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### Patterns of within-host spread of *Chlamydia trachomatis* between vagina, endocervix and rectum revealed by comparative genomic analysis

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**Introduction:** Chlamydia trachomatis, a gram-negative obligate intracellular bacterium, commonly causes sexually transmitted infections (STIs). Little is known about *C. trachomatis* transmission within the host, which is important for understanding disease epidemiology and progression.

**Methods:** We used RNA-bait enrichment and whole-genome sequencing to compare rectal, vaginal and endocervical samples collected at the same time from 26 study participants who attended Fijian Ministry of Health and Medical Services clinics and tested positive for *C. trachomatis* at each anatomic site.

**Results:** The 78 *C. trachomatis* genomes from participants resolved into two major clades of the *C. trachomatis* phylogeny (the "prevalent urogenital and anorectal" clade and "non-prevalent urogenital and anorectal" clade). For 21 participants, genome sequences were almost identical in each anatomic site. For the other five participants, two distinct *C. trachomatis* strains were present in different sites; in two cases, the vaginal sample was a mixture of strains.

**Discussion:** The absence of large numbers of fixed SNPs between *C. trachomatis* genomes within many of the participants could indicate recent acquisition of infection prior to the clinic visit without sufficient time to accumulate significant genetic variation in different body sites. This model suggests that many *C. trachomatis* infections may be resolved relatively quickly in the Fijian population, possibly reflecting common prescription or over-the-counter antibiotics usage.

#### KEYWORDS

*Chlamydia trachomatis*, single nucleotide polymorphisms, single variable polymorphisms, sexually transmitted diseases, chlamydiae

#### Highlights

- Chlamydia trachomatis is a bacterial pathogen that causes millions of sexually transmitted infections (STIs) annually across the globe. Because C. trachomatis lives inside human cells, it has historically been hard to study. We know little about how the bacterium spreads between body sites. Here, samples from 26 study participants who were simultaneously postive in their vagina, rectum and endocervix were genetically analyzed using an improved method to extract C. trachomatis DNA directly from clinical samples for genome sequencing. By analyzing patterns of mutations in the genomes, we found that 21 participants shared very similar C. trachomatis strains in all three anatomic sites, suggesting recent infection and spread. For five participants, two C. trachomatis strains were evident, indicating multiple infections. This study is significant in that improved enrichment methods for genome sequencing provides robust data to genetically trace patterns of C. trachomatis infection and transmission within an individual for epidemiologic and pathogenesis interrogations.

#### Introduction

The obligate intracellular bacterium *Chlamydia trachomatis* is the most common worldwide cause of bacterial sexually transmitted infections (STIs) with over 129 million annual cases in 2020 (World Health Organization, 2020). In 2019, 1.8 million cases were reported in the United States alone, representing a 19% increase since 2015 (Centers for Disease Control Prevention and Department of Health Human Services, 2021). Approximately 80% of female and 50% of male *C. trachomatis* STIs are asymptomatic (Batteiger, 2020), increasing the risk of transmission and complications at a yearly cost of billions of dollars (Satterwhite et al., 2013).

The endocervix is considered the most common initial site of chlamydial sexually transmitted, non-lymphogranuloma venereum (LGV) infections. Sloughed C. trachomatis infected cells and the organism itself can be secreted into the vagina but neither are known to infect the squamous epithelium of that organ (Batteiger, 2020). Cervicitis, an inflammation of the uterine endocervix, is a strong predictor of upper genital tract inflammation and disease (Peipert et al., 2000), including pelvic inflammatory disease, tubalfactor infertility, ectopic pregnancy and poor pregnancy outcomes (Haggerty et al., 2010). The rectum is another site of infection. A growing number of studies now show that C. trachomatis rectal infections are more common than previously thought, ranging from 2 to 77% of women seen in clinical settings (Chan et al., 2016). In one study, over 70% of women with urogenital C. trachomatis also had rectal C. trachomatis infection (van Liere et al., 2015). Of the 24 studies reporting on both urogenital and rectal infections in the same women, six showed a higher prevalence of C. trachomatis in the rectum (Chan et al., 2016). These data suggest that, while the rectum is known to be a common site of infection with LGV strains among men who have sex with men (Stoner and Cohen, 2015), it may also be a more frequent primary site of non-LGV strain infections among women. However, no studies to date have evaluated this issue.

There are several hypotheses for *C. trachomatis* transmission between sexual partners and within anatomic sites of the same

individual given our fragmentary knowledge of the genetic structure of C. trachomatis populations in natural human infections. The ascertainment of C. trachomatis infection in females could be affected by rectal infections persisting longer than endocervical infections and/or increased transmissibility during receptive anal intercourse. However, a recent study found no association between receptive anal intercourse and rectal C. trachomatis infections (Chandra et al., 2018) and another found that screening given a history of receptive anal intercourse did not significantly influence the rate of detection of C. trachomatis infections in the rectum (van Liere et al., 2015). We also know that women may develop urinary tract infections from enteric bacteria that are transferred from the perineum or anorectal area during sex (van Liere et al., 2015). It is therefore possible that rectal C. trachomatis infections could similarly be spread to the endocervix and urethra and possibly vice versa from the endocervix and urethra to the rectum. The concern here is that single dose treatment that is effective for uncomplicated urogenital tract infections is inadequate for rectal infections, as has been shown in recent studies (Drummond et al., 2011; Khosropour et al., 2014; Lanjouw et al., 2016; van Liere et al., 2017; Foschi et al., 2018). Indeed, a study that followed cervicovaginal and anorectal C. trachomatis loads following treatment with one gram of azithromycin found consistently higher loads in the anorectal site at 16 days after therapy with increasing loads up to 51 days when the study was terminated (Dukers-Muijrers et al., 2013). Due to the requirement to treat non-LGV C. trachomatis infections of the rectum for seven days and LGV strains for 21 days, adherence to treatment and/or treatment failure, as a result of lack of adherence, are also concerns (Kong et al., 2014). These studies show that rectal infection, if not treated appropriately, could have a significant effect on persistence and within-host transmission and disease. Therefore, it is important to understand the pathways of transmission between anatomic sites.

To understand the dynamics and pathobiology of withinhost transmission of *C. trachomatis*, we explored the relationships among *C. trachomatis* genomes sequenced using DNA purified directly from endocervical, vaginal and rectal swabs from the same women. Our cohort comprised a population of Fijian women that have an unusually high prevalence of *C. trachomatis* STIs (Svigals et al., 2020). We sought to reveal evidence of withinhost dissemination that may promote maintenance of infection in the rectum and increase transmission both within the host and to sexual partners in addition to providing data to select optimal anatomic sites for diagnostic screening, appropriate treatment and duration of therapy.

#### Results

#### Direct enrichment and sequencing of *Chlamydia trachomatis* genomes and comparison of bacterial loads between anatomic sites

Clinical endocervical, rectal, and vaginal swab samples collected from 26 women who attended the Fijian Ministry of Health and Medical Services clinics and tested positive for *C. trachomatis* at each anatomic site simultaneously were supplied

de-identified from an ongoing parent study (Svigals et al., 2020). The women ranged in age from 19 to 38 years (mean 26.69 years) of whom 13 (34.6%) had signs and/or symptoms of STIs. There was no association of age (i.e., <25 years vs  $\geq$ 25 years) with signs or symptoms, *omp*A genotype or plasmid strain (Supplementary Table 1).

We successfully extracted DNA from clinical swabs and used our recently redesigned Agilent RNA bait library (Bowden et al., 2021) to enrich C. trachomatis genomic sequences from Illumina sequencing libraries (see Methods). We defined a threshold for a "good quality" genome of at least 10× average C. trachomatis genome read redundancy ("coverage") postenrichment and at least 5 reads mapped to > 900,000 bases of the 1,042,519 bp C. trachomatis reference D/UW-3/CX chromosome (Supplementary Table 1). The median coverage of these 78 samples was  $127 \times$  with an average of  $308 \times$ ; only three samples were lower than 20×. The RNA bait method was therefore able to enrich C. trachomatis genomic DNA even though the samples from the three anatomic sites likely contain high levels of other viral and bacterial organisms. These data are supported by our previous study using the same methodology that successfully generated genomes derived from DNA purified directly from clinical vaginalrectal pairs from Fijian participants (Bowden et al., 2021).

Using qPCR with conserved ompA primers, the chromosomal yield for 25/26 women with C. trachomatis successfully sequenced from each body site ranged from 69 to 9,600,000 copies/µL. Given the obligate intracellular nature of C. trachomatis, and to normalize the sample against the number of human cells collected in the sample, the ratio of the C. trachomatis genomic copy numberbased on the single copy ompA gene in the C. trachomatis genome to the human beta-actin (a single gene in the human genome) copy number was calculated as an estimated relative load of the organism in each anatomic site. In comparing the vaginal with the rectal site for each woman using a paired t-test, there was a statistically significant higher load in the rectum than the vagina (P = 0.0124; Supplementary Figure 1). However, there were no statistically significant differences between rectum/endocervix and vagina/endocervix sites. When comparing body sites from the same person, 21 of the 26 women had a higher load in the rectum compared to the vagina (Figure 1). However, the differences in qPCR loads across body sites were not reflected in the redundancy of genome coverage. Within the 78 genomes, there was a significantly higher coverage in the endocervical samples compared to rectal (T-test; P = 0.031) and vaginal (P = 0.0016) samples (Supplementary Figure 2).

# Fiji sample genomes in the context of the global *Chlamydia trachomatis* phylogeny

We investigated the phylogenetic distribution of assembled genomes from this study and selected chlamydial reference and other clinical genomes representing known global *C. trachomatis* clades corresponding to four major *C. trachomatis* clades: LGV, ocular, "prevalent urogenital and anorectal (P-UA) and "non-prevalent urogenital and anorectal" (NP-UA) (Smelov et al., 2017; Figure 2 and Table 1). The reference genome D/UW-3/CX was in the NP-UA clade. All Fiji genomes were in the NP-UA and

P-UA clades, forming two subclades of NP-UA and one in P-UA, suggesting that the Fiji genomes were derived from at least two independent introductions in NP-UA and one in P-UA (Figure 2). Based on sequencing of the ompA gene, referred to as the ompA genotype, 32 genomes in NP-UA had ompA genotype D (4), F (3), G (23) and Ja (1) plus one that was not possible to determine, and the 46 genomes in P-UA had E (21), G (2), and Ja (23) ompA genotypes. Twenty-four Fiji samples dominated a sub-lineage of NP-UA (ompA genotypes G and F) that included one publicly submitted genome sequence G/11222 (BioSample: SAMN02603694, Assembly NC\_017430.1) (Jeffrey et al., 2010), which was a cervical sample but with no notation of geographic source. This Fijian subclade may represent a local endemic clone. We also found genomes with ompA genotype Ja with an E backbone that we had previously described in the Fiji population (Bowden et al., 2021) and also a plasmid genotype E.

Numerous studies have shown that ompA alleles recombine frequently between C. trachomatis genomic backbones (Gomes et al., 2004; Somboonna et al., 2011; Joseph et al., 2012; Hadfield et al., 2017; Seth-Smith et al., 2021). While the association of ompA genotypes with clades in Fiji strains was broadly consistent with patterns found in the Hadfield et al. study (Hadfield et al., 2017), there were some combinations of genomic clade and ompA in this work not previously reported: G in P-UA and F in NP-UA (Figure 2). fastGEAR (Mostowy et al., 2017) inferred recombination events in ancestors of the global P-UA clade (primarily from NP-UA into P-UA) as well as recent recombinational exchange of DNA within the branches of the tree containing Fiji strains (Supplementary Figure 3). Recent inferred events included donors from all clades, including a small number of importation events from LGV and ocular clades, respectively, at recombination hotspots in the chromosome (Supplementary Table 2).

#### Participants with samples from three anatomic body sites fell into two groups based on levels of *Chlamydia trachomatis* genome diversity

Of the 26 study participants, there was good quality genome sequence data across the three anatomic sites, and 21 had the same ompA genotype strain consistent with the rest of its genome that formed a monophyletic clade on the global C. trachomatis phylogenetic tree (Figure 2 and Supplementary Table 3). We inferred these strains shared a recent common ancestor. We termed these 21 participants "Group A". Five participants ("Group B") had three samples that appeared not to derive from a single recent infection event. For participant #1078, the rectal sample and vaginal/endocervical samples were different ompA genotypes/genomes from different clades (E in P-UA and D in NP-UA, respectively). For participant #564, all samples were in P-UA but the vaginal and rectal samples were both E while the endocervical sample was Ja and more distantly related on the core genome phylogeny than the other two (Figure 2 and Supplementary Figure 3). The rectal and endocervical samples of participant #1176 were both Ja in P-UA, but the vaginal sample was a G in NP-UA. In participant #32, all of the strains were ompA



genotype G. However, the endocervical and rectal genomes were closely related in the P-UA clade while the vaginal strain was in NP-UA. For participant #1182, all strains were *omp*A genotype Ja but in this case, while the vaginal and endocervical genomes were closely related in P-UA, the rectal genome was in NP-UA. The *omp*A genotype E is rare in NP-UA strains (Figure 2), suggesting the rectal strain acquired the allele through recent recombination.

The differences in *C. trachomatis* strains between the vagina and endocervix of the same individual confirm that these sites can be effectively sampled without cross-contamination. In addition, shotgun metagenomics from some of the same samples as in this study also revealed related but diverged communities at each site (Bommana et al., 2022). Further, while the endocervix is the site of infection and secretions along with the infected cells flow into the vagina, the vaginal environment may promote unique pressures on the genomes that are then detected as noted above.

The *C. trachomatis* ~7 kb virulence plasmid was amplified and sequenced in 66/78 samples. For each participant, the genotype based on comparison with reference strain plasmid sequences was identical across the anatomic sites (Supplementary Table 1). All plasmids were either E genotype or "D/G" genotype (D and G plasmids had identical sequences in our typing scheme). Plasmid genotype E was linked to P-UA genomes (36 out of 37 samples with data) and D/G linked to NP-UA (26/29 samples with data). The strong association between chromosome and plasmid genotype suggested that vertical transmission was the dominant mode for plasmid inheritance (Hadfield et al., 2017). Only in Group B patients were incongruent combinations seen (plasmid genotype E-P-UA for 32V, 1176V, and 1182R samples and plasmid D/G-NP-UA for 1078R). These samples likely have had plasmid replacement events, with the donor strain containing the transferred plasmid infecting another anatomic site.

#### Patterns of shared fixed single nucleotide polymorphisms (SNPs) and single nucleotide variants (SNVs) in *Chlamydia trachomatis* from anatomic body sites of the same participant are different in group A and group B participants

We looked first at the Group A participants to see what the patterns of SNPs revealed about the relationships between the body sites. We defined "fixed" SNPs to mean nucleotide positions on the reference genome where 10% or less of the mapped sequence read coverage matched the reference base. The number of fixed SNPs in all three body sites was 512-1944 for NP-UA samples and 2169-5229 SNPs for P-UA (**Supplementary Table 3**). The higher number for P-UA was because the reference strain D/UW-3/CX was in the NP-UA clade. This pattern was consistent with these SNPs being shared by the common ancestor of the sample that infected the three body sites of each participant.

Fixed SNPs found in only one or two body site samples were rare in Group A participants. The presence of these SNPs would be suggestive of independently evolving populations at different sites. Only five Group A participants had a rectal sample with a fixed SNP, one had a fixed SNP in the endocervix but zero had fixed SNPs unique to the vaginal sample (Figure 3 and Supplementary Table 3). One participant had a SNP shared by rectal and vaginal samples and one shared between rectal and endocervical samples. There were three SNPs shared between endocervical and vaginal pairs that were fixed in one of the sites but intermediate frequency in the other (see below) (Figure 3). Since these mutations probably occurred within the host, these data point to a recent common ancestor of the bacterium in each body site of the Group A participants.

Next, we looked at intermediate frequency single nucleotide variants (SNVs), which we defined as having reference allele frequencies in the 10–90% range. Reference alleles over 90% were inferred to be the same as the reference while less than 10% were defined as fixed, as in the paragraph above. Across the 78 high-quality Fiji genomes, we found 8,694 SNVs. Most SNVs were found in a small number of samples, with 2,039 (23.5%) found in only one. Of particular note were the 3,818 "rare SNVs" that were only found in one or more anatomic sites of the same participant. The remaining "common" SNVs (found in 4 + of the 78 samples) appeared to be frequently occurring polymorphic sites within C. trachomatis populations. They were distributed across the genome but there was a peak in regions around the highly recombinogenic ompA gene. SNVs could be generated by genetic drift and/or sharing of populations between body sites. Alternatively, they could be artifacts of random sequencing error. Artifacts would be more likely to occur where there was lower coverage, as one or two miscalled bases could put the position in the 10-90% range for SNV calling. Some Group A participants with lower coverage had as many as 500 SNVs in only one of the body site samples but on inspection we found that SNVs at these positions were close to the 90% reference threshold, suggesting that they were likely to be false positives generated by sequencing error. Positions that had SNPs that were either fixed in two sites and SNV in the other, or fixed in one and SNV in the other two also were likely artifacts. In this case the SNVs were found at the 10% threshold and probably represented false positive SNPs that were fixed in all three sites. However, positions that were fixed SNPs in one body site but SNV at one other would be expected to be generated infrequently by sequence error. This pattern only occurred in three participants where, in each case, the body site that shared the mutations were the endocervix and vagina (Figure 3).

