

Assembly Report

Experiment Details

ExperimentID:	Experiment 60
Sequencing Coverage:	29
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	476

Assembly Details

Number of Contigs:	16
Contig N50:	1176
Contig N90:	1051
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	257
Total Reads Count(Repeat):	140
Retetitive Read Count based on (Partitions Identifier):	139
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1129
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4200												
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions										
1	10080	CGGTCGAAAA	4	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															
					<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1376</td><td>1725</td></tr><tr><td>4127</td><td>4476</td></tr><tr><td>6570</td><td>6919</td></tr><tr><td>8665</td><td>9014</td></tr></table>	Start Position	End Position	1376	1725	4127	4476	6570	6919	8665	9014
Start Position	End Position														
1376	1725														
4127	4476														
6570	6919														
8665	9014														

1	10080	GATTCATTTCGG	4	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
3285	3634
4858	5207
7202	7551
9332	9681

1	10080	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
799	1148
2039	2388
8043	8392

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	397

Reads Count after Overlapping:	218
Initial Dataset Size in (Base):	301119
Dataset Siset after Removing Duplication:	126674
Dataset Size after Overlapping:	61872

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:01m:53s:000ms
Reads Alignment Time:	00h:00m:08s:000ms
Total Hybrid Assembly Time:	00h:02m:01s:000ms
Repeat Annotation Time:	00h:00m:25s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
247	66049	23	1	0
226	65536	253	119	0
221	18769	10	1	0
206	18496	9	1	0
201	18225	17	7	0
176	16384	105	50	0