

Reports for Job pb_359_6-15000



SMRT Cells: 1 Movies: 1

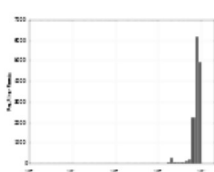
Overview

Job Metric

Value

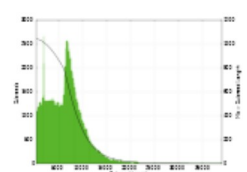
Polished Contigs	19
Adapter Dimers (0-10bp)	0.01%
Short Inserts (11-100bp)	0.0%
Number of Bases	1,055,734,106
Number of Reads	94,470
N50 Read Length	17,774
Mean Read Length	11,175
Mean Read Score	0.87
Mapped Reads	89,054
Mapped Read Length of Insert	5,537
Average Reference Length	269,562
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.97%
Average Reference Coverage	165.79

Adapters



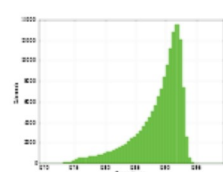
Observed Insert Length Distribution Histogram

Subread Filtering



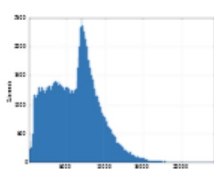
Subread Filtering

Mapping



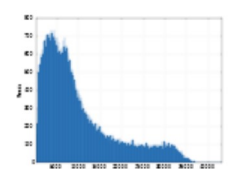
Mapped Subread Concordance

Mapping



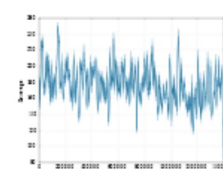
Mapped Subread Length

Mapping



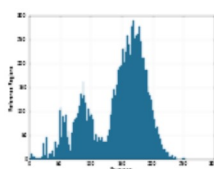
Mapped Polymerase Read Length

Coverage



Coverage Across Reference

Coverage



Depth of Coverage

Corrections



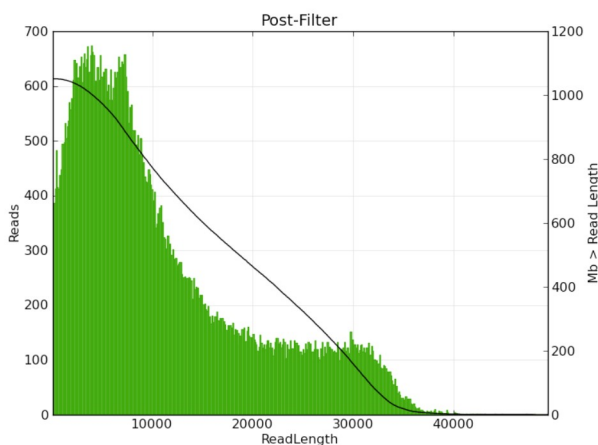
Corrections Across Contigs

Filtering

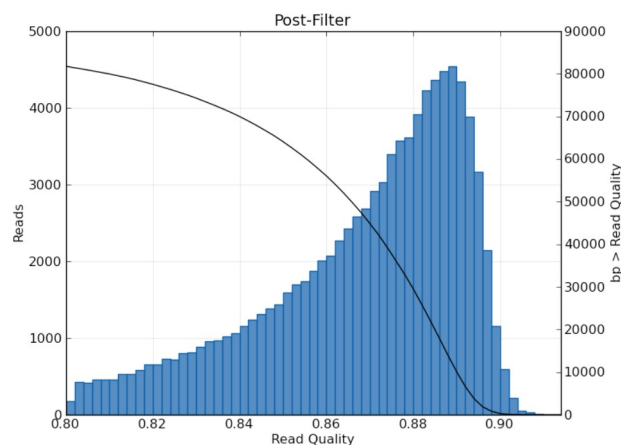
Filtering

Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	1134474684	1055734106
Polymerase Reads	150292	94470
Polymerase Read N50	17374	17774
Polymerase Read Length	7548	11175
Polymerase Read Quality	0.588	0.867

