

# Reports for Job pb\_359\_5-25000

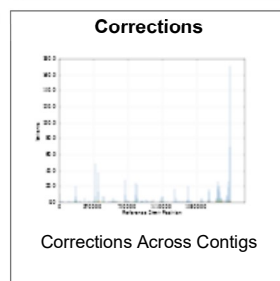
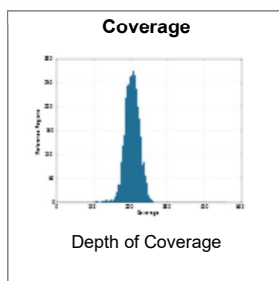
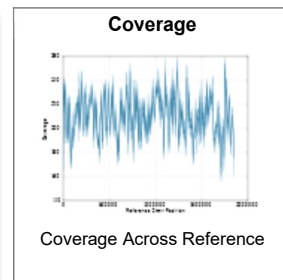
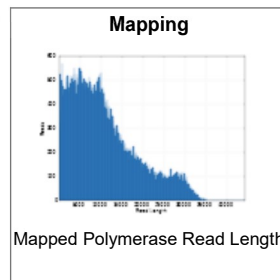
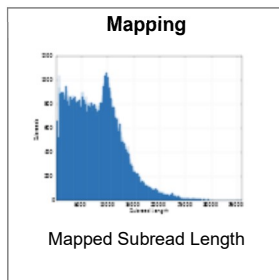
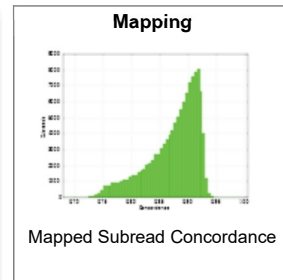
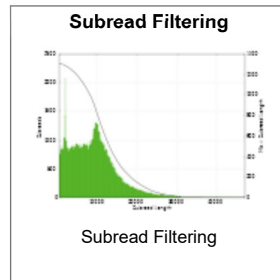
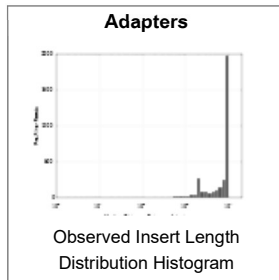


SMRT Cells: 1 Movies: 1

## Overview

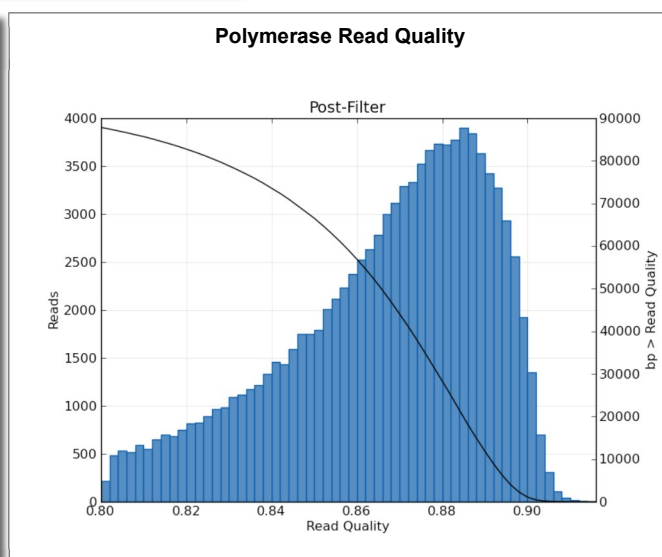
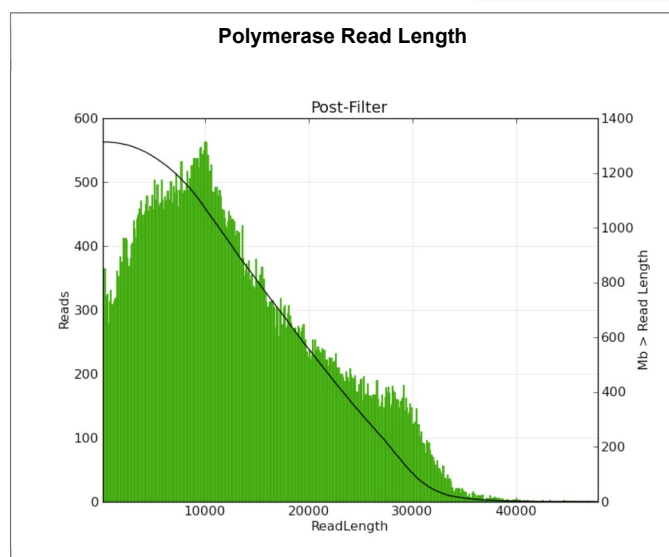
### Job Metric

