Reports for Job Sm_RO5_3_cells-10000

PACIFIC BIOSCIENCES™

SMRT Cells: 3   Movies: 3

Overview

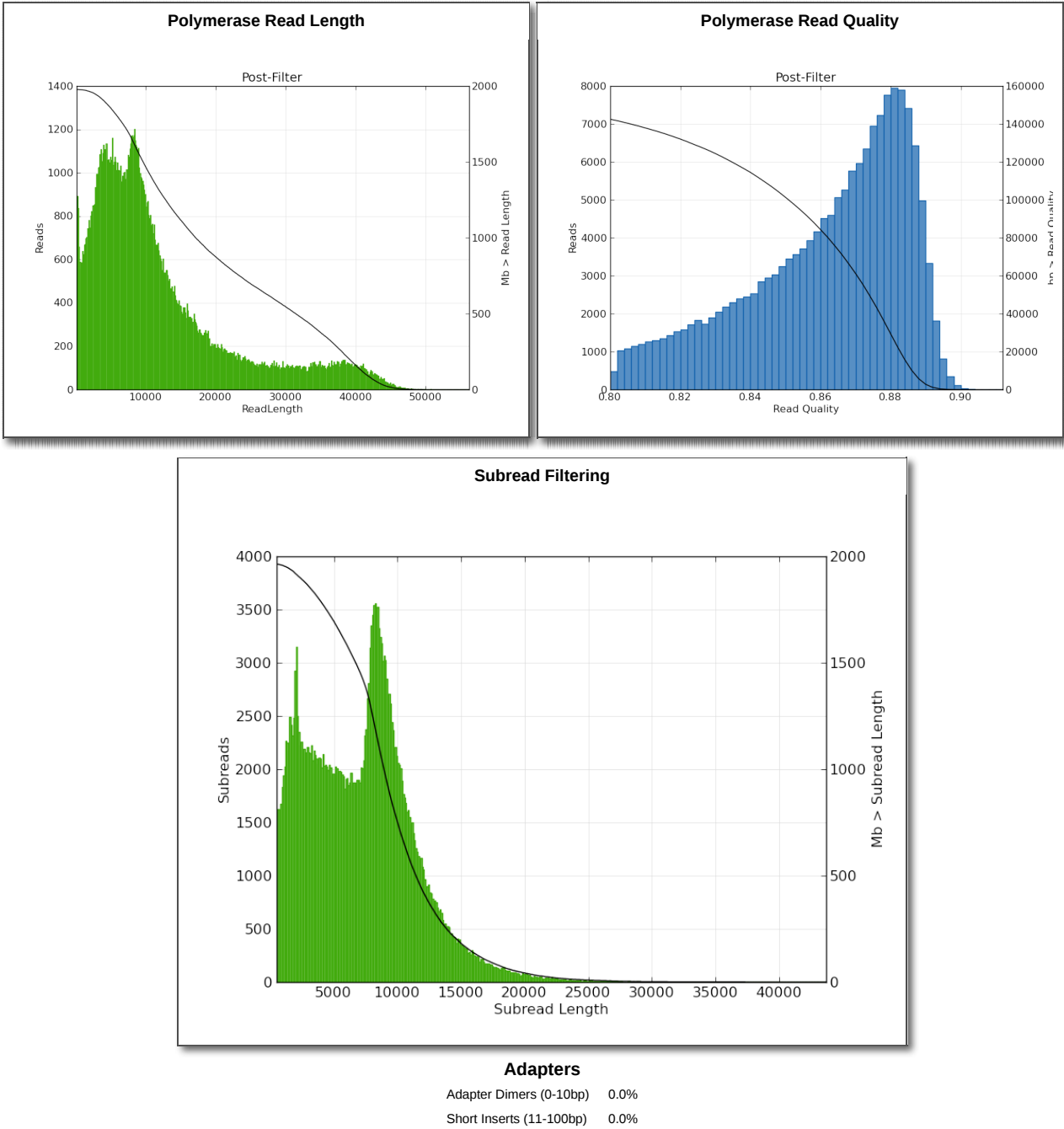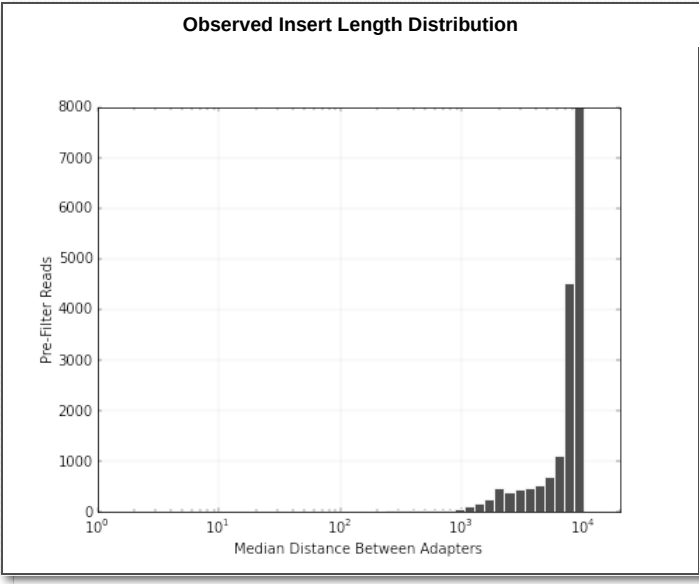| Job Metric	Value
Polished Contigs	3,331
Adapter Dimers (0-10bp)	0.0%
Short Inserts (11-100bp)	0.0%
Number of Bases	1,985,823,340
Number of Reads	166,095
N50 Read Length	17,404
Mean Read Length	11,955
Mean Read Score	0.86
Mapped Reads	159,187
Mapped Read Length of Insert	6,261
Average Reference Length	315,444
Average Reference Bases Called	99.95%
Average Reference Consensus Concordance	99.91%
Average Reference Coverage	28.54

