

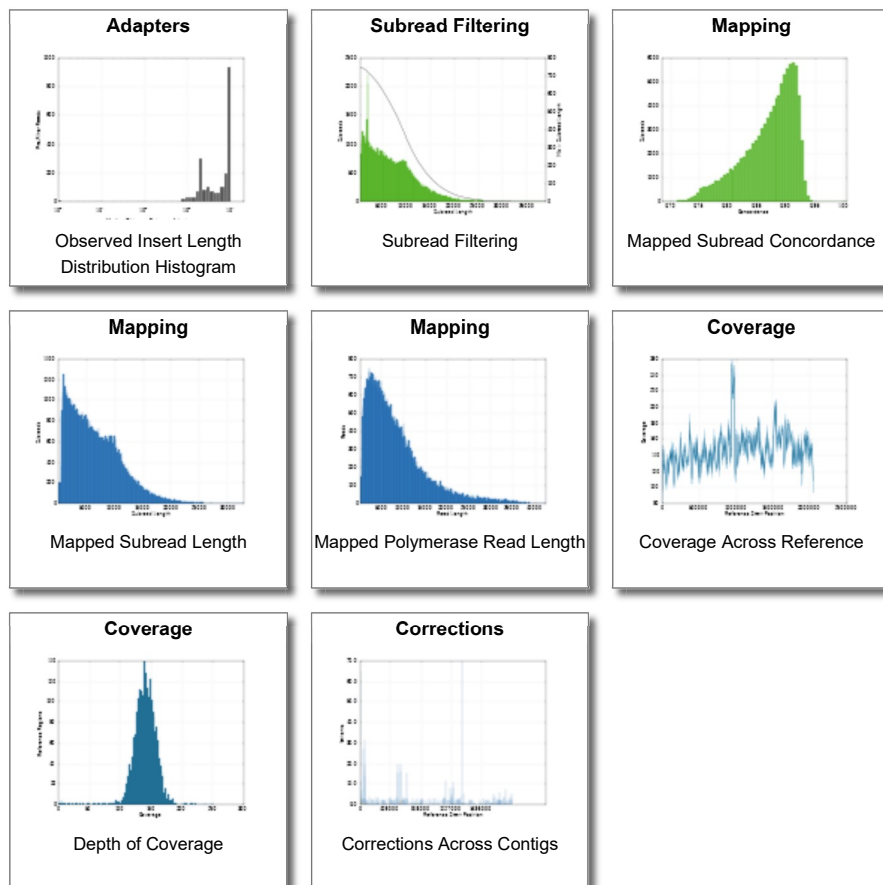
Reports for Job pb_359_2-20000



SMRT Cells: 1 Movies: 1

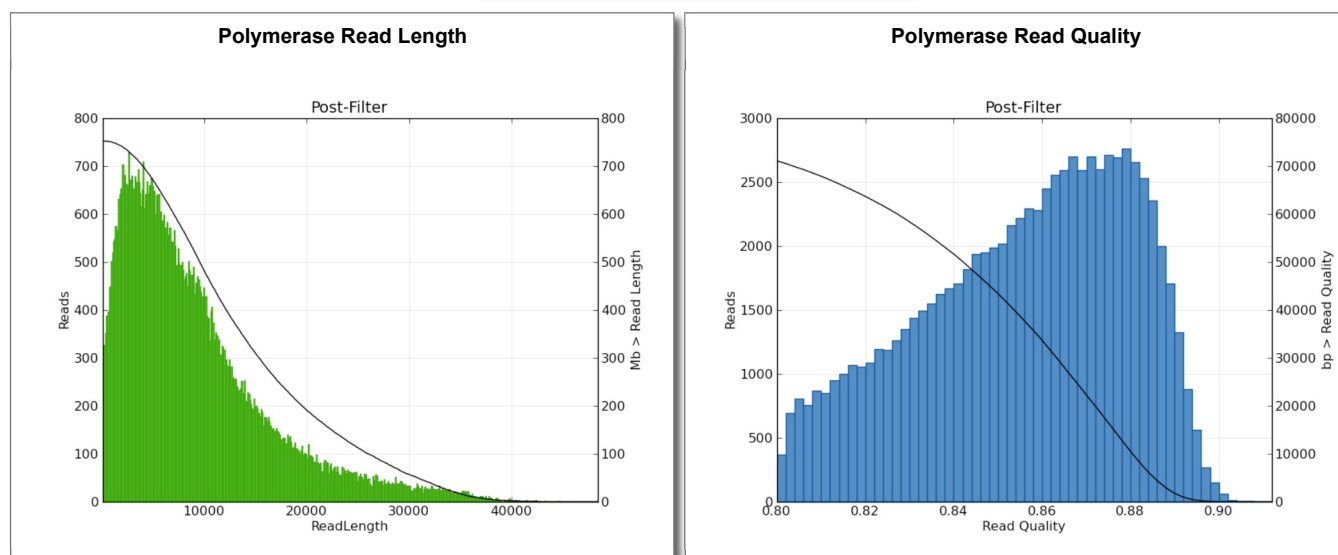
Overview

Job Metric	Value
Polished Contigs	5
Adapter Dimers (0-10bp)	0.02%
Short Inserts (11-100bp)	0.0%
Number of Bases	756,426,295
Number of Reads	83,546
N50 Read Length	12,916
Mean Read Length	9,054
Mean Read Score	0.85
Mapped Reads	78,262
Mapped Read Length of Insert	6,397
