

Reports for Job pb_359_7-20000



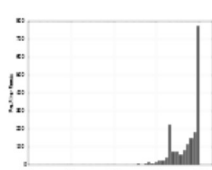
SMRT Cells: 1 Movies: 1

Overview

Job Metric

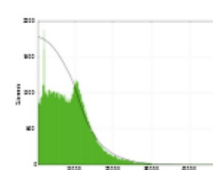
Job Metric	Value
Polished Contigs	4
Adapter Dimers (0-10bp)	0.01%
Short Inserts (11-100bp)	0.0%
Number of Bases	1,255,903,408
Number of Reads	107,814
N50 Read Length	16,269
Mean Read Length	11,648
Mean Read Score	0.86
Mapped Reads	100,376
Mapped Read Length of Insert	7,372
Average Reference Length	1,351,391
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.99%
Average Reference Coverage	182.4

Adapters



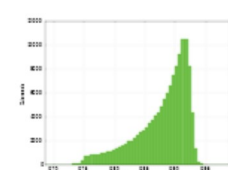
Observed Insert Length Distribution Histogram

Subread Filtering



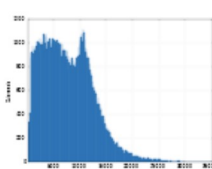
Subread Filtering

Mapping



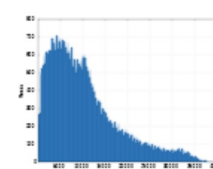
Mapped Subread Concordance

Mapping



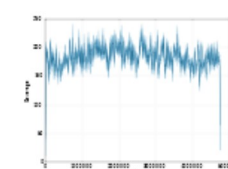
Mapped Subread Length

Mapping



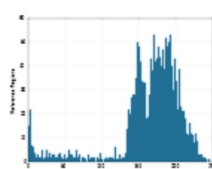
Mapped Polymerase Read Length

Coverage



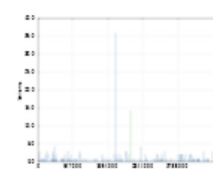
Coverage Across Reference

Coverage



Depth of Coverage

Corrections



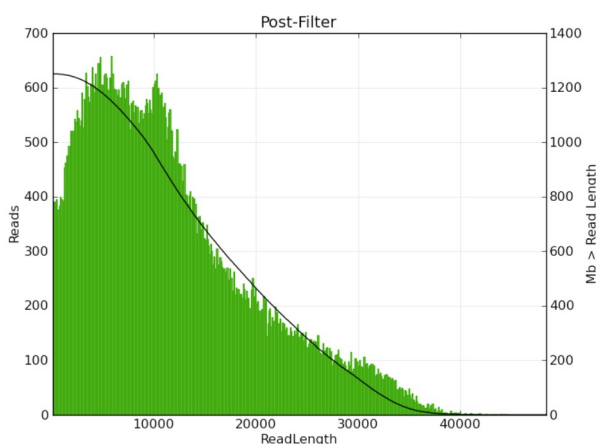
Corrections Across Contigs

Filtering

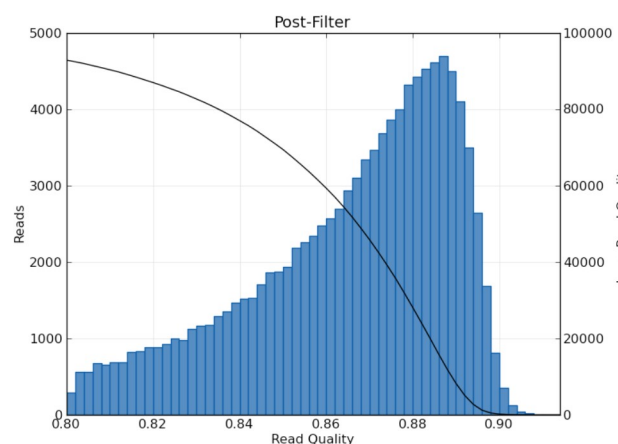
Filtering

Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	1363324689	1255903408
Polymerase Reads	150292	107814
Polymerase Read N50	15986	16269
Polymerase Read Length	9071	11648
Polymerase Read Quality	0.674	0.864

