

Assembly Report

Experiment Details

ExperimentID:	Experiment 56
Sequencing Coverage:	29
Number of Partitions:	1
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	251

Reads Dataset Details

Total Reads Count:	1209
Total Dataset Size in (Base):	301119
Valid Read Count:	1209
Rejected Read Count:	0
Maximum Read Length:	251
Minimum Read Length:	212

Reference Genome Details

Length of Reference Genome (Base):	10080
Number of K-mers:	9830
Length of K-mer	515

Assembly Details

Number of Contigs:	19
Contig N50:	1452
Contig N90:	1276
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	391
Total Reads Count(Repeat):	6
Retetitive Read Count based on (Partitions Identifier):	0
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	9
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	<table><tr><th>Start Position</th><th>End Position</th></tr><tr><td>3285</td><td>3634</td></tr><tr><td>4858</td><td>5207</td></tr><tr><td>7202</td><td>7551</td></tr><tr><td>9332</td><td>9681</td></tr></table>	Start Position	End Position	3285	3634	4858	5207	7202	7551	9332	9681
		Start Position				End Position									
		3285				3634									
		4858				5207									
		7202				7551									
		9332				9681									
		GATGGTCTGT													
		GTGGATTAAAA													
		AAAGAGTGTCT													
		GATAGCAGCTT													
		CTGAACTGGTT													
		ACCTGCCGTG													
		AGTAAATTTAAA													
		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															

1	10080	GCTTTTCATTC	4	350		
		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						

Start Positio n	End Positio n
1	350
799	1148
2039	2388
8043	8392

SRGD Performance Metrics

Initial Reads Count:	1209
Reads Count after Removing Duplication:	397

Reads Count after Overlapping:	106
Initial Dataset Size in (Base):	301119
Dataset Siset after Removing Duplication:	126674
Dataset Size after Overlapping:	36803

Overlapping Metrics

Repeat Identification Time:	00h:00m:06s:000ms
Overlapping Time:	00h:04m:40s:000ms
Reads Alignment Time:	00h:00m:14s:000ms
Total Hybrid Assembly Time:	00h:04m:54s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	152881	89	7	0
249	147456	83	7	0
247	142129	60	5	0
246	138384	86	7	0
245	133225	102	8	0
244	127449	84	1	0
238	126736	79	4	0
237	123904	71	1	0
236	123201	60	1	0
234	122500	78	2	0
233	121104	61	1	0
229	120409	48	1	0

226	119716	371	165	0
211	32761	11	1	0
209	32400	23	1	0
207	32041	21	1	0
204	31684	10	1	0
201	31329	11	5	0
188	29584	22	2	0
184	28900	14	1	0
181	28561	17	1	0
176	28224	160	68	0