

Assembly Report

Experiment Details

ExperimentID:	Experiment 99
Sequencing Coverage:	21
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

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	326

Assembly Details

Number of Contigs:	51
Contig N50:	1076
Contig N90:	826
Number of Scaffold	2
Scaffold N50:	7946
Scaffold N90:	7946
Mis-assembly Count:	0
TotalAssembly Size:	20401

Repeat Details

Total Reads Count(Non-Repeat) :	608
Total Reads Count(Repeat):	184
Retetitive Read Count based on (Partitions Identifier):	184
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	944
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			2500		
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions
1	12455	ATTACAGAGTA	5	220	
		CACAACATCCT			
		CAAAGCCTAC			
		CGGTGACAGT			
		GCGGGCTTTTT			
		TTTCGACCAAA			
		GGTAACGAGG			Start Position
		TAACAACTCAT			End Position
		GGCATGCGAG			1378
		TGTTGAAGTTT			1597
		TCAGGAGATC			4583
		CTAAAGGCAG			4802
		GCTGTACCCG			6820
		TTACCTAGCCA			7039
		GTTGGCATTAA			10076
		ACGTATCCTAG			10295
		ACGGTACCTA			12215
		GGCATGCCCT			12434
		ACGTAATCGTA			
		GCCTTAGCAAT			
		CTCCAGTCC			

1	12455	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	5	280		
					Start Positio n	End Positio n
					1	280
					1693	1972
					2328	2607
					5350	5629
					9123	9402

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	792
Reads Count after Overlapping:	476
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	180168

Dataset Size after Overlapping:	103275
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Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:03m:34s:000ms
Reads Alignment Time:	00h:00m:54s:000ms
Total Hybrid Assembly Time:	00h:04m:28s:000ms
Repeat Annotation Time:	00h:01m:56s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
198	369664	146	10	0
197	357604	138	7	0
196	349281	132	1	0
193	348100	133	4	0
192	343396	109	1	0
188	342225	109	1	0
187	341056	129	2	0
184	338724	109	1	0
183	337561	124	4	0
180	332929	121	1	0
179	331776	117	1	0
176	330625	621	272	0
162	91809	34	1	0
160	91204	29	1	0
159	90601	26	1	0
154	90000	27	1	0
151	89401	19	6	0

147

85849

31

1

0