Polymerase Read Length

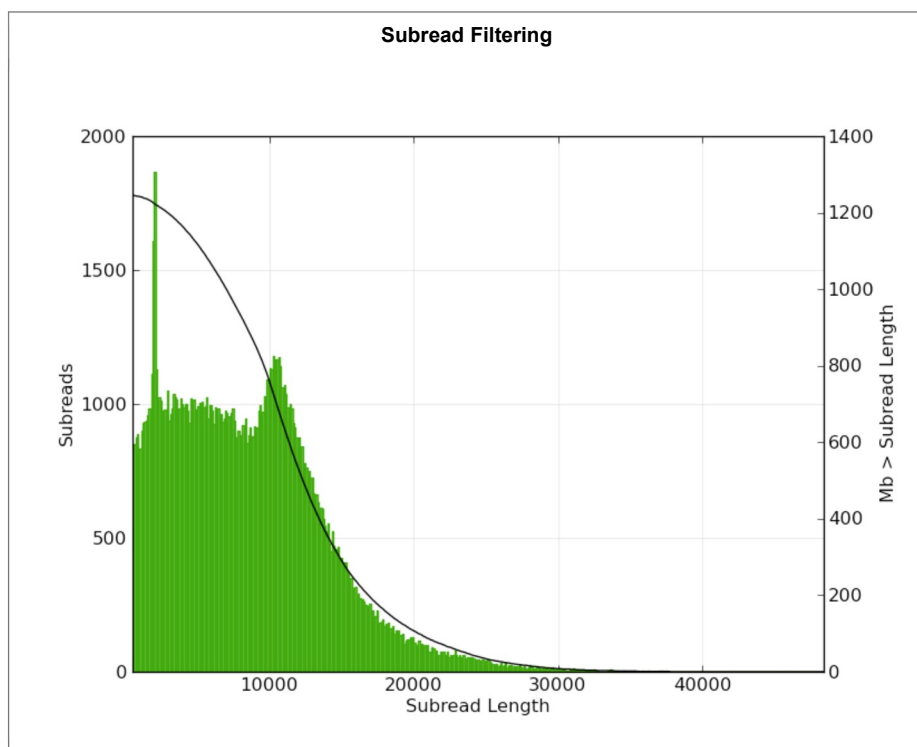


Polymerase Read Quality



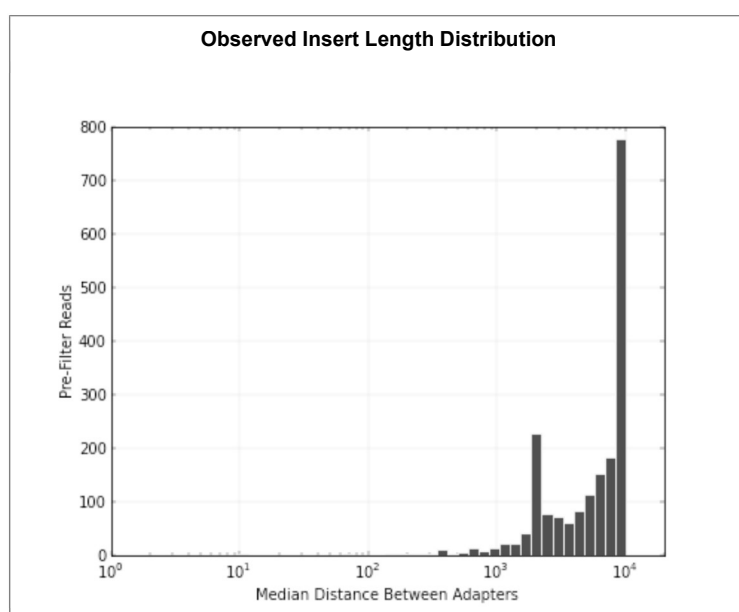
Subread Filtering

Mean Subread length	8,479	N50	11,231
Total Number of Bases	1,252,753,682	Number of Reads	147,747



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_150917_42237_c101088372550000001823265803091781	150,292	14.15%	76.9%	8.95%

