

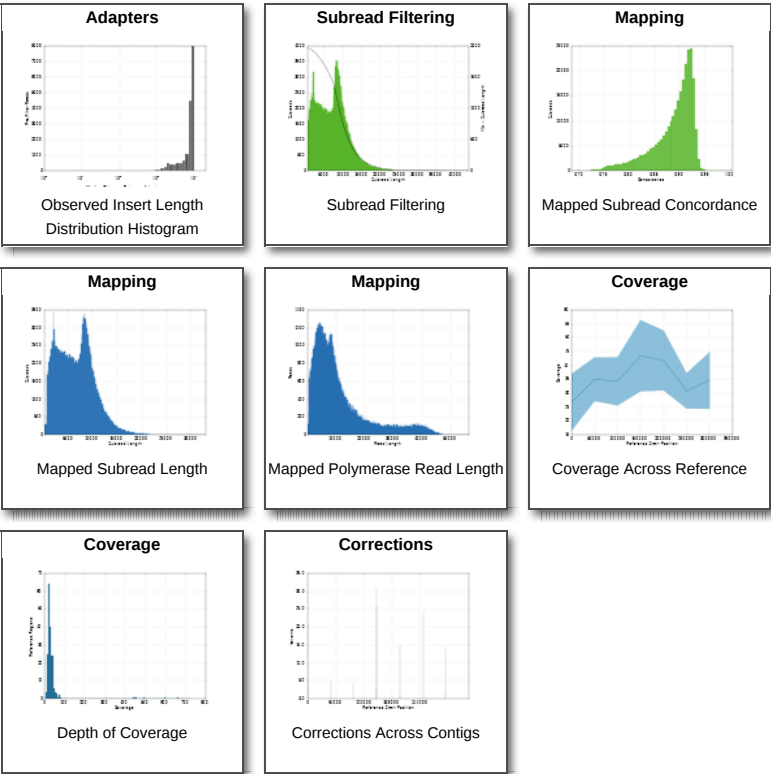
Reports for Job Skeletonema_RO5_3_cells



SMRT Cells: 3 Movies: 3

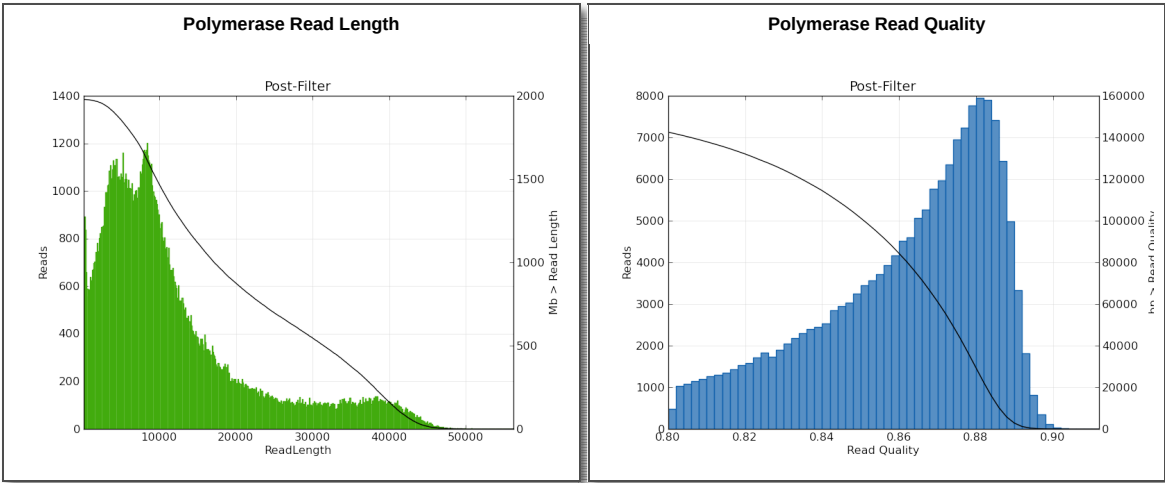
Overview

Job Metric	Value
Polished Contigs	4,392
Adapter Dimers (0-10bp)	0.0%
Short Inserts (11-100bp)	0.0%
Number of Bases	1,985,823,340
Number of Reads	166,095
N50 Read Length	17,404
Mean Read Length	11,955
Mean Read Score	0.86
Mapped Reads	159,174
Mapped Read Length of Insert	6,193
Average Reference Length	206,025
Average Reference Bases Called	99.93%
Average Reference Consensus Concordance	99.95%
Average Reference Coverage	44.35



