

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 66
Sequencing Coverage:	23
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	201

## 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	414

## Assembly Details

Number of Contigs:	37
Contig N50:	776
Contig N90:	614
Number of Scaffold	8
Scaffold N50:	2164
Scaffold N90:	1450
Mis-assembly Count:	0
TotalAssembly Size:	12099

## Repeat Details

Total Reads Count(Non-Repeat) :	381
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)			6300			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4348	CGGTCGAAAA	3	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						

1	4348	GATTCATTTCGG	3	350	
		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					
GGCATTAAAC					
GTATACGGTAC					
CTAGGCATGTA					
CGTAATCGTAG					
CCTTAGCAATC					
TCCAGTCC					

Start Positio n	End Positio n
409	758
2228	2577
3182	3531



4276	6262	CGGTCGAAAA	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>5117</td><td>5466</td></tr><tr><td>5910</td><td>6259</td></tr></table>	Start Position	End Position	5117	5466	5910	6259
		Start Position				End Position					
		5117				5466					
		5910				6259					
		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											



7776	9939	CGGTCGAAAA	2	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
8386	8735
9149	9498



7776	9939	GATTCATTTCGG	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>8014</td><td>8363</td></tr><tr><td>9552</td><td>9901</td></tr></table>	Start Position	End Position	8014	8363	9552	9901
		Start Position				End Position					
		8014				8363					
		9552				9901					
		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											
GGCATTAAAC											
GTATACGGTAC											
CTAGGCATGTA											
CGTAATCGTAG											
CCTTAGCAATC											
TCCAGTCC											

### SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	388

Reads Count after Overlapping:	134
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	99165
Dataset Size after Overlapping:	30984

Overlapping Metrics

Repeat Identification Time:	00h:00m:04s:000ms
Overlapping Time:	00h:01m:39s:000ms
Reads Alignment Time:	00h:00m:09s:000ms
Total Hybrid Assembly Time:	00h:01m:48s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	145161	207	33	0
199	121104	201	19	0
198	108241	172	15	0
197	98596	150	21	0
196	85849	114	6	0
195	82369	79	2	0
194	81225	119	8	0
193	76729	78	6	0
191	73441	70	1	0
188	72900	83	4	0
187	70756	87	1	0
186	70225	84	2	0

183	69169	108	1	0
181	68644	88	2	0
180	67600	116	1	0
179	67081	116	2	0
178	66049	121	1	0
177	65536	111	1	0
176	65025	302	114	0
175	19881	33	1	0
174	19600	45	1	0
171	19321	23	1	0
170	19044	14	1	0
169	18769	27	3	0
155	17956	21	1	0
151	17689	25	3	0
146	16900	23	1	0
144	16641	22	1	0
141	16384	21	1	0