

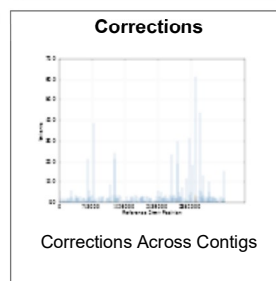
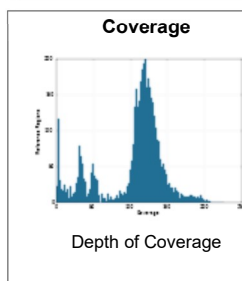
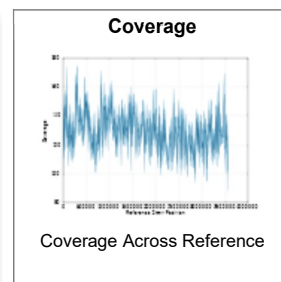
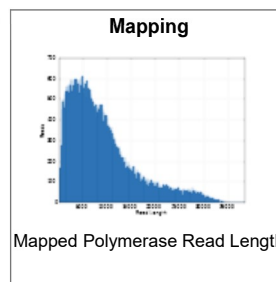
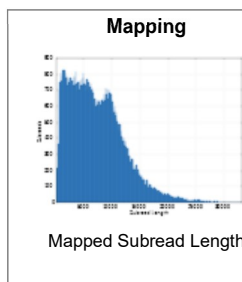
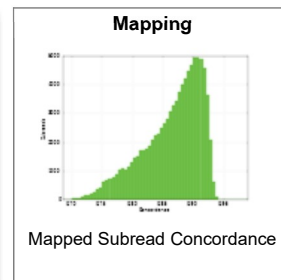
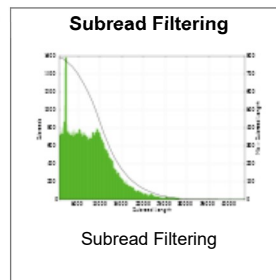
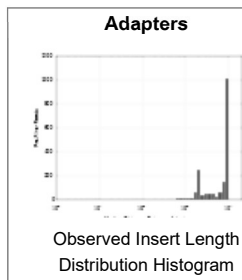
# Reports for Job pb\_359\_1-20000



SMRT Cells: 1 Movies: 1

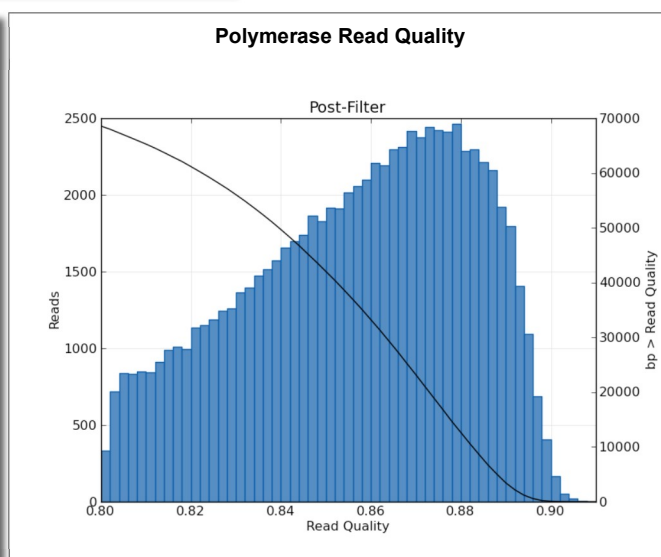
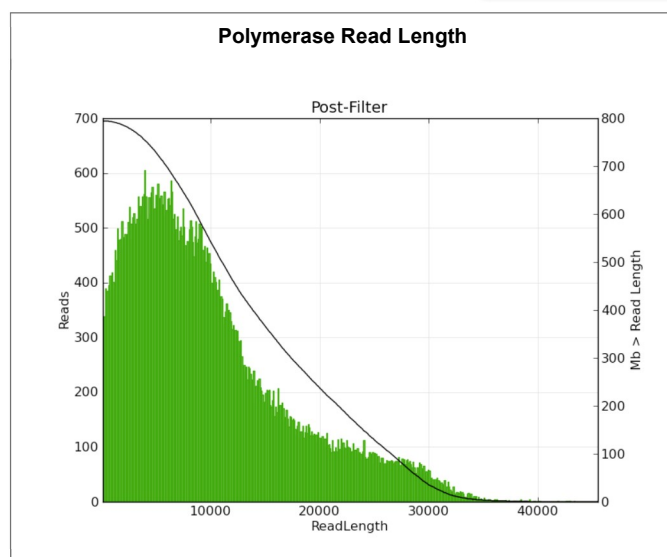
## Overview