Mapping

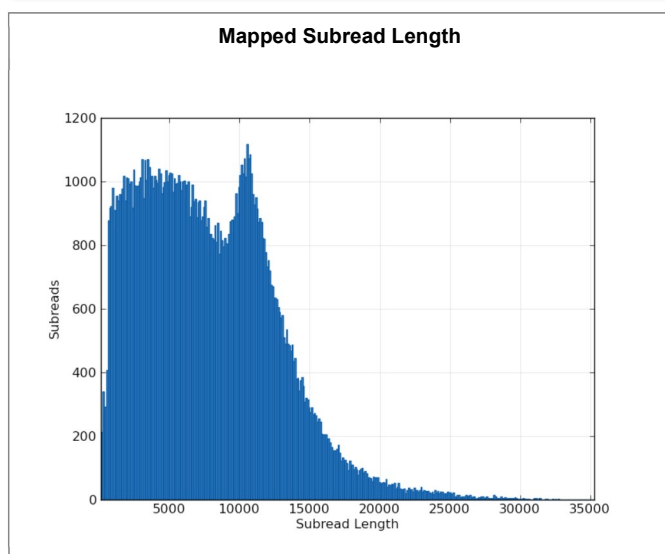
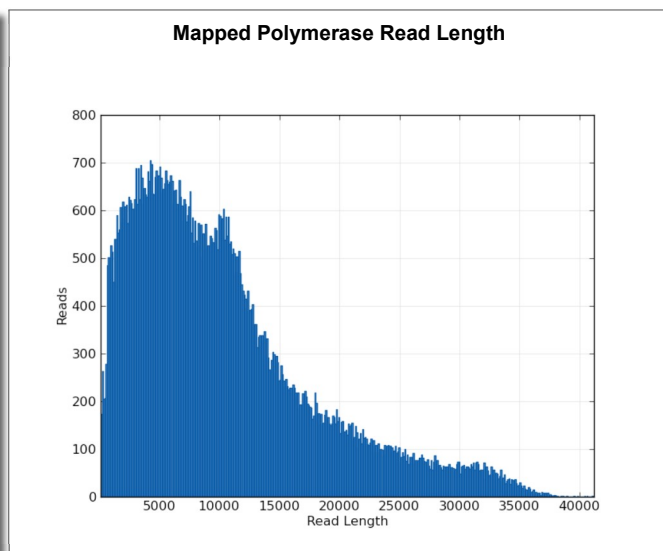
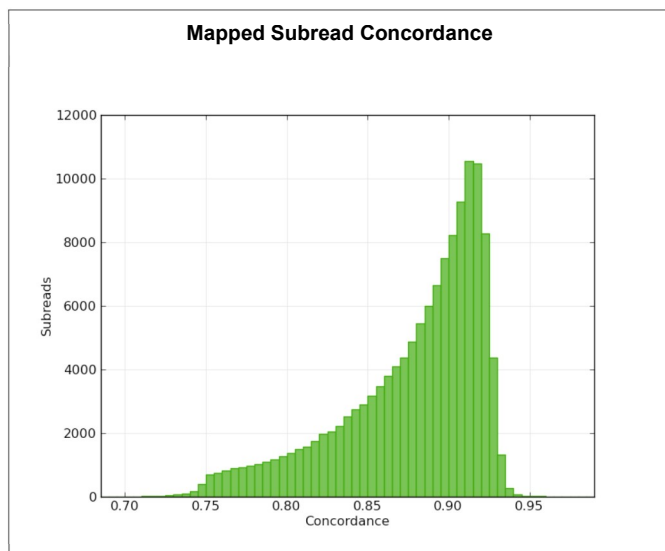
Mapped Subread Length N50 (bp) 10,467 Mapped Polymerase Read Length 95% (bp) 26,690
Mapped Subread Length Mean (bp) 7,662 Mapped Polymerase Read Length Max (bp) 41,092

