Assembly Report

Experiment Details

ExperimentID:	Experiment 102
Sequencing Coverage:	21
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

Total Reads Count:	2205
Total Dataset Size in (Base):	440864
Valid Read Count:	2205
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19960
Length of K-mer	472

Assembly Details

Number of Contigs:	53
Contig N50:	1112
Contig N90:	926
Number of Scaffold	4
Scaffold N50:	6301
Scaffold N90:	5208
Mis-assembly Count:	0
TotalAssembly Size:	20885

Repeat Details

Total Reads Count(Non-Repeat) :	774
Total Reads Count(Repeat):	30
Retetitve Read Count based on (Partitions Identifier):	24
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	29
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			1100		

Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
11542	17842	ATTACAGAGTA CACAACATCCT CAAAGCCTAC CGGTGACAGT GCGGGCTTTTT TTTCGACCAAA GGTAACGAGG TAACAACTCAT GGCATGCGAG TGTTGAAGTTT TCAGGAGATC CTAAAGGCAG GCTGTACCCG TTACCTAGCCA GTTGGCATTAA ACGTATCCTAG ACGGTACCTA GGCATGCCCT ACGTAATCGTA GCCTTAGCAAT CTCCAGTCC	5	220	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>11805</td><td>12024</td></tr><tr><td>12025</td><td>12244</td></tr><tr><td>14483</td><td>14702</td></tr><tr><td>15074</td><td>15293</td></tr><tr><td>17242</td><td>17461</td></tr></table>

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	804
Reads Count after Overlapping:	382
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	182580

Dataset Size after Overlapping:		86555		

Overlapping Metrics

Repeat Identification Time:		00h:00m:04s:000ms		
Overlapping Time:		00h:01m:38s:000ms		
Reads Alignment Time:		00h:00m:12s:000ms		
Total Hybrid Assembly Time:		00h:01m:50s:000ms		
Repeat Annotation Time:		00h:00m:02s:000ms		

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	599076	219	5	0
199	591361	278	18	0
198	564001	226	9	0
197	550564	222	1	0
195	549081	207	6	0
194	540225	211	7	0
193	529984	181	2	0
192	527076	218	1	0
189	525625	197	5	0
187	518400	180	1	0
185	516961	194	1	0
180	515524	202	2	0
178	512656	214	1	0
176	511225	822	344	0
174	137641	70	2	0
173	136161	41	1	0
169	135424	51	1	0

168	134689	48	1	0
166	133956	36	1	0
161	133225	51	1	0
158	132496	62	1	0
155	131769	60	1	0
151	131044	36	7	0
144	126025	43	1	0
143	125316	36	1	0
140	124609	50	1	0