

Assembly Report

Experiment Details

ExperimentID:	Experiment 34
Sequencing Coverage:	26
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	63

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	495

Assembly Details

Number of Contigs:	18
Contig N50:	1625
Contig N90:	926
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	315
Total Reads Count(Repeat):	73
Retetitive Read Count based on (Partitions Identifier):	73
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	533
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			2800			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	GCTTTTCATTC	8	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				
		GGCTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Initial Reads Count:	1051
Reads Count after Removing Duplication:	388
Reads Count after Overlapping:	171
Initial Dataset Size in (Base):	263021
Dataset Siset after Removing Duplication:	106397
Dataset Size after Overlapping:	51094

Overlapping Metrics

Repeat Identification Time:	00h:00m:42s:000ms
Overlapping Time:	00h:05m:46s:000ms
Reads Alignment Time:	00h:00m:07s:000ms
Total Hybrid Assembly Time:	00h:05m:53s:000ms
Repeat Annotation Time:	00h:00m:15s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
249	99225	59	3	0
247	97344	49	5	0
232	94249	48	2	0
230	93025	47	1	0
226	92416	341	146	0
205	24964	12	1	0
203	24649	10	1	0
182	24336	13	1	0
176	24025	152	57	0