Assembly Report

Experiment Details

ExperimentID:	Experiment 70
Sequencing Coverage:	23
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

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	301

Assembly Details

Number of Contigs:	24
Contig N50:	951
Contig N90:	676
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	39
Total Reads Count(Repeat):	349
Retetitve Read Count based on (Partitions Identifier):	349
Retetitve Read Count (Entire Read Frequency Identifier):	4
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	7317
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			8806		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	10080	CGGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCGTCGATATTGCTGAGTCCACCCGCCGTATTGCGGCAAGTCGTATTCCGGCTGATCACATGGTGCTGATGGCAGGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCC	8	350	

Start Position	End Position
1756	2105
3561	3910
3964	4313
5117	5466
5910	6259
7138	7487
8386	8735
9149	9498

1	10080	GATTCATTCGGGATGGTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCTCAAAGCCTACCGGTGACAGTGCGGGCTTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGTCAGGAGATCCTAAAGGCCTGTACCCGTTACCTAGCCAGTTGGCATTAAACGTATACGGTACCTAGGCATGTACGTAATCGTAGCCTTAGCAATCTCCAGTCC	8	350		

Start Position	End Position
409	758
2228	2577
3182	3531
4730	5079
5529	5878
6730	7079
8014	8363
9552	9901

| 1 | 10080 | GCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTGGTTACCTGCCGTGAGTAAATTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGTAACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTCGACCAAAGGTAACGAGGTAACAACCATGCGAGTGTTGAAGT | 8 | 350 |

<table>
Start Position	End Position
1	350
854	1203
1295	1644
2705	3054
4337	4686
6359	6708
7574	7923
8752	9101
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1	10080	GTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTGCCTGTTTACGCGCCGATTGTTGCGAGATTTGGACGGACGTTGACGGGGTCTATACCTGCGACCCGCGTCAGGTGCCCGATGCGAGGTTGTTGAAGTCGATGTCCTACCAGGAAGCGATGGAGCTTTCCTACTTCGGCGCTCTAGGTCAGGCCTA	2	203	Start Position	End Position
					1905	2107
					7287	7489

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388
Reads Count after Overlapping:	370
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	99165
Dataset Size after Overlapping:	74824

Overlapping Metrics

Repeat Identification Time:	00h:00m:21s:000ms

Overlapping Time:		00h:03m:28s:000ms		
Reads Alignment Time:		00h:01m:14s:000ms		
Total Hybrid Assembly Time:		00h:04m:42s:000ms		
Repeat Annotation Time:		00h:39m:25s:000ms		
Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	1521	3	1	0
176	1444	28	16	0
151	484	1	1	0