Average Reference Length	871,133
Average Reference Bases Called	100.0%
Average Reference Consensus Concordance	99.96%
Average Reference Coverage	144.64



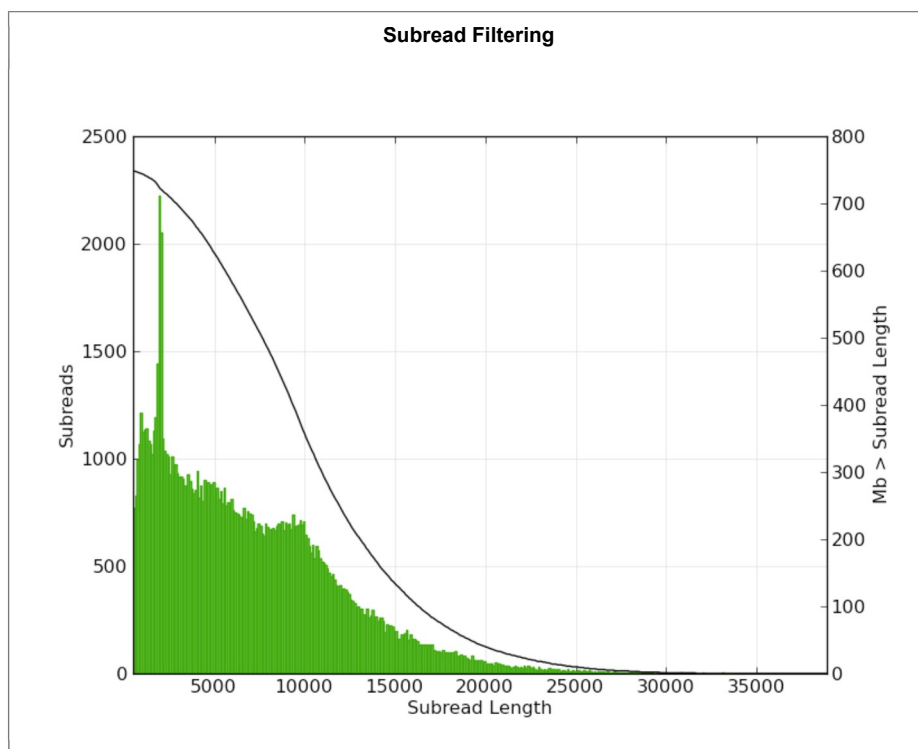
Filtering

Filtering		
Metrics	Pre-Filter	Post-Filter
Polymerase Read Bases	844379722	756426295
Polymerase Reads	150292	83546
Polymerase Read N50	12545	12916
Polymerase Read Length	5618	9054
Polymerase Read Quality	0.538	0.854