To help understand patterns of sharing within individuals we identified 5,520 genome positions that differentiated NP-UA and P-UA Fiji strains (see Methods). Because of pervasive recombination in *C. trachomatis* every strain had some alleles assigned to both clades but were overrepresented in alleles common in their own clade. In Group A samples, these clonal SNP sites (CSS) segregated across the chromosome as fixed differences (i.e., either mostly > 90% or < 10% reference allele frequency). The pattern seen in participant #1201 (**Figure 4**) is representative of the simple relationships seen in Group A. In this case, CSSs were dominated by NP-UA alleles (>90% reads aligning to reference bases) with few intermediate frequency SNVs. In Group A participants where the dominant strain was from the P-NP clade, the majority of CSS alleles were different from the reference genome (<10% reads aligning).

We saw more complex patterns of SNPs and SNVs in Group B participants compared to Group A. The simplest Group B participant was #564 where all genomes were in P-UA: the rectal and vaginal genomes were genotype E while the endocervix was genotype Ja. Therefore, the CSS showed all three sites exhibited a pattern typical of P-UA but the rectal and vaginal samples shared a large number of fixed SNPs (179 SNPs) not found in the endocervical sample. Conversely, the endocervical sample had unique fixed SNPs (231 SNPs) not found in the other two body sites (**Supplementary Table 3** and **Supplementary Figure 4**). Approximately 50% of these unique SNPs were found within blocks predicted by fastGEAR, suggesting that recombination was a major contributor to genetic differences between the two strains. A simple explanation of these patterns was that participant #564 contained multiple strains: caused by a P-UA Ja strain coinfecting the



endocervix after another P-UAE strain had previously infected the rectum and vagina; the reverse order, with E strains coinfecting was also possible. The recombination events between genotypes could have occurred pre- or post-coinfection as natural transformation only requires that chlamydial DNA from a prior, non-viable infection or co-occurring infection be present that can be taken up by a newly infected cell.

In participants #32 and #1176, CSS patterns clearly showed strain mixing in the vaginal genome (Figures 5, 6). While the endocervical and rectal genomes were dominated by alleles typical of P-UA strains, the vaginal genomes, located in the NP-UAs clade, had intermediate allele frequency across the length of the chromosome. Our interpretation of this pattern is that the vaginal samples contain a mixture of strains with P-UA and NP-UA chromosomes.

In participant #1078 interpretation was complicated by the lower data quality of endocervical and rectal samples: (only 249,618 and 875,018 bases with >  $10 \times$  redundancy, respectively) (**Supplementary Figure 5**). There were many fixed SNPs in the rectal E genome, indicating it was from a different clade to the vaginal D genome. The pattern of CSS suggested some mixing of P-UA and NP-UA backgrounds in the vaginal genome. In #1078 all samples had the same plasmid subtype "D" despite differences in chromosome backgrounds suggesting possible plasmid transmission.

#### Discussion

The Fijian genomes sequenced in this study represent a sampling from the globally distributed P-UA and NP-UA clades. Although the phylogeny suggested multiple introductions of C. trachomatis strains from outside Fiji, there was also evidence for clonal expansion in both clades, presumably due to endemic local transmission (Svigals et al., 2020). There was evidence of recent DNA exchange between P-UA and NP-UA clades and possible local introductions of DNA from LGV and ocular clades into both clades of Fijian strains. This suggests that LGV and ocular strains might be present locally in Fiji but not common in the cohort we sampled, which would be expected as LGV is more common in Men who have Sex with Men, and the ocular strains are associated with the non-STI disease trachoma. However, trachoma is endemic to the Pacific Islands of the Western Pacific Region, and previous research has shown that both ocular and urogenital strains can be present at the same time in trachoma patients (Dean et al., 2008), which would provide an opportunity for genetic exchange.

This work is centered around sequencing *C. trachomatis* genomes directly from clinical samples using Agilent RNA bait libraries. This approach has been used to sequence bacterial species such as *C. trachomatis* and *Treponema pallidum* that are difficult to

#### TABLE 1 Terms used specific to this work.

Term	Explanation
CSS	"Clonal SNP sites". A set of 5,520 SNPs that were used to differentiate Fijian NP-UA from P-UA chromosomal backgrounds. They were defined at positions where 90% NP-UA had one allele and 90% P-UA had the other (reference C. trachomatis D/UW-3/CX is in the NP-UA clade).
"fixed SNP"	Single Nucleotide Polymorphism is defined here as a position with an allele frequency of less than 0.1 compared to the reference C. trachomatis D/UW-3/CX chromosome. For example, if the reference nucleotide at a position is "A", a fixed SNP would have $> 90\%$ sequencing reads as either "G", "C" or "T" aligning to that position.
LGV	"Lymphogranuloma venereum".
NP-UA	""non-prevalent urogenital and anorectal" clade in the <i>C. trachomatis</i> species phylogeny
P-UA	"Prevalent urogenital and anorectal" clade.
SNV	"Single nucleotide variant". Defined here as an allele frequency of $> 0.1-0.9 <$ compared to the reference.
STI	"Sexually transmitted infection"

culture and are present in only small fractions of the metagenome (Seth-Smith et al., 2013, 2021; Hadfield et al., 2017; Pickering et al., 2020; Beale et al., 2021; Bowden et al., 2021). Here, we showed that the newly redesigned bait library (Bowden et al., 2021) could be used efficiently to produce high-quality genome sequences from samples with low yields of *C. trachomatis*, as measured by qPCR. Some samples had a high proportion of human DNA even after enrichment, leaving lower-coverage regions in the *C. trachomatis* genomes. However, we achieved good sequence data

from 78 samples representing all three anatomic sites from 26 study participants.

There were complexities in the bioinformatic interpretation of the data, which arose because what was being sequenced was actually a within-species pool of strains rather than the pure cultures normally used in bacterial genomics projects. We showed that SNVs, which we defined here as having an allele frequency of 10-90%, were common across all samples but unevenly distributed, with some having many thousands more than the average due to random sequence errors in low-coverage regions. Non-artifactual SNVs could theoretically come from two sources: (1) the presence of more than one C. trachomatis strain through mixed infections; (2) mutation accumulation over time through population growth. Interpretation of the sequence pools in the absence of being able to culture pure cell lines is complex as multiple processes may be occurring, especially allowing for the possibility of recombination between subpopulations of strains within the sample pool (Somboonna et al., 2011). We also found that SNVs complicated analysis based on calling consensus nucleotide positions (e.g., de novo assembly or reference mapping using tools such as SNIPPY). While these methods worked well for placing samples on a phylogenetic tree, detailed analysis can be confused if SNVs are around the 50% consensus line. Consensus base calling means that distinct subpopulations are not recognized if they are distributed at significantly less than 50% frequency or alternatively, if over 50%, they are incorporated into the consensus.

To our knowledge, this is the first study to use genomics to assess within-host transmission dynamics for *C. trachomatis* STIs. Our analysis revealed two strikingly different patterns within participants: "Group A" (n = 21) had three anatomic samples with similar genetic background and *omp*A genotype or known





Patterns of SNP and SNV frequency across anatomic sites for representative Group A participant #1201. (A–C) Percent reference scores versus position on reference genome for "clonal SNPs" (CSSs) by body site. The set of 5,520 CSSs were chosen to differentiate NP-UA and P-UA genetic backgrounds. Each point shows the percentage of reads that mapped with the reference allele at each CSS position. The strains from #1201 are from the NP-UA clade and therefore, at most, CSSs are close to 100% match to the reference (D) allele, which is also in the NP-UA clade. The gaps in the distribution of CSSs across the chromosome are where there were regions of low variation or high recombination. (D) Box plot of distribution of% reference for clonal SNPs by body site. The minority of the CSSs with alternative alleles (<10% of reference genome) were likely the product of recombination events that have occurred since the divergence of the strains. Notably there is an intermediate frequency of SNVs.

recombinant (i.e., Ja *omp*A but E backbone), while "Group B" (n = 5) had one sample with a different background, implying a coinfection event. In the case of Group A, it was notable that only a minority of participants had samples with any fixed SNP differences and, if present, the modal number of SNPs was one (Figure 3 and Supplementary Table 3). We argue that positions that were SNPs or rare SNVs shared between two samples from different anatomic sites were likely to be real. These, too, were rare in Group A women (Figure 3). As the mutation rate of *C. trachomatis* inferred from dated whole genome comparison is ~0.2 SNPs per genome per year (Hadfield et al., 2017; Seth-Smith et al., 2021), the most likely implication of these patterns is that there has been recent acquisition and transmission between anatomic sites in these participants. The simplest explanation is that these infections are quite transient and resolve before there has been time to accumulate

significant variation between sites. This resolution may be due to recent infection and prescribed treatment proximal to a clinic visit or self-treatment with antibiotics that are available over-thecounter, limiting the longitudinal acquisition of SNPs. Either of these scenarios could result from symptomatic infection and health care seeking behavior—as would be presumed for the nine women (34.6%) in the study who were symptomatic—or asymptomatic infection with concern over sexual exposure to someone with an STI. These patterns could also be explained by more complex alternative models, for example, population contractions across all body sites followed by rapid re-seeding from one site with a small bottleneck.

The patterns of mutation might reveal pathways of transfer of *C. trachomatis* between anatomic sites, although care must be taken to not over-interpret the findings as the number of participants



in this pilot study was small. SNPs and SNVs have been used to infer transmission between individuals (Worby et al., 2017) and in theory could also be used for potential events occurring between body sites of the same individual. It is possibly a sign of the biases in transmission between sites that unique fixed SNPs in Group A participants were more common in rectal samples, and that vaginal and endocervical samples more often had shared fixed and SNVs (**Figure 3**). The accumulation of SNPs in one site could be seen as a sign of population stratification caused by anatomy: The vaginal and endocervical *C. trachomatis* populations transmit between each other more frequently, given their proximity, than *C. trachomatis* in the rectum.

The Group B participant samples had much greater numbers of fixed and intermediate SNPs in pairwise comparisons than Group A. The simplest explanation for these is the coinfection of one anatomic site. The site with the divergent strain was not constant: in two cases it was the rectum (participants #1078R and #1082R), in two cases the vagina (participants #32V and #1176V) and in one case the endocervix (#564C). In four of these samples (#32V, #1078R, #1176V, #1182R) there was evidence of mixtures between *C. trachomatis* strains from different clades. These data show that sequencing of enriched *C. trachomatis genomes* directly from DNA of clinical samples can be used to identify co-infections, which are necessary for inter-strain recombination events to occur. The harmonization of plasmid genotypes in women containing *C. trachomatis* from different clades suggested that the process of plasmid replacement can be rapid. However, the caveat is that plasmid sequences in this study are based on PCR amplification and Sanger sequencing rather than Agilent bait pulldown, so it may not be possible to identify minor plasmid subpopulations.

This study revealed the intricacies of *C. trachomatis* withinhost diversity and transmission during natural human infections and suggested that further investigation will yield information that



will help understand infection spread and disease processes. More samples are needed from a global sample set to know if these results can be extrapolated across human populations. Integration with additional bio-behavioral data will also be important to fully understand causes and direction of C. trachomatis transmission, although partner and sexual history are not always reliable. It would be ideal to expand individual datasets by conducting longitudinal studies to help resolve the dynamics of recombination and determine if multiple cycles of cross-infection occur between sites, but this would not be ethical as identification of infection requires treatment to eradicate C. trachomatis. Genomic approaches that resolve the potential subpopulations, such as single-cell sequencing (Zheng et al., 2022) and Hi-C (Kent et al., 2020), are hampered by C. trachomatis being only a minor component of the DNA in the clinical metagenomic sample. It may be possible to dissect recombination by isolating clonal C. trachomatis populations from individual samples and sequencing them independently. The technique commonly used for this is the plaque assay that is labor-intensive and not always guaranteed to completely separate out subpopulations (Somboonna et al., 2008). The most productive near-term strategy may be to continue to build up our picture of *C. trachomatis* natural infection by taking more "snapshots" of populations at single time points across multiple anatomic sites from a larger sample sizes of participants across Fiji, using the efficient RNA-bait methodology, to see if the patterns hold or diverge across a more global population, especially as tourism is a major part of the economy in Fiji.

#### Materials and methods

#### Study design and sample collection

The parent study was cross-sectional in design, enrolling women 18 years of age and older attending Ministry of Health and Medical Services (MoHMS) Health Centers in Fiji following

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written informed consent as described (Svigals et al., 2020). Appropriate IRB approval had been obtained from UCSF (21-33864) and the Fijian MoHMS (FNHRERC 2015.100.MC) prior to commencement of the parent study. Women attended the Health Centers for various reasons including family planning, contraception, annual pap test, infertilty, a general check-up or interest in STI testing. Only women who did not use antibiotics within the prior month were consented and enrolled.

The current study was supplied with C. trachomatis positive endocervical, vaginal and rectal swab samples that had all been collected at the same time during the parent study to determine whether C. trachomatis was present in all three sites, especially the rectum as reported in other countries. All samples were de-identified with a unique ID number. All endocervical samples were collected by trained clinicians after cleaning the exocervix with a large cotton swab prior to inserting the collection swab directly into the endocervix, avoiding contact with the exocervix, vaginal wall or speculum. In addition, data on age and signs and/or symptoms of STIs were provided at the time of sample collection. The women were of iTauki ethnicity. None of the women engaged in transactional sex or reported anal intercourse or had a history of anal intercourse or any extragenital sex. All women were heterosexual and had one reported sexual partner who was also reported to be heterosexual.

Paired vaginal and rectal swabs were screened for *C. trachomatis* using the Cepheid Xpert CT/NG assay (Sunnyvale, CA) according to manufacturer's instructions. *C. trachomatis* positive endocervical samples were identified using a *C. trachomatis*-specific in-house qPCR assay as described (Bowden et al., 2021).

# DNA extraction and determination of *Chlamydia trachomatis* copy number and load

Genomic (g)DNA was extracted from remnant Xpert CT/NG transport media for vaginal swabs and remnant M4 transport media (Thermo Fisher, South San Francisco, CA) for endocervical and rectal swabs as described previously (Bowden et al., 2021). Briefly, 59  $\mu$ l consisting of 50  $\mu$ L lysozyme (10 mg/mL; MilliporeSigma, St. Louis, MO), 3  $\mu$ l of lysostaphin (4,000 U/mL in sodium acetate; MilliporeSigma) and 6  $\mu$ l of mutanolysin (25,000 U/mL; MilliporeSigma) was added to 200  $\mu$ l of remnant transport media and incubated for 1 h at 37°C as described (Bommana et al., 2022). The QIAamp DNA mini kit (Qiagen, California) was then used for DNA extraction, according to manufacturer's instructions. 5  $\mu$ L of the resulting DNA underwent one or more displacement amplifications using the Repli-G MDA kit (Qiagen), to enrich microbial DNA. DNA concentration was measured using the Qubit dsDNA broad-range assay kit (Invitrogen).

Quantitative PCR (qPCR) was used to determine *C. trachomatis* genomic copy number and *C. trachomatis* load as described (Gomes et al., 2006; Sharma et al., 2018). Primers specific for the *C. trachomatis ompA* gene and for human Beta-Actin were used to generate standard curves of 10-fold serial increases in

plasmids containing a single copy of each gene, respectively. Copy number of *C. trachomatis* and Beta-Actin for the clinical sample was determined based on comparison with the standard curve for the respective control plasmid. *C. trachomatis* load was estimated based on the ratio of bacteria (*C. trachomatis* genome copy number) per human cell (Beta-actin genome copy number) for each clinical sample to normalize the data against the host cell.

### Chlamydia trachomatis ompA genotyping and plasmid sequencing

The *omp*A genotype was determined for each clinical sample as described previously (Somboonna et al., 2008). PCR was performed using primer pairs that flank the *omp*A gene; the product was sequenced in both directions and aligned using MAFFT v7.45062 to create the consensus sequence, which was then aligned with the 19 known *C. trachomatis* reference sequences to determine the *omp*A genotype. The reference strains were A/HAR-13, B/TW-5/OT, Ba/Apache-2, C/TW-3/OT, D/UW-3/Cx, Da/TW-448, E/Bour, F/IC-Cal-13, G/UW-57/Cx, H/UW-4/Cx, I/UW-12/Ur, Ia/UW-202, J/UW-36/Cx, Ja/UW-92, K/UW-31/Cx, L1/440, L2/434, L2a/UW-396, L2b/UCH-1/proctitis, L2c, and L3/404.

