

Assembly Report

Experiment Details

ExperimentID:	Experiment 5
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	386

Assembly Details

Number of Contigs:	28
Contig N50:	976
Contig N90:	826
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	371
Total Reads Count(Repeat):	27
Retetitive Read Count based on (Partitions Identifier):	27
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	160
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			1000			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	GCTTTTCATTC	4	250		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCBA				
		TATAGGCATAG				
		CGCACAGACA				
		GATAAAAATTA				
		CAGAGTACAC				
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
CACCACCATCA						
CCATTACCACA						
GGTAACGGTG						
CGGG						

SRGD Performance Metrics

Initial Reads Count:	1054
Reads Count after Removing Duplication:	398
Reads Count after Overlapping:	209
Initial Dataset Size in (Base):	211074

Dataset Siset after Removing Duplication:	87057
Dataset Size after Overlapping:	46773

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:01m:47s:000ms
Reads Alignment Time:	00h:00m:06s:000ms
Total Hybrid Assembly Time:	00h:01m:53s:000ms
Repeat Annotation Time:	00h:00m:03s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	137641	49	1	0
197	136900	58	1	0
177	136161	59	1	0
176	135424	390	183	0
151	34225	10	2	0
141	33489	15	1	0