	Value
Polished Contigs	7
Adapter Dimers (0-10bp)	0.01%
Short Inserts (11-100bp)	0.01%
Number of Bases	1,318,128,196
Number of Reads	101,723
N50 Read Length	18,054
Mean Read Length	12,958
Mean Read Score	0.86
Mapped Reads	87,241
Mapped Read Length of Insert	7,490
Average Reference Length	624,193
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.96%
Average Reference Coverage	206.08



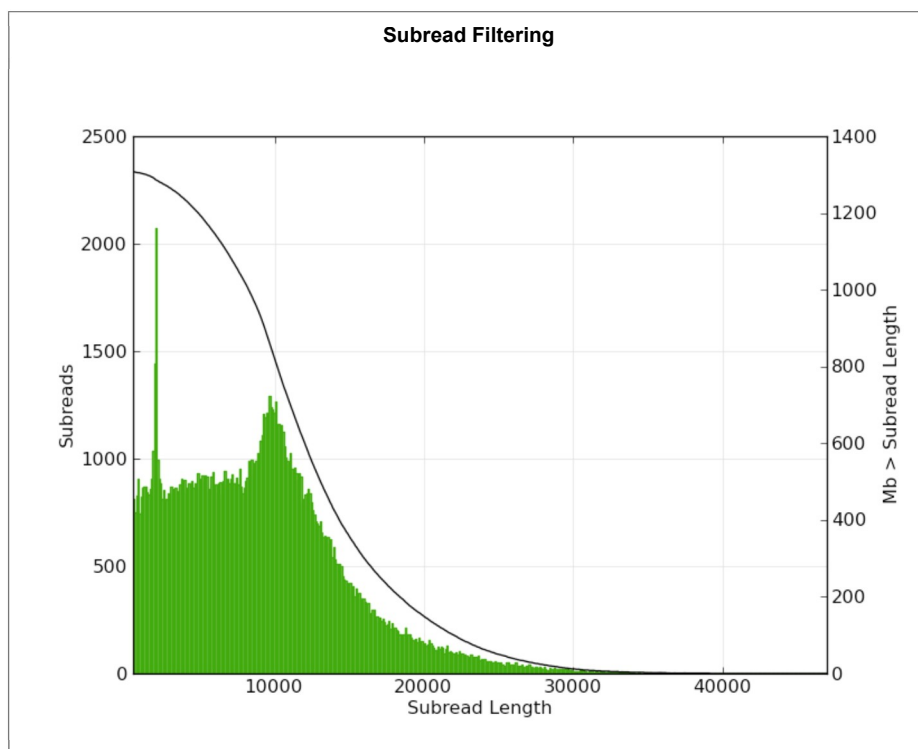
## Filtering

Filtering		
Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	1424795029	1318128196
Polymerase Reads	150292	101723
Polymerase Read N50	17725	18054
Polymerase Read Length	9480	12958
Polymerase Read Quality	0.63	0.865



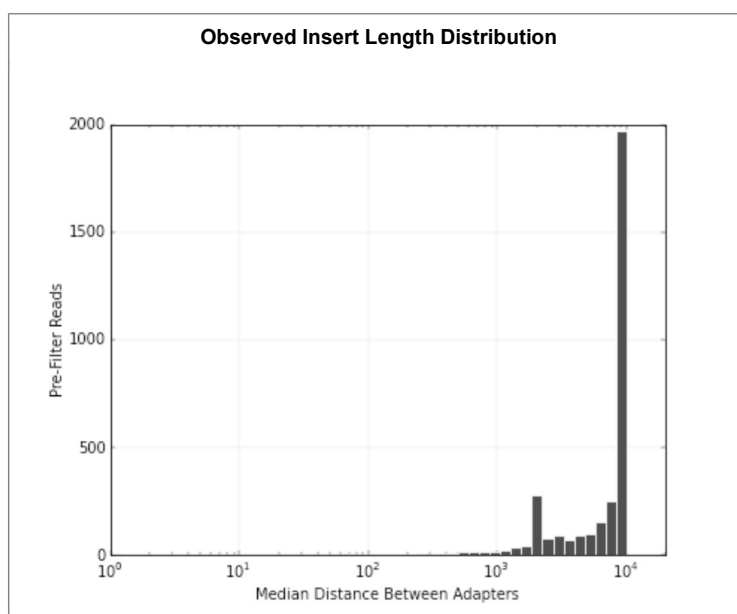
## Subread Filtering

Mean Subread length	8,964	N50	11,566
Total Number of Bases	1,314,793,812	Number of Reads	146,668



