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Investigation of SeqA as a transcription regulator of bacteriophages and host genes in
Salmonella enterica and *Escherichia coli* and the phages potential role in genome
duplications

A dissertation submitted in partial satisfaction of the requirements for the degree

Doctor of Philosophy

in

Biology

by

Gregory Alexander Peters

Committee in charge:

University of California San Diego

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Professor Barbara Bailey
Professor Stanley Maloy
Professor Forest Rohwer

2019

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Chair

University of California San Diego

San Diego State University

2019

Dedication

This dissertation is dedicated to my family and friends.

Epigraph

“The field of bacterial viruses is a fine playground for serious children who ask ambitious questions.”

Max Delbrück

[...] “our knowledge of bacteriophages is an inch wide and a mile deep.”

Ry Young

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List of Abbreviations

AMR	Antimicrobial resistance
ANOVA	Analysis of Variance
BED	Browser Extensible Data
BLAST	Basic Local Alignment Search Tool
bp	Basepair
ChIP-Chip	Chromatin immunoprecipitation with DNA microarray
Chip-Seq	ChIP-sequencing
cm	Centimeter
DNA	Deoxyribonucleic Acid
DNase	Deoxyribonuclease
EBU	Evans Blue Uranine
EDTA	Ethylenediaminetetraacetic acid
FDR	False Discovery Rate
GCT	Gene Cluster Text
GEO	Gene Expression Omnibus
GFF	General Feature Format
GFP	Green Fluorescent Protein
IGV	Integrative Genomics Viewer
IPTG	Isopropyl β -D-1-thiogalactopyranoside
KB	Kilobase
KEGG	Kyoto Encyclopedia of Genes and Genomes
LB	Lysogeny Broth
M	Molar
Mb	Megabase
mm	Millimeter
mL	Milliliter
MHB	Mueller-Hinton Broth
MMC	Mitomycin
MOPS	(3-(N-morpholino) propanesulfonic acid)
ORF	Open Reading Frame
OriC	Origin of Replication
padj	Adjusted p value
PCR	Polymerase Chain Reaction
PFU	Plaque Forming Unit
Phage	Bacteriophage
RFP	Red Fluorescent Protein
RNA	Ribonucleic Acid
RNAP	RNA Polymerase

RNase	Ribonuclease
RPM	Revolutions per minute
<i>rrn</i>	Ribosomal RNA gene
SAM	Sequence Alignment Map
SDS	Sodium dodecyl sulfate
TBE	Tris-Borate-EDTA
Ter	Terminus
λ	Lambda
μL	microliter
UV	Ultraviolet
μg	Microgram
V	Volt

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ASCB: The American Society for Cell Biology
ASM: American Society for Microbiology
CES: Cancer Epigenetics Society
GK: Golden Key
ISCB: International Society for Computational Biology
ISPE: International Society for Pharmaceutical Engineering
NPA: National Postdoctoral Association
PKP: Phi Kappa Phi
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Presentations

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Prophages contribute to the formation of duplications in *Salmonella enterica* LT2. **G A. Peters.** P Parks, and A Segall. - Poster Presentation

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Investigating the Interplay between Chromosome Segregation, Recombination, and Phages in *Salmonella Typhimurium*. **G A. Peters.** N Agrawal, and A Segall. - Poster Presentation

Southern California American Society for Microbiology 79th Annual Meeting – October 2015

Investigating the Interplay between Chromosome Segregation, Recombination, and Phages in *Salmonella Typhimurium*. **G A. Peters.** N Agrawal, and A Segall. - Poster Presentation

San Diego State University – Cell and Molecular Biology Graduate Student Symposium – April 2015

Investigating Prophage Induction in *Salmonella enterica* serovar *Typhimurium* LT2. **G A. Peters.** N Agrawal, and A Segall. - Poster Presentation

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Development of Highly Efficient Synthetic Biology Cloning System: LBC For Use In High Throughput Cloning on Automated Robots. **G A. Peters.**- Oral Presentation

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Programmable Pulse Generator: Engineering a Synthetic Gene Network. **G A. Peters**, J J. Barr, R Auro, and F Rohwer - Oral Presentation

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Publications

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Subdiffusive motion of bacteriophage in mucosal surfaces increases the frequency of bacterial encounters. Proc Natl Acad Sci U S A 112:13675–80.

Knowles B, Bailey B, Boling L, Breitbart M, Cobián-Güemes A, del Campo J, Edwards R, Felts B, Grasis J, Haas AF, Katira P, Kelly LW, Luque A, Nulton J, Paul L, **Peters G**, Robinett N, Sandin S, Segall A, Silveira C, Youle M, Rohwer F. 2017. Variability and host density independence in inductions-based estimates of environmental lysogeny.

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Abstract of the Dissertation

Investigation of SeqA as a transcription regulator of bacteriophages and host genes in *Salmonella enterica* and *Escherichia coli* and the phages potential role in genome duplications

by

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Doctor of Philosophy in Biology

University of California San Diego, 2019

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An estimated 10^{24} infections per second occur between bacteriophages and bacteria. This dissertation investigates these interactions of *E.coli* and *Salmonella* and their prophages. Chapter 1 is an introduction to the history of bacteriophages and their influence on molecular biology and studies of DNA replication. Chapter 2 includes an analysis of the binding of SeqA, a negative regulator of replication, throughout the bacterial chromosome and introduces a new mechanism of how SeqA is potentially

involved in transcription regulation and regulating prophage life cycles. This mechanism was found by reanalyzing protein binding data from multiple ChIP-Chip studies and analyzing them with new bioinformatics programs BEDOPS and BEDTools and Markov modeling. The ChIP-Chip data is randomized and both random and observed signals filtered into varying signal strengths. The signals are chopped to 1 bp “regions” in order to get a fine-detailed analysis of the signals and comparison of randomized vs. observed. A method for analyzing GATCs based on pairing is developed and GATCs are randomized GATC locations are compared to observed GATCs. Multiple phage are very low in GATC content. Chapter 3 involves Illumina RNA-Seq analysis of *Salmonella* and its prophages to observe the *Salmonella* prophage activity. A workflow was developed using Galaxy and DEBrowser to observe differential expression using DESeq2, EdgeR, and Limma. Chapter 4 involves the investigation and development of an assay to observe genome duplications *in vivo* using the ParB:*parS* system and see if prophages recombination proteins are involved in this process. A P1 *parS* was placed in a region in which duplications occur frequently *purH* in between *rrn* operons *rrnE* and *rrnB* and compared to a region in which duplications do not occur frequently at *argD*. A second pMT1 *parS* is placed in a region in which duplications do not occur frequently at *putA*. Gifsy-1 prophage recombination genes (*recE*, *recT*, *ninG*) were cloned onto pRHA109-Kan^R plasmid and duplications can be assayed using pFH4034, which encodes for multiple fluorescent ParB fusions. Chapter 5 is the conclusion and is a perspective on the future of phage-related research. Appendix 1 contains programs and additional RNA-Seq analysis for Chapter 2 and Chapter 3.

Chapter 1: Introduction

Bacteriophages (Phages)

Bacteriophages, viruses that infect bacteria, are the most abundant biological entity on earth, with an estimated 10^{32} present throughout the world (1–3). An estimated 10^{24} infections per second occur throughout the world (4, 5). This dissertation aims to further investigate the roles of phages with their bacteria hosts and focuses on the phages of *Escherichia coli* and *Salmonella enterica*. When a phage infects a cell it can undergo different life cycle stages, either lytic or lysogenic growth (Fig. 1) (6–12). In the lytic cycle, the phage replicates its DNA and lyses the cell to release progeny which can go on to infect other cells (13). In the lysogenic cycle, the phage injects its DNA and integrates into the host genome or replicates as a low-copy plasmid. During the lysogenic cycle the phage can replicate with the host chromosome without producing new virions, or upon an induction event, the virus can switch into the lytic phase. Here I will introduce some pertinent history on phages and put the dissertation in context with the interesting field of phages and emphasize the importance of phage research over the past 104 years since their discovery.

Phage history and molecular biology

Phages and lysis were first discovered in 1915 and 1917 by Frederick Twort and Félix d'Herelle respectively (14, 15, 24, 16–23). There was a dispute over who discovered phages, and the lysis phenomenon was later referred to as the Twort-d'Herelle phenomenon (17, 25). Ernest Hankin also found evidence of what was likely phage lysis in 1896 (26, 27). Lysogeny was discovered shortly after the lysis phenomenon and as lysis, it was also controversial. The first evidence of Lysogeny was

discovered in 1921 when Jules Bordet and Mihai Ciuca found bacteria produced self lysing phages (28). This was also found in 1921 by E. Gildemeister and Herzberg and in 1925 by Oskar Bail (29–31). In 1925 Bordet later named this phenomenon ‘pouvoir lysogène’ which in English is translated as lysogenic power (32). Felix d’Herelle and Jules Bordet had disagreements over the phenomena as they are in direct contrast with each other. How could a phage virus do both?

Phage research initially was focused in two areas, one for phage therapy where phage were to be used to lyse pathogenic bacteria in a patient and the other for diagnostic tools for typing bacteria. Initial phage therapy worked but large scale clinical trials failed because of lack of knowledge of how to handle and dose the phages (33–36). Antibiotics were discovered and were very effective and more simple to use and this led to a decline in phage therapy research (37). Phage therapy was still pursued in France, Russia, India, and countries of the former Soviet Union including Georgia, Poland, and Slovenia (38). Two key centers focused on phage therapy were founded and one of them is the Polish Academy of Sciences in Wroclaw where Stefan Slopek published detailed phage therapy studies. A second key center, the Eliava Institute, was founded by Felix d’Herelle and George Eliava in Tbilisi, Georgia. For technical and economic reasons phage therapy was furthered pursued in these countries became a standard of care and was used during World War II. The United States distanced itself from Soviet Union related research after the war and during the Cold war and phage therapy became politically unsound for the United States to pursue.

Research on phages led to the advent of molecular biology and many important discoveries including DNA as the genetic material, solving of the structure of DNA,

elucidation of the genetic code, operons, and many others (21). Multiple Nobel Prizes have been awarded for the uncovering of biological phenomenon by researchers that have either been pursued phage research or have been influenced by it. Phages have also played an important role in the knowledge about the nature of viruses as whole. Phage research has greatly influenced society as a whole and will continue to do so.

The advent of molecular biology started in 1938, around the time of World War 2 which started in 1939 (39). Max Delbrück was a physicist who pursued biological questions and he formed and led the American phage group which met in Cold Spring Harbor in New York (21, 39, 40). This American phage group set out to study *Escherichia coli* phages T1 - T7 and work out in great detail phage-related biological processes (39). Salvador Luria worked with Max Delbrück and they studied the randomness of mutations (41). Alfred Hershey and Martha Chase were also in this group and performed experiments showing that DNA is the genetic material. Max Delbrück, Alfred Hershey, and Salvador Luria won the Nobel Prize in Physiology or Medicine in 1969 for their work (42).

A French phage group also formed in France at the Institute Pasteur and was led by André Lwoff, Jacques Monod, and François Jacob (43). André Lwoff studied lysogeny and investigated how this phenomenon occurs using *Bacillus Megaterium* and found it was possible to induce lysogenic phages to the lytic phase using UV light (6, 44, 45). André Lwoff also coined the term prophage which and he defines in a review as the following; the “Prophage is the form in which lysogenic bacteria to perpetuate the power to produce phage” (6). Jacob and Monod developed the operon model which greatly helped to understand how genes were regulated (46–48). The three won the Nobel

Prize in Physiology or Medicine in 1965 for their work on the genetic control of enzymes and virus synthesis (49).

***E. coli* and prophages**

Escherichia coli K-12 was first isolated in 1922 and its lineages are well studied (50). In 1951 Esther Lederberg serendipitously discovered that *E. coli* K-12 contains a lysogenic phage, Lambda (λ) phage, when she shined UV light on the strain and it lysed (51). New *E. coli* strains were made and Lambda was cured from the bacteria and *E. coli* K-12 MG1655 became a main lab workhorse. Lambda phage was introduced to the American phage group but they did not initially want to study lambda because they did want to study lysogenic phage (39, 43). Lysogeny later became a major area of focus and Lambda phage served as a model phage for understanding lysogeny (39, 43). Lambda like phages are called lambdoid phage. After infection Lambda phage makes a decision to go into the lytic phase or a lysogenic phase and this has been called the genetic switch.

Mark Ptashne discovered the cI repressor in Lambda phage in 1967 (52). The cI plays a major role in the control of the life cycle of the phage and switching from one life cycle to another (9, 10, 53, 54). In the lysogenic life cycle, the cI repressor binds to operator sites at the promoters of genes involved in lysis and represses the lytic growth phase. Upon DNA damaged by UV light or another DNA damaging agent RecA* is produced, which is an activated form of the recombination RecA. RecA* cleaves the cI repressor and cI repression is relieved. This loss of repression causes an increase of genes involved in lysis and the switch into the lytic phase. Phage progeny are produced and go on to infect other cells.

Lambda phage was also used to study how the phage integrates its genome into the host (55–59). After the phage injects its DNA and decides to enter the lysogenic state, it uses Integrase to integrate its genome into the chromosome using site-specific recombination. In this reaction, *attP* sites on the phage chromosome and *attB* sites in the bacteria undergo recombination catalyzed by Integrase and the phage is then integrated into the genome. During the recombination event, the *attP* and *attB* sites are converted into *attL* and *attR* sites. After integration, the cI repressor represses genes involved in replication and lysis, and the phage remains stably integrated into the genome. Excisionase genes are involved in the reverse step of this reaction and are necessary to promote excision of the phage.

When the *E. coli* K-12 MG1655 genome was sequenced in 1997, multiple cryptic prophages were found integrated into the genome which are inactive and unable to produce virions (60–62). This extra DNA does not appear to be detrimental to the cell, but instead can be advantageous to the bacteria (63). Genes from cryptic prophages are expressed and used by their bacterial hosts (63). It is likely that active phages also influence the host and make it more pathogenic. In studies of *E. coli* K-12 MG1655, cells with prophages were found to grow faster in lab conditions than isogenic cured cells (63). Phages also spread toxin genes by transduction (i.e. lateral gene transfer), which can make bacteria more virulent (64, 65). Bacterial pathogens are a major public health concern and phages also can increase antibiotic resistance through horizontal gene transfer (66). Lysogenic conversion is the process where a prophage changes the phenotype of its host; for example, an avirulent strain can be converted into a virulent strain through expression of genes gained via a prophage (9). Lysogenic conversion

occurred in *E. coli* HO157:H7, where Shiga toxin genes were transferred to *E. coli* by a phage carrying the Shiga toxin gene (67). *E. coli* strains containing Shiga toxin genes are denoted STEC for Shiga toxin-producing *E. coli*. These strains cause Hemorrhagic Colitis and Hemolytic Uremic Syndrome (HUS) and are a major public health concern with an estimated 2.8 million infections and 230 deaths annually. The pathogen first emerged in 1982 and has continued to cause outbreaks with the most recent outbreak in 2018 being related to Romaine lettuce (68, 69). Multiple strains have been isolated and sequenced *E. coli* O157:H7 strain EDL933 from the 1982 multi-state outbreak in Michigan associated with Hamburgers was sequenced in 2001(70). A second strain of *E. coli* O157:H7 strain Sakai from the 1996 Sakai outbreak in Osaka, Japan was sequenced in 2001. EDL933 and Sakai have many prophages (12 in EDL933 and 18 in Sakai) and Shiga toxin-encoding genes *stx1* and *stx2* are found in prophages (64, 71). Prophages are linked to the virulence of these strains and having more prophages has been correlated to increased pathogenicity (64, 71, 72).

***Salmonella enterica* and prophages**

The *Salmonella* genus is also very well studied and *Salmonella enterica* serovar Typhimurium, originally known as *Salmonella typhimurium* (STm for short), became one of the organisms studied as a model pathogenic enteric bacterium. In the 1950s, around the same time as the Phage group was formed, fundamental studies on the growth of bacteria were being performed using *Salmonella* (73, 74). These studies were performed by Moselio Schaechter, Ole Maaløe, and Nils Ole Kjeldgaard and they introduced quantitative growth laws (75–77). Jaques Monod was also influential in this field and was one of the first scientists to quantitatively study the growth of *E. coli* cells

(77, 78). *Salmonella* species also have well-established genetics, including transduction with P22 phage, discovered by Norton Zinder and Joshua Lederberg, and this aids in the study and creation of new strains (79).

Salmonella species of bacteria are highly diverse, with over 2500 serovars, and infect a broad range of organisms including humans, chickens, and amphibians (80–82). *Salmonella enterica* subspecies *enterica* serovar Typhi causes Typhoid fever in humans, but Non-Typhoidal serovars are also major public health concerns. Serovars are typed using antibodies and typed according to the Kaufmann-White classification scheme. Antibodies are used and these antibodies are targeted to the outermost portion of the Lipopolysaccharide named the O antigen or to flagella regions named H antigens. *Salmonella* are able to change the polysaccharides on the surface of their cells, and this allows for the pathogen to evade the host immune response. This diversity mechanism has been correlated with *Salmonella* phages and other horizontal gene transfer events. More recently strains are being sequenced which gives more insight of what makes the strains different, and many *Salmonella* have prophages integrated in their genomes.

Salmonella enterica subspecies *enterica* (Non-Typhoidal) causes 153 million cases of gastroenteritis and 57,000 deaths annually (83). The most well-studied lab strain is *Salmonella enterica* serovar Typhimurium LT2. This strain is used as a model organism for studying Typhoid Fever in mice. The strain was sequenced in 2001 and its genome is 4.8 Mb and it contains 4 active prophages, Gifsy-1, Gifsy-2, Fels-1 and Fels-2 (84–86). Gifsy-1, Gifsy-2 are known to be linked to virulence and are similar in genome structure and regulation to phage lambda. The Gifsy-2 prophage in this strain carries a *sodC* gene, which encodes a superoxide dismutase that permits intracellular

survival when the *Salmonella* is engulfed by macrophages (65, 87). Fels-1 is also lambdoid, whereas Fels-2 shares similarity to the *E. coli* P2 phage, a myophage. The genetic switch between lysogeny and lysis is also similar to phage lambda's cI repressor-based switch, but these phages have antirepressor proteins (Tum) which bind to the the cI repressor and prevents the cI repressor from binding to operator sites leading to induction of the phage and active phage (88–90). Gifsy-1 and Gifsy-2 are highly similar and share 99% similarity over long homologies. Their repressors and antirepressors can act in trans to each other, leading to complicated life cycles which overlap. There are also multiple cryptic/defective prophages which are unable to form active virions. Another well studied strain is *Salmonella enterica* serovar Typhimurium 14028s and this strain causes virulence in mice and also contains prophages, including a Gifsy-2 homolog (91).

Salmonella enterica serovar Typhi strains are pathogenic and cause typhoid fever and cause multiple outbreaks (92, 93). According to the CDC data from May 31, 2017, there are 26 million cases of typhoid fever globally with 250,000 deaths (93). *Salmonella enterica* serovar Typhi CT18 was isolated in December 1993 from Vietnam from a 9-year-old girl suffering from typhoid fever (94). The genome was sequenced in 2001 and it is multidrug resistant and contains seven prophages (94). One of the *Salmonella* pathogenicity islands SPI7 contains a *sopE* containing phage and *sopE* is a virulence gene which encodes a Type III secretion effector (T3SS) protein that is a strong inducer of intestinal inflammation (95–97). A second *Salmonella enterica* serovar Typhi Ty2 was sequenced in 2003 (98). Comparing the two strains shows that both contain seven prophages, one of which encodes a *sopE* gene. The two genomes differ

from each other by a large inversion spanning almost half the genome. The *Salmonella* genome is dynamic and an inversion is one example that occurs, other events such as duplications and deletions can also occur and will further be expanded upon.

Dissertation aims

This dissertation covers two main projects with an overall goal to better understand how phages in *E. coli* and *Salmonella* interact with their hosts. In Chapter 2, we uncover a new mechanism of how a bacterial protein involved in DNA replication, SeqA, may interact with the prophages in the genomes of *E. coli* and *Salmonella*. In Chapters 3 and 4 we develop a system to investigate if phages are involved in genome duplications and amplifications (a known mechanism of antibiotic resistance) using RNA-Seq analysis and fluorescence microscopy.

DNA replication and the cell cycle

DNA replication is a fundamental process of the cell and is orchestrated by numerous processes and works in concert with processes regulating the cell cycle (99–102). The cell cycle requires replication of the bacterial chromosome and the segregation of the second chromosome into the daughter cell. The mechanisms of DNA replication were uncovered by studying mutants of bacteria and aided by phage (74, 99, 103).

Stephen Cooper and Charles Helmstetter worked on the timing of the cell cycle in *E. coli* (103–105). They defined the cell cycle as the sum of different periods $I + C + D$, where I is the time before initiation of DNA replication, C is the time necessary to replicate the chromosome and D is the time to for the division of the cell. C and D were found to be constants, whereas I was variable. Donachie found cells divide at constant

mass (106–108). All of these processes must be coordinated in the cell, and bacteria served as a useful model organism due to their fast generation times. Many of the growth laws are thought to be universal to all cellular life.

DnaA is one of the major bacterial proteins involved in initiation of DNA replication. It binds to the origin of replication, *oriC*, and changes the topology of this region. Its binding recruits a cascade of multiple other proteins, including DnaC, DnaB, DNA polymerase, and DNA topoisomerases that work in concert to faithfully replicate the chromosome (103, 109–113). DnaA is both autoregulated and regulated by multiple other proteins (99, 109, 114). Several rounds of replication can occur at one time depending on the growth phase of the cell.

Prophages in the chromosome are replicated with the rest of the chromosome using their hosts' cellular processes. This method of phage replication does not directly yield progeny but has the advantage that the phages can replicate without having to form infectious particles and search for bacterial prey. Recently a Piggyback-the-Winner model has been proposed that shows that phage lysogeny of bacteria (piggybacking) that grow faster than their competitors (i.e., the winners) is one of the most widespread lifestyle strategies of phages in a broad range of environments (115). This model contrasts the earlier Kill-the-Winner model, which proposed that phages infect and kill the winner by lysis (116).

DNA replication and SeqA

The DNA replication cycle is not fully understood and the complete details of how the initiation of DNA replication is regulated are still not known (99). The conversion of DnaA-ATP to DnaA-ADP plays a role, along with other mechanisms; nevertheless, there

is still much more to be researched in this area (99, 117). SeqA was discovered and characterized as a protein that prevents overinitiation of DNA replication, it also plays roles in other cellular processes such as chromosome organization and segregation (109, 118, 119). In *seqA* mutants the DNA cycle is misregulated: too many copies of the chromosome are made in an asynchronous manner, which also misregulates the cell cycle (118).

A number of studies, using *in vitro* biochemistry assays and *in vivo* tracking the distribution of SeqA binding in *E. coli* cells, have shown that SeqA binds to GATC sites in DNA (120–124). *In vitro* biochemical reactions with purified SeqA protein and DNA showed that it binds to DNA optimally when pairs of GATC sites are found close together (< 41 basepairs apart). SeqA protein can also bind GATCs at much longer distances, even across the chromosome, through protein-protein interactions to other SeqA proteins. SeqA proteins have been shown to cluster together and form higher order structures in a positive cooperative manner. GATC sites are distributed throughout the chromosome, with the highest concentration near the origin of replication at *oriC* and *dnaA* promoters. Current models propose that SeqA regulates the DNA cycle by sequestering origin-proximal DNA to the membrane, thereby preventing overinitiation of replication.

During the DNA cycle, the chromosome starts fully methylated. Immediately after replication the DNA is transiently hemimethylated, until Dam methylase, which follows the replication fork, adds methyl groups to the adenine within all chromosomal GATC sequences. SeqA binds with higher affinity to hemimethylated than fully methylated DNA, and has the lowest affinity for unmethylated DNA (125). The highest SeqA binding

follows the replication fork and this has been shown *in vivo* with SeqA fused to GFP (122, 126).

Two different labs have assessed SeqA binding to the chromosome in *E. coli* using chromatin immunoprecipitation (ChIP-Chip) (120–122). These ChIP-Chip assays were performed by growing bacteria, crosslinking DNA using formaldehyde, and then using anti-SeqA antibodies to immunoprecipitate SeqA-bound DNA. This DNA was then hybridized onto a microarray chip with short oligonucleotides of *E. coli* DNA sequences spanning the chromosome. The SeqA-immunoprecipitated DNA hybridized to these regions was measured using fluorescent dyes. Two reports of SeqA binding using ChIP-Chip were published in 2010 and a third was published in 2012 (120–122). SeqA had the highest binding in regions with high GATC counts in the 2010 studies and the 2012 study (120–122). These reports showed that high SeqA binding correlated with a high density of GATC sites. The highest peaks of the signal were near the origin of replication at *oriC*, *dnaA*, and the *dnaA* promoter, all of which have numerous and clustered GATC sites. It is possible that SeqA binds to the *oriC* region and affects binding of DnaA but this has not been shown directly. Sánchez-Romero et al. suggested that SeqA binds the GATC sites in the promoter, thereby repressing transcription of the *dnaA* gene (120). This may not be the case, since mutations of GATC sites in the *dnaA* promoter region do not appear to affect the DNA and cell cycles. Zyskind and colleagues mutated the GATCs sites in the major *dnaAp2* promoter and found no change in the synchrony of replication initiation in either minimal or enriched media; thus it is unclear if SeqA directly affects the *dnaA* gene (127).

Transcription and SeqA

Multiple studies have been performed to study SeqA's potential effect on transcription using quantitative assays in both *E. coli* and *Salmonella*. Transcription of *dnaA* was previously shown to increase 1.8 fold in *E. coli seqA* mutants using quantitative S1 nuclease transcription assays (128). Protein levels of DnaA in *E. coli seqA* mutants were also shown to increase over 1.8 fold in a separate study using immunoblotting (129).

In 2003, a microarray study of *E. coli* measuring total transcription effects of wildtype and *seqA* mutants was performed. In contrast to the previous *dnaA* transcription studies, this one found no significant increase of *dnaA* transcription in *seqA* mutants (130). They showed that SOS genes (*recA*, *oraA*, *recN*, *sulA*, *dinI*, and *umuDC*) were upregulated in *seqA* mutants. They also found that the *seqA* mutants share similar transcription profiles to Dam-overproducing cells (130).

In 2007 Prieto et al. published a paper that included microarray data of *seqA* mutants of *Salmonella* Typhimurium 14028s (131). They found that the *seqA* mutants had decreased virulence in mice and displayed membrane instability, but the absence of SeqA had no effect on lysogenization by P22. In the microarray data, they did not show a significant increase of *dnaA* transcription (130, 131). The SOS response was moderately increased in both exponential and stationary phases. The study showed that two genes were repressed and four were activated in exponential phase, whereas four genes were repressed and 16 were activated in stationary phase. Interestingly, they noted that ~30% (16/42) of the genes that were either activated or repressed by SeqA were *Salmonella*-specific genes and many of these had unknown functions. One of the

genes activated by SeqA is STM4212, a phage tail core gene of a phage remnant in the genome (72).

In chapter 2 we studied SeqA's role in the cell and suggest another mechanism of how SeqA acts. We also propose a model that provides a link between SeqA and the regulation of the exit from lysogeny into lytic replication. SeqA protein binding studies and microscopy studies have shown that SeqA and RNA Polymerase (RNAP) binding is mutually exclusive, and we propose that SeqA affects RNAP transcription (121, 132). We integrate the three Chip-ChIP studies and use bioinformatics tools to uncover the likelihood that SeqA interferes with transcription. In addition, we focused further on comparing GATC site distribution within the chromosome versus phage sequences.

Genome duplications

In Chapter 3 we further investigated the active prophages in *Salmonella* LT2 (those that can form infectious virions) and look at their activity specifically to see if they contribute to the formation of genome duplications (133–136). *Salmonella* LT2 is the most well-studied organism for how genome duplications and amplifications arise. The formation of these rearrangements is thought to be universal and has been implicated in antibiotic resistance and cancer. When an antibiotic resistance gene is duplicated, selection for the function of the gene can result in further amplification and higher number of gene copies that “answer” the selection.

Genome duplications occur frequently between regions of the genome that have high homology or homeology (imperfect similarity). In both *E. coli* and *Salmonella* Typhimurium, duplications often occur between the seven *rrn* operons (ribosomal RNA

operons) (Figs. 2 - 3). The RecBCD and RecFOR are major recombination pathways implicated in genome duplications (137, 138). RecA-dependent and RecA-independent mechanisms have been proposed for the formation of genome duplications.

Amplifications are thought to be highly dependent on RecA and *recA* mutations decrease the frequency of both duplications and amplifications. The Gifsy-1 and Gifsy-2 prophages carry recombination genes (*recE*, *recT*, and *ninG*) that could influence the formation of genome duplications and amplifications. We used next Illumina next-generation sequencing (RNA-Seq) to investigate if the prophage-encoded recombination genes are active and investigate if prophage functions are involved in genome duplications.

In Chapter 4, we developed methods to investigate if the phages are involved in genome duplications using fluorescence based microscopy. We inserted *parS* sites at multiple regions in the chromosome and used ParB proteins fused to fluorescent proteins. These ParB fusions bind specifically to the *parS* sites and form foci. We created a system where we can quantify the foci at one location in a region known to be duplicated (*purH*) and compared this frequency to another location expected to have a low frequency of duplications (139). We compared strains with prophages with strains from which the prophages were cured in order to quantify the contribution of the phages to the generation of rearrangements between *rrn* operons. We also tested the effect of a *recA* mutation on the formation of duplications (140). In order to see if the prophage recombination genes (*recE*, *recT*, and *ninG*) were involved, we cloned them into a tightly regulated plasmid and designed a system to test if these proteins can complement the loss of RecA function in duplication and amplification formation.

A

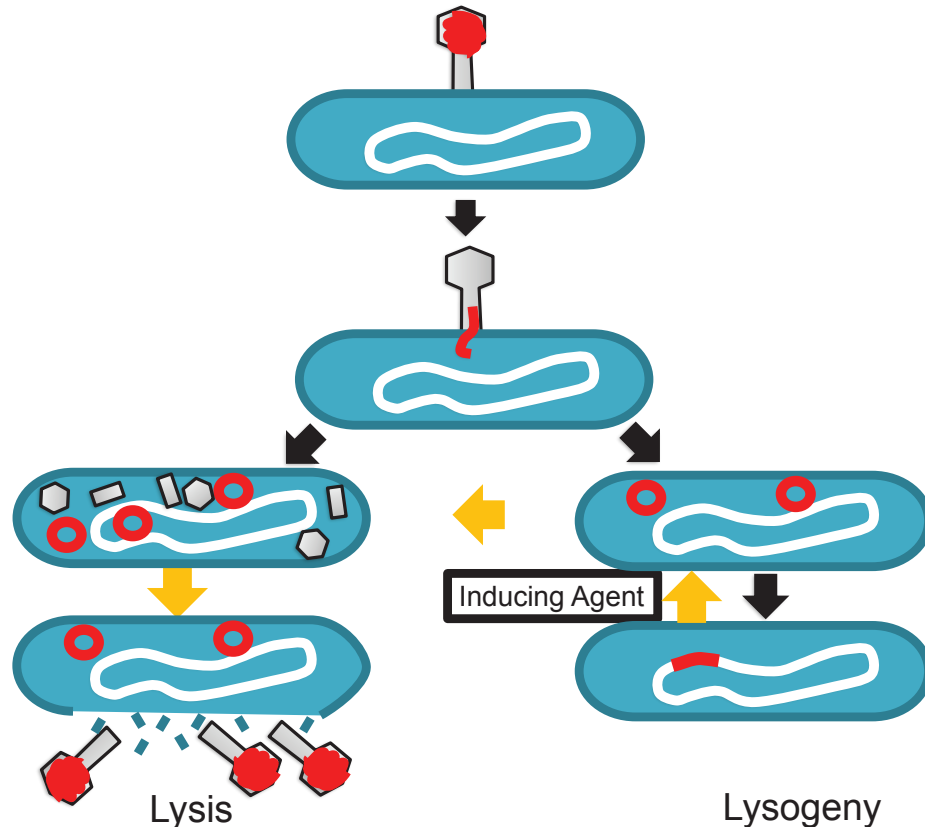


Figure 1: Prophage induction. A. Bacteriophage life cycle: When a phage infects it can inject its DNA and this can be integrated into the chromosome in the lysogenic life cycle or it can undergo lysis and replicate and can lyse the cell and release phage progeny. An inducing agent can induce the switch from the lysogenic to the lytic life cycle. Adapted from (10).

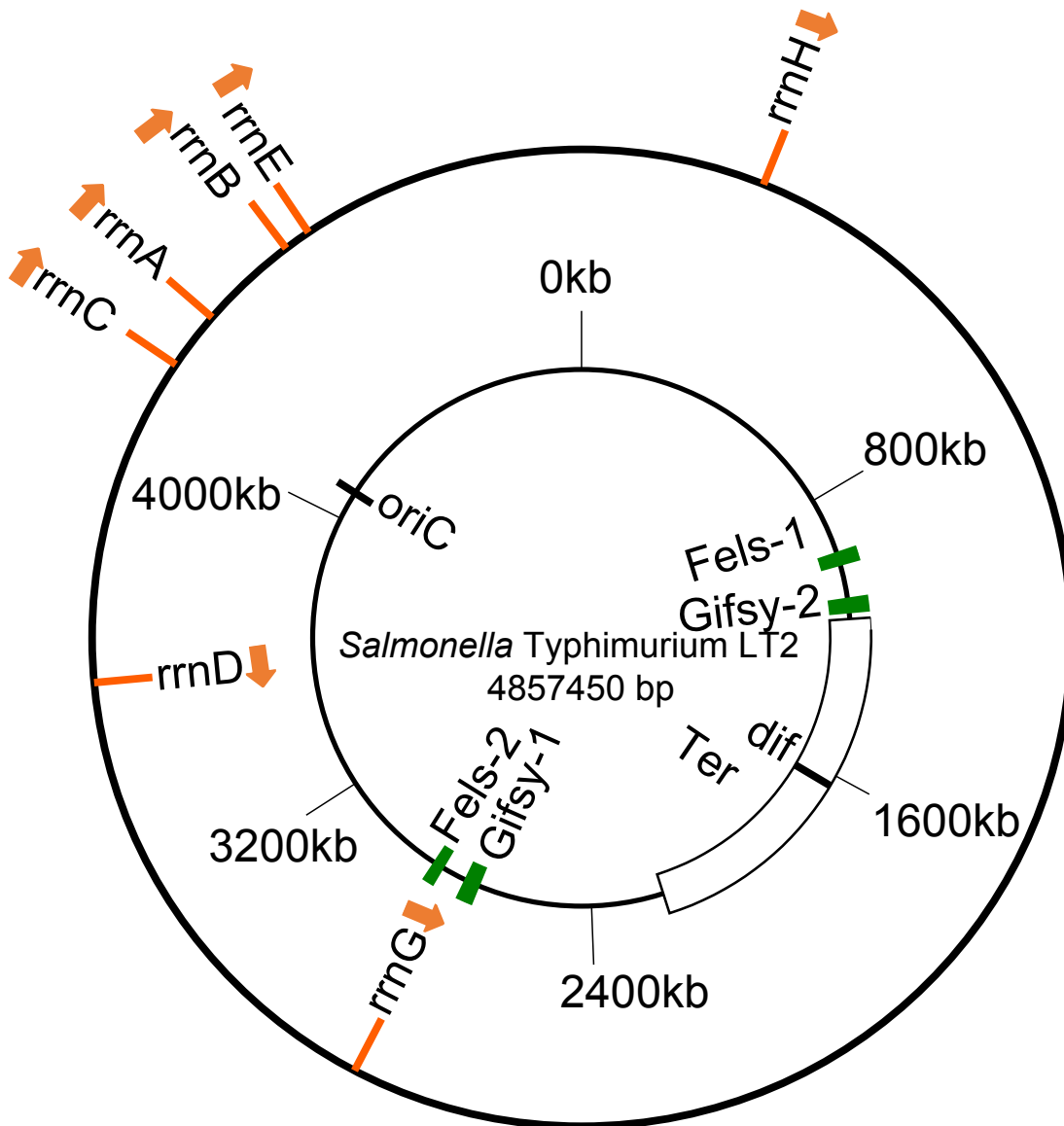


Figure 2: *Salmonella* LT2 chromosome organization. A. *Salmonella* LT2 chromosome with regions mapped and not drawn to scale using GenomeVX (141). The outside circle shows sites facing outwards and these are in the opposite orientation of sites facing inwards. Locations of the 7 *rrn* operons on the *Salmonella* LT2 chromosome are shown in orange on the outside of the circle; orange arrows indicate *rrn* operon direction. *Gifsy-1*, *Gifsy-2*, *Fels-1*, *Fels-2* active prophages are shown in dark green. *oriC* was found from BLAST with the *E. coli* MG1655 *oriC* site and is the origin of replication. The *Ter* macrodomain where replication ends is indicated and was identified from (142, 143). *Dif* site was located from (144).

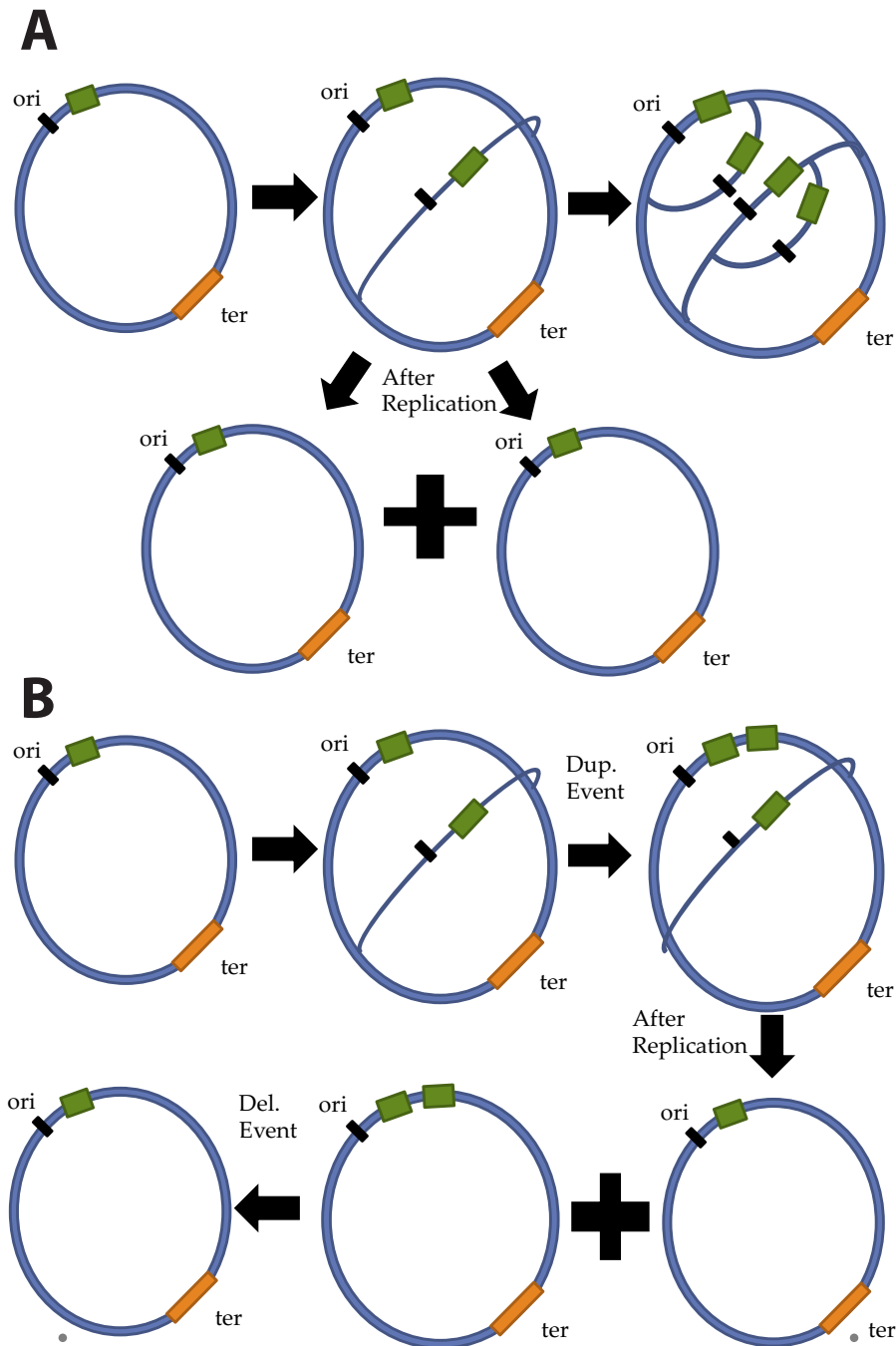


Figure 3: DNA replication vs. DNA replication with a duplication event. A. A circular chromosome with an ori site (origin of replication) denoted with a black box and a ter (terminus) denoted with an orange rectangle. A gene is shown in green box to the right of the origin of replication. Replication starts at oriC and proceeds in both directions bidirectionally and can have a second firing of the origin in high amounts of growth. After replication a second chromosome is made **A.** DNA replication with a duplication event. After a duplication event a second green is formed and the second copy of the chromosome has two copies whereas the original has one copy. A duplication event can then delete the duplication.

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Chapter 2: SeqA as a regulator of genes and bacteriophages

SeqA as a regulator of genes and bacteriophage replication and life cycles in *Salmonella enterica* serovars Typhimurium and Typhi and *Escherichia coli* K-12 and O157:H7

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Abstract

In gammaproteobacteria, SeqA is a protein that prevents overinitiation of DNA replication and is involved in chromosome organization and segregation. SeqA binds DNA at GATC sites throughout the chromosome that are close together with highest binding around the origin of replication and *dnaA*. While working with *seqA* mutants of *Salmonella* LT2, we found increased induction of prophages and investigated the mechanism of how this was occurring. The SOS response is constitutively induced in these mutants and this could allow for increased replication of the prophages. We provide evidence that SeqA directly affects prophage gene expression. A search within the prophage DNA revealed pairs of GATCs in the open reading frames (ORFs) of prophage lifecycle genes (integrase, excisionase, cI repressor, *dnaA*, and *dnaC* analogs). Previous microarray and microscopy studies of SeqA in *Escherichia coli* found that RNA polymerase and SeqA mutually exclude each other. After reanalyzing the previous CHIP-Chip data we find that SeqA signals are over-represented inside ORFs despite being generally under-represented in prophage sequences. SeqA may downregulate gene expression by excluding RNA polymerase and impede transcript elongation. Phage may have evolved to escape this down-regulation although SeqA binding sites and exclusion of RNA polymerase are present in phage genes important for the maintenance of lysogeny and phage DNA replication initiation. This study presents evidence of SeqA acting as a secondary mechanism to prevent spurious prophage induction. SeqA exclusion of RNAP polymerase appears to occur in phage ORFs and bacterial ORFs involved in the cell cycle (*dnaA*, *mioC*, *mnmG*) and these

ORFs have pairs of GATC inside them. This study provides evidence that SeqA affects gene regulation and phages directly.

Importance

SeqA is an important and abundant chromosome organizing protein in gammaproteobacteria and has been best studied in *E. coli* K-12 MG1655 and *Salmonella* Typhimurium LT2. SeqA was identified as a protein necessary to prevent overinitiation of DNA replication. SeqA binds to GATC sites, which occur throughout the chromosome, but are organized in clusters near the origin of replication, leading to increased SeqA binding in these regions. Both the Grainger and Skarstad labs have published binding data of SeqA binding in the chromosome and also RNAP polymerase binding (120–122). In this paper we reanalyze this data using recently developed bioinformatic tools and present new insights into how SeqA acts. In *seqA* mutants of *Salmonella* LT2 we find increased bacteriophage replication of prophages that are integrated in the chromosome. The default hypothesis is that the *seqA* mutation leads to induction of the SOS response, which consequently leads to prophage instability and entry into the lytic cycle. However, we wanted to investigate whether SeqA might have a more direct role in the lysis-lysogeny decision, and/or in the maintenance of the lysogenic state. Because *seqA* mutants are highly pleiotropic, however a bioinformatic analysis of SeqA binding and differential interactions with the bacterial chromosome offered a more promising approach. SeqA binding has been examined in detail. SeqA binding sites occur inside many ORFs important for the replication and life cycle of these viruses. SeqA appears to affect these genes by binding inside the ORF and occluding RNA Polymerase, impeding transcription of the ORF. Our analysis of the occurrence of multiple GATC sites indicates significantly lower than average in prophage ORFs. Some lytic bacteriophages have very few GATC sites and the viruses

could evolve in order to decrease SeqA binding. Gene regulation is primarily thought to occur outside the ORFs in promoter regions. We find evidence for transcription regulation by interfering with the elongation process.

Keywords

SeqA, Bacteriophages, Prophages, Chromosome Organization, Chromosome Structure, Epigenetics, Gene Regulation, RNA Polymerase, Transcription Regulation

Introduction

Bacteriophages are abundant and can increase pathogenicity of hosts

There are huge numbers of bacteriophages an estimated 10^{32} , however, despite their abundance we do not know relatively little about their interactions with their hosts (1, 145). A recent analysis of the SEED database spanning phyla of Bacteria and Archaea with the prophage-finding program PhiSpy revealed that 82.76% of the bacteria have at least one prophage (146, 147). Many have more with an average of 3 prophages per bacterial genome (36,488 prophages / 11,941 bacteria) (146, 147). 43.23% have an annotated integrase gene (*int*) of the tyrosine and serine recombinase families suggesting they integrate into their hosts. Prophages can increase pathogenicity of the host by transferring virulence factors such as antibiotic resistance genes, between bacteria, a major health concern. *Escherichia coli* O157:H7 - EDL933 and *Escherichia coli* O157:H7 - Sakai have caused multiple outbreaks and contain 18 and 24 prophages respectively (64, 70, 71, 148, 149). *Salmonella* Typhi - CT18 and *Salmonella* Typhi - Ty2 also cause outbreaks and contain 7 and 6 prophages respectively (64, 94, 98, 149). Some prophages can have suffered deletion events to form cryptic prophages, which are unable to form active infectious particles, but which provide genetic material to the host. For example, the common laboratory strain *Escherichia coli* MG1655 K-12 has 11 cryptic prophages. *Salmonella enterica* serovar Typhimurium LT2 has four active prophages, which have temperate life cycles: Gifsy-1,

Gifsy-2, Fels-1, and Fels-2, as well as two likely cryptic prophage fragments (63, 86). We have found that the SeqA protein, which is involved in chromosome replication and segregation, also binds to prophage regions and is likely regulating bacteriophage replication and the lysis/lysogeny decision in *Escherichia coli* K-12, *Escherichia coli* O157:H7, *Salmonella* LT2, and *Salmonella* Typhi.

SeqA and DNA Methylation

SeqA was identified as a negative regulator of DNA replication in *E. coli* that binds to methylated GATC sites in the chromosome (118, 119, 129). While GATC sites are spread throughout the chromosome, their highest density is near the origin of replication (150). SeqA is thought to bind to these sites and sequester the origin of replication from the DNA replication initiation protein, DnaA, thus preventing overinitiation of replication (151, 152).

Biochemical studies *in vitro* show that two SeqA monomers form a dimer that binds hemimethylated GATC sites in DNA with greater affinity than fully methylated DNA, and does not bind to unmethylated DNA (123, 124, 153, 154). SeqA has been shown *in vitro* to bind most efficiently GATC sites that are close together separated by fewer than 41 bp and introduces positive supercoils when bound (123, 124, 126, 155–159).

To assess SeqA binding to the *E. coli* chromosome in two separate labs used chromatin immunoprecipitation (ChIP-Chip) (120–122). In these reports, they showed high SeqA binding correlated with a high density of GATC sites. The highest peaks of signal were near the origin of replication at *oriC*, and in the *dnaA* gene and the *dnaA* promoter all of which have numerous and clustered GATC sites. The *dnaA* gene is both

autoregulated and regulated by multiple other proteins (99, 109, 114). Sánchez-Romero et al. suggested SeqA that binds the GATC sites in the promoter, thereby repressing transcription of *dnaA* (120). However there was no significant increase of *dnaA* transcription in *seqA* mutants of either *E. coli* and *Salmonella* (130, 131). In addition, mutation of the GATCs sites in the *dnaAp2* promoter does not change the synchrony of initiation in either minimal or enriched media, thus it is unclear if SeqA directly affects the *dnaA* gene (127).

One of the most striking results in the 2010 Sánchez-Romero et al. ChIP-Chip data is that the *rrn* operons, which are the most highly transcribed operons in *E. coli*, lack GATC sites and thus have little if any SeqA binding (120). RNA polymerase has a strong signal at the *rrn* operons, as expected. The *rrnC* operon is unusual: it is very close to *oriC*, where a higher SeqA binding would be expected. Instead, *rrnC* has a lower SeqA binding signal than the surrounding area. The authors suggest that SeqA binds within genes and affects their transcription and point to low RNAP signals in SeqA-bound regions, but many regions with no SeqA bound have low RNAP signals. They show a weak inverse correlation when they compare data from this experiment of SeqA binding to RNAP binding data from a 2006 RNAP ChIP-Chip experiment (-0.13 correlation coefficient).

SeqA and RNAP are also mutually exclusive in the 2010 Waldminghaus et al. ChIP-Chip data (121). Of the genes with a detectable signal, 998 (48.26%) showed high RNAP binding, 1058 (51.16%) showed high SeqA binding and only 12 (0.58%) had overlapping RNAP and SeqA signals. In 2014 this was confirmed *in vivo* using super-resolution-structured illumination microscopy (132). Together, these studies together

suggest that SeqA binding to DNA may exclude RNA Polymerase and in turn reduce or prevent transcription.

The 2012 Waldminghaus et al. ChIP-Chip data shows SeqA binds to regions with newly synthesized hemimethylated DNA more frequently near the terminus (122). During exponential growth, genes near the origin of replication, such as *mioC* and *mnmG*, were more likely to be affected by SeqA. The data show very high binding signals at *oriC*, *dnaA*, and in the *dnaA* promoters in synchronized *dnaC2* mutant cells 5 minutes after the initiation of replication (121). The signal “travels” bidirectionally around the chromosome following the replication fork. However, signals at *oriC*, *mioC*, *mnmG*, *dnaA*, and the *dnaA* promoters are constant and persist after 15 minutes, 35 minutes, and 50 minutes. It is likely that SeqA is bound to newly synthesized hemimethylated DNA at *dnaA* and *oriC* and that SeqA this affects transcription as well as replication. Over time the SeqA signal “travels” along the chromosome and appears to bind within other coding sequences, which would likely affect the transcription of these other genes. When SeqA binds it would introduce positive supercoils and thereby exclude RNA polymerase.

Here we reanalyze the 2010 and 2012 ChIP-Chip data and show that it is likely that SeqA is binding within Open Reading Frames (ORFs), excluding RNA polymerase and presumably reducing transcription. This phenomenon is likely to affect bacteriophage genes and influencing the phages’ life cycles.

Results

Prophages are highly induced in *Salmonella* LT2 *seqA* mutants

For our study we used *Salmonella* LT2 since it has four active prophages and allows for the study of regulation of its prophages. Our experiments show higher levels of bacteriophage induction in our *Salmonella* LT2 *seqA* mutant than wildtype LT2 (Fig. 4). This effect could be due either to the constitutive SOS response induction in *seqA* mutants and/or a LexA-independent mechanism affected by SeqA. The transcription repressor LexA controls the SOS response. To test whether the high induction in *seqA* mutants is SOS-related, we introduced a noncleavable allele of the LexA repressor, *lexAind3*. LT2, *seqA*, *seqA lexAind3* strains were grown in LB without treatment or treated with 0.1 µg/mL mitomycin C (MMC) a known inducer of the SOS regulon. Cells were lysed with chloroform, and lysates were tittered on a recipient strain lacking Fels and Gifsy prophages (SDT2739). Numerous very small (~1 mm) plaques characteristic of Gifsy-2 formed and a 1 cm² sector was counted with three 1 cm² sectors counted for each plate (Fig. 1) (160). The increase of phages in the *seqA* mutants could result either from the induced SOS response and/or due to a direct effect of the absence of SeqA see discussion.

Pairs of GATC Sites are in or near Gifsy-1 and Gifsy-2 prophage ORFs including cI repressor analogs, *dnaA* analogs, and *dnaC* analogs

In order to investigate whether SeqA may have a direct effect on the regulation of induction, we identified potential SeqA binding sites (i.e. pairs of GATCs) with respect to the prophages. We searched for pairs of GATC motifs within 41 basepairs in or near prophage ORFs, because SeqA binding to these motifs has been well characterized *in vitro* (123, 124, 126, 155, 156). Pairs of GATCs were found inside or near ORFs that

could potentially regulate the lysis/lysogeny switch, and phage replication, including the analogs of integrases, excisionases, *ci* lambda repressor, *dnaA*, and *dnaC* (Fig. 5). An analysis of GATC sites was also done for *E. coli* prophage related regions. The occurrence of pairs at this distance is not likely to occur by chance: after shuffling the genome 1000 times with a k-mer size of four, to keep the same number of GATCs, the occurrence of any pairs and pairs within 41 bp in the whole genome decreased by 20% in both *E. coli* and *Salmonella* LT2 (P value: <0.0001, ****) (Fig. 13/S1).

To further explore SeqA protein binding chromosome wide, *E. coli* ChIP-Chip data was analyzed and no SeqA binding data is available for *Salmonella*. SeqA binding was compared to RNAP binding using the 2010 ChIP-Chip data from both Sánchez-Romero et al. and from Waldminghaus et al. (120, 121). A two-tailed t-test was performed on both data sets which revealed loci in which SeqA binding was enriched and RNAP binding was depleted (Fig. 6) (120). The 2012 Waldminghaus et al. data was also processed to compare overall SeqA binding and a two tailed t-test was used to compare signals at 0 min vs. 50 min. The 0 min time point was chosen since it had little to no SeqA binding and the 50 min time point had SeqA binding distributed throughout the chromosome. The data was sorted by % rank, yielding the most highly occupied (Top) SeqA binding sites (122). The Top 50%, Top 25%, and Top 10% were obtained by filtering the signals into their respective ranks and these signals were used to create independent files to compare against the total signals. These tracks for the three data sets were co-visualized with GATC sites to give a better overall view of overall where SeqA is acting (Fig. 6, Table 1). Pairs of GATC sites were also found within the

integrase ORF of the *E. coli* cryptic prophage CP4-6 (Fig. 6). This provided evidence that SeqA binds prophage ORFs and excludes RNAP.

SeqA binding signals and GATCs are over-represented in ORFs and under-represented in prophage

In order to quantify and compare the signals in prophage sequences and in ORFs throughout the whole genome, BEDOPs and BEDTools were used (161, 162). These computational tools provide a range of functions to further analyze the signals and genomic features such as GATC sites. The BEDOPs “element-of” function was used to find GATCs that were elements of the SeqA ChIP-Chip data sets for the weak Top 50% and the strong Top 10% interactions (Fig. 14/S2). Even pairs of GATC sites had an increase in SeqA signal of 10-15%, showing that SeqA interacts with pairs of GATC within bacteriophage ORFs. A new method of analysis of GATCs was developed based on pairing of GATCs *in vitro*, see methods and Han J.S and Hwang D.S. 2003 (123). Further pairing into higher order GATCs increased the SeqA microarray signals 10-15% for each GATC site to a GATC site pair (GATC₂) to form the (GATC₃) third GATC was paired, to form the (GATC₄) a fourth GATC pair was formed (Fig. 14/S2).

To see how often pairing and formation of higher order structures occurs we compared the observed counts vs. shuffled counts. Shuffling of the genome of *E. coli* and *Salmonella* LT2 was done using uShuffle with a k-mer size of four in order to keep the same number of GATCs (Fig. 13/S1) (163). After 1000 shuffles, there was a 20% decrease of GATC₂ instances both *E. coli* and *Salmonella* LT2 and a further 20% decrease of GATC₃ and GATC₄ higher order complexes, indicating that pairing of

GATCs is not random. These observations suggest that the role of paired and higher multiple of GATCs is biologically important (Fig. 13/S1).

The SeqA Signals for SeqA Only 1 (Waldminhaus et al. 2010), SeqA Only 2 (Sánchez-Romero et al. 2010), and SeqA Binding (Waldminhaus et al. 2012) (120–122) and the GATCs occurrences were quantified using BEDTools and BEDOPS (161, 162) to see overall binding to regions in the genome in prophage, ORFs, and promoters. The signals were shuffled 1000 times and randomized in order to compare randomized SeqA signals to the actual SeqA signals. GATC locations were also randomized to compare these to the observed GATCs. Cryptic prophage locations were identified in *E. coli* and both cryptic and active locations were identified in *Salmonella* LT2. BEDTools complement was used to create regions opposite (inverse) of prophage ORFs, and promoters and named nonprophage, noncoding, and nonpromoters respectively. The signals were divided into 1 basepair “regions” and BEDOPS “element-of” was used to quantify signals in regions vs. their complement.

There was a decrease of all of the signals (SeqA Only 1, SeqA Only 2, SeqA binding) and GATCs in prophage-related regions in both *E. coli* and *Salmonella* LT2 and these decreases were significant using χ^2 statistics comparing random vs. observed (Fig. 7). In addition, there are decreasing strong signals apparent in all of the signals (SeqA Only 1, SeqA Only 2, SeqA binding) and higher order GATCs (Fig. 7). SeqA signals and GATCs were all increased in ORFs in both *E. coli* and *Salmonella* LT2 and significant using χ^2 statistics of random vs. observed for *E. coli* and not *Salmonella* LT2 (Fig. 8). There was an increasing trend of the SeqA signals inside ORFs with no apparent trend in the GATCs (Fig. 8). There was a decreasing trend of SeqA Only 1

(Waldminhaus et al. 2010) and GATCs in promoters and no trend in SeqA Only 2 (Sánchez-Romero et al. 2010), or SeqA Binding (Waldminhaus et al. 2012)(120–122) and these trends were significant using χ^2 of random vs. observed(Fig. 15/S3).

Both SeqA signals and phages correlate with GATC Odds Markov ratio

After finding that phage have decreased GATCs, pairing, and signals we further analyzed the sequences using tetranucleotide frequencies on the microarray signals, signals, and bacteriophages. GATC tetranucleotide frequencies are lower in phage when calculated using a second order Markov model and pairing is less frequent in phage (164, 165). We used the CMBL Signature web server and calculated GATC tetranucleotide relative abundances with second order Markov modeling (166). The formula used for GATC Odds Markov ratio is $\tilde{t}_{GATC} = \frac{f_{GATC}^* f_{AT}^*}{f_{GAT}^* f_{ATC}^*}$ (167–169). Conservative statistical cutoffs of extremely high/low occurrences were previously developed by the Karlin lab (167–170). The cutoffs are based on statistical theory and on sequence motifs present in bacteriophage, bacteria, large human viruses, eukaryotes, and mitochondria in the European Molecular Biology Laboratory database in June 1991 (167–170).

Increasing SeqA signals correlate with increasing GATC Odds Markov ratio modeling (Fig. 9A). RNAP signals are always significantly low in GATC Odds Markov ratio (Fig. 9A). In order to see if this occurred in other phage both lytic and lysogenic phage were analyzed. Multiple lytic phage (T4, T7, P22, Felix O1) are extremely low for GATC Odds Markov ratio, and multiple cryptic phage are significantly lower but not as low as the fully lytic phage (Fig. 9). It is likely that phage evolve to avoid the effect of transcriptional regulation of SeqA on their life cycles.

To see an effect in virulent strains of *E. coli* and *Salmonella* an GATC Odds Markov ratio analysis was performed. *E. coli* O157:H7 - EDL933, *E. coli* O157:H7 – Sakai, *Salmonella* Typhi Ty2 and CT18. Many *E. coli* O157:H7 prophage are significantly low in GATC Odds Markov ratio for both EDL933 and Sakai including the shiga toxin encoding phage: CP-933V-stx1 , BP-933W-stx2, Sp15-stx1 and SP5-stx2 (Fig. 10A-B). Many *Salmonella* Typhi prophage are significantly low in GATC Odds Markov ratio as well for both CT18 and Ty2 (Fig. 10C-D).

Pairs of GATC sites are in cell cycle ORFs (*dnaA*, *mioC*, *mnmG/gidA*)

It was interesting that phage are very low in GATCs and that there were pairs of GATC sites in *dnaA* analogs, so we also investigated the *E. coli dnaA*, *mioC*, and *mnmG (gidA)* cell cycle ORFs. A search for GATC sites in them in *E. coli* yields clusters of GATCs with high binding by SeqA (Fig. 11). When SeqA is present in these locations RNAP polymerase is excluded and it is likely that transcription is regulated. It could bind directly inside these ORFs it could repress transcription of *dnaA*, other cell cycle ORFs, and preventing overinitiation of replication.

Discussion

High prophage induction in *seqA* mutants of *Salmonella* LT2 led to the finding that there are pairs of GATC sites inside important prophage life cycle ORFs and these do not appear to be random for both *E. coli* and *Salmonella*. SeqA binding inside an ORF and affecting transcription has not been shown before so it was unclear if SeqA was acting directly on the prophages or if it was because the SOS response was constitutively on. In Fels-2 and both Gifsy prophages, SOS regulation of prophage induction differs from that in *E. coli* λ . In λ , cI repressor controls the lysis-lysogeny

switch and when the SOS response is on the phage switch to the lytic life cycle. The Fels-2 and Gifsy prophages have an antirepressor tum that prevents *cl* analog from binding to its operator sites, thus keeping the phage active. There are *lexA* boxes upstream of the antirepressor tum gene for Gifsy-1, Gifsy-2, and Fels-2 and a capsid gene of Gifsy-1 and tail ORFs of Gifsy-2 and these have previously been shown to be strongly repressed by LexA overexpression (90). LexAind3 is an allele of the protein that is resistant to proteolysis and functions as a constitutive repressor. LexAind3 could have a negative effect on the genes of the prophages reducing their induction independently of the SOS response. *lexA* null mutants were shown to be lethal due to induction of the prophage. Therefore it is difficult to separate the effects of the *seqA* mutation and the SOS response (90).

After reanalyzing *E. coli* SeqA ChIP-Chip signals we found they are under-represented in prophages. These cryptic prophages do not form virions and thus it would be difficult to study the effect of SeqA on their life cycles. It appears the increased prophage induction is both direct and indirect. The SeqA signals are over-represented in ORFs. Our model is that SeqA binds inside ORFs causing positive supercoiling which interferes with RNA Polymerase transcription elongation (Fig. 12). SeqA might act to repress prophage induction directly, which could provide benefits to the host. SeqA might be acting to prevent overinitiation of replication by phage and stabilize phage lysogeny. SeqA could be acting to dysregulate phage leading to the formation of cryptic prophages. Interestingly some phage have extremely low GATC Odds Markov ratio, so it is possible phage evolve to escape the effect of SeqA.

In eukaryotes, CpG DNA methylation can cause increased compaction of DNA into inactive heterochromatin regions and transcriptionally silenced regions of DNA (171–176). SeqA could act similarly to histones and nucleosomes, providing another link between gene regulation in prokaryotes and eukaryotes. In addition, in yeast, forkhead box proteins are highly homologous to human forkhead box proteins and act similarly to SeqA (177–179). Forkhead 1 (Fkh1) and Forkhead 2 (Fkh2) bind to DNA and are involved in regulation of DNA replication initiation timing (177–179). Fkh1 and Fkh2 also bind throughout the chromosome and are slightly enriched in ORFs compared to flanking regions (177–179). Interestingly Fkh1 and Fkh2 have been shown *in vitro* to inhibit transcription elongation of RNAPII in coding regions of multiple genes (180). Further studies could further elucidate the effect of chromosome binding proteins on transcription regulation and similarities with eukaryotes and prokaryotes.

Materials and Methods

Recombineering

Recombineering was carried out using established protocols and the pSIM6 plasmid (181). The tetracycline resistance regulon (TetRA) was PCR amplified from Tn10dTet with primers with 40 basepairs of homology targeting SeqA. Forward primer SeqA - tetRA – Forward and SeqA - tetRA – Reverse (Table 3). Q5® High-Fidelity DNA polymerase was used with 1 µL purified genomic DNA of the G270 strain (*recD543::Tn10dTet*) and forward and reverse primers. 2 µL of the PCR product was electroporated into electrocompetent cells which had been grown at in low salt LB (2.5 g NaCl, 5 g Tryptone, 2.5 g Yeast Extract in 500 mL H₂O) at 30 °C with pSIM6 and with recombineering genes induced for 15 minutes at 42°C. Cells were recovered for 2 hours

at 30°C and on LB + 15 µg/mL tetracycline plates. The pSIM6 plasmids were cured from recombinants by subculturing cells with a 1:1000 dilution into 2 mL LB and grown for 8 hours at 37 °C. Cells were streaked from the culture onto an LB plate and then let to grow overnight and colonies were patch plated onto LB and LB + 30 µg/mL chloramphenicol. Cells that were sensitive to chloramphenicol were streak isolated and used for downstream assays.

P22 Transductions

Phage P22 was used for transductions and phage lysates were made according to previous protocols (182). Lysates were made by inoculating 2 mL of pre-phage broth (100 mL LB + 2 mL 50X NCE salts + 1 mL 20% glucose) with 0.5 mL donor cells and infecting with 5 µL P22HT. Cells were allowed to grow at 30 °C for 6 to 16 hours. Cultures were transferred to two 1.5 mL microcentrifuge tubes and lysed with 0.25 mL chloroform (CHCl₃). The tubes were vortexed, incubated on the bench for 10 minutes at room temperature and spun down at 13200 RPM for 5 minutes. Two phases formed, and the top phase was transferred to new tubes and treated with CHCl₃ vortexed, incubated, and spun down again. This was repeated until the lysate was clear and lysates were stored with drops of CHCl₃ in a 4 °C refrigerator. Transductions of *lexAind3* were set up on LB plates by adding 100 µL recipient cells with 20 µL, 10 µL, or 5 µL lysates. Plates were spread and incubated at 37 °C for 4 hours. They were then replica plated using sterile autoclaved velvets and transferred to LB plates + 30 µg/mL chloramphenicol. Transductants were streak purified twice on EBU agar plates. P22H5 was used to test for P22 sensitivity and sensitive colonies were streak purified onto LB plates.

Phage Induction

A sterile toothpick was used to streak out the glycerol freezer stock of G905, SDT2991, and SDT2993 onto LB Agar Plates (5 g NaCl, 5 g Tryptone, 2.5 g Yeast Extract, 7 g Agar in 500 mL H₂O) and allowed to grow at 37 °C for 12 hours. Single colonies were picked and inoculated into 1 mL Mueller Hinton Broth (MHB) and grown overnight for 16 hours. Overnights were subcultured 1:100 into 2 mL MHB and grown at 37 °C to Optical Density (OD₆₀₀) 0.17. Cells were diluted 1:3 into LB or different treatments of Mitomycin C (MilliporeSigma) to get final concentrations of 0.1 µg/mL to a final volume of 150 µL in microtiter plates (183). Cells were grown overnight for 20 hours at 37 °C with shaking in VersaMax™ Microplate Reader to monitor growth. The cells were taken out of the VersaMax™ Microplate Reader and were transferred to microcentrifuge tubes and whole cell lysates were made with the addition of 15 µL CHCl₃ (184). The lysates were centrifuged at 13200 RPM for 5 minutes in an Eppendorf 5415 D centrifuge and two layers formed. 0.6% Top agar (5g NaCl, 5g Tryptone, 2.5g Yeast Extract, 3g Agar in 500 mL H₂O) was melted in a microwave at 30% power and transferred to glass tubes in a water bath set at 50 °C (185). For full plate plaque assays 100 µL lysates was added with 100 µL of LT2 –phage and 3 mL of top agar and mixed together and plated onto EBU-Agar plates. Plates were incubated facing up overnight at 37 °C and checked the next day for plaques. 10 biological replicates were performed and plaques in a 1 cm² sector for each plate were counted with three technical replicates per plate. Using GraphPad Prism 6, two-way repeated measures ANOVA with matching was performed on averages of the three technical replicates. For strains

and treatments, Tukey's multiple comparisons with 95% confidence interval was performed.

Differential Binding of SeqA vs. RNAP and Analysis of SeqA Binding from ChIP-Chip data

Integrative Genomics Viewer (IGV) version 2.4.6 was used to view the *Salmonella enterica subsp. enterica serovar* Typhimurium str. LT2 (ASM694v2), and *Escherichia coli* str. K-12 substr. MG1655 (ASM584v2) genome assemblies (62, 186–191). GATC positive strand motifs were identified using find motif and searching for “GATC”. Prophage locations and ORFs were identified from assembly annotations and PHASTER (<https://phaster.ca/>) (149, 191). Gene annotations and KEGG was used to identify functions of ORFs in prophages (192). ChIP-Chip Data was obtained from the Gene Expression Omnibus (GEO) for the 2010 (GSE19053) and 2012 (GSE28280) Waldminghaus et al. data (121, 122, 193–195) using GenePattern (193). ChIP-Chip data from Sánchez-Romero et al. was downloaded from supplemental data and manually converted to a GCT file (120). Microarray loci were converted from U00096.2 to U00096.3 locations using the EcoGene: Gene Interval Updater (61). Updated ChIP-Chip data was uploaded to GenePattern and Sánchez-Romero et al. data were preprocessed to obtain \log_2 transformed data and GSE19053/GSE28280 data were already \log_2 transformed. SeqA vs. RNAP differential binding was assessed by using ComparativeMarkerSelection (196). A two-tailed t-test was performed on the SeqA-new vs. RNAP old duplicate samples for GSE19053: (GSM471486 SeqA new rep1, GSM471487 SeqA new rep2 vs. GSM471482 RNAP old rep1 GSM471483 RNAP old rep2). A two-tailed t-test was also performed on the SeqA timepoint 1 vs. RNAP

duplicate samples for the Sánchez-Romero et al. data. To assess SeqA binding a two-tailed t-test was performed on the SeqA 0-minute timepoint vs. SeqA 50-minute timepoint duplicate samples for GSE28280: (GSM699908 SeqA in 0 min dnaC2 rep1, GSM699909 SeqA in 0 min dnaC2 rep2, GSM699921 SeqA in 50 min dnaC2 rep1, GSM699922 SeqA in 50 min dnaC2 rep2). 50-minutes was selected as it has the most SeqA binding coverage compared to other time points.

ComparativeMarkerSelectionViewer was used to download the data and then sorted by rank of the test statistic (P value) (196). GCT files were made for all ranks 100% and the top ranks (5%, 10%, 25%, 50%) were obtained by filtering for the specified percentage in Microsoft Excel. In IGV the GCT files were used to make tracks onto the genome assembly with the updated probe locations and compared to GATC motifs and ORF locations.

GATC Odds Markov Ratio on Signals and Regions

The GCT files created from Waldminghaus et al. 2010 and Sánchez-Romero for all ranks and 5%, 10%, 25%, and 50% for both RNAP Only and SeqA Only were converted to BED files using Microsoft Excel (120, 121). The GCT files created from Waldminghaus et al. 2012 for SeqA Binding all ranks and the top ranks (5%, 10%, 25% and 50%) were converted to BED files using Microsoft Excel (122). Prophage regions for *E. coli* and *Salmonella* were annotated on Integrative Genomics Viewer and exported to BED files (186, 187). To obtain ORFs, GFF files from the *E. coli* MG1655 (ASM584v2) and LT2 (ASM694v2) assemblies were converted into Microsoft Excel files and duplicate annotations, annotations that were internal to other annotations, and ID annotations were deleted (62, 188–191). BEDTools v2.27.1 was downloaded from

<https://bedtools.readthedocs.io/> and BEDOPS v2.3.45 was downloaded from <https://bedops.readthedocs.io/en/latest/> and both were installed on a local computer (161, 162). The ORFs were then converted into BED files and overlapping ORFs were merged using BEDOPS with the "--merge" command (161). Noncoding BED files for both *E. coli* and *Salmonella* were made using BEDTools and the "complement" command on the ORFs BED file and two .genome files containing the genome sizes and chromosomes (162). Cryptic prophage locations for *E. coli* K-12 were identified from the RefSeq assembly, a patent, and PHASTER (62, 149, 188, 190, 191, 197). Prophage locations for *E. coli* O157:H7 were identified from the RefSeq assemblies, the literature, and PHASTER (64, 70, 71, 148, 149). Five new prophages of *E. coli* O157:H7 - EDL933 were identified using PHASTER in locations NC_002655.2:1748351-1756006, NC_002655.2:2142479-2177204, NC_002655.2:2272752-2342415, NC_002655.2:3260475-3274334, NC_002655.2:3544753-3565707 and named GP-9338, GP-93311, GP-93312, GP-93316, GP-93317 respectively. Prophage locations for *Salmonella* LT2 were identified from the RefSeq assembly, Defective prophages 1-4 were identified using the literature and PHASTER (85, 189). A fifth defective prophage was identified using PHASTER in location: "AE006468.2:2,899,841-2,931,190" and named SD-9 (149). Prophage locations for *Salmonella* Typhi were identified from the RefSeq assemblies, the literature, and PHASTER (64, 94, 98, 149). Prophage locations for *E. coli* and *Salmonella* were annotated on Integrative Genomics Viewer and saved as BED files. Active prophages for *Salmonella* LT2 were distinguished from cryptic in an active prophage BED file containing regions for Gifsy-1, Gifsy-2, Fels-1, and Fels-2. The all prophage BED file contains the regions for the

Salmonella LT2 active prophages and the five defective prophages. Nonprophage regions for *E. coli* and *Salmonella* were created using BEDtools “complement” with the prophage BED file for *E. coli* and the all prophage BED file for *Salmonella* and their respective genome files (162). All promoter sequences for *E. coli* K-12 were obtained from RegulonDB 9.0 and converted to FASTA files using Microsoft Excel (198). Bowtie2 version 2.3.4.1 was downloaded from <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml> and installed on a local computer (199, 200). The FASTA promoter files were aligned to the *E. coli* genome using Bowtie2 (199, 200). The SAM output file from Bowtie2 was converted to a BED file using the BEDOPS “sam2bed” command (161). EMBOSS seqret was used to convert BED files for the signals, prophage regions, and promoters to GenBank files using the FNA files from the *E. coli* MG1655 (ASM584v2), *E. coli* O157:H7-EDL933 (ASM666v1), *E. coli* O157:H7-Sakai (ASM886v2), *Salmonella* LT2 (ASM694v2), *Salmonella* CT18 (ASM19599v1), and *Salmonella* Ty2 (ASM754v1) assemblies (62, 70, 94, 98, 148, 188–191). *E. coli* infecting phage genome sequences of GenBank files were downloaded from NCBI with the following names and accession numbers: T1 (GenBank: AY216660.1), T4 (Refseq: NC_000866.4), T5 (Refseq: NC_005859.1), T7 (Refseq: NC_001604.1) and Lambda (Refseq: NC_001416.1) (191, 201–205). *Salmonella* infecting phage genome GenBank files were downloaded from NCBI with the following names and accession numbers, P22 (Refseq: NC_002371.2), Felix O1 (Refseq: NC_005282.1) (191, 206). All GenBank files for all regions and phage were run on the CMBL Signature web server (<http://cdbl.uga.edu/software/signature.html>) to calculate GATC Odds Markov Ratio:

$$\tilde{\tau}_{GATC} = \frac{f_{GATC}^* f_{AT}^*}{f_{GAT}^* f_{ATC}^*} \quad (167-169).$$

GenBank files for signals with over 10,000 sequences 50

Min All, RNAP Only 1, RNAP Only 2), were converted into separate GenBank files of less than 10,000 and then the GATC Odds Markov ratio were averaged across the runs. *E. coli* cryptic prophage PR-X was not included in GATC Odds Markov Ratio analysis because of the small size.

Shuffling and Randomization of Signals and Genomes

The BED files created from Waldminghaus et al. 2010 and Sánchez-Romero for all ranks and 5%, 10%, 25%, and 50% for SeqA Only and Waldminghaus et al. 2012 for SeqA Binding all ranks and the top ranks (5%, 10%, 25% and 50%) were shuffled 1000 times using a shell script written in Python3 (120–122, 207). The BEDtools “shuffle” command with seed 1 and sort the bed file using the Unix sort command “sort -k1,1 -k2,2n” (162). The signals were then placed in locations in the microarray sorted by a cell created by the Microsoft Excel RAND function to create random locations. The locations were then sorted in Microsoft Excel using sort for the start site of the microarray probe and then the Excel files were converted to BED files.

GATC Sites, GATC Pairs, and Higher Order GATCs and Randomization

Integrative Genomics Viewer (IGV) was used to view the *Salmonella enterica* *subsp. enterica* serovar Typhimurium str. LT2 (ASM694v2), and *Escherichia coli* str. K-12 substr. MG1655 (ASM584v2) genome assemblies and Ushuffle sorted genome assemblies (62, 163, 186–191). GATC positive strand motifs were identified using find motif and searching for “GATC”. The GATC locations were saved as BED files and converted to Microsoft Excel spreadsheets. To analyze pairing *in vivo* GATCs were grouped in five different categories: GATCs on the positive sense strand were labeled as GATC All; GATCs within 41 basepairs were categorized as GATC Pairs, GATC Pairs

that were near within 41 basepairs third GATC were categorized as GATC Higher Order 1 (i.e., two pairs of GATCs). If the GATC Higher Order 1 had a fourth GATC within 41 basepairs, it was categorized as a GATC Higher Order 2 (i.e., three pairs of GATCs). Microsoft Excel was used to find GATC sites were that were < 41 basepairs from the middle of the another GATC site ($GA^{\downarrow}TC < 41$ basepairs from a $GA^{\downarrow}TC$) and placed in a column and defined GATC Pairs. A second column was created to find GATC Pairs < 41 basepairs from the middle of the first GATC site and defined GATC Higher Order 1. A third column was created to find GATC Higher Order 1 sites < 41 basepairs from the middle of the first GATC site and defined GATC Higher Order 2. GATCs were sorted for All GATCs, GATC Pairs, GATC Higher Order 1, and GATC Higher Order 2 were copied into new spreadsheets and then sorted by location. GATC spreadsheets were then converted into BED files. Random GATC locations for *E. coli* and *Salmonella* LT2 were created using BEDtools “random” function using a “.genome” text file with the “-n” option followed by the number containing the count of all GATCs (162). The random locations for GATC pairs, GATC Higher Order 1, GATC Higher Order 2 were created the same way using a “.genome” text file and the “-n” option followed by the original counts of GATC pairs, GATC Higher Order 1, GATC Higher Order 2 respectively (162).

Genome Arithmetic

Bash shell scripts were created to run BEDOPS on microarray BED observed and randomized signals. The “--chop” function with the “1” option to chop the signals into single basepairs (161). Scripts were run using the BEDOPS “--element-of” function to find counts of observed chopped signals, randomized chopped signals, observed GATCs, and randomized GATCs in the ORFs and prophage regions (161). Scripts were

also run using BEDOPS and the “--element-of” function and range 75 to find counts of GATCs, GATC Pairs, and Higher Order GATCs with signals (161). Contingency tables of random vs. observed were made in GraphPad Prism 6 and χ^2 statistics were performed using a 95% confidence interval. Results were graphed as percentage of counts vs. total of counts for the regions:

$$\left(\frac{\text{Signals in ORFs}}{\text{Signals in ORFs} + \text{Signals in Noncoding}}\right) * 100, \left(\frac{\text{GATCs in Noncoding}}{\text{GATCs in ORFs} + \text{GATCs in Noncoding}}\right) * 100$$

$$\left(\frac{\text{Signals in Prophage}}{\text{Signals in Prophage} + \text{Signals in Nonprophage}}\right) * 100, \left(\frac{\text{GATCs in Nonprophage}}{\text{GATCs in ORFs} + \text{GATCs in Noncoding}}\right) * 100$$

$$\left(\frac{\text{Signals in Promoters}}{\text{Signals in Promoters} + \text{Signals in Nonpromoters}}\right) * 100, \left(\frac{\text{GATCs in Nonpromoters}}{\text{GATCs in Promoters} + \text{GATCs in Nonpromoters}}\right) * 100$$

Table 1: Supplemental File S1: ChIP-Chip IGV Tracks and Bed Files.

GCT_files_and_BED_files.zip. Zip files containing .gct and .bed files for each track and region.

Track/Bed	File	Source
SeqA Only 1_Top 5%	SeqAOnlyTop5PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
SeqA Only 1_Top 10%	SeqAOnlyTop10PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
SeqA Only 1_Top 25%	SeqAOnlyTop25PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
SeqA Only 1_Top 50%	SeqAOnlyTop50PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
SeqA Only 1_100%	SeqAOnly_W_2010_GSE19053.zip	Waldminghaus et al. 2010
RNAP Only 1_100%	RNAPOnly_W_2010_GSE19053.zip	Waldminghaus et al. 2010
RNAP Only 1_Top 50%	RNAPOnlyTop50PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
RNAP Only 1_Top 25%	RNAPOnlyTop25PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
RNAP Only 1_Top 10%	RNAPOnlyTop10PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
RNAP Only 1_Top 5%	RNAPOnlyTop5PercentRank_W_2010_GSE19053.zip	Waldminghaus et al. 2010
SeqA Only 2_Top 5%	SeqAOnlyTop5PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
SeqA Only 2_Top 10%	SeqAOnlyTop10PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
SeqA Only 2_Top 25%	SeqAOnlyTop25PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
SeqA Only 2_Top 50%	SeqAOnlyTop50PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
SeqA Only 2_100%	SeqAOnly_SR_2010.zip	Sánchez-Romero et al. 2010

Table 1: Supplemental File S1: ChIP-Chip IGV Tracks and Bed Files.

GCT_files_and_BED_files.zip. Zip files containing .gct and .bed files for each track and region.

Track/Bed	File	Source
RNAP Only 2 100%	RNAPOnly_SR_2010.zip	Sánchez-Romero et al. 2010
RNAP Only 2_Top 50%	RNAPOnlyTop50PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
RNAP Only 2_Top 25%	RNAPOnlyTop25PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
RNAP Only 2_Top 10%	RNAPOnlyTop10PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
RNAP Only 1_Top 5%	RNAPOnlyTop5PercentRank_SR_2010.zip	Sánchez-Romero et al. 2010
SeqA Binding 5%	0vs50MinTop5PercentSignal_W_2012.zip	Waldminghaus et al. 2012
SeqA Binding 10%	0vs50MinTop10PercentSignal_W_2012.zip	Waldminghaus et al. 2012
SeqA Binding 25%	0vs50MinTop25PercentSignal_W_2012.zip	Waldminghaus et al. 2012
SeqA Binding 50%	0vs50MinTop50PercentSignal_W_2012.zip	Waldminghaus et al. 2012
SeqA Binding 100%	0vs50Min_W_2012.zip	This study
<i>E. coli</i> GATC	EcoliGATC_All.zip	This study
<i>E. coli</i> GATC₂	EcoliGATC_HigherO1.zip	This study
<i>E. coli</i> GATC₃	EcoliGATC_HigherO2.zip	This study
<i>E. coli</i> GATC₄	EcoliGATC_HigherO3.zip	This study
LT2 GATC	LT2GATC_All.zip	This study
LT2 GATC₂	LT2GATC_HigherO1.zip	This study
LT2 GATC₃	LT2GATC_HigherO2.zip	This study
LT2 GATC₄	LT2GATC_HigherO3.zip	This study
<i>E. coli</i> ORFs	EcoliORFs.zip	This study
<i>E. coli</i> Prophage	EcoliProphage.zip	This study
<i>E. coli</i> Promoters	EcoliPromoters.zip	This study

Table 1: Supplemental File S1: ChIP-Chip IGV Tracks and Bed Files.

GCT_files_and_BED_files.zip. Zip files containing .gct and .bed files for each track and region.

Track/Bed	File	Source
<i>E. coli</i> Noncoding	EcoliNoncoding.zip	This study
<i>E. coli</i> Nonphage	EcoliNonphage.zip	This study
<i>E. coli</i> Nonpromoters	EcoliNonpromoters.zip	This study
LT2 ORFs	LT2ORFs.zip	This study
LT2 Prophage	LT2Prophage.zip	This study
LT2 Promoters	LT2Promoters.zip	This study
LT2 Noncoding	LT2Noncoding.zip	This study

Table 2: Supplemental File S2: Strain List.

Strain_list.zip. Zip files containing strain list.

Strain		Genotype
G905	LT2	Lab collection
SDT2937	LT2 <i>lexA33::(Cm^R lexA3IND)(sw)</i>	This study
SDT2991	LT2 Δ <i>seqA::Tet^R</i>	This study
SDT2993	LT2 Δ <i>seqA::Tet^R lexA33::(Cm^R lexA3IND)(sw)</i>	This study

Table 3: Primers (5' -> 3'):

Name	Sequence
SeqA - tetRA - Forward	GTTGATGATGAACTCTATAGCTAAGCACTTGTCTCCTGTT
SeqA - tetRA - Reverse	TGGTCCTTCTAATGCAAGGAGCTGCTTTTAAGACCCACTT

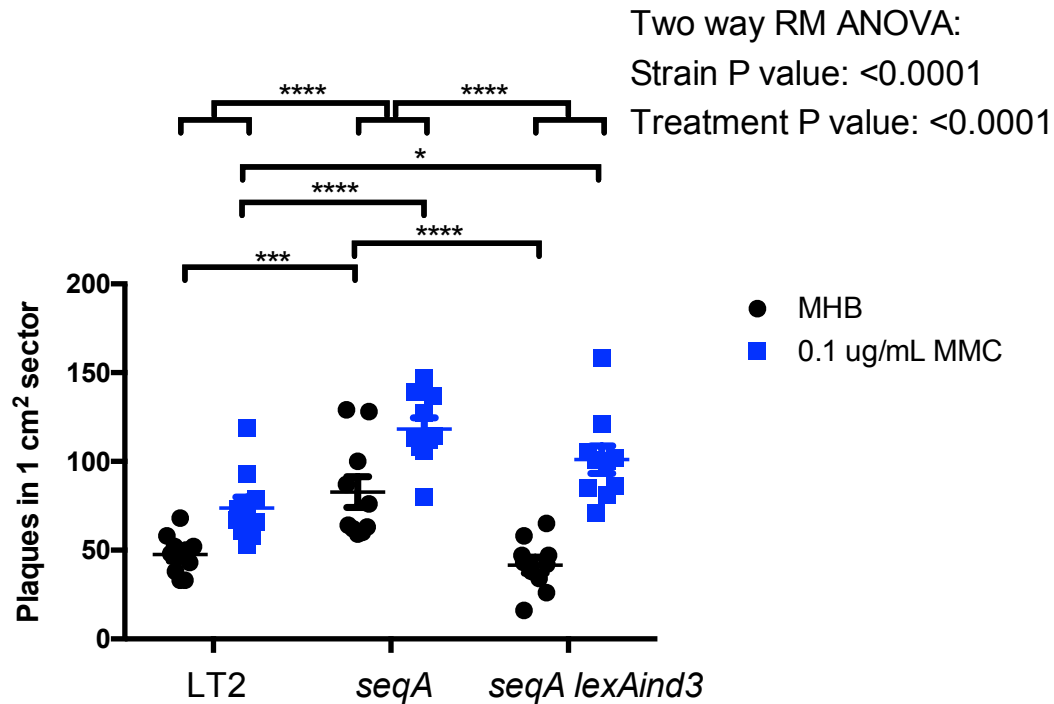


Figure 4: Prophage induction in LT2, *seqA*, and *seqA lexAind3* strains. A. Gifsy-2 size (~1 mm) plaque counts in a 1 cm² sector on an Evans Blue Uranine (EBU) plate of G905 LT2 strains, SDT2991 *seqA* strains, and SDT2993 *seqA lexAind3*. Cultures were treated with MHB (●) alone or 0.1 μg/mL MMC (■). Experiments are done with ten biological replicates with three technical replicates from each plate and error bars indicating standard error of the mean. Two-way repeated measures (RM) ANOVA for strain (P Value: <0.0001) and treatment (P Value: <0.0001). Tukey's multiple comparisons test: MHB[LT2:*seqA*] (***), MHB[*seqA*:*seqA lexAind3*] (****), 0.1 μg/mL MMC[LT2:*seqA*] (***), 0.1 μg/mL MMC[LT2:*seqA lexAind3*] (*), MHB and 0.1 μg/mL [LT2:*seqA*] (****), MHB and 0.1 μg/mL [*seqA*: *seqA lexAind3*] (****) all other comparisons were not significant.

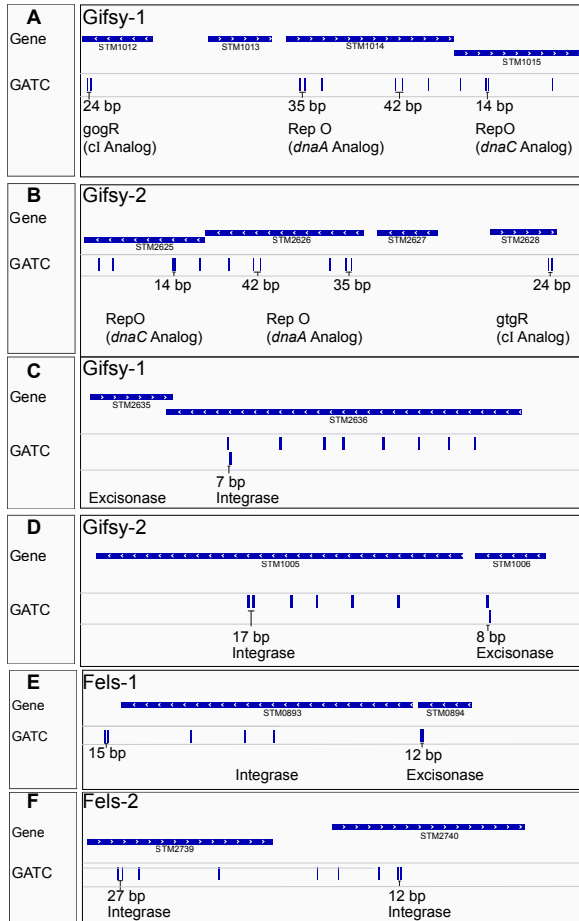


Figure 5: Pairs of GATC sites in active *Salmonella* LT2 prophages: Gifsy-1, Gifsy-2, Fels-1 and Fels-2 regulatory ORFs. GATC sites are denoted by vertical lines. **A.** Gifsy-1: STM1012 (Lambda *ci* repressor analog) - GATC pair 24 bp apart in ORF; STM1014 (*dnaA* analog) – two GATC pairs 35 bp and 42 bp apart in ORF; STM1015 (*dnaC* analog) - GATC pair 14 bp apart in ORF. **B.** Gifsy-1: STM2628 (Lambda *ci* repressor analog) - GATC pair 24 bp apart in ORF; STM2626 (*dnaA* analog) – two GATC pairs 35 bp and 42 bp apart in ORF; STM2625 (*dnaC* analog) - GATC pair 14 bp apart in ORF. Gifsy-1 and Gifsy-2 are integrated into the chromosome in opposite orientations and are highly homologous between the A and B. **C.** Gifsy-1: STM2636 (Integrase) - GATC pair 7 bp apart in ORF; STM2635 (Excisionase). STM2635 does not have a pair of GATC sites. **D.** Gifsy-1: STM1005 (Integrase) - GATC pair 17 bp apart in ORF; STM1006 (Excisionase) - GATC pair 8 bp apart in ORF. **E.** Fels-1: STM0893 (Integrase) - GATC pair 15 bp apart downstream of ORF; STM0894 (Excisionase) - GATC pair 12 bp apart in ORF. **F.** Fels-2: STM2740 (Integrase) - GATC pair 12 bp apart in ORF; STM2739 (Integrase) - GATC pair 27 bp apart in ORF. An excisionase was not identified in Fels-2. Fels-1 and Fels-2 are in different bacteriophage families and are not highly homologous between the regions.

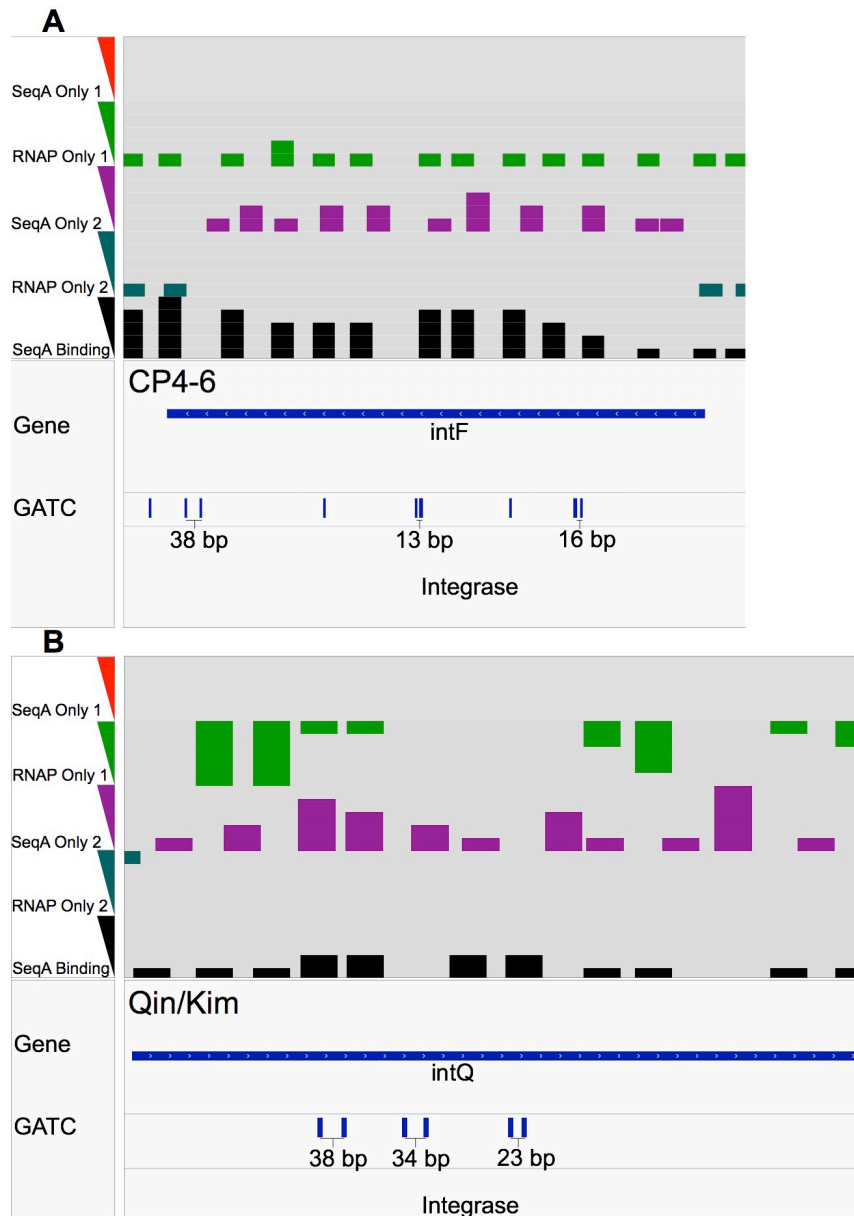


Figure 6: Pairs of GATC sites in cryptic *E. coli* prophage CP4-6 and Qin/Kim Integrase ORFs. GATC sites are denoted by vertical lines. SeqA vs. RNAP differential binding and SeqA binding signals are shown in rank by two-tailed t-test by the test statistic (P value) with top ranks (5%, 10%, 25%, 50%) and all ranks (100%) (120, 122). SeqA Only 2 rows in purple and RNAP Only 2 rows in dark green indicate differential binding by the rank of ChIP-Chip data from Sánchez-Romero et al. 2010 (120). SeqA Binding rows in black indicate SeqA binding by the rank of 50-minute ChIP-Chip data from Waldminghaus et al. 2012 (122). GATC sites on the positive strand are shown. A. CP4-6: intF (Integrase) - three GATC pairs 38 bp and 13 bp and 16 bp apart in ORF. B. Qin/Kim: intF (Integrase) - three GATC pairs 38 bp and 34 bp and 23 bp apart in ORF.

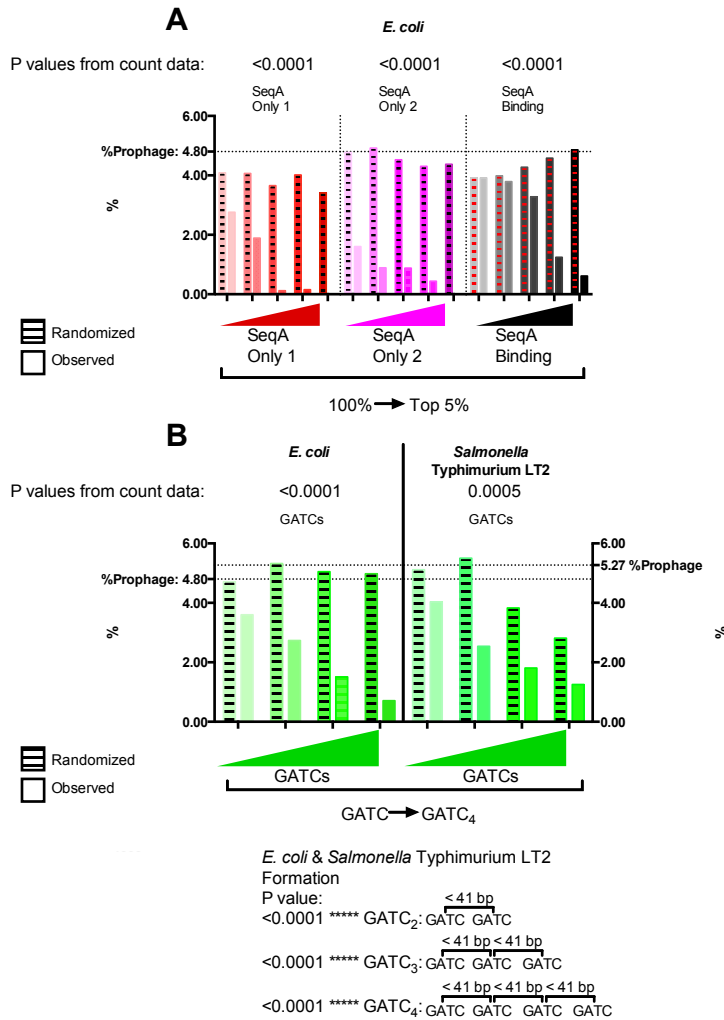


Figure 7: SeqA signals and GATCs in prophages of *E. coli* and *Salmonella* LT2. BEDOPS frequency counts of signals in prophages (161). Signals were chopped to 1 bp regions and results graphed as a percentage of signals in prophage regions. Bars are shaded light to dark to indicate increasing strength of signal from weak to strong. %Prophage for *E. coli* of 4.8% is indicated on the left Y axis with a dashed bar and %Prophage for *Salmonella* LT2 of 5.27% is indicated on the right Y axis. χ^2 statistics were performed on counts and P values were calculated and shown on graph. **A.** *E. coli* ChIP-Chip of SeqA Only 1 (Red) from Waldminghaus et al. 2010 (121). ChIP-Chip of SeqA Only 2 (Purple) from Sánchez-Romero et al. 2010 (120). *E. coli* ChIP-Chip of SeqA Binding (Black) from Waldminghaus et al. 2012 (122). Dashed bars for signals indicate signals that had been shuffled 1000 times and placed in random locations. **B.** GATCs (Green) in prophage for both *E. coli* and *Salmonella* LT2. Dashed bars for GATCs indicate GATCs that had been placed in random locations in the genome.

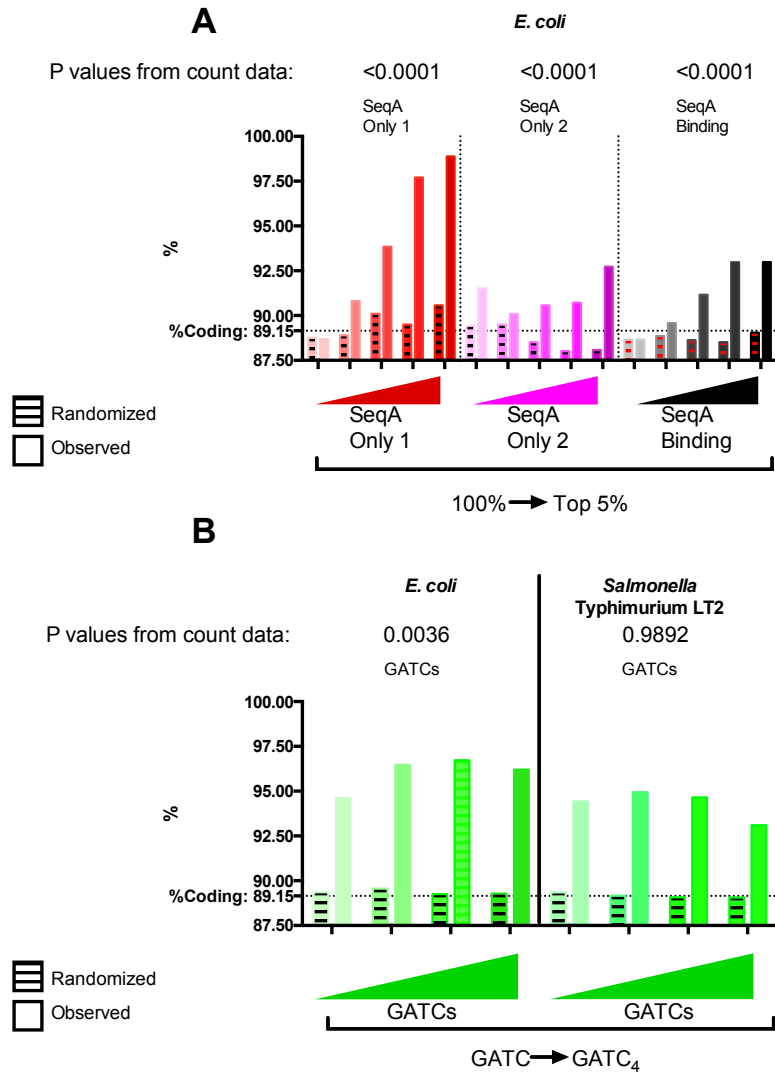
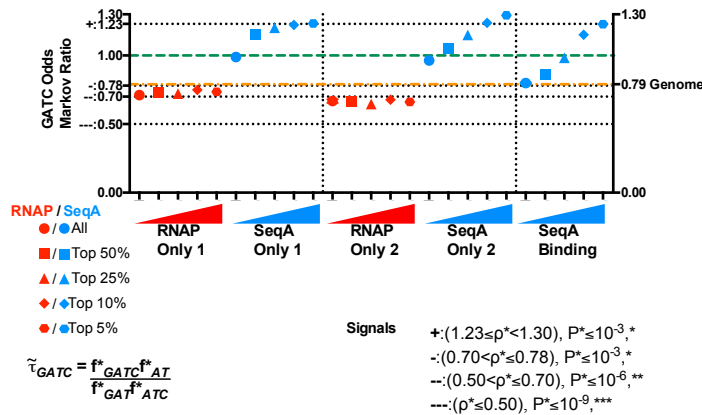


Figure 8: SeqA signals and GATCs in ORFs of *E. coli* and *Salmonella* LT2. BEDOPS frequency counts of signals in ORFs (161). Signals were chopped to 1 bp regions and results graphed as a percentage of signals in ORFs. Bars are shaded light to dark to indicate increasing strength of signal from weak to strong. %Coding for *E. coli* and *Salmonella* LT2 of 89.15% is indicated on the left Y axis. χ^2 statistics were performed on counts and P values were calculated and shown on graph. **A.** ChIP-Chip of SeqA Only 1 (Red) from Waldminghaus et al. 2010 (121). ChIP-Chip of SeqA Only 2 (Purple) from Sánchez-Romero et al. 2010 (120). *E. coli* ChIP-Chip of SeqA Binding (Black) from Waldminghaus et al. 2012 (122). Dashed bars for signals indicate signals that had been shuffled 1000 times and placed in random locations. **B.** GATCs (Green) in coding sequence for both *E. coli* and *Salmonella* LT2. Dashed bars for GATCs indicate GATCs that had been placed in random locations in the genome.

A



B

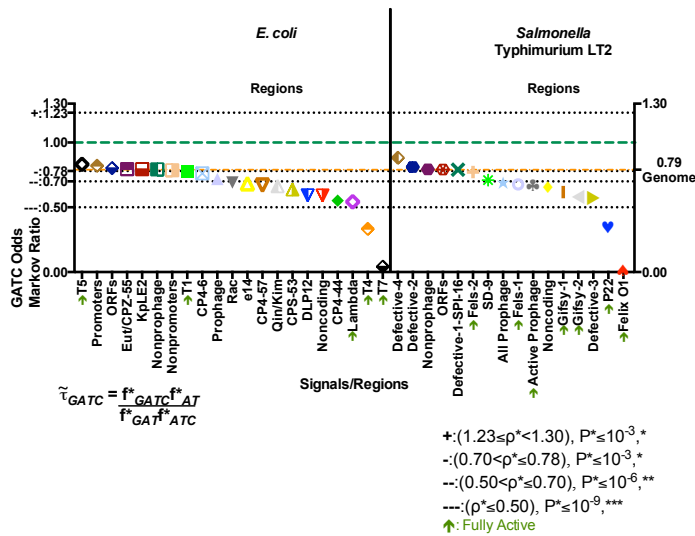


Figure 9: GATC Odds Markov ratio of SeqA signals and genomic regions of *E. coli* K-12 and *Salmonella* LT2.

GATC Odds Markov Ratio ρ^* calculated using the Signature web interface on signals of *E. coli* regions of *E. coli* K-12 and *Salmonella* LT2 using equation:

$$\tilde{\rho}_{GATC} = \frac{f^*_{GATC} f^*_{AT}}{f^*_{GAT} f^*_{ATC}} \quad (167-169).$$

1.0 denotes average relative abundance and is indicated. Significance cutoffs are +1.23 for overrepresented GATCs (+), P^* value $\leq 10^{-3}$, -0.78 underrepresented (-), value $\leq 10^{-3}$, -0.70 highly underrepresented (--), P^* value $\leq 10^{-6}$, -0.50 very highly underrepresented (---), P value $\leq 10^{-9}$ (167–169). The ratios for both the *E. coli* and *Salmonella* LT2 genomes are 0.79 and is indicated. **A.** *E. coli* ChIP-Chip of RNAP Only 1 (Red) and SeqA Only 1 (Blue) from Waldminghaus et al. 2010 (121). *E. coli* ChIP-Chip RNAP Only 2 (Red) and SeqA Only 2 (Blue) from Sánchez-Romero et al. 2010 (120). *E. coli* ChIP-Chip of SeqA Binding Waldminghaus et al. 2012 (122). **B.** Regions of *E. coli* and *Salmonella* Typhimurium and bacteriophages are included. Fully active phage are denoted by green arrow.

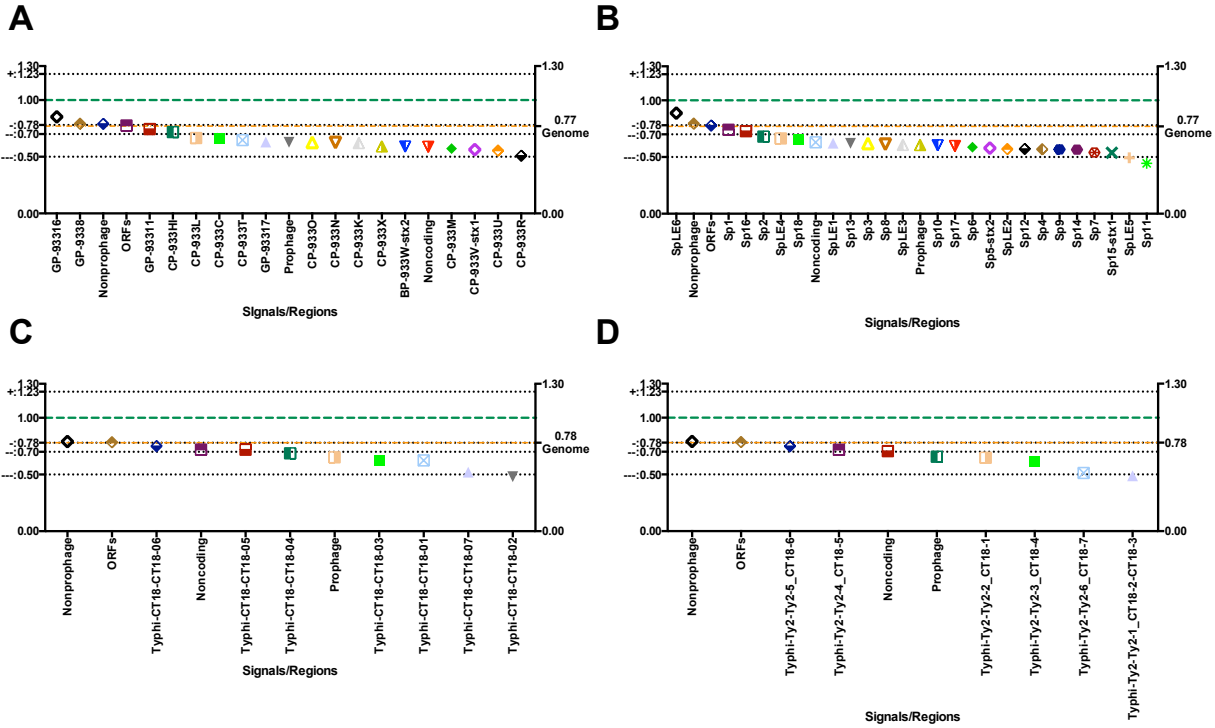


Figure 10: GATC Odds Markov ratio of genomic regions of *E. coli* O157:H7 and *Salmonella* Typhi. GATC Odds Markov Ratio ρ^* calculated using the Signature web interface on signals of *E. coli* regions of *E. coli* O157:H7 and *Salmonella* Typhi using equation: $\tilde{\tau}_{GATC} = \frac{f^*_{GATC} f^*_{AT}}{f^*_{GAT} f^*_{ATC}}$ (167–169). 1.0 denotes average relative abundance and is indicated. Significance cutoffs are +1.23 for overrepresented GATCs (+), P^* value $\leq 10^{-3}$, -0.78 underrepresented (-), value $\leq 10^{-3}$, -0.70 highly underrepresented (--), P^* value $\leq 10^{-6}$, -0.50 very highly underrepresented (---), P value $\leq 10^{-9}$ (167–169). The ratios for *E. coli* O157:H7 and *Salmonella* Typhi genomes are 0.77 and 0.78 respectively and are indicated. **A.** *E. coli* O157:H7 - EDL933 **B.** *E. coli* O157:H7 - Sakai **C.** *Salmonella* Typhi CT18 **D.** *Salmonella* Typhi Ty2.

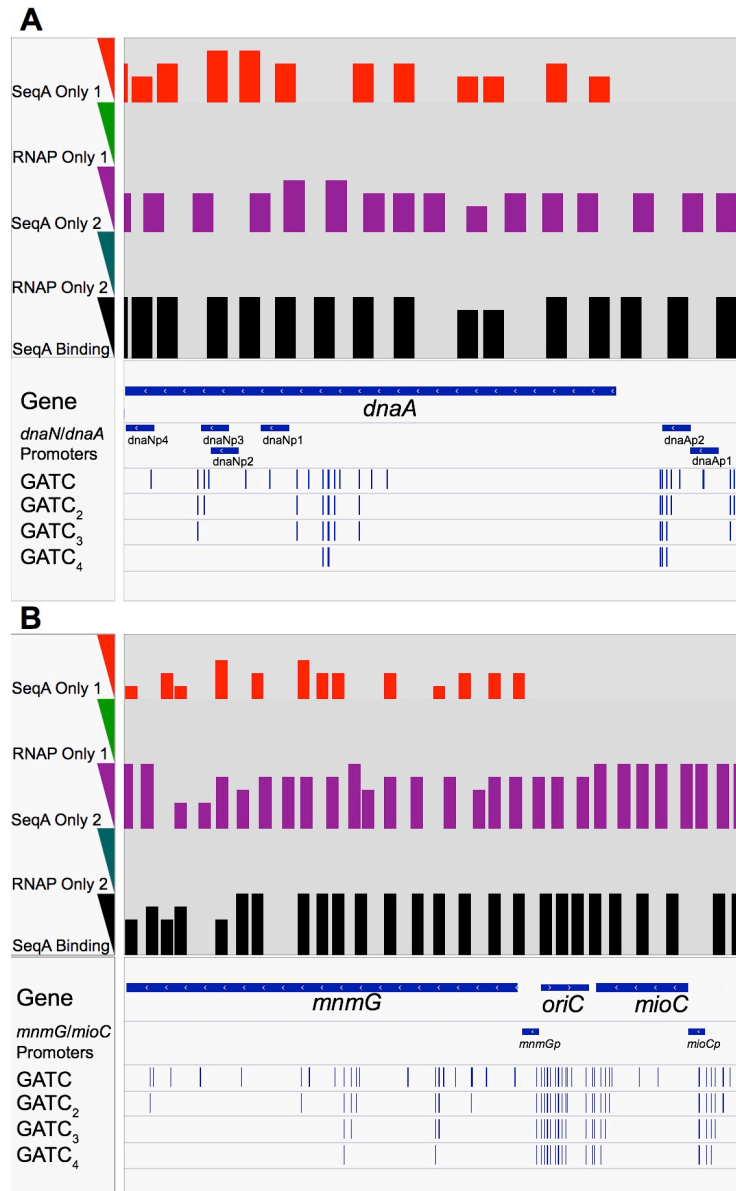


Figure 11: Pairs of GATC sites in *E. coli* cell cycle ORFs: *dnaA*, *mioC*, *mnmG* (*gidA*). GATC sites, pairs, and higher order GATCs are denoted by vertical lines. SeqA vs. RNAP differential binding and SeqA binding signals are shown in rank by two-tailed t-test by the test statistic (P value) with top ranks (5%, 10%, 25%, 50%) and all ranks (100%) (120–122). SeqA Only 1 rows in red and RNAP Only 1 rows in light green indicate differential binding by the rank of ChIP-Chip data from Waldminghaus et al. 2010 (121). SeqA Only 2 rows in purple and RNAP Only 2 rows in dark green indicate differential binding by the rank of ChIP-Chip data from Sánchez-Romero et al. 2010 (120). SeqA Binding rows in black indicate SeqA binding by the rank of 50-minute ChIP-Chip data from Waldminghaus et al. 2012 (122). GATC sites on positive strand are shown with GATC Pairs, GATC Higher Order 1 to GATC Higher Order 4. **A.** *dnaA* **B.** *mnmG*, *mioC*. *oriC* is labeled.

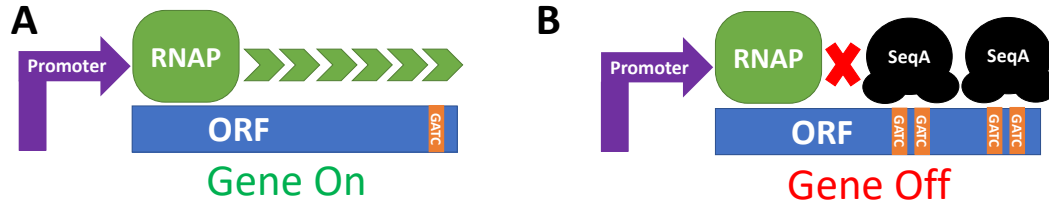


Figure 12: Model of how SeqA regulates genes. **A.** In phage or bacteria genes with few GATC sites (Orange) in the ORF (Blue), RNA Polymerase (Green) is able to freely access a coding sequence and the gene is on. **B.** When SeqA (Black) is bound to pairs of GATC sites it introduces positive supercoils in the ORF which limits the accessibility by RNA Polymerase and the gene is off.

Supplemental Materials

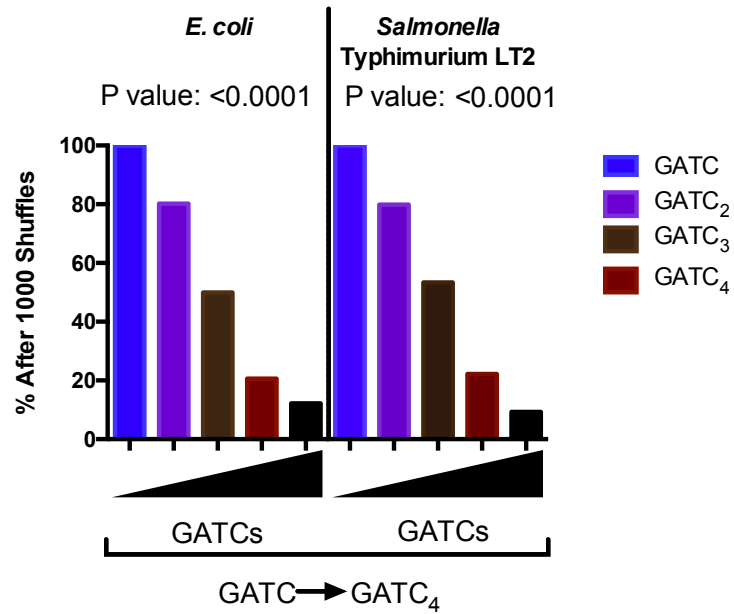
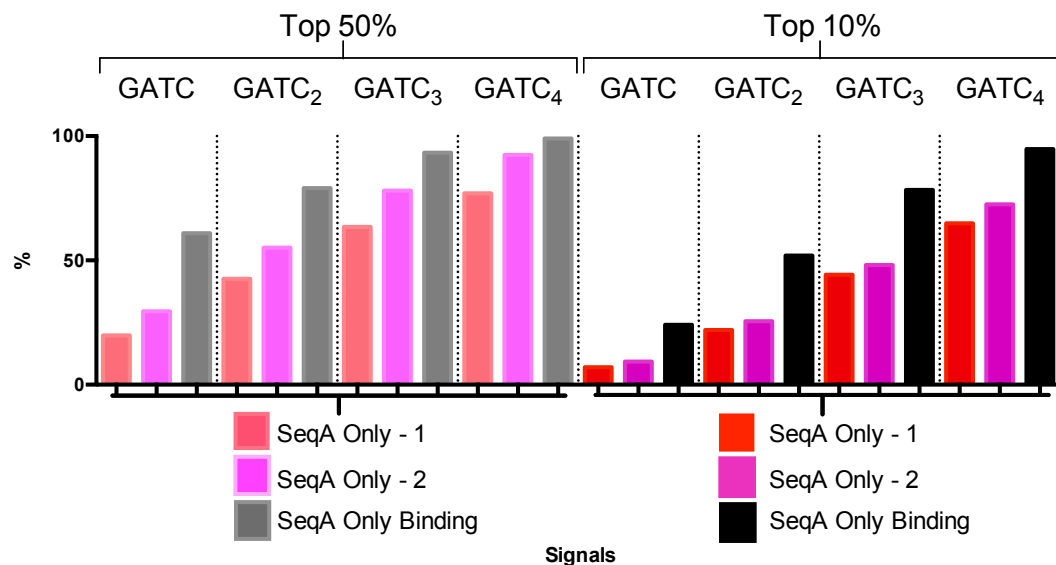


Figure 13/S1: GATC pairing in *E. coli* and *Salmonella* LT2 after 1000 times shuffling. The genomes of *E. coli* and *Salmonella* LT2 were shuffled with ushuffle 1000 times and a k-mer size of four in order to preserve GATCs (163). Pairs of < 41 basepairs and higher order GATCs, were counted and compared to counts before shuffling and percentage decrease after 1000 shuffles was graphed. χ^2 statistics were performed on counts of shuffled counts vs. observed counts. P values were calculated and shown on the graph.



