

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 11
Sequencing Coverage:	20
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

## Reads Dataset Details

Total Reads Count:	1054
Total Dataset Size in (Base):	211074
Valid Read Count:	1054
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	312

## Assembly Details

Number of Contigs:	25
Contig N50:	1176
Contig N90:	976
Number of Scaffold	2
Scaffold N50:	1811
Scaffold N90:	1811
Mis-assembly Count:	0
TotalAssembly Size:	10566

## Repeat Details

Total Reads Count(Non-Repeat) :	396
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)			1750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	1811	GCTTTTCATTC	3	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA				
		TATAGGCATAG				
		CGCACAGACA				
		GATAAAAATTA				
		CAGAGTACAC				
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						
					Start Position	End Position
					1	350
					799	1148
					1434	1783

1326	10080	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1434</td><td>1783</td></tr><tr><td>8510</td><td>8859</td></tr></table>	Start Position	End Position	1434	1783	8510	8859
		Start Position				End Position					
		1434				1783					
		8510				8859					
		TGACTGCAAC									
		GGGCAATATG									
		TCTCTGTGTGG									
		ATTAAAAAAG									
		AGTGTCTGATA									
		GCAGCTTCTG									
		AACTGGTTACC									
		TGCCGTGAGT									
		AAATTAAAATT									
		TTATTGACTTA									
		GGTCACTAAAT									
		ACTTTAACCAA									
		TATAGGCATAG									
		CGCACAGACA									
		GATAAAAATTA									
		CAGAGTACAC									
AACATCCATGA											
AACGCATTAGC											
ACCACCATTAC											
CACCACCATCA											
CCATTACCACA											
GGTAACGGTG											
CGGGCTGACG											
CGTACAGGAA											
ACACAGAAAAA											
AGCCCGCACCC											
TGACAGTGCG											
GGCTTTTTTTTT											
CGACCAAAGG											
TAACGAGGTAA											
CAACCATGCG											
AGTGTTGAAGT											

### SRGD Performance Metrics

Initial Reads Count:	1054
Reads Count after Removing Duplication:	398

Reads Count after Overlapping:	190
Initial Dataset Size in (Base):	211074
Dataset Siset after Removing Duplication:	87057
Dataset Size after Overlapping:	43024

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:04m:08s:000ms
Reads Alignment Time:	00h:00m:30s:000ms
Total Hybrid Assembly Time:	00h:04m:38s:000ms
Repeat Annotation Time:	00h:00m:00s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	156816	68	6	0
199	152100	59	5	0
197	148225	56	1	0
193	147456	65	6	0
191	142884	61	1	0
187	142129	62	3	0
176	139876	396	183	0
162	36481	11	1	0
151	36100	9	2	0