Job Metric	Value
Polished Contigs	9
Adapter Dimers (0-10bp)	0.01%
Short Inserts (11-100bp)	0.0%
Number of Bases	798,420,648
Number of Reads	80,471
N50 Read Length	14,006
Mean Read Length	9,921
Mean Read Score	0.86
Mapped Reads	75,008
Mapped Read Length of Insert	7,011
Average Reference Length	583,727
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.98%
Average Reference Coverage	125.21



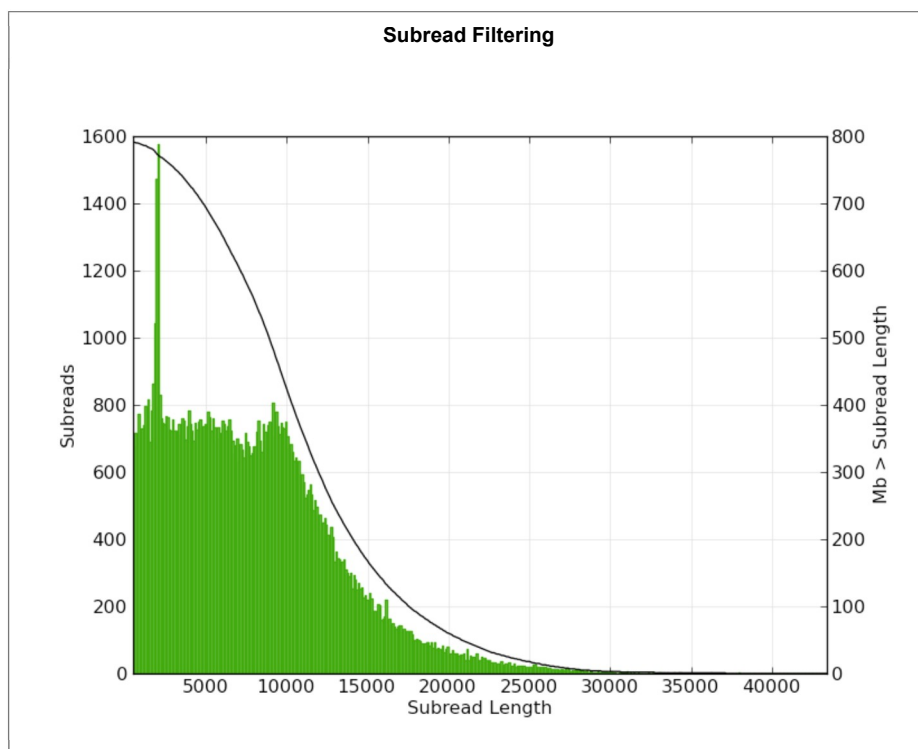
## Filtering

Filtering		
Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	909729460	798420648
Polymerase Reads	150292	80471
Polymerase Read N50	13545	14006
Polymerase Read Length	6053	9921
Polymerase Read Quality	0.524	0.855



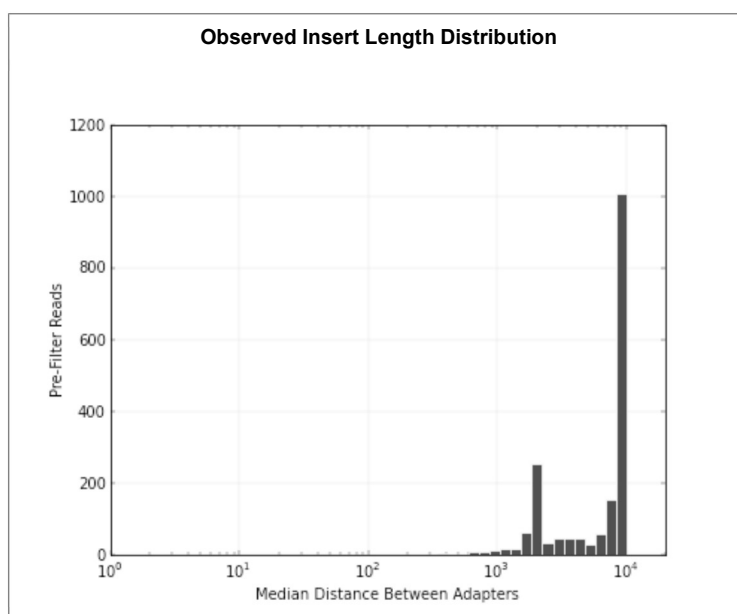
## Subread Filtering

Mean Subread length	7,815	N50	10,495
Total Number of Bases	796,566,107	Number of Reads	101,915



