

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 40
Sequencing Coverage:	31
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	61

## 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	426

## Assembly Details

Number of Contigs:	12
Contig N50:	2001
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) :	262
Total Reads Count(Repeat):	128
Retetitive Read Count based on (Partitions Identifier):	128
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	2729
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			1056			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CTGCTTTTCAT	3	352		
		TCTGACTGCAA				
		CGGGCAATAT				
		GTCTCTGTGTG				
		GATTAAAAAAA				
		GAGTGTCTGAT				
		AGCAGCTTCT				
		GAACTGGTTAC				
		CTGCCGTGAG				
		TAAATTAAAAT				
		TTTATTGACTT				
		AGGTCACTAAA				
		TACTTTAACCA				
		ATATAGGCATA				
		GCGCACAGAC				
		AGATAAAAATT				
		ACAGAGTACA				
		CAACATCCATG				
		AAACGCATTAG				
		CACCACCATTA				
		CCACCACCAT				
		CACCATTACCA				
		CAGGTAACGG				
		TGCGGGGCTGA				
		CGCGTACAGG				
		AAACACAGAAA				
		AAAGCCCGCA				
		CCTGACAGTG				
		CGGGCTTTTTT				
		TTCGACCAAAG				
		GTAACGAGGT				
		AACAACCATGC				
GAGTGTTGAA						
GT						
					Start Position	End Position
					763	1114
					1398	1749
					7648	7999

SRGD Performance Metrics

Initial Reads Count:	1045
Reads Count after Removing Duplication:	390
Reads Count after Overlapping:	213
Initial Dataset Size in (Base):	313765
Dataset Siset after Removing Duplication:	128349
Dataset Size after Overlapping:	71017

Overlapping Metrics

Repeat Identification Time:	00h:00m:17s:000ms
Overlapping Time:	00h:04m:42s:000ms
Reads Alignment Time:	00h:00m:19s:000ms
Total Hybrid Assembly Time:	00h:05m:01s:000ms
Repeat Annotation Time:	00h:10m:25s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
297	68644	31	1	0
276	68121	285	126	0
226	18225	130	50	0