

Assembly Report

Experiment Details

ExperimentID:	Experiment 68
Sequencing Coverage:	23
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

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	397

Assembly Details

Number of Contigs:	22
Contig N50:	916
Contig N90:	651
Number of Scaffold	2
Scaffold N50:	4171
Scaffold N90:	4171
Mis-assembly Count:	0
TotalAssembly Size:	10433

Repeat Details

Total Reads Count(Non-Repeat) :	170
Total Reads Count(Repeat):	218
Retetitive Read Count based on (Partitions Identifier):	216
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	2952
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	6262	CGGTCGAAAA	5	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG			Start Position	End Position
		AAAAAGGCGA			1756	2105
		ACTGGTGGTG			3561	3910
		CTTGGACGCA			3964	4313
		ACGGTTCCGA			5117	5466
		CTACTCTGCTG			5910	6259
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
AAGCGATGGA						
GCTTTCCTACT						
TCGGCGCTCT						
AGGTCAGGCC						

1	6262	GATTCATTTCGG	5	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 Positio n	End Positio n
409	758
2228	2577
3182	3531
4730	5079
5529	5878

1	6262	GCTTTTCATTC TGA CTGCAAC 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	5	350		
					Start Positio n	End Positio n
					1	350
					854	1203
					1295	1644
					2705	3054
					4337	4686

5910	10080	CGGTCGAAAA	4	350	<table><tr><th>Start Position</th><th>End Position</th></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	5910	6259	7138	7487	8386	8735	9149	9498
		Start Position				End Position									
		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															

5910	10080	GATTCATTCGG	3	350		
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTAAA				
		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				

5910	10080	GCTTTTCATTC	3	350	<table><tr><td>Start Position</td><td>End Position</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	6359	6708	7574	7923	8752	9101
		Start Position				End Position							
		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													

SRGD Performance Metrics

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

Reads Count after Overlapping:	283
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	99165
Dataset Size after Overlapping:	58983

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:01m:40s:000ms
Reads Alignment Time:	00h:00m:21s:000ms
Total Hybrid Assembly Time:	00h:02m:01s:000ms
Repeat Annotation Time:	00h:04m:30s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	28900	63	7	0
199	26569	61	7	0
198	24336	58	4	0
197	23104	46	6	0
195	21316	33	1	0
194	21025	51	5	0
190	19600	40	4	0
187	18496	29	1	0
183	18225	41	2	0
182	17689	28	1	0
179	17424	45	1	0
176	17161	133	57	0

165	5476	12	1	0
162	5329	9	1	0
156	5184	9	1	0
151	5041	10	4	0
140	4489	8	2	0