Assembly Report

Experiment Details

ExperimentID:	Experiment 39
Sequencing Coverage:	31
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

Reads Dataset Details

Total Reads Count:	1045
Total Dataset Size in (Base):	313765
Valid Read Count:	1045
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	501

Assembly Details

Number of Contigs:	13
Contig N50:	1726
Contig N90:	1426
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	289
Total Reads Count(Repeat):	101
Retetitve Read Count based on (Partitions Identifier):	101
Retetitve Read Count (Entire Read Frequency Identifier):	1
Retetitve Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	775
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			2800		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	10080	GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	8	350	

Start Position	End Position
1	350
765	1114
1400	1749
3146	3495
4226	4575
6742	7091
7650	7999
8549	8898

SRGD Performance Metrics

Initial Reads Count:	1045
Reads Count after Removing Duplication:	390
Reads Count after Overlapping:	191
Initial Dataset Size in (Base):	313765
Dataset Sizet after Removing Duplication:	128349
Dataset Size after Overlapping:	65189

Overlapping Metrics

Repeat Identification Time:	00h:00m:15s:000ms
Overlapping Time:	00h:05m:48s:000ms
Reads Alignment Time:	00h:00m:19s:000ms
Total Hybrid Assembly Time:	00h:06m:07s:000ms
Repeat Annotation Time:	00h:01m:05s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
297	83521	45	1	0
282	82944	33	1	0
276	82369	348	141	0
251	21316	13	2	0
226	20736	139	54	0