Assembly Report

Experiment Details

ExperimentID:	Experiment 103
Sequencing Coverage:	21
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

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	376

Assembly Details

Number of Contigs:	43
Contig N50:	1126
Contig N90:	926
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	596
Total Reads Count(Repeat):	208
Retetitve Read Count based on (Partitions Identifier):	207
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	2103
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			6350		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	20160	ATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACTCATGGCATGCGAGTGTTGAAGTTTCAGGAGATCCTAAAGGCAGGCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATCCTAGACGGTACCTAGGCATGCCCTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	12	220	(see sub-table below)

Start Position	End Position
1378	1597
4303	4522
6540	6759
9446	9665
10326	10545
11805	12024
12025	12244
14483	14702
15074	15293
17242	17461
18978	19197
19552	19771

1	20160	CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC	5	350		
					Start Position	End Position
					2991	3340
					7647	7996
					11393	11742
					15570	15919
					17484	17833

					Start Position	End Position
1	20160	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGC	7	280	1	280
					2048	2327
					5070	5349
					8493	8772
					13510	13789
					16232	16511
					18474	18753

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	804
Reads Count after Overlapping:	503
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	182580

Dataset Size after Overlapping:	108530

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:01m:37s:000ms
Reads Alignment Time:	00h:00m:20s:000ms
Total Hybrid Assembly Time:	00h:01m:57s:000ms
Repeat Annotation Time:	00h:02m:25s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
199	355216	135	6	0
197	348100	121	6	0
189	341056	109	1	0
182	339889	121	3	0
179	336400	112	1	0
176	335241	620	274	0
173	93025	25	1	0
163	92416	32	1	0
157	91809	31	1	0
156	91204	29	1	0
155	90601	32	1	0
151	90000	21	5	0