P values from count data for SeqA Only - 1	P values from count data for SeqA Only - 2	P values from count data for SeqA Only Binding
GATC ₂ : <0.0001	GATC ₂ : <0.0001	GATC ₂ : <0.0001
GATC ₃ : <0.0001	GATC ₃ : <0.0001	GATC ₃ : <0.0001
GATC ₄ : <0.0001	GATC ₄ : <0.0001	GATC ₄ : <0.0001

Figure 14/S2: SeqA signals with higher order GATCs. A. In phage or bacteria genes with few GATC sites (Orange) in the ORF (Blue), RNA Polymerase (Green) is able to freely access a coding sequence and the gene is on. **B.** When SeqA (Black) is bound to pairs of GATC sites it introduces positive supercoils in the ORF which limits the accessibility by RNA Polymerase and the gene is off.

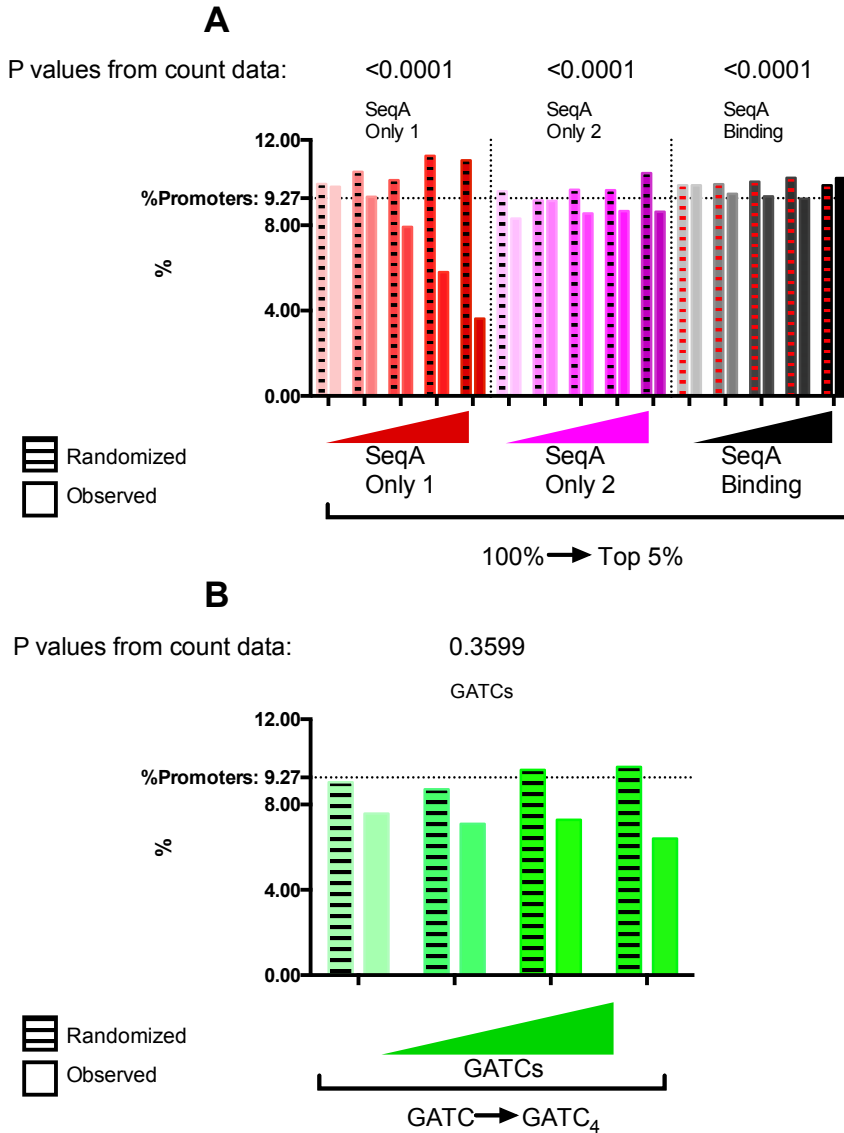


Figure 15/S3: SeqA signals and GATCs in promoters. BEDOPS frequency counts of signals in promoter regions (161). Signals were chopped to 1 bp regions and results graphed as a percentage of signals in promoter regions. %Promoters for *E. coli* is 4.8%. χ^2 statistics were performed on counts and P values were calculated and shown on the graph. A. *E. coli* ChIP-Chip of SeqA Only 1 (Red) from Waldminghaus et al. 2010 (121). ChIP-Chip of SeqA Only 2 (Purple) from Sánchez-Romero et al. 2010 (120). *E. coli* ChIP-Chip of SeqA Binding (Black) from Waldminghaus et al. 2012 (122). Dashed bars for signals indicate signals that had been shuffled 1000 times and placed in random locations. B. GATCs (Green) in prophage for both *E. coli* and *Salmonella* LT2. Dashed bars for GATCs indicate GATCs that had been placed in random locations in the genome.

Acknowledgements

Chapter 2, in part, is currently being prepared for submission for publication of the material. Peters, Gregory; Agrawal, Nishtha; Bailey, Barbara; Nulton, Jim; Rohwer Forest; Segall Anca. The dissertation/thesis author was the primary investigator and author of this material.

Introduction

Genome duplications and recombination pathways

The chromosome is dynamic and during active growth, mutations arise in the form of insertions, deletions, point changes, duplications, and large genome duplications (134, 135, 139, 140, 208, 209). Genome duplications are a major driving force in evolution and are well studied (210–212). It is thought that gene duplications occur by conserved mechanisms in all domains of life. In Eukaryotes genome duplications occur in cancers and may give rise to resistance to chemotherapeutics (134). Genome duplications are also intermediates in the evolution of new genes with novel functions and lead to the adaptation of the organism to environmental stresses or resistance to antibiotics (209, 213, 214). As cells undergo DNA damage during growth, the pathways involved in DNA repair and recombination may contribute to genome duplications (215).

Recombination, strand annealing, and transposition may all give rise to genome duplications (134, 140) by exchanges between sister chromatids at replication forks or by insertion of a replicated region of DNA into a new location in the same chromatid (Fig. 16A)(134). The mechanism of giving rise to a duplication by an exchange between regions (a) and (b) to duplicate a gene and the concomitant formation of a (b/a) duplication join point is shown (Fig. 16A). Due to high homology between both the original sequence and the duplicated regions, a gene duplication event can subsequently be deleted. If the gene duplication confers an advantage under selection during growth, the duplication may persist in the chromosome. This duplication can then

undergo further amplification (Fig. 16A), an event that is thought to be highly dependent on recombination and RecA-like functions. Genome amplifications of up to 100 copies have been reported (134, 216).

Bacterial genomes also contain multiple mobile elements such as prophages and insertion elements (60, 71, 217, 218). *Salmonella* LT2 has four active prophages, Gifsy-1, Gifsy-2, Fels-1, and Fels-2, which are temperate phages and which are able to form infectious virions (86, 89, 90, 219, 220). Gifsy-1 and Gifsy-2 were discovered due to their ability to suppress a *recB* mutation (219). Because these prophages encode several recombination-related genes, we hypothesized that they may contribute to the formation of genome duplications. We performed RNA-Seq analysis on wildtype STm and isogenic recombination mutants in order to see whether prophage-associated genes are transcribed during growth.

Recombination pathways

Recombination pathways are thought to play an important role in genome duplications between long regions of homology (134, 138–140, 215). These recombination pathways are involved in DNA repair of double-strand breaks and single-stranded breaks or gaps (Fig. 16B) (221). RecBCD acts on the break and degrades the DNA to form a long single-stranded DNA “tail,” until the RecBCD complex reaches a Chi site, where RecA is loaded onto the DNA and catalyzes strand invasion into a region of homology. A Holliday junction is formed, allowing branch migration and formation of stretches of heterologous DNA. The RuvABC complex resolves Holliday junctions, creating recombinant chromosomes. During gap repair, the RecJ nuclease enlarges

DNA gaps sufficiently to permit binding of RecFOR, leading to the subsequent loading of RecA and the catalysis of strand invasion into a homologous DNA region (Fig. 16B). One or two Holliday junctions are formed, again permitting branch migration; these Holliday junction intermediates must also be resolved by RuvABC. In 2014 Reams et al. published a report studying multiple recombination mutants and the effect on duplication rates between *rrn* operons (139). One locus they tested was *purHD*, between the *rrnE* and *rrnH* operons, and found a high (2.5%) frequency of duplications. They also found that a *recA* mutation did not significantly decrease the duplication rate, whereas mutations in *ruvC* and *ruvAB* did significantly decrease the duplication rate. Interestingly when a *recA* mutation was introduced into *ruvC* mutants, the frequency of duplications was increased back to wild-type. They reasoned that there are likely other pathways involved in duplication formation and suggested an alternate single-stranded annealing pathway to explain the results.

Results

RNA-Seq

We further investigated alternative sources of RecA function and whether prophage-associated recombination genes could complement for the missing cellular functions. To do this, we compared wild-type LT2 and *recA*, *ruvAB*, and *ruvC* mutants in strains that either had the four Gifsy and Fels prophages or were cured of these prophages. All of the strains had a shortened *parS* site inserted into the chromosome between the *rrnA* and *rrnC* operons at the *metE* locus (222). The strains also contained the pALA2702 plasmid that encodes a fused GFP-ParB protein. When expressed, the

GFP-ParB protein binds to *parS* sites and forms a filament that fluoresces green when excited with an appropriate laser (223, 224). Data obtained from analysis of fluorescent foci suggested that genes encoded by one or more of the prophages are partly active in the recombination mutants and contribute to the copy number of the ParB foci (Polly Parks, Master's thesis, 2015) (225). Our hypothesis is that *recE* and *recT* genes from Gifsy-1 and/or Gifsy-2 are able to at least partially replace RecA function and suppress a *recA* mutant phenotype. Induction of the SOS response may also affect duplication formation as well.

In order to investigate the expression of genes and test if any prophage genes were upregulated or downregulated in the wild-type and recombination mutants, we performed an Illumina RNA-Seq experiment on RNA from strains SDT2913 "wt Lysogens", SDT2914 "wt Cured", SDT2917 "*recA* Lysogens", SDT2918 "*recA* Cured", SDT2925 "*ruvC* Lysogens", SDT2927 "*ruvC* Cured", SDT2930 "*ruvAB* Cured", SDT2939 "*ruvAB* Lysogens" (226). The sequencing produced 32.6 million paired-end reads. These reads were processed after quality checks to remove primer sequences and were aligned against the *Salmonella* LT2 genome. Differential Expression Analysis was performed using the DEBrowser with Harman batch correction and DESeq2, EdgeR, and Limma functions (227–231). Tables 7-9 show the genes differentially expressed using DESeq2, EdgeR, and Limma respectively in wild-type lysogens, *recA* lysogens, *ruvAB* lysogens, and *ruvC* lysogens vs. the isogenic prophage-cured wild-type, *recA*, *ruvAB*, and *ruvC* strains (Figs. 16 - 18). The combinations compared were *ruvAB* lysogens *ruvAB* cured vs. *ruvC* Lysogens *ruvC* cured (Table 7); *ruvAB* cured *ruvC* cured vs. *ruvAB* Lysogens *ruvC* lysogens (Table 8); wild-type cured *recA*

cured vs. wild-type Lysogens *recA* lysogens (Table 9); and wild-type lysogens wild-type cured vs. *recA* cured *recA* lysogens. Appendix 1 contains more data on prophage activities and comparisons of wild-type cured *recA* cured *ruvAB* cured *ruvC* cured.

Conclusions

Prophage genes are active in the lysogens vs. cured using each of the methods. Using all three methods is important as it gives a more complete view of the actual differential gene expression than each method alone. DEBrowser permits the dynamic viewing of the results and obtaining these results all in one R program.

STM2632 is a recombination gene and encodes the Gifsy-1 recombinase. This gene was upregulated in *ruvC* Lysogens *ruvC* cured vs. *ruvAB* lysogens *ruvAB* cured and also *ruvAB* lysogens *ruvC* lysogens vs. *ruvAB* cured *ruvC* cured. This indicates the prophage recombination genes are active.

One virulence gene not coded by the prophages, *sodC-2*, was found to be overexpressed by both DESeq2 and Limma analyses. This gene is a superoxide dismutase and is similar to *sodC-1* is found in Gifsy-2, it is possible that this gene is being expressed in Gifsy-2 and that there is a misalignment of the transcripts to the duplicate gene outside Gifsy-2.

There were multiple groups of strains for which RNA was purified from cells grown on different days, and DEBrowser's built-in Harman Batch removal functionality was applied which normalizes batch effects based on Principal Components Analysis (PCA) among the groups. There was only one replicate per sample and it would be useful to redo this experiment and add replicates (ideally biologically independent triplicates would be analyzed). This same "purification through analysis" workflow can

be used for analysis on the triplicate samples. Follow-up experiments will be needed to be performed in order to see if the prophage genes are directly involved in genome duplications and Chapter 4.

Methods

RNA purification and library preparation for RNA-Seq

Recombination mutants with and without the prophages were grown for RNA purification and RNA Sequencing. Single colonies were picked and inoculated into 1 mL MGCV media [3-(N-morpholino) propanesulfonate (MOPS)/glucose/casamino acids/vitamins] with 50 µg/mL ampicillin and grown overnight at 37°C for 16 hours (232). Cells were subcultured 1:100 by adding 50 µL into 5 mL of MGCV media with 50 µg/mL ampicillin and 100 µM IPTG in 15 mL Falcon tubes. Cells were grown for 3.5 hours at 37°C and then harvested by centrifugation for 5 minutes at 4000 rpm in an Eppendorf Centrifuge 5810. Cells were transferred to microcentrifuge tubes and flash frozen using a dry ice-ethanol bath. The *RNAsnap*[™] RNA isolation method for Gram-negative bacteria protocol was followed (233). Media was aspirated and pellets were resuspended in 100 µL or RNA extraction solution (18 mM EDTA, 0.025% SDS, 1% β-mercaptoethanol, 95% formamide) and then vortexed. Cells were lysed by incubating at 95°C in a Bio-Rad PTC-100 thermal cycler. The tubes were centrifuged at 13200 RPM for 5 minutes in an Eppendorf 5415 R centrifuge. RNA was precipitated using Ethanol purification and 10 µL 3M Sodium Acetate was added to samples. 330 µL of ice-cold 100% Ethanol was added and incubated on ice for 2 hours. Samples were centrifuged for 1 hour at 12000 RPM at room temperature and ethanol was aspirated from samples. Pellets were washed with 250 µL ice-cold 70% Ethanol and samples briefly vortexed

and centrifuged at 12000 RPM for 5 minutes. Ethanol was aspirated and pellets were dried for 5 minutes and resuspended in 80 μ L of HyClone™ HyPure™ molecular biology grade water. Samples were further dissolved by heating at 60°C in a Bio-Rad PTC-100 Thermal Cycler. 2 Units of Thermo Scientific RNase-Free DNase I was used with the Thermo Scientific 1x buffer to a total volume of 100 μ L and treated for 30 minutes at room temperature in a Bio-Rad PTC-100 Thermal cycler (234). DNase-treated samples were purified using QIAGEN (Valencia, CA) RNeasy® Mini spin columns according to the manufacturer's protocol (235). Columns were washed with QIAGEN Buffers and eluted for 10 minutes twice in 30 μ L to maximize RNA quantity. Samples were run on an Agilent 2100 Bioanalyzer using an RNA 6000 Pico chip on the Eukaryote Total RNA Pico protocol (236). Ribosomal RNA was depleted from samples using the Illumina Ribo-Zero Gold rRNA Removal Kit (Epidemiology) according to the manufacturer's protocol (237). Ribo-Zero treated RNA was purified using the Ethanol/Sodium acetate precipitation protocol. 16s PCR with Q5® High-Fidelity DNA polymerase was performed according to manufacturer's protocols with purified RNA and universal 27F and 1492R and verified there was no bacterial DNA contamination (Table 5) (238). Libraries were prepared using the Illumina TruSeq Stranded mRNA Library Prep Kit according to manufacturer's High Sample protocol and a 1-minute library insert fragmentation time (226). Libraries were quantified using a Qubit® 2.0 fluorometer and pooled and 0.4x size selected using Agencourt® AMPure® XP beads (Beckman Coulter, Inc.) and the Size Selection of Adaptor-ligated DNA (E7370) protocol (New England Biolabs) (239–241). Libraries were run on an Illumina HiSeq 2500 sequencer

using dual indexing and the PE250 Rapid Run Protocol by the UC Irvine Genomics High-Throughput Facility (242, 243).

RNA-Seq analysis

FastQ files were uploaded to Galaxy and quality checked using FastQC (244, 245). PEAR was used to assemble paired-end reads (246). FASTQ Groomer was used to convert to fastqsanger format (247). Trimmomatic was used to trim ends using ILLUMINACLIP with TruSeq3 adapters with Sliding Window trimming (SLIDINGWINDOW) on assembled and unassembled reads. Concatenate tail to head was used to concatenate assembled and unassembled reads. HISAT2 was used to align reads to the Salmonella LT2 ASM694v2 reference genome (fna file) from NCBI FTP (248). Picard SortSam was used to sort alignments by coordinate order (249). StringTie was used to assemble transcripts to the ASM694v2 reference annotation genome (gff file) from NCBI FTP with the Forward stranded option (250). Gene count tables were produced, and gene IDs were column joined in Galaxy. The count tables were downloaded and manually converted to TSV (Tab separated values) files. RStudio Version 1.1.456 with R version 3.5.2 was used and DEBrowser v1.10.2 was used for Differential Expression analysis (227, 251, 252). In DEBrowser the TSV file was uploaded as a Count Data File and a metadata file was uploaded with sample names, batch, and condition information. Low count filtering was performed using Max and Max Value < 1. Batch effect correction and normalization was performed using TMM normalization (Trimmed mean of M-values normalization method) and Harman batch correction with samples option for treatment and batch option for batch (231). DESeq2 was run using parametric fit type, False betaPrior option and LRT Test type (228).

EdgeR was run using TMM Normalization, 0 Dispersion and exactTest Test type (229).

Limma was run using TMM Normalization, ls Fit Type, None option chose for Norm. Bet.

Arrays (230). DEBrowser was used to produce scatter, volcano, and MA plots (253).

Table 4: Strains:

Strain	Genotype
SDT2913	LT2 pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ <i>fliC7716</i> (no drug), Δ (<i>hin-fljA7731</i>) (no drug) a.k.a. “wt Lysogens”
SDT2914	LT2 pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), MOD Gifsy-1:: <i>FRT</i> scar, Δ Fels-1:: <i>FRT</i> scar, Gifsy-2 [-], Fels-2 [-] a.k.a. “wt Cured”
SDT2917	LT2 <i>recA651::rif</i> (Rif ^R), pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ <i>fliC7716</i> (no drug), Δ (<i>hin-fljA7731</i>) (no drug) a.k.a. “ <i>recA</i> Lysogens”
SDT2918	LT2 <i>recA651::rif</i> (Rif ^R), pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), MOD Gifsy-1:: <i>FRT</i> scar, Δ Fels-1:: <i>FRT</i> scar, Gifsy-2 [-], Fels-2 [-] a.k.a. “ <i>recA</i> Cured”
SDT2925	LT2 <i>ruvC4::Cm^R</i> , pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ <i>fliC7716</i> (no drug), Δ (<i>hin-fljA7731</i>) (no drug) a.k.a. “ <i>ruvC</i> Lysogens”
SDT2927	LT2 <i>ruvC4::Cm^R</i> , pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), MOD Gifsy-1:: <i>FRT</i> scar, Δ Fels-1:: <i>FRT</i> scar, Gifsy-2 [-], Fels-2 [-] a.k.a. “ <i>ruvC</i> Cured”
SDT2930	LT2 <i>ruvAB::Cm^R</i> , pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), MOD Gifsy-1:: <i>FRT</i> scar, Δ Fels-1:: <i>FRT</i> scar, Gifsy-2 [-], Fels-2 [-] a.k.a. “ <i>ruvAB</i> Cured”
SDT2939	LT2 <i>ruvAB::Cm^R</i> , pALA2702 (Amp ^R) <i>gfp::parB</i> , <i>metE::parS-FRT</i> scar, Δ <i>fliC7716</i> (no drug), Δ (<i>hin-fljA7731</i>) (no drug) a.k.a. “ <i>ruvAB</i> Lysogens”

Table 5: 16s Primers (5' -> 3'):

Name	Sequence
27F	AGAGTTTGATCTGGCTCAG
1492R	GGTACCTTGTTACGACTT

Table 6: Samples with Illumina Primer Index IDs and Sequences (5' -> 3')

Name	I7_Index_ID	I7 Sequence	I5_Index_ID	I5 Sequence
SDT2913	D705	ATTCAGAA	D508	GTA CTGAC
SDT2913	D706	GAATTCGT	D508	GTA CTGAC
SDT2914	D707	CTGAAGCT	D508	GTA CTGAC
SDT2914	D708	TAATGCGC	D508	GTA CTGAC
SDT2917	D709	CGGCTATG	D508	GTA CTGAC
SDT2918	D710	TCCGCGAA	D508	GTA CTGAC
SDT2925	D711	TCTCGCGC	D508	GTA CTGAC
SDT2927	D712	AGCGATAG	D508	GTA CTGAC
SDT2930	D711	TCTCGCGC	D508	GTA CTGAC
SDT2939	D705	ATTCAGAA	D508	GTA CTGAC

Table 7: RNA-Seq differential expression using DESeq2, EdgeR, and Limma of *ruvAB* lysogens *ruvAB* cured vs. *ruvC* Lysogens *ruvC* cured.

Type indicates DESeq2, EdgeR, or Limma. The description indicates the KEGG annotation (p adj/adjusted p value <0.01). A positive fold change indicates an increase in *ruvC* Lysogens *ruvC* cured vs. *ruvAB* lysogens *ruvAB* cured.

Type	Gene	Log ₂ fold change	KEGG annotation
Limma	STM0904	9.58	no KO assigned (RefSeq) Fels-1 prophage protein
Limma	<i>nanH</i> - STM0928	8.71	K01186 sialidase-1 [EC:3.2.1.18] (RefSeq) <i>nanH</i> ; sialidase; Fels-1 associated (based on RefSeq annotn)
Limma	STM0913	7.1	no KO assigned (RefSeq) Fels-1 prophage protein
Limma	STM0929	6.87	putative inner membrane protein; Fels-1 associated
Limma	STM1025	6.52	no KO assigned (RefSeq) Gifsy-2 prophage protein
Limma	<i>yaaU</i> - STM0079	5.99	K08368 MFS family transporter, putative metabolite transport protein (RefSeq) <i>yaaU</i> ; MFS transporter
Limma	STM2632	5.89	K10906 exodeoxyribonuclease VIII [EC:3.1.11.-] (RefSeq) Gifsy-1 prophage <i>recE</i>
Limma	STM1053	5.78	no KO assigned (RefSeq) Gifsy-2 prophage protein
Limma	<i>sipD</i> - STM2883	5.74	K13287 invasin D (RefSeq) <i>sipD</i> ; cell invasion protein SipD
Limma	STM2724	5.69	Fels-2 prophage protein
EdgeR	STM2870	8.94	no KO assigned (RefSeq) putative inner membrane protein

Table 8: RNA-Seq differential expression using DESeq2, EdgeR, and Limma of *ruvAB* cured *ruvC* cured vs. *ruvAB* Lysogens *ruvC* lysogens.

Type indicates DESeq2, EdgeR, or Limma. The description indicates the KEGG annotation (p adj/adjusted p value <0.01). A positive fold change indicates an increase in *ruvAB* lysogens *ruvC* lysogens vs. *ruvAB* cured *ruvC* cured.

Type	Gene	Log ₂ fold change	KEGG annotation
DESeq2	STM2734	8.35	no KO assigned (RefSeq) Fels-2 prophage protein
DESeq2	STM1025	8.04	no KO assigned (RefSeq) Gifsy-2 prophage protein
DESeq2	STM1026	7.58	no KO assigned (RefSeq) Gifsy-2 prophage protein
DESeq2	<i>yaaU</i> - STM0079	7.5	K08368 MFS transporter, putative metabolite transport protein (RefSeq) <i>yaaU</i> ; MFS transporter
DESeq2	STM4204	7.28	no KO assigned (RefSeq) hypothetical protein; defective 4 prophage-related; inner membrane protein; same operon glucose translocase / glycosyltransferase
DESeq2	STM2614	7.02	no KO assigned (RefSeq) Gifsy-1 prophage protein
DESeq2	STM1005	7	K14059 integrase (RefSeq) Gifsy-2 prophage integrase
DESeq2	STM2600	6.62	no KO assigned (RefSeq) hypothetical protein
DESeq2	<i>cysU</i> - STM2443	5.39	K02046 sulfate/thiosulfate transport system permease protein (RefSeq) <i>cysU</i> ; sulfate ABC transporter permease subunit CysT
DESeq2	<i>dcuR</i> - STM4303	4.98	K07703 two-component system, CitB family, response regulator DcuR (RefSeq) <i>dcuR</i> ; two-component system response regulator
EdgeR	STM1005	9.78	K14059 integrase (RefSeq) Gifsy-2 prophage integrase
EdgeR	STM1025	12.27	no KO assigned (RefSeq) Gifsy-2 prophage protein
EdgeR	STM2705	11.93	no KO assigned (RefSeq) Fels-2 prophage protein
EdgeR	STM2734	11.73	no KO assigned (RefSeq) Fels-2 prophage protein
EdgeR	STM1026	10.38	no KO assigned (RefSeq) Gifsy-2 prophage protein
EdgeR	STM4204	9.95	no KO assigned (RefSeq) hypothetical protein; defective 4 prophage-related; inner membrane protein; same operon glucose translocase / glycosyltransferase
EdgeR	STM2614	9.59	no KO assigned (RefSeq) Gifsy-1 prophage protein
EdgeR	STM2588	9.41	no KO assigned (RefSeq) Gifsy-1 prophage protein
EdgeR	STM2600	9.01	no KO assigned (RefSeq) hypothetical protein - Gifsy-1 protein
EdgeR	<i>cysU</i> - STM2443	7.56	K02046 sulfate/thiosulfate transport system permease protein (RefSeq) <i>cysU</i> ; sulfate ABC transporter permease subunit CysT
EdgeR	STM2585 A	-6.21	K07801 PhoPQ-activated protein (RefSeq) Gifsy-1 prophage protein
Limma	STM0904	9.58	no KO assigned (RefSeq) Fels-1 prophage protein
Limma	<i>nanH</i> - STM0928	8.71	K01186 sialidase-1 [EC:3.2.1.18] (RefSeq) <i>nanH</i> ; sialidase Fels-1 associated
Limma	STM0913	7.1	no KO assigned (RefSeq) Fels-1 prophage protein
Limma	STM0929	6.87	putative inner membrane protein; Fels-1 associated
Limma	STM1025	6.52	no KO assigned (RefSeq) Gifsy-2 prophage protein
Limma	<i>yaaU</i> - STM0079	5.99	K08368 MFS transporter, putative metabolite transport protein (RefSeq) <i>yaaU</i> ; MFS transporter
Limma	STM2632	5.89	K10906 exodeoxyribonuclease VIII [EC:3.1.11.-] (RefSeq) Gifsy-1 prophage protein
Limma	STM1053	5.78	no KO assigned (RefSeq) Gifsy-2 prophage protein
Limma	<i>sipD</i> - STM2883	5.74	K13287 invasins D (RefSeq) <i>sipD</i> ; cell invasion protein SipD
Limma	STM2724	5.69	Fels-2 prophage protein

Table 91: RNA-Seq differential expression using DESeq2, EdgeR, and Limma of wild-type cured *recA* cured vs. wild-type lysogens *recA* lysogens.

Type indicates DESeq2, EdgeR, or Limma. The description indicates the KEGG annotation (p adj/adjusted p value <0.01). A positive fold change indicates an increase in wild-type lysogens *recA* lysogens compared to wild-type cured *recA* cured.

Type	Gene	Log ₂ fold change	KEGG annotation
DESeq2	STM2870	9.62	no KO assigned (RefSeq) putative inner membrane protein
DESeq2	STM1049	8.6	no KO assigned (RefSeq) Gifsy-2 prophage probable tail fiber protein
DESeq2	<i>nagC</i> - STM0682	8.02	K02565 N-acetylglucosamine repressor (RefSeq) <i>nagC</i> ; transcriptional regulator
DESeq2	STM1043	7.89	no KO assigned (RefSeq) Gifsy-2 prophage attachment and invasion protein homolog
DESeq2	<i>yjdB</i> -> <i>eptA</i> STM4293	7.87	no entry in KEGG LT2; EcoCyc phosphoethanolamine transferase
DESeq2	STM2600	6.68	no KO assigned (RefSeq) hypothetical protein; Gifsy-1 protein
DESeq2	STM2585A	-7.63	K07801 PhoPQ-activated protein (RefSeq) Gifsy-1 prophage protein
EdgeR	STM1049	13.15	no KO assigned (RefSeq) Gifsy-2 prophage probable tail fiber protein
EdgeR	<i>nagC</i> - STM0682	12.32	K02565 N-acetylglucosamine repressor (RefSeq) <i>nagC</i> ; transcriptional regulator
EdgeR	STM1043	12.15	no KO assigned (RefSeq) Gifsy-2 prophage attachment and invasion protein homolog
EdgeR	<i>yjdB</i> -> <i>eptA</i> STM4293	12.08	no entry in KEGG LT2; EcoCyc phosphoethanolamine transferase
EdgeR	<i>sspH2</i> - STM2241	11.67	K15353 E3 ubiquitin-protein ligase SspH2 (RefSeq) <i>sspH2</i> ; E3 ubiquitin--protein ligase - def-3 prophage associated
EdgeR	STM2735	11.3	no KO assigned (RefSeq) Fels-2 prophage protein
EdgeR	STM2600	9.37	no KO assigned (RefSeq) hypothetical protein; Gifsy-1 protein
EdgeR	STM2585A	-10.56	K07801 PhoPQ-activated protein (RefSeq) Gifsy-1 prophage protein

Table 102: RNA-Seq differential expression using DESeq2, EdgeR, and Limma of wild-type lysogens wild-type cured vs. *recA* cured *recA* lysogens.

Type indicates DESeq2, EdgeR, or Limma. The description indicates the KEGG annotation. (p adj/adjusted p value <0.01). NA indicates there were no significant changes observed.

Type	Gene	Log ₂ fold change	KEGG annotation
DESeq2	NA	NA	NA
EdgeR	NA	NA	NA
Limma	NA	NA	NA

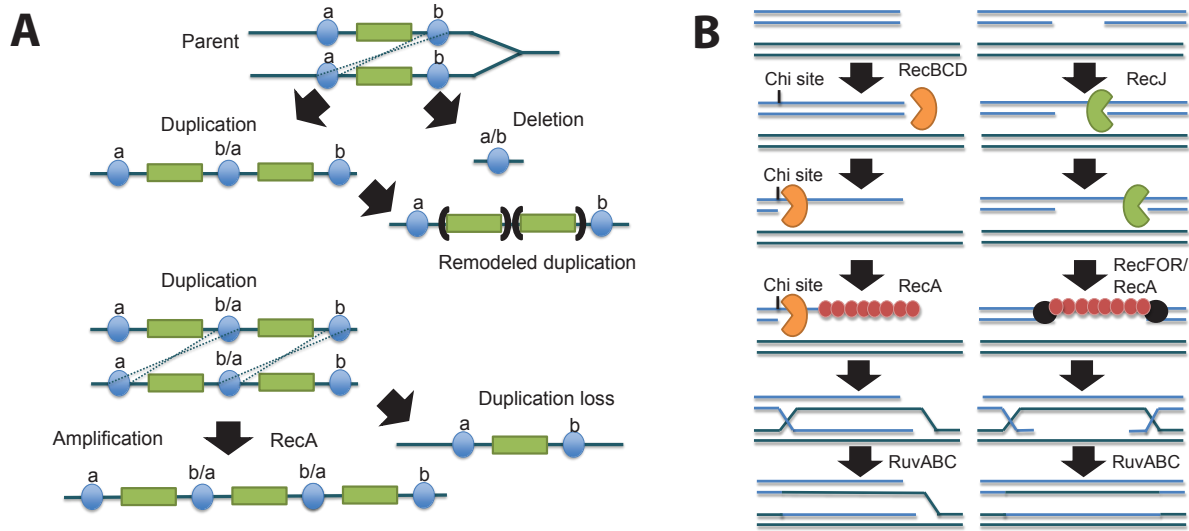


Figure 16: Genome duplications and amplifications are mediated by recombination proteins. **A.** Mechanisms of gene duplication and amplification. A gene shown as a green box can be duplicated in the chromosome. During replication if (b) recombines with (a) a duplication can occur with a (b/a) join point to form a duplicated gene, this can be remodeled with a loss of the join point. Deletions of the gene can occur. After duplication occurs, amplification of the duplication can occur, and this process is thought to be mediated by RecA protein. Due to high homologies, the duplication is frequently lost. Adapted from (134). **B.** Proteins involved in DNA repair and recombination. RecBCD acts on a double-strand break in DNA and acts as an exonuclease degrading DNA until it reaches a Chi site and forms ssDNA. RecA protein binds to the ssDNA and catalyzes strand invasion to a region of homology on another strand of DNA. Holliday junctions are formed and must be resolved by the resolvase RuvABC. RecJ acts on gaps in DNA and acts as an exonuclease and degrades DNA. RecFOR proteins bind and load RecA onto the ssDNA. RecA catalyzes strand invasion to a homologous sequence and RuvABC resolves the Holliday junctions (221, 225).

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Introduction

Strategy to observe genome duplications

Genome duplications in *E. coli* and *Salmonella* have been observed between the regions of long homology present within the 7 *rrn* operons, first detected in *Salmonella* by Anderson *et al.* in 1981 (133, 135, 139, 254) (Fig. 17A) (134, 135, 139, 255). The *rrn* operons are highly transcribed and encode the genes for ribosomal RNAs, which have regions of high secondary structure (134, 139, 143, 256). Duplications occur frequently between the *rrn* operons, at rates as high as 10^{-3} between *rrnE* and *rrnB* (133, 134, 139). Duplications occur much less frequently (rates of 10^{-6}) between *rrnH* and *rrnG* at *pyrD*, near the Ter region.

We developed an *in vivo* assay to study genome duplications using fluorescence microscopy, by using fluorescently-labeled DNA binding proteins to mark specific sites in the chromosome. We have taken advantage of the ParB-*parS* system, in which a ParB protein (originally encoded by a phage and/or plasmid) fused to a fluorescent protein domain binds to its specific *parS* site (Fig. 17B). To monitor duplication frequency in real time, these sites can be placed in different locations around the chromosome in regions in which duplications are known to occur (223, 224). The pFH4034 plasmid encodes several fusion genes between distinct fluorescent proteins fused to ParB proteins that recognize different *parS* sequences: the P1parB-RFPch that binds to the P1 *parS* sequence and the yGFP-pMT1ParB that binds to the pMT1 plasmid's *parS* site (257, 258). A P1 *parS* site was placed at *purH*, which is located between *rrnE* and *rrnH*, where duplications occur frequently (Fig. 17A). To compare the

frequency of duplications at this site with the frequency of duplications in locations within the origin domain that do not duplicate frequently, a P1 *parS* site was placed at *argD*, between *rrnC* and *rrnD*. The *argD* gene was between two *rrn* operons that are in inverse orientation with respect to each other, and thus recombination cannot form duplications between them. (While inversion rearrangements could arise by recombination between *rrnC* and *rrnD*, this rearrangement would not change the copy number of the *argD* locus.) Another pMT1 *parS* site is placed at *putA*, between *rrnH* and *rrnG*; these *rrn* operons are far apart and duplications occur much less frequently between them (157). When duplication of a *parS* site occurs, the parent will have 1X fluorescence intensity and the cells with a duplication of the relevant region will have 2X fluorescence intensity (Fig. 17B).

Potential involvement of prophages

Our hypothesis is that under certain physiological conditions, the recombination genes encoded by the Gifsy and/or Fels prophages may be transcribed sufficiently to contribute to the frequency of duplication formation in the host, and thus help mitigate environmental stresses that may slow or prevent the growth of the host. We will focus on testing the involvement of Gifsy-1 prophage's recombination genes. Gifsy-1 encodes *recE* and *recT*, which function similarly to RecBCD and RecA, respectively. Gifsy-1 also encodes a *ninG* gene. NinG is similar to the NinG protein encoded by phage λ , which was also named Rap (86, 259–261). NinG has been shown to be involved in recombination and acts as an endonuclease similar to RuvC. NinG has been shown to

increase RecBCD mediated recombination. It is likely these proteins are involved in forming genome duplications.

Results

Cloning and strain construction

Strains were constructed in order to assay duplications in lysogenic strains and in strains cured of the prophages; in addition, all of the strains have mutations that render the cells nonmotile due to removal of the two flagellin genes, which would permit us to analyze these strains in real time in microfluidic chambers called the “mother machine”. The mutations that knock out the two *Salmonella* LT2 flagellin genes allow the strains to be analyzed in real time in the mother machine (262). The cured nonmotile strain contained a modified Gifsy-1 prophage, which was completely cured from the set of strains in Table 11. Recombineering was performed using a FRT-Cm^R-FRT cassette with homology to regions flanking Gifsy-1 (181, 263). P22 transduction was used to move this marker into the nonmotile cured strain and pCP20 was used to Flp out the Cm^R cassette (182, 264).

The wild type LT2 genetic background, from which the nonmotile lysogen and cured strains were derived, contains the low copy number virulence plasmid pSLT, which encodes a *parS* site. This *parS* has the same specificity as the P1 *parS* site and interfered with the fluorescence focus assay, and therefore the pSLT plasmid was cured from the set of strains shown in Table 13. A recombineering selection of *tetA-sacB* to delete the *samAB* operon, which overlaps *parS*, and the *parS* was performed (181,

265). This *tetA-sacB* was transduced into the nonmotile lysogens and phage-cured strains in which the whole of Gifsy-1 prophage was deleted. Subsequently pSLT was cured from these strains using a counterselection against the Tet/SacB cassette on counter-selection medium (265).

P1 *parS* sites and pMT1 *parS* sites were chosen to insert between *rrn* operons because the two sequences are recognized by their cognate ParB protein, and because the P1 *parS* site would appear red and the pMT1 *parS* site would appear green. This combination of GFP proteins allows greater resolution for the microscopy experiments. The P1 *parS* was synthesized as part of an oligonucleotide and then integrated with FRT-Cm^R-FRT at *metE*, using recombineering (181, 263). This P1 *parS* site FRT-Cm^R-FRT was then moved to *argD* and *purH*. The pMT1 *parS* site was synthesized into a different oligonucleotide and integrated with FRT-Cm^R-FRT, as above, into the genome at *putA*. P22 transductions were used to move P1 *parS* FRT:Cm^R FRT and pMT1 *parS*::FRT-Kan^R-FRT into strains with different genetic backgrounds, as necessary (182, 263).

Finally, to test whether phage recombination functions are able to complement the chromosomal *rec* mutations, appropriate pRHA109-Kan^R constructs (described below) were transformed into the relevant different strains (.1). The pRHA109 vector is a medium copy plasmid (266) which was used for cloning the Gifsy-1 prophage recombination genes. However, both pRHA109 and pFH4034 encode β -lactamase mediated ampicillin resistance, so the *bla* gene of pRHA109 was changed to knock out its function and insert a kanamycin resistance cassette (266). PstI cuts once inside the *bla* gene; the kanamycin resistance gene of the pUC4K plasmid was liberated using the

flanking PstI sites and moved into pRHA109 using the NEB Instant Ligation (266, 267). This new pRHA109-Kan^R was used for cloning of the Gifsy-1 recombination genes (Fig. 18A). PCR was performed using the genome of a strain cured of Gifsy-2 as the template to produce PCR fragments. These fragments encoding the *recE*, *recT*, *ninG*, *recET* and the *recET* and *ninG* genes were digested with BamHI and Sall and introduced into pRHA109-Kan^R cut with BamHI and Sall using the NEB HiFi DNA Assembly kit (268). In the case of *recET* and *recET ninG* constructs, they are arranged as an operon transcribed by the *prha* promoter of the plasmid. All clones were Sanger sequenced verified (Fig. 18B-F).

Microscopy

The presence of ParB foci in the strains was confirmed using agar pad microscopy at 1000x (Figs. 19– 22). Strains with single P1 *parS* sites formed red foci and strains with pMT1 *parS* sites formed green foci. Strains with P1 *parS* sites formed red foci and strains with pMT1 *parS* sites formed green foci. Strains with a combination of P1 *parS* sites with pMT1 *parS* sites formed red and green foci in the same cell.

Conclusions

Multiple strains were constructed to test the genome duplications at regions in the chromosome *in vivo*. The strains were verified by microscopy and are now ready for further assays. These duplication or amplification of various chromosomal regions in these strains can now be quantified in real time using a quantitative microfluidic device such as the mother machine (262). The program Oufiti or a similar program can be used to quantify foci in the cells during growth (269). Rhamnose will be used to induce

expression of prophage recombination genes from pRHA109 in order to test whether these genes affect the duplication rate.

Methods

Strains

Salmonella strains are listed in Tables 11 and *E. coli* strains are listed in Table 12.

Cloning to create pRHA109-Kan^R and pRHA109-Kan^R with Gifsy-1 prophage recombination genes

For high copy plasmid purification of pUC4K, a QIAGEN Plasmid Miniprep protocol was followed (267, 270). For medium copy plasmid purification of pRHA109, a QIAGEN Plasmid Midiprep protocol was followed with the low copy plasmid protocol (271). Restriction enzyme digestion of plasmid DNA of 1 µg pUC4K and 1 µg pRHA109 was performed using 10 units of PstI-HF (NEB) and 1X CutSmart® buffer (NEB) (267). 1 µL of Quick CIP (NEB) was included in the pRHA109 digestion reaction. Digests were incubated at 37°C for 1 hour in a Bio-Rad PTC-100 thermal cycler. pUC4K DNA was run on 0.8% agarose gel in 0.5X TBE with 0.25x SYBR™ Safe in the gel for 2 hours at 100V (267). Two bands formed, and the 1.2 KB band was cut out with a sterile razor blade and placed in a microcentrifuge tube. The 1.2KB gel cut band and digestion reaction were further purified using the Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). Ligations of pUC4K gel purified DNA and pRHA109 were set up with purified DNA using the NEB Quick Ligation™ Kit using 3:1 vector:insert ratio (267, 273). Chemically competent DH5α cells were transformed with reactions and successful clones were obtained.

pRHA109-Kan^R was further used for cloning of phage genes and to purify DNA a QIAGEN Plasmid Midiprep protocol was followed with the low copy plasmid protocol (271). Genomic DNA of strain lacking Gifsy-2 (G756) was purified by CTAB-NaCl genomic DNA purification. PCRs were performed using primers using Q5® High-Fidelity DNA polymerase by manufacturers protocols (Table 14) (238). PCR sizes were verified by running DNA on a 1% agarose gel in 0.5X TBE with 0.25x SYBR™ Safe in the gel for 1 hour at 100V (274). *recE* produced a band of 2930 bp, *recT* produced a band of 1198 bp, *ninG* produced a band of 657 bp, *recET* produced a band of 4046 bp, and RecETNinG PCR blocks produced two separate blocks of 4046 bp and 657 bp. Restriction enzyme digestion of plasmid DNA of 1 µg pRHA109-Kan^R and 100 ng PCR fragments was performed using 20 units of BamHI-HF (NEB), 20 units of Sall-HF (NEB), 1 µL of Quick CIP (NEB), and 1X CutSmart® buffer (NEB). Digests were incubated at 37°C for 1 hour with a 65°C restriction enzyme inactivation for 20 minutes in a Bio-Rad PTC-100 thermal cycler. Digests were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). NEBuilder® HiFi DNA Assembly Master Mix was used to set up cloning reactions with cut pRHA109-Kan^R and insert fragments with a vector:insert ratio of 1:2 (268). Electrocompetent DH5α cells were transformed with reactions and successful clones were obtained. QIAGEN plasmid minipreps were performed with clones and plasmid inserts were verified using Sanger sequencing (270).

Recombineering to delete Gifsy-1 Mod with FRT-Cm^R-FRT

Nonmotile LT2 strains were used with prophages “Lysogens” and strains cured of prophages “Cured”. The nonmotile “cured” strain contains a modified Gifsy-1 and this

was completely cured using recombineering protocols (181). pSIM29 was transformed into both Lysogens strain and the strain with the modified Gifsy-1 (275). PCR was performed to amplify FRT-Cm^R-FRT from pKD3 with 40 bps of homology to the beginning and end of Gifsy-1 (263). PCR was performed off of 1 pg pKD3 using the Q5® High-Fidelity DNA polymerase protocol (263). PCR products were run on 1.5% agarose gel in 0.5X TBE for 1 hour at 100V with 0.25x SYBR™ Safe and an 1113 bp band formed (274). PCRs were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). The nonmotile strain with modified Gifsy-1 was grown and recombineering was performed according to established protocol and successful recombinants were obtained (181).

Recombineering to insert *tetA sacB* in pSLT plasmid at *samAB parS*

The *tetA sacB* cassette was amplified from T-SACK with primers with 40 bp primers to target *samAB parS* (Table 14). PCR was performed off genomic DNA of T-SACK purified by CTAB-NaCl protocol using the Q5® High-Fidelity DNA polymerase protocol (238). PCRs were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). PCR products were run on a 1.5% agarose gel in 0.5X TBE for 1 hour at 100V with 0.25x SYBR™ Safe and a 3527 bp band formed (274). Recombineering was performed using nonmotile strains with pSIM29 and cured of Gifsy-1 and prophages according to established protocols (181, 275).

Recombineering to insert P1 *parS*::FRT-Cm^R-FRT in the genome at *metE*, *argD*, and *purH*

The P1 *parS* was synthesized in an Ultramer® DNA Oligonucleotide (IDT) and used in overlap extension PCR with a second block from pKD3 to amplify FRT-Cm^R-FRT (263). PCR was performed off of the Ultramer® DNA Oligonucleotide (IDT) for block 1 and 100 pg pKD3 DNA for block 2 using the Q5® High-Fidelity DNA polymerase protocol (238, 263). PCRs were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). DpnI Restriction enzyme digestion of PCR for block 2 was set up with PCR products and 20 units of DpnI (NEB) in 1X CutSmart® buffer (NEB). Digests were incubated at 37°C for 3 hours with an 80°C restriction enzyme inactivation for 20 minutes in a Bio-Rad PTC-100 thermal cycler. Digests were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). A second DpnI digest was performed with the same protocol, and a second PCR cleanup was performed using the Wizard® SV Gel and PCR Clean-Up System (Promega) (272). A second overlap extension PCR was performed and introduced homology to target *metE*. PCR products were run on a 1.5% agarose gel in 0.5X TBE for 1 hour at 100V with 0.25x SYBR™ Safe and a 1650 bp band formed (274). Recombineering was performed using nonmotile strains with pSIM29 and cured of Gifsy-1 and prophages according to established protocols (181, 275). Successful recombinants were obtained, and this strain was used as a template for PCR to move P1 *parS*::FRT-Cm^R-FRT to *argD* and *purH*. PCR primers with 40 bp homology to target *argD* and *purH* were used (Table 14). PCR was performed off of cultures with P1 *parS*::FRT-Cm^R-FRT at *metE* diluted 1:10 in

water using the Q5® High-Fidelity DNA polymerase protocol (238). PCR products were run on 1.5% agarose gel in 0.5X TBE for 1 hour at 100V with 0.25x SYBR™ Safe and 1232 bp bands formed (274). Recombineering was performed using nonmotile strains with pSIM29 and cured of Gifsy-1 and prophages according to established protocols (181, 275).

Recombineering to insert pMT1 *parS*::FRT-Kan^R-FRT in the genome at *putA*

The pMT1 *parS* was synthesized in an Ultramer® DNA Oligonucleotide (IDT) and used to amplify FRT-Kan^R-FRT from pKD4 with 40 bp homology in recombineering primers to target *putA* (Table 14) (181, 263). PCR was performed off of 1 pg pKD4 using the Q5® High-Fidelity DNA polymerase protocol (238, 263). PCR products were run on 1.5% agarose gel in 0.5X TBE for 1 hour at 100V with 0.25x SYBR™ Safe and a 1650 bp band formed (274). DpnI Restriction enzyme digestion of PCR was set up with PCR products and 20 units of DpnI (NEB) in 1X CutSmart® buffer (NEB). Digests were incubated at 37°C for 3 hours with an 80°C restriction enzyme inactivation for 20 minutes in a Bio-Rad PTC-100 thermal cycler. Digests were purified using a Wizard® SV Gel and PCR Clean-Up System (Promega) according to the manufacturer's protocols (272). Recombineering was performed using nonmotile strains with pSIM29 and cured of Gifsy-1 and prophages according to established protocols (181, 275).

P22 transductions of *samAB parS::FRT-Cm^R-FRT*, Gifsy-1 Mod::*FRT-Cm^R-FRT*, P1 *parS::FRT-Cm^R-FRT* at *argD*, P1 *parS::FRT-Cm^R-FRT* at *purH*, pMT1 *parS::FRT-Kan^R-FRT* at *putA*, Rif^R at *recA* and strain construction

P22 lysates of *samAB parS::FRT-Cm^R-FRT*, Gifsy-1 Mod::*FRT-Cm^R-FRT*, P1 *parS::FRT-Cm^R-FRT* at *argD*, P1 *parS::FRT-Cm^R-FRT* at *purH*, pMT1 *parS::FRT-Kan^R-FRT* at *putA*, Rif^R at *recA* were made according to protocols (182). After recombineering, a P22 lysate was made to transduce the markers to the nonmotile Lysogens and nonmotile Cured strains. 5 µL P22HT was added to 2 mL Pre-phage broth and 500 µL overnight culture of the donor cells. Cells were grown for 16 hours and transferred to microcentrifuge tubes and lysed with the addition of 250 µL chloroform. Tubes were incubated at room temperature for 10 minutes, vortexed briefly, and were then centrifuged at 13200 RPM for 5 minutes in an Eppendorf 5415 D centrifuge. Lysates were transferred to new microcentrifuge tubes and treated with a second addition of 250 µL chloroform. Tubes were incubated at room temperature for 10 minutes, vortexed briefly, and were then centrifuged at 13200 RPM for 5 minutes in an Eppendorf 5415 D centrifuge. Lysates were transferred to new microcentrifuge tubes and used in transductions according to established protocols. Transductions to nonmotile lysogens and nonmotile cured strains were set up in microcentrifuge tubes using 100 µL recipient strains in tubes and varying amounts of the P22 lysates (20 µL, 10 µL, 5 µL, 5 µL of 1:10 dilution of phage lysate, 5 µL of 1:100 dilution of phage lysate, 5 µL of 1:1000 dilution of phage lysate). Tubes were incubated on the bench for 15 minutes and 1 mL of LB was added to tubes. Tubes were incubated at 37°C with shaking at 200 RPM for 1 hour. After 1 hour tubes were taken out and were then

centrifuged at 13200 RPM for 5 minutes in an Eppendorf 5415 D centrifuge. The supernatant was removed and cells were resuspended with 100 μ L and plated onto selective LB plates (30 μ g/mL chloramphenicol, 50 μ g/mL kanamycin, 15 μ g/mL tetracycline, or 100 μ g/mL rifampicin) and incubated overnight for 16 hours at 37°C. Successful transductants formed and colonies from the transduction with the lowest amount of phage were picked with a sterile toothpick and streaked onto EBU plates. Plates were incubated overnight for 16 hours at 37°C and colonies formed. The light whitish colonies were streaked a second time onto EBU plates. Plates were incubated overnight for 16 hours at 37°C and colonies formed. To verify P22 was no longer present a P22 cross streak test was performed. 20 μ L P22H5 was dropped on an EBU plate and inverted to create a line across the plate. Plates were allowed to dry for 5 minutes and white colonies from the second EBU were used in the cross-streak test. Colonies were picked with a sterile toothpick and the toothpick was touched to one side of the EBU plate with P22H5 and then picked up and streaked across the plate perpendicular to P22H5. Plates were incubated overnight for 16 hours at 37°C and P22 sensitive streaks formed.

Curing of pSLT plasmid with Tet/SacB counter selection, Flip out of FRT-Cm^R-FRT and FRT-Kan^R-FRT using pCP20, the transformation of pFH4034 and pRHA109-Kan^R constructs

The pSLT plasmid was cured with a Tet/SacB counter-selection according to protocols (265). Cells were streaked onto Tet/SacB counter-selection agar plates and grown at 16 hours at 42°C (265). Cells were streaked a second time onto Tet/SacB counter-selection agar plates and grown at 16 hours at 42°C (265). Colonies formed

and were patch patched onto LB plates, LB plate with 15 µg/mL tetracycline, 30 µg/mL chloramphenicol. Streaks formed and colonies sensitive to 15 µg/mL tetracycline, 30 µg/mL chloramphenicol were picked and streaked onto new LB plates.

pCP20 was used to Flip out FRT-Cm^R-FRT and FRT-Kan^R-FRT according to protocols (263, 264). Single colonies were picked from plates and inoculated with sterile sticks into 1 mL LB medium with 100 µg/mL ampicillin and grown for 16 hours at 30°C. Cells were subcultured 1:100 in LB medium and grown for 1 hour at 30°C. The culture was shifted to a shaking 42°C water bath for 2 hours at 300 RPM to cure pCP20 from strains (264). Cells were streaked onto LB plates and grown for 16 hours at 37°C. Colonies were then patch plated onto LB and LB + 100 µg/mL ampicillin. Streaks that were sensitive to ampicillin formed and were used in transformations. pFH4034 was electroporated into strains onto selective LB plates with 100 µg/mL ampicillin according to protocols (257, 258). pRHA109-Kan^R and constructs with Gifsy-1 prophage genes cloned were electroporated into strains onto selective LB plates with 50 µg/mL kanamycin according to protocols.

Microscopy

Single colonies were picked and inoculated into 1 mL MGCV media [3-(N-morpholino) propanesulfonate (MOPS)/glucose/casamino acids/vitamins] with 50 µg/mL ampicillin and 0.75 mM adenine and grown overnight at 37°C for 16 hours (232). Cells were subcultured 1:100 by adding 10 µL into 1 mL of MGCV media with 50 µg/mL ampicillin, 0.75 mM adenine, and 100 µM IPTG in 1 mL glass culture tubes. Cells were grown for 3 hours at 37°C and transferred to sterile microcentrifuge tubes. To fix cells

formamide was added to tubes at a final concentration of 0.25% and let to sit for 5 minutes. To concentrate the cells, the tubes were centrifuged at 13200 RPM for 1 minute in an Eppendorf 5415 D centrifuge. The supernatant was removed and cells were resuspended by pipetting 50 μ L MGCV media with 50 μ g/mL ampicillin, 0.75 mM adenine, and 100 μ M IPTG. 5 μ L of cells were transferred to agar pads made with 2% agarose and coverslips were placed over cells. Cells were then visualized at 100x magnification using a ZEISS Axio Observer Z.1 inverted microscope.

Table 11: Salmonella Strains:

Strain	Genotype
SDT3065	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) $\$pSLT-$ #COM -GAP
SDT3098	LT2 $\$pSLT-$ $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM: Flp out FRT:Cm ^R and cure pCP20 -GAP
SDT3159	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) $\$pSLT-$ pMT1 $parS(FRT:Scar)::\Delta putA$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3160	LT2 $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] $\$pSLT-$ pMT1 $parS(FRT:Scar)::\Delta putA$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3161	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 $parS(FRT:Scar)::\Delta argD$ $\$pSLT-$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3162	LT2 $\$pSLT-$ $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 $parS(FRT:Scar)::\Delta argD$ $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3163	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 $parS(FRT:Scar)::\Delta purH$ $\$pSLT-$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3164	LT2 $\$pSLT-$ $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 $parS(FRT:Scar)::\Delta purH$ $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3165	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 $parS(FRT:Scar)::\Delta argD$ pMT1 $parS(FRT:Scar)::\Delta putA$ $\$pSLT-$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3166	LT2 $\$pSLT-$ $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 $parS(FRT:Scar)::\Delta argD$ pMT1 $parS(FRT:Scar)::\Delta putA$ $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3167	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 $parS(FRT:Scar)::\Delta purH$ pMT1 $parS(FRT:Scar)::\Delta putA$ $\$pSLT-$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3168	LT2 $\$pSLT-$ $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 $parS(FRT:Scar)::\Delta purH$ pMT1 $parS(FRT:Scar)::\Delta putA$ $\Delta(MOD$ Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3169	LT2 $recA::rif$ (Rif ^R) $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 $parS(FRT:Scar)::\Delta argD$ pMT1 $parS(FRT:Scar)::\Delta putA$ $\$pSLT-$ #COM Flp Out FRT Cassettes and cure pCP20 -GAP

Table 113: Salmonella Strains:

Strain	Genotype
SDT3170	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 <i>parS</i> (FRT:Scar):: $\Delta argD$ pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3171	LT2 <i>recA::rif</i> (Rif ^R) $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 <i>parS</i> (FRT:Scar):: $\Delta purH$ pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ \$pSLT- #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3172	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 <i>parS</i> (FRT:Scar):: $\Delta purH$ pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and #COM Flp Out FRT Cassettes and cure pCP20 -GAP
SDT3173	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) \$pSLT- pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3174	LT2 $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] \$pSLT- pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3175	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 <i>parS</i> (FRT:Scar):: $\Delta argD$ \$pSLT- / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3176	LT2 \$pSLT- $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 <i>parS</i> (FRT:Scar):: $\Delta argD$ Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3177	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 <i>parS</i> (FRT:Scar):: $\Delta purH$ \$pSLT- / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3178	LT2 \$pSLT- $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 <i>parS</i> (FRT:Scar):: $\Delta purH$ Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3179	LT2 $\Delta fliC7716$ (no drug), $\Delta(hin-fljA7731)$ (no drug) P1 <i>parS</i> (FRT:Scar):: $\Delta argD$ pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ \$pSLT- / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP
SDT3180	LT2 \$pSLT- $\Delta(hin-fljA7731)::tetRA$ (Tet ^R), $\Delta fliC7716$ (no drug), P1 <i>parS</i> (FRT:Scar):: $\Delta argD$ pMT1 <i>parS</i> (FRT:Scar):: $\Delta putA$ Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, $\Delta Fels-1::FRT$ scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP

Table 114: Salmonella Strains:

Strain	Genotype
SDT3181	LT2 Δ fliC7716 (no drug), Δ (hin-fljA7731) (no drug) P1 <i>parS</i> (FRT:Scar):: Δ purH pMT1 <i>parS</i> (FRT:Scar):: Δ putA \$pSLT- / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3182	LT2 \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ purH pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3183	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) Δ fliC7716 (no drug), Δ (hin-fljA7731) (no drug) P1 <i>parS</i> (FRT:Scar):: Δ argD pMT1 <i>parS</i> (FRT:Scar):: Δ putA \$pSLT- / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3184	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ argD pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3185	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) Δ fliC7716 (no drug), Δ (hin-fljA7731) (no drug) P1 <i>parS</i> (FRT:Scar):: Δ purH pMT1 <i>parS</i> (FRT:Scar):: Δ putA \$pSLT- / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3186	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ purH pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] and / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3205	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ argD pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> #COM Empty Vector-GAP
SDT3206	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ argD pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recE</i> / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3207	LT2 <i>recA</i> :: <i>rif</i> (Rif ^R) \$pSLT- Δ (hin-fljA7731)::tetRA (Tet ^R), Δ fliC7716 (no drug), P1 <i>parS</i> (FRT:Scar):: Δ argD pMT1 <i>parS</i> (FRT:Scar):: Δ putA Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recT</i> / pFH4034 #COM (Amp ^R) :cfp::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP

Table 115: Salmonella Strains:

Strain	Genotype
SDT3208	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>argD</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>ninG</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3209	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>argD</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recET</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3210	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>argD</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recET_ninG</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3211	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> #COM Empty Vector-GAP
SDT3212	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recE</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3213	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recT</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3214	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>ninG</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP
SDT3215	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gifsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gifsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gifsy-1 <i>recET</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygfp</i> ::pMT1 <i>parB</i> -GAP

Table 116: *Salmonella* Strains:

Strain	Genotype
SDT3216	LT2 <i>recA::rif</i> (Rif ^R) \$pSLT- Δ (<i>hin-fljA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> (no drug), P1 <i>parS</i> (FRT:Scar):: Δ <i>purH</i> pMT1 <i>parS</i> (FRT:Scar):: Δ <i>putA</i> Δ (MOD Gfsy-1 (Kan ^R))::FRT:scar, Δ Fels-1::FRT scar, Gfsy-2 [-], Fels-2 [-] / pRHA109-Kan ^R -Gfsy-1 <i>recET_ninG</i> / pFH4034 #COM (Amp ^R) : <i>cfp</i> ::P7 <i>parB</i> , P1 <i>parB</i> :: <i>rfpch</i> , <i>ygf</i> p::pMT1 <i>parB</i> -GAP

Table 127: *E. coli* Strains:

Strain	Genotype
EDT2822	DH5α pRHA109-Kan ^R from pUC4K PstI-Kan ^R #COM Medium copy # ~50 copies Gel Purified 1.2KB Kan ^R Insert - Ligation Cloned - and BamHI/Sall Cuts - GAP
EDT2825	DH5α pRHA109-Kan ^R -Gifsy-1 <i>recE</i> #COM Cloned with NEB HiFi cloning Q5® High-Fidelity DNA Polymerase and BamHI/Sall restriction enzymes and Sanger Sequence Verified -GAP
EDT2826	DH5α pRHA109-Kan ^R -Gifsy-1 <i>recT</i> #COM Cloned with NEB HiFi cloning Q5® High-Fidelity DNA Polymerase and BamHI/Sall restriction enzymes and Sanger Sequence Verified -GAP
EDT2827	DH5α pRHA109-Kan ^R -Gifsy-1 <i>ninG</i> #COM Cloned with NEB HiFi cloning Q5® High-Fidelity DNA Polymerase and BamHI/Sall restriction enzymes and Sanger Sequence Verified -GAP
EDT2828	DH5α pRHA109-Kan ^R -Gifsy-1 <i>recET</i> #COM Cloned with NEB HiFi cloning Q5® High-Fidelity DNA Polymerase and BamHI/Sall restriction enzymes and Sanger Sequence Verified -GAP
EDT2829	DH5α pRHA109-Kan ^R -Gifsy-1 <i>recET_ninG</i> #COM Cloned with NEB HiFi cloning Q5® High-Fidelity DNA Polymerase and BamHI/Sall restriction enzymes and Sanger Sequence Verified-GAP

Table 138: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1 <i>parS</i>	pFH4034	Rec Genes	1 mM IPTG Red ^b	1 mM IPTG Green ^b
SDT3065 ^a	LT2 No <i>parS</i> Δ <i>fliC7716</i> , Δ (<i>hin-fliA7731</i>) Φ pSLT- Lysogens	No	No	No	No	No	No
SDT3098 ^a	LT2 No <i>parS</i> Δ (<i>hin-fliA7731</i>):: <i>tetRA</i> (Tet ^R), Δ <i>fliC7716</i> Φ pSLT- Cured	No	No	No	No	No	No
SDT3159	<i>putA</i> ::pMT1 <i>parS</i> Lysogens	No	Yes	No	No	No	No
SDT3160	<i>putA</i> ::pMT1 <i>parS</i> Cured	No	Yes	No	No	No	No
SDT3161	<i>argD</i> ::P1 <i>parS</i> Lysogens	Yes	No	No	No	No	No
SDT3162	<i>argD</i> ::P1 <i>parS</i> Cured	Yes	No	No	No	No	No
SDT3163	<i>purH</i> ::P1 <i>parS</i> Lysogens	Yes	No	No	No	No	No
SDT3164	<i>purH</i> ::P1 <i>parS</i> Cured	Yes	No	No	No	No	No
SDT3165	<i>argD</i> ::P1 <i>parS</i> <i>putA</i> ::pMT1 <i>parS</i> Lysogens	Yes	Yes	No	No	No	No
SDT3166	<i>argD</i> ::P1 <i>parS</i> <i>putA</i> ::pMT1 <i>parS</i> Cured	Yes	Yes	No	No	No	No

Table 139: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1		Rec Genes	1 mM	1 mM
			<i>parS</i>	pFH4034		IPTG Red ^b	IPTG Green ^b
SDT3167	<i>purH::P1 parS putA::pMT1 parS</i> Lysogens	Yes	Yes	No	No	No	No
SDT3168	<i>purH::P1 parS putA::pMT1 parS</i> Cured	Yes	Yes	No	No	No	No
SDT3169	<i>recA argD::P1 parS putA::pMT1 parS</i> Lysogens	Yes	Yes	No	No	No	No
SDT3170	<i>recA argD::P1 parS putA::pMT1 parS</i> Cured	Yes	Yes	No	No	No	No
SDT3171	<i>recA purH::P1 parS putA::pMT1 parS</i> Lysogens	Yes	Yes	No	No	No	No
SDT3172	<i>recA purH::P1 parS putA::pMT1 parS</i> Cured	Yes	Yes	No	No	No	No
SDT3187	No <i>parS</i> Lysogens / pFH4034	No	No	Yes	No	No	No
SDT3188	No <i>parS</i> Cured /pFH4034	No	No	Yes	No	No	No

Table 1310: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells.

Strain Number	Genotype	P1 <i>parS</i>	pMT1		Rec Genes	1 mM	1 mM
			<i>parS</i>	pFH4034		IPTG Red ^b	IPTG Green ^b
SDT3173	<i>putA::pMT1 parS</i> Lysogens / pFH4034	No	Yes	Yes	No	No	Yes
SDT3174	<i>putA::pMT1 parS</i> Cured / pFH4034	No	Yes	Yes	No	No	Yes
SDT3175	<i>argD::P1 parS</i> Lysogens / pFH4034	Yes	No	Yes	No	Yes	No
SDT3176	<i>argD::P1 parS</i> Cured / pFH4034	Yes	No	Yes	No	Yes	No
SDT3177	<i>purH::P1 parS</i> Lysogens / pFH4034	Yes	No	Yes	No	Yes	No
SDT3178	<i>purH::P1 parS</i> Cured / pFH4034	Yes	No	Yes	No	Yes	No
SDT3179	<i>argD::P1 parS</i> <i>putA::pMT1 parS</i> Lysogens / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3180	<i>argD::P1 parS</i> <i>putA::pMT1 parS</i> Cured / pFH4034	Yes	Yes	Yes	No	Yes	Yes

Table 1311: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1		Rec Genes	1 mM	1 mM
			<i>parS</i>	pFH4034		IPTG Red ^b	IPTG Green ^b
SDT3181	<i>purH::P1 parS putA::pMT1 parS</i> Lysogens / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3182	<i>purH::P1 parS putA::pMT1 parS</i> Cured / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3183	<i>recA argD::P1 parS putA::pMT1 parS</i> Lysogens / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3184	<i>recA argD::P1 parS putA::pMT1 parS</i> Cured / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3185	<i>recA purH::P1 parS putA::pMT1 parS</i> Lysogens / pFH4034	Yes	Yes	Yes	No	Yes	Yes
SDT3186	<i>recA purH::P1 parS putA::pMT1 parS</i> Cured / pFH4034	Yes	Yes	Yes	No	Yes	Yes

Table 1312: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1 <i>parS</i>	pFH4034	Rec Genes	1 mM	1 mM
						IPTG Red ^b	IPTG Green ^b
SDT3205	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R</i>	Yes	Yes	Yes	No	Yes	Yes
SDT3206	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recE</i>	Yes	Yes	Yes	<i>recE</i>	Yes	Yes
SDT3207	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recT</i>	Yes	Yes	Yes	<i>recT</i>	Yes	Yes
SDT3208	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-ninG</i>	Yes	Yes	Yes	<i>ninG</i>	Yes	Yes

Table 1313: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1		Rec Genes	1 mM IPTG	1 mM IPTG
			<i>parS</i>	pFH4034		Red ^b	Green ^b
SDT3209	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recET</i>	Yes	Yes	Yes	<i>recET</i>	Yes	Yes
SDT3210	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recET ninG</i>	Yes	Yes	Yes	<i>recET ninG</i>	Yes	Yes
SDT3211	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R</i>	Yes	Yes	Yes	No	Yes	Yes
SDT3212	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recE</i>	Yes	Yes	Yes	<i>recE</i>	Yes	Yes

Table 1314: Duplication strain table.

Containing strain numbers, genotypes, and *parS* location. All of these strains were cured of pSLT plasmid and harbor mutations that render the cells nonmotile, The presence or absence of prophages is indicated, as is the presence of the pRHA109 plasmid with the relevant phage recombination gene (or the absence of any cloned insert) and NA denotes plasmid is absent. ^aAll subsequent strains were constructed in either the SDT3065 or SDT3098 genetic background, as indicated by the “lysogen” or “cured” designation. ^bColor of ParB foci expected when IPTG is added to the cells..

Strain Number	Genotype	P1 <i>parS</i>	pMT1		Rec Genes	1 mM IPTG	1 mM IPTG
			<i>parS</i>	pFH4034		Red ^b	Green ^b
SDT3213	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recT</i>	Yes	Yes	Yes	<i>recT</i>	Yes	Yes
SDT3214	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-ninG</i>	Yes	Yes	Yes	<i>ninG</i>	Yes	Yes
SDT3215	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recET</i>	Yes	Yes	Yes	<i>recET</i>	Yes	Yes
SDT3216	<i>recA argD::P1 parS putA::pMT1 parS Cured / pFH4034 / pRHA109-Kan^R-recET ninG</i>	Yes	Yes	Yes	<i>recET ninG</i>	Yes	Yes

Table 1415: Primers (5' -> 3'):

Name	Sequence
<i>recT</i> FWD	GAAATTCAGGAGGTTGTCGAATGTGCGCCGCTTGAAGCG
<i>recT</i> REV	CGGATGAGGGCGCGGGGATCTTAG CCGATGTATTCCGGTTTCATATCG
<i>recE</i> FWD	GAAATTCAGGAGGTTGTCGAATGAGT GGAACATAATCCTGTATTTTTAGTCCG
<i>recE</i> REV	CGGATGAGGGCGCGGGGATCTTAA TTATGCCTGTACGCGCAACGCTTC
<i>ninG</i> FWD	GAAATTCAGGAGGTTGTCGAATGGCTAAATTACCGCGCCG
<i>ninG</i> REV	CGGATGAGGGCGCGGGGATCTTATT TCATGCGGCCTCCAGCTTTTTTAGC
<i>recT_recE</i> REV (1)	CACTCATTGACAACCTCCTTTAG CCGATGTATTCCGGTTTCATATCG
<i>recT_recE</i> FWD (2)	CGGCTAAAGGAGGTTGTCGAATGAGT GGAACATAATCCTGTATTTTTAGTCCG
<i>recT_recE_ninG</i> FWD (2)	CGGCTAAAGGAGGTTGTCGAATGA GTGGAACATAATCCTGTATTTTTAG
<i>recT_recE_ninG</i> REV (2)	CATTGACAACCTCCTTTAATTATGCCTGTACGCGCAACG
<i>recT_recE_ninG</i> FWD (3)	TAATTAAGGAGGTTGTCGAATGGCTAAATTACCGCGCCG
delGifsy-1_andattL-Forward	TGGCGTGCATATTACACTGTAGCTTTGAAAT CGTCAGCATGTGTAGGCTGGAGCTGCTTC
delGifsy-1_andattL-Reverse	TAAAACAGACGTTAAGCTCAGAACAGCGAC CTCTAAAGTCATGGGAATTAGCCATGGTCC
pSLT delete <i>samABparS tetA sacB</i> F	AGCTATCAACGAGGTCCTTGAGAGAAATTTG AGTCAATAATCCTAATTTTTGTTGACTCTA
pSLT delete <i>samAB tetA sacB</i> R	TAATGCTGTATATAAAAACAGGCATTTAAGA GGTATGCCATCAAAGGGAAAACGTCCATAT
P1 <i>parS metE</i> Ultramer F	TATTGACTCATACCTCGGTTTTCTCGCGTTGGCCTGCGAA ACTTTGCCATTCAAATTTCACTATTAAGTACTGTTTAAAA GTAAATTAATCTAAAATTTCAAGGTGAAATCGCCACGATTTT ACCTGGGTGTAGGCTGGAGCTGCTTC

Table 1416: Primers (5' -> 3'):

Name	Sequence
P1 <i>parS metE</i> Block 1 Forward	TATTGACTCATACCCTCGGTTTTCTCGCG TTGGCCTGCGAAACTTTTCGCCATTCAAATT
P1 <i>parS metE</i> Block 2 Forward	TCTAAAATTTCAAGGTGAAATCGCCACGATT TCACCTTGGGTGTAGGCTGGAGCTGCTTC
P1 <i>parS metE</i> Block 1 Reverse	CTAGAAAGTATAGGAACTTCGAAGCAGCTCC AGCCTACACCCAAGGTGAAATCGTGGCGA
P1 <i>parS metE</i> Block 2 Reverse	CACGCCTTCAAATAGGTCGTCAGCAACAG CTTCACCTGGATGGGAATTAGCCATGGTCC
<i>argD</i> P1 <i>parS</i> F	CCGACCGCCGGATGCGCTACGCTTATCCGG CAATCCGCCAAGTGTCCAGGTTTGGCGTCA
<i>argD</i> P1 <i>parS</i> R	GCTGAAAAATTTCTCCGGCGTTGATTTGT GGTTGCTATTCTCGGTTTTCTCGCGTTGG
<i>purH</i> P1 <i>parS</i> F	CGTTACCAATCACTAATACTTTCATGTTTCG CTCCATTAACTCGGTTTTCTCGCGTTGG
<i>purH</i> P1 <i>parS</i> R	TCTTTCAGGGATAAAAGCGGGGCCAGAATT TAAAAAGAAAAGTGTCCAGGTTTGGCGTCA
pMT1 <i>putA</i> F	AGCCTTAATTAACACAGTAGAGGTTGAAA AGCGTGGTGATTTCAAGTGTGAAAGAATTTT CAATTTTCCTTTATAATCAAACAAATAACCA TGAAATTGGCGTGGTGAAAAACAGTGTAG GCTGGAGCTGCTTC
pMT1 <i>putA</i> R	AAAATAAATCCAGATGGTTTTCTCGTCAGA CACTCCCTTAATGGGAATTAGCCATGGTCC

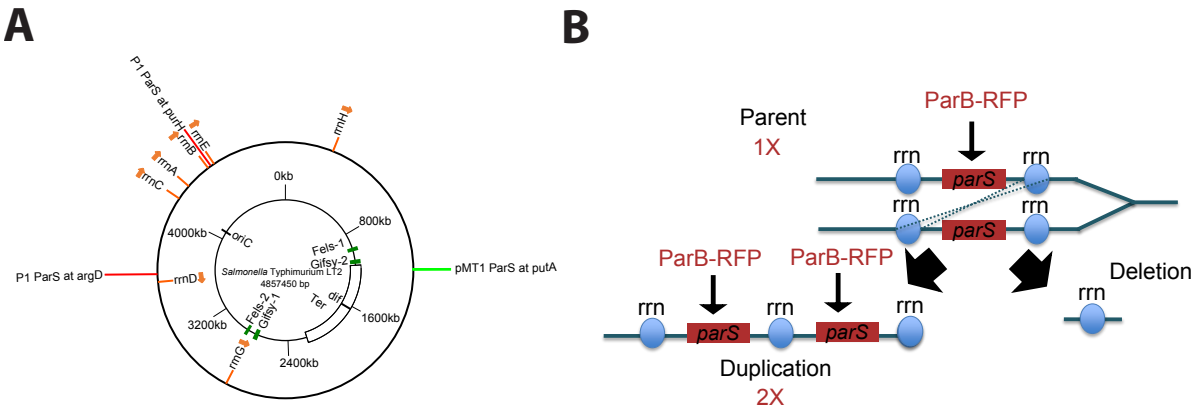


Figure 17: Chromosome organization and assay used to detect duplications. *Salmonella* LT2 chromosome with regions mapped and not drawn to scale using GenomeVX (141). The outside circle shows sites facing outwards and these are in the opposite orientation of sites facing inwards. Locations of the 7 *rrn* operons on the *Salmonella* LT2 chromosome are shown in orange on the outside of the circle; orange arrows indicate *rrn* operon direction. Gifsy-1, Gifsy-2, Fels-1, Fels-2 active prophages are shown in dark green. A P1 *parS* site was recombineered into the chromosome at *argD* or *purH* and is shown in red (223). A pMT1 *parS* site was recombineered into *putA* and is shown in green (223). *oriC* was found from BLAST with the *E. coli* MG1655 *oriC* site and is the origin of replication. The Ter macrodomain where replication ends is indicated and was identified from (142, 143). Dif site was located from (144). **B.** A P1 *parS* site was placed between *rrn* operons and ParB-RFP can bind specifically and fluoresce red when excited with a laser with 1x signal intensity. This site can be duplicated and fluoresce red with 2x or higher signal intensity if the *parS* site undergoes a duplication or amplification. Adapted from (134).

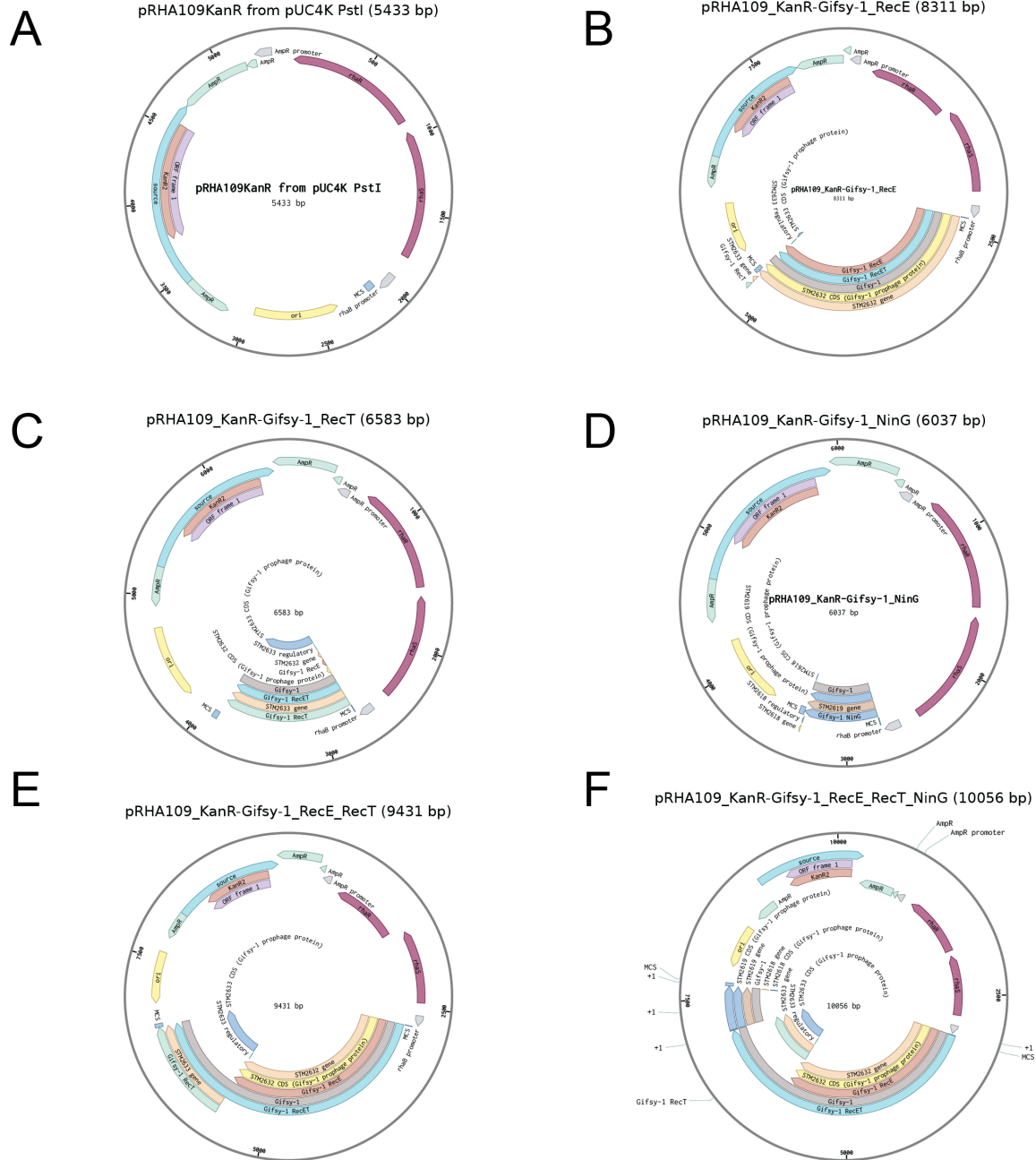


Figure 18: pRHA109-Kan^R plasmids with Gifsy-1 recombination proteins. **A.** pRHA109-Kan^R. **B.** pRHA109-Kan^R_Gifsy-1_recE. **C.** pRHA109-Kan^R_Gifsy-1_recT. **D.** pRHA109-Kan^R_Gifsy-1_ninG. **E.** pRHA109-Kan^R_Gifsy-1_recE_recT. **F.** pRHA109-Kan^R_Gifsy-1_recE_recT_ninG.

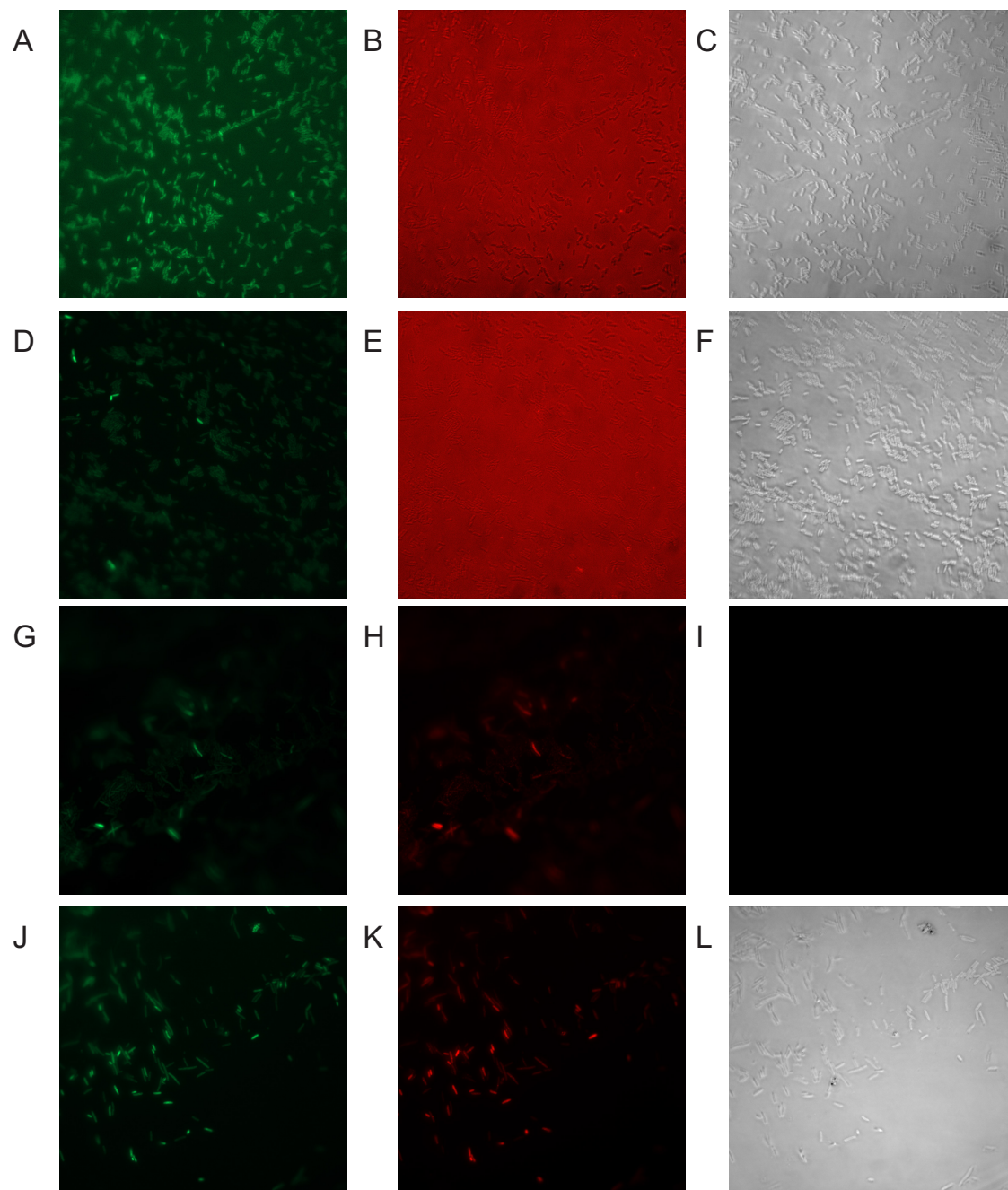


Figure 19: Microscopy – SDT3173 – SDT3176
A. SDT3173 - Green Channel **B.** SDT3173 - Red Channel. **C.** SDT3173 - Phase Channel. **D.** SDT3174 - Green Channel. **E.** SDT3174 - Red Channel. **F.** SDT3174 - Phase Channel. **G.** SDT3175 - Green Channel. **H.** SDT3175 - Red Channel. **I.** SDT3175 - Phase Channel. **J.** SDT3176 - Green Channel. **K.** SDT3176 - Red Channel. **L.** SDT3176 - Phase Channel.

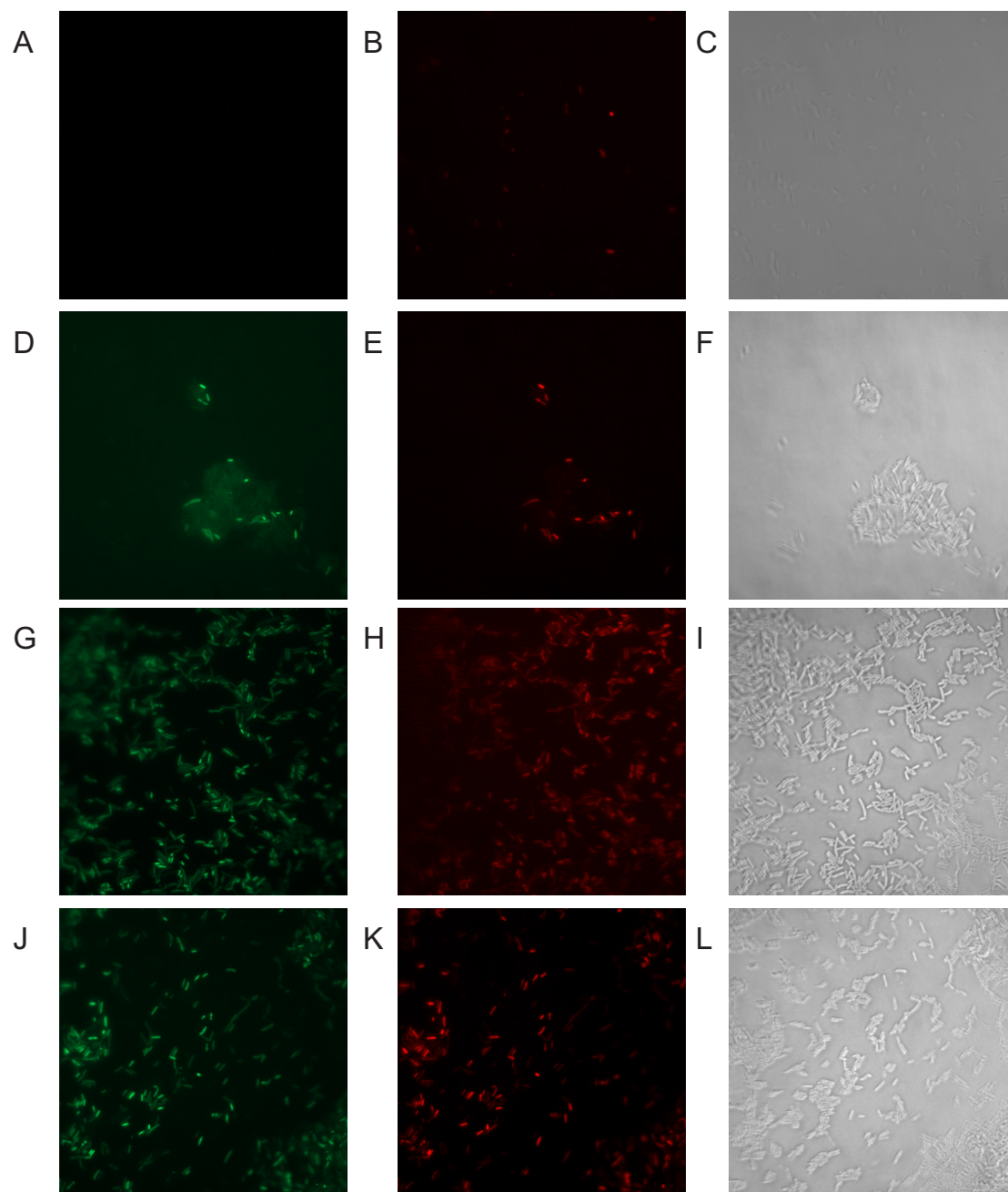


Figure 20: Microscopy – SDT3177 – SDT3180
A. SDT3177 - Green Channel **B.** SDT3177 - Red Channel. **C.** SDT3177 - Phase Channel. **D.** SDT3178 - Green Channel. **E.** SDT3178 - Red Channel. **F.** SDT3178 - Phase Channel. **G.** SDT3179 - Green Channel. **H.** SDT3179 - Red Channel. **I.** SDT3179 - Phase Channel. **J.** SDT3180 - Green Channel. **K.** SDT3180 - Red Channel. **L.** SDT3180 - Phase Channel.

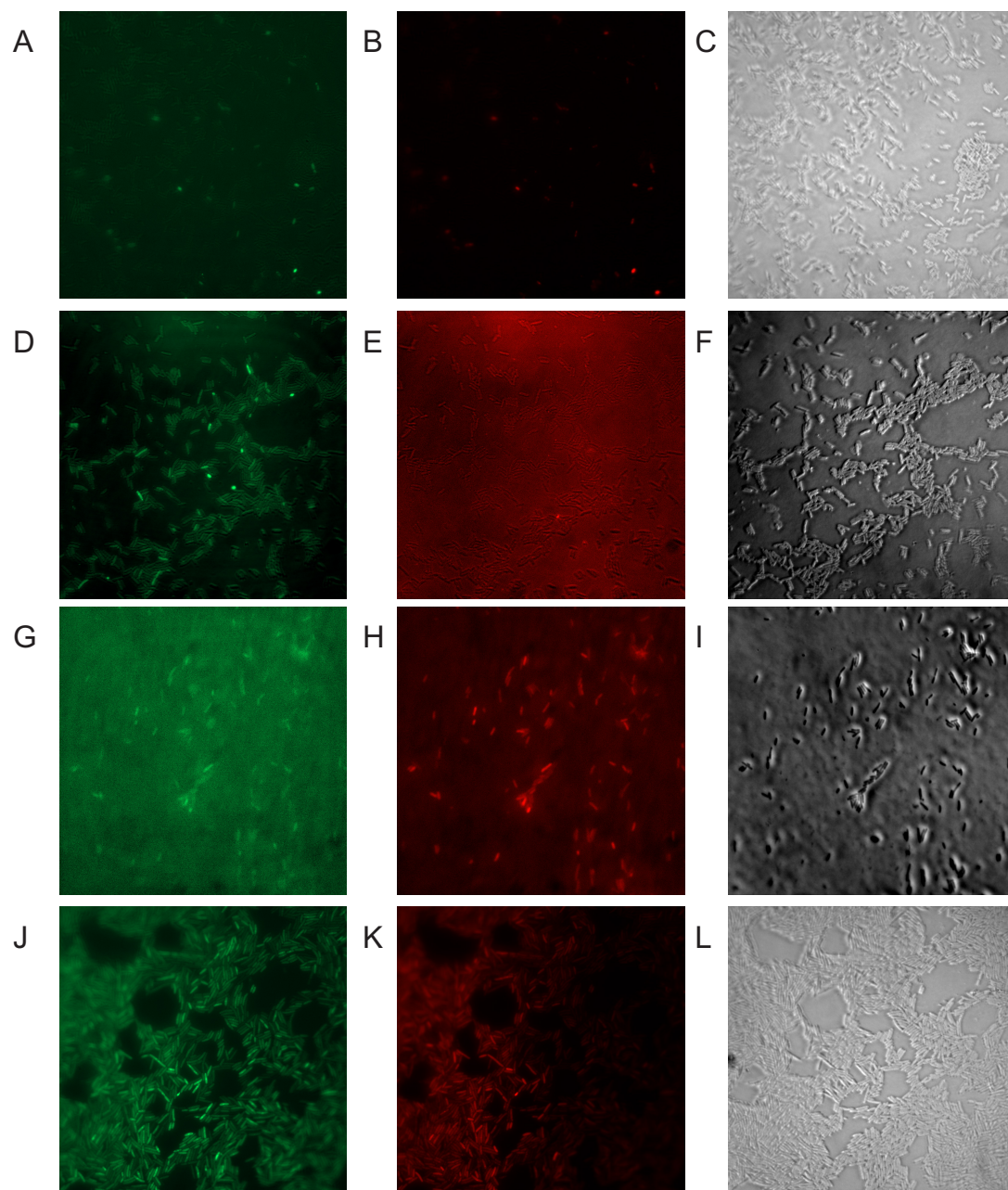


Figure 21: Microscopy – SDT3181 – SDT3184
A. SDT3181 - Green Channel **B.** SDT3181 - Red Channel. **C.** SDT3181 - Phase Channel. **D.** SDT3182 - Green Channel. **E.** SDT3182 - Red Channel. **F.** SDT3182 - Phase Channel. **G.** SDT3183 - Green Channel. **H.** SDT3183 - Red Channel. **I.** SDT3183 - Phase Channel. **J.** SDT3184 - Green Channel. **K.** SDT3184 - Red Channel. **L.** SDT3184 - Phase Channel.

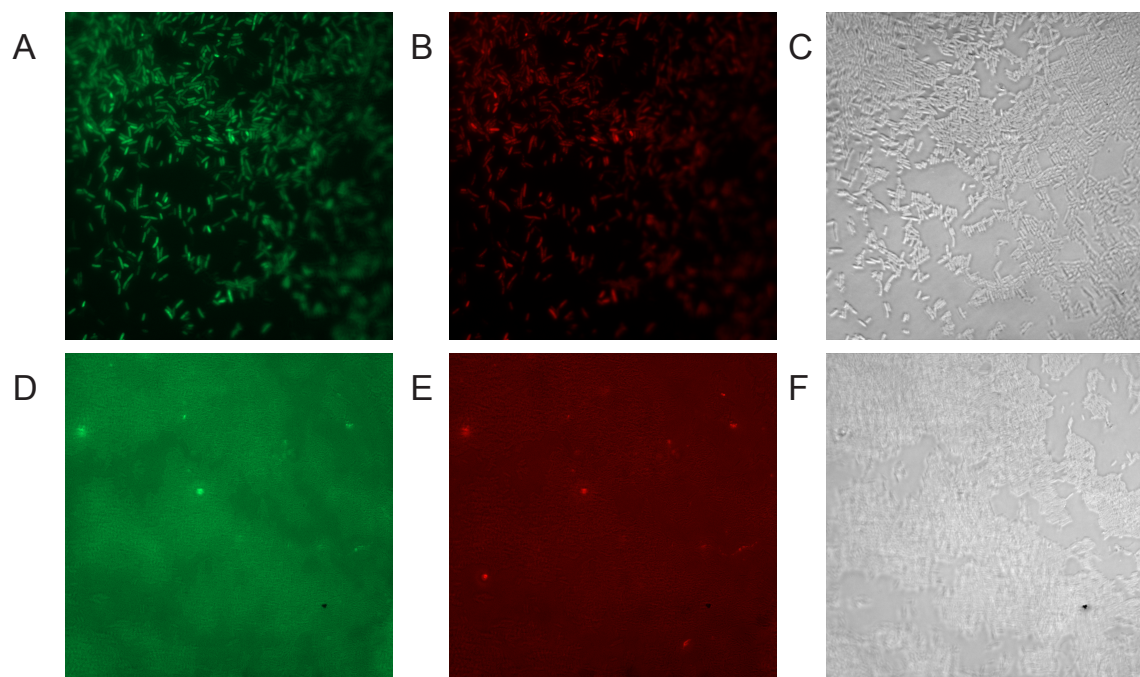


Figure 22: Microscopy– SDT3185 – SDT3186**A.** SDT3185 - Green Channel **B.** SDT3185 - Red Channel. **C.** SDT3185 - Phase Channel. **D.** SDT3186 - Green - Channel. **E.** SDT3186 - Red Channel. **F.** SDT3186 - Phase Channel.

Acknowledgements

Chapter 4, in part, is currently being prepared for submission for publication of the material. Peters, Gregory; Segall, Anca. The dissertation/thesis author was the primary investigator and author of this material.

Chapter 5: Conclusion

SeqA, GATCs, transcription and phage regulation

This dissertation helps to uncover some of the intricacies of interactions between phage and bacteria. While pursuing research from a Phage-centric point of view we were able to uncover a new transcription regulation mechanism and found a connection between a host gene, SeqA, and control of the life cycle of phage. Previously it was known that the binding site of SeqA, GATC motifs, were low in phage but now we have a better idea and found a connection with the host protein SeqA. SeqA is involved in numerous cell processes and while working with *Salmonella* LT2 which has four active prophages we found that SeqA mutants of *Salmonella* LT2 had increased prophage induction compared to wildtype. This led to the investigation into and finding that the SeqA is likely to affect the transcription regulation of viruses. This was found by investigating where GATC motifs are in comparison to genes and integrating multiple sources of protein binding data from different labs. Pairs of GATC sites are in multiple genes which likely could affect regulation of prophages. Pairs of GATC sites occur in both the host *dnaA* gene and also prophage *dnaA* and *dnaC* analogs. After investigating protein binding data of SeqA vs. RNAP polymerase in *E. coli* we find many regions across the genome in which SeqA binding affects RNAP binding. SeqA binds to and likely affects and occludes RNA Polymerase from completing transcription regulation in important genes such as *dnaA* and phage life cycle genes. SeqA is likely binding and affecting regulation of phages could cause dysregulation of phage life cycles.

SeqA could bind to phage and prevent a phage from replicating and be a defense mechanism against phage. It is not clear if SeqA acts by stabilizing lysogeny or

lysis, but phage genes are appeared to be regulated to an extent. From the phage “point of view”, having a “connection” to a host cellular process involved in DNA replication would be useful to “sense” the growth level of the bacteria. From the bacteria point of view, it would be useful to have a control on the phages infecting it. This might be an immune mechanism and SeqA might act to dysregulate the phage life cycle and prevent it from replicating. One hypothesis along this line is that SeqA “traps” phages and this can lead to the acquisition of new genes by the bacteria. SeqA could allow for brief and quick bursts of otherwise toxic genes which could aid in pathogenicity of the host. From either point of view, both are in a way advantage both the virus and host.

This study could lead to a new mechanism of how SeqA prevents overinitiation of DNA replication and further investigation into this would be useful. One way to study this would be to make mutations of the GATCs into synonymous codons and see if there is an effect on DNA initiation and the cell cycle. Another way to study this would be to synthesize genes with GATC in them and with no GATCs and clone onto a plasmid and compare and monitor transcription or RNA lengths. If SeqA binds it is likely that numerous short RNAs are produced in the wildtype in comparison to the full-length RNAs in the GATC mutant. It is likely there is a gradient of both sizes and at this is dependent on the cell cycle and stage of growth the bacteria is in. Exponential and stationary phases are likely to both have different effects of SeqA transcription regulation. There are many other host genes in which SeqA transcription regulation yielding many new genes to study of how SeqA potentially regulates.

During this study we developed two statistical approaches to investigate SeqA binding, the first involved a t-test of SeqA binding vs. RNAP binding and SeqA binding

from 0 minutes and 50-minutes and then filtering the signals into different strengths and comparing them against randomized signals using BEDOPS (161). BEDOPS allows the chopping of signals into one basepair and this allowed for higher resolution of where the signals bind (161). The BEDOPS shuffle allows for the creation of randomized signals which allowed for the comparison of randomized signals helping to identify where the signals localize to (161). The differences are very difficult to observe unless these steps are taken and can be missed. This method could also be applied to ChIP-Seq data in the future and randomize sequencing read locations. Both experimental data of ChIP-Chip microarray data and theoretical data of the location of paired GATC sites follow the same trends, reinforcing each other.

The second new statistical method involved using the GATC Odds Markov ratio on the ChIP-Chip signals, this could be applied to Chip-Seq signals as well. This allowed us to get an idea of SeqA signals compares to the Odds Markov ratio of the genomes of the phage and bacteria. Phage have previously been shown to have very low GATC Odds Ratios and this provides a link to SeqA binding. Multiple lytic phages have the lowest GATC odds ratio and some phage have extremely low amounts of GATC sites and maybe evolved to avoid SeqA binding.

During this study, it became even more apparent that the line between virus genes and host genes is very fine. How do we know which gene comes from a virus and which gene comes from the host? Currently, phage sequences are located by experienced scientists that search for phage features like attR and attL or known phage genes. Multiple bioinformatics programs have been developed that aid with this program such as PhiSpy and PHASTER. But what if the attR and attL are deleted from a host

event, it is likely both experienced and intuitive scientists and programs will miss the identification of the phage genes. This seems to have occurred during the annotation of *E. coli* O157-H7 EDL933 strain. In the EDL933 strain, there were numerous prophage regions that had been previously missed and PHASTER readily identified these (149). These regions shared homology with the Sakai strain in phage regions that were previously annotated. Most of the regions in the EDL933 had been annotated as bacteria genes so it is likely there are many more misannotations that occur during the annotation of genomes. It is important to improve this process so we can better clarify what is virus and what is host. Even bigger questions arise along this line; how do we distinguish the virus from the host if many of the genes are shared or evolved from rapidly replicating and evolving viruses?

It would be interesting to search for SeqA like proteins in other organisms such as Eukaryotes and other Bacteria which don't have SeqA homologs. The forkhead box protein 1 and 2 proteins act similarly to SeqA and are involved in the initiation of DNA replication in Eukaryotes. The motif is different and regions, where the protein binds, are different, but it is possible these or other transcription factors bind within the coding sequence of important genes. Retroviruses infect multiple organisms and make up 8% of the Human genome (276). The retroviruses are RNA viruses and integrate reverse transcribed DNA their DNA these are similar to bacterial prophages, so it is possible there is a protein that binds to and effects retroviruses life cycles and other genes (276–278).

Genome duplications

The active viruses in Bacteria are likely to be involved in genome duplications and amplifications. The mechanism of genome duplications and amplifications is thought to be universal in all organisms and involve recombination genes. The viruses contain genes which are involved in recombination and likely to affect these mechanisms. In Chapters 3 and 4 we developed assays to study the viruses potential roll in genome duplications. We performed RNA-Seq on Bacteria with and without lysogens to see what genes were differentially expressed and see if the lysogens could potentially compensate for a recombination mutant defect. We also developed a system to monitor the effects using fluorescence of specific sites in the genome. It would be interesting to see if expressing the prophage genes were able to recover genome duplications from a recombination defect. It would also be interesting to see if expressing the genes alone causes duplications or amplifications to arise.

Duplications and amplifications are becoming even more important since cancers that are sequenced exhibit chromosomal rearrangements and amplifications. It is not known what causes these and viruses could potentially play a larger role than previously thought. A recent study of Alzheimer's disease shows a link with the disease and gene recombination. What if a virus infects the cells and rearranges the genome to produce misfolded proteins? Other diseases of unknown etiology could also be linked to viruses.

The phast, phresent, and phuture of Phages

The study of Phages are over 100 years old but and there likely will be many new discoveries over the next 100 years (279). The Year of the Phage meeting occurred in 2015 at SDSU celebrating 100 years since the discovery of Phages (280). A meeting

website is here: <http://2015phage.org/>. Videos of lectures of the history and future of phages are located at this website: <http://2015phage.org/program.php> and https://www.youtube.com/user/rohwerlab/videos?sort=dd&shelf_id=0&view=0. An illustrated timeline is located here: http://2015phage.org/phage_art.php. A Second meeting occurred in 2017 at the Pasteur Institute (281). More information about phages can also be found on the ASM:Division M website archived here: <https://web.archive.org/web/20170302164211/http://www.asm.org:80/division/m/OfcMem.html>

We are coming on into a new age of phage research as evidenced by recent research considerable drop in DNA sequencing revealing many more DNA sequences, many of which have viruses. In addition, phage therapy is making a comeback and will be more important as antibiotic resistance is rapidly spreading and becoming a public health concern. A recent report by “The Review on Antimicrobial Resistance (AMR)” predicted that cases of antimicrobial resistant superbugs will cause more deaths than cancer in 2050 (282). Recently in 2017, there was a case study with a patient who had acquired an MDR *Actinobacter baumannii* infection which was resistant to all known antibiotics who was successfully treated by phage (283). This shows the success of phage therapy in times of dire need and more phage therapy studies are currently underway (284). Cancer has had a dramatic reduction of phases and this year on January 8, 2019, the American Cancer Society reports show that cancer deaths have decreased 27% in the past 25 years from 1991 to 2016 (285). Perhaps it is time to switch the funding into other areas of research such as phage-oriented research and stimulate the economy to tackle the large antimicrobial threat.

Phage are becoming more popular as well by recent talks on YouTube. Dr. Steffanie Strathdee, a professor at UCSD, whose Husband Dr. Tom Patterson was treated by Phage Therapy in the 2014 case study. Steffanie Strathdee gave a TedXTalk talk at TedXNashville titled “How Sewage Saved My Husband's Life from a Superbug” (286). The video link is here: <https://www.youtube.com/watch?v=AbAZU8FqzX4>. In 2018, Stephanie Strathdee was named to TIME’s 50 Most Influential People in Health Care (287). Also on May 13, 2018, a YouTube video titled “The Deadliest Being on Planet Earth – The Bacteriophage” was published by Kurzgesagt – In a Nutshell (288). The video link is here: <https://www.youtube.com/watch?v=YI3tsmFsrOg>. This video was #2 trending on YouTube when it was first published and has reached millions of views and is at 7.5 million views as of January 2019. These videos will likely inspire more phage researchers. The reader is also suggested to read the recent books Life in Our Phage World published in December 2014 and Thinking Like a Phage: The Genius of the Viruses That Infect Bacteria and Archaea published in May 2017 (4, 289). These books help the public and scientists gain an even greater appreciation and inspiration from the wonderful phages. We have entered into the next century of phage may the super cool and important phages yield many new insights of how life works.

Acknowledgements

Chapter 5, in part, is currently being prepared for submission for publication of the material. Peters, Gregory. The dissertation/thesis author was the primary investigator and author of this material.

