Reports for Job pb_359_3-20000

PACIFIC BIOSCIENCES™

SMRT Cells: 1   Movies: 1

Overview

| Job Metric	Value
Polished Contigs	5
Adapter Dimers (0-10bp)	0.02%
Short Inserts (11-100bp)	0.01%
Number of Bases	845,426,581
Number of Reads	81,585
N50 Read Length	15,049
Mean Read Length	10,362
Mean Read Score	0.85
Mapped Reads	75,702
Mapped Read Length of Insert	6,931
Average Reference Length	818,724
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.97%
Average Reference Coverage	174.71

Adapters
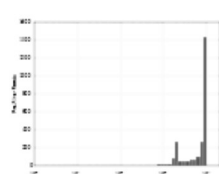
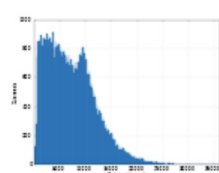Observed Insert Length Distribution Histogram

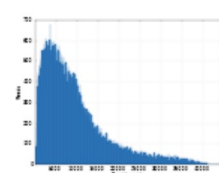**Subread Filtering**
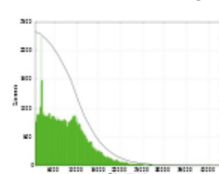
Subread Filtering
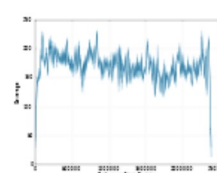
Mapping
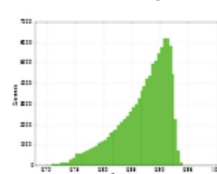
Mapped Subread Concordance

Mapping
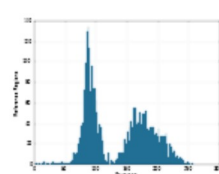
Mapped Subread Length

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	935427792	845426581
Polymerase Reads	150292	81585
Polymerase Read N50	14608	15049
Polymerase Read Length	6224	10362
Polymerase Read Quality	0.523	0.854

Polymerase Read Length

Post-Filter

Polymerase Read Quality

Post-Filter
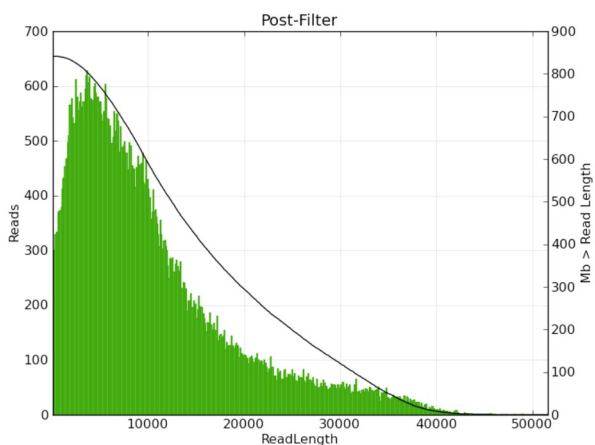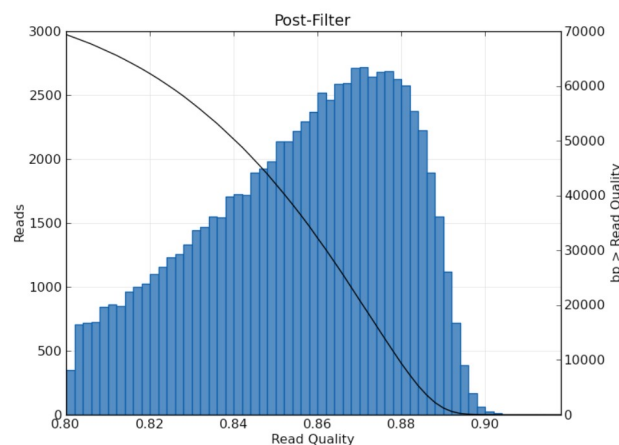
Subread Filtering

