Reports for Job pb_359_4-10000

**PACIFIC BIOSCIENCES**

SMRT Cells: 1   Movies: 1

Overview

Job Metric	Value
Polished Contigs	1
Adapter Dimers (0-10bp)	0.02%
Short Inserts (11-100bp)	0.0%
Number of Bases	413,668,254
Number of Reads	68,619
N50 Read Length	8,265
Mean Read Length	6,028
Mean Read Score	0.85
Mapped Reads	64,950
Mapped Read Length of Insert	4,155
Average Reference Length	3,492,185
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.99%
Average Reference Coverage	100.41

**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
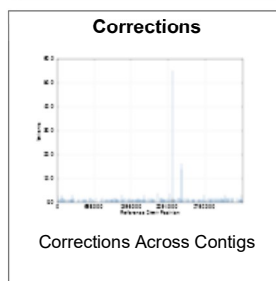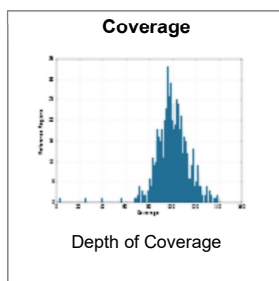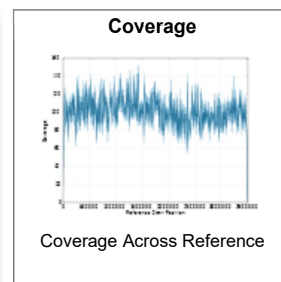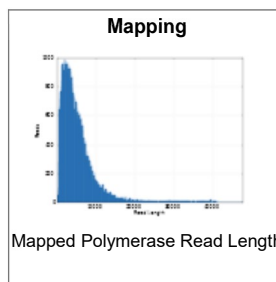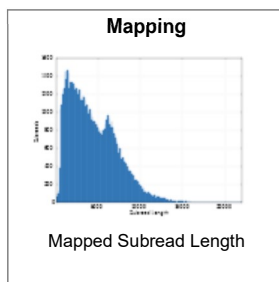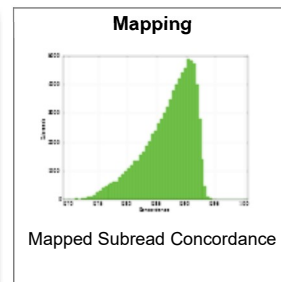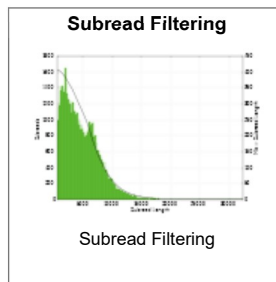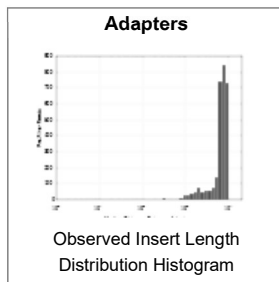
Filtering

Filtering

Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	464955476	413668254
Polymerase Reads	150292	68619
Polymerase Read N50	8005	8265
Polymerase Read Length	3093	6028
Polymerase Read Quality	0.446	0.854

Polymerase Read Length

Polymerase Read Quality
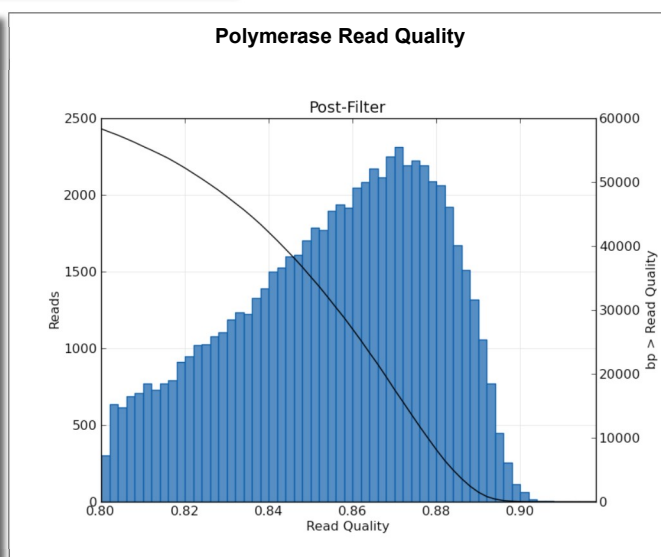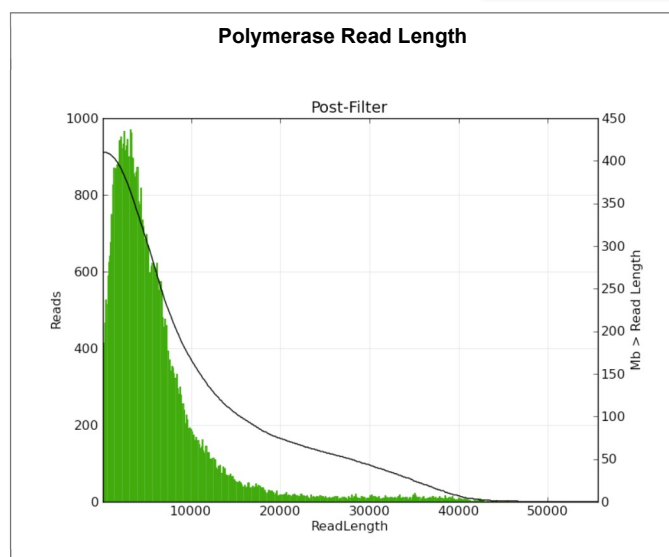
Subread Filtering