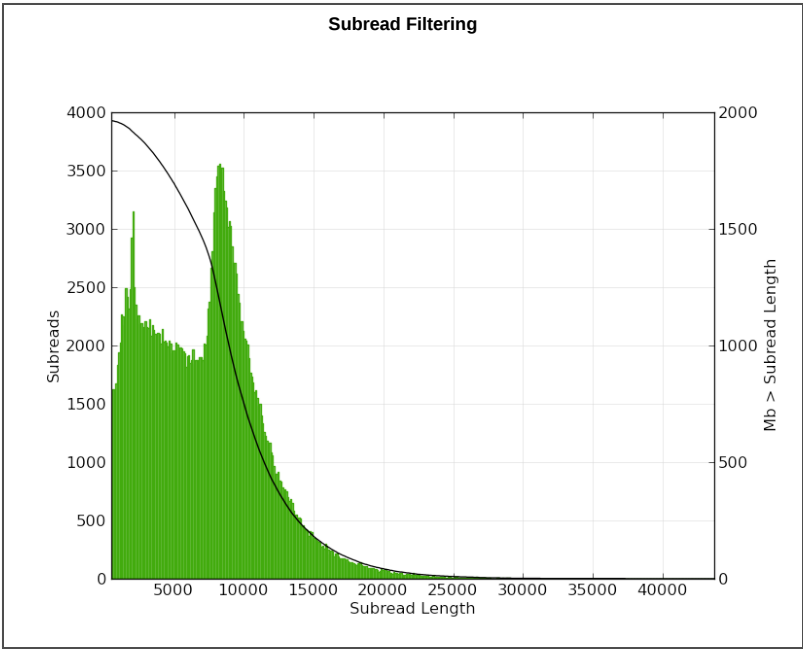
Filtering

Filtering		
Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	2114161164	1985823340
Polymerase Reads	450876	166095
Polymerase Read N50	16843	17404
Polymerase Read Length	4689	11955
Polymerase Read Quality	0.352	0.86



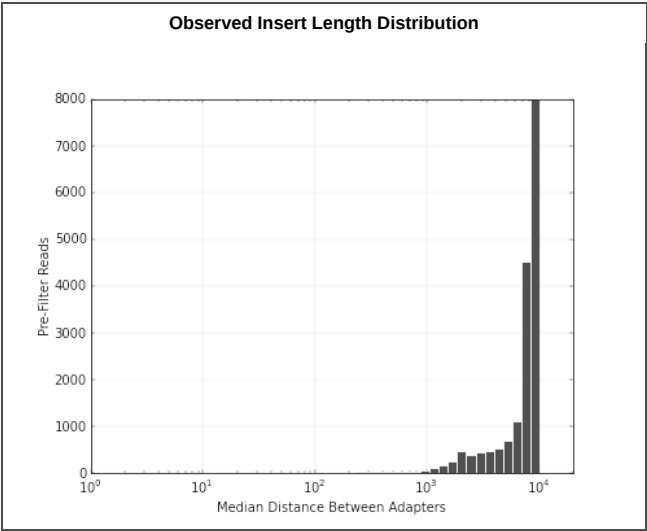
Subread Filtering

Mean Subread length	7,104	N50	9,091
Total Number of Bases	1,978,157,185	Number of Reads	278,430