Mean Subread length	7,522	N50	10,244
Total Number of Bases	843,064,733	Number of Reads	112,068

Subread Filtering
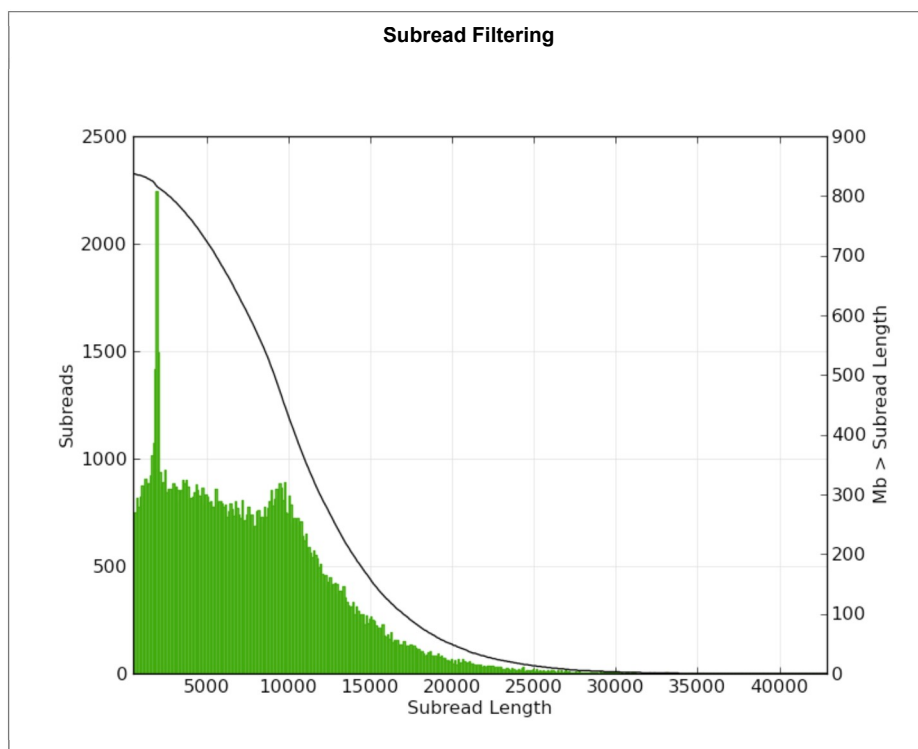
Adapters

Adapter Dimers (0-10bp)   0.02%

Short Inserts (11-100bp)   0.01%

Observed Insert Length Distribution
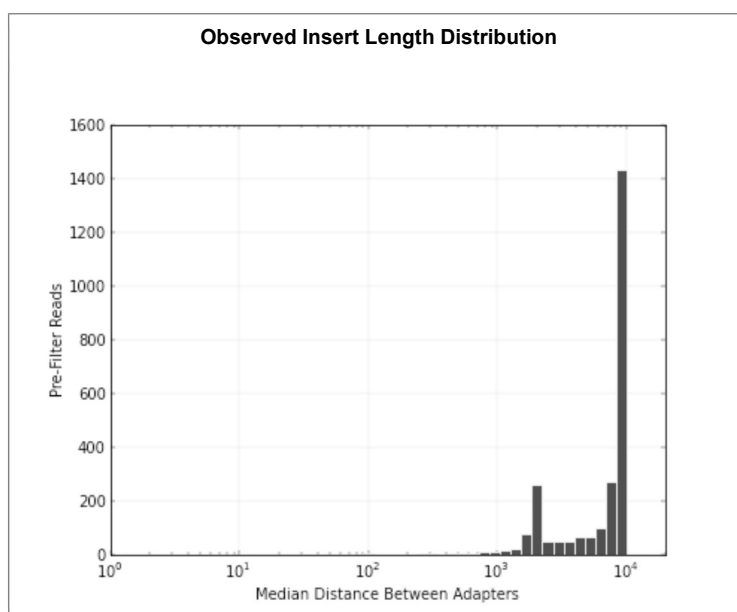
Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160816_232118_42203_c101086032550000001823265803091733	150,292	25.64%	60.12%	14.24%