The plasmid for each clinical sample was sequenced as described (Bowden et al., 2021). Five primer pairs that flanked and covered the entire plasmid sequence were used, and the PCR products were sanger sequenced and aligned as above using MAFFT v7.45062 (Katoh and Standley, 2013). Each plasmid sequence was aligned to the 19 reference sequences to determine the plasmid identity.

#### Enrichment of *Chlamydia trachomatis* sequences from clinical samples using an agilent bait library

We used a methodology for RNA bait capture of C. trachomatis described in detail by Bowden et al. (2021). Human gDNA (Promega, San Luis Obispo, CA) was added to the extracted gDNA from the clinical swabs to reach a total input of 3  $\mu$ g/130  $\mu$ L for fragmentation and library prep. Samples were sheared on the Covaris LE220 plus (Covaris, Woburn, MA). After shearing and magnetic bead purification, the SureSelectXT Target Enrichment System for Illumina Paired-End Multiplexed Sequencing Library (VC2 Dec 2018) and all recommended quality control steps were performed on all gDNA samples. The 2.698 Mbp RNA bait library consisted of 34,795 120-mer probes spanning 85 GenBank C. trachomatis reference genomes (Bowden et al., 2021)(Agilent Technologies, INC, Santa Clara, CA, reference: ELID: 3173001). A 16-hour incubation at 65°C was performed for RNA bait library hybridization. Post-capture PCR cycling was set at 12 cycles based on a capture library size > 1.5 Mb. The libraries were paired end sequenced for 150 nt using an Illumina HiSeq instrument. Sequence data from this project was submitted to the NCBI Sequence Read Archive under the BioProject accession ID: PRJNA609714.

## Post-sequencing bioinformatic isolation of *Chlamydia trachomatis* sequences

The post-enrichment raw sequencing reads were processed to remove the host genome and *C. trachomatis reads* were extracted and assembled into contigs as described in Bowden et al. (2021). We used an arbitrary threshold for good quality sequence data if the samples had at least  $10 \times$  average *C. trachomatis* genome coverage post-enrichment and at least 5 reads mapped to > 900,000 bases of the 1,042,519 Mbp *C. trachomatis* reference D/UW-3/CX chromosome. To genotype the patient samples, *de novo* contigs were used to extract and compare the *omp*A genes against a customized BLAST (Altschul et al., 1990) database of the 21 reference *omp*A sequences as we described (Bowden et al., 2021).

#### Phylogeny and recombination inference

For the global phylogenetic analysis of the main chromosomes (total n = 176), we included all "good quality" genome sequences from the 26 participants (n = 77, with the exception of 1078C, which assembled into too many small contigs); and a collection of diverse C. trachomatis chromosomes available in NCBI (n = 99). We used a reference mapping approach with a custom version of C. trachomatis D/UW-3/CX by masking the 6 rRNA genes present in the repeated rRNA operons as described in Bowden et al. (2021), and generated a full-length whole genome alignment using snippy v4.3.8<sup>1</sup>. Snippy mapped the C. trachomatis reads from each sample to the reference genome using bwa and identified variants using Freebayes v1.0.2 (Garrison and Marth, 2012). The length of the region common to all samples with at least 10× read coverage and 90% read concordance at each site was 699,239 nucleotides with 11,971 polymorphic sites. Regions of increased density of homoplasious SNPs introduced by possible recombination events were predicted iteratively and masked using Gubbins (Croucher et al., 2014). The final maximum-likelihood (ML) global phylogenetic tree on 10,045 polymorphic sites was reconstructed using RAxML v8.2.9 (Kozlov et al., 2019) on the recombination removed (MRE) convergence criterion, along with ascertainment bias corrected using Stamatakis method. Lineagespecific phylogenetic trees were inferred as described above by using only the genomes from Fiji samples from their respective lineages.

fastGEAR (Mostowy et al., 2017) was run on a whole alignment that contained all "good quality" Fiji *C. trachomatis* genomes along with representative reference genomes from the clade on the global phylogenetic tree. This software infers the population structure and detects the "ancestral" and "recent" recombinations between the genomes present in the alignment. FastGEAR was run by clades with 100 iterations and checking for convergence. The statistical significance of the inferred recombination events (changes in SNP density between the two lineages) were assessed based on the natural log of Bayes factor calculated within FastGEAR. To understand the recombination events within group A individuals, we generated individual whole genome alignments from each of the three body sites by reference mapping the *C. trachomatis* reads to *C. trachomatis* D/UW-3/CX genomes using snippy and the within individual recombination events were inferred using Gubbins as described above.

# Comparison of SNPs patterns between samples from the same participant

We used samtools mpileup (Li et al., 1000) to process the BAM files created by aligning sample FASTQ files against the reference chromosome to create tables of the numbers of each base (A, C, T, G) mapped to each individual base of reference. For each pair of samples from the same participant, we used R tidyverse tools (R Core Team, 2016; Wickham et al., 2019) to merge the positions with at least  $10 \times$  read mapping redundancy. Code for analysis of the merged mpileup output was deposited to GitHub.<sup>2</sup>

To create a list of clonal SNP positions (CSSs), we performed Snippy alignment of all contigs from Fiji samples against the reference and identified positions where at least 90% of P-UA strains were identical but different to at least 90% of NP-UA strains. We then filtered out those falling in recombinant regions identified by Gubbins (see section above), leaving 5,520 CSS positions.

#### Data availability statement

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found below: https://www.ncbi.nlm. nih.gov/bioproject/?term=PRJNA609714, PRJNA609714.

#### **Ethics statement**

Appropriate IRB approval had been obtained from UCSF (21-33864) and the Fijian MoHMS (FNHRERC 2015.100.MC) prior to commencement of the parent study. The participants provided their written informed consent to participate in this study.

#### Author contributions

DD, MK, and NZ: sample collection. TR and SJ: primary bioinformatic analysis. TR, SJ, SB, and DD: writing. DD and TR: study concept and design. All authors contributed to the article and approved the submitted version.

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<sup>1</sup> https://github.com/tseemann/snippy

<sup>2</sup> https://github.com/Read-Lab-Confederation/Ct\_MAP\_analysis

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#### **Conflict of interest**

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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#### Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fmicb.2023. 1154664/full#supplementary-material

#### SUPPLEMENTARY FIGURE 1

Distribution of log-transformed ratio of the *C. trachomatis ompA* genome copy number to the beta-actin genome copy number (y-axis) is shown for each site. The load was significantly higher in the rectum compared to the vagina (P = 0.0124). C, endocervix; R, rectum; V, vagina.

#### SUPPLEMENTARY FIGURE 2

Comparison of the mean depth of sequencing coverage based on mapping of quality trimmed reads to the reference genome. Significant differences for endocervical depth compared to rectal and vaginal depth are shown. C, endocervix; R, rectum; V, vagina.

#### SUPPLEMENTARY FIGURE 3

Whole genome phylogenies of strains from this study from clades (a) P-UA and (b) NP-UA. Two G strains were found in the P-UA clade while three F and four D strains were found in the NP-UA clade. P-UA, prevalent urogenital and anorectal; NP-UA, non-prevalent urogenital and anorectal.

#### SUPPLEMENTARY FIGURE 4

Patterns of CSS frequency across anatomic sites for participant 1,078. For details of the plots see **Figure 4**. In this case, strains from the endocervix and vagina were in the NP-UA clade, and the rectum in the P-NP clade.

#### SUPPLEMENTARY FIGURE 5

Patterns of CSS frequency across anatomic sites for participant 564. For details of the plots see **Figure 3**. The high number of SNVs seen in this strain were a result of random errors in low sequence coverage regions.

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Supplemental Tab	le 1. Me	tadata, typing an	d genome sec	uence quality c	ontrol statistics associate	d with the sa	mples from 2	6 women with good qu	ality genomic seq	uences in three	anatomic sit	tes.				
					# of read pairs after	paired	per base on	positions covered in	positions	nucleotide						Load
		Signs &	Anatomic	# of Raw Read	adaptor trimming and	classified as	Ct	the reference with	covered in the	positions	ompA		plasmid	Ct ompA	Ct b-actin	(ompA/b-
Sample_name	Age*	Symptoms**	Site	pairs	Quality score (>=15)	C.	reference	>=10 reads	reference with	covered in	genotype	Clade***	genotype	(copies/µl)	(copies/µl)	actin)
26C 26B	20	yes	Rectum	3881771	1973633	607714	309.7515	1030529	1030662	1030986	F	P-UA P-IIA	NO data F	534.5 3075 5	233.672	2.287
26V	20	no	Vagina	2538201	875282	360482	98.48688	1029795	1030419	1030997	E	P-UA	E	1645	NA	NA
32C	26	no	Endocervix	2768653	1300007	1047385	284.9352	979976	1011880	1029955	G	P-UA	E	452.382	2103.437	0.215
32R	26	yes	Rectum	8518792	4120862	1249195	341.3122	1030360	1030575	1031049	G	P-UA	No data	828.676	1617.977	0.512
32V 68C	26	yes	Fndocervix	3493014	1038876	575175	227 504	1031261	1031464	1031627	G la	P-UA P-UA	F	1683 931	1021 489	2.868
68R	26	no	Rectum	3964230	2171942	300439	82.32851	1028335	1029607	1030976	Ja	P-UA	No data	262.311	2008.173	0.131
68V	26	no	Vagina	2399972	825022	232670	63.32957	1029398	1030136	1030693	Ja	P-UA	E	2005.341	1433.92	1.399
72C	32	no	Endocervix	9061129	5449349	5188999	1418.151	1031271	1031313	1031928	G	NP-UA	D/G	2107.48	482.501	4.368
72R	32	no	Rectum Vagina	1764699	1429554	53096	13.99784	778741	1002017	1030750	G	NP-UA	D/G	1664	41.292	40.299
870	24	10	Endocervix	3379564	403007	584847	156.5297	1028273	1030168	1031293	G	NP-UA	D/G	186.8	2233.7	0.084
87R	24	no	Rectum	4378845	2091933	125227	33.88708	1026633	1030429	1031485	G	NP-UA	D/G	953.3	778.639	1.224
87V	24	yes	Vagina	3583086	639211	142218	38.48257	1027794	1030251	1031481	G	NP-UA	D/G	151.5	1666.666	0.091
98C	22	yes	Endocervix	10110856	6618509	6510165	1742.018	1031308	1031462	1031966	G	NP-UA	D/G	344	3947.599	0.087
98K 98V	22	ves	Vagina	1259385	791372	307678	262.0773	1031377	1031487	1031574	G	NP-UA NP-UA	D/G	434.4	1809.354	0.24
107C	29	no	Endocervix	33923070	2934946	324782	86.66605	859337	928194	994243	Ja	P-UA	E	2218	1301.548	1.704
107R	29	no	Rectum	2302152	1924399	705294	190.4395	1030324	1030537	1030800	Ja	P-UA	E	18377	708.586	25.935
107V	29	no	Vagina	1347716	942944	175198	47.05494	1028088	1029717	1030586	Ja	P-UA	E	120.18	815.621	0.147
192C 192R	26	10	Rectum	2175904	215/9/3	1184836	312 305	1030173	1030356	1031167	la la	P-UA P-IIA	F	43905	2363.433	28 32
192V	26	no	Vagina	1390989	940352	331250	90.01676	1030137	1030378	1030584	Ja	P-UA	E	275.1	NA	NA
227C	21	yes	Endocervix	4827086	2972494	2651587	728.0298	1031271	1031343	1031864	G	NP-UA	D/G	1824	2790.564	0.654
227R	21	yes	Rectum	17615509	5210586	86270	22.26701	987852	1026120	1030982	G	NP-UA	D/G	470.5	NA	NA
227V 262C	21	no	Vagina	4115404	1431140	402322	220 4672	1030961	1031102	1031458	G	NP-UA	D/G	3257.49	NA 820.484	2 3 3 1
362R	35	no	Rectum	7028809	3899905	613008	165.2597	1029180	1031012	1031524	F	NP-UA	D/G	576.25	1236.356	0.466
362V	35	no	Vagina	2785894	1277347	297558	80.73862	1030914	1031031	1031456	F	NP-UA	D/G	136.42	1067.452	0.128
519C	19	no	Endocervix	10915045	7121754	7083988	1933.492	1030759	1030904	1031711	E	P-UA	No data	532.044	1918.343	0.277
519R	19	no	Rectum	23015761	3637332	175582	46.22006	927851	995316	1027451	E	P-UA	E	185.797	136.429	1.362
5640	32	yes no	Endocervix	4201603	1928478	1393171	379.1702	1029979	1030347	1031041	la	P-UA	F	894.99	2781.221	0.322
564R	32	no	Rectum	4643615	1954793	259807	70.08115	1029757	1030218	1030957	E	P-UA	No data	404.064	2515.309	0.161
564V	32	no	Vagina	3677998	1262700	128965	34.80634	1024900	1028851	1030891	E	P-UA	E	2953.966	794.379	3.719
753C	23	no	Endocervix	4811591	2477195	351316	94.55193	1030538	1031074	1031552	G	NP-UA	No data	772.9	3714.723	0.208
753K 753V	23	no	Vagina	3858570	2348430	75702	20.22568	925660	1016985	1030573	G	NP-UA	D/G	570.39	5.158 NA	23.033 NA
908C	31	no	Endocervix	3044175	587948	351365	95.79307	1028111	1029501	1031150	Ja	P-UA	E	116.754	2771.414	0.042
908R	31	no	Rectum	3595960	2193839	802050	219.5479	1029593	1029970	1030676	Ja	P-UA	E	483.091	779.604	0.62
908V	31	no	Vagina	25289804	2368406	342739	87.13967	1027162	1029070	1030287	Ja	P-UA	E	1477.985	NA	NA
927C	38	no	Endocervix	4153249	2063566	1804757	488.6605	1030526	1030707	1031018	E	P-UA P-UA	No data E	1295.605	2437.583 NA	0.532 NA
927V	38	ves	Vagina	4960468	2505383	1894046	518.5069	1030516	1030630	1031226	E	P-UA	E	2350.484	NA	NA
951C	30	no	Endocervix	3002396	1697833	1591389	434.9692	1030210	1030390	1031095	E	P-UA	No data	840.525	2249.041	0.374
951R	30	no	Rectum	11964131	7658027	4952271	1345.959	1030963	1031735	1032243	E	P-UA	E	1159.613	651.188	1.781
951V	30	no	Vagina	4113765	2118273	555930	151.452	1030100	1030593	1031837	E	P-UA	E No data	2638.747	NA 6159 419	0.141
968R	22	ves	Rectum	4395902	2364069	65255	17.4249	882607	1009672	1032082	G	NP-UA	No data	1201.895	18.175	66.129
968V	22	yes	Vagina	4098543	1864162	742576	201.6281	1031096	1031313	1031790	G	NP-UA	D/G	15179.26	NA	NA
1077C	30	no	Endocervix	2707271	1379498	973867	265.4235	1030256	1030606	1031899	Ja	P-UA	No data	122.744	2572.965	0.048
1077R	30	no	Rectum	4536604	2112188	146444	36.00623	966434	1021812	1030909	Ja	P-UA	No data	368.139	NA	NA
1077V	26	no	Endocervix	44313968	8314392	62220	18.3445	437082	751250	1030334	na	na	D/G	77.516	1113.549	0.07
1078R	26	no	Rectum	30823554	10871094	104468	30.8532	987934	1025420	1030651	E	P-UA	D/G	123.705	15.964	7.749
1078V	26	yes	Vagina	15664189	2304311	149052	38.30531	1026002	1030627	1031695	D	NP-UA	D/G	118.389	NA	NA
1079C	32	no	Endocervix	3518444	1377695	483959	131.2056	1030045	1030473	1031026	E	P-UA	E	103.751	2800.482	0.037
1079K	32	no	Vagina	35435/5	795669	264367	40.54158	1026667	1030411	1031639	E	P-UA P-UA	E	402.732	367.255 NA	0.791 NA
1106C	26	yes	Endocervix	7390409	4895814	4867637	1330.369	1031633	1031676	1032115	D	NP-UA	D/G	2362.054	2419.986	0.976
1106R	26	no	Rectum	7878537	4880882	3546987	967.0821	1031652	1031738	1032043	D	NP-UA	D/G	2018.854	1201.252	1.681
1106V	26	yes	Vagina	2673088	1497698	1177170	320.2839	1031568	1031628	1031896	D	NP-UA	D/G	20731.73	1444.637	14.351
1145C 1145R	27	no	Rectum	3245911 6315303	6U5268 3675922	542941 2839618	93.50092 772.0722	1029412	1029994	1031149	el B	P-UA P-UA	F	249.978	507.37	2.609
1145V	27	no	Vagina	4261594	1499177	133698	36.1844	992587	1026948	1031199	Ja	P-UA	E	1771.264	1528.859	1.159
1176C	28	no	Endocervix	1704397	402441	290255	78.88034	1029623	1030448	1031097	Ja	P-UA	E	84.805	1951.951	0.043
1176R	28	no	Rectum	3079956	1095024	304242	82.72563	1030642	1031200	1031893	Ja	P-UA	E	641.326	1003.104	0.639
1176V	28	no	Vagina	3031154	537031	145531	39.68367	1026976	1030621	1031844	G	NP-UA	E	331.935	2495.802	0.133
1182R	25	no	Rectum	2578932	1335796	186473	51.01578	1030301	1030332	1031354	Ja	NP-UA	E	540.352	787.653	0.686
1182V	25	no	Vagina	4025248	1989224	1675784	455.4528	1031233	1031630	1031873	Ja	P-UA	E	351.756	241.598	1.456
1201C	20	yes	Endocervix	5865884	3620178	3577270	979.1686	1031246	1031480	1032125	G	NP-UA	D/G	1029.991	2832.509	0.364
1201R	20	no	Rectum	3035709	1400669	447950	122.1489	1030976	1031407	1031829	G	NP-UA	D/G	413.114	293.635	1.407
1226C	20	no	Endocervix	2940/41	721573	360904	342.8366 98,11438	1031186	1031311	10318/1	F	P-UA	D/G F	2431.069	1919.655	1.266
1226R	24	no	Rectum	4552437	2653408	88464	23.96163	868261	999909	1030018	E	P-UA	E	454.206	NA	NA
1226V	24	no	Vagina	3779246	1735200	518926	141.4167	1028643	1029935	1030975	E	P-UA	E	69.292	60.915	1.138

 1226v
 24
 no
 Vagina
 3779246
 1735200
 51892b
 141.41o7
 1026043
 2027.5

 \*Age, participant age when samples were taken.