#### Adapters

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



#### Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160814_063117_42237_c101088342550000001823265803091717	150,292	21.64%	71.91%	6.45%

#### Mapping

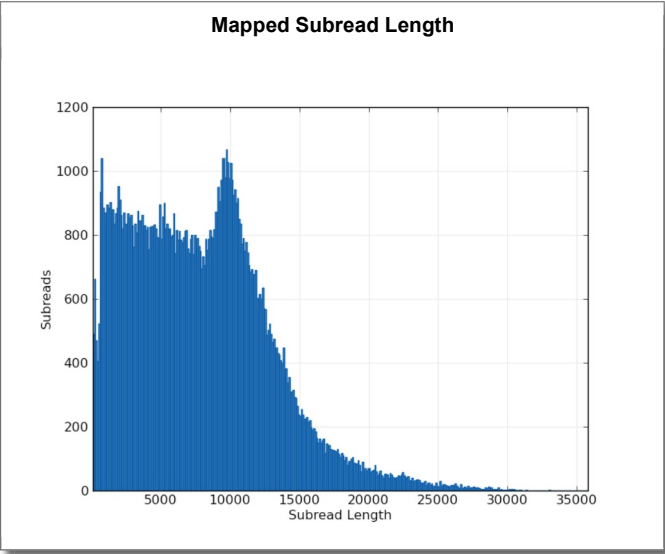
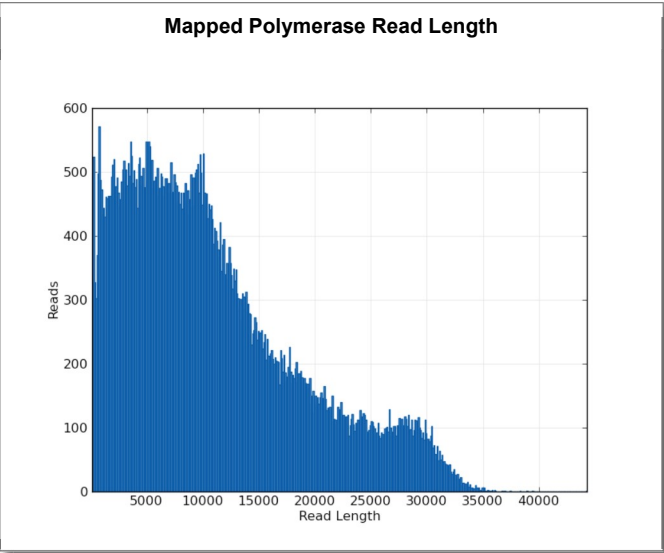
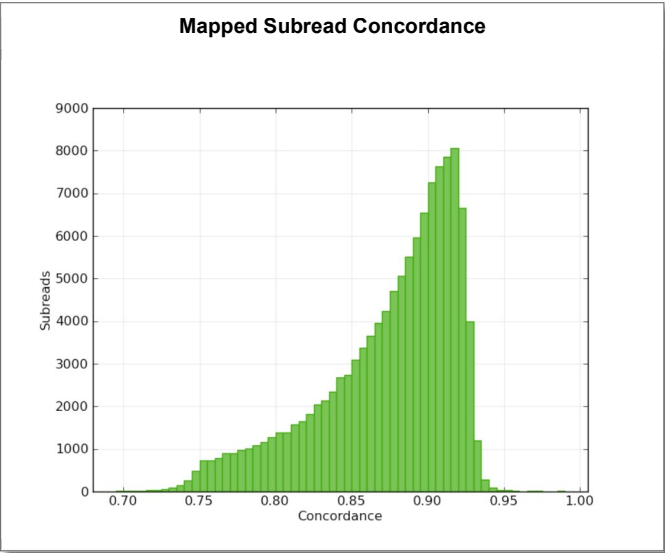
Mapped Subread Length N50 (bp) 10,457 Mapped Polymerase Read Length 95% (bp) 27,320  
Mapped Subread Length Mean (bp) 7,749 Mapped Polymerase Read Length Max (bp) 44,113