#### 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
m160816_143842_42203_c101086032550000001823265803091731	150,292	30.23%	59.83%	9.94%

#### Mapping

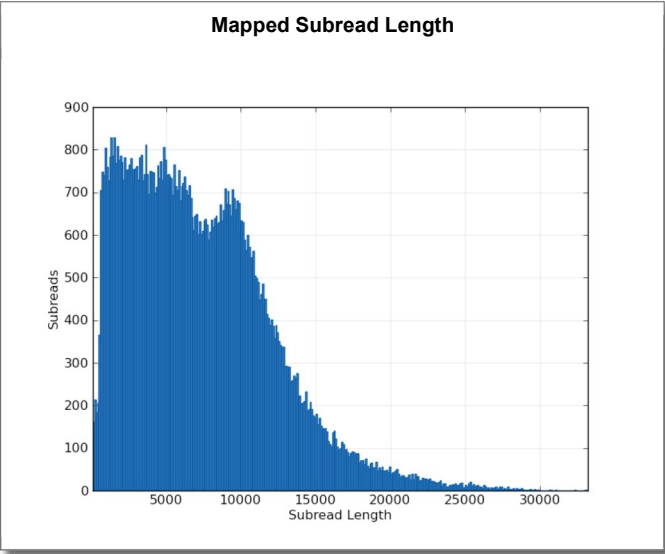
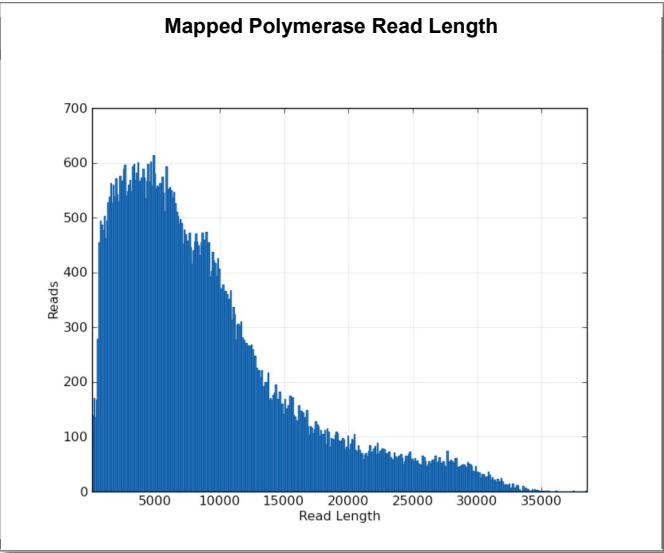
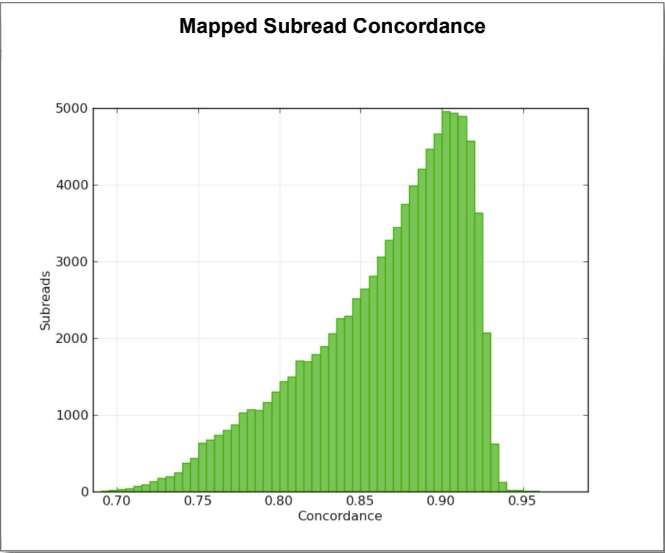
Mapped Subread Length N50 (bp) 9,862 Mapped Polymerase Read Length 95% (bp) 24,250  
Mapped Subread Length Mean (bp) 7,214 Mapped Polymerase Read Length Max (bp) 38,368

