

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 104
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	383

## Assembly Details

Number of Contigs:	47
Contig N50:	1076
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) :	591
Total Reads Count(Repeat):	213
Retetitive Read Count based on (Partitions Identifier):	211
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1109
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3710			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	20160	CGGTCGAAAA	5	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	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	7	280		
					Start Positio n	End Positio n
					1	280
					2048	2327
					5070	5349
					8493	8772
					13510	13789
					16232	16511
					18474	18753

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	804
Reads Count after Overlapping:	508
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	182580

Dataset Size after Overlapping:	109578
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Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:01m:47s:000ms
Reads Alignment Time:	00h:00m:22s:000ms
Total Hybrid Assembly Time:	00h:02m:09s:000ms
Repeat Annotation Time:	00h:01m:17s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
198	349281	119	3	0
192	345744	120	1	0
189	344569	113	2	0
188	342225	129	1	0
179	341056	112	2	0
176	338724	633	279	0
168	91809	26	1	0
151	91204	25	5	0
144	88209	27	2	0