

Assembly Report

Experiment Details

ExperimentID:	Experiment 73
Sequencing Coverage:	29
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	84

Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	549

Assembly Details

Number of Contigs:	15
Contig N50:	1358
Contig N90:	1130
Number of Scaffold	4
Scaffold N50:	2859
Scaffold N90:	2140
Mis-assembly Count:	0
TotalAssembly Size:	11191

Repeat Details

Total Reads Count(Non-Repeat) :	251
Total Reads Count(Repeat):	139
Retetitive Read Count based on (Partitions Identifier):	138
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	1099
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			7350			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	2140	GCTTTTCATTC	3	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 Position	End Position
					1	350
					854	1203
					1295	1644

2626	7490	CGGTCGAAAA	5	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>3561</td><td>3910</td></tr><tr><td>3964</td><td>4313</td></tr><tr><td>5117</td><td>5466</td></tr><tr><td>5910</td><td>6259</td></tr><tr><td>7138</td><td>7487</td></tr></table>	Start Position	End Position	3561	3910	3964	4313	5117	5466	5910	6259	7138	7487
		Start Position				End Position											
		3561				3910											
		3964				4313											
		5117				5466											
		5910				6259											
		7138				7487											
		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																	

2626	7490	GATTCATTTCGG	4	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>3182</td><td>3531</td></tr><tr><td>4730</td><td>5079</td></tr><tr><td>5529</td><td>5878</td></tr><tr><td>6730</td><td>7079</td></tr></table>	Start Position	End Position	3182	3531	4730	5079	5529	5878	6730	7079
		Start Position				End Position									
		3182				3531									
		4730				5079									
		5529				5878									
		6730				7079									
		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															

2626	7490	GCTTTTCATTC	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>2705</td><td>3054</td></tr><tr><td>4337</td><td>4686</td></tr><tr><td>6359</td><td>6708</td></tr></table>	Start Position	End Position	2705	3054	4337	4686	6359	6708
		Start Position				End Position							
		2705				3054							
		4337				4686							
		6359				6708							
		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													
AGCCCGCACC													
TGACAGTGCG													
GGCTTTTTTTTT													
CGACCAAAGG													
TAACGAGGTAA													
CAACCATGCG													
AGTGTTGAAGT													

7222	10080	CGGTCGAAAA	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>8386</td><td>8735</td></tr><tr><td>9149</td><td>9498</td></tr></table>	Start Position	End Position	8386	8735	9149	9498
		Start Position				End Position					
		8386				8735					
		9149				9498					
		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											

7222	10080	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAAA 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 Positio n	End Positio n
					8014	8363
					9552	9901

7222	10080	GCTTTTCATTC	2	350	<table><tr><td>Start Position</td><td>End Position</td></tr><tr><td>7574</td><td>7923</td></tr><tr><td>8752</td><td>9101</td></tr></table>	Start Position	End Position	7574	7923	8752	9101
		Start Position				End Position					
		7574				7923					
		8752				9101					
		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:	1209
Reads Count after Removing Duplication:	390

Reads Count after Overlapping:	204
Initial Dataset Size in (Base):	301119
Dataset Siset after Removing Duplication:	124917
Dataset Size after Overlapping:	57251

Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:06m:25s:000ms
Reads Alignment Time:	00h:01m:20s:000ms
Total Hybrid Assembly Time:	00h:07m:45s:000ms
Repeat Annotation Time:	00h:03m:10s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	63001	104	9	0
249	58564	83	5	0
248	56169	97	5	0
247	53824	88	8	0
245	50176	57	3	0
244	48841	91	6	0
241	46225	47	1	0
237	45796	70	2	0
236	44944	46	2	0
233	44100	82	3	0
232	42849	51	1	0
229	42436	78	1	0

228	42025	64	1	0
226	41616	221	90	0
219	12996	25	1	0
201	12769	20	4	0
194	11881	18	1	0
189	11664	5	1	0
184	11449	9	1	0
180	11236	18	2	0
176	10816	71	39	0