

Assembly Report

Experiment Details

ExperimentID:	Experiment 33
Sequencing Coverage:	26
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	84

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:	15
Contig N50:	1376
Contig N90:	1026
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	307
Total Reads Count(Repeat):	81
Retetitive Read Count based on (Partitions Identifier):	80
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	668
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:	176
Initial Dataset Size in (Base):	263021
Dataset Sizet after Removing Duplication:	106397
Dataset Size after Overlapping:	52270

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:01m:57s:000ms
Reads Alignment Time:	00h:00m:08s:000ms
Total Hybrid Assembly Time:	00h:02m:05s:000ms
Repeat Annotation Time:	00h:00m:34s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
247	94249	46	5	0
236	91204	44	1	0
230	90601	46	1	0
226	90000	360	145	0
209	24025	9	1	0
201	23716	13	2	0
180	23104	12	1	0
176	22801	148	56	0