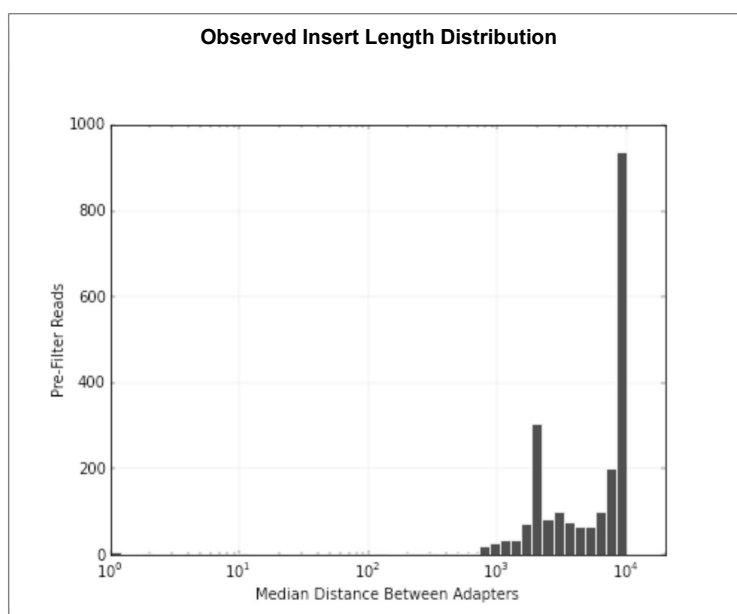
Subread Filtering

Mean Subread length	6,938	N50	9,822
Total Number of Bases	754,186,317	Number of Reads	108,700



Adapters

Adapter Dimers (0-10bp) 0.02%
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
m160816_190022_42203_c101086032550000001823265803091732	150,292	24.34%	61.81%	13.84%

Mapping

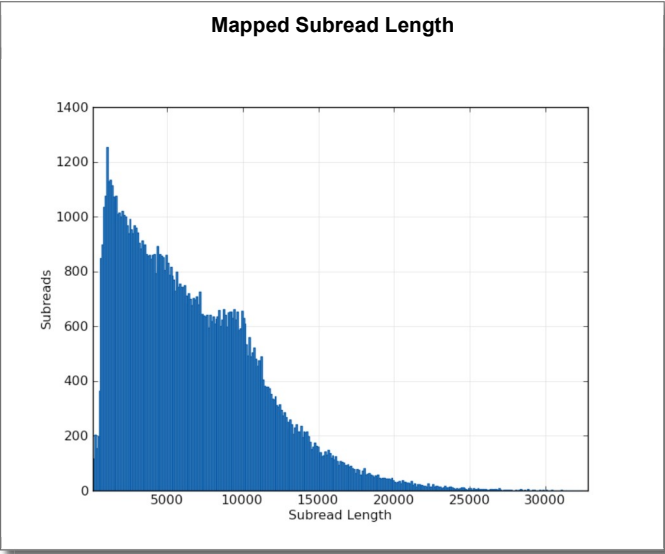
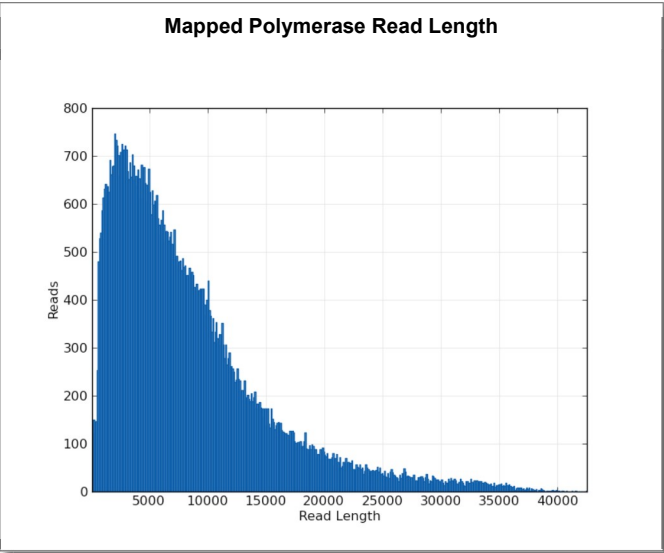
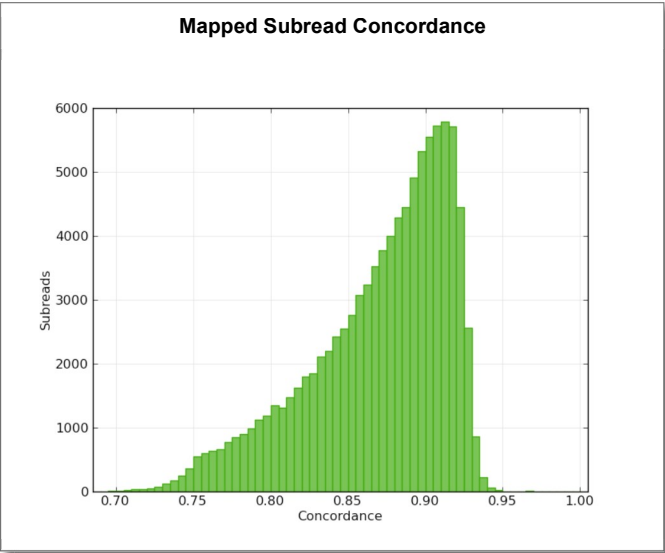
Mapped Subread Length N50 (bp) 9,347 Mapped Polymerase Read Length 95% (bp) 22,380
Mapped Subread Length Mean (bp) 6,559 Mapped Polymerase Read Length Max (bp) 42,377

