

Assembly Report

Experiment Details

ExperimentID:	Experiment 90
Sequencing Coverage:	27
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	51

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	476

Assembly Details

Number of Contigs:	32
Contig N50:	1426
Contig N90:	1121
Number of Scaffold	2
Scaffold N50:	4085
Scaffold N90:	4085
Mis-assembly Count:	0
TotalAssembly Size:	20481

Repeat Details

Total Reads Count(Non-Repeat) :	422
Total Reads Count(Repeat):	365
Retetitive Read Count based on (Partitions Identifier):	365
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	6683
Total Unique Repetitive Sequences Count	3

Total Repeat Size (Base)			6650			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	16396	CGGTCGAAAA	6	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	16396	GATTCATTTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTTAA 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	6	350		
					Start Positio n	End Positio n
					871	1220
					4144	4493
					6008	6357
					9464	9813
					11173	11522
					13704	14053

1	16396	GCTTTTCATTC	7	350	<table><tr><th>Start Positio n</th><th>End Positio n</th></tr><tr><td>1</td><td>350</td></tr><tr><td>1316</td><td>1665</td></tr><tr><td>2021</td><td>2370</td></tr><tr><td>5041</td><td>5390</td></tr><tr><td>8441</td><td>8790</td></tr><tr><td>13123</td><td>13472</td></tr><tr><td>15543</td><td>15892</td></tr></table>	Start Positio n	End Positio n	1	350	1316	1665	2021	2370	5041	5390	8441	8790	13123	13472	15543	15892
		Start Positio n				End Positio n															
		1				350															
		1316				1665															
		2021				2370															
		5041				5390															
		8441				8790															
		13123				13472															
		15543				15892															
		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:	2200
Reads Count after Removing Duplication:	787

Reads Count after Overlapping:	496
Initial Dataset Size in (Base):	549860
Dataset Siset after Removing Duplication:	224564
Dataset Size after Overlapping:	136065

Overlapping Metrics

Repeat Identification Time:	00h:00m:16s:000ms
Overlapping Time:	00h:02m:54s:000ms
Reads Alignment Time:	00h:00m:39s:000ms
Total Hybrid Assembly Time:	00h:03m:33s:000ms
Repeat Annotation Time:	00h:12m:42s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
242	178084	80	1	0
226	177241	444	199	0
211	49284	16	1	0
201	48841	19	8	0
181	45369	17	1	0
176	44944	181	81	0