Polymerase Read Length

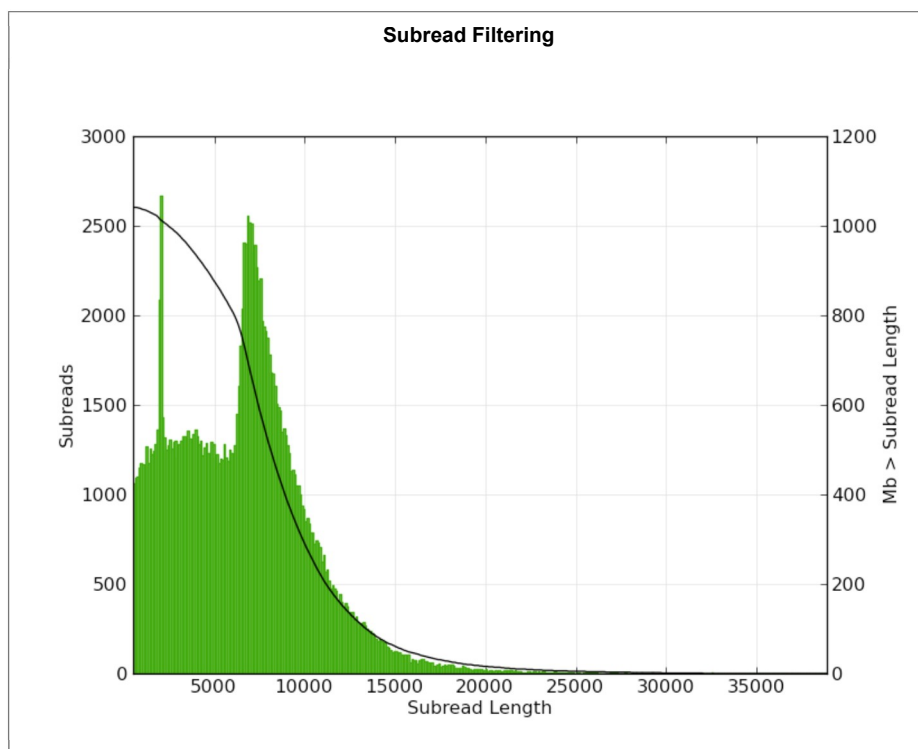


Polymerase Read Quality



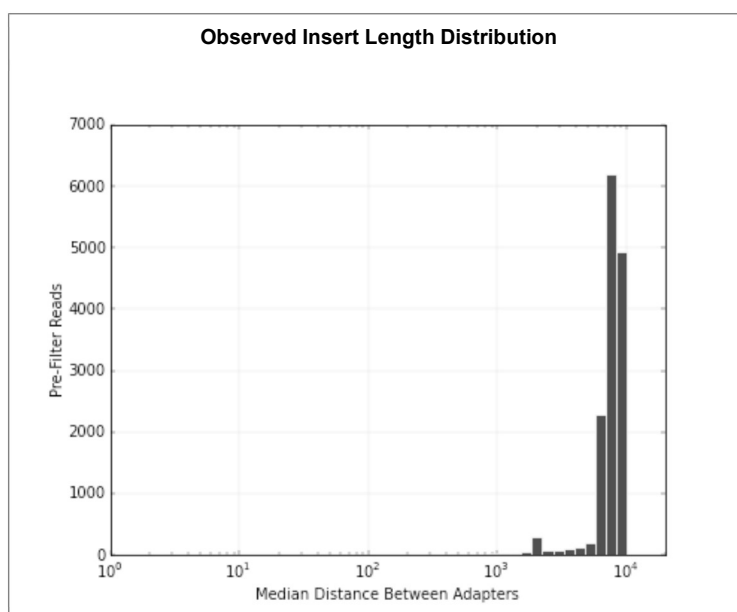
Subread Filtering

Mean Subread length	6,489	N50	8,048
Total Number of Bases	1,050,985,941	Number of Reads	161,958



Adapters

Adapter Dimers (0-10bp) 0.01%
Short Inserts (11-100bp) 0.0%



Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160814_105004_42237_c101088372550000001823265803091780	150,292	27.13%	66.71%	6.17%