 \*Signs & Symptoms, whether or not the anatomic site was showing any signs and/or participant had symptoms suggestive of a sexually transmitted infection.

 \*\*Clades, P-UA, prevalent urogenital and anorectal; NP-UA, non prevalent urogenital and anorectal

 NOTE: plasmid genotypes D and G are identical

Suppleme	ntal Table	2. Coordinates of	reci	ent cross-c	lade recom	bination ev	vents inferred by fastGEAR.
Start	End	Donor Clade		log(BF)	Sample	Fiji omp A genotypes	
1038741	1038783	L	GV	30.8	1077C	Ja	
58310	58671	Li Li	GV	52	1078V	D	
746274	746804	1	GV	1.4	1106C	D	
58310	58686	- U	Gν	51.3	1182R	Ja	
732899	733369	U	GV	27.2	1182V	Ja	
58310	58493	U	GV	35.7	1201R	G	
1039115	1042519	Li Li	GV	1.2	192C	Ja	
1039115	1042519	1	GV	1.2	192K	Ja	
1038578	1038783	- U	GV	97.1	32C	G	
1038758	1038783	Li	GV	19	32R	G	
58310	58686	U	GV	51.6	32V	G	
1038558	1038783	L	GV	103.9	519V	E	
160233	98346	Li Li	GV GV	39.5	Ct_refDa		
195737	220733	5	GV	48	Ct_refDa		
233403	237307	U	GV	0.7	Ct_refDa		
784059	785445	U	Gν	0.7	Ct_refDa		
786670	788427	U	GV	2	Ct_refDa		
790699	791639	Li Li	GV	5.7	Ct_refDa		
1026738	1029022	1	GV	96.4	Ct_refDa		
1031970	1035741	- U	GV	3.6	Ct_refDa		
1037401	1042312	U	GV	182.5	Ct_refDa		
236999	240719	U	Gν	0.8	F_70		
255752	256238	U	GV	3.7	F_70		
697276	699446	U	GV	5.7	F_70		
58310	163994		GV GV	48.2	D_43ni E 38ni		
58310	58748	10	GV	48.2	G G		
58310	58748	-	GV	47.7	H		
1022818	1026750	U	Gν	52.6	J		
448581	450045	U	GV	0.2	Ja_26s		
473619	474831	L	GV	1.6	Ja_26s		
732899	733258	Li Li	GV	24	Ja_26s		
58310	58748	1	GV	47.5	D UW3		
825804	849082	- U	GV	102.1	L2C		
1022890	1027524	L	Gν	140.4	G_9768		
1022890	1027524	U	GV	139.9	G_9301		
58310	58748	L	GV	48.3	D-EC		
58310	58748	Li Li	GV	48.2	D-LC		
1023318	1027501	1	GV	140.1	G 11074		
155911	163894	- U	GV	5.5	E IU824		
155911	163894	U	Gν	5.5	E_IU888		
749035	749094	U	GV	4.2	L1_115		
58310	58748	U	GV	48.2	SotonG1		
767990 58310	59749	Li Li	GV GV	16.5	SotonD5		
155911	163894	5	GV	5.6	E Bour		
58310	58748	Li Li	GV	48.3	CS637_11		
155441	163894	U	Gν	4.3	S1025_11		
58310	58748	U	GV	48.4	CS190_96		
166185	170075	Li Li	GV	1	E-32931		
255752	256238		SV	3.8	5032		
58310	58748	10	GV	48.5	5020		
58310	58748	- U	Gν	48.5	SQ24		
58406	58748	U	Gν	21.3	SQ15		
58406	58748	U	GV	20.6	SQ19		
58310	58748	Li Li	GV	48.3	chxRP4F1		
58310	58748		GV GV	48.2	chyPP1H1		
57817	58298	NP-I	UA	57.6	1077C	Ja	
747018	747565	NP-I	UA	124	1077C	Ja	
770942	771475	NP-I	UA	37.9	1077C	Ja	
771727	772398	NP-I	UA	53	1077C	Ja	
744966	745205	NP-I	UA	53.1	1077R	Ja	
771727	//14/5	NP-I		38 53 7	1077R	Ja	
770942	771475	NP-I	UA	38	1077	ьс sl	
772005	772374	NP-I	UA	48.6	1077V	Ja	
1038531	1038783	NP-	UA	109.7	1077V	Ja	
719232	732487	NP-I	UA	39.1	1078R	Е	
791507	791761	NP-	UA	36	1078R	E	
768502	1034464	NP-I	UA IIA	108.2	1078V	D	
57213	58309	NP-I	UA	20.2	10780	F	
770942	771475	NP-	UA	37.6	1079C	E	
772005	772374	NP-I	UA	48.2	1079C	E	
1029706	1033303	NP-I	UΑ	97.1	1079C	Е	

57213			1/0.8	10/90	E
	57860	NP-UA	37.3	1079R	E
57861	58748	NP-UA	46.1	1079R	E
744966	745167	NP-UA	43.5	1079R	E
770942	771475	NP-UA	37.8	1079R	E
1029706	1033303	NP-UA	97.7	1079R	E
1037307	1042519	NP-UA	180.1	1079R	E
57213	58598	NP-UA	75.7	1079V	Е
58599	58686	NP-UA	7.6	1079V	Е
744966	745227	NP-LIA	55.4	1079V	F
744500	743227	NP-UA	04.7	10791	-
747018	/4/362	NP-UA	94.7	10790	E
770942	771475	NP-UA	37.8	1079V	E
1029706	1033303	NP-UA	97.8	1079V	E
1037307	1042519	NP-UA	180.3	1079V	E
770942	771475	NP-UA	38.4	107C	Ja
770942	771475	NP-IIA	38.4	107R	la la
770042	771475	ND LIA	20.4	1071/	-
770942	771475	NP-UA	38.4	10/0	Ja
768502	//2831	NP-UA	107.8	1106C	D
1024613	1034464	NP-UA	25.9	1106C	D
768502	772831	NP-UA	107.9	1106R	D
1024613	1034464	NP-UA	26	1106R	D
768502	772831	NP-IIA	108.2	1106V	D
1034613	1024464	ND LIA	26.2	11061	5
1024613	1034464	NP-UA	20.2	11060	D
58083	58298	NP-UA	9.5	1145C	Ja
747285	747565	NP-UA	50.6	1145C	Ja
770942	771475	NP-UA	38.5	1145C	Ja
7709/2	771475	NP-IIA	38.4	11/50	15
1029461	1029734	ND LIA	96 C	11/50	10
1038461	1038/21	NP-UA	60.5	1145K	19
57963	58139	NP-UA	37.8	1145V	Ja
770942	771475	NP-UA	38.5	1145V	Ja
1	20947	NP-UA	10.8	1176C	Ja
57213	58298	NP-IIA	73.2	1176C	la
111506	120244	NID_I I A	10	11760	12
111500	774 424	NP-UA	1.7	11700	10
770942	//1421	NP-UA	40.5	11/60	Ja
1013693	1025311	NP-UA	23.8	1176C	Ja
1026984	1028007	NP-UA	5.1	1176C	Ja
1028570	1029449	NP-UA	0.4	1176C	Ja
1029706	1031027	NP-UA	4.7	1176C	Ja
1037224	1042519	NP-IIA	184 7	11760	la
E 2017	2072313	ND LIA	104.7	11760	10
5/213	112517	NP-UA	/3	11700	10
111814	112517	NP-UA	6	1176R	Ja
744990	745386	NP-UA	40.3	1176R	Ja
770942	771421	NP-UA	40.4	1176R	Ja
1013809	1016084	NP-UA	1.2	1176R	Ja
10191/5	1024440	NP-UA	0.2	1176P	
1018145	1024440	INP-UA	U.3	11/0K	bt
1010145	4000075	100.000		44765	
1027274	1029229	NP-UA	7.7	1176R	Ja
1027274 1037946	1029229 1039376	NP-UA NP-UA	7.7 265.1	1176R 1176R	Ja Ja
1027274 1037946 57020	1029229 1039376 58493	NP-UA NP-UA NP-UA	7.7 265.1 27.7	1176R 1176R 1176V	Ja Ja G
1027274 1037946 57020 770942	1029229 1039376 58493 772415	NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87	1176R 1176R 1176V 1182C	Ja Ja G Ja
1027274 1037946 57020 770942 768502	1029229 1039376 58493 772415 772831	NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87	1176R 1176R 1176V 1182C	et G E
1027274 1027274 1037946 57020 770942 768502	1029229 1039376 58493 772415 772831	NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5	1176R 1176R 1176V 1182C 1182R	Ja Ja G Ja Ja
1027274 1037946 57020 	1029229 1039376 58493 772415 772831 1034464	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5 24.5	1176R 1176R 1176V 1182C 1182R 1182R	Ja Ja Ja Ja Ja
1027274 1037946 57020 <u>770942</u> 768502 1024613 25851	1029229 1039376 58493 772415 772831 1034464 26192	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5 24.5 21.6	1176R 1176R 1176V <u>1182C</u> 1182R 1182R 1182V	Ja Ja G Ja Ja Ja Ja
1027274 1037946 57020 770942 768502 1024613 25851 57757	1029229 1039376 58493 772415 772831 1034464 26192 58298	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5 24.5 21.6 89.1	1176R 1176R 1176V 1182C 1182R 1182R 1182V 1182V	Ja Ja G Ja Ja Ja Ja Ja
1027274 1037946 570200 770942 7768502 1024613 25851 57757 161219	1029229 1039376 58493 772415 772831 1034464 26192 58298 161530	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5 24.5 21.6 89.1 16.1	1176R 1176V 1176V 1182C 1182R 1182R 1182V 1182V 1182V 1182V	Ja Ja G Ja Ja Ja Ja Ja Ja
1027274 1037946 57020 776942 768502 1024613 25851 57757 161219 321995	1029229 1039376 58493 772415 772831 1034464 26192 58298 161530 322235	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	7.7 265.1 27.7 87 102.5 24.5 21.6 89.1 16.1 8.7	1176R 1176R 1176V 1182C 1182R 1182R 1182V 1182V 1182V 1182V 1182V	Ja Ja Ja Ja Ja Ja Ja Ja Ja Ja Ja
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1027274 1037946 57020 770942 768502 1024613 25851 57757 161219 321995 342202 358309 408332 410039 408332 410039 540891 540891 540891 547014 547014 547014 741420 741420 741420 741420 741420 741420 770515 770527 77055 771277 786960 791507 795467 895259 966526 1001738 1026422 1038181	1029229 1039376 1039376 772815 1034464 26192 58298 161530 322235 348418 358607 3408583 440372 541245 597625 697564 701180 741711 742367 751321 770914 770914 771726 774463 7787168 791761 7746887 996687 996687 9966887 91002840 91002840 1002840	الباط           الباط<	7.7 7.7 87 102.5 24.5 24.5 89.1 161.1 89.1 161.1 8.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1176R 1176R 1176V 1182C 1182R 1182R 1182V	
1027274 1037946 570200 770942 768502 1024613 27851 162199 321995 348202 358309 408332 410089 540891 547014 742134 747144 74420 742134 74024 74025 770551 77127 786560 791507 779545 771127 786560 791507 795467 795457 719557 779545 71127 786560 791507 795467 79557 9966526 1001738 1002422 10038181 1002422 1038181	1029229 1039376 58493 772415 772831 1034464 26192 58298 161530 322235 348418 358607 40853 410372 40853 410372 541245 547456 597564 701180 741711 742367 751321 770914 771463 787168 791761 796602 895681 796602 895681 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 791761 791761 791761 791761 7917777777777	АЦ-94 NP-UA N	777 777 87 1025 2451 1025 2452 2452 245 245 245 245 245 245 245	1176R 1176R 1176V 1182R 1182R 1182R 1182V	
1027274 1037946 57020 770942 768502 1024613 25851 57757 161219 321995 342902 358309 408322 410089 408322 410089 540891 540891 540891 540891 547014 597494 697276 770427 774120 774120 774120 774120 774120 770515 770525 770525 7795467 895259 966526 1001738 1026422 1038181 1026422 1038181 575600 575600	1029229 1039376 1039376 772815 1034464 26192 58298 161530 322235 348418 358607 3408583 440372 541245 547456 597625 697564 701180 741711 742367 751321 770914 770914 770914 770914 770914 770914 770914 770914 770914 770914 770915 71463 774765 77463 774765 77463 787168 795687 1002840 9966887 1002840 10028537 1002845 1002845 1002845 78482 58482 58482	NP-UA NP-N NP-N NP-N NP-N NP-N NP-N	7.7 7.7 87 102.5 24.5 24.5 89.1 161.1 89.1 161.1 8.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1176R 1176R 1176V 1182C 1182R 1182R 1182V	
1027274 1037246 57020 770942 776942 7768502 1024613 25851 57757 161219 321995 348202 358309 4408332 410089 4408332 410089 540891 547014 547014 547041 741240 740241 741240 770513 770513 770513 770513 770513 770513 770523 771527 778690 789529 966526 1001738 1026427 289529 966526 1001738	1029229 1039376 1039376 772415 772415 1034464 26192 58298 161530 322235 348418 358607 408587 40553 440372 440372 440372 440372 547456 597564 70180 741711 742367 751321 770914 77126 774613 787168 787168 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 796602 895681 791761 79602 895681 791761 79602 895681 791761 79602 895681 791761 7996887 10029537 10029537	NP-UA           NP-UA<	77,77 77,78 7265.1 102.5 24.7 24.5 24.7 24.5 24.5 24.7 24.5 24.5 24.7 24.5 24.5 24.7 24.5 24.5 24.7 24.5 24.5 24.7 24.5 24.5 24.5 24.5 24.7 24.5 24.5 24.7 24.5 24.7 24.5 2	1176R 1176R 1176V 11827 11827 11828 11827	
1027274 1037946 57020 770942 768502 768502 768502 1024613 25851 57757 161219 321995 342902 358309 408312 410089 408312 410089 540891 540891 540914 547014 547014 547014 74120 742120 7450000 7450000 7450000 74500000 7450000000000	1029229 1039376 1039376 772815 1034464 26192 58298 161530 322235 348418 358607 3408583 440372 541245 547456 597625 697564 701180 7447111 742367 751321 77476 751321 779144 779176 779144 7791761 7791761 7791761 7471761 795602 895581 9966887 1002840 1029537 1002840 1000840 1000840 1000840 1000840 1000840 1000840 1000800 1000800000000	۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰۰         ۱۹۰۰۰         ۱۹	7.7 7.7 87 102.5 24.5 24.5 89.1 16.1 18.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1176R 1176R 1176V 1182C 1182R 1182R 1182V	
1027274 103746 57020 770942 7768502 1024613 25851 57757 161219 321995 348202 358309 4408332 410089 4408332 410089 540891 547014 5747014 5747014 5747014 5747014 740149 770231 770251 77127 7785960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77127 7786960 771527 77551 77127 7786960 775611 77127 7786960 775610 77560 77560 77560 77560 77560 77560 77560 77560 77560 75777 757777777777	1029229 1039376 58493 772415 772831 1034464 26192 58298 161530 322235 348418 358607 408583 440372 541245 547456 597564 701180 741717 742367 751321 770914 774263 787168 791761 774662 787168 791761 79966887 791761 7996682 791761 7996887 1029537 1029547 1029577 1029577 1029577 1029577 1029577 1029577 10295777 10005777 100057	Ν-U.4	7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,	1176R 1176R 1176V 11827 11827 11828 11827	
1027274 1037946 57020 770942 768502 768502 768502 1024613 25851 57757 161219 321995 348202 358309 408312 410089 408312 410089 540914 547014 547014 547014 547014 74120 742124 74120 742124 74420 742124 7444 744	1029229 1039376 1039376 772815 1034464 26192 58298 161530 322235 348418 358607 322235 348418 358607 408583 410372 547456 597625 697564 701180 7447111 742367 751321 771726 774463 791761 779144 7797014 7791761 779146 7791761 7791761 779164 791761 74463 791761 7985881 1002840 1002840 1002840 1002840 1002840 1002840 1002840 10038464 1034464 1034464	۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰	7.7 7.7 87 102.5 24.5 24.5 89.1 16.1 18.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1176R 1176R 1176V 1182C 1182R 1182R 1182V	
1027274 103746 57020 770942 7768502 1024613 25851 57757 161219 31195 34202 358309 4408322 410089 540891 547014 5747014 597494 697276 700241 774120 7742134 774124 774124 774124 774124 774124 774125 771727 7786960 771557 771727 7786960 771567 771577 7786960 771567 771577 7786960 771567 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 771577 786960 7715777 786960 771577777 786960 77157777777777777777777777777777777777	1029229 1039376 1039376 1039376 1034464 26192 58298 161530 322235 348418 358607 408583 440372 541245 547456 597564 697564 701180 74171726 774163 787168 791761 774662 8966837 791761 774662 8966837 791761 1029537 1039376 56849 1034464 1034464 1034464 1034464	Ν-U.4	7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,	1176R 1176R 1176V 1182R 1182R 1182R 1182V 1226C	
1027274 1037946 57020 770942 768502 768502 768502 1024613 25851 57757 161219 321995 342902 358309 408312 410089 400891 540144 597494 697276 770274 74120 7412400 74140000000000	1029229 1039376 1039376 772815 1034464 26192 58298 161530 322235 348418 358607 408583 440372 541245 597625 697564 701180 7447111 742367 751321 771726 751321 771726 774463 791761 77476 791761 795602 895681 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 1002840 10028537 1002840 1002857 1002840 1002857 1002840 1002840 1002857 10005757 10005757 10005757 10005757 1000575757 100057575757 100057575757	۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰۰۰         ۱۹۰	7.7 7.7 87 102.5 24.5 24.5 89.1 16.1 18.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1176R 1176R 1176V 1182C 1182R 1182R 1182V 1201C 1201C 1226C 1226C	
1027274 103746 57020 770942 776942 7768502 1024613 25851 57757 161219 321995 348202 358309 440832 410089 440832 440839 440832 440839 440832 440839 540891 547014 740241 740241 740241 770531 770531 770531 770531 77157 7786960 789529 966526 1001738 1026427 2103749 789529 966526 1001738 1026427 2103749 776800 57680 1030034 1030034 1030034 1030034 1030034 1030034 1030034	1029229 1039376 1039376 772415 772415 772831 1034464 26192 58298 161530 322235 348418 358607 408587 408587 408587 409564 40375 547456 597564 597564 70180 741711 742367 751321 770914 7417726 774463 787168 791761 79602 895681 79602 895681 79602 895681 9966887 10029537 1002957 1000000000000000000000000000000000000	NP-UA NP-UA	77,7 77,7 87 102,5 245,1 102,5 245,5 245,5 245,5 245,5 245,5 245,7 27 2,7 2,7 2,7 2,7 2,7 2,7 2,7 2,7 2,	1176R 1176R 1176V 11827 11828 11827 11828 11827 12016 1206 12268 12686 12686 12686 12686 12686 12686 12686 12686 12686 12686 12686 1	

