Assembly Report

Experiment Details

ExperimentID:	Experiment 75
Sequencing Coverage:	29
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	576

Assembly Details

Number of Contigs:	15
Contig N50:	1576
Contig N90:	1349
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	53
Total Reads Count(Repeat):	337
Retetitve Read Count based on (Partitions Identifier):	337
Retetitve Read Count (Entire Read Frequency Identifier):	3
Retetitve Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	6529
Total Unique Repetitive Sequences Count	6

Total Repeat Size (Base)			8400		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	10080	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	

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

1	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	8	350		
					Start Position	End Position
					409	758
					2228	2577
					3182	3531
					4730	5079
					5529	5878
					6730	7079
					8014	8363
					9552	9901

1	10080	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 GGCTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	8	350	

Start Position	End Position
1	350
854	1203
1295	1644
2705	3054
4337	4686
6359	6708
7574	7923
8752	9101

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	359
Initial Dataset Size in (Base):	301119
Dataset Sizet after Removing Duplication:	124917
Dataset Size after Overlapping:	91159

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:01m:55s:000ms
Reads Alignment Time:	00h:00m:18s:000ms
Total Hybrid Assembly Time:	00h:02m:13s:000ms
Repeat Annotation Time:	00h:15m:39s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
244	2809	15	4	0
233	2401	15	2	0
226	2209	32	16	0
208	961	3	1	0
201	900	2	2	0
183	784	5	1	0
176	729	9	5	0