Mapping Stats Summary

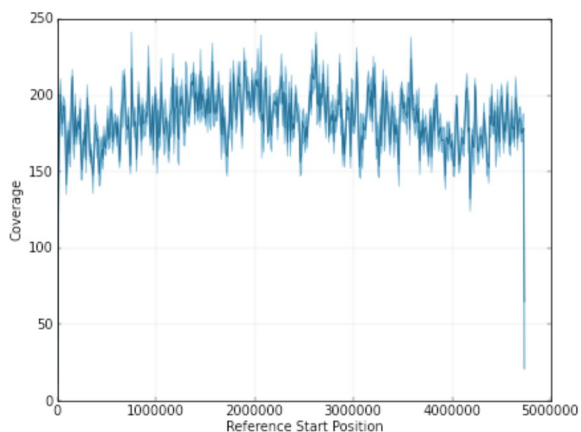
Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	100,376	10,270	14308	133,452	1022558450	7,662	0.872
m160814_150917_42237_c101088372550000001823265803091781_s1_p0	100,376	10,270	14308	133,452	1022558450	7,662	0.872

Coverage

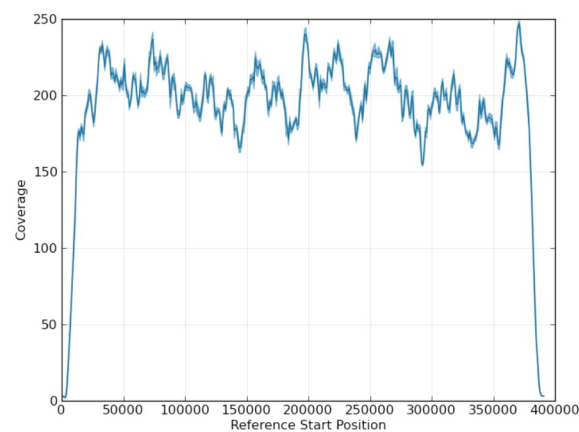
Mean Coverage 182.4
Missing Bases (%) 0.0



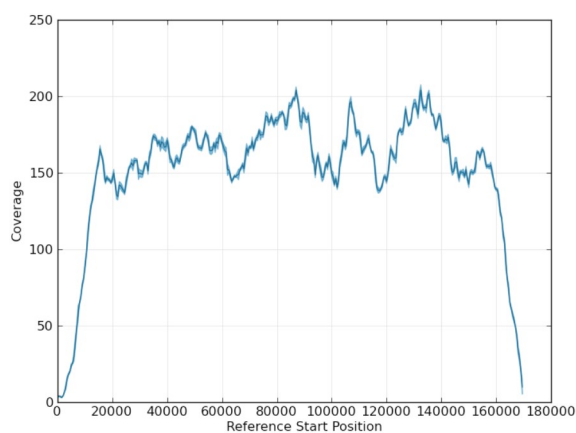
Coverage Across Reference



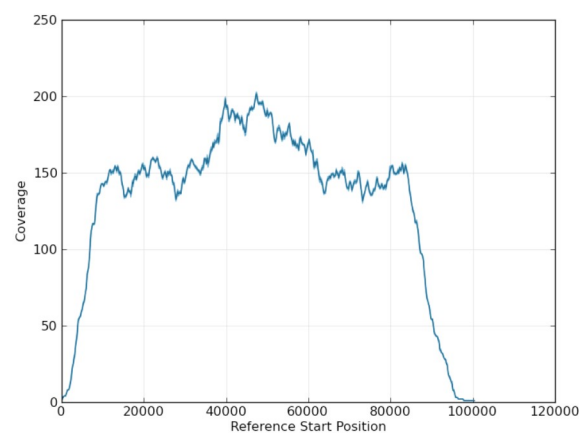
Observed depth of coverage across scf7180000000008 (window size = 10004bp).



Observed depth of coverage across scf7180000000009 (window size = 1000bp).

