

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 83
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):	440865
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	390

## Assembly Details

Number of Contigs:	46
Contig N50:	976
Contig N90:	876
Number of Scaffold	2
Scaffold N50:	3660
Scaffold N90:	3660
Mis-assembly Count:	0
TotalAssembly Size:	20690

## Repeat Details

Total Reads Count(Non-Repeat) :	496
Total Reads Count(Repeat):	285
Retetitive Read Count based on (Partitions Identifier):	284
Retetitive Read Count (Entire Read Frequency Identifier):	5
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3897
Total Unique Repetitive Sequences Count	4

Total Repeat Size (Base)			7000			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	17030	CGGTCGAAAA	6	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC			Start Position	End Position
		GCCGGTAATG			2832	3181
		AAAAAGGCGA			7245	7594
		ACTGGTGGTG			8068	8417
		CTTGGACGCA			10761	11110
		ACGGTTCCGA			11904	12253
		CTACTCTGCTG			14881	15230
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
AAGCGATGGA						
GCTTTCCTACT						
TCGGCGCTCT						
AGGTCAGGCC						

1	17030	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC	7	350		
					Start Positio n	End Positio n
					871	1220
					4144	4493
					6008	6357
					9464	9813
					11173	11522
					13704	14053
					16623	16972

1	17030	GCTTTTCATTC	7	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCAA				
		TATAGGCATAG				
		CGCACAGACA				
GATAAAAATTA						
CAGAGTACAC						
AACATCCATGA						
AACGCATTAGC						
ACCACCATTAC						
CACCACCATCA						
CCATTACCACA						
GGTAACGGTG						
CGGGCTGACG						
CGTACAGGAA						
ACACAGAAAAA						
AGCCCGCACCC						
TGACAGTGCG						
GGCTTTTTTTTT						
CGACCAAAGG						
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

Start Positio n	End Positio n
1	350
1316	1665
2021	2370
5041	5390
8441	8790
13123	13472
15543	15892

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	781

Reads Count after Overlapping:	526
Initial Dataset Size in (Base):	440865
Dataset Siset after Removing Duplication:	178158
Dataset Size after Overlapping:	112216

Overlapping Metrics

Repeat Identification Time:	00h:00m:09s:000ms
Overlapping Time:	00h:03m:27s:000ms
Reads Alignment Time:	00h:01m:30s:000ms
Total Hybrid Assembly Time:	00h:04m:57s:000ms
Repeat Annotation Time:	00h:20m:44s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	246016	99	6	0
196	240100	87	1	0
190	239121	100	2	0
188	237169	90	1	0
187	236196	86	1	0
181	235225	93	1	0
177	234256	89	3	0
176	231361	515	226	0
162	65025	23	1	0
152	64516	21	1	0
151	64009	29	12	0