Adapters

Adapter Dimers (0-10bp) 0.0%
Short Inserts (11-100bp) 0.0%



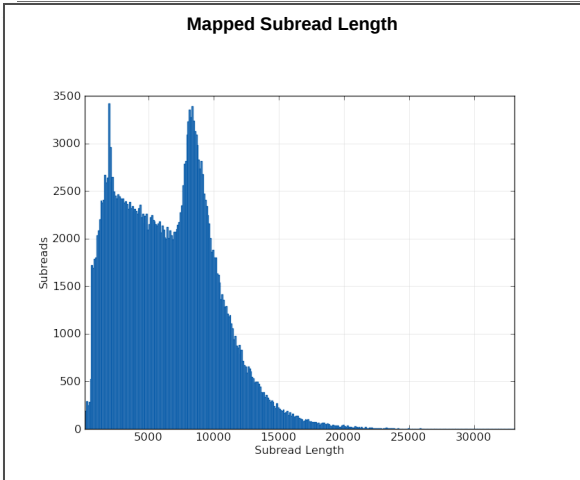
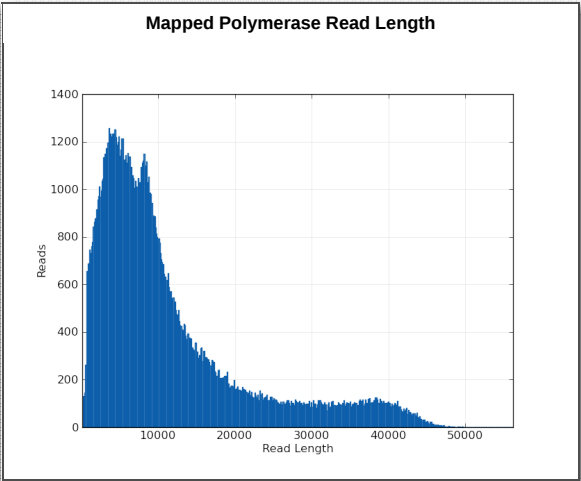
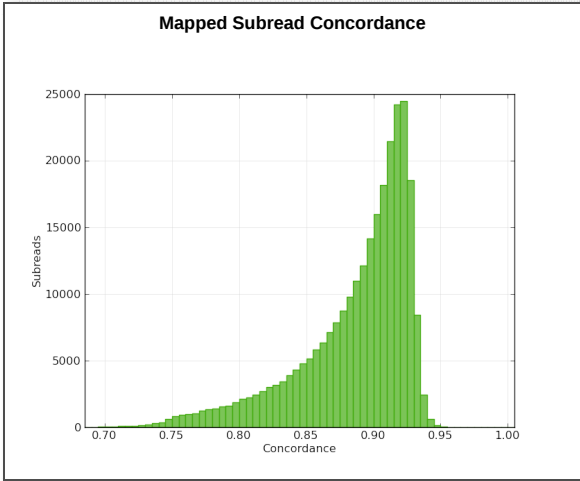
Loading

SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160809_233148_42203_c101084512550000001823238903091753	150,292	54.2%	41.51%	4.28%
m160810_080809_42203_c1010845125500000001823238903091755	150,292	56.17%	39.43%	4.4%
m160810_035054_42203_c101084512550000001823238903091754	150,292	56.7%	38.87%	4.43%