#### Mapping Stats Summary

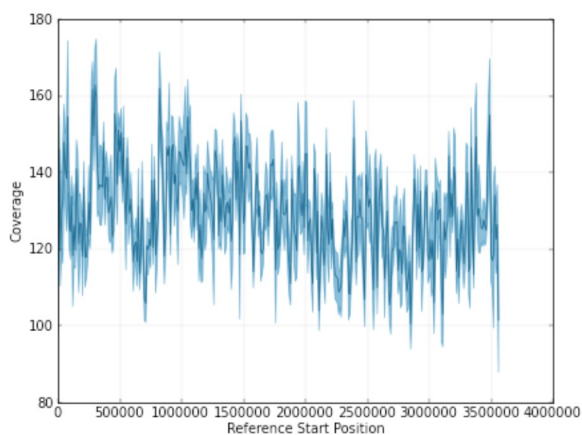
Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	75,008	8,961	12,597	92,619	668,124,656	7,214	0.860
m160816_143842_42203_c101086032550000001823265803091731_s1_p0	75,008	8,961	12,597	92,619	668,124,656	7,214	0.860

#### Coverage

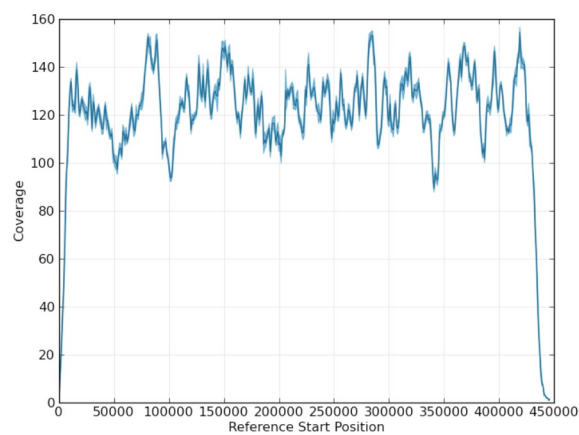
Mean Coverage 125.21  
Missing Bases (%) 0.0



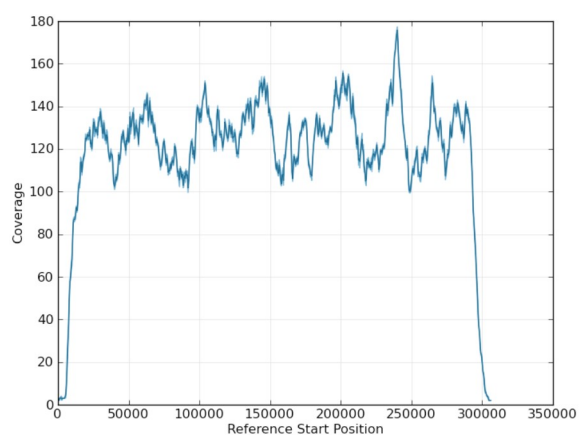
### Coverage Across Reference



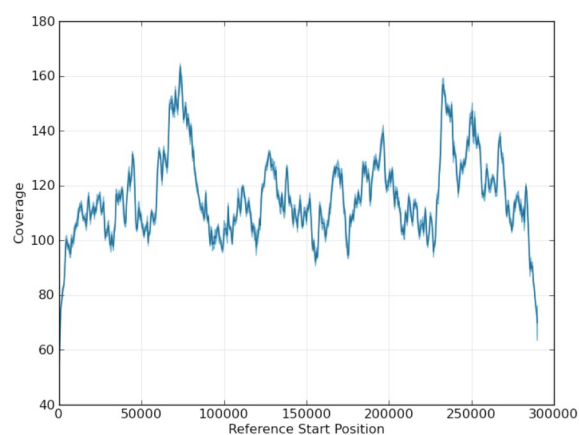
Observed depth of coverage across scf7180000000018 (window size = 10002bp).



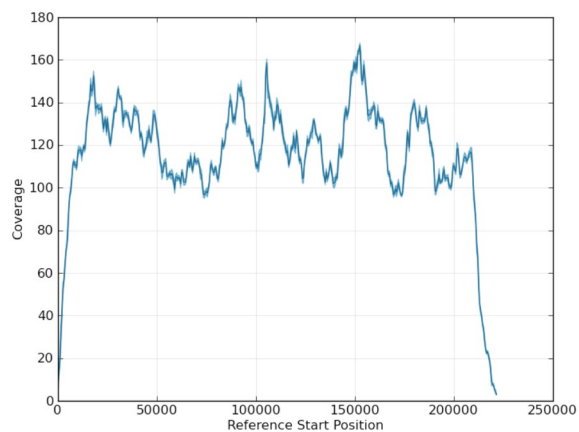
Observed depth of coverage across scf7180000000019 (window size = 1001bp).