313206	348342	NP-UA	108	1920	Ja
261477	266640	NDUA	10.0	1020	
3014//	300040	NP-UA	10.9	1920	Ja
747047	/4/2/1	NP-UA		192C	Ja
771159	772415	NP-UA	80.9	192C	Ja
57213	57962	NP-UA	51.2	192R	Ja
57963	58748	NP-UA	34.4	192R	Ja
91094	92117	NP-UA	5.1	192R	Ja
313206	348342	NP-IIA	107.8	192R	12
313200	340342	ND UA	107.0	1020	10
361477	366640	NP-UA	10.9	192R	Ja
771159	772415	NP-UA	80.9	192R	Ja
57213	57962	NP-UA	51.2	192V	Ja
57963	58748	NP-UA	34.4	192V	Ja
91094	92117	NP-IIA	5.1	192V	la
212206	3/83/7	NP-UA	107.7	1021/	12
313200	340342	ND UA	107.7	1021	10
3014//	300040	NP-UA	10.9	1920	Ja
771159	772415	NP-UA	80.8	192V	Ja
125050	140910	NP-UA	6.6	227C	G
126602	140910	NP-UA	7.8	227R	G
126602	140910	NP-UA	7.8	227V	G
	209/17	NP-UA	11.4	260	-
57313	57062	ND UA	50.4	200	
5/213	5/962	NP-UA	50.4	26C	E
57963	58748	NP-UA	33.8	26C	E
1037832	1038008	NP-UA	33.3	26C	E
1039130	1042519	NP-UA	4.8	26C	E
1	20947	NP-UA	11.4	26R	F
57212	57062	NDUA	E0.4	260	-
37213	37902	NF-UA	30.4	206	E
57963	58748	NP-UA	33.8	26R	E
1037832	1038008	NP-UA	33.3	26R	E
1039130	1042519	NP-UA	4.8	26R	E
1	20947	NP-UA	11.4	26V	Е
57212	57962	NP-11A	50.4	261/	F
57215	57502	NI-UA	50.4	201	-
57963	58748	NP-UA	33.8	26V	E
1037832	1038008	NP-UA	33.3	26V	E
1039130	1042519	NP-UA	4.8	26V	E
770942	772415	NP-UA	85.9	32C	G
770942	772415	NP-LIA	85.9	32R	6
130070	121240	ND UA	1 0	2620	-
125578	131240	NP-UA	1.6	3620	-
125578	131240	NP-UA	1.6	362R	F
125578	131240	NP-UA	1.6	362V	F
774153	774250	NP-UA	14.8	519C	E
1030034	1034464	NP-UA	0.3	5190	F
1029461	1020757	ND LIA	00.0	5100	
1038401	1038/5/	NP-UA	99.9	519C	E
1030034	1034464	NP-UA	0.2	519R	E
1030034	1034464	NP-UA	0.3	519V	E
770942	772415	NP-UA	86.3	564C	Ja
1	7520	NP-LIA	0.3	564R	5
1020010	1042510	ND UA	226.2	5640	
1026818	1042519	NP-UA	226.3	564K	E
1	7529	NP-UA	0.3	564V	E
1026818	1042519	NP-UA	226	564V	E
770942	772415	NP-UA	86.3	68C	Ja
1029209	1029445	NDUA	45.7	690	
1036356	1038443	NF-UA	43.7	080	bt
57757	57962	NP-UA	51.9	68R	Ja
770942	772415	NP-UA	86.3	68R	Ja
770942	772415	NP-UA	86.3	68V	Ja
57680	58530	NP-UA	58.7	720	G
770043	772426	ND UA	06.7	0000	-
//0942	//2426	INP-UA	80.2	9080	la
57757	57962	NP-UA	52	908R	Ja
770942	772426	NP-UA	86.2	908R	Ja
770942	772426	NP-UA	86.2	908V	Ja
1	209/7	NP-11A	13.2	9270	F
111505	120245	ND	13.5	0270	
111506	120245	NP-UA	0.2	927C	E
1013693	1025125	NP-UA	20.5	927C	E
1026738	1042519	NP-UA	237.4	927C	E
1	20947	NP-IIA	13 2	977P	F
111500	120245	ND LIA	13.5	0270	-
111200	120245	INP-UA	0.2	32/K	E
1013693	1025125	NP-UA	20.5	927R	E
1026728		NP-UA	203.7	927R	E
1020750	1042519			0271/	E
1020738	1042519 20947	NP-UA	13.3	5270	
111615	1042519 20947 120245	NP-UA NP-UA	13.3 0.4	9271	F
111615 1012602	1042519 20947 120245 1025125	NP-UA NP-UA	13.3 0.4	927V	E
1 111615 1013693	1042519 20947 120245 1025125	NP-UA NP-UA NP-UA	13.3 0.4 20.5	927V 927V	E
1 111615 1013693 1026738	1042519 20947 120245 1025125 1042519	NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4	927V 927V 927V 927V	E E
1 111615 1013693 1026738 719232	1042519 20947 120245 1025125 1042519 732487	NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2	927V 927V 927V 927V 927V 951C	E E E
1020730 11 111615 1013693 1026738 719232 57757	1042519 20947 120245 1025125 1042519 732487 58309	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8	927V 927V 927V 927V 951C 951R	E E E E
1026736 1 111615 1013693 1026738 719232 57757 719232	1042519 20947 120245 1025125 1042519 732487 58309 732612	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2	927V 927V 927V 927V 951C 951R 951P	E E E E
1126738 1 111615 1013693 1026738 719232 57757 719232	1042519 20947 120245 1025125 1042519 732487 58309 732612 732632	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2	927V 927V 927V 927V 951C 951R 951R	E E E E
1026738 1111615 1013693 1026738 719232 57757 719232 733061	1042519 20947 120245 1025125 1042519 732487 58309 732612 735089	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8	927V 927V 927V 951C 951R 951R	E E E E E
1 1 111615 1013693 1026738 719232 57757 719232 733061 748462	1042519 20947 120245 1025125 1042519 732487 58309 732612 735089 749152	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8 1.9	927V 927V 927V 951C 951R 951R 951R 951R	E E E E E E
1 1 111615 1013693 1026738 719232 57757 719232 733061 748462 	1042519 20947 120245 1025125 1042519 732487 58309 732612 735089 749152 1038517	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8 1.9 111	927V 927V 927V 951C 951R 951R 951R 951R 951R	E E E E E E E
1 1 111615 10136938 719232 57757 719232 733061 748462 1038268 719232	1042519 20947 120245 1025125 1042519 732487 58309 732612 735089 749152 1038517 732487	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8 1.9 111 43.2	927V 927V 927V 951C 951R 951R 951R 951R 951R 951R 951R	E E E E E E E E E
1020730 1 111615 1013693 1026738 719232 57757 719232 733061 748462 <u>1038268</u> 719232 56796	1042519 20947 120245 1025125 1042519 732487 58309 732612 735089 749152 1038517 732487 57816	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8 1.9 111 43.2 4.9	927V 927V 927V 951C 951R 951R 951R 951R 951R 951R 951V 968V	E E E E E E E E E G
1 111615 1013693 1026738 719232 57757 719232 733061 748462 1038268 719232 56796	1042519 20947 120245 1025125 1042519 732487 732612 735089 749152 1038517 732487 57816 59740	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	13.3 0.4 20.5 237.4 43.2 88.8 46.2 14.8 1.9 111 43.2 4.9 26.1	927V 927V 927V 951C 951R 951R 951R 951R 951R 951R 951V 968V	E E E E E E E E C
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774194			INF-UA	80.7	ва
	94 775753	3	NP-UA	42.2	Ct_RefC
1030673	/3 1035390	0	NP-UA	84.5	Ct_RefC
57213	13 57962	2	NP-UA	50.8	Ct_refDa
57963	53 58748	8	NP-UA	25.3	Ct_refDa
412356	36 44848t	6	NP-UA	66	Ct_refDa
44848/	37 454822	2	NP-UA	21.7	Ct_refDa
4/3918	.8 4/5218	8	NP-UA	1.2	Ct_retDa
581883	J3 582242	2	NP-UA	3.4	Ct_refDa
632048	48 032202	2	NP-UA	0.6	Ct_refDa
642496	Jb b/484t	6	NP-UA	23.3	Ct_retDa
831688	38 834931	1	NP-UA	2.9	Ct_refDa
1030689	39 1031469	9	NP-UA	40.3	Ct_refDa
57213	L3 57962	2	NP-UA	50.7	D_2923
57963	3 58748	8	NP-UA	25.3	D_2923
61351	J 62117	/	NP-UA	1.1	D_2923
96678	/8 120155	5	NP-UA	5.4	D_2923
195090	30 204801	1	NP-UA	13	D_2923
412356	36 442321	1	NP-UA	49.6	D_2923
532095	35 534130	0	NP-UA	3.7	D_2923
1025905	)5 1034464	4	NP-UA	27.9	D_2923
69317	L7 88069	9	NP-UA	19.4	F_70
177751	51 181271	1	NP-UA	14.5	F_70
183935	35 192026	6	NP-UA	6.4	F_70
251546	46 255658	8	NP-UA	12.9	F_70
498976	/6 502720	0	NP-UA	4.4	F_70
511159	i9 513562	2	NP-UA	9.4	F_70
518973	/3 520574	4	NP-UA	4.1	F_70
538742	42 539300	0	NP-UA	5.1	F_70
628901	J1 629159	9	NP-UA	2.3	F_70
638304	)4 641356	6	NP-UA	7.4	F_70
646039	39 65531?	3	NP-UA	15.7	F_70
719592	32 73428	3	NP-UA	54.1	F_70
1012132	32 1020476	6	NP-UA	8.1	F 70
1020427	27 1025348	8	NP-UA	1.9	F 70
1026756	56 102823	3	NP-UA	12.6	F 70
78602	1020230	4	NP-UA	15.1	D 43nl
140811	11 16087	3	NP-UA	2.1	D_43nl
196511	78 23842	7	NP-IIA	12 2	D_43rl
768360	50 77782	1	NP-UA	93.0	D 43nl
/06300	12 5704	2	ND-IIA	50 A	D 8/c
5/213	5/962	2	ND LLA	50.4	D 045
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100669	19 120155	5	NP-UA	2.7	U_84s
195030	JU 199995	5	NP-UA	3.3	D_84s
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412356	6 442321	1	NP-UA	52.1	D_84s
532095	5 534130	0	NP-UA	3.6	D_84s
650218	18 659457	7	NP-UA	2.4	D_84s
700800	JO 701180	0	NP-UA	37.1	D_84s
732899	J9 733258	8	ND LLA	24.4	D_84s
772663	53 774999		INF-UA	24.1	
1025905	J5 103446/	9	NP-UA	39.5	D_84s
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57215	13 57962	9   4   2	NP-UA NP-UA NP-UA	24.1 39.5 27.5 50.8	D_84s D_84s E_55
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57963 96678	13 57962 53 58820 78 120155	9   2   5   3	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	24.1 39.5 27.5 50.8 23.9 7.8	D_84s D_84s E_5s E_5s E_5s
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1024613	1034464	NP-UA	25.5	G	
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768502	773345	NP-UA	102.2	Н	
920081	920415	NP-UA	3.4	н	
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184815	773345	NP-UA	101.3	H 19c	
1024613	1028007	NP-UA	61.7	H 18s	
743302	747173	NP-UA	3		
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739057	751267	NP-UA	163.1	Ja	
1026738	1028233	NP-UA	0.6	Ja	
1028234	1042519	NP-UA	24.1	Ja	
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57169	57962	NP-UA	52.2	Ja_26s	
5/903	120155	NP-UA	23.0	Ja_205	
195090	198531	NP-UA	1.9	la 26s	
198532	204801	NP-UA	4.1	Ja 26s	
335988	336927	NP-UA	3.5	Ja 26s	
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700800	701180	NP-UA	37	Ja_26s	
1025905	1042519	NP-UA	162	Ja_26s	
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54059	551/3	NP-UA	4.1	Ja_4/nL	
55460	58300	NP-UA NP-IIA	5.1 79.5	Ja_470L Ja_47nl	
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259420	305251	NP-UA	12.4	G_9768	
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1255/8	11655	NP-UA NP-IIA	1.0	F 11023	
700800	701180	NP-UA	37.5	E 11023	
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700800	701180	NP-UA	37.7	E_150	
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57213	57962	NP-UA	51.2 F_SW4
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1	20947	NP-UA	13 E SW3
57213	57962	NP-UA	51.4 E SW3
57963	58832	NP-UA	24.1 E SW3
111506	120245	NP-UA	1.3 E SW3
700800	701180	NP-UA	37.7 E SW3
732899	733258	NP-UA	24.6 E SW3
1013693	1025311	NP-UA	21.7 F SW3
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1028234	1042519	NP-IIA	132.6 F SW3
1020204	11655	NP-UA	1 F SW5
57213	57962	NP-UA	50.8 F SW5
57063	59932	NP-UA	23.7 E SW/5
96678	120155	ND-UA	5.6 E SW5
105000	204901	ND UA	12.2 E SWE
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768360	772831	NP-UA	93 )_SotonD5
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1028234	1042519	NP-UA	132.3 E_SotonE4
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700800	701180	NP-UA	37.4 E_Bour
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57154	58349	NP-UA	82.4 F_1-93
96678	120155	NP-UA	5.8 F_1-93
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532095	534130	NP-UA	3.7 D_13-96
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581/6	58298	NP-UA	28.9 C_TW3
293124	302319	NP-UA	1.1 C_1W3
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251912	258094	NP-UA	7.3 (\$637_11
768309	772831	NP-IIA	102.2 (\$637_11
1024613	1034464	NP-UA	25.8 (\$637_11
58191	58349	NP-UA	39.2) CS19 08
58191	58349	NP-UA	39.1 CS784 08
1	11655	NP-UA	1.51025 11
700800	701180	NP-UA	37.3 \$1025_11
732899	733258	NP-UA	24.3 S1025_11
1025905	1042519	NP-UA	164.9 S1025_11
1	11655	NP-UA	1_CS847_08
57169	58349	NP-UA	82.7 CS847_08
412356	442321	NP-UA	50_CS847_08
532095	534130	NP-UA	5.3 CS847_08
644228	654822	NP-UA	20.3 CS847_08
700800	701180	NP-UA	37.3 CS847_08
/32899	/33258	NP-UA	24.3 CS847_08
768066	772119	NP-UA	104.8 CS847_08
1024613	1034464	NP-UA	25.9 (\$190.96
1024015	20947	NP-IIA	11.9 F-103
57169	58349	NP-UA	83.4 E-103
111506	120245	NP-UA	
700800		NDUA	0.3 E-103
	701180	NP-UA	0.3 E-103 37.6 E-103
732899	701180 733258	NP-UA	0.3 E-103 37.6 E-103 24.5 E-103
732899 1013693	701180 733258 1026008	NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103
732899 1013693 1026009	701180 733258 1026008 1042519	NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103
732899 1013693 1026009 1	701180 733258 1026008 1042519 20947	NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103 12.5 E-160
732899 1013693 1026009 1 57169	701180 733258 1026008 1042519 20947 58349	NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103 12.5 E-160 83.2 E-160
732899 1013693 1026099 1 57169 111506	701180 733258 1026008 1042519 20947 58349 120245	NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 168.4 E-103 12.5 E-160 83.2 E-160 1.1 E-160
732899 1013693 1026009 1 57169 111506 700800	701180 733258 1026008 1042519 20947 58349 120245 701180	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103 12.5 E-100 83.2 E-160 37.5 E-160 37.5 E-160
732899 1013693 1026009 1 57169 111506 700800 732899	701180 733258 1026008 1042519 20947 58349 120245 701180 733258	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103 12.5 E-160 83.2 E-160 37.5 E-160 24.4 E-160 24.4 E-160
732899 1013693 1026009 1 57169 111506 700800 732899 1013693	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 168.4 E-103 12.5 E-160 33.2 E-160 37.5 E-160 24.4 E-160 24.4 E-160 21.3 E-160
732899 1013693 1026009 1 57169 111506 700800 732899 1013693 1026738	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 168.4 E-103 12.5 E-160 83.2 E-160 37.5 E-160 24.4 E-160 21.3 E-160 1.3 E-160 1.3 E-160
732899 1013693 1026009 1 57169 111506 700800 732899 1013693 1026738 1028234	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20047	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 21.8 E-103 12.5 E-160 83.2 E-160 37.5 E-160 24.4 E-160 21.3 E-160 13.3 E-160 13.3 E-160
732899 1013693 1026009 1 157169 700800 732899 1013693 1026738 1028234 1 57169	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20947 58349	NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	0.3 E-103 37.6 E-103 24.5 E-103 168.4 E-103 12.5 E-160 37.5 E-160 37.5 E-160 24.4 E-160 21.3 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-547
732899 1013693 1026009 1 1 57169 111506 700800 732899 1013693 1026738 1028234 1 57169 111506	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20947 58349 120245	NU-341 AU-340 AU-40 NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA NP-UA	$\begin{array}{cccc} 0.3 & E \cdot 103 \\ 37.6 & E \cdot 103 \\ 24.8 & E \cdot 103 \\ 168.4 & E \cdot 103 \\ 12.8 & E \cdot 160 \\ 3.2 & E \cdot 160 \\ 3.7.5 & E \cdot 160 \\ 24.4 & E \cdot 160 \\ 24.3 & E \cdot 160 \\ 24.3 & E \cdot 160 \\ 13.3 & E \cdot 160 \\ 13.3 & E \cdot 160 \\ 13.3 & E \cdot 547 \\ 83.6 & E \cdot 547 \\ 1.3 & F \cdot 547 \end{array}$
732899 1013693 1026009 11 57169 1013693 1026738 1026738 1026234 1 57169 111506 700800	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1024519 20947 58349 120245 701180	NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA NU-UA	0.3 E-103 37.6 E-103 24.8 E-103 168.4 E-103 12.5 E-160 37.5 E-160 24.4 E-160 24.4 E-160 23.3 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-547 8.3.6 E-547 1.3 E-547
732899 1013693 1026009 1 157169 111506 702800 732899 1013693 1026738 1026738 1026738 1026738 1026738 111506 702800 732899	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20947 58349 120245 701180 733306	40-94 AU-94	$\begin{array}{ccccc} 0.3 & E-103 \\ 37.6 & E-103 \\ 24.8 & E-103 \\ 124.8 & E-103 \\ 168.4 & E-103 \\ 12.5 & E-160 \\ 1.1 & E-160 \\ 13.7 & E-160 \\ 24.4 & E-160 \\ 13.3 & E-160 \\ 13.1 & E-160 \\ 13.1 & E-160 \\ 13.1 & E-160 \\ 13.1 & E-160 \\ 12.9 & E-547 \\ 1.3 & E-547 \\ 1.4 & E-547 \\ 1.5 $
722899 1013693 1026009 1 157169 111506 700800 732899 1013693 1026234 112506 700800 732899 111506 700800 732899 1013693	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20947 58349 120245 701180 733306 1025311	4U-9N AU-9NA	$\begin{array}{cccc} 0.3 & E-103 \\ 37.6 & E-103 \\ 24.5 & E-103 \\ 168.4 & E-103 \\ 12.8 & E-160 \\ 1.1 & E-160 \\ 1.2 & E-160 \\ 1.3 & E-160 \\ 24.4 & E-150 \\ 24.4 & E-150 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-547 \\ 13.6 & E-547 \\ 13.7 & E-547 \\ 23 & E-547 \\ 23 & E-547 \\ 24 & E-547 \\ 25 & E-$
732899 1013693 1026009 1 157169 111506 700800 732899 1013693 1026738 111506 700800 732899 1013693 1026738	701180 733258 1042519 20947 58349 120245 701180 733258 1025311 1028233 1042519 20947 58349 120245 701180 733306 1025311 1028233	40-9N AU-9NA	$\begin{array}{ccccc} 0.3 & E-103\\ 37.6 & E-103\\ 24.5 & E-103\\ 168.4 & E-103\\ 12.5 & E-160\\ 37.5 & E-160\\ 37.5 & E-160\\ 24.4 & E-160\\ 13.3 & E-547\\ 1.3 & E-547\\ 1.3 & E-547\\ 2.2 & E-547\\ 2.16 & E-547\\ 1.3 & $
722899 1013693 1026009 11506 700800 722899 1013693 1026738 1026738 1026738 11506 700800 732899 1013693 1026738 1026738	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1025311 1042519 20947 58349 120245 701180 733306 1025311 1028233	AU-9N AU-9NA	$\begin{array}{ccccc} 0.3 & E-103\\ 3.7.6 & E-103\\ 24.8 & E-103\\ 168.4 & E-103\\ 168.4 & E-103\\ 12.5 & E-160\\ 3.7.5 & E-160\\ 24.4 & E-160\\ 21.3 & E-160\\ 21.3 & E-160\\ 13.3 & E-160\\ 13.3 & E-160\\ 13.3 & E-547\\ 3.7.7 & E-547\\ 3.7.7 & E-547\\ 23 & E-547\\ 13.4 & E-547\\ 13.2 & E-547\\ 13$
722899 1013693 1026009 1 157169 111506 700800 722899 1013693 1026738 115506 700800 722899 1013693 1026738 1026738 1026738 1026738	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1024517 20947 58349 120245 701180 733306 1025311 1025311 1025311 1025311	հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹۸ հԱ-۹4 AL-94	$\begin{array}{ccccc} 0.3 & E-103 \\ 37.6 & E-103 \\ 24.5 & E-103 \\ 12.8 & E-103 \\ 12.5 & E-160 \\ 8.12 & E-160 \\ 1.1 & E-160 \\ 24.4 & E-160 \\ 24.4 & E-160 \\ 24.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-547 \\ 13.4 & E-547 \\ 13.7 & E-547 \\ 23 & E-547 \\ 13.4 & E-547 \\ 13.4 & E-547 \\ 13.2 & E-547 \\ 13.4 & E-547 \\$
722899 101693 1026009 1 157169 111506 700800 722899 1013693 1026788 1028234 1 15506 700800 732899 1013693 1026788 1026788 1026788 1026788	701180 733258 1042519 20947 58349 120245 701180 733258 1028233 1042519 20947 58349 120245 701180 733306 1028233 1042519 1028233 1042519 11655 58349	КU-9N AU-9N	$\begin{array}{ccccc} 0.3 & E-103 \\ 37.6 & E-103 \\ 24.8 & E-103 \\ 124.8 & E-103 \\ 168.4 & E-103 \\ 12.5 & E-160 \\ 1.1 & E-160 \\ 37.5 & E-160 \\ 24.4 & E-160 \\ 13.3 & E-160 \\ 13.1 & E-160 \\ 13.1 & E-160 \\ 13.1 & E-160 \\ 13.3 & E-547 \\ 35.6 & E-547 \\ 1.3 & E-547 \\ 1.4 & E-547 \\ 1.5 $
722899 1013693 1005609 1 15769 711506 700800 732899 1013693 1026234 1 57169 111506 700800 722899 1013693 1026738 1026234 1026234 1 57154	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 10025311 102233 1042519 20947 58349 120245 701180 733306 1025311 1028233 10242519 11655 58349 120116	КU-94 AU-94	$\begin{array}{cccc} 0.3 & E-103 \\ 37.6 & E-103 \\ 24.8 & E-103 \\ 168.4 & E-103 \\ 121.8 & E-103 \\ 122.8 & E-160 \\ 13.1 & E-160 \\ 13.2 & E-160 \\ 24.4 & E-160 \\ 24.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-547 \\ 13.3 & E-547 \\ 23 & E-547 \\ 23 & E-547 \\ 23 & E-547 \\ 13.4 & E-547 \\ 13.2 & E-547 \\ 13.2 & E-547 \\ 13.2 & E-547 \\ 13.3 & E-547 \\ 13.3 & E-547 \\ 13.4 & E-547 \\ 13.4 & E-547 \\ 13.2 & E-547 \\ 13.2 & E-547 \\ 13.2 & E-547 \\ 13.3 & E-547 \\ 13.3 & E-547 \\ 13.4 & E-547 \\ $
722899 1013693 1026009 1 157169 111506 700800 722899 1013693 1026234 115506 700800 722899 1013693 1026234 1026234 1357154 96678 125590	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1042519 1042519 1042519 1042519 120245 701180 733306 1025311 10255511 10255511 10255511 102555511 1025555511 1025555555555	КU-9N AU-9N	$\begin{array}{ccccc} 0.3 & E-103\\ 3.7.6 & E-103\\ 24.8 & E-103\\ 168.4 & E-103\\ 12.5 & E-160\\ 3.2 & E-160\\ 3.7.5 & E-160\\ 3.7.5 & E-160\\ 24.4 & E-160\\ 13.3 & E-547\\ 3.7.7 & E-547\\ 1.3 & E-547\\ 1.$
722899 1013693 10136009 1 11506 700800 722899 1013693 1026738 1026234 1 57169 111506 700800 732899 1013693 1026738 1026234 1 57154 1026738 1026234 1 57154	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 1042519 20947 58349 120245 701180 733306 1025311 1028233 1042519 11655 58349 120116 25849 120116 701180 7012017 70120000000000	AU-9N AU-9NA	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
722899 1013693 1026009 1 157169 111506 700800 732899 1013693 1026238 102638 1005658 1005658 1005658 1005658 1005658 1005658 1005658 100	701180 733258 1026008 1042519 20947 701180 733258 1025311 1028233 1042519 102453 1042519 120245 701180 733306 1028233 1042519 11055 58349 120116 204801 701180 733306	АU-9N AU-9N	$\begin{array}{cccccc} 0.3 & E-103 \\ 3.7.6 & E-103 \\ 24.8 & E-103 \\ 12.8 & E-103 \\ 12.5 & E-160 \\ 1.1 & E-160 \\ 1.1 & E-160 \\ 24.4 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-160 \\ 13.3 & E-547 \\ 13.6 & E-547 \\ 13.7 & E-547 \\ 23 & E-547 \\ 13.4 & E-547 \\ 13.2 & E-547 \\ 13.3 & E-547 \\ 13.2 & E-547 \\ 13.2 & E-547 \\ 13.3 & E-547 \\ 13.3 & E-547 \\ 13.4 & E-547 \\ 13.5 & E-8873 \\ 13.5 & E-8873 \\ 13.5 & E-8873 \\ 22.8 & E-8873 \\ 2$
722899 101693 1026009 1 157169 111506 700800 722899 1013693 1026788 1028234 1 157169 111506 700800 732899 1013693 1026788 1026788 1026788 1026788 1055780 700800 702800 702800 702800	701180 733258 1026008 1042519 20947 58349 120245 701180 733258 102231 102231 102231 1022519 120245 701180 733306 1025311 1028233 1042519 120155 58349 12016 204801 701180 733306 1024519	КU-9N AU-9N	$\begin{array}{cccccc} 0.3 & E-103 \\ 3.7.6 & E-103 \\ 24.8 & E-103 \\ 12.8 & E-103 \\ 12.5 & E-160 \\ 1.1 & E-160 \\ 3.7.5 & E-160 \\ 24.4 & E-160 \\ 13.3 & E-160 \\ 13.1 & E-547 \\ 3.6 & E-547 \\ 1.3 & E-547 \\ 1.3 & E-547 \\ 1.2 & E-8473 \\ 3.7.7 & E-547 \\ 1.2 & E-8473 \\ 3.7.7 & E-547 \\ 1.2 & E-8873 \\ 3.7.5 & E-8873 \\ 3.7.5$
722899 1013693 1005609 111506 700800 722899 1013693 1026234 115506 700800 722899 1013693 1026738 1026234 1026738 1026234 1026738 102678 102678 105905 700800 700800 702899 1015955 15595	701180 733258 1026008 1042519 20947 701180 733258 1025311 1028233 1042519 20947 701180 733306 1025311 1028233 1042519 110525 58349 120116 204801 701180 733306 1042519 20947 59247	КU-9N AU-9N	0.3 E-103 37.6 E-103 24.8 E-103 168.4 E-103 121.8 E-103 121.8 E-103 125.5 E-160 83.2 E-160 13.1 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-547 13.3 E-547 1.3 E-6873 1.5
722899 1013693 1005609 111506 700800 702809 1013693 1026738 1026234 1026234 1026234 1026234 1026738 1026738 1026738 1026234 115506 700800 702899 1025905 1025905 1155754	701180 733258 1026008 1042519 20947 758349 120245 701180 733258 1042519 20947 58349 120245 701180 733306 120245 701180 733306 1042519 20947 120245 58349 120145 204801 701180 733306 1042519 20947 758349 120245	AU-9N	0.3         E-103           37.6         E-103           24.8         E-103           168.4         E-103           12.5         E-160           3.2         E-160           3.2         E-160           3.5         E-160           3.5         E-160           3.5         E-160           3.5         E-160           3.3         E-547           3.7         E-547           3.3         E-547           3.3         E-547           3.2         E-547           3.2         E-547           3.2         E-547           3.2         E-547           3.2         E-547           3.
722899 1013633 1026009 1 11506 700800 722899 1013633 1026738 1028234 1 57159 1013693 1026738 1026738 1028234 1 57154 96678 105795 10575	701180 733258 1026008 1042519 20947 53349 120245 701180 733258 1042519 20947 733268 1042519 120245 701180 733306 1025311 1028233 1042519 120116 53349 120116 701180 733306 1042519 20947 735306	AU-9N	0.3 E-103 37.6 E-103 24.8 E-103 168.4 E-103 168.4 E-103 168.4 E-103 17.5 E-160 1.1 E-160 13.5 E-160 13.3 E-160 13.3 E-160 13.3 E-160 13.3 E-547 13.3 E-547 1.3 E-547 1.2 E-8873 1.5 E-8873 1.5 E-8873 1.5 E-8873 1.5 E-8873 1.5 E-8873 1.6 E-8873 1.5 E-8873 1.5 E-8873 1.6 E-8873 1.6 E-8873 1.6 E-8873 1.6 E-8873 1.7 E-8873 1.8 E-8873 1.9 E-32981 0.4 E-32
722899 1013693 1005609 1 11506 700800 732899 10056738 1028234 1028234 105738 10128234 115506 700800 732899 1013693 1026738 1026738 1028234 96678 155950 700800 700800 700800 702899 1025905 1 1557154 111556 164296 184768	701180 733258 1026008 20947 733258 70180 733258 120245 70180 733268 1025311 102231 1022531 1022531 1022531 1022531 1022531 102253 1022531 102253 102253 102253 102253 102253 10225 10225 10225 10253 10255 10055 10055 10055 100555 10055 100555 100555 100555 100555 100555 1	AU-9N	0.3         E-103           37.6         E-103           24.8         E-103           121.8         E-103           121.8         E-103           122.5         E-160           13.2         E-160           13.2         E-160           13.3         E-160           13.4         E-547           13.5         E-547           13.4         E-547           13.5         E-8873           15.5         E-8873           15.5         E-8873           15.5         E-8873           16.6         E-8873           16.7         E-32931