Appendix 1: Source code and RNA-Seq analysis of prophage activity

Introduction

Protocol to run programs used in Chapter 2

The appendix contains Python programs and shell scripts used in the analysis of Chapter 2. The Python programs `bedtools_shuffle_sort_SeqAOnly.py`, `bedtools_shuffle_sort_SeqAOnly_Grainger`, `http://bedtools_shuffle_sort_0vs50Min.py` are Python3 programs that prints to standard output a shell script to randomize the SeqA Only 1, SeqA Only 2, and SeqA Binding signals respectively 1000 times. In order to run the following command is run in the terminal:

```
python3 ./Filename.py > ./Filename.sh
```

The “Filename” denotes the Python program being run and creates a `.sh` file or shell script file of the same name. The appendix also contains shell scripts to run these a file with the same filename listed in the comments section, the second comment in all comment shell scripts denotes the filename and ends in `.sh` (comment lines begin with `#` and the first comment line is always `#!/bin/bash` for a bash shell script). In order to run the created shell script and all shell scripts the Unix permissions must first be changed to enable execute using the change mode command:

```
chmod +x ./Filename.sh
```

In order to run the shell script the following command would be run:

./Filename.sh

Additional RNA-Seq analysis for prophage activity for Chapter 3

The appendix also contains additional analysis of prophage activity. Tables 15 - 17 show the genes differentially expressed using DESeq2, EdgeR, and Limma respectively in wild-type lysogens, *recA* lysogens, *ruvAB* lysogens, and *ruvC* lysogens vs. the isogenic prophage-cured wild-type, *recA*, *ruvAB*, and *ruvC* strains (Figs. 23 - 25)

Python programs

Python program to make shell script to shuffle SeqA Only signals (SeqA Only 1)

1000 times

```
1. #bedtools_shuffle_sort_SeqAOnly.py
2. #Python 3.6.5 [Anaconda, Inc.] (default, Apr 26 2018, 08:42:37)
3. #[GCC 4.2.1 Compatible Clang 4.0.1 (tags/RELEASE_401/final)] on darwin
4.
5. #Python 3 script to make shell script to run uShuffle 1000 times on SeqAOnly signal
6.
7.
8. import sys
9. sys.stdout.flush()
10.
11. sys.stdout.write('cp ./SeqAOnly.bed ./SeqAOnly_r0s0.bed')
12. print()
13. for a in range(1, 1001):
14.     b = a-1
15.     sys.stdout.write('bedtools shuffle -seed 1 -i SeqAOnly_r')
16.     sys.stdout.write(str(b))
17.     sys.stdout.write('s')
18.     sys.stdout.write(str(b))
19.     sys.stdout.write('.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r')
20.     sys.stdout.write(str(a))
21.     sys.stdout.write('s')
22.     sys.stdout.write(str(b))
23.     sys.stdout.write('.bed')
24.     print()
25.     sys.stdout.write('sort -k1,1 -k2,2n ./SeqAOnly_r')
26.     sys.stdout.write(str(a))
27.     sys.stdout.write('s')
28.     sys.stdout.write(str(b))
29.     sys.stdout.write('.bed > ./SeqAOnly_r')
30.     sys.stdout.write(str(a))
31.     sys.stdout.write('s')
32.     sys.stdout.write(str(a))
33.     sys.stdout.write('.bed')
34.     print()
```


Python program to make shell script to shuffle SeqA Only (Grainger) signals (SeqA Only 2) 1000 times

```
1. #bedtools_shuffle_sort_SeqAOnly_Grainger.py
2. #Python 3.6.5 |Anaconda, Inc.| (default, Apr 26 2018, 08:42:37)
3. #[GCC 4.2.1 Compatible Clang 4.0.1 (tags/RELEASE_401/final)] on darwin
4.
5. #Python 3 script to make shell script to run uShuffle 1000 times on SeqAOnly_Grainger signal
6.
7.
8. import sys
9. sys.stdout.flush()
10.
11. sys.stdout.write('cp ./SeqAOnly_Grainger.bed ./SeqAOnly_Grainger_r0s0.bed')
12. print()
13. for a in range (1, 1001):
14.     b = a-1
15.     sys.stdout.write('bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r')
16.     sys.stdout.write(str(b))
17.     sys.stdout.write('s')
18.     sys.stdout.write(str(b))
19.     sys.stdout.write('.bed -g Ecoli-genomesize.txt > ./SeqAOnly_Grainger_r')
20.     sys.stdout.write(str(a))
21.     sys.stdout.write('s')
22.     sys.stdout.write(str(b))
23.     sys.stdout.write('.bed')
24.     print()
25.     sys.stdout.write('sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r')
26.     sys.stdout.write(str(a))
27.     sys.stdout.write('s')
28.     sys.stdout.write(str(b))
29.     sys.stdout.write('.bed > ./SeqAOnly_Grainger_r')
30.     sys.stdout.write(str(a))
31.     sys.stdout.write('s')
32.     sys.stdout.write(str(a))
33.     sys.stdout.write('.bed')
34.     print()
```

Python program to make shell script to shuffle 0 vs. 50 Min signals (SeqA Binding) 1000 times

```
1. #bedtools_shuffle_sort_0vs50Min.py
2. #Python 3.6.5 |Anaconda, Inc.| (default, Apr 26 2018, 08:42:37)
3. #[GCC 4.2.1 Compatible Clang 4.0.1 (tags/RELEASE_401/final)] on darwin
4.
5. #Python 3 script to make shell script to run uShuffle 1000 times on 0vs50Min signal
6.
7.
8. import sys
9. sys.stdout.flush()
10.
11. sys.stdout.write('cp ./0vs50Min.bed ./0vs50Min_r0s0.bed')
12. print()
13. for a in range (1, 1001):
14.     b = a-1
15.     sys.stdout.write('bedtools shuffle -seed 1 -i 0vs50Min_r')
16.     sys.stdout.write(str(b))
17.     sys.stdout.write('s')
18.     sys.stdout.write(str(b))
19.     sys.stdout.write('.bed -g Ecoli-genomesize.txt > ./0vs50Min_r')
20.     sys.stdout.write(str(a))
21.     sys.stdout.write('s')
22.     sys.stdout.write(str(b))
23.     sys.stdout.write('.bed')
24.     print()
25.     sys.stdout.write('sort -k1,1 -k2,2n ./0vs50Min_r')
26.     sys.stdout.write(str(a))
27.     sys.stdout.write('s')
28.     sys.stdout.write(str(b))
29.     sys.stdout.write('.bed > ./0vs50Min_r')
30.     sys.stdout.write(str(a))
31.     sys.stdout.write('s')
32.     sys.stdout.write(str(a))
33.     sys.stdout.write('.bed')
34.     print()
```

Python program to parse and rename CMBL signature output from unzipped zip file to zip file name

```
1. #RenameSignatureFilesInFolders.py
2. #Python 3.6.5 |Anaconda, Inc.| (default, Apr 26 2018, 08:42:37)
3. #[GCC 4.2.1 Compatible Clang 4.0.1 (tags/RELEASE_401/final)] on darwin
4.
5. #Python 3 script to rename signature output from: "http://www.cmbl.uga.edu/software/signature.html"
6. #Email output is sent after signature is run
7. #Download and name the Zip file with a descriptive name of the DNA sequence being analyzed.
8. #Unzip zip file
9. #This script recursively renames individual files from unzipped zip file to name of unzipped folder
10.
11. import os
12.
13. for root, dirs, files in os.walk("."):
14.     path = root.split(os.sep)
15.     print(os.path.basename(root))
16.     for file in files:
17.         for filename in os.listdir("."):
18.             if filename.endswith(".txt"):
19.                 os.rename(filename, "Changed-", + filename ".txt")
```

Shell scripts

BEDTools shuffle SeqA Only signals (SeqA Only 1) 1000 times

```
1. #!/bin/bash
2.
3. #bedtools_shuffle_sort_SeqAOnly.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to shuffle SeqAOnly signals 1000 times
6.
7. cp ./SeqAOnly.bed ./SeqAOnly_r0s0.bed
8. bedtools shuffle -seed 1 -i SeqAOnly_r0s0.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r1s0.bed
9. sort -k1,1 -k2,2n ./SeqAOnly_r1s0.bed > ./SeqAOnly_r1s1.bed
10. bedtools shuffle -seed 1 -i SeqAOnly_r1s1.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r2s1.bed
11. sort -k1,1 -k2,2n ./SeqAOnly_r2s1.bed > ./SeqAOnly_r2s2.bed
12. bedtools shuffle -seed 1 -i SeqAOnly_r2s2.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r3s2.bed
13. sort -k1,1 -k2,2n ./SeqAOnly_r3s2.bed > ./SeqAOnly_r3s3.bed
14. bedtools shuffle -seed 1 -i SeqAOnly_r3s3.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r4s3.bed
15. sort -k1,1 -k2,2n ./SeqAOnly_r4s3.bed > ./SeqAOnly_r4s4.bed
16. bedtools shuffle -seed 1 -i SeqAOnly_r4s4.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r5s4.bed
17. sort -k1,1 -k2,2n ./SeqAOnly_r5s4.bed > ./SeqAOnly_r5s5.bed
18. bedtools shuffle -seed 1 -i SeqAOnly_r5s5.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r6s5.bed
19. sort -k1,1 -k2,2n ./SeqAOnly_r6s5.bed > ./SeqAOnly_r6s6.bed
20. bedtools shuffle -seed 1 -i SeqAOnly_r6s6.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r7s6.bed
21. sort -k1,1 -k2,2n ./SeqAOnly_r7s6.bed > ./SeqAOnly_r7s7.bed
22. bedtools shuffle -seed 1 -i SeqAOnly_r7s7.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r8s7.bed
23. sort -k1,1 -k2,2n ./SeqAOnly_r8s7.bed > ./SeqAOnly_r8s8.bed
24. bedtools shuffle -seed 1 -i SeqAOnly_r8s8.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r9s8.bed
25. sort -k1,1 -k2,2n ./SeqAOnly_r9s8.bed > ./SeqAOnly_r9s9.bed
26. bedtools shuffle -seed 1 -i SeqAOnly_r9s9.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r10s9.bed
27. sort -k1,1 -k2,2n ./SeqAOnly_r10s9.bed > ./SeqAOnly_r10s10.bed
28. bedtools shuffle -seed 1 -i SeqAOnly_r10s10.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r11s10.bed
29. sort -k1,1 -k2,2n ./SeqAOnly_r11s10.bed > ./SeqAOnly_r11s11.bed
30. bedtools shuffle -seed 1 -i SeqAOnly_r11s11.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r12s11.bed
31. sort -k1,1 -k2,2n ./SeqAOnly_r12s11.bed > ./SeqAOnly_r12s12.bed
32. bedtools shuffle -seed 1 -i SeqAOnly_r12s12.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r13s12.bed
33. sort -k1,1 -k2,2n ./SeqAOnly_r13s12.bed > ./SeqAOnly_r13s13.bed
34. bedtools shuffle -seed 1 -i SeqAOnly_r13s13.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r14s13.bed
35. sort -k1,1 -k2,2n ./SeqAOnly_r14s13.bed > ./SeqAOnly_r14s14.bed
36. bedtools shuffle -seed 1 -i SeqAOnly_r14s14.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r15s14.bed
37. sort -k1,1 -k2,2n ./SeqAOnly_r15s14.bed > ./SeqAOnly_r15s15.bed
38. bedtools shuffle -seed 1 -i SeqAOnly_r15s15.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r16s15.bed
39. sort -k1,1 -k2,2n ./SeqAOnly_r16s15.bed > ./SeqAOnly_r16s16.bed
40. bedtools shuffle -seed 1 -i SeqAOnly_r16s16.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r17s16.bed
41. sort -k1,1 -k2,2n ./SeqAOnly_r17s16.bed > ./SeqAOnly_r17s17.bed
```

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42. bedtools shuffle -seed 1 -i SeqAOnly_r17s17.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r18s17.bed
43. sort -k1,1 -k2,2n ./SeqAOnly_r18s17.bed > ./SeqAOnly_r18s18.bed
44. bedtools shuffle -seed 1 -i SeqAOnly_r18s18.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r19s18.bed
45. sort -k1,1 -k2,2n ./SeqAOnly_r19s18.bed > ./SeqAOnly_r19s19.bed
46. bedtools shuffle -seed 1 -i SeqAOnly_r19s19.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r20s19.bed
47. sort -k1,1 -k2,2n ./SeqAOnly_r20s19.bed > ./SeqAOnly_r20s20.bed
48. bedtools shuffle -seed 1 -i SeqAOnly_r20s20.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r21s20.bed
49. sort -k1,1 -k2,2n ./SeqAOnly_r21s20.bed > ./SeqAOnly_r21s21.bed
50. bedtools shuffle -seed 1 -i SeqAOnly_r21s21.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r22s21.bed
51. sort -k1,1 -k2,2n ./SeqAOnly_r22s21.bed > ./SeqAOnly_r22s22.bed
52. bedtools shuffle -seed 1 -i SeqAOnly_r22s22.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r23s22.bed
53. sort -k1,1 -k2,2n ./SeqAOnly_r23s22.bed > ./SeqAOnly_r23s23.bed
54. bedtools shuffle -seed 1 -i SeqAOnly_r23s23.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r24s23.bed
55. sort -k1,1 -k2,2n ./SeqAOnly_r24s23.bed > ./SeqAOnly_r24s24.bed
56. bedtools shuffle -seed 1 -i SeqAOnly_r24s24.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r25s24.bed
57. sort -k1,1 -k2,2n ./SeqAOnly_r25s24.bed > ./SeqAOnly_r25s25.bed
58. bedtools shuffle -seed 1 -i SeqAOnly_r25s25.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r26s25.bed
59. sort -k1,1 -k2,2n ./SeqAOnly_r26s25.bed > ./SeqAOnly_r26s26.bed
60. bedtools shuffle -seed 1 -i SeqAOnly_r26s26.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r27s26.bed
61. sort -k1,1 -k2,2n ./SeqAOnly_r27s26.bed > ./SeqAOnly_r27s27.bed
62. bedtools shuffle -seed 1 -i SeqAOnly_r27s27.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r28s27.bed
63. sort -k1,1 -k2,2n ./SeqAOnly_r28s27.bed > ./SeqAOnly_r28s28.bed
64. bedtools shuffle -seed 1 -i SeqAOnly_r28s28.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r29s28.bed
65. sort -k1,1 -k2,2n ./SeqAOnly_r29s28.bed > ./SeqAOnly_r29s29.bed
66. bedtools shuffle -seed 1 -i SeqAOnly_r29s29.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r30s29.bed
67. sort -k1,1 -k2,2n ./SeqAOnly_r30s29.bed > ./SeqAOnly_r30s30.bed
68. bedtools shuffle -seed 1 -i SeqAOnly_r30s30.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r31s30.bed
69. sort -k1,1 -k2,2n ./SeqAOnly_r31s30.bed > ./SeqAOnly_r31s31.bed
70. bedtools shuffle -seed 1 -i SeqAOnly_r31s31.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r32s31.bed
71. sort -k1,1 -k2,2n ./SeqAOnly_r32s31.bed > ./SeqAOnly_r32s32.bed
72. bedtools shuffle -seed 1 -i SeqAOnly_r32s32.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r33s32.bed
73. sort -k1,1 -k2,2n ./SeqAOnly_r33s32.bed > ./SeqAOnly_r33s33.bed
74. bedtools shuffle -seed 1 -i SeqAOnly_r33s33.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r34s33.bed
75. sort -k1,1 -k2,2n ./SeqAOnly_r34s33.bed > ./SeqAOnly_r34s34.bed
76. bedtools shuffle -seed 1 -i SeqAOnly_r34s34.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r35s34.bed
77. sort -k1,1 -k2,2n ./SeqAOnly_r35s34.bed > ./SeqAOnly_r35s35.bed
78. bedtools shuffle -seed 1 -i SeqAOnly_r35s35.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r36s35.bed

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79. sort -k1,1 -k2,2n ./SeqAOnly_r36s35.bed > ./SeqAOnly_r36s36.bed
80. bedtools shuffle -seed 1 -i SeqAOnly_r36s36.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r37s36.bed
81. sort -k1,1 -k2,2n ./SeqAOnly_r37s36.bed > ./SeqAOnly_r37s37.bed
82. bedtools shuffle -seed 1 -i SeqAOnly_r37s37.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r38s37.bed
83. sort -k1,1 -k2,2n ./SeqAOnly_r38s37.bed > ./SeqAOnly_r38s38.bed
84. bedtools shuffle -seed 1 -i SeqAOnly_r38s38.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r39s38.bed
85. sort -k1,1 -k2,2n ./SeqAOnly_r39s38.bed > ./SeqAOnly_r39s39.bed
86. bedtools shuffle -seed 1 -i SeqAOnly_r39s39.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r40s39.bed
87. sort -k1,1 -k2,2n ./SeqAOnly_r40s39.bed > ./SeqAOnly_r40s40.bed
88. bedtools shuffle -seed 1 -i SeqAOnly_r40s40.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r41s40.bed
89. sort -k1,1 -k2,2n ./SeqAOnly_r41s40.bed > ./SeqAOnly_r41s41.bed
90. bedtools shuffle -seed 1 -i SeqAOnly_r41s41.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r42s41.bed
91. sort -k1,1 -k2,2n ./SeqAOnly_r42s41.bed > ./SeqAOnly_r42s42.bed
92. bedtools shuffle -seed 1 -i SeqAOnly_r42s42.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r43s42.bed
93. sort -k1,1 -k2,2n ./SeqAOnly_r43s42.bed > ./SeqAOnly_r43s43.bed
94. bedtools shuffle -seed 1 -i SeqAOnly_r43s43.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r44s43.bed
95. sort -k1,1 -k2,2n ./SeqAOnly_r44s43.bed > ./SeqAOnly_r44s44.bed
96. bedtools shuffle -seed 1 -i SeqAOnly_r44s44.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r45s44.bed
97. sort -k1,1 -k2,2n ./SeqAOnly_r45s44.bed > ./SeqAOnly_r45s45.bed
98. bedtools shuffle -seed 1 -i SeqAOnly_r45s45.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r46s45.bed
99. sort -k1,1 -k2,2n ./SeqAOnly_r46s45.bed > ./SeqAOnly_r46s46.bed
100. bedtools shuffle -seed 1 -i SeqAOnly_r46s46.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r47s46.bed
101. sort -k1,1 -k2,2n ./SeqAOnly_r47s46.bed > ./SeqAOnly_r47s47.bed
102. bedtools shuffle -seed 1 -i SeqAOnly_r47s47.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r48s47.bed
103. sort -k1,1 -k2,2n ./SeqAOnly_r48s47.bed > ./SeqAOnly_r48s48.bed
104. bedtools shuffle -seed 1 -i SeqAOnly_r48s48.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r49s48.bed
105. sort -k1,1 -k2,2n ./SeqAOnly_r49s48.bed > ./SeqAOnly_r49s49.bed
106. bedtools shuffle -seed 1 -i SeqAOnly_r49s49.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r50s49.bed
107. sort -k1,1 -k2,2n ./SeqAOnly_r50s49.bed > ./SeqAOnly_r50s50.bed
108. bedtools shuffle -seed 1 -i SeqAOnly_r50s50.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r51s50.bed
109. sort -k1,1 -k2,2n ./SeqAOnly_r51s50.bed > ./SeqAOnly_r51s51.bed
110. bedtools shuffle -seed 1 -i SeqAOnly_r51s51.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r52s51.bed
111. sort -k1,1 -k2,2n ./SeqAOnly_r52s51.bed > ./SeqAOnly_r52s52.bed
112. bedtools shuffle -seed 1 -i SeqAOnly_r52s52.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r53s52.bed
113. sort -k1,1 -k2,2n ./SeqAOnly_r53s52.bed > ./SeqAOnly_r53s53.bed
114. bedtools shuffle -seed 1 -i SeqAOnly_r53s53.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r54s53.bed
115. sort -k1,1 -k2,2n ./SeqAOnly_r54s53.bed > ./SeqAOnly_r54s54.bed

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116. bedtools shuffle -seed 1 -i SeqAOnly_r54s54.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r55s54.bed
117. sort -k1,1 -k2,2n ./SeqAOnly_r55s54.bed > ./SeqAOnly_r55s55.bed
118. bedtools shuffle -seed 1 -i SeqAOnly_r55s55.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r56s55.bed
119. sort -k1,1 -k2,2n ./SeqAOnly_r56s55.bed > ./SeqAOnly_r56s56.bed
120. bedtools shuffle -seed 1 -i SeqAOnly_r56s56.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r57s56.bed
121. sort -k1,1 -k2,2n ./SeqAOnly_r57s56.bed > ./SeqAOnly_r57s57.bed
122. bedtools shuffle -seed 1 -i SeqAOnly_r57s57.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r58s57.bed
123. sort -k1,1 -k2,2n ./SeqAOnly_r58s57.bed > ./SeqAOnly_r58s58.bed
124. bedtools shuffle -seed 1 -i SeqAOnly_r58s58.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r59s58.bed
125. sort -k1,1 -k2,2n ./SeqAOnly_r59s58.bed > ./SeqAOnly_r59s59.bed
126. bedtools shuffle -seed 1 -i SeqAOnly_r59s59.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r60s59.bed
127. sort -k1,1 -k2,2n ./SeqAOnly_r60s59.bed > ./SeqAOnly_r60s60.bed
128. bedtools shuffle -seed 1 -i SeqAOnly_r60s60.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r61s60.bed
129. sort -k1,1 -k2,2n ./SeqAOnly_r61s60.bed > ./SeqAOnly_r61s61.bed
130. bedtools shuffle -seed 1 -i SeqAOnly_r61s61.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r62s61.bed
131. sort -k1,1 -k2,2n ./SeqAOnly_r62s61.bed > ./SeqAOnly_r62s62.bed
132. bedtools shuffle -seed 1 -i SeqAOnly_r62s62.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r63s62.bed
133. sort -k1,1 -k2,2n ./SeqAOnly_r63s62.bed > ./SeqAOnly_r63s63.bed
134. bedtools shuffle -seed 1 -i SeqAOnly_r63s63.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r64s63.bed
135. sort -k1,1 -k2,2n ./SeqAOnly_r64s63.bed > ./SeqAOnly_r64s64.bed
136. bedtools shuffle -seed 1 -i SeqAOnly_r64s64.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r65s64.bed
137. sort -k1,1 -k2,2n ./SeqAOnly_r65s64.bed > ./SeqAOnly_r65s65.bed
138. bedtools shuffle -seed 1 -i SeqAOnly_r65s65.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r66s65.bed
139. sort -k1,1 -k2,2n ./SeqAOnly_r66s65.bed > ./SeqAOnly_r66s66.bed
140. bedtools shuffle -seed 1 -i SeqAOnly_r66s66.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r67s66.bed
141. sort -k1,1 -k2,2n ./SeqAOnly_r67s66.bed > ./SeqAOnly_r67s67.bed
142. bedtools shuffle -seed 1 -i SeqAOnly_r67s67.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r68s67.bed
143. sort -k1,1 -k2,2n ./SeqAOnly_r68s67.bed > ./SeqAOnly_r68s68.bed
144. bedtools shuffle -seed 1 -i SeqAOnly_r68s68.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r69s68.bed
145. sort -k1,1 -k2,2n ./SeqAOnly_r69s68.bed > ./SeqAOnly_r69s69.bed
146. bedtools shuffle -seed 1 -i SeqAOnly_r69s69.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r70s69.bed
147. sort -k1,1 -k2,2n ./SeqAOnly_r70s69.bed > ./SeqAOnly_r70s70.bed
148. bedtools shuffle -seed 1 -i SeqAOnly_r70s70.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r71s70.bed
149. sort -k1,1 -k2,2n ./SeqAOnly_r71s70.bed > ./SeqAOnly_r71s71.bed
150. bedtools shuffle -seed 1 -i SeqAOnly_r71s71.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r72s71.bed
151. sort -k1,1 -k2,2n ./SeqAOnly_r72s71.bed > ./SeqAOnly_r72s72.bed
152. bedtools shuffle -seed 1 -i SeqAOnly_r72s72.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r73s72.bed

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153.      sort -k1,1 -k2,2n ./SeqAOnly_r73s72.bed > ./SeqAOnly_r73s73.bed
154.      bedtools shuffle -seed 1 -i SeqAOnly_r73s73.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r74s73.bed
155.      sort -k1,1 -k2,2n ./SeqAOnly_r74s73.bed > ./SeqAOnly_r74s74.bed
156.      bedtools shuffle -seed 1 -i SeqAOnly_r74s74.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r75s74.bed
157.      sort -k1,1 -k2,2n ./SeqAOnly_r75s74.bed > ./SeqAOnly_r75s75.bed
158.      bedtools shuffle -seed 1 -i SeqAOnly_r75s75.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r76s75.bed
159.      sort -k1,1 -k2,2n ./SeqAOnly_r76s75.bed > ./SeqAOnly_r76s76.bed
160.      bedtools shuffle -seed 1 -i SeqAOnly_r76s76.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r77s76.bed
161.      sort -k1,1 -k2,2n ./SeqAOnly_r77s76.bed > ./SeqAOnly_r77s77.bed
162.      bedtools shuffle -seed 1 -i SeqAOnly_r77s77.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r78s77.bed
163.      sort -k1,1 -k2,2n ./SeqAOnly_r78s77.bed > ./SeqAOnly_r78s78.bed
164.      bedtools shuffle -seed 1 -i SeqAOnly_r78s78.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r79s78.bed
165.      sort -k1,1 -k2,2n ./SeqAOnly_r79s78.bed > ./SeqAOnly_r79s79.bed
166.      bedtools shuffle -seed 1 -i SeqAOnly_r79s79.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r80s79.bed
167.      sort -k1,1 -k2,2n ./SeqAOnly_r80s79.bed > ./SeqAOnly_r80s80.bed
168.      bedtools shuffle -seed 1 -i SeqAOnly_r80s80.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r81s80.bed
169.      sort -k1,1 -k2,2n ./SeqAOnly_r81s80.bed > ./SeqAOnly_r81s81.bed
170.      bedtools shuffle -seed 1 -i SeqAOnly_r81s81.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r82s81.bed
171.      sort -k1,1 -k2,2n ./SeqAOnly_r82s81.bed > ./SeqAOnly_r82s82.bed
172.      bedtools shuffle -seed 1 -i SeqAOnly_r82s82.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r83s82.bed
173.      sort -k1,1 -k2,2n ./SeqAOnly_r83s82.bed > ./SeqAOnly_r83s83.bed
174.      bedtools shuffle -seed 1 -i SeqAOnly_r83s83.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r84s83.bed
175.      sort -k1,1 -k2,2n ./SeqAOnly_r84s83.bed > ./SeqAOnly_r84s84.bed
176.      bedtools shuffle -seed 1 -i SeqAOnly_r84s84.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r85s84.bed
177.      sort -k1,1 -k2,2n ./SeqAOnly_r85s84.bed > ./SeqAOnly_r85s85.bed
178.      bedtools shuffle -seed 1 -i SeqAOnly_r85s85.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r86s85.bed
179.      sort -k1,1 -k2,2n ./SeqAOnly_r86s85.bed > ./SeqAOnly_r86s86.bed
180.      bedtools shuffle -seed 1 -i SeqAOnly_r86s86.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r87s86.bed
181.      sort -k1,1 -k2,2n ./SeqAOnly_r87s86.bed > ./SeqAOnly_r87s87.bed
182.      bedtools shuffle -seed 1 -i SeqAOnly_r87s87.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r88s87.bed
183.      sort -k1,1 -k2,2n ./SeqAOnly_r88s87.bed > ./SeqAOnly_r88s88.bed
184.      bedtools shuffle -seed 1 -i SeqAOnly_r88s88.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r89s88.bed
185.      sort -k1,1 -k2,2n ./SeqAOnly_r89s88.bed > ./SeqAOnly_r89s89.bed
186.      bedtools shuffle -seed 1 -i SeqAOnly_r89s89.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r90s89.bed
187.      sort -k1,1 -k2,2n ./SeqAOnly_r90s89.bed > ./SeqAOnly_r90s90.bed
188.      bedtools shuffle -seed 1 -i SeqAOnly_r90s90.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r91s90.bed
189.      sort -k1,1 -k2,2n ./SeqAOnly_r91s90.bed > ./SeqAOnly_r91s91.bed
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190. bedtools shuffle -seed 1 -i SeqAOnly_r91s91.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r92s91.bed
191. sort -k1,1 -k2,2n ./SeqAOnly_r92s91.bed > ./SeqAOnly_r92s92.bed
192. bedtools shuffle -seed 1 -i SeqAOnly_r92s92.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r93s92.bed
193. sort -k1,1 -k2,2n ./SeqAOnly_r93s92.bed > ./SeqAOnly_r93s93.bed
194. bedtools shuffle -seed 1 -i SeqAOnly_r93s93.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r94s93.bed
195. sort -k1,1 -k2,2n ./SeqAOnly_r94s93.bed > ./SeqAOnly_r94s94.bed
196. bedtools shuffle -seed 1 -i SeqAOnly_r94s94.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r95s94.bed
197. sort -k1,1 -k2,2n ./SeqAOnly_r95s94.bed > ./SeqAOnly_r95s95.bed
198. bedtools shuffle -seed 1 -i SeqAOnly_r95s95.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r96s95.bed
199. sort -k1,1 -k2,2n ./SeqAOnly_r96s95.bed > ./SeqAOnly_r96s96.bed
200. bedtools shuffle -seed 1 -i SeqAOnly_r96s96.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r97s96.bed
201. sort -k1,1 -k2,2n ./SeqAOnly_r97s96.bed > ./SeqAOnly_r97s97.bed
202. bedtools shuffle -seed 1 -i SeqAOnly_r97s97.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r98s97.bed
203. sort -k1,1 -k2,2n ./SeqAOnly_r98s97.bed > ./SeqAOnly_r98s98.bed
204. bedtools shuffle -seed 1 -i SeqAOnly_r98s98.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r99s98.bed
205. sort -k1,1 -k2,2n ./SeqAOnly_r99s98.bed > ./SeqAOnly_r99s99.bed
206. bedtools shuffle -seed 1 -i SeqAOnly_r99s99.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r100s99.bed
207. sort -k1,1 -k2,2n ./SeqAOnly_r100s99.bed > ./SeqAOnly_r100s100.bed
208. bedtools shuffle -seed 1 -i SeqAOnly_r100s100.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r101s100.bed
209. sort -k1,1 -k2,2n ./SeqAOnly_r101s100.bed > ./SeqAOnly_r101s101.bed
210. bedtools shuffle -seed 1 -i SeqAOnly_r101s101.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r102s101.bed
211. sort -k1,1 -k2,2n ./SeqAOnly_r102s101.bed > ./SeqAOnly_r102s102.bed
212. bedtools shuffle -seed 1 -i SeqAOnly_r102s102.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r103s102.bed
213. sort -k1,1 -k2,2n ./SeqAOnly_r103s102.bed > ./SeqAOnly_r103s103.bed
214. bedtools shuffle -seed 1 -i SeqAOnly_r103s103.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r104s103.bed
215. sort -k1,1 -k2,2n ./SeqAOnly_r104s103.bed > ./SeqAOnly_r104s104.bed
216. bedtools shuffle -seed 1 -i SeqAOnly_r104s104.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r105s104.bed
217. sort -k1,1 -k2,2n ./SeqAOnly_r105s104.bed > ./SeqAOnly_r105s105.bed
218. bedtools shuffle -seed 1 -i SeqAOnly_r105s105.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r106s105.bed
219. sort -k1,1 -k2,2n ./SeqAOnly_r106s105.bed > ./SeqAOnly_r106s106.bed
220. bedtools shuffle -seed 1 -i SeqAOnly_r106s106.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r107s106.bed
221. sort -k1,1 -k2,2n ./SeqAOnly_r107s106.bed > ./SeqAOnly_r107s107.bed
222. bedtools shuffle -seed 1 -i SeqAOnly_r107s107.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r108s107.bed
223. sort -k1,1 -k2,2n ./SeqAOnly_r108s107.bed > ./SeqAOnly_r108s108.bed
224. bedtools shuffle -seed 1 -i SeqAOnly_r108s108.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r109s108.bed
225. sort -k1,1 -k2,2n ./SeqAOnly_r109s108.bed > ./SeqAOnly_r109s109.bed
226. bedtools shuffle -seed 1 -i SeqAOnly_r109s109.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r110s109.bed

```

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227.      sort -k1,1 -k2,2n ./SeqAOnly_r110s109.bed > ./SeqAOnly_r110s110.bed
228.      bedtools shuffle -seed 1 -i SeqAOnly_r110s110.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r111s110.bed
229.      sort -k1,1 -k2,2n ./SeqAOnly_r111s110.bed > ./SeqAOnly_r111s111.bed
230.      bedtools shuffle -seed 1 -i SeqAOnly_r111s111.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r112s111.bed
231.      sort -k1,1 -k2,2n ./SeqAOnly_r112s111.bed > ./SeqAOnly_r112s112.bed
232.      bedtools shuffle -seed 1 -i SeqAOnly_r112s112.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r113s112.bed
233.      sort -k1,1 -k2,2n ./SeqAOnly_r113s112.bed > ./SeqAOnly_r113s113.bed
234.      bedtools shuffle -seed 1 -i SeqAOnly_r113s113.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r114s113.bed
235.      sort -k1,1 -k2,2n ./SeqAOnly_r114s113.bed > ./SeqAOnly_r114s114.bed
236.      bedtools shuffle -seed 1 -i SeqAOnly_r114s114.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r115s114.bed
237.      sort -k1,1 -k2,2n ./SeqAOnly_r115s114.bed > ./SeqAOnly_r115s115.bed
238.      bedtools shuffle -seed 1 -i SeqAOnly_r115s115.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r116s115.bed
239.      sort -k1,1 -k2,2n ./SeqAOnly_r116s115.bed > ./SeqAOnly_r116s116.bed
240.      bedtools shuffle -seed 1 -i SeqAOnly_r116s116.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r117s116.bed
241.      sort -k1,1 -k2,2n ./SeqAOnly_r117s116.bed > ./SeqAOnly_r117s117.bed
242.      bedtools shuffle -seed 1 -i SeqAOnly_r117s117.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r118s117.bed
243.      sort -k1,1 -k2,2n ./SeqAOnly_r118s117.bed > ./SeqAOnly_r118s118.bed
244.      bedtools shuffle -seed 1 -i SeqAOnly_r118s118.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r119s118.bed
245.      sort -k1,1 -k2,2n ./SeqAOnly_r119s118.bed > ./SeqAOnly_r119s119.bed
246.      bedtools shuffle -seed 1 -i SeqAOnly_r119s119.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r120s119.bed
247.      sort -k1,1 -k2,2n ./SeqAOnly_r120s119.bed > ./SeqAOnly_r120s120.bed
248.      bedtools shuffle -seed 1 -i SeqAOnly_r120s120.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r121s120.bed
249.      sort -k1,1 -k2,2n ./SeqAOnly_r121s120.bed > ./SeqAOnly_r121s121.bed
250.      bedtools shuffle -seed 1 -i SeqAOnly_r121s121.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r122s121.bed
251.      sort -k1,1 -k2,2n ./SeqAOnly_r122s121.bed > ./SeqAOnly_r122s122.bed
252.      bedtools shuffle -seed 1 -i SeqAOnly_r122s122.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r123s122.bed
253.      sort -k1,1 -k2,2n ./SeqAOnly_r123s122.bed > ./SeqAOnly_r123s123.bed
254.      bedtools shuffle -seed 1 -i SeqAOnly_r123s123.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r124s123.bed
255.      sort -k1,1 -k2,2n ./SeqAOnly_r124s123.bed > ./SeqAOnly_r124s124.bed
256.      bedtools shuffle -seed 1 -i SeqAOnly_r124s124.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r125s124.bed
257.      sort -k1,1 -k2,2n ./SeqAOnly_r125s124.bed > ./SeqAOnly_r125s125.bed
258.      bedtools shuffle -seed 1 -i SeqAOnly_r125s125.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r126s125.bed
259.      sort -k1,1 -k2,2n ./SeqAOnly_r126s125.bed > ./SeqAOnly_r126s126.bed
260.      bedtools shuffle -seed 1 -i SeqAOnly_r126s126.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r127s126.bed
261.      sort -k1,1 -k2,2n ./SeqAOnly_r127s126.bed > ./SeqAOnly_r127s127.bed
262.      bedtools shuffle -seed 1 -i SeqAOnly_r127s127.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r128s127.bed
263.      sort -k1,1 -k2,2n ./SeqAOnly_r128s127.bed > ./SeqAOnly_r128s128.bed
```

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264.     bedtools shuffle -seed 1 -i SeqAOnly_r128s128.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r129s128.bed
265.     sort -k1,1 -k2,2n ./SeqAOnly_r129s128.bed > ./SeqAOnly_r129s129.bed
266.     bedtools shuffle -seed 1 -i SeqAOnly_r129s129.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r130s129.bed
267.     sort -k1,1 -k2,2n ./SeqAOnly_r130s129.bed > ./SeqAOnly_r130s130.bed
268.     bedtools shuffle -seed 1 -i SeqAOnly_r130s130.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r131s130.bed
269.     sort -k1,1 -k2,2n ./SeqAOnly_r131s130.bed > ./SeqAOnly_r131s131.bed
270.     bedtools shuffle -seed 1 -i SeqAOnly_r131s131.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r132s131.bed
271.     sort -k1,1 -k2,2n ./SeqAOnly_r132s131.bed > ./SeqAOnly_r132s132.bed
272.     bedtools shuffle -seed 1 -i SeqAOnly_r132s132.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r133s132.bed
273.     sort -k1,1 -k2,2n ./SeqAOnly_r133s132.bed > ./SeqAOnly_r133s133.bed
274.     bedtools shuffle -seed 1 -i SeqAOnly_r133s133.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r134s133.bed
275.     sort -k1,1 -k2,2n ./SeqAOnly_r134s133.bed > ./SeqAOnly_r134s134.bed
276.     bedtools shuffle -seed 1 -i SeqAOnly_r134s134.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r135s134.bed
277.     sort -k1,1 -k2,2n ./SeqAOnly_r135s134.bed > ./SeqAOnly_r135s135.bed
278.     bedtools shuffle -seed 1 -i SeqAOnly_r135s135.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r136s135.bed
279.     sort -k1,1 -k2,2n ./SeqAOnly_r136s135.bed > ./SeqAOnly_r136s136.bed
280.     bedtools shuffle -seed 1 -i SeqAOnly_r136s136.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r137s136.bed
281.     sort -k1,1 -k2,2n ./SeqAOnly_r137s136.bed > ./SeqAOnly_r137s137.bed
282.     bedtools shuffle -seed 1 -i SeqAOnly_r137s137.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r138s137.bed
283.     sort -k1,1 -k2,2n ./SeqAOnly_r138s137.bed > ./SeqAOnly_r138s138.bed
284.     bedtools shuffle -seed 1 -i SeqAOnly_r138s138.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r139s138.bed
285.     sort -k1,1 -k2,2n ./SeqAOnly_r139s138.bed > ./SeqAOnly_r139s139.bed
286.     bedtools shuffle -seed 1 -i SeqAOnly_r139s139.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r140s139.bed
287.     sort -k1,1 -k2,2n ./SeqAOnly_r140s139.bed > ./SeqAOnly_r140s140.bed
288.     bedtools shuffle -seed 1 -i SeqAOnly_r140s140.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r141s140.bed
289.     sort -k1,1 -k2,2n ./SeqAOnly_r141s140.bed > ./SeqAOnly_r141s141.bed
290.     bedtools shuffle -seed 1 -i SeqAOnly_r141s141.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r142s141.bed
291.     sort -k1,1 -k2,2n ./SeqAOnly_r142s141.bed > ./SeqAOnly_r142s142.bed
292.     bedtools shuffle -seed 1 -i SeqAOnly_r142s142.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r143s142.bed
293.     sort -k1,1 -k2,2n ./SeqAOnly_r143s142.bed > ./SeqAOnly_r143s143.bed
294.     bedtools shuffle -seed 1 -i SeqAOnly_r143s143.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r144s143.bed
295.     sort -k1,1 -k2,2n ./SeqAOnly_r144s143.bed > ./SeqAOnly_r144s144.bed
296.     bedtools shuffle -seed 1 -i SeqAOnly_r144s144.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r145s144.bed
297.     sort -k1,1 -k2,2n ./SeqAOnly_r145s144.bed > ./SeqAOnly_r145s145.bed
298.     bedtools shuffle -seed 1 -i SeqAOnly_r145s145.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r146s145.bed
299.     sort -k1,1 -k2,2n ./SeqAOnly_r146s145.bed > ./SeqAOnly_r146s146.bed
300.     bedtools shuffle -seed 1 -i SeqAOnly_r146s146.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r147s146.bed

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301.      sort -k1,1 -k2,2n ./SeqAOnly_r147s146.bed > ./SeqAOnly_r147s147.bed
302.      bedtools shuffle -seed 1 -i SeqAOnly_r147s147.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r148s147.bed
303.      sort -k1,1 -k2,2n ./SeqAOnly_r148s147.bed > ./SeqAOnly_r148s148.bed
304.      bedtools shuffle -seed 1 -i SeqAOnly_r148s148.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r149s148.bed
305.      sort -k1,1 -k2,2n ./SeqAOnly_r149s148.bed > ./SeqAOnly_r149s149.bed
306.      bedtools shuffle -seed 1 -i SeqAOnly_r149s149.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r150s149.bed
307.      sort -k1,1 -k2,2n ./SeqAOnly_r150s149.bed > ./SeqAOnly_r150s150.bed
308.      bedtools shuffle -seed 1 -i SeqAOnly_r150s150.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r151s150.bed
309.      sort -k1,1 -k2,2n ./SeqAOnly_r151s150.bed > ./SeqAOnly_r151s151.bed
310.      bedtools shuffle -seed 1 -i SeqAOnly_r151s151.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r152s151.bed
311.      sort -k1,1 -k2,2n ./SeqAOnly_r152s151.bed > ./SeqAOnly_r152s152.bed
312.      bedtools shuffle -seed 1 -i SeqAOnly_r152s152.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r153s152.bed
313.      sort -k1,1 -k2,2n ./SeqAOnly_r153s152.bed > ./SeqAOnly_r153s153.bed
314.      bedtools shuffle -seed 1 -i SeqAOnly_r153s153.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r154s153.bed
315.      sort -k1,1 -k2,2n ./SeqAOnly_r154s153.bed > ./SeqAOnly_r154s154.bed
316.      bedtools shuffle -seed 1 -i SeqAOnly_r154s154.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r155s154.bed
317.      sort -k1,1 -k2,2n ./SeqAOnly_r155s154.bed > ./SeqAOnly_r155s155.bed
318.      bedtools shuffle -seed 1 -i SeqAOnly_r155s155.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r156s155.bed
319.      sort -k1,1 -k2,2n ./SeqAOnly_r156s155.bed > ./SeqAOnly_r156s156.bed
320.      bedtools shuffle -seed 1 -i SeqAOnly_r156s156.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r157s156.bed
321.      sort -k1,1 -k2,2n ./SeqAOnly_r157s156.bed > ./SeqAOnly_r157s157.bed
322.      bedtools shuffle -seed 1 -i SeqAOnly_r157s157.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r158s157.bed
323.      sort -k1,1 -k2,2n ./SeqAOnly_r158s157.bed > ./SeqAOnly_r158s158.bed
324.      bedtools shuffle -seed 1 -i SeqAOnly_r158s158.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r159s158.bed
325.      sort -k1,1 -k2,2n ./SeqAOnly_r159s158.bed > ./SeqAOnly_r159s159.bed
326.      bedtools shuffle -seed 1 -i SeqAOnly_r159s159.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r160s159.bed
327.      sort -k1,1 -k2,2n ./SeqAOnly_r160s159.bed > ./SeqAOnly_r160s160.bed
328.      bedtools shuffle -seed 1 -i SeqAOnly_r160s160.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r161s160.bed
329.      sort -k1,1 -k2,2n ./SeqAOnly_r161s160.bed > ./SeqAOnly_r161s161.bed
330.      bedtools shuffle -seed 1 -i SeqAOnly_r161s161.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r162s161.bed
331.      sort -k1,1 -k2,2n ./SeqAOnly_r162s161.bed > ./SeqAOnly_r162s162.bed
332.      bedtools shuffle -seed 1 -i SeqAOnly_r162s162.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r163s162.bed
333.      sort -k1,1 -k2,2n ./SeqAOnly_r163s162.bed > ./SeqAOnly_r163s163.bed
334.      bedtools shuffle -seed 1 -i SeqAOnly_r163s163.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r164s163.bed
335.      sort -k1,1 -k2,2n ./SeqAOnly_r164s163.bed > ./SeqAOnly_r164s164.bed
336.      bedtools shuffle -seed 1 -i SeqAOnly_r164s164.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r165s164.bed
337.      sort -k1,1 -k2,2n ./SeqAOnly_r165s164.bed > ./SeqAOnly_r165s165.bed
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338. bedtools shuffle -seed 1 -i SeqAOnly_r165s165.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r166s165.bed
339. sort -k1,1 -k2,2n ./SeqAOnly_r166s165.bed > ./SeqAOnly_r166s166.bed
340. bedtools shuffle -seed 1 -i SeqAOnly_r166s166.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r167s166.bed
341. sort -k1,1 -k2,2n ./SeqAOnly_r167s166.bed > ./SeqAOnly_r167s167.bed
342. bedtools shuffle -seed 1 -i SeqAOnly_r167s167.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r168s167.bed
343. sort -k1,1 -k2,2n ./SeqAOnly_r168s167.bed > ./SeqAOnly_r168s168.bed
344. bedtools shuffle -seed 1 -i SeqAOnly_r168s168.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r169s168.bed
345. sort -k1,1 -k2,2n ./SeqAOnly_r169s168.bed > ./SeqAOnly_r169s169.bed
346. bedtools shuffle -seed 1 -i SeqAOnly_r169s169.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r170s169.bed
347. sort -k1,1 -k2,2n ./SeqAOnly_r170s169.bed > ./SeqAOnly_r170s170.bed
348. bedtools shuffle -seed 1 -i SeqAOnly_r170s170.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r171s170.bed
349. sort -k1,1 -k2,2n ./SeqAOnly_r171s170.bed > ./SeqAOnly_r171s171.bed
350. bedtools shuffle -seed 1 -i SeqAOnly_r171s171.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r172s171.bed
351. sort -k1,1 -k2,2n ./SeqAOnly_r172s171.bed > ./SeqAOnly_r172s172.bed
352. bedtools shuffle -seed 1 -i SeqAOnly_r172s172.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r173s172.bed
353. sort -k1,1 -k2,2n ./SeqAOnly_r173s172.bed > ./SeqAOnly_r173s173.bed
354. bedtools shuffle -seed 1 -i SeqAOnly_r173s173.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r174s173.bed
355. sort -k1,1 -k2,2n ./SeqAOnly_r174s173.bed > ./SeqAOnly_r174s174.bed
356. bedtools shuffle -seed 1 -i SeqAOnly_r174s174.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r175s174.bed
357. sort -k1,1 -k2,2n ./SeqAOnly_r175s174.bed > ./SeqAOnly_r175s175.bed
358. bedtools shuffle -seed 1 -i SeqAOnly_r175s175.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r176s175.bed
359. sort -k1,1 -k2,2n ./SeqAOnly_r176s175.bed > ./SeqAOnly_r176s176.bed
360. bedtools shuffle -seed 1 -i SeqAOnly_r176s176.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r177s176.bed
361. sort -k1,1 -k2,2n ./SeqAOnly_r177s176.bed > ./SeqAOnly_r177s177.bed
362. bedtools shuffle -seed 1 -i SeqAOnly_r177s177.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r178s177.bed
363. sort -k1,1 -k2,2n ./SeqAOnly_r178s177.bed > ./SeqAOnly_r178s178.bed
364. bedtools shuffle -seed 1 -i SeqAOnly_r178s178.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r179s178.bed
365. sort -k1,1 -k2,2n ./SeqAOnly_r179s178.bed > ./SeqAOnly_r179s179.bed
366. bedtools shuffle -seed 1 -i SeqAOnly_r179s179.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r180s179.bed
367. sort -k1,1 -k2,2n ./SeqAOnly_r180s179.bed > ./SeqAOnly_r180s180.bed
368. bedtools shuffle -seed 1 -i SeqAOnly_r180s180.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r181s180.bed
369. sort -k1,1 -k2,2n ./SeqAOnly_r181s180.bed > ./SeqAOnly_r181s181.bed
370. bedtools shuffle -seed 1 -i SeqAOnly_r181s181.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r182s181.bed
371. sort -k1,1 -k2,2n ./SeqAOnly_r182s181.bed > ./SeqAOnly_r182s182.bed
372. bedtools shuffle -seed 1 -i SeqAOnly_r182s182.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r183s182.bed
373. sort -k1,1 -k2,2n ./SeqAOnly_r183s182.bed > ./SeqAOnly_r183s183.bed
374. bedtools shuffle -seed 1 -i SeqAOnly_r183s183.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r184s183.bed
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375.      sort -k1,1 -k2,2n ./SeqAOnly_r184s183.bed > ./SeqAOnly_r184s184.bed
376.      bedtools shuffle -seed 1 -i SeqAOnly_r184s184.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r185s184.bed
377.      sort -k1,1 -k2,2n ./SeqAOnly_r185s184.bed > ./SeqAOnly_r185s185.bed
378.      bedtools shuffle -seed 1 -i SeqAOnly_r185s185.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r186s185.bed
379.      sort -k1,1 -k2,2n ./SeqAOnly_r186s185.bed > ./SeqAOnly_r186s186.bed
380.      bedtools shuffle -seed 1 -i SeqAOnly_r186s186.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r187s186.bed
381.      sort -k1,1 -k2,2n ./SeqAOnly_r187s186.bed > ./SeqAOnly_r187s187.bed
382.      bedtools shuffle -seed 1 -i SeqAOnly_r187s187.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r188s187.bed
383.      sort -k1,1 -k2,2n ./SeqAOnly_r188s187.bed > ./SeqAOnly_r188s188.bed
384.      bedtools shuffle -seed 1 -i SeqAOnly_r188s188.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r189s188.bed
385.      sort -k1,1 -k2,2n ./SeqAOnly_r189s188.bed > ./SeqAOnly_r189s189.bed
386.      bedtools shuffle -seed 1 -i SeqAOnly_r189s189.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r190s189.bed
387.      sort -k1,1 -k2,2n ./SeqAOnly_r190s189.bed > ./SeqAOnly_r190s190.bed
388.      bedtools shuffle -seed 1 -i SeqAOnly_r190s190.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r191s190.bed
389.      sort -k1,1 -k2,2n ./SeqAOnly_r191s190.bed > ./SeqAOnly_r191s191.bed
390.      bedtools shuffle -seed 1 -i SeqAOnly_r191s191.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r192s191.bed
391.      sort -k1,1 -k2,2n ./SeqAOnly_r192s191.bed > ./SeqAOnly_r192s192.bed
392.      bedtools shuffle -seed 1 -i SeqAOnly_r192s192.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r193s192.bed
393.      sort -k1,1 -k2,2n ./SeqAOnly_r193s192.bed > ./SeqAOnly_r193s193.bed
394.      bedtools shuffle -seed 1 -i SeqAOnly_r193s193.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r194s193.bed
395.      sort -k1,1 -k2,2n ./SeqAOnly_r194s193.bed > ./SeqAOnly_r194s194.bed
396.      bedtools shuffle -seed 1 -i SeqAOnly_r194s194.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r195s194.bed
397.      sort -k1,1 -k2,2n ./SeqAOnly_r195s194.bed > ./SeqAOnly_r195s195.bed
398.      bedtools shuffle -seed 1 -i SeqAOnly_r195s195.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r196s195.bed
399.      sort -k1,1 -k2,2n ./SeqAOnly_r196s195.bed > ./SeqAOnly_r196s196.bed
400.      bedtools shuffle -seed 1 -i SeqAOnly_r196s196.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r197s196.bed
401.      sort -k1,1 -k2,2n ./SeqAOnly_r197s196.bed > ./SeqAOnly_r197s197.bed
402.      bedtools shuffle -seed 1 -i SeqAOnly_r197s197.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r198s197.bed
403.      sort -k1,1 -k2,2n ./SeqAOnly_r198s197.bed > ./SeqAOnly_r198s198.bed
404.      bedtools shuffle -seed 1 -i SeqAOnly_r198s198.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r199s198.bed
405.      sort -k1,1 -k2,2n ./SeqAOnly_r199s198.bed > ./SeqAOnly_r199s199.bed
406.      bedtools shuffle -seed 1 -i SeqAOnly_r199s199.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r200s199.bed
407.      sort -k1,1 -k2,2n ./SeqAOnly_r200s199.bed > ./SeqAOnly_r200s200.bed
408.      bedtools shuffle -seed 1 -i SeqAOnly_r200s200.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r201s200.bed
409.      sort -k1,1 -k2,2n ./SeqAOnly_r201s200.bed > ./SeqAOnly_r201s201.bed
410.      bedtools shuffle -seed 1 -i SeqAOnly_r201s201.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r202s201.bed
411.      sort -k1,1 -k2,2n ./SeqAOnly_r202s201.bed > ./SeqAOnly_r202s202.bed
```

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412. bedtools shuffle -seed 1 -i SeqAOnly_r202s202.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r203s202.bed
413. sort -k1,1 -k2,2n ./SeqAOnly_r203s202.bed > ./SeqAOnly_r203s203.bed
414. bedtools shuffle -seed 1 -i SeqAOnly_r203s203.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r204s203.bed
415. sort -k1,1 -k2,2n ./SeqAOnly_r204s203.bed > ./SeqAOnly_r204s204.bed
416. bedtools shuffle -seed 1 -i SeqAOnly_r204s204.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r205s204.bed
417. sort -k1,1 -k2,2n ./SeqAOnly_r205s204.bed > ./SeqAOnly_r205s205.bed
418. bedtools shuffle -seed 1 -i SeqAOnly_r205s205.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r206s205.bed
419. sort -k1,1 -k2,2n ./SeqAOnly_r206s205.bed > ./SeqAOnly_r206s206.bed
420. bedtools shuffle -seed 1 -i SeqAOnly_r206s206.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r207s206.bed
421. sort -k1,1 -k2,2n ./SeqAOnly_r207s206.bed > ./SeqAOnly_r207s207.bed
422. bedtools shuffle -seed 1 -i SeqAOnly_r207s207.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r208s207.bed
423. sort -k1,1 -k2,2n ./SeqAOnly_r208s207.bed > ./SeqAOnly_r208s208.bed
424. bedtools shuffle -seed 1 -i SeqAOnly_r208s208.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r209s208.bed
425. sort -k1,1 -k2,2n ./SeqAOnly_r209s208.bed > ./SeqAOnly_r209s209.bed
426. bedtools shuffle -seed 1 -i SeqAOnly_r209s209.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r210s209.bed
427. sort -k1,1 -k2,2n ./SeqAOnly_r210s209.bed > ./SeqAOnly_r210s210.bed
428. bedtools shuffle -seed 1 -i SeqAOnly_r210s210.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r211s210.bed
429. sort -k1,1 -k2,2n ./SeqAOnly_r211s210.bed > ./SeqAOnly_r211s211.bed
430. bedtools shuffle -seed 1 -i SeqAOnly_r211s211.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r212s211.bed
431. sort -k1,1 -k2,2n ./SeqAOnly_r212s211.bed > ./SeqAOnly_r212s212.bed
432. bedtools shuffle -seed 1 -i SeqAOnly_r212s212.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r213s212.bed
433. sort -k1,1 -k2,2n ./SeqAOnly_r213s212.bed > ./SeqAOnly_r213s213.bed
434. bedtools shuffle -seed 1 -i SeqAOnly_r213s213.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r214s213.bed
435. sort -k1,1 -k2,2n ./SeqAOnly_r214s213.bed > ./SeqAOnly_r214s214.bed
436. bedtools shuffle -seed 1 -i SeqAOnly_r214s214.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r215s214.bed
437. sort -k1,1 -k2,2n ./SeqAOnly_r215s214.bed > ./SeqAOnly_r215s215.bed
438. bedtools shuffle -seed 1 -i SeqAOnly_r215s215.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r216s215.bed
439. sort -k1,1 -k2,2n ./SeqAOnly_r216s215.bed > ./SeqAOnly_r216s216.bed
440. bedtools shuffle -seed 1 -i SeqAOnly_r216s216.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r217s216.bed
441. sort -k1,1 -k2,2n ./SeqAOnly_r217s216.bed > ./SeqAOnly_r217s217.bed
442. bedtools shuffle -seed 1 -i SeqAOnly_r217s217.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r218s217.bed
443. sort -k1,1 -k2,2n ./SeqAOnly_r218s217.bed > ./SeqAOnly_r218s218.bed
444. bedtools shuffle -seed 1 -i SeqAOnly_r218s218.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r219s218.bed
445. sort -k1,1 -k2,2n ./SeqAOnly_r219s218.bed > ./SeqAOnly_r219s219.bed
446. bedtools shuffle -seed 1 -i SeqAOnly_r219s219.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r220s219.bed
447. sort -k1,1 -k2,2n ./SeqAOnly_r220s219.bed > ./SeqAOnly_r220s220.bed
448. bedtools shuffle -seed 1 -i SeqAOnly_r220s220.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r221s220.bed
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449.      sort -k1,1 -k2,2n ./SeqAOnly_r221s220.bed > ./SeqAOnly_r221s221.bed
450.      bedtools shuffle -seed 1 -i SeqAOnly_r221s221.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r222s221.bed
451.      sort -k1,1 -k2,2n ./SeqAOnly_r222s221.bed > ./SeqAOnly_r222s222.bed
452.      bedtools shuffle -seed 1 -i SeqAOnly_r222s222.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r223s222.bed
453.      sort -k1,1 -k2,2n ./SeqAOnly_r223s222.bed > ./SeqAOnly_r223s223.bed
454.      bedtools shuffle -seed 1 -i SeqAOnly_r223s223.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r224s223.bed
455.      sort -k1,1 -k2,2n ./SeqAOnly_r224s223.bed > ./SeqAOnly_r224s224.bed
456.      bedtools shuffle -seed 1 -i SeqAOnly_r224s224.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r225s224.bed
457.      sort -k1,1 -k2,2n ./SeqAOnly_r225s224.bed > ./SeqAOnly_r225s225.bed
458.      bedtools shuffle -seed 1 -i SeqAOnly_r225s225.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r226s225.bed
459.      sort -k1,1 -k2,2n ./SeqAOnly_r226s225.bed > ./SeqAOnly_r226s226.bed
460.      bedtools shuffle -seed 1 -i SeqAOnly_r226s226.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r227s226.bed
461.      sort -k1,1 -k2,2n ./SeqAOnly_r227s226.bed > ./SeqAOnly_r227s227.bed
462.      bedtools shuffle -seed 1 -i SeqAOnly_r227s227.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r228s227.bed
463.      sort -k1,1 -k2,2n ./SeqAOnly_r228s227.bed > ./SeqAOnly_r228s228.bed
464.      bedtools shuffle -seed 1 -i SeqAOnly_r228s228.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r229s228.bed
465.      sort -k1,1 -k2,2n ./SeqAOnly_r229s228.bed > ./SeqAOnly_r229s229.bed
466.      bedtools shuffle -seed 1 -i SeqAOnly_r229s229.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r230s229.bed
467.      sort -k1,1 -k2,2n ./SeqAOnly_r230s229.bed > ./SeqAOnly_r230s230.bed
468.      bedtools shuffle -seed 1 -i SeqAOnly_r230s230.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r231s230.bed
469.      sort -k1,1 -k2,2n ./SeqAOnly_r231s230.bed > ./SeqAOnly_r231s231.bed
470.      bedtools shuffle -seed 1 -i SeqAOnly_r231s231.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r232s231.bed
471.      sort -k1,1 -k2,2n ./SeqAOnly_r232s231.bed > ./SeqAOnly_r232s232.bed
472.      bedtools shuffle -seed 1 -i SeqAOnly_r232s232.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r233s232.bed
473.      sort -k1,1 -k2,2n ./SeqAOnly_r233s232.bed > ./SeqAOnly_r233s233.bed
474.      bedtools shuffle -seed 1 -i SeqAOnly_r233s233.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r234s233.bed
475.      sort -k1,1 -k2,2n ./SeqAOnly_r234s233.bed > ./SeqAOnly_r234s234.bed
476.      bedtools shuffle -seed 1 -i SeqAOnly_r234s234.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r235s234.bed
477.      sort -k1,1 -k2,2n ./SeqAOnly_r235s234.bed > ./SeqAOnly_r235s235.bed
478.      bedtools shuffle -seed 1 -i SeqAOnly_r235s235.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r236s235.bed
479.      sort -k1,1 -k2,2n ./SeqAOnly_r236s235.bed > ./SeqAOnly_r236s236.bed
480.      bedtools shuffle -seed 1 -i SeqAOnly_r236s236.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r237s236.bed
481.      sort -k1,1 -k2,2n ./SeqAOnly_r237s236.bed > ./SeqAOnly_r237s237.bed
482.      bedtools shuffle -seed 1 -i SeqAOnly_r237s237.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r238s237.bed
483.      sort -k1,1 -k2,2n ./SeqAOnly_r238s237.bed > ./SeqAOnly_r238s238.bed
484.      bedtools shuffle -seed 1 -i SeqAOnly_r238s238.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r239s238.bed
485.      sort -k1,1 -k2,2n ./SeqAOnly_r239s238.bed > ./SeqAOnly_r239s239.bed
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486.      bedtools shuffle -seed 1 -i SeqAOnly_r239s239.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r240s239.bed
487.      sort -k1,1 -k2,2n ./SeqAOnly_r240s239.bed > ./SeqAOnly_r240s240.bed
488.      bedtools shuffle -seed 1 -i SeqAOnly_r240s240.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r241s240.bed
489.      sort -k1,1 -k2,2n ./SeqAOnly_r241s240.bed > ./SeqAOnly_r241s241.bed
490.      bedtools shuffle -seed 1 -i SeqAOnly_r241s241.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r242s241.bed
491.      sort -k1,1 -k2,2n ./SeqAOnly_r242s241.bed > ./SeqAOnly_r242s242.bed
492.      bedtools shuffle -seed 1 -i SeqAOnly_r242s242.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r243s242.bed
493.      sort -k1,1 -k2,2n ./SeqAOnly_r243s242.bed > ./SeqAOnly_r243s243.bed
494.      bedtools shuffle -seed 1 -i SeqAOnly_r243s243.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r244s243.bed
495.      sort -k1,1 -k2,2n ./SeqAOnly_r244s243.bed > ./SeqAOnly_r244s244.bed
496.      bedtools shuffle -seed 1 -i SeqAOnly_r244s244.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r245s244.bed
497.      sort -k1,1 -k2,2n ./SeqAOnly_r245s244.bed > ./SeqAOnly_r245s245.bed
498.      bedtools shuffle -seed 1 -i SeqAOnly_r245s245.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r246s245.bed
499.      sort -k1,1 -k2,2n ./SeqAOnly_r246s245.bed > ./SeqAOnly_r246s246.bed
500.      bedtools shuffle -seed 1 -i SeqAOnly_r246s246.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r247s246.bed
501.      sort -k1,1 -k2,2n ./SeqAOnly_r247s246.bed > ./SeqAOnly_r247s247.bed
502.      bedtools shuffle -seed 1 -i SeqAOnly_r247s247.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r248s247.bed
503.      sort -k1,1 -k2,2n ./SeqAOnly_r248s247.bed > ./SeqAOnly_r248s248.bed
504.      bedtools shuffle -seed 1 -i SeqAOnly_r248s248.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r249s248.bed
505.      sort -k1,1 -k2,2n ./SeqAOnly_r249s248.bed > ./SeqAOnly_r249s249.bed
506.      bedtools shuffle -seed 1 -i SeqAOnly_r249s249.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r250s249.bed
507.      sort -k1,1 -k2,2n ./SeqAOnly_r250s249.bed > ./SeqAOnly_r250s250.bed
508.      bedtools shuffle -seed 1 -i SeqAOnly_r250s250.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r251s250.bed
509.      sort -k1,1 -k2,2n ./SeqAOnly_r251s250.bed > ./SeqAOnly_r251s251.bed
510.      bedtools shuffle -seed 1 -i SeqAOnly_r251s251.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r252s251.bed
511.      sort -k1,1 -k2,2n ./SeqAOnly_r252s251.bed > ./SeqAOnly_r252s252.bed
512.      bedtools shuffle -seed 1 -i SeqAOnly_r252s252.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r253s252.bed
513.      sort -k1,1 -k2,2n ./SeqAOnly_r253s252.bed > ./SeqAOnly_r253s253.bed
514.      bedtools shuffle -seed 1 -i SeqAOnly_r253s253.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r254s253.bed
515.      sort -k1,1 -k2,2n ./SeqAOnly_r254s253.bed > ./SeqAOnly_r254s254.bed
516.      bedtools shuffle -seed 1 -i SeqAOnly_r254s254.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r255s254.bed
517.      sort -k1,1 -k2,2n ./SeqAOnly_r255s254.bed > ./SeqAOnly_r255s255.bed
518.      bedtools shuffle -seed 1 -i SeqAOnly_r255s255.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r256s255.bed
519.      sort -k1,1 -k2,2n ./SeqAOnly_r256s255.bed > ./SeqAOnly_r256s256.bed
520.      bedtools shuffle -seed 1 -i SeqAOnly_r256s256.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r257s256.bed
521.      sort -k1,1 -k2,2n ./SeqAOnly_r257s256.bed > ./SeqAOnly_r257s257.bed
522.      bedtools shuffle -seed 1 -i SeqAOnly_r257s257.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r258s257.bed
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523.      sort -k1,1 -k2,2n ./SeqAOnly_r258s257.bed > ./SeqAOnly_r258s258.bed
524.      bedtools shuffle -seed 1 -i SeqAOnly_r258s258.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r259s258.bed
525.      sort -k1,1 -k2,2n ./SeqAOnly_r259s258.bed > ./SeqAOnly_r259s259.bed
526.      bedtools shuffle -seed 1 -i SeqAOnly_r259s259.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r260s259.bed
527.      sort -k1,1 -k2,2n ./SeqAOnly_r260s259.bed > ./SeqAOnly_r260s260.bed
528.      bedtools shuffle -seed 1 -i SeqAOnly_r260s260.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r261s260.bed
529.      sort -k1,1 -k2,2n ./SeqAOnly_r261s260.bed > ./SeqAOnly_r261s261.bed
530.      bedtools shuffle -seed 1 -i SeqAOnly_r261s261.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r262s261.bed
531.      sort -k1,1 -k2,2n ./SeqAOnly_r262s261.bed > ./SeqAOnly_r262s262.bed
532.      bedtools shuffle -seed 1 -i SeqAOnly_r262s262.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r263s262.bed
533.      sort -k1,1 -k2,2n ./SeqAOnly_r263s262.bed > ./SeqAOnly_r263s263.bed
534.      bedtools shuffle -seed 1 -i SeqAOnly_r263s263.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r264s263.bed
535.      sort -k1,1 -k2,2n ./SeqAOnly_r264s263.bed > ./SeqAOnly_r264s264.bed
536.      bedtools shuffle -seed 1 -i SeqAOnly_r264s264.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r265s264.bed
537.      sort -k1,1 -k2,2n ./SeqAOnly_r265s264.bed > ./SeqAOnly_r265s265.bed
538.      bedtools shuffle -seed 1 -i SeqAOnly_r265s265.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r266s265.bed
539.      sort -k1,1 -k2,2n ./SeqAOnly_r266s265.bed > ./SeqAOnly_r266s266.bed
540.      bedtools shuffle -seed 1 -i SeqAOnly_r266s266.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r267s266.bed
541.      sort -k1,1 -k2,2n ./SeqAOnly_r267s266.bed > ./SeqAOnly_r267s267.bed
542.      bedtools shuffle -seed 1 -i SeqAOnly_r267s267.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r268s267.bed
543.      sort -k1,1 -k2,2n ./SeqAOnly_r268s267.bed > ./SeqAOnly_r268s268.bed
544.      bedtools shuffle -seed 1 -i SeqAOnly_r268s268.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r269s268.bed
545.      sort -k1,1 -k2,2n ./SeqAOnly_r269s268.bed > ./SeqAOnly_r269s269.bed
546.      bedtools shuffle -seed 1 -i SeqAOnly_r269s269.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r270s269.bed
547.      sort -k1,1 -k2,2n ./SeqAOnly_r270s269.bed > ./SeqAOnly_r270s270.bed
548.      bedtools shuffle -seed 1 -i SeqAOnly_r270s270.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r271s270.bed
549.      sort -k1,1 -k2,2n ./SeqAOnly_r271s270.bed > ./SeqAOnly_r271s271.bed
550.      bedtools shuffle -seed 1 -i SeqAOnly_r271s271.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r272s271.bed
551.      sort -k1,1 -k2,2n ./SeqAOnly_r272s271.bed > ./SeqAOnly_r272s272.bed
552.      bedtools shuffle -seed 1 -i SeqAOnly_r272s272.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r273s272.bed
553.      sort -k1,1 -k2,2n ./SeqAOnly_r273s272.bed > ./SeqAOnly_r273s273.bed
554.      bedtools shuffle -seed 1 -i SeqAOnly_r273s273.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r274s273.bed
555.      sort -k1,1 -k2,2n ./SeqAOnly_r274s273.bed > ./SeqAOnly_r274s274.bed
556.      bedtools shuffle -seed 1 -i SeqAOnly_r274s274.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r275s274.bed
557.      sort -k1,1 -k2,2n ./SeqAOnly_r275s274.bed > ./SeqAOnly_r275s275.bed
558.      bedtools shuffle -seed 1 -i SeqAOnly_r275s275.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r276s275.bed
559.      sort -k1,1 -k2,2n ./SeqAOnly_r276s275.bed > ./SeqAOnly_r276s276.bed

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560. bedtools shuffle -seed 1 -i SeqAOnly_r276s276.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r277s276.bed
561. sort -k1,1 -k2,2n ./SeqAOnly_r277s276.bed > ./SeqAOnly_r277s277.bed
562. bedtools shuffle -seed 1 -i SeqAOnly_r277s277.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r278s277.bed
563. sort -k1,1 -k2,2n ./SeqAOnly_r278s277.bed > ./SeqAOnly_r278s278.bed
564. bedtools shuffle -seed 1 -i SeqAOnly_r278s278.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r279s278.bed
565. sort -k1,1 -k2,2n ./SeqAOnly_r279s278.bed > ./SeqAOnly_r279s279.bed
566. bedtools shuffle -seed 1 -i SeqAOnly_r279s279.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r280s279.bed
567. sort -k1,1 -k2,2n ./SeqAOnly_r280s279.bed > ./SeqAOnly_r280s280.bed
568. bedtools shuffle -seed 1 -i SeqAOnly_r280s280.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r281s280.bed
569. sort -k1,1 -k2,2n ./SeqAOnly_r281s280.bed > ./SeqAOnly_r281s281.bed
570. bedtools shuffle -seed 1 -i SeqAOnly_r281s281.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r282s281.bed
571. sort -k1,1 -k2,2n ./SeqAOnly_r282s281.bed > ./SeqAOnly_r282s282.bed
572. bedtools shuffle -seed 1 -i SeqAOnly_r282s282.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r283s282.bed
573. sort -k1,1 -k2,2n ./SeqAOnly_r283s282.bed > ./SeqAOnly_r283s283.bed
574. bedtools shuffle -seed 1 -i SeqAOnly_r283s283.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r284s283.bed
575. sort -k1,1 -k2,2n ./SeqAOnly_r284s283.bed > ./SeqAOnly_r284s284.bed
576. bedtools shuffle -seed 1 -i SeqAOnly_r284s284.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r285s284.bed
577. sort -k1,1 -k2,2n ./SeqAOnly_r285s284.bed > ./SeqAOnly_r285s285.bed
578. bedtools shuffle -seed 1 -i SeqAOnly_r285s285.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r286s285.bed
579. sort -k1,1 -k2,2n ./SeqAOnly_r286s285.bed > ./SeqAOnly_r286s286.bed
580. bedtools shuffle -seed 1 -i SeqAOnly_r286s286.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r287s286.bed
581. sort -k1,1 -k2,2n ./SeqAOnly_r287s286.bed > ./SeqAOnly_r287s287.bed
582. bedtools shuffle -seed 1 -i SeqAOnly_r287s287.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r288s287.bed
583. sort -k1,1 -k2,2n ./SeqAOnly_r288s287.bed > ./SeqAOnly_r288s288.bed
584. bedtools shuffle -seed 1 -i SeqAOnly_r288s288.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r289s288.bed
585. sort -k1,1 -k2,2n ./SeqAOnly_r289s288.bed > ./SeqAOnly_r289s289.bed
586. bedtools shuffle -seed 1 -i SeqAOnly_r289s289.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r290s289.bed
587. sort -k1,1 -k2,2n ./SeqAOnly_r290s289.bed > ./SeqAOnly_r290s290.bed
588. bedtools shuffle -seed 1 -i SeqAOnly_r290s290.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r291s290.bed
589. sort -k1,1 -k2,2n ./SeqAOnly_r291s290.bed > ./SeqAOnly_r291s291.bed
590. bedtools shuffle -seed 1 -i SeqAOnly_r291s291.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r292s291.bed
591. sort -k1,1 -k2,2n ./SeqAOnly_r292s291.bed > ./SeqAOnly_r292s292.bed
592. bedtools shuffle -seed 1 -i SeqAOnly_r292s292.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r293s292.bed
593. sort -k1,1 -k2,2n ./SeqAOnly_r293s292.bed > ./SeqAOnly_r293s293.bed
594. bedtools shuffle -seed 1 -i SeqAOnly_r293s293.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r294s293.bed
595. sort -k1,1 -k2,2n ./SeqAOnly_r294s293.bed > ./SeqAOnly_r294s294.bed
596. bedtools shuffle -seed 1 -i SeqAOnly_r294s294.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r295s294.bed

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597.      sort -k1,1 -k2,2n ./SeqAOnly_r295s294.bed > ./SeqAOnly_r295s295.bed
598.      bedtools shuffle -seed 1 -i SeqAOnly_r295s295.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r296s295.bed
599.      sort -k1,1 -k2,2n ./SeqAOnly_r296s295.bed > ./SeqAOnly_r296s296.bed
600.      bedtools shuffle -seed 1 -i SeqAOnly_r296s296.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r297s296.bed
601.      sort -k1,1 -k2,2n ./SeqAOnly_r297s296.bed > ./SeqAOnly_r297s297.bed
602.      bedtools shuffle -seed 1 -i SeqAOnly_r297s297.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r298s297.bed
603.      sort -k1,1 -k2,2n ./SeqAOnly_r298s297.bed > ./SeqAOnly_r298s298.bed
604.      bedtools shuffle -seed 1 -i SeqAOnly_r298s298.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r299s298.bed
605.      sort -k1,1 -k2,2n ./SeqAOnly_r299s298.bed > ./SeqAOnly_r299s299.bed
606.      bedtools shuffle -seed 1 -i SeqAOnly_r299s299.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r300s299.bed
607.      sort -k1,1 -k2,2n ./SeqAOnly_r300s299.bed > ./SeqAOnly_r300s300.bed
608.      bedtools shuffle -seed 1 -i SeqAOnly_r300s300.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r301s300.bed
609.      sort -k1,1 -k2,2n ./SeqAOnly_r301s300.bed > ./SeqAOnly_r301s301.bed
610.      bedtools shuffle -seed 1 -i SeqAOnly_r301s301.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r302s301.bed
611.      sort -k1,1 -k2,2n ./SeqAOnly_r302s301.bed > ./SeqAOnly_r302s302.bed
612.      bedtools shuffle -seed 1 -i SeqAOnly_r302s302.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r303s302.bed
613.      sort -k1,1 -k2,2n ./SeqAOnly_r303s302.bed > ./SeqAOnly_r303s303.bed
614.      bedtools shuffle -seed 1 -i SeqAOnly_r303s303.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r304s303.bed
615.      sort -k1,1 -k2,2n ./SeqAOnly_r304s303.bed > ./SeqAOnly_r304s304.bed
616.      bedtools shuffle -seed 1 -i SeqAOnly_r304s304.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r305s304.bed
617.      sort -k1,1 -k2,2n ./SeqAOnly_r305s304.bed > ./SeqAOnly_r305s305.bed
618.      bedtools shuffle -seed 1 -i SeqAOnly_r305s305.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r306s305.bed
619.      sort -k1,1 -k2,2n ./SeqAOnly_r306s305.bed > ./SeqAOnly_r306s306.bed
620.      bedtools shuffle -seed 1 -i SeqAOnly_r306s306.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r307s306.bed
621.      sort -k1,1 -k2,2n ./SeqAOnly_r307s306.bed > ./SeqAOnly_r307s307.bed
622.      bedtools shuffle -seed 1 -i SeqAOnly_r307s307.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r308s307.bed
623.      sort -k1,1 -k2,2n ./SeqAOnly_r308s307.bed > ./SeqAOnly_r308s308.bed
624.      bedtools shuffle -seed 1 -i SeqAOnly_r308s308.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r309s308.bed
625.      sort -k1,1 -k2,2n ./SeqAOnly_r309s308.bed > ./SeqAOnly_r309s309.bed
626.      bedtools shuffle -seed 1 -i SeqAOnly_r309s309.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r310s309.bed
627.      sort -k1,1 -k2,2n ./SeqAOnly_r310s309.bed > ./SeqAOnly_r310s310.bed
628.      bedtools shuffle -seed 1 -i SeqAOnly_r310s310.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r311s310.bed
629.      sort -k1,1 -k2,2n ./SeqAOnly_r311s310.bed > ./SeqAOnly_r311s311.bed
630.      bedtools shuffle -seed 1 -i SeqAOnly_r311s311.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r312s311.bed
631.      sort -k1,1 -k2,2n ./SeqAOnly_r312s311.bed > ./SeqAOnly_r312s312.bed
632.      bedtools shuffle -seed 1 -i SeqAOnly_r312s312.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r313s312.bed
633.      sort -k1,1 -k2,2n ./SeqAOnly_r313s312.bed > ./SeqAOnly_r313s313.bed
```

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634.     bedtools shuffle -seed 1 -i SeqAOnly_r313s313.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r314s313.bed
635.     sort -k1,1 -k2,2n ./SeqAOnly_r314s313.bed > ./SeqAOnly_r314s314.bed
636.     bedtools shuffle -seed 1 -i SeqAOnly_r314s314.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r315s314.bed
637.     sort -k1,1 -k2,2n ./SeqAOnly_r315s314.bed > ./SeqAOnly_r315s315.bed
638.     bedtools shuffle -seed 1 -i SeqAOnly_r315s315.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r316s315.bed
639.     sort -k1,1 -k2,2n ./SeqAOnly_r316s315.bed > ./SeqAOnly_r316s316.bed
640.     bedtools shuffle -seed 1 -i SeqAOnly_r316s316.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r317s316.bed
641.     sort -k1,1 -k2,2n ./SeqAOnly_r317s316.bed > ./SeqAOnly_r317s317.bed
642.     bedtools shuffle -seed 1 -i SeqAOnly_r317s317.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r318s317.bed
643.     sort -k1,1 -k2,2n ./SeqAOnly_r318s317.bed > ./SeqAOnly_r318s318.bed
644.     bedtools shuffle -seed 1 -i SeqAOnly_r318s318.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r319s318.bed
645.     sort -k1,1 -k2,2n ./SeqAOnly_r319s318.bed > ./SeqAOnly_r319s319.bed
646.     bedtools shuffle -seed 1 -i SeqAOnly_r319s319.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r320s319.bed
647.     sort -k1,1 -k2,2n ./SeqAOnly_r320s319.bed > ./SeqAOnly_r320s320.bed
648.     bedtools shuffle -seed 1 -i SeqAOnly_r320s320.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r321s320.bed
649.     sort -k1,1 -k2,2n ./SeqAOnly_r321s320.bed > ./SeqAOnly_r321s321.bed
650.     bedtools shuffle -seed 1 -i SeqAOnly_r321s321.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r322s321.bed
651.     sort -k1,1 -k2,2n ./SeqAOnly_r322s321.bed > ./SeqAOnly_r322s322.bed
652.     bedtools shuffle -seed 1 -i SeqAOnly_r322s322.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r323s322.bed
653.     sort -k1,1 -k2,2n ./SeqAOnly_r323s322.bed > ./SeqAOnly_r323s323.bed
654.     bedtools shuffle -seed 1 -i SeqAOnly_r323s323.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r324s323.bed
655.     sort -k1,1 -k2,2n ./SeqAOnly_r324s323.bed > ./SeqAOnly_r324s324.bed
656.     bedtools shuffle -seed 1 -i SeqAOnly_r324s324.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r325s324.bed
657.     sort -k1,1 -k2,2n ./SeqAOnly_r325s324.bed > ./SeqAOnly_r325s325.bed
658.     bedtools shuffle -seed 1 -i SeqAOnly_r325s325.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r326s325.bed
659.     sort -k1,1 -k2,2n ./SeqAOnly_r326s325.bed > ./SeqAOnly_r326s326.bed
660.     bedtools shuffle -seed 1 -i SeqAOnly_r326s326.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r327s326.bed
661.     sort -k1,1 -k2,2n ./SeqAOnly_r327s326.bed > ./SeqAOnly_r327s327.bed
662.     bedtools shuffle -seed 1 -i SeqAOnly_r327s327.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r328s327.bed
663.     sort -k1,1 -k2,2n ./SeqAOnly_r328s327.bed > ./SeqAOnly_r328s328.bed
664.     bedtools shuffle -seed 1 -i SeqAOnly_r328s328.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r329s328.bed
665.     sort -k1,1 -k2,2n ./SeqAOnly_r329s328.bed > ./SeqAOnly_r329s329.bed
666.     bedtools shuffle -seed 1 -i SeqAOnly_r329s329.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r330s329.bed
667.     sort -k1,1 -k2,2n ./SeqAOnly_r330s329.bed > ./SeqAOnly_r330s330.bed
668.     bedtools shuffle -seed 1 -i SeqAOnly_r330s330.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r331s330.bed
669.     sort -k1,1 -k2,2n ./SeqAOnly_r331s330.bed > ./SeqAOnly_r331s331.bed
670.     bedtools shuffle -seed 1 -i SeqAOnly_r331s331.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r332s331.bed

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671.      sort -k1,1 -k2,2n ./SeqAOnly_r332s331.bed > ./SeqAOnly_r332s332.bed
672.      bedtools shuffle -seed 1 -i SeqAOnly_r332s332.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r333s332.bed
673.      sort -k1,1 -k2,2n ./SeqAOnly_r333s332.bed > ./SeqAOnly_r333s333.bed
674.      bedtools shuffle -seed 1 -i SeqAOnly_r333s333.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r334s333.bed
675.      sort -k1,1 -k2,2n ./SeqAOnly_r334s333.bed > ./SeqAOnly_r334s334.bed
676.      bedtools shuffle -seed 1 -i SeqAOnly_r334s334.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r335s334.bed
677.      sort -k1,1 -k2,2n ./SeqAOnly_r335s334.bed > ./SeqAOnly_r335s335.bed
678.      bedtools shuffle -seed 1 -i SeqAOnly_r335s335.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r336s335.bed
679.      sort -k1,1 -k2,2n ./SeqAOnly_r336s335.bed > ./SeqAOnly_r336s336.bed
680.      bedtools shuffle -seed 1 -i SeqAOnly_r336s336.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r337s336.bed
681.      sort -k1,1 -k2,2n ./SeqAOnly_r337s336.bed > ./SeqAOnly_r337s337.bed
682.      bedtools shuffle -seed 1 -i SeqAOnly_r337s337.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r338s337.bed
683.      sort -k1,1 -k2,2n ./SeqAOnly_r338s337.bed > ./SeqAOnly_r338s338.bed
684.      bedtools shuffle -seed 1 -i SeqAOnly_r338s338.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r339s338.bed
685.      sort -k1,1 -k2,2n ./SeqAOnly_r339s338.bed > ./SeqAOnly_r339s339.bed
686.      bedtools shuffle -seed 1 -i SeqAOnly_r339s339.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r340s339.bed
687.      sort -k1,1 -k2,2n ./SeqAOnly_r340s339.bed > ./SeqAOnly_r340s340.bed
688.      bedtools shuffle -seed 1 -i SeqAOnly_r340s340.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r341s340.bed
689.      sort -k1,1 -k2,2n ./SeqAOnly_r341s340.bed > ./SeqAOnly_r341s341.bed
690.      bedtools shuffle -seed 1 -i SeqAOnly_r341s341.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r342s341.bed
691.      sort -k1,1 -k2,2n ./SeqAOnly_r342s341.bed > ./SeqAOnly_r342s342.bed
692.      bedtools shuffle -seed 1 -i SeqAOnly_r342s342.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r343s342.bed
693.      sort -k1,1 -k2,2n ./SeqAOnly_r343s342.bed > ./SeqAOnly_r343s343.bed
694.      bedtools shuffle -seed 1 -i SeqAOnly_r343s343.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r344s343.bed
695.      sort -k1,1 -k2,2n ./SeqAOnly_r344s343.bed > ./SeqAOnly_r344s344.bed
696.      bedtools shuffle -seed 1 -i SeqAOnly_r344s344.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r345s344.bed
697.      sort -k1,1 -k2,2n ./SeqAOnly_r345s344.bed > ./SeqAOnly_r345s345.bed
698.      bedtools shuffle -seed 1 -i SeqAOnly_r345s345.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r346s345.bed
699.      sort -k1,1 -k2,2n ./SeqAOnly_r346s345.bed > ./SeqAOnly_r346s346.bed
700.      bedtools shuffle -seed 1 -i SeqAOnly_r346s346.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r347s346.bed
701.      sort -k1,1 -k2,2n ./SeqAOnly_r347s346.bed > ./SeqAOnly_r347s347.bed
702.      bedtools shuffle -seed 1 -i SeqAOnly_r347s347.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r348s347.bed
703.      sort -k1,1 -k2,2n ./SeqAOnly_r348s347.bed > ./SeqAOnly_r348s348.bed
704.      bedtools shuffle -seed 1 -i SeqAOnly_r348s348.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r349s348.bed
705.      sort -k1,1 -k2,2n ./SeqAOnly_r349s348.bed > ./SeqAOnly_r349s349.bed
706.      bedtools shuffle -seed 1 -i SeqAOnly_r349s349.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r350s349.bed
707.      sort -k1,1 -k2,2n ./SeqAOnly_r350s349.bed > ./SeqAOnly_r350s350.bed
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708. bedtools shuffle -seed 1 -i SeqAOnly_r350s350.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r351s350.bed
709. sort -k1,1 -k2,2n ./SeqAOnly_r351s350.bed > ./SeqAOnly_r351s351.bed
710. bedtools shuffle -seed 1 -i SeqAOnly_r351s351.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r352s351.bed
711. sort -k1,1 -k2,2n ./SeqAOnly_r352s351.bed > ./SeqAOnly_r352s352.bed
712. bedtools shuffle -seed 1 -i SeqAOnly_r352s352.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r353s352.bed
713. sort -k1,1 -k2,2n ./SeqAOnly_r353s352.bed > ./SeqAOnly_r353s353.bed
714. bedtools shuffle -seed 1 -i SeqAOnly_r353s353.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r354s353.bed
715. sort -k1,1 -k2,2n ./SeqAOnly_r354s353.bed > ./SeqAOnly_r354s354.bed
716. bedtools shuffle -seed 1 -i SeqAOnly_r354s354.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r355s354.bed
717. sort -k1,1 -k2,2n ./SeqAOnly_r355s354.bed > ./SeqAOnly_r355s355.bed
718. bedtools shuffle -seed 1 -i SeqAOnly_r355s355.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r356s355.bed
719. sort -k1,1 -k2,2n ./SeqAOnly_r356s355.bed > ./SeqAOnly_r356s356.bed
720. bedtools shuffle -seed 1 -i SeqAOnly_r356s356.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r357s356.bed
721. sort -k1,1 -k2,2n ./SeqAOnly_r357s356.bed > ./SeqAOnly_r357s357.bed
722. bedtools shuffle -seed 1 -i SeqAOnly_r357s357.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r358s357.bed
723. sort -k1,1 -k2,2n ./SeqAOnly_r358s357.bed > ./SeqAOnly_r358s358.bed
724. bedtools shuffle -seed 1 -i SeqAOnly_r358s358.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r359s358.bed
725. sort -k1,1 -k2,2n ./SeqAOnly_r359s358.bed > ./SeqAOnly_r359s359.bed
726. bedtools shuffle -seed 1 -i SeqAOnly_r359s359.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r360s359.bed
727. sort -k1,1 -k2,2n ./SeqAOnly_r360s359.bed > ./SeqAOnly_r360s360.bed
728. bedtools shuffle -seed 1 -i SeqAOnly_r360s360.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r361s360.bed
729. sort -k1,1 -k2,2n ./SeqAOnly_r361s360.bed > ./SeqAOnly_r361s361.bed
730. bedtools shuffle -seed 1 -i SeqAOnly_r361s361.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r362s361.bed
731. sort -k1,1 -k2,2n ./SeqAOnly_r362s361.bed > ./SeqAOnly_r362s362.bed
732. bedtools shuffle -seed 1 -i SeqAOnly_r362s362.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r363s362.bed
733. sort -k1,1 -k2,2n ./SeqAOnly_r363s362.bed > ./SeqAOnly_r363s363.bed
734. bedtools shuffle -seed 1 -i SeqAOnly_r363s363.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r364s363.bed
735. sort -k1,1 -k2,2n ./SeqAOnly_r364s363.bed > ./SeqAOnly_r364s364.bed
736. bedtools shuffle -seed 1 -i SeqAOnly_r364s364.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r365s364.bed
737. sort -k1,1 -k2,2n ./SeqAOnly_r365s364.bed > ./SeqAOnly_r365s365.bed
738. bedtools shuffle -seed 1 -i SeqAOnly_r365s365.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r366s365.bed
739. sort -k1,1 -k2,2n ./SeqAOnly_r366s365.bed > ./SeqAOnly_r366s366.bed
740. bedtools shuffle -seed 1 -i SeqAOnly_r366s366.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r367s366.bed
741. sort -k1,1 -k2,2n ./SeqAOnly_r367s366.bed > ./SeqAOnly_r367s367.bed
742. bedtools shuffle -seed 1 -i SeqAOnly_r367s367.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r368s367.bed
743. sort -k1,1 -k2,2n ./SeqAOnly_r368s367.bed > ./SeqAOnly_r368s368.bed
744. bedtools shuffle -seed 1 -i SeqAOnly_r368s368.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_r369s368.bed

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745.      sort -k1,1 -k2,2n ./SeqAOnly_r369s368.bed > ./SeqAOnly_r369s369.bed
746.      bedtools shuffle -seed 1 -i SeqAOnly_r369s369.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r370s369.bed
747.      sort -k1,1 -k2,2n ./SeqAOnly_r370s369.bed > ./SeqAOnly_r370s370.bed
748.      bedtools shuffle -seed 1 -i SeqAOnly_r370s370.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r371s370.bed
749.      sort -k1,1 -k2,2n ./SeqAOnly_r371s370.bed > ./SeqAOnly_r371s371.bed
750.      bedtools shuffle -seed 1 -i SeqAOnly_r371s371.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r372s371.bed
751.      sort -k1,1 -k2,2n ./SeqAOnly_r372s371.bed > ./SeqAOnly_r372s372.bed
752.      bedtools shuffle -seed 1 -i SeqAOnly_r372s372.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r373s372.bed
753.      sort -k1,1 -k2,2n ./SeqAOnly_r373s372.bed > ./SeqAOnly_r373s373.bed
754.      bedtools shuffle -seed 1 -i SeqAOnly_r373s373.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r374s373.bed
755.      sort -k1,1 -k2,2n ./SeqAOnly_r374s373.bed > ./SeqAOnly_r374s374.bed
756.      bedtools shuffle -seed 1 -i SeqAOnly_r374s374.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r375s374.bed
757.      sort -k1,1 -k2,2n ./SeqAOnly_r375s374.bed > ./SeqAOnly_r375s375.bed
758.      bedtools shuffle -seed 1 -i SeqAOnly_r375s375.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r376s375.bed
759.      sort -k1,1 -k2,2n ./SeqAOnly_r376s375.bed > ./SeqAOnly_r376s376.bed
760.      bedtools shuffle -seed 1 -i SeqAOnly_r376s376.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r377s376.bed
761.      sort -k1,1 -k2,2n ./SeqAOnly_r377s376.bed > ./SeqAOnly_r377s377.bed
762.      bedtools shuffle -seed 1 -i SeqAOnly_r377s377.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r378s377.bed
763.      sort -k1,1 -k2,2n ./SeqAOnly_r378s377.bed > ./SeqAOnly_r378s378.bed
764.      bedtools shuffle -seed 1 -i SeqAOnly_r378s378.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r379s378.bed
765.      sort -k1,1 -k2,2n ./SeqAOnly_r379s378.bed > ./SeqAOnly_r379s379.bed
766.      bedtools shuffle -seed 1 -i SeqAOnly_r379s379.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r380s379.bed
767.      sort -k1,1 -k2,2n ./SeqAOnly_r380s379.bed > ./SeqAOnly_r380s380.bed
768.      bedtools shuffle -seed 1 -i SeqAOnly_r380s380.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r381s380.bed
769.      sort -k1,1 -k2,2n ./SeqAOnly_r381s380.bed > ./SeqAOnly_r381s381.bed
770.      bedtools shuffle -seed 1 -i SeqAOnly_r381s381.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r382s381.bed
771.      sort -k1,1 -k2,2n ./SeqAOnly_r382s381.bed > ./SeqAOnly_r382s382.bed
772.      bedtools shuffle -seed 1 -i SeqAOnly_r382s382.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r383s382.bed
773.      sort -k1,1 -k2,2n ./SeqAOnly_r383s382.bed > ./SeqAOnly_r383s383.bed
774.      bedtools shuffle -seed 1 -i SeqAOnly_r383s383.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r384s383.bed
775.      sort -k1,1 -k2,2n ./SeqAOnly_r384s383.bed > ./SeqAOnly_r384s384.bed
776.      bedtools shuffle -seed 1 -i SeqAOnly_r384s384.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r385s384.bed
777.      sort -k1,1 -k2,2n ./SeqAOnly_r385s384.bed > ./SeqAOnly_r385s385.bed
778.      bedtools shuffle -seed 1 -i SeqAOnly_r385s385.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r386s385.bed
779.      sort -k1,1 -k2,2n ./SeqAOnly_r386s385.bed > ./SeqAOnly_r386s386.bed
780.      bedtools shuffle -seed 1 -i SeqAOnly_r386s386.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r387s386.bed
781.      sort -k1,1 -k2,2n ./SeqAOnly_r387s386.bed > ./SeqAOnly_r387s387.bed
```



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782.     bedtools shuffle -seed 1 -i SeqAOnly_r387s387.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r388s387.bed
783.     sort -k1,1 -k2,2n ./SeqAOnly_r388s387.bed > ./SeqAOnly_r388s388.bed
784.     bedtools shuffle -seed 1 -i SeqAOnly_r388s388.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r389s388.bed
785.     sort -k1,1 -k2,2n ./SeqAOnly_r389s388.bed > ./SeqAOnly_r389s389.bed
786.     bedtools shuffle -seed 1 -i SeqAOnly_r389s389.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r390s389.bed
787.     sort -k1,1 -k2,2n ./SeqAOnly_r390s389.bed > ./SeqAOnly_r390s390.bed
788.     bedtools shuffle -seed 1 -i SeqAOnly_r390s390.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r391s390.bed
789.     sort -k1,1 -k2,2n ./SeqAOnly_r391s390.bed > ./SeqAOnly_r391s391.bed
790.     bedtools shuffle -seed 1 -i SeqAOnly_r391s391.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r392s391.bed
791.     sort -k1,1 -k2,2n ./SeqAOnly_r392s391.bed > ./SeqAOnly_r392s392.bed
792.     bedtools shuffle -seed 1 -i SeqAOnly_r392s392.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r393s392.bed
793.     sort -k1,1 -k2,2n ./SeqAOnly_r393s392.bed > ./SeqAOnly_r393s393.bed
794.     bedtools shuffle -seed 1 -i SeqAOnly_r393s393.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r394s393.bed
795.     sort -k1,1 -k2,2n ./SeqAOnly_r394s393.bed > ./SeqAOnly_r394s394.bed
796.     bedtools shuffle -seed 1 -i SeqAOnly_r394s394.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r395s394.bed
797.     sort -k1,1 -k2,2n ./SeqAOnly_r395s394.bed > ./SeqAOnly_r395s395.bed
798.     bedtools shuffle -seed 1 -i SeqAOnly_r395s395.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r396s395.bed
799.     sort -k1,1 -k2,2n ./SeqAOnly_r396s395.bed > ./SeqAOnly_r396s396.bed
800.     bedtools shuffle -seed 1 -i SeqAOnly_r396s396.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r397s396.bed
801.     sort -k1,1 -k2,2n ./SeqAOnly_r397s396.bed > ./SeqAOnly_r397s397.bed
802.     bedtools shuffle -seed 1 -i SeqAOnly_r397s397.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r398s397.bed
803.     sort -k1,1 -k2,2n ./SeqAOnly_r398s397.bed > ./SeqAOnly_r398s398.bed
804.     bedtools shuffle -seed 1 -i SeqAOnly_r398s398.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r399s398.bed
805.     sort -k1,1 -k2,2n ./SeqAOnly_r399s398.bed > ./SeqAOnly_r399s399.bed
806.     bedtools shuffle -seed 1 -i SeqAOnly_r399s399.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r400s399.bed
807.     sort -k1,1 -k2,2n ./SeqAOnly_r400s399.bed > ./SeqAOnly_r400s400.bed
808.     bedtools shuffle -seed 1 -i SeqAOnly_r400s400.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r401s400.bed
809.     sort -k1,1 -k2,2n ./SeqAOnly_r401s400.bed > ./SeqAOnly_r401s401.bed
810.     bedtools shuffle -seed 1 -i SeqAOnly_r401s401.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r402s401.bed
811.     sort -k1,1 -k2,2n ./SeqAOnly_r402s401.bed > ./SeqAOnly_r402s402.bed
812.     bedtools shuffle -seed 1 -i SeqAOnly_r402s402.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r403s402.bed
813.     sort -k1,1 -k2,2n ./SeqAOnly_r403s402.bed > ./SeqAOnly_r403s403.bed
814.     bedtools shuffle -seed 1 -i SeqAOnly_r403s403.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r404s403.bed
815.     sort -k1,1 -k2,2n ./SeqAOnly_r404s403.bed > ./SeqAOnly_r404s404.bed
816.     bedtools shuffle -seed 1 -i SeqAOnly_r404s404.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r405s404.bed
817.     sort -k1,1 -k2,2n ./SeqAOnly_r405s404.bed > ./SeqAOnly_r405s405.bed
818.     bedtools shuffle -seed 1 -i SeqAOnly_r405s405.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r406s405.bed

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819.      sort -k1,1 -k2,2n ./SeqAOnly_r406s405.bed > ./SeqAOnly_r406s406.bed
820.      bedtools shuffle -seed 1 -i SeqAOnly_r406s406.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r407s406.bed
821.      sort -k1,1 -k2,2n ./SeqAOnly_r407s406.bed > ./SeqAOnly_r407s407.bed
822.      bedtools shuffle -seed 1 -i SeqAOnly_r407s407.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r408s407.bed
823.      sort -k1,1 -k2,2n ./SeqAOnly_r408s407.bed > ./SeqAOnly_r408s408.bed
824.      bedtools shuffle -seed 1 -i SeqAOnly_r408s408.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r409s408.bed
825.      sort -k1,1 -k2,2n ./SeqAOnly_r409s408.bed > ./SeqAOnly_r409s409.bed
826.      bedtools shuffle -seed 1 -i SeqAOnly_r409s409.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r410s409.bed
827.      sort -k1,1 -k2,2n ./SeqAOnly_r410s409.bed > ./SeqAOnly_r410s410.bed
828.      bedtools shuffle -seed 1 -i SeqAOnly_r410s410.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r411s410.bed
829.      sort -k1,1 -k2,2n ./SeqAOnly_r411s410.bed > ./SeqAOnly_r411s411.bed
830.      bedtools shuffle -seed 1 -i SeqAOnly_r411s411.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r412s411.bed
831.      sort -k1,1 -k2,2n ./SeqAOnly_r412s411.bed > ./SeqAOnly_r412s412.bed
832.      bedtools shuffle -seed 1 -i SeqAOnly_r412s412.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r413s412.bed
833.      sort -k1,1 -k2,2n ./SeqAOnly_r413s412.bed > ./SeqAOnly_r413s413.bed
834.      bedtools shuffle -seed 1 -i SeqAOnly_r413s413.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r414s413.bed
835.      sort -k1,1 -k2,2n ./SeqAOnly_r414s413.bed > ./SeqAOnly_r414s414.bed
836.      bedtools shuffle -seed 1 -i SeqAOnly_r414s414.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r415s414.bed
837.      sort -k1,1 -k2,2n ./SeqAOnly_r415s414.bed > ./SeqAOnly_r415s415.bed
838.      bedtools shuffle -seed 1 -i SeqAOnly_r415s415.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r416s415.bed
839.      sort -k1,1 -k2,2n ./SeqAOnly_r416s415.bed > ./SeqAOnly_r416s416.bed
840.      bedtools shuffle -seed 1 -i SeqAOnly_r416s416.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r417s416.bed
841.      sort -k1,1 -k2,2n ./SeqAOnly_r417s416.bed > ./SeqAOnly_r417s417.bed
842.      bedtools shuffle -seed 1 -i SeqAOnly_r417s417.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r418s417.bed
843.      sort -k1,1 -k2,2n ./SeqAOnly_r418s417.bed > ./SeqAOnly_r418s418.bed
844.      bedtools shuffle -seed 1 -i SeqAOnly_r418s418.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r419s418.bed
845.      sort -k1,1 -k2,2n ./SeqAOnly_r419s418.bed > ./SeqAOnly_r419s419.bed
846.      bedtools shuffle -seed 1 -i SeqAOnly_r419s419.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r420s419.bed
847.      sort -k1,1 -k2,2n ./SeqAOnly_r420s419.bed > ./SeqAOnly_r420s420.bed
848.      bedtools shuffle -seed 1 -i SeqAOnly_r420s420.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r421s420.bed
849.      sort -k1,1 -k2,2n ./SeqAOnly_r421s420.bed > ./SeqAOnly_r421s421.bed
850.      bedtools shuffle -seed 1 -i SeqAOnly_r421s421.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r422s421.bed
851.      sort -k1,1 -k2,2n ./SeqAOnly_r422s421.bed > ./SeqAOnly_r422s422.bed
852.      bedtools shuffle -seed 1 -i SeqAOnly_r422s422.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r423s422.bed
853.      sort -k1,1 -k2,2n ./SeqAOnly_r423s422.bed > ./SeqAOnly_r423s423.bed
854.      bedtools shuffle -seed 1 -i SeqAOnly_r423s423.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r424s423.bed
855.      sort -k1,1 -k2,2n ./SeqAOnly_r424s423.bed > ./SeqAOnly_r424s424.bed
```

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856.      bedtools shuffle -seed 1 -i SeqAOnly_r424s424.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r425s424.bed
857.      sort -k1,1 -k2,2n ./SeqAOnly_r425s424.bed > ./SeqAOnly_r425s425.bed
858.      bedtools shuffle -seed 1 -i SeqAOnly_r425s425.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r426s425.bed
859.      sort -k1,1 -k2,2n ./SeqAOnly_r426s425.bed > ./SeqAOnly_r426s426.bed
860.      bedtools shuffle -seed 1 -i SeqAOnly_r426s426.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r427s426.bed
861.      sort -k1,1 -k2,2n ./SeqAOnly_r427s426.bed > ./SeqAOnly_r427s427.bed
862.      bedtools shuffle -seed 1 -i SeqAOnly_r427s427.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r428s427.bed
863.      sort -k1,1 -k2,2n ./SeqAOnly_r428s427.bed > ./SeqAOnly_r428s428.bed
864.      bedtools shuffle -seed 1 -i SeqAOnly_r428s428.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r429s428.bed
865.      sort -k1,1 -k2,2n ./SeqAOnly_r429s428.bed > ./SeqAOnly_r429s429.bed
866.      bedtools shuffle -seed 1 -i SeqAOnly_r429s429.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r430s429.bed
867.      sort -k1,1 -k2,2n ./SeqAOnly_r430s429.bed > ./SeqAOnly_r430s430.bed
868.      bedtools shuffle -seed 1 -i SeqAOnly_r430s430.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r431s430.bed
869.      sort -k1,1 -k2,2n ./SeqAOnly_r431s430.bed > ./SeqAOnly_r431s431.bed
870.      bedtools shuffle -seed 1 -i SeqAOnly_r431s431.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r432s431.bed
871.      sort -k1,1 -k2,2n ./SeqAOnly_r432s431.bed > ./SeqAOnly_r432s432.bed
872.      bedtools shuffle -seed 1 -i SeqAOnly_r432s432.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r433s432.bed
873.      sort -k1,1 -k2,2n ./SeqAOnly_r433s432.bed > ./SeqAOnly_r433s433.bed
874.      bedtools shuffle -seed 1 -i SeqAOnly_r433s433.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r434s433.bed
875.      sort -k1,1 -k2,2n ./SeqAOnly_r434s433.bed > ./SeqAOnly_r434s434.bed
876.      bedtools shuffle -seed 1 -i SeqAOnly_r434s434.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r435s434.bed
877.      sort -k1,1 -k2,2n ./SeqAOnly_r435s434.bed > ./SeqAOnly_r435s435.bed
878.      bedtools shuffle -seed 1 -i SeqAOnly_r435s435.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r436s435.bed
879.      sort -k1,1 -k2,2n ./SeqAOnly_r436s435.bed > ./SeqAOnly_r436s436.bed
880.      bedtools shuffle -seed 1 -i SeqAOnly_r436s436.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r437s436.bed
881.      sort -k1,1 -k2,2n ./SeqAOnly_r437s436.bed > ./SeqAOnly_r437s437.bed
882.      bedtools shuffle -seed 1 -i SeqAOnly_r437s437.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r438s437.bed
883.      sort -k1,1 -k2,2n ./SeqAOnly_r438s437.bed > ./SeqAOnly_r438s438.bed
884.      bedtools shuffle -seed 1 -i SeqAOnly_r438s438.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r439s438.bed
885.      sort -k1,1 -k2,2n ./SeqAOnly_r439s438.bed > ./SeqAOnly_r439s439.bed
886.      bedtools shuffle -seed 1 -i SeqAOnly_r439s439.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r440s439.bed
887.      sort -k1,1 -k2,2n ./SeqAOnly_r440s439.bed > ./SeqAOnly_r440s440.bed
888.      bedtools shuffle -seed 1 -i SeqAOnly_r440s440.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r441s440.bed
889.      sort -k1,1 -k2,2n ./SeqAOnly_r441s440.bed > ./SeqAOnly_r441s441.bed
890.      bedtools shuffle -seed 1 -i SeqAOnly_r441s441.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r442s441.bed
891.      sort -k1,1 -k2,2n ./SeqAOnly_r442s441.bed > ./SeqAOnly_r442s442.bed
892.      bedtools shuffle -seed 1 -i SeqAOnly_r442s442.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r443s442.bed

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893.      sort -k1,1 -k2,2n ./SeqAOnly_r443s442.bed > ./SeqAOnly_r443s443.bed
894.      bedtools shuffle -seed 1 -i SeqAOnly_r443s443.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r444s443.bed
895.      sort -k1,1 -k2,2n ./SeqAOnly_r444s443.bed > ./SeqAOnly_r444s444.bed
896.      bedtools shuffle -seed 1 -i SeqAOnly_r444s444.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r445s444.bed
897.      sort -k1,1 -k2,2n ./SeqAOnly_r445s444.bed > ./SeqAOnly_r445s445.bed
898.      bedtools shuffle -seed 1 -i SeqAOnly_r445s445.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r446s445.bed
899.      sort -k1,1 -k2,2n ./SeqAOnly_r446s445.bed > ./SeqAOnly_r446s446.bed
900.      bedtools shuffle -seed 1 -i SeqAOnly_r446s446.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r447s446.bed
901.      sort -k1,1 -k2,2n ./SeqAOnly_r447s446.bed > ./SeqAOnly_r447s447.bed
902.      bedtools shuffle -seed 1 -i SeqAOnly_r447s447.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r448s447.bed
903.      sort -k1,1 -k2,2n ./SeqAOnly_r448s447.bed > ./SeqAOnly_r448s448.bed
904.      bedtools shuffle -seed 1 -i SeqAOnly_r448s448.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r449s448.bed
905.      sort -k1,1 -k2,2n ./SeqAOnly_r449s448.bed > ./SeqAOnly_r449s449.bed
906.      bedtools shuffle -seed 1 -i SeqAOnly_r449s449.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r450s449.bed
907.      sort -k1,1 -k2,2n ./SeqAOnly_r450s449.bed > ./SeqAOnly_r450s450.bed
908.      bedtools shuffle -seed 1 -i SeqAOnly_r450s450.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r451s450.bed
909.      sort -k1,1 -k2,2n ./SeqAOnly_r451s450.bed > ./SeqAOnly_r451s451.bed
910.      bedtools shuffle -seed 1 -i SeqAOnly_r451s451.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r452s451.bed
911.      sort -k1,1 -k2,2n ./SeqAOnly_r452s451.bed > ./SeqAOnly_r452s452.bed
912.      bedtools shuffle -seed 1 -i SeqAOnly_r452s452.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r453s452.bed
913.      sort -k1,1 -k2,2n ./SeqAOnly_r453s452.bed > ./SeqAOnly_r453s453.bed
914.      bedtools shuffle -seed 1 -i SeqAOnly_r453s453.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r454s453.bed
915.      sort -k1,1 -k2,2n ./SeqAOnly_r454s453.bed > ./SeqAOnly_r454s454.bed
916.      bedtools shuffle -seed 1 -i SeqAOnly_r454s454.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r455s454.bed
917.      sort -k1,1 -k2,2n ./SeqAOnly_r455s454.bed > ./SeqAOnly_r455s455.bed
918.      bedtools shuffle -seed 1 -i SeqAOnly_r455s455.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r456s455.bed
919.      sort -k1,1 -k2,2n ./SeqAOnly_r456s455.bed > ./SeqAOnly_r456s456.bed
920.      bedtools shuffle -seed 1 -i SeqAOnly_r456s456.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r457s456.bed
921.      sort -k1,1 -k2,2n ./SeqAOnly_r457s456.bed > ./SeqAOnly_r457s457.bed
922.      bedtools shuffle -seed 1 -i SeqAOnly_r457s457.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r458s457.bed
923.      sort -k1,1 -k2,2n ./SeqAOnly_r458s457.bed > ./SeqAOnly_r458s458.bed
924.      bedtools shuffle -seed 1 -i SeqAOnly_r458s458.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r459s458.bed
925.      sort -k1,1 -k2,2n ./SeqAOnly_r459s458.bed > ./SeqAOnly_r459s459.bed
926.      bedtools shuffle -seed 1 -i SeqAOnly_r459s459.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r460s459.bed
927.      sort -k1,1 -k2,2n ./SeqAOnly_r460s459.bed > ./SeqAOnly_r460s460.bed
928.      bedtools shuffle -seed 1 -i SeqAOnly_r460s460.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r461s460.bed
929.      sort -k1,1 -k2,2n ./SeqAOnly_r461s460.bed > ./SeqAOnly_r461s461.bed
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930. bedtools shuffle -seed 1 -i SeqAOnly_r461s461.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r462s461.bed
931. sort -k1,1 -k2,2n ./SeqAOnly_r462s461.bed > ./SeqAOnly_r462s462.bed
932. bedtools shuffle -seed 1 -i SeqAOnly_r462s462.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r463s462.bed
933. sort -k1,1 -k2,2n ./SeqAOnly_r463s462.bed > ./SeqAOnly_r463s463.bed
934. bedtools shuffle -seed 1 -i SeqAOnly_r463s463.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r464s463.bed
935. sort -k1,1 -k2,2n ./SeqAOnly_r464s463.bed > ./SeqAOnly_r464s464.bed
936. bedtools shuffle -seed 1 -i SeqAOnly_r464s464.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r465s464.bed
937. sort -k1,1 -k2,2n ./SeqAOnly_r465s464.bed > ./SeqAOnly_r465s465.bed
938. bedtools shuffle -seed 1 -i SeqAOnly_r465s465.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r466s465.bed
939. sort -k1,1 -k2,2n ./SeqAOnly_r466s465.bed > ./SeqAOnly_r466s466.bed
940. bedtools shuffle -seed 1 -i SeqAOnly_r466s466.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r467s466.bed
941. sort -k1,1 -k2,2n ./SeqAOnly_r467s466.bed > ./SeqAOnly_r467s467.bed
942. bedtools shuffle -seed 1 -i SeqAOnly_r467s467.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r468s467.bed
943. sort -k1,1 -k2,2n ./SeqAOnly_r468s467.bed > ./SeqAOnly_r468s468.bed
944. bedtools shuffle -seed 1 -i SeqAOnly_r468s468.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r469s468.bed
945. sort -k1,1 -k2,2n ./SeqAOnly_r469s468.bed > ./SeqAOnly_r469s469.bed
946. bedtools shuffle -seed 1 -i SeqAOnly_r469s469.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r470s469.bed
947. sort -k1,1 -k2,2n ./SeqAOnly_r470s469.bed > ./SeqAOnly_r470s470.bed
948. bedtools shuffle -seed 1 -i SeqAOnly_r470s470.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r471s470.bed
949. sort -k1,1 -k2,2n ./SeqAOnly_r471s470.bed > ./SeqAOnly_r471s471.bed
950. bedtools shuffle -seed 1 -i SeqAOnly_r471s471.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r472s471.bed
951. sort -k1,1 -k2,2n ./SeqAOnly_r472s471.bed > ./SeqAOnly_r472s472.bed
952. bedtools shuffle -seed 1 -i SeqAOnly_r472s472.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r473s472.bed
953. sort -k1,1 -k2,2n ./SeqAOnly_r473s472.bed > ./SeqAOnly_r473s473.bed
954. bedtools shuffle -seed 1 -i SeqAOnly_r473s473.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r474s473.bed
955. sort -k1,1 -k2,2n ./SeqAOnly_r474s473.bed > ./SeqAOnly_r474s474.bed
956. bedtools shuffle -seed 1 -i SeqAOnly_r474s474.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r475s474.bed
957. sort -k1,1 -k2,2n ./SeqAOnly_r475s474.bed > ./SeqAOnly_r475s475.bed
958. bedtools shuffle -seed 1 -i SeqAOnly_r475s475.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r476s475.bed
959. sort -k1,1 -k2,2n ./SeqAOnly_r476s475.bed > ./SeqAOnly_r476s476.bed
960. bedtools shuffle -seed 1 -i SeqAOnly_r476s476.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r477s476.bed
961. sort -k1,1 -k2,2n ./SeqAOnly_r477s476.bed > ./SeqAOnly_r477s477.bed
962. bedtools shuffle -seed 1 -i SeqAOnly_r477s477.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r478s477.bed
963. sort -k1,1 -k2,2n ./SeqAOnly_r478s477.bed > ./SeqAOnly_r478s478.bed
964. bedtools shuffle -seed 1 -i SeqAOnly_r478s478.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r479s478.bed
965. sort -k1,1 -k2,2n ./SeqAOnly_r479s478.bed > ./SeqAOnly_r479s479.bed
966. bedtools shuffle -seed 1 -i SeqAOnly_r479s479.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r480s479.bed

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967.      sort -k1,1 -k2,2n ./SeqAOnly_r480s479.bed > ./SeqAOnly_r480s480.bed
968.      bedtools shuffle -seed 1 -i SeqAOnly_r480s480.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r481s480.bed
969.      sort -k1,1 -k2,2n ./SeqAOnly_r481s480.bed > ./SeqAOnly_r481s481.bed
970.      bedtools shuffle -seed 1 -i SeqAOnly_r481s481.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r482s481.bed
971.      sort -k1,1 -k2,2n ./SeqAOnly_r482s481.bed > ./SeqAOnly_r482s482.bed
972.      bedtools shuffle -seed 1 -i SeqAOnly_r482s482.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r483s482.bed
973.      sort -k1,1 -k2,2n ./SeqAOnly_r483s482.bed > ./SeqAOnly_r483s483.bed
974.      bedtools shuffle -seed 1 -i SeqAOnly_r483s483.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r484s483.bed
975.      sort -k1,1 -k2,2n ./SeqAOnly_r484s483.bed > ./SeqAOnly_r484s484.bed
976.      bedtools shuffle -seed 1 -i SeqAOnly_r484s484.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r485s484.bed
977.      sort -k1,1 -k2,2n ./SeqAOnly_r485s484.bed > ./SeqAOnly_r485s485.bed
978.      bedtools shuffle -seed 1 -i SeqAOnly_r485s485.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r486s485.bed
979.      sort -k1,1 -k2,2n ./SeqAOnly_r486s485.bed > ./SeqAOnly_r486s486.bed
980.      bedtools shuffle -seed 1 -i SeqAOnly_r486s486.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r487s486.bed
981.      sort -k1,1 -k2,2n ./SeqAOnly_r487s486.bed > ./SeqAOnly_r487s487.bed
982.      bedtools shuffle -seed 1 -i SeqAOnly_r487s487.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r488s487.bed
983.      sort -k1,1 -k2,2n ./SeqAOnly_r488s487.bed > ./SeqAOnly_r488s488.bed
984.      bedtools shuffle -seed 1 -i SeqAOnly_r488s488.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r489s488.bed
985.      sort -k1,1 -k2,2n ./SeqAOnly_r489s488.bed > ./SeqAOnly_r489s489.bed
986.      bedtools shuffle -seed 1 -i SeqAOnly_r489s489.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r490s489.bed
987.      sort -k1,1 -k2,2n ./SeqAOnly_r490s489.bed > ./SeqAOnly_r490s490.bed
988.      bedtools shuffle -seed 1 -i SeqAOnly_r490s490.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r491s490.bed
989.      sort -k1,1 -k2,2n ./SeqAOnly_r491s490.bed > ./SeqAOnly_r491s491.bed
990.      bedtools shuffle -seed 1 -i SeqAOnly_r491s491.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r492s491.bed
991.      sort -k1,1 -k2,2n ./SeqAOnly_r492s491.bed > ./SeqAOnly_r492s492.bed
992.      bedtools shuffle -seed 1 -i SeqAOnly_r492s492.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r493s492.bed
993.      sort -k1,1 -k2,2n ./SeqAOnly_r493s492.bed > ./SeqAOnly_r493s493.bed
994.      bedtools shuffle -seed 1 -i SeqAOnly_r493s493.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r494s493.bed
995.      sort -k1,1 -k2,2n ./SeqAOnly_r494s493.bed > ./SeqAOnly_r494s494.bed
996.      bedtools shuffle -seed 1 -i SeqAOnly_r494s494.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r495s494.bed
997.      sort -k1,1 -k2,2n ./SeqAOnly_r495s494.bed > ./SeqAOnly_r495s495.bed
998.      bedtools shuffle -seed 1 -i SeqAOnly_r495s495.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r496s495.bed
999.      sort -k1,1 -k2,2n ./SeqAOnly_r496s495.bed > ./SeqAOnly_r496s496.bed
1000.     bedtools shuffle -seed 1 -i SeqAOnly_r496s496.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r497s496.bed
1001.     sort -k1,1 -k2,2n ./SeqAOnly_r497s496.bed > ./SeqAOnly_r497s497.bed
1002.     bedtools shuffle -seed 1 -i SeqAOnly_r497s497.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r498s497.bed
1003.     sort -k1,1 -k2,2n ./SeqAOnly_r498s497.bed > ./SeqAOnly_r498s498.bed
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1004. bedtools shuffle -seed 1 -i SeqAOnly_r498s498.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r499s498.bed
1005. sort -k1,1 -k2,2n ./SeqAOnly_r499s498.bed > ./SeqAOnly_r499s499.bed
1006. bedtools shuffle -seed 1 -i SeqAOnly_r499s499.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r500s499.bed
1007. sort -k1,1 -k2,2n ./SeqAOnly_r500s499.bed > ./SeqAOnly_r500s500.bed
1008. bedtools shuffle -seed 1 -i SeqAOnly_r500s500.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r501s500.bed
1009. sort -k1,1 -k2,2n ./SeqAOnly_r501s500.bed > ./SeqAOnly_r501s501.bed
1010. bedtools shuffle -seed 1 -i SeqAOnly_r501s501.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r502s501.bed
1011. sort -k1,1 -k2,2n ./SeqAOnly_r502s501.bed > ./SeqAOnly_r502s502.bed
1012. bedtools shuffle -seed 1 -i SeqAOnly_r502s502.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r503s502.bed
1013. sort -k1,1 -k2,2n ./SeqAOnly_r503s502.bed > ./SeqAOnly_r503s503.bed
1014. bedtools shuffle -seed 1 -i SeqAOnly_r503s503.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r504s503.bed
1015. sort -k1,1 -k2,2n ./SeqAOnly_r504s503.bed > ./SeqAOnly_r504s504.bed
1016. bedtools shuffle -seed 1 -i SeqAOnly_r504s504.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r505s504.bed
1017. sort -k1,1 -k2,2n ./SeqAOnly_r505s504.bed > ./SeqAOnly_r505s505.bed
1018. bedtools shuffle -seed 1 -i SeqAOnly_r505s505.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r506s505.bed
1019. sort -k1,1 -k2,2n ./SeqAOnly_r506s505.bed > ./SeqAOnly_r506s506.bed
1020. bedtools shuffle -seed 1 -i SeqAOnly_r506s506.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r507s506.bed
1021. sort -k1,1 -k2,2n ./SeqAOnly_r507s506.bed > ./SeqAOnly_r507s507.bed
1022. bedtools shuffle -seed 1 -i SeqAOnly_r507s507.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r508s507.bed
1023. sort -k1,1 -k2,2n ./SeqAOnly_r508s507.bed > ./SeqAOnly_r508s508.bed
1024. bedtools shuffle -seed 1 -i SeqAOnly_r508s508.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r509s508.bed
1025. sort -k1,1 -k2,2n ./SeqAOnly_r509s508.bed > ./SeqAOnly_r509s509.bed
1026. bedtools shuffle -seed 1 -i SeqAOnly_r509s509.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r510s509.bed
1027. sort -k1,1 -k2,2n ./SeqAOnly_r510s509.bed > ./SeqAOnly_r510s510.bed
1028. bedtools shuffle -seed 1 -i SeqAOnly_r510s510.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r511s510.bed
1029. sort -k1,1 -k2,2n ./SeqAOnly_r511s510.bed > ./SeqAOnly_r511s511.bed
1030. bedtools shuffle -seed 1 -i SeqAOnly_r511s511.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r512s511.bed
1031. sort -k1,1 -k2,2n ./SeqAOnly_r512s511.bed > ./SeqAOnly_r512s512.bed
1032. bedtools shuffle -seed 1 -i SeqAOnly_r512s512.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r513s512.bed
1033. sort -k1,1 -k2,2n ./SeqAOnly_r513s512.bed > ./SeqAOnly_r513s513.bed
1034. bedtools shuffle -seed 1 -i SeqAOnly_r513s513.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r514s513.bed
1035. sort -k1,1 -k2,2n ./SeqAOnly_r514s513.bed > ./SeqAOnly_r514s514.bed
1036. bedtools shuffle -seed 1 -i SeqAOnly_r514s514.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r515s514.bed
1037. sort -k1,1 -k2,2n ./SeqAOnly_r515s514.bed > ./SeqAOnly_r515s515.bed
1038. bedtools shuffle -seed 1 -i SeqAOnly_r515s515.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r516s515.bed
1039. sort -k1,1 -k2,2n ./SeqAOnly_r516s515.bed > ./SeqAOnly_r516s516.bed
1040. bedtools shuffle -seed 1 -i SeqAOnly_r516s516.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r517s516.bed

1041. sort -k1,1 -k2,2n ./SeqAOnly_r517s516.bed > ./SeqAOnly_r517s517.bed
1042. bedtools shuffle -seed 1 -i SeqAOnly_r517s517.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r518s517.bed
1043. sort -k1,1 -k2,2n ./SeqAOnly_r518s517.bed > ./SeqAOnly_r518s518.bed
1044. bedtools shuffle -seed 1 -i SeqAOnly_r518s518.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r519s518.bed
1045. sort -k1,1 -k2,2n ./SeqAOnly_r519s518.bed > ./SeqAOnly_r519s519.bed
1046. bedtools shuffle -seed 1 -i SeqAOnly_r519s519.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r520s519.bed
1047. sort -k1,1 -k2,2n ./SeqAOnly_r520s519.bed > ./SeqAOnly_r520s520.bed
1048. bedtools shuffle -seed 1 -i SeqAOnly_r520s520.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r521s520.bed
1049. sort -k1,1 -k2,2n ./SeqAOnly_r521s520.bed > ./SeqAOnly_r521s521.bed
1050. bedtools shuffle -seed 1 -i SeqAOnly_r521s521.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r522s521.bed
1051. sort -k1,1 -k2,2n ./SeqAOnly_r522s521.bed > ./SeqAOnly_r522s522.bed
1052. bedtools shuffle -seed 1 -i SeqAOnly_r522s522.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r523s522.bed
1053. sort -k1,1 -k2,2n ./SeqAOnly_r523s522.bed > ./SeqAOnly_r523s523.bed
1054. bedtools shuffle -seed 1 -i SeqAOnly_r523s523.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r524s523.bed
1055. sort -k1,1 -k2,2n ./SeqAOnly_r524s523.bed > ./SeqAOnly_r524s524.bed
1056. bedtools shuffle -seed 1 -i SeqAOnly_r524s524.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r525s524.bed
1057. sort -k1,1 -k2,2n ./SeqAOnly_r525s524.bed > ./SeqAOnly_r525s525.bed
1058. bedtools shuffle -seed 1 -i SeqAOnly_r525s525.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r526s525.bed
1059. sort -k1,1 -k2,2n ./SeqAOnly_r526s525.bed > ./SeqAOnly_r526s526.bed
1060. bedtools shuffle -seed 1 -i SeqAOnly_r526s526.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r527s526.bed
1061. sort -k1,1 -k2,2n ./SeqAOnly_r527s526.bed > ./SeqAOnly_r527s527.bed
1062. bedtools shuffle -seed 1 -i SeqAOnly_r527s527.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r528s527.bed
1063. sort -k1,1 -k2,2n ./SeqAOnly_r528s527.bed > ./SeqAOnly_r528s528.bed
1064. bedtools shuffle -seed 1 -i SeqAOnly_r528s528.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r529s528.bed
1065. sort -k1,1 -k2,2n ./SeqAOnly_r529s528.bed > ./SeqAOnly_r529s529.bed
1066. bedtools shuffle -seed 1 -i SeqAOnly_r529s529.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r530s529.bed
1067. sort -k1,1 -k2,2n ./SeqAOnly_r530s529.bed > ./SeqAOnly_r530s530.bed
1068. bedtools shuffle -seed 1 -i SeqAOnly_r530s530.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r531s530.bed
1069. sort -k1,1 -k2,2n ./SeqAOnly_r531s530.bed > ./SeqAOnly_r531s531.bed
1070. bedtools shuffle -seed 1 -i SeqAOnly_r531s531.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r532s531.bed
1071. sort -k1,1 -k2,2n ./SeqAOnly_r532s531.bed > ./SeqAOnly_r532s532.bed
1072. bedtools shuffle -seed 1 -i SeqAOnly_r532s532.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r533s532.bed
1073. sort -k1,1 -k2,2n ./SeqAOnly_r533s532.bed > ./SeqAOnly_r533s533.bed
1074. bedtools shuffle -seed 1 -i SeqAOnly_r533s533.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r534s533.bed
1075. sort -k1,1 -k2,2n ./SeqAOnly_r534s533.bed > ./SeqAOnly_r534s534.bed
1076. bedtools shuffle -seed 1 -i SeqAOnly_r534s534.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r535s534.bed
1077. sort -k1,1 -k2,2n ./SeqAOnly_r535s534.bed > ./SeqAOnly_r535s535.bed

1078. bedtools shuffle -seed 1 -i SeqAOnly_r535s535.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r536s535.bed
1079. sort -k1,1 -k2,2n ./SeqAOnly_r536s535.bed > ./SeqAOnly_r536s536.bed
1080. bedtools shuffle -seed 1 -i SeqAOnly_r536s536.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r537s536.bed
1081. sort -k1,1 -k2,2n ./SeqAOnly_r537s536.bed > ./SeqAOnly_r537s537.bed
1082. bedtools shuffle -seed 1 -i SeqAOnly_r537s537.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r538s537.bed
1083. sort -k1,1 -k2,2n ./SeqAOnly_r538s537.bed > ./SeqAOnly_r538s538.bed
1084. bedtools shuffle -seed 1 -i SeqAOnly_r538s538.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r539s538.bed
1085. sort -k1,1 -k2,2n ./SeqAOnly_r539s538.bed > ./SeqAOnly_r539s539.bed
1086. bedtools shuffle -seed 1 -i SeqAOnly_r539s539.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r540s539.bed
1087. sort -k1,1 -k2,2n ./SeqAOnly_r540s539.bed > ./SeqAOnly_r540s540.bed
1088. bedtools shuffle -seed 1 -i SeqAOnly_r540s540.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r541s540.bed
1089. sort -k1,1 -k2,2n ./SeqAOnly_r541s540.bed > ./SeqAOnly_r541s541.bed
1090. bedtools shuffle -seed 1 -i SeqAOnly_r541s541.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r542s541.bed
1091. sort -k1,1 -k2,2n ./SeqAOnly_r542s541.bed > ./SeqAOnly_r542s542.bed
1092. bedtools shuffle -seed 1 -i SeqAOnly_r542s542.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r543s542.bed
1093. sort -k1,1 -k2,2n ./SeqAOnly_r543s542.bed > ./SeqAOnly_r543s543.bed
1094. bedtools shuffle -seed 1 -i SeqAOnly_r543s543.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r544s543.bed
1095. sort -k1,1 -k2,2n ./SeqAOnly_r544s543.bed > ./SeqAOnly_r544s544.bed
1096. bedtools shuffle -seed 1 -i SeqAOnly_r544s544.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r545s544.bed
1097. sort -k1,1 -k2,2n ./SeqAOnly_r545s544.bed > ./SeqAOnly_r545s545.bed
1098. bedtools shuffle -seed 1 -i SeqAOnly_r545s545.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r546s545.bed
1099. sort -k1,1 -k2,2n ./SeqAOnly_r546s545.bed > ./SeqAOnly_r546s546.bed
1100. bedtools shuffle -seed 1 -i SeqAOnly_r546s546.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r547s546.bed
1101. sort -k1,1 -k2,2n ./SeqAOnly_r547s546.bed > ./SeqAOnly_r547s547.bed
1102. bedtools shuffle -seed 1 -i SeqAOnly_r547s547.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r548s547.bed
1103. sort -k1,1 -k2,2n ./SeqAOnly_r548s547.bed > ./SeqAOnly_r548s548.bed
1104. bedtools shuffle -seed 1 -i SeqAOnly_r548s548.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r549s548.bed
1105. sort -k1,1 -k2,2n ./SeqAOnly_r549s548.bed > ./SeqAOnly_r549s549.bed
1106. bedtools shuffle -seed 1 -i SeqAOnly_r549s549.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r550s549.bed
1107. sort -k1,1 -k2,2n ./SeqAOnly_r550s549.bed > ./SeqAOnly_r550s550.bed
1108. bedtools shuffle -seed 1 -i SeqAOnly_r550s550.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r551s550.bed
1109. sort -k1,1 -k2,2n ./SeqAOnly_r551s550.bed > ./SeqAOnly_r551s551.bed
1110. bedtools shuffle -seed 1 -i SeqAOnly_r551s551.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r552s551.bed
1111. sort -k1,1 -k2,2n ./SeqAOnly_r552s551.bed > ./SeqAOnly_r552s552.bed
1112. bedtools shuffle -seed 1 -i SeqAOnly_r552s552.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r553s552.bed
1113. sort -k1,1 -k2,2n ./SeqAOnly_r553s552.bed > ./SeqAOnly_r553s553.bed
1114. bedtools shuffle -seed 1 -i SeqAOnly_r553s553.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r554s553.bed

