

Assembly Report

Experiment Details

ExperimentID:	Experiment 71
Sequencing Coverage:	29
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	251

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	469

Assembly Details

Number of Contigs:	16
Contig N50:	1513
Contig N90:	1413
Number of Scaffold	3
Scaffold N50:	4693
Scaffold N90:	4693
Mis-assembly Count:	0
TotalAssembly Size:	11154

Repeat Details

Total Reads Count(Non-Repeat) :	384
Total Reads Count(Repeat):	6
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			8400			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4693	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						
					Start Position	End Position
					1756	2105
					3561	3910
					3964	4313

1	4693	GATTCATTTCGG	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>409</td><td>758</td></tr><tr><td>2228</td><td>2577</td></tr><tr><td>3182</td><td>3531</td></tr></table>	Start Position	End Position	409	758	2228	2577	3182	3531
		Start Position				End Position							
		409				758							
		2228				2577							
		3182				3531							
		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													

1	4693	GCTTTTCATTC TGA CTGCAAC 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	5	350		
					Start Positio n	End Positio n
					1	350
					854	1203
					1295	1644
					2705	3054
					4337	4686

4451	10080	CGGTCGAAAA	5	350	<table><tr><th>Start Position</th><th>End Position</th></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><tr><td>8386</td><td>8735</td></tr><tr><td>9149</td><td>9498</td></tr></table>	Start Position	End Position	5117	5466	5910	6259	7138	7487	8386	8735	9149	9498
		Start Position				End Position											
		5117				5466											
		5910				6259											
		7138				7487											
		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																	

4451	10080	GATTCATTTCGG	5	350		
		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						

Start Positio n	End Positio n
4730	5079
5529	5878
6730	7079
8014	8363
9552	9901

4451	10080	GCTTTTCATTC	3	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>6359</td><td>6708</td></tr><tr><td>7574</td><td>7923</td></tr><tr><td>8752</td><td>9101</td></tr></table>	Start Position	End Position	6359	6708	7574	7923	8752	9101
		Start Position				End Position							
		6359				6708							
		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:	102
Initial Dataset Size in (Base):	301119
Dataset Siset after Removing Duplication:	124917
Dataset Size after Overlapping:	33904

Overlapping Metrics

Repeat Identification Time:	00h:00m:09s:000ms
Overlapping Time:	00h:04m:07s:000ms
Reads Alignment Time:	00h:00m:12s:000ms
Total Hybrid Assembly Time:	00h:04m:19s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	147456	212	22	0
249	131044	212	13	0
248	121801	192	10	0
247	114921	170	15	0
246	104976	132	4	0
245	102400	98	1	0
244	101761	143	6	0
243	97969	98	4	0
241	95481	97	1	0
238	94864	107	2	0
237	93636	126	1	0
236	93025	110	2	0

233	91809	140	1	0
231	91204	111	2	0
230	90000	143	1	0
229	89401	141	1	0
228	88804	152	1	0
227	88209	139	1	0
226	87616	363	135	0
224	25921	52	1	0
221	25600	25	1	0
219	25281	39	2	0
217	24649	22	1	0
216	24336	18	1	0
205	24025	26	1	0
201	23716	38	5	0
176	22201	119	53	0