

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 49
Sequencing Coverage:	23
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

## Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

## Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	326

## Assembly Details

Number of Contigs:	25
Contig N50:	901
Contig N90:	676
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	165
Total Reads Count(Repeat):	231
Retetitive Read Count based on (Partitions Identifier):	231
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	2904
Total Unique Repetitive Sequences Count	5

Total Repeat Size (Base)			7215			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	AAAGAGTGTCT	3	202		
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA			Start	End
		AATACTTTAAC			Positio	Positio
		CAATATAGGCA			n	n
		TAGCGCACAG			1227	1428
		ACAGATAAAAA			5951	6152
		TTACAGAGTAC			8498	8699
		ACAACATCCAT				
		GAAACGCATTA				
		GCACCACCATT				
		ACCACCACCAT				
		CACCATTACCA				
CAGGTAACGG						
TGCGGGA						

1	10080	CGGTCGAAAA	8	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
AAAAAGGCGA						
ACTGGTGGTG						
CTTGGACGCA						
ACGGTTCCGA						
CTACTCTGCTG						
CGGTGCTGGC						
TGCCTGTTTAC						
GCGCCGATTG						
TTGCGAGATTT						
GGACGGACGT						
TGACGGGGTC						
TA						

Start Positio n	End Positio n
1539	1788
3069	3318
3377	3626
4616	4865
5414	5663
6700	6949
7986	8235
8904	9153

1	10080	CTGCTTTTCAT TCTGACTGCAA CGGGCAATAT GTCTCTGTGTG GATTAAAAAA GAGTGTCTGAT AGCAGCTTCT GAACTGGTTAC CTGCCGTGAG TAAATTAAAAT TTTATTGACTT AGGTCACTAAA TACTTTAACCA ATATAGGCATA GCGCACAGAC AGATAAAAATT ACAGAGTACA CAACATCCATG AAACGCATTA	3	203		
					Start Positio n	End Positio n
					777	979
					1176	1378
					7168	7370

1	10080	GATTCATTTCGG	8	250		
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA				
		TAGCGCACAG				
ACAGATAAAAA						
TTACAGAGTAC						
ACAACATCCTC						
AAAGCCTACC						
GGTGACAGTG						
CGGGCTTTTTT						
TTCGACCAAAG						
GTAACGAGGT						
AACAACCATGC						
GAGTGTTGAA						
GTCA						

1	10080	GCTTTTCATTC TGA CTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGG	8	250		
					Start Positio n	End Positio n
					1	250
					779	1028
					1178	1427
					2353	2602
					3783	4032
					5902	6151
					7170	7419
					8449	8698

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	314
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	100773
Dataset Size after Overlapping:	65243

Overlapping Metrics

Repeat Identification Time:		00h:00m:12s:000ms		
Overlapping Time:		00h:03m:19s:000ms		
Reads Alignment Time:		00h:00m:36s:000ms		
Total Hybrid Assembly Time:		00h:03m:55s:000ms		
Repeat Annotation Time:		00h:14m:49s:000ms		
Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	27225	23	1	0
193	26896	20	2	0
184	26244	24	2	0
176	25600	141	71	0
151	7921	6	6	0