Assembly Report

Experiment Details

ExperimentID:	Experiment 89
Sequencing Coverage:	27
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	63

Reads Dataset Details

Total Reads Count:	2200
Total Dataset Size in (Base):	549860
Valid Read Count:	2200
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19910
Length of K-mer	591

Assembly Details

Number of Contigs:	31
Contig N50:	1576
Contig N90:	1270
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	536
Total Reads Count(Repeat):	251
Retetitve Read Count based on (Partitions Identifier):	248
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	2959
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			8400		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	20160	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	8	350	See positions table below

Start Position	End Position
2832	3181
7245	7594
8068	8417
10761	11110
11904	12253
14881	15230
16995	17344
18809	19158

| 1 | 20160 | GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC | 8 | 350 | Start/End table |

Start Position	End Position
871	1220
4144	4493
6008	6357
9464	9813
11173	11522
13704	14053
16623	16972
19422	19771

| 1 | 20160 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT | 8 | 350 |

Start Position	End Position
1	350
1316	1665
2021	2370
5041	5390
8441	8790
13123	13472
15543	15892
18132	18481

SRGD Performance Metrics

Initial Reads Count:	2200
Reads Count after Removing Duplication:	787

Reads Count after Overlapping:	407
Initial Dataset Size in (Base):	549860
Dataset Sizet after Removing Duplication:	224564
Dataset Size after Overlapping:	116498

Overlapping Metrics

Repeat Identification Time:	00h:00m:09s:000ms
Overlapping Time:	00h:03m:48s:000ms
Reads Alignment Time:	00h:00m:30s:000ms
Total Hybrid Assembly Time:	00h:04m:18s:000ms
Repeat Annotation Time:	00h:04m:39s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
249	287296	108	6	0
248	280900	104	1	0
246	279841	134	5	0
245	274576	93	1	0
242	273529	118	3	0
241	270400	121	3	0
237	267289	120	1	0
236	266256	101	1	0
235	265225	114	1	0
233	264196	85	2	0
231	262144	133	2	0
228	260100	95	2	0

226	258064	562	242	0
201	70756	24	7	0
196	67081	29	1	0
191	66564	27	1	0
183	66049	26	2	0
181	65025	25	1	0
176	64516	230	98	0