Mapping Stats Summary

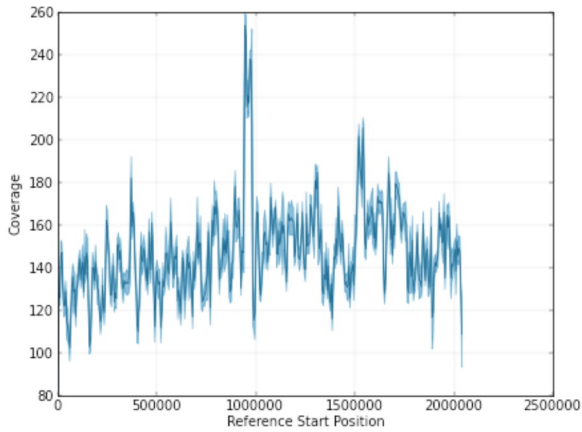
Movie	Mapped Read	Mapped Polymerase Read Length	Mapped Polymerase Read Length N50	Mapped Subreads	Mapped Subread Bases	Mapped Subread Length	Mean Mapped Subread Concordance
All Movies	78,262	8,305	11795	98,462	645786155	6,559	0.865
m160816_190022_42203_c101086032550000001823265803091732_s1_p0	78,262	8,305	11795	98,462	645786155	6,559	0.865

Coverage

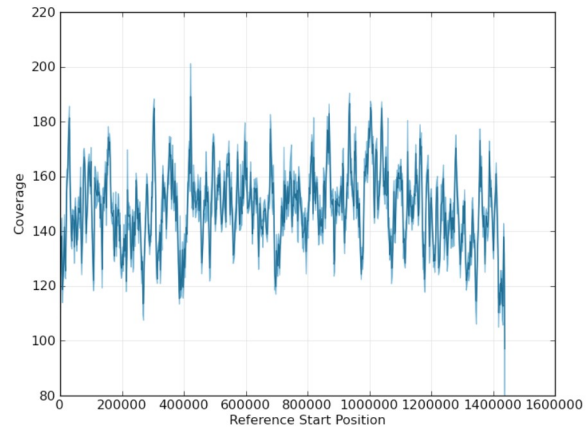
Mean Coverage 144.64
Missing Bases (%) 0.0