700800	701180	NP-UA	37.7	E-32931
732899	733306	NP-UA	23	E-32931
1013693	1025311	NP-UA	21.6	E-32931
1026738	1028233	NP-UA	13.4	E-32931
1028234	20047	NP-UA	132.2	E-32931
121260	123640	NP-UA	12.5	E_DK20
179423	179834	NP-UA	0.4	E_DK20
247629	258599	NP-UA	2.3	E DK20
700800	701180	NP-UA	37.4	E_DK20
732899	733306	NP-UA	22.8	E_DK20
1015715	1025311	NP-UA	11.4	E_DK20
1026716	1028233	NP-UA	15.1	E_DK20
1028234	1042519	NP-UA	130.6	E_DK20
1	11655	NP-UA	0.9	F-6068
5/154	120116	NP-UA	81.9	F-6068
157904	163060	NP-UA NP-UA	19.5	F-6068
195090	204801	NP-UA	13	F-6068
412356	442321	NP-UA	54	F-6068
532095	534130	NP-UA	3.6	F-6068
700800	701180	NP-UA	37.2	F-6068
732899	733306	NP-UA	22.6	F-6068
1025876	1042519	NP-UA	163.6	F-6068
1	11655	NP-UA	0.4	SQ32
5/143	58349	NP-UA	80.6	SQ32
96678 170473	120155	NP-UA	4.6	SQ32 SQ32
2/7300	255658	NP-UA	12.2	5032
700800	701180	NP-UA	36.8	SQ32
732899	733306	NP-UA	22.3	SQ32
1026422	1042519	NP-UA	153.4	SQ32
1	11655	NP-UA	0.4	SQ29
57143	58349	NP-UA	80.6	SQ29
96678	120155	NP-UA	4.6	SQ29
179423	179834	NP-UA	0.2	SQ29
247390	255658	NP-UA	13.1	SQ29
722800	722206	NP-UA	22.2	5029
1026422	1042519	NP-UA	153.3	5029
55290	56443	NP-UA	6.3	5020
184369	189727	NP-UA	11.5	SQ20
768502	773345	NP-UA	101.9	SQ20
1024613	1034464	NP-UA	26.1	SQ20
55290	56443	NP-UA	6.3	SQ24
184369	189727	NP-UA	11.5	SQ24
768502	1024464	NP-UA	101.9	SQ24
7/20/7	747172	NP-UA	20.1	SQ24 SO01
1	11655	NP-UA	1.1	5025
57143	58349	NP-UA	82.2	SQ25
96678	120155	NP-UA	5.9	SQ25
160877	161749	NP-UA	13.4	SQ25
700800	701180	NP-UA	37.4	SQ25
732899	733306	NP-UA	22.8	SQ25
1025905	1042519	NP-UA	166	SQ25
1	52385	NP-UA	0	SQ15
55460	56443	NP-UA	12.7	SQ15
99774	133032	NP-UA NP-UA	13.7	SQ15 SQ15
161146	164916	NP-UA	7.5	5015
219432	219821	NP-UA	6.2	SQ15
553069	558653	NP-UA	2.7	SQ15
55460	56443	NP-UA	7.8	SQ19
57118	58405	NP-UA	13	SQ19
161146	164916	NP-UA	6.6	SQ19
219432	219821	NP-UA	5.9	SQ19
553048	558653	NP-UA	1.9	SQ19
23957	40177	NP-UA	8.4	QH111L 0H111L
57/97	57816	NP-UA	18.2	OH111L
58176	58275	NP-UA	30.2	OH111
66045	67698	NP-UA	3.2	QH111L
72139	76886	NP-UA	7.3	QH111L
179656	191627	NP-UA	22.6	QH111L
240720	243829	NP-UA	20.2	QH111L
246875	257350	NP-UA	63.3	QH111L
258952	271304	NP-UA	4.7	QH111L
2/7645	280981	NP-UA	7.8	QH111L
420020	380284	NP-UA	0.1	QH111L OH1111
423029	450039	NP-UA	39.1	0H111
481583	482294	NP-UA	5.7	QH1111
526117	528445	NP-UA	5.3	QH111L
635952	645097	NP-UA	2	QH111L
757409	771312	NP-UA	7.2	QH111L