#### Mapping Stats Summary

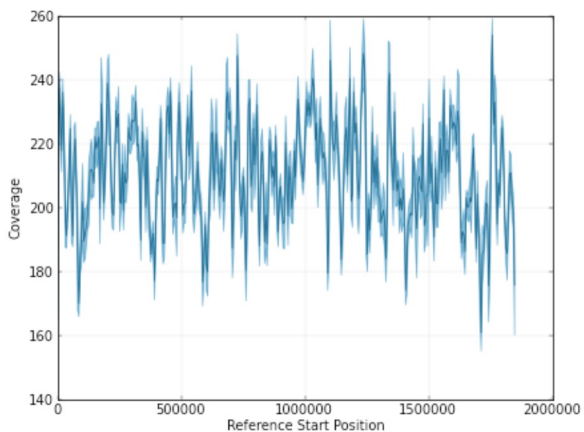
Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	87,241	10,773	15537	119,887	929036481	7,749	0.869
m160814_063117_42237_c101088342550000001823265803091717_s1_p0	87,241	10,773	15537	119,887	929036481	7,749	0.869

#### Coverage

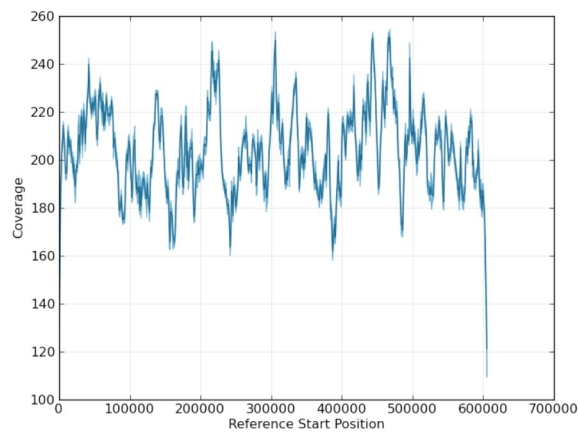
Mean Coverage 206.08  
Missing Bases (%) 0.0



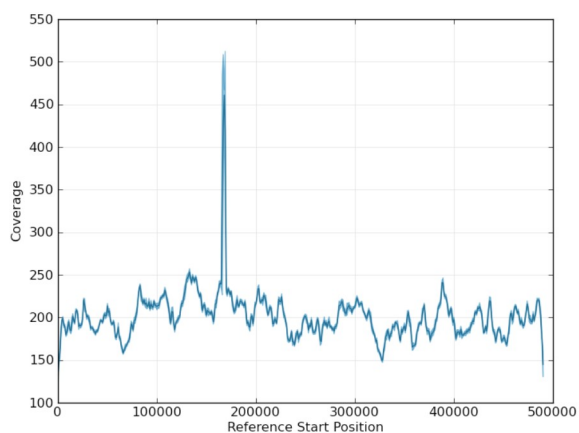
### Coverage Across Reference



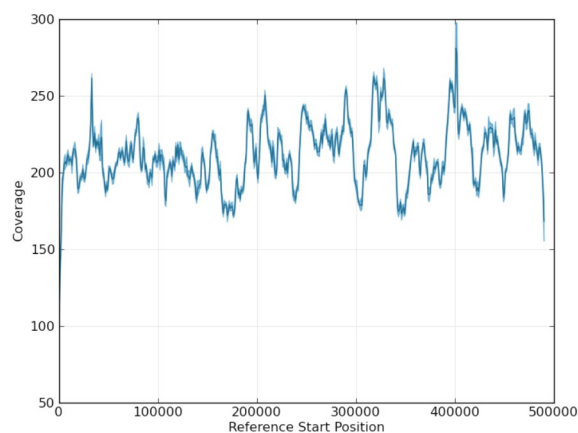
Observed depth of coverage across scf7180000000016 (window size = 5002bp).



