

Assembly Report

Experiment Details

ExperimentID:	Experiment 50
Sequencing Coverage:	23
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

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:	24
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) :	108
Total Reads Count(Repeat):	288
Retetitive Read Count based on (Partitions Identifier):	288
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	6242
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			6808			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	8	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA			Start Positio n	End Positio n
		TTGCGGCAAG			1539	1788
		TCGTATTCCGG			3069	3318
		CTGATCACATG			3377	3626
		GTGCTGATGG			4616	4865
		CAGGTTTCACC			5414	5663
		GCCGGTAATG			6700	6949
		AAAAAGGCGA			7986	8235
		ACTGGTGGTG			8904	9153
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGGTC				
		TA				

1	10080	GATTCATTTCGG	8	250		
		GATGGTCTGT				
		GTGGATTAAAA				
		AAAGAGTGTCT				
		GATAGCAGCTT				
		CTGAACTGGTT				
		ACCTGCCGTG				
		AGTAAATTTAAA				
		ATTTTATTGAC				
		TTAGGTCACTA				
		AATACTTTAAC				
		CAATATAGGCA				
		TAGCGCACAG				
ACAGATAAAAA						
TTACAGAGTAC						
ACAACATCCTC						
AAAGCCTACC						
GGTGACAGTG						
CGGGCTTTTTT						
TTCGACCAAAG						
GTAACGAGGT						
AACAACCATGC						
GAGTGTTGAA						
GTCA						

1	10080	GCTTTTCATTC	8	250		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACC				
		CAATAGGCATAG				
CGCACAGACA						
GATAAAAATTA						
CAGAGTACAC						
AACATCCATGA						
AACGCATTAGC						
ACCACCATTAC						
CACCACCATCA						
CCATTACCACA						
GGTAACGGTG						
CGGG						
					Start Positio n	End Positio n
					1	250
					779	1028
					1178	1427
					2353	2602
					3783	4032
					5902	6151
					7170	7419
					8449	8698

1	10080	TATTGCTGAGT CCACCCGCCG TATTGCGGCAA GTCGTATTCCG GCTGATCACAT GGTGCTGATG GCAGGTTTCA CCGCCGGTAA TGAAAAAGGC GAACTGGTGG TGCTTGGACG CAACGGTTCC GACTACTCTGC TGCGGTGCTG GCTGCCTGTTT ACGCGCCGAT TGTTGCGAGAT TTGGACGGAC GTTGACGGGG TCTAT	4	202		
					Start Positio n	End Positio n
					1588	1789
					4665	4866
					5463	5664
					6749	6950

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	349
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	100773
Dataset Size after Overlapping:	71428

Overlapping Metrics

Repeat Identification Time:	00h:00m:13s:000ms
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Overlapping Time:		00h:03m:05s:000ms		
Reads Alignment Time:		00h:00m:45s:000ms		
Total Hybrid Assembly Time:		00h:03m:50s:000ms		
Repeat Annotation Time:		00h:45m:53s:000ms		
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	11664	11	1	0
176	11449	85	41	0
151	4356	5	5	0