

# Assembly Report

## Experiment Details

ExperimentID:	Experiment 67
Sequencing Coverage:	23
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

## 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	419

## Assembly Details

Number of Contigs:	28
Contig N50:	911
Contig N90:	826
Number of Scaffold	5
Scaffold N50:	2695
Scaffold N90:	2150
Mis-assembly Count:	0
TotalAssembly Size:	11208

## Repeat Details

Total Reads Count(Non-Repeat) :	341
Total Reads Count(Repeat):	47
Retetitive Read Count based on (Partitions Identifier):	40
Retetitive Read Count (Entire Read Frequency Identifier):	4
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	81
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			7000											
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions									
1	4348	CGGTCGAAAA	3	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>1756</td><td>2105</td></tr><tr><td>3561</td><td>3910</td></tr><tr><td>3964</td><td>4313</td></tr></table>		Start Position	End Position	1756	2105	3561	3910	3964	4313
		Start Position					End Position							
		1756					2105							
		3561					3910							
		3964			4313									
		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

1	4348	GCTTTTCATTC TGACTGCAAC GGGCAATATG TCTCTGTGTGG ATTAAAAAAG AGTGTCTGATA GCAGCTTCTG AACTGGTTACC TGCCGTGAGT AAATTAAAATT TTATTGACTTA GGTCACTAAAT ACTTTAACC TATAGGCATAG CGCACAGACA GATAAAAATTA CAGAGTACAC AACATCCATGA AACGCATTAGC ACCACCATTAC CACCACCATCA CCATTACCACA GGTAACGGTG CGGGCTGACG CGTACAGGAA ACACAGAAAAA AGCCCGCACC TGACAGTGCG GGCTTTTTTTT CGACCAAAGG TAACGAGGTAA CAACCATGCG AGTGTTGAAGT	4	350	Start Position	End Position
					1	350
					854	1203
					1295	1644
					2705	3054

4113	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											

4113	6262	GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA 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	2	350		
					Start Position	End Position
					4730	5079
					5529	5878

6076	8770	CGGTCGAAAA	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>7138</td><td>7487</td></tr><tr><td>8386</td><td>8735</td></tr></table>	Start Position	End Position	7138	7487	8386	8735
		Start Position				End Position					
		7138				7487					
		8386				8735					
		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											



6076	8770	GATTCATTTCGG	2	350	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAA			
		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			

Start Position	End Position
6730	7079
8014	8363

6076	8770	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>6359</td><td>6708</td></tr><tr><td>7574</td><td>7923</td></tr></table>	Start Position	End Position	6359	6708	7574	7923
		Start Position				End Position					
		6359				6708					
		7574				7923					
		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											

SRGD Performance Metrics

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

Reads Count after Overlapping:	158
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	99165
Dataset Size after Overlapping:	35306

Overlapping Metrics

Repeat Identification Time:	00h:00m:08s:000ms
Overlapping Time:	00h:03m:14s:000ms
Reads Alignment Time:	00h:00m:19s:000ms
Total Hybrid Assembly Time:	00h:03m:33s:000ms
Repeat Annotation Time:	00h:00m:10s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	116281	158	31	0
199	96100	140	20	0
198	84100	124	13	0
197	76729	109	20	0
196	66049	88	6	0
195	63001	64	1	0
194	62500	107	8	0
193	58564	56	4	0
191	56644	56	1	0
190	56169	68	2	0
188	55225	64	5	0
187	52900	73	1	0

186	52441	53	1	0
183	51984	82	1	0
181	51529	66	1	0
180	51076	81	1	0
179	50625	80	2	0
178	49729	68	1	0
177	49284	77	1	0
176	48841	242	96	0
174	15625	30	2	0
172	15129	26	1	0
171	14884	17	1	0
170	14641	13	1	0
169	14400	27	3	0
155	13689	18	1	0
151	13456	16	2	0
146	12996	26	1	0
144	12769	19	1	0
141	12544	19	1	0