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
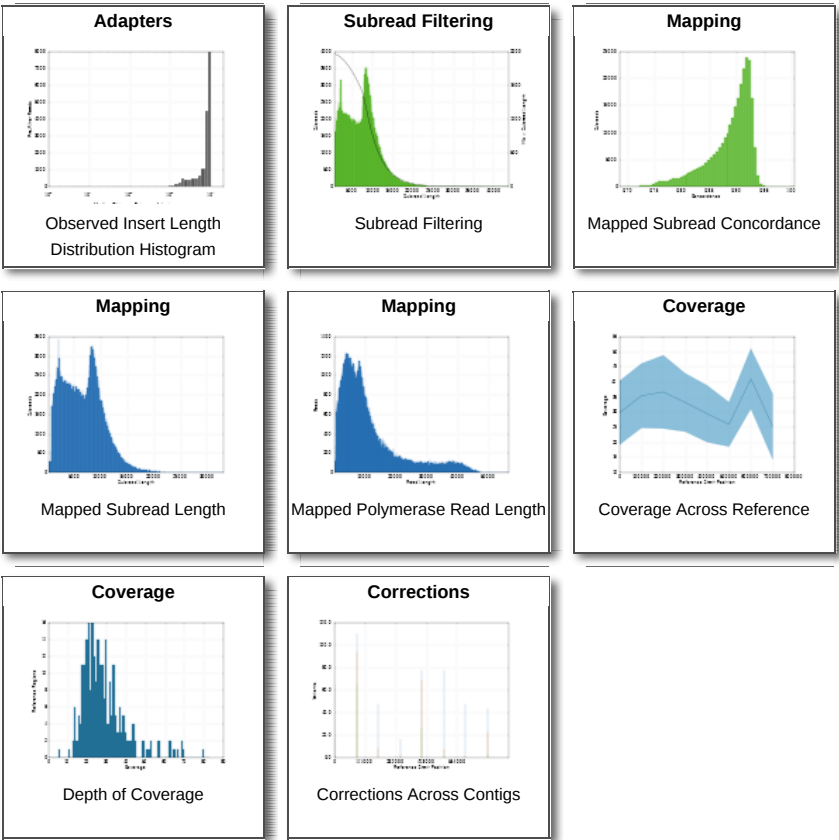
Filtering

Filtering

Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	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

