

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 55
Sequencing Coverage:	23
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	41

## Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

## Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	305

## Assembly Details

Number of Contigs:	20
Contig N50:	1051
Contig N90:	976
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	247
Total Reads Count(Repeat):	152
Retetitive Read Count based on (Partitions Identifier):	151
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1342
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4200			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	4	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						

Start Position	End Position
1376	1725
4127	4476
6570	6919
8665	9014

1	10080	GATTCATTTCGG	4	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>3285</td><td>3634</td></tr><tr><td>4858</td><td>5207</td></tr><tr><td>7202</td><td>7551</td></tr><tr><td>9332</td><td>9681</td></tr></table>	Start Position	End Position	3285	3634	4858	5207	7202	7551	9332	9681
		Start Position				End Position									
		3285				3634									
		4858				5207									
		7202				7551									
		9332				9681									
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
ACAACATCCTC															
AAAGCCTACC															
GGTGACAGTG															
CGGGCTTTTTT															
TTCGACCAAAG															
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCAGGAGAT															
CCTAAAGGCC															
TGTACCCGTTA															
CCTAGCCAGTT															
GGCATTTAAC															
GTATACGGTAC															
CTAGGCATGTA															
CGTAATCGTAG															
CCTTAGCAATC															
TCCAGTCC															

1	10080	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 AGCCCGCACCC TGACAGTGCG GGCTTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	4	350		
					Start Positio n	End Positio n
					1	350
					799	1148
					2039	2388
					8043	8392

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	399

Reads Count after Overlapping:	278
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	101376
Dataset Size after Overlapping:	59008

Overlapping Metrics

Repeat Identification Time:	00h:00m:18s:000ms
Overlapping Time:	00h:03m:35s:000ms
Reads Alignment Time:	00h:00m:31s:000ms
Total Hybrid Assembly Time:	00h:04m:06s:000ms
Repeat Annotation Time:	00h:02m:14s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	61009	28	1	0
190	60516	26	1	0
187	60025	29	1	0
180	59536	18	1	0
176	59049	235	111	0
151	17424	13	5	0
146	16129	8	1	0