Assembly Report

Experiment Details

ExperimentID:	Experiment 100
Sequencing Coverage:	21
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

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	313

Assembly Details

Number of Contigs:	51
Contig N50:	1176
Contig N90:	876
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	505
Total Reads Count(Repeat):	287
Retetitve Read Count based on (Partitions Identifier):	287
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3650
Total Unique Repetitive Sequences Count	6

Total Repeat Size (Base)			6800		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	20160	ATTACAGAGTA CACAACATCCT CAAAGCCTAC CGGTGACAGT GCGGGCTTTTT TTTCGACCAAA GGTAACGAGG TAACAACTCAT GGCATGCGAG TGTTGAAGTTT TCAGGAGATC CTAAAGGCAG GCTGTACCCG TTACCTAGCCA GTTGGCATTAA ACGTATCCTAG ACGGTACCTA GGCATGCCCT ACGTAATCGTA GCCTTAGCAAT CTCCAGTCC	8	220	(see positions table below)

Start Position	End Position
1378	1597
4583	4802
6820	7039
10076	10295
12215	12434
14561	14780
17100	17319
19552	19771

1	20160	CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC	8	350		

Start Position	End Position
3271	3620
7927	8276
8750	9099
11803	12152
13026	13375
15428	15777
17342	17691
18939	19288

1	20160	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGC	8	280	Start Position	End Position
					1	280
					1693	1972
					2328	2607
					5350	5629
					9123	9402
					14050	14329
					16090	16369
					18332	18611

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	792
Reads Count after Overlapping:	544
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	180168

Dataset Size after Overlapping:	115589

Overlapping Metrics

Repeat Identification Time:	00h:00m:15s:000ms
Overlapping Time:	00h:03m:45s:000ms
Reads Alignment Time:	00h:01m:11s:000ms
Total Hybrid Assembly Time:	00h:04m:56s:000ms
Repeat Annotation Time:	00h:11m:48s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
193	255025	80	1	0
192	254016	75	1	0
189	253009	80	3	0
188	250000	72	2	0
184	248004	74	1	0
176	247009	537	234	0
151	69169	17	6	0