Assembly Report

Experiment Details

ExperimentID:	Experiment 46
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:	24
Contig N50:	989
Contig N90:	876
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	390
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)			6000		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	10080	CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTA	8	250	Start Position / End Position

Start Position	End Position
1539	1788
3069	3318
3377	3626
4616	4865
5414	5663
6700	6949
7986	8235
8904	9153

					Start Position	End Position
1	10080	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCA	8	250	374	623
					1975	2224
					2790	3039
					4278	4527
					5006	5255
					6355	6604
					7714	7963
					9343	9592

1	10080	GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGG	8	250	Start Position	End Position
					1	250
					779	1028
					1178	1427
					2353	2602
					3783	4032
					5902	6151
					7170	7419
					8449	8698

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	180
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	100773
Dataset Size after Overlapping:	40767

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:03m:02s:000ms
Reads Alignment Time:	00h:00m:15s:000ms
Total Hybrid Assembly Time:	00h:03m:17s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	152100	140	10	0
199	144400	170	8	0
198	138384	154	8	0
197	132496	122	6	0
195	128164	130	5	0
194	124609	107	2	0
193	123201	101	1	0
190	122500	113	1	0
189	121801	125	3	0
188	119716	110	1	0
186	119025	118	1	0
185	118336	111	1	0
182	117649	116	1	0
181	116964	109	1	0
179	116281	109	1	0
176	115600	383	158	0
172	33124	34	1	0
170	32761	24	1	0
152	32400	28	1	0

| 151 | 32041 | 23 | 5 | 0 |