

Assembly Report

Experiment Details

ExperimentID:	Experiment 91
Sequencing Coverage:	32
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	301

Reads Dataset Details

Total Reads Count:	2195
Total Dataset Size in (Base):	658355
Valid Read Count:	2195
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19860
Length of K-mer	540

Assembly Details

Number of Contigs:	30
Contig N50:	1826
Contig N90:	1489
Number of Scaffold	3
Scaffold N50:	6363
Scaffold N90:	4096
Mis-assembly Count:	0
TotalAssembly Size:	21444

Repeat Details

Total Reads Count(Non-Repeat) :	787
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)			3500			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
9176	20160	CGGTCGAAAA	5	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG			Start Position	End Position
		AAAAAGGCGA			10761	11110
		ACTGGTGGTG			11904	12253
		CTTGGACGCA			14881	15230
		ACGGTTCCGA			16995	17344
		CTACTCTGCTG			18809	19158
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
AAGCGATGGA						
GCTTTCCTACT						
TCGGCGCTCT						
AGGTCAGGCC						

9176	20160	GATTCATTTCGG	5	350	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>9464</td><td>9813</td></tr><tr><td>11173</td><td>11522</td></tr><tr><td>13704</td><td>14053</td></tr><tr><td>16623</td><td>16972</td></tr><tr><td>19422</td><td>19771</td></tr></table>	Start Position	End Position	9464	9813	11173	11522	13704	14053	16623	16972	19422	19771
		Start Position				End Position											
		9464				9813											
		11173				11522											
		13704				14053											
		16623				16972											
		19422				19771											
		GATGGTCTGT															
		GTGGATTAAAA															
		AAAGAGTGTCT															
		GATAGCAGCTT															
		CTGAACTGGTT															
		ACCTGCCGTG															
		AGTAAATTTAA															
		ATTTTATTGAC															
		TTAGGTCACATA															
		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:	2195
Reads Count after Removing Duplication:	793

Reads Count after Overlapping:	235
Initial Dataset Size in (Base):	658355
Dataset Siset after Removing Duplication:	271570
Dataset Size after Overlapping:	91326

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:03m:31s:000ms
Reads Alignment Time:	00h:00m:14s:000ms
Total Hybrid Assembly Time:	00h:03m:45s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
300	619369	264	4	0
299	613089	328	12	0
298	594441	238	2	0
297	591361	263	2	0
296	588289	308	2	0
295	585225	254	5	0
294	577600	260	3	0
293	573049	227	2	0
292	570025	326	5	0
290	562500	330	1	0
289	561001	230	1	0
278	559504	303	3	0

277	555025	230	2	0
276	552049	1002	363	0
275	144400	68	1	0
274	143641	70	1	0
265	142884	62	1	0
251	142129	51	1	0
231	141376	76	1	0
228	140625	77	1	0
226	139876	425	139	0
224	55225	20	1	0
221	54756	24	2	0
213	53824	25	1	0
212	53361	34	1	0
210	52900	27	1	0