

Assembly Report

Experiment Details

ExperimentID:	1
Species:	E.Coli
Sequencing Coverage:	17
Number of Partitions:	5
Allowed Mismatch Count in (Base):	0
Length of Sliding Window:	61

Reads Dataset Details

Total Reads Count:	153
Total Dataset Size in (Base):	44181
Valid Read Count:	152
Rejected Read Count:	1
Maximum Read Length:	301
Minimum Read Length:	41

Reference Genome Details

Length of Reference Genome (Base):	2520
Number of K-mers:	2220

Length of K-mer	438
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Assembly Details

Number of Contigs:	6
Contig N50:	1086
Contig N90:	1086
Number of Scaffold	1
Scaffold N50:	2520
Scaffold N90:	2520
Mis-assembly Count:	0
TotalAssembly Size:	2520

Repeat Details

Total Reads Count(Non-Repeat) :	31
Total Reads Count(Repeat):	17
Retetitive Read Count based on (Partitions Identifier):	16
Retetitive Read Count (Entire Read Frequency Identifier):	2
Retetitive Read Count (Contained Read Frequency Identifier):	1
Total Repetitive Sequences Count	38

Total Unique Repetitive Sequences Count			1			
Total Repeat Size (Base)			1750			
Starting	Ending	Repetitive Sequences	Repeat Count	Length	Positions	
1	2520	GCTTTTCATTC	5	350		
		TGACTGCAAC				
		GGGCAATATG				
		TCTCTGTGTGG				
		ATTAAAAAAG				
		AGTGTCTGATA				
		GCAGCTTCTG				
		AACTGGTTACC				
		TGCCGTGAGT				
		AAATTAAAATT				
		TTATTGACTTA				
		GGTCACTAAAT				
		ACTTTAACCBA				
		TATAGGCATAG				
		CGCACAGACA				
		GATAAAAATTA				
		CAGAGTACAC				
		AACATCCATGA				
		AACGCATTAGC				
		ACCACCATTAC				
		CACCACCATCA				
		CCATTACCACA				
		GGTAACGGTG				
		CGGGCTGACG				
		CGTACAGGAA				
		ACACAGAAAAA				
		AGCCCGCACC				
TGACAGTGCG						
GGCTTTTTTTT						
CGACCAAAGG						
TAACGAGGTAA						
CAACCATGCG						
AGTGTTGAAGT						

SRGD Performance Metrics

Initial Reads Count:	153
Reads Count after Removing Duplication:	48
Reads Count after Overlapping:	33
Initial Dataset Size in (Base):	44181
Dataset Sizet after Removing Duplication:	17392
Dataset Size after Overlapping:	10570

Overlapping Metrics

Repeat Identification Time:	00h:00m:17s:000ms
Overlapping Time:	00h:04m:01s:000ms
Reads Alignment Time:	00h:00m:05s:000ms
Total Hybrid Assembly Time:	00h:04m:06s:000ms
Repeat Annotation Time:	00h:00m:01s:000ms

Overlapping Length	O(N)2 Time Complexity	Hit Index Count	Overlapping Matched Count	RI
299	961	1	1	0
293	900	5	1	0
265	841	1	1	0
259	784	5	1	0
251	729	22	11	0