

Assembly Report

Experiment Details

ExperimentID:	Experiment 69
Sequencing Coverage:	23
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
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	426

Assembly Details

Number of Contigs:	23
Contig N50:	976
Contig N90:	916
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	99
Total Reads Count(Repeat):	289
Retetitive Read Count based on (Partitions Identifier):	288
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3506
Total Unique Repetitive Sequences Count	5

Total Repeat Size (Base)			9412											
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions									
1	10080	AATTACAGAGT	3	202										
		ACACAACATCC												
		TCAAAGCCTAC												
		CGGTGACAGT												
		GCGGGCTTTTT			<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>2377</td><td>2578</td></tr><tr><td>4879</td><td>5080</td></tr><tr><td>9701</td><td>9902</td></tr></table>		Start Position	End Position	2377	2578	4879	5080	9701	9902
		Start Position					End Position							
		2377					2578							
		4879					5080							
		9701			9902									
		TTTCGACCAAA												
		GGTAACGAGG												
		TAACAACCATG												
		CGAGTGTTGA												
		AGTCAGGAGA												
		TCCTAAAGGC												
		CTGTACCCGTT												
		ACCTAGCCAG												
TTGGCATTAAA														
CGTATACGGTA														
CCTAGGCATG														
TACGTAATCGT														
AGCCTTAGCAA														
TCTCCAGTCCC														

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	8	350	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAAA			
		ATTTTATTGAC			
		TTAGGTCACTA			
		AATACTTTAAC			
		CAATATAGGCA			
		TAGCGCACAG			
		ACAGATAAAAA			
TTACAGAGTAC					
ACAACATCCTC					
AAAGCCTACC					
GGTGACAGTG					
CGGGCTTTTTT					
TTCGACCAAAG					
GTAACGAGGT					
AACAACCATGC					
GAGTGTTGAA					
GTCAGGAGAT					
CCTAAAGGCC					
TGTACCCGTTA					
CCTAGCCAGTT					
GGCATTAAAC					
GTATACGGTAC					
CTAGGCATGTA					
CGTAATCGTAG					
CCTTAGCAATC					
TCCAGTCC					

Start Position	End Position
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						
GGCTTTTTTTTT						
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	2	203	
		GGGATGGTCT			
		GTGTGGATTAA			
		AAAAAGAGTGT			
		CTGATAGCAG			
		CTTCTGAACTG			
		GTTACCTGCC			
		GTGAGTAAATT			
		AAAATTTTATT			
		GACTTAGGTCA			
CTAAATACTTT					
AACCAATATAG					
GCATAGCGCA					
CAGACAGATAA					
AAATTACAGAG					
TACACAACATC					
CTCAAAGCCTA					
CCGGTGACAG					
TGCGGGCTTT					

Start Positio n	End Positio n
2226	2428
4728	4930

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388
Reads Count after Overlapping:	331
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	99165
Dataset Size after Overlapping:	67920

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:01m:40s:000ms

Reads Alignment Time:			00h:00m:29s:000ms	
Total Hybrid Assembly Time:			00h:02m:09s:000ms	
Repeat Annotation Time:			00h:06m:40s:000ms	
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	9801	11	1	0
194	9604	35	6	0
190	8464	22	6	0
187	7396	18	2	0
180	7056	14	1	0
176	6889	60	31	0
169	2704	5	2	0
162	2500	3	1	0
151	2401	7	7	0