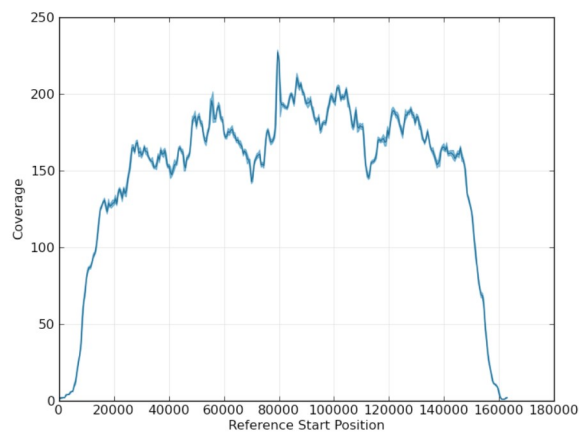
Observed depth of coverage across scf7180000000021 (window size = 500bp).



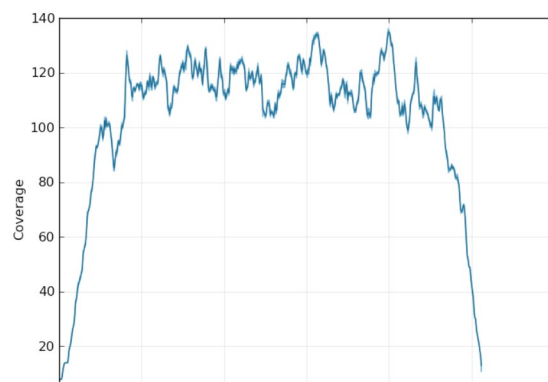
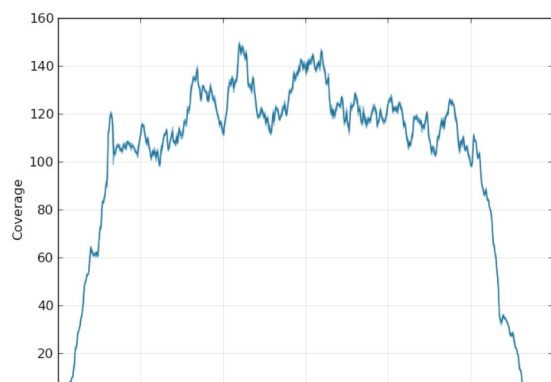
Observed depth of coverage across scf7180000000020 (window size = 500bp).

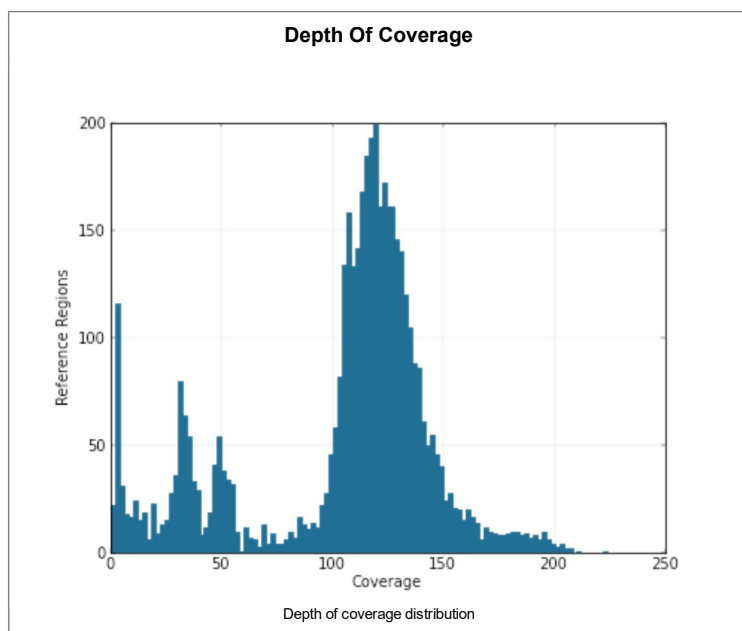


Observed depth of coverage across scf7180000000022 (window size = 500bp).



Observed depth of coverage across scf7180000000023 (window size = 501bp).