Mean Subread length	4,671	N50	6,392
Total Number of Bases	411,362,288	Number of Reads	88,061

Subread Filtering
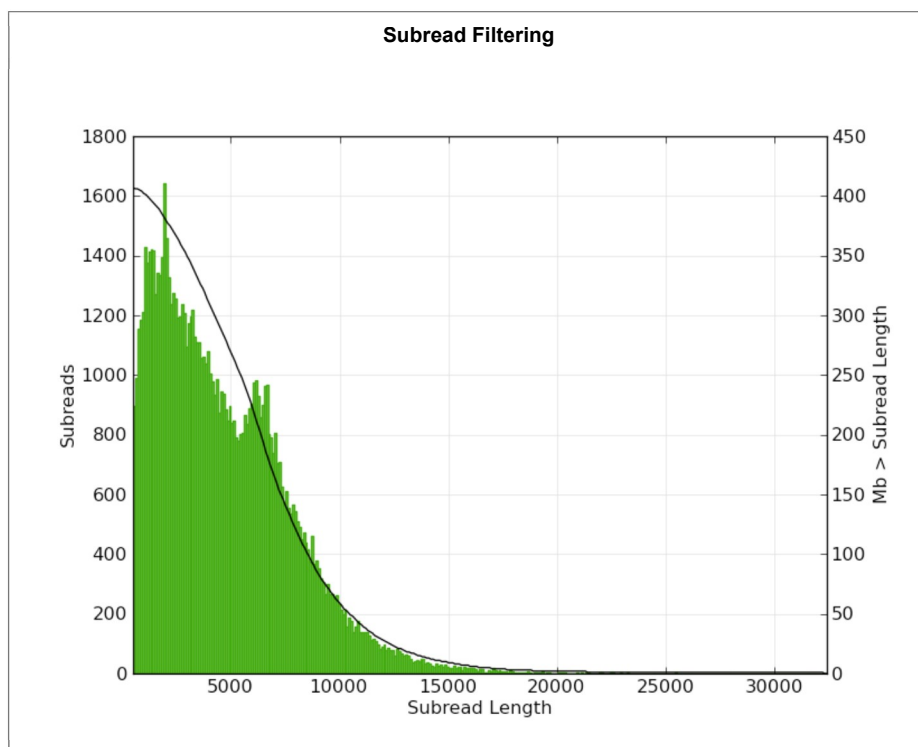
Adapters

Adapter Dimers (0-10bp)   0.02%

Short Inserts (11-100bp)   0.0%

Observed Insert Length Distribution
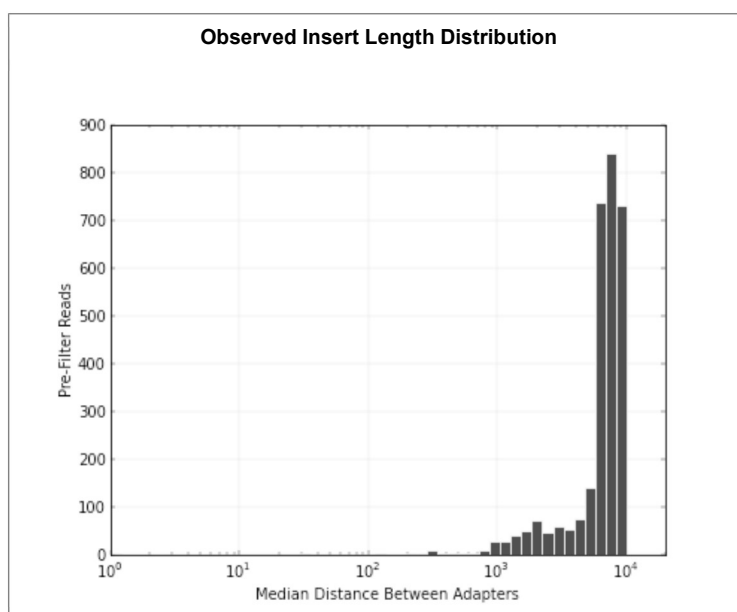
Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160817_034130_42203_c101086032550000001823265803091734	150,292	36.72%	51.03%	12.26%

Mapping

Mapped Subread Length N50 (bp)	6,056	Mapped Polymerase Read Length 95% (bp)	15,090