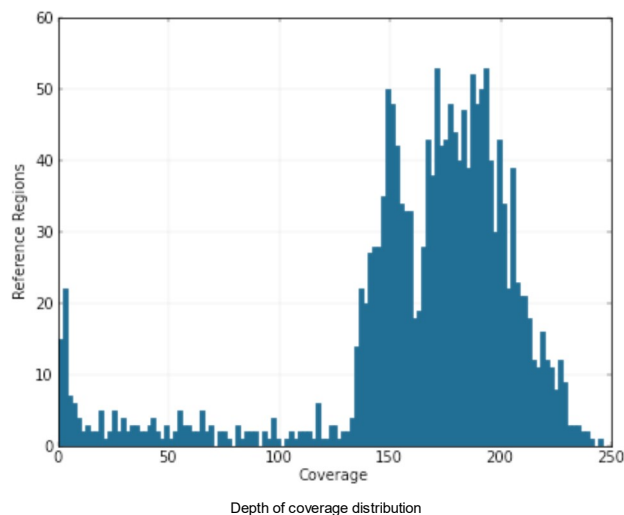


Observed depth of coverage across scf7180000000010 (window size = 501bp).



Observed depth of coverage across scf7180000000011 (window size = 200bp).

Depth Of Coverage

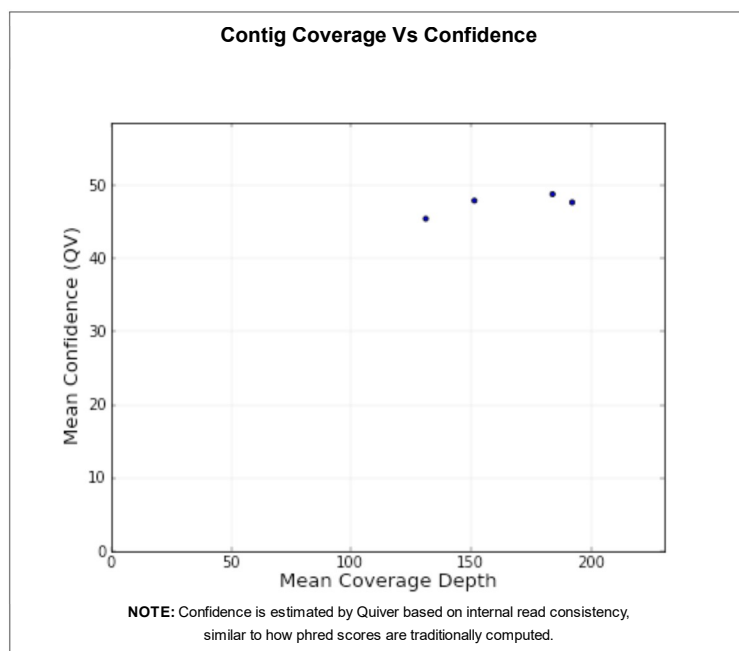


Pre-Assembler Report

Polymerase Read Bases	1,252,753,682	Length Cutoff	20,000
Seed Bases	108,986,412	Pre-Assembled bases	69,464,615
Pre-Assembled Yield	.637	Pre-Assembled Reads	5,988
Pre-Assembled Reads Length	11,600	Pre-Assembled N50	19,662

Polished Assembly

Polished Contigs	4	Max Contig Length	4,742,396
N50 Contig Length	4,742,396	Sum of Contig Lengths	5,405,917