Polymerase Read Length

Polymerase Read Quality

Subread Filtering

Adapters

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

Observed Insert Length Distribution

Loading

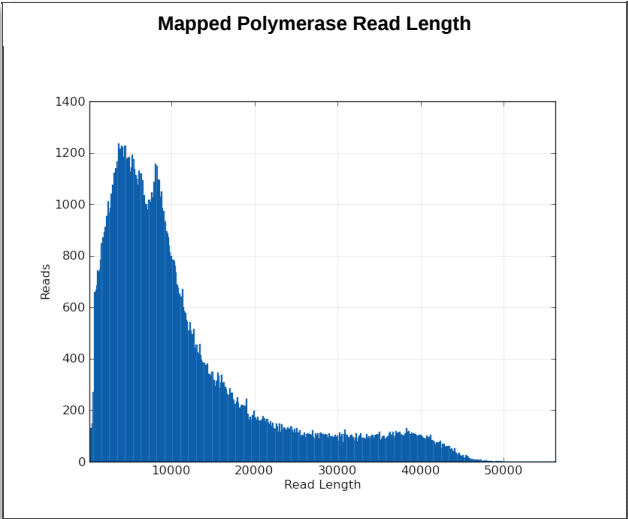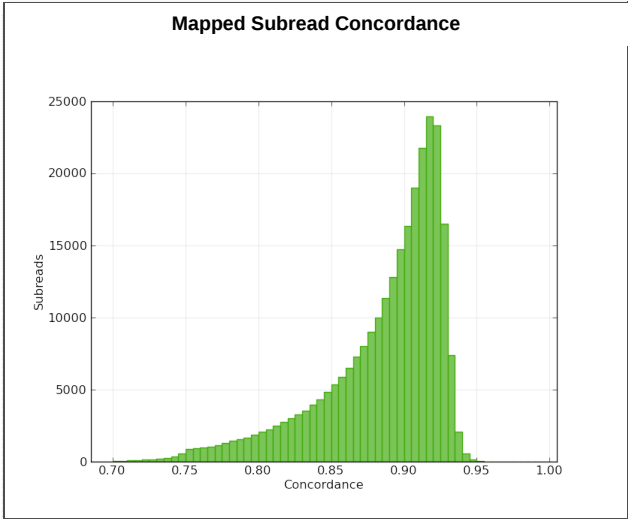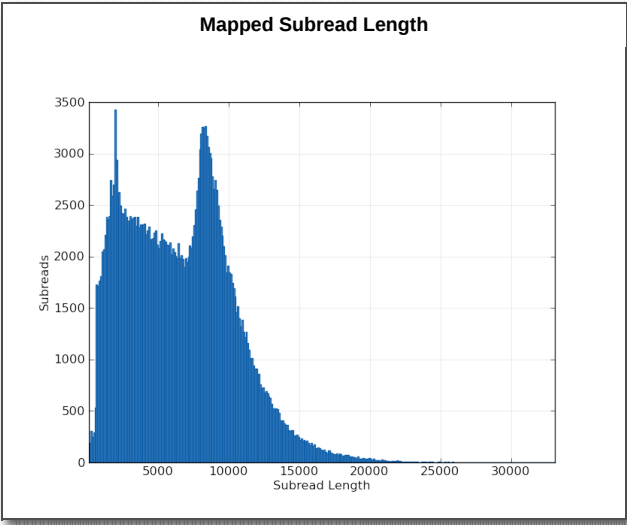| SMRT Cell ID	Productive ZMWs	ZMW Loading For Productivity 0	ZMW Loading For Productivity 1	ZMW Loading For Productivity 2
m160809_233148_42203_c10108451255000000182323903091753	150,292	54.2%	41.51%	4.28%
m160810_080809_42203_c10108451255000000182323903091755	150,292	56.17%	39.43%	4.4%
m160810_035054_42203_c10108451255000000182323903091754	150,292	56.7%	38.87%	4.43%

