

Assembly Report

Experiment Details

ExperimentID:	Experiment 27
Sequencing Coverage:	20
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

Total Reads Count:	1054
Total Dataset Size in (Base):	211074
Valid Read Count:	1054
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	395

Assembly Details

Number of Contigs:	26
Contig N50:	970
Contig N90:	876
Number of Scaffold	2
Scaffold N50:	4603
Scaffold N90:	4603
Mis-assembly Count:	0
TotalAssembly Size:	10309

Repeat Details

Total Reads Count(Non-Repeat) :	360
Total Reads Count(Repeat):	26
Retetitive Read Count based on (Partitions Identifier):	24
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	56
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			2800			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4603	GCTTTTCATTC	5	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA			Start Position	End Position
		TATAGGCATAG			1	350
		CGCACAGACA			765	1114
		GATAAAAATTA			1400	1749
		CAGAGTACAC			3146	3495
		AACATCCATGA			4226	4575
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
		TGACAGTGCG				
		GGCTTTTTTTT				
		CGACCAAAGG				
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

4375	10080	GCTTTTCATTC	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>6742</td><td>7091</td></tr><tr><td>7650</td><td>7999</td></tr><tr><td>8549</td><td>8898</td></tr></table>	Start Position	End Position	6742	7091	7650	7999	8549	8898
		Start Position				End Position							
		6742				7091							
		7650				7999							
		8549				8898							
		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:	1054
Reads Count after Removing Duplication:	386

Reads Count after Overlapping:	190
Initial Dataset Size in (Base):	211074
Dataset Siset after Removing Duplication:	84645
Dataset Size after Overlapping:	42564

Overlapping Metrics

Repeat Identification Time:	00h:00m:08s:000ms
Overlapping Time:	00h:03m:21s:000ms
Reads Alignment Time:	00h:00m:15s:000ms
Total Hybrid Assembly Time:	00h:03m:36s:000ms
Repeat Annotation Time:	00h:00m:05s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	129600	88	6	0
199	125316	72	6	0
198	121104	49	6	0
197	116964	58	7	0
187	112225	53	5	0
186	108900	56	1	0
185	108241	65	1	0
176	107584	393	157	0
175	29241	15	1	0
174	28900	14	1	0
171	28561	12	1	0
158	28224	9	1	0

151	27889	19	2	0
143	27225	8	1	0