

Assembly Report

Experiment Details

ExperimentID:	Experiment 98
Sequencing Coverage:	21
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

Reads Dataset Details

Total Reads Count:	2205
Total Dataset Size in (Base):	440864
Valid Read Count:	2205
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19960
Length of K-mer	376

Assembly Details

Number of Contigs:	47
Contig N50:	1126
Contig N90:	876
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

Repeat Details

Total Reads Count(Non-Repeat) :	574
Total Reads Count(Repeat):	218
Retetitive Read Count based on (Partitions Identifier):	214
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1922
Total Unique Repetitive Sequences Count	7

Total Repeat Size (Base)			6800			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	20160	ATTACAGAGTA	8	220		
		CACAACATCCT				
		CAAAGCCTAC				
		CGGTGACAGT				
		GCGGGCTTTTT				
		TTTCGACCAAA			Start Position	End Position
		GGTAACGAGG				
		TAACAACTCAT			1378	1597
		GGCATGCGAG			4583	4802
		TGTTGAAGTTT				
		TCAGGAGATC			6820	7039
		CTAAAGGCAG			10076	10295
		GCTGTACCCG			12215	12434
		TTACCTAGCCA				
		GTTGGCATTAA			14561	14780
		ACGTATCCTAG			17100	17319
		ACGGTACCTA			19552	19771
		GGCATGCCCT				
		ACGTAATCGTA				
		GCCTTAGCAAT				
CTCCAGTCC						

1	20160	CGGTCGAAAA 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	8	350		
					Start Positio n	End Positio n
					3271	3620
					7927	8276
					8750	9099
					11803	12152
					13026	13375
					15428	15777
					17342	17691
					18939	19288

1	20160	GCTTTTCATTC TGA CTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACCAA TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGC	8	280		
					Start Positio n	End Positio n
					1	280
					1693	1972
					2328	2607
					5350	5629
					9123	9402
					14050	14329
					16090	16369
					18332	18611

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	792
Reads Count after Overlapping:	491
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	180168

Dataset Size after Overlapping:	105976
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Overlapping Metrics

Repeat Identification Time:	00h:00m:17s:000ms
Overlapping Time:	00h:03m:55s:000ms
Reads Alignment Time:	00h:00m:58s:000ms
Total Hybrid Assembly Time:	00h:04m:53s:000ms
Repeat Annotation Time:	00h:04m:54s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	329476	117	5	0
199	323761	145	1	0
198	322624	108	3	0
196	319225	129	1	0
195	318096	115	6	0
194	311364	141	6	0
190	304704	105	3	0
189	301401	109	2	0
187	299209	111	1	0
179	298116	90	2	0
176	295936	599	259	0
165	81225	32	1	0
151	80656	29	10	0
140	75076	21	1	0