783800	786478	NP-UA	0.7	QH111L
981635	1019101	NP-UA	23.3	QH111L
768090	772831	NP-UA	91.3	chxRP4F1
1024613	1034464	NP-UA	25.7	chxRP4F1
1024613	1034464	NP-UA NP-UA	25.6	hxRP4D10
768090	772831	NP-UA	91.1	chxRP1H1
1024613	1034464	NP-UA	25.6	chxRP1H1
56342	57312	P-UA	48	1078V
183216	189371	P-UA	7.6	1078V
444988	448392	P-UA	17.6	1078V
192216	5/312	P-UA	43.8	1106C
183210	1893/1	P-UA P-UA	17.5	11060
56138	57312	P-UA	43.8	1106C
183216	189371	P-UA	7.5	1106R
444988	448392	P-UA	17.5	1106R
56138	57312	P-UA	43.9	1106V
183216	189371	P-UA	7.6	1106V
444988	448392	P-UA	17.6	1106V
101026	5/019	P-UA	107.7	1176V
1026793	1027561	P-UA	7.2	1176V
54294	55173	P-UA	32.8	1182R
55624	57312	P-UA	39.2	1182R
183216	189371	P-UA	7.6	1182R
444988	448392	P-UA	15.5	1182R
1026984	1027561	P-UA	12.2	227C
1026984	1027561	P-UA	12.2	227R
54294	57019	P-114	58.9	321
183068	189274	P-UA	6.2	32V
760234	761754	P-UA	6.4	32V
790344	797331	P-UA	87.9	32V
799963	819898	P-UA	7.8	32V
825301	826002	P-UA	2.5	32V
827105	871020	P-UA	99	32V
772002	775803	P-UA P-UA	125.0	3620
783109	883485	P-UA	253.5	362C
923775	941098	P-UA	39.8	362C
942211	962496	P-UA	29.7	362C
981310	985396	P-UA	10.6	362C
990878	1007315	P-UA	59.1	362C
133033	134933	P-UA	6.3	362R
7/3993	//5893	P-UA	135.9	362K
923775	941098	P-UA P-IIA	253.5	362R
942211	962496	P-UA	29.7	362R
981310	985396	P-UA	10.6	362R
990878	1007315	P-UA	59.1	362R
133033	134933	P-UA	6.3	362V
773993	775893	P-UA	135.9	362V
783109	883485	P-UA	253.5	362V
942319	962496	P-114	29.0	362V
981310	985396	P-UA	10.6	362V
990878	1007315	P-UA	59.1	362V
760234	761621	P-UA	5	72C
790344	797331	P-UA	90.8	72C
799963	819898	P-UA	11.2	72C
825301	826002	P-UA	2.b 104.7	720
760234	761621	P-114	104.7	72C 72R
790344	797331	P-UA	90.3	72R
799963	819898	P-UA	10.9	72R
825301	826002	P-UA	2.5	72R
827105	870700	P-UA	104	72R
760234	761621	P-UA	4.9	72V
790344	/9/331	P-UA	90.3	720
825301	826002	P-114	2.5	720
827105	870700	P-UA	104	72V
159603	163454	P-UA	8.1	Ba
160316	163454	P-UA	15.5	Ct_RefC
774014	774193	P-UA	9.2	Ct_RefC
4437	7334	P-UA	8.2	Ct_refL3
775667	775005	P-UA	22.2	Ct_refL3
56607	57019	P-UA P-IIA	37.2	D 43nl
183216	189371	P-UA	8.8	D_43nl
56607	57019	P-UA	37.2	G
183216	189371	P-UA	7.3	G
56607	57019	P-UA	36.8	н
444988	448392	P-UA	14.7	Н
56607	5/312	P-UA	47.1	H_185

556834	558381	P-UA	5.3 J
56607	57019	P-UA	36.9 K
183216	189371	P-UA	10.2 K
56607	57019	P-UA	37.3 D_UW3
183216	189371	P-UA	7.5 D_UW3
158321	104185	P-UA D LIA	5.4 A_RAK15
160618	163454	P-UA P-IIA	10.8 B Jali20
56607	56740	P-UA	10.8 B_Jali20
56607	57212	P-UA P-UA	02.3 L2C
159/09	161052	P-UA	5 0 G 9768
183068	186806	P-114	48.8 G 9768
230981	259419	P-UA	12.5 G 9768
133033	134933	P-UA	6.3 G 11222
56607	57312	P-UA	43.8 G 9301
158498	161953	P-UA	5.8 G 9301
183068	186806	P-UA	48.5 G 9301
230981	259419	P-UA	12.2 G_9301
56607	57019	P-UA	37.2 D-EC
183216	189371	P-UA	7.4 D-EC
56607	57019	P-UA	37.2 D-LC
183216	189371	P-UA	7.3 D-LC
56607	57312	P-UA	43.9 G_11074
158498	161953	P-UA	5.8 G_11074
183068	186806	P-UA	48.6 G_11074
230981	259419	P-UA	12.3 G_11074
56607	56749	P-UA	62.3!_SF25667
56607	56749	P-UA	62.9 L1_440
56607	57019	P-UA	3/.1i_SotonG1
103210	1093/1	P-UA	7.51_SOLONG1
200U/	5/UI9 190271	P-UA	30.9 /_SOTOND5
103210 56444	57212	P-UA D_IIA	38.8 K SotonK1
183216	189371	P-11Δ	6.8K SotonK1
759982	768192	P-UA	32.3 J 31-98
160349	163454	P-UA	13.8 C TW3
56444	57312	P-UA	39.6 CS637 11
183216	189371	P-UA	7.4 CS637_11
56607	57019	P-UA	37.3 CS190_96
65929	72014	P-UA	31.1 CS190_96
183216	189371	P-UA	7.5 CS190_96
56444	57312	P-UA	39.8 SQ20
56444	57312	P-UA	39.8 SQ24
886192	887789	P-UA	2.6 SQ09
556834	558441	P-UA	5 SQ01
556834	558441	P-UA	4.9 SQ02
556834	558441	P-UA	4.9 SQ05
56444	5/11/	P-UA	31.5 SQ15
56444	5/11/	P-UA	30.5 SQ19
155621	162454	P-UA	20.4 UNIIIL 7 OU1111
100031	103434	P-UA	27.2 chupp454
183216	189371	P-UA D_IIA	7.2 CHXRP4F1
56607	57010	P-UA D_IIA	37.9 UIXNF4F1
183216	189371	P-11Δ	7.3 hxRP4D10
56607	57019	P-11Δ	37.2 cbxRP1H1
183216	189371	P-11Δ	7.3 cbxRP1H1
547176	547381	Trachoma	12.9 1079R
25451	25733	Trachoma	10.6 1182V
55340	55372	Trachoma	28.1 927V
782882	784058	Trachoma	5.7 Ct_refDa
788428	788439	Trachoma	1.7 Ct_refDa
111229	111548	Trachoma	1.3 F_70
54204	55451	Trachoma	65.7 D_43nl
54204	55451	Trachoma	65.7 G
690319	690410	Trachoma	18.8 G
55174	55451	Trachoma	38.4 H
55174	55459	Trachoma	30.6 Ja_47nL
782093	783896	Trachoma	1.6 Ja_47nL
54204	55451	Trachoma	65.3 K
54204	55451	Trachoma	66 D_UW3
54204	55451	Trachoma	65.8 D-EC
54204	55451	Trachoma	65.7 D-LC
54204	55451	Trachoma	65.6 SotonG1
54204	55451	Trachoma	65.1 )_SotonD5
869427	893862	Trachoma	// J_6276
54204	55451	Trachoma	66_CS190_96
111229	111548	i rachoma	1.5 E_DK20
113026	114074	Trachoma	1 E_DK20
52380	22429	Trachoma	25.7 SQ15
52380	22429	Trachoma	24.3 SQ19
54204	55459	Trachoma	43.9 QH111L
54204	55451	Trachoma	65.7 hvpp4p10
54204	55451	Trachoma	65.7 cbvRP1H1
757409	759981	Unknown	0.1 10781/