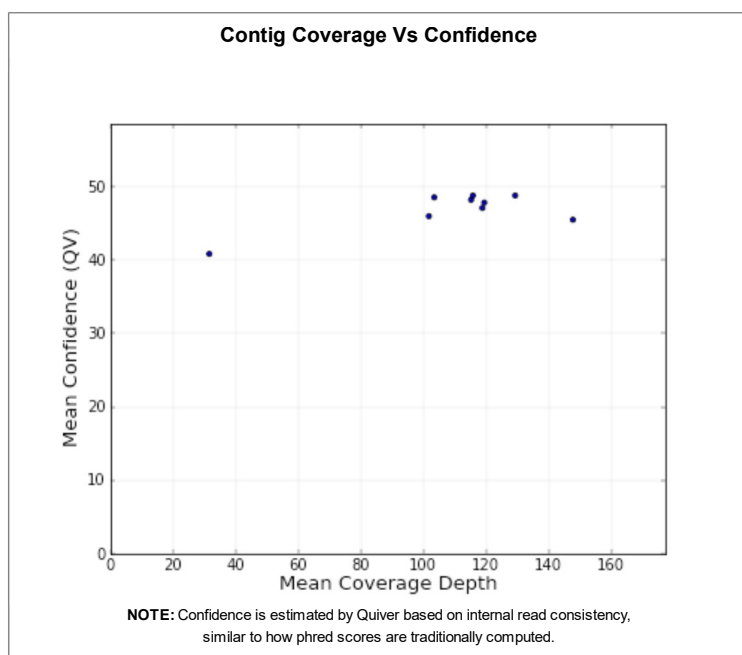


#### Pre-Assembler Report

Polymerase Read Bases	796,566,107	Length Cutoff	20,000
Seed Bases	61,575,526	Pre-Assembled bases	42,280,716
Pre-Assembled Yield	.687	Pre-Assembled Reads	3,334
Pre-Assembled Reads Length	12,681	Pre-Assembled N50	20,613

#### Polished Assembly

Polished Contigs	9	Max Contig Length	3,571,750
N50 Contig Length	3,571,750	Sum of Contig Lengths	5,254,996



