

Assembly Report

Experiment Details

ExperimentID:	Experiment 54
Sequencing Coverage:	23
Number of Partitions:	4
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

Reads Dataset Details

Total Reads Count:	1212
Total Dataset Size in (Base):	241272
Valid Read Count:	1212
Rejected Read Count:	0
Maximum Read Length:	201
Minimum Read Length:	162

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9880
Length of K-mer	305

Assembly Details

Number of Contigs:	21
Contig N50:	976
Contig N90:	776
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	277
Total Reads Count(Repeat):	122
Retetitive Read Count based on (Partitions Identifier):	121
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	663
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	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:	1212
Reads Count after Removing Duplication:	399

Reads Count after Overlapping:	257
Initial Dataset Size in (Base):	241272
Dataset Siset after Removing Duplication:	101376
Dataset Size after Overlapping:	55316

Overlapping Metrics

Repeat Identification Time:	00h:00m:19s:000ms
Overlapping Time:	00h:03m:52s:000ms
Reads Alignment Time:	00h:00m:32s:000ms
Total Hybrid Assembly Time:	00h:04m:24s:000ms
Repeat Annotation Time:	00h:01m:06s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
197	76729	33	1	0
196	76176	44	3	0
181	74529	42	2	0
176	73441	275	128	0
151	20449	18	8	0