Mapped Subread Length Mean (bp)	4,343	Mapped Polymerase Read Length Max (bp)	47,431

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	64,950	5,629	7523	83,361	362024128	4,343	0.864
m160817_034130_42203_c101086032550000001823265803091734_s1_p0	64,950	5,629	7523	83,361	362024128	4,343	0.864

Coverage

Mean Coverage   100.41

Missing Bases (%)   0.0

Mapped Subread Concordance

Mapped Polymerase Read Length

Mapped Subread Length
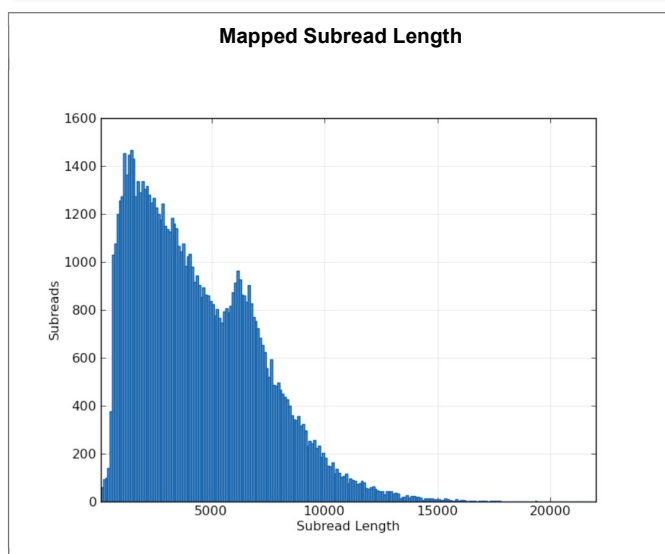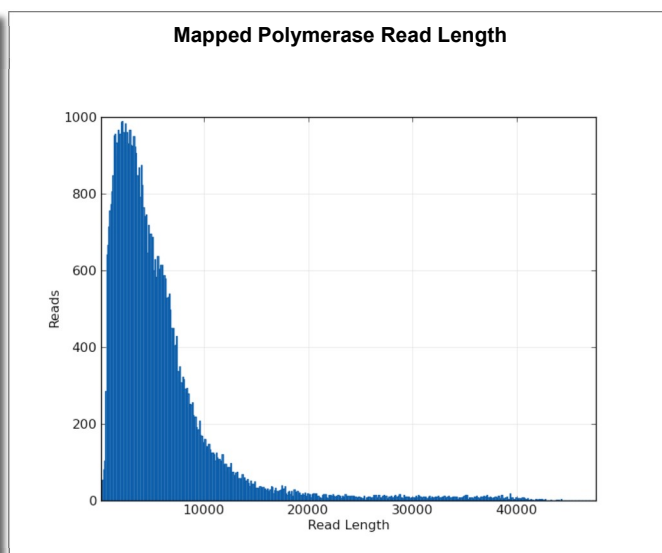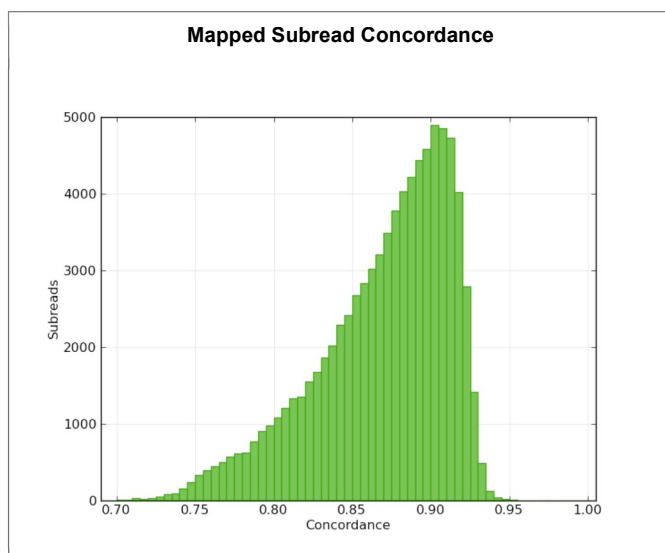
Pre-Assembler Report

