

Assembly Report

Experiment Details

ExperimentID:	Experiment 82
Sequencing Coverage:	21
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	101

Reads Dataset Details

Total Reads Count:	2205
Total Dataset Size in (Base):	440865
Valid Read Count:	2205
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	20160
Number of K-mers:	19960
Length of K-mer	418

Assembly Details

Number of Contigs:	46
Contig N50:	1153
Contig N90:	901
Number of Scaffold	5
Scaffold N50:	3360
Scaffold N90:	2328
Mis-assembly Count:	0
TotalAssembly Size:	21986

Repeat Details

Total Reads Count(Non-Repeat) :	709
Total Reads Count(Repeat):	72
Retetitive Read Count based on (Partitions Identifier):	65
Retetitive Read Count (Entire Read Frequency Identifier):	5
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	134
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			1750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
2776	13553	CGGTCGAAAA	5	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG			Start Position	End Position
		AAAAAGGCGA			2832	3181
		ACTGGTGGTG			7245	7594
		CTTGGACGCA			8068	8417
		ACGGTTCCGA			10761	11110
		CTACTCTGCTG			11904	12253
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
AAGCGATGGA						
GCTTTCCTACT						
TCGGCGCTCT						
AGGTCAGGCC						

SRGD Performance Metrics

Initial Reads Count:	2205
Reads Count after Removing Duplication:	781
Reads Count after Overlapping:	371
Initial Dataset Size in (Base):	440865
Dataset Sizet after Removing Duplication:	178158
Dataset Size after Overlapping:	83027

Overlapping Metrics

Repeat Identification Time:	00h:00m:10s:000ms
Overlapping Time:	00h:04m:07s:000ms
Reads Alignment Time:	00h:00m:38s:000ms
Total Hybrid Assembly Time:	00h:04m:45s:000ms
Repeat Annotation Time:	00h:00m:22s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	502681	220	12	0
199	485809	225	31	0
198	443556	177	6	0
197	435600	177	3	0
196	431649	183	7	0
195	422500	161	13	0
194	405769	167	8	0
193	395641	160	1	0

192	394384	182	9	0
191	383161	170	3	0
190	379456	182	5	0
189	373321	129	1	0
186	372100	142	1	0
184	370881	153	1	0
181	369664	184	1	0
178	368449	167	3	0
177	364816	148	3	0
176	361201	690	286	0
175	99225	41	1	0
174	98596	46	3	0
171	96721	36	1	0
168	96100	38	1	0
165	95481	52	1	0
159	94864	33	1	0
151	94249	30	5	0
150	91204	32	1	0
149	90601	45	1	0
148	90000	41	1	0