

Assembly Report

Experiment Details

ExperimentID:	Experiment 43
Sequencing Coverage:	23
Number of Partitions:	3
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	67

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	349

Assembly Details

Number of Contigs:	22
Contig N50:	1172
Contig N90:	1020
Number of Scaffold	2
Scaffold N50:	1995
Scaffold N90:	1995
Mis-assembly Count:	0
TotalAssembly Size:	10500

Repeat Details

Total Reads Count(Non-Repeat) :	352
Total Reads Count(Repeat):	49
Retetitive Read Count based on (Partitions Identifier):	48
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	222
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			3000			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	1995	GCTTTTCATTC	3	250		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCBA				
		TATAGGCATAG				
		CGCACAGACA				
		GATAAAAATTA				
		CAGAGTACAC				
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
CACCACCATCA						
CCATTACCACA						
GGTAACGGTG						
CGGG						

1576	10080	CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGGACGT TGACGGGGTC TA	3	250	Start Position	End Position
					3630	3879
					5894	6143
					8864	9113

1576	10080	GATTCATTTCGG	4	250											
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAA													
		ATTTTATTGAC													
		TTAGGTCACTA													
		AATACTTTAAC													
		CAATATAGGCA													
		TAGCGCACAG													
		ACAGATAAAAA													
		TTACAGAGTAC													
		ACAACATCCTC													
		AAAGCCTACC													
		GGTGACAGTG													
		CGGGCTTTTTT													
		TTCGACCAAAG													
GTAACGAGGT															
AACAACCATGC															
GAGTGTTGAA															
GTCA															
					<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>2885</td><td>3134</td></tr><tr><td>4257</td><td>4506</td></tr><tr><td>6796</td><td>7045</td></tr><tr><td>9434</td><td>9683</td></tr></table>	Start Positio n	End Positio n	2885	3134	4257	4506	6796	7045	9434	9683
Start Positio n	End Positio n														
2885	3134														
4257	4506														
6796	7045														
9434	9683														

1576	10080	GCTTTTCATTC	2	250	<table><tr><td>Start Positio n</td><td>End Positio n</td></tr><tr><td>1738</td><td>1987</td></tr><tr><td>8344</td><td>8593</td></tr></table>		Start Positio n	End Positio n	1738	1987	8344	8593
		Start Positio n					End Positio n					
		1738					1987					
		8344			8593							
		TGACTGCAAC										
		GGGCAATATG										
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		ATTAAAAAAG										
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		GCAGCTTCTG										
		AACTGGTTACC										
		TGCCGTGAGT										
		AAATTAAAATT										
		TTATTGACTTA										
		GGTCACTAAAT										
ACTTTAACCAA												
TATAGGCATAG												
CGCACAGACA												
GATAAAAATTA												
CAGAGTACAC												
AACATCCATGA												
AACGCATTAGC												
ACCACCATTAC												
CACCACCATCA												
CCATTACCACA												
GGTAACGGTG												
CGGG												

SRGD Performance Metrics

Initial Reads Count:	1212
Reads Count after Removing Duplication:	401
Reads Count after Overlapping:	217
Initial Dataset Size in (Base):	241272
Dataset Sizet after Removing Duplication:	101778
Dataset Size after Overlapping:	48199

Overlapping Metrics

Repeat Identification Time:		00h:00m:14s:000ms		
Overlapping Time:		00h:02m:37s:000ms		
Reads Alignment Time:		00h:00m:12s:000ms		
Total Hybrid Assembly Time:		00h:02m:49s:000ms		
Repeat Annotation Time:		00h:00m:11s:000ms		
Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
200	123904	47	1	0
197	123201	47	1	0
196	122500	62	2	0
195	121104	63	2	0
194	119716	72	1	0
190	119025	72	2	0
189	117649	64	1	0
187	116964	73	2	0
183	115600	55	1	0
177	114921	37	1	0
176	114244	359	162	0
157	30976	16	1	0
151	30625	18	7	0