

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 36
Sequencing Coverage:	31
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

## 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	510

## Assembly Details

Number of Contigs:	15
Contig N50:	1826
Contig N90:	1501
Number of Scaffold	3
Scaffold N50:	3755
Scaffold N90:	3755
Mis-assembly Count:	0
TotalAssembly Size:	11253

## Repeat Details

Total Reads Count(Non-Repeat) :	388
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)			3150			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	7093	GCTTTTCATTC	6	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT			Start Position	End Position
		ACTTTAACCAA			1	350
		TATAGGCATAG			765	1114
		CGCACAGACA			1400	1749
		GATAAAAATTA			3146	3495
		CAGAGTACAC			4226	4575
		AACATCCATGA			6742	7091
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACCC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

6326	10080	GCTTTTCATTC	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>6742</td><td>7091</td></tr><tr><td>7650</td><td>7999</td></tr><tr><td>8549</td><td>8898</td></tr></table>	Start Position	End Position	6742	7091	7650	7999	8549	8898
		Start Position				End Position							
		6742				7091							
		7650				7999							
		8549				8898							
		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:	1045
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	123
Initial Dataset Size in (Base):	313765
Dataset Sizet after Removing Duplication:	128349
Dataset Size after Overlapping:	46929

Overlapping Metrics

Repeat Identification Time:	00h:00m:03s:000ms
Overlapping Time:	00h:05m:18s:000ms
Reads Alignment Time:	00h:00m:24s:000ms
Total Hybrid Assembly Time:	00h:05m:42s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	150544	137	3	0
299	148225	99	2	0
298	146689	59	2	0
297	145161	83	3	0
296	142884	73	1	0
287	142129	73	1	0
286	141376	77	2	0
276	139876	478	181	0
275	37249	35	1	0
258	36864	10	1	0
251	36481	28	1	0
226	36100	200	67	0

222	15129	12	1	0
217	14884	10	1	0