Mapping

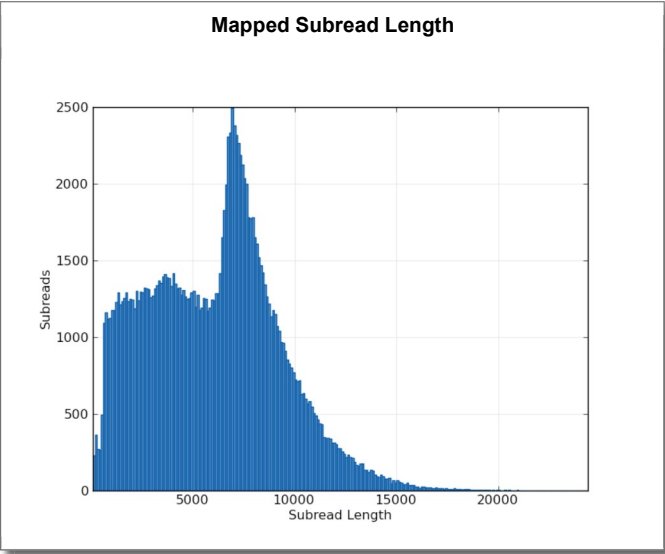
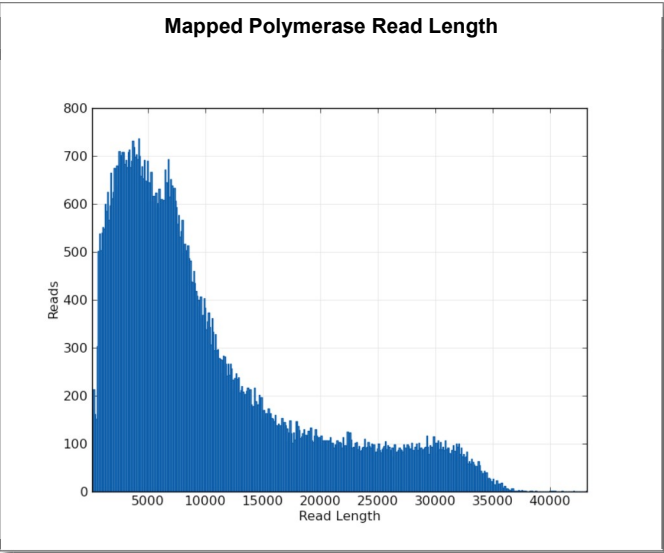
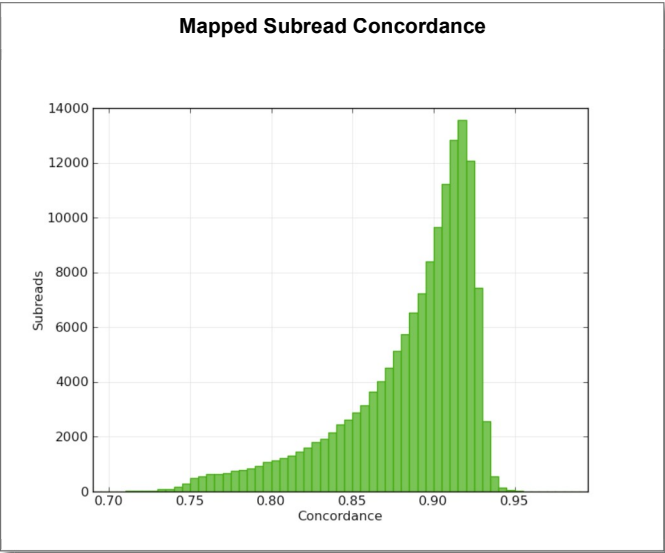
Mapped Subread Length N50 (bp) 7,537 Mapped Polymerase Read Length 95% (bp) 29,120
Mapped Subread Length Mean (bp) 5,943 Mapped Polymerase Read Length Max (bp) 43,085

Mapping Stats Summary

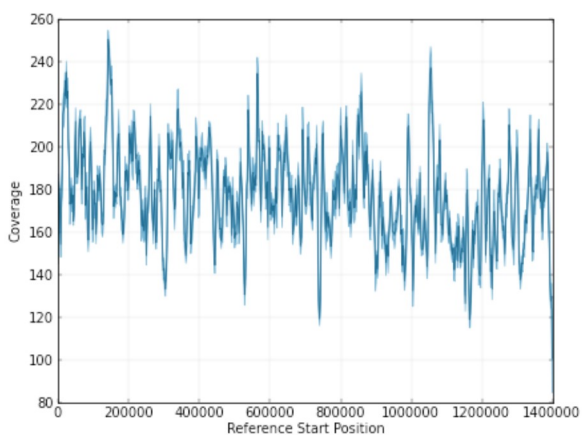
Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	89,054	10,037	15800	147,416	876102260	5,943	0.880
m160814_105004_42237_c101088372550000001823265803091780_s1_p0	89,054	10,037	15800	147,416	876102260	5,943	0.880

