

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 21
Sequencing Coverage:	31
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

## 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	574

## Assembly Details

Number of Contigs:	13
Contig N50:	1626
Contig N90:	1576
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	392
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:	1045
Reads Count after Removing Duplication:	394
Reads Count after Overlapping:	126
Initial Dataset Size in (Base):	313765
Dataset Sizet after Removing Duplication:	129553
Dataset Size after Overlapping:	47939

### Overlapping Metrics

Repeat Identification Time:	00h:00m:04s:000ms
Overlapping Time:	00h:02m:13s:000ms
Reads Alignment Time:	00h:00m:06s:000ms
Total Hybrid Assembly Time:	00h:02m:19s:000ms
Repeat Annotation Time:	00h:00m:00s:000ms

Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	153664	67	2	0
299	152100	59	1	0
297	151321	55	1	0
293	150544	64	2	0
291	148996	71	1	0
287	148225	66	1	0
276	147456	415	189	0
262	38025	11	1	0
251	37636	8	2	0

226	36864	194	67	0
225	15625	10	1	0