

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 24
Sequencing Coverage:	31
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

## Reads Dataset Details

Total Reads Count:	1045
Total Dataset Size in (Base):	313765
Valid Read Count:	1045
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

## Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9780
Length of K-mer	426

## Assembly Details

Number of Contigs:	13
Contig N50:	1576
Contig N90:	1326
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	354
Total Reads Count(Repeat):	40
Retetitive Read Count based on (Partitions Identifier):	40
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	221
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			1400													
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions											
1	10080	GCTTTTCATTC	4	350	<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											
		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:	1045
Reads Count after Removing Duplication:	394
Reads Count after Overlapping:	156
Initial Dataset Size in (Base):	313765
Dataset Siset after Removing Duplication:	129553
Dataset Size after Overlapping:	55985

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:02m:34s:000ms
Reads Alignment Time:	00h:00m:10s:000ms
Total Hybrid Assembly Time:	00h:02m:44s:000ms
Repeat Annotation Time:	00h:00m:03s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
297	125316	50	1	0
276	124609	373	175	0
226	31684	175	62	0