Mapping

Mapped Subread Length N50 (bp)	9,832	Mapped Polymerase Read Length 95% (bp)	27,200
Mapped Subread Length Mean (bp)	7,215	Mapped Polymerase Read Length Max (bp)	44,023

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	75,702	9,667	13841	100,694	726519050	7,215	0.865
m160816_232118_42203_c101086032550000001823265803091733_s1_p0	75,702	9,667	13841	100,694	726519050	7,215	0.865

Coverage

Mean Coverage   174.71

Missing Bases (%)   0.0

Mapped Subread Concordance

Mapped Polymerase Read Length

Mapped Subread Length
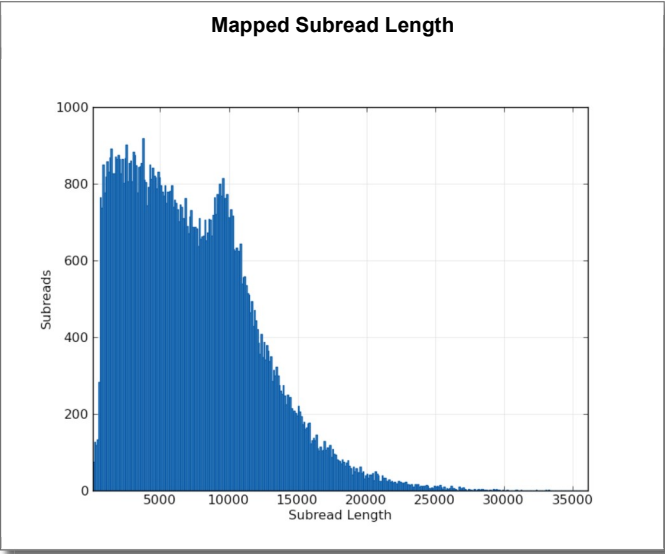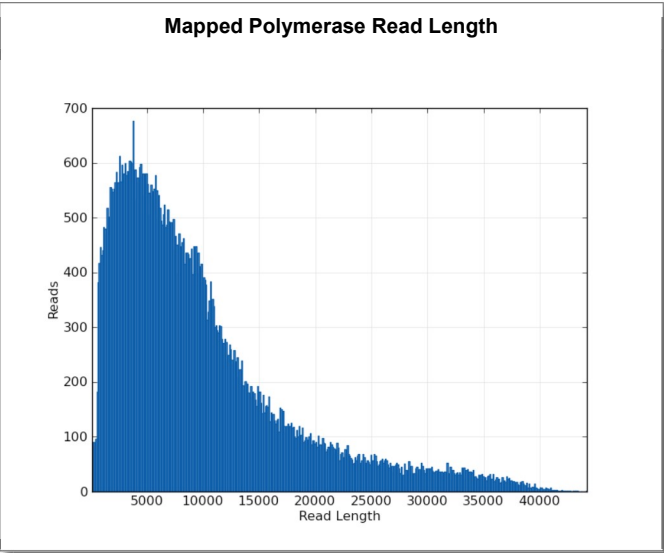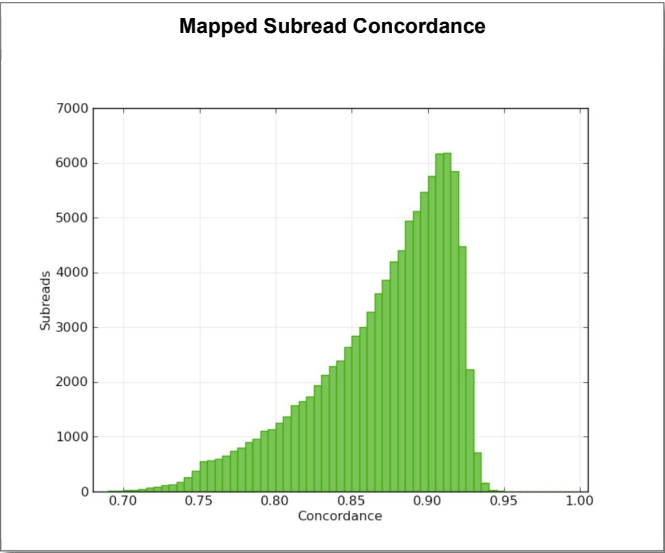
