

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 105
Sequencing Coverage:	21
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

## 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	301

## Assembly Details

Number of Contigs:	45
Contig N50:	1026
Contig N90:	901
Number of Scaffold	1
Scaffold N50:	20160
Scaffold N90:	20160
Mis-assembly Count:	0
TotalAssembly Size:	20160

## Repeat Details

Total Reads Count(Non-Repeat) :	490
Total Reads Count(Repeat):	314
Retetitive Read Count based on (Partitions Identifier):	313
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3547
Total Unique Repetitive Sequences Count	14

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:	566
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	182580

Dataset Size after Overlapping:	119784
---------------------------------	--------

Overlapping Metrics

Repeat Identification Time:	00h:00m:20s:000ms
Overlapping Time:	00h:04m:15s:000ms
Reads Alignment Time:	00h:00m:59s:000ms
Total Hybrid Assembly Time:	00h:05m:14s:000ms
Repeat Annotation Time:	00h:09m:51s:000ms

Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
192	240100	71	1	0
176	239121	508	233	0
166	65536	18	1	0
151	65025	15	3	0