

Assembly Report

Experiment Details

ExperimentID:	Experiment 26
Sequencing Coverage:	20
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

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	399

Assembly Details

Number of Contigs:	26
Contig N50:	1021
Contig N90:	925
Number of Scaffold	3
Scaffold N50:	3155
Scaffold N90:	2819
Mis-assembly Count:	0
TotalAssembly Size:	10651

Repeat Details

Total Reads Count(Non-Repeat) :	384
Total Reads Count(Repeat):	2
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	3
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			2450															
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions													
1	4677	GCTTTTCATTC	5	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>1</td><td>350</td></tr><tr><td>765</td><td>1114</td></tr><tr><td>1400</td><td>1749</td></tr><tr><td>3146</td><td>3495</td></tr><tr><td>4226</td><td>4575</td></tr></table>		Start Position	End Position	1	350	765	1114	1400	1749	3146	3495	4226	4575
		Start Position					End Position											
		1					350											
		765					1114											
		1400					1749											
		3146					3495											
		4226					4575											
		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																		

6926	10080	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>7650</td><td>7999</td></tr><tr><td>8549</td><td>8898</td></tr></table>	Start Position	End Position	7650	7999	8549	8898
		Start Position				End Position					
		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:	177
Initial Dataset Size in (Base):	211074
Dataset Sizet after Removing Duplication:	84645
Dataset Size after Overlapping:	40228

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:05m:11s:000ms
Reads Alignment Time:	00h:00m:15s:000ms
Total Hybrid Assembly Time:	00h:05m:26s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	147456	120	7	0
199	142129	89	6	0
198	137641	53	6	0
197	133225	70	7	0
196	128164	58	1	0
187	127449	64	5	0
186	123904	67	2	0
176	122500	431	168	0
175	33124	25	1	0
174	32761	21	1	0
167	32400	17	1	0
158	32041	8	1	0

151	31684	24	2	0
150	30976	16	1	0