

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 23
Sequencing Coverage:	31
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

## 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	499

## Assembly Details

Number of Contigs:	15
Contig N50:	1576
Contig N90:	1426
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):	23
Retetitive Read Count based on (Partitions Identifier):	22
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	50
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:	1045
Reads Count after Removing Duplication:	394
Reads Count after Overlapping:	142
Initial Dataset Size in (Base):	313765
Dataset Siset after Removing Duplication:	129553
Dataset Size after Overlapping:	52254

### Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:05m:10s:000ms
Reads Alignment Time:	00h:00m:18s:000ms
Total Hybrid Assembly Time:	00h:05m:28s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	137641	54	1	0
297	136900	53	1	0
291	136161	56	1	0
278	135424	64	1	0
276	134689	392	181	0
253	34596	15	1	0
251	34225	9	2	0
226	33489	182	64	0