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1115.    sort -k1,1 -k2,2n ./SeqAOnly_r554s553.bed > ./SeqAOnly_r554s554.bed
1116.    bedtools shuffle -seed 1 -i SeqAOnly_r554s554.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r555s554.bed
1117.    sort -k1,1 -k2,2n ./SeqAOnly_r555s554.bed > ./SeqAOnly_r555s555.bed
1118.    bedtools shuffle -seed 1 -i SeqAOnly_r555s555.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r556s555.bed
1119.    sort -k1,1 -k2,2n ./SeqAOnly_r556s555.bed > ./SeqAOnly_r556s556.bed
1120.    bedtools shuffle -seed 1 -i SeqAOnly_r556s556.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r557s556.bed
1121.    sort -k1,1 -k2,2n ./SeqAOnly_r557s556.bed > ./SeqAOnly_r557s557.bed
1122.    bedtools shuffle -seed 1 -i SeqAOnly_r557s557.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r558s557.bed
1123.    sort -k1,1 -k2,2n ./SeqAOnly_r558s557.bed > ./SeqAOnly_r558s558.bed
1124.    bedtools shuffle -seed 1 -i SeqAOnly_r558s558.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r559s558.bed
1125.    sort -k1,1 -k2,2n ./SeqAOnly_r559s558.bed > ./SeqAOnly_r559s559.bed
1126.    bedtools shuffle -seed 1 -i SeqAOnly_r559s559.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r560s559.bed
1127.    sort -k1,1 -k2,2n ./SeqAOnly_r560s559.bed > ./SeqAOnly_r560s560.bed
1128.    bedtools shuffle -seed 1 -i SeqAOnly_r560s560.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r561s560.bed
1129.    sort -k1,1 -k2,2n ./SeqAOnly_r561s560.bed > ./SeqAOnly_r561s561.bed
1130.    bedtools shuffle -seed 1 -i SeqAOnly_r561s561.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r562s561.bed
1131.    sort -k1,1 -k2,2n ./SeqAOnly_r562s561.bed > ./SeqAOnly_r562s562.bed
1132.    bedtools shuffle -seed 1 -i SeqAOnly_r562s562.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r563s562.bed
1133.    sort -k1,1 -k2,2n ./SeqAOnly_r563s562.bed > ./SeqAOnly_r563s563.bed
1134.    bedtools shuffle -seed 1 -i SeqAOnly_r563s563.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r564s563.bed
1135.    sort -k1,1 -k2,2n ./SeqAOnly_r564s563.bed > ./SeqAOnly_r564s564.bed
1136.    bedtools shuffle -seed 1 -i SeqAOnly_r564s564.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r565s564.bed
1137.    sort -k1,1 -k2,2n ./SeqAOnly_r565s564.bed > ./SeqAOnly_r565s565.bed
1138.    bedtools shuffle -seed 1 -i SeqAOnly_r565s565.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r566s565.bed
1139.    sort -k1,1 -k2,2n ./SeqAOnly_r566s565.bed > ./SeqAOnly_r566s566.bed
1140.    bedtools shuffle -seed 1 -i SeqAOnly_r566s566.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r567s566.bed
1141.    sort -k1,1 -k2,2n ./SeqAOnly_r567s566.bed > ./SeqAOnly_r567s567.bed
1142.    bedtools shuffle -seed 1 -i SeqAOnly_r567s567.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r568s567.bed
1143.    sort -k1,1 -k2,2n ./SeqAOnly_r568s567.bed > ./SeqAOnly_r568s568.bed
1144.    bedtools shuffle -seed 1 -i SeqAOnly_r568s568.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r569s568.bed
1145.    sort -k1,1 -k2,2n ./SeqAOnly_r569s568.bed > ./SeqAOnly_r569s569.bed
1146.    bedtools shuffle -seed 1 -i SeqAOnly_r569s569.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r570s569.bed
1147.    sort -k1,1 -k2,2n ./SeqAOnly_r570s569.bed > ./SeqAOnly_r570s570.bed
1148.    bedtools shuffle -seed 1 -i SeqAOnly_r570s570.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r571s570.bed
1149.    sort -k1,1 -k2,2n ./SeqAOnly_r571s570.bed > ./SeqAOnly_r571s571.bed
1150.    bedtools shuffle -seed 1 -i SeqAOnly_r571s571.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r572s571.bed
1151.    sort -k1,1 -k2,2n ./SeqAOnly_r572s571.bed > ./SeqAOnly_r572s572.bed
```

1152. bedtools shuffle -seed 1 -i SeqAOnly_r572s572.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r573s572.bed
1153. sort -k1,1 -k2,2n ./SeqAOnly_r573s572.bed > ./SeqAOnly_r573s573.bed
1154. bedtools shuffle -seed 1 -i SeqAOnly_r573s573.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r574s573.bed
1155. sort -k1,1 -k2,2n ./SeqAOnly_r574s573.bed > ./SeqAOnly_r574s574.bed
1156. bedtools shuffle -seed 1 -i SeqAOnly_r574s574.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r575s574.bed
1157. sort -k1,1 -k2,2n ./SeqAOnly_r575s574.bed > ./SeqAOnly_r575s575.bed
1158. bedtools shuffle -seed 1 -i SeqAOnly_r575s575.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r576s575.bed
1159. sort -k1,1 -k2,2n ./SeqAOnly_r576s575.bed > ./SeqAOnly_r576s576.bed
1160. bedtools shuffle -seed 1 -i SeqAOnly_r576s576.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r577s576.bed
1161. sort -k1,1 -k2,2n ./SeqAOnly_r577s576.bed > ./SeqAOnly_r577s577.bed
1162. bedtools shuffle -seed 1 -i SeqAOnly_r577s577.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r578s577.bed
1163. sort -k1,1 -k2,2n ./SeqAOnly_r578s577.bed > ./SeqAOnly_r578s578.bed
1164. bedtools shuffle -seed 1 -i SeqAOnly_r578s578.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r579s578.bed
1165. sort -k1,1 -k2,2n ./SeqAOnly_r579s578.bed > ./SeqAOnly_r579s579.bed
1166. bedtools shuffle -seed 1 -i SeqAOnly_r579s579.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r580s579.bed
1167. sort -k1,1 -k2,2n ./SeqAOnly_r580s579.bed > ./SeqAOnly_r580s580.bed
1168. bedtools shuffle -seed 1 -i SeqAOnly_r580s580.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r581s580.bed
1169. sort -k1,1 -k2,2n ./SeqAOnly_r581s580.bed > ./SeqAOnly_r581s581.bed
1170. bedtools shuffle -seed 1 -i SeqAOnly_r581s581.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r582s581.bed
1171. sort -k1,1 -k2,2n ./SeqAOnly_r582s581.bed > ./SeqAOnly_r582s582.bed
1172. bedtools shuffle -seed 1 -i SeqAOnly_r582s582.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r583s582.bed
1173. sort -k1,1 -k2,2n ./SeqAOnly_r583s582.bed > ./SeqAOnly_r583s583.bed
1174. bedtools shuffle -seed 1 -i SeqAOnly_r583s583.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r584s583.bed
1175. sort -k1,1 -k2,2n ./SeqAOnly_r584s583.bed > ./SeqAOnly_r584s584.bed
1176. bedtools shuffle -seed 1 -i SeqAOnly_r584s584.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r585s584.bed
1177. sort -k1,1 -k2,2n ./SeqAOnly_r585s584.bed > ./SeqAOnly_r585s585.bed
1178. bedtools shuffle -seed 1 -i SeqAOnly_r585s585.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r586s585.bed
1179. sort -k1,1 -k2,2n ./SeqAOnly_r586s585.bed > ./SeqAOnly_r586s586.bed
1180. bedtools shuffle -seed 1 -i SeqAOnly_r586s586.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r587s586.bed
1181. sort -k1,1 -k2,2n ./SeqAOnly_r587s586.bed > ./SeqAOnly_r587s587.bed
1182. bedtools shuffle -seed 1 -i SeqAOnly_r587s587.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r588s587.bed
1183. sort -k1,1 -k2,2n ./SeqAOnly_r588s587.bed > ./SeqAOnly_r588s588.bed
1184. bedtools shuffle -seed 1 -i SeqAOnly_r588s588.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r589s588.bed
1185. sort -k1,1 -k2,2n ./SeqAOnly_r589s588.bed > ./SeqAOnly_r589s589.bed
1186. bedtools shuffle -seed 1 -i SeqAOnly_r589s589.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r590s589.bed
1187. sort -k1,1 -k2,2n ./SeqAOnly_r590s589.bed > ./SeqAOnly_r590s590.bed
1188. bedtools shuffle -seed 1 -i SeqAOnly_r590s590.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r591s590.bed

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1189.    sort -k1,1 -k2,2n ./SeqAOnly_r591s590.bed > ./SeqAOnly_r591s591.bed
1190.    bedtools shuffle -seed 1 -i SeqAOnly_r591s591.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r592s591.bed
1191.    sort -k1,1 -k2,2n ./SeqAOnly_r592s591.bed > ./SeqAOnly_r592s592.bed
1192.    bedtools shuffle -seed 1 -i SeqAOnly_r592s592.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r593s592.bed
1193.    sort -k1,1 -k2,2n ./SeqAOnly_r593s592.bed > ./SeqAOnly_r593s593.bed
1194.    bedtools shuffle -seed 1 -i SeqAOnly_r593s593.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r594s593.bed
1195.    sort -k1,1 -k2,2n ./SeqAOnly_r594s593.bed > ./SeqAOnly_r594s594.bed
1196.    bedtools shuffle -seed 1 -i SeqAOnly_r594s594.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r595s594.bed
1197.    sort -k1,1 -k2,2n ./SeqAOnly_r595s594.bed > ./SeqAOnly_r595s595.bed
1198.    bedtools shuffle -seed 1 -i SeqAOnly_r595s595.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r596s595.bed
1199.    sort -k1,1 -k2,2n ./SeqAOnly_r596s595.bed > ./SeqAOnly_r596s596.bed
1200.    bedtools shuffle -seed 1 -i SeqAOnly_r596s596.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r597s596.bed
1201.    sort -k1,1 -k2,2n ./SeqAOnly_r597s596.bed > ./SeqAOnly_r597s597.bed
1202.    bedtools shuffle -seed 1 -i SeqAOnly_r597s597.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r598s597.bed
1203.    sort -k1,1 -k2,2n ./SeqAOnly_r598s597.bed > ./SeqAOnly_r598s598.bed
1204.    bedtools shuffle -seed 1 -i SeqAOnly_r598s598.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r599s598.bed
1205.    sort -k1,1 -k2,2n ./SeqAOnly_r599s598.bed > ./SeqAOnly_r599s599.bed
1206.    bedtools shuffle -seed 1 -i SeqAOnly_r599s599.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r600s599.bed
1207.    sort -k1,1 -k2,2n ./SeqAOnly_r600s599.bed > ./SeqAOnly_r600s600.bed
1208.    bedtools shuffle -seed 1 -i SeqAOnly_r600s600.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r601s600.bed
1209.    sort -k1,1 -k2,2n ./SeqAOnly_r601s600.bed > ./SeqAOnly_r601s601.bed
1210.    bedtools shuffle -seed 1 -i SeqAOnly_r601s601.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r602s601.bed
1211.    sort -k1,1 -k2,2n ./SeqAOnly_r602s601.bed > ./SeqAOnly_r602s602.bed
1212.    bedtools shuffle -seed 1 -i SeqAOnly_r602s602.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r603s602.bed
1213.    sort -k1,1 -k2,2n ./SeqAOnly_r603s602.bed > ./SeqAOnly_r603s603.bed
1214.    bedtools shuffle -seed 1 -i SeqAOnly_r603s603.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r604s603.bed
1215.    sort -k1,1 -k2,2n ./SeqAOnly_r604s603.bed > ./SeqAOnly_r604s604.bed
1216.    bedtools shuffle -seed 1 -i SeqAOnly_r604s604.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r605s604.bed
1217.    sort -k1,1 -k2,2n ./SeqAOnly_r605s604.bed > ./SeqAOnly_r605s605.bed
1218.    bedtools shuffle -seed 1 -i SeqAOnly_r605s605.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r606s605.bed
1219.    sort -k1,1 -k2,2n ./SeqAOnly_r606s605.bed > ./SeqAOnly_r606s606.bed
1220.    bedtools shuffle -seed 1 -i SeqAOnly_r606s606.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r607s606.bed
1221.    sort -k1,1 -k2,2n ./SeqAOnly_r607s606.bed > ./SeqAOnly_r607s607.bed
1222.    bedtools shuffle -seed 1 -i SeqAOnly_r607s607.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r608s607.bed
1223.    sort -k1,1 -k2,2n ./SeqAOnly_r608s607.bed > ./SeqAOnly_r608s608.bed
1224.    bedtools shuffle -seed 1 -i SeqAOnly_r608s608.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r609s608.bed
1225.    sort -k1,1 -k2,2n ./SeqAOnly_r609s608.bed > ./SeqAOnly_r609s609.bed
```

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1226. bedtools shuffle -seed 1 -i SeqAOnly_r609s609.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r610s609.bed
1227. sort -k1,1 -k2,2n ./SeqAOnly_r610s609.bed > ./SeqAOnly_r610s610.bed
1228. bedtools shuffle -seed 1 -i SeqAOnly_r610s610.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r611s610.bed
1229. sort -k1,1 -k2,2n ./SeqAOnly_r611s610.bed > ./SeqAOnly_r611s611.bed
1230. bedtools shuffle -seed 1 -i SeqAOnly_r611s611.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r612s611.bed
1231. sort -k1,1 -k2,2n ./SeqAOnly_r612s611.bed > ./SeqAOnly_r612s612.bed
1232. bedtools shuffle -seed 1 -i SeqAOnly_r612s612.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r613s612.bed
1233. sort -k1,1 -k2,2n ./SeqAOnly_r613s612.bed > ./SeqAOnly_r613s613.bed
1234. bedtools shuffle -seed 1 -i SeqAOnly_r613s613.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r614s613.bed
1235. sort -k1,1 -k2,2n ./SeqAOnly_r614s613.bed > ./SeqAOnly_r614s614.bed
1236. bedtools shuffle -seed 1 -i SeqAOnly_r614s614.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r615s614.bed
1237. sort -k1,1 -k2,2n ./SeqAOnly_r615s614.bed > ./SeqAOnly_r615s615.bed
1238. bedtools shuffle -seed 1 -i SeqAOnly_r615s615.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r616s615.bed
1239. sort -k1,1 -k2,2n ./SeqAOnly_r616s615.bed > ./SeqAOnly_r616s616.bed
1240. bedtools shuffle -seed 1 -i SeqAOnly_r616s616.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r617s616.bed
1241. sort -k1,1 -k2,2n ./SeqAOnly_r617s616.bed > ./SeqAOnly_r617s617.bed
1242. bedtools shuffle -seed 1 -i SeqAOnly_r617s617.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r618s617.bed
1243. sort -k1,1 -k2,2n ./SeqAOnly_r618s617.bed > ./SeqAOnly_r618s618.bed
1244. bedtools shuffle -seed 1 -i SeqAOnly_r618s618.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r619s618.bed
1245. sort -k1,1 -k2,2n ./SeqAOnly_r619s618.bed > ./SeqAOnly_r619s619.bed
1246. bedtools shuffle -seed 1 -i SeqAOnly_r619s619.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r620s619.bed
1247. sort -k1,1 -k2,2n ./SeqAOnly_r620s619.bed > ./SeqAOnly_r620s620.bed
1248. bedtools shuffle -seed 1 -i SeqAOnly_r620s620.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r621s620.bed
1249. sort -k1,1 -k2,2n ./SeqAOnly_r621s620.bed > ./SeqAOnly_r621s621.bed
1250. bedtools shuffle -seed 1 -i SeqAOnly_r621s621.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r622s621.bed
1251. sort -k1,1 -k2,2n ./SeqAOnly_r622s621.bed > ./SeqAOnly_r622s622.bed
1252. bedtools shuffle -seed 1 -i SeqAOnly_r622s622.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r623s622.bed
1253. sort -k1,1 -k2,2n ./SeqAOnly_r623s622.bed > ./SeqAOnly_r623s623.bed
1254. bedtools shuffle -seed 1 -i SeqAOnly_r623s623.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r624s623.bed
1255. sort -k1,1 -k2,2n ./SeqAOnly_r624s623.bed > ./SeqAOnly_r624s624.bed
1256. bedtools shuffle -seed 1 -i SeqAOnly_r624s624.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r625s624.bed
1257. sort -k1,1 -k2,2n ./SeqAOnly_r625s624.bed > ./SeqAOnly_r625s625.bed
1258. bedtools shuffle -seed 1 -i SeqAOnly_r625s625.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r626s625.bed
1259. sort -k1,1 -k2,2n ./SeqAOnly_r626s625.bed > ./SeqAOnly_r626s626.bed
1260. bedtools shuffle -seed 1 -i SeqAOnly_r626s626.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r627s626.bed
1261. sort -k1,1 -k2,2n ./SeqAOnly_r627s626.bed > ./SeqAOnly_r627s627.bed
1262. bedtools shuffle -seed 1 -i SeqAOnly_r627s627.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r628s627.bed

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1263.    sort -k1,1 -k2,2n ./SeqAOnly_r628s627.bed > ./SeqAOnly_r628s628.bed
1264.    bedtools shuffle -seed 1 -i SeqAOnly_r628s628.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r629s628.bed
1265.    sort -k1,1 -k2,2n ./SeqAOnly_r629s628.bed > ./SeqAOnly_r629s629.bed
1266.    bedtools shuffle -seed 1 -i SeqAOnly_r629s629.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r630s629.bed
1267.    sort -k1,1 -k2,2n ./SeqAOnly_r630s629.bed > ./SeqAOnly_r630s630.bed
1268.    bedtools shuffle -seed 1 -i SeqAOnly_r630s630.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r631s630.bed
1269.    sort -k1,1 -k2,2n ./SeqAOnly_r631s630.bed > ./SeqAOnly_r631s631.bed
1270.    bedtools shuffle -seed 1 -i SeqAOnly_r631s631.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r632s631.bed
1271.    sort -k1,1 -k2,2n ./SeqAOnly_r632s631.bed > ./SeqAOnly_r632s632.bed
1272.    bedtools shuffle -seed 1 -i SeqAOnly_r632s632.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r633s632.bed
1273.    sort -k1,1 -k2,2n ./SeqAOnly_r633s632.bed > ./SeqAOnly_r633s633.bed
1274.    bedtools shuffle -seed 1 -i SeqAOnly_r633s633.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r634s633.bed
1275.    sort -k1,1 -k2,2n ./SeqAOnly_r634s633.bed > ./SeqAOnly_r634s634.bed
1276.    bedtools shuffle -seed 1 -i SeqAOnly_r634s634.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r635s634.bed
1277.    sort -k1,1 -k2,2n ./SeqAOnly_r635s634.bed > ./SeqAOnly_r635s635.bed
1278.    bedtools shuffle -seed 1 -i SeqAOnly_r635s635.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r636s635.bed
1279.    sort -k1,1 -k2,2n ./SeqAOnly_r636s635.bed > ./SeqAOnly_r636s636.bed
1280.    bedtools shuffle -seed 1 -i SeqAOnly_r636s636.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r637s636.bed
1281.    sort -k1,1 -k2,2n ./SeqAOnly_r637s636.bed > ./SeqAOnly_r637s637.bed
1282.    bedtools shuffle -seed 1 -i SeqAOnly_r637s637.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r638s637.bed
1283.    sort -k1,1 -k2,2n ./SeqAOnly_r638s637.bed > ./SeqAOnly_r638s638.bed
1284.    bedtools shuffle -seed 1 -i SeqAOnly_r638s638.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r639s638.bed
1285.    sort -k1,1 -k2,2n ./SeqAOnly_r639s638.bed > ./SeqAOnly_r639s639.bed
1286.    bedtools shuffle -seed 1 -i SeqAOnly_r639s639.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r640s639.bed
1287.    sort -k1,1 -k2,2n ./SeqAOnly_r640s639.bed > ./SeqAOnly_r640s640.bed
1288.    bedtools shuffle -seed 1 -i SeqAOnly_r640s640.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r641s640.bed
1289.    sort -k1,1 -k2,2n ./SeqAOnly_r641s640.bed > ./SeqAOnly_r641s641.bed
1290.    bedtools shuffle -seed 1 -i SeqAOnly_r641s641.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r642s641.bed
1291.    sort -k1,1 -k2,2n ./SeqAOnly_r642s641.bed > ./SeqAOnly_r642s642.bed
1292.    bedtools shuffle -seed 1 -i SeqAOnly_r642s642.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r643s642.bed
1293.    sort -k1,1 -k2,2n ./SeqAOnly_r643s642.bed > ./SeqAOnly_r643s643.bed
1294.    bedtools shuffle -seed 1 -i SeqAOnly_r643s643.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r644s643.bed
1295.    sort -k1,1 -k2,2n ./SeqAOnly_r644s643.bed > ./SeqAOnly_r644s644.bed
1296.    bedtools shuffle -seed 1 -i SeqAOnly_r644s644.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r645s644.bed
1297.    sort -k1,1 -k2,2n ./SeqAOnly_r645s644.bed > ./SeqAOnly_r645s645.bed
1298.    bedtools shuffle -seed 1 -i SeqAOnly_r645s645.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r646s645.bed
1299.    sort -k1,1 -k2,2n ./SeqAOnly_r646s645.bed > ./SeqAOnly_r646s646.bed
```

1300. bedtools shuffle -seed 1 -i SeqAOnly_r646s646.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r647s646.bed
1301. sort -k1,1 -k2,2n ./SeqAOnly_r647s646.bed > ./SeqAOnly_r647s647.bed
1302. bedtools shuffle -seed 1 -i SeqAOnly_r647s647.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r648s647.bed
1303. sort -k1,1 -k2,2n ./SeqAOnly_r648s647.bed > ./SeqAOnly_r648s648.bed
1304. bedtools shuffle -seed 1 -i SeqAOnly_r648s648.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r649s648.bed
1305. sort -k1,1 -k2,2n ./SeqAOnly_r649s648.bed > ./SeqAOnly_r649s649.bed
1306. bedtools shuffle -seed 1 -i SeqAOnly_r649s649.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r650s649.bed
1307. sort -k1,1 -k2,2n ./SeqAOnly_r650s649.bed > ./SeqAOnly_r650s650.bed
1308. bedtools shuffle -seed 1 -i SeqAOnly_r650s650.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r651s650.bed
1309. sort -k1,1 -k2,2n ./SeqAOnly_r651s650.bed > ./SeqAOnly_r651s651.bed
1310. bedtools shuffle -seed 1 -i SeqAOnly_r651s651.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r652s651.bed
1311. sort -k1,1 -k2,2n ./SeqAOnly_r652s651.bed > ./SeqAOnly_r652s652.bed
1312. bedtools shuffle -seed 1 -i SeqAOnly_r652s652.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r653s652.bed
1313. sort -k1,1 -k2,2n ./SeqAOnly_r653s652.bed > ./SeqAOnly_r653s653.bed
1314. bedtools shuffle -seed 1 -i SeqAOnly_r653s653.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r654s653.bed
1315. sort -k1,1 -k2,2n ./SeqAOnly_r654s653.bed > ./SeqAOnly_r654s654.bed
1316. bedtools shuffle -seed 1 -i SeqAOnly_r654s654.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r655s654.bed
1317. sort -k1,1 -k2,2n ./SeqAOnly_r655s654.bed > ./SeqAOnly_r655s655.bed
1318. bedtools shuffle -seed 1 -i SeqAOnly_r655s655.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r656s655.bed
1319. sort -k1,1 -k2,2n ./SeqAOnly_r656s655.bed > ./SeqAOnly_r656s656.bed
1320. bedtools shuffle -seed 1 -i SeqAOnly_r656s656.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r657s656.bed
1321. sort -k1,1 -k2,2n ./SeqAOnly_r657s656.bed > ./SeqAOnly_r657s657.bed
1322. bedtools shuffle -seed 1 -i SeqAOnly_r657s657.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r658s657.bed
1323. sort -k1,1 -k2,2n ./SeqAOnly_r658s657.bed > ./SeqAOnly_r658s658.bed
1324. bedtools shuffle -seed 1 -i SeqAOnly_r658s658.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r659s658.bed
1325. sort -k1,1 -k2,2n ./SeqAOnly_r659s658.bed > ./SeqAOnly_r659s659.bed
1326. bedtools shuffle -seed 1 -i SeqAOnly_r659s659.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r660s659.bed
1327. sort -k1,1 -k2,2n ./SeqAOnly_r660s659.bed > ./SeqAOnly_r660s660.bed
1328. bedtools shuffle -seed 1 -i SeqAOnly_r660s660.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r661s660.bed
1329. sort -k1,1 -k2,2n ./SeqAOnly_r661s660.bed > ./SeqAOnly_r661s661.bed
1330. bedtools shuffle -seed 1 -i SeqAOnly_r661s661.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r662s661.bed
1331. sort -k1,1 -k2,2n ./SeqAOnly_r662s661.bed > ./SeqAOnly_r662s662.bed
1332. bedtools shuffle -seed 1 -i SeqAOnly_r662s662.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r663s662.bed
1333. sort -k1,1 -k2,2n ./SeqAOnly_r663s662.bed > ./SeqAOnly_r663s663.bed
1334. bedtools shuffle -seed 1 -i SeqAOnly_r663s663.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r664s663.bed
1335. sort -k1,1 -k2,2n ./SeqAOnly_r664s663.bed > ./SeqAOnly_r664s664.bed
1336. bedtools shuffle -seed 1 -i SeqAOnly_r664s664.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r665s664.bed

1337. sort -k1,1 -k2,2n ./SeqAOnly_r665s664.bed > ./SeqAOnly_r665s665.bed
1338. bedtools shuffle -seed 1 -i SeqAOnly_r665s665.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r666s665.bed
1339. sort -k1,1 -k2,2n ./SeqAOnly_r666s665.bed > ./SeqAOnly_r666s666.bed
1340. bedtools shuffle -seed 1 -i SeqAOnly_r666s666.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r667s666.bed
1341. sort -k1,1 -k2,2n ./SeqAOnly_r667s666.bed > ./SeqAOnly_r667s667.bed
1342. bedtools shuffle -seed 1 -i SeqAOnly_r667s667.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r668s667.bed
1343. sort -k1,1 -k2,2n ./SeqAOnly_r668s667.bed > ./SeqAOnly_r668s668.bed
1344. bedtools shuffle -seed 1 -i SeqAOnly_r668s668.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r669s668.bed
1345. sort -k1,1 -k2,2n ./SeqAOnly_r669s668.bed > ./SeqAOnly_r669s669.bed
1346. bedtools shuffle -seed 1 -i SeqAOnly_r669s669.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r670s669.bed
1347. sort -k1,1 -k2,2n ./SeqAOnly_r670s669.bed > ./SeqAOnly_r670s670.bed
1348. bedtools shuffle -seed 1 -i SeqAOnly_r670s670.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r671s670.bed
1349. sort -k1,1 -k2,2n ./SeqAOnly_r671s670.bed > ./SeqAOnly_r671s671.bed
1350. bedtools shuffle -seed 1 -i SeqAOnly_r671s671.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r672s671.bed
1351. sort -k1,1 -k2,2n ./SeqAOnly_r672s671.bed > ./SeqAOnly_r672s672.bed
1352. bedtools shuffle -seed 1 -i SeqAOnly_r672s672.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r673s672.bed
1353. sort -k1,1 -k2,2n ./SeqAOnly_r673s672.bed > ./SeqAOnly_r673s673.bed
1354. bedtools shuffle -seed 1 -i SeqAOnly_r673s673.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r674s673.bed
1355. sort -k1,1 -k2,2n ./SeqAOnly_r674s673.bed > ./SeqAOnly_r674s674.bed
1356. bedtools shuffle -seed 1 -i SeqAOnly_r674s674.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r675s674.bed
1357. sort -k1,1 -k2,2n ./SeqAOnly_r675s674.bed > ./SeqAOnly_r675s675.bed
1358. bedtools shuffle -seed 1 -i SeqAOnly_r675s675.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r676s675.bed
1359. sort -k1,1 -k2,2n ./SeqAOnly_r676s675.bed > ./SeqAOnly_r676s676.bed
1360. bedtools shuffle -seed 1 -i SeqAOnly_r676s676.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r677s676.bed
1361. sort -k1,1 -k2,2n ./SeqAOnly_r677s676.bed > ./SeqAOnly_r677s677.bed
1362. bedtools shuffle -seed 1 -i SeqAOnly_r677s677.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r678s677.bed
1363. sort -k1,1 -k2,2n ./SeqAOnly_r678s677.bed > ./SeqAOnly_r678s678.bed
1364. bedtools shuffle -seed 1 -i SeqAOnly_r678s678.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r679s678.bed
1365. sort -k1,1 -k2,2n ./SeqAOnly_r679s678.bed > ./SeqAOnly_r679s679.bed
1366. bedtools shuffle -seed 1 -i SeqAOnly_r679s679.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r680s679.bed
1367. sort -k1,1 -k2,2n ./SeqAOnly_r680s679.bed > ./SeqAOnly_r680s680.bed
1368. bedtools shuffle -seed 1 -i SeqAOnly_r680s680.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r681s680.bed
1369. sort -k1,1 -k2,2n ./SeqAOnly_r681s680.bed > ./SeqAOnly_r681s681.bed
1370. bedtools shuffle -seed 1 -i SeqAOnly_r681s681.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r682s681.bed
1371. sort -k1,1 -k2,2n ./SeqAOnly_r682s681.bed > ./SeqAOnly_r682s682.bed
1372. bedtools shuffle -seed 1 -i SeqAOnly_r682s682.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r683s682.bed
1373. sort -k1,1 -k2,2n ./SeqAOnly_r683s682.bed > ./SeqAOnly_r683s683.bed


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1374. bedtools shuffle -seed 1 -i SeqAOnly_r683s683.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r684s683.bed
1375. sort -k1,1 -k2,2n ./SeqAOnly_r684s683.bed > ./SeqAOnly_r684s684.bed
1376. bedtools shuffle -seed 1 -i SeqAOnly_r684s684.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r685s684.bed
1377. sort -k1,1 -k2,2n ./SeqAOnly_r685s684.bed > ./SeqAOnly_r685s685.bed
1378. bedtools shuffle -seed 1 -i SeqAOnly_r685s685.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r686s685.bed
1379. sort -k1,1 -k2,2n ./SeqAOnly_r686s685.bed > ./SeqAOnly_r686s686.bed
1380. bedtools shuffle -seed 1 -i SeqAOnly_r686s686.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r687s686.bed
1381. sort -k1,1 -k2,2n ./SeqAOnly_r687s686.bed > ./SeqAOnly_r687s687.bed
1382. bedtools shuffle -seed 1 -i SeqAOnly_r687s687.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r688s687.bed
1383. sort -k1,1 -k2,2n ./SeqAOnly_r688s687.bed > ./SeqAOnly_r688s688.bed
1384. bedtools shuffle -seed 1 -i SeqAOnly_r688s688.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r689s688.bed
1385. sort -k1,1 -k2,2n ./SeqAOnly_r689s688.bed > ./SeqAOnly_r689s689.bed
1386. bedtools shuffle -seed 1 -i SeqAOnly_r689s689.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r690s689.bed
1387. sort -k1,1 -k2,2n ./SeqAOnly_r690s689.bed > ./SeqAOnly_r690s690.bed
1388. bedtools shuffle -seed 1 -i SeqAOnly_r690s690.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r691s690.bed
1389. sort -k1,1 -k2,2n ./SeqAOnly_r691s690.bed > ./SeqAOnly_r691s691.bed
1390. bedtools shuffle -seed 1 -i SeqAOnly_r691s691.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r692s691.bed
1391. sort -k1,1 -k2,2n ./SeqAOnly_r692s691.bed > ./SeqAOnly_r692s692.bed
1392. bedtools shuffle -seed 1 -i SeqAOnly_r692s692.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r693s692.bed
1393. sort -k1,1 -k2,2n ./SeqAOnly_r693s692.bed > ./SeqAOnly_r693s693.bed
1394. bedtools shuffle -seed 1 -i SeqAOnly_r693s693.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r694s693.bed
1395. sort -k1,1 -k2,2n ./SeqAOnly_r694s693.bed > ./SeqAOnly_r694s694.bed
1396. bedtools shuffle -seed 1 -i SeqAOnly_r694s694.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r695s694.bed
1397. sort -k1,1 -k2,2n ./SeqAOnly_r695s694.bed > ./SeqAOnly_r695s695.bed
1398. bedtools shuffle -seed 1 -i SeqAOnly_r695s695.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r696s695.bed
1399. sort -k1,1 -k2,2n ./SeqAOnly_r696s695.bed > ./SeqAOnly_r696s696.bed
1400. bedtools shuffle -seed 1 -i SeqAOnly_r696s696.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r697s696.bed
1401. sort -k1,1 -k2,2n ./SeqAOnly_r697s696.bed > ./SeqAOnly_r697s697.bed
1402. bedtools shuffle -seed 1 -i SeqAOnly_r697s697.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r698s697.bed
1403. sort -k1,1 -k2,2n ./SeqAOnly_r698s697.bed > ./SeqAOnly_r698s698.bed
1404. bedtools shuffle -seed 1 -i SeqAOnly_r698s698.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r699s698.bed
1405. sort -k1,1 -k2,2n ./SeqAOnly_r699s698.bed > ./SeqAOnly_r699s699.bed
1406. bedtools shuffle -seed 1 -i SeqAOnly_r699s699.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r700s699.bed
1407. sort -k1,1 -k2,2n ./SeqAOnly_r700s699.bed > ./SeqAOnly_r700s700.bed
1408. bedtools shuffle -seed 1 -i SeqAOnly_r700s700.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r701s700.bed
1409. sort -k1,1 -k2,2n ./SeqAOnly_r701s700.bed > ./SeqAOnly_r701s701.bed
1410. bedtools shuffle -seed 1 -i SeqAOnly_r701s701.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r702s701.bed

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1411.    sort -k1,1 -k2,2n ./SeqAOnly_r702s701.bed > ./SeqAOnly_r702s702.bed
1412.    bedtools shuffle -seed 1 -i SeqAOnly_r702s702.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r703s702.bed
1413.    sort -k1,1 -k2,2n ./SeqAOnly_r703s702.bed > ./SeqAOnly_r703s703.bed
1414.    bedtools shuffle -seed 1 -i SeqAOnly_r703s703.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r704s703.bed
1415.    sort -k1,1 -k2,2n ./SeqAOnly_r704s703.bed > ./SeqAOnly_r704s704.bed
1416.    bedtools shuffle -seed 1 -i SeqAOnly_r704s704.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r705s704.bed
1417.    sort -k1,1 -k2,2n ./SeqAOnly_r705s704.bed > ./SeqAOnly_r705s705.bed
1418.    bedtools shuffle -seed 1 -i SeqAOnly_r705s705.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r706s705.bed
1419.    sort -k1,1 -k2,2n ./SeqAOnly_r706s705.bed > ./SeqAOnly_r706s706.bed
1420.    bedtools shuffle -seed 1 -i SeqAOnly_r706s706.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r707s706.bed
1421.    sort -k1,1 -k2,2n ./SeqAOnly_r707s706.bed > ./SeqAOnly_r707s707.bed
1422.    bedtools shuffle -seed 1 -i SeqAOnly_r707s707.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r708s707.bed
1423.    sort -k1,1 -k2,2n ./SeqAOnly_r708s707.bed > ./SeqAOnly_r708s708.bed
1424.    bedtools shuffle -seed 1 -i SeqAOnly_r708s708.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r709s708.bed
1425.    sort -k1,1 -k2,2n ./SeqAOnly_r709s708.bed > ./SeqAOnly_r709s709.bed
1426.    bedtools shuffle -seed 1 -i SeqAOnly_r709s709.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r710s709.bed
1427.    sort -k1,1 -k2,2n ./SeqAOnly_r710s709.bed > ./SeqAOnly_r710s710.bed
1428.    bedtools shuffle -seed 1 -i SeqAOnly_r710s710.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r711s710.bed
1429.    sort -k1,1 -k2,2n ./SeqAOnly_r711s710.bed > ./SeqAOnly_r711s711.bed
1430.    bedtools shuffle -seed 1 -i SeqAOnly_r711s711.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r712s711.bed
1431.    sort -k1,1 -k2,2n ./SeqAOnly_r712s711.bed > ./SeqAOnly_r712s712.bed
1432.    bedtools shuffle -seed 1 -i SeqAOnly_r712s712.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r713s712.bed
1433.    sort -k1,1 -k2,2n ./SeqAOnly_r713s712.bed > ./SeqAOnly_r713s713.bed
1434.    bedtools shuffle -seed 1 -i SeqAOnly_r713s713.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r714s713.bed
1435.    sort -k1,1 -k2,2n ./SeqAOnly_r714s713.bed > ./SeqAOnly_r714s714.bed
1436.    bedtools shuffle -seed 1 -i SeqAOnly_r714s714.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r715s714.bed
1437.    sort -k1,1 -k2,2n ./SeqAOnly_r715s714.bed > ./SeqAOnly_r715s715.bed
1438.    bedtools shuffle -seed 1 -i SeqAOnly_r715s715.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r716s715.bed
1439.    sort -k1,1 -k2,2n ./SeqAOnly_r716s715.bed > ./SeqAOnly_r716s716.bed
1440.    bedtools shuffle -seed 1 -i SeqAOnly_r716s716.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r717s716.bed
1441.    sort -k1,1 -k2,2n ./SeqAOnly_r717s716.bed > ./SeqAOnly_r717s717.bed
1442.    bedtools shuffle -seed 1 -i SeqAOnly_r717s717.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r718s717.bed
1443.    sort -k1,1 -k2,2n ./SeqAOnly_r718s717.bed > ./SeqAOnly_r718s718.bed
1444.    bedtools shuffle -seed 1 -i SeqAOnly_r718s718.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r719s718.bed
1445.    sort -k1,1 -k2,2n ./SeqAOnly_r719s718.bed > ./SeqAOnly_r719s719.bed
1446.    bedtools shuffle -seed 1 -i SeqAOnly_r719s719.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r720s719.bed
1447.    sort -k1,1 -k2,2n ./SeqAOnly_r720s719.bed > ./SeqAOnly_r720s720.bed
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1448. bedtools shuffle -seed 1 -i SeqAOnly_r720s720.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r721s720.bed
1449. sort -k1,1 -k2,2n ./SeqAOnly_r721s720.bed > ./SeqAOnly_r721s721.bed
1450. bedtools shuffle -seed 1 -i SeqAOnly_r721s721.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r722s721.bed
1451. sort -k1,1 -k2,2n ./SeqAOnly_r722s721.bed > ./SeqAOnly_r722s722.bed
1452. bedtools shuffle -seed 1 -i SeqAOnly_r722s722.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r723s722.bed
1453. sort -k1,1 -k2,2n ./SeqAOnly_r723s722.bed > ./SeqAOnly_r723s723.bed
1454. bedtools shuffle -seed 1 -i SeqAOnly_r723s723.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r724s723.bed
1455. sort -k1,1 -k2,2n ./SeqAOnly_r724s723.bed > ./SeqAOnly_r724s724.bed
1456. bedtools shuffle -seed 1 -i SeqAOnly_r724s724.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r725s724.bed
1457. sort -k1,1 -k2,2n ./SeqAOnly_r725s724.bed > ./SeqAOnly_r725s725.bed
1458. bedtools shuffle -seed 1 -i SeqAOnly_r725s725.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r726s725.bed
1459. sort -k1,1 -k2,2n ./SeqAOnly_r726s725.bed > ./SeqAOnly_r726s726.bed
1460. bedtools shuffle -seed 1 -i SeqAOnly_r726s726.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r727s726.bed
1461. sort -k1,1 -k2,2n ./SeqAOnly_r727s726.bed > ./SeqAOnly_r727s727.bed
1462. bedtools shuffle -seed 1 -i SeqAOnly_r727s727.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r728s727.bed
1463. sort -k1,1 -k2,2n ./SeqAOnly_r728s727.bed > ./SeqAOnly_r728s728.bed
1464. bedtools shuffle -seed 1 -i SeqAOnly_r728s728.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r729s728.bed
1465. sort -k1,1 -k2,2n ./SeqAOnly_r729s728.bed > ./SeqAOnly_r729s729.bed
1466. bedtools shuffle -seed 1 -i SeqAOnly_r729s729.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r730s729.bed
1467. sort -k1,1 -k2,2n ./SeqAOnly_r730s729.bed > ./SeqAOnly_r730s730.bed
1468. bedtools shuffle -seed 1 -i SeqAOnly_r730s730.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r731s730.bed
1469. sort -k1,1 -k2,2n ./SeqAOnly_r731s730.bed > ./SeqAOnly_r731s731.bed
1470. bedtools shuffle -seed 1 -i SeqAOnly_r731s731.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r732s731.bed
1471. sort -k1,1 -k2,2n ./SeqAOnly_r732s731.bed > ./SeqAOnly_r732s732.bed
1472. bedtools shuffle -seed 1 -i SeqAOnly_r732s732.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r733s732.bed
1473. sort -k1,1 -k2,2n ./SeqAOnly_r733s732.bed > ./SeqAOnly_r733s733.bed
1474. bedtools shuffle -seed 1 -i SeqAOnly_r733s733.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r734s733.bed
1475. sort -k1,1 -k2,2n ./SeqAOnly_r734s733.bed > ./SeqAOnly_r734s734.bed
1476. bedtools shuffle -seed 1 -i SeqAOnly_r734s734.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r735s734.bed
1477. sort -k1,1 -k2,2n ./SeqAOnly_r735s734.bed > ./SeqAOnly_r735s735.bed
1478. bedtools shuffle -seed 1 -i SeqAOnly_r735s735.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r736s735.bed
1479. sort -k1,1 -k2,2n ./SeqAOnly_r736s735.bed > ./SeqAOnly_r736s736.bed
1480. bedtools shuffle -seed 1 -i SeqAOnly_r736s736.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r737s736.bed
1481. sort -k1,1 -k2,2n ./SeqAOnly_r737s736.bed > ./SeqAOnly_r737s737.bed
1482. bedtools shuffle -seed 1 -i SeqAOnly_r737s737.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r738s737.bed
1483. sort -k1,1 -k2,2n ./SeqAOnly_r738s737.bed > ./SeqAOnly_r738s738.bed
1484. bedtools shuffle -seed 1 -i SeqAOnly_r738s738.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r739s738.bed

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1485.    sort -k1,1 -k2,2n ./SeqAOnly_r739s738.bed > ./SeqAOnly_r739s739.bed
1486.    bedtools shuffle -seed 1 -i SeqAOnly_r739s739.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r740s739.bed
1487.    sort -k1,1 -k2,2n ./SeqAOnly_r740s739.bed > ./SeqAOnly_r740s740.bed
1488.    bedtools shuffle -seed 1 -i SeqAOnly_r740s740.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r741s740.bed
1489.    sort -k1,1 -k2,2n ./SeqAOnly_r741s740.bed > ./SeqAOnly_r741s741.bed
1490.    bedtools shuffle -seed 1 -i SeqAOnly_r741s741.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r742s741.bed
1491.    sort -k1,1 -k2,2n ./SeqAOnly_r742s741.bed > ./SeqAOnly_r742s742.bed
1492.    bedtools shuffle -seed 1 -i SeqAOnly_r742s742.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r743s742.bed
1493.    sort -k1,1 -k2,2n ./SeqAOnly_r743s742.bed > ./SeqAOnly_r743s743.bed
1494.    bedtools shuffle -seed 1 -i SeqAOnly_r743s743.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r744s743.bed
1495.    sort -k1,1 -k2,2n ./SeqAOnly_r744s743.bed > ./SeqAOnly_r744s744.bed
1496.    bedtools shuffle -seed 1 -i SeqAOnly_r744s744.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r745s744.bed
1497.    sort -k1,1 -k2,2n ./SeqAOnly_r745s744.bed > ./SeqAOnly_r745s745.bed
1498.    bedtools shuffle -seed 1 -i SeqAOnly_r745s745.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r746s745.bed
1499.    sort -k1,1 -k2,2n ./SeqAOnly_r746s745.bed > ./SeqAOnly_r746s746.bed
1500.    bedtools shuffle -seed 1 -i SeqAOnly_r746s746.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r747s746.bed
1501.    sort -k1,1 -k2,2n ./SeqAOnly_r747s746.bed > ./SeqAOnly_r747s747.bed
1502.    bedtools shuffle -seed 1 -i SeqAOnly_r747s747.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r748s747.bed
1503.    sort -k1,1 -k2,2n ./SeqAOnly_r748s747.bed > ./SeqAOnly_r748s748.bed
1504.    bedtools shuffle -seed 1 -i SeqAOnly_r748s748.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r749s748.bed
1505.    sort -k1,1 -k2,2n ./SeqAOnly_r749s748.bed > ./SeqAOnly_r749s749.bed
1506.    bedtools shuffle -seed 1 -i SeqAOnly_r749s749.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r750s749.bed
1507.    sort -k1,1 -k2,2n ./SeqAOnly_r750s749.bed > ./SeqAOnly_r750s750.bed
1508.    bedtools shuffle -seed 1 -i SeqAOnly_r750s750.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r751s750.bed
1509.    sort -k1,1 -k2,2n ./SeqAOnly_r751s750.bed > ./SeqAOnly_r751s751.bed
1510.    bedtools shuffle -seed 1 -i SeqAOnly_r751s751.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r752s751.bed
1511.    sort -k1,1 -k2,2n ./SeqAOnly_r752s751.bed > ./SeqAOnly_r752s752.bed
1512.    bedtools shuffle -seed 1 -i SeqAOnly_r752s752.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r753s752.bed
1513.    sort -k1,1 -k2,2n ./SeqAOnly_r753s752.bed > ./SeqAOnly_r753s753.bed
1514.    bedtools shuffle -seed 1 -i SeqAOnly_r753s753.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r754s753.bed
1515.    sort -k1,1 -k2,2n ./SeqAOnly_r754s753.bed > ./SeqAOnly_r754s754.bed
1516.    bedtools shuffle -seed 1 -i SeqAOnly_r754s754.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r755s754.bed
1517.    sort -k1,1 -k2,2n ./SeqAOnly_r755s754.bed > ./SeqAOnly_r755s755.bed
1518.    bedtools shuffle -seed 1 -i SeqAOnly_r755s755.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r756s755.bed
1519.    sort -k1,1 -k2,2n ./SeqAOnly_r756s755.bed > ./SeqAOnly_r756s756.bed
1520.    bedtools shuffle -seed 1 -i SeqAOnly_r756s756.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r757s756.bed
1521.    sort -k1,1 -k2,2n ./SeqAOnly_r757s756.bed > ./SeqAOnly_r757s757.bed
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1522. bedtools shuffle -seed 1 -i SeqAOnly_r757s757.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r758s757.bed
1523. sort -k1,1 -k2,2n ./SeqAOnly_r758s757.bed > ./SeqAOnly_r758s758.bed
1524. bedtools shuffle -seed 1 -i SeqAOnly_r758s758.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r759s758.bed
1525. sort -k1,1 -k2,2n ./SeqAOnly_r759s758.bed > ./SeqAOnly_r759s759.bed
1526. bedtools shuffle -seed 1 -i SeqAOnly_r759s759.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r760s759.bed
1527. sort -k1,1 -k2,2n ./SeqAOnly_r760s759.bed > ./SeqAOnly_r760s760.bed
1528. bedtools shuffle -seed 1 -i SeqAOnly_r760s760.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r761s760.bed
1529. sort -k1,1 -k2,2n ./SeqAOnly_r761s760.bed > ./SeqAOnly_r761s761.bed
1530. bedtools shuffle -seed 1 -i SeqAOnly_r761s761.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r762s761.bed
1531. sort -k1,1 -k2,2n ./SeqAOnly_r762s761.bed > ./SeqAOnly_r762s762.bed
1532. bedtools shuffle -seed 1 -i SeqAOnly_r762s762.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r763s762.bed
1533. sort -k1,1 -k2,2n ./SeqAOnly_r763s762.bed > ./SeqAOnly_r763s763.bed
1534. bedtools shuffle -seed 1 -i SeqAOnly_r763s763.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r764s763.bed
1535. sort -k1,1 -k2,2n ./SeqAOnly_r764s763.bed > ./SeqAOnly_r764s764.bed
1536. bedtools shuffle -seed 1 -i SeqAOnly_r764s764.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r765s764.bed
1537. sort -k1,1 -k2,2n ./SeqAOnly_r765s764.bed > ./SeqAOnly_r765s765.bed
1538. bedtools shuffle -seed 1 -i SeqAOnly_r765s765.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r766s765.bed
1539. sort -k1,1 -k2,2n ./SeqAOnly_r766s765.bed > ./SeqAOnly_r766s766.bed
1540. bedtools shuffle -seed 1 -i SeqAOnly_r766s766.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r767s766.bed
1541. sort -k1,1 -k2,2n ./SeqAOnly_r767s766.bed > ./SeqAOnly_r767s767.bed
1542. bedtools shuffle -seed 1 -i SeqAOnly_r767s767.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r768s767.bed
1543. sort -k1,1 -k2,2n ./SeqAOnly_r768s767.bed > ./SeqAOnly_r768s768.bed
1544. bedtools shuffle -seed 1 -i SeqAOnly_r768s768.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r769s768.bed
1545. sort -k1,1 -k2,2n ./SeqAOnly_r769s768.bed > ./SeqAOnly_r769s769.bed
1546. bedtools shuffle -seed 1 -i SeqAOnly_r769s769.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r770s769.bed
1547. sort -k1,1 -k2,2n ./SeqAOnly_r770s769.bed > ./SeqAOnly_r770s770.bed
1548. bedtools shuffle -seed 1 -i SeqAOnly_r770s770.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r771s770.bed
1549. sort -k1,1 -k2,2n ./SeqAOnly_r771s770.bed > ./SeqAOnly_r771s771.bed
1550. bedtools shuffle -seed 1 -i SeqAOnly_r771s771.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r772s771.bed
1551. sort -k1,1 -k2,2n ./SeqAOnly_r772s771.bed > ./SeqAOnly_r772s772.bed
1552. bedtools shuffle -seed 1 -i SeqAOnly_r772s772.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r773s772.bed
1553. sort -k1,1 -k2,2n ./SeqAOnly_r773s772.bed > ./SeqAOnly_r773s773.bed
1554. bedtools shuffle -seed 1 -i SeqAOnly_r773s773.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r774s773.bed
1555. sort -k1,1 -k2,2n ./SeqAOnly_r774s773.bed > ./SeqAOnly_r774s774.bed
1556. bedtools shuffle -seed 1 -i SeqAOnly_r774s774.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r775s774.bed
1557. sort -k1,1 -k2,2n ./SeqAOnly_r775s774.bed > ./SeqAOnly_r775s775.bed
1558. bedtools shuffle -seed 1 -i SeqAOnly_r775s775.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r776s775.bed

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1559.    sort -k1,1 -k2,2n ./SeqAOnly_r776s775.bed > ./SeqAOnly_r776s776.bed
1560.    bedtools shuffle -seed 1 -i SeqAOnly_r776s776.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r777s776.bed
1561.    sort -k1,1 -k2,2n ./SeqAOnly_r777s776.bed > ./SeqAOnly_r777s777.bed
1562.    bedtools shuffle -seed 1 -i SeqAOnly_r777s777.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r778s777.bed
1563.    sort -k1,1 -k2,2n ./SeqAOnly_r778s777.bed > ./SeqAOnly_r778s778.bed
1564.    bedtools shuffle -seed 1 -i SeqAOnly_r778s778.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r779s778.bed
1565.    sort -k1,1 -k2,2n ./SeqAOnly_r779s778.bed > ./SeqAOnly_r779s779.bed
1566.    bedtools shuffle -seed 1 -i SeqAOnly_r779s779.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r780s779.bed
1567.    sort -k1,1 -k2,2n ./SeqAOnly_r780s779.bed > ./SeqAOnly_r780s780.bed
1568.    bedtools shuffle -seed 1 -i SeqAOnly_r780s780.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r781s780.bed
1569.    sort -k1,1 -k2,2n ./SeqAOnly_r781s780.bed > ./SeqAOnly_r781s781.bed
1570.    bedtools shuffle -seed 1 -i SeqAOnly_r781s781.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r782s781.bed
1571.    sort -k1,1 -k2,2n ./SeqAOnly_r782s781.bed > ./SeqAOnly_r782s782.bed
1572.    bedtools shuffle -seed 1 -i SeqAOnly_r782s782.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r783s782.bed
1573.    sort -k1,1 -k2,2n ./SeqAOnly_r783s782.bed > ./SeqAOnly_r783s783.bed
1574.    bedtools shuffle -seed 1 -i SeqAOnly_r783s783.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r784s783.bed
1575.    sort -k1,1 -k2,2n ./SeqAOnly_r784s783.bed > ./SeqAOnly_r784s784.bed
1576.    bedtools shuffle -seed 1 -i SeqAOnly_r784s784.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r785s784.bed
1577.    sort -k1,1 -k2,2n ./SeqAOnly_r785s784.bed > ./SeqAOnly_r785s785.bed
1578.    bedtools shuffle -seed 1 -i SeqAOnly_r785s785.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r786s785.bed
1579.    sort -k1,1 -k2,2n ./SeqAOnly_r786s785.bed > ./SeqAOnly_r786s786.bed
1580.    bedtools shuffle -seed 1 -i SeqAOnly_r786s786.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r787s786.bed
1581.    sort -k1,1 -k2,2n ./SeqAOnly_r787s786.bed > ./SeqAOnly_r787s787.bed
1582.    bedtools shuffle -seed 1 -i SeqAOnly_r787s787.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r788s787.bed
1583.    sort -k1,1 -k2,2n ./SeqAOnly_r788s787.bed > ./SeqAOnly_r788s788.bed
1584.    bedtools shuffle -seed 1 -i SeqAOnly_r788s788.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r789s788.bed
1585.    sort -k1,1 -k2,2n ./SeqAOnly_r789s788.bed > ./SeqAOnly_r789s789.bed
1586.    bedtools shuffle -seed 1 -i SeqAOnly_r789s789.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r790s789.bed
1587.    sort -k1,1 -k2,2n ./SeqAOnly_r790s789.bed > ./SeqAOnly_r790s790.bed
1588.    bedtools shuffle -seed 1 -i SeqAOnly_r790s790.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r791s790.bed
1589.    sort -k1,1 -k2,2n ./SeqAOnly_r791s790.bed > ./SeqAOnly_r791s791.bed
1590.    bedtools shuffle -seed 1 -i SeqAOnly_r791s791.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r792s791.bed
1591.    sort -k1,1 -k2,2n ./SeqAOnly_r792s791.bed > ./SeqAOnly_r792s792.bed
1592.    bedtools shuffle -seed 1 -i SeqAOnly_r792s792.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r793s792.bed
1593.    sort -k1,1 -k2,2n ./SeqAOnly_r793s792.bed > ./SeqAOnly_r793s793.bed
1594.    bedtools shuffle -seed 1 -i SeqAOnly_r793s793.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r794s793.bed
1595.    sort -k1,1 -k2,2n ./SeqAOnly_r794s793.bed > ./SeqAOnly_r794s794.bed
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1596.     bedtools shuffle -seed 1 -i SeqAOnly_r794s794.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r795s794.bed
1597.     sort -k1,1 -k2,2n ./SeqAOnly_r795s794.bed > ./SeqAOnly_r795s795.bed
1598.     bedtools shuffle -seed 1 -i SeqAOnly_r795s795.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r796s795.bed
1599.     sort -k1,1 -k2,2n ./SeqAOnly_r796s795.bed > ./SeqAOnly_r796s796.bed
1600.     bedtools shuffle -seed 1 -i SeqAOnly_r796s796.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r797s796.bed
1601.     sort -k1,1 -k2,2n ./SeqAOnly_r797s796.bed > ./SeqAOnly_r797s797.bed
1602.     bedtools shuffle -seed 1 -i SeqAOnly_r797s797.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r798s797.bed
1603.     sort -k1,1 -k2,2n ./SeqAOnly_r798s797.bed > ./SeqAOnly_r798s798.bed
1604.     bedtools shuffle -seed 1 -i SeqAOnly_r798s798.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r799s798.bed
1605.     sort -k1,1 -k2,2n ./SeqAOnly_r799s798.bed > ./SeqAOnly_r799s799.bed
1606.     bedtools shuffle -seed 1 -i SeqAOnly_r799s799.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r800s799.bed
1607.     sort -k1,1 -k2,2n ./SeqAOnly_r800s799.bed > ./SeqAOnly_r800s800.bed
1608.     bedtools shuffle -seed 1 -i SeqAOnly_r800s800.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r801s800.bed
1609.     sort -k1,1 -k2,2n ./SeqAOnly_r801s800.bed > ./SeqAOnly_r801s801.bed
1610.     bedtools shuffle -seed 1 -i SeqAOnly_r801s801.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r802s801.bed
1611.     sort -k1,1 -k2,2n ./SeqAOnly_r802s801.bed > ./SeqAOnly_r802s802.bed
1612.     bedtools shuffle -seed 1 -i SeqAOnly_r802s802.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r803s802.bed
1613.     sort -k1,1 -k2,2n ./SeqAOnly_r803s802.bed > ./SeqAOnly_r803s803.bed
1614.     bedtools shuffle -seed 1 -i SeqAOnly_r803s803.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r804s803.bed
1615.     sort -k1,1 -k2,2n ./SeqAOnly_r804s803.bed > ./SeqAOnly_r804s804.bed
1616.     bedtools shuffle -seed 1 -i SeqAOnly_r804s804.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r805s804.bed
1617.     sort -k1,1 -k2,2n ./SeqAOnly_r805s804.bed > ./SeqAOnly_r805s805.bed
1618.     bedtools shuffle -seed 1 -i SeqAOnly_r805s805.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r806s805.bed
1619.     sort -k1,1 -k2,2n ./SeqAOnly_r806s805.bed > ./SeqAOnly_r806s806.bed
1620.     bedtools shuffle -seed 1 -i SeqAOnly_r806s806.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r807s806.bed
1621.     sort -k1,1 -k2,2n ./SeqAOnly_r807s806.bed > ./SeqAOnly_r807s807.bed
1622.     bedtools shuffle -seed 1 -i SeqAOnly_r807s807.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r808s807.bed
1623.     sort -k1,1 -k2,2n ./SeqAOnly_r808s807.bed > ./SeqAOnly_r808s808.bed
1624.     bedtools shuffle -seed 1 -i SeqAOnly_r808s808.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r809s808.bed
1625.     sort -k1,1 -k2,2n ./SeqAOnly_r809s808.bed > ./SeqAOnly_r809s809.bed
1626.     bedtools shuffle -seed 1 -i SeqAOnly_r809s809.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r810s809.bed
1627.     sort -k1,1 -k2,2n ./SeqAOnly_r810s809.bed > ./SeqAOnly_r810s810.bed
1628.     bedtools shuffle -seed 1 -i SeqAOnly_r810s810.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r811s810.bed
1629.     sort -k1,1 -k2,2n ./SeqAOnly_r811s810.bed > ./SeqAOnly_r811s811.bed
1630.     bedtools shuffle -seed 1 -i SeqAOnly_r811s811.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r812s811.bed
1631.     sort -k1,1 -k2,2n ./SeqAOnly_r812s811.bed > ./SeqAOnly_r812s812.bed
1632.     bedtools shuffle -seed 1 -i SeqAOnly_r812s812.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r813s812.bed

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1633.    sort -k1,1 -k2,2n ./SeqAOnly_r813s812.bed > ./SeqAOnly_r813s813.bed
1634.    bedtools shuffle -seed 1 -i SeqAOnly_r813s813.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r814s813.bed
1635.    sort -k1,1 -k2,2n ./SeqAOnly_r814s813.bed > ./SeqAOnly_r814s814.bed
1636.    bedtools shuffle -seed 1 -i SeqAOnly_r814s814.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r815s814.bed
1637.    sort -k1,1 -k2,2n ./SeqAOnly_r815s814.bed > ./SeqAOnly_r815s815.bed
1638.    bedtools shuffle -seed 1 -i SeqAOnly_r815s815.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r816s815.bed
1639.    sort -k1,1 -k2,2n ./SeqAOnly_r816s815.bed > ./SeqAOnly_r816s816.bed
1640.    bedtools shuffle -seed 1 -i SeqAOnly_r816s816.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r817s816.bed
1641.    sort -k1,1 -k2,2n ./SeqAOnly_r817s816.bed > ./SeqAOnly_r817s817.bed
1642.    bedtools shuffle -seed 1 -i SeqAOnly_r817s817.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r818s817.bed
1643.    sort -k1,1 -k2,2n ./SeqAOnly_r818s817.bed > ./SeqAOnly_r818s818.bed
1644.    bedtools shuffle -seed 1 -i SeqAOnly_r818s818.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r819s818.bed
1645.    sort -k1,1 -k2,2n ./SeqAOnly_r819s818.bed > ./SeqAOnly_r819s819.bed
1646.    bedtools shuffle -seed 1 -i SeqAOnly_r819s819.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r820s819.bed
1647.    sort -k1,1 -k2,2n ./SeqAOnly_r820s819.bed > ./SeqAOnly_r820s820.bed
1648.    bedtools shuffle -seed 1 -i SeqAOnly_r820s820.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r821s820.bed
1649.    sort -k1,1 -k2,2n ./SeqAOnly_r821s820.bed > ./SeqAOnly_r821s821.bed
1650.    bedtools shuffle -seed 1 -i SeqAOnly_r821s821.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r822s821.bed
1651.    sort -k1,1 -k2,2n ./SeqAOnly_r822s821.bed > ./SeqAOnly_r822s822.bed
1652.    bedtools shuffle -seed 1 -i SeqAOnly_r822s822.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r823s822.bed
1653.    sort -k1,1 -k2,2n ./SeqAOnly_r823s822.bed > ./SeqAOnly_r823s823.bed
1654.    bedtools shuffle -seed 1 -i SeqAOnly_r823s823.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r824s823.bed
1655.    sort -k1,1 -k2,2n ./SeqAOnly_r824s823.bed > ./SeqAOnly_r824s824.bed
1656.    bedtools shuffle -seed 1 -i SeqAOnly_r824s824.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r825s824.bed
1657.    sort -k1,1 -k2,2n ./SeqAOnly_r825s824.bed > ./SeqAOnly_r825s825.bed
1658.    bedtools shuffle -seed 1 -i SeqAOnly_r825s825.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r826s825.bed
1659.    sort -k1,1 -k2,2n ./SeqAOnly_r826s825.bed > ./SeqAOnly_r826s826.bed
1660.    bedtools shuffle -seed 1 -i SeqAOnly_r826s826.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r827s826.bed
1661.    sort -k1,1 -k2,2n ./SeqAOnly_r827s826.bed > ./SeqAOnly_r827s827.bed
1662.    bedtools shuffle -seed 1 -i SeqAOnly_r827s827.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r828s827.bed
1663.    sort -k1,1 -k2,2n ./SeqAOnly_r828s827.bed > ./SeqAOnly_r828s828.bed
1664.    bedtools shuffle -seed 1 -i SeqAOnly_r828s828.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r829s828.bed
1665.    sort -k1,1 -k2,2n ./SeqAOnly_r829s828.bed > ./SeqAOnly_r829s829.bed
1666.    bedtools shuffle -seed 1 -i SeqAOnly_r829s829.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r830s829.bed
1667.    sort -k1,1 -k2,2n ./SeqAOnly_r830s829.bed > ./SeqAOnly_r830s830.bed
1668.    bedtools shuffle -seed 1 -i SeqAOnly_r830s830.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r831s830.bed
1669.    sort -k1,1 -k2,2n ./SeqAOnly_r831s830.bed > ./SeqAOnly_r831s831.bed
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1670. bedtools shuffle -seed 1 -i SeqAOnly_r831s831.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r832s831.bed
1671. sort -k1,1 -k2,2n ./SeqAOnly_r832s831.bed > ./SeqAOnly_r832s832.bed
1672. bedtools shuffle -seed 1 -i SeqAOnly_r832s832.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r833s832.bed
1673. sort -k1,1 -k2,2n ./SeqAOnly_r833s832.bed > ./SeqAOnly_r833s833.bed
1674. bedtools shuffle -seed 1 -i SeqAOnly_r833s833.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r834s833.bed
1675. sort -k1,1 -k2,2n ./SeqAOnly_r834s833.bed > ./SeqAOnly_r834s834.bed
1676. bedtools shuffle -seed 1 -i SeqAOnly_r834s834.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r835s834.bed
1677. sort -k1,1 -k2,2n ./SeqAOnly_r835s834.bed > ./SeqAOnly_r835s835.bed
1678. bedtools shuffle -seed 1 -i SeqAOnly_r835s835.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r836s835.bed
1679. sort -k1,1 -k2,2n ./SeqAOnly_r836s835.bed > ./SeqAOnly_r836s836.bed
1680. bedtools shuffle -seed 1 -i SeqAOnly_r836s836.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r837s836.bed
1681. sort -k1,1 -k2,2n ./SeqAOnly_r837s836.bed > ./SeqAOnly_r837s837.bed
1682. bedtools shuffle -seed 1 -i SeqAOnly_r837s837.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r838s837.bed
1683. sort -k1,1 -k2,2n ./SeqAOnly_r838s837.bed > ./SeqAOnly_r838s838.bed
1684. bedtools shuffle -seed 1 -i SeqAOnly_r838s838.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r839s838.bed
1685. sort -k1,1 -k2,2n ./SeqAOnly_r839s838.bed > ./SeqAOnly_r839s839.bed
1686. bedtools shuffle -seed 1 -i SeqAOnly_r839s839.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r840s839.bed
1687. sort -k1,1 -k2,2n ./SeqAOnly_r840s839.bed > ./SeqAOnly_r840s840.bed
1688. bedtools shuffle -seed 1 -i SeqAOnly_r840s840.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r841s840.bed
1689. sort -k1,1 -k2,2n ./SeqAOnly_r841s840.bed > ./SeqAOnly_r841s841.bed
1690. bedtools shuffle -seed 1 -i SeqAOnly_r841s841.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r842s841.bed
1691. sort -k1,1 -k2,2n ./SeqAOnly_r842s841.bed > ./SeqAOnly_r842s842.bed
1692. bedtools shuffle -seed 1 -i SeqAOnly_r842s842.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r843s842.bed
1693. sort -k1,1 -k2,2n ./SeqAOnly_r843s842.bed > ./SeqAOnly_r843s843.bed
1694. bedtools shuffle -seed 1 -i SeqAOnly_r843s843.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r844s843.bed
1695. sort -k1,1 -k2,2n ./SeqAOnly_r844s843.bed > ./SeqAOnly_r844s844.bed
1696. bedtools shuffle -seed 1 -i SeqAOnly_r844s844.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r845s844.bed
1697. sort -k1,1 -k2,2n ./SeqAOnly_r845s844.bed > ./SeqAOnly_r845s845.bed
1698. bedtools shuffle -seed 1 -i SeqAOnly_r845s845.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r846s845.bed
1699. sort -k1,1 -k2,2n ./SeqAOnly_r846s845.bed > ./SeqAOnly_r846s846.bed
1700. bedtools shuffle -seed 1 -i SeqAOnly_r846s846.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r847s846.bed
1701. sort -k1,1 -k2,2n ./SeqAOnly_r847s846.bed > ./SeqAOnly_r847s847.bed
1702. bedtools shuffle -seed 1 -i SeqAOnly_r847s847.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r848s847.bed
1703. sort -k1,1 -k2,2n ./SeqAOnly_r848s847.bed > ./SeqAOnly_r848s848.bed
1704. bedtools shuffle -seed 1 -i SeqAOnly_r848s848.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r849s848.bed
1705. sort -k1,1 -k2,2n ./SeqAOnly_r849s848.bed > ./SeqAOnly_r849s849.bed
1706. bedtools shuffle -seed 1 -i SeqAOnly_r849s849.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r850s849.bed

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1707.    sort -k1,1 -k2,2n ./SeqAOnly_r850s849.bed > ./SeqAOnly_r850s850.bed
1708.    bedtools shuffle -seed 1 -i SeqAOnly_r850s850.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r851s850.bed
1709.    sort -k1,1 -k2,2n ./SeqAOnly_r851s850.bed > ./SeqAOnly_r851s851.bed
1710.    bedtools shuffle -seed 1 -i SeqAOnly_r851s851.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r852s851.bed
1711.    sort -k1,1 -k2,2n ./SeqAOnly_r852s851.bed > ./SeqAOnly_r852s852.bed
1712.    bedtools shuffle -seed 1 -i SeqAOnly_r852s852.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r853s852.bed
1713.    sort -k1,1 -k2,2n ./SeqAOnly_r853s852.bed > ./SeqAOnly_r853s853.bed
1714.    bedtools shuffle -seed 1 -i SeqAOnly_r853s853.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r854s853.bed
1715.    sort -k1,1 -k2,2n ./SeqAOnly_r854s853.bed > ./SeqAOnly_r854s854.bed
1716.    bedtools shuffle -seed 1 -i SeqAOnly_r854s854.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r855s854.bed
1717.    sort -k1,1 -k2,2n ./SeqAOnly_r855s854.bed > ./SeqAOnly_r855s855.bed
1718.    bedtools shuffle -seed 1 -i SeqAOnly_r855s855.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r856s855.bed
1719.    sort -k1,1 -k2,2n ./SeqAOnly_r856s855.bed > ./SeqAOnly_r856s856.bed
1720.    bedtools shuffle -seed 1 -i SeqAOnly_r856s856.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r857s856.bed
1721.    sort -k1,1 -k2,2n ./SeqAOnly_r857s856.bed > ./SeqAOnly_r857s857.bed
1722.    bedtools shuffle -seed 1 -i SeqAOnly_r857s857.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r858s857.bed
1723.    sort -k1,1 -k2,2n ./SeqAOnly_r858s857.bed > ./SeqAOnly_r858s858.bed
1724.    bedtools shuffle -seed 1 -i SeqAOnly_r858s858.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r859s858.bed
1725.    sort -k1,1 -k2,2n ./SeqAOnly_r859s858.bed > ./SeqAOnly_r859s859.bed
1726.    bedtools shuffle -seed 1 -i SeqAOnly_r859s859.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r860s859.bed
1727.    sort -k1,1 -k2,2n ./SeqAOnly_r860s859.bed > ./SeqAOnly_r860s860.bed
1728.    bedtools shuffle -seed 1 -i SeqAOnly_r860s860.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r861s860.bed
1729.    sort -k1,1 -k2,2n ./SeqAOnly_r861s860.bed > ./SeqAOnly_r861s861.bed
1730.    bedtools shuffle -seed 1 -i SeqAOnly_r861s861.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r862s861.bed
1731.    sort -k1,1 -k2,2n ./SeqAOnly_r862s861.bed > ./SeqAOnly_r862s862.bed
1732.    bedtools shuffle -seed 1 -i SeqAOnly_r862s862.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r863s862.bed
1733.    sort -k1,1 -k2,2n ./SeqAOnly_r863s862.bed > ./SeqAOnly_r863s863.bed
1734.    bedtools shuffle -seed 1 -i SeqAOnly_r863s863.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r864s863.bed
1735.    sort -k1,1 -k2,2n ./SeqAOnly_r864s863.bed > ./SeqAOnly_r864s864.bed
1736.    bedtools shuffle -seed 1 -i SeqAOnly_r864s864.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r865s864.bed
1737.    sort -k1,1 -k2,2n ./SeqAOnly_r865s864.bed > ./SeqAOnly_r865s865.bed
1738.    bedtools shuffle -seed 1 -i SeqAOnly_r865s865.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r866s865.bed
1739.    sort -k1,1 -k2,2n ./SeqAOnly_r866s865.bed > ./SeqAOnly_r866s866.bed
1740.    bedtools shuffle -seed 1 -i SeqAOnly_r866s866.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r867s866.bed
1741.    sort -k1,1 -k2,2n ./SeqAOnly_r867s866.bed > ./SeqAOnly_r867s867.bed
1742.    bedtools shuffle -seed 1 -i SeqAOnly_r867s867.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r868s867.bed
1743.    sort -k1,1 -k2,2n ./SeqAOnly_r868s867.bed > ./SeqAOnly_r868s868.bed
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1744. bedtools shuffle -seed 1 -i SeqAOnly_r868s868.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r869s868.bed
1745. sort -k1,1 -k2,2n ./SeqAOnly_r869s868.bed > ./SeqAOnly_r869s869.bed
1746. bedtools shuffle -seed 1 -i SeqAOnly_r869s869.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r870s869.bed
1747. sort -k1,1 -k2,2n ./SeqAOnly_r870s869.bed > ./SeqAOnly_r870s870.bed
1748. bedtools shuffle -seed 1 -i SeqAOnly_r870s870.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r871s870.bed
1749. sort -k1,1 -k2,2n ./SeqAOnly_r871s870.bed > ./SeqAOnly_r871s871.bed
1750. bedtools shuffle -seed 1 -i SeqAOnly_r871s871.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r872s871.bed
1751. sort -k1,1 -k2,2n ./SeqAOnly_r872s871.bed > ./SeqAOnly_r872s872.bed
1752. bedtools shuffle -seed 1 -i SeqAOnly_r872s872.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r873s872.bed
1753. sort -k1,1 -k2,2n ./SeqAOnly_r873s872.bed > ./SeqAOnly_r873s873.bed
1754. bedtools shuffle -seed 1 -i SeqAOnly_r873s873.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r874s873.bed
1755. sort -k1,1 -k2,2n ./SeqAOnly_r874s873.bed > ./SeqAOnly_r874s874.bed
1756. bedtools shuffle -seed 1 -i SeqAOnly_r874s874.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r875s874.bed
1757. sort -k1,1 -k2,2n ./SeqAOnly_r875s874.bed > ./SeqAOnly_r875s875.bed
1758. bedtools shuffle -seed 1 -i SeqAOnly_r875s875.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r876s875.bed
1759. sort -k1,1 -k2,2n ./SeqAOnly_r876s875.bed > ./SeqAOnly_r876s876.bed
1760. bedtools shuffle -seed 1 -i SeqAOnly_r876s876.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r877s876.bed
1761. sort -k1,1 -k2,2n ./SeqAOnly_r877s876.bed > ./SeqAOnly_r877s877.bed
1762. bedtools shuffle -seed 1 -i SeqAOnly_r877s877.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r878s877.bed
1763. sort -k1,1 -k2,2n ./SeqAOnly_r878s877.bed > ./SeqAOnly_r878s878.bed
1764. bedtools shuffle -seed 1 -i SeqAOnly_r878s878.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r879s878.bed
1765. sort -k1,1 -k2,2n ./SeqAOnly_r879s878.bed > ./SeqAOnly_r879s879.bed
1766. bedtools shuffle -seed 1 -i SeqAOnly_r879s879.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r880s879.bed
1767. sort -k1,1 -k2,2n ./SeqAOnly_r880s879.bed > ./SeqAOnly_r880s880.bed
1768. bedtools shuffle -seed 1 -i SeqAOnly_r880s880.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r881s880.bed
1769. sort -k1,1 -k2,2n ./SeqAOnly_r881s880.bed > ./SeqAOnly_r881s881.bed
1770. bedtools shuffle -seed 1 -i SeqAOnly_r881s881.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r882s881.bed
1771. sort -k1,1 -k2,2n ./SeqAOnly_r882s881.bed > ./SeqAOnly_r882s882.bed
1772. bedtools shuffle -seed 1 -i SeqAOnly_r882s882.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r883s882.bed
1773. sort -k1,1 -k2,2n ./SeqAOnly_r883s882.bed > ./SeqAOnly_r883s883.bed
1774. bedtools shuffle -seed 1 -i SeqAOnly_r883s883.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r884s883.bed
1775. sort -k1,1 -k2,2n ./SeqAOnly_r884s883.bed > ./SeqAOnly_r884s884.bed
1776. bedtools shuffle -seed 1 -i SeqAOnly_r884s884.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r885s884.bed
1777. sort -k1,1 -k2,2n ./SeqAOnly_r885s884.bed > ./SeqAOnly_r885s885.bed
1778. bedtools shuffle -seed 1 -i SeqAOnly_r885s885.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r886s885.bed
1779. sort -k1,1 -k2,2n ./SeqAOnly_r886s885.bed > ./SeqAOnly_r886s886.bed
1780. bedtools shuffle -seed 1 -i SeqAOnly_r886s886.bed -g Ecoli-genomesize.txt > ./SeqAOnly_r887s886.bed

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1781.    sort -k1,1 -k2,2n ./SeqAOnly_r887s886.bed > ./SeqAOnly_r887s887.bed
1782.    bedtools shuffle -seed 1 -i SeqAOnly_r887s887.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r888s887.bed
1783.    sort -k1,1 -k2,2n ./SeqAOnly_r888s887.bed > ./SeqAOnly_r888s888.bed
1784.    bedtools shuffle -seed 1 -i SeqAOnly_r888s888.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r889s888.bed
1785.    sort -k1,1 -k2,2n ./SeqAOnly_r889s888.bed > ./SeqAOnly_r889s889.bed
1786.    bedtools shuffle -seed 1 -i SeqAOnly_r889s889.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r890s889.bed
1787.    sort -k1,1 -k2,2n ./SeqAOnly_r890s889.bed > ./SeqAOnly_r890s890.bed
1788.    bedtools shuffle -seed 1 -i SeqAOnly_r890s890.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r891s890.bed
1789.    sort -k1,1 -k2,2n ./SeqAOnly_r891s890.bed > ./SeqAOnly_r891s891.bed
1790.    bedtools shuffle -seed 1 -i SeqAOnly_r891s891.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r892s891.bed
1791.    sort -k1,1 -k2,2n ./SeqAOnly_r892s891.bed > ./SeqAOnly_r892s892.bed
1792.    bedtools shuffle -seed 1 -i SeqAOnly_r892s892.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r893s892.bed
1793.    sort -k1,1 -k2,2n ./SeqAOnly_r893s892.bed > ./SeqAOnly_r893s893.bed
1794.    bedtools shuffle -seed 1 -i SeqAOnly_r893s893.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r894s893.bed
1795.    sort -k1,1 -k2,2n ./SeqAOnly_r894s893.bed > ./SeqAOnly_r894s894.bed
1796.    bedtools shuffle -seed 1 -i SeqAOnly_r894s894.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r895s894.bed
1797.    sort -k1,1 -k2,2n ./SeqAOnly_r895s894.bed > ./SeqAOnly_r895s895.bed
1798.    bedtools shuffle -seed 1 -i SeqAOnly_r895s895.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r896s895.bed
1799.    sort -k1,1 -k2,2n ./SeqAOnly_r896s895.bed > ./SeqAOnly_r896s896.bed
1800.    bedtools shuffle -seed 1 -i SeqAOnly_r896s896.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r897s896.bed
1801.    sort -k1,1 -k2,2n ./SeqAOnly_r897s896.bed > ./SeqAOnly_r897s897.bed
1802.    bedtools shuffle -seed 1 -i SeqAOnly_r897s897.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r898s897.bed
1803.    sort -k1,1 -k2,2n ./SeqAOnly_r898s897.bed > ./SeqAOnly_r898s898.bed
1804.    bedtools shuffle -seed 1 -i SeqAOnly_r898s898.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r899s898.bed
1805.    sort -k1,1 -k2,2n ./SeqAOnly_r899s898.bed > ./SeqAOnly_r899s899.bed
1806.    bedtools shuffle -seed 1 -i SeqAOnly_r899s899.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r900s899.bed
1807.    sort -k1,1 -k2,2n ./SeqAOnly_r900s899.bed > ./SeqAOnly_r900s900.bed
1808.    bedtools shuffle -seed 1 -i SeqAOnly_r900s900.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r901s900.bed
1809.    sort -k1,1 -k2,2n ./SeqAOnly_r901s900.bed > ./SeqAOnly_r901s901.bed
1810.    bedtools shuffle -seed 1 -i SeqAOnly_r901s901.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r902s901.bed
1811.    sort -k1,1 -k2,2n ./SeqAOnly_r902s901.bed > ./SeqAOnly_r902s902.bed
1812.    bedtools shuffle -seed 1 -i SeqAOnly_r902s902.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r903s902.bed
1813.    sort -k1,1 -k2,2n ./SeqAOnly_r903s902.bed > ./SeqAOnly_r903s903.bed
1814.    bedtools shuffle -seed 1 -i SeqAOnly_r903s903.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r904s903.bed
1815.    sort -k1,1 -k2,2n ./SeqAOnly_r904s903.bed > ./SeqAOnly_r904s904.bed
1816.    bedtools shuffle -seed 1 -i SeqAOnly_r904s904.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_r905s904.bed
1817.    sort -k1,1 -k2,2n ./SeqAOnly_r905s904.bed > ./SeqAOnly_r905s905.bed
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1818.     bedtools shuffle -seed 1 -i SeqAOnly_r905s905.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r906s905.bed
1819.     sort -k1,1 -k2,2n ./SeqAOnly_r906s905.bed > ./SeqAOnly_r906s906.bed
1820.     bedtools shuffle -seed 1 -i SeqAOnly_r906s906.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r907s906.bed
1821.     sort -k1,1 -k2,2n ./SeqAOnly_r907s906.bed > ./SeqAOnly_r907s907.bed
1822.     bedtools shuffle -seed 1 -i SeqAOnly_r907s907.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r908s907.bed
1823.     sort -k1,1 -k2,2n ./SeqAOnly_r908s907.bed > ./SeqAOnly_r908s908.bed
1824.     bedtools shuffle -seed 1 -i SeqAOnly_r908s908.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r909s908.bed
1825.     sort -k1,1 -k2,2n ./SeqAOnly_r909s908.bed > ./SeqAOnly_r909s909.bed
1826.     bedtools shuffle -seed 1 -i SeqAOnly_r909s909.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r910s909.bed
1827.     sort -k1,1 -k2,2n ./SeqAOnly_r910s909.bed > ./SeqAOnly_r910s910.bed
1828.     bedtools shuffle -seed 1 -i SeqAOnly_r910s910.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r911s910.bed
1829.     sort -k1,1 -k2,2n ./SeqAOnly_r911s910.bed > ./SeqAOnly_r911s911.bed
1830.     bedtools shuffle -seed 1 -i SeqAOnly_r911s911.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r912s911.bed
1831.     sort -k1,1 -k2,2n ./SeqAOnly_r912s911.bed > ./SeqAOnly_r912s912.bed
1832.     bedtools shuffle -seed 1 -i SeqAOnly_r912s912.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r913s912.bed
1833.     sort -k1,1 -k2,2n ./SeqAOnly_r913s912.bed > ./SeqAOnly_r913s913.bed
1834.     bedtools shuffle -seed 1 -i SeqAOnly_r913s913.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r914s913.bed
1835.     sort -k1,1 -k2,2n ./SeqAOnly_r914s913.bed > ./SeqAOnly_r914s914.bed
1836.     bedtools shuffle -seed 1 -i SeqAOnly_r914s914.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r915s914.bed
1837.     sort -k1,1 -k2,2n ./SeqAOnly_r915s914.bed > ./SeqAOnly_r915s915.bed
1838.     bedtools shuffle -seed 1 -i SeqAOnly_r915s915.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r916s915.bed
1839.     sort -k1,1 -k2,2n ./SeqAOnly_r916s915.bed > ./SeqAOnly_r916s916.bed
1840.     bedtools shuffle -seed 1 -i SeqAOnly_r916s916.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r917s916.bed
1841.     sort -k1,1 -k2,2n ./SeqAOnly_r917s916.bed > ./SeqAOnly_r917s917.bed
1842.     bedtools shuffle -seed 1 -i SeqAOnly_r917s917.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r918s917.bed
1843.     sort -k1,1 -k2,2n ./SeqAOnly_r918s917.bed > ./SeqAOnly_r918s918.bed
1844.     bedtools shuffle -seed 1 -i SeqAOnly_r918s918.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r919s918.bed
1845.     sort -k1,1 -k2,2n ./SeqAOnly_r919s918.bed > ./SeqAOnly_r919s919.bed
1846.     bedtools shuffle -seed 1 -i SeqAOnly_r919s919.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r920s919.bed
1847.     sort -k1,1 -k2,2n ./SeqAOnly_r920s919.bed > ./SeqAOnly_r920s920.bed
1848.     bedtools shuffle -seed 1 -i SeqAOnly_r920s920.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r921s920.bed
1849.     sort -k1,1 -k2,2n ./SeqAOnly_r921s920.bed > ./SeqAOnly_r921s921.bed
1850.     bedtools shuffle -seed 1 -i SeqAOnly_r921s921.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r922s921.bed
1851.     sort -k1,1 -k2,2n ./SeqAOnly_r922s921.bed > ./SeqAOnly_r922s922.bed
1852.     bedtools shuffle -seed 1 -i SeqAOnly_r922s922.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r923s922.bed
1853.     sort -k1,1 -k2,2n ./SeqAOnly_r923s922.bed > ./SeqAOnly_r923s923.bed
1854.     bedtools shuffle -seed 1 -i SeqAOnly_r923s923.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r924s923.bed

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1855. sort -k1,1 -k2,2n ./SeqAOnly_r924s923.bed > ./SeqAOnly_r924s924.bed
1856. bedtools shuffle -seed 1 -i SeqAOnly_r924s924.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r925s924.bed
1857. sort -k1,1 -k2,2n ./SeqAOnly_r925s924.bed > ./SeqAOnly_r925s925.bed
1858. bedtools shuffle -seed 1 -i SeqAOnly_r925s925.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r926s925.bed
1859. sort -k1,1 -k2,2n ./SeqAOnly_r926s925.bed > ./SeqAOnly_r926s926.bed
1860. bedtools shuffle -seed 1 -i SeqAOnly_r926s926.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r927s926.bed
1861. sort -k1,1 -k2,2n ./SeqAOnly_r927s926.bed > ./SeqAOnly_r927s927.bed
1862. bedtools shuffle -seed 1 -i SeqAOnly_r927s927.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r928s927.bed
1863. sort -k1,1 -k2,2n ./SeqAOnly_r928s927.bed > ./SeqAOnly_r928s928.bed
1864. bedtools shuffle -seed 1 -i SeqAOnly_r928s928.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r929s928.bed
1865. sort -k1,1 -k2,2n ./SeqAOnly_r929s928.bed > ./SeqAOnly_r929s929.bed
1866. bedtools shuffle -seed 1 -i SeqAOnly_r929s929.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r930s929.bed
1867. sort -k1,1 -k2,2n ./SeqAOnly_r930s929.bed > ./SeqAOnly_r930s930.bed
1868. bedtools shuffle -seed 1 -i SeqAOnly_r930s930.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r931s930.bed
1869. sort -k1,1 -k2,2n ./SeqAOnly_r931s930.bed > ./SeqAOnly_r931s931.bed
1870. bedtools shuffle -seed 1 -i SeqAOnly_r931s931.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r932s931.bed
1871. sort -k1,1 -k2,2n ./SeqAOnly_r932s931.bed > ./SeqAOnly_r932s932.bed
1872. bedtools shuffle -seed 1 -i SeqAOnly_r932s932.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r933s932.bed
1873. sort -k1,1 -k2,2n ./SeqAOnly_r933s932.bed > ./SeqAOnly_r933s933.bed
1874. bedtools shuffle -seed 1 -i SeqAOnly_r933s933.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r934s933.bed
1875. sort -k1,1 -k2,2n ./SeqAOnly_r934s933.bed > ./SeqAOnly_r934s934.bed
1876. bedtools shuffle -seed 1 -i SeqAOnly_r934s934.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r935s934.bed
1877. sort -k1,1 -k2,2n ./SeqAOnly_r935s934.bed > ./SeqAOnly_r935s935.bed
1878. bedtools shuffle -seed 1 -i SeqAOnly_r935s935.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r936s935.bed
1879. sort -k1,1 -k2,2n ./SeqAOnly_r936s935.bed > ./SeqAOnly_r936s936.bed
1880. bedtools shuffle -seed 1 -i SeqAOnly_r936s936.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r937s936.bed
1881. sort -k1,1 -k2,2n ./SeqAOnly_r937s936.bed > ./SeqAOnly_r937s937.bed
1882. bedtools shuffle -seed 1 -i SeqAOnly_r937s937.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r938s937.bed
1883. sort -k1,1 -k2,2n ./SeqAOnly_r938s937.bed > ./SeqAOnly_r938s938.bed
1884. bedtools shuffle -seed 1 -i SeqAOnly_r938s938.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r939s938.bed
1885. sort -k1,1 -k2,2n ./SeqAOnly_r939s938.bed > ./SeqAOnly_r939s939.bed
1886. bedtools shuffle -seed 1 -i SeqAOnly_r939s939.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r940s939.bed
1887. sort -k1,1 -k2,2n ./SeqAOnly_r940s939.bed > ./SeqAOnly_r940s940.bed
1888. bedtools shuffle -seed 1 -i SeqAOnly_r940s940.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r941s940.bed
1889. sort -k1,1 -k2,2n ./SeqAOnly_r941s940.bed > ./SeqAOnly_r941s941.bed
1890. bedtools shuffle -seed 1 -i SeqAOnly_r941s941.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_r942s941.bed
1891. sort -k1,1 -k2,2n ./SeqAOnly_r942s941.bed > ./SeqAOnly_r942s942.bed

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1892.     bedtools shuffle -seed 1 -i SeqAOnly_r942s942.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r943s942.bed
1893.     sort -k1,1 -k2,2n ./SeqAOnly_r943s942.bed > ./SeqAOnly_r943s943.bed
1894.     bedtools shuffle -seed 1 -i SeqAOnly_r943s943.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r944s943.bed
1895.     sort -k1,1 -k2,2n ./SeqAOnly_r944s943.bed > ./SeqAOnly_r944s944.bed
1896.     bedtools shuffle -seed 1 -i SeqAOnly_r944s944.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r945s944.bed
1897.     sort -k1,1 -k2,2n ./SeqAOnly_r945s944.bed > ./SeqAOnly_r945s945.bed
1898.     bedtools shuffle -seed 1 -i SeqAOnly_r945s945.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r946s945.bed
1899.     sort -k1,1 -k2,2n ./SeqAOnly_r946s945.bed > ./SeqAOnly_r946s946.bed
1900.     bedtools shuffle -seed 1 -i SeqAOnly_r946s946.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r947s946.bed
1901.     sort -k1,1 -k2,2n ./SeqAOnly_r947s946.bed > ./SeqAOnly_r947s947.bed
1902.     bedtools shuffle -seed 1 -i SeqAOnly_r947s947.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r948s947.bed
1903.     sort -k1,1 -k2,2n ./SeqAOnly_r948s947.bed > ./SeqAOnly_r948s948.bed
1904.     bedtools shuffle -seed 1 -i SeqAOnly_r948s948.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r949s948.bed
1905.     sort -k1,1 -k2,2n ./SeqAOnly_r949s948.bed > ./SeqAOnly_r949s949.bed
1906.     bedtools shuffle -seed 1 -i SeqAOnly_r949s949.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r950s949.bed
1907.     sort -k1,1 -k2,2n ./SeqAOnly_r950s949.bed > ./SeqAOnly_r950s950.bed
1908.     bedtools shuffle -seed 1 -i SeqAOnly_r950s950.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r951s950.bed
1909.     sort -k1,1 -k2,2n ./SeqAOnly_r951s950.bed > ./SeqAOnly_r951s951.bed
1910.     bedtools shuffle -seed 1 -i SeqAOnly_r951s951.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r952s951.bed
1911.     sort -k1,1 -k2,2n ./SeqAOnly_r952s951.bed > ./SeqAOnly_r952s952.bed
1912.     bedtools shuffle -seed 1 -i SeqAOnly_r952s952.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r953s952.bed
1913.     sort -k1,1 -k2,2n ./SeqAOnly_r953s952.bed > ./SeqAOnly_r953s953.bed
1914.     bedtools shuffle -seed 1 -i SeqAOnly_r953s953.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r954s953.bed
1915.     sort -k1,1 -k2,2n ./SeqAOnly_r954s953.bed > ./SeqAOnly_r954s954.bed
1916.     bedtools shuffle -seed 1 -i SeqAOnly_r954s954.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r955s954.bed
1917.     sort -k1,1 -k2,2n ./SeqAOnly_r955s954.bed > ./SeqAOnly_r955s955.bed
1918.     bedtools shuffle -seed 1 -i SeqAOnly_r955s955.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r956s955.bed
1919.     sort -k1,1 -k2,2n ./SeqAOnly_r956s955.bed > ./SeqAOnly_r956s956.bed
1920.     bedtools shuffle -seed 1 -i SeqAOnly_r956s956.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r957s956.bed
1921.     sort -k1,1 -k2,2n ./SeqAOnly_r957s956.bed > ./SeqAOnly_r957s957.bed
1922.     bedtools shuffle -seed 1 -i SeqAOnly_r957s957.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r958s957.bed
1923.     sort -k1,1 -k2,2n ./SeqAOnly_r958s957.bed > ./SeqAOnly_r958s958.bed
1924.     bedtools shuffle -seed 1 -i SeqAOnly_r958s958.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r959s958.bed
1925.     sort -k1,1 -k2,2n ./SeqAOnly_r959s958.bed > ./SeqAOnly_r959s959.bed
1926.     bedtools shuffle -seed 1 -i SeqAOnly_r959s959.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r960s959.bed
1927.     sort -k1,1 -k2,2n ./SeqAOnly_r960s959.bed > ./SeqAOnly_r960s960.bed
1928.     bedtools shuffle -seed 1 -i SeqAOnly_r960s960.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_r961s960.bed

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1929.    sort -k1,1 -k2,2n ./SeqAOnly_r961s960.bed > ./SeqAOnly_r961s961.bed
1930.    bedtools shuffle -seed 1 -i SeqAOnly_r961s961.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r962s961.bed
1931.    sort -k1,1 -k2,2n ./SeqAOnly_r962s961.bed > ./SeqAOnly_r962s962.bed
1932.    bedtools shuffle -seed 1 -i SeqAOnly_r962s962.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r963s962.bed
1933.    sort -k1,1 -k2,2n ./SeqAOnly_r963s962.bed > ./SeqAOnly_r963s963.bed
1934.    bedtools shuffle -seed 1 -i SeqAOnly_r963s963.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r964s963.bed
1935.    sort -k1,1 -k2,2n ./SeqAOnly_r964s963.bed > ./SeqAOnly_r964s964.bed
1936.    bedtools shuffle -seed 1 -i SeqAOnly_r964s964.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r965s964.bed
1937.    sort -k1,1 -k2,2n ./SeqAOnly_r965s964.bed > ./SeqAOnly_r965s965.bed
1938.    bedtools shuffle -seed 1 -i SeqAOnly_r965s965.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r966s965.bed
1939.    sort -k1,1 -k2,2n ./SeqAOnly_r966s965.bed > ./SeqAOnly_r966s966.bed
1940.    bedtools shuffle -seed 1 -i SeqAOnly_r966s966.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r967s966.bed
1941.    sort -k1,1 -k2,2n ./SeqAOnly_r967s966.bed > ./SeqAOnly_r967s967.bed
1942.    bedtools shuffle -seed 1 -i SeqAOnly_r967s967.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r968s967.bed
1943.    sort -k1,1 -k2,2n ./SeqAOnly_r968s967.bed > ./SeqAOnly_r968s968.bed
1944.    bedtools shuffle -seed 1 -i SeqAOnly_r968s968.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r969s968.bed
1945.    sort -k1,1 -k2,2n ./SeqAOnly_r969s968.bed > ./SeqAOnly_r969s969.bed
1946.    bedtools shuffle -seed 1 -i SeqAOnly_r969s969.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r970s969.bed
1947.    sort -k1,1 -k2,2n ./SeqAOnly_r970s969.bed > ./SeqAOnly_r970s970.bed
1948.    bedtools shuffle -seed 1 -i SeqAOnly_r970s970.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r971s970.bed
1949.    sort -k1,1 -k2,2n ./SeqAOnly_r971s970.bed > ./SeqAOnly_r971s971.bed
1950.    bedtools shuffle -seed 1 -i SeqAOnly_r971s971.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r972s971.bed
1951.    sort -k1,1 -k2,2n ./SeqAOnly_r972s971.bed > ./SeqAOnly_r972s972.bed
1952.    bedtools shuffle -seed 1 -i SeqAOnly_r972s972.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r973s972.bed
1953.    sort -k1,1 -k2,2n ./SeqAOnly_r973s972.bed > ./SeqAOnly_r973s973.bed
1954.    bedtools shuffle -seed 1 -i SeqAOnly_r973s973.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r974s973.bed
1955.    sort -k1,1 -k2,2n ./SeqAOnly_r974s973.bed > ./SeqAOnly_r974s974.bed
1956.    bedtools shuffle -seed 1 -i SeqAOnly_r974s974.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r975s974.bed
1957.    sort -k1,1 -k2,2n ./SeqAOnly_r975s974.bed > ./SeqAOnly_r975s975.bed
1958.    bedtools shuffle -seed 1 -i SeqAOnly_r975s975.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r976s975.bed
1959.    sort -k1,1 -k2,2n ./SeqAOnly_r976s975.bed > ./SeqAOnly_r976s976.bed
1960.    bedtools shuffle -seed 1 -i SeqAOnly_r976s976.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r977s976.bed
1961.    sort -k1,1 -k2,2n ./SeqAOnly_r977s976.bed > ./SeqAOnly_r977s977.bed
1962.    bedtools shuffle -seed 1 -i SeqAOnly_r977s977.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r978s977.bed
1963.    sort -k1,1 -k2,2n ./SeqAOnly_r978s977.bed > ./SeqAOnly_r978s978.bed
1964.    bedtools shuffle -seed 1 -i SeqAOnly_r978s978.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r979s978.bed
1965.    sort -k1,1 -k2,2n ./SeqAOnly_r979s978.bed > ./SeqAOnly_r979s979.bed
```



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1966. bedtools shuffle -seed 1 -i SeqAOnly_r979s979.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r980s979.bed
1967. sort -k1,1 -k2,2n ./SeqAOnly_r980s979.bed > ./SeqAOnly_r980s980.bed
1968. bedtools shuffle -seed 1 -i SeqAOnly_r980s980.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r981s980.bed
1969. sort -k1,1 -k2,2n ./SeqAOnly_r981s980.bed > ./SeqAOnly_r981s981.bed
1970. bedtools shuffle -seed 1 -i SeqAOnly_r981s981.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r982s981.bed
1971. sort -k1,1 -k2,2n ./SeqAOnly_r982s981.bed > ./SeqAOnly_r982s982.bed
1972. bedtools shuffle -seed 1 -i SeqAOnly_r982s982.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r983s982.bed
1973. sort -k1,1 -k2,2n ./SeqAOnly_r983s982.bed > ./SeqAOnly_r983s983.bed
1974. bedtools shuffle -seed 1 -i SeqAOnly_r983s983.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r984s983.bed
1975. sort -k1,1 -k2,2n ./SeqAOnly_r984s983.bed > ./SeqAOnly_r984s984.bed
1976. bedtools shuffle -seed 1 -i SeqAOnly_r984s984.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r985s984.bed
1977. sort -k1,1 -k2,2n ./SeqAOnly_r985s984.bed > ./SeqAOnly_r985s985.bed
1978. bedtools shuffle -seed 1 -i SeqAOnly_r985s985.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r986s985.bed
1979. sort -k1,1 -k2,2n ./SeqAOnly_r986s985.bed > ./SeqAOnly_r986s986.bed
1980. bedtools shuffle -seed 1 -i SeqAOnly_r986s986.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r987s986.bed
1981. sort -k1,1 -k2,2n ./SeqAOnly_r987s986.bed > ./SeqAOnly_r987s987.bed
1982. bedtools shuffle -seed 1 -i SeqAOnly_r987s987.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r988s987.bed
1983. sort -k1,1 -k2,2n ./SeqAOnly_r988s987.bed > ./SeqAOnly_r988s988.bed
1984. bedtools shuffle -seed 1 -i SeqAOnly_r988s988.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r989s988.bed
1985. sort -k1,1 -k2,2n ./SeqAOnly_r989s988.bed > ./SeqAOnly_r989s989.bed
1986. bedtools shuffle -seed 1 -i SeqAOnly_r989s989.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r990s989.bed
1987. sort -k1,1 -k2,2n ./SeqAOnly_r990s989.bed > ./SeqAOnly_r990s990.bed
1988. bedtools shuffle -seed 1 -i SeqAOnly_r990s990.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r991s990.bed
1989. sort -k1,1 -k2,2n ./SeqAOnly_r991s990.bed > ./SeqAOnly_r991s991.bed
1990. bedtools shuffle -seed 1 -i SeqAOnly_r991s991.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r992s991.bed
1991. sort -k1,1 -k2,2n ./SeqAOnly_r992s991.bed > ./SeqAOnly_r992s992.bed
1992. bedtools shuffle -seed 1 -i SeqAOnly_r992s992.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r993s992.bed
1993. sort -k1,1 -k2,2n ./SeqAOnly_r993s992.bed > ./SeqAOnly_r993s993.bed
1994. bedtools shuffle -seed 1 -i SeqAOnly_r993s993.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r994s993.bed
1995. sort -k1,1 -k2,2n ./SeqAOnly_r994s993.bed > ./SeqAOnly_r994s994.bed
1996. bedtools shuffle -seed 1 -i SeqAOnly_r994s994.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r995s994.bed
1997. sort -k1,1 -k2,2n ./SeqAOnly_r995s994.bed > ./SeqAOnly_r995s995.bed
1998. bedtools shuffle -seed 1 -i SeqAOnly_r995s995.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r996s995.bed
1999. sort -k1,1 -k2,2n ./SeqAOnly_r996s995.bed > ./SeqAOnly_r996s996.bed
2000. bedtools shuffle -seed 1 -i SeqAOnly_r996s996.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r997s996.bed
2001. sort -k1,1 -k2,2n ./SeqAOnly_r997s996.bed > ./SeqAOnly_r997s997.bed
2002. bedtools shuffle -seed 1 -i SeqAOnly_r997s997.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_r998s997.bed

```

```
2003.    sort -k1,1 -k2,2n ./SeqAOnly_r998s997.bed > ./SeqAOnly_r998s998.bed
2004.    bedtools shuffle -seed 1 -i SeqAOnly_r998s998.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r999s998.bed
2005.    sort -k1,1 -k2,2n ./SeqAOnly_r999s998.bed > ./SeqAOnly_r999s999.bed
2006.    bedtools shuffle -seed 1 -i SeqAOnly_r999s999.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_r1000s999.bed
2007.    sort -k1,1 -k2,2n ./SeqAOnly_r1000s999.bed > ./SeqAOnly_r1000s1000.bed
```

BEDTools shuffle SeqA Only (Grainger) signals (SeqA Only 2) 1000 times

```
1. #!/bin/bash
2.
3. #bedtools_shuffle_sort_SeqAOnly_Grainger.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to shuffle SeqAOnly_Grainger signals 1000 times
6.
7. cp ./SeqAOnly_Grainger.bed ./SeqAOnly_Grainger_r0s0.bed
8. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r0s0.bed -g Ecoli-
   genomesize.txt > ./SeqAOnly_Grainger_r1s0.bed
9. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r1s0.bed > ./SeqAOnly_Grainger_r1s1.bed
10. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r1s1.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r2s1.bed
11. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r2s1.bed > ./SeqAOnly_Grainger_r2s2.bed
12. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r2s2.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r3s2.bed
13. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r3s2.bed > ./SeqAOnly_Grainger_r3s3.bed
14. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r3s3.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r4s3.bed
15. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r4s3.bed > ./SeqAOnly_Grainger_r4s4.bed
16. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r4s4.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r5s4.bed
17. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r5s4.bed > ./SeqAOnly_Grainger_r5s5.bed
18. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r5s5.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r6s5.bed
19. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r6s5.bed > ./SeqAOnly_Grainger_r6s6.bed
20. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r6s6.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r7s6.bed
21. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r7s6.bed > ./SeqAOnly_Grainger_r7s7.bed
22. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r7s7.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r8s7.bed
23. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r8s7.bed > ./SeqAOnly_Grainger_r8s8.bed
24. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r8s8.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r9s8.bed
25. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r9s8.bed > ./SeqAOnly_Grainger_r9s9.bed
26. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r9s9.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r10s9.bed
27. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r10s9.bed > ./SeqAOnly_Grainger_r10s10.bed
28. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r10s10.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r11s10.bed
29. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r11s10.bed > ./SeqAOnly_Grainger_r11s11.bed
30. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r11s11.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r12s11.bed
31. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r12s11.bed > ./SeqAOnly_Grainger_r12s12.bed
32. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r12s12.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r13s12.bed
33. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r13s12.bed > ./SeqAOnly_Grainger_r13s13.bed
34. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r13s13.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r14s13.bed
35. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r14s13.bed > ./SeqAOnly_Grainger_r14s14.bed
36. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r14s14.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r15s14.bed
37. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r15s14.bed > ./SeqAOnly_Grainger_r15s15.bed
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38. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r15s15.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r16s15.bed
39. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r16s15.bed > ./SeqAOnly_Grainger_r16s16.bed
40. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r16s16.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r17s16.bed
41. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r17s16.bed > ./SeqAOnly_Grainger_r17s17.bed
42. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r17s17.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r18s17.bed
43. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r18s17.bed > ./SeqAOnly_Grainger_r18s18.bed
44. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r18s18.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r19s18.bed
45. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r19s18.bed > ./SeqAOnly_Grainger_r19s19.bed
46. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r19s19.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r20s19.bed
47. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r20s19.bed > ./SeqAOnly_Grainger_r20s20.bed
48. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r20s20.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r21s20.bed
49. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r21s20.bed > ./SeqAOnly_Grainger_r21s21.bed
50. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r21s21.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r22s21.bed
51. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r22s21.bed > ./SeqAOnly_Grainger_r22s22.bed
52. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r22s22.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r23s22.bed
53. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r23s22.bed > ./SeqAOnly_Grainger_r23s23.bed
54. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r23s23.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r24s23.bed
55. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r24s23.bed > ./SeqAOnly_Grainger_r24s24.bed
56. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r24s24.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r25s24.bed
57. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r25s24.bed > ./SeqAOnly_Grainger_r25s25.bed
58. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r25s25.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r26s25.bed
59. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r26s25.bed > ./SeqAOnly_Grainger_r26s26.bed
60. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r26s26.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r27s26.bed
61. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r27s26.bed > ./SeqAOnly_Grainger_r27s27.bed
62. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r27s27.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r28s27.bed
63. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r28s27.bed > ./SeqAOnly_Grainger_r28s28.bed
64. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r28s28.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r29s28.bed
65. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r29s28.bed > ./SeqAOnly_Grainger_r29s29.bed
66. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r29s29.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r30s29.bed
67. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r30s29.bed > ./SeqAOnly_Grainger_r30s30.bed
68. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r30s30.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r31s30.bed
69. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r31s30.bed > ./SeqAOnly_Grainger_r31s31.bed
70. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r31s31.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r32s31.bed
71. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r32s31.bed > ./SeqAOnly_Grainger_r32s32.bed
72. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r32s32.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r33s32.bed
73. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r33s32.bed > ./SeqAOnly_Grainger_r33s33.bed
74. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r33s33.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r34s33.bed

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75. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r34s33.bed > ./SeqAOnly_Grainger_r34s34.bed
76. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r34s34.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r35s34.bed
77. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r35s34.bed > ./SeqAOnly_Grainger_r35s35.bed
78. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r35s35.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r36s35.bed
79. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r36s35.bed > ./SeqAOnly_Grainger_r36s36.bed
80. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r36s36.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r37s36.bed
81. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r37s36.bed > ./SeqAOnly_Grainger_r37s37.bed
82. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r37s37.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r38s37.bed
83. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r38s37.bed > ./SeqAOnly_Grainger_r38s38.bed
84. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r38s38.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r39s38.bed
85. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r39s38.bed > ./SeqAOnly_Grainger_r39s39.bed
86. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r39s39.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r40s39.bed
87. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r40s39.bed > ./SeqAOnly_Grainger_r40s40.bed
88. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r40s40.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r41s40.bed
89. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r41s40.bed > ./SeqAOnly_Grainger_r41s41.bed
90. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r41s41.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r42s41.bed
91. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r42s41.bed > ./SeqAOnly_Grainger_r42s42.bed
92. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r42s42.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r43s42.bed
93. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r43s42.bed > ./SeqAOnly_Grainger_r43s43.bed
94. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r43s43.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r44s43.bed
95. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r44s43.bed > ./SeqAOnly_Grainger_r44s44.bed
96. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r44s44.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r45s44.bed
97. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r45s44.bed > ./SeqAOnly_Grainger_r45s45.bed
98. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r45s45.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r46s45.bed
99. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r46s45.bed > ./SeqAOnly_Grainger_r46s46.bed
100. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r46s46.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r47s46.bed
101. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r47s46.bed > ./SeqAOnly_Grainger_r47s47.bed
102. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r47s47.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r48s47.bed
103. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r48s47.bed > ./SeqAOnly_Grainger_r48s48.bed
104. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r48s48.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r49s48.bed
105. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r49s48.bed > ./SeqAOnly_Grainger_r49s49.bed
106. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r49s49.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r50s49.bed
107. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r50s49.bed > ./SeqAOnly_Grainger_r50s50.bed
108. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r50s50.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r51s50.bed
109. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r51s50.bed > ./SeqAOnly_Grainger_r51s51.bed
110. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r51s51.bed -g Ecoli-
    genomesize.txt > ./SeqAOnly_Grainger_r52s51.bed
111. sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r52s51.bed > ./SeqAOnly_Grainger_r52s52.bed
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112.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r52s52.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r53s52.bed
113.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r53s52.bed > ./SeqAOnly_Grainger_r53s53.bed
114.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r53s53.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r54s53.bed
115.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r54s53.bed > ./SeqAOnly_Grainger_r54s54.bed
116.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r54s54.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r55s54.bed
117.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r55s54.bed > ./SeqAOnly_Grainger_r55s55.bed
118.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r55s55.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r56s55.bed
119.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r56s55.bed > ./SeqAOnly_Grainger_r56s56.bed
120.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r56s56.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r57s56.bed
121.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r57s56.bed > ./SeqAOnly_Grainger_r57s57.bed
122.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r57s57.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r58s57.bed
123.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r58s57.bed > ./SeqAOnly_Grainger_r58s58.bed
124.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r58s58.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r59s58.bed
125.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r59s58.bed > ./SeqAOnly_Grainger_r59s59.bed
126.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r59s59.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r60s59.bed
127.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r60s59.bed > ./SeqAOnly_Grainger_r60s60.bed
128.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r60s60.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r61s60.bed
129.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r61s60.bed > ./SeqAOnly_Grainger_r61s61.bed
130.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r61s61.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r62s61.bed
131.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r62s61.bed > ./SeqAOnly_Grainger_r62s62.bed
132.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r62s62.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r63s62.bed
133.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r63s62.bed > ./SeqAOnly_Grainger_r63s63.bed
134.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r63s63.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r64s63.bed
135.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r64s63.bed > ./SeqAOnly_Grainger_r64s64.bed
136.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r64s64.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r65s64.bed
137.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r65s64.bed > ./SeqAOnly_Grainger_r65s65.bed
138.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r65s65.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r66s65.bed
139.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r66s65.bed > ./SeqAOnly_Grainger_r66s66.bed
140.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r66s66.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r67s66.bed
141.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r67s66.bed > ./SeqAOnly_Grainger_r67s67.bed
142.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r67s67.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r68s67.bed
143.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r68s67.bed > ./SeqAOnly_Grainger_r68s68.bed
144.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r68s68.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r69s68.bed
145.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r69s68.bed > ./SeqAOnly_Grainger_r69s69.bed
146.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r69s69.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r70s69.bed
147.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r70s69.bed > ./SeqAOnly_Grainger_r70s70.bed
148.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r70s70.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r71s70.bed

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149.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r71s70.bed > ./SeqAOnly_Grainger_r71s71.bed
150.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r71s71.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r72s71.bed
151.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r72s71.bed > ./SeqAOnly_Grainger_r72s72.bed
152.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r72s72.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r73s72.bed
153.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r73s72.bed > ./SeqAOnly_Grainger_r73s73.bed
154.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r73s73.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r74s73.bed
155.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r74s73.bed > ./SeqAOnly_Grainger_r74s74.bed
156.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r74s74.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r75s74.bed
157.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r75s74.bed > ./SeqAOnly_Grainger_r75s75.bed
158.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r75s75.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r76s75.bed
159.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r76s75.bed > ./SeqAOnly_Grainger_r76s76.bed
160.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r76s76.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r77s76.bed
161.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r77s76.bed > ./SeqAOnly_Grainger_r77s77.bed
162.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r77s77.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r78s77.bed
163.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r78s77.bed > ./SeqAOnly_Grainger_r78s78.bed
164.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r78s78.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r79s78.bed
165.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r79s78.bed > ./SeqAOnly_Grainger_r79s79.bed
166.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r79s79.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r80s79.bed
167.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r80s79.bed > ./SeqAOnly_Grainger_r80s80.bed
168.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r80s80.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r81s80.bed
169.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r81s80.bed > ./SeqAOnly_Grainger_r81s81.bed
170.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r81s81.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r82s81.bed
171.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r82s81.bed > ./SeqAOnly_Grainger_r82s82.bed
172.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r82s82.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r83s82.bed
173.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r83s82.bed > ./SeqAOnly_Grainger_r83s83.bed
174.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r83s83.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r84s83.bed
175.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r84s83.bed > ./SeqAOnly_Grainger_r84s84.bed
176.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r84s84.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r85s84.bed
177.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r85s84.bed > ./SeqAOnly_Grainger_r85s85.bed
178.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r85s85.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r86s85.bed
179.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r86s85.bed > ./SeqAOnly_Grainger_r86s86.bed
180.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r86s86.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r87s86.bed
181.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r87s86.bed > ./SeqAOnly_Grainger_r87s87.bed
182.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r87s87.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r88s87.bed
183.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r88s87.bed > ./SeqAOnly_Grainger_r88s88.bed
184.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r88s88.bed -g Ecoli-
      genomesize.txt > ./SeqAOnly_Grainger_r89s88.bed
185.      sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r89s88.bed > ./SeqAOnly_Grainger_r89s89.bed

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186.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r89s89.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r90s89.bed
187.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r90s89.bed > ./SeqAOnly_Grainger_r90s90.bed
188.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r90s90.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r91s90.bed
189.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r91s90.bed > ./SeqAOnly_Grainger_r91s91.bed
190.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r91s91.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r92s91.bed
191.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r92s91.bed > ./SeqAOnly_Grainger_r92s92.bed
192.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r92s92.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r93s92.bed
193.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r93s92.bed > ./SeqAOnly_Grainger_r93s93.bed
194.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r93s93.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r94s93.bed
195.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r94s93.bed > ./SeqAOnly_Grainger_r94s94.bed
196.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r94s94.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r95s94.bed
197.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r95s94.bed > ./SeqAOnly_Grainger_r95s95.bed
198.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r95s95.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r96s95.bed
199.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r96s95.bed > ./SeqAOnly_Grainger_r96s96.bed
200.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r96s96.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r97s96.bed
201.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r97s96.bed > ./SeqAOnly_Grainger_r97s97.bed
202.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r97s97.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r98s97.bed
203.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r98s97.bed > ./SeqAOnly_Grainger_r98s98.bed
204.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r98s98.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r99s98.bed
205.     sort -k1,1 -k2,2n ./SeqAOnly_Grainger_r99s98.bed > ./SeqAOnly_Grainger_r99s99.bed
206.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r99s99.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r100s99.bed
207.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r100s99.bed > ./SeqAOnly_Grainger_r100s100.bed
208.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r100s100.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r101s100.bed
209.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r101s100.bed > ./SeqAOnly_Grainger_r101s101.bed
210.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r101s101.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r102s101.bed
211.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r102s101.bed > ./SeqAOnly_Grainger_r102s102.bed
212.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r102s102.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r103s102.bed
213.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r103s102.bed > ./SeqAOnly_Grainger_r103s103.bed
214.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r103s103.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r104s103.bed
215.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r104s103.bed > ./SeqAOnly_Grainger_r104s104.bed
216.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r104s104.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r105s104.bed
217.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r105s104.bed > ./SeqAOnly_Grainger_r105s105.bed
218.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r105s105.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r106s105.bed

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219.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r106s105.bed > ./SeqAOnly_Grainger_r106s106.bed
220.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r106s106.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r107s106.bed
221.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r107s106.bed > ./SeqAOnly_Grainger_r107s107.bed
222.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r107s107.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r108s107.bed
223.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r108s107.bed > ./SeqAOnly_Grainger_r108s108.bed
224.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r108s108.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r109s108.bed
225.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r109s108.bed > ./SeqAOnly_Grainger_r109s109.bed
226.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r109s109.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r110s109.bed
227.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r110s109.bed > ./SeqAOnly_Grainger_r110s110.bed
228.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r110s110.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r111s110.bed
229.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r111s110.bed > ./SeqAOnly_Grainger_r111s111.bed
230.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r111s111.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r112s111.bed
231.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r112s111.bed > ./SeqAOnly_Grainger_r112s112.bed
232.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r112s112.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r113s112.bed
233.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r113s112.bed > ./SeqAOnly_Grainger_r113s113.bed
234.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r113s113.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r114s113.bed
235.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r114s113.bed > ./SeqAOnly_Grainger_r114s114.bed
236.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r114s114.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r115s114.bed
237.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r115s114.bed > ./SeqAOnly_Grainger_r115s115.bed
238.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r115s115.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r116s115.bed
239.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r116s115.bed > ./SeqAOnly_Grainger_r116s116.bed
240.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r116s116.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r117s116.bed
241.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r117s116.bed > ./SeqAOnly_Grainger_r117s117.bed
242.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r117s117.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r118s117.bed
243.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r118s117.bed > ./SeqAOnly_Grainger_r118s118.bed
244.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r118s118.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r119s118.bed
245.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r119s118.bed > ./SeqAOnly_Grainger_r119s119.bed
246.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r119s119.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r120s119.bed

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247.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r120s119.bed > ./SeqAOnly_Grainger_r120s120.bed
248.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r120s120.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r121s120.bed
249.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r121s120.bed > ./SeqAOnly_Grainger_r121s121.bed
250.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r121s121.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r122s121.bed
251.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r122s121.bed > ./SeqAOnly_Grainger_r122s122.bed
252.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r122s122.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r123s122.bed
253.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r123s122.bed > ./SeqAOnly_Grainger_r123s123.bed
254.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r123s123.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r124s123.bed
255.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r124s123.bed > ./SeqAOnly_Grainger_r124s124.bed
256.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r124s124.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r125s124.bed
257.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r125s124.bed > ./SeqAOnly_Grainger_r125s125.bed
258.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r125s125.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r126s125.bed
259.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r126s125.bed > ./SeqAOnly_Grainger_r126s126.bed
260.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r126s126.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r127s126.bed
261.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r127s126.bed > ./SeqAOnly_Grainger_r127s127.bed
262.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r127s127.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r128s127.bed
263.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r128s127.bed > ./SeqAOnly_Grainger_r128s128.bed
264.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r128s128.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r129s128.bed
265.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r129s128.bed > ./SeqAOnly_Grainger_r129s129.bed
266.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r129s129.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r130s129.bed
267.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r130s129.bed > ./SeqAOnly_Grainger_r130s130.bed
268.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r130s130.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r131s130.bed
269.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r131s130.bed > ./SeqAOnly_Grainger_r131s131.bed
270.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r131s131.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r132s131.bed
271.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r132s131.bed > ./SeqAOnly_Grainger_r132s132.bed
272.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r132s132.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r133s132.bed
273.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r133s132.bed > ./SeqAOnly_Grainger_r133s133.bed
274.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r133s133.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r134s133.bed

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275.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r134s133.bed > ./SeqAOnly_Grainger_r134s134.bed
276.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r134s134.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r135s134.bed
277.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r135s134.bed > ./SeqAOnly_Grainger_r135s135.bed
278.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r135s135.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r136s135.bed
279.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r136s135.bed > ./SeqAOnly_Grainger_r136s136.bed
280.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r136s136.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r137s136.bed
281.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r137s136.bed > ./SeqAOnly_Grainger_r137s137.bed
282.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r137s137.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r138s137.bed
283.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r138s137.bed > ./SeqAOnly_Grainger_r138s138.bed
284.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r138s138.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r139s138.bed
285.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r139s138.bed > ./SeqAOnly_Grainger_r139s139.bed
286.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r139s139.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r140s139.bed
287.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r140s139.bed > ./SeqAOnly_Grainger_r140s140.bed
288.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r140s140.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r141s140.bed
289.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r141s140.bed > ./SeqAOnly_Grainger_r141s141.bed
290.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r141s141.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r142s141.bed
291.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r142s141.bed > ./SeqAOnly_Grainger_r142s142.bed
292.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r142s142.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r143s142.bed
293.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r143s142.bed > ./SeqAOnly_Grainger_r143s143.bed
294.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r143s143.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r144s143.bed
295.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r144s143.bed > ./SeqAOnly_Grainger_r144s144.bed
296.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r144s144.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r145s144.bed
297.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r145s144.bed > ./SeqAOnly_Grainger_r145s145.bed
298.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r145s145.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r146s145.bed
299.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r146s145.bed > ./SeqAOnly_Grainger_r146s146.bed
300.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r146s146.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r147s146.bed
301.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r147s146.bed > ./SeqAOnly_Grainger_r147s147.bed
302.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r147s147.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r148s147.bed

