

Assembly Report

Experiment Details

ExperimentID:	Experiment 95
Sequencing Coverage:	32
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	61

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	501

Assembly Details

Number of Contigs:	22
Contig N50:	1576
Contig N90:	1460
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	397
Total Reads Count(Repeat):	396
Retetitive Read Count based on (Partitions Identifier):	395
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	8610
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			5600			
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	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:	521
Initial Dataset Size in (Base):	658355
Dataset Siset after Removing Duplication:	271570
Dataset Size after Overlapping:	167596

Overlapping Metrics

Repeat Identification Time:	00h:00m:12s:000ms
Overlapping Time:	00h:04m:16s:000ms
Reads Alignment Time:	00h:00m:38s:000ms
Total Hybrid Assembly Time:	00h:04m:54s:000ms
Repeat Annotation Time:	00h:55m:52s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
292	157609	66	1	0
276	156816	418	187	0
260	43681	15	1	0
251	43264	19	7	0
226	40401	171	76	0