

Assembly Report

Experiment Details

ExperimentID:	Experiment 16
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	476

Assembly Details

Number of Contigs:	17
Contig N50:	1376
Contig N90:	1201
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	394
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)			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:	125
Initial Dataset Size in (Base):	263021
Dataset Siset after Removing Duplication:	108405
Dataset Size after Overlapping:	41262

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:04m:19s:000ms
Reads Alignment Time:	00h:00m:13s:000ms
Total Hybrid Assembly Time:	00h:04m:32s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	155236	67	4	0
249	152100	58	3	0
247	149769	55	1	0
243	148996	64	4	0
241	145924	67	1	0
237	145161	63	2	0
226	143641	406	186	0
212	37249	11	1	0
201	36864	10	2	0

187	36100	20	1	0
176	35721	189	66	0