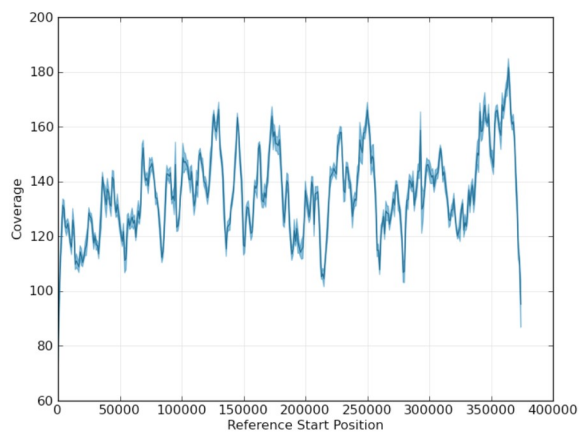
Coverage Across Reference



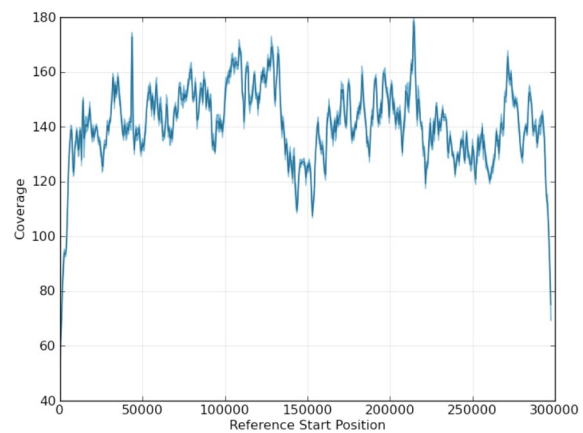
Observed depth of coverage across scf718000000012 (window size = 5002bp).



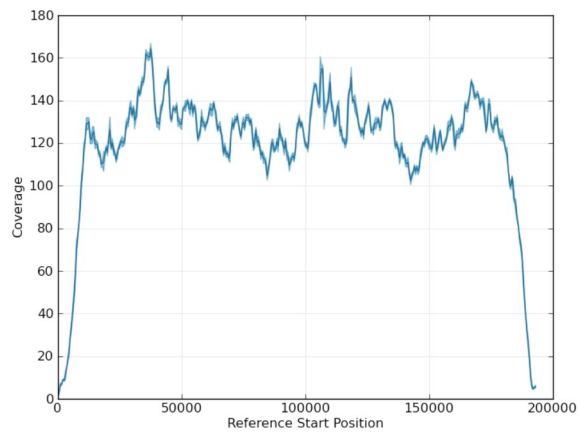
Observed depth of coverage across scf718000000013 (window size = 2002bp).



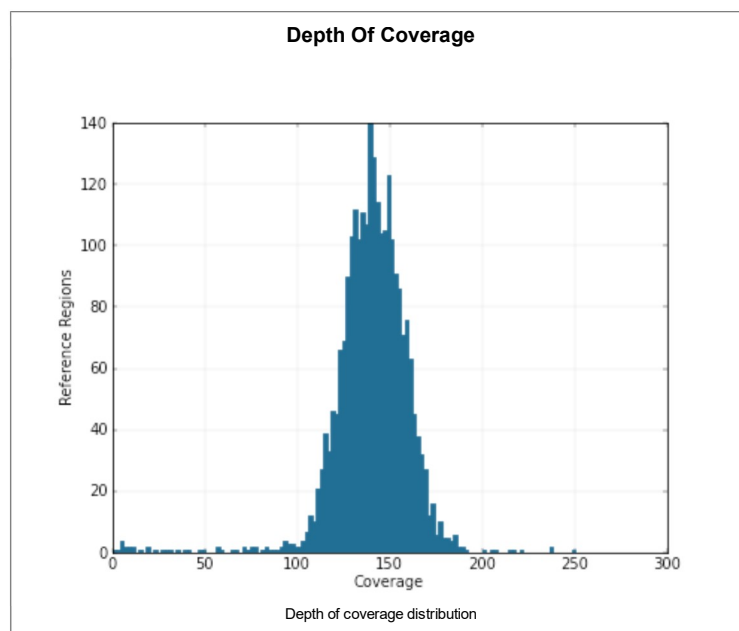
Observed depth of coverage across scf718000000014 (window size = 1002bp).



