

Assembly Report

Experiment Details

ExperimentID:	Experiment 86
Sequencing Coverage:	27
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	251

Reads Dataset Details

Total Reads Count:	2200
Total Dataset Size in (Base):	549860
Valid Read Count:	2200
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19910
Length of K-mer	586

Assembly Details

Number of Contigs:	36
Contig N50:	1276
Contig N90:	1176
Number of Scaffold	4
Scaffold N50:	3438
Scaffold N90:	2499
Mis-assembly Count:	0
TotalAssembly Size:	21362

Repeat Details

Total Reads Count(Non-Repeat) :	781
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)			4200			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
6126	20160	CGGTCGAAAA	7	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC			Start Position	End Position
		GCCGGTAATG			7245	7594
		AAAAAGGCGA			8068	8417
		ACTGGTGGTG			10761	11110
		CTTGGACGCA			11904	12253
		ACGGTTCCGA			14881	15230
		CTACTCTGCTG			16995	17344
		CGGTGCTGGC			18809	19158
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
AAGCGATGGA						
GCTTTCCTACT						
TCGGCGCTCT						
AGGTCAGGCC						

6126	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															
		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																	

SRGD Performance Metrics

Initial Reads Count:	2200
Reads Count after Removing Duplication:	787

Reads Count after Overlapping:	226
Initial Dataset Size in (Base):	549860
Dataset Siset after Removing Duplication:	224564
Dataset Size after Overlapping:	75966

Overlapping Metrics

Repeat Identification Time:	00h:00m:09s:000ms
Overlapping Time:	00h:02m:41s:000ms
Reads Alignment Time:	00h:00m:12s:000ms
Total Hybrid Assembly Time:	00h:02m:53s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	609961	259	8	0
249	597529	315	24	0
248	561001	216	4	0
247	555025	243	4	0
246	549081	276	4	0
245	543169	230	9	0
244	529984	232	6	0
243	521284	207	2	0
242	518400	289	9	0
240	505521	270	1	0
239	504100	192	1	0
236	502681	229	1	0

233	501264	215	1	0
228	499849	260	3	0
227	495616	203	2	0
226	492804	907	340	0
225	131044	57	1	0
224	130321	67	2	0
218	128881	49	1	0
215	128164	58	1	0
201	127449	45	5	0
198	123904	52	1	0
181	123201	57	1	0
178	122500	58	1	0
176	121801	371	129	0