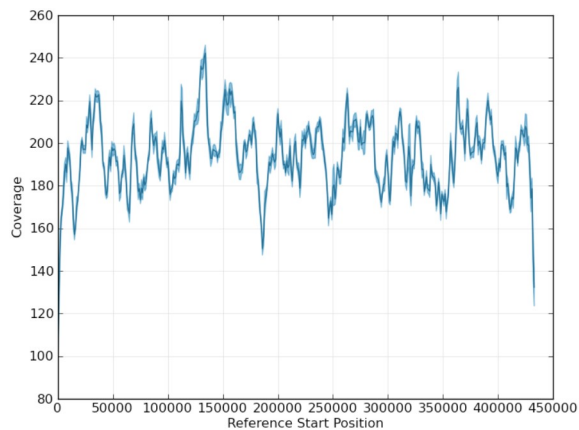
Observed depth of coverage across scf7180000000017 (window size = 1000bp).



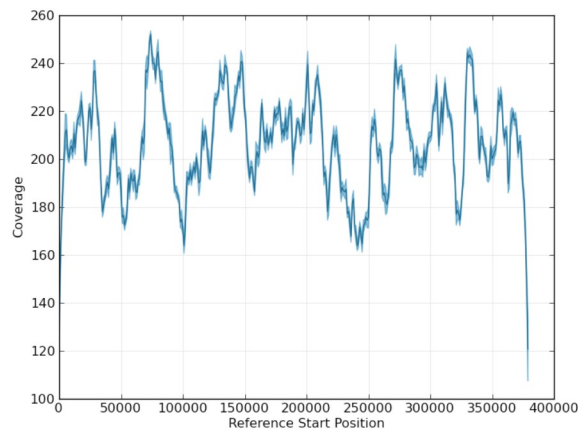
Observed depth of coverage across scf7180000000018 (window size = 1001bp).



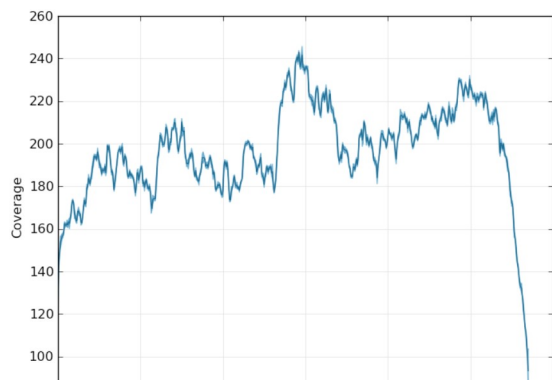
Observed depth of coverage across scf7180000000019 (window size = 1000bp).

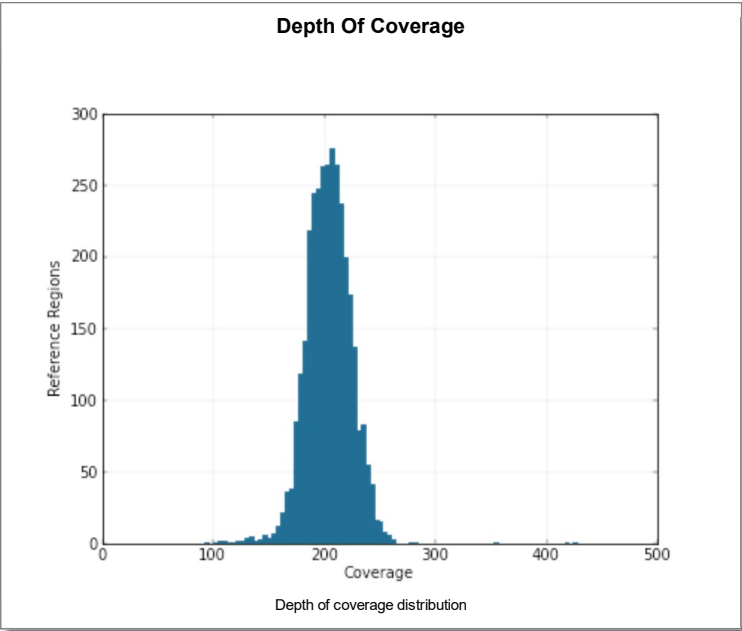


Observed depth of coverage across scf7180000000020 (window size = 1000bp).



Observed depth of coverage across scf7180000000021 (window size = 1001bp).



