

Assembly Report

Experiment Details

ExperimentID:	Experiment 64
Sequencing Coverage:	35
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	76

Reads Dataset Details

Total Reads Count:	1203
Total Dataset Size in (Base):	359763
Valid Read Count:	1203
Rejected Read Count:	0
Maximum Read Length:	301
Minimum Read Length:	262

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9780
Length of K-mer	531

Assembly Details

Number of Contigs:	14
Contig N50:	1401
Contig N90:	1201
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	280
Total Reads Count(Repeat):	115
Retetitive Read Count based on (Partitions Identifier):	114
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	729
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			4200			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	10080	CGGTCGAAAA	4	350		
		ACTGCTGGCA				
		GTGGGGCATT				
		ACCTCGAATCT				
		ACCGTCGATAT				
		TGCTGAGTCC				
		ACCCGCCGTA				
		TTGCGGCAAG				
		TCGTATTCCGG				
		CTGATCACATG				
		GTGCTGATGG				
		CAGGTTTCACC				
		GCCGGTAATG				
		AAAAAGGCGA				
		ACTGGTGGTG				
		CTTGGACGCA				
		ACGGTTCCGA				
		CTACTCTGCTG				
		CGGTGCTGGC				
		TGCCTGTTTAC				
		GCGCCGATTG				
		TTGCGAGATTT				
		GGACGGACGT				
		TGACGGGGTC				
		TATACCTGCGA				
		CCCGCGTCAG				
		GTGCCCCGATG				
		CGAGGTTGTT				
		GAAGTCGATG				
		TCCTACCAGG				
		AAGCGATGGA				
		GCTTTCCTACT				
TCGGCGCTCT						
AGGTCAGGCC						

1	10080	GATTCATTTCGG	4	350	
		GATGGTCTGT			
		GTGGATTAAAA			
		AAAGAGTGTCT			
		GATAGCAGCTT			
		CTGAACTGGTT			
		ACCTGCCGTG			
		AGTAAATTTAA			
		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					

Start Position	End Position
3285	3634
4858	5207
7202	7551
9332	9681

1	10080	GCTTTTCATTC	4	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>1</td><td>350</td></tr><tr><td>799</td><td>1148</td></tr><tr><td>2039</td><td>2388</td></tr><tr><td>8043</td><td>8392</td></tr></table>	Start Positio n	End Positio n	1	350	799	1148	2039	2388	8043	8392
		Start Positio n				End Positio n									
		1				350									
		799				1148									
		2039				2388									
		8043				8392									
		TGACTGCAAC													
		GGGCAATATG													
		TCTCTGTGTGG													
		ATTAAAAAAG													
		AGTGTCTGATA													
		GCAGCTTCTG													
		AACTGGTTACC													
		TGCCGTGAGT													
		AAATTAAAATT													
		TTATTGACTTA													
		GGTCACTAAAT													
		ACTTTAACCAA													
		TATAGGCATAG													
		CGCACAGACA													
GATAAAAATTA															
CAGAGTACAC															
AACATCCATGA															
AACGCATTAGC															
ACCACCATTAC															
CACCACCATCA															
CCATTACCACA															
GGTAACGGTG															
CGGGCTGACG															
CGTACAGGAA															
ACACAGAAAAA															
AGCCCGCACCC															
TGACAGTGCG															
GGCTTTTTTTTT															
CGACCAAAGG															
TAACGAGGTAA															
CAACCATGCG															
AGTGTTGAAGT															

SRGD Performance Metrics

Initial Reads Count:	1203
Reads Count after Removing Duplication:	395

Reads Count after Overlapping:	195
Initial Dataset Size in (Base):	359763
Dataset Siset after Removing Duplication:	151772
Dataset Size after Overlapping:	66789

Overlapping Metrics

Repeat Identification Time:	00h:00m:10s:000ms
Overlapping Time:	00h:04m:53s:000ms
Reads Alignment Time:	00h:00m:15s:000ms
Total Hybrid Assembly Time:	00h:05m:08s:000ms
Repeat Annotation Time:	00h:00m:57s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
297	78400	33	1	0
296	77841	44	1	0
281	77284	46	1	0
276	76729	286	132	0
256	21025	14	1	0
251	20736	7	4	0
226	19600	122	58	0
221	6724	3	1	0
211	6561	2	1	0