

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 79
Sequencing Coverage:	35
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

## Reads Dataset Details

Total Reads Count:	1203
Total Dataset Size in (Base):	359763
Valid Read Count:	1203
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	565

## Assembly Details

Number of Contigs:	13
Contig N50:	2651
Contig N90:	2101
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	100
Total Reads Count(Repeat):	292
Retetitive Read Count based on (Partitions Identifier):	291
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3874
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			7357			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	8	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
TCGGCGCTCT						
AGGTCAGGCC						



1	10080	GCTTTTCATTC	8	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>1</td><td>350</td></tr><tr><td>854</td><td>1203</td></tr><tr><td>1295</td><td>1644</td></tr><tr><td>2705</td><td>3054</td></tr><tr><td>4337</td><td>4686</td></tr><tr><td>6359</td><td>6708</td></tr><tr><td>7574</td><td>7923</td></tr><tr><td>8752</td><td>9101</td></tr></table>	Start Position	End Position	1	350	854	1203	1295	1644	2705	3054	4337	4686	6359	6708	7574	7923	8752	9101
		Start Position				End Position																	
		1				350																	
		854				1203																	
		1295				1644																	
		2705				3054																	
		4337				4686																	
		6359				6708																	
		7574				7923																	
		8752				9101																	
		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																							

1	10080	GTGATTCATTC	2	352		
		GGGATGGTCT				
		GTGTGGATTAA				
		AAAAAGAGTGT				
		CTGATAGCAG				
		CTTCTGAACTG				
		GTTACCTGCC				
		GTGAGTAAATT				
		AAAATTTTATT				
		GACTTAGGTCA				
		CTAAATACTTT				
		AACCAATATAG				
		GCATAGCGCA				
		CAGACAGATAA				
		AAATTACAGAG				
TACACAACATC						
CTCAAAGCCTA						
CCGGTGACAG						
TGCGGGCTTTT						
TTTTCGACCAA						
AGGTAACGAG						
GTAACAACCAT						
GCGAGTGTTG						
AAGTCAGGAG						
ATCCTAAAGGC						
CTGTACCCGTT						
ACCTAGCCAG						
TTGGCATTAAA						
CGTATACGGTA						
CCTAGGCATG						
TACGTAATCGT						
AGCCTTAGCAA						
TCTCCAGTCC						

Start Positio n	End Positio n
2226	2577
4728	5079

## SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	392

Reads Count after Overlapping:	326
Initial Dataset Size in (Base):	359763
Dataset Siset after Removing Duplication:	150869
Dataset Size after Overlapping:	100358

Overlapping Metrics

Repeat Identification Time:	00h:00m:19s:000ms
Overlapping Time:	00h:05m:12s:000ms
Reads Alignment Time:	00h:00m:28s:000ms
Total Hybrid Assembly Time:	00h:05m:40s:000ms
Repeat Annotation Time:	00h:22m:03s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
297	10000	14	2	0
294	9604	27	3	0
290	9025	16	2	0
280	8649	16	2	0
276	8281	72	40	0
269	2601	8	2	0
251	2401	4	2	0
237	2209	4	1	0
226	2116	15	11	0
215	1225	4	1	0