

Assembly Report

Experiment Details

ExperimentID:	Experiment 48
Sequencing Coverage:	23
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	305

Assembly Details

Number of Contigs:	25
Contig N50:	951
Contig N90:	801
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	167
Total Reads Count(Repeat):	229
Retetitive Read Count based on (Partitions Identifier):	228
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3944
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4756			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	8	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGGTC				
		TA				

1	10080	CTGCTTTTCAT TCTGACTGCAA CGGGCAATAT GTCTCTGTGTG GATTAAAAAAA GAGTGTCTGAT AGCAGCTTCT GAACTGGTTAC CTGCCGTGAG TAAATTAAAAT TTTATTGACTT AGGTCACTAAA TACTTTAACCA ATATAGGCATA GCGCACAGAC AGATAAAAATT ACAGAGTACA CAACATCCATG AAACGCATTAG CACCACCATTA CCACCACCAT CACCATTACCA CAGGTAACGG TGCGGG	3	252		
					Start Positio n	End Positio n
					777	1028
					1176	1427
					7168	7419

1	10080	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAAA ATTTTATTGAC TTAGGTCACATA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCA	8	250		
					Start Positio n	End Positio n
					374	623
					1975	2224
					2790	3039
					4278	4527
					5006	5255
					6355	6604
					7714	7963
					9343	9592

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	318
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	100773
Dataset Size after Overlapping:	65888

Overlapping Metrics

Repeat Identification Time:		00h:00m:11s:000ms		
Overlapping Time:		00h:03m:09s:000ms		
Reads Alignment Time:		00h:00m:33s:000ms		
Total Hybrid Assembly Time:		00h:03m:42s:000ms		
Repeat Annotation Time:		00h:23m:26s:000ms		
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	27889	36	2	0
191	27225	19	2	0
189	26569	27	1	0
186	26244	24	1	0
176	25921	151	67	0
161	8836	7	1	0
151	8649	8	4	0