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303.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r148s147.bed > ./SeqAOnly_Grainger_r148s148.bed
304.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r148s148.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r149s148.bed
305.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r149s148.bed > ./SeqAOnly_Grainger_r149s149.bed
306.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r149s149.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r150s149.bed
307.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r150s149.bed > ./SeqAOnly_Grainger_r150s150.bed
308.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r150s150.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r151s150.bed
309.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r151s150.bed > ./SeqAOnly_Grainger_r151s151.bed
310.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r151s151.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r152s151.bed
311.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r152s151.bed > ./SeqAOnly_Grainger_r152s152.bed
312.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r152s152.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r153s152.bed
313.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r153s152.bed > ./SeqAOnly_Grainger_r153s153.bed
314.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r153s153.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r154s153.bed
315.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r154s153.bed > ./SeqAOnly_Grainger_r154s154.bed
316.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r154s154.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r155s154.bed
317.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r155s154.bed > ./SeqAOnly_Grainger_r155s155.bed
318.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r155s155.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r156s155.bed
319.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r156s155.bed > ./SeqAOnly_Grainger_r156s156.bed
320.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r156s156.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r157s156.bed
321.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r157s156.bed > ./SeqAOnly_Grainger_r157s157.bed
322.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r157s157.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r158s157.bed
323.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r158s157.bed > ./SeqAOnly_Grainger_r158s158.bed
324.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r158s158.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r159s158.bed
325.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r159s158.bed > ./SeqAOnly_Grainger_r159s159.bed
326.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r159s159.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r160s159.bed
327.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r160s159.bed > ./SeqAOnly_Grainger_r160s160.bed
328.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r160s160.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r161s160.bed
329.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r161s160.bed > ./SeqAOnly_Grainger_r161s161.bed
330.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r161s161.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r162s161.bed

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331.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r162s161.bed > ./SeqAOnly_Grainger_r162s162.bed
332.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r162s162.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r163s162.bed
333.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r163s162.bed > ./SeqAOnly_Grainger_r163s163.bed
334.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r163s163.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r164s163.bed
335.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r164s163.bed > ./SeqAOnly_Grainger_r164s164.bed
336.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r164s164.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r165s164.bed
337.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r165s164.bed > ./SeqAOnly_Grainger_r165s165.bed
338.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r165s165.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r166s165.bed
339.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r166s165.bed > ./SeqAOnly_Grainger_r166s166.bed
340.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r166s166.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r167s166.bed
341.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r167s166.bed > ./SeqAOnly_Grainger_r167s167.bed
342.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r167s167.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r168s167.bed
343.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r168s167.bed > ./SeqAOnly_Grainger_r168s168.bed
344.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r168s168.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r169s168.bed
345.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r169s168.bed > ./SeqAOnly_Grainger_r169s169.bed
346.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r169s169.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r170s169.bed
347.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r170s169.bed > ./SeqAOnly_Grainger_r170s170.bed
348.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r170s170.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r171s170.bed
349.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r171s170.bed > ./SeqAOnly_Grainger_r171s171.bed
350.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r171s171.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r172s171.bed
351.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r172s171.bed > ./SeqAOnly_Grainger_r172s172.bed
352.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r172s172.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r173s172.bed
353.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r173s172.bed > ./SeqAOnly_Grainger_r173s173.bed
354.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r173s173.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r174s173.bed
355.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r174s173.bed > ./SeqAOnly_Grainger_r174s174.bed
356.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r174s174.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r175s174.bed
357.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r175s174.bed > ./SeqAOnly_Grainger_r175s175.bed
358.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r175s175.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r176s175.bed

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359.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r176s175.bed > ./SeqAOnly_Grainger_r176s176.bed
360.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r176s176.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r177s176.bed
361.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r177s176.bed > ./SeqAOnly_Grainger_r177s177.bed
362.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r177s177.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r178s177.bed
363.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r178s177.bed > ./SeqAOnly_Grainger_r178s178.bed
364.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r178s178.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r179s178.bed
365.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r179s178.bed > ./SeqAOnly_Grainger_r179s179.bed
366.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r179s179.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r180s179.bed
367.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r180s179.bed > ./SeqAOnly_Grainger_r180s180.bed
368.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r180s180.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r181s180.bed
369.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r181s180.bed > ./SeqAOnly_Grainger_r181s181.bed
370.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r181s181.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r182s181.bed
371.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r182s181.bed > ./SeqAOnly_Grainger_r182s182.bed
372.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r182s182.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r183s182.bed
373.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r183s182.bed > ./SeqAOnly_Grainger_r183s183.bed
374.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r183s183.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r184s183.bed
375.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r184s183.bed > ./SeqAOnly_Grainger_r184s184.bed
376.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r184s184.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r185s184.bed
377.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r185s184.bed > ./SeqAOnly_Grainger_r185s185.bed
378.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r185s185.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r186s185.bed
379.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r186s185.bed > ./SeqAOnly_Grainger_r186s186.bed
380.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r186s186.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r187s186.bed
381.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r187s186.bed > ./SeqAOnly_Grainger_r187s187.bed
382.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r187s187.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r188s187.bed
383.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r188s187.bed > ./SeqAOnly_Grainger_r188s188.bed
384.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r188s188.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r189s188.bed
385.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r189s188.bed > ./SeqAOnly_Grainger_r189s189.bed
386.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r189s189.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r190s189.bed

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387.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r190s189.bed > ./SeqAOnly_Grainger_r190s190.bed
388.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r190s190.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r191s190.bed
389.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r191s190.bed > ./SeqAOnly_Grainger_r191s191.bed
390.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r191s191.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r192s191.bed
391.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r192s191.bed > ./SeqAOnly_Grainger_r192s192.bed
392.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r192s192.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r193s192.bed
393.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r193s192.bed > ./SeqAOnly_Grainger_r193s193.bed
394.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r193s193.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r194s193.bed
395.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r194s193.bed > ./SeqAOnly_Grainger_r194s194.bed
396.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r194s194.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r195s194.bed
397.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r195s194.bed > ./SeqAOnly_Grainger_r195s195.bed
398.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r195s195.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r196s195.bed
399.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r196s195.bed > ./SeqAOnly_Grainger_r196s196.bed
400.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r196s196.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r197s196.bed
401.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r197s196.bed > ./SeqAOnly_Grainger_r197s197.bed
402.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r197s197.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r198s197.bed
403.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r198s197.bed > ./SeqAOnly_Grainger_r198s198.bed
404.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r198s198.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r199s198.bed
405.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r199s198.bed > ./SeqAOnly_Grainger_r199s199.bed
406.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r199s199.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r200s199.bed
407.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r200s199.bed > ./SeqAOnly_Grainger_r200s200.bed
408.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r200s200.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r201s200.bed
409.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r201s200.bed > ./SeqAOnly_Grainger_r201s201.bed
410.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r201s201.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r202s201.bed
411.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r202s201.bed > ./SeqAOnly_Grainger_r202s202.bed
412.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r202s202.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r203s202.bed
413.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r203s202.bed > ./SeqAOnly_Grainger_r203s203.bed
414.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r203s203.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r204s203.bed

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415.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r204s203.bed > ./SeqAOnly_Grainger_r204s204.bed
416.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r204s204.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r205s204.bed
417.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r205s204.bed > ./SeqAOnly_Grainger_r205s205.bed
418.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r205s205.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r206s205.bed
419.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r206s205.bed > ./SeqAOnly_Grainger_r206s206.bed
420.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r206s206.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r207s206.bed
421.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r207s206.bed > ./SeqAOnly_Grainger_r207s207.bed
422.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r207s207.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r208s207.bed
423.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r208s207.bed > ./SeqAOnly_Grainger_r208s208.bed
424.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r208s208.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r209s208.bed
425.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r209s208.bed > ./SeqAOnly_Grainger_r209s209.bed
426.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r209s209.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r210s209.bed
427.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r210s209.bed > ./SeqAOnly_Grainger_r210s210.bed
428.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r210s210.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r211s210.bed
429.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r211s210.bed > ./SeqAOnly_Grainger_r211s211.bed
430.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r211s211.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r212s211.bed
431.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r212s211.bed > ./SeqAOnly_Grainger_r212s212.bed
432.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r212s212.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r213s212.bed
433.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r213s212.bed > ./SeqAOnly_Grainger_r213s213.bed
434.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r213s213.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r214s213.bed
435.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r214s213.bed > ./SeqAOnly_Grainger_r214s214.bed
436.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r214s214.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r215s214.bed
437.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r215s214.bed > ./SeqAOnly_Grainger_r215s215.bed
438.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r215s215.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r216s215.bed
439.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r216s215.bed > ./SeqAOnly_Grainger_r216s216.bed
440.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r216s216.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r217s216.bed
441.      sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r217s216.bed > ./SeqAOnly_Grainger_r217s217.bed
442.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r217s217.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r218s217.bed

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443.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r218s217.bed > ./SeqAOnly_Grainger_r218s218.bed
444.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r218s218.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r219s218.bed
445.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r219s218.bed > ./SeqAOnly_Grainger_r219s219.bed
446.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r219s219.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r220s219.bed
447.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r220s219.bed > ./SeqAOnly_Grainger_r220s220.bed
448.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r220s220.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r221s220.bed
449.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r221s220.bed > ./SeqAOnly_Grainger_r221s221.bed
450.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r221s221.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r222s221.bed
451.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r222s221.bed > ./SeqAOnly_Grainger_r222s222.bed
452.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r222s222.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r223s222.bed
453.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r223s222.bed > ./SeqAOnly_Grainger_r223s223.bed
454.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r223s223.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r224s223.bed
455.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r224s223.bed > ./SeqAOnly_Grainger_r224s224.bed
456.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r224s224.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r225s224.bed
457.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r225s224.bed > ./SeqAOnly_Grainger_r225s225.bed
458.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r225s225.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r226s225.bed
459.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r226s225.bed > ./SeqAOnly_Grainger_r226s226.bed
460.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r226s226.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r227s226.bed
461.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r227s226.bed > ./SeqAOnly_Grainger_r227s227.bed
462.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r227s227.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r228s227.bed
463.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r228s227.bed > ./SeqAOnly_Grainger_r228s228.bed
464.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r228s228.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r229s228.bed
465.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r229s228.bed > ./SeqAOnly_Grainger_r229s229.bed
466.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r229s229.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r230s229.bed
467.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r230s229.bed > ./SeqAOnly_Grainger_r230s230.bed
468.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r230s230.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r231s230.bed
469.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r231s230.bed > ./SeqAOnly_Grainger_r231s231.bed
470.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r231s231.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r232s231.bed

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471.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r232s231.bed > ./SeqAOnly_Grainger_r232s232.bed
472.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r232s232.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r233s232.bed
473.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r233s232.bed > ./SeqAOnly_Grainger_r233s233.bed
474.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r233s233.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r234s233.bed
475.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r234s233.bed > ./SeqAOnly_Grainger_r234s234.bed
476.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r234s234.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r235s234.bed
477.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r235s234.bed > ./SeqAOnly_Grainger_r235s235.bed
478.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r235s235.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r236s235.bed
479.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r236s235.bed > ./SeqAOnly_Grainger_r236s236.bed
480.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r236s236.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r237s236.bed
481.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r237s236.bed > ./SeqAOnly_Grainger_r237s237.bed
482.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r237s237.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r238s237.bed
483.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r238s237.bed > ./SeqAOnly_Grainger_r238s238.bed
484.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r238s238.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r239s238.bed
485.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r239s238.bed > ./SeqAOnly_Grainger_r239s239.bed
486.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r239s239.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r240s239.bed
487.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r240s239.bed > ./SeqAOnly_Grainger_r240s240.bed
488.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r240s240.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r241s240.bed
489.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r241s240.bed > ./SeqAOnly_Grainger_r241s241.bed
490.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r241s241.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r242s241.bed
491.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r242s241.bed > ./SeqAOnly_Grainger_r242s242.bed
492.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r242s242.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r243s242.bed
493.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r243s242.bed > ./SeqAOnly_Grainger_r243s243.bed
494.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r243s243.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r244s243.bed
495.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r244s243.bed > ./SeqAOnly_Grainger_r244s244.bed
496.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r244s244.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r245s244.bed
497.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r245s244.bed > ./SeqAOnly_Grainger_r245s245.bed
498.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r245s245.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r246s245.bed

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499.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r246s245.bed > ./SeqAOnly_Grainger_r246s246.bed
500.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r246s246.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r247s246.bed
501.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r247s246.bed > ./SeqAOnly_Grainger_r247s247.bed
502.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r247s247.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r248s247.bed
503.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r248s247.bed > ./SeqAOnly_Grainger_r248s248.bed
504.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r248s248.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r249s248.bed
505.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r249s248.bed > ./SeqAOnly_Grainger_r249s249.bed
506.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r249s249.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r250s249.bed
507.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r250s249.bed > ./SeqAOnly_Grainger_r250s250.bed
508.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r250s250.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r251s250.bed
509.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r251s250.bed > ./SeqAOnly_Grainger_r251s251.bed
510.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r251s251.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r252s251.bed
511.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r252s251.bed > ./SeqAOnly_Grainger_r252s252.bed
512.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r252s252.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r253s252.bed
513.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r253s252.bed > ./SeqAOnly_Grainger_r253s253.bed
514.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r253s253.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r254s253.bed
515.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r254s253.bed > ./SeqAOnly_Grainger_r254s254.bed
516.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r254s254.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r255s254.bed
517.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r255s254.bed > ./SeqAOnly_Grainger_r255s255.bed
518.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r255s255.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r256s255.bed
519.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r256s255.bed > ./SeqAOnly_Grainger_r256s256.bed
520.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r256s256.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r257s256.bed
521.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r257s256.bed > ./SeqAOnly_Grainger_r257s257.bed
522.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r257s257.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r258s257.bed
523.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r258s257.bed > ./SeqAOnly_Grainger_r258s258.bed
524.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r258s258.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r259s258.bed
525.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r259s258.bed > ./SeqAOnly_Grainger_r259s259.bed
526.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r259s259.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r260s259.bed

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527.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r260s259.bed > ./SeqAOnly_Grainger_r260s260.bed
528.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r260s260.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r261s260.bed
529.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r261s260.bed > ./SeqAOnly_Grainger_r261s261.bed
530.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r261s261.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r262s261.bed
531.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r262s261.bed > ./SeqAOnly_Grainger_r262s262.bed
532.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r262s262.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r263s262.bed
533.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r263s262.bed > ./SeqAOnly_Grainger_r263s263.bed
534.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r263s263.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r264s263.bed
535.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r264s263.bed > ./SeqAOnly_Grainger_r264s264.bed
536.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r264s264.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r265s264.bed
537.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r265s264.bed > ./SeqAOnly_Grainger_r265s265.bed
538.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r265s265.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r266s265.bed
539.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r266s265.bed > ./SeqAOnly_Grainger_r266s266.bed
540.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r266s266.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r267s266.bed
541.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r267s266.bed > ./SeqAOnly_Grainger_r267s267.bed
542.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r267s267.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r268s267.bed
543.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r268s267.bed > ./SeqAOnly_Grainger_r268s268.bed
544.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r268s268.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r269s268.bed
545.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r269s268.bed > ./SeqAOnly_Grainger_r269s269.bed
546.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r269s269.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r270s269.bed
547.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r270s269.bed > ./SeqAOnly_Grainger_r270s270.bed
548.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r270s270.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r271s270.bed
549.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r271s270.bed > ./SeqAOnly_Grainger_r271s271.bed
550.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r271s271.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r272s271.bed
551.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r272s271.bed > ./SeqAOnly_Grainger_r272s272.bed
552.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r272s272.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r273s272.bed
553.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r273s272.bed > ./SeqAOnly_Grainger_r273s273.bed
554.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r273s273.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r274s273.bed

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555.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r274s273.bed > ./SeqAOnly_Grainger_r274s274.bed
556.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r274s274.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r275s274.bed
557.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r275s274.bed > ./SeqAOnly_Grainger_r275s275.bed
558.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r275s275.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r276s275.bed
559.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r276s275.bed > ./SeqAOnly_Grainger_r276s276.bed
560.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r276s276.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r277s276.bed
561.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r277s276.bed > ./SeqAOnly_Grainger_r277s277.bed
562.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r277s277.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r278s277.bed
563.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r278s277.bed > ./SeqAOnly_Grainger_r278s278.bed
564.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r278s278.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r279s278.bed
565.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r279s278.bed > ./SeqAOnly_Grainger_r279s279.bed
566.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r279s279.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r280s279.bed
567.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r280s279.bed > ./SeqAOnly_Grainger_r280s280.bed
568.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r280s280.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r281s280.bed
569.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r281s280.bed > ./SeqAOnly_Grainger_r281s281.bed
570.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r281s281.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r282s281.bed
571.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r282s281.bed > ./SeqAOnly_Grainger_r282s282.bed
572.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r282s282.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r283s282.bed
573.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r283s282.bed > ./SeqAOnly_Grainger_r283s283.bed
574.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r283s283.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r284s283.bed
575.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r284s283.bed > ./SeqAOnly_Grainger_r284s284.bed
576.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r284s284.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r285s284.bed
577.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r285s284.bed > ./SeqAOnly_Grainger_r285s285.bed
578.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r285s285.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r286s285.bed
579.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r286s285.bed > ./SeqAOnly_Grainger_r286s286.bed
580.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r286s286.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r287s286.bed
581.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r287s286.bed > ./SeqAOnly_Grainger_r287s287.bed
582.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r287s287.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r288s287.bed

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583.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r288s287.bed > ./SeqAOnly_Grainger_r288s288.bed
584.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r288s288.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r289s288.bed
585.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r289s288.bed > ./SeqAOnly_Grainger_r289s289.bed
586.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r289s289.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r290s289.bed
587.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r290s289.bed > ./SeqAOnly_Grainger_r290s290.bed
588.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r290s290.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r291s290.bed
589.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r291s290.bed > ./SeqAOnly_Grainger_r291s291.bed
590.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r291s291.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r292s291.bed
591.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r292s291.bed > ./SeqAOnly_Grainger_r292s292.bed
592.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r292s292.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r293s292.bed
593.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r293s292.bed > ./SeqAOnly_Grainger_r293s293.bed
594.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r293s293.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r294s293.bed
595.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r294s293.bed > ./SeqAOnly_Grainger_r294s294.bed
596.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r294s294.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r295s294.bed
597.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r295s294.bed > ./SeqAOnly_Grainger_r295s295.bed
598.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r295s295.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r296s295.bed
599.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r296s295.bed > ./SeqAOnly_Grainger_r296s296.bed
600.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r296s296.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r297s296.bed
601.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r297s296.bed > ./SeqAOnly_Grainger_r297s297.bed
602.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r297s297.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r298s297.bed
603.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r298s297.bed > ./SeqAOnly_Grainger_r298s298.bed
604.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r298s298.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r299s298.bed
605.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r299s298.bed > ./SeqAOnly_Grainger_r299s299.bed
606.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r299s299.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r300s299.bed
607.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r300s299.bed > ./SeqAOnly_Grainger_r300s300.bed
608.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r300s300.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r301s300.bed
609.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r301s300.bed > ./SeqAOnly_Grainger_r301s301.bed
610.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r301s301.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r302s301.bed

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611.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r302s301.bed > ./SeqAOnly_Grainger_r302s302.bed
612.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r302s302.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r303s302.bed
613.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r303s302.bed > ./SeqAOnly_Grainger_r303s303.bed
614.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r303s303.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r304s303.bed
615.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r304s303.bed > ./SeqAOnly_Grainger_r304s304.bed
616.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r304s304.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r305s304.bed
617.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r305s304.bed > ./SeqAOnly_Grainger_r305s305.bed
618.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r305s305.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r306s305.bed
619.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r306s305.bed > ./SeqAOnly_Grainger_r306s306.bed
620.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r306s306.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r307s306.bed
621.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r307s306.bed > ./SeqAOnly_Grainger_r307s307.bed
622.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r307s307.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r308s307.bed
623.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r308s307.bed > ./SeqAOnly_Grainger_r308s308.bed
624.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r308s308.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r309s308.bed
625.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r309s308.bed > ./SeqAOnly_Grainger_r309s309.bed
626.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r309s309.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r310s309.bed
627.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r310s309.bed > ./SeqAOnly_Grainger_r310s310.bed
628.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r310s310.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r311s310.bed
629.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r311s310.bed > ./SeqAOnly_Grainger_r311s311.bed
630.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r311s311.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r312s311.bed
631.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r312s311.bed > ./SeqAOnly_Grainger_r312s312.bed
632.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r312s312.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r313s312.bed
633.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r313s312.bed > ./SeqAOnly_Grainger_r313s313.bed
634.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r313s313.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r314s313.bed
635.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r314s313.bed > ./SeqAOnly_Grainger_r314s314.bed
636.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r314s314.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r315s314.bed
637.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r315s314.bed > ./SeqAOnly_Grainger_r315s315.bed
638.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r315s315.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r316s315.bed

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639.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r316s315.bed > ./SeqAOnly_Grainger_r316s316.bed
640.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r316s316.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r317s316.bed
641.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r317s316.bed > ./SeqAOnly_Grainger_r317s317.bed
642.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r317s317.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r318s317.bed
643.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r318s317.bed > ./SeqAOnly_Grainger_r318s318.bed
644.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r318s318.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r319s318.bed
645.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r319s318.bed > ./SeqAOnly_Grainger_r319s319.bed
646.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r319s319.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r320s319.bed
647.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r320s319.bed > ./SeqAOnly_Grainger_r320s320.bed
648.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r320s320.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r321s320.bed
649.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r321s320.bed > ./SeqAOnly_Grainger_r321s321.bed
650.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r321s321.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r322s321.bed
651.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r322s321.bed > ./SeqAOnly_Grainger_r322s322.bed
652.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r322s322.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r323s322.bed
653.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r323s322.bed > ./SeqAOnly_Grainger_r323s323.bed
654.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r323s323.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r324s323.bed
655.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r324s323.bed > ./SeqAOnly_Grainger_r324s324.bed
656.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r324s324.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r325s324.bed
657.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r325s324.bed > ./SeqAOnly_Grainger_r325s325.bed
658.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r325s325.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r326s325.bed
659.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r326s325.bed > ./SeqAOnly_Grainger_r326s326.bed
660.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r326s326.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r327s326.bed
661.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r327s326.bed > ./SeqAOnly_Grainger_r327s327.bed
662.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r327s327.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r328s327.bed
663.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r328s327.bed > ./SeqAOnly_Grainger_r328s328.bed
664.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r328s328.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r329s328.bed
665.     sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r329s328.bed > ./SeqAOnly_Grainger_r329s329.bed
666.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r329s329.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r330s329.bed

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667.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r330s329.bed > ./SeqAOnly_Grainger_r330s330.bed
668.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r330s330.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r331s330.bed
669.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r331s330.bed > ./SeqAOnly_Grainger_r331s331.bed
670.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r331s331.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r332s331.bed
671.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r332s331.bed > ./SeqAOnly_Grainger_r332s332.bed
672.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r332s332.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r333s332.bed
673.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r333s332.bed > ./SeqAOnly_Grainger_r333s333.bed
674.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r333s333.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r334s333.bed
675.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r334s333.bed > ./SeqAOnly_Grainger_r334s334.bed
676.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r334s334.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r335s334.bed
677.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r335s334.bed > ./SeqAOnly_Grainger_r335s335.bed
678.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r335s335.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r336s335.bed
679.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r336s335.bed > ./SeqAOnly_Grainger_r336s336.bed
680.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r336s336.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r337s336.bed
681.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r337s336.bed > ./SeqAOnly_Grainger_r337s337.bed
682.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r337s337.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r338s337.bed
683.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r338s337.bed > ./SeqAOnly_Grainger_r338s338.bed
684.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r338s338.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r339s338.bed
685.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r339s338.bed > ./SeqAOnly_Grainger_r339s339.bed
686.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r339s339.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r340s339.bed
687.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r340s339.bed > ./SeqAOnly_Grainger_r340s340.bed
688.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r340s340.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r341s340.bed
689.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r341s340.bed > ./SeqAOnly_Grainger_r341s341.bed
690.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r341s341.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r342s341.bed
691.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r342s341.bed > ./SeqAOnly_Grainger_r342s342.bed
692.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r342s342.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r343s342.bed
693.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r343s342.bed > ./SeqAOnly_Grainger_r343s343.bed
694.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r343s343.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r344s343.bed

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695.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r344s343.bed > ./SeqAOnly_Grainger_r344s344.bed
696.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r344s344.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r345s344.bed
697.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r345s344.bed > ./SeqAOnly_Grainger_r345s345.bed
698.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r345s345.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r346s345.bed
699.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r346s345.bed > ./SeqAOnly_Grainger_r346s346.bed
700.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r346s346.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r347s346.bed
701.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r347s346.bed > ./SeqAOnly_Grainger_r347s347.bed
702.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r347s347.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r348s347.bed
703.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r348s347.bed > ./SeqAOnly_Grainger_r348s348.bed
704.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r348s348.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r349s348.bed
705.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r349s348.bed > ./SeqAOnly_Grainger_r349s349.bed
706.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r349s349.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r350s349.bed
707.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r350s349.bed > ./SeqAOnly_Grainger_r350s350.bed
708.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r350s350.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r351s350.bed
709.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r351s350.bed > ./SeqAOnly_Grainger_r351s351.bed
710.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r351s351.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r352s351.bed
711.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r352s351.bed > ./SeqAOnly_Grainger_r352s352.bed
712.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r352s352.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r353s352.bed
713.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r353s352.bed > ./SeqAOnly_Grainger_r353s353.bed
714.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r353s353.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r354s353.bed
715.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r354s353.bed > ./SeqAOnly_Grainger_r354s354.bed
716.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r354s354.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r355s354.bed
717.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r355s354.bed > ./SeqAOnly_Grainger_r355s355.bed
718.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r355s355.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r356s355.bed
719.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r356s355.bed > ./SeqAOnly_Grainger_r356s356.bed
720.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r356s356.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r357s356.bed
721.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r357s356.bed > ./SeqAOnly_Grainger_r357s357.bed
722.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r357s357.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r358s357.bed

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723.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r358s357.bed > ./SeqAOnly_Grainger_r358s358.bed
724.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r358s358.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r359s358.bed
725.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r359s358.bed > ./SeqAOnly_Grainger_r359s359.bed
726.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r359s359.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r360s359.bed
727.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r360s359.bed > ./SeqAOnly_Grainger_r360s360.bed
728.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r360s360.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r361s360.bed
729.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r361s360.bed > ./SeqAOnly_Grainger_r361s361.bed
730.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r361s361.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r362s361.bed
731.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r362s361.bed > ./SeqAOnly_Grainger_r362s362.bed
732.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r362s362.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r363s362.bed
733.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r363s362.bed > ./SeqAOnly_Grainger_r363s363.bed
734.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r363s363.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r364s363.bed
735.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r364s363.bed > ./SeqAOnly_Grainger_r364s364.bed
736.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r364s364.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r365s364.bed
737.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r365s364.bed > ./SeqAOnly_Grainger_r365s365.bed
738.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r365s365.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r366s365.bed
739.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r366s365.bed > ./SeqAOnly_Grainger_r366s366.bed
740.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r366s366.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r367s366.bed
741.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r367s366.bed > ./SeqAOnly_Grainger_r367s367.bed
742.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r367s367.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r368s367.bed
743.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r368s367.bed > ./SeqAOnly_Grainger_r368s368.bed
744.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r368s368.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r369s368.bed
745.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r369s368.bed > ./SeqAOnly_Grainger_r369s369.bed
746.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r369s369.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r370s369.bed
747.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r370s369.bed > ./SeqAOnly_Grainger_r370s370.bed
748.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r370s370.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r371s370.bed
749.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r371s370.bed > ./SeqAOnly_Grainger_r371s371.bed
750.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r371s371.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r372s371.bed

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751.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r372s371.bed > ./SeqAOnly_Grainger_r372s372.bed
752.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r372s372.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r373s372.bed
753.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r373s372.bed > ./SeqAOnly_Grainger_r373s373.bed
754.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r373s373.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r374s373.bed
755.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r374s373.bed > ./SeqAOnly_Grainger_r374s374.bed
756.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r374s374.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r375s374.bed
757.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r375s374.bed > ./SeqAOnly_Grainger_r375s375.bed
758.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r375s375.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r376s375.bed
759.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r376s375.bed > ./SeqAOnly_Grainger_r376s376.bed
760.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r376s376.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r377s376.bed
761.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r377s376.bed > ./SeqAOnly_Grainger_r377s377.bed
762.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r377s377.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r378s377.bed
763.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r378s377.bed > ./SeqAOnly_Grainger_r378s378.bed
764.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r378s378.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r379s378.bed
765.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r379s378.bed > ./SeqAOnly_Grainger_r379s379.bed
766.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r379s379.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r380s379.bed
767.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r380s379.bed > ./SeqAOnly_Grainger_r380s380.bed
768.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r380s380.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r381s380.bed
769.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r381s380.bed > ./SeqAOnly_Grainger_r381s381.bed
770.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r381s381.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r382s381.bed
771.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r382s381.bed > ./SeqAOnly_Grainger_r382s382.bed
772.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r382s382.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r383s382.bed
773.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r383s382.bed > ./SeqAOnly_Grainger_r383s383.bed
774.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r383s383.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r384s383.bed
775.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r384s383.bed > ./SeqAOnly_Grainger_r384s384.bed
776.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r384s384.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r385s384.bed
777.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r385s384.bed > ./SeqAOnly_Grainger_r385s385.bed
778.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r385s385.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r386s385.bed

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779.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r386s385.bed > ./SeqAOnly_Grainger_r386s386.bed
780.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r386s386.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r387s386.bed
781.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r387s386.bed > ./SeqAOnly_Grainger_r387s387.bed
782.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r387s387.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r388s387.bed
783.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r388s387.bed > ./SeqAOnly_Grainger_r388s388.bed
784.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r388s388.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r389s388.bed
785.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r389s388.bed > ./SeqAOnly_Grainger_r389s389.bed
786.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r389s389.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r390s389.bed
787.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r390s389.bed > ./SeqAOnly_Grainger_r390s390.bed
788.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r390s390.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r391s390.bed
789.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r391s390.bed > ./SeqAOnly_Grainger_r391s391.bed
790.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r391s391.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r392s391.bed
791.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r392s391.bed > ./SeqAOnly_Grainger_r392s392.bed
792.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r392s392.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r393s392.bed
793.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r393s392.bed > ./SeqAOnly_Grainger_r393s393.bed
794.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r393s393.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r394s393.bed
795.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r394s393.bed > ./SeqAOnly_Grainger_r394s394.bed
796.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r394s394.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r395s394.bed
797.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r395s394.bed > ./SeqAOnly_Grainger_r395s395.bed
798.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r395s395.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r396s395.bed
799.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r396s395.bed > ./SeqAOnly_Grainger_r396s396.bed
800.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r396s396.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r397s396.bed
801.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r397s396.bed > ./SeqAOnly_Grainger_r397s397.bed
802.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r397s397.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r398s397.bed
803.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r398s397.bed > ./SeqAOnly_Grainger_r398s398.bed
804.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r398s398.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r399s398.bed
805.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r399s398.bed > ./SeqAOnly_Grainger_r399s399.bed
806.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r399s399.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r400s399.bed

```

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807.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r400s399.bed > ./SeqAOnly_Grainger_r400s400.bed
808.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r400s400.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r401s400.bed
809.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r401s400.bed > ./SeqAOnly_Grainger_r401s401.bed
810.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r401s401.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r402s401.bed
811.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r402s401.bed > ./SeqAOnly_Grainger_r402s402.bed
812.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r402s402.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r403s402.bed
813.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r403s402.bed > ./SeqAOnly_Grainger_r403s403.bed
814.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r403s403.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r404s403.bed
815.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r404s403.bed > ./SeqAOnly_Grainger_r404s404.bed
816.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r404s404.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r405s404.bed
817.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r405s404.bed > ./SeqAOnly_Grainger_r405s405.bed
818.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r405s405.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r406s405.bed
819.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r406s405.bed > ./SeqAOnly_Grainger_r406s406.bed
820.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r406s406.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r407s406.bed
821.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r407s406.bed > ./SeqAOnly_Grainger_r407s407.bed
822.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r407s407.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r408s407.bed
823.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r408s407.bed > ./SeqAOnly_Grainger_r408s408.bed
824.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r408s408.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r409s408.bed
825.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r409s408.bed > ./SeqAOnly_Grainger_r409s409.bed
826.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r409s409.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r410s409.bed
827.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r410s409.bed > ./SeqAOnly_Grainger_r410s410.bed
828.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r410s410.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r411s410.bed
829.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r411s410.bed > ./SeqAOnly_Grainger_r411s411.bed
830.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r411s411.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r412s411.bed
831.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r412s411.bed > ./SeqAOnly_Grainger_r412s412.bed
832.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r412s412.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r413s412.bed
833.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r413s412.bed > ./SeqAOnly_Grainger_r413s413.bed
834.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r413s413.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r414s413.bed

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835.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r414s413.bed > ./SeqAOnly_Grainger_r414s414.bed
836.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r414s414.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r415s414.bed
837.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r415s414.bed > ./SeqAOnly_Grainger_r415s415.bed
838.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r415s415.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r416s415.bed
839.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r416s415.bed > ./SeqAOnly_Grainger_r416s416.bed
840.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r416s416.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r417s416.bed
841.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r417s416.bed > ./SeqAOnly_Grainger_r417s417.bed
842.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r417s417.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r418s417.bed
843.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r418s417.bed > ./SeqAOnly_Grainger_r418s418.bed
844.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r418s418.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r419s418.bed
845.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r419s418.bed > ./SeqAOnly_Grainger_r419s419.bed
846.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r419s419.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r420s419.bed
847.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r420s419.bed > ./SeqAOnly_Grainger_r420s420.bed
848.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r420s420.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r421s420.bed
849.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r421s420.bed > ./SeqAOnly_Grainger_r421s421.bed
850.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r421s421.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r422s421.bed
851.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r422s421.bed > ./SeqAOnly_Grainger_r422s422.bed
852.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r422s422.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r423s422.bed
853.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r423s422.bed > ./SeqAOnly_Grainger_r423s423.bed
854.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r423s423.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r424s423.bed
855.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r424s423.bed > ./SeqAOnly_Grainger_r424s424.bed
856.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r424s424.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r425s424.bed
857.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r425s424.bed > ./SeqAOnly_Grainger_r425s425.bed
858.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r425s425.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r426s425.bed
859.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r426s425.bed > ./SeqAOnly_Grainger_r426s426.bed
860.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r426s426.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r427s426.bed
861.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r427s426.bed > ./SeqAOnly_Grainger_r427s427.bed
862.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r427s427.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r428s427.bed

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863.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r428s427.bed > ./SeqAOnly_Grainger_r428s428.bed
864.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r428s428.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r429s428.bed
865.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r429s428.bed > ./SeqAOnly_Grainger_r429s429.bed
866.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r429s429.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r430s429.bed
867.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r430s429.bed > ./SeqAOnly_Grainger_r430s430.bed
868.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r430s430.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r431s430.bed
869.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r431s430.bed > ./SeqAOnly_Grainger_r431s431.bed
870.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r431s431.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r432s431.bed
871.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r432s431.bed > ./SeqAOnly_Grainger_r432s432.bed
872.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r432s432.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r433s432.bed
873.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r433s432.bed > ./SeqAOnly_Grainger_r433s433.bed
874.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r433s433.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r434s433.bed
875.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r434s433.bed > ./SeqAOnly_Grainger_r434s434.bed
876.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r434s434.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r435s434.bed
877.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r435s434.bed > ./SeqAOnly_Grainger_r435s435.bed
878.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r435s435.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r436s435.bed
879.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r436s435.bed > ./SeqAOnly_Grainger_r436s436.bed
880.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r436s436.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r437s436.bed
881.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r437s436.bed > ./SeqAOnly_Grainger_r437s437.bed
882.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r437s437.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r438s437.bed
883.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r438s437.bed > ./SeqAOnly_Grainger_r438s438.bed
884.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r438s438.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r439s438.bed
885.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r439s438.bed > ./SeqAOnly_Grainger_r439s439.bed
886.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r439s439.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r440s439.bed
887.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r440s439.bed > ./SeqAOnly_Grainger_r440s440.bed
888.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r440s440.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r441s440.bed
889.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r441s440.bed > ./SeqAOnly_Grainger_r441s441.bed
890.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r441s441.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r442s441.bed

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891.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r442s441.bed > ./SeqAOnly_Grainger_r442s442.bed
892.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r442s442.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r443s442.bed
893.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r443s442.bed > ./SeqAOnly_Grainger_r443s443.bed
894.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r443s443.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r444s443.bed
895.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r444s443.bed > ./SeqAOnly_Grainger_r444s444.bed
896.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r444s444.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r445s444.bed
897.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r445s444.bed > ./SeqAOnly_Grainger_r445s445.bed
898.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r445s445.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r446s445.bed
899.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r446s445.bed > ./SeqAOnly_Grainger_r446s446.bed
900.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r446s446.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r447s446.bed
901.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r447s446.bed > ./SeqAOnly_Grainger_r447s447.bed
902.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r447s447.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r448s447.bed
903.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r448s447.bed > ./SeqAOnly_Grainger_r448s448.bed
904.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r448s448.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r449s448.bed
905.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r449s448.bed > ./SeqAOnly_Grainger_r449s449.bed
906.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r449s449.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r450s449.bed
907.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r450s449.bed > ./SeqAOnly_Grainger_r450s450.bed
908.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r450s450.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r451s450.bed
909.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r451s450.bed > ./SeqAOnly_Grainger_r451s451.bed
910.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r451s451.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r452s451.bed
911.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r452s451.bed > ./SeqAOnly_Grainger_r452s452.bed
912.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r452s452.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r453s452.bed
913.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r453s452.bed > ./SeqAOnly_Grainger_r453s453.bed
914.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r453s453.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r454s453.bed
915.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r454s453.bed > ./SeqAOnly_Grainger_r454s454.bed
916.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r454s454.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r455s454.bed
917.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r455s454.bed > ./SeqAOnly_Grainger_r455s455.bed
918.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r455s455.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r456s455.bed

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919.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r456s455.bed > ./SeqAOnly_Grainger_r456s456.bed
920.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r456s456.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r457s456.bed
921.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r457s456.bed > ./SeqAOnly_Grainger_r457s457.bed
922.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r457s457.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r458s457.bed
923.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r458s457.bed > ./SeqAOnly_Grainger_r458s458.bed
924.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r458s458.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r459s458.bed
925.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r459s458.bed > ./SeqAOnly_Grainger_r459s459.bed
926.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r459s459.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r460s459.bed
927.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r460s459.bed > ./SeqAOnly_Grainger_r460s460.bed
928.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r460s460.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r461s460.bed
929.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r461s460.bed > ./SeqAOnly_Grainger_r461s461.bed
930.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r461s461.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r462s461.bed
931.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r462s461.bed > ./SeqAOnly_Grainger_r462s462.bed
932.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r462s462.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r463s462.bed
933.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r463s462.bed > ./SeqAOnly_Grainger_r463s463.bed
934.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r463s463.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r464s463.bed
935.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r464s463.bed > ./SeqAOnly_Grainger_r464s464.bed
936.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r464s464.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r465s464.bed
937.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r465s464.bed > ./SeqAOnly_Grainger_r465s465.bed
938.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r465s465.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r466s465.bed
939.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r466s465.bed > ./SeqAOnly_Grainger_r466s466.bed
940.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r466s466.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r467s466.bed
941.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r467s466.bed > ./SeqAOnly_Grainger_r467s467.bed
942.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r467s467.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r468s467.bed
943.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r468s467.bed > ./SeqAOnly_Grainger_r468s468.bed
944.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r468s468.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r469s468.bed
945.      sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r469s468.bed > ./SeqAOnly_Grainger_r469s469.bed
946.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r469s469.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r470s469.bed

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947.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r470s469.bed > ./SeqAOnly_Grainger_r470s470.bed
948.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r470s470.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r471s470.bed
949.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r471s470.bed > ./SeqAOnly_Grainger_r471s471.bed
950.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r471s471.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r472s471.bed
951.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r472s471.bed > ./SeqAOnly_Grainger_r472s472.bed
952.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r472s472.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r473s472.bed
953.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r473s472.bed > ./SeqAOnly_Grainger_r473s473.bed
954.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r473s473.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r474s473.bed
955.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r474s473.bed > ./SeqAOnly_Grainger_r474s474.bed
956.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r474s474.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r475s474.bed
957.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r475s474.bed > ./SeqAOnly_Grainger_r475s475.bed
958.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r475s475.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r476s475.bed
959.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r476s475.bed > ./SeqAOnly_Grainger_r476s476.bed
960.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r476s476.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r477s476.bed
961.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r477s476.bed > ./SeqAOnly_Grainger_r477s477.bed
962.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r477s477.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r478s477.bed
963.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r478s477.bed > ./SeqAOnly_Grainger_r478s478.bed
964.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r478s478.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r479s478.bed
965.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r479s478.bed > ./SeqAOnly_Grainger_r479s479.bed
966.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r479s479.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r480s479.bed
967.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r480s479.bed > ./SeqAOnly_Grainger_r480s480.bed
968.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r480s480.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r481s480.bed
969.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r481s480.bed > ./SeqAOnly_Grainger_r481s481.bed
970.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r481s481.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r482s481.bed
971.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r482s481.bed > ./SeqAOnly_Grainger_r482s482.bed
972.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r482s482.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r483s482.bed
973.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r483s482.bed > ./SeqAOnly_Grainger_r483s483.bed
974.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r483s483.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r484s483.bed

```

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975.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r484s483.bed > ./SeqAOnly_Grainger_r484s484.bed
976.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r484s484.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r485s484.bed
977.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r485s484.bed > ./SeqAOnly_Grainger_r485s485.bed
978.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r485s485.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r486s485.bed
979.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r486s485.bed > ./SeqAOnly_Grainger_r486s486.bed
980.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r486s486.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r487s486.bed
981.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r487s486.bed > ./SeqAOnly_Grainger_r487s487.bed
982.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r487s487.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r488s487.bed
983.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r488s487.bed > ./SeqAOnly_Grainger_r488s488.bed
984.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r488s488.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r489s488.bed
985.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r489s488.bed > ./SeqAOnly_Grainger_r489s489.bed
986.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r489s489.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r490s489.bed
987.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r490s489.bed > ./SeqAOnly_Grainger_r490s490.bed
988.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r490s490.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r491s490.bed
989.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r491s490.bed > ./SeqAOnly_Grainger_r491s491.bed
990.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r491s491.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r492s491.bed
991.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r492s491.bed > ./SeqAOnly_Grainger_r492s492.bed
992.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r492s492.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r493s492.bed
993.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r493s492.bed > ./SeqAOnly_Grainger_r493s493.bed
994.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r493s493.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r494s493.bed
995.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r494s493.bed > ./SeqAOnly_Grainger_r494s494.bed
996.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r494s494.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r495s494.bed
997.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r495s494.bed > ./SeqAOnly_Grainger_r495s495.bed
998.      bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r495s495.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r496s495.bed
999.      sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r496s495.bed > ./SeqAOnly_Grainger_r496s496.bed
1000.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r496s496.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r497s496.bed
1001.     sort -k1,1 -
          k2,2n ./SeqAOnly_Grainger_r497s496.bed > ./SeqAOnly_Grainger_r497s497.bed
1002.     bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r497s497.bed -g Ecoli-
          genomesize.txt > ./SeqAOnly_Grainger_r498s497.bed

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1003.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r498s497.bed > ./SeqAOnly_Grainger_r498s498.bed
1004.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r498s498.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r499s498.bed
1005.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r499s498.bed > ./SeqAOnly_Grainger_r499s499.bed
1006.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r499s499.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r500s499.bed
1007.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r500s499.bed > ./SeqAOnly_Grainger_r500s500.bed
1008.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r500s500.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r501s500.bed
1009.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r501s500.bed > ./SeqAOnly_Grainger_r501s501.bed
1010.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r501s501.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r502s501.bed
1011.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r502s501.bed > ./SeqAOnly_Grainger_r502s502.bed
1012.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r502s502.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r503s502.bed
1013.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r503s502.bed > ./SeqAOnly_Grainger_r503s503.bed
1014.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r503s503.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r504s503.bed
1015.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r504s503.bed > ./SeqAOnly_Grainger_r504s504.bed
1016.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r504s504.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r505s504.bed
1017.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r505s504.bed > ./SeqAOnly_Grainger_r505s505.bed
1018.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r505s505.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r506s505.bed
1019.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r506s505.bed > ./SeqAOnly_Grainger_r506s506.bed
1020.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r506s506.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r507s506.bed
1021.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r507s506.bed > ./SeqAOnly_Grainger_r507s507.bed
1022.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r507s507.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r508s507.bed
1023.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r508s507.bed > ./SeqAOnly_Grainger_r508s508.bed
1024.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r508s508.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r509s508.bed
1025.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r509s508.bed > ./SeqAOnly_Grainger_r509s509.bed
1026.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r509s509.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r510s509.bed
1027.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r510s509.bed > ./SeqAOnly_Grainger_r510s510.bed
1028.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r510s510.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r511s510.bed
1029.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r511s510.bed > ./SeqAOnly_Grainger_r511s511.bed
1030.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r511s511.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r512s511.bed

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1031.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r512s511.bed > ./SeqAOnly_Grainger_r512s512.bed
1032.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r512s512.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r513s512.bed
1033.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r513s512.bed > ./SeqAOnly_Grainger_r513s513.bed
1034.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r513s513.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r514s513.bed
1035.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r514s513.bed > ./SeqAOnly_Grainger_r514s514.bed
1036.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r514s514.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r515s514.bed
1037.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r515s514.bed > ./SeqAOnly_Grainger_r515s515.bed
1038.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r515s515.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r516s515.bed
1039.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r516s515.bed > ./SeqAOnly_Grainger_r516s516.bed
1040.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r516s516.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r517s516.bed
1041.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r517s516.bed > ./SeqAOnly_Grainger_r517s517.bed
1042.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r517s517.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r518s517.bed
1043.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r518s517.bed > ./SeqAOnly_Grainger_r518s518.bed
1044.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r518s518.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r519s518.bed
1045.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r519s518.bed > ./SeqAOnly_Grainger_r519s519.bed
1046.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r519s519.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r520s519.bed
1047.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r520s519.bed > ./SeqAOnly_Grainger_r520s520.bed
1048.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r520s520.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r521s520.bed
1049.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r521s520.bed > ./SeqAOnly_Grainger_r521s521.bed
1050.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r521s521.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r522s521.bed
1051.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r522s521.bed > ./SeqAOnly_Grainger_r522s522.bed
1052.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r522s522.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r523s522.bed
1053.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r523s522.bed > ./SeqAOnly_Grainger_r523s523.bed
1054.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r523s523.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r524s523.bed
1055.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r524s523.bed > ./SeqAOnly_Grainger_r524s524.bed
1056.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r524s524.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r525s524.bed
1057.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r525s524.bed > ./SeqAOnly_Grainger_r525s525.bed
1058.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r525s525.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r526s525.bed

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1059.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r526s525.bed > ./SeqAOnly_Grainger_r526s526.bed
1060.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r526s526.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r527s526.bed
1061.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r527s526.bed > ./SeqAOnly_Grainger_r527s527.bed
1062.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r527s527.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r528s527.bed
1063.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r528s527.bed > ./SeqAOnly_Grainger_r528s528.bed
1064.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r528s528.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r529s528.bed
1065.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r529s528.bed > ./SeqAOnly_Grainger_r529s529.bed
1066.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r529s529.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r530s529.bed
1067.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r530s529.bed > ./SeqAOnly_Grainger_r530s530.bed
1068.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r530s530.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r531s530.bed
1069.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r531s530.bed > ./SeqAOnly_Grainger_r531s531.bed
1070.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r531s531.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r532s531.bed
1071.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r532s531.bed > ./SeqAOnly_Grainger_r532s532.bed
1072.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r532s532.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r533s532.bed
1073.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r533s532.bed > ./SeqAOnly_Grainger_r533s533.bed
1074.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r533s533.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r534s533.bed
1075.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r534s533.bed > ./SeqAOnly_Grainger_r534s534.bed
1076.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r534s534.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r535s534.bed
1077.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r535s534.bed > ./SeqAOnly_Grainger_r535s535.bed
1078.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r535s535.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r536s535.bed
1079.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r536s535.bed > ./SeqAOnly_Grainger_r536s536.bed
1080.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r536s536.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r537s536.bed
1081.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r537s536.bed > ./SeqAOnly_Grainger_r537s537.bed
1082.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r537s537.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r538s537.bed
1083.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r538s537.bed > ./SeqAOnly_Grainger_r538s538.bed
1084.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r538s538.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r539s538.bed
1085.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r539s538.bed > ./SeqAOnly_Grainger_r539s539.bed
1086.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r539s539.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r540s539.bed

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1087.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r540s539.bed > ./SeqAOnly_Grainger_r540s540.bed
1088.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r540s540.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r541s540.bed
1089.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r541s540.bed > ./SeqAOnly_Grainger_r541s541.bed
1090.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r541s541.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r542s541.bed
1091.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r542s541.bed > ./SeqAOnly_Grainger_r542s542.bed
1092.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r542s542.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r543s542.bed
1093.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r543s542.bed > ./SeqAOnly_Grainger_r543s543.bed
1094.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r543s543.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r544s543.bed
1095.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r544s543.bed > ./SeqAOnly_Grainger_r544s544.bed
1096.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r544s544.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r545s544.bed
1097.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r545s544.bed > ./SeqAOnly_Grainger_r545s545.bed
1098.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r545s545.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r546s545.bed
1099.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r546s545.bed > ./SeqAOnly_Grainger_r546s546.bed
1100.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r546s546.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r547s546.bed
1101.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r547s546.bed > ./SeqAOnly_Grainger_r547s547.bed
1102.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r547s547.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r548s547.bed
1103.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r548s547.bed > ./SeqAOnly_Grainger_r548s548.bed
1104.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r548s548.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r549s548.bed
1105.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r549s548.bed > ./SeqAOnly_Grainger_r549s549.bed
1106.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r549s549.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r550s549.bed
1107.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r550s549.bed > ./SeqAOnly_Grainger_r550s550.bed
1108.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r550s550.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r551s550.bed
1109.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r551s550.bed > ./SeqAOnly_Grainger_r551s551.bed
1110.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r551s551.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r552s551.bed
1111.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r552s551.bed > ./SeqAOnly_Grainger_r552s552.bed
1112.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r552s552.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r553s552.bed
1113.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r553s552.bed > ./SeqAOnly_Grainger_r553s553.bed
1114.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r553s553.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r554s553.bed

```



```

1115.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r554s553.bed > ./SeqAOnly_Grainger_r554s554.bed
1116.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r554s554.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r555s554.bed
1117.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r555s554.bed > ./SeqAOnly_Grainger_r555s555.bed
1118.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r555s555.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r556s555.bed
1119.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r556s555.bed > ./SeqAOnly_Grainger_r556s556.bed
1120.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r556s556.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r557s556.bed
1121.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r557s556.bed > ./SeqAOnly_Grainger_r557s557.bed
1122.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r557s557.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r558s557.bed
1123.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r558s557.bed > ./SeqAOnly_Grainger_r558s558.bed
1124.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r558s558.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r559s558.bed
1125.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r559s558.bed > ./SeqAOnly_Grainger_r559s559.bed
1126.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r559s559.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r560s559.bed
1127.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r560s559.bed > ./SeqAOnly_Grainger_r560s560.bed
1128.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r560s560.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r561s560.bed
1129.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r561s560.bed > ./SeqAOnly_Grainger_r561s561.bed
1130.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r561s561.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r562s561.bed
1131.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r562s561.bed > ./SeqAOnly_Grainger_r562s562.bed
1132.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r562s562.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r563s562.bed
1133.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r563s562.bed > ./SeqAOnly_Grainger_r563s563.bed
1134.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r563s563.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r564s563.bed
1135.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r564s563.bed > ./SeqAOnly_Grainger_r564s564.bed
1136.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r564s564.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r565s564.bed
1137.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r565s564.bed > ./SeqAOnly_Grainger_r565s565.bed
1138.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r565s565.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r566s565.bed
1139.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r566s565.bed > ./SeqAOnly_Grainger_r566s566.bed
1140.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r566s566.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r567s566.bed
1141.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r567s566.bed > ./SeqAOnly_Grainger_r567s567.bed
1142.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r567s567.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r568s567.bed

```

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1143.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r568s567.bed > ./SeqAOnly_Grainger_r568s568.bed
1144.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r568s568.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r569s568.bed
1145.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r569s568.bed > ./SeqAOnly_Grainger_r569s569.bed
1146.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r569s569.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r570s569.bed
1147.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r570s569.bed > ./SeqAOnly_Grainger_r570s570.bed
1148.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r570s570.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r571s570.bed
1149.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r571s570.bed > ./SeqAOnly_Grainger_r571s571.bed
1150.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r571s571.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r572s571.bed
1151.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r572s571.bed > ./SeqAOnly_Grainger_r572s572.bed
1152.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r572s572.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r573s572.bed
1153.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r573s572.bed > ./SeqAOnly_Grainger_r573s573.bed
1154.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r573s573.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r574s573.bed
1155.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r574s573.bed > ./SeqAOnly_Grainger_r574s574.bed
1156.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r574s574.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r575s574.bed
1157.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r575s574.bed > ./SeqAOnly_Grainger_r575s575.bed
1158.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r575s575.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r576s575.bed
1159.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r576s575.bed > ./SeqAOnly_Grainger_r576s576.bed
1160.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r576s576.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r577s576.bed
1161.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r577s576.bed > ./SeqAOnly_Grainger_r577s577.bed
1162.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r577s577.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r578s577.bed
1163.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r578s577.bed > ./SeqAOnly_Grainger_r578s578.bed
1164.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r578s578.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r579s578.bed
1165.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r579s578.bed > ./SeqAOnly_Grainger_r579s579.bed
1166.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r579s579.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r580s579.bed
1167.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r580s579.bed > ./SeqAOnly_Grainger_r580s580.bed
1168.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r580s580.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r581s580.bed
1169.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r581s580.bed > ./SeqAOnly_Grainger_r581s581.bed
1170.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r581s581.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r582s581.bed

```

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1171.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r582s581.bed > ./SeqAOnly_Grainger_r582s582.bed
1172.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r582s582.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r583s582.bed
1173.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r583s582.bed > ./SeqAOnly_Grainger_r583s583.bed
1174.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r583s583.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r584s583.bed
1175.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r584s583.bed > ./SeqAOnly_Grainger_r584s584.bed
1176.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r584s584.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r585s584.bed
1177.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r585s584.bed > ./SeqAOnly_Grainger_r585s585.bed
1178.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r585s585.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r586s585.bed
1179.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r586s585.bed > ./SeqAOnly_Grainger_r586s586.bed
1180.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r586s586.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r587s586.bed
1181.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r587s586.bed > ./SeqAOnly_Grainger_r587s587.bed
1182.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r587s587.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r588s587.bed
1183.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r588s587.bed > ./SeqAOnly_Grainger_r588s588.bed
1184.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r588s588.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r589s588.bed
1185.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r589s588.bed > ./SeqAOnly_Grainger_r589s589.bed
1186.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r589s589.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r590s589.bed
1187.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r590s589.bed > ./SeqAOnly_Grainger_r590s590.bed
1188.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r590s590.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r591s590.bed
1189.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r591s590.bed > ./SeqAOnly_Grainger_r591s591.bed
1190.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r591s591.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r592s591.bed
1191.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r592s591.bed > ./SeqAOnly_Grainger_r592s592.bed
1192.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r592s592.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r593s592.bed
1193.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r593s592.bed > ./SeqAOnly_Grainger_r593s593.bed
1194.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r593s593.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r594s593.bed
1195.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r594s593.bed > ./SeqAOnly_Grainger_r594s594.bed
1196.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r594s594.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r595s594.bed
1197.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r595s594.bed > ./SeqAOnly_Grainger_r595s595.bed
1198.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r595s595.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r596s595.bed

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1199.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r596s595.bed > ./SeqAOnly_Grainger_r596s596.bed
1200.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r596s596.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r597s596.bed
1201.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r597s596.bed > ./SeqAOnly_Grainger_r597s597.bed
1202.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r597s597.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r598s597.bed
1203.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r598s597.bed > ./SeqAOnly_Grainger_r598s598.bed
1204.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r598s598.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r599s598.bed
1205.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r599s598.bed > ./SeqAOnly_Grainger_r599s599.bed
1206.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r599s599.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r600s599.bed
1207.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r600s599.bed > ./SeqAOnly_Grainger_r600s600.bed
1208.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r600s600.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r601s600.bed
1209.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r601s600.bed > ./SeqAOnly_Grainger_r601s601.bed
1210.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r601s601.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r602s601.bed
1211.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r602s601.bed > ./SeqAOnly_Grainger_r602s602.bed
1212.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r602s602.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r603s602.bed
1213.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r603s602.bed > ./SeqAOnly_Grainger_r603s603.bed
1214.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r603s603.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r604s603.bed
1215.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r604s603.bed > ./SeqAOnly_Grainger_r604s604.bed
1216.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r604s604.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r605s604.bed
1217.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r605s604.bed > ./SeqAOnly_Grainger_r605s605.bed
1218.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r605s605.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r606s605.bed
1219.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r606s605.bed > ./SeqAOnly_Grainger_r606s606.bed
1220.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r606s606.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r607s606.bed
1221.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r607s606.bed > ./SeqAOnly_Grainger_r607s607.bed
1222.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r607s607.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r608s607.bed
1223.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r608s607.bed > ./SeqAOnly_Grainger_r608s608.bed
1224.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r608s608.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r609s608.bed
1225.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r609s608.bed > ./SeqAOnly_Grainger_r609s609.bed
1226.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r609s609.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r610s609.bed

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1227.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r610s609.bed > ./SeqAOnly_Grainger_r610s610.bed
1228.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r610s610.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r611s610.bed
1229.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r611s610.bed > ./SeqAOnly_Grainger_r611s611.bed
1230.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r611s611.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r612s611.bed
1231.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r612s611.bed > ./SeqAOnly_Grainger_r612s612.bed
1232.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r612s612.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r613s612.bed
1233.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r613s612.bed > ./SeqAOnly_Grainger_r613s613.bed
1234.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r613s613.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r614s613.bed
1235.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r614s613.bed > ./SeqAOnly_Grainger_r614s614.bed
1236.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r614s614.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r615s614.bed
1237.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r615s614.bed > ./SeqAOnly_Grainger_r615s615.bed
1238.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r615s615.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r616s615.bed
1239.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r616s615.bed > ./SeqAOnly_Grainger_r616s616.bed
1240.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r616s616.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r617s616.bed
1241.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r617s616.bed > ./SeqAOnly_Grainger_r617s617.bed
1242.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r617s617.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r618s617.bed
1243.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r618s617.bed > ./SeqAOnly_Grainger_r618s618.bed
1244.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r618s618.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r619s618.bed
1245.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r619s618.bed > ./SeqAOnly_Grainger_r619s619.bed
1246.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r619s619.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r620s619.bed
1247.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r620s619.bed > ./SeqAOnly_Grainger_r620s620.bed
1248.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r620s620.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r621s620.bed
1249.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r621s620.bed > ./SeqAOnly_Grainger_r621s621.bed
1250.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r621s621.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r622s621.bed
1251.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r622s621.bed > ./SeqAOnly_Grainger_r622s622.bed
1252.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r622s622.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r623s622.bed
1253.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r623s622.bed > ./SeqAOnly_Grainger_r623s623.bed
1254.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r623s623.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r624s623.bed

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1255.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r624s623.bed > ./SeqAOnly_Grainger_r624s624.bed
1256.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r624s624.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r625s624.bed
1257.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r625s624.bed > ./SeqAOnly_Grainger_r625s625.bed
1258.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r625s625.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r626s625.bed
1259.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r626s625.bed > ./SeqAOnly_Grainger_r626s626.bed
1260.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r626s626.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r627s626.bed
1261.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r627s626.bed > ./SeqAOnly_Grainger_r627s627.bed
1262.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r627s627.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r628s627.bed
1263.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r628s627.bed > ./SeqAOnly_Grainger_r628s628.bed
1264.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r628s628.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r629s628.bed
1265.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r629s628.bed > ./SeqAOnly_Grainger_r629s629.bed
1266.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r629s629.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r630s629.bed
1267.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r630s629.bed > ./SeqAOnly_Grainger_r630s630.bed
1268.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r630s630.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r631s630.bed
1269.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r631s630.bed > ./SeqAOnly_Grainger_r631s631.bed
1270.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r631s631.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r632s631.bed
1271.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r632s631.bed > ./SeqAOnly_Grainger_r632s632.bed
1272.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r632s632.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r633s632.bed
1273.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r633s632.bed > ./SeqAOnly_Grainger_r633s633.bed
1274.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r633s633.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r634s633.bed
1275.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r634s633.bed > ./SeqAOnly_Grainger_r634s634.bed
1276.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r634s634.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r635s634.bed
1277.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r635s634.bed > ./SeqAOnly_Grainger_r635s635.bed
1278.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r635s635.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r636s635.bed
1279.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r636s635.bed > ./SeqAOnly_Grainger_r636s636.bed
1280.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r636s636.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r637s636.bed
1281.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r637s636.bed > ./SeqAOnly_Grainger_r637s637.bed
1282.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r637s637.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r638s637.bed

```

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1283.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r638s637.bed > ./SeqAOnly_Grainger_r638s638.bed
1284.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r638s638.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r639s638.bed
1285.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r639s638.bed > ./SeqAOnly_Grainger_r639s639.bed
1286.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r639s639.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r640s639.bed
1287.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r640s639.bed > ./SeqAOnly_Grainger_r640s640.bed
1288.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r640s640.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r641s640.bed
1289.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r641s640.bed > ./SeqAOnly_Grainger_r641s641.bed
1290.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r641s641.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r642s641.bed
1291.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r642s641.bed > ./SeqAOnly_Grainger_r642s642.bed
1292.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r642s642.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r643s642.bed
1293.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r643s642.bed > ./SeqAOnly_Grainger_r643s643.bed
1294.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r643s643.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r644s643.bed
1295.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r644s643.bed > ./SeqAOnly_Grainger_r644s644.bed
1296.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r644s644.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r645s644.bed
1297.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r645s644.bed > ./SeqAOnly_Grainger_r645s645.bed
1298.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r645s645.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r646s645.bed
1299.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r646s645.bed > ./SeqAOnly_Grainger_r646s646.bed
1300.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r646s646.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r647s646.bed
1301.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r647s646.bed > ./SeqAOnly_Grainger_r647s647.bed
1302.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r647s647.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r648s647.bed
1303.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r648s647.bed > ./SeqAOnly_Grainger_r648s648.bed
1304.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r648s648.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r649s648.bed
1305.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r649s648.bed > ./SeqAOnly_Grainger_r649s649.bed
1306.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r649s649.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r650s649.bed
1307.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r650s649.bed > ./SeqAOnly_Grainger_r650s650.bed
1308.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r650s650.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r651s650.bed
1309.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r651s650.bed > ./SeqAOnly_Grainger_r651s651.bed
1310.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r651s651.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r652s651.bed

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1311.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r652s651.bed > ./SeqAOnly_Grainger_r652s652.bed
1312.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r652s652.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r653s652.bed
1313.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r653s652.bed > ./SeqAOnly_Grainger_r653s653.bed
1314.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r653s653.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r654s653.bed
1315.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r654s653.bed > ./SeqAOnly_Grainger_r654s654.bed
1316.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r654s654.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r655s654.bed
1317.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r655s654.bed > ./SeqAOnly_Grainger_r655s655.bed
1318.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r655s655.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r656s655.bed
1319.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r656s655.bed > ./SeqAOnly_Grainger_r656s656.bed
1320.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r656s656.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r657s656.bed
1321.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r657s656.bed > ./SeqAOnly_Grainger_r657s657.bed
1322.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r657s657.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r658s657.bed
1323.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r658s657.bed > ./SeqAOnly_Grainger_r658s658.bed
1324.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r658s658.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r659s658.bed
1325.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r659s658.bed > ./SeqAOnly_Grainger_r659s659.bed
1326.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r659s659.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r660s659.bed
1327.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r660s659.bed > ./SeqAOnly_Grainger_r660s660.bed
1328.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r660s660.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r661s660.bed
1329.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r661s660.bed > ./SeqAOnly_Grainger_r661s661.bed
1330.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r661s661.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r662s661.bed
1331.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r662s661.bed > ./SeqAOnly_Grainger_r662s662.bed
1332.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r662s662.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r663s662.bed
1333.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r663s662.bed > ./SeqAOnly_Grainger_r663s663.bed
1334.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r663s663.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r664s663.bed
1335.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r664s663.bed > ./SeqAOnly_Grainger_r664s664.bed
1336.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r664s664.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r665s664.bed
1337.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r665s664.bed > ./SeqAOnly_Grainger_r665s665.bed
1338.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r665s665.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r666s665.bed

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1339.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r666s665.bed > ./SeqAOnly_Grainger_r666s666.bed
1340.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r666s666.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r667s666.bed
1341.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r667s666.bed > ./SeqAOnly_Grainger_r667s667.bed
1342.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r667s667.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r668s667.bed
1343.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r668s667.bed > ./SeqAOnly_Grainger_r668s668.bed
1344.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r668s668.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r669s668.bed
1345.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r669s668.bed > ./SeqAOnly_Grainger_r669s669.bed
1346.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r669s669.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r670s669.bed
1347.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r670s669.bed > ./SeqAOnly_Grainger_r670s670.bed
1348.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r670s670.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r671s670.bed
1349.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r671s670.bed > ./SeqAOnly_Grainger_r671s671.bed
1350.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r671s671.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r672s671.bed
1351.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r672s671.bed > ./SeqAOnly_Grainger_r672s672.bed
1352.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r672s672.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r673s672.bed
1353.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r673s672.bed > ./SeqAOnly_Grainger_r673s673.bed
1354.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r673s673.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r674s673.bed
1355.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r674s673.bed > ./SeqAOnly_Grainger_r674s674.bed
1356.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r674s674.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r675s674.bed
1357.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r675s674.bed > ./SeqAOnly_Grainger_r675s675.bed
1358.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r675s675.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r676s675.bed
1359.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r676s675.bed > ./SeqAOnly_Grainger_r676s676.bed
1360.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r676s676.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r677s676.bed
1361.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r677s676.bed > ./SeqAOnly_Grainger_r677s677.bed
1362.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r677s677.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r678s677.bed
1363.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r678s677.bed > ./SeqAOnly_Grainger_r678s678.bed
1364.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r678s678.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r679s678.bed
1365.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r679s678.bed > ./SeqAOnly_Grainger_r679s679.bed
1366.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r679s679.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r680s679.bed

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1367.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r680s679.bed > ./SeqAOnly_Grainger_r680s680.bed
1368.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r680s680.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r681s680.bed
1369.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r681s680.bed > ./SeqAOnly_Grainger_r681s681.bed
1370.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r681s681.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r682s681.bed
1371.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r682s681.bed > ./SeqAOnly_Grainger_r682s682.bed
1372.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r682s682.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r683s682.bed
1373.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r683s682.bed > ./SeqAOnly_Grainger_r683s683.bed
1374.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r683s683.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r684s683.bed
1375.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r684s683.bed > ./SeqAOnly_Grainger_r684s684.bed
1376.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r684s684.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r685s684.bed
1377.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r685s684.bed > ./SeqAOnly_Grainger_r685s685.bed
1378.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r685s685.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r686s685.bed
1379.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r686s685.bed > ./SeqAOnly_Grainger_r686s686.bed
1380.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r686s686.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r687s686.bed
1381.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r687s686.bed > ./SeqAOnly_Grainger_r687s687.bed
1382.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r687s687.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r688s687.bed
1383.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r688s687.bed > ./SeqAOnly_Grainger_r688s688.bed
1384.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r688s688.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r689s688.bed
1385.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r689s688.bed > ./SeqAOnly_Grainger_r689s689.bed
1386.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r689s689.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r690s689.bed
1387.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r690s689.bed > ./SeqAOnly_Grainger_r690s690.bed
1388.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r690s690.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r691s690.bed
1389.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r691s690.bed > ./SeqAOnly_Grainger_r691s691.bed
1390.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r691s691.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r692s691.bed
1391.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r692s691.bed > ./SeqAOnly_Grainger_r692s692.bed
1392.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r692s692.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r693s692.bed
1393.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r693s692.bed > ./SeqAOnly_Grainger_r693s693.bed
1394.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r693s693.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r694s693.bed

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1395.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r694s693.bed > ./SeqAOnly_Grainger_r694s694.bed
1396.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r694s694.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r695s694.bed
1397.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r695s694.bed > ./SeqAOnly_Grainger_r695s695.bed
1398.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r695s695.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r696s695.bed
1399.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r696s695.bed > ./SeqAOnly_Grainger_r696s696.bed
1400.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r696s696.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r697s696.bed
1401.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r697s696.bed > ./SeqAOnly_Grainger_r697s697.bed
1402.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r697s697.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r698s697.bed
1403.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r698s697.bed > ./SeqAOnly_Grainger_r698s698.bed
1404.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r698s698.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r699s698.bed
1405.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r699s698.bed > ./SeqAOnly_Grainger_r699s699.bed
1406.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r699s699.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r700s699.bed
1407.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r700s699.bed > ./SeqAOnly_Grainger_r700s700.bed
1408.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r700s700.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r701s700.bed
1409.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r701s700.bed > ./SeqAOnly_Grainger_r701s701.bed
1410.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r701s701.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r702s701.bed
1411.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r702s701.bed > ./SeqAOnly_Grainger_r702s702.bed
1412.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r702s702.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r703s702.bed
1413.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r703s702.bed > ./SeqAOnly_Grainger_r703s703.bed
1414.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r703s703.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r704s703.bed
1415.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r704s703.bed > ./SeqAOnly_Grainger_r704s704.bed
1416.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r704s704.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r705s704.bed
1417.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r705s704.bed > ./SeqAOnly_Grainger_r705s705.bed
1418.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r705s705.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r706s705.bed
1419.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r706s705.bed > ./SeqAOnly_Grainger_r706s706.bed
1420.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r706s706.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r707s706.bed
1421.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r707s706.bed > ./SeqAOnly_Grainger_r707s707.bed
1422.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r707s707.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r708s707.bed

```

1423. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r708s707.bed > ./SeqAOnly_Grainger_r708s708.bed
1424. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r708s708.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r709s708.bed
1425. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r709s708.bed > ./SeqAOnly_Grainger_r709s709.bed
1426. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r709s709.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r710s709.bed
1427. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r710s709.bed > ./SeqAOnly_Grainger_r710s710.bed
1428. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r710s710.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r711s710.bed
1429. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r711s710.bed > ./SeqAOnly_Grainger_r711s711.bed
1430. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r711s711.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r712s711.bed
1431. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r712s711.bed > ./SeqAOnly_Grainger_r712s712.bed
1432. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r712s712.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r713s712.bed
1433. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r713s712.bed > ./SeqAOnly_Grainger_r713s713.bed
1434. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r713s713.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r714s713.bed
1435. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r714s713.bed > ./SeqAOnly_Grainger_r714s714.bed
1436. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r714s714.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r715s714.bed
1437. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r715s714.bed > ./SeqAOnly_Grainger_r715s715.bed
1438. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r715s715.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r716s715.bed
1439. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r716s715.bed > ./SeqAOnly_Grainger_r716s716.bed
1440. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r716s716.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r717s716.bed
1441. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r717s716.bed > ./SeqAOnly_Grainger_r717s717.bed
1442. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r717s717.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r718s717.bed
1443. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r718s717.bed > ./SeqAOnly_Grainger_r718s718.bed
1444. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r718s718.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r719s718.bed
1445. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r719s718.bed > ./SeqAOnly_Grainger_r719s719.bed
1446. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r719s719.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r720s719.bed
1447. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r720s719.bed > ./SeqAOnly_Grainger_r720s720.bed
1448. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r720s720.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r721s720.bed
1449. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r721s720.bed > ./SeqAOnly_Grainger_r721s721.bed
1450. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r721s721.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r722s721.bed

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1451.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r722s721.bed > ./SeqAOnly_Grainger_r722s722.bed
1452.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r722s722.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r723s722.bed
1453.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r723s722.bed > ./SeqAOnly_Grainger_r723s723.bed
1454.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r723s723.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r724s723.bed
1455.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r724s723.bed > ./SeqAOnly_Grainger_r724s724.bed
1456.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r724s724.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r725s724.bed
1457.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r725s724.bed > ./SeqAOnly_Grainger_r725s725.bed
1458.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r725s725.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r726s725.bed
1459.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r726s725.bed > ./SeqAOnly_Grainger_r726s726.bed
1460.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r726s726.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r727s726.bed
1461.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r727s726.bed > ./SeqAOnly_Grainger_r727s727.bed
1462.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r727s727.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r728s727.bed
1463.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r728s727.bed > ./SeqAOnly_Grainger_r728s728.bed
1464.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r728s728.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r729s728.bed
1465.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r729s728.bed > ./SeqAOnly_Grainger_r729s729.bed
1466.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r729s729.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r730s729.bed
1467.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r730s729.bed > ./SeqAOnly_Grainger_r730s730.bed
1468.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r730s730.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r731s730.bed
1469.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r731s730.bed > ./SeqAOnly_Grainger_r731s731.bed
1470.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r731s731.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r732s731.bed
1471.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r732s731.bed > ./SeqAOnly_Grainger_r732s732.bed
1472.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r732s732.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r733s732.bed
1473.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r733s732.bed > ./SeqAOnly_Grainger_r733s733.bed
1474.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r733s733.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r734s733.bed
1475.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r734s733.bed > ./SeqAOnly_Grainger_r734s734.bed
1476.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r734s734.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r735s734.bed
1477.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r735s734.bed > ./SeqAOnly_Grainger_r735s735.bed
1478.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r735s735.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r736s735.bed

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1479.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r736s735.bed > ./SeqAOnly_Grainger_r736s736.bed
1480.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r736s736.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r737s736.bed
1481.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r737s736.bed > ./SeqAOnly_Grainger_r737s737.bed
1482.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r737s737.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r738s737.bed
1483.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r738s737.bed > ./SeqAOnly_Grainger_r738s738.bed
1484.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r738s738.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r739s738.bed
1485.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r739s738.bed > ./SeqAOnly_Grainger_r739s739.bed
1486.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r739s739.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r740s739.bed
1487.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r740s739.bed > ./SeqAOnly_Grainger_r740s740.bed
1488.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r740s740.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r741s740.bed
1489.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r741s740.bed > ./SeqAOnly_Grainger_r741s741.bed
1490.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r741s741.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r742s741.bed
1491.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r742s741.bed > ./SeqAOnly_Grainger_r742s742.bed
1492.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r742s742.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r743s742.bed
1493.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r743s742.bed > ./SeqAOnly_Grainger_r743s743.bed
1494.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r743s743.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r744s743.bed
1495.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r744s743.bed > ./SeqAOnly_Grainger_r744s744.bed
1496.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r744s744.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r745s744.bed
1497.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r745s744.bed > ./SeqAOnly_Grainger_r745s745.bed
1498.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r745s745.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r746s745.bed
1499.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r746s745.bed > ./SeqAOnly_Grainger_r746s746.bed
1500.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r746s746.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r747s746.bed
1501.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r747s746.bed > ./SeqAOnly_Grainger_r747s747.bed
1502.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r747s747.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r748s747.bed
1503.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r748s747.bed > ./SeqAOnly_Grainger_r748s748.bed
1504.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r748s748.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r749s748.bed
1505.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r749s748.bed > ./SeqAOnly_Grainger_r749s749.bed
1506.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r749s749.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r750s749.bed

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1507.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r750s749.bed > ./SeqAOnly_Grainger_r750s750.bed
1508.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r750s750.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r751s750.bed
1509.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r751s750.bed > ./SeqAOnly_Grainger_r751s751.bed
1510.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r751s751.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r752s751.bed
1511.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r752s751.bed > ./SeqAOnly_Grainger_r752s752.bed
1512.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r752s752.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r753s752.bed
1513.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r753s752.bed > ./SeqAOnly_Grainger_r753s753.bed
1514.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r753s753.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r754s753.bed
1515.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r754s753.bed > ./SeqAOnly_Grainger_r754s754.bed
1516.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r754s754.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r755s754.bed
1517.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r755s754.bed > ./SeqAOnly_Grainger_r755s755.bed
1518.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r755s755.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r756s755.bed
1519.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r756s755.bed > ./SeqAOnly_Grainger_r756s756.bed
1520.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r756s756.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r757s756.bed
1521.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r757s756.bed > ./SeqAOnly_Grainger_r757s757.bed
1522.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r757s757.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r758s757.bed
1523.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r758s757.bed > ./SeqAOnly_Grainger_r758s758.bed
1524.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r758s758.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r759s758.bed
1525.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r759s758.bed > ./SeqAOnly_Grainger_r759s759.bed
1526.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r759s759.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r760s759.bed
1527.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r760s759.bed > ./SeqAOnly_Grainger_r760s760.bed
1528.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r760s760.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r761s760.bed
1529.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r761s760.bed > ./SeqAOnly_Grainger_r761s761.bed
1530.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r761s761.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r762s761.bed
1531.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r762s761.bed > ./SeqAOnly_Grainger_r762s762.bed
1532.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r762s762.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r763s762.bed
1533.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r763s762.bed > ./SeqAOnly_Grainger_r763s763.bed
1534.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r763s763.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r764s763.bed

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1535. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r764s763.bed > ./SeqAOnly_Grainger_r764s764.bed
1536. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r764s764.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r765s764.bed
1537. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r765s764.bed > ./SeqAOnly_Grainger_r765s765.bed
1538. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r765s765.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r766s765.bed
1539. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r766s765.bed > ./SeqAOnly_Grainger_r766s766.bed
1540. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r766s766.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r767s766.bed
1541. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r767s766.bed > ./SeqAOnly_Grainger_r767s767.bed
1542. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r767s767.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r768s767.bed
1543. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r768s767.bed > ./SeqAOnly_Grainger_r768s768.bed
1544. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r768s768.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r769s768.bed
1545. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r769s768.bed > ./SeqAOnly_Grainger_r769s769.bed
1546. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r769s769.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r770s769.bed
1547. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r770s769.bed > ./SeqAOnly_Grainger_r770s770.bed
1548. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r770s770.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r771s770.bed
1549. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r771s770.bed > ./SeqAOnly_Grainger_r771s771.bed
1550. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r771s771.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r772s771.bed
1551. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r772s771.bed > ./SeqAOnly_Grainger_r772s772.bed
1552. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r772s772.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r773s772.bed
1553. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r773s772.bed > ./SeqAOnly_Grainger_r773s773.bed
1554. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r773s773.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r774s773.bed
1555. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r774s773.bed > ./SeqAOnly_Grainger_r774s774.bed
1556. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r774s774.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r775s774.bed
1557. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r775s774.bed > ./SeqAOnly_Grainger_r775s775.bed
1558. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r775s775.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r776s775.bed
1559. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r776s775.bed > ./SeqAOnly_Grainger_r776s776.bed
1560. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r776s776.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r777s776.bed
1561. sort -k1,1 -
k2,2n ./SeqAOnly_Grainger_r777s776.bed > ./SeqAOnly_Grainger_r777s777.bed
1562. bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r777s777.bed -g Ecoli-
genomesize.txt > ./SeqAOnly_Grainger_r778s777.bed


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1563.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r778s777.bed > ./SeqAOnly_Grainger_r778s778.bed
1564.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r778s778.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r779s778.bed
1565.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r779s778.bed > ./SeqAOnly_Grainger_r779s779.bed
1566.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r779s779.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r780s779.bed
1567.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r780s779.bed > ./SeqAOnly_Grainger_r780s780.bed
1568.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r780s780.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r781s780.bed
1569.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r781s780.bed > ./SeqAOnly_Grainger_r781s781.bed
1570.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r781s781.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r782s781.bed
1571.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r782s781.bed > ./SeqAOnly_Grainger_r782s782.bed
1572.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r782s782.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r783s782.bed
1573.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r783s782.bed > ./SeqAOnly_Grainger_r783s783.bed
1574.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r783s783.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r784s783.bed
1575.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r784s783.bed > ./SeqAOnly_Grainger_r784s784.bed
1576.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r784s784.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r785s784.bed
1577.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r785s784.bed > ./SeqAOnly_Grainger_r785s785.bed
1578.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r785s785.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r786s785.bed
1579.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r786s785.bed > ./SeqAOnly_Grainger_r786s786.bed
1580.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r786s786.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r787s786.bed
1581.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r787s786.bed > ./SeqAOnly_Grainger_r787s787.bed
1582.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r787s787.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r788s787.bed
1583.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r788s787.bed > ./SeqAOnly_Grainger_r788s788.bed
1584.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r788s788.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r789s788.bed
1585.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r789s788.bed > ./SeqAOnly_Grainger_r789s789.bed
1586.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r789s789.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r790s789.bed
1587.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r790s789.bed > ./SeqAOnly_Grainger_r790s790.bed
1588.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r790s790.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r791s790.bed
1589.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r791s790.bed > ./SeqAOnly_Grainger_r791s791.bed
1590.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r791s791.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r792s791.bed

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1591.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r792s791.bed > ./SeqAOnly_Grainger_r792s792.bed
1592.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r792s792.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r793s792.bed
1593.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r793s792.bed > ./SeqAOnly_Grainger_r793s793.bed
1594.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r793s793.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r794s793.bed
1595.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r794s793.bed > ./SeqAOnly_Grainger_r794s794.bed
1596.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r794s794.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r795s794.bed
1597.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r795s794.bed > ./SeqAOnly_Grainger_r795s795.bed
1598.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r795s795.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r796s795.bed
1599.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r796s795.bed > ./SeqAOnly_Grainger_r796s796.bed
1600.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r796s796.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r797s796.bed
1601.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r797s796.bed > ./SeqAOnly_Grainger_r797s797.bed
1602.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r797s797.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r798s797.bed
1603.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r798s797.bed > ./SeqAOnly_Grainger_r798s798.bed
1604.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r798s798.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r799s798.bed
1605.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r799s798.bed > ./SeqAOnly_Grainger_r799s799.bed
1606.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r799s799.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r800s799.bed
1607.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r800s799.bed > ./SeqAOnly_Grainger_r800s800.bed
1608.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r800s800.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r801s800.bed
1609.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r801s800.bed > ./SeqAOnly_Grainger_r801s801.bed
1610.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r801s801.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r802s801.bed
1611.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r802s801.bed > ./SeqAOnly_Grainger_r802s802.bed
1612.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r802s802.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r803s802.bed
1613.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r803s802.bed > ./SeqAOnly_Grainger_r803s803.bed
1614.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r803s803.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r804s803.bed
1615.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r804s803.bed > ./SeqAOnly_Grainger_r804s804.bed
1616.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r804s804.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r805s804.bed
1617.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r805s804.bed > ./SeqAOnly_Grainger_r805s805.bed
1618.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r805s805.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r806s805.bed

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1619.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r806s805.bed > ./SeqAOnly_Grainger_r806s806.bed
1620.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r806s806.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r807s806.bed
1621.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r807s806.bed > ./SeqAOnly_Grainger_r807s807.bed
1622.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r807s807.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r808s807.bed
1623.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r808s807.bed > ./SeqAOnly_Grainger_r808s808.bed
1624.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r808s808.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r809s808.bed
1625.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r809s808.bed > ./SeqAOnly_Grainger_r809s809.bed
1626.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r809s809.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r810s809.bed
1627.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r810s809.bed > ./SeqAOnly_Grainger_r810s810.bed
1628.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r810s810.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r811s810.bed
1629.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r811s810.bed > ./SeqAOnly_Grainger_r811s811.bed
1630.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r811s811.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r812s811.bed
1631.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r812s811.bed > ./SeqAOnly_Grainger_r812s812.bed
1632.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r812s812.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r813s812.bed
1633.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r813s812.bed > ./SeqAOnly_Grainger_r813s813.bed
1634.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r813s813.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r814s813.bed
1635.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r814s813.bed > ./SeqAOnly_Grainger_r814s814.bed
1636.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r814s814.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r815s814.bed
1637.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r815s814.bed > ./SeqAOnly_Grainger_r815s815.bed
1638.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r815s815.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r816s815.bed
1639.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r816s815.bed > ./SeqAOnly_Grainger_r816s816.bed
1640.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r816s816.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r817s816.bed
1641.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r817s816.bed > ./SeqAOnly_Grainger_r817s817.bed
1642.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r817s817.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r818s817.bed
1643.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r818s817.bed > ./SeqAOnly_Grainger_r818s818.bed
1644.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r818s818.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r819s818.bed
1645.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r819s818.bed > ./SeqAOnly_Grainger_r819s819.bed
1646.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r819s819.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r820s819.bed

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1647.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r820s819.bed > ./SeqAOnly_Grainger_r820s820.bed
1648.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r820s820.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r821s820.bed
1649.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r821s820.bed > ./SeqAOnly_Grainger_r821s821.bed
1650.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r821s821.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r822s821.bed
1651.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r822s821.bed > ./SeqAOnly_Grainger_r822s822.bed
1652.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r822s822.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r823s822.bed
1653.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r823s822.bed > ./SeqAOnly_Grainger_r823s823.bed
1654.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r823s823.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r824s823.bed
1655.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r824s823.bed > ./SeqAOnly_Grainger_r824s824.bed
1656.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r824s824.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r825s824.bed
1657.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r825s824.bed > ./SeqAOnly_Grainger_r825s825.bed
1658.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r825s825.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r826s825.bed
1659.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r826s825.bed > ./SeqAOnly_Grainger_r826s826.bed
1660.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r826s826.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r827s826.bed
1661.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r827s826.bed > ./SeqAOnly_Grainger_r827s827.bed
1662.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r827s827.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r828s827.bed
1663.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r828s827.bed > ./SeqAOnly_Grainger_r828s828.bed
1664.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r828s828.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r829s828.bed
1665.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r829s828.bed > ./SeqAOnly_Grainger_r829s829.bed
1666.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r829s829.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r830s829.bed
1667.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r830s829.bed > ./SeqAOnly_Grainger_r830s830.bed
1668.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r830s830.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r831s830.bed
1669.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r831s830.bed > ./SeqAOnly_Grainger_r831s831.bed
1670.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r831s831.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r832s831.bed
1671.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r832s831.bed > ./SeqAOnly_Grainger_r832s832.bed
1672.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r832s832.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r833s832.bed
1673.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r833s832.bed > ./SeqAOnly_Grainger_r833s833.bed
1674.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r833s833.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r834s833.bed

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1675.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r834s833.bed > ./SeqAOnly_Grainger_r834s834.bed
1676.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r834s834.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r835s834.bed
1677.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r835s834.bed > ./SeqAOnly_Grainger_r835s835.bed
1678.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r835s835.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r836s835.bed
1679.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r836s835.bed > ./SeqAOnly_Grainger_r836s836.bed
1680.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r836s836.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r837s836.bed
1681.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r837s836.bed > ./SeqAOnly_Grainger_r837s837.bed
1682.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r837s837.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r838s837.bed
1683.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r838s837.bed > ./SeqAOnly_Grainger_r838s838.bed
1684.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r838s838.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r839s838.bed
1685.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r839s838.bed > ./SeqAOnly_Grainger_r839s839.bed
1686.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r839s839.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r840s839.bed
1687.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r840s839.bed > ./SeqAOnly_Grainger_r840s840.bed
1688.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r840s840.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r841s840.bed
1689.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r841s840.bed > ./SeqAOnly_Grainger_r841s841.bed
1690.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r841s841.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r842s841.bed
1691.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r842s841.bed > ./SeqAOnly_Grainger_r842s842.bed
1692.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r842s842.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r843s842.bed
1693.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r843s842.bed > ./SeqAOnly_Grainger_r843s843.bed
1694.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r843s843.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r844s843.bed
1695.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r844s843.bed > ./SeqAOnly_Grainger_r844s844.bed
1696.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r844s844.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r845s844.bed
1697.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r845s844.bed > ./SeqAOnly_Grainger_r845s845.bed
1698.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r845s845.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r846s845.bed
1699.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r846s845.bed > ./SeqAOnly_Grainger_r846s846.bed
1700.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r846s846.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r847s846.bed
1701.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r847s846.bed > ./SeqAOnly_Grainger_r847s847.bed
1702.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r847s847.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r848s847.bed

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1703.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r848s847.bed > ./SeqAOnly_Grainger_r848s848.bed
1704.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r848s848.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r849s848.bed
1705.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r849s848.bed > ./SeqAOnly_Grainger_r849s849.bed
1706.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r849s849.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r850s849.bed
1707.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r850s849.bed > ./SeqAOnly_Grainger_r850s850.bed
1708.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r850s850.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r851s850.bed
1709.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r851s850.bed > ./SeqAOnly_Grainger_r851s851.bed
1710.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r851s851.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r852s851.bed
1711.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r852s851.bed > ./SeqAOnly_Grainger_r852s852.bed
1712.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r852s852.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r853s852.bed
1713.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r853s852.bed > ./SeqAOnly_Grainger_r853s853.bed
1714.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r853s853.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r854s853.bed
1715.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r854s853.bed > ./SeqAOnly_Grainger_r854s854.bed
1716.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r854s854.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r855s854.bed
1717.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r855s854.bed > ./SeqAOnly_Grainger_r855s855.bed
1718.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r855s855.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r856s855.bed
1719.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r856s855.bed > ./SeqAOnly_Grainger_r856s856.bed
1720.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r856s856.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r857s856.bed
1721.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r857s856.bed > ./SeqAOnly_Grainger_r857s857.bed
1722.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r857s857.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r858s857.bed
1723.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r858s857.bed > ./SeqAOnly_Grainger_r858s858.bed
1724.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r858s858.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r859s858.bed
1725.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r859s858.bed > ./SeqAOnly_Grainger_r859s859.bed
1726.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r859s859.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r860s859.bed
1727.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r860s859.bed > ./SeqAOnly_Grainger_r860s860.bed
1728.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r860s860.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r861s860.bed
1729.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r861s860.bed > ./SeqAOnly_Grainger_r861s861.bed
1730.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r861s861.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r862s861.bed

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1731.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r862s861.bed > ./SeqAOnly_Grainger_r862s862.bed
1732.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r862s862.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r863s862.bed
1733.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r863s862.bed > ./SeqAOnly_Grainger_r863s863.bed
1734.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r863s863.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r864s863.bed
1735.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r864s863.bed > ./SeqAOnly_Grainger_r864s864.bed
1736.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r864s864.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r865s864.bed
1737.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r865s864.bed > ./SeqAOnly_Grainger_r865s865.bed
1738.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r865s865.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r866s865.bed
1739.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r866s865.bed > ./SeqAOnly_Grainger_r866s866.bed
1740.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r866s866.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r867s866.bed
1741.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r867s866.bed > ./SeqAOnly_Grainger_r867s867.bed
1742.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r867s867.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r868s867.bed
1743.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r868s867.bed > ./SeqAOnly_Grainger_r868s868.bed
1744.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r868s868.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r869s868.bed
1745.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r869s868.bed > ./SeqAOnly_Grainger_r869s869.bed
1746.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r869s869.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r870s869.bed
1747.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r870s869.bed > ./SeqAOnly_Grainger_r870s870.bed
1748.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r870s870.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r871s870.bed
1749.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r871s870.bed > ./SeqAOnly_Grainger_r871s871.bed
1750.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r871s871.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r872s871.bed
1751.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r872s871.bed > ./SeqAOnly_Grainger_r872s872.bed
1752.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r872s872.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r873s872.bed
1753.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r873s872.bed > ./SeqAOnly_Grainger_r873s873.bed
1754.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r873s873.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r874s873.bed
1755.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r874s873.bed > ./SeqAOnly_Grainger_r874s874.bed
1756.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r874s874.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r875s874.bed
1757.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r875s874.bed > ./SeqAOnly_Grainger_r875s875.bed
1758.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r875s875.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r876s875.bed

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1759.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r876s875.bed > ./SeqAOnly_Grainger_r876s876.bed
1760.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r876s876.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r877s876.bed
1761.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r877s876.bed > ./SeqAOnly_Grainger_r877s877.bed
1762.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r877s877.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r878s877.bed
1763.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r878s877.bed > ./SeqAOnly_Grainger_r878s878.bed
1764.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r878s878.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r879s878.bed
1765.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r879s878.bed > ./SeqAOnly_Grainger_r879s879.bed
1766.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r879s879.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r880s879.bed
1767.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r880s879.bed > ./SeqAOnly_Grainger_r880s880.bed
1768.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r880s880.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r881s880.bed
1769.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r881s880.bed > ./SeqAOnly_Grainger_r881s881.bed
1770.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r881s881.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r882s881.bed
1771.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r882s881.bed > ./SeqAOnly_Grainger_r882s882.bed
1772.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r882s882.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r883s882.bed
1773.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r883s882.bed > ./SeqAOnly_Grainger_r883s883.bed
1774.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r883s883.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r884s883.bed
1775.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r884s883.bed > ./SeqAOnly_Grainger_r884s884.bed
1776.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r884s884.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r885s884.bed
1777.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r885s884.bed > ./SeqAOnly_Grainger_r885s885.bed
1778.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r885s885.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r886s885.bed
1779.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r886s885.bed > ./SeqAOnly_Grainger_r886s886.bed
1780.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r886s886.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r887s886.bed
1781.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r887s886.bed > ./SeqAOnly_Grainger_r887s887.bed
1782.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r887s887.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r888s887.bed
1783.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r888s887.bed > ./SeqAOnly_Grainger_r888s888.bed
1784.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r888s888.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r889s888.bed
1785.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r889s888.bed > ./SeqAOnly_Grainger_r889s889.bed
1786.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r889s889.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r890s889.bed

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1787.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r890s889.bed > ./SeqAOnly_Grainger_r890s890.bed
1788.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r890s890.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r891s890.bed
1789.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r891s890.bed > ./SeqAOnly_Grainger_r891s891.bed
1790.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r891s891.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r892s891.bed
1791.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r892s891.bed > ./SeqAOnly_Grainger_r892s892.bed
1792.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r892s892.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r893s892.bed
1793.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r893s892.bed > ./SeqAOnly_Grainger_r893s893.bed
1794.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r893s893.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r894s893.bed
1795.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r894s893.bed > ./SeqAOnly_Grainger_r894s894.bed
1796.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r894s894.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r895s894.bed
1797.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r895s894.bed > ./SeqAOnly_Grainger_r895s895.bed
1798.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r895s895.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r896s895.bed
1799.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r896s895.bed > ./SeqAOnly_Grainger_r896s896.bed
1800.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r896s896.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r897s896.bed
1801.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r897s896.bed > ./SeqAOnly_Grainger_r897s897.bed
1802.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r897s897.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r898s897.bed
1803.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r898s897.bed > ./SeqAOnly_Grainger_r898s898.bed
1804.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r898s898.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r899s898.bed
1805.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r899s898.bed > ./SeqAOnly_Grainger_r899s899.bed
1806.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r899s899.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r900s899.bed
1807.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r900s899.bed > ./SeqAOnly_Grainger_r900s900.bed
1808.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r900s900.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r901s900.bed
1809.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r901s900.bed > ./SeqAOnly_Grainger_r901s901.bed
1810.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r901s901.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r902s901.bed
1811.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r902s901.bed > ./SeqAOnly_Grainger_r902s902.bed
1812.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r902s902.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r903s902.bed
1813.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r903s902.bed > ./SeqAOnly_Grainger_r903s903.bed
1814.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r903s903.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r904s903.bed

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1815.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r904s903.bed > ./SeqAOnly_Grainger_r904s904.bed
1816.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r904s904.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r905s904.bed
1817.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r905s904.bed > ./SeqAOnly_Grainger_r905s905.bed
1818.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r905s905.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r906s905.bed
1819.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r906s905.bed > ./SeqAOnly_Grainger_r906s906.bed
1820.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r906s906.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r907s906.bed
1821.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r907s906.bed > ./SeqAOnly_Grainger_r907s907.bed
1822.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r907s907.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r908s907.bed
1823.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r908s907.bed > ./SeqAOnly_Grainger_r908s908.bed
1824.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r908s908.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r909s908.bed
1825.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r909s908.bed > ./SeqAOnly_Grainger_r909s909.bed
1826.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r909s909.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r910s909.bed
1827.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r910s909.bed > ./SeqAOnly_Grainger_r910s910.bed
1828.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r910s910.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r911s910.bed
1829.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r911s910.bed > ./SeqAOnly_Grainger_r911s911.bed
1830.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r911s911.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r912s911.bed
1831.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r912s911.bed > ./SeqAOnly_Grainger_r912s912.bed
1832.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r912s912.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r913s912.bed
1833.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r913s912.bed > ./SeqAOnly_Grainger_r913s913.bed
1834.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r913s913.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r914s913.bed
1835.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r914s913.bed > ./SeqAOnly_Grainger_r914s914.bed
1836.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r914s914.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r915s914.bed
1837.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r915s914.bed > ./SeqAOnly_Grainger_r915s915.bed
1838.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r915s915.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r916s915.bed
1839.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r916s915.bed > ./SeqAOnly_Grainger_r916s916.bed
1840.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r916s916.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r917s916.bed
1841.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r917s916.bed > ./SeqAOnly_Grainger_r917s917.bed
1842.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r917s917.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r918s917.bed

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1843.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r918s917.bed > ./SeqAOnly_Grainger_r918s918.bed
1844.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r918s918.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r919s918.bed
1845.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r919s918.bed > ./SeqAOnly_Grainger_r919s919.bed
1846.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r919s919.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r920s919.bed
1847.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r920s919.bed > ./SeqAOnly_Grainger_r920s920.bed
1848.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r920s920.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r921s920.bed
1849.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r921s920.bed > ./SeqAOnly_Grainger_r921s921.bed
1850.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r921s921.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r922s921.bed
1851.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r922s921.bed > ./SeqAOnly_Grainger_r922s922.bed
1852.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r922s922.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r923s922.bed
1853.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r923s922.bed > ./SeqAOnly_Grainger_r923s923.bed
1854.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r923s923.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r924s923.bed
1855.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r924s923.bed > ./SeqAOnly_Grainger_r924s924.bed
1856.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r924s924.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r925s924.bed
1857.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r925s924.bed > ./SeqAOnly_Grainger_r925s925.bed
1858.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r925s925.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r926s925.bed
1859.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r926s925.bed > ./SeqAOnly_Grainger_r926s926.bed
1860.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r926s926.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r927s926.bed
1861.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r927s926.bed > ./SeqAOnly_Grainger_r927s927.bed
1862.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r927s927.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r928s927.bed
1863.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r928s927.bed > ./SeqAOnly_Grainger_r928s928.bed
1864.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r928s928.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r929s928.bed
1865.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r929s928.bed > ./SeqAOnly_Grainger_r929s929.bed
1866.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r929s929.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r930s929.bed
1867.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r930s929.bed > ./SeqAOnly_Grainger_r930s930.bed
1868.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r930s930.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r931s930.bed
1869.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r931s930.bed > ./SeqAOnly_Grainger_r931s931.bed
1870.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r931s931.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r932s931.bed

```

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1871.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r932s931.bed > ./SeqAOnly_Grainger_r932s932.bed
1872.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r932s932.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r933s932.bed
1873.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r933s932.bed > ./SeqAOnly_Grainger_r933s933.bed
1874.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r933s933.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r934s933.bed
1875.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r934s933.bed > ./SeqAOnly_Grainger_r934s934.bed
1876.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r934s934.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r935s934.bed
1877.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r935s934.bed > ./SeqAOnly_Grainger_r935s935.bed
1878.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r935s935.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r936s935.bed
1879.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r936s935.bed > ./SeqAOnly_Grainger_r936s936.bed
1880.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r936s936.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r937s936.bed
1881.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r937s936.bed > ./SeqAOnly_Grainger_r937s937.bed
1882.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r937s937.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r938s937.bed
1883.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r938s937.bed > ./SeqAOnly_Grainger_r938s938.bed
1884.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r938s938.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r939s938.bed
1885.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r939s938.bed > ./SeqAOnly_Grainger_r939s939.bed
1886.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r939s939.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r940s939.bed
1887.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r940s939.bed > ./SeqAOnly_Grainger_r940s940.bed
1888.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r940s940.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r941s940.bed
1889.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r941s940.bed > ./SeqAOnly_Grainger_r941s941.bed
1890.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r941s941.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r942s941.bed
1891.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r942s941.bed > ./SeqAOnly_Grainger_r942s942.bed
1892.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r942s942.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r943s942.bed
1893.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r943s942.bed > ./SeqAOnly_Grainger_r943s943.bed
1894.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r943s943.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r944s943.bed
1895.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r944s943.bed > ./SeqAOnly_Grainger_r944s944.bed
1896.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r944s944.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r945s944.bed
1897.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r945s944.bed > ./SeqAOnly_Grainger_r945s945.bed
1898.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r945s945.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r946s945.bed

```

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1899.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r946s945.bed > ./SeqAOnly_Grainger_r946s946.bed
1900.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r946s946.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r947s946.bed
1901.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r947s946.bed > ./SeqAOnly_Grainger_r947s947.bed
1902.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r947s947.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r948s947.bed
1903.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r948s947.bed > ./SeqAOnly_Grainger_r948s948.bed
1904.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r948s948.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r949s948.bed
1905.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r949s948.bed > ./SeqAOnly_Grainger_r949s949.bed
1906.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r949s949.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r950s949.bed
1907.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r950s949.bed > ./SeqAOnly_Grainger_r950s950.bed
1908.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r950s950.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r951s950.bed
1909.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r951s950.bed > ./SeqAOnly_Grainger_r951s951.bed
1910.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r951s951.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r952s951.bed
1911.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r952s951.bed > ./SeqAOnly_Grainger_r952s952.bed
1912.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r952s952.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r953s952.bed
1913.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r953s952.bed > ./SeqAOnly_Grainger_r953s953.bed
1914.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r953s953.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r954s953.bed
1915.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r954s953.bed > ./SeqAOnly_Grainger_r954s954.bed
1916.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r954s954.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r955s954.bed
1917.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r955s954.bed > ./SeqAOnly_Grainger_r955s955.bed
1918.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r955s955.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r956s955.bed
1919.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r956s955.bed > ./SeqAOnly_Grainger_r956s956.bed
1920.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r956s956.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r957s956.bed
1921.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r957s956.bed > ./SeqAOnly_Grainger_r957s957.bed
1922.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r957s957.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r958s957.bed
1923.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r958s957.bed > ./SeqAOnly_Grainger_r958s958.bed
1924.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r958s958.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r959s958.bed
1925.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r959s958.bed > ./SeqAOnly_Grainger_r959s959.bed
1926.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r959s959.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r960s959.bed

```

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1927.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r960s959.bed > ./SeqAOnly_Grainger_r960s960.bed
1928.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r960s960.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r961s960.bed
1929.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r961s960.bed > ./SeqAOnly_Grainger_r961s961.bed
1930.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r961s961.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r962s961.bed
1931.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r962s961.bed > ./SeqAOnly_Grainger_r962s962.bed
1932.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r962s962.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r963s962.bed
1933.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r963s962.bed > ./SeqAOnly_Grainger_r963s963.bed
1934.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r963s963.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r964s963.bed
1935.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r964s963.bed > ./SeqAOnly_Grainger_r964s964.bed
1936.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r964s964.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r965s964.bed
1937.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r965s964.bed > ./SeqAOnly_Grainger_r965s965.bed
1938.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r965s965.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r966s965.bed
1939.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r966s965.bed > ./SeqAOnly_Grainger_r966s966.bed
1940.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r966s966.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r967s966.bed
1941.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r967s966.bed > ./SeqAOnly_Grainger_r967s967.bed
1942.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r967s967.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r968s967.bed
1943.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r968s967.bed > ./SeqAOnly_Grainger_r968s968.bed
1944.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r968s968.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r969s968.bed
1945.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r969s968.bed > ./SeqAOnly_Grainger_r969s969.bed
1946.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r969s969.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r970s969.bed
1947.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r970s969.bed > ./SeqAOnly_Grainger_r970s970.bed
1948.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r970s970.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r971s970.bed
1949.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r971s970.bed > ./SeqAOnly_Grainger_r971s971.bed
1950.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r971s971.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r972s971.bed
1951.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r972s971.bed > ./SeqAOnly_Grainger_r972s972.bed
1952.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r972s972.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r973s972.bed
1953.    sort -k1,1 -
        k2,2n ./SeqAOnly_Grainger_r973s972.bed > ./SeqAOnly_Grainger_r973s973.bed
1954.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r973s973.bed -g Ecoli-
        genomesize.txt > ./SeqAOnly_Grainger_r974s973.bed

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1955.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r974s973.bed > ./SeqAOnly_Grainger_r974s974.bed
1956.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r974s974.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r975s974.bed
1957.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r975s974.bed > ./SeqAOnly_Grainger_r975s975.bed
1958.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r975s975.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r976s975.bed
1959.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r976s975.bed > ./SeqAOnly_Grainger_r976s976.bed
1960.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r976s976.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r977s976.bed
1961.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r977s976.bed > ./SeqAOnly_Grainger_r977s977.bed
1962.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r977s977.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r978s977.bed
1963.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r978s977.bed > ./SeqAOnly_Grainger_r978s978.bed
1964.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r978s978.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r979s978.bed
1965.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r979s978.bed > ./SeqAOnly_Grainger_r979s979.bed
1966.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r979s979.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r980s979.bed
1967.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r980s979.bed > ./SeqAOnly_Grainger_r980s980.bed
1968.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r980s980.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r981s980.bed
1969.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r981s980.bed > ./SeqAOnly_Grainger_r981s981.bed
1970.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r981s981.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r982s981.bed
1971.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r982s981.bed > ./SeqAOnly_Grainger_r982s982.bed
1972.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r982s982.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r983s982.bed
1973.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r983s982.bed > ./SeqAOnly_Grainger_r983s983.bed
1974.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r983s983.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r984s983.bed
1975.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r984s983.bed > ./SeqAOnly_Grainger_r984s984.bed
1976.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r984s984.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r985s984.bed
1977.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r985s984.bed > ./SeqAOnly_Grainger_r985s985.bed
1978.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r985s985.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r986s985.bed
1979.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r986s985.bed > ./SeqAOnly_Grainger_r986s986.bed
1980.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r986s986.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r987s986.bed
1981.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r987s986.bed > ./SeqAOnly_Grainger_r987s987.bed
1982.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r987s987.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r988s987.bed

```

```
1983.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r988s987.bed > ./SeqAOnly_Grainger_r988s988.bed
1984.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r988s988.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r989s988.bed
1985.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r989s988.bed > ./SeqAOnly_Grainger_r989s989.bed
1986.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r989s989.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r990s989.bed
1987.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r990s989.bed > ./SeqAOnly_Grainger_r990s990.bed
1988.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r990s990.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r991s990.bed
1989.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r991s990.bed > ./SeqAOnly_Grainger_r991s991.bed
1990.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r991s991.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r992s991.bed
1991.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r992s991.bed > ./SeqAOnly_Grainger_r992s992.bed
1992.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r992s992.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r993s992.bed
1993.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r993s992.bed > ./SeqAOnly_Grainger_r993s993.bed
1994.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r993s993.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r994s993.bed
1995.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r994s993.bed > ./SeqAOnly_Grainger_r994s994.bed
1996.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r994s994.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r995s994.bed
1997.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r995s994.bed > ./SeqAOnly_Grainger_r995s995.bed
1998.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r995s995.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r996s995.bed
1999.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r996s995.bed > ./SeqAOnly_Grainger_r996s996.bed
2000.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r996s996.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r997s996.bed
2001.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r997s996.bed > ./SeqAOnly_Grainger_r997s997.bed
2002.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r997s997.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r998s997.bed
2003.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r998s997.bed > ./SeqAOnly_Grainger_r998s998.bed
2004.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r998s998.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r999s998.bed
2005.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r999s998.bed > ./SeqAOnly_Grainger_r999s999.bed
2006.    bedtools shuffle -seed 1 -i SeqAOnly_Grainger_r999s999.bed -g Ecoli-
         genomesize.txt > ./SeqAOnly_Grainger_r1000s999.bed
2007.    sort -k1,1 -
         k2,2n ./SeqAOnly_Grainger_r1000s999.bed > ./SeqAOnly_Grainger_r1000s1000.bed
```