Top Corrections

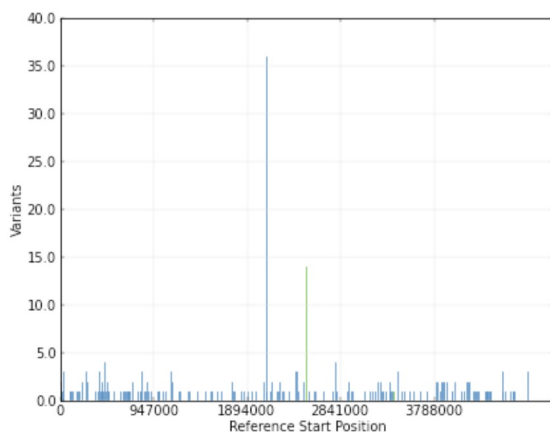
Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000008	1,132,785	1132785_1132786insC	INS	100	53	haploid
scf7180000000008	4,232,299	4232299_4232300insG	INS	100	53	haploid
scf7180000000008	1,291,892	1291892_1291893insG	INS	100	52	haploid
scf7180000000008	3,712,221	3712221_3712222insG	INS	100	52	haploid
scf7180000000009	386,396	386396_386397insT	INS	20	52	haploid
scf7180000000011	89,558	89558_89559insG	INS	62	52	haploid
scf7180000000008	32,052	32052_32053insC	INS	100	51	haploid
scf7180000000008	166,584	166584_166585insG	INS	100	51	haploid
scf7180000000008	418,769	418769_418770insC	INS	100	51	haploid
scf7180000000008	473,868	473868_473869insC	INS	100	51	haploid
scf7180000000008	879,279	879279_879280insC	INS	100	51	haploid
scf7180000000008	2,087,644	2087644_2087645insG	INS	100	51	haploid
scf7180000000008	2,191,736	2191736_2191737insG	INS	100	51	haploid
scf7180000000008	3,212,507	3212507_3212508insC	INS	100	51	haploid
scf7180000000008	3,248,353	3248353_3248354insC	INS	100	51	haploid
scf7180000000008	3,257,485	3257485_3257486insG	INS	100	51	haploid
scf7180000000008	3,993,479	3993479_3993480insG	INS	100	51	haploid
scf7180000000008	4,111,367	4111367_4111368insC	INS	100	51	haploid
scf7180000000008	4,303,910	4303910_4303911insG	INS	100	51	haploid
scf7180000000008	4,332,256	4332256_4332257insC	INS	100	51	haploid
scf7180000000008	4,361,721	4361721_4361722insC	INS	100	51	haploid
scf7180000000010	17,005	17005_17006insG	INS	100	51	haploid
scf7180000000010	31,563	31563_31564insG	INS	100	51	haploid
scf7180000000010	33,722	33722_33723insG	INS	100	51	haploid
scf7180000000010	125,027	125027_125028insG	INS	100	51	haploid
scf7180000000011	73,386	73386_73387insG	INS	100	51	haploid
scf7180000000011	90,468	90468_90469insT	INS	50	51	haploid
scf7180000000011	92,168	92168_92169insC	INS	32	51	haploid
scf7180000000011	94,038	94038_94039insCCGATC	INS	20	51	haploid
scf7180000000008	3,185	3185_3186insC	INS	13	50	haploid
scf7180000000008	36,800	36800_36801insG	INS	100	50	haploid
scf7180000000008	192,323	192323_192324insG	INS	100	50	haploid
scf7180000000008	254,159	254159_254160insG	INS	100	50	haploid
scf7180000000008	352,831	352831_352832insG	INS	100	50	haploid
scf7180000000008	395,247	395247_395248insC	INS	100	50	haploid
scf7180000000008	407,815	407815_407816insC	INS	100	50	haploid
scf7180000000008	419,920	419920_419921insC	INS	100	50	haploid
scf7180000000008	430,208	430208_430209insC	INS	100	50	haploid
scf7180000000008	440,266	440266_440267insG	INS	100	50	haploid
scf7180000000008	473,111	473111_473112insC	INS	100	50	haploid
scf7180000000008	497,032	497032_497033insC	INS	100	50	haploid
scf7180000000008	610,197	610197_610198insC	INS	100	50	haploid
scf7180000000008	697,653	697653_697654insG	INS	100	50	haploid
scf7180000000008	782,706	782706_782707insC	INS	100	50	haploid
scf7180000000008	818,779	818779_818780insC	INS	100	50	haploid
scf7180000000008	825,263	825263_825264insG	INS	100	50	haploid
scf7180000000008	829,110	829110_829111insC	INS	100	50	haploid
scf7180000000008	857,683	857683_857684insC	INS	100	50	haploid
scf7180000000008	911,803	911803_911804insC	INS	100	50	haploid
scf7180000000008	997,490	997490_997491insC	INS	100	50	haploid
scf7180000000008	1,068,705	1068705_1068706insC	INS	100	50	haploid
scf7180000000008	1,122,317	1122317_1122318insG	INS	100	50	haploid
scf7180000000008	1,125,473	1125473_1125474insC	INS	100	50	haploid
scf7180000000008	1,125,657	1125657_1125658insC	INS	100	50	haploid
scf7180000000008	1,463,727	1463727_1463728insC	INS	100	50	haploid
scf7180000000008	1,527,810	1527810_1527811insG	INS	100	50	haploid
scf7180000000008	1,757,267	1757267_1757268insC	INS	100	50	haploid
scf7180000000008	1,868,888	1868888_1868889insG	INS	100	50	haploid
scf7180000000008	1,988,628	1988628_1988629insC	INS	100	50	haploid
scf7180000000008	2,050,537	2050537_2050538insG	INS	100	50	haploid
scf7180000000008	2,055,978	2055978_2055979insG	INS	100	50	haploid
scf7180000000008	2,093,122	2093122_2093123insGACCCGACCGACGGTACG	INS	100	50	haploid
scf7180000000008	2,129,508	2129508_2129509insC	INS	100	50	haploid
scf7180000000008	2,221,557	2221557_2221558insC	INS	100	50	haploid
scf7180000000008	2,391,557	2391557_2391558insG	INS	100	50	haploid
scf7180000000008	2,462,993	2462993_2462994insG	INS	100	50	haploid