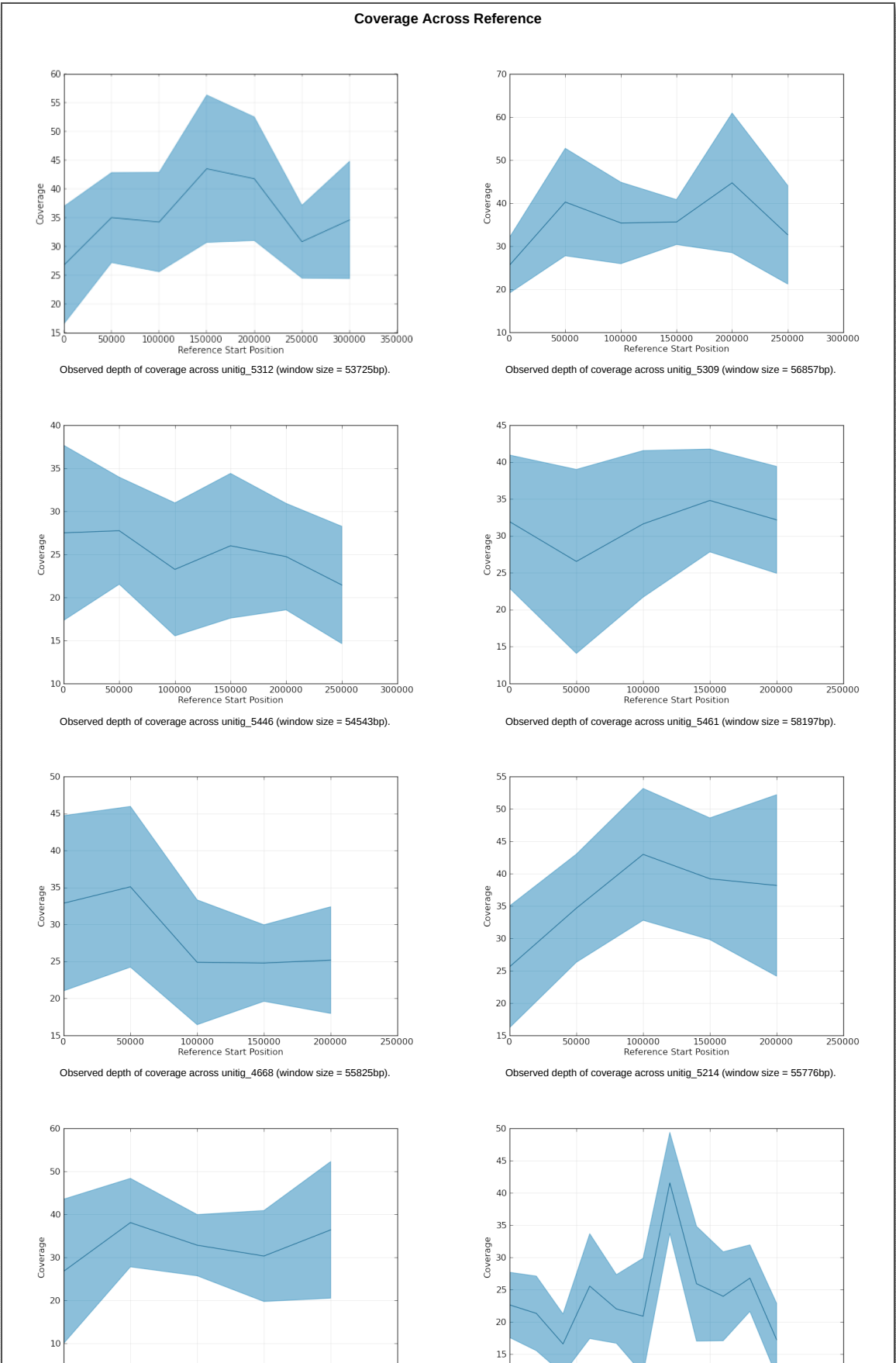
Mapping

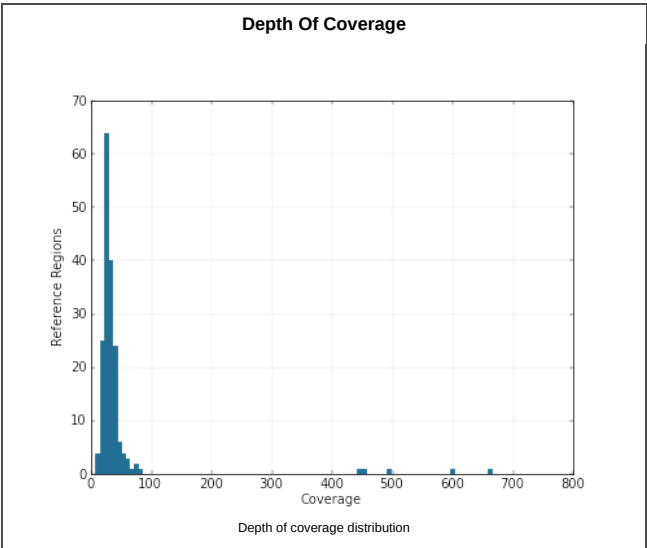
Mapped Subread Length N50 (bp) 8,481 Mapped Polymerase Read Length 95% (bp) 35,670
Mapped Subread Length Mean (bp) 6,417 Mapped Polymerase Read Length Max (bp) 56,097

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	159,174	11,287	16909	269,775	1731045012	6,417	0.881
m160810_035054_42203_c101084512550000001823238903091754_s1_p0	51,645	11,554	17850	89,441	572993512	6,406	0.877
m160809_233148_42203_c101084512550000001823238903091753_s1_p0	55,007	10,950	15988	90,796	582255214	6,413	0.884
m160810_080809_42203_c101084512550000001823238903091755_s1_p0	52,522	11,377	17035	89,538	575796286	6,431	0.883



