

Assembly Report

Experiment Details

ExperimentID:	Experiment 38
Sequencing Coverage:	31
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

Total Reads Count:	1045
Total Dataset Size in (Base):	313765
Valid Read Count:	1045
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9780
Length of K-mer	572

Assembly Details

Number of Contigs:	17
Contig N50:	1276
Contig N90:	1176
Number of Scaffold	4
Scaffold N50:	3755
Scaffold N90:	3007
Mis-assembly Count:	0
TotalAssembly Size:	11833

Repeat Details

Total Reads Count(Non-Repeat) :	323
Total Reads Count(Repeat):	67
Retetitive Read Count based on (Partitions Identifier):	67
Retetitive Read Count (Entire Read Frequency Identifier):	1
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	340
Total Unique Repetitive Sequences Count	1

Total Repeat Size (Base)			3500			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	1124	GCTTTTCATTC	2	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				
		GGCTTTTTTTT				
		CGACCAAAGG				
		TAACGAGGTAA				
		CAACCATGCG				
		AGTGTTGAAGT				

526	3532	GCTTTTCATTC	3	350		<table><tr><th>Start Position</th><th>End Position</th></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></table>	Start Position	End Position	765	1114	1400	1749	3146	3495
		Start Position					End Position							
		765					1114							
		1400					1749							
		3146					3495							
		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														
AGCCCGCACC														
TGACAGTGCG														
GGCTTTTTTTTT														
CGACCAAAGG														
TAACGAGGTAA														
CAACCATGCG														
AGTGTTGAAGT														

3251	7197	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>4226</td><td>4575</td></tr><tr><td>6742</td><td>7091</td></tr></table>	Start Position	End Position	4226	4575	6742	7091
		Start Position				End Position					
		4226				4575					
		6742				7091					
		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											

6326	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:	1045
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	169
Initial Dataset Size in (Base):	313765
Dataset Siset after Removing Duplication:	128349
Dataset Size after Overlapping:	59273

Overlapping Metrics

Repeat Identification Time:	00h:00m:08s:000ms
Overlapping Time:	00h:04m:41s:000ms
Reads Alignment Time:	00h:00m:17s:000ms
Total Hybrid Assembly Time:	00h:04m:58s:000ms
Repeat Annotation Time:	00h:01m:15s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	104329	62	2	0
297	103041	54	3	0
282	101124	55	2	0
276	99856	387	152	0
255	26896	14	1	0
253	26569	12	1	0
251	26244	21	2	0
226	25600	160	57	0
220	10609	4	1	0