

Assembly Report

Experiment Details

ExperimentID:	Experiment 47
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	308

Assembly Details

Number of Contigs:	26
Contig N50:	1139
Contig N90:	851
Number of Scaffold	2
Scaffold N50:	4867
Scaffold N90:	4867
Mis-assembly Count:	0
TotalAssembly Size:	10644

Repeat Details

Total Reads Count(Non-Repeat) :	344
Total Reads Count(Repeat):	52
Retetitive Read Count based on (Partitions Identifier):	46
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	129
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			5003			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	4867	CGGTCGAAAA	4	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
GCGCCGATTG						
TTGCGAGATTT						
GGACGGACGT						
TGACGGGGGTC						
TA						

1	4867	GATTCATTTCGG	4	250											
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
		ACAACATCCTC													
		AAAGCCTACC													
		GGTGACAGTG													
		CGGGCTTTTTT													
		TTCGACCAAAG													
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCA															
					<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>374</td><td>623</td></tr><tr><td>1975</td><td>2224</td></tr><tr><td>2790</td><td>3039</td></tr><tr><td>4278</td><td>4527</td></tr></table>	Start Positio n	End Positio n	374	623	1975	2224	2790	3039	4278	4527
Start Positio n	End Positio n														
374	623														
1975	2224														
2790	3039														
4278	4527														

1	4867	TGCTTTTCATT CTGACTGCAA CGGGCAATAT GTCTCTGTGTG GATTAAAAAAA GAGTGTCTGAT AGCAGCTTCT GAACTGGTTAC CTGCCGTGAG TAAATTAAAAT TTTATTGACTT AGGTCACTAAA TACTTTAACCA ATATAGGCATA GCGCACAGAC AGATAAAAATT ACAGAGTACA CAACATCCATG AAACGCATTAG CACCACCATTA CCACCACCAT CACCATTACCA CAGGTAACGG TGCGGG	3	251		
					Start Positio n	End Positio n
					778	1028
					1177	1427
					2352	2602

4304	10080	CGGTCGAAAA	5	250		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
ACGGTTCCGA						
CTACTCTGCTG						
CGGTGCTGGC						
TGCCTGTTTAC						
GCGCCGATTG						
TTGCGAGATTT						
GGACGGACGT						
TGACGGGGTC						
TA						

Start Positio n	End Positio n
4616	4865
5414	5663
6700	6949
7986	8235
8904	9153

4304	10080	GATTCATTTCGG	4	250											
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
		ACAACATCCTC													
		AAAGCCTACC													
		GGTGACAGTG													
		CGGGCTTTTTT													
		TTCGACCAAAG													
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCA															
					<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>5006</td><td>5255</td></tr><tr><td>6355</td><td>6604</td></tr><tr><td>7714</td><td>7963</td></tr><tr><td>9343</td><td>9592</td></tr></table>	Start Positio n	End Positio n	5006	5255	6355	6604	7714	7963	9343	9592
Start Positio n	End Positio n														
5006	5255														
6355	6604														
7714	7963														
9343	9592														

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	396
Reads Count after Overlapping:	210
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	100773
Dataset Size after Overlapping:	46051

Overlapping Metrics

Repeat Identification Time:		00h:00m:09s:000ms		
Overlapping Time:		00h:03m:19s:000ms		
Reads Alignment Time:		00h:00m:18s:000ms		
Total Hybrid Assembly Time:		00h:03m:37s:000ms		
Repeat Annotation Time:		00h:00m:13s:000ms		
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	118336	100	8	0
199	112896	117	7	0
198	108241	123	5	0
197	104976	93	8	0
195	99856	100	3	0
194	97969	85	2	0
193	96721	69	2	0
192	95481	91	1	0
189	94864	106	2	0
188	93636	86	1	0
185	93025	95	2	0
182	91809	95	1	0
181	91204	67	1	0
179	90601	85	1	0
176	90000	310	139	0
174	25921	21	1	0
168	25600	20	1	0
151	25281	10	1	0