Coverage

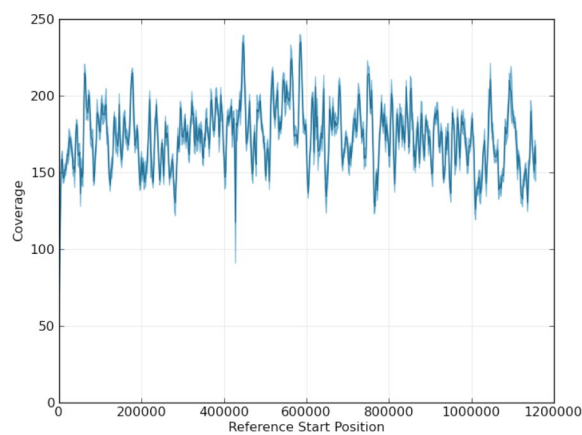
Mean Coverage 165.79
Missing Bases (%) 0.0



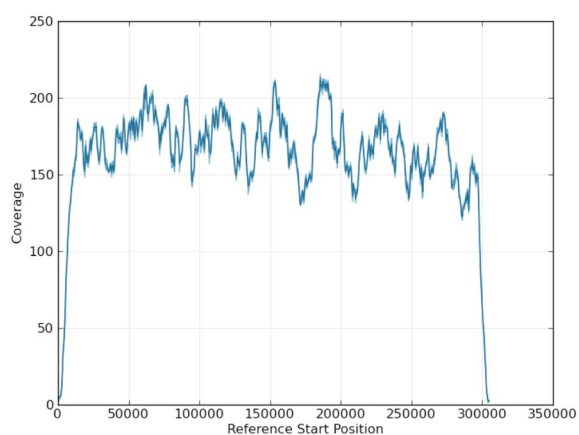
Coverage Across Reference



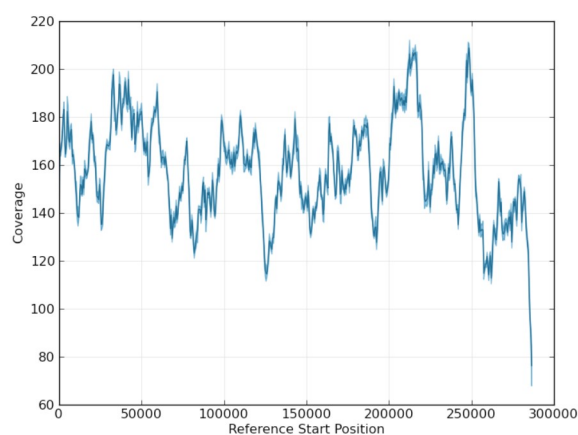
Observed depth of coverage across scf7180000000040 (window size = 2000bp).



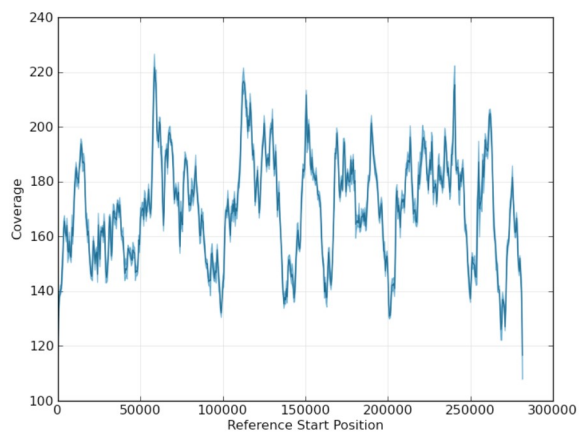
Observed depth of coverage across scf7180000000041 (window size = 2002bp).



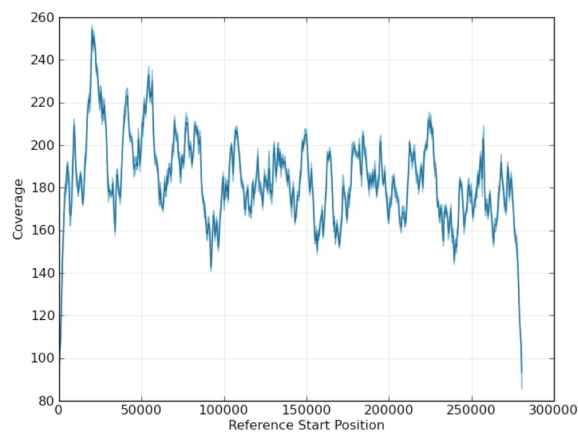
Observed depth of coverage across scf7180000000042 (window size = 500bp).