Mapping

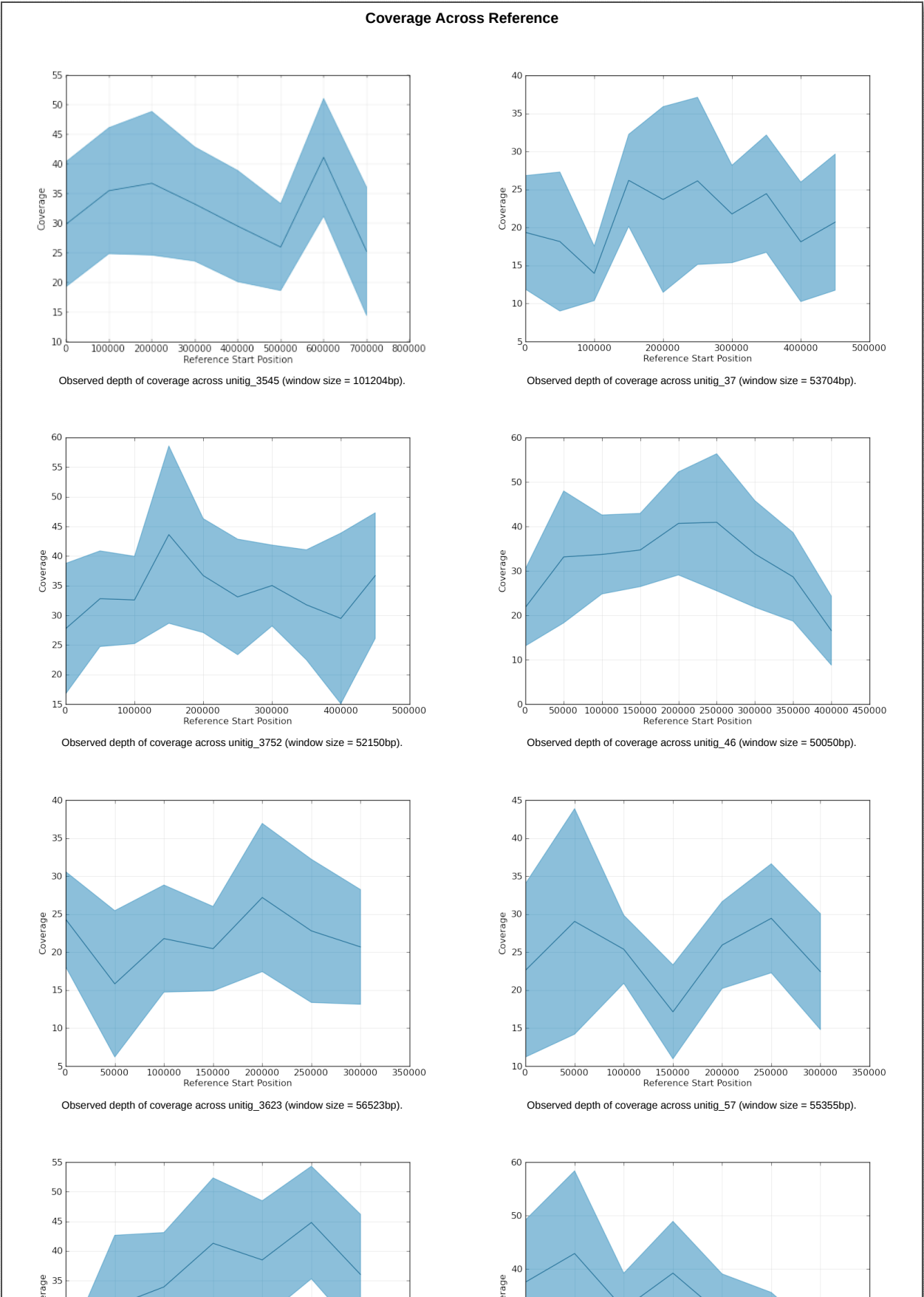|			
Mapped Subread Length N50 (bp)	8,580	Mapped Polymerase Read Length 95% (bp)	35,720
Mapped Subread Length Mean (bp)	6,485	Mapped Polymerase Read Length Max (bp)	56,097

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	159,187	11,360	16981	269,617	1748565802	6,485	0.881
m160810_035054_42203_c10108451255000000182323903091754_s1_p0	51,627	11,632	17964	89,362	578782604	6,477	0.877
m160809_233148_42203_c10108451255000000182323903091753_s1_p0	54,989	11,028	16067	90,740	587823523	6,478	0.883
m160810_080809_42203_c10108451255000000182323903091755_s1_p0	52,571	11,442	17085	89,515	581959675	6,501	0.882

Mapped Subread Concordance

Mapped Polymerase Read Length

Coverage

Mapped Subread Length

Mean Coverage   28.54
Missing Bases (%)   0.05

Coverage Across Reference

Observed depth of coverage across unitig_3545 (window size = 101204bp).

Observed depth of coverage across unitig_37 (window size = 53704bp).