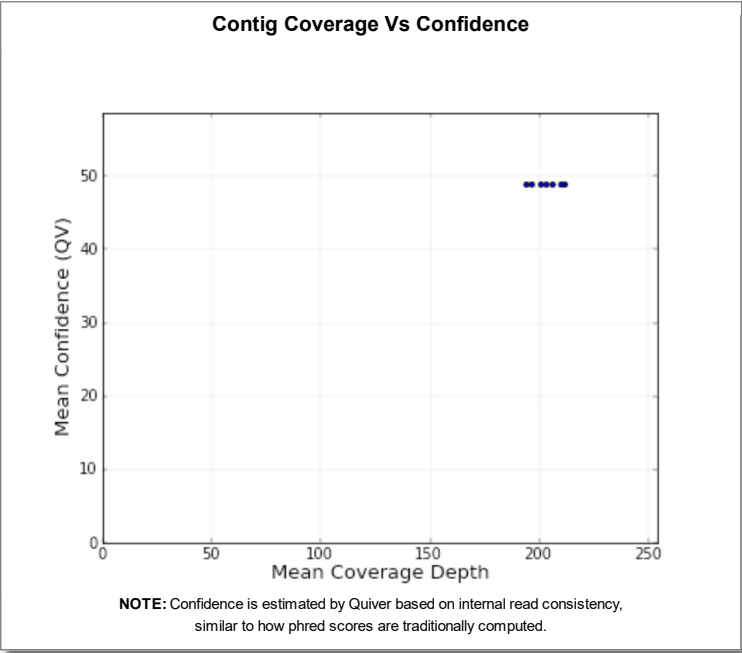


#### Pre-Assembler Report

Polymerase Read Bases	1,314,793,812	Length Cutoff	25,000
Seed Bases	51,293,422	Pre-Assembled bases	24,007,172
Pre-Assembled Yield	.468	Pre-Assembled Reads	2,249
Pre-Assembled Reads Length	10,674	Pre-Assembled N50	24,218

#### Polished Assembly

Polished Contigs	7	Max Contig Length	1,851,986
N50 Contig Length	606,868	Sum of Contig Lengths	4,371,673