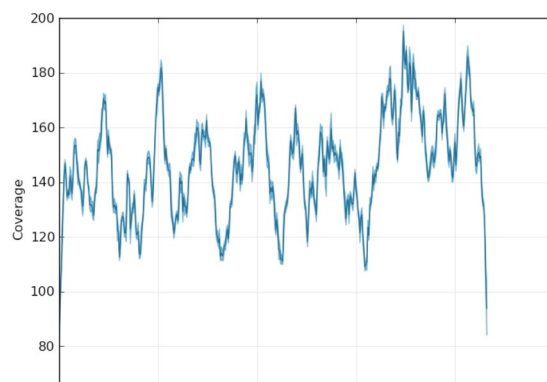
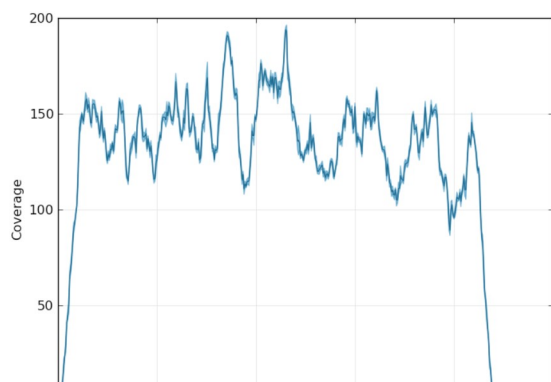
Observed depth of coverage across scf7180000000046 (window size = 500bp).

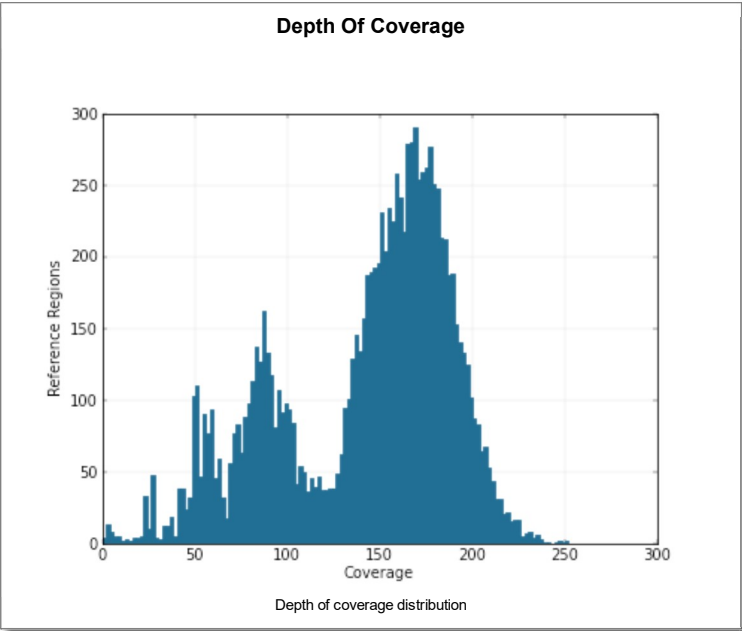


Observed depth of coverage across scf7180000000045 (window size = 500bp).



Observed depth of coverage across scf7180000000044 (window size = 500bp).



