Assembly Report

Experiment Details

ExperimentID:	Experiment 51
Sequencing Coverage:	23
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	378

Assembly Details

Number of Contigs:	28
Contig N50:	926
Contig N90:	826
Number of Scaffold	2
Scaffold N50:	2491
Scaffold N90:	2491
Mis-assembly Count:	0
TotalAssembly Size:	10371

Repeat Details

Total Reads Count(Non-Repeat) :	393
Total Reads Count(Repeat):	6
Retetitve Read Count based on (Partitions Identifier):	0
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3500		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	2491	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	3	350	(see positions table)

Positions:

Start Position	End Position
1	350
799	1148
2039	2388

| 2201 | 10080 | CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC | 3 | 350 |

Start Position	End Position
4127	4476
6570	6919
8665	9014

2201	10080	GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC	4	350		

Start Position	End Position
3285	3634
4858	5207
7202	7551
9332	9681

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	399

Reads Count after Overlapping:	169
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	101376
Dataset Size after Overlapping:	38685

Overlapping Metrics

Repeat Identification Time:	00h:00m:17s:000ms
Overlapping Time:	00h:04m:38s:000ms
Reads Alignment Time:	00h:00m:19s:000ms
Total Hybrid Assembly Time:	00h:04m:57s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	154449	90	11	0
199	145924	81	11	0
197	137641	61	7	0
196	132496	87	11	0
195	124609	97	12	0
194	116281	73	1	0
188	115600	74	6	0
187	111556	57	1	0
186	110889	55	1	0
184	110224	69	3	0
183	108241	54	1	0
179	107584	42	1	0

176	106929	345	154	0
161	29929	10	1	0
159	29584	18	1	0
157	29241	20	1	0
154	28900	8	1	0
151	28561	10	6	0