Observed depth of coverage across unitig_3752 (window size = 52150bp).

Observed depth of coverage across unitig_46 (window size = 50050bp).

Observed depth of coverage across unitig_3623 (window size = 56523bp).

Observed depth of coverage across unitig_57 (window size = 55355bp).

Depth Of Coverage

Depth of coverage distribution

Pre-Assembler Report

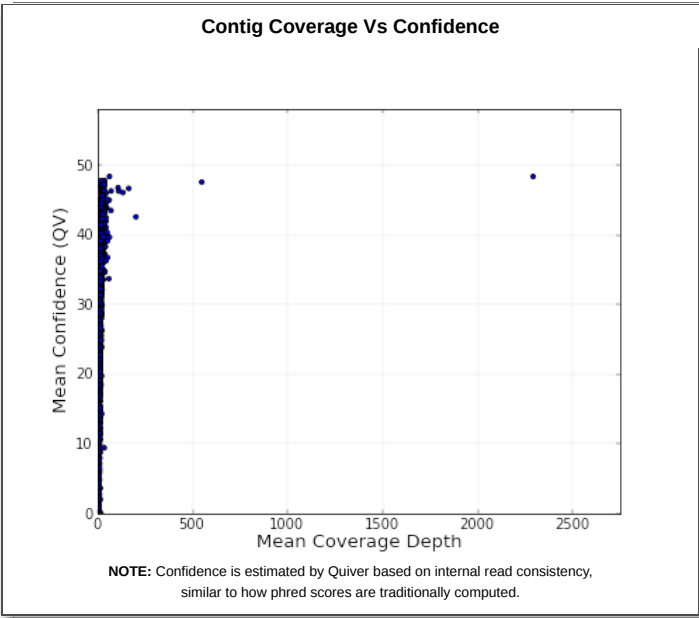|			
Polymerase Read Bases	1,978,157,185	Length Cutoff	10,000
Seed Bases	775,115,084	Pre-Assembled bases	501,060,993
Pre-Assembled Yield	.646	Pre-Assembled Reads	85,632
Pre-Assembled Reads Length	5,851	Pre-Assembled N50	10,224

Polished Assembly

Polished Contigs	3,331	Max Contig Length	810,089
N50 Contig Length	41,080	Sum of Contig Lengths	87,883,232