#### Top Corrections

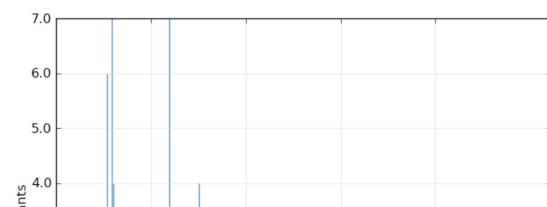
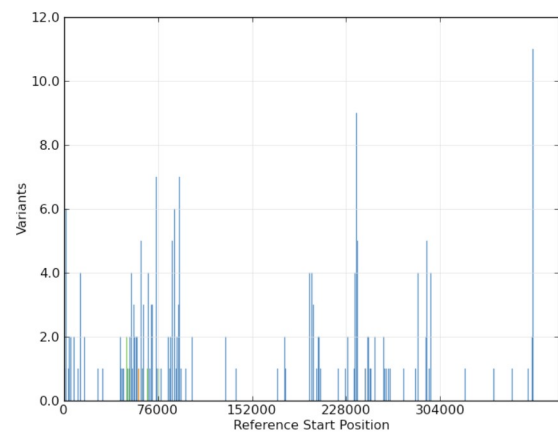
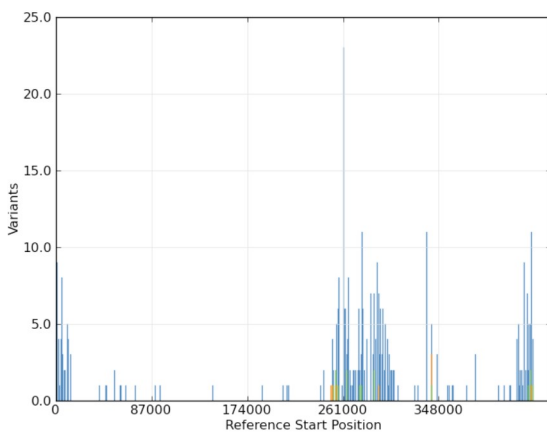
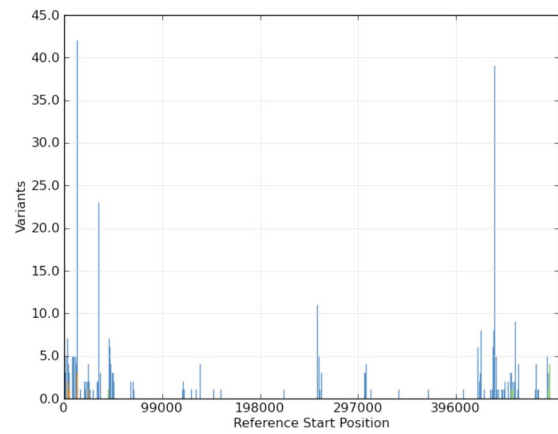
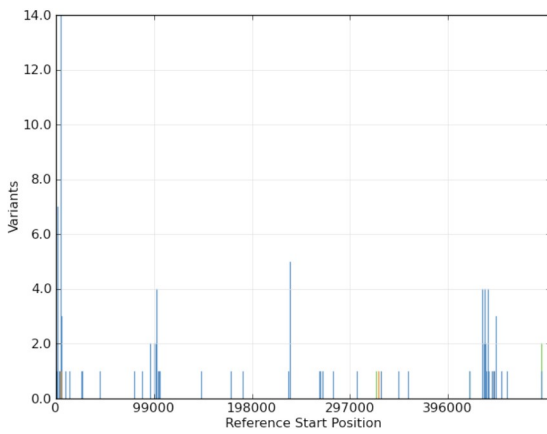
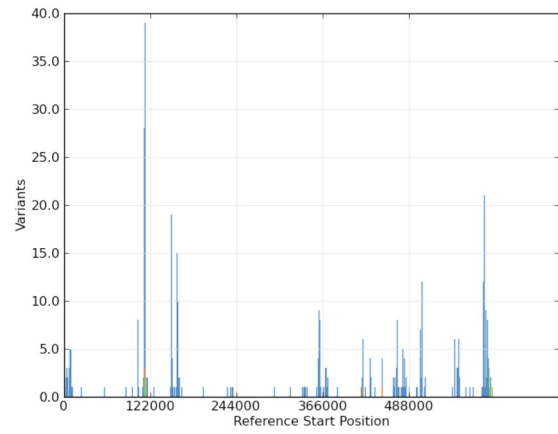
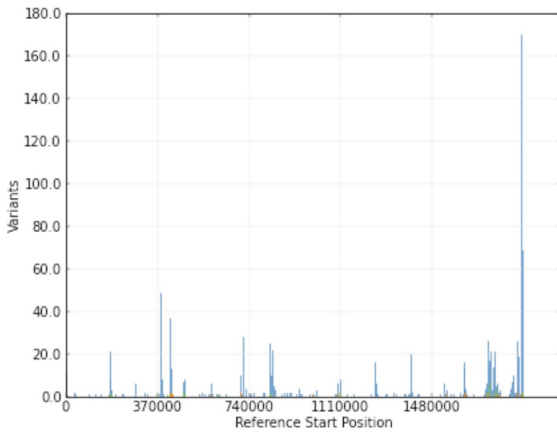
Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000017	56,098	56098_56099insC	INS	100	54	haploid
scf7180000000016	483,836	483836_483837insA	INS	100	53	haploid
scf7180000000016	1,822,654	1822654_1822655insA	INS	100	53	haploid
scf7180000000016	1,822,958	1822958_1822959insGTG	INS	100	53	haploid
scf7180000000017	113,499	113499_113500insG	INS	100	53	haploid
scf7180000000017	159,439	159439_159440insGTC	INS	100	53	haploid
scf7180000000019	434,082	434082_434083insC	INS	100	53	haploid
scf7180000000020	264,045	264045_264046insG	INS	100	53	haploid
scf7180000000020	293,637	293637_293638insT	INS	100	53	haploid
scf7180000000021	53,894	53894_53895insG	INS	100	53	haploid
scf7180000000021	234,907	234907_234908insT	INS	100	53	haploid
scf7180000000016	219	219_220insC	INS	100	52	haploid
scf7180000000016	179,846	179846_179847insC	INS	100	52	haploid
scf7180000000016	283,889	283889_283890insG	INS	100	52	haploid
scf7180000000016	383,567	383567_383568insG	INS	100	52	haploid
scf7180000000016	586,461	586461_586462insG	INS	100	52	haploid
scf7180000000016	833,662	833662_833663insG	INS	100	52	haploid
scf7180000000016	834,072	834072_834073insG	INS	100	52	haploid
scf7180000000016	912,543	912543_912544insC	INS	100	52	haploid
scf7180000000016	1,137,763	1137763_1137764insC	INS	100	52	haploid
scf7180000000016	1,321,713	1321713_1321714insG	INS	100	52	haploid
scf7180000000016	1,421,528	1421528_1421529insC	INS	100	52	haploid
scf7180000000016	1,605,942	1605942_1605943insG	INS	100	52	haploid
scf7180000000016	1,732,494	1732494_1732495insC	INS	100	52	haploid
scf7180000000016	1,801,747	1801747_1801748insC	INS	100	52	haploid
scf7180000000016	1,808,478	1808478_1808479insG	INS	100	52	haploid
scf7180000000016	1,808,658	1808658_1808659insC	INS	100	52	haploid
scf7180000000016	1,814,272	1814272_1814273insG	INS	100	52	haploid
scf7180000000016	1,844,375	1844375_1844376insC	INS	100	52	haploid
scf7180000000016	1,844,415	1844415_1844416insTGGGT	INS	100	52	haploid
scf7180000000017	24,680	24680_24681insC	INS	100	52	haploid
scf7180000000017	158,968	158968_158969insA	INS	100	52	haploid
scf7180000000017	361,022	361022_361023insG	INS	100	52	haploid
scf7180000000017	362,038	362038_362039insC	INS	100	52	haploid
