

Assembly Report

Experiment Details

ExperimentID:	Experiment 93
Sequencing Coverage:	32
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

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	533

Assembly Details

Number of Contigs:	27
Contig N50:	1626
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) :	606
Total Reads Count(Repeat):	187
Retetitive Read Count based on (Partitions Identifier):	182
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1202
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				
		AGTAAATTTAA				
		ATTTTATTGAC				
		TTAGGTCACCTA				
		AATACTTTAAC				
		CAATATAGGCA				
		TAGCGCACAG				
		ACAGATAAAAA				
		TTACAGAGTAC				
ACAACATCCTC						
AAAGCCTACC						
GGTGACAGTG						
CGGGCTTTTTT						
TTCGACCAAAG						
GTAACGAGGT						
AACAACCATGC						
GAGTGTTGAA						
GTCAGGAGAT						
CCTAAAGGCC						
TGTACCCGTTA						
CCTAGCCAGTT						
GGCATTTAAAC						
GTATACGGTAC						
CTAGGCATGTA						
CGTAATCGTAG						
CCTTAGCAATC						
TCCAGTCC						

Start Position	End Position
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					
GGCTTTTTTTTT					
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:	369
Initial Dataset Size in (Base):	658355
Dataset Siset after Removing Duplication:	271570
Dataset Size after Overlapping:	127003

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:03m:03s:000ms
Reads Alignment Time:	00h:00m:17s:000ms
Total Hybrid Assembly Time:	00h:03m:20s:000ms
Repeat Annotation Time:	00h:01m:59s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	367236	142	7	0
298	358801	129	2	0
296	356409	176	3	0
295	352836	131	1	0
294	351649	135	2	0
292	349281	170	4	0
291	344569	162	2	0
290	342225	164	2	0
287	339889	163	1	0
278	338724	136	1	0
276	337561	659	280	0
273	90601	24	1	0

265	90000	56	2	0
258	88804	30	1	0
251	88209	25	1	0
226	87616	282	112	0
219	33856	11	1	0
212	33489	11	1	0