

Assembly Report

Experiment Details

ExperimentID:	Experiment 57
Sequencing Coverage:	29
Number of Partitions:	2
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	126

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:	21
Contig N50:	1305
Contig N90:	1101
Number of Scaffold	1
Scaffold N50:	10080
Scaffold N90:	10080
Mis-assembly Count:	0
TotalAssembly Size:	10080

Repeat Details

Total Reads Count(Non-Repeat) :	383
Total Reads Count(Repeat):	14
Retetitive Read Count based on (Partitions Identifier):	8
Retetitive Read Count (Entire Read Frequency Identifier):	3
Retetitive Read Count (Contained Read Frequency Identifier):	3
Total Repetitive Sequences Count	23
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 TGA CTGCAAC 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	4	350		
					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:	115
Initial Dataset Size in (Base):	301119
Dataset Siset after Removing Duplication:	126674
Dataset Size after Overlapping:	38812

Overlapping Metrics

Repeat Identification Time:	00h:00m:11s:000ms
Overlapping Time:	00h:04m:46s:000ms
Reads Alignment Time:	00h:00m:17s:000ms
Total Hybrid Assembly Time:	00h:05m:03s:000ms
Repeat Annotation Time:	00h:00m:02s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
250	146689	88	7	0
249	141376	79	5	0
247	137641	58	3	0
246	135424	84	7	0
245	130321	97	6	0
244	126025	84	1	0
241	125316	64	2	0
238	123904	79	4	0
237	121104	70	1	0
236	120409	57	1	0
234	119716	76	1	0
233	119025	59	1	0

232	118336	81	1	0
229	117649	48	1	0
226	116964	362	163	0
211	32041	11	1	0
209	31684	26	2	0
202	30976	17	1	0
201	30625	8	4	0
188	29241	22	2	0
182	28561	26	1	0
181	28224	17	1	0
176	27889	161	66	0