

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 88
Sequencing Coverage:	27
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	84

## Reads Dataset Details

Total Reads Count:	2200
Total Dataset Size in (Base):	549860
Valid Read Count:	2200
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

## Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19910
Length of K-mer	548

## Assembly Details

Number of Contigs:	33
Contig N50:	1276
Contig N90:	976
Number of Scaffold	3
Scaffold N50:	6935
Scaffold N90:	4448
Mis-assembly Count:	0
TotalAssembly Size:	21226

## Repeat Details

Total Reads Count(Non-Repeat) :	570
Total Reads Count(Repeat):	217
Retetitive Read Count based on (Partitions Identifier):	213
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1532
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			1750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	9843	GCTTTTCATTC	5	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA			Start Position	End Position
		TATAGGCATAG			1	350
		CGCACAGACA			1316	1665
		GATAAAAATTA			2021	2370
		CAGAGTACAC			5041	5390
		AACATCCATGA			8441	8790
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Initial Reads Count:	2200
Reads Count after Removing Duplication:	787
Reads Count after Overlapping:	388
Initial Dataset Size in (Base):	549860
Dataset Sizet after Removing Duplication:	224564
Dataset Size after Overlapping:	112362

Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:03m:32s:000ms
Reads Alignment Time:	00h:00m:26s:000ms
Total Hybrid Assembly Time:	00h:03m:58s:000ms
Repeat Annotation Time:	00h:03m:13s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	324900	144	8	0
249	315844	123	3	0
247	312481	113	1	0
246	311364	120	1	0
244	310249	119	2	0
243	308025	122	1	0
238	306916	118	1	0
234	305809	123	1	0
231	304704	139	1	0

229	303601	150	2	0
227	301401	122	3	0
226	298116	615	263	0
221	80089	33	1	0
201	79524	26	6	0
184	76176	27	1	0
181	75625	30	1	0
178	75076	25	1	0
177	74529	25	2	0
176	73441	248	100	0