#### Top Corrections

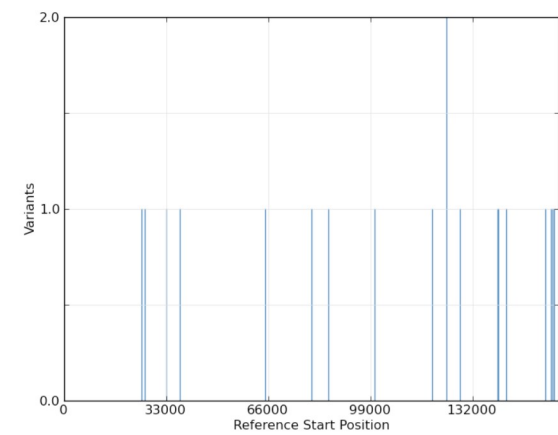
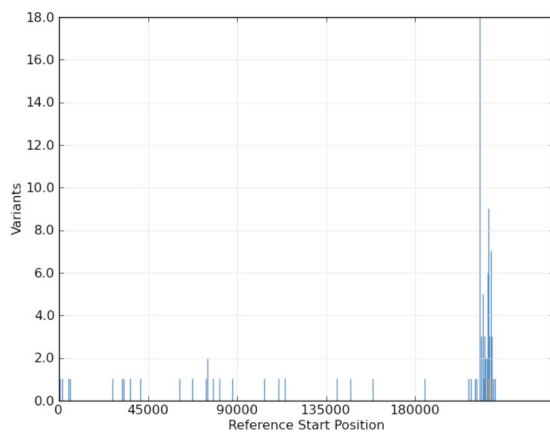
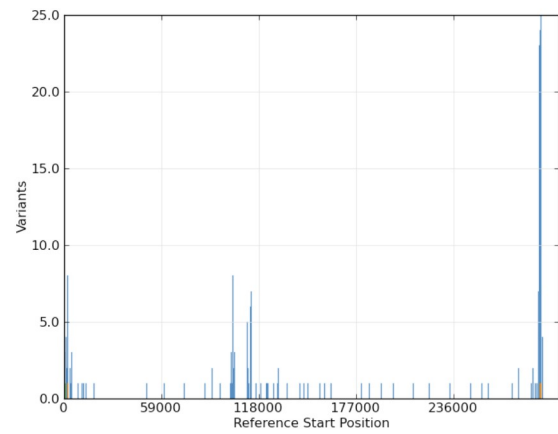
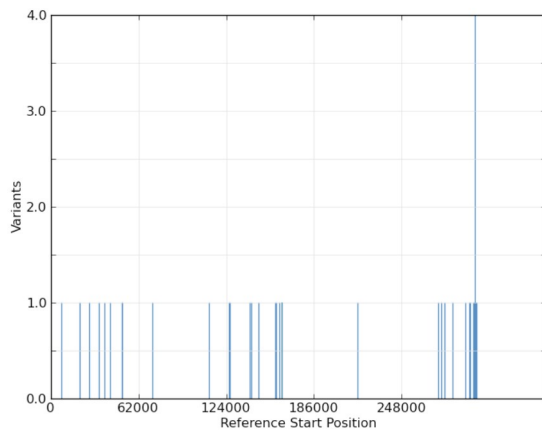
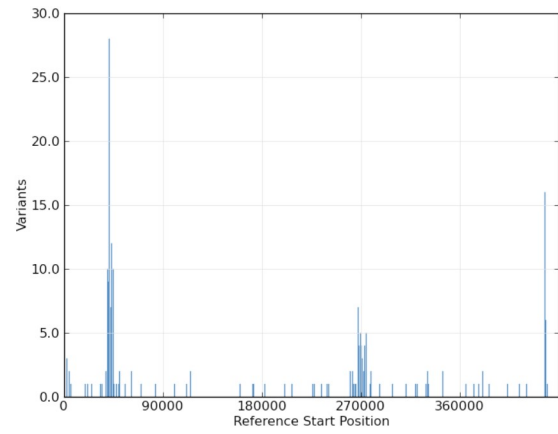
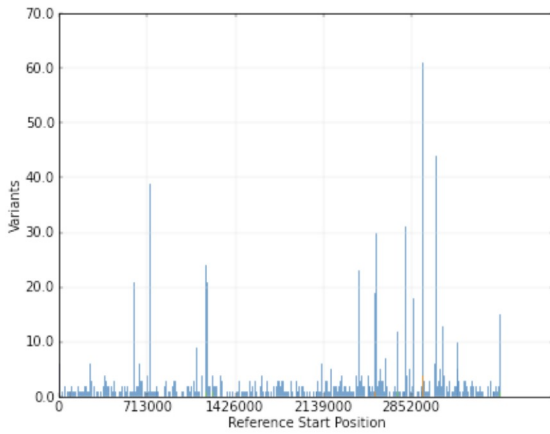
Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000018	251,194	251194_251195insC	INS	100	53	haploid
scf7180000000018	914,637	914637_914638insC	INS	100	53	haploid
scf7180000000018	3,228,706	3228706_3228707insG	INS	100	53	haploid
scf7180000000018	3,291,020	3291020_3291021insC	INS	100	53	haploid
scf7180000000020	275,839	275839_275840insG	INS	100	53	haploid
scf7180000000021	299,805	299805_299806insC	INS	23	53	haploid
scf7180000000018	180,611	180611_180612insG	INS	100	52	haploid
scf7180000000018	1,117,941	1117941_1117942insG	INS	100	52	haploid
scf7180000000018	1,186,960	1186960_1186961insCGC	INS	100	52	haploid
scf7180000000018	1,190,305	1190305_1190306insT	INS	100	52	haploid
scf7180000000018	1,195,460	1195460_1195461insG	INS	100	52	haploid
scf7180000000018	1,264,520	1264520_1264521insC	INS	100	52	haploid
scf7180000000018	2,236,713	2236713_2236714insC	INS	100	52	haploid
scf7180000000018	2,557,464	2557464_2557465insC	INS	95	52	haploid
scf7180000000018	2,713,560	2713560_2713561insG	INS	100	52	haploid
scf7180000000018	2,859,477	2859477_2859478insC	INS	93	52	haploid
scf7180000000018	2,945,932	2945932A>G	SUB	97	52	haploid
scf7180000000018	2,958,632	2958632_2958633insC	INS	100	52	haploid
scf7180000000018	2,990,945	2990945_2990946insC	INS	100	52	haploid
scf7180000000018	3,045,399	3045399_3045400insGCTG	INS	98	52	haploid
scf7180000000019	41,719	41719_41720insC	INS	100	52	haploid
scf7180000000019	269,977	269977_269978insA	INS	100	52	haploid
scf7180000000019	270,571	270571_270572insCGC	INS	100	52	haploid
scf7180000000020	3,575	3575_3576insC	INS	86	52	haploid
scf7180000000020	4,486	4486_4487insC	INS	98	52	haploid
scf7180000000020	123,444	123444_123445insG	INS	100	52	haploid
scf7180000000020	185,422	185422_185423insC	INS	100	52	haploid
scf7180000000022	212,645	212645_212646insC	INS	56	52	haploid
scf7180000000018	175	175_176insC	INS	74	51	haploid
scf7180000000018	9,993	9993_9994insC	INS	100	51	haploid
scf7180000000018	106,625	106625_106626insC	INS	100	51	haploid
scf7180000000018	108,476	108476_108477insC	INS	100	51	haploid
scf7180000000018	259,545	259545_259546insC	INS	100	51	haploid
scf7180000000018	350,975	350975_350976insG	INS	100	51	haploid
scf7180000000018	450,204	450204_450205insG	INS	100	51	haploid
scf7180000000018	537,186	537186_537187insA	INS	100	51	haploid
scf7180000000018	583,198	583198_583199insG	INS	100	51	haploid
