

Assembly Report

Experiment Details

ExperimentID:	Experiment 94
Sequencing Coverage:	32
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

Reads Dataset Details

Total Reads Count:	2195
Total Dataset Size in (Base):	658355
Valid Read Count:	2195
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19860
Length of K-mer	615

Assembly Details

Number of Contigs:	28
Contig N50:	1476
Contig N90:	1326
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	465
Total Reads Count(Repeat):	328
Retetitive Read Count based on (Partitions Identifier):	326
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	4439
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8400			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	20160	CGGTCGAAAA	8	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						

1	20160	GATTCATTTCGG	8	350	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAAA			
		ATTTTATTGAC			
		TTAGGTCACCTA			
		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
871	1220
4144	4493
6008	6357
9464	9813
11173	11522
13704	14053
16623	16972
19422	19771

1	20160	GCTTTTCATTC	8	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						

Start Positio n	End Positio n
1	350
1316	1665
2021	2370
5041	5390
8441	8790
13123	13472
15543	15892
18132	18481

SRGD Performance Metrics

Initial Reads Count:	2195
Reads Count after Removing Duplication:	793

Reads Count after Overlapping:	474
Initial Dataset Size in (Base):	658355
Dataset Siset after Removing Duplication:	271570
Dataset Size after Overlapping:	155262

Overlapping Metrics

Repeat Identification Time:	00h:00m:10s:000ms
Overlapping Time:	00h:04m:23s:000ms
Reads Alignment Time:	00h:00m:36s:000ms
Total Hybrid Assembly Time:	00h:04m:59s:000ms
Repeat Annotation Time:	00h:09m:57s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
292	216225	100	1	0
276	215296	511	223	0
251	58081	17	5	0
236	55696	20	1	0
226	55225	208	88	0
212	21609	6	1	0