

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 75
Sequencing Coverage:	29
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

## Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
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	576

## Assembly Details

Number of Contigs:	16
Contig N50:	1539
Contig N90:	1176
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	53
Total Reads Count(Repeat):	337
Retetitive Read Count based on (Partitions Identifier):	337
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	6529
Total Unique Repetitive Sequences Count	6

Total Repeat Size (Base)			10673			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	AGGTCACTAAA	3	253		
		TACTTTAACCA				
		ATATAGGCATA				
		GCGCACAGAC				
		AGATAAAAATT				
		ACAGAGTACA				
		CAACATCCTCA				
		AAGCCTACCG				
		GTGACAGTGC				
		GGGCTTTTTTT				
		TCGACCAAAG				
		GTAACGAGGT				
		AACAACCATGC				
		GAGTGTTGAA				
		GTCAGGAGAT				
		CCTAAAGGCC				
		TGTACCCGTTA				
		CCTAGCCAGTT				
		GGCATTAAAC				
		GTATACGGTAC				
CTAGGCATGTA						
CGTAATCGTAG						
CCTTAGCAATC						
TCCAGTCCCA						

1	10080	CGGTCGAAAA	8	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>1756</td><td>2105</td></tr><tr><td>3561</td><td>3910</td></tr><tr><td>3964</td><td>4313</td></tr><tr><td>5117</td><td>5466</td></tr><tr><td>5910</td><td>6259</td></tr><tr><td>7138</td><td>7487</td></tr><tr><td>8386</td><td>8735</td></tr><tr><td>9149</td><td>9498</td></tr></table>	Start Position	End Position	1756	2105	3561	3910	3964	4313	5117	5466	5910	6259	7138	7487	8386	8735	9149	9498
		Start Position				End Position																	
		1756				2105																	
		3561				3910																	
		3964				4313																	
		5117				5466																	
		5910				6259																	
		7138				7487																	
		8386				8735																	
		9149				9498																	
		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	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAAA ATTTTATTGAC TTAGGTCACCTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC	8	350		
					Start Positio n	End Positio n
					409	758
					2228	2577
					3182	3531
					4730	5079
					5529	5878
					6730	7079
					8014	8363
					9552	9901

1	10080	GCTTTTCATTC	8	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						
GGCTTTTTTTT						
CGACCAAAGG						
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Start Positio n	End Positio n
1	350
854	1203
1295	1644
2705	3054
4337	4686
6359	6708
7574	7923
8752	9101

1	10080	GTGATTCATTC GGGATGGTCT GTGTGGATTAA AAAAAGAGTGT CTGATAGCAG CTTCTGAACTG GTTACCTGCC GTGAGTAAATT AAAATTTTATT GACTTAGGTCA CTAAATACTTT AACCAATATAG GCATAGCGCA CAGACAGATAA AAATTACAGAG TACACAACATC CTCAAAGCCTA CCGGTGACAG TGCGGGCTTTT TTTTCGACCAA AGGTAACGAG GTAACAACCAT GCGAGTGTTG AAGTCAG	2	253		
					Start Positio n	End Positio n
					2226	2478
					4728	4980

1	10080	TGCTTTTCATT	4	252		
		CTGACTGCAA				
		CGGGCAATAT				
		GTCTCTGTGTG				
		GATTAAAAAAA				
		GAGTGTCTGAT				
		AGCAGCTTCT				
		GAACTGGTTAC				
		CTGCCGTGAG				
		TAAATTAAAAT				
TTTATTGACTT						
AGGTCACTAAA						
TACTTTAACCA						
ATATAGGCATA						
GCGCACAGAC						
AGATAAAAATT						
ACAGAGTACA						
CAACATCCATG						
AAACGCATTAG						
CACCACCATTA						
CCACCACCAT						
CACCATTACCA						
CAGGTAACGG						
TGCGGGC						
					Start Positio n	End Positio n
					853	1104
					1294	1545
					2704	2955
					7573	7824

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	390
Reads Count after Overlapping:	359
Initial Dataset Size in (Base):	301119
Dataset Sizet after Removing Duplication:	124917
Dataset Size after Overlapping:	91159



Overlapping Metrics

Repeat Identification Time:		00h:00m:07s:000ms		
Overlapping Time:		00h:01m:54s:000ms		
Reads Alignment Time:		00h:00m:21s:000ms		
Total Hybrid Assembly Time:		00h:02m:15s:000ms		
Repeat Annotation Time:		00h:19m:37s:000ms		
Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
244	2809	15	4	0
233	2401	15	2	0
226	2209	32	16	0
208	961	3	1	0
201	900	2	2	0
183	784	5	1	0
176	729	9	5	0