Assembly Report

Experiment Details

ExperimentID:	Experiment 61
Sequencing Coverage:	35
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

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:	16
Contig N50:	1776
Contig N90:	1326
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	389
Total Reads Count(Repeat):	6
Retetitve Read Count based on (Partitions Identifier):	0
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
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

1	10080	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	4	350	Start Position	End Position
					3285	3634
					4858	5207
					7202	7551
					9332	9681

| 1 | 10080 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT | 4 | 350 | |

| 1 | 10080 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT | 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:	113
Initial Dataset Size in (Base):	359763
Dataset Sizet after Removing Duplication:	151772
Dataset Size after Overlapping:	44555

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:05m:52s:000ms
Reads Alignment Time:	00h:00m:11s:000ms
Total Hybrid Assembly Time:	00h:06m:03s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	151321	89	3	0
299	148996	85	3	0
297	146689	64	3	0
296	144400	89	3	0
295	142129	106	4	0
294	139129	88	1	0
288	138384	86	2	0
287	136900	79	1	0
286	136161	63	1	0
284	135424	91	1	0
283	134689	71	1	0
279	133956	54	1	0

276	133225	397	175	0
261	36100	10	1	0
259	35721	24	1	0
257	35344	19	1	0
254	34969	11	1	0
251	34596	12	5	0
231	32761	18	1	0
226	32400	176	70	0
223	12100	6	1	0
220	11881	11	1	0
215	11664	5	1	0