Coverage
Mean Coverage 44.35
Missing Bases (%) 0.07



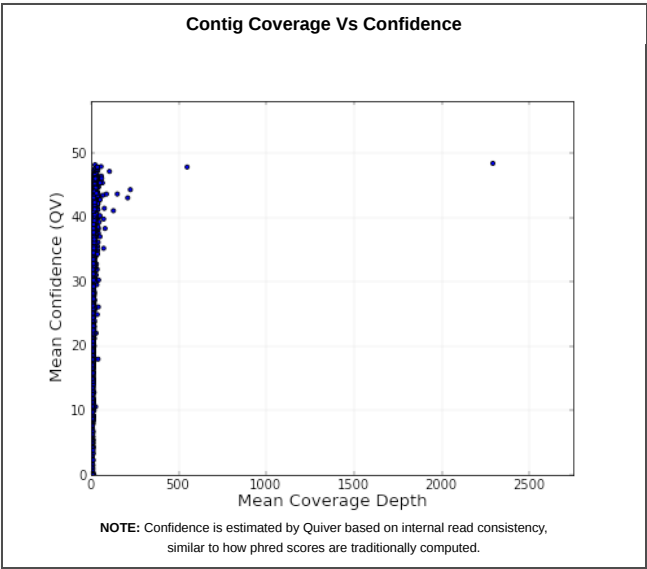


Pre-Assembler Report

Polymerase Read Bases	1,978,157,185	Length Cutoff	6,880
Seed Bases	1,500,041,066	Pre-Assembled bases	633,187,391
Pre-Assembled Yield	.422	Pre-Assembled Reads	177,540
Pre-Assembled Reads Length	3,566	Pre-Assembled N50	7,714

Polished Assembly

Polished Contigs	4,392	Max Contig Length	376,227
N50 Contig Length	29,241	Sum of Contig Lengths	87,662,760