Observed depth of coverage across scf718000000016 (window size = 500bp).



Observed depth of coverage across scf718000000015 (window size = 500bp).

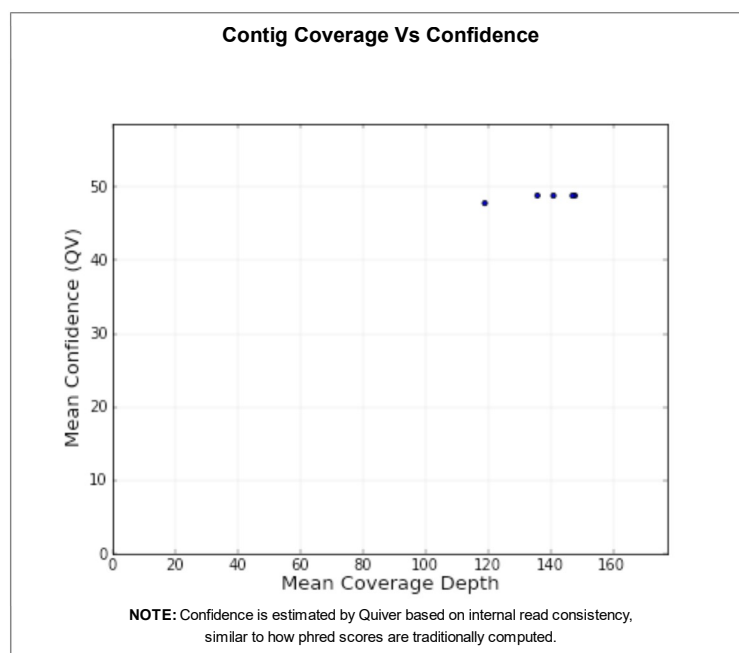


Pre-Assembler Report

Polymerase Read Bases	754,186,317	Length Cutoff	20,000
Seed Bases	41,228,974	Pre-Assembled bases	30,899,087
Pre-Assembled Yield	.749	Pre-Assembled Reads	2,440
Pre-Assembled Reads Length	12,663	Pre-Assembled N50	20,080

Polished Assembly

Polished Contigs	5	Max Contig Length	2,046,678
N50 Contig Length	1,442,524	Sum of Contig Lengths	4,357,721