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
unitig_3930	134,744	134744_134745insT	INS	17	52	haploid
unitig_3976	106,740	106740_106741insT	INS	45	52	haploid
unitig_817	57,942	57942_57943insC	INS	18	52	haploid
unitig_1587	32,089	32089G>A	SUB	42	52	haploid
unitig_3405	43,858	43858_43859insT	INS	16	52	haploid
unitig_1896	7,780	7780_7781insT	INS	24	52	haploid
unitig_3338	3,221	3221_3222insG	INS	18	52	haploid
unitig_665	17,489	17489_17490insT	INS	21	52	haploid
unitig_477	11,622	11622_11623insA	INS	24	52	haploid
unitig_3545	201,987	201987T>A	SUB	30	51	haploid
unitig_3545	426,733	426733_426734insC	INS	36	51	haploid
unitig_3545	575,888	575888_575889insG	INS	25	51	haploid
unitig_3545	764,957	764957_764958insTG	INS	15	51	haploid
unitig_3545	769,707	769707_769708insC	INS	21	51	haploid
unitig_3545	779,016	779016_779017insT	INS	20	51	haploid
unitig_3752	141,442	141442_141443insG	INS	28	51	haploid
unitig_3752	446,561	446561_446562insT	INS	41	51	haploid
unitig_4010	324,942	324942_324943insT	INS	100	51	haploid
unitig_37	22,104	22104G>T	SUB	14	51	haploid
unitig_37	249,545	249545_249546insA	INS	20	51	haploid
unitig_37	339,851	339851_339852insC	INS	25	51	haploid
unitig_51	44,516	44516_44517insG	INS	15	51	haploid
unitig_51	367,143	367143_367144insG	INS	43	51	haploid
unitig_46	212,973	212973_212974insG	INS	30	51	haploid
unitig_46	228,161	228161_228162insA	INS	38	51	haploid
unitig_46	319,486	319486delG	DEL	33	51	haploid
unitig_46	331,773	331773_331774insA	INS	29	51	haploid
unitig_46	364,801	364801G>A	SUB	23	51	haploid
unitig_46	400,367	400367C>T	SUB	14	51	haploid
unitig_46	444,927	444927_444928insA	INS	14	51	haploid
unitig_4003	149,228	149228_149229insC	INS	24	51	haploid
unitig_4002	271,537	271537_271538insT	INS	26	51	haploid
unitig_4002	326,814	326814_326815insC	INS	19	51	haploid
unitig_57	65,164	65164C>A	SUB	53	51	haploid
unitig_3623	18,953	18953_18954insT	INS	19	51	haploid
unitig_3623	287,906	287906_287907insA	INS	22	51	haploid
unitig_3623	380,880	380880_380881insC	INS	16	51	haploid
unitig_3712	164,442	164442T>A	SUB	24	51	haploid
unitig_3712	201,652	201652_201653insG	INS	31	51	haploid
unitig_3984	141,135	141135_141136insT	INS	21	51	haploid
unitig_142	40,965	40965_40966insGCTCTCCACCACGCTCCC	INS	16	51	haploid
unitig_142	180,403	180403_180404insT	INS	26	51	haploid
unitig_142	194,431	194431_194432insT	INS	41	51	haploid
unitig_3968	105,437	105437_105438insA	INS	29	51	haploid
unitig_3968	175,875	175875_175876insT	INS	33	51	haploid
unitig_44	44,845	44845delCT	DEL	40	51	haploid
unitig_44	58,604	58604_58605insT	INS	31	51	haploid
unitig_44	94,886	94886_94887insT	INS	17	51	haploid
unitig_44	96,966	96966T>G	SUB	15	51	haploid
unitig_44	225,904	225904_225905insAAACA	INS	24	51	haploid
unitig_44	225,905	225905T>A	SUB	24	51	haploid
unitig_3817	12,560	12560_12561insA	INS	25	51	haploid
unitig_3817	115,732	115732_115733insA	INS	22	51	haploid
unitig_3890	41,445	41445_41446insC	INS	16	51	haploid
unitig_3930	150,934	150934T>A	SUB	18	51	haploid
unitig_3571	19,874	19874_19875insA	INS	21	51	haploid
unitig_3571	84,691	84691_84692insG	INS	19	51	haploid
unitig_3571	98,219	98219_98220insC	INS	20	51	haploid
unitig_3382	161,169	161169_161170insC	INS	26	51	haploid
unitig_169	33,333	33333_33334insA	INS	39	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
unitig_3545	809,634	99.98%	99.9192%	32.06
unitig_37	537,043	100.0%	99.8477%	21.21
unitig_3752	521,501	100.0%	99.9436%	34.06
unitig_46	450,455	100.0%	99.9056%	31.53
unitig_3623	395,665	100.0%	99.9219%	21.73
unitig_57	387,489	99.58%	99.9103%	24.36
unitig_51	387,366	100.0%	99.9479%	34.9
unitig_4002	352,537	100.0%	99.9314%	32.77
unitig_4003	343,049	100.0%	99.9612%	36.91
unitig_4010	330,279	100.0%	99.9761%	62.17
unitig_3712	274,827	100.0%	99.9138%	22.71
unitig_3632	247,086	100.0%	99.8822%	26.25
unitig_44	240,679	100.0%	99.8700%	28.06
unitig_3888	235,561	100.0%	99.8884%	20.61
unitig_3930	231,977	100.0%	99.8815%	22.85
unitig_3968	230,444	100.0%	99.8919%	25.85
unitig_3984	229,146	100.0%	99.9206%	22.45
unitig_142	228,882	100.0%	99.9183%	22.87
unitig_3890	224,208	100.0%	99.9269%	22.69
unitig_203	219,446	100.0%	99.8929%	25.82
unitig_3477	212,493	98.97%	99.9025%	23.29
unitig_3571	201,822	100.0%	99.9232%	23.89
unitig_263	199,421	100.0%	99.8440%	20.85
unitig_239	198,065	100.0%	99.9101%	22.7
unitig_3656	197,023	100.0%	99.8828%	21.94

Corrections Across Reference

Observed variants across unitig_3545.

Observed variants across unitig_37.

Observed variants across unitig_3752.

Observed variants across unitig_46.

Observed variants across unitig_3623.

Observed variants across unitig_57.