**Coverage Across Reference**
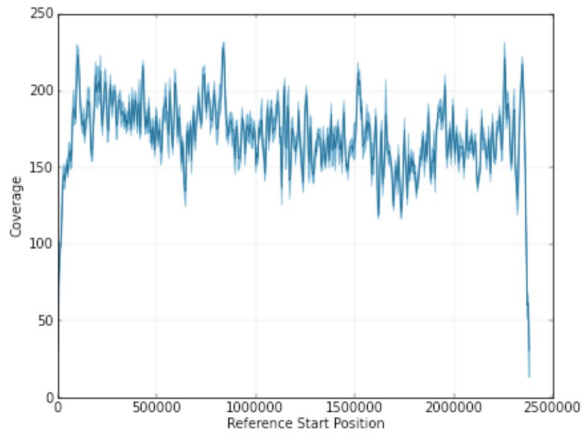
Observed depth of coverage across scf7180000000010 (window size = 5006bp).
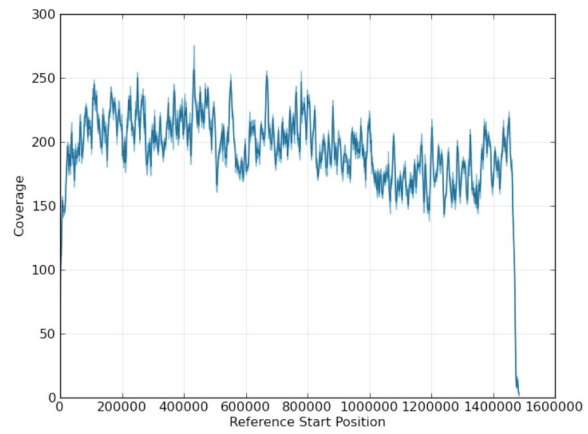
Observed depth of coverage across scf7180000000011 (window size = 2001bp).
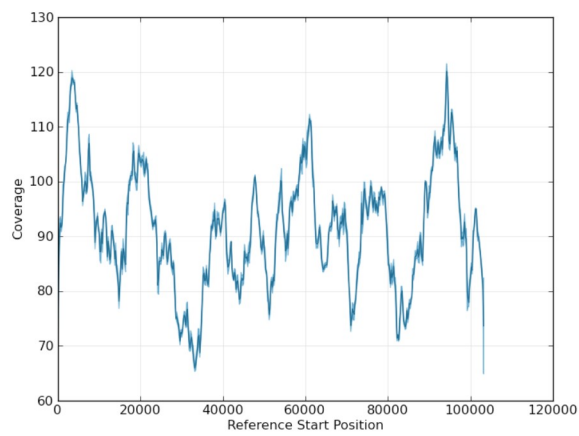
Observed depth of coverage across scf7180000000013 (window size = 200bp).
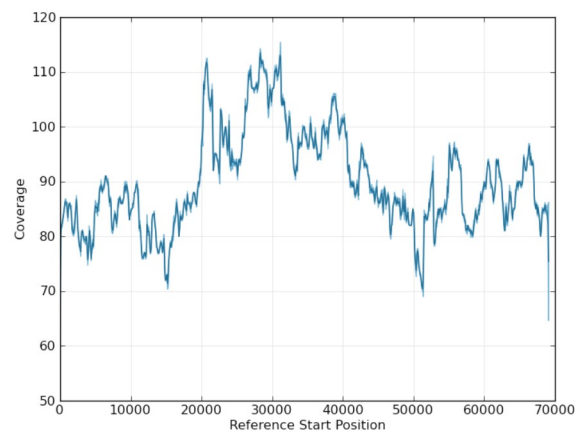
Observed depth of coverage across scf7180000000014 (window size = 100bp).
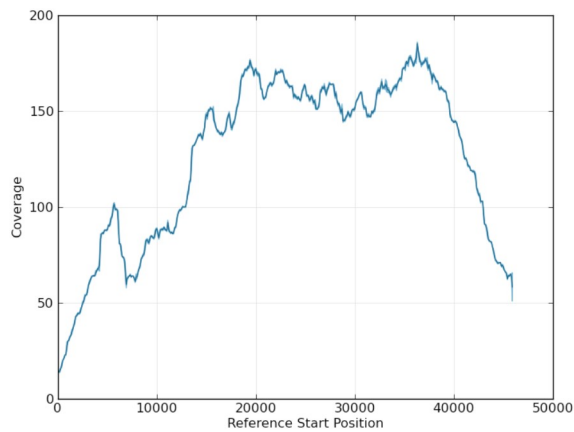
Observed depth of coverage across scf7180000000012 (window size = 100bp).