775878	782794	Unknown	0.1	1079C	E	
368170	375328	Unknown	0.2	1078R	E	
228878	230623	Unknown	0.2	F_70		
368170	375328	Unknown	0.3	1079R	E	
368170	375328	Unknown	0.3	1079V	E	
368170	375328	Unknown	0.4	1079C	E	
546715	547318	Unknown	0.5	Ja_26s		
228878	230560	Unknown	0.6	SQ32		
228878	230560	Unknown	0.6	SQ29		
234361	234931	Unknown	0.9	E_DK20		
564829	572854	Unknown	1.1	1077V	Ja	
997249	997589	Unknown	1.1	1077V	Ja	
997249	997589	Unknown	1.1	1078R	E	
771476	772004	Unknown	1.1	1079C	E	
564829	572854	Unknown	1.2	1077C	Ja	
564829	572854	Unknown	1.2	1077R	Ja	
771476	772004	Unknown	1.2	1077V	Ja	
564829	572854	Unknown	1.2	1078R	E	
564829	572854	Unknown	1.3	1079R	E	
564829	572854	Unknown	1.3	1079V	E	
564829	572854	Unknown	1.4	1079C	E	
240720	242279	Unknown	1.5	E_DK20		
179835	180770	Unknown	1.6	SQ32		
179835	180770	Unknown	1.6	SQ29		
908055	909649	Unknown	1.7	1078V	D	
183776	183934	Unknown	1.7	F_70		
234320	234786	Unknown	1.7	F 70		
179835	180770	Unknown	1.8	E_DK20		
234320	234786	Unknown	1.8	SQ32		
234320	234786	Unknown	1.8	SQ29		
410939	412132	Unknown	1.9	1176R	Ja	
410939	412132	Unknown	1.9	1182C	Ja	
113026	116013	Unknown	2	F_70		
670547	673508	Unknown	2.2	1079C	E	
670547	673508	Unknown	2.3	1079R	E	
670547	673508	Unknown	2.3	1079V	E	
1	4436	Unknown	14.7	Ct_refL3		
54539	56341	Unknown	208.6	1078V	D	
54539	56137	Unknown	216.6	1106C	D	
54539	56137	Unknown	216.8	1106R	D	
54539	56137	Unknown	217.1	1106V	D	
55174	55623	Unknown	82.3	1182R	Ja	
105937	111228	Unknown	5	E_DK20		
105937 124692	111228 125577	Unknown Unknown	5 8.5	E_DK20 362C	F	
105937 124692 124692	111228 125577 125577	Unknown Unknown Unknown	5 8.5 8.5	E_DK20 362C 362R	F	
105937 124692 124692 124692	111228 125577 125577 125577	Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5	E_DK20 362C 362R 362V	F F F	
105937 124692 124692 124692 124692	111228 125577 125577 125577 125577	Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 8.5	E_DK20 362C 362R 362V G_11222	F F F	
105937 124692 124692 124692 124692 124692 183068	111228 125577 125577 125577 125577 185466	Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 8.5 33.7	E_DK20 362C 362R 362V G_11222 SQ32	F F	
105937 124692 124692 124692 124692 124692 183068 183068	111228 125577 125577 125577 125577 185466 185466	Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 33.7 33.7	E_DK20 362C 362R 362V G_11222 SQ32 SQ29	F F	
105937 124692 124692 124692 124692 183068 183068 183068	111228 125577 125577 125577 125577 125577 185466 185466 185466	Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 33.7 33.7 34.8	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20	F F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 187879	111228 125577 125577 125577 125577 125577 185466 185466 185466 185466 191434	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 33.7 34.8 6.3	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC	F F	
105937 124692 124692 124692 124692 183068 183068 183068 187879 187879	111228 125577 125577 125577 125577 185466 185466 185466 191434 191434	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba	F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 187879 187879 187879	111228 125577 125577 125577 125577 185466 185466 185466 191434 191434 191434	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L	F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 187879 187879 191628 191628	111228 125577 125577 125577 125577 185466 185466 185466 185466 191434 191434 191434 192722 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70	F F	
105937 124692 124692 124692 124692 183068 183068 183068 187879 187879 191628 192027 192027	111228 125577 125577 125577 125577 185466 185466 191434 191434 191434 192722 192606 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 2.7	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32	F F	
105937 124692 124692 124692 183068 183068 183068 183068 18308 193027 191628 192027 192027 192027	111228 125577 125577 125577 185466 185466 191434 191434 191434 192722 192606 192606 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 2.7 2.7	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32 SQ29 SQ29 SQ29 SQ29 SQ29 SQ20	F	
105937 124692 124692 124692 124692 1883068 183068 183068 183068 187879 191628 192027 192027 192027 192027	111228 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 125576 125466 191434 191434 192722 192606 192606 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 6.2.7 2.7 2.7 2.7	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32 SQ29 E_DK20 C22 SQ29 E_DK20 C22 SQ29 SQ29 SQ29 SQ29 SQ29 C22 SQ29 C22 SQ29 C22 SQ29	F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 183068 183068 183068 183068 183068 194027 192027 192027 192027 192027 192027	111228 125577 12556 125606 122606 1292606 1292606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 2.7 2.7 2.7 2.9 7.6	E_DK20 362C 3627 3627 3627 G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32 SQ29 E_DK20 SQ32 SQ32 SQ32	F F	
105937 124692 124692 124692 183068 183068 183068 183068 187879 191628 192027 192027 192027 192027 192027 192027	111228 125577 125577 125577 125577 185466 185466 191434 191434 191434 192722 192606 192606 192606 192606 192606 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 33.7 34.8 6.3 9.3 9.1 2.6 2.7 2.7 2.7 7.6 7.6	E_DK20 362C 3627 3627 9621222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32 SQ29 E_DK20 SQ32 SQ29 SQ22	F F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 183086 183086 183087 194027 192027 192027 192027 192027 192027 192027 194157 194157 194157	111228 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 125577 191434 191434 191434 192722 192606 192606 192606 192606 192606 192606 192606 192606 192606	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 2.7 2.7 2.7 2.9 7.6 7.6 9.4	E_DK20 362C 362R 362Y G_11222 SQ32 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ32 SQ29 E_DK20 SQ32 SQ29 E_702 F_70 F_70	F F	
105937 124692 124692 124692 124692 183068 183068 183068 183068 183068 183068 183068 183068 183068 193027 192027 192027 192027 192027 192027 192027 194157 194157 194157	111228 125577 125577 125577 125577 185466 191434 191434 191434 192426 192606 192606 192606 192606 192606 192606 192697 194897 194897	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 33.7 33.7 33.8 6.3 9.3 9.1 2.6 2.7 2.7 2.7 2.9 7.6 7.6 9.4 9.9	E_DK20 362C 362R 362V G_11222 SQ32 SQ29 E_DK20 CC_RefC Ba QH111L F_70 SQ32 SQ29 E_DK20 SQ22 SQ29 F_70 E_DK20	F F	
105937 124692 124692 124692 124692 183068 183068 183068 187879 191628 192027 192027 192027 192027 192027 192027 194157 194299 194299 194299	111228 125577 125577 125577 125577 185466 191434 191434 192406 192606 192606 192606 192606 192606 192606 192606 194897 194897 194897 194897	Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown Unknown	5 8.5 8.5 8.5 33.7 33.8 9.1 2.6 2.7 2.9 7.6 7.6 9.4 9.9 9.2 3.2 22.2	E_DK20 362C 362C 362V G_11222 SQ29 E_DK20 Ct_RefC Ba QH1111 F_70 SQ22 SQ29 E_DK20 SQ32 SQ29 E_DK20 SQ32 SQ29 F_700 E_DK20 F_70 E_DK20 SQ32 SQ29 F_70 SQ32	F F	
105937 124692 124692 124692 183068 183068 183068 187879 191628 192027 192027 192027 192027 192027 192027 194157 194299 194299 194299 240720 240720	111228 125577 125577 125577 125577 185466 185466 185466 191434 191434 191434 192722 192606 192606 192606 192606 192606 192606 192606 194897 194897 194897 243742 243742 243742	Unknown Unknown	5 8.5 8.5 33.7 34.8 6.3 9.1 2.6 2.7 2.9 7.6 7.6 9.4 9.9 23.3 23.6	E_DK20 362C 362R 362V G_11222 SQ29 E_DK20 Ct_REa QH111L F_70 SQ32 SQ29 E_DK20 SQ29 E_DK20 SQ29 F_70 E_DK20 SQ32 SQ29 F_70 SQ32 SQ3	FF	
105937 124692 124692 124692 183068 183068 183068 187879 191628 192027 192027 192027 192027 192027 192027 194157 194157 194157 194159 194152 240720 240720	111228 125577 125577 125577 185466 185466 191434 191434 191434 192722 192606 192606 192606 192606 192606 192606 194897 194897 194897 194897 243742 243742 243742	Unknown Unknown	5 8.5 8.5 8.5 33.7 34.8 6.3 9.3 9.1 2.6 2.7 2.9 7.6 7.6 9.4 9.9 9.2 3.3 23.6 23.6	E_DK20 362C 362C 362V G_11222 SQ29 E_DK20 Ct_RefC Ba QH111L F_70 SQ29 E_DK20 SQ29 F_70 E_DK20 SQ29 F_70 SQ22 SQ29	FF	
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410020	410100	Unio	44.0	44451	
410939	412132	Unknown	11.9	1145V	J
4/5/04	477304	Unknown	107.3	Ja_265	
553192	534985	Unknown	12.2	1a_20S	
552194	553288	Unknown	6.2	Ja_26s	
560155	564195	Unknown	11.7	F_70	
562294	563151	Unknown	4.2	Ja_26s	
607013	610302	Unknown	11.3	Ja_26s	
670547	673508	Unknown	2.4	1077C	1
670547	673508	Unknown	2.4	1077R	1
670547	673508	Unknown	2.4	1077V	1
670547	673508	Unknown	3.8	1078R	
699525	700240	Unknown	3.7	1182V	J
700608	701180	Unknown	132.4	Ct_refL3	
708134	709277	Unknown	61.6	1078V	6
708134	708338	Unknown	87.5	1106C	
708134	708338	Unknown	87.5	1106R	
708134	708338	Unknown	87.7	1106V	
708707	709277	Unknown	5.2	1078R	
708707	708980	Unknown	10.7	1077C	J
708707	708980	Unknown	10.7	1077R	j
708707	708980	Unknown	10.7	1077V	j
732899	733258	Unknown	39.5	Ct refl 3	
747566	747913	Unknown	6.1	10770	
747639	747913	Unknown	7.6	1078R	
747639	747913	Unknown	77	1077R	
747639	747913	Unknown	77	1077	
752032	7551/2	Linknown	23.7	10781/	
770865	771562	Linknown	13.7	10789	
771476	772/26	Unknown	13.2	10700	
771476	772420	Linknown	44.4	10791	
771476	772413	Unknown	45.0	1070	
771470	772420	Unknown	45.2	1070	
714/6	772426	Unknown	45.3	107K	
771476	772426	Unknown	45.3	11450	
771476	772426	Unknown	45.3	1145R	1
1476	772426	Unknown	45.3	1145V	J
/14/6	772426	Unknown	45.4	1145C	J
305980	806131	Unknown	4.9	Ja_47nL	
347368	847574	Unknown	16.3	Ja_26s	
96817	901645	Unknown	2.8	SQ25	
)26738	1026792	Unknown	33.7	1176V	
028008	1028569	Unknown	10.5	1176C	1
028570	1042519	Unknown	763	Ct_refL3	
028881	1029705	Unknown	16.1	1079C	
028881	1029705	Unknown	16.2	1079R	
028881	1029705	Unknown	16.2	1079V	
029023	1030688	Unknown	115.8	Ct_refDa	
029050	1030672	Unknown	137.4	Ct_RefC	
029050	1030672	Unknown	139.7	Ba	
031470	1031969	Unknown	60.8	Ct refDa	
035391	1037320	Unknown	169.4	Ba	
035391	1037333	Unknown	174.2	Ct RefC	
035742	1036028	Unknown	42.1	Ct_refDa	
036354	1037400	Unknown	104.4	Ct_refDa	
038578	1038595	Unknown	21.4	680	
			T		

 1038578
 1038595
 Unknown
 21.4
 68C
 Ja

 Start & End, coordinates of the putative recombination region on the reference chromosome
 P-UA, prevalent urogenital and anorectal; NP-UA, non-prevalent urogenital and anorectal (as described in Figure 2)

 Unknown, in some cases, the donor is unknown or uncertain, probably representing unsampled lineages of *C. trachomatis* liogBF, log of the Bayes Factor sore
 Fiji genome names, as in Supplemental Table 1

 mpA gendypes, based on complete sequence of the *omp* A gene and provided for each Fiji genome
 Blocks of shared recombination events with "unknown donor" assignments are highlighted in different colors.

Supplemental Table 3. Sample information from Group A and B participants

												Rare fixed				Rare fixed											
												SNPs found	Rare iSNPs	Rare fixed	Rare iSNPs	SNPs found	Rare iSNPs										
												in	found in	SNPs found	found in	in vaginal	found in				Fixed SNP	Fixed SNP	Fixed SNP				
						Rare fixed		Rare fixed	Rare iSNPs	Rare fixed		endocervic	a endocervica	in vaginal	vaginal and	and	vaginal and	Fixed SNP	Fixed SNP	Fixed SNP	in	in	in	Fixed SNP	Fixed SNP	Fixed SN <sup>4</sup>	ş
	Endocervica					SNPs found	Rare iSNPs	SNPs found	found only	SNPs found	Rare iSNP	s I and rectal	I and rectal	and rectal	rectal but	endocervic	a endocervica	in rectal	in rectal	in rectal	endocervix	endocervix	endocervix	in vagina	in vagina	in vagina	
	I	Rectal	Vaginal	Fixed SNPs R	are Fixed	only in	found only	only in	in	only in	found only	but not	but not	but not	not	I but not	I but not	sample rare	e sample rare	e sample rare	e sample rare	sample rare	sample rare	sample rare	e sample rar	e sample ra	are
	clade/omp4	A clade/ompA	A clade/ompA	found in all S	NPs in 3	rectal	in rectal	endocervica	endocervic	a vaginalsam	in vaginal	vaginal	vaginal	endocervica	endocervica	a rectal	rectal	iSNP in	iSNP in	iSNP in	iSNP in	iSNP in	iSNP in	iSNP in	iSNP in	iSNP in	
Participant Group	genotype	genotype	genotype	3 sites si	ites	sample	sample	I sample	l sample	ple	sample	sample	sample	I sample	I sample	sample	sample	vagina	endocervix	others	vagina	rectum	others	endocervix	rectum	others	
927 A	P-UA/E	P-UA/E	P-UA/E	5464	1388	. C	) 2	7 (	) 1	3	0 2	22	0 1	1 0	) :	8	0 (	5 (	) (	0 0	) (	) (	) (	(	)	0	1
26 A	P-UA/E	P-UA/E	P-UA/E	5316	1264	. C	) 9	1 (	1	6	0 5	50	0 10	0 C	) :	2	0 (	5 (	) (	0 0	) (	) (	) з	(	)	0	1
951 A	P-UA/E	P-UA/E	P-UA/E	5291	1192		2	3	L 1	5	0 8	88	0 1	3 0		4	0 (	5 (	) (	0 0	) (	) (	) 7		0	0	1
192 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	5245	1330	2	2 2	5 (	) 8	1	0 9	90	D !	5 <mark>1</mark>	L 1	1	0 2	2 (	) (	0 0	) (	) (	) (	1	2	0	2
68 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	5241	1085	0	5	3 (	) 1	В	0 5	57	0 1	7 0	) :	3	0 2	2 (	) (	0 0	) (	) (	) (	(	)	0	0
1226 A	P-UA/E	P-UA/E	P-UA/E	5187	1123	1	L 18	3 (	) 3	5	0 7	72	D 3	з о	)	5	0 3	3 (	) (	D 2	2 (	) (	) 1	(	)	0	0
908 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	4911	1010	0	) 5	1 (	0 12	D	0 22	28	D 4	4 0	) .	4	0 :	L (	) (	D 1	1 (	) (	) (	(	)	0	3
564 B	P-UA/Ja	P-UA/E	P-UA/E	4750	949	C	) 10	5 72	2 4	3	0 12	28	، c	4 107	/ 1	6	0 3	3 (	) (	D 1	1 (	) (	) (	(	)	0	0
1145 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	4242	841	1	L 1	7 (	) 4	7	0 24	44	D 3	з о	) .	4	0 2	2 (	) (	0 0	) (	) (	) (	(	)	0	1
519 A	P-UA/E	P-UA/E	P-UA/E	4066	860	0	25	0 (	) .	2	0 20	00	D 3	з о	) :	1	0 3	3 (	) (	D 1	1 (	) (	) (	(	)	0	0
107 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	3600	729	2	2 3	0 (	27	4	0 7	74	D :	2 0	)	5	0 :	L (	) (	0 0	) (	) (	) 1	(	)	0	0
1077 A	P-UA/Ja	P-UA/Ja	P-UA/Ja	3172	670	C	) 22	6 (	) (	9	0 7	79	D :	1 0	) (	0	0 (	) (	) (	0 0	) (	) (	) (	(	)	0	0
1079 A	P-UA/E	P-UA/E	P-UA/E	2189	917	0	) 32	9 (	) 3	1	0 7	78	D !	5 0	) 1	1	0 !	5 (	) (	D 1	L (	) (	0 16	(	)	0	1
362 A	NP-UA/F	NP-UA/F	NP-UA/F	1986	939	C	) 19	5 (	) 12	4	0 7	76	5 C	e o	) :	3	0 2	2 (	) (	D 2	2 (	) (	) 2	(	)	0	1
98 A	NP-UA/G	NP-UA/G	NP-UA/G	1247	880	0	2	7 (	) 3	D	06	59	D :	з о	) .	7	0 2	2 (	) (	0 0	) (	) (	) (	(	)	0	1
1201 A	NP-UA/G	NP-UA/G	NP-UA/G	1139	788	1	L 5	8 (	)	6	0	6	<b>)</b> :	1 0	) :	3	0 !	5 (	) (	0 0	) (	) (	) 8	(	)	0	0
87 A	NP-UA/G	NP-UA/G	NP-UA/G	1006	721		) 12	6 (	0 14	9	0 1	10	1 (	D 0	) (	0	0 3	3 (	) (	0 0	0 1	. (	) (	(	)	0	0
227 A	NP-UA/G	NP-UA/G	NP-UA/G	825	582		) 19	2 (	)	1	0 3	35	D (	o a	)	1	0 :		) (	0 0	) (	) (	) (	(	)	0	0
32 B	P-UA/G	P-UA/G	NP-UA/G	759	547	0	) 1	8 (	) 25	1	0 43	15 1	4 14	4 0	)	1	0 !	5 (	) (	D 1	1 (	) (	) 1	(	)	0	0
1106 A	NP-UA/D	NP-UA/D	NP-UA/D	695	452		) 1	7 (	) .	3	0 :	18	، C	4 0	)	1	0 (	) (	) (	D 1	1 (	) (	) (	(	)	0	2
753 A	NP-UA/G	NP-UA/G	NP-UA/G	633	451		) 17	6 (	) 2	6	0 2	25	، C	4 0	) (	0	0 (	) (	) (	0 0	) (	) (	) (	(	)	0	0
968 A	NP-UA/G	NP-UA/G	NP-UA/G	605	436		) 20	8 (	)	1	0	9	D (	D 0	) (	0	0 2	2 (	) (	0 0	0 1	. (	) 1	(	)	0	1
72 A	NP-UA/G	NP-UA/G	NP-UA/G	554	341		) 6	5 (	0 1	3	0 4	40	D :	2 0	) :	3	0 !	5 (	) (	D 1	L (	) (	) (	(	)	0	0
1176 B	P-UA/Ja	P-UA/Ja	NP-UA/G	385	378		) 7	8 :	1 5	4	1 40	02 2	5 11	7 0	) 1	2	0 4	1 (	) (	0 0	) (	) !	9 8	(	)	0	52
1182 B	P-UA/Ja	NP-UA/Ja	P-UA/Ja	250	231	13	3 25	2 (	56	1	0 2	21	D :	2 0	) 1	3 21	8 93	3 1	L (	0 0	0 125	i (	) 37	(	)	0	0
1078 B	nd	P-UA/E	NP-UA/D	32	32	41	l 11	9 (	0 11	В	1 4	44	D :	з о	) 1	2	2 13	5 53	3 5	7 63	3 9	) (	) (	-	5	0	0

NOTE: "Fixed" SNPs are defined as < 10% reference allele frequency and not in fastGEAR defined recombination blocks. SNVs have 10-90% reference allele frequency. "Rare" SNPs or SNVs are only found in <= 3 samples, which in almost all cases means that they only appeared in samples isolated from one study participant.