

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 69
Sequencing Coverage:	23
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

## 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	426

## Assembly Details

Number of Contigs:	19
Contig N50:	1098
Contig N90:	916
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

## Repeat Details

Total Reads Count(Non-Repeat) :	99
Total Reads Count(Repeat):	289
Retetitive Read Count based on (Partitions Identifier):	288
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	3506
Total Unique Repetitive Sequences Count	5

Total Repeat Size (Base)			9412			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	AATTACAGAGT	3	202		
		ACACAACATCC				
		TCAAAGCCTAC				
		CGGTGACAGT				
		GCGGGCTTTTT				
		TTTCGACCAAA				
		GGTAACGAGG			Start Position	End Position
		TAACAACCATG			2377	2578
		CGAGTGTTGA			4879	5080
		AGTCAGGAGA			9701	9902
		TCCTAAAGGC				
		CTGTACCCGTT				
		ACCTAGCCAG				
		TTGGCATTAAA				
		CGTATACGGTA				
		CCTAGGCATG				
		TACGTAATCGT				
AGCCTTAGCAA						
TCTCCAGTCCC						

1	10080	CGGTCGAAAA 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	8	350		
					Start	End
					Positio	Positio
					n	n
					1756	2105
					3561	3910
					3964	4313
					5117	5466
					5910	6259
					7138	7487
					8386	8735
					9149	9498

1	10080	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAAA ATTTTATTGAC TTAGGTCACCTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CGTAATCGTAG CCTTAGCAATC TCCAGTCC	8	350		
					Start Positio n	End Positio n
					409	758
					2228	2577
					3182	3531
					4730	5079
					5529	5878
					6730	7079
					8014	8363
					9552	9901

1	10080	GCTTTTCATTC	8	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
854	1203
1295	1644
2705	3054
4337	4686
6359	6708
7574	7923
8752	9101

1	10080	GTGATTCATTC GGGATGGTCT GTGTGGATTAA AAAAAGAGTGT CTGATAGCAG CTTCTGAACTG GTTACCTGCC GTGAGTAAATT AAAATTTTATT GACTTAGGTCA CTAAATACTTT AACCAATATAG GCATAGCGCA CAGACAGATAA AAATTACAGAG TACACAACATC CTCAAAGCCTA CCGGTGACAG TGCGGGCTTT	2	203		
					Start Positio n	End Positio n
					2226	2428
					4728	4930

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388
Reads Count after Overlapping:	331
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	99165
Dataset Size after Overlapping:	67920

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:01m:34s:000ms

Reads Alignment Time:		00h:00m:28s:000ms		
Total Hybrid Assembly Time:		00h:02m:02s:000ms		
Repeat Annotation Time:		00h:15m:30s:000ms		
Overlapping Length	O(N) <sup>2</sup> Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	9801	11	1	0
194	9604	35	6	0
190	8464	22	6	0
187	7396	18	2	0
180	7056	14	1	0
176	6889	60	31	0
169	2704	5	2	0
162	2500	3	1	0
151	2401	7	7	0