Depth of coverage distribution
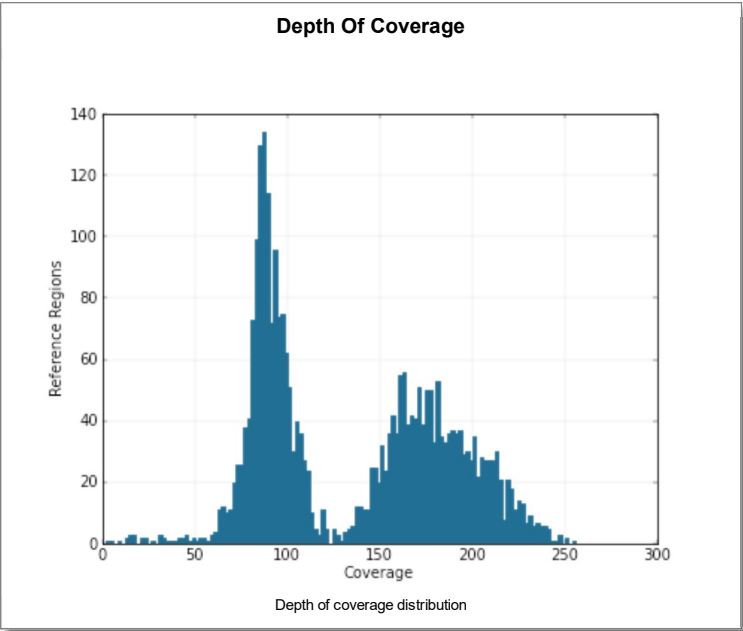
Pre-Assembler Report

Polymerase Read Bases	843,064,733	Length Cutoff	20,000
Seed Bases	49,766,027	Pre-Assembled bases	37,009,814
Pre-Assembled Yield	.744	Pre-Assembled Reads	2,744
Pre-Assembled Reads Length	13,487	Pre-Assembled N50	20,445

Polished Assembly

Polished Contigs	5	Max Contig Length	2,388,684
N50 Contig Length	2,388,684	Sum of Contig Lengths	4,095,113

