

Assembly Report

Experiment Details

ExperimentID:	Experiment 20
Sequencing Coverage:	26
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

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	451

Assembly Details

Number of Contigs:	18
Contig N50:	1226
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) :	347
Total Reads Count(Repeat):	49
Retetitive Read Count based on (Partitions Identifier):	49
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	433
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			<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1</td><td>350</td></tr><tr><td>799</td><td>1148</td></tr><tr><td>1434</td><td>1783</td></tr><tr><td>8510</td><td>8859</td></tr></table>		Start Position	End Position	1	350	799	1148	1434	1783	8510	8859
		Start Position					End Position									
		1					350									
		799					1148									
		1434			1783											
		8510			8859											
		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:	164
Initial Dataset Size in (Base):	263021
Dataset Siset after Removing Duplication:	108405
Dataset Size after Overlapping:	49968

Overlapping Metrics

Repeat Identification Time:	00h:00m:14s:000ms
Overlapping Time:	00h:04m:50s:000ms
Reads Alignment Time:	00h:00m:15s:000ms
Total Hybrid Assembly Time:	00h:05m:05s:000ms
Repeat Annotation Time:	00h:00m:24s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
247	120409	48	1	0
226	119716	364	170	0
201	30976	8	1	0
176	30625	171	60	0