

Assembly Report

Experiment Details

ExperimentID:	Experiment 67
Sequencing Coverage:	23
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

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	419

Assembly Details

Number of Contigs:	26
Contig N50:	937
Contig N90:	892
Number of Scaffold	9
Scaffold N50:	1887
Scaffold N90:	1470
Mis-assembly Count:	0
TotalAssembly Size:	13429

Repeat Details

Total Reads Count(Non-Repeat) :	341
Total Reads Count(Repeat):	47
Retetitive Read Count based on (Partitions Identifier):	40
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	81
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			5600			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4348	CGGTCGAAAA	3	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	4348	GATTCATTTCGG	3	350	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAA			
		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 Positio n	End Positio n
409	758
2228	2577
3182	3531

1	4348	GCTTTTCATTC	4	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

4376	6262	CGGTCGAAAA	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>5117</td><td>5466</td></tr><tr><td>5910</td><td>6259</td></tr></table>	Start Position	End Position	5117	5466	5910	6259
		Start Position				End Position					
		5117				5466					
		5910				6259					
		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											

8276	9944	CGGTCGAAAA	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>8386</td><td>8735</td></tr><tr><td>9149</td><td>9498</td></tr></table>	Start Position	End Position	8386	8735	9149	9498
		Start Position				End Position					
		8386				8735					
		9149				9498					
		ACTGCTGGCA									
		GTGGGGCATT									
		ACCTCGAATCT									
		ACCGTCGATAT									
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		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											

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388

Reads Count after Overlapping:	158
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	99165
Dataset Size after Overlapping:	35306

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:01m:35s:000ms
Reads Alignment Time:	00h:00m:10s:000ms
Total Hybrid Assembly Time:	00h:01m:45s:000ms
Repeat Annotation Time:	00h:00m:07s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	116281	158	31	0
199	96100	140	20	0
198	84100	124	13	0
197	76729	109	20	0
196	66049	88	6	0
195	63001	64	1	0
194	62500	107	8	0
193	58564	56	4	0
191	56644	56	1	0
190	56169	68	2	0
188	55225	64	5	0
187	52900	73	1	0

186	52441	53	1	0
183	51984	82	1	0
181	51529	66	1	0
180	51076	81	1	0
179	50625	80	2	0
178	49729	68	1	0
177	49284	77	1	0
176	48841	242	96	0
174	15625	30	2	0
172	15129	26	1	0
171	14884	17	1	0
170	14641	13	1	0
169	14400	27	3	0
155	13689	18	1	0
151	13456	16	2	0
146	12996	26	1	0
144	12769	19	1	0
141	12544	19	1	0