

Assembly Report

Experiment Details

ExperimentID:	Experiment 30
Sequencing Coverage:	20
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

Reads Dataset Details

Total Reads Count:	1054
Total Dataset Size in (Base):	211074
Valid Read Count:	1054
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	305

Assembly Details

Number of Contigs:	21
Contig N50:	1076
Contig N90:	976
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	281
Total Reads Count(Repeat):	105
Retetitive Read Count based on (Partitions Identifier):	105
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	1452
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3682			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGGTCTGCT GGCGAAGTCA CTCGGTCTGC CGGTGAA	2	37	Start Positio n	End Positio n
					2565	2601
					5765	5801

1	10080	GCTTTTCATTC TGA CTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACCC TGACAGTGCG GGCTTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	8	350		
					Start Positio n	End Positio n
					1	350
					765	1114
					1400	1749
					3146	3495
					4226	4575
					6742	7091
					7650	7999
					8549	8898

1	10080	TGCTTTTCATT CTGACTGCAA CGGGCAATAT GTCTCTGTGTG GATTAAAAAAA GAGTGTCTGAT AGCAGCTTCT GAACTGGTTAC CTGCCGTGAG TAAATTAAAAT TTTATTGACTT AGGTCACTAAA TACTTTAACCA ATATAGGCATA GCGCACAGAC AGATAAAAATT ACAGAGTACA CAACATCCATG AAACGCATTA	4	202		
					Start Positio n	End Positio n
					764	965
					1399	1600
					3145	3346
					7649	7850

SRGD Performance Metrics

Initial Reads Count:	1054
Reads Count after Removing Duplication:	386
Reads Count after Overlapping:	241
Initial Dataset Size in (Base):	211074
Dataset Sizet after Removing Duplication:	84645
Dataset Size after Overlapping:	52053

Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:03m:25s:000ms

Reads Alignment Time:		00h:00m:32s:000ms		
Total Hybrid Assembly Time:		00h:03m:57s:000ms		
Repeat Annotation Time:		00h:03m:19s:000ms		
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	78961	38	6	0
180	75625	32	3	0
176	73984	280	131	0
151	19881	10	5	0