

Assembly Report

Experiment Details

ExperimentID:	Experiment 87
Sequencing Coverage:	27
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	126

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	565

Assembly Details

Number of Contigs:	36
Contig N50:	1276
Contig N90:	1101
Number of Scaffold	3
Scaffold N50:	6894
Scaffold N90:	3215
Mis-assembly Count:	0
TotalAssembly Size:	21094

Repeat Details

Total Reads Count(Non-Repeat) :	705
Total Reads Count(Repeat):	82
Retetitive Read Count based on (Partitions Identifier):	76
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	198
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	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAAA			
		ATTTTATTGAC			
		TTAGGTCACCTA			
		AATACTTTAAC			
		CAATATAGGCA			
		TAGCGCACAG			
		ACAGATAAAAA			
		TTACAGAGTAC			
		ACAACATCCTC			
		AAAGCCTACC			
		GGTGACAGTG			
		CGGGCTTTTTT			
		TTCGACCAAAG			
GTAACGAGGT					
AACAACCATGC					
GAGTGTTGAA					
GTCAGGAGAT					
CCTAAAGGCC					
TGTACCCGTTA					
CCTAGCCAGTT					
GGCATTAAAC					
GTATACGGTAC					
CTAGGCATGTA					
CGTAATCGTAG					
CCTTAGCAATC					
TCCAGTCC					

Start Position	End Position
9464	9813
11173	11522
13704	14053
16623	16972
19422	19771

SRGD Performance Metrics

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

Reads Count after Overlapping:	276
Initial Dataset Size in (Base):	549860
Dataset Siset after Removing Duplication:	224564
Dataset Size after Overlapping:	86779

Overlapping Metrics

Repeat Identification Time:	00h:00m:05s:000ms
Overlapping Time:	00h:04m:50s:000ms
Reads Alignment Time:	00h:00m:13s:000ms
Total Hybrid Assembly Time:	00h:05m:03s:000ms
Repeat Annotation Time:	00h:00m:09s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	497025	222	8	0
249	485809	228	22	0
248	455625	196	4	0
247	450241	187	2	0
246	447561	218	4	0
245	442225	166	9	0
244	430336	184	5	0
243	423801	175	2	0
242	421201	201	7	0
241	412164	191	2	0
240	409600	204	3	0
239	405769	142	1	0

228	404496	187	3	0
227	400689	167	2	0
226	398161	737	305	0
225	106276	51	1	0
224	105625	51	3	0
218	103684	45	1	0
215	103041	48	1	0
209	102400	38	1	0
201	101761	36	6	0
181	97969	44	1	0
178	97344	41	1	0
176	96721	300	117	0