Assembly Report

Experiment Details

ExperimentID:	Experiment 62
Sequencing Coverage:	35
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	151

Reads Dataset Details

Total Reads Count:	1203
Total Dataset Size in (Base):	359763
Valid Read Count:	1203
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9780
Length of K-mer	637

Assembly Details

Number of Contigs:	13
Contig N50:	1751
Contig N90:	1416
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	385
Total Reads Count(Repeat):	10
Retetitve Read Count based on (Partitions Identifier):	4
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	15
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4200		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	10080	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TATACCTGCGA CCCGCGTCAG GTGCCCGATG CGAGGTTGTT GAAGTCGATG TCCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC	4	350	

Start Position	End Position
1376	1725
4127	4476
6570	6919
8665	9014

					Start Position	End Position
1	10080	GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC	4	350	3285	3634
					4858	5207
					7202	7551
					9332	9681

1	10080	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT	4	350	Start Position	End Position
					1	350
					799	1148
					2039	2388
					8043	8392

SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	395

Reads Count after Overlapping:	118
Initial Dataset Size in (Base):	359763
Dataset Sizet after Removing Duplication:	151772
Dataset Size after Overlapping:	45935

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:04m:52s:000ms
Reads Alignment Time:	00h:00m:12s:000ms
Total Hybrid Assembly Time:	00h:05m:04s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	148225	89	3	0
299	145924	83	2	0
297	144400	63	2	0
296	142884	89	3	0
295	140625	103	3	0
294	138384	87	1	0
291	137641	70	1	0
288	136900	86	2	0
287	135424	78	1	0
286	134689	63	1	0
284	133956	90	1	0
283	133225	71	1	0

282	132496	96	1	0
279	131769	54	1	0
276	131044	391	173	0
261	35721	9	1	0
259	35344	24	1	0
251	34969	16	5	0
231	33124	19	1	0
227	32761	22	1	0
226	32400	171	69	0
223	12321	7	1	0
220	12100	11	1	0
215	11881	6	1	0