scf7180000000018	606,495	606495_606496insA	INS	100	51	haploid
scf7180000000018	657,067	657067_657068insAC	INS	100	51	haploid
scf7180000000018	736,015	736015_736016insGCC	INS	100	51	haploid
scf7180000000018	750,679	750679_750680insG	INS	100	51	haploid
scf7180000000018	1,039,070	1039070_1039071insG	INS	100	51	haploid
scf7180000000018	1,051,242	1051242_1051243insG	INS	100	51	haploid
scf7180000000018	1,116,638	1116638_1116639insC	INS	100	51	haploid
scf7180000000018	1,187,447	1187447_1187448insC	INS	100	51	haploid
scf7180000000018	1,188,460	1188460_1188461insC	INS	100	51	haploid
scf7180000000018	1,189,066	1189066_1189067insG	INS	100	51	haploid
scf7180000000018	1,193,003	1193003_1193004insG	INS	100	51	haploid
scf7180000000018	1,202,125	1202125_1202126insC	INS	100	51	haploid
scf7180000000018	1,310,488	1310488_1310489insG	INS	100	51	haploid
scf7180000000018	1,440,686	1440686_1440687insG	INS	100	51	haploid
scf7180000000018	1,517,116	1517116_1517117insC	INS	100	51	haploid
scf7180000000018	1,543,597	1543597_1543598insC	INS	100	51	haploid
scf7180000000018	1,583,925	1583925_1583926insG	INS	100	51	haploid
scf7180000000018	1,596,738	1596738_1596739insC	INS	100	51	haploid
scf7180000000018	1,653,202	1653202_1653203insC	INS	100	51	haploid
scf7180000000018	1,735,372	1735372_1735373insG	INS	100	51	haploid
scf7180000000018	1,802,570	1802570_1802571insC	INS	100	51	haploid
scf7180000000018	1,910,419	1910419_1910420insG	INS	100	51	haploid
scf7180000000018	1,966,733	1966733_1966734insG	INS	100	51	haploid
scf7180000000018	2,121,324	2121324_2121325insC	INS	100	51	haploid
scf7180000000018	2,175,644	2175644_2175645insG	INS	100	51	haploid
scf7180000000018	2,187,976	2187976_2187977insG	INS	100	51	haploid
scf7180000000018	2,232,776	2232776_2232777insC	INS	100	51	haploid
scf7180000000018	2,244,751	2244751_2244752insC	INS	100	51	haploid
scf7180000000018	2,267,390	2267390_2267391insG	INS	100	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000018	3,570,902	100.0%	99.9802%	129.15
scf7180000000019	447,811	100.0%	99.9665%	119.27
scf7180000000021	306,631	100.0%	99.9886%	118.67
scf7180000000020	290,723	100.0%	99.9584%	115.65
scf7180000000022	222,381	100.0%	99.9694%	115.06
scf7180000000023	163,969	99.99%	99.9884%	147.58
scf7180000000024	116,206	99.95%	99.9923%	101.59
scf7180000000025	102,744	100.0%	99.9737%	103.31
scf7180000000026	32,179	100.0%	99.8633%	31.49

### Corrections Across Reference

- Insertions
- Deletions
- Substitutions





---

Generated by SMRT® Portal. Mon Aug 29 09:16:14 CEST 2016  
For Research Use Only. Not for use in diagnostic procedures.