Polymerase Read Bases	411,362,288	Length Cutoff	10,000
Seed Bases	60,470,354	Pre-Assembled bases	45,688,129
Pre-Assembled Yield	.756	Pre-Assembled Reads	6,184
Pre-Assembled Reads Length	7,388	Pre-Assembled N50	10,130

Polished Assembly

Polished Contigs	1	Max Contig Length	3,492,548
N50 Contig Length	3,492,548	Sum of Contig Lengths	3,492,548

Coverage Across Reference

Observed depth of coverage across scf7180000000002 (window size = 5003bp).

Depth Of Coverage

Depth of coverage distribution

Contig Coverage Vs Confidence

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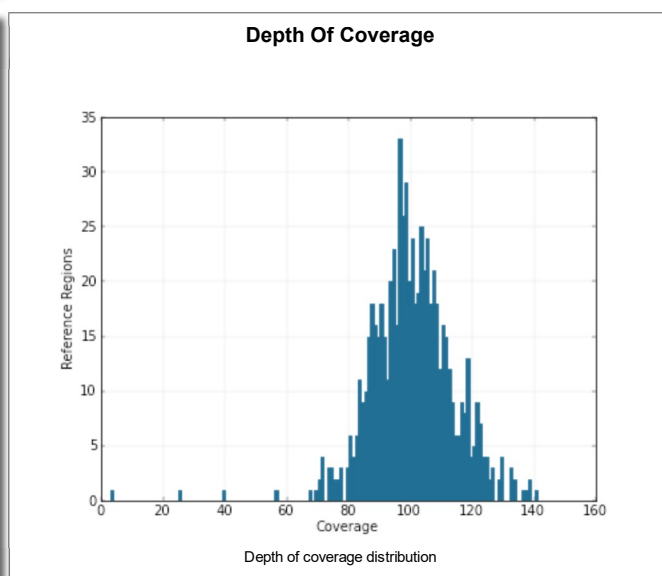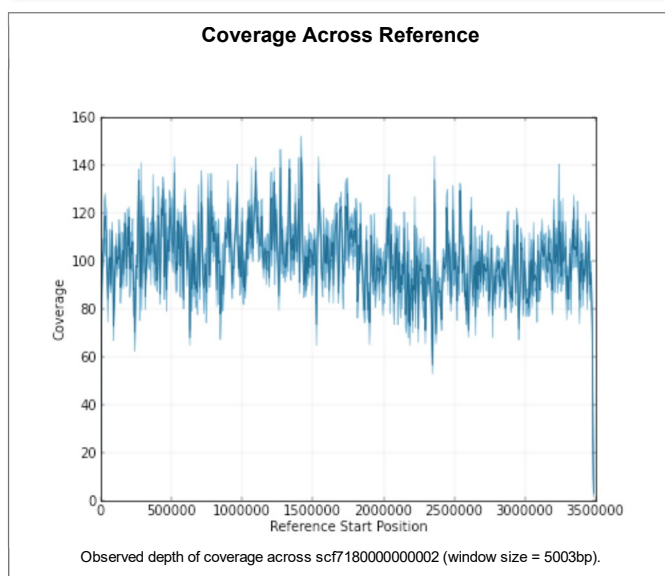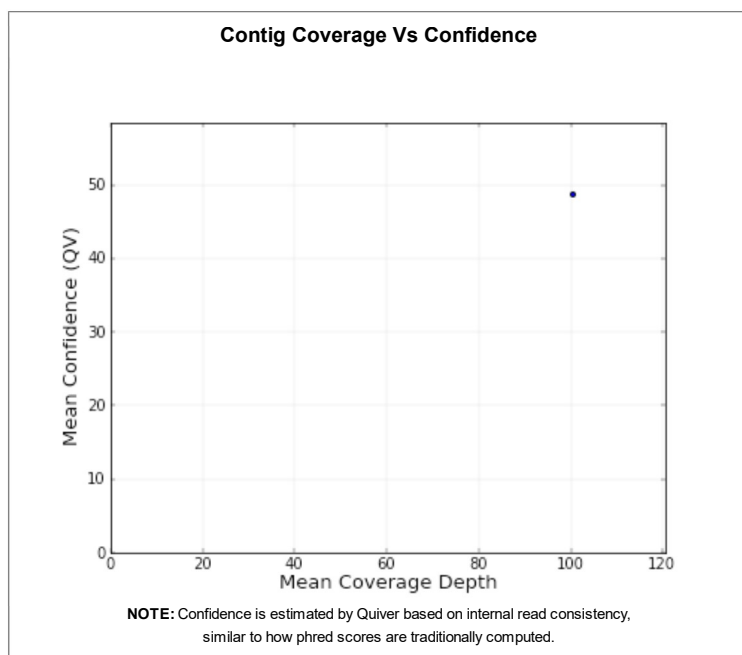
Top Corrections

Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000002	550,234	550234_550235insG	INS	100	53	haploid
scf7180000000002	1,513,653	1513653_1513654insC	INS	100	53	haploid
scf7180000000002	2,154,290	2154290_2154291insG	INS	89	53	haploid
scf7180000000002	2,594,223	2594223_2594224insG	INS	93	53	haploid
scf7180000000002	198,477	198477_198478insC	INS	98	52	haploid
scf7180000000002	294,038	294038_294039insA	INS	83	52	haploid
scf7180000000002	1,094,215	1094215_1094216insC	INS	100	52	haploid
scf7180000000002	1,439,385	1439385_1439386insC	INS	91	52	haploid
scf7180000000002	1,616,591	1616591_1616592insG	INS	89	52	haploid
scf7180000000002	1,648,193	1648193_1648194insG	INS	89	52	haploid
scf7180000000002	1,888,311	1888311_1888312insG	INS	92	52	haploid
scf7180000000002	89,176	89176_89177insC	INS	81	51	haploid
scf7180000000002	91,505	91505_91506insG	INS	74	51	haploid
scf7180000000002	123,145	123145_123146insC	INS	96	51	haploid
scf7180000000002	134,754	134754_134755insG	INS	100	51	haploid
scf7180000000002	147,736	147736_147737insG	INS	91	51	haploid
scf7180000000002	283,559	283559_283560insC	INS	94	51	haploid
scf7180000000002	318,447	318447_318448insC	INS	81	51	haploid
scf7180000000002	416,266	416266_416267insG	INS	95	51	haploid
scf7180000000002	535,135	535135_535136insG	INS	100	51	haploid
scf7180000000002	614,298	614298_614299insC	INS	100	51	haploid
scf7180000000002	692,015	692015_692016insC	INS	100	51	haploid
scf7180000000002	998,415	998415_998416insG	INS	100	51	haploid
scf7180000000002	1,109,478	1109478_1109479insG	INS	100	51	haploid
scf7180000000002	1,172,992	1172992_1172993insC	INS	92	51	haploid
scf7180000000002	1,354,465	1354465_1354466insG	INS	95	51	haploid
scf7180000000002	1,453,355	1453355_1453356insC	INS	87	51	haploid
scf7180000000002	1,501,292	1501292_1501293insC	INS	100	51	haploid
scf7180000000002	1,557,512	1557512_1557513insG	INS	99	51	haploid
scf7180000000002	1,629,044	1629044_1629045insC	INS	91	51	haploid
scf7180000000002	1,846,534	1846534_1846535insC	INS	94	51	haploid
scf7180000000002	1,982,057	1982057_1982058insG	INS	96	51	haploid
scf7180000000002	2,119,048	2119048_2119049insG	INS	83	51	haploid
scf7180000000002	2,167,126	2167126_2167127insC	INS	84	51	haploid
scf7180000000002	2,337,602	2337602_2337603insT	INS	84	51	haploid
scf7180000000002	2,498,337	2498337_2498338insG	INS	88	51	haploid
scf7180000000002	2,740,005	2740005_2740006insG	INS	100	51	haploid
scf7180000000002	2,872,227	2872227_2872228insG	INS	100	51	haploid
scf7180000000002	3,082,990	3082990_3082991insC	INS	89	51	haploid
scf7180000000002	3,121,078	3121078_3121079insC	INS	100	51	haploid
scf7180000000002	3,161,450	3161450_3161451insG	INS	88	51	haploid
scf7180000000002	3,388,776	3388776_3388777insG	INS	71	51	haploid
scf7180000000002	15,244	15244_15245insC	INS	91	50	haploid
scf7180000000002	62,312	62312_62313insC	INS	98	50	haploid
scf7180000000002	84,993	84993_84994insG	INS	100	50	haploid
scf7180000000002	93,341	93341_93342insC	INS	67	50	haploid
scf7180000000002	243,743	243743_243744insC	INS	64	50	haploid
scf7180000000002	264,007	264007_264008insG	INS	100	50	haploid
scf7180000000002	280,031	280031_280032insG	INS	76	50	haploid
scf7180000000002	390,177	390177_390178insC	INS	100	50	haploid
scf7180000000002	477,906	477906_477907insC	INS	98	50	haploid
scf7180000000002	514,218	514218_514219insG	INS	100	50	haploid
scf7180000000002	528,991	528991_528992insG	INS	93	50	haploid
scf7180000000002	611,127	611127_611128insG	INS	92	50	haploid
scf7180000000002	675,639	675639_675640insC	INS	79	50	haploid
scf7180000000002	818,456	818456_818457insC	INS	94	50	haploid
scf7180000000002	906,257	906257_906258insG	INS	100	50	haploid
scf7180000000002	932,732	932732_932733insG	INS	80	50	haploid
scf7180000000002	966,101	966101_966102insG	INS	100	50	haploid
scf7180000000002	1,122,788	1122788_1122789insG	INS	100	50	haplotp
scf7180000000002	1,216,327	1216327_1216328insG	INS	100	50	haploid
scf7180000000002	1,222,495	1222495_1222496insG	INS	100	50	haploid
scf7180000000002	1,251,458	1251458_1251459insG	INS	96	50	haploid
scf7180000000002	1,269,748	1269748_1269749insG	INS	100	50	haploid
scf7180000000002	1,347,382	1347382_1347383insT	INS	91	50	haploid
scf7180000000002	1,427,601	1427601_1427602insG	INS	100	50	haploid

