

Assembly Report

Experiment Details

ExperimentID:	Experiment 31
Sequencing Coverage:	26
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	251

Reads Dataset Details

Total Reads Count:	1051
Total Dataset Size in (Base):	263021
Valid Read Count:	1051
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	492

Assembly Details

Number of Contigs:	18
Contig N50:	1468
Contig N90:	1376
Number of Scaffold	2
Scaffold N50:	3755
Scaffold N90:	3755
Mis-assembly Count:	0
TotalAssembly Size:	10848

Repeat Details

Total Reads Count(Non-Repeat) :	386
Total Reads Count(Repeat):	2
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	3
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			3150			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	7093	GCTTTTCATTC	6	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT			Start Position	End Position
		ACTTTAACCAA			1	350
		TATAGGCATAG			765	1114
		CGCACAGACA			1400	1749
		GATAAAAATTA			3146	3495
		CAGAGTACAC			4226	4575
		AACATCCATGA			6742	7091
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

6326	10080	GCTTTTCATTC	3	350		
		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						
AGCCCGCACCC						
TGACAGTGCG						
GGCTTTTTTTTT						
CGACCAAAGG						
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Start Positio n	End Positio n
6742	7091
7650	7999
8549	8898

SRGD Performance Metrics

Initial Reads Count:	1051
Reads Count after Removing Duplication:	388

Reads Count after Overlapping:	120
Initial Dataset Size in (Base):	263021
Dataset Siset after Removing Duplication:	106397
Dataset Size after Overlapping:	39663

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:02m:18s:000ms
Reads Alignment Time:	00h:00m:06s:000ms
Total Hybrid Assembly Time:	00h:02m:24s:000ms
Repeat Annotation Time:	00h:00m:00s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	148996	127	5	0
249	145161	95	4	0
248	142129	57	4	0
247	139129	78	5	0
246	135424	65	1	0
237	134689	70	3	0
236	132496	71	2	0
226	131044	455	175	0
225	34969	29	1	0
224	34596	22	1	0
208	34225	8	1	0
176	33856	192	66	0