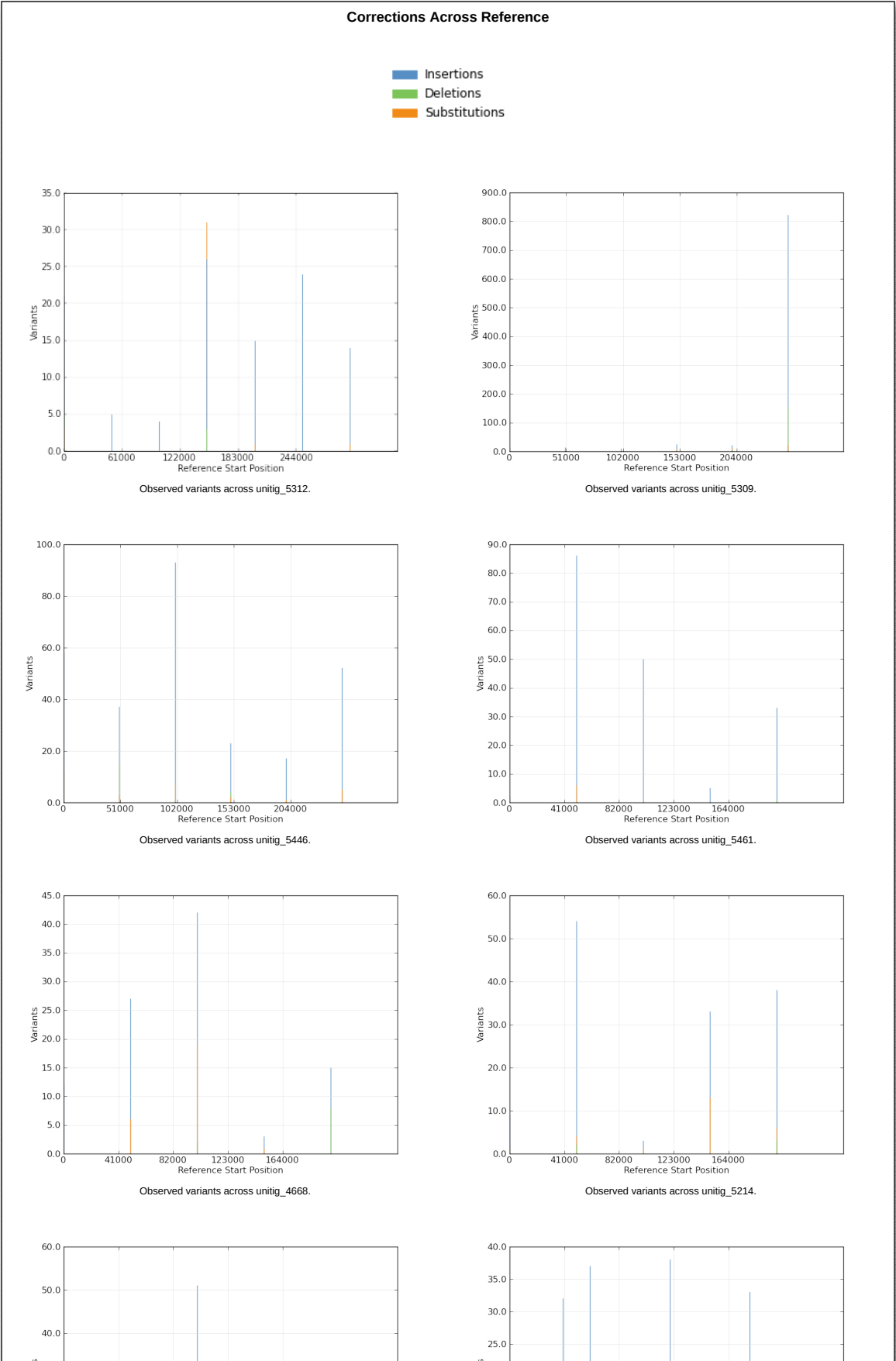


Top Corrections

Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
unitig_119	43,878	43878_43879insT	INS	26	52	haploid
unitig_4994	18,810	18810_18811insA	INS	15	52	haploid
unitig_642	42,000	42000_42001insT	INS	20	52	haploid
unitig_4557	15,040	15040_15041insTGT	INS	23	52	haploid
unitig_167	2,563	2563_2564insA	INS	14	52	haploid
unitig_2326	14,452	14452_14453insT	INS	15	52	haploid
unitig_5223	22,091	22091_22092insA	INS	14	52	haploid
unitig_467	15,270	15270_15271insT	INS	17	52	haploid
unitig_5312	40,581	40581G>T	SUB	22	51	haploid
unitig_5312	96,526	96526_96527insG	INS	42	51	haploid
unitig_5309	185,961	185961_185962insG	INS	30	51	haploid
unitig_5309	316,831	316831_316832insT	INS	40	51	haploid
unitig_5446	24,590	24590_24591insG	INS	22	51	haploid
unitig_5446	28,518	28518_28519insT	INS	27	51	haploid
unitig_5446	141,022	141022_141023insC	INS	22	51	haploid
unitig_5461	57,314	57314_57315insC	INS	19	51	haploid
unitig_5461	100,029	100029_100030insCGTATATTGGTTATAACAACCAATAAAACCAC	INS	33	51	haploid
unitig_4667	197,165	197165_197166insT	INS	23	51	haploid
unitig_123	76,915	76915_76916insC	INS	20	51	haploid
unitig_5435	64,256	64256_64257insATA	INS	44	51	haploid
unitig_8	167,103	167103_167104insA	INS	33	51	haploid
unitig_5269	174,311	174311_174312insC	INS	19	51	haploid
unitig_186	52,833	52833T>G	SUB	32	51	haploid
unitig_352	85,101	85101_85102insG	INS	19	51	haploid
unitig_261	85,920	85920_85921insG	INS	20	51	haploid
unitig_524	2,756	2756_2757insC	INS	18	51	haploid
unitig_233	63,746	63746_63747insT	INS	44	51	haploid
unitig_5218	23,633	23633_23634insT	INS	40	51	haploid
unitig_5218	104,732	104732_104733insA	INS	19	51	haploid
unitig_5419	80,537	80537_80538insA	INS	19	51	haploid
unitig_4259	49,225	49225G>A	SUB	21	51	haploid
unitig_4965	71,562	71562GT>TG	SUB	28	51	haploid
unitig_5427	84,173	84173_84174insA	INS	20	51	haploid
unitig_4551	25,451	25451_25452insA	INS	16	51	haploid
unitig_535	40,359	40359delAA	DEL	39	51	haploid
unitig_535	68,409	68409_68410insC	INS	22	51	haploid
unitig_5401	87,327	87327G>A	SUB	48	51	haploid
unitig_4685	59,246	59246_59247insG	INS	25	51	haploid
unitig_4685	115,097	115097_115098insC	INS	20	51	haploid
unitig_697	13,676	13676C>G	SUB	29	51	haploid
unitig_783	50,313	50313_50314insA	INS	32	51	haploid
unitig_135	58,229	58229_58230insACA	INS	32	51	haploid