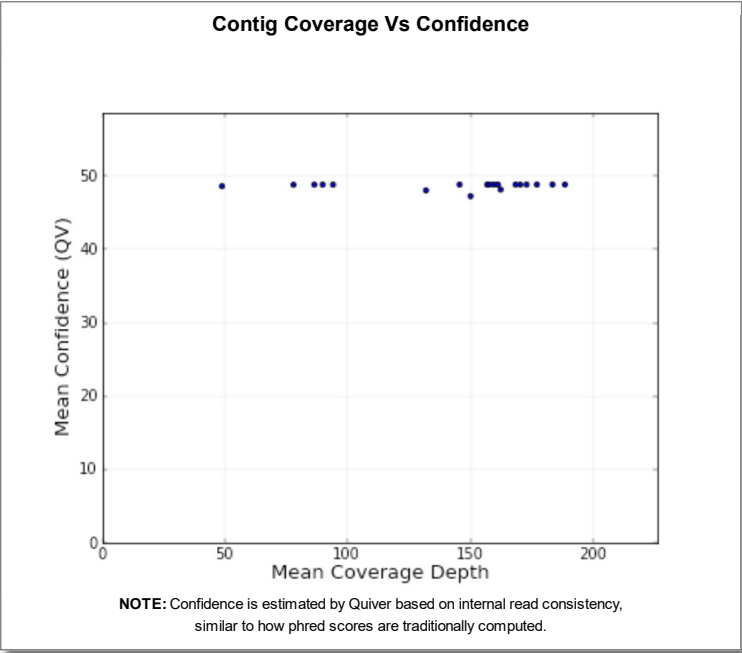


Pre-Assembler Report

Polymerase Read Bases	1,050,985,941	Length Cutoff	15,000
Seed Bases	63,345,748	Pre-Assembled bases	31,569,082
Pre-Assembled Yield	.498	Pre-Assembled Reads	4,426
Pre-Assembled Reads Length	7,132	Pre-Assembled N50	10,875

Polished Assembly

Polished Contigs	19	Max Contig Length	1,400,708
N50 Contig Length	305,879	Sum of Contig Lengths	5,123,604



