Exploring Variation Detection Within a Wide Range of Bioenergy-Relevant Species Via Short Read Technology

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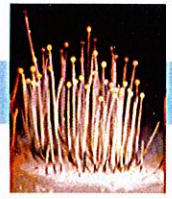
Plants

Microbes

+

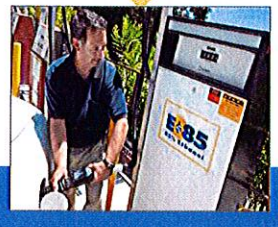
Fungi



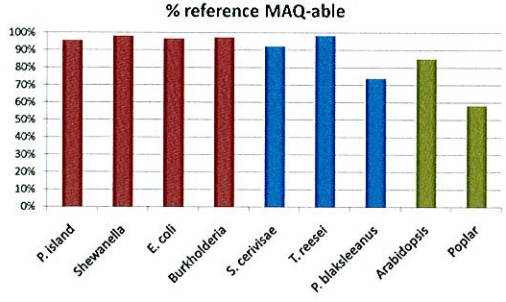
Variation Detection

	Sample	Genome Size (Mb)	Depth	bp covered (Mb)	%ref MAQ-able	% simSNP	# SNP hap/homo	SNP/BP	# SNP hets	% simIndels	# indels hap/homo	# indels het
Canonical	*Dehalococcoides sp.*	1.3	1566X	1.3	92%	89%	0	0	9	96%	346	348
	Desulfovibrio vulgaris	3.7	112X	3.7	97%	98%	0	0	0	85%	0	0
	Shewanella amazonensis	4.3	176X	4.3	98%	98%	0	0	0	86%	1	2
	Rhodopseudomonas palustris	5.3	113X	5.3	98%	99%	0	0	0	83%	0	0
	Verminephrobacter eiseniae	5.6	52X	5.6	98%	97%	0	0	0	77%	7	7
	Burkholderia cepacia	7.5	62X	7.5	97%	99%	0	0	0	75%	0	0
	Pyrobaculum islandicum	1.8	500X	1.8	96%	98%	0	0	0	NA	NA	NA
	E. coli Rad CB1012	4.6	23X	4.6	97%	96%	71	1/64,788	0	NA	NA	NA
	E. coli Rad CB1013	4.6	47X	4.6	97%	97%	47	1/97,872	2	NA	NA	NA
	E. coli Rad CB1014	4.6	57X	4.6	97%	97%	54	1/85,185	2	NA	NA	NA
	E. coli Rad CB1015	4.6	33X	4.6	97%	97%	57	1/80,701	1	NA	NA	NA
	E. coli Rad CB1024	4.6	57X	4.6	97%	97%	64	1/71,875	1	NA	NA	NA
	E. coli Rad CB1025	4.6	45X	4.6	97%	97%	43	1/106,976	2	NA	NA	NA
	S. cerivisae BY4742	12.2	25X	12.1	92%	92%	361	1/33,795	17	NA	NA	NA
	S. cerivisae EPY330	12.2	20X	12.1	92%	93%	519	1/23,507	40	NA	NA	NA
	Trichoderma reesei	33.4	33X	33.1	98%	97%	410	1/81,463	1210	49%	56	376
	Phycomyces blaeksleeanus	51.0	40X	50.8	72%	72%	73,997	1/687	5745	NA	NA	NA
Canonical	*Arabidopsis thaliana* Col-0	119.5	13X	117.9	85%	73%	829	1/144,150	458	NA	NA	NA
	Arabidopsis thaliana Shadara	119.5	24X	112.9	85%	73%	435,130	1/258	13995	NA	NA	NA
	Arabidopsis thaliana Bay	119.5	20X	113.7	85%	71%	343,295	1/331	9529	NA	NA	NA
	Poplar BESC-79	427.6	33X	411.7	59%	67%	1,098,163	1/375	1539795	43%	184,020	198,744
	Poplar 93-968	427.6	24X	412.6	59%	61%	844,197	1/489	1,089,779	24%	70,805	49,722
	Poplar BESC-52	427.6	19X	409.6	59%	67%	994,608	1/412	1,281,829	40%	152,052	143,099

Better Biofuels!



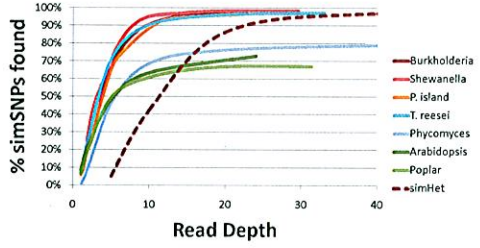
Short Reads Can Capture a Wide Range of Genome Complexity



Conclusion:

- A significant percentage of all genomes are accessible using 35bp reads.

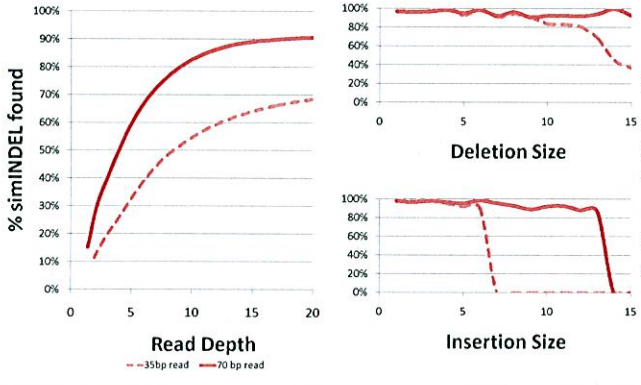
Simulated SNP Analysis Determines Required Depth



Conclusion:

- ~15X depth is sufficient to capture the majority of haploid or homozygous variants.
- ~20x depth is sufficient to capture the majority of heterozygous variants.

Longer Reads Find More Indels



Conclusion:

- 70bp read length give significantly more indel detection.
- Majority of short indels can be found, longer indels can not be found.

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