

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 17
Sequencing Coverage:	26
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	126

## 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	476

## Assembly Details

Number of Contigs:	16
Contig N50:	1676
Contig N90:	1201
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	394
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			Start Position	End Position
		TATAGGCATAG			1	350
		CGCACAGACA			799	1148
		GATAAAAATTA			1434	1783
		CAGAGTACAC			8510	8859
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
AGTGTTGAAGT						

Initial Reads Count:	1051
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	125
Initial Dataset Size in (Base):	263021
Dataset Sizet after Removing Duplication:	108405
Dataset Size after Overlapping:	41262

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:04m:12s:000ms
Reads Alignment Time:	00h:00m:12s:000ms
Total Hybrid Assembly Time:	00h:04m:24s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	155236	67	4	0
249	152100	58	3	0
247	149769	55	1	0
243	148996	64	4	0
241	145924	67	1	0
237	145161	63	2	0
226	143641	406	186	0
212	37249	11	1	0
201	36864	10	2	0

187	36100	20	1	0
176	35721	189	66	0