Top Corrections

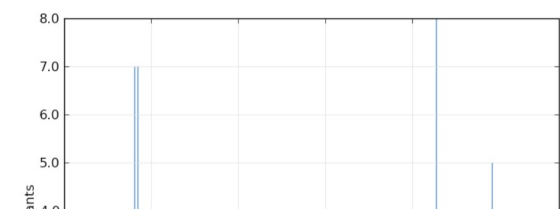
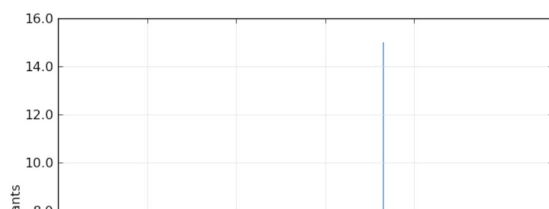
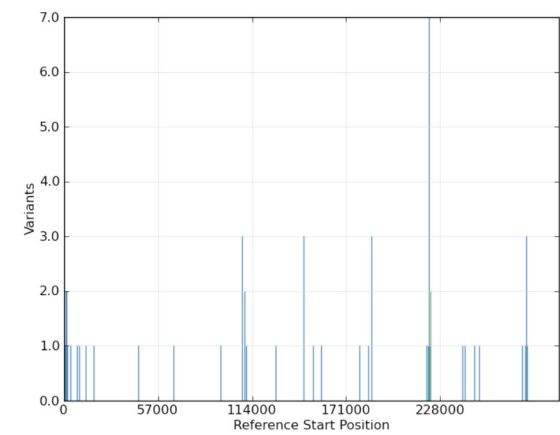
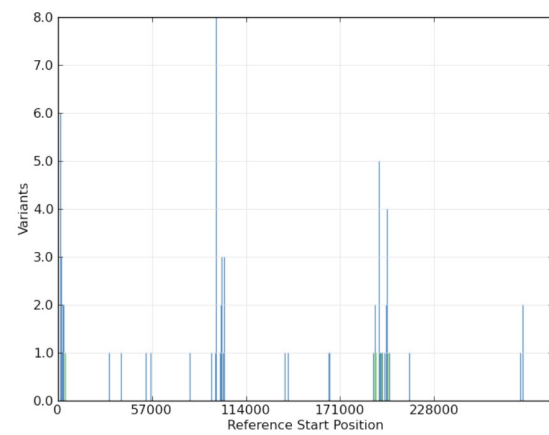
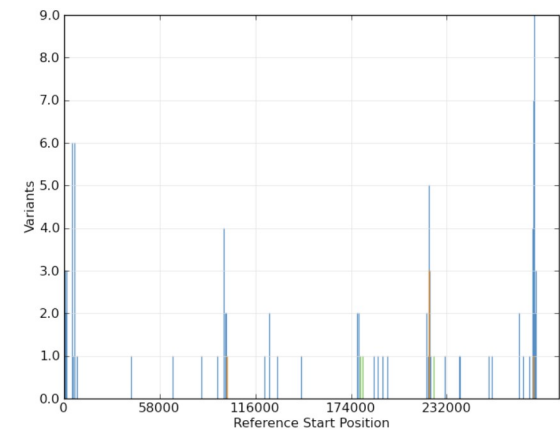
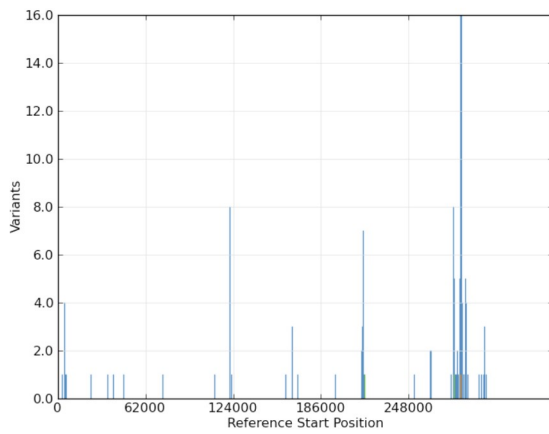
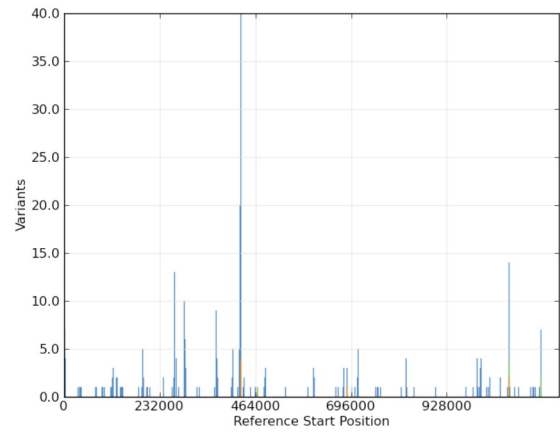
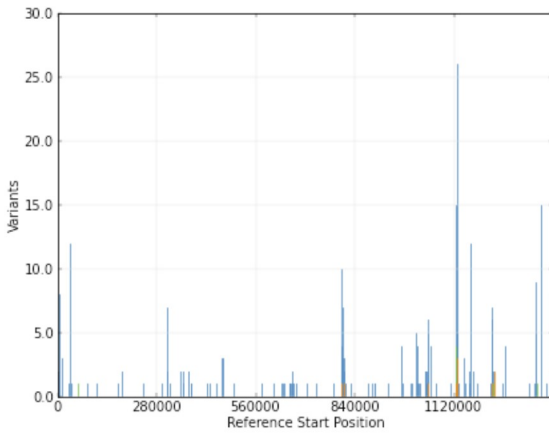
Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000054	41,316	41316_41317insCCTTTTC	INS	86	54	haploid
scf7180000000040	33,151	33151_33152insC	INS	100	53	haploid
scf7180000000040	422,019	422019_422020insG	INS	100	53	haploid
scf7180000000040	1,367,439	1367439_1367440insA	INS	100	53	haploid
scf7180000000048	940	940_941insG	INS	98	53	haploid
scf7180000000050	129,946	129946_129947insA	INS	100	53	haploid
scf7180000000040	355,973	355973_355974insG	INS	100	52	haploid
scf7180000000040	1,047,121	1047121_1047122insTG	INS	100	52	haploid
scf7180000000040	1,176,372	1176372_1176373insC	INS	100	52	haploid
scf7180000000040	1,234,465	1234465CG>GC	SUB	100	52	haploid
scf7180000000041	424,531	424531_424532insC	INS	100	52	haploid
scf7180000000041	485,053	485053_485054insG	INS	100	52	haploid
scf7180000000041	1,074,273	1074273_1074274insT	INS	100	52	haploid
scf7180000000041	1,158,569	1158569_1158570insG	INS	100	52	haploid
scf7180000000042	161,317	161317_161318insG	INS	100	52	haploid
scf7180000000042	165,890	165890_165891insG	INS	100	52	haploid
scf7180000000043	5,824	5824_5825insG	INS	39	52	haploid
scf7180000000043	26,924	26924_26925insG	INS	100	52	haploid
scf7180000000043	32,456	32456_32457insG	INS	100	52	haploid
scf7180000000043	148,667	148667_148668insG	INS	100	52	haploid
scf7180000000043	178,409	178409_178410insC	INS	100	52	haploid
scf7180000000043	216,198	216198_216199insC	INS	47	52	haploid
scf7180000000043	219,060	219060delC	DEL	10	52	haploid
scf7180000000044	108,009	108009_108010insG	INS	100	52	haploid
scf7180000000044	128,248	128248_128249insC	INS	100	52	haploid
scf7180000000045	280,415	280415_280416insG	INS	100	52	haploid
scf7180000000046	412	412_413insG	INS	100	52	haploid
scf7180000000046	286,305	286305_286306insC	INS	89	52	haploid
scf7180000000048	156,205	156205_156206insG	INS	100	52	haploid
scf7180000000048	193,774	193774_193775insC	INS	100	52	haploid
scf7180000000049	52,336	52336_52337insGCG	INS	100	52	haploid
scf7180000000049	72,728	72728_72729insG	INS	100	52	haploid
scf7180000000052	48,789	48789_48790insT	INS	100	52	haploid
scf7180000000054	16,443	16443_16444insC	INS	98	52	haploid
scf7180000000054	16,562	16562_16563insC	INS	99	52	haploid
scf7180000000056	4,919	4919_4920insG	INS	90	52	haploid
scf7180000000056	9,161	9161_9162insG	INS	98	52	haploid
scf7180000000057	7,363	7363_7364insG	INS	96	52	haploid
scf7180000000040	2,025	2025_2026insA	INS	100	51	haploid