Top Corrections

Sequence	Position	Correction	Type	Coverage	Confidence	Genotype
scf7180000000012	1,377,410	1377410_1377411insG	INS	100	54	haploid
scf7180000000013	886,596	886596_886597insG	INS	100	54	haploid
scf7180000000012	63,351	63351_63352insG	INS	100	53	haploid
scf7180000000012	552,686	552686_552687insC	INS	100	53	haploid
scf7180000000013	1,264,480	1264480_1264481insC	INS	100	53	haploid
scf7180000000013	1,327,821	1327821_1327822insG	INS	100	53	haploid
scf7180000000013	1,434,225	1434225_1434226insG	INS	100	53	haploid
scf7180000000016	915	915_916insC	INS	67	53	haploid
scf7180000000016	213,931	213931_213932insC	INS	100	53	haploid
scf7180000000016	295,316	295316_295317insC	INS	100	53	haploid
scf7180000000012	291	291_292insC	INS	71	52	haploid
scf7180000000012	52,604	52604_52605insA	INS	100	52	haploid
scf7180000000012	55,406	55406_55407insG	INS	100	52	haploid
scf7180000000012	168,048	168048_168049insG	INS	100	52	haploid
scf7180000000012	399,152	399152_399153insC	INS	100	52	haploid
scf7180000000012	510,499	510499_510500insG	INS	100	52	haploid
scf7180000000012	545,694	545694_545695insC	INS	100	52	haploid
scf7180000000012	589,360	589360_589361insC	INS	100	52	haploid
scf7180000000012	806,993	806993_806994insG	INS	100	52	haploid
scf7180000000012	947,679	947679_947680insC	INS	100	52	haploid
scf7180000000012	1,028,802	1028802_1028803insG	INS	100	52	haploid
scf7180000000012	1,132,483	1132483_1132484insC	INS	100	52	haploid
scf7180000000012	1,657,369	1657369_1657370insT	INS	100	52	haploid
scf7180000000012	1,735,541	1735541_1735542insC	INS	100	52	haploid
scf7180000000013	93,301	93301_93302insC	INS	100	52	haploid
scf7180000000013	168,188	168188_168189insG	INS	100	52	haploid
scf7180000000013	201,214	201214_201215insC	INS	100	52	haploid
scf7180000000013	238,172	238172_238173insG	INS	100	52	haploid
scf7180000000013	449,744	449744_449745insG	INS	100	52	haploid
scf7180000000013	637,638	637638_637639insG	INS	100	52	haploid
scf7180000000013	756,433	756433_756434insC	INS	100	52	haploid
scf7180000000013	788,512	788512_788513insT	INS	100	52	haploid
scf7180000000013	806,984	806984_806985insC	INS	100	52	haploid
scf7180000000013	832,333	832333_832334insC	INS	100	52	haploid
scf7180000000013	940,302	940302_940303insG	INS	100	52	haploid
scf7180000000013	1,130,542	1130542_1130543insA	INS	100	52	haploid
scf7180000000013	1,229,339	1229339_1229340insC	INS	100	52	haploid
scf7180000000013	1,321,763	1321763_1321764insC	INS	100	52	haploid
scf7180000000013	1,414,260	1414260_1414261insC	INS	100	52	haploid
scf7180000000013	1,429,806	1429806_1429807insC	INS	100	52	haploid
scf7180000000013	1,440,308	1440308_1440309insC	INS	93	52	haploid
scf7180000000014	186,615	186615_186616insC	INS	100	52	haploid
scf7180000000015	137,046	137046_137047insA	INS	100	52	haploid
scf7180000000016	239	239_240insC	INS	61	52	haploid
scf7180000000016	72,990	72990_72991insG	INS	100	52	haploid
scf7180000000016	116,394	116394_116395insC	INS	100	52	haploid
scf7180000000016	143,340	143340_143341insG	INS	100	52	haploid
scf7180000000016	174,342	174342_174343insC	INS	100	52	haploid
scf7180000000016	295,482	295482_295483insC	INS	100	52	haploid
scf7180000000012	32	32_33insA	INS	45	51	haploid
scf7180000000012	1,085	1085_1086insG	INS	83	51	haploid
scf7180000000012	2,274	2274_2275insC	INS	98	51	haploid
scf7180000000012	5,304	5304_5305insG	INS	100	51	haploid
scf7180000000012	5,403	5403_5404insA	INS	100	51	haploid
scf7180000000012	11,244	11244_11245insG	INS	100	51	haploid
scf7180000000012	14,806	14806_14807insG	INS	100	51	haploid
scf7180000000012	25,977	25977_25978insG	INS	100	51	haploid
scf7180000000012	42,420	42420_42421insG	INS	100	51	haploid
scf7180000000012	46,662	46662_46663insG	INS	100	51	haploid
scf7180000000012	52,637	52637_52638insC	INS	100	51	haploid
scf7180000000012	53,139	53139_53140insG	INS	100	51	haploid
scf7180000000012	53,477	53477_53478insG	INS	100	51	haploid
scf7180000000012	53,496	53496_53497insC	INS	100	51	haploid
scf7180000000012	53,545	53545_53546insT	INS	100	51	haploid
scf7180000000012	58,761	58761_58762insC	INS	100	51	haploid
scf7180000000012	67,078	67078_67079insG	INS	100	51	haploid

Corrections

Consensus Calling Results				
Reference	Reference Length	Bases Called	Consensus Concordance	Coverage
scf7180000000012	2,045,874	100.0%	99.9675%	147.03
scf7180000000013	1,441,836	100.0%	99.9589%	147.79
scf7180000000014	375,927	100.0%	99.9649%	135.78
scf7180000000016	298,189	100.0%	99.9366%	140.91
scf7180000000015	193,841	99.92%	99.9494%	118.97

Corrections Across Reference

Insertions
Deletions
Substitutions

