

Assembly Report

Experiment Details

ExperimentID:	0
Species:	
Sequencing Coverage:	29
Number of Partitions:	5
Allowed Mismatch Count in (Base):	
Length of Sliding Window:	61

Dataset Reads Details

TotalReadCount:	502172
Total Dataset Size in (Base):	151153471
ValidReadCount:	502171
RejectedReadCount:	1
Maximum Read Length:	301
Minimum Read Length:	301

Reference Genome Details

Length of Reference Genome:	
Number of K-mers:	

K-mer Length

Assembly Details

Number of Contigs:	
Contog N50:	
Contig N90:	
Number of Scaffold	
Scaffold N50:	
Scaffold N90:	
Mis-assembly Count:	
TotalAssembly Size:	0

Repeat Details

Total Reads Count(Non-Repeat) :	218796
Total Reads Count(Repeat):	281716
Retetitive Read Count based on (Partitions Identifier):	281716
Retetitive Read Count (Entire Read Frequency Identifier):	0
Retetitive Read Count (Contained Read Frequency Identifier):	0
Total Repetitive Sequences Count	
Total Unique Repetitive Sequences Count	

Starting	Ending	Repetitive Sequences	Repeat Count	Positions
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SRGD Performance Metrics

Initial Reads Count:	502172
Reads Count after Removing Duplication:	500512
Reads Count after Overlapping:	499838
Initial Dataset Size in (Base):	151153471
Dataset Siset after Removing Duplication:	150654112
Dataset Size after Overlapping:	150633892

Overlapping Metrics

Overlapping Time:	00h:00m:05s:000ms
Total Assembly Time:	00h:11m:46s:000ms

Overlapping Length	O(N) ² Time Complexity	Hit Index Count	Overlapping Matched Count	RI
30	47871689616	12217490	674	0

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