scf7180000000040	3,178	3178_3179insC	INS	100	51	haploid
scf7180000000040	12,690	12690_12691insAC	INS	100	51	haploid
scf7180000000040	111,367	111367_111368insA	INS	100	51	haploid
scf7180000000040	241,641	241641_241642insG	INS	100	51	haploid
scf7180000000040	309,557	309557_309558insC	INS	100	51	haploid
scf7180000000040	655,149	655149_655150insG	INS	100	51	haploid
scf7180000000040	704,834	704834_704835insG	INS	100	51	haploid
scf7180000000040	803,806	803806_803807insA	INS	100	51	haploid
scf7180000000040	891,459	891459_891460insC	INS	100	51	haploid
scf7180000000040	1,014,781	1014781_1014782insC	INS	100	51	haploid
scf7180000000040	1,049,663	1049663_1049664insC	INS	100	51	haploid
scf7180000000040	1,126,232	1126232_1126233insG	INS	100	51	haploid
scf7180000000040	1,128,086	1128086_1128087insG	INS	100	51	haploid
scf7180000000040	1,129,944	1129944_1129945insA	INS	100	51	haploid
scf7180000000040	1,351,761	1351761_1351762insG	INS	100	51	haploid
scf7180000000040	1,398,862	1398862_1398863insTGG	INS	100	51	haploid
scf7180000000041	76,473	76473_76474insG	INS	100	51	haploid
scf7180000000041	118,045	118045_118046insT	INS	100	51	haploid
scf7180000000041	140,455	140455_140456insT	INS	100	51	haploid
scf7180000000041	269,896	269896_269897insC	INS	100	51	haploid
scf7180000000041	269,964	269964_269965insC	INS	100	51	haploid
scf7180000000041	291,350	291350_291351insA	INS	100	51	haploid
scf7180000000041	292,153	292153_292154insC	INS	100	51	haploid
scf7180000000041	369,201	369201_369202insC	INS	100	51	haploid
scf7180000000041	371,548	371548_371549insG	INS	100	51	haploid
scf7180000000041	420,696	420696_420697insC	INS	100	51	haploid
scf7180000000041	424,077	424077_424078insC	INS	100	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000040	1,400,422	100.0%	99.9834%	177.16
scf7180000000041	1,159,722	100.0%	99.9803%	172.94
scf7180000000042	305,750	100.0%	99.9712%	162.35
scf7180000000046	287,119	100.0%	99.9721%	157.81
scf7180000000045	282,106	100.0%	99.9801%	170.35
scf7180000000044	281,359	100.0%	99.9822%	183.48
scf7180000000043	220,994	100.0%	99.9615%	131.87
scf7180000000048	216,813	100.0%	99.9709%	145.61
scf7180000000049	177,785	100.0%	99.9291%	161.27
scf7180000000047	155,179	100.0%	99.9845%	150.07
scf7180000000050	152,477	100.0%	99.9836%	188.57
scf7180000000051	137,892	100.0%	99.9761%	156.86
scf7180000000052	116,229	100.0%	99.9682%	168.42
scf7180000000054	60,897	100.0%	99.8703%	93.98
scf7180000000055	51,714	100.0%	99.9362%	89.76
scf7180000000053	51,133	100.0%	99.9687%	159.62
scf7180000000056	29,858	100.0%	99.7555%	77.84
scf7180000000057	18,870	100.0%	99.8145%	86.33
scf7180000000058	15,364	100.0%	99.6030%	48.71

Corrections Across Reference

- Insertions
- Deletions
- Substitutions



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