Corrections

Consensus Calling Results

Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000002	3,492,185	100.0%	99.9911%	100.41

Observed variants across scf7180000000002.
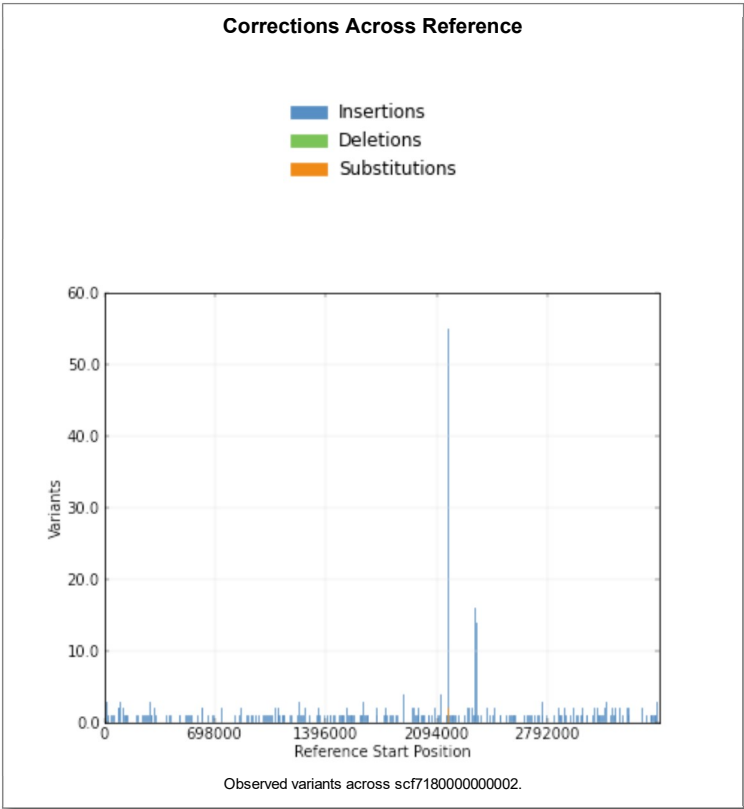
Generated by SMRT® Portal. Mon Aug 29 09:23:43 CEST 2016
For Research Use Only. Not for use in diagnostic procedures.