

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 45
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:	28
Contig N50:	1226
Contig N90:	776
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	272
Total Reads Count(Repeat):	129
Retetitive Read Count based on (Partitions Identifier):	128
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1564
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3000			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	4	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
GCGCCGATTG						
TTGCGAGATTT						
GGACGGACGT						
TGACGGGGGTC						
TA						

1	10080	GATTCATTCGG	4	250	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>2885</td><td>3134</td></tr><tr><td>4257</td><td>4506</td></tr><tr><td>6796</td><td>7045</td></tr><tr><td>9434</td><td>9683</td></tr></table>	Start Positio n	End Positio n	2885	3134	4257	4506	6796	7045	9434	9683
		Start Positio n				End Positio n									
		2885				3134									
		4257				4506									
		6796				7045									
		9434				9683									
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTAAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
ACAACATCCTC															
AAAGCCTACC															
GGTGACAGTG															
CGGGCTTTTTT															
TTCGACCAAAG															
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCA															

1	10080	GCTTTTCATTC	4	250											
		TGACTGCAAC													
		GGGCAATATG													
		TCTCTGTGTGG													
		ATTAAAAAAG													
		AGTGTCTGATA													
		GCAGCTTCTG													
		AACTGGTTACC													
		TGCCGTGAGT													
		AAATTAAAATT													
TTATTGACTTA															
GGTCACTAAAT															
ACTTTAACC															
TATAGGCATAG															
CGCACAGACA															
GATAAAAATTA															
CAGAGTACAC															
AACATCCATGA															
AACGCATTAGC															
ACCACCATTAC															
CACCACCATCA															
CCATTACCACA															
GGTAACGGTG															
CGGG															
					<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>1</td><td>250</td></tr><tr><td>699</td><td>948</td></tr><tr><td>1738</td><td>1987</td></tr><tr><td>8344</td><td>8593</td></tr></table>	Start Positio n	End Positio n	1	250	699	948	1738	1987	8344	8593
Start Positio n	End Positio n														
1	250														
699	948														
1738	1987														
8344	8593														

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	401
Reads Count after Overlapping:	267
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	101778
Dataset Size after Overlapping:	57121

Overlapping Metrics

Repeat Identification Time:		00h:00m:17s:000ms		
Overlapping Time:		00h:02m:30s:000ms		
Reads Alignment Time:		00h:00m:12s:000ms		
Total Hybrid Assembly Time:		00h:02m:42s:000ms		
Repeat Annotation Time:		00h:01m:26s:000ms		
Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	73984	25	1	0
176	73441	290	128	0
151	20449	16	5	0