

Assembly Report

Experiment Details

ExperimentID:	Experiment 19
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	476

Assembly Details

Number of Contigs:	17
Contig N50:	1376
Contig N90:	1126
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):	25
Retetitive Read Count based on (Partitions Identifier):	24
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	46
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			1400			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	GCTTTTCATTC	4	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						

Initial Reads Count:	1051
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	142
Initial Dataset Size in (Base):	263021
Dataset Sizet after Removing Duplication:	108405
Dataset Size after Overlapping:	45229

Overlapping Metrics

Repeat Identification Time:	00h:00m:13s:000ms
Overlapping Time:	00h:04m:24s:000ms
Reads Alignment Time:	00h:00m:14s:000ms
Total Hybrid Assembly Time:	00h:04m:38s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
249	137641	53	3	0
247	135424	52	1	0
241	134689	56	1	0
228	133956	62	2	0
226	132496	386	178	0
203	34596	16	1	0
201	34225	11	3	0
178	33124	15	1	0
176	32761	180	64	0