BEDTools shuffle 0 vs. 50 Min signals (SeqA Binding) 1000 times

```
1. #!/bin/bash
2.
3. #bedtools_shuffle_sort_Ovs50Min.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to shuffle Ovs50Min signals 1000 times
6.
7. cp ./Ovs50Min.bed ./Ovs50Min_r0s0.bed
8. bedtools shuffle -seed 1 -i Ovs50Min_r0s0.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r1s0.bed
9. sort -k1,1 -k2,2n ./Ovs50Min_r1s0.bed > ./Ovs50Min_r1s1.bed
10. bedtools shuffle -seed 1 -i Ovs50Min_r1s1.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r2s1.bed
11. sort -k1,1 -k2,2n ./Ovs50Min_r2s1.bed > ./Ovs50Min_r2s2.bed
12. bedtools shuffle -seed 1 -i Ovs50Min_r2s2.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r3s2.bed
13. sort -k1,1 -k2,2n ./Ovs50Min_r3s2.bed > ./Ovs50Min_r3s3.bed
14. bedtools shuffle -seed 1 -i Ovs50Min_r3s3.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r4s3.bed
15. sort -k1,1 -k2,2n ./Ovs50Min_r4s3.bed > ./Ovs50Min_r4s4.bed
16. bedtools shuffle -seed 1 -i Ovs50Min_r4s4.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r5s4.bed
17. sort -k1,1 -k2,2n ./Ovs50Min_r5s4.bed > ./Ovs50Min_r5s5.bed
18. bedtools shuffle -seed 1 -i Ovs50Min_r5s5.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r6s5.bed
19. sort -k1,1 -k2,2n ./Ovs50Min_r6s5.bed > ./Ovs50Min_r6s6.bed
20. bedtools shuffle -seed 1 -i Ovs50Min_r6s6.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r7s6.bed
21. sort -k1,1 -k2,2n ./Ovs50Min_r7s6.bed > ./Ovs50Min_r7s7.bed
22. bedtools shuffle -seed 1 -i Ovs50Min_r7s7.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r8s7.bed
23. sort -k1,1 -k2,2n ./Ovs50Min_r8s7.bed > ./Ovs50Min_r8s8.bed
24. bedtools shuffle -seed 1 -i Ovs50Min_r8s8.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r9s8.bed
25. sort -k1,1 -k2,2n ./Ovs50Min_r9s8.bed > ./Ovs50Min_r9s9.bed
26. bedtools shuffle -seed 1 -i Ovs50Min_r9s9.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r10s9.bed
27. sort -k1,1 -k2,2n ./Ovs50Min_r10s9.bed > ./Ovs50Min_r10s10.bed
28. bedtools shuffle -seed 1 -i Ovs50Min_r10s10.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r11s10.bed
29. sort -k1,1 -k2,2n ./Ovs50Min_r11s10.bed > ./Ovs50Min_r11s11.bed
30. bedtools shuffle -seed 1 -i Ovs50Min_r11s11.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r12s11.bed
31. sort -k1,1 -k2,2n ./Ovs50Min_r12s11.bed > ./Ovs50Min_r12s12.bed
32. bedtools shuffle -seed 1 -i Ovs50Min_r12s12.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r13s12.bed
33. sort -k1,1 -k2,2n ./Ovs50Min_r13s12.bed > ./Ovs50Min_r13s13.bed
34. bedtools shuffle -seed 1 -i Ovs50Min_r13s13.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r14s13.bed
35. sort -k1,1 -k2,2n ./Ovs50Min_r14s13.bed > ./Ovs50Min_r14s14.bed
36. bedtools shuffle -seed 1 -i Ovs50Min_r14s14.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r15s14.bed
37. sort -k1,1 -k2,2n ./Ovs50Min_r15s14.bed > ./Ovs50Min_r15s15.bed
38. bedtools shuffle -seed 1 -i Ovs50Min_r15s15.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r16s15.bed
39. sort -k1,1 -k2,2n ./Ovs50Min_r16s15.bed > ./Ovs50Min_r16s16.bed
40. bedtools shuffle -seed 1 -i Ovs50Min_r16s16.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r17s16.bed
41. sort -k1,1 -k2,2n ./Ovs50Min_r17s16.bed > ./Ovs50Min_r17s17.bed
42. bedtools shuffle -seed 1 -i Ovs50Min_r17s17.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r18s17.bed
43. sort -k1,1 -k2,2n ./Ovs50Min_r18s17.bed > ./Ovs50Min_r18s18.bed
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44. bedtools shuffle -seed 1 -i 0vs50Min_r18s18.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r19s18.bed
45. sort -k1,1 -k2,2n ./0vs50Min_r19s18.bed > ./0vs50Min_r19s19.bed
46. bedtools shuffle -seed 1 -i 0vs50Min_r19s19.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r20s19.bed
47. sort -k1,1 -k2,2n ./0vs50Min_r20s19.bed > ./0vs50Min_r20s20.bed
48. bedtools shuffle -seed 1 -i 0vs50Min_r20s20.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r21s20.bed
49. sort -k1,1 -k2,2n ./0vs50Min_r21s20.bed > ./0vs50Min_r21s21.bed
50. bedtools shuffle -seed 1 -i 0vs50Min_r21s21.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r22s21.bed
51. sort -k1,1 -k2,2n ./0vs50Min_r22s21.bed > ./0vs50Min_r22s22.bed
52. bedtools shuffle -seed 1 -i 0vs50Min_r22s22.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r23s22.bed
53. sort -k1,1 -k2,2n ./0vs50Min_r23s22.bed > ./0vs50Min_r23s23.bed
54. bedtools shuffle -seed 1 -i 0vs50Min_r23s23.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r24s23.bed
55. sort -k1,1 -k2,2n ./0vs50Min_r24s23.bed > ./0vs50Min_r24s24.bed
56. bedtools shuffle -seed 1 -i 0vs50Min_r24s24.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r25s24.bed
57. sort -k1,1 -k2,2n ./0vs50Min_r25s24.bed > ./0vs50Min_r25s25.bed
58. bedtools shuffle -seed 1 -i 0vs50Min_r25s25.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r26s25.bed
59. sort -k1,1 -k2,2n ./0vs50Min_r26s25.bed > ./0vs50Min_r26s26.bed
60. bedtools shuffle -seed 1 -i 0vs50Min_r26s26.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r27s26.bed
61. sort -k1,1 -k2,2n ./0vs50Min_r27s26.bed > ./0vs50Min_r27s27.bed
62. bedtools shuffle -seed 1 -i 0vs50Min_r27s27.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r28s27.bed
63. sort -k1,1 -k2,2n ./0vs50Min_r28s27.bed > ./0vs50Min_r28s28.bed
64. bedtools shuffle -seed 1 -i 0vs50Min_r28s28.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r29s28.bed
65. sort -k1,1 -k2,2n ./0vs50Min_r29s28.bed > ./0vs50Min_r29s29.bed
66. bedtools shuffle -seed 1 -i 0vs50Min_r29s29.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r30s29.bed
67. sort -k1,1 -k2,2n ./0vs50Min_r30s29.bed > ./0vs50Min_r30s30.bed
68. bedtools shuffle -seed 1 -i 0vs50Min_r30s30.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r31s30.bed
69. sort -k1,1 -k2,2n ./0vs50Min_r31s30.bed > ./0vs50Min_r31s31.bed
70. bedtools shuffle -seed 1 -i 0vs50Min_r31s31.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r32s31.bed
71. sort -k1,1 -k2,2n ./0vs50Min_r32s31.bed > ./0vs50Min_r32s32.bed
72. bedtools shuffle -seed 1 -i 0vs50Min_r32s32.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r33s32.bed
73. sort -k1,1 -k2,2n ./0vs50Min_r33s32.bed > ./0vs50Min_r33s33.bed
74. bedtools shuffle -seed 1 -i 0vs50Min_r33s33.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r34s33.bed
75. sort -k1,1 -k2,2n ./0vs50Min_r34s33.bed > ./0vs50Min_r34s34.bed
76. bedtools shuffle -seed 1 -i 0vs50Min_r34s34.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r35s34.bed
77. sort -k1,1 -k2,2n ./0vs50Min_r35s34.bed > ./0vs50Min_r35s35.bed
78. bedtools shuffle -seed 1 -i 0vs50Min_r35s35.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r36s35.bed
79. sort -k1,1 -k2,2n ./0vs50Min_r36s35.bed > ./0vs50Min_r36s36.bed
80. bedtools shuffle -seed 1 -i 0vs50Min_r36s36.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r37s36.bed

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81. sort -k1,1 -k2,2n ./0vs50Min_r37s36.bed > ./0vs50Min_r37s37.bed
82. bedtools shuffle -seed 1 -i 0vs50Min_r37s37.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r38s37.bed
83. sort -k1,1 -k2,2n ./0vs50Min_r38s37.bed > ./0vs50Min_r38s38.bed
84. bedtools shuffle -seed 1 -i 0vs50Min_r38s38.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r39s38.bed
85. sort -k1,1 -k2,2n ./0vs50Min_r39s38.bed > ./0vs50Min_r39s39.bed
86. bedtools shuffle -seed 1 -i 0vs50Min_r39s39.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r40s39.bed
87. sort -k1,1 -k2,2n ./0vs50Min_r40s39.bed > ./0vs50Min_r40s40.bed
88. bedtools shuffle -seed 1 -i 0vs50Min_r40s40.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r41s40.bed
89. sort -k1,1 -k2,2n ./0vs50Min_r41s40.bed > ./0vs50Min_r41s41.bed
90. bedtools shuffle -seed 1 -i 0vs50Min_r41s41.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r42s41.bed
91. sort -k1,1 -k2,2n ./0vs50Min_r42s41.bed > ./0vs50Min_r42s42.bed
92. bedtools shuffle -seed 1 -i 0vs50Min_r42s42.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r43s42.bed
93. sort -k1,1 -k2,2n ./0vs50Min_r43s42.bed > ./0vs50Min_r43s43.bed
94. bedtools shuffle -seed 1 -i 0vs50Min_r43s43.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r44s43.bed
95. sort -k1,1 -k2,2n ./0vs50Min_r44s43.bed > ./0vs50Min_r44s44.bed
96. bedtools shuffle -seed 1 -i 0vs50Min_r44s44.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r45s44.bed
97. sort -k1,1 -k2,2n ./0vs50Min_r45s44.bed > ./0vs50Min_r45s45.bed
98. bedtools shuffle -seed 1 -i 0vs50Min_r45s45.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r46s45.bed
99. sort -k1,1 -k2,2n ./0vs50Min_r46s45.bed > ./0vs50Min_r46s46.bed
100. bedtools shuffle -seed 1 -i 0vs50Min_r46s46.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r47s46.bed
101. sort -k1,1 -k2,2n ./0vs50Min_r47s46.bed > ./0vs50Min_r47s47.bed
102. bedtools shuffle -seed 1 -i 0vs50Min_r47s47.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r48s47.bed
103. sort -k1,1 -k2,2n ./0vs50Min_r48s47.bed > ./0vs50Min_r48s48.bed
104. bedtools shuffle -seed 1 -i 0vs50Min_r48s48.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r49s48.bed
105. sort -k1,1 -k2,2n ./0vs50Min_r49s48.bed > ./0vs50Min_r49s49.bed
106. bedtools shuffle -seed 1 -i 0vs50Min_r49s49.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r50s49.bed
107. sort -k1,1 -k2,2n ./0vs50Min_r50s49.bed > ./0vs50Min_r50s50.bed
108. bedtools shuffle -seed 1 -i 0vs50Min_r50s50.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r51s50.bed
109. sort -k1,1 -k2,2n ./0vs50Min_r51s50.bed > ./0vs50Min_r51s51.bed
110. bedtools shuffle -seed 1 -i 0vs50Min_r51s51.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r52s51.bed
111. sort -k1,1 -k2,2n ./0vs50Min_r52s51.bed > ./0vs50Min_r52s52.bed
112. bedtools shuffle -seed 1 -i 0vs50Min_r52s52.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r53s52.bed
113. sort -k1,1 -k2,2n ./0vs50Min_r53s52.bed > ./0vs50Min_r53s53.bed
114. bedtools shuffle -seed 1 -i 0vs50Min_r53s53.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r54s53.bed
115. sort -k1,1 -k2,2n ./0vs50Min_r54s53.bed > ./0vs50Min_r54s54.bed
116. bedtools shuffle -seed 1 -i 0vs50Min_r54s54.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r55s54.bed
117. sort -k1,1 -k2,2n ./0vs50Min_r55s54.bed > ./0vs50Min_r55s55.bed

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118. bedtools shuffle -seed 1 -i Ovs50Min_r55s55.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r56s55.bed
119. sort -k1,1 -k2,2n ./Ovs50Min_r56s55.bed > ./Ovs50Min_r56s56.bed
120. bedtools shuffle -seed 1 -i Ovs50Min_r56s56.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r57s56.bed
121. sort -k1,1 -k2,2n ./Ovs50Min_r57s56.bed > ./Ovs50Min_r57s57.bed
122. bedtools shuffle -seed 1 -i Ovs50Min_r57s57.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r58s57.bed
123. sort -k1,1 -k2,2n ./Ovs50Min_r58s57.bed > ./Ovs50Min_r58s58.bed
124. bedtools shuffle -seed 1 -i Ovs50Min_r58s58.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r59s58.bed
125. sort -k1,1 -k2,2n ./Ovs50Min_r59s58.bed > ./Ovs50Min_r59s59.bed
126. bedtools shuffle -seed 1 -i Ovs50Min_r59s59.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r60s59.bed
127. sort -k1,1 -k2,2n ./Ovs50Min_r60s59.bed > ./Ovs50Min_r60s60.bed
128. bedtools shuffle -seed 1 -i Ovs50Min_r60s60.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r61s60.bed
129. sort -k1,1 -k2,2n ./Ovs50Min_r61s60.bed > ./Ovs50Min_r61s61.bed
130. bedtools shuffle -seed 1 -i Ovs50Min_r61s61.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r62s61.bed
131. sort -k1,1 -k2,2n ./Ovs50Min_r62s61.bed > ./Ovs50Min_r62s62.bed
132. bedtools shuffle -seed 1 -i Ovs50Min_r62s62.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r63s62.bed
133. sort -k1,1 -k2,2n ./Ovs50Min_r63s62.bed > ./Ovs50Min_r63s63.bed
134. bedtools shuffle -seed 1 -i Ovs50Min_r63s63.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r64s63.bed
135. sort -k1,1 -k2,2n ./Ovs50Min_r64s63.bed > ./Ovs50Min_r64s64.bed
136. bedtools shuffle -seed 1 -i Ovs50Min_r64s64.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r65s64.bed
137. sort -k1,1 -k2,2n ./Ovs50Min_r65s64.bed > ./Ovs50Min_r65s65.bed
138. bedtools shuffle -seed 1 -i Ovs50Min_r65s65.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r66s65.bed
139. sort -k1,1 -k2,2n ./Ovs50Min_r66s65.bed > ./Ovs50Min_r66s66.bed
140. bedtools shuffle -seed 1 -i Ovs50Min_r66s66.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r67s66.bed
141. sort -k1,1 -k2,2n ./Ovs50Min_r67s66.bed > ./Ovs50Min_r67s67.bed
142. bedtools shuffle -seed 1 -i Ovs50Min_r67s67.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r68s67.bed
143. sort -k1,1 -k2,2n ./Ovs50Min_r68s67.bed > ./Ovs50Min_r68s68.bed
144. bedtools shuffle -seed 1 -i Ovs50Min_r68s68.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r69s68.bed
145. sort -k1,1 -k2,2n ./Ovs50Min_r69s68.bed > ./Ovs50Min_r69s69.bed
146. bedtools shuffle -seed 1 -i Ovs50Min_r69s69.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r70s69.bed
147. sort -k1,1 -k2,2n ./Ovs50Min_r70s69.bed > ./Ovs50Min_r70s70.bed
148. bedtools shuffle -seed 1 -i Ovs50Min_r70s70.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r71s70.bed
149. sort -k1,1 -k2,2n ./Ovs50Min_r71s70.bed > ./Ovs50Min_r71s71.bed
150. bedtools shuffle -seed 1 -i Ovs50Min_r71s71.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r72s71.bed
151. sort -k1,1 -k2,2n ./Ovs50Min_r72s71.bed > ./Ovs50Min_r72s72.bed
152. bedtools shuffle -seed 1 -i Ovs50Min_r72s72.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r73s72.bed
153. sort -k1,1 -k2,2n ./Ovs50Min_r73s72.bed > ./Ovs50Min_r73s73.bed
154. bedtools shuffle -seed 1 -i Ovs50Min_r73s73.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r74s73.bed
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155.      sort -k1,1 -k2,2n ./0vs50Min_r74s73.bed > ./0vs50Min_r74s74.bed
156.      bedtools shuffle -seed 1 -i 0vs50Min_r74s74.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r75s74.bed
157.      sort -k1,1 -k2,2n ./0vs50Min_r75s74.bed > ./0vs50Min_r75s75.bed
158.      bedtools shuffle -seed 1 -i 0vs50Min_r75s75.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r76s75.bed
159.      sort -k1,1 -k2,2n ./0vs50Min_r76s75.bed > ./0vs50Min_r76s76.bed
160.      bedtools shuffle -seed 1 -i 0vs50Min_r76s76.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r77s76.bed
161.      sort -k1,1 -k2,2n ./0vs50Min_r77s76.bed > ./0vs50Min_r77s77.bed
162.      bedtools shuffle -seed 1 -i 0vs50Min_r77s77.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r78s77.bed
163.      sort -k1,1 -k2,2n ./0vs50Min_r78s77.bed > ./0vs50Min_r78s78.bed
164.      bedtools shuffle -seed 1 -i 0vs50Min_r78s78.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r79s78.bed
165.      sort -k1,1 -k2,2n ./0vs50Min_r79s78.bed > ./0vs50Min_r79s79.bed
166.      bedtools shuffle -seed 1 -i 0vs50Min_r79s79.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r80s79.bed
167.      sort -k1,1 -k2,2n ./0vs50Min_r80s79.bed > ./0vs50Min_r80s80.bed
168.      bedtools shuffle -seed 1 -i 0vs50Min_r80s80.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r81s80.bed
169.      sort -k1,1 -k2,2n ./0vs50Min_r81s80.bed > ./0vs50Min_r81s81.bed
170.      bedtools shuffle -seed 1 -i 0vs50Min_r81s81.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r82s81.bed
171.      sort -k1,1 -k2,2n ./0vs50Min_r82s81.bed > ./0vs50Min_r82s82.bed
172.      bedtools shuffle -seed 1 -i 0vs50Min_r82s82.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r83s82.bed
173.      sort -k1,1 -k2,2n ./0vs50Min_r83s82.bed > ./0vs50Min_r83s83.bed
174.      bedtools shuffle -seed 1 -i 0vs50Min_r83s83.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r84s83.bed
175.      sort -k1,1 -k2,2n ./0vs50Min_r84s83.bed > ./0vs50Min_r84s84.bed
176.      bedtools shuffle -seed 1 -i 0vs50Min_r84s84.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r85s84.bed
177.      sort -k1,1 -k2,2n ./0vs50Min_r85s84.bed > ./0vs50Min_r85s85.bed
178.      bedtools shuffle -seed 1 -i 0vs50Min_r85s85.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r86s85.bed
179.      sort -k1,1 -k2,2n ./0vs50Min_r86s85.bed > ./0vs50Min_r86s86.bed
180.      bedtools shuffle -seed 1 -i 0vs50Min_r86s86.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r87s86.bed
181.      sort -k1,1 -k2,2n ./0vs50Min_r87s86.bed > ./0vs50Min_r87s87.bed
182.      bedtools shuffle -seed 1 -i 0vs50Min_r87s87.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r88s87.bed
183.      sort -k1,1 -k2,2n ./0vs50Min_r88s87.bed > ./0vs50Min_r88s88.bed
184.      bedtools shuffle -seed 1 -i 0vs50Min_r88s88.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r89s88.bed
185.      sort -k1,1 -k2,2n ./0vs50Min_r89s88.bed > ./0vs50Min_r89s89.bed
186.      bedtools shuffle -seed 1 -i 0vs50Min_r89s89.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r90s89.bed
187.      sort -k1,1 -k2,2n ./0vs50Min_r90s89.bed > ./0vs50Min_r90s90.bed
188.      bedtools shuffle -seed 1 -i 0vs50Min_r90s90.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r91s90.bed
189.      sort -k1,1 -k2,2n ./0vs50Min_r91s90.bed > ./0vs50Min_r91s91.bed
190.      bedtools shuffle -seed 1 -i 0vs50Min_r91s91.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r92s91.bed
191.      sort -k1,1 -k2,2n ./0vs50Min_r92s91.bed > ./0vs50Min_r92s92.bed

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192. bedtools shuffle -seed 1 -i Ovs50Min_r92s92.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r93s92.bed
193. sort -k1,1 -k2,2n ./Ovs50Min_r93s92.bed > ./Ovs50Min_r93s93.bed
194. bedtools shuffle -seed 1 -i Ovs50Min_r93s93.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r94s93.bed
195. sort -k1,1 -k2,2n ./Ovs50Min_r94s93.bed > ./Ovs50Min_r94s94.bed
196. bedtools shuffle -seed 1 -i Ovs50Min_r94s94.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r95s94.bed
197. sort -k1,1 -k2,2n ./Ovs50Min_r95s94.bed > ./Ovs50Min_r95s95.bed
198. bedtools shuffle -seed 1 -i Ovs50Min_r95s95.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r96s95.bed
199. sort -k1,1 -k2,2n ./Ovs50Min_r96s95.bed > ./Ovs50Min_r96s96.bed
200. bedtools shuffle -seed 1 -i Ovs50Min_r96s96.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r97s96.bed
201. sort -k1,1 -k2,2n ./Ovs50Min_r97s96.bed > ./Ovs50Min_r97s97.bed
202. bedtools shuffle -seed 1 -i Ovs50Min_r97s97.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r98s97.bed
203. sort -k1,1 -k2,2n ./Ovs50Min_r98s97.bed > ./Ovs50Min_r98s98.bed
204. bedtools shuffle -seed 1 -i Ovs50Min_r98s98.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r99s98.bed
205. sort -k1,1 -k2,2n ./Ovs50Min_r99s98.bed > ./Ovs50Min_r99s99.bed
206. bedtools shuffle -seed 1 -i Ovs50Min_r99s99.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r100s99.bed
207. sort -k1,1 -k2,2n ./Ovs50Min_r100s99.bed > ./Ovs50Min_r100s100.bed
208. bedtools shuffle -seed 1 -i Ovs50Min_r100s100.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r101s100.bed
209. sort -k1,1 -k2,2n ./Ovs50Min_r101s100.bed > ./Ovs50Min_r101s101.bed
210. bedtools shuffle -seed 1 -i Ovs50Min_r101s101.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r102s101.bed
211. sort -k1,1 -k2,2n ./Ovs50Min_r102s101.bed > ./Ovs50Min_r102s102.bed
212. bedtools shuffle -seed 1 -i Ovs50Min_r102s102.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r103s102.bed
213. sort -k1,1 -k2,2n ./Ovs50Min_r103s102.bed > ./Ovs50Min_r103s103.bed
214. bedtools shuffle -seed 1 -i Ovs50Min_r103s103.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r104s103.bed
215. sort -k1,1 -k2,2n ./Ovs50Min_r104s103.bed > ./Ovs50Min_r104s104.bed
216. bedtools shuffle -seed 1 -i Ovs50Min_r104s104.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r105s104.bed
217. sort -k1,1 -k2,2n ./Ovs50Min_r105s104.bed > ./Ovs50Min_r105s105.bed
218. bedtools shuffle -seed 1 -i Ovs50Min_r105s105.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r106s105.bed
219. sort -k1,1 -k2,2n ./Ovs50Min_r106s105.bed > ./Ovs50Min_r106s106.bed
220. bedtools shuffle -seed 1 -i Ovs50Min_r106s106.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r107s106.bed
221. sort -k1,1 -k2,2n ./Ovs50Min_r107s106.bed > ./Ovs50Min_r107s107.bed
222. bedtools shuffle -seed 1 -i Ovs50Min_r107s107.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r108s107.bed
223. sort -k1,1 -k2,2n ./Ovs50Min_r108s107.bed > ./Ovs50Min_r108s108.bed
224. bedtools shuffle -seed 1 -i Ovs50Min_r108s108.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r109s108.bed
225. sort -k1,1 -k2,2n ./Ovs50Min_r109s108.bed > ./Ovs50Min_r109s109.bed
226. bedtools shuffle -seed 1 -i Ovs50Min_r109s109.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r110s109.bed
227. sort -k1,1 -k2,2n ./Ovs50Min_r110s109.bed > ./Ovs50Min_r110s110.bed
228. bedtools shuffle -seed 1 -i Ovs50Min_r110s110.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r111s110.bed

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229.      sort -k1,1 -k2,2n ./Ovs50Min_r111s110.bed > ./Ovs50Min_r111s111.bed
230.      bedtools shuffle -seed 1 -i Ovs50Min_r111s111.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r112s111.bed
231.      sort -k1,1 -k2,2n ./Ovs50Min_r112s111.bed > ./Ovs50Min_r112s112.bed
232.      bedtools shuffle -seed 1 -i Ovs50Min_r112s112.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r113s112.bed
233.      sort -k1,1 -k2,2n ./Ovs50Min_r113s112.bed > ./Ovs50Min_r113s113.bed
234.      bedtools shuffle -seed 1 -i Ovs50Min_r113s113.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r114s113.bed
235.      sort -k1,1 -k2,2n ./Ovs50Min_r114s113.bed > ./Ovs50Min_r114s114.bed
236.      bedtools shuffle -seed 1 -i Ovs50Min_r114s114.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r115s114.bed
237.      sort -k1,1 -k2,2n ./Ovs50Min_r115s114.bed > ./Ovs50Min_r115s115.bed
238.      bedtools shuffle -seed 1 -i Ovs50Min_r115s115.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r116s115.bed
239.      sort -k1,1 -k2,2n ./Ovs50Min_r116s115.bed > ./Ovs50Min_r116s116.bed
240.      bedtools shuffle -seed 1 -i Ovs50Min_r116s116.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r117s116.bed
241.      sort -k1,1 -k2,2n ./Ovs50Min_r117s116.bed > ./Ovs50Min_r117s117.bed
242.      bedtools shuffle -seed 1 -i Ovs50Min_r117s117.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r118s117.bed
243.      sort -k1,1 -k2,2n ./Ovs50Min_r118s117.bed > ./Ovs50Min_r118s118.bed
244.      bedtools shuffle -seed 1 -i Ovs50Min_r118s118.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r119s118.bed
245.      sort -k1,1 -k2,2n ./Ovs50Min_r119s118.bed > ./Ovs50Min_r119s119.bed
246.      bedtools shuffle -seed 1 -i Ovs50Min_r119s119.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r120s119.bed
247.      sort -k1,1 -k2,2n ./Ovs50Min_r120s119.bed > ./Ovs50Min_r120s120.bed
248.      bedtools shuffle -seed 1 -i Ovs50Min_r120s120.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r121s120.bed
249.      sort -k1,1 -k2,2n ./Ovs50Min_r121s120.bed > ./Ovs50Min_r121s121.bed
250.      bedtools shuffle -seed 1 -i Ovs50Min_r121s121.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r122s121.bed
251.      sort -k1,1 -k2,2n ./Ovs50Min_r122s121.bed > ./Ovs50Min_r122s122.bed
252.      bedtools shuffle -seed 1 -i Ovs50Min_r122s122.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r123s122.bed
253.      sort -k1,1 -k2,2n ./Ovs50Min_r123s122.bed > ./Ovs50Min_r123s123.bed
254.      bedtools shuffle -seed 1 -i Ovs50Min_r123s123.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r124s123.bed
255.      sort -k1,1 -k2,2n ./Ovs50Min_r124s123.bed > ./Ovs50Min_r124s124.bed
256.      bedtools shuffle -seed 1 -i Ovs50Min_r124s124.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r125s124.bed
257.      sort -k1,1 -k2,2n ./Ovs50Min_r125s124.bed > ./Ovs50Min_r125s125.bed
258.      bedtools shuffle -seed 1 -i Ovs50Min_r125s125.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r126s125.bed
259.      sort -k1,1 -k2,2n ./Ovs50Min_r126s125.bed > ./Ovs50Min_r126s126.bed
260.      bedtools shuffle -seed 1 -i Ovs50Min_r126s126.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r127s126.bed
261.      sort -k1,1 -k2,2n ./Ovs50Min_r127s126.bed > ./Ovs50Min_r127s127.bed
262.      bedtools shuffle -seed 1 -i Ovs50Min_r127s127.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r128s127.bed
263.      sort -k1,1 -k2,2n ./Ovs50Min_r128s127.bed > ./Ovs50Min_r128s128.bed
264.      bedtools shuffle -seed 1 -i Ovs50Min_r128s128.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r129s128.bed
265.      sort -k1,1 -k2,2n ./Ovs50Min_r129s128.bed > ./Ovs50Min_r129s129.bed
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266. bedtools shuffle -seed 1 -i Ovs50Min_r129s129.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r130s129.bed
267. sort -k1,1 -k2,2n ./Ovs50Min_r130s129.bed > ./Ovs50Min_r130s130.bed
268. bedtools shuffle -seed 1 -i Ovs50Min_r130s130.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r131s130.bed
269. sort -k1,1 -k2,2n ./Ovs50Min_r131s130.bed > ./Ovs50Min_r131s131.bed
270. bedtools shuffle -seed 1 -i Ovs50Min_r131s131.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r132s131.bed
271. sort -k1,1 -k2,2n ./Ovs50Min_r132s131.bed > ./Ovs50Min_r132s132.bed
272. bedtools shuffle -seed 1 -i Ovs50Min_r132s132.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r133s132.bed
273. sort -k1,1 -k2,2n ./Ovs50Min_r133s132.bed > ./Ovs50Min_r133s133.bed
274. bedtools shuffle -seed 1 -i Ovs50Min_r133s133.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r134s133.bed
275. sort -k1,1 -k2,2n ./Ovs50Min_r134s133.bed > ./Ovs50Min_r134s134.bed
276. bedtools shuffle -seed 1 -i Ovs50Min_r134s134.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r135s134.bed
277. sort -k1,1 -k2,2n ./Ovs50Min_r135s134.bed > ./Ovs50Min_r135s135.bed
278. bedtools shuffle -seed 1 -i Ovs50Min_r135s135.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r136s135.bed
279. sort -k1,1 -k2,2n ./Ovs50Min_r136s135.bed > ./Ovs50Min_r136s136.bed
280. bedtools shuffle -seed 1 -i Ovs50Min_r136s136.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r137s136.bed
281. sort -k1,1 -k2,2n ./Ovs50Min_r137s136.bed > ./Ovs50Min_r137s137.bed
282. bedtools shuffle -seed 1 -i Ovs50Min_r137s137.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r138s137.bed
283. sort -k1,1 -k2,2n ./Ovs50Min_r138s137.bed > ./Ovs50Min_r138s138.bed
284. bedtools shuffle -seed 1 -i Ovs50Min_r138s138.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r139s138.bed
285. sort -k1,1 -k2,2n ./Ovs50Min_r139s138.bed > ./Ovs50Min_r139s139.bed
286. bedtools shuffle -seed 1 -i Ovs50Min_r139s139.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r140s139.bed
287. sort -k1,1 -k2,2n ./Ovs50Min_r140s139.bed > ./Ovs50Min_r140s140.bed
288. bedtools shuffle -seed 1 -i Ovs50Min_r140s140.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r141s140.bed
289. sort -k1,1 -k2,2n ./Ovs50Min_r141s140.bed > ./Ovs50Min_r141s141.bed
290. bedtools shuffle -seed 1 -i Ovs50Min_r141s141.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r142s141.bed
291. sort -k1,1 -k2,2n ./Ovs50Min_r142s141.bed > ./Ovs50Min_r142s142.bed
292. bedtools shuffle -seed 1 -i Ovs50Min_r142s142.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r143s142.bed
293. sort -k1,1 -k2,2n ./Ovs50Min_r143s142.bed > ./Ovs50Min_r143s143.bed
294. bedtools shuffle -seed 1 -i Ovs50Min_r143s143.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r144s143.bed
295. sort -k1,1 -k2,2n ./Ovs50Min_r144s143.bed > ./Ovs50Min_r144s144.bed
296. bedtools shuffle -seed 1 -i Ovs50Min_r144s144.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r145s144.bed
297. sort -k1,1 -k2,2n ./Ovs50Min_r145s144.bed > ./Ovs50Min_r145s145.bed
298. bedtools shuffle -seed 1 -i Ovs50Min_r145s145.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r146s145.bed
299. sort -k1,1 -k2,2n ./Ovs50Min_r146s145.bed > ./Ovs50Min_r146s146.bed
300. bedtools shuffle -seed 1 -i Ovs50Min_r146s146.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r147s146.bed
301. sort -k1,1 -k2,2n ./Ovs50Min_r147s146.bed > ./Ovs50Min_r147s147.bed
302. bedtools shuffle -seed 1 -i Ovs50Min_r147s147.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r148s147.bed

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303.      sort -k1,1 -k2,2n ./Ovs50Min_r148s147.bed > ./Ovs50Min_r148s148.bed
304.      bedtools shuffle -seed 1 -i Ovs50Min_r148s148.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r149s148.bed
305.      sort -k1,1 -k2,2n ./Ovs50Min_r149s148.bed > ./Ovs50Min_r149s149.bed
306.      bedtools shuffle -seed 1 -i Ovs50Min_r149s149.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r150s149.bed
307.      sort -k1,1 -k2,2n ./Ovs50Min_r150s149.bed > ./Ovs50Min_r150s150.bed
308.      bedtools shuffle -seed 1 -i Ovs50Min_r150s150.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r151s150.bed
309.      sort -k1,1 -k2,2n ./Ovs50Min_r151s150.bed > ./Ovs50Min_r151s151.bed
310.      bedtools shuffle -seed 1 -i Ovs50Min_r151s151.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r152s151.bed
311.      sort -k1,1 -k2,2n ./Ovs50Min_r152s151.bed > ./Ovs50Min_r152s152.bed
312.      bedtools shuffle -seed 1 -i Ovs50Min_r152s152.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r153s152.bed
313.      sort -k1,1 -k2,2n ./Ovs50Min_r153s152.bed > ./Ovs50Min_r153s153.bed
314.      bedtools shuffle -seed 1 -i Ovs50Min_r153s153.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r154s153.bed
315.      sort -k1,1 -k2,2n ./Ovs50Min_r154s153.bed > ./Ovs50Min_r154s154.bed
316.      bedtools shuffle -seed 1 -i Ovs50Min_r154s154.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r155s154.bed
317.      sort -k1,1 -k2,2n ./Ovs50Min_r155s154.bed > ./Ovs50Min_r155s155.bed
318.      bedtools shuffle -seed 1 -i Ovs50Min_r155s155.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r156s155.bed
319.      sort -k1,1 -k2,2n ./Ovs50Min_r156s155.bed > ./Ovs50Min_r156s156.bed
320.      bedtools shuffle -seed 1 -i Ovs50Min_r156s156.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r157s156.bed
321.      sort -k1,1 -k2,2n ./Ovs50Min_r157s156.bed > ./Ovs50Min_r157s157.bed
322.      bedtools shuffle -seed 1 -i Ovs50Min_r157s157.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r158s157.bed
323.      sort -k1,1 -k2,2n ./Ovs50Min_r158s157.bed > ./Ovs50Min_r158s158.bed
324.      bedtools shuffle -seed 1 -i Ovs50Min_r158s158.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r159s158.bed
325.      sort -k1,1 -k2,2n ./Ovs50Min_r159s158.bed > ./Ovs50Min_r159s159.bed
326.      bedtools shuffle -seed 1 -i Ovs50Min_r159s159.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r160s159.bed
327.      sort -k1,1 -k2,2n ./Ovs50Min_r160s159.bed > ./Ovs50Min_r160s160.bed
328.      bedtools shuffle -seed 1 -i Ovs50Min_r160s160.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r161s160.bed
329.      sort -k1,1 -k2,2n ./Ovs50Min_r161s160.bed > ./Ovs50Min_r161s161.bed
330.      bedtools shuffle -seed 1 -i Ovs50Min_r161s161.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r162s161.bed
331.      sort -k1,1 -k2,2n ./Ovs50Min_r162s161.bed > ./Ovs50Min_r162s162.bed
332.      bedtools shuffle -seed 1 -i Ovs50Min_r162s162.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r163s162.bed
333.      sort -k1,1 -k2,2n ./Ovs50Min_r163s162.bed > ./Ovs50Min_r163s163.bed
334.      bedtools shuffle -seed 1 -i Ovs50Min_r163s163.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r164s163.bed
335.      sort -k1,1 -k2,2n ./Ovs50Min_r164s163.bed > ./Ovs50Min_r164s164.bed
336.      bedtools shuffle -seed 1 -i Ovs50Min_r164s164.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r165s164.bed
337.      sort -k1,1 -k2,2n ./Ovs50Min_r165s164.bed > ./Ovs50Min_r165s165.bed
338.      bedtools shuffle -seed 1 -i Ovs50Min_r165s165.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r166s165.bed
339.      sort -k1,1 -k2,2n ./Ovs50Min_r166s165.bed > ./Ovs50Min_r166s166.bed

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340.     bedtools shuffle -seed 1 -i Ovs50Min_r166s166.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r167s166.bed
341.     sort -k1,1 -k2,2n ./Ovs50Min_r167s166.bed > ./Ovs50Min_r167s167.bed
342.     bedtools shuffle -seed 1 -i Ovs50Min_r167s167.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r168s167.bed
343.     sort -k1,1 -k2,2n ./Ovs50Min_r168s167.bed > ./Ovs50Min_r168s168.bed
344.     bedtools shuffle -seed 1 -i Ovs50Min_r168s168.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r169s168.bed
345.     sort -k1,1 -k2,2n ./Ovs50Min_r169s168.bed > ./Ovs50Min_r169s169.bed
346.     bedtools shuffle -seed 1 -i Ovs50Min_r169s169.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r170s169.bed
347.     sort -k1,1 -k2,2n ./Ovs50Min_r170s169.bed > ./Ovs50Min_r170s170.bed
348.     bedtools shuffle -seed 1 -i Ovs50Min_r170s170.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r171s170.bed
349.     sort -k1,1 -k2,2n ./Ovs50Min_r171s170.bed > ./Ovs50Min_r171s171.bed
350.     bedtools shuffle -seed 1 -i Ovs50Min_r171s171.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r172s171.bed
351.     sort -k1,1 -k2,2n ./Ovs50Min_r172s171.bed > ./Ovs50Min_r172s172.bed
352.     bedtools shuffle -seed 1 -i Ovs50Min_r172s172.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r173s172.bed
353.     sort -k1,1 -k2,2n ./Ovs50Min_r173s172.bed > ./Ovs50Min_r173s173.bed
354.     bedtools shuffle -seed 1 -i Ovs50Min_r173s173.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r174s173.bed
355.     sort -k1,1 -k2,2n ./Ovs50Min_r174s173.bed > ./Ovs50Min_r174s174.bed
356.     bedtools shuffle -seed 1 -i Ovs50Min_r174s174.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r175s174.bed
357.     sort -k1,1 -k2,2n ./Ovs50Min_r175s174.bed > ./Ovs50Min_r175s175.bed
358.     bedtools shuffle -seed 1 -i Ovs50Min_r175s175.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r176s175.bed
359.     sort -k1,1 -k2,2n ./Ovs50Min_r176s175.bed > ./Ovs50Min_r176s176.bed
360.     bedtools shuffle -seed 1 -i Ovs50Min_r176s176.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r177s176.bed
361.     sort -k1,1 -k2,2n ./Ovs50Min_r177s176.bed > ./Ovs50Min_r177s177.bed
362.     bedtools shuffle -seed 1 -i Ovs50Min_r177s177.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r178s177.bed
363.     sort -k1,1 -k2,2n ./Ovs50Min_r178s177.bed > ./Ovs50Min_r178s178.bed
364.     bedtools shuffle -seed 1 -i Ovs50Min_r178s178.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r179s178.bed
365.     sort -k1,1 -k2,2n ./Ovs50Min_r179s178.bed > ./Ovs50Min_r179s179.bed
366.     bedtools shuffle -seed 1 -i Ovs50Min_r179s179.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r180s179.bed
367.     sort -k1,1 -k2,2n ./Ovs50Min_r180s179.bed > ./Ovs50Min_r180s180.bed
368.     bedtools shuffle -seed 1 -i Ovs50Min_r180s180.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r181s180.bed
369.     sort -k1,1 -k2,2n ./Ovs50Min_r181s180.bed > ./Ovs50Min_r181s181.bed
370.     bedtools shuffle -seed 1 -i Ovs50Min_r181s181.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r182s181.bed
371.     sort -k1,1 -k2,2n ./Ovs50Min_r182s181.bed > ./Ovs50Min_r182s182.bed
372.     bedtools shuffle -seed 1 -i Ovs50Min_r182s182.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r183s182.bed
373.     sort -k1,1 -k2,2n ./Ovs50Min_r183s182.bed > ./Ovs50Min_r183s183.bed
374.     bedtools shuffle -seed 1 -i Ovs50Min_r183s183.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r184s183.bed
375.     sort -k1,1 -k2,2n ./Ovs50Min_r184s183.bed > ./Ovs50Min_r184s184.bed
376.     bedtools shuffle -seed 1 -i Ovs50Min_r184s184.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r185s184.bed

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377.      sort -k1,1 -k2,2n ./0vs50Min_r185s184.bed > ./0vs50Min_r185s185.bed
378.      bedtools shuffle -seed 1 -i 0vs50Min_r185s185.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r186s185.bed
379.      sort -k1,1 -k2,2n ./0vs50Min_r186s185.bed > ./0vs50Min_r186s186.bed
380.      bedtools shuffle -seed 1 -i 0vs50Min_r186s186.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r187s186.bed
381.      sort -k1,1 -k2,2n ./0vs50Min_r187s186.bed > ./0vs50Min_r187s187.bed
382.      bedtools shuffle -seed 1 -i 0vs50Min_r187s187.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r188s187.bed
383.      sort -k1,1 -k2,2n ./0vs50Min_r188s187.bed > ./0vs50Min_r188s188.bed
384.      bedtools shuffle -seed 1 -i 0vs50Min_r188s188.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r189s188.bed
385.      sort -k1,1 -k2,2n ./0vs50Min_r189s188.bed > ./0vs50Min_r189s189.bed
386.      bedtools shuffle -seed 1 -i 0vs50Min_r189s189.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r190s189.bed
387.      sort -k1,1 -k2,2n ./0vs50Min_r190s189.bed > ./0vs50Min_r190s190.bed
388.      bedtools shuffle -seed 1 -i 0vs50Min_r190s190.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r191s190.bed
389.      sort -k1,1 -k2,2n ./0vs50Min_r191s190.bed > ./0vs50Min_r191s191.bed
390.      bedtools shuffle -seed 1 -i 0vs50Min_r191s191.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r192s191.bed
391.      sort -k1,1 -k2,2n ./0vs50Min_r192s191.bed > ./0vs50Min_r192s192.bed
392.      bedtools shuffle -seed 1 -i 0vs50Min_r192s192.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r193s192.bed
393.      sort -k1,1 -k2,2n ./0vs50Min_r193s192.bed > ./0vs50Min_r193s193.bed
394.      bedtools shuffle -seed 1 -i 0vs50Min_r193s193.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r194s193.bed
395.      sort -k1,1 -k2,2n ./0vs50Min_r194s193.bed > ./0vs50Min_r194s194.bed
396.      bedtools shuffle -seed 1 -i 0vs50Min_r194s194.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r195s194.bed
397.      sort -k1,1 -k2,2n ./0vs50Min_r195s194.bed > ./0vs50Min_r195s195.bed
398.      bedtools shuffle -seed 1 -i 0vs50Min_r195s195.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r196s195.bed
399.      sort -k1,1 -k2,2n ./0vs50Min_r196s195.bed > ./0vs50Min_r196s196.bed
400.      bedtools shuffle -seed 1 -i 0vs50Min_r196s196.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r197s196.bed
401.      sort -k1,1 -k2,2n ./0vs50Min_r197s196.bed > ./0vs50Min_r197s197.bed
402.      bedtools shuffle -seed 1 -i 0vs50Min_r197s197.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r198s197.bed
403.      sort -k1,1 -k2,2n ./0vs50Min_r198s197.bed > ./0vs50Min_r198s198.bed
404.      bedtools shuffle -seed 1 -i 0vs50Min_r198s198.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r199s198.bed
405.      sort -k1,1 -k2,2n ./0vs50Min_r199s198.bed > ./0vs50Min_r199s199.bed
406.      bedtools shuffle -seed 1 -i 0vs50Min_r199s199.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r200s199.bed
407.      sort -k1,1 -k2,2n ./0vs50Min_r200s199.bed > ./0vs50Min_r200s200.bed
408.      bedtools shuffle -seed 1 -i 0vs50Min_r200s200.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r201s200.bed
409.      sort -k1,1 -k2,2n ./0vs50Min_r201s200.bed > ./0vs50Min_r201s201.bed
410.      bedtools shuffle -seed 1 -i 0vs50Min_r201s201.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r202s201.bed
411.      sort -k1,1 -k2,2n ./0vs50Min_r202s201.bed > ./0vs50Min_r202s202.bed
412.      bedtools shuffle -seed 1 -i 0vs50Min_r202s202.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r203s202.bed
413.      sort -k1,1 -k2,2n ./0vs50Min_r203s202.bed > ./0vs50Min_r203s203.bed
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414.      bedtools shuffle -seed 1 -i 0vs50Min_r203s203.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r204s203.bed
415.      sort -k1,1 -k2,2n ./0vs50Min_r204s203.bed > ./0vs50Min_r204s204.bed
416.      bedtools shuffle -seed 1 -i 0vs50Min_r204s204.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r205s204.bed
417.      sort -k1,1 -k2,2n ./0vs50Min_r205s204.bed > ./0vs50Min_r205s205.bed
418.      bedtools shuffle -seed 1 -i 0vs50Min_r205s205.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r206s205.bed
419.      sort -k1,1 -k2,2n ./0vs50Min_r206s205.bed > ./0vs50Min_r206s206.bed
420.      bedtools shuffle -seed 1 -i 0vs50Min_r206s206.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r207s206.bed
421.      sort -k1,1 -k2,2n ./0vs50Min_r207s206.bed > ./0vs50Min_r207s207.bed
422.      bedtools shuffle -seed 1 -i 0vs50Min_r207s207.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r208s207.bed
423.      sort -k1,1 -k2,2n ./0vs50Min_r208s207.bed > ./0vs50Min_r208s208.bed
424.      bedtools shuffle -seed 1 -i 0vs50Min_r208s208.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r209s208.bed
425.      sort -k1,1 -k2,2n ./0vs50Min_r209s208.bed > ./0vs50Min_r209s209.bed
426.      bedtools shuffle -seed 1 -i 0vs50Min_r209s209.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r210s209.bed
427.      sort -k1,1 -k2,2n ./0vs50Min_r210s209.bed > ./0vs50Min_r210s210.bed
428.      bedtools shuffle -seed 1 -i 0vs50Min_r210s210.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r211s210.bed
429.      sort -k1,1 -k2,2n ./0vs50Min_r211s210.bed > ./0vs50Min_r211s211.bed
430.      bedtools shuffle -seed 1 -i 0vs50Min_r211s211.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r212s211.bed
431.      sort -k1,1 -k2,2n ./0vs50Min_r212s211.bed > ./0vs50Min_r212s212.bed
432.      bedtools shuffle -seed 1 -i 0vs50Min_r212s212.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r213s212.bed
433.      sort -k1,1 -k2,2n ./0vs50Min_r213s212.bed > ./0vs50Min_r213s213.bed
434.      bedtools shuffle -seed 1 -i 0vs50Min_r213s213.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r214s213.bed
435.      sort -k1,1 -k2,2n ./0vs50Min_r214s213.bed > ./0vs50Min_r214s214.bed
436.      bedtools shuffle -seed 1 -i 0vs50Min_r214s214.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r215s214.bed
437.      sort -k1,1 -k2,2n ./0vs50Min_r215s214.bed > ./0vs50Min_r215s215.bed
438.      bedtools shuffle -seed 1 -i 0vs50Min_r215s215.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r216s215.bed
439.      sort -k1,1 -k2,2n ./0vs50Min_r216s215.bed > ./0vs50Min_r216s216.bed
440.      bedtools shuffle -seed 1 -i 0vs50Min_r216s216.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r217s216.bed
441.      sort -k1,1 -k2,2n ./0vs50Min_r217s216.bed > ./0vs50Min_r217s217.bed
442.      bedtools shuffle -seed 1 -i 0vs50Min_r217s217.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r218s217.bed
443.      sort -k1,1 -k2,2n ./0vs50Min_r218s217.bed > ./0vs50Min_r218s218.bed
444.      bedtools shuffle -seed 1 -i 0vs50Min_r218s218.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r219s218.bed
445.      sort -k1,1 -k2,2n ./0vs50Min_r219s218.bed > ./0vs50Min_r219s219.bed
446.      bedtools shuffle -seed 1 -i 0vs50Min_r219s219.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r220s219.bed
447.      sort -k1,1 -k2,2n ./0vs50Min_r220s219.bed > ./0vs50Min_r220s220.bed
448.      bedtools shuffle -seed 1 -i 0vs50Min_r220s220.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r221s220.bed
449.      sort -k1,1 -k2,2n ./0vs50Min_r221s220.bed > ./0vs50Min_r221s221.bed
450.      bedtools shuffle -seed 1 -i 0vs50Min_r221s221.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r222s221.bed

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451.      sort -k1,1 -k2,2n ./Ovs50Min_r222s221.bed > ./Ovs50Min_r222s222.bed
452.      bedtools shuffle -seed 1 -i Ovs50Min_r222s222.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r223s222.bed
453.      sort -k1,1 -k2,2n ./Ovs50Min_r223s222.bed > ./Ovs50Min_r223s223.bed
454.      bedtools shuffle -seed 1 -i Ovs50Min_r223s223.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r224s223.bed
455.      sort -k1,1 -k2,2n ./Ovs50Min_r224s223.bed > ./Ovs50Min_r224s224.bed
456.      bedtools shuffle -seed 1 -i Ovs50Min_r224s224.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r225s224.bed
457.      sort -k1,1 -k2,2n ./Ovs50Min_r225s224.bed > ./Ovs50Min_r225s225.bed
458.      bedtools shuffle -seed 1 -i Ovs50Min_r225s225.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r226s225.bed
459.      sort -k1,1 -k2,2n ./Ovs50Min_r226s225.bed > ./Ovs50Min_r226s226.bed
460.      bedtools shuffle -seed 1 -i Ovs50Min_r226s226.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r227s226.bed
461.      sort -k1,1 -k2,2n ./Ovs50Min_r227s226.bed > ./Ovs50Min_r227s227.bed
462.      bedtools shuffle -seed 1 -i Ovs50Min_r227s227.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r228s227.bed
463.      sort -k1,1 -k2,2n ./Ovs50Min_r228s227.bed > ./Ovs50Min_r228s228.bed
464.      bedtools shuffle -seed 1 -i Ovs50Min_r228s228.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r229s228.bed
465.      sort -k1,1 -k2,2n ./Ovs50Min_r229s228.bed > ./Ovs50Min_r229s229.bed
466.      bedtools shuffle -seed 1 -i Ovs50Min_r229s229.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r230s229.bed
467.      sort -k1,1 -k2,2n ./Ovs50Min_r230s229.bed > ./Ovs50Min_r230s230.bed
468.      bedtools shuffle -seed 1 -i Ovs50Min_r230s230.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r231s230.bed
469.      sort -k1,1 -k2,2n ./Ovs50Min_r231s230.bed > ./Ovs50Min_r231s231.bed
470.      bedtools shuffle -seed 1 -i Ovs50Min_r231s231.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r232s231.bed
471.      sort -k1,1 -k2,2n ./Ovs50Min_r232s231.bed > ./Ovs50Min_r232s232.bed
472.      bedtools shuffle -seed 1 -i Ovs50Min_r232s232.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r233s232.bed
473.      sort -k1,1 -k2,2n ./Ovs50Min_r233s232.bed > ./Ovs50Min_r233s233.bed
474.      bedtools shuffle -seed 1 -i Ovs50Min_r233s233.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r234s233.bed
475.      sort -k1,1 -k2,2n ./Ovs50Min_r234s233.bed > ./Ovs50Min_r234s234.bed
476.      bedtools shuffle -seed 1 -i Ovs50Min_r234s234.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r235s234.bed
477.      sort -k1,1 -k2,2n ./Ovs50Min_r235s234.bed > ./Ovs50Min_r235s235.bed
478.      bedtools shuffle -seed 1 -i Ovs50Min_r235s235.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r236s235.bed
479.      sort -k1,1 -k2,2n ./Ovs50Min_r236s235.bed > ./Ovs50Min_r236s236.bed
480.      bedtools shuffle -seed 1 -i Ovs50Min_r236s236.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r237s236.bed
481.      sort -k1,1 -k2,2n ./Ovs50Min_r237s236.bed > ./Ovs50Min_r237s237.bed
482.      bedtools shuffle -seed 1 -i Ovs50Min_r237s237.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r238s237.bed
483.      sort -k1,1 -k2,2n ./Ovs50Min_r238s237.bed > ./Ovs50Min_r238s238.bed
484.      bedtools shuffle -seed 1 -i Ovs50Min_r238s238.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r239s238.bed
485.      sort -k1,1 -k2,2n ./Ovs50Min_r239s238.bed > ./Ovs50Min_r239s239.bed
486.      bedtools shuffle -seed 1 -i Ovs50Min_r239s239.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r240s239.bed
487.      sort -k1,1 -k2,2n ./Ovs50Min_r240s239.bed > ./Ovs50Min_r240s240.bed

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488. bedtools shuffle -seed 1 -i 0vs50Min_r240s240.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r241s240.bed
489. sort -k1,1 -k2,2n ./0vs50Min_r241s240.bed > ./0vs50Min_r241s241.bed
490. bedtools shuffle -seed 1 -i 0vs50Min_r241s241.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r242s241.bed
491. sort -k1,1 -k2,2n ./0vs50Min_r242s241.bed > ./0vs50Min_r242s242.bed
492. bedtools shuffle -seed 1 -i 0vs50Min_r242s242.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r243s242.bed
493. sort -k1,1 -k2,2n ./0vs50Min_r243s242.bed > ./0vs50Min_r243s243.bed
494. bedtools shuffle -seed 1 -i 0vs50Min_r243s243.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r244s243.bed
495. sort -k1,1 -k2,2n ./0vs50Min_r244s243.bed > ./0vs50Min_r244s244.bed
496. bedtools shuffle -seed 1 -i 0vs50Min_r244s244.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r245s244.bed
497. sort -k1,1 -k2,2n ./0vs50Min_r245s244.bed > ./0vs50Min_r245s245.bed
498. bedtools shuffle -seed 1 -i 0vs50Min_r245s245.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r246s245.bed
499. sort -k1,1 -k2,2n ./0vs50Min_r246s245.bed > ./0vs50Min_r246s246.bed
500. bedtools shuffle -seed 1 -i 0vs50Min_r246s246.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r247s246.bed
501. sort -k1,1 -k2,2n ./0vs50Min_r247s246.bed > ./0vs50Min_r247s247.bed
502. bedtools shuffle -seed 1 -i 0vs50Min_r247s247.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r248s247.bed
503. sort -k1,1 -k2,2n ./0vs50Min_r248s247.bed > ./0vs50Min_r248s248.bed
504. bedtools shuffle -seed 1 -i 0vs50Min_r248s248.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r249s248.bed
505. sort -k1,1 -k2,2n ./0vs50Min_r249s248.bed > ./0vs50Min_r249s249.bed
506. bedtools shuffle -seed 1 -i 0vs50Min_r249s249.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r250s249.bed
507. sort -k1,1 -k2,2n ./0vs50Min_r250s249.bed > ./0vs50Min_r250s250.bed
508. bedtools shuffle -seed 1 -i 0vs50Min_r250s250.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r251s250.bed
509. sort -k1,1 -k2,2n ./0vs50Min_r251s250.bed > ./0vs50Min_r251s251.bed
510. bedtools shuffle -seed 1 -i 0vs50Min_r251s251.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r252s251.bed
511. sort -k1,1 -k2,2n ./0vs50Min_r252s251.bed > ./0vs50Min_r252s252.bed
512. bedtools shuffle -seed 1 -i 0vs50Min_r252s252.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r253s252.bed
513. sort -k1,1 -k2,2n ./0vs50Min_r253s252.bed > ./0vs50Min_r253s253.bed
514. bedtools shuffle -seed 1 -i 0vs50Min_r253s253.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r254s253.bed
515. sort -k1,1 -k2,2n ./0vs50Min_r254s253.bed > ./0vs50Min_r254s254.bed
516. bedtools shuffle -seed 1 -i 0vs50Min_r254s254.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r255s254.bed
517. sort -k1,1 -k2,2n ./0vs50Min_r255s254.bed > ./0vs50Min_r255s255.bed
518. bedtools shuffle -seed 1 -i 0vs50Min_r255s255.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r256s255.bed
519. sort -k1,1 -k2,2n ./0vs50Min_r256s255.bed > ./0vs50Min_r256s256.bed
520. bedtools shuffle -seed 1 -i 0vs50Min_r256s256.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r257s256.bed
521. sort -k1,1 -k2,2n ./0vs50Min_r257s256.bed > ./0vs50Min_r257s257.bed
522. bedtools shuffle -seed 1 -i 0vs50Min_r257s257.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r258s257.bed
523. sort -k1,1 -k2,2n ./0vs50Min_r258s257.bed > ./0vs50Min_r258s258.bed
524. bedtools shuffle -seed 1 -i 0vs50Min_r258s258.bed -g Ecoli-
    genomesize.txt > ./0vs50Min_r259s258.bed
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525.      sort -k1,1 -k2,2n ./0vs50Min_r259s258.bed > ./0vs50Min_r259s259.bed
526.      bedtools shuffle -seed 1 -i 0vs50Min_r259s259.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r260s259.bed
527.      sort -k1,1 -k2,2n ./0vs50Min_r260s259.bed > ./0vs50Min_r260s260.bed
528.      bedtools shuffle -seed 1 -i 0vs50Min_r260s260.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r261s260.bed
529.      sort -k1,1 -k2,2n ./0vs50Min_r261s260.bed > ./0vs50Min_r261s261.bed
530.      bedtools shuffle -seed 1 -i 0vs50Min_r261s261.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r262s261.bed
531.      sort -k1,1 -k2,2n ./0vs50Min_r262s261.bed > ./0vs50Min_r262s262.bed
532.      bedtools shuffle -seed 1 -i 0vs50Min_r262s262.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r263s262.bed
533.      sort -k1,1 -k2,2n ./0vs50Min_r263s262.bed > ./0vs50Min_r263s263.bed
534.      bedtools shuffle -seed 1 -i 0vs50Min_r263s263.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r264s263.bed
535.      sort -k1,1 -k2,2n ./0vs50Min_r264s263.bed > ./0vs50Min_r264s264.bed
536.      bedtools shuffle -seed 1 -i 0vs50Min_r264s264.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r265s264.bed
537.      sort -k1,1 -k2,2n ./0vs50Min_r265s264.bed > ./0vs50Min_r265s265.bed
538.      bedtools shuffle -seed 1 -i 0vs50Min_r265s265.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r266s265.bed
539.      sort -k1,1 -k2,2n ./0vs50Min_r266s265.bed > ./0vs50Min_r266s266.bed
540.      bedtools shuffle -seed 1 -i 0vs50Min_r266s266.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r267s266.bed
541.      sort -k1,1 -k2,2n ./0vs50Min_r267s266.bed > ./0vs50Min_r267s267.bed
542.      bedtools shuffle -seed 1 -i 0vs50Min_r267s267.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r268s267.bed
543.      sort -k1,1 -k2,2n ./0vs50Min_r268s267.bed > ./0vs50Min_r268s268.bed
544.      bedtools shuffle -seed 1 -i 0vs50Min_r268s268.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r269s268.bed
545.      sort -k1,1 -k2,2n ./0vs50Min_r269s268.bed > ./0vs50Min_r269s269.bed
546.      bedtools shuffle -seed 1 -i 0vs50Min_r269s269.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r270s269.bed
547.      sort -k1,1 -k2,2n ./0vs50Min_r270s269.bed > ./0vs50Min_r270s270.bed
548.      bedtools shuffle -seed 1 -i 0vs50Min_r270s270.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r271s270.bed
549.      sort -k1,1 -k2,2n ./0vs50Min_r271s270.bed > ./0vs50Min_r271s271.bed
550.      bedtools shuffle -seed 1 -i 0vs50Min_r271s271.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r272s271.bed
551.      sort -k1,1 -k2,2n ./0vs50Min_r272s271.bed > ./0vs50Min_r272s272.bed
552.      bedtools shuffle -seed 1 -i 0vs50Min_r272s272.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r273s272.bed
553.      sort -k1,1 -k2,2n ./0vs50Min_r273s272.bed > ./0vs50Min_r273s273.bed
554.      bedtools shuffle -seed 1 -i 0vs50Min_r273s273.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r274s273.bed
555.      sort -k1,1 -k2,2n ./0vs50Min_r274s273.bed > ./0vs50Min_r274s274.bed
556.      bedtools shuffle -seed 1 -i 0vs50Min_r274s274.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r275s274.bed
557.      sort -k1,1 -k2,2n ./0vs50Min_r275s274.bed > ./0vs50Min_r275s275.bed
558.      bedtools shuffle -seed 1 -i 0vs50Min_r275s275.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r276s275.bed
559.      sort -k1,1 -k2,2n ./0vs50Min_r276s275.bed > ./0vs50Min_r276s276.bed
560.      bedtools shuffle -seed 1 -i 0vs50Min_r276s276.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r277s276.bed
561.      sort -k1,1 -k2,2n ./0vs50Min_r277s276.bed > ./0vs50Min_r277s277.bed
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562.     bedtools shuffle -seed 1 -i 0vs50Min_r277s277.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r278s277.bed
563.     sort -k1,1 -k2,2n ./0vs50Min_r278s277.bed > ./0vs50Min_r278s278.bed
564.     bedtools shuffle -seed 1 -i 0vs50Min_r278s278.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r279s278.bed
565.     sort -k1,1 -k2,2n ./0vs50Min_r279s278.bed > ./0vs50Min_r279s279.bed
566.     bedtools shuffle -seed 1 -i 0vs50Min_r279s279.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r280s279.bed
567.     sort -k1,1 -k2,2n ./0vs50Min_r280s279.bed > ./0vs50Min_r280s280.bed
568.     bedtools shuffle -seed 1 -i 0vs50Min_r280s280.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r281s280.bed
569.     sort -k1,1 -k2,2n ./0vs50Min_r281s280.bed > ./0vs50Min_r281s281.bed
570.     bedtools shuffle -seed 1 -i 0vs50Min_r281s281.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r282s281.bed
571.     sort -k1,1 -k2,2n ./0vs50Min_r282s281.bed > ./0vs50Min_r282s282.bed
572.     bedtools shuffle -seed 1 -i 0vs50Min_r282s282.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r283s282.bed
573.     sort -k1,1 -k2,2n ./0vs50Min_r283s282.bed > ./0vs50Min_r283s283.bed
574.     bedtools shuffle -seed 1 -i 0vs50Min_r283s283.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r284s283.bed
575.     sort -k1,1 -k2,2n ./0vs50Min_r284s283.bed > ./0vs50Min_r284s284.bed
576.     bedtools shuffle -seed 1 -i 0vs50Min_r284s284.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r285s284.bed
577.     sort -k1,1 -k2,2n ./0vs50Min_r285s284.bed > ./0vs50Min_r285s285.bed
578.     bedtools shuffle -seed 1 -i 0vs50Min_r285s285.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r286s285.bed
579.     sort -k1,1 -k2,2n ./0vs50Min_r286s285.bed > ./0vs50Min_r286s286.bed
580.     bedtools shuffle -seed 1 -i 0vs50Min_r286s286.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r287s286.bed
581.     sort -k1,1 -k2,2n ./0vs50Min_r287s286.bed > ./0vs50Min_r287s287.bed
582.     bedtools shuffle -seed 1 -i 0vs50Min_r287s287.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r288s287.bed
583.     sort -k1,1 -k2,2n ./0vs50Min_r288s287.bed > ./0vs50Min_r288s288.bed
584.     bedtools shuffle -seed 1 -i 0vs50Min_r288s288.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r289s288.bed
585.     sort -k1,1 -k2,2n ./0vs50Min_r289s288.bed > ./0vs50Min_r289s289.bed
586.     bedtools shuffle -seed 1 -i 0vs50Min_r289s289.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r290s289.bed
587.     sort -k1,1 -k2,2n ./0vs50Min_r290s289.bed > ./0vs50Min_r290s290.bed
588.     bedtools shuffle -seed 1 -i 0vs50Min_r290s290.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r291s290.bed
589.     sort -k1,1 -k2,2n ./0vs50Min_r291s290.bed > ./0vs50Min_r291s291.bed
590.     bedtools shuffle -seed 1 -i 0vs50Min_r291s291.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r292s291.bed
591.     sort -k1,1 -k2,2n ./0vs50Min_r292s291.bed > ./0vs50Min_r292s292.bed
592.     bedtools shuffle -seed 1 -i 0vs50Min_r292s292.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r293s292.bed
593.     sort -k1,1 -k2,2n ./0vs50Min_r293s292.bed > ./0vs50Min_r293s293.bed
594.     bedtools shuffle -seed 1 -i 0vs50Min_r293s293.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r294s293.bed
595.     sort -k1,1 -k2,2n ./0vs50Min_r294s293.bed > ./0vs50Min_r294s294.bed
596.     bedtools shuffle -seed 1 -i 0vs50Min_r294s294.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r295s294.bed
597.     sort -k1,1 -k2,2n ./0vs50Min_r295s294.bed > ./0vs50Min_r295s295.bed
598.     bedtools shuffle -seed 1 -i 0vs50Min_r295s295.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r296s295.bed

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599.      sort -k1,1 -k2,2n ./0vs50Min_r296s295.bed > ./0vs50Min_r296s296.bed
600.      bedtools shuffle -seed 1 -i 0vs50Min_r296s296.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r297s296.bed
601.      sort -k1,1 -k2,2n ./0vs50Min_r297s296.bed > ./0vs50Min_r297s297.bed
602.      bedtools shuffle -seed 1 -i 0vs50Min_r297s297.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r298s297.bed
603.      sort -k1,1 -k2,2n ./0vs50Min_r298s297.bed > ./0vs50Min_r298s298.bed
604.      bedtools shuffle -seed 1 -i 0vs50Min_r298s298.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r299s298.bed
605.      sort -k1,1 -k2,2n ./0vs50Min_r299s298.bed > ./0vs50Min_r299s299.bed
606.      bedtools shuffle -seed 1 -i 0vs50Min_r299s299.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r300s299.bed
607.      sort -k1,1 -k2,2n ./0vs50Min_r300s299.bed > ./0vs50Min_r300s300.bed
608.      bedtools shuffle -seed 1 -i 0vs50Min_r300s300.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r301s300.bed
609.      sort -k1,1 -k2,2n ./0vs50Min_r301s300.bed > ./0vs50Min_r301s301.bed
610.      bedtools shuffle -seed 1 -i 0vs50Min_r301s301.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r302s301.bed
611.      sort -k1,1 -k2,2n ./0vs50Min_r302s301.bed > ./0vs50Min_r302s302.bed
612.      bedtools shuffle -seed 1 -i 0vs50Min_r302s302.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r303s302.bed
613.      sort -k1,1 -k2,2n ./0vs50Min_r303s302.bed > ./0vs50Min_r303s303.bed
614.      bedtools shuffle -seed 1 -i 0vs50Min_r303s303.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r304s303.bed
615.      sort -k1,1 -k2,2n ./0vs50Min_r304s303.bed > ./0vs50Min_r304s304.bed
616.      bedtools shuffle -seed 1 -i 0vs50Min_r304s304.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r305s304.bed
617.      sort -k1,1 -k2,2n ./0vs50Min_r305s304.bed > ./0vs50Min_r305s305.bed
618.      bedtools shuffle -seed 1 -i 0vs50Min_r305s305.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r306s305.bed
619.      sort -k1,1 -k2,2n ./0vs50Min_r306s305.bed > ./0vs50Min_r306s306.bed
620.      bedtools shuffle -seed 1 -i 0vs50Min_r306s306.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r307s306.bed
621.      sort -k1,1 -k2,2n ./0vs50Min_r307s306.bed > ./0vs50Min_r307s307.bed
622.      bedtools shuffle -seed 1 -i 0vs50Min_r307s307.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r308s307.bed
623.      sort -k1,1 -k2,2n ./0vs50Min_r308s307.bed > ./0vs50Min_r308s308.bed
624.      bedtools shuffle -seed 1 -i 0vs50Min_r308s308.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r309s308.bed
625.      sort -k1,1 -k2,2n ./0vs50Min_r309s308.bed > ./0vs50Min_r309s309.bed
626.      bedtools shuffle -seed 1 -i 0vs50Min_r309s309.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r310s309.bed
627.      sort -k1,1 -k2,2n ./0vs50Min_r310s309.bed > ./0vs50Min_r310s310.bed
628.      bedtools shuffle -seed 1 -i 0vs50Min_r310s310.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r311s310.bed
629.      sort -k1,1 -k2,2n ./0vs50Min_r311s310.bed > ./0vs50Min_r311s311.bed
630.      bedtools shuffle -seed 1 -i 0vs50Min_r311s311.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r312s311.bed
631.      sort -k1,1 -k2,2n ./0vs50Min_r312s311.bed > ./0vs50Min_r312s312.bed
632.      bedtools shuffle -seed 1 -i 0vs50Min_r312s312.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r313s312.bed
633.      sort -k1,1 -k2,2n ./0vs50Min_r313s312.bed > ./0vs50Min_r313s313.bed
634.      bedtools shuffle -seed 1 -i 0vs50Min_r313s313.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r314s313.bed
635.      sort -k1,1 -k2,2n ./0vs50Min_r314s313.bed > ./0vs50Min_r314s314.bed
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636.      bedtools shuffle -seed 1 -i Ovs50Min_r314s314.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r315s314.bed
637.      sort -k1,1 -k2,2n ./Ovs50Min_r315s314.bed > ./Ovs50Min_r315s315.bed
638.      bedtools shuffle -seed 1 -i Ovs50Min_r315s315.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r316s315.bed
639.      sort -k1,1 -k2,2n ./Ovs50Min_r316s315.bed > ./Ovs50Min_r316s316.bed
640.      bedtools shuffle -seed 1 -i Ovs50Min_r316s316.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r317s316.bed
641.      sort -k1,1 -k2,2n ./Ovs50Min_r317s316.bed > ./Ovs50Min_r317s317.bed
642.      bedtools shuffle -seed 1 -i Ovs50Min_r317s317.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r318s317.bed
643.      sort -k1,1 -k2,2n ./Ovs50Min_r318s317.bed > ./Ovs50Min_r318s318.bed
644.      bedtools shuffle -seed 1 -i Ovs50Min_r318s318.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r319s318.bed
645.      sort -k1,1 -k2,2n ./Ovs50Min_r319s318.bed > ./Ovs50Min_r319s319.bed
646.      bedtools shuffle -seed 1 -i Ovs50Min_r319s319.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r320s319.bed
647.      sort -k1,1 -k2,2n ./Ovs50Min_r320s319.bed > ./Ovs50Min_r320s320.bed
648.      bedtools shuffle -seed 1 -i Ovs50Min_r320s320.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r321s320.bed
649.      sort -k1,1 -k2,2n ./Ovs50Min_r321s320.bed > ./Ovs50Min_r321s321.bed
650.      bedtools shuffle -seed 1 -i Ovs50Min_r321s321.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r322s321.bed
651.      sort -k1,1 -k2,2n ./Ovs50Min_r322s321.bed > ./Ovs50Min_r322s322.bed
652.      bedtools shuffle -seed 1 -i Ovs50Min_r322s322.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r323s322.bed
653.      sort -k1,1 -k2,2n ./Ovs50Min_r323s322.bed > ./Ovs50Min_r323s323.bed
654.      bedtools shuffle -seed 1 -i Ovs50Min_r323s323.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r324s323.bed
655.      sort -k1,1 -k2,2n ./Ovs50Min_r324s323.bed > ./Ovs50Min_r324s324.bed
656.      bedtools shuffle -seed 1 -i Ovs50Min_r324s324.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r325s324.bed
657.      sort -k1,1 -k2,2n ./Ovs50Min_r325s324.bed > ./Ovs50Min_r325s325.bed
658.      bedtools shuffle -seed 1 -i Ovs50Min_r325s325.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r326s325.bed
659.      sort -k1,1 -k2,2n ./Ovs50Min_r326s325.bed > ./Ovs50Min_r326s326.bed
660.      bedtools shuffle -seed 1 -i Ovs50Min_r326s326.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r327s326.bed
661.      sort -k1,1 -k2,2n ./Ovs50Min_r327s326.bed > ./Ovs50Min_r327s327.bed
662.      bedtools shuffle -seed 1 -i Ovs50Min_r327s327.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r328s327.bed
663.      sort -k1,1 -k2,2n ./Ovs50Min_r328s327.bed > ./Ovs50Min_r328s328.bed
664.      bedtools shuffle -seed 1 -i Ovs50Min_r328s328.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r329s328.bed
665.      sort -k1,1 -k2,2n ./Ovs50Min_r329s328.bed > ./Ovs50Min_r329s329.bed
666.      bedtools shuffle -seed 1 -i Ovs50Min_r329s329.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r330s329.bed
667.      sort -k1,1 -k2,2n ./Ovs50Min_r330s329.bed > ./Ovs50Min_r330s330.bed
668.      bedtools shuffle -seed 1 -i Ovs50Min_r330s330.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r331s330.bed
669.      sort -k1,1 -k2,2n ./Ovs50Min_r331s330.bed > ./Ovs50Min_r331s331.bed
670.      bedtools shuffle -seed 1 -i Ovs50Min_r331s331.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r332s331.bed
671.      sort -k1,1 -k2,2n ./Ovs50Min_r332s331.bed > ./Ovs50Min_r332s332.bed
672.      bedtools shuffle -seed 1 -i Ovs50Min_r332s332.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r333s332.bed

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673.      sort -k1,1 -k2,2n ./Ovs50Min_r333s332.bed > ./Ovs50Min_r333s333.bed
674.      bedtools shuffle -seed 1 -i Ovs50Min_r333s333.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r334s333.bed
675.      sort -k1,1 -k2,2n ./Ovs50Min_r334s333.bed > ./Ovs50Min_r334s334.bed
676.      bedtools shuffle -seed 1 -i Ovs50Min_r334s334.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r335s334.bed
677.      sort -k1,1 -k2,2n ./Ovs50Min_r335s334.bed > ./Ovs50Min_r335s335.bed
678.      bedtools shuffle -seed 1 -i Ovs50Min_r335s335.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r336s335.bed
679.      sort -k1,1 -k2,2n ./Ovs50Min_r336s335.bed > ./Ovs50Min_r336s336.bed
680.      bedtools shuffle -seed 1 -i Ovs50Min_r336s336.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r337s336.bed
681.      sort -k1,1 -k2,2n ./Ovs50Min_r337s336.bed > ./Ovs50Min_r337s337.bed
682.      bedtools shuffle -seed 1 -i Ovs50Min_r337s337.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r338s337.bed
683.      sort -k1,1 -k2,2n ./Ovs50Min_r338s337.bed > ./Ovs50Min_r338s338.bed
684.      bedtools shuffle -seed 1 -i Ovs50Min_r338s338.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r339s338.bed
685.      sort -k1,1 -k2,2n ./Ovs50Min_r339s338.bed > ./Ovs50Min_r339s339.bed
686.      bedtools shuffle -seed 1 -i Ovs50Min_r339s339.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r340s339.bed
687.      sort -k1,1 -k2,2n ./Ovs50Min_r340s339.bed > ./Ovs50Min_r340s340.bed
688.      bedtools shuffle -seed 1 -i Ovs50Min_r340s340.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r341s340.bed
689.      sort -k1,1 -k2,2n ./Ovs50Min_r341s340.bed > ./Ovs50Min_r341s341.bed
690.      bedtools shuffle -seed 1 -i Ovs50Min_r341s341.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r342s341.bed
691.      sort -k1,1 -k2,2n ./Ovs50Min_r342s341.bed > ./Ovs50Min_r342s342.bed
692.      bedtools shuffle -seed 1 -i Ovs50Min_r342s342.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r343s342.bed
693.      sort -k1,1 -k2,2n ./Ovs50Min_r343s342.bed > ./Ovs50Min_r343s343.bed
694.      bedtools shuffle -seed 1 -i Ovs50Min_r343s343.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r344s343.bed
695.      sort -k1,1 -k2,2n ./Ovs50Min_r344s343.bed > ./Ovs50Min_r344s344.bed
696.      bedtools shuffle -seed 1 -i Ovs50Min_r344s344.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r345s344.bed
697.      sort -k1,1 -k2,2n ./Ovs50Min_r345s344.bed > ./Ovs50Min_r345s345.bed
698.      bedtools shuffle -seed 1 -i Ovs50Min_r345s345.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r346s345.bed
699.      sort -k1,1 -k2,2n ./Ovs50Min_r346s345.bed > ./Ovs50Min_r346s346.bed
700.      bedtools shuffle -seed 1 -i Ovs50Min_r346s346.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r347s346.bed
701.      sort -k1,1 -k2,2n ./Ovs50Min_r347s346.bed > ./Ovs50Min_r347s347.bed
702.      bedtools shuffle -seed 1 -i Ovs50Min_r347s347.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r348s347.bed
703.      sort -k1,1 -k2,2n ./Ovs50Min_r348s347.bed > ./Ovs50Min_r348s348.bed
704.      bedtools shuffle -seed 1 -i Ovs50Min_r348s348.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r349s348.bed
705.      sort -k1,1 -k2,2n ./Ovs50Min_r349s348.bed > ./Ovs50Min_r349s349.bed
706.      bedtools shuffle -seed 1 -i Ovs50Min_r349s349.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r350s349.bed
707.      sort -k1,1 -k2,2n ./Ovs50Min_r350s349.bed > ./Ovs50Min_r350s350.bed
708.      bedtools shuffle -seed 1 -i Ovs50Min_r350s350.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r351s350.bed
709.      sort -k1,1 -k2,2n ./Ovs50Min_r351s350.bed > ./Ovs50Min_r351s351.bed

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710. bedtools shuffle -seed 1 -i Ovs50Min_r351s351.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r352s351.bed
711. sort -k1,1 -k2,2n ./Ovs50Min_r352s351.bed > ./Ovs50Min_r352s352.bed
712. bedtools shuffle -seed 1 -i Ovs50Min_r352s352.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r353s352.bed
713. sort -k1,1 -k2,2n ./Ovs50Min_r353s352.bed > ./Ovs50Min_r353s353.bed
714. bedtools shuffle -seed 1 -i Ovs50Min_r353s353.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r354s353.bed
715. sort -k1,1 -k2,2n ./Ovs50Min_r354s353.bed > ./Ovs50Min_r354s354.bed
716. bedtools shuffle -seed 1 -i Ovs50Min_r354s354.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r355s354.bed
717. sort -k1,1 -k2,2n ./Ovs50Min_r355s354.bed > ./Ovs50Min_r355s355.bed
718. bedtools shuffle -seed 1 -i Ovs50Min_r355s355.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r356s355.bed
719. sort -k1,1 -k2,2n ./Ovs50Min_r356s355.bed > ./Ovs50Min_r356s356.bed
720. bedtools shuffle -seed 1 -i Ovs50Min_r356s356.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r357s356.bed
721. sort -k1,1 -k2,2n ./Ovs50Min_r357s356.bed > ./Ovs50Min_r357s357.bed
722. bedtools shuffle -seed 1 -i Ovs50Min_r357s357.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r358s357.bed
723. sort -k1,1 -k2,2n ./Ovs50Min_r358s357.bed > ./Ovs50Min_r358s358.bed
724. bedtools shuffle -seed 1 -i Ovs50Min_r358s358.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r359s358.bed
725. sort -k1,1 -k2,2n ./Ovs50Min_r359s358.bed > ./Ovs50Min_r359s359.bed
726. bedtools shuffle -seed 1 -i Ovs50Min_r359s359.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r360s359.bed
727. sort -k1,1 -k2,2n ./Ovs50Min_r360s359.bed > ./Ovs50Min_r360s360.bed
728. bedtools shuffle -seed 1 -i Ovs50Min_r360s360.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r361s360.bed
729. sort -k1,1 -k2,2n ./Ovs50Min_r361s360.bed > ./Ovs50Min_r361s361.bed
730. bedtools shuffle -seed 1 -i Ovs50Min_r361s361.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r362s361.bed
731. sort -k1,1 -k2,2n ./Ovs50Min_r362s361.bed > ./Ovs50Min_r362s362.bed
732. bedtools shuffle -seed 1 -i Ovs50Min_r362s362.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r363s362.bed
733. sort -k1,1 -k2,2n ./Ovs50Min_r363s362.bed > ./Ovs50Min_r363s363.bed
734. bedtools shuffle -seed 1 -i Ovs50Min_r363s363.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r364s363.bed
735. sort -k1,1 -k2,2n ./Ovs50Min_r364s363.bed > ./Ovs50Min_r364s364.bed
736. bedtools shuffle -seed 1 -i Ovs50Min_r364s364.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r365s364.bed
737. sort -k1,1 -k2,2n ./Ovs50Min_r365s364.bed > ./Ovs50Min_r365s365.bed
738. bedtools shuffle -seed 1 -i Ovs50Min_r365s365.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r366s365.bed
739. sort -k1,1 -k2,2n ./Ovs50Min_r366s365.bed > ./Ovs50Min_r366s366.bed
740. bedtools shuffle -seed 1 -i Ovs50Min_r366s366.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r367s366.bed
741. sort -k1,1 -k2,2n ./Ovs50Min_r367s366.bed > ./Ovs50Min_r367s367.bed
742. bedtools shuffle -seed 1 -i Ovs50Min_r367s367.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r368s367.bed
743. sort -k1,1 -k2,2n ./Ovs50Min_r368s367.bed > ./Ovs50Min_r368s368.bed
744. bedtools shuffle -seed 1 -i Ovs50Min_r368s368.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r369s368.bed
745. sort -k1,1 -k2,2n ./Ovs50Min_r369s368.bed > ./Ovs50Min_r369s369.bed
746. bedtools shuffle -seed 1 -i Ovs50Min_r369s369.bed -g Ecoli-
    genomesize.txt > ./Ovs50Min_r370s369.bed

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747.      sort -k1,1 -k2,2n ./0vs50Min_r370s369.bed > ./0vs50Min_r370s370.bed
748.      bedtools shuffle -seed 1 -i 0vs50Min_r370s370.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r371s370.bed
749.      sort -k1,1 -k2,2n ./0vs50Min_r371s370.bed > ./0vs50Min_r371s371.bed
750.      bedtools shuffle -seed 1 -i 0vs50Min_r371s371.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r372s371.bed
751.      sort -k1,1 -k2,2n ./0vs50Min_r372s371.bed > ./0vs50Min_r372s372.bed
752.      bedtools shuffle -seed 1 -i 0vs50Min_r372s372.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r373s372.bed
753.      sort -k1,1 -k2,2n ./0vs50Min_r373s372.bed > ./0vs50Min_r373s373.bed
754.      bedtools shuffle -seed 1 -i 0vs50Min_r373s373.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r374s373.bed
755.      sort -k1,1 -k2,2n ./0vs50Min_r374s373.bed > ./0vs50Min_r374s374.bed
756.      bedtools shuffle -seed 1 -i 0vs50Min_r374s374.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r375s374.bed
757.      sort -k1,1 -k2,2n ./0vs50Min_r375s374.bed > ./0vs50Min_r375s375.bed
758.      bedtools shuffle -seed 1 -i 0vs50Min_r375s375.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r376s375.bed
759.      sort -k1,1 -k2,2n ./0vs50Min_r376s375.bed > ./0vs50Min_r376s376.bed
760.      bedtools shuffle -seed 1 -i 0vs50Min_r376s376.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r377s376.bed
761.      sort -k1,1 -k2,2n ./0vs50Min_r377s376.bed > ./0vs50Min_r377s377.bed
762.      bedtools shuffle -seed 1 -i 0vs50Min_r377s377.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r378s377.bed
763.      sort -k1,1 -k2,2n ./0vs50Min_r378s377.bed > ./0vs50Min_r378s378.bed
764.      bedtools shuffle -seed 1 -i 0vs50Min_r378s378.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r379s378.bed
765.      sort -k1,1 -k2,2n ./0vs50Min_r379s378.bed > ./0vs50Min_r379s379.bed
766.      bedtools shuffle -seed 1 -i 0vs50Min_r379s379.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r380s379.bed
767.      sort -k1,1 -k2,2n ./0vs50Min_r380s379.bed > ./0vs50Min_r380s380.bed
768.      bedtools shuffle -seed 1 -i 0vs50Min_r380s380.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r381s380.bed
769.      sort -k1,1 -k2,2n ./0vs50Min_r381s380.bed > ./0vs50Min_r381s381.bed
770.      bedtools shuffle -seed 1 -i 0vs50Min_r381s381.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r382s381.bed
771.      sort -k1,1 -k2,2n ./0vs50Min_r382s381.bed > ./0vs50Min_r382s382.bed
772.      bedtools shuffle -seed 1 -i 0vs50Min_r382s382.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r383s382.bed
773.      sort -k1,1 -k2,2n ./0vs50Min_r383s382.bed > ./0vs50Min_r383s383.bed
774.      bedtools shuffle -seed 1 -i 0vs50Min_r383s383.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r384s383.bed
775.      sort -k1,1 -k2,2n ./0vs50Min_r384s383.bed > ./0vs50Min_r384s384.bed
776.      bedtools shuffle -seed 1 -i 0vs50Min_r384s384.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r385s384.bed
777.      sort -k1,1 -k2,2n ./0vs50Min_r385s384.bed > ./0vs50Min_r385s385.bed
778.      bedtools shuffle -seed 1 -i 0vs50Min_r385s385.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r386s385.bed
779.      sort -k1,1 -k2,2n ./0vs50Min_r386s385.bed > ./0vs50Min_r386s386.bed
780.      bedtools shuffle -seed 1 -i 0vs50Min_r386s386.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r387s386.bed
781.      sort -k1,1 -k2,2n ./0vs50Min_r387s386.bed > ./0vs50Min_r387s387.bed
782.      bedtools shuffle -seed 1 -i 0vs50Min_r387s387.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r388s387.bed
783.      sort -k1,1 -k2,2n ./0vs50Min_r388s387.bed > ./0vs50Min_r388s388.bed

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784.     bedtools shuffle -seed 1 -i Ovs50Min_r388s388.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r389s388.bed
785.     sort -k1,1 -k2,2n ./Ovs50Min_r389s388.bed > ./Ovs50Min_r389s389.bed
786.     bedtools shuffle -seed 1 -i Ovs50Min_r389s389.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r390s389.bed
787.     sort -k1,1 -k2,2n ./Ovs50Min_r390s389.bed > ./Ovs50Min_r390s390.bed
788.     bedtools shuffle -seed 1 -i Ovs50Min_r390s390.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r391s390.bed
789.     sort -k1,1 -k2,2n ./Ovs50Min_r391s390.bed > ./Ovs50Min_r391s391.bed
790.     bedtools shuffle -seed 1 -i Ovs50Min_r391s391.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r392s391.bed
791.     sort -k1,1 -k2,2n ./Ovs50Min_r392s391.bed > ./Ovs50Min_r392s392.bed
792.     bedtools shuffle -seed 1 -i Ovs50Min_r392s392.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r393s392.bed
793.     sort -k1,1 -k2,2n ./Ovs50Min_r393s392.bed > ./Ovs50Min_r393s393.bed
794.     bedtools shuffle -seed 1 -i Ovs50Min_r393s393.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r394s393.bed
795.     sort -k1,1 -k2,2n ./Ovs50Min_r394s393.bed > ./Ovs50Min_r394s394.bed
796.     bedtools shuffle -seed 1 -i Ovs50Min_r394s394.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r395s394.bed
797.     sort -k1,1 -k2,2n ./Ovs50Min_r395s394.bed > ./Ovs50Min_r395s395.bed
798.     bedtools shuffle -seed 1 -i Ovs50Min_r395s395.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r396s395.bed
799.     sort -k1,1 -k2,2n ./Ovs50Min_r396s395.bed > ./Ovs50Min_r396s396.bed
800.     bedtools shuffle -seed 1 -i Ovs50Min_r396s396.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r397s396.bed
801.     sort -k1,1 -k2,2n ./Ovs50Min_r397s396.bed > ./Ovs50Min_r397s397.bed
802.     bedtools shuffle -seed 1 -i Ovs50Min_r397s397.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r398s397.bed
803.     sort -k1,1 -k2,2n ./Ovs50Min_r398s397.bed > ./Ovs50Min_r398s398.bed
804.     bedtools shuffle -seed 1 -i Ovs50Min_r398s398.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r399s398.bed
805.     sort -k1,1 -k2,2n ./Ovs50Min_r399s398.bed > ./Ovs50Min_r399s399.bed
806.     bedtools shuffle -seed 1 -i Ovs50Min_r399s399.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r400s399.bed
807.     sort -k1,1 -k2,2n ./Ovs50Min_r400s399.bed > ./Ovs50Min_r400s400.bed
808.     bedtools shuffle -seed 1 -i Ovs50Min_r400s400.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r401s400.bed
809.     sort -k1,1 -k2,2n ./Ovs50Min_r401s400.bed > ./Ovs50Min_r401s401.bed
810.     bedtools shuffle -seed 1 -i Ovs50Min_r401s401.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r402s401.bed
811.     sort -k1,1 -k2,2n ./Ovs50Min_r402s401.bed > ./Ovs50Min_r402s402.bed
812.     bedtools shuffle -seed 1 -i Ovs50Min_r402s402.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r403s402.bed
813.     sort -k1,1 -k2,2n ./Ovs50Min_r403s402.bed > ./Ovs50Min_r403s403.bed
814.     bedtools shuffle -seed 1 -i Ovs50Min_r403s403.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r404s403.bed
815.     sort -k1,1 -k2,2n ./Ovs50Min_r404s403.bed > ./Ovs50Min_r404s404.bed
816.     bedtools shuffle -seed 1 -i Ovs50Min_r404s404.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r405s404.bed
817.     sort -k1,1 -k2,2n ./Ovs50Min_r405s404.bed > ./Ovs50Min_r405s405.bed
818.     bedtools shuffle -seed 1 -i Ovs50Min_r405s405.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r406s405.bed
819.     sort -k1,1 -k2,2n ./Ovs50Min_r406s405.bed > ./Ovs50Min_r406s406.bed
820.     bedtools shuffle -seed 1 -i Ovs50Min_r406s406.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r407s406.bed

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821.      sort -k1,1 -k2,2n ./Ovs50Min_r407s406.bed > ./Ovs50Min_r407s407.bed
822.      bedtools shuffle -seed 1 -i Ovs50Min_r407s407.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r408s407.bed
823.      sort -k1,1 -k2,2n ./Ovs50Min_r408s407.bed > ./Ovs50Min_r408s408.bed
824.      bedtools shuffle -seed 1 -i Ovs50Min_r408s408.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r409s408.bed
825.      sort -k1,1 -k2,2n ./Ovs50Min_r409s408.bed > ./Ovs50Min_r409s409.bed
826.      bedtools shuffle -seed 1 -i Ovs50Min_r409s409.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r410s409.bed
827.      sort -k1,1 -k2,2n ./Ovs50Min_r410s409.bed > ./Ovs50Min_r410s410.bed
828.      bedtools shuffle -seed 1 -i Ovs50Min_r410s410.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r411s410.bed
829.      sort -k1,1 -k2,2n ./Ovs50Min_r411s410.bed > ./Ovs50Min_r411s411.bed
830.      bedtools shuffle -seed 1 -i Ovs50Min_r411s411.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r412s411.bed
831.      sort -k1,1 -k2,2n ./Ovs50Min_r412s411.bed > ./Ovs50Min_r412s412.bed
832.      bedtools shuffle -seed 1 -i Ovs50Min_r412s412.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r413s412.bed
833.      sort -k1,1 -k2,2n ./Ovs50Min_r413s412.bed > ./Ovs50Min_r413s413.bed
834.      bedtools shuffle -seed 1 -i Ovs50Min_r413s413.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r414s413.bed
835.      sort -k1,1 -k2,2n ./Ovs50Min_r414s413.bed > ./Ovs50Min_r414s414.bed
836.      bedtools shuffle -seed 1 -i Ovs50Min_r414s414.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r415s414.bed
837.      sort -k1,1 -k2,2n ./Ovs50Min_r415s414.bed > ./Ovs50Min_r415s415.bed
838.      bedtools shuffle -seed 1 -i Ovs50Min_r415s415.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r416s415.bed
839.      sort -k1,1 -k2,2n ./Ovs50Min_r416s415.bed > ./Ovs50Min_r416s416.bed
840.      bedtools shuffle -seed 1 -i Ovs50Min_r416s416.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r417s416.bed
841.      sort -k1,1 -k2,2n ./Ovs50Min_r417s416.bed > ./Ovs50Min_r417s417.bed
842.      bedtools shuffle -seed 1 -i Ovs50Min_r417s417.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r418s417.bed
843.      sort -k1,1 -k2,2n ./Ovs50Min_r418s417.bed > ./Ovs50Min_r418s418.bed
844.      bedtools shuffle -seed 1 -i Ovs50Min_r418s418.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r419s418.bed
845.      sort -k1,1 -k2,2n ./Ovs50Min_r419s418.bed > ./Ovs50Min_r419s419.bed
846.      bedtools shuffle -seed 1 -i Ovs50Min_r419s419.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r420s419.bed
847.      sort -k1,1 -k2,2n ./Ovs50Min_r420s419.bed > ./Ovs50Min_r420s420.bed
848.      bedtools shuffle -seed 1 -i Ovs50Min_r420s420.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r421s420.bed
849.      sort -k1,1 -k2,2n ./Ovs50Min_r421s420.bed > ./Ovs50Min_r421s421.bed
850.      bedtools shuffle -seed 1 -i Ovs50Min_r421s421.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r422s421.bed
851.      sort -k1,1 -k2,2n ./Ovs50Min_r422s421.bed > ./Ovs50Min_r422s422.bed
852.      bedtools shuffle -seed 1 -i Ovs50Min_r422s422.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r423s422.bed
853.      sort -k1,1 -k2,2n ./Ovs50Min_r423s422.bed > ./Ovs50Min_r423s423.bed
854.      bedtools shuffle -seed 1 -i Ovs50Min_r423s423.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r424s423.bed
855.      sort -k1,1 -k2,2n ./Ovs50Min_r424s423.bed > ./Ovs50Min_r424s424.bed
856.      bedtools shuffle -seed 1 -i Ovs50Min_r424s424.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r425s424.bed
857.      sort -k1,1 -k2,2n ./Ovs50Min_r425s424.bed > ./Ovs50Min_r425s425.bed
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858.      bedtools shuffle -seed 1 -i Ovs50Min_r425s425.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r426s425.bed
859.      sort -k1,1 -k2,2n ./Ovs50Min_r426s425.bed > ./Ovs50Min_r426s426.bed
860.      bedtools shuffle -seed 1 -i Ovs50Min_r426s426.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r427s426.bed
861.      sort -k1,1 -k2,2n ./Ovs50Min_r427s426.bed > ./Ovs50Min_r427s427.bed
862.      bedtools shuffle -seed 1 -i Ovs50Min_r427s427.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r428s427.bed
863.      sort -k1,1 -k2,2n ./Ovs50Min_r428s427.bed > ./Ovs50Min_r428s428.bed
864.      bedtools shuffle -seed 1 -i Ovs50Min_r428s428.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r429s428.bed
865.      sort -k1,1 -k2,2n ./Ovs50Min_r429s428.bed > ./Ovs50Min_r429s429.bed
866.      bedtools shuffle -seed 1 -i Ovs50Min_r429s429.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r430s429.bed
867.      sort -k1,1 -k2,2n ./Ovs50Min_r430s429.bed > ./Ovs50Min_r430s430.bed
868.      bedtools shuffle -seed 1 -i Ovs50Min_r430s430.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r431s430.bed
869.      sort -k1,1 -k2,2n ./Ovs50Min_r431s430.bed > ./Ovs50Min_r431s431.bed
870.      bedtools shuffle -seed 1 -i Ovs50Min_r431s431.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r432s431.bed
871.      sort -k1,1 -k2,2n ./Ovs50Min_r432s431.bed > ./Ovs50Min_r432s432.bed
872.      bedtools shuffle -seed 1 -i Ovs50Min_r432s432.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r433s432.bed
873.      sort -k1,1 -k2,2n ./Ovs50Min_r433s432.bed > ./Ovs50Min_r433s433.bed
874.      bedtools shuffle -seed 1 -i Ovs50Min_r433s433.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r434s433.bed
875.      sort -k1,1 -k2,2n ./Ovs50Min_r434s433.bed > ./Ovs50Min_r434s434.bed
876.      bedtools shuffle -seed 1 -i Ovs50Min_r434s434.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r435s434.bed
877.      sort -k1,1 -k2,2n ./Ovs50Min_r435s434.bed > ./Ovs50Min_r435s435.bed
878.      bedtools shuffle -seed 1 -i Ovs50Min_r435s435.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r436s435.bed
879.      sort -k1,1 -k2,2n ./Ovs50Min_r436s435.bed > ./Ovs50Min_r436s436.bed
880.      bedtools shuffle -seed 1 -i Ovs50Min_r436s436.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r437s436.bed
881.      sort -k1,1 -k2,2n ./Ovs50Min_r437s436.bed > ./Ovs50Min_r437s437.bed
882.      bedtools shuffle -seed 1 -i Ovs50Min_r437s437.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r438s437.bed
883.      sort -k1,1 -k2,2n ./Ovs50Min_r438s437.bed > ./Ovs50Min_r438s438.bed
884.      bedtools shuffle -seed 1 -i Ovs50Min_r438s438.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r439s438.bed
885.      sort -k1,1 -k2,2n ./Ovs50Min_r439s438.bed > ./Ovs50Min_r439s439.bed
886.      bedtools shuffle -seed 1 -i Ovs50Min_r439s439.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r440s439.bed
887.      sort -k1,1 -k2,2n ./Ovs50Min_r440s439.bed > ./Ovs50Min_r440s440.bed
888.      bedtools shuffle -seed 1 -i Ovs50Min_r440s440.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r441s440.bed
889.      sort -k1,1 -k2,2n ./Ovs50Min_r441s440.bed > ./Ovs50Min_r441s441.bed
890.      bedtools shuffle -seed 1 -i Ovs50Min_r441s441.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r442s441.bed
891.      sort -k1,1 -k2,2n ./Ovs50Min_r442s441.bed > ./Ovs50Min_r442s442.bed
892.      bedtools shuffle -seed 1 -i Ovs50Min_r442s442.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r443s442.bed
893.      sort -k1,1 -k2,2n ./Ovs50Min_r443s442.bed > ./Ovs50Min_r443s443.bed
894.      bedtools shuffle -seed 1 -i Ovs50Min_r443s443.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r444s443.bed

```



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895.      sort -k1,1 -k2,2n ./Ovs50Min_r444s443.bed > ./Ovs50Min_r444s444.bed
896.      bedtools shuffle -seed 1 -i Ovs50Min_r444s444.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r445s444.bed
897.      sort -k1,1 -k2,2n ./Ovs50Min_r445s444.bed > ./Ovs50Min_r445s445.bed
898.      bedtools shuffle -seed 1 -i Ovs50Min_r445s445.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r446s445.bed
899.      sort -k1,1 -k2,2n ./Ovs50Min_r446s445.bed > ./Ovs50Min_r446s446.bed
900.      bedtools shuffle -seed 1 -i Ovs50Min_r446s446.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r447s446.bed
901.      sort -k1,1 -k2,2n ./Ovs50Min_r447s446.bed > ./Ovs50Min_r447s447.bed
902.      bedtools shuffle -seed 1 -i Ovs50Min_r447s447.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r448s447.bed
903.      sort -k1,1 -k2,2n ./Ovs50Min_r448s447.bed > ./Ovs50Min_r448s448.bed
904.      bedtools shuffle -seed 1 -i Ovs50Min_r448s448.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r449s448.bed
905.      sort -k1,1 -k2,2n ./Ovs50Min_r449s448.bed > ./Ovs50Min_r449s449.bed
906.      bedtools shuffle -seed 1 -i Ovs50Min_r449s449.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r450s449.bed
907.      sort -k1,1 -k2,2n ./Ovs50Min_r450s449.bed > ./Ovs50Min_r450s450.bed
908.      bedtools shuffle -seed 1 -i Ovs50Min_r450s450.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r451s450.bed
909.      sort -k1,1 -k2,2n ./Ovs50Min_r451s450.bed > ./Ovs50Min_r451s451.bed
910.      bedtools shuffle -seed 1 -i Ovs50Min_r451s451.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r452s451.bed
911.      sort -k1,1 -k2,2n ./Ovs50Min_r452s451.bed > ./Ovs50Min_r452s452.bed
912.      bedtools shuffle -seed 1 -i Ovs50Min_r452s452.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r453s452.bed
913.      sort -k1,1 -k2,2n ./Ovs50Min_r453s452.bed > ./Ovs50Min_r453s453.bed
914.      bedtools shuffle -seed 1 -i Ovs50Min_r453s453.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r454s453.bed
915.      sort -k1,1 -k2,2n ./Ovs50Min_r454s453.bed > ./Ovs50Min_r454s454.bed
916.      bedtools shuffle -seed 1 -i Ovs50Min_r454s454.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r455s454.bed
917.      sort -k1,1 -k2,2n ./Ovs50Min_r455s454.bed > ./Ovs50Min_r455s455.bed
918.      bedtools shuffle -seed 1 -i Ovs50Min_r455s455.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r456s455.bed
919.      sort -k1,1 -k2,2n ./Ovs50Min_r456s455.bed > ./Ovs50Min_r456s456.bed
920.      bedtools shuffle -seed 1 -i Ovs50Min_r456s456.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r457s456.bed
921.      sort -k1,1 -k2,2n ./Ovs50Min_r457s456.bed > ./Ovs50Min_r457s457.bed
922.      bedtools shuffle -seed 1 -i Ovs50Min_r457s457.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r458s457.bed
923.      sort -k1,1 -k2,2n ./Ovs50Min_r458s457.bed > ./Ovs50Min_r458s458.bed
924.      bedtools shuffle -seed 1 -i Ovs50Min_r458s458.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r459s458.bed
925.      sort -k1,1 -k2,2n ./Ovs50Min_r459s458.bed > ./Ovs50Min_r459s459.bed
926.      bedtools shuffle -seed 1 -i Ovs50Min_r459s459.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r460s459.bed
927.      sort -k1,1 -k2,2n ./Ovs50Min_r460s459.bed > ./Ovs50Min_r460s460.bed
928.      bedtools shuffle -seed 1 -i Ovs50Min_r460s460.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r461s460.bed
929.      sort -k1,1 -k2,2n ./Ovs50Min_r461s460.bed > ./Ovs50Min_r461s461.bed
930.      bedtools shuffle -seed 1 -i Ovs50Min_r461s461.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r462s461.bed
931.      sort -k1,1 -k2,2n ./Ovs50Min_r462s461.bed > ./Ovs50Min_r462s462.bed
```

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932.      bedtools shuffle -seed 1 -i Ovs50Min_r462s462.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r463s462.bed
933.      sort -k1,1 -k2,2n ./Ovs50Min_r463s462.bed > ./Ovs50Min_r463s463.bed
934.      bedtools shuffle -seed 1 -i Ovs50Min_r463s463.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r464s463.bed
935.      sort -k1,1 -k2,2n ./Ovs50Min_r464s463.bed > ./Ovs50Min_r464s464.bed
936.      bedtools shuffle -seed 1 -i Ovs50Min_r464s464.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r465s464.bed
937.      sort -k1,1 -k2,2n ./Ovs50Min_r465s464.bed > ./Ovs50Min_r465s465.bed
938.      bedtools shuffle -seed 1 -i Ovs50Min_r465s465.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r466s465.bed
939.      sort -k1,1 -k2,2n ./Ovs50Min_r466s465.bed > ./Ovs50Min_r466s466.bed
940.      bedtools shuffle -seed 1 -i Ovs50Min_r466s466.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r467s466.bed
941.      sort -k1,1 -k2,2n ./Ovs50Min_r467s466.bed > ./Ovs50Min_r467s467.bed
942.      bedtools shuffle -seed 1 -i Ovs50Min_r467s467.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r468s467.bed
943.      sort -k1,1 -k2,2n ./Ovs50Min_r468s467.bed > ./Ovs50Min_r468s468.bed
944.      bedtools shuffle -seed 1 -i Ovs50Min_r468s468.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r469s468.bed
945.      sort -k1,1 -k2,2n ./Ovs50Min_r469s468.bed > ./Ovs50Min_r469s469.bed
946.      bedtools shuffle -seed 1 -i Ovs50Min_r469s469.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r470s469.bed
947.      sort -k1,1 -k2,2n ./Ovs50Min_r470s469.bed > ./Ovs50Min_r470s470.bed
948.      bedtools shuffle -seed 1 -i Ovs50Min_r470s470.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r471s470.bed
949.      sort -k1,1 -k2,2n ./Ovs50Min_r471s470.bed > ./Ovs50Min_r471s471.bed
950.      bedtools shuffle -seed 1 -i Ovs50Min_r471s471.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r472s471.bed
951.      sort -k1,1 -k2,2n ./Ovs50Min_r472s471.bed > ./Ovs50Min_r472s472.bed
952.      bedtools shuffle -seed 1 -i Ovs50Min_r472s472.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r473s472.bed
953.      sort -k1,1 -k2,2n ./Ovs50Min_r473s472.bed > ./Ovs50Min_r473s473.bed
954.      bedtools shuffle -seed 1 -i Ovs50Min_r473s473.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r474s473.bed
955.      sort -k1,1 -k2,2n ./Ovs50Min_r474s473.bed > ./Ovs50Min_r474s474.bed
956.      bedtools shuffle -seed 1 -i Ovs50Min_r474s474.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r475s474.bed
957.      sort -k1,1 -k2,2n ./Ovs50Min_r475s474.bed > ./Ovs50Min_r475s475.bed
958.      bedtools shuffle -seed 1 -i Ovs50Min_r475s475.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r476s475.bed
959.      sort -k1,1 -k2,2n ./Ovs50Min_r476s475.bed > ./Ovs50Min_r476s476.bed
960.      bedtools shuffle -seed 1 -i Ovs50Min_r476s476.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r477s476.bed
961.      sort -k1,1 -k2,2n ./Ovs50Min_r477s476.bed > ./Ovs50Min_r477s477.bed
962.      bedtools shuffle -seed 1 -i Ovs50Min_r477s477.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r478s477.bed
963.      sort -k1,1 -k2,2n ./Ovs50Min_r478s477.bed > ./Ovs50Min_r478s478.bed
964.      bedtools shuffle -seed 1 -i Ovs50Min_r478s478.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r479s478.bed
965.      sort -k1,1 -k2,2n ./Ovs50Min_r479s478.bed > ./Ovs50Min_r479s479.bed
966.      bedtools shuffle -seed 1 -i Ovs50Min_r479s479.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r480s479.bed
967.      sort -k1,1 -k2,2n ./Ovs50Min_r480s479.bed > ./Ovs50Min_r480s480.bed
968.      bedtools shuffle -seed 1 -i Ovs50Min_r480s480.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r481s480.bed

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969.      sort -k1,1 -k2,2n ./Ovs50Min_r481s480.bed > ./Ovs50Min_r481s481.bed
970.      bedtools shuffle -seed 1 -i Ovs50Min_r481s481.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r482s481.bed
971.      sort -k1,1 -k2,2n ./Ovs50Min_r482s481.bed > ./Ovs50Min_r482s482.bed
972.      bedtools shuffle -seed 1 -i Ovs50Min_r482s482.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r483s482.bed
973.      sort -k1,1 -k2,2n ./Ovs50Min_r483s482.bed > ./Ovs50Min_r483s483.bed
974.      bedtools shuffle -seed 1 -i Ovs50Min_r483s483.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r484s483.bed
975.      sort -k1,1 -k2,2n ./Ovs50Min_r484s483.bed > ./Ovs50Min_r484s484.bed
976.      bedtools shuffle -seed 1 -i Ovs50Min_r484s484.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r485s484.bed
977.      sort -k1,1 -k2,2n ./Ovs50Min_r485s484.bed > ./Ovs50Min_r485s485.bed
978.      bedtools shuffle -seed 1 -i Ovs50Min_r485s485.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r486s485.bed
979.      sort -k1,1 -k2,2n ./Ovs50Min_r486s485.bed > ./Ovs50Min_r486s486.bed
980.      bedtools shuffle -seed 1 -i Ovs50Min_r486s486.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r487s486.bed
981.      sort -k1,1 -k2,2n ./Ovs50Min_r487s486.bed > ./Ovs50Min_r487s487.bed
982.      bedtools shuffle -seed 1 -i Ovs50Min_r487s487.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r488s487.bed
983.      sort -k1,1 -k2,2n ./Ovs50Min_r488s487.bed > ./Ovs50Min_r488s488.bed
984.      bedtools shuffle -seed 1 -i Ovs50Min_r488s488.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r489s488.bed
985.      sort -k1,1 -k2,2n ./Ovs50Min_r489s488.bed > ./Ovs50Min_r489s489.bed
986.      bedtools shuffle -seed 1 -i Ovs50Min_r489s489.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r490s489.bed
987.      sort -k1,1 -k2,2n ./Ovs50Min_r490s489.bed > ./Ovs50Min_r490s490.bed
988.      bedtools shuffle -seed 1 -i Ovs50Min_r490s490.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r491s490.bed
989.      sort -k1,1 -k2,2n ./Ovs50Min_r491s490.bed > ./Ovs50Min_r491s491.bed
990.      bedtools shuffle -seed 1 -i Ovs50Min_r491s491.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r492s491.bed
991.      sort -k1,1 -k2,2n ./Ovs50Min_r492s491.bed > ./Ovs50Min_r492s492.bed
992.      bedtools shuffle -seed 1 -i Ovs50Min_r492s492.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r493s492.bed
993.      sort -k1,1 -k2,2n ./Ovs50Min_r493s492.bed > ./Ovs50Min_r493s493.bed
994.      bedtools shuffle -seed 1 -i Ovs50Min_r493s493.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r494s493.bed
995.      sort -k1,1 -k2,2n ./Ovs50Min_r494s493.bed > ./Ovs50Min_r494s494.bed
996.      bedtools shuffle -seed 1 -i Ovs50Min_r494s494.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r495s494.bed
997.      sort -k1,1 -k2,2n ./Ovs50Min_r495s494.bed > ./Ovs50Min_r495s495.bed
998.      bedtools shuffle -seed 1 -i Ovs50Min_r495s495.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r496s495.bed
999.      sort -k1,1 -k2,2n ./Ovs50Min_r496s495.bed > ./Ovs50Min_r496s496.bed
1000.     bedtools shuffle -seed 1 -i Ovs50Min_r496s496.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r497s496.bed
1001.     sort -k1,1 -k2,2n ./Ovs50Min_r497s496.bed > ./Ovs50Min_r497s497.bed
1002.     bedtools shuffle -seed 1 -i Ovs50Min_r497s497.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r498s497.bed
1003.     sort -k1,1 -k2,2n ./Ovs50Min_r498s497.bed > ./Ovs50Min_r498s498.bed
1004.     bedtools shuffle -seed 1 -i Ovs50Min_r498s498.bed -g Ecoli-
          genomesize.txt > ./Ovs50Min_r499s498.bed
1005.     sort -k1,1 -k2,2n ./Ovs50Min_r499s498.bed > ./Ovs50Min_r499s499.bed
```

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1006. bedtools shuffle -seed 1 -i Ovs50Min_r499s499.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r500s499.bed
1007. sort -k1,1 -k2,2n ./Ovs50Min_r500s499.bed > ./Ovs50Min_r500s500.bed
1008. bedtools shuffle -seed 1 -i Ovs50Min_r500s500.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r501s500.bed
1009. sort -k1,1 -k2,2n ./Ovs50Min_r501s500.bed > ./Ovs50Min_r501s501.bed
1010. bedtools shuffle -seed 1 -i Ovs50Min_r501s501.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r502s501.bed
1011. sort -k1,1 -k2,2n ./Ovs50Min_r502s501.bed > ./Ovs50Min_r502s502.bed
1012. bedtools shuffle -seed 1 -i Ovs50Min_r502s502.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r503s502.bed
1013. sort -k1,1 -k2,2n ./Ovs50Min_r503s502.bed > ./Ovs50Min_r503s503.bed
1014. bedtools shuffle -seed 1 -i Ovs50Min_r503s503.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r504s503.bed
1015. sort -k1,1 -k2,2n ./Ovs50Min_r504s503.bed > ./Ovs50Min_r504s504.bed
1016. bedtools shuffle -seed 1 -i Ovs50Min_r504s504.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r505s504.bed
1017. sort -k1,1 -k2,2n ./Ovs50Min_r505s504.bed > ./Ovs50Min_r505s505.bed
1018. bedtools shuffle -seed 1 -i Ovs50Min_r505s505.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r506s505.bed
1019. sort -k1,1 -k2,2n ./Ovs50Min_r506s505.bed > ./Ovs50Min_r506s506.bed
1020. bedtools shuffle -seed 1 -i Ovs50Min_r506s506.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r507s506.bed
1021. sort -k1,1 -k2,2n ./Ovs50Min_r507s506.bed > ./Ovs50Min_r507s507.bed
1022. bedtools shuffle -seed 1 -i Ovs50Min_r507s507.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r508s507.bed
1023. sort -k1,1 -k2,2n ./Ovs50Min_r508s507.bed > ./Ovs50Min_r508s508.bed
1024. bedtools shuffle -seed 1 -i Ovs50Min_r508s508.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r509s508.bed
1025. sort -k1,1 -k2,2n ./Ovs50Min_r509s508.bed > ./Ovs50Min_r509s509.bed
1026. bedtools shuffle -seed 1 -i Ovs50Min_r509s509.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r510s509.bed
1027. sort -k1,1 -k2,2n ./Ovs50Min_r510s509.bed > ./Ovs50Min_r510s510.bed
1028. bedtools shuffle -seed 1 -i Ovs50Min_r510s510.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r511s510.bed
1029. sort -k1,1 -k2,2n ./Ovs50Min_r511s510.bed > ./Ovs50Min_r511s511.bed
1030. bedtools shuffle -seed 1 -i Ovs50Min_r511s511.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r512s511.bed
1031. sort -k1,1 -k2,2n ./Ovs50Min_r512s511.bed > ./Ovs50Min_r512s512.bed
1032. bedtools shuffle -seed 1 -i Ovs50Min_r512s512.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r513s512.bed
1033. sort -k1,1 -k2,2n ./Ovs50Min_r513s512.bed > ./Ovs50Min_r513s513.bed
1034. bedtools shuffle -seed 1 -i Ovs50Min_r513s513.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r514s513.bed
1035. sort -k1,1 -k2,2n ./Ovs50Min_r514s513.bed > ./Ovs50Min_r514s514.bed
1036. bedtools shuffle -seed 1 -i Ovs50Min_r514s514.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r515s514.bed
1037. sort -k1,1 -k2,2n ./Ovs50Min_r515s514.bed > ./Ovs50Min_r515s515.bed
1038. bedtools shuffle -seed 1 -i Ovs50Min_r515s515.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r516s515.bed
1039. sort -k1,1 -k2,2n ./Ovs50Min_r516s515.bed > ./Ovs50Min_r516s516.bed
1040. bedtools shuffle -seed 1 -i Ovs50Min_r516s516.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r517s516.bed
1041. sort -k1,1 -k2,2n ./Ovs50Min_r517s516.bed > ./Ovs50Min_r517s517.bed
1042. bedtools shuffle -seed 1 -i Ovs50Min_r517s517.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r518s517.bed