Corrections

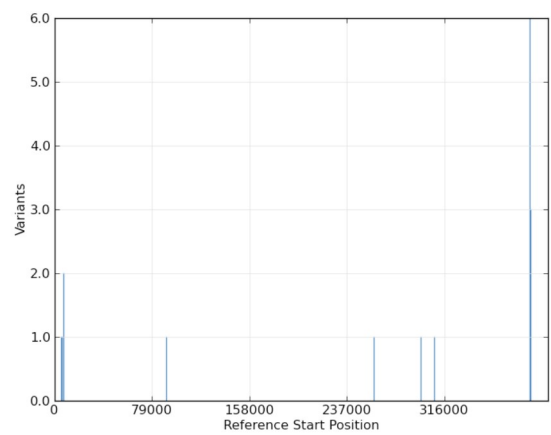
Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000008	4,742,171	100.0%	99.9954%	183.81
scf7180000000009	392,188	100.0%	99.9967%	192.01
scf7180000000010	170,470	100.0%	99.9830%	151.28
scf7180000000011	100,735	99.95%	99.9781%	131.02

Corrections Across Reference

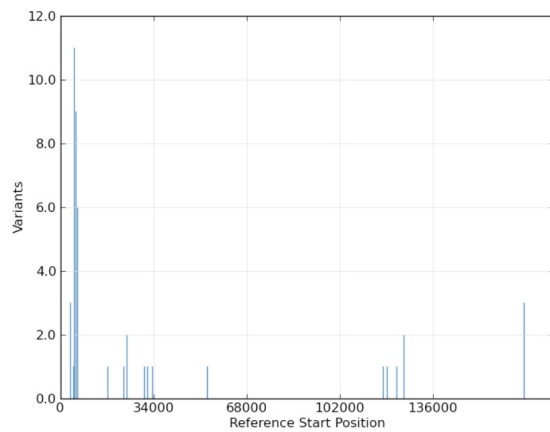
■ Insertions
■ Deletions
■ Substitutions



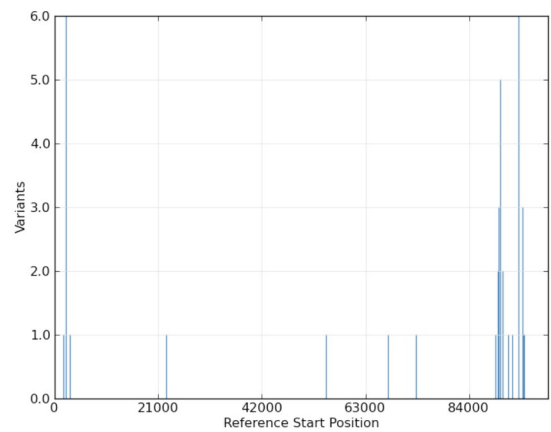
Observed variants across scf7180000000008.



Observed variants across scf7180000000009.



Observed variants across scf7180000000010.



Observed variants across scf7180000000011.