

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 96
Sequencing Coverage:	21
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

## 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	476

## Assembly Details

Number of Contigs:	57
Contig N50:	1076
Contig N90:	876
Number of Scaffold	3
Scaffold N50:	7056
Scaffold N90:	5921
Mis-assembly Count:	0
TotalAssembly Size:	21862

## Repeat Details

Total Reads Count(Non-Repeat) :	785
Total Reads Count(Repeat):	7
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	12
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			1750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
11276	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						

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	792
Reads Count after Overlapping:	361
Initial Dataset Size in (Base):	440864
Dataset Sizet after Removing Duplication:	180168
Dataset Size after Overlapping:	82219

Overlapping Metrics

Repeat Identification Time:	00h:00m:07s:000ms
Overlapping Time:	00h:07m:43s:000ms
Reads Alignment Time:	00h:00m:29s:000ms
Total Hybrid Assembly Time:	00h:08m:12s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	616225	268	8	0
199	603729	285	7	0
198	592900	263	16	0
197	568516	218	10	0
196	553536	235	9	0
195	540225	177	1	0
193	538756	220	3	0
192	534361	181	3	0

190	529984	211	5	0
189	522729	197	3	0
188	518400	183	2	0
187	515524	234	1	0
184	514089	208	1	0
183	512656	222	1	0
182	511225	185	1	0
180	509796	184	1	0
179	508369	210	1	0
178	506944	203	2	0
177	504100	208	1	0
176	502681	842	341	0
172	135424	48	1	0
170	134689	38	1	0
169	133956	55	1	0
165	133225	66	1	0
156	132496	61	1	0
155	131769	56	1	0
151	131044	37	7	0
146	126025	46	1	0