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1043.    sort -k1,1 -k2,2n ./Ovs50Min_r518s517.bed > ./Ovs50Min_r518s518.bed
1044.    bedtools shuffle -seed 1 -i Ovs50Min_r518s518.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r519s518.bed
1045.    sort -k1,1 -k2,2n ./Ovs50Min_r519s518.bed > ./Ovs50Min_r519s519.bed
1046.    bedtools shuffle -seed 1 -i Ovs50Min_r519s519.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r520s519.bed
1047.    sort -k1,1 -k2,2n ./Ovs50Min_r520s519.bed > ./Ovs50Min_r520s520.bed
1048.    bedtools shuffle -seed 1 -i Ovs50Min_r520s520.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r521s520.bed
1049.    sort -k1,1 -k2,2n ./Ovs50Min_r521s520.bed > ./Ovs50Min_r521s521.bed
1050.    bedtools shuffle -seed 1 -i Ovs50Min_r521s521.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r522s521.bed
1051.    sort -k1,1 -k2,2n ./Ovs50Min_r522s521.bed > ./Ovs50Min_r522s522.bed
1052.    bedtools shuffle -seed 1 -i Ovs50Min_r522s522.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r523s522.bed
1053.    sort -k1,1 -k2,2n ./Ovs50Min_r523s522.bed > ./Ovs50Min_r523s523.bed
1054.    bedtools shuffle -seed 1 -i Ovs50Min_r523s523.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r524s523.bed
1055.    sort -k1,1 -k2,2n ./Ovs50Min_r524s523.bed > ./Ovs50Min_r524s524.bed
1056.    bedtools shuffle -seed 1 -i Ovs50Min_r524s524.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r525s524.bed
1057.    sort -k1,1 -k2,2n ./Ovs50Min_r525s524.bed > ./Ovs50Min_r525s525.bed
1058.    bedtools shuffle -seed 1 -i Ovs50Min_r525s525.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r526s525.bed
1059.    sort -k1,1 -k2,2n ./Ovs50Min_r526s525.bed > ./Ovs50Min_r526s526.bed
1060.    bedtools shuffle -seed 1 -i Ovs50Min_r526s526.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r527s526.bed
1061.    sort -k1,1 -k2,2n ./Ovs50Min_r527s526.bed > ./Ovs50Min_r527s527.bed
1062.    bedtools shuffle -seed 1 -i Ovs50Min_r527s527.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r528s527.bed
1063.    sort -k1,1 -k2,2n ./Ovs50Min_r528s527.bed > ./Ovs50Min_r528s528.bed
1064.    bedtools shuffle -seed 1 -i Ovs50Min_r528s528.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r529s528.bed
1065.    sort -k1,1 -k2,2n ./Ovs50Min_r529s528.bed > ./Ovs50Min_r529s529.bed
1066.    bedtools shuffle -seed 1 -i Ovs50Min_r529s529.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r530s529.bed
1067.    sort -k1,1 -k2,2n ./Ovs50Min_r530s529.bed > ./Ovs50Min_r530s530.bed
1068.    bedtools shuffle -seed 1 -i Ovs50Min_r530s530.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r531s530.bed
1069.    sort -k1,1 -k2,2n ./Ovs50Min_r531s530.bed > ./Ovs50Min_r531s531.bed
1070.    bedtools shuffle -seed 1 -i Ovs50Min_r531s531.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r532s531.bed
1071.    sort -k1,1 -k2,2n ./Ovs50Min_r532s531.bed > ./Ovs50Min_r532s532.bed
1072.    bedtools shuffle -seed 1 -i Ovs50Min_r532s532.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r533s532.bed
1073.    sort -k1,1 -k2,2n ./Ovs50Min_r533s532.bed > ./Ovs50Min_r533s533.bed
1074.    bedtools shuffle -seed 1 -i Ovs50Min_r533s533.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r534s533.bed
1075.    sort -k1,1 -k2,2n ./Ovs50Min_r534s533.bed > ./Ovs50Min_r534s534.bed
1076.    bedtools shuffle -seed 1 -i Ovs50Min_r534s534.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r535s534.bed
1077.    sort -k1,1 -k2,2n ./Ovs50Min_r535s534.bed > ./Ovs50Min_r535s535.bed
1078.    bedtools shuffle -seed 1 -i Ovs50Min_r535s535.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r536s535.bed
1079.    sort -k1,1 -k2,2n ./Ovs50Min_r536s535.bed > ./Ovs50Min_r536s536.bed

```

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1080. bedtools shuffle -seed 1 -i Ovs50Min_r536s536.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r537s536.bed
1081. sort -k1,1 -k2,2n ./Ovs50Min_r537s536.bed > ./Ovs50Min_r537s537.bed
1082. bedtools shuffle -seed 1 -i Ovs50Min_r537s537.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r538s537.bed
1083. sort -k1,1 -k2,2n ./Ovs50Min_r538s537.bed > ./Ovs50Min_r538s538.bed
1084. bedtools shuffle -seed 1 -i Ovs50Min_r538s538.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r539s538.bed
1085. sort -k1,1 -k2,2n ./Ovs50Min_r539s538.bed > ./Ovs50Min_r539s539.bed
1086. bedtools shuffle -seed 1 -i Ovs50Min_r539s539.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r540s539.bed
1087. sort -k1,1 -k2,2n ./Ovs50Min_r540s539.bed > ./Ovs50Min_r540s540.bed
1088. bedtools shuffle -seed 1 -i Ovs50Min_r540s540.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r541s540.bed
1089. sort -k1,1 -k2,2n ./Ovs50Min_r541s540.bed > ./Ovs50Min_r541s541.bed
1090. bedtools shuffle -seed 1 -i Ovs50Min_r541s541.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r542s541.bed
1091. sort -k1,1 -k2,2n ./Ovs50Min_r542s541.bed > ./Ovs50Min_r542s542.bed
1092. bedtools shuffle -seed 1 -i Ovs50Min_r542s542.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r543s542.bed
1093. sort -k1,1 -k2,2n ./Ovs50Min_r543s542.bed > ./Ovs50Min_r543s543.bed
1094. bedtools shuffle -seed 1 -i Ovs50Min_r543s543.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r544s543.bed
1095. sort -k1,1 -k2,2n ./Ovs50Min_r544s543.bed > ./Ovs50Min_r544s544.bed
1096. bedtools shuffle -seed 1 -i Ovs50Min_r544s544.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r545s544.bed
1097. sort -k1,1 -k2,2n ./Ovs50Min_r545s544.bed > ./Ovs50Min_r545s545.bed
1098. bedtools shuffle -seed 1 -i Ovs50Min_r545s545.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r546s545.bed
1099. sort -k1,1 -k2,2n ./Ovs50Min_r546s545.bed > ./Ovs50Min_r546s546.bed
1100. bedtools shuffle -seed 1 -i Ovs50Min_r546s546.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r547s546.bed
1101. sort -k1,1 -k2,2n ./Ovs50Min_r547s546.bed > ./Ovs50Min_r547s547.bed
1102. bedtools shuffle -seed 1 -i Ovs50Min_r547s547.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r548s547.bed
1103. sort -k1,1 -k2,2n ./Ovs50Min_r548s547.bed > ./Ovs50Min_r548s548.bed
1104. bedtools shuffle -seed 1 -i Ovs50Min_r548s548.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r549s548.bed
1105. sort -k1,1 -k2,2n ./Ovs50Min_r549s548.bed > ./Ovs50Min_r549s549.bed
1106. bedtools shuffle -seed 1 -i Ovs50Min_r549s549.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r550s549.bed
1107. sort -k1,1 -k2,2n ./Ovs50Min_r550s549.bed > ./Ovs50Min_r550s550.bed
1108. bedtools shuffle -seed 1 -i Ovs50Min_r550s550.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r551s550.bed
1109. sort -k1,1 -k2,2n ./Ovs50Min_r551s550.bed > ./Ovs50Min_r551s551.bed
1110. bedtools shuffle -seed 1 -i Ovs50Min_r551s551.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r552s551.bed
1111. sort -k1,1 -k2,2n ./Ovs50Min_r552s551.bed > ./Ovs50Min_r552s552.bed
1112. bedtools shuffle -seed 1 -i Ovs50Min_r552s552.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r553s552.bed
1113. sort -k1,1 -k2,2n ./Ovs50Min_r553s552.bed > ./Ovs50Min_r553s553.bed
1114. bedtools shuffle -seed 1 -i Ovs50Min_r553s553.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r554s553.bed
1115. sort -k1,1 -k2,2n ./Ovs50Min_r554s553.bed > ./Ovs50Min_r554s554.bed
1116. bedtools shuffle -seed 1 -i Ovs50Min_r554s554.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r555s554.bed

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1117.    sort -k1,1 -k2,2n ./Ovs50Min_r555s554.bed > ./Ovs50Min_r555s555.bed
1118.    bedtools shuffle -seed 1 -i Ovs50Min_r555s555.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r556s555.bed
1119.    sort -k1,1 -k2,2n ./Ovs50Min_r556s555.bed > ./Ovs50Min_r556s556.bed
1120.    bedtools shuffle -seed 1 -i Ovs50Min_r556s556.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r557s556.bed
1121.    sort -k1,1 -k2,2n ./Ovs50Min_r557s556.bed > ./Ovs50Min_r557s557.bed
1122.    bedtools shuffle -seed 1 -i Ovs50Min_r557s557.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r558s557.bed
1123.    sort -k1,1 -k2,2n ./Ovs50Min_r558s557.bed > ./Ovs50Min_r558s558.bed
1124.    bedtools shuffle -seed 1 -i Ovs50Min_r558s558.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r559s558.bed
1125.    sort -k1,1 -k2,2n ./Ovs50Min_r559s558.bed > ./Ovs50Min_r559s559.bed
1126.    bedtools shuffle -seed 1 -i Ovs50Min_r559s559.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r560s559.bed
1127.    sort -k1,1 -k2,2n ./Ovs50Min_r560s559.bed > ./Ovs50Min_r560s560.bed
1128.    bedtools shuffle -seed 1 -i Ovs50Min_r560s560.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r561s560.bed
1129.    sort -k1,1 -k2,2n ./Ovs50Min_r561s560.bed > ./Ovs50Min_r561s561.bed
1130.    bedtools shuffle -seed 1 -i Ovs50Min_r561s561.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r562s561.bed
1131.    sort -k1,1 -k2,2n ./Ovs50Min_r562s561.bed > ./Ovs50Min_r562s562.bed
1132.    bedtools shuffle -seed 1 -i Ovs50Min_r562s562.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r563s562.bed
1133.    sort -k1,1 -k2,2n ./Ovs50Min_r563s562.bed > ./Ovs50Min_r563s563.bed
1134.    bedtools shuffle -seed 1 -i Ovs50Min_r563s563.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r564s563.bed
1135.    sort -k1,1 -k2,2n ./Ovs50Min_r564s563.bed > ./Ovs50Min_r564s564.bed
1136.    bedtools shuffle -seed 1 -i Ovs50Min_r564s564.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r565s564.bed
1137.    sort -k1,1 -k2,2n ./Ovs50Min_r565s564.bed > ./Ovs50Min_r565s565.bed
1138.    bedtools shuffle -seed 1 -i Ovs50Min_r565s565.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r566s565.bed
1139.    sort -k1,1 -k2,2n ./Ovs50Min_r566s565.bed > ./Ovs50Min_r566s566.bed
1140.    bedtools shuffle -seed 1 -i Ovs50Min_r566s566.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r567s566.bed
1141.    sort -k1,1 -k2,2n ./Ovs50Min_r567s566.bed > ./Ovs50Min_r567s567.bed
1142.    bedtools shuffle -seed 1 -i Ovs50Min_r567s567.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r568s567.bed
1143.    sort -k1,1 -k2,2n ./Ovs50Min_r568s567.bed > ./Ovs50Min_r568s568.bed
1144.    bedtools shuffle -seed 1 -i Ovs50Min_r568s568.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r569s568.bed
1145.    sort -k1,1 -k2,2n ./Ovs50Min_r569s568.bed > ./Ovs50Min_r569s569.bed
1146.    bedtools shuffle -seed 1 -i Ovs50Min_r569s569.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r570s569.bed
1147.    sort -k1,1 -k2,2n ./Ovs50Min_r570s569.bed > ./Ovs50Min_r570s570.bed
1148.    bedtools shuffle -seed 1 -i Ovs50Min_r570s570.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r571s570.bed
1149.    sort -k1,1 -k2,2n ./Ovs50Min_r571s570.bed > ./Ovs50Min_r571s571.bed
1150.    bedtools shuffle -seed 1 -i Ovs50Min_r571s571.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r572s571.bed
1151.    sort -k1,1 -k2,2n ./Ovs50Min_r572s571.bed > ./Ovs50Min_r572s572.bed
1152.    bedtools shuffle -seed 1 -i Ovs50Min_r572s572.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r573s572.bed
1153.    sort -k1,1 -k2,2n ./Ovs50Min_r573s572.bed > ./Ovs50Min_r573s573.bed

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1154. bedtools shuffle -seed 1 -i Ovs50Min_r573s573.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r574s573.bed
1155. sort -k1,1 -k2,2n ./Ovs50Min_r574s573.bed > ./Ovs50Min_r574s574.bed
1156. bedtools shuffle -seed 1 -i Ovs50Min_r574s574.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r575s574.bed
1157. sort -k1,1 -k2,2n ./Ovs50Min_r575s574.bed > ./Ovs50Min_r575s575.bed
1158. bedtools shuffle -seed 1 -i Ovs50Min_r575s575.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r576s575.bed
1159. sort -k1,1 -k2,2n ./Ovs50Min_r576s575.bed > ./Ovs50Min_r576s576.bed
1160. bedtools shuffle -seed 1 -i Ovs50Min_r576s576.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r577s576.bed
1161. sort -k1,1 -k2,2n ./Ovs50Min_r577s576.bed > ./Ovs50Min_r577s577.bed
1162. bedtools shuffle -seed 1 -i Ovs50Min_r577s577.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r578s577.bed
1163. sort -k1,1 -k2,2n ./Ovs50Min_r578s577.bed > ./Ovs50Min_r578s578.bed
1164. bedtools shuffle -seed 1 -i Ovs50Min_r578s578.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r579s578.bed
1165. sort -k1,1 -k2,2n ./Ovs50Min_r579s578.bed > ./Ovs50Min_r579s579.bed
1166. bedtools shuffle -seed 1 -i Ovs50Min_r579s579.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r580s579.bed
1167. sort -k1,1 -k2,2n ./Ovs50Min_r580s579.bed > ./Ovs50Min_r580s580.bed
1168. bedtools shuffle -seed 1 -i Ovs50Min_r580s580.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r581s580.bed
1169. sort -k1,1 -k2,2n ./Ovs50Min_r581s580.bed > ./Ovs50Min_r581s581.bed
1170. bedtools shuffle -seed 1 -i Ovs50Min_r581s581.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r582s581.bed
1171. sort -k1,1 -k2,2n ./Ovs50Min_r582s581.bed > ./Ovs50Min_r582s582.bed
1172. bedtools shuffle -seed 1 -i Ovs50Min_r582s582.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r583s582.bed
1173. sort -k1,1 -k2,2n ./Ovs50Min_r583s582.bed > ./Ovs50Min_r583s583.bed
1174. bedtools shuffle -seed 1 -i Ovs50Min_r583s583.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r584s583.bed
1175. sort -k1,1 -k2,2n ./Ovs50Min_r584s583.bed > ./Ovs50Min_r584s584.bed
1176. bedtools shuffle -seed 1 -i Ovs50Min_r584s584.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r585s584.bed
1177. sort -k1,1 -k2,2n ./Ovs50Min_r585s584.bed > ./Ovs50Min_r585s585.bed
1178. bedtools shuffle -seed 1 -i Ovs50Min_r585s585.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r586s585.bed
1179. sort -k1,1 -k2,2n ./Ovs50Min_r586s585.bed > ./Ovs50Min_r586s586.bed
1180. bedtools shuffle -seed 1 -i Ovs50Min_r586s586.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r587s586.bed
1181. sort -k1,1 -k2,2n ./Ovs50Min_r587s586.bed > ./Ovs50Min_r587s587.bed
1182. bedtools shuffle -seed 1 -i Ovs50Min_r587s587.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r588s587.bed
1183. sort -k1,1 -k2,2n ./Ovs50Min_r588s587.bed > ./Ovs50Min_r588s588.bed
1184. bedtools shuffle -seed 1 -i Ovs50Min_r588s588.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r589s588.bed
1185. sort -k1,1 -k2,2n ./Ovs50Min_r589s588.bed > ./Ovs50Min_r589s589.bed
1186. bedtools shuffle -seed 1 -i Ovs50Min_r589s589.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r590s589.bed
1187. sort -k1,1 -k2,2n ./Ovs50Min_r590s589.bed > ./Ovs50Min_r590s590.bed
1188. bedtools shuffle -seed 1 -i Ovs50Min_r590s590.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r591s590.bed
1189. sort -k1,1 -k2,2n ./Ovs50Min_r591s590.bed > ./Ovs50Min_r591s591.bed
1190. bedtools shuffle -seed 1 -i Ovs50Min_r591s591.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r592s591.bed

1191. sort -k1,1 -k2,2n ./0vs50Min_r592s591.bed > ./0vs50Min_r592s592.bed
1192. bedtools shuffle -seed 1 -i 0vs50Min_r592s592.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r593s592.bed
1193. sort -k1,1 -k2,2n ./0vs50Min_r593s592.bed > ./0vs50Min_r593s593.bed
1194. bedtools shuffle -seed 1 -i 0vs50Min_r593s593.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r594s593.bed
1195. sort -k1,1 -k2,2n ./0vs50Min_r594s593.bed > ./0vs50Min_r594s594.bed
1196. bedtools shuffle -seed 1 -i 0vs50Min_r594s594.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r595s594.bed
1197. sort -k1,1 -k2,2n ./0vs50Min_r595s594.bed > ./0vs50Min_r595s595.bed
1198. bedtools shuffle -seed 1 -i 0vs50Min_r595s595.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r596s595.bed
1199. sort -k1,1 -k2,2n ./0vs50Min_r596s595.bed > ./0vs50Min_r596s596.bed
1200. bedtools shuffle -seed 1 -i 0vs50Min_r596s596.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r597s596.bed
1201. sort -k1,1 -k2,2n ./0vs50Min_r597s596.bed > ./0vs50Min_r597s597.bed
1202. bedtools shuffle -seed 1 -i 0vs50Min_r597s597.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r598s597.bed
1203. sort -k1,1 -k2,2n ./0vs50Min_r598s597.bed > ./0vs50Min_r598s598.bed
1204. bedtools shuffle -seed 1 -i 0vs50Min_r598s598.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r599s598.bed
1205. sort -k1,1 -k2,2n ./0vs50Min_r599s598.bed > ./0vs50Min_r599s599.bed
1206. bedtools shuffle -seed 1 -i 0vs50Min_r599s599.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r600s599.bed
1207. sort -k1,1 -k2,2n ./0vs50Min_r600s599.bed > ./0vs50Min_r600s600.bed
1208. bedtools shuffle -seed 1 -i 0vs50Min_r600s600.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r601s600.bed
1209. sort -k1,1 -k2,2n ./0vs50Min_r601s600.bed > ./0vs50Min_r601s601.bed
1210. bedtools shuffle -seed 1 -i 0vs50Min_r601s601.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r602s601.bed
1211. sort -k1,1 -k2,2n ./0vs50Min_r602s601.bed > ./0vs50Min_r602s602.bed
1212. bedtools shuffle -seed 1 -i 0vs50Min_r602s602.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r603s602.bed
1213. sort -k1,1 -k2,2n ./0vs50Min_r603s602.bed > ./0vs50Min_r603s603.bed
1214. bedtools shuffle -seed 1 -i 0vs50Min_r603s603.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r604s603.bed
1215. sort -k1,1 -k2,2n ./0vs50Min_r604s603.bed > ./0vs50Min_r604s604.bed
1216. bedtools shuffle -seed 1 -i 0vs50Min_r604s604.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r605s604.bed
1217. sort -k1,1 -k2,2n ./0vs50Min_r605s604.bed > ./0vs50Min_r605s605.bed
1218. bedtools shuffle -seed 1 -i 0vs50Min_r605s605.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r606s605.bed
1219. sort -k1,1 -k2,2n ./0vs50Min_r606s605.bed > ./0vs50Min_r606s606.bed
1220. bedtools shuffle -seed 1 -i 0vs50Min_r606s606.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r607s606.bed
1221. sort -k1,1 -k2,2n ./0vs50Min_r607s606.bed > ./0vs50Min_r607s607.bed
1222. bedtools shuffle -seed 1 -i 0vs50Min_r607s607.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r608s607.bed
1223. sort -k1,1 -k2,2n ./0vs50Min_r608s607.bed > ./0vs50Min_r608s608.bed
1224. bedtools shuffle -seed 1 -i 0vs50Min_r608s608.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r609s608.bed
1225. sort -k1,1 -k2,2n ./0vs50Min_r609s608.bed > ./0vs50Min_r609s609.bed
1226. bedtools shuffle -seed 1 -i 0vs50Min_r609s609.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r610s609.bed
1227. sort -k1,1 -k2,2n ./0vs50Min_r610s609.bed > ./0vs50Min_r610s610.bed

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1228. bedtools shuffle -seed 1 -i Ovs50Min_r610s610.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r611s610.bed
1229. sort -k1,1 -k2,2n ./Ovs50Min_r611s610.bed > ./Ovs50Min_r611s611.bed
1230. bedtools shuffle -seed 1 -i Ovs50Min_r611s611.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r612s611.bed
1231. sort -k1,1 -k2,2n ./Ovs50Min_r612s611.bed > ./Ovs50Min_r612s612.bed
1232. bedtools shuffle -seed 1 -i Ovs50Min_r612s612.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r613s612.bed
1233. sort -k1,1 -k2,2n ./Ovs50Min_r613s612.bed > ./Ovs50Min_r613s613.bed
1234. bedtools shuffle -seed 1 -i Ovs50Min_r613s613.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r614s613.bed
1235. sort -k1,1 -k2,2n ./Ovs50Min_r614s613.bed > ./Ovs50Min_r614s614.bed
1236. bedtools shuffle -seed 1 -i Ovs50Min_r614s614.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r615s614.bed
1237. sort -k1,1 -k2,2n ./Ovs50Min_r615s614.bed > ./Ovs50Min_r615s615.bed
1238. bedtools shuffle -seed 1 -i Ovs50Min_r615s615.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r616s615.bed
1239. sort -k1,1 -k2,2n ./Ovs50Min_r616s615.bed > ./Ovs50Min_r616s616.bed
1240. bedtools shuffle -seed 1 -i Ovs50Min_r616s616.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r617s616.bed
1241. sort -k1,1 -k2,2n ./Ovs50Min_r617s616.bed > ./Ovs50Min_r617s617.bed
1242. bedtools shuffle -seed 1 -i Ovs50Min_r617s617.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r618s617.bed
1243. sort -k1,1 -k2,2n ./Ovs50Min_r618s617.bed > ./Ovs50Min_r618s618.bed
1244. bedtools shuffle -seed 1 -i Ovs50Min_r618s618.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r619s618.bed
1245. sort -k1,1 -k2,2n ./Ovs50Min_r619s618.bed > ./Ovs50Min_r619s619.bed
1246. bedtools shuffle -seed 1 -i Ovs50Min_r619s619.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r620s619.bed
1247. sort -k1,1 -k2,2n ./Ovs50Min_r620s619.bed > ./Ovs50Min_r620s620.bed
1248. bedtools shuffle -seed 1 -i Ovs50Min_r620s620.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r621s620.bed
1249. sort -k1,1 -k2,2n ./Ovs50Min_r621s620.bed > ./Ovs50Min_r621s621.bed
1250. bedtools shuffle -seed 1 -i Ovs50Min_r621s621.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r622s621.bed
1251. sort -k1,1 -k2,2n ./Ovs50Min_r622s621.bed > ./Ovs50Min_r622s622.bed
1252. bedtools shuffle -seed 1 -i Ovs50Min_r622s622.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r623s622.bed
1253. sort -k1,1 -k2,2n ./Ovs50Min_r623s622.bed > ./Ovs50Min_r623s623.bed
1254. bedtools shuffle -seed 1 -i Ovs50Min_r623s623.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r624s623.bed
1255. sort -k1,1 -k2,2n ./Ovs50Min_r624s623.bed > ./Ovs50Min_r624s624.bed
1256. bedtools shuffle -seed 1 -i Ovs50Min_r624s624.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r625s624.bed
1257. sort -k1,1 -k2,2n ./Ovs50Min_r625s624.bed > ./Ovs50Min_r625s625.bed
1258. bedtools shuffle -seed 1 -i Ovs50Min_r625s625.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r626s625.bed
1259. sort -k1,1 -k2,2n ./Ovs50Min_r626s625.bed > ./Ovs50Min_r626s626.bed
1260. bedtools shuffle -seed 1 -i Ovs50Min_r626s626.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r627s626.bed
1261. sort -k1,1 -k2,2n ./Ovs50Min_r627s626.bed > ./Ovs50Min_r627s627.bed
1262. bedtools shuffle -seed 1 -i Ovs50Min_r627s627.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r628s627.bed
1263. sort -k1,1 -k2,2n ./Ovs50Min_r628s627.bed > ./Ovs50Min_r628s628.bed
1264. bedtools shuffle -seed 1 -i Ovs50Min_r628s628.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r629s628.bed

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1265.    sort -k1,1 -k2,2n ./Ovs50Min_r629s628.bed > ./Ovs50Min_r629s629.bed
1266.    bedtools shuffle -seed 1 -i Ovs50Min_r629s629.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r630s629.bed
1267.    sort -k1,1 -k2,2n ./Ovs50Min_r630s629.bed > ./Ovs50Min_r630s630.bed
1268.    bedtools shuffle -seed 1 -i Ovs50Min_r630s630.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r631s630.bed
1269.    sort -k1,1 -k2,2n ./Ovs50Min_r631s630.bed > ./Ovs50Min_r631s631.bed
1270.    bedtools shuffle -seed 1 -i Ovs50Min_r631s631.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r632s631.bed
1271.    sort -k1,1 -k2,2n ./Ovs50Min_r632s631.bed > ./Ovs50Min_r632s632.bed
1272.    bedtools shuffle -seed 1 -i Ovs50Min_r632s632.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r633s632.bed
1273.    sort -k1,1 -k2,2n ./Ovs50Min_r633s632.bed > ./Ovs50Min_r633s633.bed
1274.    bedtools shuffle -seed 1 -i Ovs50Min_r633s633.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r634s633.bed
1275.    sort -k1,1 -k2,2n ./Ovs50Min_r634s633.bed > ./Ovs50Min_r634s634.bed
1276.    bedtools shuffle -seed 1 -i Ovs50Min_r634s634.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r635s634.bed
1277.    sort -k1,1 -k2,2n ./Ovs50Min_r635s634.bed > ./Ovs50Min_r635s635.bed
1278.    bedtools shuffle -seed 1 -i Ovs50Min_r635s635.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r636s635.bed
1279.    sort -k1,1 -k2,2n ./Ovs50Min_r636s635.bed > ./Ovs50Min_r636s636.bed
1280.    bedtools shuffle -seed 1 -i Ovs50Min_r636s636.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r637s636.bed
1281.    sort -k1,1 -k2,2n ./Ovs50Min_r637s636.bed > ./Ovs50Min_r637s637.bed
1282.    bedtools shuffle -seed 1 -i Ovs50Min_r637s637.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r638s637.bed
1283.    sort -k1,1 -k2,2n ./Ovs50Min_r638s637.bed > ./Ovs50Min_r638s638.bed
1284.    bedtools shuffle -seed 1 -i Ovs50Min_r638s638.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r639s638.bed
1285.    sort -k1,1 -k2,2n ./Ovs50Min_r639s638.bed > ./Ovs50Min_r639s639.bed
1286.    bedtools shuffle -seed 1 -i Ovs50Min_r639s639.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r640s639.bed
1287.    sort -k1,1 -k2,2n ./Ovs50Min_r640s639.bed > ./Ovs50Min_r640s640.bed
1288.    bedtools shuffle -seed 1 -i Ovs50Min_r640s640.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r641s640.bed
1289.    sort -k1,1 -k2,2n ./Ovs50Min_r641s640.bed > ./Ovs50Min_r641s641.bed
1290.    bedtools shuffle -seed 1 -i Ovs50Min_r641s641.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r642s641.bed
1291.    sort -k1,1 -k2,2n ./Ovs50Min_r642s641.bed > ./Ovs50Min_r642s642.bed
1292.    bedtools shuffle -seed 1 -i Ovs50Min_r642s642.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r643s642.bed
1293.    sort -k1,1 -k2,2n ./Ovs50Min_r643s642.bed > ./Ovs50Min_r643s643.bed
1294.    bedtools shuffle -seed 1 -i Ovs50Min_r643s643.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r644s643.bed
1295.    sort -k1,1 -k2,2n ./Ovs50Min_r644s643.bed > ./Ovs50Min_r644s644.bed
1296.    bedtools shuffle -seed 1 -i Ovs50Min_r644s644.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r645s644.bed
1297.    sort -k1,1 -k2,2n ./Ovs50Min_r645s644.bed > ./Ovs50Min_r645s645.bed
1298.    bedtools shuffle -seed 1 -i Ovs50Min_r645s645.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r646s645.bed
1299.    sort -k1,1 -k2,2n ./Ovs50Min_r646s645.bed > ./Ovs50Min_r646s646.bed
1300.    bedtools shuffle -seed 1 -i Ovs50Min_r646s646.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r647s646.bed
1301.    sort -k1,1 -k2,2n ./Ovs50Min_r647s646.bed > ./Ovs50Min_r647s647.bed

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1302. bedtools shuffle -seed 1 -i Ovs50Min_r647s647.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r648s647.bed
1303. sort -k1,1 -k2,2n ./Ovs50Min_r648s647.bed > ./Ovs50Min_r648s648.bed
1304. bedtools shuffle -seed 1 -i Ovs50Min_r648s648.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r649s648.bed
1305. sort -k1,1 -k2,2n ./Ovs50Min_r649s648.bed > ./Ovs50Min_r649s649.bed
1306. bedtools shuffle -seed 1 -i Ovs50Min_r649s649.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r650s649.bed
1307. sort -k1,1 -k2,2n ./Ovs50Min_r650s649.bed > ./Ovs50Min_r650s650.bed
1308. bedtools shuffle -seed 1 -i Ovs50Min_r650s650.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r651s650.bed
1309. sort -k1,1 -k2,2n ./Ovs50Min_r651s650.bed > ./Ovs50Min_r651s651.bed
1310. bedtools shuffle -seed 1 -i Ovs50Min_r651s651.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r652s651.bed
1311. sort -k1,1 -k2,2n ./Ovs50Min_r652s651.bed > ./Ovs50Min_r652s652.bed
1312. bedtools shuffle -seed 1 -i Ovs50Min_r652s652.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r653s652.bed
1313. sort -k1,1 -k2,2n ./Ovs50Min_r653s652.bed > ./Ovs50Min_r653s653.bed
1314. bedtools shuffle -seed 1 -i Ovs50Min_r653s653.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r654s653.bed
1315. sort -k1,1 -k2,2n ./Ovs50Min_r654s653.bed > ./Ovs50Min_r654s654.bed
1316. bedtools shuffle -seed 1 -i Ovs50Min_r654s654.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r655s654.bed
1317. sort -k1,1 -k2,2n ./Ovs50Min_r655s654.bed > ./Ovs50Min_r655s655.bed
1318. bedtools shuffle -seed 1 -i Ovs50Min_r655s655.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r656s655.bed
1319. sort -k1,1 -k2,2n ./Ovs50Min_r656s655.bed > ./Ovs50Min_r656s656.bed
1320. bedtools shuffle -seed 1 -i Ovs50Min_r656s656.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r657s656.bed
1321. sort -k1,1 -k2,2n ./Ovs50Min_r657s656.bed > ./Ovs50Min_r657s657.bed
1322. bedtools shuffle -seed 1 -i Ovs50Min_r657s657.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r658s657.bed
1323. sort -k1,1 -k2,2n ./Ovs50Min_r658s657.bed > ./Ovs50Min_r658s658.bed
1324. bedtools shuffle -seed 1 -i Ovs50Min_r658s658.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r659s658.bed
1325. sort -k1,1 -k2,2n ./Ovs50Min_r659s658.bed > ./Ovs50Min_r659s659.bed
1326. bedtools shuffle -seed 1 -i Ovs50Min_r659s659.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r660s659.bed
1327. sort -k1,1 -k2,2n ./Ovs50Min_r660s659.bed > ./Ovs50Min_r660s660.bed
1328. bedtools shuffle -seed 1 -i Ovs50Min_r660s660.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r661s660.bed
1329. sort -k1,1 -k2,2n ./Ovs50Min_r661s660.bed > ./Ovs50Min_r661s661.bed
1330. bedtools shuffle -seed 1 -i Ovs50Min_r661s661.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r662s661.bed
1331. sort -k1,1 -k2,2n ./Ovs50Min_r662s661.bed > ./Ovs50Min_r662s662.bed
1332. bedtools shuffle -seed 1 -i Ovs50Min_r662s662.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r663s662.bed
1333. sort -k1,1 -k2,2n ./Ovs50Min_r663s662.bed > ./Ovs50Min_r663s663.bed
1334. bedtools shuffle -seed 1 -i Ovs50Min_r663s663.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r664s663.bed
1335. sort -k1,1 -k2,2n ./Ovs50Min_r664s663.bed > ./Ovs50Min_r664s664.bed
1336. bedtools shuffle -seed 1 -i Ovs50Min_r664s664.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r665s664.bed
1337. sort -k1,1 -k2,2n ./Ovs50Min_r665s664.bed > ./Ovs50Min_r665s665.bed
1338. bedtools shuffle -seed 1 -i Ovs50Min_r665s665.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r666s665.bed

1339. sort -k1,1 -k2,2n ./Ovs50Min_r666s665.bed > ./Ovs50Min_r666s666.bed
1340. bedtools shuffle -seed 1 -i Ovs50Min_r666s666.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r667s666.bed
1341. sort -k1,1 -k2,2n ./Ovs50Min_r667s666.bed > ./Ovs50Min_r667s667.bed
1342. bedtools shuffle -seed 1 -i Ovs50Min_r667s667.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r668s667.bed
1343. sort -k1,1 -k2,2n ./Ovs50Min_r668s667.bed > ./Ovs50Min_r668s668.bed
1344. bedtools shuffle -seed 1 -i Ovs50Min_r668s668.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r669s668.bed
1345. sort -k1,1 -k2,2n ./Ovs50Min_r669s668.bed > ./Ovs50Min_r669s669.bed
1346. bedtools shuffle -seed 1 -i Ovs50Min_r669s669.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r670s669.bed
1347. sort -k1,1 -k2,2n ./Ovs50Min_r670s669.bed > ./Ovs50Min_r670s670.bed
1348. bedtools shuffle -seed 1 -i Ovs50Min_r670s670.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r671s670.bed
1349. sort -k1,1 -k2,2n ./Ovs50Min_r671s670.bed > ./Ovs50Min_r671s671.bed
1350. bedtools shuffle -seed 1 -i Ovs50Min_r671s671.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r672s671.bed
1351. sort -k1,1 -k2,2n ./Ovs50Min_r672s671.bed > ./Ovs50Min_r672s672.bed
1352. bedtools shuffle -seed 1 -i Ovs50Min_r672s672.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r673s672.bed
1353. sort -k1,1 -k2,2n ./Ovs50Min_r673s672.bed > ./Ovs50Min_r673s673.bed
1354. bedtools shuffle -seed 1 -i Ovs50Min_r673s673.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r674s673.bed
1355. sort -k1,1 -k2,2n ./Ovs50Min_r674s673.bed > ./Ovs50Min_r674s674.bed
1356. bedtools shuffle -seed 1 -i Ovs50Min_r674s674.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r675s674.bed
1357. sort -k1,1 -k2,2n ./Ovs50Min_r675s674.bed > ./Ovs50Min_r675s675.bed
1358. bedtools shuffle -seed 1 -i Ovs50Min_r675s675.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r676s675.bed
1359. sort -k1,1 -k2,2n ./Ovs50Min_r676s675.bed > ./Ovs50Min_r676s676.bed
1360. bedtools shuffle -seed 1 -i Ovs50Min_r676s676.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r677s676.bed
1361. sort -k1,1 -k2,2n ./Ovs50Min_r677s676.bed > ./Ovs50Min_r677s677.bed
1362. bedtools shuffle -seed 1 -i Ovs50Min_r677s677.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r678s677.bed
1363. sort -k1,1 -k2,2n ./Ovs50Min_r678s677.bed > ./Ovs50Min_r678s678.bed
1364. bedtools shuffle -seed 1 -i Ovs50Min_r678s678.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r679s678.bed
1365. sort -k1,1 -k2,2n ./Ovs50Min_r679s678.bed > ./Ovs50Min_r679s679.bed
1366. bedtools shuffle -seed 1 -i Ovs50Min_r679s679.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r680s679.bed
1367. sort -k1,1 -k2,2n ./Ovs50Min_r680s679.bed > ./Ovs50Min_r680s680.bed
1368. bedtools shuffle -seed 1 -i Ovs50Min_r680s680.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r681s680.bed
1369. sort -k1,1 -k2,2n ./Ovs50Min_r681s680.bed > ./Ovs50Min_r681s681.bed
1370. bedtools shuffle -seed 1 -i Ovs50Min_r681s681.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r682s681.bed
1371. sort -k1,1 -k2,2n ./Ovs50Min_r682s681.bed > ./Ovs50Min_r682s682.bed
1372. bedtools shuffle -seed 1 -i Ovs50Min_r682s682.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r683s682.bed
1373. sort -k1,1 -k2,2n ./Ovs50Min_r683s682.bed > ./Ovs50Min_r683s683.bed
1374. bedtools shuffle -seed 1 -i Ovs50Min_r683s683.bed -g Ecoli-
genomesize.txt > ./Ovs50Min_r684s683.bed
1375. sort -k1,1 -k2,2n ./Ovs50Min_r684s683.bed > ./Ovs50Min_r684s684.bed

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1376. bedtools shuffle -seed 1 -i Ovs50Min_r684s684.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r685s684.bed
1377. sort -k1,1 -k2,2n ./Ovs50Min_r685s684.bed > ./Ovs50Min_r685s685.bed
1378. bedtools shuffle -seed 1 -i Ovs50Min_r685s685.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r686s685.bed
1379. sort -k1,1 -k2,2n ./Ovs50Min_r686s685.bed > ./Ovs50Min_r686s686.bed
1380. bedtools shuffle -seed 1 -i Ovs50Min_r686s686.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r687s686.bed
1381. sort -k1,1 -k2,2n ./Ovs50Min_r687s686.bed > ./Ovs50Min_r687s687.bed
1382. bedtools shuffle -seed 1 -i Ovs50Min_r687s687.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r688s687.bed
1383. sort -k1,1 -k2,2n ./Ovs50Min_r688s687.bed > ./Ovs50Min_r688s688.bed
1384. bedtools shuffle -seed 1 -i Ovs50Min_r688s688.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r689s688.bed
1385. sort -k1,1 -k2,2n ./Ovs50Min_r689s688.bed > ./Ovs50Min_r689s689.bed
1386. bedtools shuffle -seed 1 -i Ovs50Min_r689s689.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r690s689.bed
1387. sort -k1,1 -k2,2n ./Ovs50Min_r690s689.bed > ./Ovs50Min_r690s690.bed
1388. bedtools shuffle -seed 1 -i Ovs50Min_r690s690.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r691s690.bed
1389. sort -k1,1 -k2,2n ./Ovs50Min_r691s690.bed > ./Ovs50Min_r691s691.bed
1390. bedtools shuffle -seed 1 -i Ovs50Min_r691s691.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r692s691.bed
1391. sort -k1,1 -k2,2n ./Ovs50Min_r692s691.bed > ./Ovs50Min_r692s692.bed
1392. bedtools shuffle -seed 1 -i Ovs50Min_r692s692.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r693s692.bed
1393. sort -k1,1 -k2,2n ./Ovs50Min_r693s692.bed > ./Ovs50Min_r693s693.bed
1394. bedtools shuffle -seed 1 -i Ovs50Min_r693s693.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r694s693.bed
1395. sort -k1,1 -k2,2n ./Ovs50Min_r694s693.bed > ./Ovs50Min_r694s694.bed
1396. bedtools shuffle -seed 1 -i Ovs50Min_r694s694.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r695s694.bed
1397. sort -k1,1 -k2,2n ./Ovs50Min_r695s694.bed > ./Ovs50Min_r695s695.bed
1398. bedtools shuffle -seed 1 -i Ovs50Min_r695s695.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r696s695.bed
1399. sort -k1,1 -k2,2n ./Ovs50Min_r696s695.bed > ./Ovs50Min_r696s696.bed
1400. bedtools shuffle -seed 1 -i Ovs50Min_r696s696.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r697s696.bed
1401. sort -k1,1 -k2,2n ./Ovs50Min_r697s696.bed > ./Ovs50Min_r697s697.bed
1402. bedtools shuffle -seed 1 -i Ovs50Min_r697s697.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r698s697.bed
1403. sort -k1,1 -k2,2n ./Ovs50Min_r698s697.bed > ./Ovs50Min_r698s698.bed
1404. bedtools shuffle -seed 1 -i Ovs50Min_r698s698.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r699s698.bed
1405. sort -k1,1 -k2,2n ./Ovs50Min_r699s698.bed > ./Ovs50Min_r699s699.bed
1406. bedtools shuffle -seed 1 -i Ovs50Min_r699s699.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r700s699.bed
1407. sort -k1,1 -k2,2n ./Ovs50Min_r700s699.bed > ./Ovs50Min_r700s700.bed
1408. bedtools shuffle -seed 1 -i Ovs50Min_r700s700.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r701s700.bed
1409. sort -k1,1 -k2,2n ./Ovs50Min_r701s700.bed > ./Ovs50Min_r701s701.bed
1410. bedtools shuffle -seed 1 -i Ovs50Min_r701s701.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r702s701.bed
1411. sort -k1,1 -k2,2n ./Ovs50Min_r702s701.bed > ./Ovs50Min_r702s702.bed
1412. bedtools shuffle -seed 1 -i Ovs50Min_r702s702.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r703s702.bed

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1413.    sort -k1,1 -k2,2n ./0vs50Min_r703s702.bed > ./0vs50Min_r703s703.bed
1414.    bedtools shuffle -seed 1 -i 0vs50Min_r703s703.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r704s703.bed
1415.    sort -k1,1 -k2,2n ./0vs50Min_r704s703.bed > ./0vs50Min_r704s704.bed
1416.    bedtools shuffle -seed 1 -i 0vs50Min_r704s704.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r705s704.bed
1417.    sort -k1,1 -k2,2n ./0vs50Min_r705s704.bed > ./0vs50Min_r705s705.bed
1418.    bedtools shuffle -seed 1 -i 0vs50Min_r705s705.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r706s705.bed
1419.    sort -k1,1 -k2,2n ./0vs50Min_r706s705.bed > ./0vs50Min_r706s706.bed
1420.    bedtools shuffle -seed 1 -i 0vs50Min_r706s706.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r707s706.bed
1421.    sort -k1,1 -k2,2n ./0vs50Min_r707s706.bed > ./0vs50Min_r707s707.bed
1422.    bedtools shuffle -seed 1 -i 0vs50Min_r707s707.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r708s707.bed
1423.    sort -k1,1 -k2,2n ./0vs50Min_r708s707.bed > ./0vs50Min_r708s708.bed
1424.    bedtools shuffle -seed 1 -i 0vs50Min_r708s708.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r709s708.bed
1425.    sort -k1,1 -k2,2n ./0vs50Min_r709s708.bed > ./0vs50Min_r709s709.bed
1426.    bedtools shuffle -seed 1 -i 0vs50Min_r709s709.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r710s709.bed
1427.    sort -k1,1 -k2,2n ./0vs50Min_r710s709.bed > ./0vs50Min_r710s710.bed
1428.    bedtools shuffle -seed 1 -i 0vs50Min_r710s710.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r711s710.bed
1429.    sort -k1,1 -k2,2n ./0vs50Min_r711s710.bed > ./0vs50Min_r711s711.bed
1430.    bedtools shuffle -seed 1 -i 0vs50Min_r711s711.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r712s711.bed
1431.    sort -k1,1 -k2,2n ./0vs50Min_r712s711.bed > ./0vs50Min_r712s712.bed
1432.    bedtools shuffle -seed 1 -i 0vs50Min_r712s712.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r713s712.bed
1433.    sort -k1,1 -k2,2n ./0vs50Min_r713s712.bed > ./0vs50Min_r713s713.bed
1434.    bedtools shuffle -seed 1 -i 0vs50Min_r713s713.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r714s713.bed
1435.    sort -k1,1 -k2,2n ./0vs50Min_r714s713.bed > ./0vs50Min_r714s714.bed
1436.    bedtools shuffle -seed 1 -i 0vs50Min_r714s714.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r715s714.bed
1437.    sort -k1,1 -k2,2n ./0vs50Min_r715s714.bed > ./0vs50Min_r715s715.bed
1438.    bedtools shuffle -seed 1 -i 0vs50Min_r715s715.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r716s715.bed
1439.    sort -k1,1 -k2,2n ./0vs50Min_r716s715.bed > ./0vs50Min_r716s716.bed
1440.    bedtools shuffle -seed 1 -i 0vs50Min_r716s716.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r717s716.bed
1441.    sort -k1,1 -k2,2n ./0vs50Min_r717s716.bed > ./0vs50Min_r717s717.bed
1442.    bedtools shuffle -seed 1 -i 0vs50Min_r717s717.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r718s717.bed
1443.    sort -k1,1 -k2,2n ./0vs50Min_r718s717.bed > ./0vs50Min_r718s718.bed
1444.    bedtools shuffle -seed 1 -i 0vs50Min_r718s718.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r719s718.bed
1445.    sort -k1,1 -k2,2n ./0vs50Min_r719s718.bed > ./0vs50Min_r719s719.bed
1446.    bedtools shuffle -seed 1 -i 0vs50Min_r719s719.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r720s719.bed
1447.    sort -k1,1 -k2,2n ./0vs50Min_r720s719.bed > ./0vs50Min_r720s720.bed
1448.    bedtools shuffle -seed 1 -i 0vs50Min_r720s720.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r721s720.bed
1449.    sort -k1,1 -k2,2n ./0vs50Min_r721s720.bed > ./0vs50Min_r721s721.bed

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1450.     bedtools shuffle -seed 1 -i 0vs50Min_r721s721.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r722s721.bed
1451.     sort -k1,1 -k2,2n ./0vs50Min_r722s721.bed > ./0vs50Min_r722s722.bed
1452.     bedtools shuffle -seed 1 -i 0vs50Min_r722s722.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r723s722.bed
1453.     sort -k1,1 -k2,2n ./0vs50Min_r723s722.bed > ./0vs50Min_r723s723.bed
1454.     bedtools shuffle -seed 1 -i 0vs50Min_r723s723.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r724s723.bed
1455.     sort -k1,1 -k2,2n ./0vs50Min_r724s723.bed > ./0vs50Min_r724s724.bed
1456.     bedtools shuffle -seed 1 -i 0vs50Min_r724s724.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r725s724.bed
1457.     sort -k1,1 -k2,2n ./0vs50Min_r725s724.bed > ./0vs50Min_r725s725.bed
1458.     bedtools shuffle -seed 1 -i 0vs50Min_r725s725.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r726s725.bed
1459.     sort -k1,1 -k2,2n ./0vs50Min_r726s725.bed > ./0vs50Min_r726s726.bed
1460.     bedtools shuffle -seed 1 -i 0vs50Min_r726s726.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r727s726.bed
1461.     sort -k1,1 -k2,2n ./0vs50Min_r727s726.bed > ./0vs50Min_r727s727.bed
1462.     bedtools shuffle -seed 1 -i 0vs50Min_r727s727.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r728s727.bed
1463.     sort -k1,1 -k2,2n ./0vs50Min_r728s727.bed > ./0vs50Min_r728s728.bed
1464.     bedtools shuffle -seed 1 -i 0vs50Min_r728s728.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r729s728.bed
1465.     sort -k1,1 -k2,2n ./0vs50Min_r729s728.bed > ./0vs50Min_r729s729.bed
1466.     bedtools shuffle -seed 1 -i 0vs50Min_r729s729.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r730s729.bed
1467.     sort -k1,1 -k2,2n ./0vs50Min_r730s729.bed > ./0vs50Min_r730s730.bed
1468.     bedtools shuffle -seed 1 -i 0vs50Min_r730s730.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r731s730.bed
1469.     sort -k1,1 -k2,2n ./0vs50Min_r731s730.bed > ./0vs50Min_r731s731.bed
1470.     bedtools shuffle -seed 1 -i 0vs50Min_r731s731.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r732s731.bed
1471.     sort -k1,1 -k2,2n ./0vs50Min_r732s731.bed > ./0vs50Min_r732s732.bed
1472.     bedtools shuffle -seed 1 -i 0vs50Min_r732s732.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r733s732.bed
1473.     sort -k1,1 -k2,2n ./0vs50Min_r733s732.bed > ./0vs50Min_r733s733.bed
1474.     bedtools shuffle -seed 1 -i 0vs50Min_r733s733.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r734s733.bed
1475.     sort -k1,1 -k2,2n ./0vs50Min_r734s733.bed > ./0vs50Min_r734s734.bed
1476.     bedtools shuffle -seed 1 -i 0vs50Min_r734s734.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r735s734.bed
1477.     sort -k1,1 -k2,2n ./0vs50Min_r735s734.bed > ./0vs50Min_r735s735.bed
1478.     bedtools shuffle -seed 1 -i 0vs50Min_r735s735.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r736s735.bed
1479.     sort -k1,1 -k2,2n ./0vs50Min_r736s735.bed > ./0vs50Min_r736s736.bed
1480.     bedtools shuffle -seed 1 -i 0vs50Min_r736s736.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r737s736.bed
1481.     sort -k1,1 -k2,2n ./0vs50Min_r737s736.bed > ./0vs50Min_r737s737.bed
1482.     bedtools shuffle -seed 1 -i 0vs50Min_r737s737.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r738s737.bed
1483.     sort -k1,1 -k2,2n ./0vs50Min_r738s737.bed > ./0vs50Min_r738s738.bed
1484.     bedtools shuffle -seed 1 -i 0vs50Min_r738s738.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r739s738.bed
1485.     sort -k1,1 -k2,2n ./0vs50Min_r739s738.bed > ./0vs50Min_r739s739.bed
1486.     bedtools shuffle -seed 1 -i 0vs50Min_r739s739.bed -g Ecoli-
          genomesize.txt > ./0vs50Min_r740s739.bed

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1487.    sort -k1,1 -k2,2n ./Ovs50Min_r740s739.bed > ./Ovs50Min_r740s740.bed
1488.    bedtools shuffle -seed 1 -i Ovs50Min_r740s740.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r741s740.bed
1489.    sort -k1,1 -k2,2n ./Ovs50Min_r741s740.bed > ./Ovs50Min_r741s741.bed
1490.    bedtools shuffle -seed 1 -i Ovs50Min_r741s741.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r742s741.bed
1491.    sort -k1,1 -k2,2n ./Ovs50Min_r742s741.bed > ./Ovs50Min_r742s742.bed
1492.    bedtools shuffle -seed 1 -i Ovs50Min_r742s742.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r743s742.bed
1493.    sort -k1,1 -k2,2n ./Ovs50Min_r743s742.bed > ./Ovs50Min_r743s743.bed
1494.    bedtools shuffle -seed 1 -i Ovs50Min_r743s743.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r744s743.bed
1495.    sort -k1,1 -k2,2n ./Ovs50Min_r744s743.bed > ./Ovs50Min_r744s744.bed
1496.    bedtools shuffle -seed 1 -i Ovs50Min_r744s744.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r745s744.bed
1497.    sort -k1,1 -k2,2n ./Ovs50Min_r745s744.bed > ./Ovs50Min_r745s745.bed
1498.    bedtools shuffle -seed 1 -i Ovs50Min_r745s745.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r746s745.bed
1499.    sort -k1,1 -k2,2n ./Ovs50Min_r746s745.bed > ./Ovs50Min_r746s746.bed
1500.    bedtools shuffle -seed 1 -i Ovs50Min_r746s746.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r747s746.bed
1501.    sort -k1,1 -k2,2n ./Ovs50Min_r747s746.bed > ./Ovs50Min_r747s747.bed
1502.    bedtools shuffle -seed 1 -i Ovs50Min_r747s747.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r748s747.bed
1503.    sort -k1,1 -k2,2n ./Ovs50Min_r748s747.bed > ./Ovs50Min_r748s748.bed
1504.    bedtools shuffle -seed 1 -i Ovs50Min_r748s748.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r749s748.bed
1505.    sort -k1,1 -k2,2n ./Ovs50Min_r749s748.bed > ./Ovs50Min_r749s749.bed
1506.    bedtools shuffle -seed 1 -i Ovs50Min_r749s749.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r750s749.bed
1507.    sort -k1,1 -k2,2n ./Ovs50Min_r750s749.bed > ./Ovs50Min_r750s750.bed
1508.    bedtools shuffle -seed 1 -i Ovs50Min_r750s750.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r751s750.bed
1509.    sort -k1,1 -k2,2n ./Ovs50Min_r751s750.bed > ./Ovs50Min_r751s751.bed
1510.    bedtools shuffle -seed 1 -i Ovs50Min_r751s751.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r752s751.bed
1511.    sort -k1,1 -k2,2n ./Ovs50Min_r752s751.bed > ./Ovs50Min_r752s752.bed
1512.    bedtools shuffle -seed 1 -i Ovs50Min_r752s752.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r753s752.bed
1513.    sort -k1,1 -k2,2n ./Ovs50Min_r753s752.bed > ./Ovs50Min_r753s753.bed
1514.    bedtools shuffle -seed 1 -i Ovs50Min_r753s753.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r754s753.bed
1515.    sort -k1,1 -k2,2n ./Ovs50Min_r754s753.bed > ./Ovs50Min_r754s754.bed
1516.    bedtools shuffle -seed 1 -i Ovs50Min_r754s754.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r755s754.bed
1517.    sort -k1,1 -k2,2n ./Ovs50Min_r755s754.bed > ./Ovs50Min_r755s755.bed
1518.    bedtools shuffle -seed 1 -i Ovs50Min_r755s755.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r756s755.bed
1519.    sort -k1,1 -k2,2n ./Ovs50Min_r756s755.bed > ./Ovs50Min_r756s756.bed
1520.    bedtools shuffle -seed 1 -i Ovs50Min_r756s756.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r757s756.bed
1521.    sort -k1,1 -k2,2n ./Ovs50Min_r757s756.bed > ./Ovs50Min_r757s757.bed
1522.    bedtools shuffle -seed 1 -i Ovs50Min_r757s757.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r758s757.bed
1523.    sort -k1,1 -k2,2n ./Ovs50Min_r758s757.bed > ./Ovs50Min_r758s758.bed

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1524. bedtools shuffle -seed 1 -i 0vs50Min_r758s758.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r759s758.bed
1525. sort -k1,1 -k2,2n ./0vs50Min_r759s758.bed > ./0vs50Min_r759s759.bed
1526. bedtools shuffle -seed 1 -i 0vs50Min_r759s759.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r760s759.bed
1527. sort -k1,1 -k2,2n ./0vs50Min_r760s759.bed > ./0vs50Min_r760s760.bed
1528. bedtools shuffle -seed 1 -i 0vs50Min_r760s760.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r761s760.bed
1529. sort -k1,1 -k2,2n ./0vs50Min_r761s760.bed > ./0vs50Min_r761s761.bed
1530. bedtools shuffle -seed 1 -i 0vs50Min_r761s761.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r762s761.bed
1531. sort -k1,1 -k2,2n ./0vs50Min_r762s761.bed > ./0vs50Min_r762s762.bed
1532. bedtools shuffle -seed 1 -i 0vs50Min_r762s762.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r763s762.bed
1533. sort -k1,1 -k2,2n ./0vs50Min_r763s762.bed > ./0vs50Min_r763s763.bed
1534. bedtools shuffle -seed 1 -i 0vs50Min_r763s763.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r764s763.bed
1535. sort -k1,1 -k2,2n ./0vs50Min_r764s763.bed > ./0vs50Min_r764s764.bed
1536. bedtools shuffle -seed 1 -i 0vs50Min_r764s764.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r765s764.bed
1537. sort -k1,1 -k2,2n ./0vs50Min_r765s764.bed > ./0vs50Min_r765s765.bed
1538. bedtools shuffle -seed 1 -i 0vs50Min_r765s765.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r766s765.bed
1539. sort -k1,1 -k2,2n ./0vs50Min_r766s765.bed > ./0vs50Min_r766s766.bed
1540. bedtools shuffle -seed 1 -i 0vs50Min_r766s766.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r767s766.bed
1541. sort -k1,1 -k2,2n ./0vs50Min_r767s766.bed > ./0vs50Min_r767s767.bed
1542. bedtools shuffle -seed 1 -i 0vs50Min_r767s767.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r768s767.bed
1543. sort -k1,1 -k2,2n ./0vs50Min_r768s767.bed > ./0vs50Min_r768s768.bed
1544. bedtools shuffle -seed 1 -i 0vs50Min_r768s768.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r769s768.bed
1545. sort -k1,1 -k2,2n ./0vs50Min_r769s768.bed > ./0vs50Min_r769s769.bed
1546. bedtools shuffle -seed 1 -i 0vs50Min_r769s769.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r770s769.bed
1547. sort -k1,1 -k2,2n ./0vs50Min_r770s769.bed > ./0vs50Min_r770s770.bed
1548. bedtools shuffle -seed 1 -i 0vs50Min_r770s770.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r771s770.bed
1549. sort -k1,1 -k2,2n ./0vs50Min_r771s770.bed > ./0vs50Min_r771s771.bed
1550. bedtools shuffle -seed 1 -i 0vs50Min_r771s771.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r772s771.bed
1551. sort -k1,1 -k2,2n ./0vs50Min_r772s771.bed > ./0vs50Min_r772s772.bed
1552. bedtools shuffle -seed 1 -i 0vs50Min_r772s772.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r773s772.bed
1553. sort -k1,1 -k2,2n ./0vs50Min_r773s772.bed > ./0vs50Min_r773s773.bed
1554. bedtools shuffle -seed 1 -i 0vs50Min_r773s773.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r774s773.bed
1555. sort -k1,1 -k2,2n ./0vs50Min_r774s773.bed > ./0vs50Min_r774s774.bed
1556. bedtools shuffle -seed 1 -i 0vs50Min_r774s774.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r775s774.bed
1557. sort -k1,1 -k2,2n ./0vs50Min_r775s774.bed > ./0vs50Min_r775s775.bed
1558. bedtools shuffle -seed 1 -i 0vs50Min_r775s775.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r776s775.bed
1559. sort -k1,1 -k2,2n ./0vs50Min_r776s775.bed > ./0vs50Min_r776s776.bed
1560. bedtools shuffle -seed 1 -i 0vs50Min_r776s776.bed -g Ecoli-
      genomesize.txt > ./0vs50Min_r777s776.bed

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1561.    sort -k1,1 -k2,2n ./0vs50Min_r777s776.bed > ./0vs50Min_r777s777.bed
1562.    bedtools shuffle -seed 1 -i 0vs50Min_r777s777.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r778s777.bed
1563.    sort -k1,1 -k2,2n ./0vs50Min_r778s777.bed > ./0vs50Min_r778s778.bed
1564.    bedtools shuffle -seed 1 -i 0vs50Min_r778s778.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r779s778.bed
1565.    sort -k1,1 -k2,2n ./0vs50Min_r779s778.bed > ./0vs50Min_r779s779.bed
1566.    bedtools shuffle -seed 1 -i 0vs50Min_r779s779.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r780s779.bed
1567.    sort -k1,1 -k2,2n ./0vs50Min_r780s779.bed > ./0vs50Min_r780s780.bed
1568.    bedtools shuffle -seed 1 -i 0vs50Min_r780s780.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r781s780.bed
1569.    sort -k1,1 -k2,2n ./0vs50Min_r781s780.bed > ./0vs50Min_r781s781.bed
1570.    bedtools shuffle -seed 1 -i 0vs50Min_r781s781.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r782s781.bed
1571.    sort -k1,1 -k2,2n ./0vs50Min_r782s781.bed > ./0vs50Min_r782s782.bed
1572.    bedtools shuffle -seed 1 -i 0vs50Min_r782s782.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r783s782.bed
1573.    sort -k1,1 -k2,2n ./0vs50Min_r783s782.bed > ./0vs50Min_r783s783.bed
1574.    bedtools shuffle -seed 1 -i 0vs50Min_r783s783.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r784s783.bed
1575.    sort -k1,1 -k2,2n ./0vs50Min_r784s783.bed > ./0vs50Min_r784s784.bed
1576.    bedtools shuffle -seed 1 -i 0vs50Min_r784s784.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r785s784.bed
1577.    sort -k1,1 -k2,2n ./0vs50Min_r785s784.bed > ./0vs50Min_r785s785.bed
1578.    bedtools shuffle -seed 1 -i 0vs50Min_r785s785.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r786s785.bed
1579.    sort -k1,1 -k2,2n ./0vs50Min_r786s785.bed > ./0vs50Min_r786s786.bed
1580.    bedtools shuffle -seed 1 -i 0vs50Min_r786s786.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r787s786.bed
1581.    sort -k1,1 -k2,2n ./0vs50Min_r787s786.bed > ./0vs50Min_r787s787.bed
1582.    bedtools shuffle -seed 1 -i 0vs50Min_r787s787.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r788s787.bed
1583.    sort -k1,1 -k2,2n ./0vs50Min_r788s787.bed > ./0vs50Min_r788s788.bed
1584.    bedtools shuffle -seed 1 -i 0vs50Min_r788s788.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r789s788.bed
1585.    sort -k1,1 -k2,2n ./0vs50Min_r789s788.bed > ./0vs50Min_r789s789.bed
1586.    bedtools shuffle -seed 1 -i 0vs50Min_r789s789.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r790s789.bed
1587.    sort -k1,1 -k2,2n ./0vs50Min_r790s789.bed > ./0vs50Min_r790s790.bed
1588.    bedtools shuffle -seed 1 -i 0vs50Min_r790s790.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r791s790.bed
1589.    sort -k1,1 -k2,2n ./0vs50Min_r791s790.bed > ./0vs50Min_r791s791.bed
1590.    bedtools shuffle -seed 1 -i 0vs50Min_r791s791.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r792s791.bed
1591.    sort -k1,1 -k2,2n ./0vs50Min_r792s791.bed > ./0vs50Min_r792s792.bed
1592.    bedtools shuffle -seed 1 -i 0vs50Min_r792s792.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r793s792.bed
1593.    sort -k1,1 -k2,2n ./0vs50Min_r793s792.bed > ./0vs50Min_r793s793.bed
1594.    bedtools shuffle -seed 1 -i 0vs50Min_r793s793.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r794s793.bed
1595.    sort -k1,1 -k2,2n ./0vs50Min_r794s793.bed > ./0vs50Min_r794s794.bed
1596.    bedtools shuffle -seed 1 -i 0vs50Min_r794s794.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r795s794.bed
1597.    sort -k1,1 -k2,2n ./0vs50Min_r795s794.bed > ./0vs50Min_r795s795.bed

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1598. bedtools shuffle -seed 1 -i 0vs50Min_r795s795.bed -g Ecoli-genomesize.txt > ./0vs50Min_r796s795.bed
1599. sort -k1,1 -k2,2n ./0vs50Min_r796s795.bed > ./0vs50Min_r796s796.bed
1600. bedtools shuffle -seed 1 -i 0vs50Min_r796s796.bed -g Ecoli-genomesize.txt > ./0vs50Min_r797s796.bed
1601. sort -k1,1 -k2,2n ./0vs50Min_r797s796.bed > ./0vs50Min_r797s797.bed
1602. bedtools shuffle -seed 1 -i 0vs50Min_r797s797.bed -g Ecoli-genomesize.txt > ./0vs50Min_r798s797.bed
1603. sort -k1,1 -k2,2n ./0vs50Min_r798s797.bed > ./0vs50Min_r798s798.bed
1604. bedtools shuffle -seed 1 -i 0vs50Min_r798s798.bed -g Ecoli-genomesize.txt > ./0vs50Min_r799s798.bed
1605. sort -k1,1 -k2,2n ./0vs50Min_r799s798.bed > ./0vs50Min_r799s799.bed
1606. bedtools shuffle -seed 1 -i 0vs50Min_r799s799.bed -g Ecoli-genomesize.txt > ./0vs50Min_r800s799.bed
1607. sort -k1,1 -k2,2n ./0vs50Min_r800s799.bed > ./0vs50Min_r800s800.bed
1608. bedtools shuffle -seed 1 -i 0vs50Min_r800s800.bed -g Ecoli-genomesize.txt > ./0vs50Min_r801s800.bed
1609. sort -k1,1 -k2,2n ./0vs50Min_r801s800.bed > ./0vs50Min_r801s801.bed
1610. bedtools shuffle -seed 1 -i 0vs50Min_r801s801.bed -g Ecoli-genomesize.txt > ./0vs50Min_r802s801.bed
1611. sort -k1,1 -k2,2n ./0vs50Min_r802s801.bed > ./0vs50Min_r802s802.bed
1612. bedtools shuffle -seed 1 -i 0vs50Min_r802s802.bed -g Ecoli-genomesize.txt > ./0vs50Min_r803s802.bed
1613. sort -k1,1 -k2,2n ./0vs50Min_r803s802.bed > ./0vs50Min_r803s803.bed
1614. bedtools shuffle -seed 1 -i 0vs50Min_r803s803.bed -g Ecoli-genomesize.txt > ./0vs50Min_r804s803.bed
1615. sort -k1,1 -k2,2n ./0vs50Min_r804s803.bed > ./0vs50Min_r804s804.bed
1616. bedtools shuffle -seed 1 -i 0vs50Min_r804s804.bed -g Ecoli-genomesize.txt > ./0vs50Min_r805s804.bed
1617. sort -k1,1 -k2,2n ./0vs50Min_r805s804.bed > ./0vs50Min_r805s805.bed
1618. bedtools shuffle -seed 1 -i 0vs50Min_r805s805.bed -g Ecoli-genomesize.txt > ./0vs50Min_r806s805.bed
1619. sort -k1,1 -k2,2n ./0vs50Min_r806s805.bed > ./0vs50Min_r806s806.bed
1620. bedtools shuffle -seed 1 -i 0vs50Min_r806s806.bed -g Ecoli-genomesize.txt > ./0vs50Min_r807s806.bed
1621. sort -k1,1 -k2,2n ./0vs50Min_r807s806.bed > ./0vs50Min_r807s807.bed
1622. bedtools shuffle -seed 1 -i 0vs50Min_r807s807.bed -g Ecoli-genomesize.txt > ./0vs50Min_r808s807.bed
1623. sort -k1,1 -k2,2n ./0vs50Min_r808s807.bed > ./0vs50Min_r808s808.bed
1624. bedtools shuffle -seed 1 -i 0vs50Min_r808s808.bed -g Ecoli-genomesize.txt > ./0vs50Min_r809s808.bed
1625. sort -k1,1 -k2,2n ./0vs50Min_r809s808.bed > ./0vs50Min_r809s809.bed
1626. bedtools shuffle -seed 1 -i 0vs50Min_r809s809.bed -g Ecoli-genomesize.txt > ./0vs50Min_r810s809.bed
1627. sort -k1,1 -k2,2n ./0vs50Min_r810s809.bed > ./0vs50Min_r810s810.bed
1628. bedtools shuffle -seed 1 -i 0vs50Min_r810s810.bed -g Ecoli-genomesize.txt > ./0vs50Min_r811s810.bed
1629. sort -k1,1 -k2,2n ./0vs50Min_r811s810.bed > ./0vs50Min_r811s811.bed
1630. bedtools shuffle -seed 1 -i 0vs50Min_r811s811.bed -g Ecoli-genomesize.txt > ./0vs50Min_r812s811.bed
1631. sort -k1,1 -k2,2n ./0vs50Min_r812s811.bed > ./0vs50Min_r812s812.bed
1632. bedtools shuffle -seed 1 -i 0vs50Min_r812s812.bed -g Ecoli-genomesize.txt > ./0vs50Min_r813s812.bed
1633. sort -k1,1 -k2,2n ./0vs50Min_r813s812.bed > ./0vs50Min_r813s813.bed
1634. bedtools shuffle -seed 1 -i 0vs50Min_r813s813.bed -g Ecoli-genomesize.txt > ./0vs50Min_r814s813.bed

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1635.    sort -k1,1 -k2,2n ./Ovs50Min_r814s813.bed > ./Ovs50Min_r814s814.bed
1636.    bedtools shuffle -seed 1 -i Ovs50Min_r814s814.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r815s814.bed
1637.    sort -k1,1 -k2,2n ./Ovs50Min_r815s814.bed > ./Ovs50Min_r815s815.bed
1638.    bedtools shuffle -seed 1 -i Ovs50Min_r815s815.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r816s815.bed
1639.    sort -k1,1 -k2,2n ./Ovs50Min_r816s815.bed > ./Ovs50Min_r816s816.bed
1640.    bedtools shuffle -seed 1 -i Ovs50Min_r816s816.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r817s816.bed
1641.    sort -k1,1 -k2,2n ./Ovs50Min_r817s816.bed > ./Ovs50Min_r817s817.bed
1642.    bedtools shuffle -seed 1 -i Ovs50Min_r817s817.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r818s817.bed
1643.    sort -k1,1 -k2,2n ./Ovs50Min_r818s817.bed > ./Ovs50Min_r818s818.bed
1644.    bedtools shuffle -seed 1 -i Ovs50Min_r818s818.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r819s818.bed
1645.    sort -k1,1 -k2,2n ./Ovs50Min_r819s818.bed > ./Ovs50Min_r819s819.bed
1646.    bedtools shuffle -seed 1 -i Ovs50Min_r819s819.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r820s819.bed
1647.    sort -k1,1 -k2,2n ./Ovs50Min_r820s819.bed > ./Ovs50Min_r820s820.bed
1648.    bedtools shuffle -seed 1 -i Ovs50Min_r820s820.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r821s820.bed
1649.    sort -k1,1 -k2,2n ./Ovs50Min_r821s820.bed > ./Ovs50Min_r821s821.bed
1650.    bedtools shuffle -seed 1 -i Ovs50Min_r821s821.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r822s821.bed
1651.    sort -k1,1 -k2,2n ./Ovs50Min_r822s821.bed > ./Ovs50Min_r822s822.bed
1652.    bedtools shuffle -seed 1 -i Ovs50Min_r822s822.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r823s822.bed
1653.    sort -k1,1 -k2,2n ./Ovs50Min_r823s822.bed > ./Ovs50Min_r823s823.bed
1654.    bedtools shuffle -seed 1 -i Ovs50Min_r823s823.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r824s823.bed
1655.    sort -k1,1 -k2,2n ./Ovs50Min_r824s823.bed > ./Ovs50Min_r824s824.bed
1656.    bedtools shuffle -seed 1 -i Ovs50Min_r824s824.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r825s824.bed
1657.    sort -k1,1 -k2,2n ./Ovs50Min_r825s824.bed > ./Ovs50Min_r825s825.bed
1658.    bedtools shuffle -seed 1 -i Ovs50Min_r825s825.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r826s825.bed
1659.    sort -k1,1 -k2,2n ./Ovs50Min_r826s825.bed > ./Ovs50Min_r826s826.bed
1660.    bedtools shuffle -seed 1 -i Ovs50Min_r826s826.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r827s826.bed
1661.    sort -k1,1 -k2,2n ./Ovs50Min_r827s826.bed > ./Ovs50Min_r827s827.bed
1662.    bedtools shuffle -seed 1 -i Ovs50Min_r827s827.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r828s827.bed
1663.    sort -k1,1 -k2,2n ./Ovs50Min_r828s827.bed > ./Ovs50Min_r828s828.bed
1664.    bedtools shuffle -seed 1 -i Ovs50Min_r828s828.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r829s828.bed
1665.    sort -k1,1 -k2,2n ./Ovs50Min_r829s828.bed > ./Ovs50Min_r829s829.bed
1666.    bedtools shuffle -seed 1 -i Ovs50Min_r829s829.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r830s829.bed
1667.    sort -k1,1 -k2,2n ./Ovs50Min_r830s829.bed > ./Ovs50Min_r830s830.bed
1668.    bedtools shuffle -seed 1 -i Ovs50Min_r830s830.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r831s830.bed
1669.    sort -k1,1 -k2,2n ./Ovs50Min_r831s830.bed > ./Ovs50Min_r831s831.bed
1670.    bedtools shuffle -seed 1 -i Ovs50Min_r831s831.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r832s831.bed
1671.    sort -k1,1 -k2,2n ./Ovs50Min_r832s831.bed > ./Ovs50Min_r832s832.bed

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1672. bedtools shuffle -seed 1 -i Ovs50Min_r832s832.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r833s832.bed
1673. sort -k1,1 -k2,2n ./Ovs50Min_r833s832.bed > ./Ovs50Min_r833s833.bed
1674. bedtools shuffle -seed 1 -i Ovs50Min_r833s833.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r834s833.bed
1675. sort -k1,1 -k2,2n ./Ovs50Min_r834s833.bed > ./Ovs50Min_r834s834.bed
1676. bedtools shuffle -seed 1 -i Ovs50Min_r834s834.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r835s834.bed
1677. sort -k1,1 -k2,2n ./Ovs50Min_r835s834.bed > ./Ovs50Min_r835s835.bed
1678. bedtools shuffle -seed 1 -i Ovs50Min_r835s835.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r836s835.bed
1679. sort -k1,1 -k2,2n ./Ovs50Min_r836s835.bed > ./Ovs50Min_r836s836.bed
1680. bedtools shuffle -seed 1 -i Ovs50Min_r836s836.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r837s836.bed
1681. sort -k1,1 -k2,2n ./Ovs50Min_r837s836.bed > ./Ovs50Min_r837s837.bed
1682. bedtools shuffle -seed 1 -i Ovs50Min_r837s837.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r838s837.bed
1683. sort -k1,1 -k2,2n ./Ovs50Min_r838s837.bed > ./Ovs50Min_r838s838.bed
1684. bedtools shuffle -seed 1 -i Ovs50Min_r838s838.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r839s838.bed
1685. sort -k1,1 -k2,2n ./Ovs50Min_r839s838.bed > ./Ovs50Min_r839s839.bed
1686. bedtools shuffle -seed 1 -i Ovs50Min_r839s839.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r840s839.bed
1687. sort -k1,1 -k2,2n ./Ovs50Min_r840s839.bed > ./Ovs50Min_r840s840.bed
1688. bedtools shuffle -seed 1 -i Ovs50Min_r840s840.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r841s840.bed
1689. sort -k1,1 -k2,2n ./Ovs50Min_r841s840.bed > ./Ovs50Min_r841s841.bed
1690. bedtools shuffle -seed 1 -i Ovs50Min_r841s841.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r842s841.bed
1691. sort -k1,1 -k2,2n ./Ovs50Min_r842s841.bed > ./Ovs50Min_r842s842.bed
1692. bedtools shuffle -seed 1 -i Ovs50Min_r842s842.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r843s842.bed
1693. sort -k1,1 -k2,2n ./Ovs50Min_r843s842.bed > ./Ovs50Min_r843s843.bed
1694. bedtools shuffle -seed 1 -i Ovs50Min_r843s843.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r844s843.bed
1695. sort -k1,1 -k2,2n ./Ovs50Min_r844s843.bed > ./Ovs50Min_r844s844.bed
1696. bedtools shuffle -seed 1 -i Ovs50Min_r844s844.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r845s844.bed
1697. sort -k1,1 -k2,2n ./Ovs50Min_r845s844.bed > ./Ovs50Min_r845s845.bed
1698. bedtools shuffle -seed 1 -i Ovs50Min_r845s845.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r846s845.bed
1699. sort -k1,1 -k2,2n ./Ovs50Min_r846s845.bed > ./Ovs50Min_r846s846.bed
1700. bedtools shuffle -seed 1 -i Ovs50Min_r846s846.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r847s846.bed
1701. sort -k1,1 -k2,2n ./Ovs50Min_r847s846.bed > ./Ovs50Min_r847s847.bed
1702. bedtools shuffle -seed 1 -i Ovs50Min_r847s847.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r848s847.bed
1703. sort -k1,1 -k2,2n ./Ovs50Min_r848s847.bed > ./Ovs50Min_r848s848.bed
1704. bedtools shuffle -seed 1 -i Ovs50Min_r848s848.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r849s848.bed
1705. sort -k1,1 -k2,2n ./Ovs50Min_r849s848.bed > ./Ovs50Min_r849s849.bed
1706. bedtools shuffle -seed 1 -i Ovs50Min_r849s849.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r850s849.bed
1707. sort -k1,1 -k2,2n ./Ovs50Min_r850s849.bed > ./Ovs50Min_r850s850.bed
1708. bedtools shuffle -seed 1 -i Ovs50Min_r850s850.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r851s850.bed

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1709.    sort -k1,1 -k2,2n ./Ovs50Min_r851s850.bed > ./Ovs50Min_r851s851.bed
1710.    bedtools shuffle -seed 1 -i Ovs50Min_r851s851.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r852s851.bed
1711.    sort -k1,1 -k2,2n ./Ovs50Min_r852s851.bed > ./Ovs50Min_r852s852.bed
1712.    bedtools shuffle -seed 1 -i Ovs50Min_r852s852.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r853s852.bed
1713.    sort -k1,1 -k2,2n ./Ovs50Min_r853s852.bed > ./Ovs50Min_r853s853.bed
1714.    bedtools shuffle -seed 1 -i Ovs50Min_r853s853.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r854s853.bed
1715.    sort -k1,1 -k2,2n ./Ovs50Min_r854s853.bed > ./Ovs50Min_r854s854.bed
1716.    bedtools shuffle -seed 1 -i Ovs50Min_r854s854.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r855s854.bed
1717.    sort -k1,1 -k2,2n ./Ovs50Min_r855s854.bed > ./Ovs50Min_r855s855.bed
1718.    bedtools shuffle -seed 1 -i Ovs50Min_r855s855.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r856s855.bed
1719.    sort -k1,1 -k2,2n ./Ovs50Min_r856s855.bed > ./Ovs50Min_r856s856.bed
1720.    bedtools shuffle -seed 1 -i Ovs50Min_r856s856.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r857s856.bed
1721.    sort -k1,1 -k2,2n ./Ovs50Min_r857s856.bed > ./Ovs50Min_r857s857.bed
1722.    bedtools shuffle -seed 1 -i Ovs50Min_r857s857.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r858s857.bed
1723.    sort -k1,1 -k2,2n ./Ovs50Min_r858s857.bed > ./Ovs50Min_r858s858.bed
1724.    bedtools shuffle -seed 1 -i Ovs50Min_r858s858.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r859s858.bed
1725.    sort -k1,1 -k2,2n ./Ovs50Min_r859s858.bed > ./Ovs50Min_r859s859.bed
1726.    bedtools shuffle -seed 1 -i Ovs50Min_r859s859.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r860s859.bed
1727.    sort -k1,1 -k2,2n ./Ovs50Min_r860s859.bed > ./Ovs50Min_r860s860.bed
1728.    bedtools shuffle -seed 1 -i Ovs50Min_r860s860.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r861s860.bed
1729.    sort -k1,1 -k2,2n ./Ovs50Min_r861s860.bed > ./Ovs50Min_r861s861.bed
1730.    bedtools shuffle -seed 1 -i Ovs50Min_r861s861.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r862s861.bed
1731.    sort -k1,1 -k2,2n ./Ovs50Min_r862s861.bed > ./Ovs50Min_r862s862.bed
1732.    bedtools shuffle -seed 1 -i Ovs50Min_r862s862.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r863s862.bed
1733.    sort -k1,1 -k2,2n ./Ovs50Min_r863s862.bed > ./Ovs50Min_r863s863.bed
1734.    bedtools shuffle -seed 1 -i Ovs50Min_r863s863.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r864s863.bed
1735.    sort -k1,1 -k2,2n ./Ovs50Min_r864s863.bed > ./Ovs50Min_r864s864.bed
1736.    bedtools shuffle -seed 1 -i Ovs50Min_r864s864.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r865s864.bed
1737.    sort -k1,1 -k2,2n ./Ovs50Min_r865s864.bed > ./Ovs50Min_r865s865.bed
1738.    bedtools shuffle -seed 1 -i Ovs50Min_r865s865.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r866s865.bed
1739.    sort -k1,1 -k2,2n ./Ovs50Min_r866s865.bed > ./Ovs50Min_r866s866.bed
1740.    bedtools shuffle -seed 1 -i Ovs50Min_r866s866.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r867s866.bed
1741.    sort -k1,1 -k2,2n ./Ovs50Min_r867s866.bed > ./Ovs50Min_r867s867.bed
1742.    bedtools shuffle -seed 1 -i Ovs50Min_r867s867.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r868s867.bed
1743.    sort -k1,1 -k2,2n ./Ovs50Min_r868s867.bed > ./Ovs50Min_r868s868.bed
1744.    bedtools shuffle -seed 1 -i Ovs50Min_r868s868.bed -g Ecoli-
        genomesize.txt > ./Ovs50Min_r869s868.bed
1745.    sort -k1,1 -k2,2n ./Ovs50Min_r869s868.bed > ./Ovs50Min_r869s869.bed

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1746. bedtools shuffle -seed 1 -i Ovs50Min_r869s869.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r870s869.bed
1747. sort -k1,1 -k2,2n ./Ovs50Min_r870s869.bed > ./Ovs50Min_r870s870.bed
1748. bedtools shuffle -seed 1 -i Ovs50Min_r870s870.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r871s870.bed
1749. sort -k1,1 -k2,2n ./Ovs50Min_r871s870.bed > ./Ovs50Min_r871s871.bed
1750. bedtools shuffle -seed 1 -i Ovs50Min_r871s871.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r872s871.bed
1751. sort -k1,1 -k2,2n ./Ovs50Min_r872s871.bed > ./Ovs50Min_r872s872.bed
1752. bedtools shuffle -seed 1 -i Ovs50Min_r872s872.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r873s872.bed
1753. sort -k1,1 -k2,2n ./Ovs50Min_r873s872.bed > ./Ovs50Min_r873s873.bed
1754. bedtools shuffle -seed 1 -i Ovs50Min_r873s873.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r874s873.bed
1755. sort -k1,1 -k2,2n ./Ovs50Min_r874s873.bed > ./Ovs50Min_r874s874.bed
1756. bedtools shuffle -seed 1 -i Ovs50Min_r874s874.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r875s874.bed
1757. sort -k1,1 -k2,2n ./Ovs50Min_r875s874.bed > ./Ovs50Min_r875s875.bed
1758. bedtools shuffle -seed 1 -i Ovs50Min_r875s875.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r876s875.bed
1759. sort -k1,1 -k2,2n ./Ovs50Min_r876s875.bed > ./Ovs50Min_r876s876.bed
1760. bedtools shuffle -seed 1 -i Ovs50Min_r876s876.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r877s876.bed
1761. sort -k1,1 -k2,2n ./Ovs50Min_r877s876.bed > ./Ovs50Min_r877s877.bed
1762. bedtools shuffle -seed 1 -i Ovs50Min_r877s877.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r878s877.bed
1763. sort -k1,1 -k2,2n ./Ovs50Min_r878s877.bed > ./Ovs50Min_r878s878.bed
1764. bedtools shuffle -seed 1 -i Ovs50Min_r878s878.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r879s878.bed
1765. sort -k1,1 -k2,2n ./Ovs50Min_r879s878.bed > ./Ovs50Min_r879s879.bed
1766. bedtools shuffle -seed 1 -i Ovs50Min_r879s879.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r880s879.bed
1767. sort -k1,1 -k2,2n ./Ovs50Min_r880s879.bed > ./Ovs50Min_r880s880.bed
1768. bedtools shuffle -seed 1 -i Ovs50Min_r880s880.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r881s880.bed
1769. sort -k1,1 -k2,2n ./Ovs50Min_r881s880.bed > ./Ovs50Min_r881s881.bed
1770. bedtools shuffle -seed 1 -i Ovs50Min_r881s881.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r882s881.bed
1771. sort -k1,1 -k2,2n ./Ovs50Min_r882s881.bed > ./Ovs50Min_r882s882.bed
1772. bedtools shuffle -seed 1 -i Ovs50Min_r882s882.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r883s882.bed
1773. sort -k1,1 -k2,2n ./Ovs50Min_r883s882.bed > ./Ovs50Min_r883s883.bed
1774. bedtools shuffle -seed 1 -i Ovs50Min_r883s883.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r884s883.bed
1775. sort -k1,1 -k2,2n ./Ovs50Min_r884s883.bed > ./Ovs50Min_r884s884.bed
1776. bedtools shuffle -seed 1 -i Ovs50Min_r884s884.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r885s884.bed
1777. sort -k1,1 -k2,2n ./Ovs50Min_r885s884.bed > ./Ovs50Min_r885s885.bed
1778. bedtools shuffle -seed 1 -i Ovs50Min_r885s885.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r886s885.bed
1779. sort -k1,1 -k2,2n ./Ovs50Min_r886s885.bed > ./Ovs50Min_r886s886.bed
1780. bedtools shuffle -seed 1 -i Ovs50Min_r886s886.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r887s886.bed
1781. sort -k1,1 -k2,2n ./Ovs50Min_r887s886.bed > ./Ovs50Min_r887s887.bed
1782. bedtools shuffle -seed 1 -i Ovs50Min_r887s887.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r888s887.bed

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1783.    sort -k1,1 -k2,2n ./0vs50Min_r888s887.bed > ./0vs50Min_r888s888.bed
1784.    bedtools shuffle -seed 1 -i 0vs50Min_r888s888.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r889s888.bed
1785.    sort -k1,1 -k2,2n ./0vs50Min_r889s888.bed > ./0vs50Min_r889s889.bed
1786.    bedtools shuffle -seed 1 -i 0vs50Min_r889s889.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r890s889.bed
1787.    sort -k1,1 -k2,2n ./0vs50Min_r890s889.bed > ./0vs50Min_r890s890.bed
1788.    bedtools shuffle -seed 1 -i 0vs50Min_r890s890.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r891s890.bed
1789.    sort -k1,1 -k2,2n ./0vs50Min_r891s890.bed > ./0vs50Min_r891s891.bed
1790.    bedtools shuffle -seed 1 -i 0vs50Min_r891s891.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r892s891.bed
1791.    sort -k1,1 -k2,2n ./0vs50Min_r892s891.bed > ./0vs50Min_r892s892.bed
1792.    bedtools shuffle -seed 1 -i 0vs50Min_r892s892.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r893s892.bed
1793.    sort -k1,1 -k2,2n ./0vs50Min_r893s892.bed > ./0vs50Min_r893s893.bed
1794.    bedtools shuffle -seed 1 -i 0vs50Min_r893s893.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r894s893.bed
1795.    sort -k1,1 -k2,2n ./0vs50Min_r894s893.bed > ./0vs50Min_r894s894.bed
1796.    bedtools shuffle -seed 1 -i 0vs50Min_r894s894.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r895s894.bed
1797.    sort -k1,1 -k2,2n ./0vs50Min_r895s894.bed > ./0vs50Min_r895s895.bed
1798.    bedtools shuffle -seed 1 -i 0vs50Min_r895s895.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r896s895.bed
1799.    sort -k1,1 -k2,2n ./0vs50Min_r896s895.bed > ./0vs50Min_r896s896.bed
1800.    bedtools shuffle -seed 1 -i 0vs50Min_r896s896.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r897s896.bed
1801.    sort -k1,1 -k2,2n ./0vs50Min_r897s896.bed > ./0vs50Min_r897s897.bed
1802.    bedtools shuffle -seed 1 -i 0vs50Min_r897s897.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r898s897.bed
1803.    sort -k1,1 -k2,2n ./0vs50Min_r898s897.bed > ./0vs50Min_r898s898.bed
1804.    bedtools shuffle -seed 1 -i 0vs50Min_r898s898.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r899s898.bed
1805.    sort -k1,1 -k2,2n ./0vs50Min_r899s898.bed > ./0vs50Min_r899s899.bed
1806.    bedtools shuffle -seed 1 -i 0vs50Min_r899s899.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r900s899.bed
1807.    sort -k1,1 -k2,2n ./0vs50Min_r900s899.bed > ./0vs50Min_r900s900.bed
1808.    bedtools shuffle -seed 1 -i 0vs50Min_r900s900.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r901s900.bed
1809.    sort -k1,1 -k2,2n ./0vs50Min_r901s900.bed > ./0vs50Min_r901s901.bed
1810.    bedtools shuffle -seed 1 -i 0vs50Min_r901s901.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r902s901.bed
1811.    sort -k1,1 -k2,2n ./0vs50Min_r902s901.bed > ./0vs50Min_r902s902.bed
1812.    bedtools shuffle -seed 1 -i 0vs50Min_r902s902.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r903s902.bed
1813.    sort -k1,1 -k2,2n ./0vs50Min_r903s902.bed > ./0vs50Min_r903s903.bed
1814.    bedtools shuffle -seed 1 -i 0vs50Min_r903s903.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r904s903.bed
1815.    sort -k1,1 -k2,2n ./0vs50Min_r904s903.bed > ./0vs50Min_r904s904.bed
1816.    bedtools shuffle -seed 1 -i 0vs50Min_r904s904.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r905s904.bed
1817.    sort -k1,1 -k2,2n ./0vs50Min_r905s904.bed > ./0vs50Min_r905s905.bed
1818.    bedtools shuffle -seed 1 -i 0vs50Min_r905s905.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r906s905.bed
1819.    sort -k1,1 -k2,2n ./0vs50Min_r906s905.bed > ./0vs50Min_r906s906.bed

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1820. bedtools shuffle -seed 1 -i Ovs50Min_r906s906.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r907s906.bed
1821. sort -k1,1 -k2,2n ./Ovs50Min_r907s906.bed > ./Ovs50Min_r907s907.bed
1822. bedtools shuffle -seed 1 -i Ovs50Min_r907s907.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r908s907.bed
1823. sort -k1,1 -k2,2n ./Ovs50Min_r908s907.bed > ./Ovs50Min_r908s908.bed
1824. bedtools shuffle -seed 1 -i Ovs50Min_r908s908.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r909s908.bed
1825. sort -k1,1 -k2,2n ./Ovs50Min_r909s908.bed > ./Ovs50Min_r909s909.bed
1826. bedtools shuffle -seed 1 -i Ovs50Min_r909s909.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r910s909.bed
1827. sort -k1,1 -k2,2n ./Ovs50Min_r910s909.bed > ./Ovs50Min_r910s910.bed
1828. bedtools shuffle -seed 1 -i Ovs50Min_r910s910.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r911s910.bed
1829. sort -k1,1 -k2,2n ./Ovs50Min_r911s910.bed > ./Ovs50Min_r911s911.bed
1830. bedtools shuffle -seed 1 -i Ovs50Min_r911s911.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r912s911.bed
1831. sort -k1,1 -k2,2n ./Ovs50Min_r912s911.bed > ./Ovs50Min_r912s912.bed
1832. bedtools shuffle -seed 1 -i Ovs50Min_r912s912.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r913s912.bed
1833. sort -k1,1 -k2,2n ./Ovs50Min_r913s912.bed > ./Ovs50Min_r913s913.bed
1834. bedtools shuffle -seed 1 -i Ovs50Min_r913s913.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r914s913.bed
1835. sort -k1,1 -k2,2n ./Ovs50Min_r914s913.bed > ./Ovs50Min_r914s914.bed
1836. bedtools shuffle -seed 1 -i Ovs50Min_r914s914.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r915s914.bed
1837. sort -k1,1 -k2,2n ./Ovs50Min_r915s914.bed > ./Ovs50Min_r915s915.bed
1838. bedtools shuffle -seed 1 -i Ovs50Min_r915s915.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r916s915.bed
1839. sort -k1,1 -k2,2n ./Ovs50Min_r916s915.bed > ./Ovs50Min_r916s916.bed
1840. bedtools shuffle -seed 1 -i Ovs50Min_r916s916.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r917s916.bed
1841. sort -k1,1 -k2,2n ./Ovs50Min_r917s916.bed > ./Ovs50Min_r917s917.bed
1842. bedtools shuffle -seed 1 -i Ovs50Min_r917s917.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r918s917.bed
1843. sort -k1,1 -k2,2n ./Ovs50Min_r918s917.bed > ./Ovs50Min_r918s918.bed
1844. bedtools shuffle -seed 1 -i Ovs50Min_r918s918.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r919s918.bed
1845. sort -k1,1 -k2,2n ./Ovs50Min_r919s918.bed > ./Ovs50Min_r919s919.bed
1846. bedtools shuffle -seed 1 -i Ovs50Min_r919s919.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r920s919.bed
1847. sort -k1,1 -k2,2n ./Ovs50Min_r920s919.bed > ./Ovs50Min_r920s920.bed
1848. bedtools shuffle -seed 1 -i Ovs50Min_r920s920.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r921s920.bed
1849. sort -k1,1 -k2,2n ./Ovs50Min_r921s920.bed > ./Ovs50Min_r921s921.bed
1850. bedtools shuffle -seed 1 -i Ovs50Min_r921s921.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r922s921.bed
1851. sort -k1,1 -k2,2n ./Ovs50Min_r922s921.bed > ./Ovs50Min_r922s922.bed
1852. bedtools shuffle -seed 1 -i Ovs50Min_r922s922.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r923s922.bed
1853. sort -k1,1 -k2,2n ./Ovs50Min_r923s922.bed > ./Ovs50Min_r923s923.bed
1854. bedtools shuffle -seed 1 -i Ovs50Min_r923s923.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r924s923.bed
1855. sort -k1,1 -k2,2n ./Ovs50Min_r924s923.bed > ./Ovs50Min_r924s924.bed
1856. bedtools shuffle -seed 1 -i Ovs50Min_r924s924.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r925s924.bed

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1857. sort -k1,1 -k2,2n ./0vs50Min_r925s924.bed > ./0vs50Min_r925s925.bed
1858. bedtools shuffle -seed 1 -i 0vs50Min_r925s925.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r926s925.bed
1859. sort -k1,1 -k2,2n ./0vs50Min_r926s925.bed > ./0vs50Min_r926s926.bed
1860. bedtools shuffle -seed 1 -i 0vs50Min_r926s926.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r927s926.bed
1861. sort -k1,1 -k2,2n ./0vs50Min_r927s926.bed > ./0vs50Min_r927s927.bed
1862. bedtools shuffle -seed 1 -i 0vs50Min_r927s927.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r928s927.bed
1863. sort -k1,1 -k2,2n ./0vs50Min_r928s927.bed > ./0vs50Min_r928s928.bed
1864. bedtools shuffle -seed 1 -i 0vs50Min_r928s928.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r929s928.bed
1865. sort -k1,1 -k2,2n ./0vs50Min_r929s928.bed > ./0vs50Min_r929s929.bed
1866. bedtools shuffle -seed 1 -i 0vs50Min_r929s929.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r930s929.bed
1867. sort -k1,1 -k2,2n ./0vs50Min_r930s929.bed > ./0vs50Min_r930s930.bed
1868. bedtools shuffle -seed 1 -i 0vs50Min_r930s930.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r931s930.bed
1869. sort -k1,1 -k2,2n ./0vs50Min_r931s930.bed > ./0vs50Min_r931s931.bed
1870. bedtools shuffle -seed 1 -i 0vs50Min_r931s931.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r932s931.bed
1871. sort -k1,1 -k2,2n ./0vs50Min_r932s931.bed > ./0vs50Min_r932s932.bed
1872. bedtools shuffle -seed 1 -i 0vs50Min_r932s932.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r933s932.bed
1873. sort -k1,1 -k2,2n ./0vs50Min_r933s932.bed > ./0vs50Min_r933s933.bed
1874. bedtools shuffle -seed 1 -i 0vs50Min_r933s933.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r934s933.bed
1875. sort -k1,1 -k2,2n ./0vs50Min_r934s933.bed > ./0vs50Min_r934s934.bed
1876. bedtools shuffle -seed 1 -i 0vs50Min_r934s934.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r935s934.bed
1877. sort -k1,1 -k2,2n ./0vs50Min_r935s934.bed > ./0vs50Min_r935s935.bed
1878. bedtools shuffle -seed 1 -i 0vs50Min_r935s935.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r936s935.bed
1879. sort -k1,1 -k2,2n ./0vs50Min_r936s935.bed > ./0vs50Min_r936s936.bed
1880. bedtools shuffle -seed 1 -i 0vs50Min_r936s936.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r937s936.bed
1881. sort -k1,1 -k2,2n ./0vs50Min_r937s936.bed > ./0vs50Min_r937s937.bed
1882. bedtools shuffle -seed 1 -i 0vs50Min_r937s937.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r938s937.bed
1883. sort -k1,1 -k2,2n ./0vs50Min_r938s937.bed > ./0vs50Min_r938s938.bed
1884. bedtools shuffle -seed 1 -i 0vs50Min_r938s938.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r939s938.bed
1885. sort -k1,1 -k2,2n ./0vs50Min_r939s938.bed > ./0vs50Min_r939s939.bed
1886. bedtools shuffle -seed 1 -i 0vs50Min_r939s939.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r940s939.bed
1887. sort -k1,1 -k2,2n ./0vs50Min_r940s939.bed > ./0vs50Min_r940s940.bed
1888. bedtools shuffle -seed 1 -i 0vs50Min_r940s940.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r941s940.bed
1889. sort -k1,1 -k2,2n ./0vs50Min_r941s940.bed > ./0vs50Min_r941s941.bed
1890. bedtools shuffle -seed 1 -i 0vs50Min_r941s941.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r942s941.bed
1891. sort -k1,1 -k2,2n ./0vs50Min_r942s941.bed > ./0vs50Min_r942s942.bed
1892. bedtools shuffle -seed 1 -i 0vs50Min_r942s942.bed -g Ecoli-
genomesize.txt > ./0vs50Min_r943s942.bed
1893. sort -k1,1 -k2,2n ./0vs50Min_r943s942.bed > ./0vs50Min_r943s943.bed

1894. bedtools shuffle -seed 1 -i Ovs50Min_r943s943.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r944s943.bed
1895. sort -k1,1 -k2,2n ./Ovs50Min_r944s943.bed > ./Ovs50Min_r944s944.bed
1896. bedtools shuffle -seed 1 -i Ovs50Min_r944s944.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r945s944.bed
1897. sort -k1,1 -k2,2n ./Ovs50Min_r945s944.bed > ./Ovs50Min_r945s945.bed
1898. bedtools shuffle -seed 1 -i Ovs50Min_r945s945.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r946s945.bed
1899. sort -k1,1 -k2,2n ./Ovs50Min_r946s945.bed > ./Ovs50Min_r946s946.bed
1900. bedtools shuffle -seed 1 -i Ovs50Min_r946s946.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r947s946.bed
1901. sort -k1,1 -k2,2n ./Ovs50Min_r947s946.bed > ./Ovs50Min_r947s947.bed
1902. bedtools shuffle -seed 1 -i Ovs50Min_r947s947.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r948s947.bed
1903. sort -k1,1 -k2,2n ./Ovs50Min_r948s947.bed > ./Ovs50Min_r948s948.bed
1904. bedtools shuffle -seed 1 -i Ovs50Min_r948s948.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r949s948.bed
1905. sort -k1,1 -k2,2n ./Ovs50Min_r949s948.bed > ./Ovs50Min_r949s949.bed
1906. bedtools shuffle -seed 1 -i Ovs50Min_r949s949.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r950s949.bed
1907. sort -k1,1 -k2,2n ./Ovs50Min_r950s949.bed > ./Ovs50Min_r950s950.bed
1908. bedtools shuffle -seed 1 -i Ovs50Min_r950s950.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r951s950.bed
1909. sort -k1,1 -k2,2n ./Ovs50Min_r951s950.bed > ./Ovs50Min_r951s951.bed
1910. bedtools shuffle -seed 1 -i Ovs50Min_r951s951.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r952s951.bed
1911. sort -k1,1 -k2,2n ./Ovs50Min_r952s951.bed > ./Ovs50Min_r952s952.bed
1912. bedtools shuffle -seed 1 -i Ovs50Min_r952s952.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r953s952.bed
1913. sort -k1,1 -k2,2n ./Ovs50Min_r953s952.bed > ./Ovs50Min_r953s953.bed
1914. bedtools shuffle -seed 1 -i Ovs50Min_r953s953.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r954s953.bed
1915. sort -k1,1 -k2,2n ./Ovs50Min_r954s953.bed > ./Ovs50Min_r954s954.bed
1916. bedtools shuffle -seed 1 -i Ovs50Min_r954s954.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r955s954.bed
1917. sort -k1,1 -k2,2n ./Ovs50Min_r955s954.bed > ./Ovs50Min_r955s955.bed
1918. bedtools shuffle -seed 1 -i Ovs50Min_r955s955.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r956s955.bed
1919. sort -k1,1 -k2,2n ./Ovs50Min_r956s955.bed > ./Ovs50Min_r956s956.bed
1920. bedtools shuffle -seed 1 -i Ovs50Min_r956s956.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r957s956.bed
1921. sort -k1,1 -k2,2n ./Ovs50Min_r957s956.bed > ./Ovs50Min_r957s957.bed
1922. bedtools shuffle -seed 1 -i Ovs50Min_r957s957.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r958s957.bed
1923. sort -k1,1 -k2,2n ./Ovs50Min_r958s957.bed > ./Ovs50Min_r958s958.bed
1924. bedtools shuffle -seed 1 -i Ovs50Min_r958s958.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r959s958.bed
1925. sort -k1,1 -k2,2n ./Ovs50Min_r959s958.bed > ./Ovs50Min_r959s959.bed
1926. bedtools shuffle -seed 1 -i Ovs50Min_r959s959.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r960s959.bed
1927. sort -k1,1 -k2,2n ./Ovs50Min_r960s959.bed > ./Ovs50Min_r960s960.bed
1928. bedtools shuffle -seed 1 -i Ovs50Min_r960s960.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r961s960.bed
1929. sort -k1,1 -k2,2n ./Ovs50Min_r961s960.bed > ./Ovs50Min_r961s961.bed
1930. bedtools shuffle -seed 1 -i Ovs50Min_r961s961.bed -g Ecoli-genomesize.txt > ./Ovs50Min_r962s961.bed

```

1931.    sort -k1,1 -k2,2n ./0vs50Min_r962s961.bed > ./0vs50Min_r962s962.bed
1932.    bedtools shuffle -seed 1 -i 0vs50Min_r962s962.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r963s962.bed
1933.    sort -k1,1 -k2,2n ./0vs50Min_r963s962.bed > ./0vs50Min_r963s963.bed
1934.    bedtools shuffle -seed 1 -i 0vs50Min_r963s963.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r964s963.bed
1935.    sort -k1,1 -k2,2n ./0vs50Min_r964s963.bed > ./0vs50Min_r964s964.bed
1936.    bedtools shuffle -seed 1 -i 0vs50Min_r964s964.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r965s964.bed
1937.    sort -k1,1 -k2,2n ./0vs50Min_r965s964.bed > ./0vs50Min_r965s965.bed
1938.    bedtools shuffle -seed 1 -i 0vs50Min_r965s965.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r966s965.bed
1939.    sort -k1,1 -k2,2n ./0vs50Min_r966s965.bed > ./0vs50Min_r966s966.bed
1940.    bedtools shuffle -seed 1 -i 0vs50Min_r966s966.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r967s966.bed
1941.    sort -k1,1 -k2,2n ./0vs50Min_r967s966.bed > ./0vs50Min_r967s967.bed
1942.    bedtools shuffle -seed 1 -i 0vs50Min_r967s967.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r968s967.bed
1943.    sort -k1,1 -k2,2n ./0vs50Min_r968s967.bed > ./0vs50Min_r968s968.bed
1944.    bedtools shuffle -seed 1 -i 0vs50Min_r968s968.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r969s968.bed
1945.    sort -k1,1 -k2,2n ./0vs50Min_r969s968.bed > ./0vs50Min_r969s969.bed
1946.    bedtools shuffle -seed 1 -i 0vs50Min_r969s969.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r970s969.bed
1947.    sort -k1,1 -k2,2n ./0vs50Min_r970s969.bed > ./0vs50Min_r970s970.bed
1948.    bedtools shuffle -seed 1 -i 0vs50Min_r970s970.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r971s970.bed
1949.    sort -k1,1 -k2,2n ./0vs50Min_r971s970.bed > ./0vs50Min_r971s971.bed
1950.    bedtools shuffle -seed 1 -i 0vs50Min_r971s971.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r972s971.bed
1951.    sort -k1,1 -k2,2n ./0vs50Min_r972s971.bed > ./0vs50Min_r972s972.bed
1952.    bedtools shuffle -seed 1 -i 0vs50Min_r972s972.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r973s972.bed
1953.    sort -k1,1 -k2,2n ./0vs50Min_r973s972.bed > ./0vs50Min_r973s973.bed
1954.    bedtools shuffle -seed 1 -i 0vs50Min_r973s973.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r974s973.bed
1955.    sort -k1,1 -k2,2n ./0vs50Min_r974s973.bed > ./0vs50Min_r974s974.bed
1956.    bedtools shuffle -seed 1 -i 0vs50Min_r974s974.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r975s974.bed
1957.    sort -k1,1 -k2,2n ./0vs50Min_r975s974.bed > ./0vs50Min_r975s975.bed
1958.    bedtools shuffle -seed 1 -i 0vs50Min_r975s975.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r976s975.bed
1959.    sort -k1,1 -k2,2n ./0vs50Min_r976s975.bed > ./0vs50Min_r976s976.bed
1960.    bedtools shuffle -seed 1 -i 0vs50Min_r976s976.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r977s976.bed
1961.    sort -k1,1 -k2,2n ./0vs50Min_r977s976.bed > ./0vs50Min_r977s977.bed
1962.    bedtools shuffle -seed 1 -i 0vs50Min_r977s977.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r978s977.bed
1963.    sort -k1,1 -k2,2n ./0vs50Min_r978s977.bed > ./0vs50Min_r978s978.bed
1964.    bedtools shuffle -seed 1 -i 0vs50Min_r978s978.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r979s978.bed
1965.    sort -k1,1 -k2,2n ./0vs50Min_r979s978.bed > ./0vs50Min_r979s979.bed
1966.    bedtools shuffle -seed 1 -i 0vs50Min_r979s979.bed -g Ecoli-
        genomesize.txt > ./0vs50Min_r980s979.bed
1967.    sort -k1,1 -k2,2n ./0vs50Min_r980s979.bed > ./0vs50Min_r980s980.bed

```

```

1968. bedtools shuffle -seed 1 -i Ovs50Min_r980s980.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r981s980.bed
1969. sort -k1,1 -k2,2n ./Ovs50Min_r981s980.bed > ./Ovs50Min_r981s981.bed
1970. bedtools shuffle -seed 1 -i Ovs50Min_r981s981.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r982s981.bed
1971. sort -k1,1 -k2,2n ./Ovs50Min_r982s981.bed > ./Ovs50Min_r982s982.bed
1972. bedtools shuffle -seed 1 -i Ovs50Min_r982s982.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r983s982.bed
1973. sort -k1,1 -k2,2n ./Ovs50Min_r983s982.bed > ./Ovs50Min_r983s983.bed
1974. bedtools shuffle -seed 1 -i Ovs50Min_r983s983.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r984s983.bed
1975. sort -k1,1 -k2,2n ./Ovs50Min_r984s983.bed > ./Ovs50Min_r984s984.bed
1976. bedtools shuffle -seed 1 -i Ovs50Min_r984s984.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r985s984.bed
1977. sort -k1,1 -k2,2n ./Ovs50Min_r985s984.bed > ./Ovs50Min_r985s985.bed
1978. bedtools shuffle -seed 1 -i Ovs50Min_r985s985.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r986s985.bed
1979. sort -k1,1 -k2,2n ./Ovs50Min_r986s985.bed > ./Ovs50Min_r986s986.bed
1980. bedtools shuffle -seed 1 -i Ovs50Min_r986s986.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r987s986.bed
1981. sort -k1,1 -k2,2n ./Ovs50Min_r987s986.bed > ./Ovs50Min_r987s987.bed
1982. bedtools shuffle -seed 1 -i Ovs50Min_r987s987.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r988s987.bed
1983. sort -k1,1 -k2,2n ./Ovs50Min_r988s987.bed > ./Ovs50Min_r988s988.bed
1984. bedtools shuffle -seed 1 -i Ovs50Min_r988s988.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r989s988.bed
1985. sort -k1,1 -k2,2n ./Ovs50Min_r989s988.bed > ./Ovs50Min_r989s989.bed
1986. bedtools shuffle -seed 1 -i Ovs50Min_r989s989.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r990s989.bed
1987. sort -k1,1 -k2,2n ./Ovs50Min_r990s989.bed > ./Ovs50Min_r990s990.bed
1988. bedtools shuffle -seed 1 -i Ovs50Min_r990s990.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r991s990.bed
1989. sort -k1,1 -k2,2n ./Ovs50Min_r991s990.bed > ./Ovs50Min_r991s991.bed
1990. bedtools shuffle -seed 1 -i Ovs50Min_r991s991.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r992s991.bed
1991. sort -k1,1 -k2,2n ./Ovs50Min_r992s991.bed > ./Ovs50Min_r992s992.bed
1992. bedtools shuffle -seed 1 -i Ovs50Min_r992s992.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r993s992.bed
1993. sort -k1,1 -k2,2n ./Ovs50Min_r993s992.bed > ./Ovs50Min_r993s993.bed
1994. bedtools shuffle -seed 1 -i Ovs50Min_r993s993.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r994s993.bed
1995. sort -k1,1 -k2,2n ./Ovs50Min_r994s993.bed > ./Ovs50Min_r994s994.bed
1996. bedtools shuffle -seed 1 -i Ovs50Min_r994s994.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r995s994.bed
1997. sort -k1,1 -k2,2n ./Ovs50Min_r995s994.bed > ./Ovs50Min_r995s995.bed
1998. bedtools shuffle -seed 1 -i Ovs50Min_r995s995.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r996s995.bed
1999. sort -k1,1 -k2,2n ./Ovs50Min_r996s995.bed > ./Ovs50Min_r996s996.bed
2000. bedtools shuffle -seed 1 -i Ovs50Min_r996s996.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r997s996.bed
2001. sort -k1,1 -k2,2n ./Ovs50Min_r997s996.bed > ./Ovs50Min_r997s997.bed
2002. bedtools shuffle -seed 1 -i Ovs50Min_r997s997.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r998s997.bed
2003. sort -k1,1 -k2,2n ./Ovs50Min_r998s997.bed > ./Ovs50Min_r998s998.bed
2004. bedtools shuffle -seed 1 -i Ovs50Min_r998s998.bed -g Ecoli-
      genomesize.txt > ./Ovs50Min_r999s998.bed

```

```
2005.    sort -k1,1 -k2,2n ./Ovs50Min_r999s998.bed > ./Ovs50Min_r999s999.bed
2006.    bedtools shuffle -seed 1 -i Ovs50Min_r999s999.bed -g Ecoli-
         genomesize.txt > ./Ovs50Min_r1000s999.bed
2007.    sort -k1,1 -k2,2n ./Ovs50Min_r1000s999.bed > ./Ovs50Min_r1000s1000.bed
```

BEDTools create random locations for *E. coli* GATCs

```
#!/bin/bash
```

- 1.
2. #bedtools_random_EcoliGATC.sh
3. #bedtools version: bedtools v2.27.1
4. #Uses Bedtools to create random locations for E. Coli GATCs
- 5.
6. bedtools random -g ./Ecoli-genomesize.txt -n 19122 -l 4 > EcoliGATC_All_r.bed
7. bedtools random -g ./Ecoli-genomesize.txt -n 3375 -l 4 > EcoliGATC_Pairs_r.bed
8. bedtools random -g ./Ecoli-genomesize.txt -n 1129 -l 4 > EcoliGATC_HigherO1_r.bed
9. bedtools random -g ./Ecoli-genomesize.txt -n 422 -l 4 > EcoliGATC_HigherO2_r.bed
10. bedtools random -g ./Ecoli-genomesize.txt -n 172 -l 4 > EcoliGATC_HigherO3_r.bed

BEDOPS chop random signals to 1 bp

```
1. #!/bin/bash
2.
3. #Bedops_ChopRandom.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find chop randomized signals into 1bp
6.
7. bedops --chop 1 ./Microarray/SeqAOnly-R1000e1.bed > ./Microarray/SeqAOnly-R1000e1-c.bed
8. bedops --chop 1 ./Microarray/SeqAOnly-R1000e1-Top50.bed > ./Microarray/SeqAOnly-R1000e1-
c-Top50.bed
9. bedops --chop 1 ./Microarray/SeqAOnly-R1000e1-Top25.bed > ./Microarray/SeqAOnly-R1000e1-
c-Top25.bed
10. bedops --chop 1 ./Microarray/SeqAOnly-R1000e1-Top10.bed > ./Microarray/SeqAOnly-R1000e1-
c-Top10.bed
11. bedops --chop 1 ./Microarray/SeqAOnly-R1000e1-Top5.bed > ./Microarray/SeqAOnly-R1000e1-
c-Top5.bed
12.
13. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Microarray/SeqAOnly_Grainger-R1000e1-c.bed
14. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-R1000e1-
Top50.bed > ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top50.bed
15. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-R1000e1-
Top25.bed > ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top25.bed
16. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-R1000e1-
Top10.bed > ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top10.bed
17. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-R1000e1-
Top5.bed > ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top5.bed
18.
19. bedops --chop 1 ./Microarray/0vs50Min-R1000e1.bed > ./Microarray/0vs50Min-R1000e1-c.bed
20. bedops --chop 1 ./Microarray/0vs50Min-R1000e1-Top50.bed > ./Microarray/0vs50Min-R1000e1-
c-Top50.bed
21. bedops --chop 1 ./Microarray/0vs50Min-R1000e1-Top25.bed > ./Microarray/0vs50Min-R1000e1-
c-Top25.bed
22. bedops --chop 1 ./Microarray/0vs50Min-R1000e1-Top10.bed > ./Microarray/0vs50Min-R1000e1-
c-Top10.bed
23. bedops --chop 1 ./Microarray/0vs50Min-R1000e1-Top5.bed > ./Microarray/0vs50Min-R1000e1-c-
Top5.bed
```

BEDOPS SeqA Only randomized signals (SeqA Only 1) in *E. coli* regions

```
1.
2. #Bedops_ElementSeqAOnly_r-cinEcoliGenes.sh
3. #bedops version: 2.4.35 (typical)
4. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli ORFs
5.
6. mkdir ./Element/
7.
8. #bedops make bed files element of
9. bedops --element-of ./Microarray/SeqAOnly-R1000e1-
c.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-R1000e1-c-
Element-EcoliGenes_RemoveIDandDups-Merged.bed
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-
R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-
R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-Merged.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-
R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-Merged.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-
R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-Merged.bed
14.
15.
16. # Copy to excel
17. cp ./Element/SeqAOnly-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
Merged.bed ./Element/SeqAOnly-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
Merged.xls
18. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-
Merged.bed ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-
Merged.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-
Merged.bed ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-
Merged.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-
Merged.bed ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-
Merged.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-
Merged.bed ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-
Merged.xls
22.
23. #Line count
24. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-
EcoliGenes_RemoveIDandDups-Merged.txt
25.
26. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged/
27. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_r-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli Noncoding r
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-R1000e1-c-Element-EcoliNoncoding-
    Complemented.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top50.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliNoncoding-
    Complemented.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top25.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliNoncoding-
    Complemented.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top10.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliNoncoding-
    Complemented.bed
14. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top5.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliNoncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-R1000e1-c-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-R1000e1-c-Element-EcoliNoncoding-
    Complemented.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliNoncoding-
    Complemented.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliNoncoding-
    Complemented.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliNoncoding-
    Complemented.xls
22. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliNoncoding-
    Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-EcoliNoncoding-
    Complemented.txt
26.
27. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_r-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli Nonpropha
   ge regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-
    c.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-R1000e1-c-Element-
    EcoliNonphage.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-R1000e1-c-Top50-Element-
    EcoliNonphage.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-R1000e1-c-Top25-Element-
    EcoliNonphage.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-R1000e1-c-Top10-Element-
    EcoliNonphage.bed
14. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-R1000e1-c-Top5-Element-
    EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-R1000e1-c-Element-EcoliNonphage.bed ./Element/SeqAOnly-R1000e1-
    c-Element-EcoliNonphage.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliNonphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top50-Element-EcoliNonphage.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliNonphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top25-Element-EcoliNonphage.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliNonphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top10-Element-EcoliNonphage.xls
22. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliNonphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top5-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-
    EcoliNonphage.txt
26.
27. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliNonphage/
28. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliNonphage/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_r-cinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli Nonpromoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.bed
14. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.xls
22. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.txt
26.
27. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement/
28. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_r-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli Promoter re
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-
   c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-R1000e1-c-
   Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
   Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-
   R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
   Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-
   R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
   Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-
   R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
   Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-R1000e1-
   c-Top5-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_r-cinEcoliProphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly randomized 1bp chopped signal in E. coli Prophage r
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-R1000e1-
    c.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly-R1000e1-c-Element-
    EcoliProphage.bed
11. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top50.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly-R1000e1-c-Top50-Element-
    EcoliProphage.bed
12. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top25.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly-R1000e1-c-Top25-Element-
    EcoliProphage.bed
13. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top10.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly-R1000e1-c-Top10-Element-
    EcoliProphage.bed
14. bedops --element-of ./Microarray/SeqAOnly-R1000e1-c-
    Top5.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly-R1000e1-c-Top5-Element-
    EcoliProphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-R1000e1-c-Element-EcoliProphage.bed ./Element/SeqAOnly-R1000e1-c-
    Element-EcoliProphage.xls
19. cp ./Element/SeqAOnly-R1000e1-c-Top50-Element-EcoliProphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top50-Element-EcoliProphage.xls
20. cp ./Element/SeqAOnly-R1000e1-c-Top25-Element-EcoliProphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top25-Element-EcoliProphage.xls
21. cp ./Element/SeqAOnly-R1000e1-c-Top10-Element-EcoliProphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top10-Element-EcoliProphage.xls
22. cp ./Element/SeqAOnly-R1000e1-c-Top5-Element-EcoliProphage.bed ./Element/SeqAOnly-
    R1000e1-c-Top5-Element-EcoliProphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-R1000e1-c-Element-
    EcoliProphage.txt
26.
27. mkdir ./SeqAOnly-R1000e1-c-Element-EcoliProphage/
28. mv ./Element/ ./SeqAOnly-R1000e1-c-Element-EcoliProphage/

```

BEDOPS SeqA Only (Grainger) randomized signals (SeqA Only 2) in *E. coli*

regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli O
   RFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-
    c.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly_Grainger-
    R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-
    EcoliGenes_RemoveIDandDups-Merged.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-
    EcoliGenes_RemoveIDandDups-Merged.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-
    EcoliGenes_RemoveIDandDups-Merged.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-
    EcoliGenes_RemoveIDandDups-Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-
    EcoliGenes_RemoveIDandDups-Merged.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-
    EcoliGenes_RemoveIDandDups-Merged.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-
    EcoliGenes_RemoveIDandDups-Merged.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-
    EcoliGenes_RemoveIDandDups-Merged.xls
23.
24. #Line count
```



```
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
    Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli N
   oncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNoncoding-
   Complemented.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top50.bed ./Genes/EcoliNoncoding-Complemented.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Top50-Element-EcoliNoncoding-Complemented.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top25.bed ./Genes/EcoliNoncoding-Complemented.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Top25-Element-EcoliNoncoding-Complemented.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top10.bed ./Genes/EcoliNoncoding-Complemented.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Top10-Element-EcoliNoncoding-Complemented.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top5.bed ./Genes/EcoliNoncoding-Complemented.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Top5-Element-EcoliNoncoding-Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNoncoding-
   Complemented.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliNoncoding-
   Complemented.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliNoncoding-
   Complemented.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliNoncoding-
   Complemented.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliNoncoding-
   Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-
   EcoliNoncoding-Complemented.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli Nonphage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliNonphage.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliNonphage.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliNonphage.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliNonphage.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliNonphage.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliNonphage.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage/
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliNonphage/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli Nonpromoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-complement.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-complement.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-complement.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-complement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement/

```

```
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli P
   romoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-
   c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainge
   r-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainge
   r-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainge
   r-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
   Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
   R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-
   Element-EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-
   Element-EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-
   Element-EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-
   Element-EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger_r-cinEcoliProphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger randomized 1bp chopped signal in E. coli P
   rophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-
    c.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Element-
    EcoliProphage.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top50.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-
    Element-EcoliProphage.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top25.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-
    Element-EcoliProphage.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top10.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-
    Element-EcoliProphage.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-R1000e1-c-
    Top5.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-
    Element-EcoliProphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Element-
    EcoliProphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Element-EcoliProphage.xls
19. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-
    EcoliProphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top50-Element-
    EcoliProphage.xls
20. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-
    EcoliProphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top25-Element-
    EcoliProphage.xls
21. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-
    EcoliProphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top10-Element-
    EcoliProphage.xls
22. cp ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-
    EcoliProphage.bed ./Element/SeqAOnly_Grainger-R1000e1-c-Top5-Element-EcoliProphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-R1000e1-c-Element-
    EcoliProphage.txt
26.
27. mkdir ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliProphage/
28. mv ./Element/ ./SeqAOnly_Grainger-R1000e1-c-Element-EcoliProphage/

```

BEDOPS 0 vs. 50 Min randomized signals (SeqA Binding) in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min_r-cinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-
    c.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-R1000e1-c-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
    Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-
    R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-Merged.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
    Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-
    R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-Merged.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
    Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-
    R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-Merged.bed
14. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
    Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-R1000e1-
    c-Top5-Element-EcoliGenes_RemoveIDandDups-Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./0vs50Min-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliGenes_RemoveIDandDups-Merged/
```



```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min_r-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli Noncoding r
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-c.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/0vs50Min-R1000e1-c-Element-EcoliNoncoding-
   Complemented.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top50.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNoncoding-
   Complemented.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top25.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNoncoding-
   Complemented.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top10.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNoncoding-
   Complemented.bed
14. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top5.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNoncoding-
   Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-R1000e1-c-Element-EcoliNoncoding-
   Complemented.bed ./Element/0vs50Min-R1000e1-c-Element-EcoliNoncoding-
   Complemented.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNoncoding-
   Complemented.bed ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNoncoding-
   Complemented.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNoncoding-
   Complemented.bed ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNoncoding-
   Complemented.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNoncoding-
   Complemented.bed ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNoncoding-
   Complemented.xls
22. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNoncoding-
   Complemented.bed ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNoncoding-
   Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-EcoliNoncoding-
   Complemented.txt
26.
27. mkdir ./0vs50Min-R1000e1-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min_r-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli Nonprophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-c.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-R1000e1-c-Element-EcoliNonphage.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNonphage.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNonphage.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNonphage.bed
14. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-R1000e1-c-Element-EcoliNonphage.bed ./Element/0vs50Min-R1000e1-c-Element-EcoliNonphage.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNonphage.bed ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliNonphage.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNonphage.bed ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliNonphage.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNonphage.bed ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliNonphage.xls
22. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNonphage.bed ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-EcoliNonphage.txt
26.
27. mkdir ./0vs50Min-R1000e1-c-Element-EcoliNonphage/
28. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliNonphage/

```

```

#!/bin/bash

1.
2. #Bedops_Element0vs50Min_r-cinEcoliNonpromoters.sh
3. #bedops version: 2.4.35 (typical)
4. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli Nonpromote
   r regions
5.
6. mkdir ./Element/
7.
8. #bedops make bed files element of
9. bedops --element-of ./Microarray/0vs50Min-R1000e1-
   c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-complement.bed > ./Element/0vs50Min-
   R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement.bed
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   complement.bed > ./Element/0vs50Min-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged-complement.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   complement.bed > ./Element/0vs50Min-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged-complement.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   complement.bed > ./Element/0vs50Min-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged-complement.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   complement.bed > ./Element/0vs50Min-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged-complement.bed
14.
15.
16. # Copy to excel
17. cp ./Element/0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-
   complement.bed ./Element/0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-
   complement.xls
18. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
   complement.bed ./Element/0vs50Min-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged-complement.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
   complement.bed ./Element/0vs50Min-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged-complement.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
   complement.bed ./Element/0vs50Min-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged-complement.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
   complement.bed ./Element/0vs50Min-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged-complement.xls
22.
23. #Line count
24. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged-complement.txt
25.
26. mkdir ./0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-complement/
27. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged-
   complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min_r-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli Promoter re
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-
   c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-R1000e1-c-
   Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-
   R1000e1-c-Top50-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-
   R1000e1-c-Top25-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-
   R1000e1-c-Top10-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-R1000e1-
   c-Top5-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-R1000e1-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-R1000e1-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-R1000e1-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-R1000e1-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-
   EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliPromotersRemoveDupsMerged/

```

```

#!/bin/bash
1.
2. #Bedops_Element0vs50Min_r-cinEcoliProphage.sh
3. #bedops version: 2.4.35 (typical)
4. #Uses Bedops to find amount of 0vs50Min randomized 1bp chopped signal in E. coli Prophage re
   gions
5.
6. mkdir ./Element/
7.
8. #bedops make bed files element of
9. bedops --element-of ./Microarray/0vs50Min-R1000e1-
   c.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-R1000e1-c-Element-
   EcoliProphage.bed
10. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top50.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-R1000e1-c-Top50-Element-
   EcoliProphage.bed
11. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top25.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-R1000e1-c-Top25-Element-
   EcoliProphage.bed
12. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top10.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-R1000e1-c-Top10-Element-
   EcoliProphage.bed
13. bedops --element-of ./Microarray/0vs50Min-R1000e1-c-
   Top5.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-R1000e1-c-Top5-Element-
   EcoliProphage.bed
14.
15.
16. # Copy to excel
17. cp ./Element/0vs50Min-R1000e1-c-Element-EcoliProphage.bed ./Element/0vs50Min-R1000e1-c-
   Element-EcoliProphage.xls
18. cp ./Element/0vs50Min-R1000e1-c-Top50-Element-EcoliProphage.bed ./Element/0vs50Min-
   R1000e1-c-Top50-Element-EcoliProphage.xls
19. cp ./Element/0vs50Min-R1000e1-c-Top25-Element-EcoliProphage.bed ./Element/0vs50Min-
   R1000e1-c-Top25-Element-EcoliProphage.xls
20. cp ./Element/0vs50Min-R1000e1-c-Top10-Element-EcoliProphage.bed ./Element/0vs50Min-
   R1000e1-c-Top10-Element-EcoliProphage.xls
21. cp ./Element/0vs50Min-R1000e1-c-Top5-Element-EcoliProphage.bed ./Element/0vs50Min-
   R1000e1-c-Top5-Element-EcoliProphage.xls
22.
23. #Line count
24. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-R1000e1-c-Element-EcoliProphage.txt
25.
26. mkdir ./0vs50Min-R1000e1-c-Element-EcoliProphage/
27. mv ./Element/ ./0vs50Min-R1000e1-c-Element-EcoliProphage/

```

BEDOPS randomized GATCs in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/EcoliGATC_All_r.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_All_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
11. bedops --element-of ./GATC/EcoliGATC_Pairs_r.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_Pairs_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
12. bedops --element-
    of ./GATC/EcoliGATC_HigherO1_r.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO1_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
13. bedops --element-
    of ./GATC/EcoliGATC_HigherO2_r.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO2_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
14. bedops --element-
    of ./GATC/EcoliGATC_HigherO3_r.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO3_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_All_r-Element-EcoliGenes_RemoveIDandDups-Merged.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_Pairs_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO1_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO2_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO3_r-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliGenes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/EcoliGATC_All_r.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_All_r-Element-EcoliNoncoding-Complemented.bed
11. bedops --element-of ./GATC/EcoliGATC_Pairs_r.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_Pairs_r-Element-EcoliNoncoding-
    Complemented.bed
12. bedops --element-of ./GATC/EcoliGATC_HigherO1_r.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO1_r-Element-EcoliNoncoding-
    Complemented.bed
13. bedops --element-of ./GATC/EcoliGATC_HigherO2_r.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO2_r-Element-EcoliNoncoding-
    Complemented.bed
14. bedops --element-of ./GATC/EcoliGATC_HigherO3_r.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO3_r-Element-EcoliNoncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_All_r-Element-EcoliNoncoding-Complemented.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_Pairs_r-Element-EcoliNoncoding-Complemented.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO1_r-Element-EcoliNoncoding-
    Complemented.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO2_r-Element-EcoliNoncoding-
    Complemented.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO3_r-Element-EcoliNoncoding-
    Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-EcoliNoncoding-
    Complemented.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli Nonphage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All_r.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_All_r-
Element-EcoliNonphage.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs_r.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_Pairs
_r-Element-EcoliNonphage.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1_r.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_
HigherO1_r-Element-EcoliNonphage.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2_r.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_
HigherO2_r-Element-EcoliNonphage.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3_r.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_
HigherO3_r-Element-EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-EcoliNonphage.bed ./Element/EcoliGATC_All_r-Element-
EcoliNonphage.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliNonphage.bed ./Element/EcoliGATC_Pairs_r-
Element-EcoliNonphage.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO1_r-Element-EcoliNonphage.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO2_r-Element-EcoliNonphage.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO3_r-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-EcoliNonphage.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliNonphage/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliNonphage/

```



```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli Nonpromoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-Complement/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-Complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli Promoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Elemen
t/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Ele
ment/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./
Element/EcoliGATC_HigherO1_r-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./
Element/EcoliGATC_HigherO2_r-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3_r.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./
Element/EcoliGATC_HigherO3_r-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_All_r-Element-
EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_Pairs_r-Element-
EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-
EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliProphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in E. coli Prophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All_r.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_All_r-
Element-EcoliProphage.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs_r.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_Pairs
_r-Element-EcoliProphage.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1_r.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_H
igherO1_r-Element-EcoliProphage.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2_r.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_H
igherO2_r-Element-EcoliProphage.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3_r.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_H
igherO3_r-Element-EcoliProphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All_r-Element-EcoliProphage.bed ./Element/EcoliGATC_All_r-Element-
EcoliProphage.xls
19. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliProphage.bed ./Element/EcoliGATC_Pairs_r-
Element-EcoliProphage.xls
20. cp ./Element/EcoliGATC_HigherO1_r-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO1_r-Element-EcoliProphage.xls
21. cp ./Element/EcoliGATC_HigherO2_r-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO2_r-Element-EcoliProphage.xls
22. cp ./Element/EcoliGATC_HigherO3_r-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO3_r-Element-EcoliProphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-EcoliProphage.txt
26.
27. mkdir ./EcoliGATC_All_r-Element-EcoliProphage/
28. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliProphage/

```

BEDOPS chop *E. coli* signals into 1 bp

```
1. #!/bin/bash
2.
3. #Bedops_ChopObserved.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find chop observed signals into 1bp
6.
7. bedops --chop 1 ./Microarray/SeqAOnly.bed > ./Microarray/SeqAOnly-c.bed
8. bedops --chop 1 ./Microarray/SeqAOnly-Top50.bed > ./Microarray/SeqAOnly-c-Top50.bed
9. bedops --chop 1 ./Microarray/SeqAOnly-Top25.bed > ./Microarray/SeqAOnly-c-Top25.bed
10. bedops --chop 1 ./Microarray/SeqAOnly-Top10.bed > ./Microarray/SeqAOnly-c-Top10.bed
11. bedops --chop 1 ./Microarray/SeqAOnly-Top5.bed > ./Microarray/SeqAOnly-c-Top5.bed
12.
13. bedops --chop 1 ./Microarray/SeqAOnly_Grainger.bed > ./Microarray/SeqAOnly_Grainger-c.bed
14. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-Top50.bed > ./Microarray/SeqAOnly_Grainger-
c-Top50.bed
15. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-Top25.bed > ./Microarray/SeqAOnly_Grainger-
c-Top25.bed
16. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-Top10.bed > ./Microarray/SeqAOnly_Grainger-
c-Top10.bed
17. bedops --chop 1 ./Microarray/SeqAOnly_Grainger-Top5.bed > ./Microarray/SeqAOnly_Grainger-
c-Top5.bed
18.
19. bedops --chop 1 ./Microarray/0vs50Min.bed > ./Microarray/0vs50Min-c.bed
20. bedops --chop 1 ./Microarray/0vs50Min-Top50.bed > ./Microarray/0vs50Min-c-Top50.bed
21. bedops --chop 1 ./Microarray/0vs50Min-Top25.bed > ./Microarray/0vs50Min-c-Top25.bed
22. bedops --chop 1 ./Microarray/0vs50Min-Top10.bed > ./Microarray/0vs50Min-c-Top10.bed
23. bedops --chop 1 ./Microarray/0vs50Min-Top5.bed > ./Microarray/0vs50Min-c-Top5.bed
```

