

Assembly Report

Experiment Details

ExperimentID:	Experiment 22
Sequencing Coverage:	31
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	151

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:	17
Contig N50:	1476
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) :	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			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:	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:06s:000ms
Overlapping Time:	00h:02m:45s:000ms
Reads Alignment Time:	00h:00m:06s:000ms
Total Hybrid Assembly Time:	00h:02m:51s:000ms
Repeat Annotation Time:	00h:00m:00s:000ms

Overlapping Length	O(N)2 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