

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 32
Sequencing Coverage:	26
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	126

## Reads Dataset Details

Total Reads Count:	1051
Total Dataset Size in (Base):	263021
Valid Read Count:	1051
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

## Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	495

## Assembly Details

Number of Contigs:	14
Contig N50:	1676
Contig N90:	1526
Number of Scaffold	2
Scaffold N50:	3755
Scaffold N90:	3755
Mis-assembly Count:	0
TotalAssembly Size:	10849

## Repeat Details

Total Reads Count(Non-Repeat) :	356
Total Reads Count(Repeat):	32
Retetitive Read Count based on (Partitions Identifier):	30
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	108
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			3150																
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions														
1	7094	GCTTTTCATTC	6	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1</td><td>350</td></tr><tr><td>765</td><td>1114</td></tr><tr><td>1400</td><td>1749</td></tr><tr><td>3146</td><td>3495</td></tr><tr><td>4226</td><td>4575</td></tr><tr><td>6742</td><td>7091</td></tr></table>	Start Position	End Position	1	350	765	1114	1400	1749	3146	3495	4226	4575	6742	7091
		Start Position				End Position													
		1				350													
		765				1114													
		1400				1749													
		3146				3495													
		4226				4575													
		6742				7091													
		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																			
GGCTTTTTTTT																			
CGACCAAAGG																			
TAACGAGGTAA																			
CAACCATGCG																			
AGTGTTGAAGT																			

6326	10080	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						
AGCCCGCACCC						
TGACAGTGCG						
GGCTTTTTTTTT						
CGACCAAAGG						
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Start Positio n	End Positio n
6742	7091
7650	7999
8549	8898

SRGD Performance Metrics

Initial Reads Count:	1051
Reads Count after Removing Duplication:	388

Reads Count after Overlapping:	139
Initial Dataset Size in (Base):	263021
Dataset Siset after Removing Duplication:	106397
Dataset Size after Overlapping:	43755

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:02m:09s:000ms
Reads Alignment Time:	00h:00m:06s:000ms
Total Hybrid Assembly Time:	00h:02m:15s:000ms
Repeat Annotation Time:	00h:00m:05s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	126736	93	4	0
249	123904	77	4	0
248	121104	50	4	0
247	118336	62	5	0
237	114921	51	3	0
236	112896	56	1	0
235	112225	71	1	0
226	111556	409	163	0
225	29241	15	1	0
221	28900	10	1	0
208	28561	7	1	0
176	28224	170	61	0