BEDOPS SeqA Only signals (SeqA Only 1) in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly-cinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly 1bp chopped signal in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-c.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly-c-Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/SeqAOnly-c-
    Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-c-
    Top50-Element-EcoliGenes_RemoveIDandDups-Merged.bed
12. bedops --element-of ./Microarray/SeqAOnly-c-
    Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-c-
    Top25-Element-EcoliGenes_RemoveIDandDups-Merged.bed
13. bedops --element-of ./Microarray/SeqAOnly-c-
    Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-c-
    Top10-Element-EcoliGenes_RemoveIDandDups-Merged.bed
14. bedops --element-of ./Microarray/SeqAOnly-c-
    Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly-c-Top5-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly-c-Element-EcoliGenes_RemoveIDandDups-Merged.xls
19. cp ./Element/SeqAOnly-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly-c-Top50-Element-EcoliGenes_RemoveIDandDups-Merged.xls
20. cp ./Element/SeqAOnly-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly-c-Top25-Element-EcoliGenes_RemoveIDandDups-Merged.xls
21. cp ./Element/SeqAOnly-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly-c-Top10-Element-EcoliGenes_RemoveIDandDups-Merged.xls
22. cp ./Element/SeqAOnly-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly-c-Top5-Element-EcoliGenes_RemoveIDandDups-Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.*bed > ./Element/OverlapStats-SeqAOnly-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./SeqAOnly-c-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./SeqAOnly-c-Element-EcoliGenes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly 1bp chopped signal in E. coli Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly-c.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-c-Element-EcoliNoncoding-Complemented.bed
11. bedops --element-of ./Microarray/SeqAOnly-c-Top50.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-c-Top50-Element-EcoliNoncoding-
    Complemented.bed
12. bedops --element-of ./Microarray/SeqAOnly-c-Top25.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-c-Top25-Element-EcoliNoncoding-
    Complemented.bed
13. bedops --element-of ./Microarray/SeqAOnly-c-Top10.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-c-Top10-Element-EcoliNoncoding-
    Complemented.bed
14. bedops --element-of ./Microarray/SeqAOnly-c-Top5.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/SeqAOnly-c-Top5-Element-EcoliNoncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly-c-Element-EcoliNoncoding-Complemented.bed ./Element/SeqAOnly-c-
    Element-EcoliNoncoding-Complemented.xls
19. cp ./Element/SeqAOnly-c-Top50-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-c-Top50-Element-EcoliNoncoding-Complemented.xls
20. cp ./Element/SeqAOnly-c-Top25-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-c-Top25-Element-EcoliNoncoding-Complemented.xls
21. cp ./Element/SeqAOnly-c-Top10-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-c-Top10-Element-EcoliNoncoding-Complemented.xls
22. cp ./Element/SeqAOnly-c-Top5-Element-EcoliNoncoding-
    Complemented.bed ./Element/SeqAOnly-c-Top5-Element-EcoliNoncoding-Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-c-Element-EcoliNoncoding-
    Complemented.txt
26.
27. mkdir ./SeqAOnly-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./SeqAOnly-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly 1bp chopped signal in E. coli Nonprophage regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/SeqAOnly-
c.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-c-Element-EcoliNonphage.bed
12. bedops --element-of ./Microarray/SeqAOnly-c-
Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-c-Top50-Element-
EcoliNonphage.bed
13. bedops --element-of ./Microarray/SeqAOnly-c-
Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-c-Top25-Element-
EcoliNonphage.bed
14. bedops --element-of ./Microarray/SeqAOnly-c-
Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-c-Top10-Element-
EcoliNonphage.bed
15. bedops --element-of ./Microarray/SeqAOnly-c-
Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly-c-Top5-Element-
EcoliNonphage.bed
16.
17.
18. # Copy to excel
19. cp ./Element/SeqAOnly-c-Element-EcoliNonphage.bed ./Element/SeqAOnly-c-Element-
EcoliNonphage.xls
20. cp ./Element/SeqAOnly-c-Top50-Element-EcoliNonphage.bed ./Element/SeqAOnly-c-Top50-
Element-EcoliNonphage.xls
21. cp ./Element/SeqAOnly-c-Top25-Element-EcoliNonphage.bed ./Element/SeqAOnly-c-Top25-
Element-EcoliNonphage.xls
22. cp ./Element/SeqAOnly-c-Top10-Element-EcoliNonphage.bed ./Element/SeqAOnly-c-Top10-
Element-EcoliNonphage.xls
23. cp ./Element/SeqAOnly-c-Top5-Element-EcoliNonphage.bed ./Element/SeqAOnly-c-Top5-
Element-EcoliNonphage.xls
24.
25. #Line count
26. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-c-Element-EcoliNonphage.txt
27.
28. mkdir ./SeqAOnly-c-Element-EcoliNonphage/
29. mv ./Element/ ./SeqAOnly-c-Element-EcoliNonphage/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly-cinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly 1bp chopped signal in E. coli Nonpromoter regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/SeqAOnly-
c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-Complement.bed > ./Element/SeqAOnly-
c-Element-EcoliPromotersRemoveDupsMerged-Complement.bed
12. bedops --element-of ./Microarray/SeqAOnly-c-
Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/SeqAOnly-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
13. bedops --element-of ./Microarray/SeqAOnly-c-
Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/SeqAOnly-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
14. bedops --element-of ./Microarray/SeqAOnly-c-
Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/SeqAOnly-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
15. bedops --element-of ./Microarray/SeqAOnly-c-
Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/SeqAOnly-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
16.
17.
18. # Copy to excel
19. cp ./Element/SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
20. cp ./Element/SeqAOnly-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/SeqAOnly-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
21. cp ./Element/SeqAOnly-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/SeqAOnly-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
22. cp ./Element/SeqAOnly-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/SeqAOnly-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
23. cp ./Element/SeqAOnly-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/SeqAOnly-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
24.
25. #Line count
26. wc -l ./Element/*.*bed > ./Element/OverlapStats-SeqAOnly-c-Element-
EcoliPromotersRemoveDupsMerged-Complement.txt
27.
28. mkdir ./SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged-Complement/
29. mv ./Element/ ./SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged-Complement/

```



```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly 1bp chopped signal in E. coli Promoter regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/SeqAOnly-
c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-c-Element-
EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/SeqAOnly-c-
Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-c-Top50-
Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/SeqAOnly-c-
Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-c-Top25-
Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/SeqAOnly-c-
Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-c-Top10-
Element-EcoliPromotersRemoveDupsMerged.bed
15. bedops --element-of ./Microarray/SeqAOnly-c-
Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly-c-Top5-
Element-EcoliPromotersRemoveDupsMerged.bed
16.
17.
18. # Copy to excel
19. cp ./Element/SeqAOnly-c-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-c-Element-
EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/SeqAOnly-c-Top50-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-c-Top50-Element-
EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/SeqAOnly-c-Top25-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-c-Top25-Element-
EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/SeqAOnly-c-Top10-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-c-Top10-Element-
EcoliPromotersRemoveDupsMerged.xls
23. cp ./Element/SeqAOnly-c-Top5-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly-c-Top5-Element-
EcoliPromotersRemoveDupsMerged.xls
24.
25. #Line count
26. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly-c-Element-
EcoliPromotersRemoveDupsMerged.txt
27.
28. mkdir ./SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged/
29. mv ./Element/ ./SeqAOnly-c-Element-EcoliPromotersRemoveDupsMerged/

```

BEDOPS SeqA Only (Grainger) signals (SeqA Only 2) in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-
    c.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/SeqAOnly_Grainger-c-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliGenes_RemoveIDandDups-Merged/
```

28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliGenes_RemoveIDandDups-Merged/

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli Noncoding re
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-c.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-c-Element-EcoliNoncoding-
   Complemented.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top50.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliNoncoding-
   Complemented.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top25.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliNoncoding-
   Complemented.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top10.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliNoncoding-
   Complemented.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top5.bed ./Genes/EcoliNoncoding-
   Complemented.bed > ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliNoncoding-
   Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-c-Element-EcoliNoncoding-
   Complemented.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliNoncoding-
   Complemented.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliNoncoding-
   Complemented.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliNoncoding-
   Complemented.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliNoncoding-
   Complemented.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliNoncoding-
   Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-EcoliNoncoding-
   Complemented.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli Nonprophage
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-
    c.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-c-Element-
    EcoliNonphage.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-c-Top50-Element-
    EcoliNonphage.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-c-Top25-Element-
    EcoliNonphage.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-c-Top10-Element-
    EcoliNonphage.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/SeqAOnly_Grainger-c-Top5-Element-
    EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-EcoliNonphage.bed ./Element/SeqAOnly_Grainger-
    c-Element-EcoliNonphage.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-
    EcoliNonphage.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliNonphage.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-
    EcoliNonphage.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliNonphage.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-
    EcoliNonphage.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliNonphage.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-
    EcoliNonphage.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-
    EcoliNonphage.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliNonphage/
28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliNonphage/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli Noncoding re
   regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-
   c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   Complement.bed > ./Element/SeqAOnly_Grainger-c-Element-
   EcoliPromotersRemoveDupsMerged-Complement.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
   Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   Complement.bed > ./Element/SeqAOnly_Grainger-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged-Complement.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
   Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   Complement.bed > ./Element/SeqAOnly_Grainger-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged-Complement.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
   Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   Complement.bed > ./Element/SeqAOnly_Grainger-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged-Complement.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
   Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
   Complement.bed > ./Element/SeqAOnly_Grainger-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged-Complement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged-
   Complement.bed ./Element/SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged-
   Complement.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
   Complement.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-
   EcoliPromotersRemoveDupsMerged-Complement.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
   Complement.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-
   EcoliPromotersRemoveDupsMerged-Complement.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
   Complement.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-
   EcoliPromotersRemoveDupsMerged-Complement.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
   Complement.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-
   EcoliPromotersRemoveDupsMerged-Complement.xls
23.
24. #Line count
25. wc -l ./Element/*.*bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-
   EcoliPromotersRemoveDupsMerged-Complement.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged-Complement/
28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged-
   Complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli Promoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-c-
    Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
    r-c-Top50-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
    r-c-Top25-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
    r-c-Top10-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-
    Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/SeqAOnly_Grainger-
    c-Top5-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-
    EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-c-Element-
    EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-
    EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-
    EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-
    EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-
    EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-
    EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-
    EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-
    EcoliPromotersRemoveDupsMerged.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-
    EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-
    EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliPromotersRemoveDupsMerged/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementSeqAOnly_Grainger-cinEcoliProphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of SeqAOnly_Grainger 1bp chopped signal in E. coli Prophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/SeqAOnly_Grainger-c.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-c-Element-EcoliProphage.bed
11. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top50.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliProphage.bed
12. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top25.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliProphage.bed
13. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top10.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliProphage.bed
14. bedops --element-of ./Microarray/SeqAOnly_Grainger-c-Top5.bed ./Prophage/EcoliProphage.bed > ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliProphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/SeqAOnly_Grainger-c-Element-EcoliProphage.bed ./Element/SeqAOnly_Grainger-c-Element-EcoliProphage.xls
19. cp ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliProphage.bed ./Element/SeqAOnly_Grainger-c-Top50-Element-EcoliProphage.xls
20. cp ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliProphage.bed ./Element/SeqAOnly_Grainger-c-Top25-Element-EcoliProphage.xls
21. cp ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliProphage.bed ./Element/SeqAOnly_Grainger-c-Top10-Element-EcoliProphage.xls
22. cp ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliProphage.bed ./Element/SeqAOnly_Grainger-c-Top5-Element-EcoliProphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-SeqAOnly_Grainger-c-Element-EcoliProphage.txt
26.
27. mkdir ./SeqAOnly_Grainger-c-Element-EcoliProphage/
28. mv ./Element/ ./SeqAOnly_Grainger-c-Element-EcoliProphage/

```


BEDOPS 0 vs. 50 Min signals (SeqA Binding) in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-c.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/0vs50Min-c-Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./Microarray/0vs50Min-c-
    Top50.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-c-Top50-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
12. bedops --element-of ./Microarray/0vs50Min-c-
    Top25.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-c-Top25-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
13. bedops --element-of ./Microarray/0vs50Min-c-
    Top10.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-c-Top10-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
14. bedops --element-of ./Microarray/0vs50Min-c-
    Top5.bed ./Genes/EcoliGenes_RemoveIDandDups-Merged.bed > ./Element/0vs50Min-c-Top5-
    Element-EcoliGenes_RemoveIDandDups-Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-c-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-c-Element-EcoliGenes_RemoveIDandDups-Merged.xls
19. cp ./Element/0vs50Min-c-Top50-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-c-Top50-Element-EcoliGenes_RemoveIDandDups-Merged.xls
20. cp ./Element/0vs50Min-c-Top25-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-c-Top25-Element-EcoliGenes_RemoveIDandDups-Merged.xls
21. cp ./Element/0vs50Min-c-Top10-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-c-Top10-Element-EcoliGenes_RemoveIDandDups-Merged.xls
22. cp ./Element/0vs50Min-c-Top5-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/0vs50Min-c-Top5-Element-EcoliGenes_RemoveIDandDups-Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./0vs50Min-c-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./0vs50Min-c-Element-EcoliGenes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-c.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/0vs50Min-c-Element-EcoliNoncoding-Complemented.bed
11. bedops --element-of ./Microarray/0vs50Min-c-Top50.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/0vs50Min-c-Top50-Element-EcoliNoncoding-
    Complemented.bed
12. bedops --element-of ./Microarray/0vs50Min-c-Top25.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/0vs50Min-c-Top25-Element-EcoliNoncoding-
    Complemented.bed
13. bedops --element-of ./Microarray/0vs50Min-c-Top10.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/0vs50Min-c-Top10-Element-EcoliNoncoding-
    Complemented.bed
14. bedops --element-of ./Microarray/0vs50Min-c-Top5.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/0vs50Min-c-Top5-Element-EcoliNoncoding-Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-c-Element-EcoliNoncoding-Complemented.bed ./Element/0vs50Min-c-
    Element-EcoliNoncoding-Complemented.xls
19. cp ./Element/0vs50Min-c-Top50-Element-EcoliNoncoding-
    Complemented.bed ./Element/0vs50Min-c-Top50-Element-EcoliNoncoding-Complemented.xls
20. cp ./Element/0vs50Min-c-Top25-Element-EcoliNoncoding-
    Complemented.bed ./Element/0vs50Min-c-Top25-Element-EcoliNoncoding-Complemented.xls
21. cp ./Element/0vs50Min-c-Top10-Element-EcoliNoncoding-
    Complemented.bed ./Element/0vs50Min-c-Top10-Element-EcoliNoncoding-Complemented.xls
22. cp ./Element/0vs50Min-c-Top5-Element-EcoliNoncoding-
    Complemented.bed ./Element/0vs50Min-c-Top5-Element-EcoliNoncoding-Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-EcoliNoncoding-
    Complemented.txt
26.
27. mkdir ./0vs50Min-c-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./0vs50Min-c-Element-EcoliNoncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli Nonprophage regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/0vs50Min-
c.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-c-Element-EcoliNonphage.bed
12. bedops --element-of ./Microarray/0vs50Min-c-
Top50.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-c-Top50-Element-
EcoliNonphage.bed
13. bedops --element-of ./Microarray/0vs50Min-c-
Top25.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-c-Top25-Element-
EcoliNonphage.bed
14. bedops --element-of ./Microarray/0vs50Min-c-
Top10.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-c-Top10-Element-
EcoliNonphage.bed
15. bedops --element-of ./Microarray/0vs50Min-c-
Top5.bed ./Prophage/EcoliNonphage.bed > ./Element/0vs50Min-c-Top5-Element-
EcoliNonphage.bed
16.
17.
18. # Copy to excel
19. cp ./Element/0vs50Min-c-Element-EcoliNonphage.bed ./Element/0vs50Min-c-Element-
EcoliNonphage.xls
20. cp ./Element/0vs50Min-c-Top50-Element-EcoliNonphage.bed ./Element/0vs50Min-c-Top50-
Element-EcoliNonphage.xls
21. cp ./Element/0vs50Min-c-Top25-Element-EcoliNonphage.bed ./Element/0vs50Min-c-Top25-
Element-EcoliNonphage.xls
22. cp ./Element/0vs50Min-c-Top10-Element-EcoliNonphage.bed ./Element/0vs50Min-c-Top10-
Element-EcoliNonphage.xls
23. cp ./Element/0vs50Min-c-Top5-Element-EcoliNonphage.bed ./Element/0vs50Min-c-Top5-
Element-EcoliNonphage.xls
24.
25. #Line count
26. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-EcoliNonphage.txt
27.
28. mkdir ./0vs50Min-c-Element-EcoliNonphage/
29. mv ./Element/ ./0vs50Min-c-Element-EcoliNonphage/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliNonpromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli Nonpromoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./Microarray/0vs50Min-
    c.bed ./Promoters/EcoliPromotersRemoveDupsMerged-Complement.bed > ./Element/0vs50Min-
    c-Element-EcoliPromotersRemoveDupsMerged-Complement.bed
11. bedops --element-of ./Microarray/0vs50Min-c-
    Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
    Complement.bed > ./Element/0vs50Min-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed
12. bedops --element-of ./Microarray/0vs50Min-c-
    Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
    Complement.bed > ./Element/0vs50Min-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed
13. bedops --element-of ./Microarray/0vs50Min-c-
    Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
    Complement.bed > ./Element/0vs50Min-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed
14. bedops --element-of ./Microarray/0vs50Min-c-
    Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
    Complement.bed > ./Element/0vs50Min-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed ./Element/0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged-
    Complement.xls
19. cp ./Element/0vs50Min-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed ./Element/0vs50Min-c-Top50-Element-EcoliPromotersRemoveDupsMerged-
    Complement.xls
20. cp ./Element/0vs50Min-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed ./Element/0vs50Min-c-Top25-Element-EcoliPromotersRemoveDupsMerged-
    Complement.xls
21. cp ./Element/0vs50Min-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed ./Element/0vs50Min-c-Top10-Element-EcoliPromotersRemoveDupsMerged-
    Complement.xls
22. cp ./Element/0vs50Min-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
    Complement.bed ./Element/0vs50Min-c-Top5-Element-EcoliPromotersRemoveDupsMerged-
    Complement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-
    EcoliPromotersRemoveDupsMerged-Complement.txt
26.
27. mkdir ./0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged-Complement/
28. mv ./Element/ ./0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged-Complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli Promoter regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/0vs50Min-
c.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-c-Element-
EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-of ./Microarray/0vs50Min-c-
Top50.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-c-Top50-
Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-of ./Microarray/0vs50Min-c-
Top25.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-c-Top25-
Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-of ./Microarray/0vs50Min-c-
Top10.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-c-Top10-
Element-EcoliPromotersRemoveDupsMerged.bed
15. bedops --element-of ./Microarray/0vs50Min-c-
Top5.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/0vs50Min-c-Top5-
Element-EcoliPromotersRemoveDupsMerged.bed
16.
17.
18. # Copy to excel
19. cp ./Element/0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-
c-Element-EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/0vs50Min-c-Top50-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-c-Top50-Element-
EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/0vs50Min-c-Top25-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-c-Top25-Element-
EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/0vs50Min-c-Top10-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-c-Top10-Element-
EcoliPromotersRemoveDupsMerged.xls
23. cp ./Element/0vs50Min-c-Top5-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/0vs50Min-c-Top5-Element-
EcoliPromotersRemoveDupsMerged.xls
24.
25. #Line count
26. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-
EcoliPromotersRemoveDupsMerged.txt
27.
28. mkdir ./0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged/
29. mv ./Element/ ./0vs50Min-c-Element-EcoliPromotersRemoveDupsMerged/

```

```

1. #!/bin/bash
2.
3. #Bedops_Element0vs50Min-cinEcoliProphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of 0vs50Min 1bp chopped signal in E. coli Prophage regions
6.
7.
8. mkdir ./Element/
9.
10. #bedops make bed files element of
11. bedops --element-of ./Microarray/0vs50Min-
c.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-c-Element-EcoliProphage.bed
12. bedops --element-of ./Microarray/0vs50Min-c-
Top50.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-c-Top50-Element-
EcoliProphage.bed
13. bedops --element-of ./Microarray/0vs50Min-c-
Top25.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-c-Top25-Element-
EcoliProphage.bed
14. bedops --element-of ./Microarray/0vs50Min-c-
Top10.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-c-Top10-Element-
EcoliProphage.bed
15. bedops --element-of ./Microarray/0vs50Min-c-
Top5.bed ./Prophage/EcoliProphage.bed > ./Element/0vs50Min-c-Top5-Element-
EcoliProphage.bed
16.
17.
18. # Copy to excel
19. cp ./Element/0vs50Min-c-Element-EcoliProphage.bed ./Element/0vs50Min-c-Element-
EcoliProphage.xls
20. cp ./Element/0vs50Min-c-Top50-Element-EcoliProphage.bed ./Element/0vs50Min-c-Top50-
Element-EcoliProphage.xls
21. cp ./Element/0vs50Min-c-Top25-Element-EcoliProphage.bed ./Element/0vs50Min-c-Top25-
Element-EcoliProphage.xls
22. cp ./Element/0vs50Min-c-Top10-Element-EcoliProphage.bed ./Element/0vs50Min-c-Top10-
Element-EcoliProphage.xls
23. cp ./Element/0vs50Min-c-Top5-Element-EcoliProphage.bed ./Element/0vs50Min-c-Top5-Element-
EcoliProphage.xls
24.
25. #Line count
26. wc -l ./Element/*.bed > ./Element/OverlapStats-0vs50Min-c-Element-EcoliProphage.txt
27.
28. mkdir ./0vs50Min-c-Element-EcoliProphage/
29. mv ./Element/ ./0vs50Min-c-Element-EcoliProphage/

```

BEDOPS GATCs in *E. coli* regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliGenes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in E. coli ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/EcoliGATC_All.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_All-Element-EcoliGenes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./GATC/EcoliGATC_Pairs.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_Pairs-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
12. bedops --element-
    of ./GATC/EcoliGATC_HigherO1.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO1-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
13. bedops --element-
    of ./GATC/EcoliGATC_HigherO2.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO2-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
14. bedops --element-
    of ./GATC/EcoliGATC_HigherO3.bed ./Genes/EcoliGenes_RemoveIDandDups-
    Merged.bed > ./Element/EcoliGATC_HigherO3-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_All-Element-EcoliGenes_RemoveIDandDups-Merged.xls
19. cp ./Element/EcoliGATC_Pairs-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_Pairs-Element-EcoliGenes_RemoveIDandDups-Merged.xls
20. cp ./Element/EcoliGATC_HigherO1-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO1-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/EcoliGATC_HigherO2-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO2-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/EcoliGATC_HigherO3-Element-EcoliGenes_RemoveIDandDups-
    Merged.bed ./Element/EcoliGATC_HigherO3-Element-EcoliGenes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All-Element-
    EcoliGenes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./EcoliGATC_All-Element-EcoliGenes_RemoveIDandDups-Merged/
28. mv ./Element/ ./EcoliGATC_All-Element-EcoliGenes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliNoncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in E. coli Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/EcoliGATC_All.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_All-Element-EcoliNoncoding-Complemented.bed
11. bedops --element-of ./GATC/EcoliGATC_Pairs.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_Pairs-Element-EcoliNoncoding-Complemented.bed
12. bedops --element-of ./GATC/EcoliGATC_HigherO1.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO1-Element-EcoliNoncoding-
    Complemented.bed
13. bedops --element-of ./GATC/EcoliGATC_HigherO2.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO2-Element-EcoliNoncoding-
    Complemented.bed
14. bedops --element-of ./GATC/EcoliGATC_HigherO3.bed ./Genes/EcoliNoncoding-
    Complemented.bed > ./Element/EcoliGATC_HigherO3-Element-EcoliNoncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_All-Element-EcoliNoncoding-Complemented.xls
19. cp ./Element/EcoliGATC_Pairs-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_Pairs-Element-EcoliNoncoding-Complemented.xls
20. cp ./Element/EcoliGATC_HigherO1-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO1-Element-EcoliNoncoding-
    Complemented.xls
21. cp ./Element/EcoliGATC_HigherO2-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO2-Element-EcoliNoncoding-
    Complemented.xls
22. cp ./Element/EcoliGATC_HigherO3-Element-EcoliNoncoding-
    Complemented.bed ./Element/EcoliGATC_HigherO3-Element-EcoliNoncoding-
    Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All-Element-EcoliNoncoding-
    Complemented.txt
26.
27. mkdir ./EcoliGATC_All-Element-EcoliNoncoding-Complemented/
28. mv ./Element/ ./EcoliGATC_All-Element-EcoliNoncoding-Complemented/

```



```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliNonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in E. coli Nonphage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_All-
Element-EcoliNonphage.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_Pairs-
Element-EcoliNonphage.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_Hi
gherO1-Element-EcoliNonphage.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_Hi
gherO2-Element-EcoliNonphage.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Prophage/EcoliNonphage.bed > ./Element/EcoliGATC_Hi
gherO3-Element-EcoliNonphage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All-Element-EcoliNonphage.bed ./Element/EcoliGATC_All-Element-
EcoliNonphage.xls
19. cp ./Element/EcoliGATC_Pairs-Element-EcoliNonphage.bed ./Element/EcoliGATC_Pairs-
Element-EcoliNonphage.xls
20. cp ./Element/EcoliGATC_HigherO1-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO1-Element-EcoliNonphage.xls
21. cp ./Element/EcoliGATC_HigherO2-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO2-Element-EcoliNonphage.xls
22. cp ./Element/EcoliGATC_HigherO3-Element-
EcoliNonphage.bed ./Element/EcoliGATC_HigherO3-Element-EcoliNonphage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All-Element-EcoliNonphage.txt
26.
27. mkdir ./EcoliGATC_All-Element-EcoliNonphage/
28. mv ./Element/ ./EcoliGATC_All-Element-EcoliNonphage/

```

```

1.
2. #Bedops_ElementGATCSinEcoliNonpromoters.sh
3. #bedops version: 2.4.35 (typical)
4. #Uses Bedops to find amount of GATCs in E. coli Nonpromoter regions
5.
6. mkdir ./Element/
7.
8. #bedops make bed files element of
9. bedops --element-
of ./GATC/EcoliGATC_All.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
10. bedops --element-
of ./GATC/EcoliGATC_Pairs.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed
11. bedops --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Promoters/EcoliPromotersRemoveDupsMerged-
Complement.bed > ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.bed
14.
15.
16. # Copy to excel
17. cp ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
18. cp ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_Pairs_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.xls
19. cp ./Element/EcoliGATC_HigherO1_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO1_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
20. cp ./Element/EcoliGATC_HigherO2_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO2_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
21. cp ./Element/EcoliGATC_HigherO3_r-Element-EcoliPromotersRemoveDupsMerged-
Complement.bed ./Element/EcoliGATC_HigherO3_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.xls
22.
23. #Line count
24. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All_r-Element-
EcoliPromotersRemoveDupsMerged-Complement.txt
25.
26. mkdir ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-Complement/
27. mv ./Element/ ./EcoliGATC_All_r-Element-EcoliPromotersRemoveDupsMerged-Complement/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinEcoliPromoters.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in E. coli Promoter regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/EcoliGATC_All.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/
EcoliGATC_All-Element-EcoliPromotersRemoveDupsMerged.bed
11. bedops --element-
of ./GATC/EcoliGATC_Pairs.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/
EcoliGATC_Pairs-Element-EcoliPromotersRemoveDupsMerged.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/
EcoliGATC_HigherO1-Element-EcoliPromotersRemoveDupsMerged.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/
EcoliGATC_HigherO2-Element-EcoliPromotersRemoveDupsMerged.bed
14. bedops --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Promoters/EcoliPromotersRemoveDupsMerged.bed > ./Element/
EcoliGATC_HigherO3-Element-EcoliPromotersRemoveDupsMerged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/EcoliGATC_All-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_All-Element-
EcoliPromotersRemoveDupsMerged.xls
19. cp ./Element/EcoliGATC_Pairs-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_Pairs-Element-
EcoliPromotersRemoveDupsMerged.xls
20. cp ./Element/EcoliGATC_HigherO1-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO1-Element-
EcoliPromotersRemoveDupsMerged.xls
21. cp ./Element/EcoliGATC_HigherO2-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO2-Element-
EcoliPromotersRemoveDupsMerged.xls
22. cp ./Element/EcoliGATC_HigherO3-Element-
EcoliPromotersRemoveDupsMerged.bed ./Element/EcoliGATC_HigherO3-Element-
EcoliPromotersRemoveDupsMerged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All-Element-
EcoliPromotersRemoveDupsMerged.txt
26.
27. mkdir ./EcoliGATC_All-Element-EcoliPromotersRemoveDupsMerged/
28. mv ./Element/ ./EcoliGATC_All-Element-EcoliPromotersRemoveDupsMerged/

```

```

1.
2. #Bedops_ElementGATCSinEcoliProphage.sh
3. #bedops version: 2.4.35 (typical)
4. #Uses Bedops to find amount of GATCs in E. coli Prophage regions
5.
6. mkdir ./Element/
7.
8. #bedops make bed files element of
9. bedops --element-
of ./GATC/EcoliGATC_All.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_All-
Element-EcoliProphage.bed
10. bedops --element-
of ./GATC/EcoliGATC_Pairs.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_Pairs-
Element-EcoliProphage.bed
11. bedops --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_Hig
herO1-Element-EcoliProphage.bed
12. bedops --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_Hig
herO2-Element-EcoliProphage.bed
13. bedops --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Prophage/EcoliProphage.bed > ./Element/EcoliGATC_Hig
herO3-Element-EcoliProphage.bed
14.
15.
16. # Copy to excel
17. cp ./Element/EcoliGATC_All-Element-EcoliProphage.bed ./Element/EcoliGATC_All-Element-
EcoliProphage.xls
18. cp ./Element/EcoliGATC_Pairs-Element-EcoliProphage.bed ./Element/EcoliGATC_Pairs-
Element-EcoliProphage.xls
19. cp ./Element/EcoliGATC_HigherO1-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO1-Element-EcoliProphage.xls
20. cp ./Element/EcoliGATC_HigherO2-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO2-Element-EcoliProphage.xls
21. cp ./Element/EcoliGATC_HigherO3-Element-
EcoliProphage.bed ./Element/EcoliGATC_HigherO3-Element-EcoliProphage.xls
22.
23. #Line count
24. wc -l ./Element/*.bed > ./Element/OverlapStats-EcoliGATC_All-Element-EcoliProphage.txt
25.
26. mkdir ./EcoliGATC_All-Element-EcoliProphage/
27. mv ./Element/ ./EcoliGATC_All-Element-EcoliProphage/

```

BEDTools create random locations for LT2 GATCs

```
1. #!/bin/bash
2.
3. # bedtools_random_LT2GATC.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to create random locations for LT2 GATCs
6.
7. bedtools random -g ./LT2-genomesize.txt -n 19168 -l 4 > LT2GATC_All_r.bed
8. bedtools random -g ./LT2-genomesize.txt -n 3271 -l 4 > LT2GATC_Pairs_r.bed
9. bedtools random -g ./LT2-genomesize.txt -n 993 -l 4 > LT2GATC_HigherO1_r.bed
10. bedtools random -g ./LT2-genomesize.txt -n 320 -l 4 > LT2GATC_HigherO2_r.bed
11. bedtools random -g ./LT2-genomesize.txt -n 108 -l 4 > LT2GATC_HigherO3_r.bed
```

BEDOPS randomized GATCs in LT2 regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementGATCS_r_inLT2Genes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in LT2 ORFs
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/LT2GATC_All_r.bed ./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./GATC/LT2GATC_Pairs_r.bed ./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
12. bedops --element-
    of ./GATC/LT2GATC_HigherO1_r.bed ./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
13. bedops --element-
    of ./GATC/LT2GATC_HigherO2_r.bed ./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
14. bedops --element-
    of ./GATC/LT2GATC_HigherO3_r.bed ./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged.xls
19. cp ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-Merged.xls
20. cp ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All_r-Element-
    LT2Genes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged/
28. mv ./Element/ ./LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCS_r_inLT2Noncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in LT2 Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/LT2GATC_All_r.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_All_r-Element-LT2Noncoding-Complemented.bed
11. bedops --element-of ./GATC/LT2GATC_Pairs_r.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_Pairs_r-Element-LT2Noncoding-Complemented.bed
12. bedops --element-of ./GATC/LT2GATC_HigherO1_r.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO1_r-Element-LT2Noncoding-
    Complemented.bed
13. bedops --element-of ./GATC/LT2GATC_HigherO2_r.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO2_r-Element-LT2Noncoding-
    Complemented.bed
14. bedops --element-of ./GATC/LT2GATC_HigherO3_r.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO3_r-Element-LT2Noncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All_r-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_All_r-Element-LT2Noncoding-Complemented.xls
19. cp ./Element/LT2GATC_Pairs_r-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_Pairs_r-Element-LT2Noncoding-Complemented.xls
20. cp ./Element/LT2GATC_HigherO1_r-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO1_r-Element-LT2Noncoding-
    Complemented.xls
21. cp ./Element/LT2GATC_HigherO2_r-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO2_r-Element-LT2Noncoding-
    Complemented.xls
22. cp ./Element/LT2GATC_HigherO3_r-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO3_r-Element-LT2Noncoding-
    Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All_r-Element-LT2Noncoding-
    Complemented.txt
26.
27. mkdir ./LT2GATC_All_r-Element-LT2Noncoding-Complemented/
28. mv ./Element/ ./LT2GATC_All_r-Element-LT2Noncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCS_r_inLT2Nonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in LT2 Nonprophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/LT2GATC_All_r.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2GATC
_All_r-Element-LT2AllPhageComplement.bed
11. bedops --element-
of ./GATC/LT2GATC_Pairs_r.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2GAT
C_Pairs_r-Element-LT2AllPhageComplement.bed
12. bedops --element-
of ./GATC/LT2GATC_HigherO1_r.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2
GATC_HigherO1_r-Element-LT2AllPhageComplement.bed
13. bedops --element-
of ./GATC/LT2GATC_HigherO2_r.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2
GATC_HigherO2_r-Element-LT2AllPhageComplement.bed
14. bedops --element-
of ./GATC/LT2GATC_HigherO3_r.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2
GATC_HigherO3_r-Element-LT2AllPhageComplement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All_r-Element-LT2AllPhageComplement.bed ./Element/LT2GATC_All_r-
Element-LT2AllPhageComplement.xls
19. cp ./Element/LT2GATC_Pairs_r-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_Pairs_r-Element-
LT2AllPhageComplement.xls
20. cp ./Element/LT2GATC_HigherO1_r-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO1_r-Element-
LT2AllPhageComplement.xls
21. cp ./Element/LT2GATC_HigherO2_r-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO2_r-Element-
LT2AllPhageComplement.xls
22. cp ./Element/LT2GATC_HigherO3_r-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO3_r-Element-
LT2AllPhageComplement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All_r-Element-
LT2AllPhageComplement.txt
26.
27. mkdir ./LT2GATC_All_r-Element-LT2AllPhageComplement/
28. mv ./Element/ ./LT2GATC_All_r-Element-LT2AllPhageComplement/

```



```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCS_r_inLT2Prophage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of random GATCs in LT2 Prophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/LT2GATC_All_r.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_All_r-
Element-LT2AllPhage.bed
11. bedops --element-
of ./GATC/LT2GATC_Pairs_r.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_Pairs_r-
Element-LT2AllPhage.bed
12. bedops --element-
of ./GATC/LT2GATC_HigherO1_r.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_High
erO1_r-Element-LT2AllPhage.bed
13. bedops --element-
of ./GATC/LT2GATC_HigherO2_r.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_High
erO2_r-Element-LT2AllPhage.bed
14. bedops --element-
of ./GATC/LT2GATC_HigherO3_r.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_High
erO3_r-Element-LT2AllPhage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All_r-Element-LT2AllPhage.bed ./Element/LT2GATC_All_r-Element-
LT2AllPhage.xls
19. cp ./Element/LT2GATC_Pairs_r-Element-LT2AllPhage.bed ./Element/LT2GATC_Pairs_r-
Element-LT2AllPhage.xls
20. cp ./Element/LT2GATC_HigherO1_r-Element-
LT2AllPhage.bed ./Element/LT2GATC_HigherO1_r-Element-LT2AllPhage.xls
21. cp ./Element/LT2GATC_HigherO2_r-Element-
LT2AllPhage.bed ./Element/LT2GATC_HigherO2_r-Element-LT2AllPhage.xls
22. cp ./Element/LT2GATC_HigherO3_r-Element-
LT2AllPhage.bed ./Element/LT2GATC_HigherO3_r-Element-LT2AllPhage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All_r-Element-LT2AllPhage.txt
26.
27. mkdir ./LT2GATC_All_r-Element-LT2AllPhage/
28. mv ./Element/ ./LT2GATC_All_r-Element-LT2AllPhage/

```

BEDOPS GATCs in LT2 regions

```
1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinLT2Genes.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in LT2 ORF
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/LT2GATC_All.bed./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged.bed
11. bedops --element-of ./GATC/LT2GATC_Pairs.bed./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
12. bedops --element-of ./GATC/LT2GATC_HigherO1.bed./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
13. bedops --element-of ./GATC/LT2GATC_HigherO2.bed./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
14. bedops --element-of ./GATC/LT2GATC_HigherO3.bed./Genes/LT2Genes_RemoveIDandDups-
    Merged.bed > ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged.xls
19. cp ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_Pairs_r-Element-LT2Genes_RemoveIDandDups-Merged.xls
20. cp ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO1_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
21. cp ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO2_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
22. cp ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.bed ./Element/LT2GATC_HigherO3_r-Element-LT2Genes_RemoveIDandDups-
    Merged.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All_r-Element-
    LT2Genes_RemoveIDandDups-Merged.txt
26.
27. mkdir ./LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged/
28. mv ./Element/ ./LT2GATC_All_r-Element-LT2Genes_RemoveIDandDups-Merged/
```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinLT2Noncoding.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in LT2 Noncoding regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-of ./GATC/LT2GATC_All.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_All-Element-LT2Noncoding-Complemented.bed
11. bedops --element-of ./GATC/LT2GATC_Pairs.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_Pairs-Element-LT2Noncoding-Complemented.bed
12. bedops --element-of ./GATC/LT2GATC_HigherO1.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO1-Element-LT2Noncoding-
    Complemented.bed
13. bedops --element-of ./GATC/LT2GATC_HigherO2.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO2-Element-LT2Noncoding-
    Complemented.bed
14. bedops --element-of ./GATC/LT2GATC_HigherO3.bed ./Genes/LT2Noncoding-
    Complemented.bed > ./Element/LT2GATC_HigherO3-Element-LT2Noncoding-
    Complemented.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All-Element-LT2Noncoding-Complemented.bed ./Element/LT2GATC_All-
    Element-LT2Noncoding-Complemented.xls
19. cp ./Element/LT2GATC_Pairs-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_Pairs-Element-LT2Noncoding-Complemented.xls
20. cp ./Element/LT2GATC_HigherO1-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO1-Element-LT2Noncoding-Complemented.xls
21. cp ./Element/LT2GATC_HigherO2-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO2-Element-LT2Noncoding-Complemented.xls
22. cp ./Element/LT2GATC_HigherO3-Element-LT2Noncoding-
    Complemented.bed ./Element/LT2GATC_HigherO3-Element-LT2Noncoding-Complemented.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All-Element-LT2Noncoding-
    Complemented.txt
26.
27. mkdir ./LT2GATC_All-Element-LT2Noncoding-Complemented/
28. mv ./Element/ ./LT2GATC_All-Element-LT2Noncoding-Complemented/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinLT2Nonphage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in LT2 Nonphage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/LT2GATC_All.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2GATC_A
ll-Element-LT2AllPhageComplement.bed
11. bedops --element-
of ./GATC/LT2GATC_Pairs.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2GATC
_Pairs-Element-LT2AllPhageComplement.bed
12. bedops --element-
of ./GATC/LT2GATC_HigherO1.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2G
ATC_HigherO1-Element-LT2AllPhageComplement.bed
13. bedops --element-
of ./GATC/LT2GATC_HigherO2.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2G
ATC_HigherO2-Element-LT2AllPhageComplement.bed
14. bedops --element-
of ./GATC/LT2GATC_HigherO3.bed ./Prophage/LT2AllPhageComplement.bed > ./Element/LT2G
ATC_HigherO3-Element-LT2AllPhageComplement.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All-Element-LT2AllPhageComplement.bed ./Element/LT2GATC_All-
Element-LT2AllPhageComplement.xls
19. cp ./Element/LT2GATC_Pairs-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_Pairs-Element-
LT2AllPhageComplement.xls
20. cp ./Element/LT2GATC_HigherO1-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO1-Element-
LT2AllPhageComplement.xls
21. cp ./Element/LT2GATC_HigherO2-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO2-Element-
LT2AllPhageComplement.xls
22. cp ./Element/LT2GATC_HigherO3-Element-
LT2AllPhageComplement.bed ./Element/LT2GATC_HigherO3-Element-
LT2AllPhageComplement.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All-Element-
LT2AllPhageComplement.txt
26.
27. mkdir ./LT2GATC_All-Element-LT2AllPhageComplement/
28. mv ./Element/ ./LT2GATC_All-Element-LT2AllPhageComplement/

```

```

1. #!/bin/bash
2.
3. #Bedops_ElementGATCSinLT2Prophage.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find amount of GATCs in LT2 Prophage regions
6.
7. mkdir ./Element/
8.
9. #bedops make bed files element of
10. bedops --element-
of ./GATC/LT2GATC_All.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_All-Element-
LT2AllPhage.bed
11. bedops --element-
of ./GATC/LT2GATC_Pairs.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_Pairs-
Element-LT2AllPhage.bed
12. bedops --element-
of ./GATC/LT2GATC_HigherO1.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_Higher
O1-Element-LT2AllPhage.bed
13. bedops --element-
of ./GATC/LT2GATC_HigherO2.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_Higher
O2-Element-LT2AllPhage.bed
14. bedops --element-
of ./GATC/LT2GATC_HigherO3.bed ./Prophage/LT2AllPhage.bed > ./Element/LT2GATC_Higher
O3-Element-LT2AllPhage.bed
15.
16.
17. # Copy to excel
18. cp ./Element/LT2GATC_All-Element-LT2AllPhage.bed ./Element/LT2GATC_All-Element-
LT2AllPhage.xls
19. cp ./Element/LT2GATC_Pairs-Element-LT2AllPhage.bed ./Element/LT2GATC_Pairs-Element-
LT2AllPhage.xls
20. cp ./Element/LT2GATC_HigherO1-Element-LT2AllPhage.bed ./Element/LT2GATC_HigherO1-
Element-LT2AllPhage.xls
21. cp ./Element/LT2GATC_HigherO2-Element-LT2AllPhage.bed ./Element/LT2GATC_HigherO2-
Element-LT2AllPhage.xls
22. cp ./Element/LT2GATC_HigherO3-Element-LT2AllPhage.bed ./Element/LT2GATC_HigherO3-
Element-LT2AllPhage.xls
23.
24. #Line count
25. wc -l ./Element/*.bed > ./Element/OverlapStats-LT2GATC_All-Element-LT2AllPhage.txt
26.
27. mkdir ./LT2GATC_All-Element-LT2AllPhage/
28. mv ./Element/ ./LT2GATC_All-Element-LT2AllPhage/

```

BEDOPS GATCs in randomized *E. coli* SeqA Only signals (SeqA Only 1)

```
1. #!/bin/bash
2.
3. #Bedops_Element-GATCSandSeqAOnly-R1000e1-All-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in randomized SeqAOnly signals
6.
7. #bedops make bed files element of
8. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-R1000e1-
  Top5.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top5.bed
9. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-R1000e1-
  Top5.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top5.bed
10. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-Top5.bed
11. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-Top5.bed
12. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-Top5.bed
13. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-R1000e1-
  Top10.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top10.bed
14. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-R1000e1-
  Top10.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top10.bed
15. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
  Top10.bed
16. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
  Top10.bed
17. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
  Top10.bed
18. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-R1000e1-
  Top25.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top25.bed
19. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-R1000e1-
  Top25.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top25.bed
20. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
  Top25.bed
21. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
  Top25.bed
22. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
  Top25.bed
23. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-R1000e1-
  Top50.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top50.bed
24. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-R1000e1-
  Top50.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top50.bed
25. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
  Top50.bed
```

```

26. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
Top50.bed
27. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
Top50.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
R1000e1.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1.bed
30. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1.bed
31. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1.bed
32. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1.bed
33.
34.
35. # Copy to excel
36. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top5.bed ./Element/EcoliGATC_All-
Element-SeqAOnly-R1000e1-Top5.xls
37. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-
Top5.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top5.xls
38. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-Top5.xls
39. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-Top5.xls
40. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-Top5.xls
41. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top10.bed ./Element/EcoliGATC_All-
Element-SeqAOnly-R1000e1-Top10.xls
42. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-
Top10.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top10.xls
43. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-Top10.xls
44. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-Top10.xls
45. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-Top10.xls
46. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top25.bed ./Element/EcoliGATC_All-
Element-SeqAOnly-R1000e1-Top25.xls
47. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-
Top25.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top25.xls
48. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-Top25.xls
49. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-Top25.xls
50. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-Top25.xls
51. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1-Top50.bed ./Element/EcoliGATC_All-
Element-SeqAOnly-R1000e1-Top50.xls
52. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-
Top50.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1-Top50.xls
53. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-
Top50.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1-Top50.xls

```

```
54. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-
    Top50.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1-Top50.xls
55. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-
    Top50.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1-Top50.xls
56. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1.bed ./Element/EcoliGATC_All-
    Element-SeqAOnly-R1000e1.xls
57. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1.xls
59. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-
    R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1.xls
60. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-
    R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1.xls
61.
62. #Line count
63. wc -l ./Element/*.bed > ./Element/OverlapStats-Bedops_Element-GATCSandSeqAOnlyAll-
    Range75.txt
64.
65. mkdir ./Bedops_Element-GATCSandSeqAOnlyAll-Range75/
66. mv ./Element/ ./Bedops_Element-GATCSandSeqAOnlyAll-Range75/
```


BEDOPS GATCs in randomized *E. coli* SeqA Only (Grainger) signals (SeqA Only

2)

```
1. #!/bin/bash
2.
3. #Bedops_Element-GATCSandSeqAOnly_Grainger-R1000e1-All-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in randomized SeqAOnly_Grainger signals
6.
7. #bedops make bed files element of
8. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top5.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed
9. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top5.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed
10. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top5.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-Top5.bed
11. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top5.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-Top5.bed
12. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top5.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-Top5.bed
13. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top10.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed
14. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top10.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed
15. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top10.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed
16. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top10.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed
17. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top10.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed
18. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top25.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top25.bed
19. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top25.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top25.bed
20. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top25.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
Top25.bed
```

```

21. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top25.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
Top25.bed
22. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top25.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
Top25.bed
23. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top50.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top50.bed
24. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1-Top50.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top50.bed
25. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top50.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
Top50.bed
26. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top50.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
Top50.bed
27. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-R1000e1-
Top50.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
Top50.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1.bed
30. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1.bed
31. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1.bed
32. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1.bed
33.
34.
35. # Copy to excel
36. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-Top5.xls
37. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-Top5.xls
38. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-Top5.xls
39. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-Top5.xls
40. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-Top5.xls
41. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-Top10.xls
42. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
Top10.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-Top10.xls

```

```

43. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
    Top10.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-Top10.xls
44. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
    Top10.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-Top10.xls
45. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
    Top10.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-Top10.xls
46. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
    Top25.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-Top25.xls
47. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
    Top25.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-Top25.xls
48. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
    Top25.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-Top25.xls
49. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
    Top25.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-Top25.xls
50. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
    Top25.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-Top25.xls
51. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-
    Top50.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1-Top50.xls
52. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-
    Top50.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1-Top50.xls
53. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-
    Top50.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1-Top50.xls
54. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-
    Top50.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1-Top50.xls
55. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-
    Top50.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1-Top50.xls
56. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1.xls
57. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1.xls
59. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1.xls
60. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1.xls
61.
62. #Line count
63. wc -l ./Element/*.bed > ./Element/OverlapStats-Bedops_Element-
    GATCSandSeqAOnly_GraingerAll-Range75.txt
64.
65. mkdir ./Bedops_Element-GATCSandSeqAOnly_GraingerAll-Range75/
66. mv ./Element/ ./Bedops_Element-GATCSandSeqAOnly_GraingerAll-Range75/

```

BEDOPS GATCs in randomized *E. coli* 0 vs. 50 Min signals (SeqA Binding)

```
1. bin/bash
2.
3. #Bedops_Element-GATCSand0vs50Min-R1000e1-All-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in randomized 0vs50Min signals
6.
7. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-R1000e1-
  Top5.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top5.bed
8. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-R1000e1-
  Top5.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top5.bed
9. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-Top5.bed
10. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-Top5.bed
11. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
  R1000e1-Top5.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-Top5.bed
12. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-R1000e1-
  Top10.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top10.bed
13. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-R1000e1-
  Top10.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top10.bed
14. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
  Top10.bed
15. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
  Top10.bed
16. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
  R1000e1-Top10.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
  Top10.bed
17. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-R1000e1-
  Top25.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top25.bed
18. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-R1000e1-
  Top25.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top25.bed
19. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
  Top25.bed
20. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
  Top25.bed
21. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
  R1000e1-Top25.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
  Top25.bed
22. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-R1000e1-
  Top50.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top50.bed
23. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-R1000e1-
  Top50.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top50.bed
24. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
  R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
  Top50.bed
25. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
  R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
  Top50.bed
```

```

26. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
R1000e1-Top50.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
Top50.bed
27. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-
R1000e1.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-
R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1.bed
30. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1.bed
31. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1.bed
32.
33.
34. # Copy to excel
35. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top5.bed ./Element/EcoliGATC_All-
Element-0vs50Min-R1000e1-Top5.xls
36. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-
Top5.bed ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top5.xls
37. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-Top5.xls
38. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-Top5.xls
39. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
Top5.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-Top5.xls
40. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top10.bed ./Element/EcoliGATC_All-
Element-0vs50Min-R1000e1-Top10.xls
41. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-
Top10.bed ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top10.xls
42. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-Top10.xls
43. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-Top10.xls
44. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
Top10.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-Top10.xls
45. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top25.bed ./Element/EcoliGATC_All-
Element-0vs50Min-R1000e1-Top25.xls
46. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-
Top25.bed ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top25.xls
47. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-Top25.xls
48. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-Top25.xls
49. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
Top25.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-Top25.xls
50. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1-Top50.bed ./Element/EcoliGATC_All-
Element-0vs50Min-R1000e1-Top50.xls
51. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-
Top50.bed ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1-Top50.xls
52. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-
Top50.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1-Top50.xls
53. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-
Top50.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1-Top50.xls
54. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-
Top50.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1-Top50.xls

```

```
55. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1.bed ./Element/EcoliGATC_All-Element-
    0vs50Min-R1000e1.xls
56. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50Min-R1000e1.xls
57. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1.xls
59. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1.xls
60.
61. #Line count
62. wc -l ./Element/*.bed > ./Element/Bedops_Element-GATCSand0vs50MinAll-Range75.txt
63.
64. mkdir ./Bedops_Element-GATCSand0vs50MinAll-Range75/
65. mv ./Element/ ./Bedops_Element-GATCSand0vs50MinAll-Range75/
```

BEDOPS GATCs in *E. coli* SeqA Only signals (SeqA Only 1)

```
1. #!/bin/bash
2.
3. #Bedops_Element-GATCSandSeqAOnly-All-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in SeqAOnly signals
6.
7. #bedops make bed files element of
8. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
  Top5.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-Top5.bed
9. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
  Top5.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top5.bed
10. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  Top5.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top5.bed
11. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  Top5.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top5.bed
12. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  Top5.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top5.bed
13. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
  Top10.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-Top10.bed
14. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
  Top10.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top10.bed
15. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  Top10.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top10.bed
16. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  Top10.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top10.bed
17. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  Top10.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top10.bed
18. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
  Top25.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-Top25.bed
19. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
  Top25.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top25.bed
20. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  Top25.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top25.bed
21. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  Top25.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top25.bed
22. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  Top25.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top25.bed
23. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
  Top50.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-Top50.bed
24. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
  Top50.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top50.bed
25. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
  Top50.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top50.bed
26. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
  Top50.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top50.bed
27. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
  Top50.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top50.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly-
  R1000e1.bed > ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly-
  R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1.bed
```

```

30. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly-
    R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1.bed
31. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly-
    R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1.bed
32. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly-
    R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1.bed
33.
34.
35. # Copy to excel
36. cp ./Element/EcoliGATC_All-Element-SeqAOnly-Top5.bed ./Element/EcoliGATC_All-Element-
    SeqAOnly-Top5.xls
37. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top5.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-Top5.xls
38. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    Top5.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top5.xls
39. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-
    Top5.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top5.xls
40. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-
    Top5.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top5.xls
41. cp ./Element/EcoliGATC_All-Element-SeqAOnly-Top10.bed ./Element/EcoliGATC_All-Element-
    SeqAOnly-Top10.xls
42. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top10.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-Top10.xls
43. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    Top10.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top10.xls
44. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-
    Top10.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top10.xls
45. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-
    Top10.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top10.xls
46. cp ./Element/EcoliGATC_All-Element-SeqAOnly-Top25.bed ./Element/EcoliGATC_All-Element-
    SeqAOnly-Top25.xls
47. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top25.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-Top25.xls
48. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    Top25.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top25.xls
49. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-
    Top25.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top25.xls
50. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-
    Top25.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top25.xls
51. cp ./Element/EcoliGATC_All-Element-SeqAOnly-Top50.bed ./Element/EcoliGATC_All-Element-
    SeqAOnly-Top50.xls
52. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-Top50.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-Top50.xls
53. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    Top50.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-Top50.xls
54. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-
    Top50.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-Top50.xls
55. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-
    Top50.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-Top50.xls
56. cp ./Element/EcoliGATC_All-Element-SeqAOnly-R1000e1.bed ./Element/EcoliGATC_All-
    Element-SeqAOnly-R1000e1.xls
57. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly-R1000e1.bed ./Element/EcoliGATC_Pairs-
    Element-SeqAOnly-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly-R1000e1.xls

```



```
59. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-  
R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly-R1000e1.xls  
60. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-  
R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly-R1000e1.xls  
61.  
62. #Line count  
63. wc -l ./Element/*.bed > ./Element/OverlapStats-Bedops_Element-GATCSandSeqAOnlyAll-  
Range75.txt  
64.  
65. mkdir ./Bedops_Element-GATCSandSeqAOnlyAll-Range75/  
66. mv ./Element/ ./Bedops_Element-GATCSandSeqAOnlyAll-Range75/
```

BEDOPS GATCs in *E. coli* SeqA Only (Grainger) signals (SeqA Only 2)

```
1. #!/bin/bash
2.
3. #Bedops_Element-GATCSandSeqAOnly_Grainger-All-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in SeqAOnly_Grainger signals
6.
7. #bedops make bed files element of
8. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
  Top5.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top5.bed
9. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
  Top5.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top5.bed
10. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
  Top5.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top5.bed
11. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
  Top5.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top5.bed
12. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
  Top5.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top5.bed
13. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
  Top10.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top10.bed
14. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
  Top10.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top10.bed
15. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
  Top10.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top10.bed
16. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
  Top10.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top10.bed
17. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
  Top10.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top10.bed
18. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
  Top25.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top25.bed
19. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
  Top25.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top25.bed
20. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
  Top25.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top25.bed
21. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
  Top25.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top25.bed
22. bedops --range 75 --element-
  of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
  Top25.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top25.bed
23. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
  Top50.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top50.bed
24. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
  Top50.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top50.bed
```

```

25. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
Top50.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top50.bed
26. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
Top50.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top50.bed
27. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
Top50.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top50.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1.bed
30. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1.bed
31. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1.bed
32. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/SeqAOnly_Grainger-
R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1.bed
33.
34.
35. # Copy to excel
36. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top5.bed ./Element/EcoliGATC_All-
Element-SeqAOnly_Grainger-Top5.xls
37. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
Top5.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top5.xls
38. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
Top5.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top5.xls
39. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
Top5.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top5.xls
40. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
Top5.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top5.xls
41. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top10.bed ./Element/EcoliGATC_All-
Element-SeqAOnly_Grainger-Top10.xls
42. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
Top10.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top10.xls
43. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
Top10.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top10.xls
44. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
Top10.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top10.xls
45. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
Top10.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top10.xls
46. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top25.bed ./Element/EcoliGATC_All-
Element-SeqAOnly_Grainger-Top25.xls
47. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
Top25.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top25.xls
48. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
Top25.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top25.xls
49. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
Top25.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top25.xls
50. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
Top25.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top25.xls

```

```

51. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-Top50.bed ./Element/EcoliGATC_All-
    Element-SeqAOnly_Grainger-Top50.xls
52. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
    Top50.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-Top50.xls
53. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
    Top50.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-Top50.xls
54. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
    Top50.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-Top50.xls
55. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
    Top50.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-Top50.xls
56. cp ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_All-Element-SeqAOnly_Grainger-R1000e1.xls
57. cp ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_Pairs-Element-SeqAOnly_Grainger-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-SeqAOnly_Grainger-R1000e1.xls
59. cp ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-SeqAOnly_Grainger-R1000e1.xls
60. cp ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-
    R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-SeqAOnly_Grainger-R1000e1.xls
61.
62. #Line count
63. wc -l ./Element/*.bed > ./Element/OverlapStats-Bedops_Element-
    GATCSandSeqAOnly_GraingerAll-Range75.txt
64.
65. mkdir ./Bedops_Element-GATCSandSeqAOnly_GraingerAll-Range75/
66. mv ./Element/ ./Bedops_Element-GATCSandSeqAOnly_GraingerAll-Range75/

```

BEDOPS GATCs in *E. coli* 0 vs. 50 Min signals (SeqA Binding)

```
1. #!/bin/bash
2.
3. #Bedops_Element-GATCSand0vs50MinAll-Range75.sh
4. #bedops version: 2.4.35 (typical)
5. #Uses Bedops to find GATCs with range 75 in 0vs50Min signals
6.
7. bedops --range 75 --element-
of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50MinTop5.bed > ./Element/EcoliGATC_All-
Element-0vs50MinTop5.bed
8. bedops --range 75 --element-
of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50MinTop5.bed > ./Element/EcoliGATC_Pairs-
Element-0vs50MinTop5.bed
9. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50MinTop5.bed > ./Element/EcoliGATC_Hi
gherO1-Element-0vs50MinTop5.bed
10. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50MinTop5.bed > ./Element/EcoliGATC_Hi
gherO2-Element-0vs50MinTop5.bed
11. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50MinTop5.bed > ./Element/EcoliGATC_Hi
gherO3-Element-0vs50MinTop5.bed
12. bedops --range 75 --element-
of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50MinTop10.bed > ./Element/EcoliGATC_All-
Element-0vs50MinTop10.bed
13. bedops --range 75 --element-
of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50MinTop10.bed > ./Element/EcoliGATC_Pairs-
Element-0vs50MinTop10.bed
14. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50MinTop10.bed > ./Element/EcoliGATC_
HigherO1-Element-0vs50MinTop10.bed
15. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50MinTop10.bed > ./Element/EcoliGATC_
HigherO2-Element-0vs50MinTop10.bed
16. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50MinTop10.bed > ./Element/EcoliGATC_
HigherO3-Element-0vs50MinTop10.bed
17. bedops --range 75 --element-
of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50MinTop25.bed > ./Element/EcoliGATC_All-
Element-0vs50MinTop25.bed
18. bedops --range 75 --element-
of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50MinTop25.bed > ./Element/EcoliGATC_Pairs-
Element-0vs50MinTop25.bed
19. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50MinTop25.bed > ./Element/EcoliGATC_
HigherO1-Element-0vs50MinTop25.bed
20. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50MinTop25.bed > ./Element/EcoliGATC_
HigherO2-Element-0vs50MinTop25.bed
21. bedops --range 75 --element-
of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50MinTop25.bed > ./Element/EcoliGATC_
HigherO3-Element-0vs50MinTop25.bed
```

```

22. bedops --range 75 --element-
    of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50MinTop50.bed > ./Element/EcoliGATC_All-
    Element-0vs50MinTop50.bed
23. bedops --range 75 --element-
    of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50MinTop50.bed > ./Element/EcoliGATC_Pairs-
    Element-0vs50MinTop50.bed
24. bedops --range 75 --element-
    of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50MinTop50.bed > ./Element/EcoliGATC_
    HigherO1-Element-0vs50MinTop50.bed
25. bedops --range 75 --element-
    of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50MinTop50.bed > ./Element/EcoliGATC_
    HigherO2-Element-0vs50MinTop50.bed
26. bedops --range 75 --element-
    of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50MinTop50.bed > ./Element/EcoliGATC_
    HigherO3-Element-0vs50MinTop50.bed
27. bedops --range 75 --element-of ./GATC/EcoliGATC_All.bed ./Microarray/0vs50Min-
    R1000e1.bed > ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1.bed
28. bedops --range 75 --element-of ./GATC/EcoliGATC_Pairs.bed ./Microarray/0vs50Min-
    R1000e1.bed > ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1.bed
29. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO1.bed ./Microarray/0vs50Min-
    R1000e1.bed > ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1.bed
30. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO2.bed ./Microarray/0vs50Min-
    R1000e1.bed > ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1.bed
31. bedops --range 75 --element-of ./GATC/EcoliGATC_HigherO3.bed ./Microarray/0vs50Min-
    R1000e1.bed > ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1.bed
32.
33.
34. # Copy to excel
35. cp ./Element/EcoliGATC_All-Element-0vs50MinTop5.bed ./Element/EcoliGATC_All-Element-
    0vs50MinTop5.xls
36. cp ./Element/EcoliGATC_Pairs-Element-0vs50MinTop5.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50MinTop5.xls
37. cp ./Element/EcoliGATC_HigherO1-Element-
    0vs50MinTop5.bed ./Element/EcoliGATC_HigherO1-Element-0vs50MinTop5.xls
38. cp ./Element/EcoliGATC_HigherO2-Element-
    0vs50MinTop5.bed ./Element/EcoliGATC_HigherO2-Element-0vs50MinTop5.xls
39. cp ./Element/EcoliGATC_HigherO3-Element-
    0vs50MinTop5.bed ./Element/EcoliGATC_HigherO3-Element-0vs50MinTop5.xls
40. cp ./Element/EcoliGATC_All-Element-0vs50MinTop10.bed ./Element/EcoliGATC_All-Element-
    0vs50MinTop10.xls
41. cp ./Element/EcoliGATC_Pairs-Element-0vs50MinTop10.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50MinTop10.xls
42. cp ./Element/EcoliGATC_HigherO1-Element-
    0vs50MinTop10.bed ./Element/EcoliGATC_HigherO1-Element-0vs50MinTop10.xls
43. cp ./Element/EcoliGATC_HigherO2-Element-
    0vs50MinTop10.bed ./Element/EcoliGATC_HigherO2-Element-0vs50MinTop10.xls
44. cp ./Element/EcoliGATC_HigherO3-Element-
    0vs50MinTop10.bed ./Element/EcoliGATC_HigherO3-Element-0vs50MinTop10.xls
45. cp ./Element/EcoliGATC_All-Element-0vs50MinTop25.bed ./Element/EcoliGATC_All-Element-
    0vs50MinTop25.xls
46. cp ./Element/EcoliGATC_Pairs-Element-0vs50MinTop25.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50MinTop25.xls
47. cp ./Element/EcoliGATC_HigherO1-Element-
    0vs50MinTop25.bed ./Element/EcoliGATC_HigherO1-Element-0vs50MinTop25.xls
48. cp ./Element/EcoliGATC_HigherO2-Element-
    0vs50MinTop25.bed ./Element/EcoliGATC_HigherO2-Element-0vs50MinTop25.xls

```

```

49. cp ./Element/EcoliGATC_HigherO3-Element-
    0vs50MinTop25.bed ./Element/EcoliGATC_HigherO3-Element-0vs50MinTop25.xls
50. cp ./Element/EcoliGATC_All-Element-0vs50MinTop50.bed ./Element/EcoliGATC_All-Element-
    0vs50MinTop50.xls
51. cp ./Element/EcoliGATC_Pairs-Element-0vs50MinTop50.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50MinTop50.xls
52. cp ./Element/EcoliGATC_HigherO1-Element-
    0vs50MinTop50.bed ./Element/EcoliGATC_HigherO1-Element-0vs50MinTop50.xls
53. cp ./Element/EcoliGATC_HigherO2-Element-
    0vs50MinTop50.bed ./Element/EcoliGATC_HigherO2-Element-0vs50MinTop50.xls
54. cp ./Element/EcoliGATC_HigherO3-Element-
    0vs50MinTop50.bed ./Element/EcoliGATC_HigherO3-Element-0vs50MinTop50.xls
55. cp ./Element/EcoliGATC_All-Element-0vs50Min-R1000e1.bed ./Element/EcoliGATC_All-Element-
    0vs50Min-R1000e1.xls
56. cp ./Element/EcoliGATC_Pairs-Element-0vs50Min-R1000e1.bed ./Element/EcoliGATC_Pairs-
    Element-0vs50Min-R1000e1.xls
57. cp ./Element/EcoliGATC_HigherO1-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO1-Element-0vs50Min-R1000e1.xls
58. cp ./Element/EcoliGATC_HigherO2-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO2-Element-0vs50Min-R1000e1.xls
59. cp ./Element/EcoliGATC_HigherO3-Element-0vs50Min-
    R1000e1.bed ./Element/EcoliGATC_HigherO3-Element-0vs50Min-R1000e1.xls
60.
61. #Line count
62. wc -l ./Element/*.bed > ./Element/Bedops_Element-GATCSand0vs50MinAll-Range75.txt
63.
64. mkdir ./Bedops_Element-GATCSand0vs50MinAll-Range75/
65. mv ./Element/ ./Bedops_Element-GATCSand0vs50MinAll-Range75/

```

uShuffle *E. coli* genome 1000 times with “4” k-mer size

```
1. #!/bin/bash
2.
3. #uShuffle1000timesScript-k4.sh
4. #fasta_ushuffle version: 0.2
5. #Uses fasta_ushuffle to shuffle E. Coli genome [>gij556503834|ref|NC_000913.3| Escherichia coli
   i str. K-12 substr. MG1655, complete genome] 1000 times
6.
7. cp ./NC_000913_Formatted.fna ./NC_000913_k4s1000_x1000a0.fna
8. ./fasta_ushuffle -k 4 -
   s 1 < ./NC_000913_k4s1000_x1000a0.fna > ./NC_000913_k4s1000_x1000a1.fna
9. ./fasta_ushuffle -k 4 -
   s 1 < ./NC_000913_k4s1000_x1000a1.fna > ./NC_000913_k4s1000_x1000a2.fna
10. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a2.fna > ./NC_000913_k4s1000_x1000a3.fna
11. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a3.fna > ./NC_000913_k4s1000_x1000a4.fna
12. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a4.fna > ./NC_000913_k4s1000_x1000a5.fna
13. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a5.fna > ./NC_000913_k4s1000_x1000a6.fna
14. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a6.fna > ./NC_000913_k4s1000_x1000a7.fna
15. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a7.fna > ./NC_000913_k4s1000_x1000a8.fna
16. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a8.fna > ./NC_000913_k4s1000_x1000a9.fna
17. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a9.fna > ./NC_000913_k4s1000_x1000a10.fna
18. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a10.fna > ./NC_000913_k4s1000_x1000a11.fna
19. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a11.fna > ./NC_000913_k4s1000_x1000a12.fna
20. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a12.fna > ./NC_000913_k4s1000_x1000a13.fna
21. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a13.fna > ./NC_000913_k4s1000_x1000a14.fna
22. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a14.fna > ./NC_000913_k4s1000_x1000a15.fna
23. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a15.fna > ./NC_000913_k4s1000_x1000a16.fna
24. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a16.fna > ./NC_000913_k4s1000_x1000a17.fna
25. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a17.fna > ./NC_000913_k4s1000_x1000a18.fna
26. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a18.fna > ./NC_000913_k4s1000_x1000a19.fna
27. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a19.fna > ./NC_000913_k4s1000_x1000a20.fna
28. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a20.fna > ./NC_000913_k4s1000_x1000a21.fna
29. ./fasta_ushuffle -k 4 -
    s 1 < ./NC_000913_k4s1000_x1000a21.fna > ./NC_000913_k4s1000_x1000a22.fna
```


uShuffle LT2 genome 1000 times with “4” k-mer size

```
1. #!/bin/bash
2.
3.
4. #uShuffle1000timesScript_LT2-k4.sh
5. #fasta_ushuffle version: 0.2
6. #Uses fasta_ushuffle to shuffle LT2 genome [>gij556503834|ref|NC_000913.3| Escherichia coli str. K-12 substr. MG1655, complete genome] 1000 times
7.
8. cp ./AE006468_2_Formatted.fna ./AE006468_2_k4s1000_x1000a0.fna
9. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a0.fna > ./AE006468_2_k4s1000_x1000a1.fna
10. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a1.fna > ./AE006468_2_k4s1000_x1000a2.fna
11. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a2.fna > ./AE006468_2_k4s1000_x1000a3.fna
12. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a3.fna > ./AE006468_2_k4s1000_x1000a4.fna
13. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a4.fna > ./AE006468_2_k4s1000_x1000a5.fna
14. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a5.fna > ./AE006468_2_k4s1000_x1000a6.fna
15. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a6.fna > ./AE006468_2_k4s1000_x1000a7.fna
16. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a7.fna > ./AE006468_2_k4s1000_x1000a8.fna
17. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a8.fna > ./AE006468_2_k4s1000_x1000a9.fna
18. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a9.fna > ./AE006468_2_k4s1000_x1000a10.fna
19. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a10.fna > ./AE006468_2_k4s1000_x1000a11.fna
20. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a11.fna > ./AE006468_2_k4s1000_x1000a12.fna
21. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a12.fna > ./AE006468_2_k4s1000_x1000a13.fna
22. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a13.fna > ./AE006468_2_k4s1000_x1000a14.fna
23. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a14.fna > ./AE006468_2_k4s1000_x1000a15.fna
24. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a15.fna > ./AE006468_2_k4s1000_x1000a16.fna
25. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a16.fna > ./AE006468_2_k4s1000_x1000a17.fna
26. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a17.fna > ./AE006468_2_k4s1000_x1000a18.fna
27. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a18.fna > ./AE006468_2_k4s1000_x1000a19.fna
28. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a19.fna > ./AE006468_2_k4s1000_x1000a20.fna
29. ./fasta_ushuffle -k 4 -
   s 1 < ./AE006468_2_k4s1000_x1000a20.fna > ./AE006468_2_k4s1000_x1000a21.fna
```


982. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a973.fna > ./AE006468_2_k4s1000_x1000a974.fna
983. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a974.fna > ./AE006468_2_k4s1000_x1000a975.fna
984. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a975.fna > ./AE006468_2_k4s1000_x1000a976.fna
985. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a976.fna > ./AE006468_2_k4s1000_x1000a977.fna
986. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a977.fna > ./AE006468_2_k4s1000_x1000a978.fna
987. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a978.fna > ./AE006468_2_k4s1000_x1000a979.fna
988. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a979.fna > ./AE006468_2_k4s1000_x1000a980.fna
989. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a980.fna > ./AE006468_2_k4s1000_x1000a981.fna
990. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a981.fna > ./AE006468_2_k4s1000_x1000a982.fna
991. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a982.fna > ./AE006468_2_k4s1000_x1000a983.fna
992. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a983.fna > ./AE006468_2_k4s1000_x1000a984.fna
993. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a984.fna > ./AE006468_2_k4s1000_x1000a985.fna
994. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a985.fna > ./AE006468_2_k4s1000_x1000a986.fna
995. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a986.fna > ./AE006468_2_k4s1000_x1000a987.fna
996. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a987.fna > ./AE006468_2_k4s1000_x1000a988.fna
997. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a988.fna > ./AE006468_2_k4s1000_x1000a989.fna
998. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a989.fna > ./AE006468_2_k4s1000_x1000a990.fna
999. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a990.fna > ./AE006468_2_k4s1000_x1000a991.fna
1000. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a991.fna > ./AE006468_2_k4s1000_x1000a992.fna
1001. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a992.fna > ./AE006468_2_k4s1000_x1000a993.fna
1002. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a993.fna > ./AE006468_2_k4s1000_x1000a994.fna
1003. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a994.fna > ./AE006468_2_k4s1000_x1000a995.fna
1004. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a995.fna > ./AE006468_2_k4s1000_x1000a996.fna
1005. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a996.fna > ./AE006468_2_k4s1000_x1000a997.fna
1006. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a997.fna > ./AE006468_2_k4s1000_x1000a998.fna
1007. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a998.fna > ./AE006468_2_k4s1000_x1000a999.fna
1008. ./fasta_ushuffle -k 4 -
s 1 < ./AE006468_2_k4s1000_x1000a999.fna > ./AE006468_2_k4s1000_x1000a1000.fna

BEDTools shell scripts to convert BED files to FASTA

```
1. #!/bin/bash
2.
3. #ConvertEcoliMicroarrayBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Ecoli ORF and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed ./Genes/EcoliGenes_RemoveIDandDups-
   Merged.bed -name+ > ./Genes/EcoliGenes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed ./Genes/EcoliNoncoding-Complemented.bed -
   name+ > ./Genes/EcoliNoncoding-Complemented.fasta
```



```

1. #!/bin/bash
2.
3. #ConvertEcoliMicroarrayBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Microarray bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly.bed -
   name+ > ./FASTA/SeqAOnly.fasta
8. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly-Top50.bed -
   name+ > ./FASTA/SeqAOnly-Top50.fasta
9. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly-Top25.bed -
   name+ > ./FASTA/SeqAOnly-Top25.fasta
10. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly-Top10.bed -
    name+ > ./FASTA/SeqAOnly-Top10.fasta
11. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly-Top5.bed -
    name+ > ./FASTA/SeqAOnly-Top5.fasta
12.
13. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly.bed -
    name+ > ./FASTA/RNAPOnly.fasta
14. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly-Top50.bed -
    name+ > ./FASTA/RNAPOnly-Top50.fasta
15. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly-Top25.bed -
    name+ > ./FASTA/RNAPOnly-Top25.fasta
16. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly-Top10.bed -
    name+ > ./FASTA/RNAPOnly-Top10.fasta
17. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly-Top5.bed -
    name+ > ./FASTA/RNAPOnly-Top5.fasta
18.
19. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_Grainger.bed -
    name+ > ./FASTA/SeqAOnly_Grainger.fasta
20. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_Grainger-Top50.bed -
    name+ > ./FASTA/SeqAOnly_Grainger-Top50.fasta
21. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_Grainger-Top25.bed -
    name+ > ./FASTA/SeqAOnly_Grainger-Top25.fasta
22. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_Grainger-Top10.bed -
    name+ > ./FASTA/SeqAOnly_Grainger-Top10.fasta
23. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_Grainger-Top5.bed -
    name+ > ./FASTA/SeqAOnly_Grainger-Top5.fasta
24.
25. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly_Grainger.bed -
    name+ > ./FASTA/RNAPOnly_Grainger.fasta
26. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly_Grainger-Top50.bed -
    name+ > ./FASTA/RNAPOnly_Grainger-Top50.fasta
27. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly_Grainger-Top25.bed -
    name+ > ./FASTA/RNAPOnly_Grainger-Top25.fasta
28. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly_Grainger-Top10.bed -
    name+ > ./FASTA/RNAPOnly_Grainger-Top10.fasta
29. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/RNAPOnly_Grainger-Top5.bed -
    name+ > ./FASTA/RNAPOnly_Grainger-Top5.fasta
30.
31. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/0vs50Min.bed -
    name+ > ./FASTA/0vs50Min.fasta
32. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/0vs50Min-Top50.bed -
    name+ > ./FASTA/0vs50Min-Top50.fasta
33. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/0vs50Min-Top25.bed -
    name+ > ./FASTA/0vs50Min-Top25.fasta

```

34. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/0vs50Min-Top10.bed -name+ > ./FASTA/0vs50Min-Top10.fasta
35. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/0vs50Min-Top5.bed -name+ > ./FASTA/0vs50Min-Top5.fasta
- 36.
37. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_All.bed -name+ > ./FASTA/SeqAOnly_All.fasta
38. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_All-Top50.bed -name+ > ./FASTA/SeqAOnly_All-Top50.fasta
39. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_All-Top25.bed -name+ > ./FASTA/SeqAOnly_All-Top25.fasta
40. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_All-Top10.bed -name+ > ./FASTA/SeqAOnly_All-Top10.fasta
41. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Microarray/SeqAOnly_All-Top5.bed -name+ > ./FASTA/SeqAOnly_All-Top5.fasta

```
1. #!/bin/bash
2.
3. #ConvertEcoliO157H7-SakaiGenesBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert EcoliO157H7-Sakai ORF and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Genes/EcoliO157H7-SakaiGenes_RemoveIDandDups-Merged.bed -
   name+ > ./FASTA/EcoliO157H7-SakaiGenes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Genes/EcoliO157H7-SakaiNoncoding-Complemented.bed -
   name+ > ./FASTA/EcoliO157H7-SakaiNoncoding-Complemented.fasta
```

```

1.  #!/bin/bash
2.
3.  #ConvertEcoliO157H7-SakaiProphageBedtoFasta.sh
4.  #bedtools version: bedtools v2.27.1
5.  #Uses Bedtools to convert EcoliO157H7-Sakai Prophage and Nonprophage bed files to fasta
6.
7.  bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-SakaiProphage.bed -name+ > ./FASTA/EcoliO157H7-
   SakaiProphage.fasta
8.  bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-SakaiNonprophage.bed -name+ > ./FASTA/EcoliO157H7-
   SakaiNonprophage.fasta
9.  bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp1.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp1.fasta
10. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp2.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp2.fasta
11. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp3.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp3.fasta
12. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp4.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp4.fasta
13. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp5-stx2.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp5-
   stx2.fasta
14. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp6.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp6.fasta
15. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp7.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp7.fasta
16. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp8.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp8.fasta
17. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp9.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp9.fasta
18. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp10.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp10.fasta
19. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp11.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp11.fasta
20. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp12.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp12.fasta
21. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp13.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp13.fasta
22. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp14.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp14.fasta
23. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp15-stx1.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp15-stx1.fasta
24. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp16.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp16.fasta
25. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -
   bed ./Prophage/EcoliO157H7-Sakai-Sp17.bed -name+ > ./FASTA/EcoliO157H7-Sakai-
   Sp17.fasta

```

26. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-Sp18.bed -name+ > ./FASTA/EcoliO157H7-Sakai-Sp18.fasta
27. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE1.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE1.fasta
28. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE2.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE2.fasta
29. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE3.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE3.fasta
30. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE4.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE4.fasta
31. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE5.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE5.fasta
32. bedtools getfasta -fi ./FASTA/O157_H7-Sakai_GCF_000008865.2_ASM886v2_genomic.fna -bed ./Prophage/EcoliO157H7-Sakai-SpLE6.bed -name+ > ./FASTA/EcoliO157H7-Sakai-SpLE6.fasta

```
1. #!/bin/bash
2.
3. #ConvertEcoliO157H7GenesBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert EcoliO157H7 ORF and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
   bed ./Genes/EcoliO157H7Genes_RemoveIDandDups-Merged.bed -
   name+ > ./FASTA/EcoliO157H7Genes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
   bed ./Genes/EcoliO157H7Noncoding-Complemented.bed -
   name+ > ./FASTA/EcoliO157H7Noncoding-Complemented.fasta
```

```

1. #!/bin/bash
2.
3. #ConvertEcoliO157H7ProphageBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert EcoliO157H7 Prophage and Nonprophage bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-BP-933W-stx2.bed -name+ > ./FASTA/EcoliO157H7-
  EDL933-BP-933W-stx2.fasta
8. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933C.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933C.fasta
9. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933HI.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933HI.fasta
10. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933K.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933K.fasta
11. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933L.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933L.fasta
12. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933M.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933M.fasta
13. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933N.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933N.fasta
14. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933O.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933O.fasta
15. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933R.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933R.fasta
16. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933T.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933T.fasta
17. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933U.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933U.fasta
18. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-CP-933X.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  CP-933X.fasta
19. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-GP-9338.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  GP-9338.fasta
20. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-GP-93311.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  GP-93311.fasta
21. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-GP-93316.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  GP-93316.fasta
22. bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -
  bed ./Prophage/EcoliO157H7-EDL933-GP-93317.bed -name+ > ./FASTA/EcoliO157H7-EDL933-
  GP-93317.fasta

```

23. `bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -bed ./Prophage/EcoliO157H7-EDL933-CP-933V-stx1.bed -name+ > ./FASTA/EcoliO157H7-EDL933-CP-933V-stx1.fasta`
24. `bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -bed ./Prophage/EcoliO157H7-EDL933NonProphage.bed -name+ > ./FASTA/EcoliO157H7-EDL933NonProphage.fasta`
25. `bedtools getfasta -fi ./FASTA/O157_H7-EDL933-GCF_000006665.1_ASM666v1_genomic.fna -bed ./Prophage/EcoliO157H7-EDL933Prophage.bed -name+ > ./FASTA/EcoliO157H7-EDL933Prophage.fasta`


```
1. #!/bin/bash
2.
3. #ConvertEcoliProphageBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert EcoliProphage and Nonprophage bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliCP4-6.bed -
   name+ > ./FASTA/EcoliCP4-6.fasta
8. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliCP4-44.bed -
   name+ > ./FASTA/EcoliCP4-44.fasta
9. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliCP4-57.bed -
   name+ > ./FASTA/EcoliCP4-57.fasta
10. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliCPS-53.bed -
    name+ > ./FASTA/EcoliCPS-53.fasta
11. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliDLP12.bed -
    name+ > ./FASTA/EcoliDLP12.fasta
12. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliEut-CPZ-55.bed -
    name+ > ./FASTA/EcoliEut-CPZ-55.fasta
13. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliKpLE2.bed -
    name+ > ./FASTA/EcoliKpLE2.fasta
14. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliNonphage.bed -
    name+ > ./FASTA/EcoliNonphage.fasta
15. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliPR-X.bed -
    name+ > ./FASTA/EcoliPR-X.fasta
16. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliProphage.bed -
    name+ > ./FASTA/EcoliProphage.fasta
17. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliQinKim.bed -
    name+ > ./FASTA/EcoliQinKim.fasta
18. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/EcoliRac.bed -
    name+ > ./FASTA/EcoliRac.fasta
19. bedtools getfasta -fi ./FASTA/NC_000913.fna -bed Prophage/Ecolie14.bed -
    name+ > ./FASTA/Ecolie14.fasta
```

```
1. #!/bin/bash
2.
3. #ConvertLT2GenesBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert LT2 ORF and and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
   bed ./Genes/LT2Genes_RemoveIDandDups-Merged.bed -
   name+ > ./FASTA/LT2Genes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
   bed ./Genes/LT2Noncoding-Complemented.bed -name+ > ./FASTA/LT2Noncoding-
   Complemented.fasta
```

```

1. #!/bin/bash
2.
3. #ConvertLT2ProphageBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert LT2 Prophage and Nonprophage bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2ActivePhage.bed -name+ > ./FASTA/LT2ActivePhage.fasta
8. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2ActivePhageComplement.bed -
  name+ > ./FASTA/LT2ActivePhageComplement.fasta
9. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2AllPhage.bed -name+ > ./FASTA/LT2AllPhage.fasta
10. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2AllPhageComplement.bed -
  name+ > ./FASTA/LT2AllPhageComplement.fasta
11. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Defective1-SPI-16.bed -name+ > ./FASTA/LT2Defective1-SPI-16.fasta
12. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Defective2.bed -name+ > ./FASTA/LT2Defective2.fasta
13. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Defective3.bed -name+ > ./FASTA/LT2Defective3.fasta
14. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Defective4.bed -name+ > ./FASTA/LT2Defective4.fasta
15. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Fels1.bed -name+ > ./FASTA/LT2Fels1.fasta
16. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Fels2.bed -name+ > ./FASTA/LT2Fels2.fasta
17. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Gifsy1.bed -name+ > ./FASTA/LT2Gifsy1.fasta
18. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Gifsy2.bed -name+ > ./FASTA/LT2Gifsy2.fasta
19. bedtools getfasta -fi ./FASTA/GCA_000006945.2_ASM694v2_genomic.fna -
  bed ./Prophage/LT2Phaster-Region8.bed -name+ > ./FASTA/SD-9.fasta

```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-CT18GenesBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Typhi-CT18 ORF and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Genes/Typhi-
   CT18Genes_RemoveIDandDups-Merged.bed -name+ > ./FASTA_Genbank/Typhi-
   CT18Genes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Genes/Typhi-CT18Noncoding-
   Complemented.bed -name+ > ./FASTA_Genbank/Typhi-CT18Noncoding-Complemented.fasta
```

```

1. #!/bin/bash
2.
3. #ConvertTyphi-CT18ProphageBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Typhi-CT18 Prophage and Nonprophage bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-01.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-01.fasta
8. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-02.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-02.fasta
9. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-03.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-03.fasta
10. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-04.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-04.fasta
11. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-05.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-05.fasta
12. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-06.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-06.fasta
13. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18-CT18-07.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18-CT18-07.fasta
14. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18NonProphage.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18NonProphage.fasta
15. bedtools getfasta -fi ./FASTA_Genbank/Typhi-CT-18-
   GCF_000195995.1_ASM19599v1_genomic.fna -bed ./Prophage/Typhi-CT18Prophage.bed -
   name+ > ./FASTA_Genbank/Typhi-CT18Prophage.fasta

```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-Ty2GenesBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Typhi-Ty2 ORF and Noncoding bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
   bed ./Genes/Typhi-Ty2Genes_RemoveIDandDups-Merged.bed -
   name+ > ./FASTA_Genbank/Typhi-Ty2Genes_RemoveIDandDups-Merged.fasta
8. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
   bed ./Genes/Typhi-Ty2Noncoding-Complemented.bed -name+ > ./FASTA_Genbank/Typhi-
   Ty2Noncoding-Complemented.fasta
```

```

1. #!/bin/bash
2.
3. #ConvertTyphi-Ty2ProphageBedtoFasta.sh
4. #bedtools version: bedtools v2.27.1
5. #Uses Bedtools to convert Typhi-Ty2 Prophage and Nonprophage bed files to fasta
6.
7. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2Nonprophage.bed -name+ > ./FASTA_Genbank/Typhi-
  Ty2Nonprophage.fasta
8. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2Prophage.bed -name+ > ./FASTA_Genbank/Typhi-Ty2Prophage.fasta
9. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-1_CT18-2-CT18-3.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-
  Ty2-1_CT18-2-CT18-3.fasta
10. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-2_CT18-1.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-Ty2-
  2_CT18-1.fasta
11. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-3_CT18-4.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-Ty2-
  3_CT18-4.fasta
12. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-4_CT18-5.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-Ty2-
  4_CT18-5.fasta
13. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-5_CT18-6.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-Ty2-
  5_CT18-6.fasta
14. bedtools getfasta -fi ./FASTA_Genbank/Typhi-Ty2-GCF_000007545.1_ASM754v1_genomic.fna -
  bed ./Prophage/Typhi-Ty2-Ty2-6_CT18-7.bed -name+ > ./FASTA_Genbank/Typhi-Ty2-Ty2-
  6_CT18-7.fasta

```

EMBOSS seqret shell scripts to convert FASTA files to GenBank

```
1. #!/bin/bash
2.
3. #ConvertEcoliGenesFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Ecoli ORF and Noncoding fasta files to genbank
6.
7. seqret -auto -sequence ./Genes/EcoliGenes_RemoveIDandDups-Merged.fasta -
osformat genbank -outseq ./Genes/EcoliGenes_RemoveIDandDups-Merged.gb
8. seqret -auto -sequence ./Genes/EcoliNoncoding-Complemented.fasta -osformat genbank -
outseq ./Genes/EcoliNoncoding-Complemented.gb
```



```

1. #!/bin/bash
2.
3. #ConvertEcoliMicroarrayFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Ecoli Microarray fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA/SeqAOnly.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly.gb
8. seqret -auto -sequence ./FASTA/SeqAOnly-Top50.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly-Top50.gb
9. seqret -auto -sequence ./FASTA/SeqAOnly-Top25.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly-Top25.gb
10. seqret -auto -sequence ./FASTA/SeqAOnly-Top10.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly-Top10.gb
11. seqret -auto -sequence ./FASTA/SeqAOnly-Top5.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly-Top5.gb
12.
13. seqret -auto -sequence ./FASTA/RNAPOnly.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly.gb
14. seqret -auto -sequence ./FASTA/RNAPOnly-Top50.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly-Top50.gb
15. seqret -auto -sequence ./FASTA/RNAPOnly-Top25.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly-Top25.gb
16. seqret -auto -sequence ./FASTA/RNAPOnly-Top10.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly-Top10.gb
17. seqret -auto -sequence ./FASTA/RNAPOnly-Top5.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly-Top5.gb
18.
19. seqret -auto -sequence ./FASTA/SeqAOnly_Grainger.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly_Grainger.gb
20. seqret -auto -sequence ./FASTA/SeqAOnly_Grainger-Top50.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly_Grainger-Top50.gb
21. seqret -auto -sequence ./FASTA/SeqAOnly_Grainger-Top25.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly_Grainger-Top25.gb
22. seqret -auto -sequence ./FASTA/SeqAOnly_Grainger-Top10.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly_Grainger-Top10.gb
23. seqret -auto -sequence ./FASTA/SeqAOnly_Grainger-Top5.fasta -osformat genbank -
  outseq ./FASTA/SeqAOnly_Grainger-Top5.gb
24.
25.
26. seqret -auto -sequence ./FASTA/RNAPOnly_Grainger.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly_Grainger.gb
27. seqret -auto -sequence ./FASTA/RNAPOnly_Grainger-Top50.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly_Grainger-Top50.gb
28. seqret -auto -sequence ./FASTA/RNAPOnly_Grainger-Top25.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly_Grainger-Top25.gb
29. seqret -auto -sequence ./FASTA/RNAPOnly_Grainger-Top10.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly_Grainger-Top10.gb
30. seqret -auto -sequence ./FASTA/RNAPOnly_Grainger-Top5.fasta -osformat genbank -
  outseq ./FASTA/RNAPOnly_Grainger-Top5.gb
31.
32. seqret -auto -sequence ./FASTA/0vs50Min.fasta -osformat genbank -
  outseq ./FASTA/0vs50Min.gb
33. seqret -auto -sequence ./FASTA/0vs50Min-Top50.fasta -osformat genbank -
  outseq ./FASTA/0vs50Min-Top50.gb

```

34. seqret -auto -sequence ./FASTA/0vs50Min-Top25.fasta -osformat genbank -
outseq ./FASTA/0vs50Min-Top25.gb
35. seqret -auto -sequence ./FASTA/0vs50Min-Top10.fasta -osformat genbank -
outseq ./FASTA/0vs50Min-Top10.gb
36. seqret -auto -sequence ./FASTA/0vs50Min-Top5.fasta -osformat genbank -
outseq ./FASTA/0vs50Min-Top5.gb
- 37.
38. seqret -auto -sequence ./FASTA/SeqAOnly_All.fasta -osformat genbank -
outseq ./FASTA/SeqAOnly_All.gb
39. seqret -auto -sequence ./FASTA/SeqAOnly_All-Top50.fasta -osformat genbank -
outseq ./FASTA/SeqAOnly_All-Top50.gb
40. seqret -auto -sequence ./FASTA/SeqAOnly_All-Top25.fasta -osformat genbank -
outseq ./FASTA/SeqAOnly_All-Top25.gb
41. seqret -auto -sequence ./FASTA/SeqAOnly_All-Top10.fasta -osformat genbank -
outseq ./FASTA/SeqAOnly_All-Top10.gb
42. seqret -auto -sequence ./FASTA/SeqAOnly_All-Top5.fasta -osformat genbank -
outseq ./FASTA/SeqAOnly_All-Top5.gb

```
1. #!/bin/bash
2.
3. #ConvertEcoliO157H7-SakaiGenesFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert EcoliO157H7-
   Sakai ORF and Noncoding fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA/EcoliO157H7-SakaiGenes_RemoveIDandDups-Merged.fasta -
   osformat genbank -outseq ./FASTA/EcoliO157H7-SakaiGenes_RemoveIDandDups-Merged.gb
8. seqret -auto -sequence ./FASTA/EcoliO157H7-SakaiNoncoding-Complemented.fasta -
   osformat genbank -outseq ./FASTA/EcoliO157H7-SakaiNoncoding-Complemented.gb
```

```

1. #!/bin/bash
2.
3. #ConvertEcoliO157H7-SakaiProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert EcoliO157H7-
   Sakai Prophage and Nonprophage fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA/EcoliO157H7-SakaiProphage.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-SakaiProphage.gb
8. seqret -auto -sequence ./FASTA/EcoliO157H7-SakaiNonprophage.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-SakaiNonprophage.gb
9. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp1.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp1.gb
10. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp2.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp2.gb
11. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp3.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp3.gb
12. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp4.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp4.gb
13. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp5-stx2.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp5-stx2.gb
14. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp6.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp6.gb
15. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp7.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp7.gb
16. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp8.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp8.gb
17. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp9.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp9.gb
18. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp10.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp10.gb
19. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp11.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp11.gb
20. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp12.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp12.gb
21. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp13.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp13.gb
22. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp14.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp14.gb
23. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp15-stx1.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp15-stx1.gb
24. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp16.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp16.gb
25. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp17.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp17.gb
26. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-Sp18.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-Sp18.gb
27. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE1.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-SpLE1.gb
28. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE2.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-SpLE2.gb
29. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE3.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-SpLE3.gb
30. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE4.fasta -osformat genbank -
   outseq ./FASTA/EcoliO157H7-Sakai-SpLE4.gb

```

31. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE5.fasta -osformat genbank -
outseq ./FASTA/EcoliO157H7-Sakai-SpLE5.gb
32. seqret -auto -sequence ./FASTA/EcoliO157H7-Sakai-SpLE6.fasta -osformat genbank -
outseq ./FASTA/EcoliO157H7-Sakai-SpLE6.gb

```
33. #!/bin/bash
34.
35. #ConvertEcoliO157H7GenesFastatoGenbank.sh
36. #seqret version: EMBOSS:6.6.0.0
37. #Uses EMBOSS seqret to convert EcoliO157H7 ORF and Noncoding fasta files to genbank
38.
39. seqret -auto -sequence ./FASTA/EcoliO157H7Genes_RemoveIDandDups-Merged.fasta -
    osformat genbank -outseq ./FASTA/EcoliO157H7Genes_RemoveIDandDups-Merged.gb
40. seqret -auto -sequence ./FASTA/EcoliO157H7Noncoding-Complemented.fasta -
    osformat genbank -outseq ./FASTA/EcoliO157H7Noncoding-Complemented.gb
```

```
1. #!/bin/bash
2.
3. #ConvertEcoliO157H7ProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert EcoliO157H7 Prophage and Nonprophage fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-BP-933W-stx2.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-BP-933W-stx2.gb
8. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933C.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933C.gb
9. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933HI.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933HI.gb
10. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933K.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933K.gb
11. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933L.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933L.gb
12. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933M.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933M.gb
13. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933N.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933N.gb
14. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933O.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933O.gb
15. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933R.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933R.gb
16. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933T.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933T.gb
17. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933U.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933U.gb
18. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933X.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933X.gb
19. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-GP-9338.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-GP-9338.gb
20. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-GP-93311.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-GP-93311.gb
21. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-GP-93316.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-GP-93316.gb
22. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-GP-93317.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-GP-93317.gb
23. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933-CP-933V-stx1.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933-CP-933V-stx1.gb
24. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933NonProphage.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933NonProphage.gb
25. seqret -auto -sequence ./FASTA/EcoliO157H7-EDL933Prophage.fasta -osformat genbank -
  outseq ./FASTA/EcoliO157H7-EDL933Prophage.gb
```

```
1. #!/bin/bash
2.
3. #ConvertEcoliPromotersRemoveDupsMergedFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Ecoli Promoters and Nonpromoters fasta files to genbank
6.
7. seqret -auto -sequence ./EcoliPromotersRemoveDupsMerged.fasta -osformat genbank -
  outseq ./EcoliPromotersRemoveDupsMerged.gb
8. seqret -auto -sequence ./EcoliPromotersRemoveDupsComplement.fasta -osformat genbank -
  outseq ./EcoliPromotersRemoveDupsComplement.gb
```



```
1. #!/bin/bash
2.
3. #ConvertEcoliProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Ecoli Prophage and Nonprophage fasta files to genbank
6.
7. seqret -auto -sequence ./Prophage/EcoliCP4-6.fasta -osformat genbank -
  outseq ./Prophage/EcoliCP4-6.gb
8. seqret -auto -sequence ./Prophage/EcoliCP4-44.fasta -osformat genbank -
  outseq ./Prophage/EcoliCP4-44.gb
9. seqret -auto -sequence ./Prophage/EcoliCP4-57.fasta -osformat genbank -
  outseq ./Prophage/EcoliCP4-57.gb
10. seqret -auto -sequence ./Prophage/EcoliCPS-53.fasta -osformat genbank -
  outseq ./Prophage/EcoliCPS-53.gb
11. seqret -auto -sequence ./Prophage/EcoliDLP12.fasta -osformat genbank -
  outseq ./Prophage/EcoliDLP12.gb
12. seqret -auto -sequence ./Prophage/EcoliEut-CPZ-55.fasta -osformat genbank -
  outseq ./Prophage/EcoliEut-CPZ-55.gb
13. seqret -auto -sequence ./Prophage/EcoliKpLE2.fasta -osformat genbank -
  outseq ./Prophage/EcoliKpLE2.gb
14. seqret -auto -sequence ./Prophage/EcoliNonphage.fasta -osformat genbank -
  outseq ./Prophage/EcoliNonphage.gb
15. seqret -auto -sequence ./Prophage/EcoliPR-X.fasta -osformat genbank -
  outseq ./Prophage/EcoliPR-X.gb
16. seqret -auto -sequence ./Prophage/EcoliProphage.fasta -osformat genbank -
  outseq ./Prophage/EcoliProphage.gb
17. seqret -auto -sequence ./Prophage/EcoliQinKim.fasta -osformat genbank -
  outseq ./Prophage/EcoliQinKim.gb
18. seqret -auto -sequence ./Prophage/EcoliRac.fasta -osformat genbank -
  outseq ./Prophage/EcoliRac.gb
19. seqret -auto -sequence ./Prophage/Ecolie14.fasta -osformat genbank -
  outseq ./Prophage/Ecolie14.gb
```

```
1. #!/bin/bash
2.
3. #ConvertLT2GenesFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert LT2 ORF and Noncoding fasta files to genbank
6.
7. seqret -auto -sequence ./Genes/LT2Genes_RemoveIDandDups-Merged.fasta -
  osformat genbank -outseq ./Genes/LT2Genes_RemoveIDandDups-Merged.gb
8. seqret -auto -sequence ./Genes/LT2Noncoding-Complemented.fasta -osformat genbank -
  outseq ./Genes/LT2Noncoding-Complemented.gb
```

```
1. #!/bin/bash
2.
3. #ConvertLT2ProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert LT2 Prophage and Nonprophage fasta files to genbank
6.
7. seqret -auto -sequence ./Prophage/LT2ActivePhage.fasta -osformat genbank -
  outseq ./Prophage/LT2ActivePhage.gb
8. seqret -auto -sequence ./Prophage/LT2ActivePhageComplement.fasta -osformat genbank -
  outseq ./Prophage/LT2ActivePhageComplement.gb
9. seqret -auto -sequence ./Prophage/LT2AllPhage.fasta -osformat genbank -
  outseq ./Prophage/LT2AllPhage.gb
10. seqret -auto -sequence ./Prophage/LT2AllPhageComplement.fasta -osformat genbank -
  outseq ./Prophage/LT2AllPhageComplement.gb
11. seqret -auto -sequence ./Prophage/LT2Defective1-SPI-16.fasta -osformat genbank -
  outseq ./Prophage/LT2Defective1-SPI-16.gb
12. seqret -auto -sequence ./Prophage/LT2Defective2.fasta -osformat genbank -
  outseq ./Prophage/LT2Defective2.gb
13. seqret -auto -sequence ./Prophage/LT2Defective3.fasta -osformat genbank -
  outseq ./Prophage/LT2Defective3.gb
14. seqret -auto -sequence ./Prophage/LT2Defective4.fasta -osformat genbank -
  outseq ./Prophage/LT2Defective4.gb
15. seqret -auto -sequence ./Prophage/LT2Fels1.fasta -osformat genbank -
  outseq ./Prophage/LT2Fels1.gb
16. seqret -auto -sequence ./Prophage/LT2Fels2.fasta -osformat genbank -
  outseq ./Prophage/LT2Fels2.gb
17. seqret -auto -sequence ./Prophage/LT2Gifsy1.fasta -osformat genbank -
  outseq ./Prophage/LT2Gifsy1.gb
18. seqret -auto -sequence ./Prophage/LT2Gifsy2.fasta -osformat genbank -
  outseq ./Prophage/LT2Gifsy2.gb
19. seqret -auto -sequence ./Prophage/LT2SD-9.fasta -osformat genbank -
  outseq ./Prophage/LT2SD-9.gb
```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-CT18GenesFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convertTyphi-CT18 ORF and Noncoding fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18Genes_RemoveIDandDups-
  Merged.fasta -osformat genbank -outseq ./FASTA_Genbank/Typhi-
  CT18Genes_RemoveIDandDups-Merged.gb
8. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18Noncoding-Complemented.fasta -
  osformat genbank -outseq ./FASTA_Genbank/Typhi-CT18Noncoding-Complemented.gb
```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-CT18ProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Typhi-
   CT18 Prophage and Nonprophage fasta files to genbank
6.
7. #convert bed files to fasta
8.
9. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-01.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-01.gb
10. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-02.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-02.gb
11. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-03.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-03.gb
12. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-04.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-04.gb
13. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-05.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-05.gb
14. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-06.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-06.gb
15. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18-CT18-07.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18-CT18-07.gb
16. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18NonProphage.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18NonProphage.gb
17. seqret -auto -sequence ./FASTA_Genbank/Typhi-CT18Prophage.fasta -osformat genbank -
   outseq ./FASTA_Genbank/Typhi-CT18Prophage.gb
```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-Ty2GenesFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Typhi-Ty2 ORF and Noncoding fasta files to genbank
6.
7. #convert bed files to fasta
8.
9. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2Genes_RemoveIDandDups-Merged.fasta -
osformat genbank -outseq ./FASTA_Genbank/Typhi-Ty2Genes_RemoveIDandDups-Merged.gb
10. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2Noncoding-Complemented.fasta -
osformat genbank -outseq ./FASTA_Genbank/Typhi-Ty2Noncoding-Complemented.gb
```

```
1. #!/bin/bash
2.
3. #ConvertTyphi-Ty2ProphageFastatoGenbank.sh
4. #seqret version: EMBOSS:6.6.0.0
5. #Uses EMBOSS seqret to convert Typhi-Ty2 Prophage and Nonprophage fasta files to genbank
6.
7. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2Nonprophage.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2Nonprophage.gb
8. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2Prophage.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2Prophage.gb
9. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-1_CT18-2-CT18-3.fasta -
  osformat genbank -outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-1_CT18-2-CT18-3.gb
10. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-2_CT18-1.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-2_CT18-1.gb
11. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-3_CT18-4.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-3_CT18-4.gb
12. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-4_CT18-5.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-4_CT18-5.gb
13. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-5_CT18-6.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-5_CT18-6.gb
14. seqret -auto -sequence ./FASTA_Genbank/Typhi-Ty2-Ty2-6_CT18-7.fasta -osformat genbank -
  outseq ./FASTA_Genbank/Typhi-Ty2-Ty2-6_CT18-7.gb
```

RNA-Seq analysis of *Salmonella* Prophage Activity

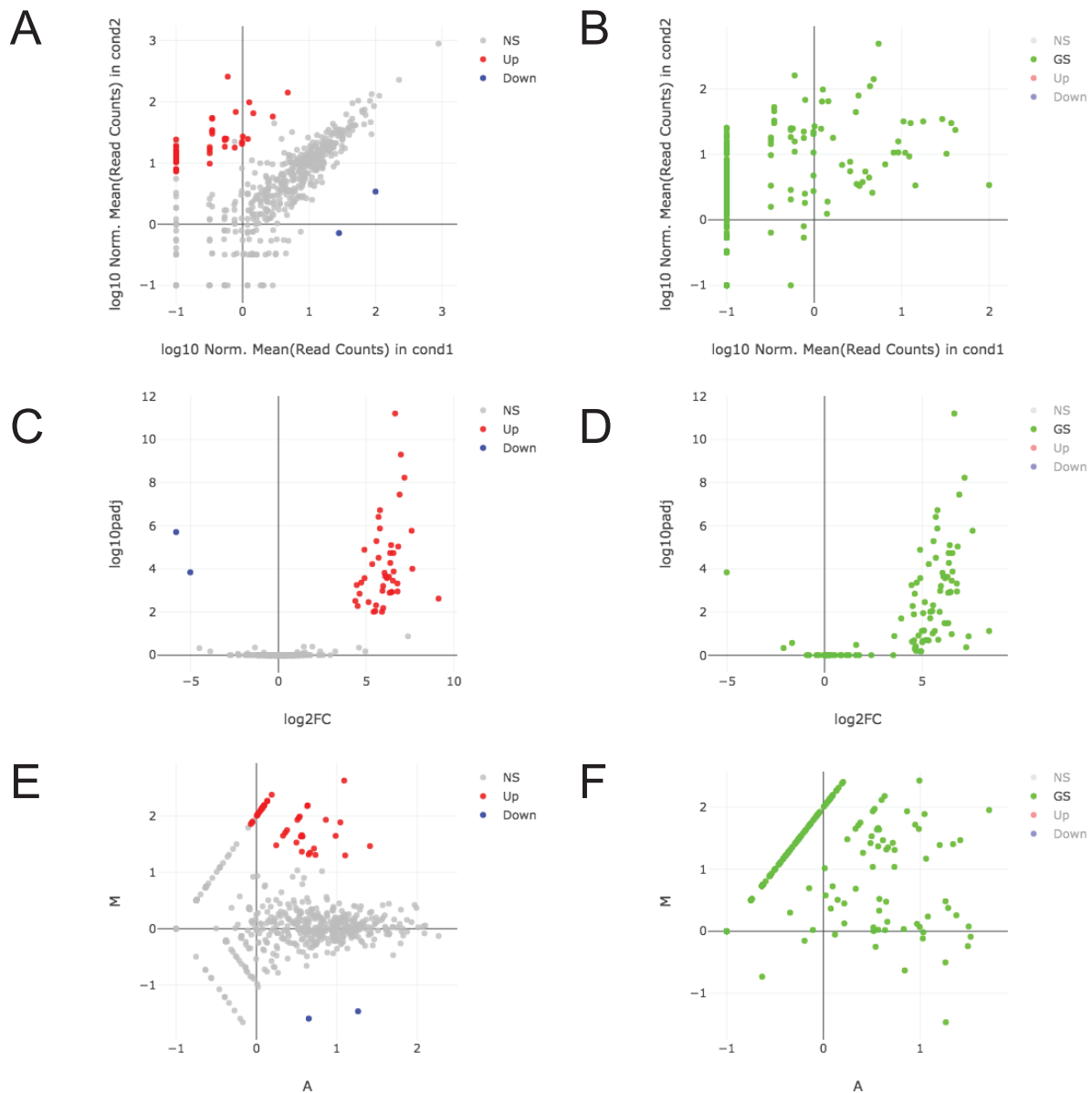


Figure 23: Prophage genes analyzed with DESeq2 in wild-type lysogens. Plots of differentially-expressed transcripts in lysogens vs. cured strains were made using the DEBrowser and DESeq2 (227, 228). GS indicates prophage genes searched. **A.** Scatter plot of all transcripts for *Salmonella* LT2 red dots are significantly upregulated and blue dots are significantly downregulated and Grey dots are nonsignificant. **B.** Scatter plot of A with prophage genes indicated with green dots. **C.** Volcano plot of all transcripts. **D.** Volcano plot of prophage transcripts. **E.** MA plot [M (log ratio) and A (mean average)] of all transcripts. **F.** MA plot of prophage transcripts.

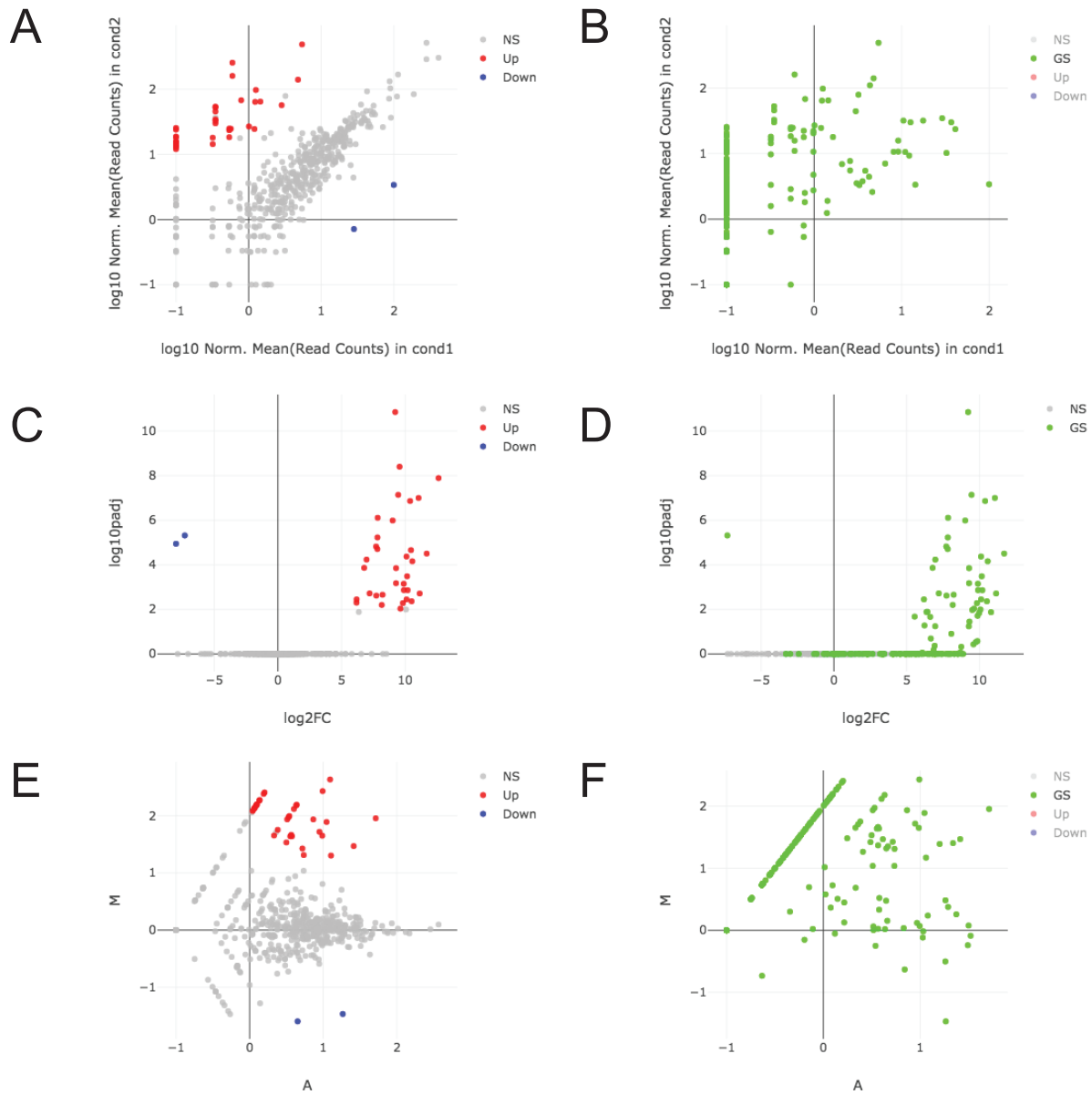


Figure 24: Prophage genes analyzed with EdgeR in wild-type lysogens. Plots of differentially-expressed transcripts in lysogens vs. cured strains were made using the DEBrowser and EdgeR (227, 229). GS indicates prophage genes searched. **A.** Scatter plot of all transcripts for *Salmonella* LT2 red dots are significantly upregulated and blue dots are significantly downregulated and Grey dots are nonsignificant. **B.** Scatter plot of A with prophage genes indicated with green dots. **C.** Volcano plot of all transcripts. **D.** Volcano plot of prophage transcripts. **D.** MA [M (log ratio) and A (mean average)] plot of all transcripts. **E.** MA plot of prophage transcripts.

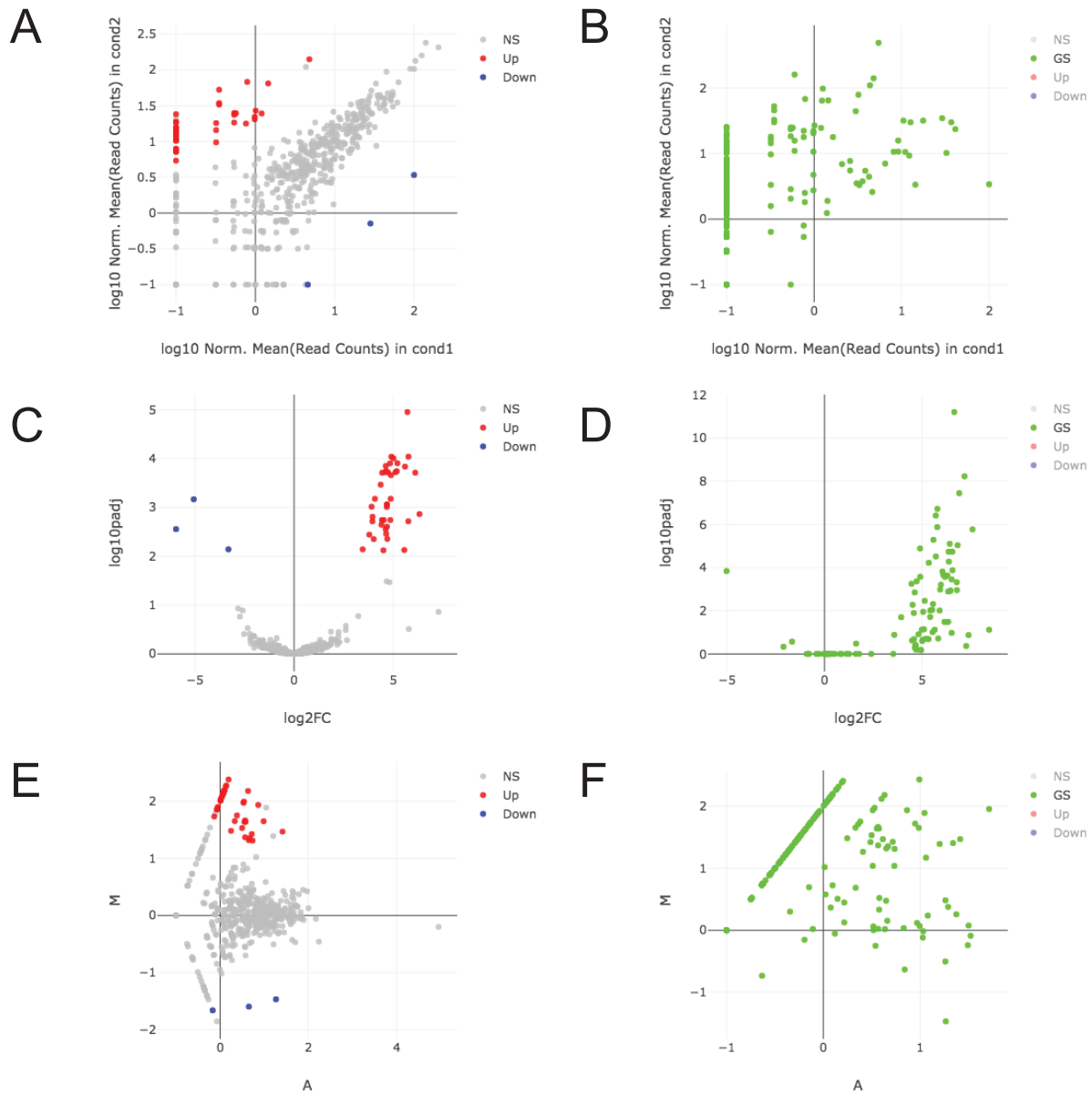


Figure 25: Prophage genes analyzed with Limma in wild-type lysogens. Plots of differentially-expressed transcripts in lysogens vs. cured strains were made using the DEBrowser and Limma (227, 230). GS indicates prophage genes searched. **A.** Scatter plot of all transcripts for *Salmonella* LT2 red dots are significantly upregulated and blue dots are significantly downregulated and Grey dots are nonsignificant. **B.** Scatter plot of A with prophage genes indicated with green dots. **C.** Volcano plot of all transcripts. **D.** Volcano plot of prophage transcripts. **D.** MA [M (log ratio) and A (mean average)] plot of all transcripts. **E.** MA plot of prophage transcripts.

Table 1517: RNA-Seq differential expression using DESeq2 of wild-type, *recA*, *ruvAB*, *ruvC* lysogens vs. wild-type, *recA*, *ruvAB*, *ruvC* cured.

Prophage-associated genes are shown in green. (p adj/adjusted p value <0.01)

Gene	Log ₂ fold change	Gene	Log ₂ fold change
<i>nanH</i>	9.12437169	<i>sodC-2</i>	5.97223704
STM0929	7.63121222	STM2620	5.96665641
STM1026	7.58891702	STM0919	5.92722728
STM2735	7.17832742	<i>ybjP</i>	5.90015782
<i>nagC</i>	6.97717116	STM2632	5.78566787
STM1043	6.90481845	STM1023	5.7794668
STM1010	6.82341145	STM2594	5.70769918
STM2592	6.78656788	STM1053	5.70429527
STM0927	6.77987866	STM0903	5.58443806
STM2600	6.65108109	STM2706	5.56336087
STM2729	6.56280224	STM1038	5.51941526
STM1013	6.55253245	STM1033	5.42125196
STM2724	6.51820242	STM0898	5.34568218
STM1031	6.45729464	STM0920	5.13683986
STM1056	6.44924088	STM0893	4.90586511
STM0924	6.41999902	STM1024	4.89718938
STM2723	6.37368173	STM1048	4.71936258
STM2726	6.36408232	STM2694	4.62311608
STM2636	6.33917544	STM2635	4.515137
STM1047	6.29817122	STM0900	4.45960403
STM2703	6.18036319	<i>dcuR</i>	4.38264146
STM2599	6.08631431	STM2585A	-5.0194594
STM2695	6.04706219	<i>citT</i>	-5.8287922

Table 1618: RNA-Seq differential expression using EdgeR of wild-type, *recA*, *ruvAB*, *ruvC* lysogens vs. wild-type, *recA*, *ruvAB*, *ruvC* cured.

Prophage-associated genes are shown in green. (p adj/adjusted p value <0.01)

Gene	Log₂ fold change	Gene	Log₂ fold change
<i>nanH</i>	12.6305514	STM0904	9.28866087
STM2734	11.699254	STM0927	9.28640148
STM1025	11.1479228	STM2600	9.22099443
STM2735	11.0614902	STM0924	9.02238017
STM1010	10.5687022	STM2695	8.22812458
STM2592	10.5129405	STM0913	8.16531643
STM0929	10.4634359	STM0903	7.84585391
STM1026	10.3924371	STM2632	7.82826105
STM2729	10.2031336	STM1023	7.82347298
STM1013	10.1588172	STM2594	7.73500481
STM2724	10.1147756	STM1053	7.7188986
STM1049	10.1119574	STM0898	7.21087253
STM2723	9.90388991	STM0893	6.96749624
STM2726	9.89322026	STM1024	6.78228225
STM1047	9.82693603	STM0900	6.18707295
STM2703	9.63152636	<i>dcuR</i>	6.18019868
<i>nagC</i>	9.56635742	STM2585A	-7.3213721
STM1043	9.45675048	<i>citT</i>	-8.0094532

Table 1719: RNA-Seq differential expression using Limma of wild-type, *recA*, *ruvAB*, *ruvC* lysogens vs. wild-type, *recA*, *ruvAB*, *ruvC* cured.

Prophage-associated genes are shown in green. (p adj/adjusted p value <0.01)

Gene	Log₂ fold change	Gene	Log₂ fold change
STM0893	6.32213961	STM2694	4.64549123
STM2600	6.10987649	STM2703	4.63993901
<i>nagC</i>	5.7685704	STM2599	4.62305315
STM1026	5.76058787	STM1031	4.61694721
STM2735	5.71513898	STM2594	4.59055082
STM1043	5.5933712	STM1048	4.52154531
STM0903	5.55847438	STM2635	4.50370207
STM1010	5.20936071	STM2620	4.43916339
STM2632	5.17753519	STM2636	4.42923291
STM1053	5.11148656	STM1056	4.40742825
STM1013	5.01056727	STM0919	4.36550883
STM2726	4.90775787	STM2706	4.07547432
STM2729	4.88337644	<i>sodC-2</i>	4.01629829
STM1023	4.86972666	STM1038	3.95612594
STM0900	4.85293331	STM0920	3.94991888
STM2723	4.83774942	STM1033	3.90877152
STM1047	4.73663507	STM2739	3.79171902
STM2592	4.69866777	STM2727	3.4595431
STM1024	4.6851338	<i>yraN</i>	-3.314713
STM0898	4.68390582	<i>citT</i>	-5.0626936
STM2695	4.6753989	STM2585A	-5.9545046
STM2724	4.67513752	STM2694	4.64549123

Acknowledgements

Appendix I, in part, is currently being prepared for submission for publication of the material. Peters, Gregory. The dissertation/thesis author was the primary investigator and author of this material.

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