NOTE: Confidence is estimated by Quiver based on internal read consistency, similar to how phred scores are traditionally computed.
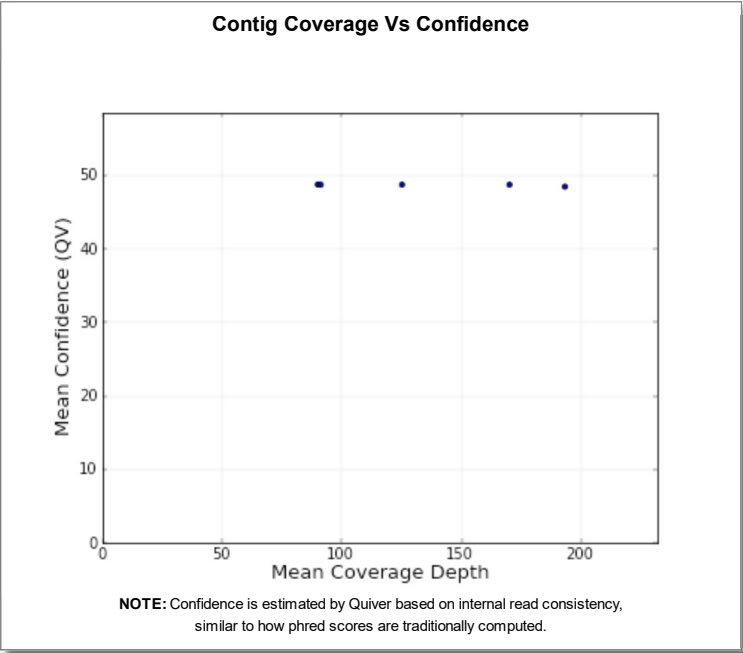
Top Corrections

Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000010	1,274,684	1274684_1274685insG	INS	100	53	haploid
scf7180000000011	598,896	598896_598897insT	INS	100	53	haploid
scf7180000000014	69,149	69149_69150insC	INS	80	53	haploid
scf7180000000010	956	956_957insG	INS	29	52	haploid
scf7180000000010	230,703	230703_230704insG	INS	100	52	haploid
scf7180000000010	234,535	234535_234536insC	INS	100	52	haploid
scf7180000000010	269,963	269963_269964insG	INS	100	52	haploid
scf7180000000010	270,396	270396A>C	SUB	100	52	haploid
scf7180000000010	354,848	354848_354849insC	INS	100	52	haploid
scf7180000000010	438,689	438689_438690insC	INS	100	52	haploid
scf7180000000010	440,558	440558_440559insG	INS	100	52	haploid
scf7180000000010	966,405	966405_966406insG	INS	100	52	haploid
scf7180000000010	997,362	997362_997363insC	INS	100	52	haploid
scf7180000000010	1,121,533	1121533_1121534insG	INS	100	52	haploid
scf7180000000010	1,136,771	1136771_1136772insA	INS	100	52	haploid
scf7180000000010	1,149,286	1149286_1149287insG	INS	100	52	haploid
scf7180000000010	1,433,725	1433725_1433726insC	INS	100	52	haploid
scf7180000000010	1,466,651	1466651_1466652insC	INS	100	52	haploid
scf7180000000010	1,621,803	1621803_1621804insG	INS	100	52	haploid
scf7180000000010	1,726,096	1726096_1726097insC	INS	100	52	haploid
scf7180000000010	2,115,242	2115242_2115243insG	INS	100	52	haploid
scf7180000000010	2,210,006	2210006_2210007insG	INS	100	52	haploid
scf7180000000010	2,210,244	2210244_2210245insG	INS	100	52	haploid
scf7180000000011	4,826	4826_4827insC	INS	100	52	haploid
scf7180000000011	5,513	5513_5514insG	INS	100	52	haploid
scf7180000000011	506,478	506478_506479insG	INS	100	52	haploid
scf7180000000011	839,636	839636_839637insA	INS	100	52	haploid
scf7180000000011	1,005,378	1005378_1005379insC	INS	100	52	haploid
scf7180000000011	1,277,953	1277953_1277954insG	INS	100	52	haploid
scf7180000000011	1,281,413	1281413_1281414insG	INS	100	52	haploid
scf7180000000011	1,295,539	1295539_1295540insG	INS	100	52	haploid
scf7180000000011	1,314,134	1314134_1314135insA	INS	100	52	haploid
scf7180000000011	1,337,882	1337882_1337883insG	INS	100	52	haploid
scf7180000000012	10,320	10320_10321insC	INS	83	52	haploid
scf7180000000012	35,915	35915_35916insG	INS	100	52	haploid
scf7180000000013	5,915	5915_5916insG	INS	100	52	haploid
scf7180000000013	90,706	90706_90707insG	INS	99	52	haploid
scf7180000000014	1,310	1310_1311insG	INS	86	52	haploid
scf7180000000014	35,139	35139_35140insA	INS	96	52	haploid
scf7180000000014	40,108	40108_40109insT	INS	98	52	haploid
scf7180000000014	43,311	43311_43312insG	INS	92	52	haploid
scf7180000000014	60,281	60281_60282insG	INS	89	52	haploid
scf7180000000014	66,162	66162_66163insG	INS	94	52	haploid
scf7180000000014	67,729	67729_67730insC	INS	84	52	haploid
scf7180000000010	1,240	1240_1241insT	INS	29	51	haploid
scf7180000000010	1,856	1856_1857insG	INS	32	51	haploid
scf7180000000010	7,162	7162_7163insG	INS	79	51	haploid
scf7180000000010	34,762	34762_34763insG	INS	100	51	haploid
scf7180000000010	55,462	55462_55463insG	INS	100	51	haploid
scf7180000000010	57,617	57617_57618insG	INS	100	51	haploid
scf7180000000010	93,537	93537_93538insG	INS	100	51	haploid
scf7180000000010	134,398	134398_134399insG	INS	100	51	haploid
scf7180000000010	161,088	161088_161089insA	INS	100	51	haploid
scf7180000000010	266,980	266980_266981insG	INS	100	51	haploid
scf7180000000010	267,792	267792_267793insT	INS	100	51	haploid
scf7180000000010	269,090	269090_269091insC	INS	100	51	haploid
scf7180000000010	304,161	304161_304162insA	INS	100	51	haploid
scf7180000000010	392,192	392192_392193insG	INS	100	51	haploid
scf7180000000010	403,560	403560_403561insC	INS	100	51	haploid
scf7180000000010	417,448	417448_417449insG	INS	100	51	haploid
scf7180000000010	440,911	440911_440912insC	INS	100	51	haploid
scf7180000000010	465,306	465306_465307insG	INS	100	51	haploid
scf7180000000010	505,603	505603_505604insG	INS	100	51	haploid
scf7180000000010	512,461	512461_512462insC	INS	100	51	haploid
scf7180000000010	607,614	607614_607615insT	INS	100	51	haploid
scf7180000000010	610,965	610965_610966insG	INS	100	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000010	2,387,884	100.0%	99.9718%	170.15
scf7180000000011	1,486,942	100.0%	99.9806%	193.34
scf7180000000013	103,460	100.0%	99.9188%	91.2
scf7180000000014	69,269	100.0%	99.7936%	89.98
scf7180000000012	46,066	100.0%	99.9284%	125.19

Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000010	2,387,884	100.0%	99.9718%	170.15
scf7180000000011	1,486,942	100.0%	99.9806%	193.34
scf7180000000013	103,460	100.0%	99.9188%	91.2
scf7180000000014	69,269	100.0%	99.7936%	89.98
scf7180000000012	46,066	100.0%	99.9284%	125.19

Corrections Across Reference

- ■ Insertions
- ■ Deletions
- ■ Substitutions

Observed variants across scf7180000000010.

Observed variants across scf7180000000011.

Observed variants across scf7180000000013.

Observed variants across scf7180000000014.

Observed variants across scf7180000000012.

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