

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 28
Sequencing Coverage:	20
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

## Reads Dataset Details

Total Reads Count:	1054
Total Dataset Size in (Base):	211074
Valid Read Count:	1054
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

## Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	305

## Assembly Details

Number of Contigs:	25
Contig N50:	976
Contig N90:	876
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	296
Total Reads Count(Repeat):	90
Retetitive Read Count based on (Partitions Identifier):	89
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	733
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				
		GGCTTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
AGTGTTGAAGT						

Initial Reads Count:	1054
Reads Count after Removing Duplication:	386
Reads Count after Overlapping:	237
Initial Dataset Size in (Base):	211074
Dataset Siset after Removing Duplication:	84645
Dataset Size after Overlapping:	51432

Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:03m:29s:000ms
Reads Alignment Time:	00h:00m:28s:000ms
Total Hybrid Assembly Time:	00h:03m:57s:000ms
Repeat Annotation Time:	00h:01m:54s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	87616	40	1	0
182	87025	34	1	0
179	86436	38	1	0
176	85849	333	142	0
151	22801	20	4	0