scf7180000000017	595,386	595386_595387insG	INS	100	52	haploid
scf7180000000019	3,698	3698_3699insG	INS	100	52	haploid
scf7180000000019	4,233	4233_4234insG	INS	100	52	haploid
scf7180000000019	12,805	12805_12806insT	INS	100	52	haploid
scf7180000000019	420,998	420998_420999insC	INS	100	52	haploid
scf7180000000019	431,275	431275_431276insC	INS	100	52	haploid
scf7180000000020	7,999	7999_8000insG	INS	100	52	haploid
scf7180000000020	13,639	13639_13640insG	INS	100	52	haploid
scf7180000000020	256,082	256082_256083insC	INS	100	52	haploid
scf7180000000020	264,630	264630_264631insC	INS	100	52	haploid
scf7180000000020	277,016	277016_277017insC	INS	100	52	haploid
scf7180000000021	513	513_514insG	INS	100	52	haploid
scf7180000000021	55,974	55974_55975insT	INS	100	52	haploid
scf7180000000021	70,435	70435_70436insT	INS	100	52	haploid
scf7180000000021	75,262	75262_75263insG	INS	100	52	haploid
scf7180000000021	86,986	86986_86987insG	INS	100	52	haploid
scf7180000000021	293,078	293078_293079insA	INS	100	52	haploid
scf7180000000021	296,086	296086_296087insA	INS	100	52	haploid
scf7180000000022	12,413	12413_12414insG	INS	100	52	haploid
scf7180000000022	13,951	13951_13952insC	INS	100	52	haploid
scf7180000000022	36,668	36668_36669insC	INS	100	52	haploid
scf7180000000016	175,967	175967_175968insC	INS	100	51	haploid
scf7180000000016	184,418	184418_184419insG	INS	100	51	haploid
scf7180000000016	185,929	185929_185930insC	INS	100	51	haploid
scf7180000000016	382,387	382387_382388insG	INS	100	51	haploid
scf7180000000016	393,880	393880_393881insC	INS	100	51	haploid
scf7180000000016	424,066	424066_424067insC	INS	100	51	haploid
scf7180000000016	424,624	424624delGT	DEL	100	51	haploid
scf7180000000016	425,170	425170_425171insG	INS	100	51	haploid
scf7180000000016	426,226	426226_426227insA	INS	100	51	haploid
scf7180000000016	483,514	483514_483515insG	INS	100	51	haploid
scf7180000000016	553,857	553857_553858insG	INS	100	51	haploid

**Corrections**

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000016	1,851,093	100.0%	99.9688%	210.15
scf7180000000017	606,486	100.0%	99.9566%	203.37
scf7180000000018	491,699	100.0%	99.9839%	200.9
scf7180000000019	491,126	100.0%	99.9548%	211.83
scf7180000000020	434,214	100.0%	99.9357%	194.22
scf7180000000021	380,460	100.0%	99.9582%	206.2
scf7180000000022	114,271	100.0%	99.9317%	196.7

Corrections Across Reference

- Insertions
- Deletions
- Substitutions





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