unitig_5422	56,356	56356_56357insA	INS	17	51	haploid
unitig_5422	105,392	105392_105393insA	INS	21	51	haploid
unitig_754	87,577	87577_87578insC	INS	16	51	haploid
unitig_5351	22,948	22948C>A	SUB	29	51	haploid
unitig_5351	23,445	23445T>A	SUB	28	51	haploid
unitig_4922	88,134	88134_88135insT	INS	23	51	haploid
unitig_5117	17,609	17609G>T	SUB	39	51	haploid
unitig_308	66,339	66339_66340insC	INS	19	51	haploid
unitig_761	53,094	53094T>C	SUB	26	51	haploid
unitig_623	66,450	66450_66451insA	INS	17	51	haploid
unitig_4994	46,009	46009_46010insC	INS	26	51	haploid
unitig_62	25,285	25285_25286insT	INS	30	51	haploid
unitig_964	80,602	80602_80603insG	INS	22	51	haploid
unitig_964	81,358	81358_81359insA	INS	18	51	haploid
unitig_5006	42,670	42670_42671insGGCATTGCGCTTACGCTGGGTTGATATGACGGCTCCGACGATGGCTCCGAGGAGGGCTGAGAAGACG	INS	22	51	haploid
unitig_4460	37,352	37352_37353insG	INS	19	51	haploid
unitig_5424	8,189	8189_8190insC	INS	27	51	haploid
unitig_642	45,117	45117_45118insC	INS	24	51	haploid
unitig_642	51,780	51780A>C	SUB	30	51	haploid
unitig_1232	47,442	47442_47443insAC	INS	33	51	haploid
unitig_1232	48,825	48825_48826insAGA	INS	26	51	haploid
unitig_932	21,632	21632_21633insC	INS	22	51	haploid
unitig_932	32,497	32497_32498insT	INS	19	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
unitig_5312	376,075	100.0%	99.9702%	35.19
unitig_5309	341,147	100.0%	99.8959%	35.34
unitig_5446	327,261	100.0%	99.9383%	24.81
unitig_5461	290,986	100.0%	99.9725%	31.52
unitig_4668	279,126	100.0%	99.9581%	28.21
unitig_5214	278,882	100.0%	99.9580%	36.34
unitig_4667	265,957	99.89%	99.9364%	33.09
unitig_5435	231,665	100.0%	99.9327%	23.69
unitig_123	214,500	100.0%	99.9193%	27.34
unitig_5269	206,974	100.0%	99.9493%	23.92
unitig_8	181,749	100.0%	99.9758%	34.6
unitig_155	177,593	100.0%	99.9702%	23.97
unitig_5325	173,279	99.99%	99.9711%	34.55
unitig_5337	173,101	100.0%	99.9671%	29.49
unitig_186	168,872	100.0%	99.9248%	26.94
unitig_5271	161,729	100.0%	99.9518%	22.02
unitig_5428	157,109	97.93%	99.9350%	23.45
unitig_261	149,143	100.0%	99.9484%	23.7
unitig_95	147,121	100.0%	99.9558%	23.17
unitig_5315	145,424	100.0%	99.9904%	51.97
unitig_334	144,292	100.0%	99.9681%	20.36
unitig_5218	141,201	100.0%	99.8916%	21.48
unitig_5316	140,001	100.0%	99.9921%	58.72
unitig_37	139,207	100.0%	100.0000%	547.68
unitig_5260	138,224	100.0%	99.9573%	31.62



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