

Project: FullAss454 copy.sqd

SeqMan NGen Assembly Report

SeqMan NGen 2.0.0 build 11

Assembly Time: 9:14:52

## Assembly Totals

Contigs: 56777  
 Contigs > 2K: 1494  
 Contigs To Reach Genome Length 25000000: 21638  
 Assembled Sequences: 1141489  
 Unassembled Sequences: 149292  
 All Sequences: 1290781  
 Contig N50: 1 Kbases  
 Average Coverage: 16

## Average Totals

Sequences per Contig: 20

## Average Lengths

Contigs: 702  
 Assembled Sequences: 350  
 Unassembled Sequences: 275  
 All Sequences: 341

## Average Quality

Assembled Sequences: 30  
 Unassembled Sequences: 28  
 All Sequences: 30

## Assembly Parameters

Match Size: 19  
 Match Spacing: 75  
 Minimum Match Percentage: 85  
 Match Score: 20  
 Mismatch Penalty: 30  
 Gap Penalty: 30  
 Max Gap: 15  
 Genome Length: 25000000  
 Expected Coverage: 2

-- SCRIPT --

setDefaultDirectory

defaultMacDirectory : /Users/UIUC/Desktop/454 Crepidula Files/Crepidula 454data/

loadSeq

file : "/Users/UIUC/Desktop/454 Crepidula Files/Crepidula 454data/linker trimmed 454A.fas"

setParameter

Parameter 'MatchSize' value '19'

setParameter

Parameter 'MatchSpacing' value '75'

setParameter

Parameter 'GapPenalty' value '30'

setParameter

Parameter 'MismatchPenalty' value '30'

setParameter

Parameter 'MatchScore' value '20'

setParameter

Parameter 'MinMatchPercentage' value '85'

setParameter

Parameter 'SNPMatchPercentage' value '85'

setParameter

Parameter 'MaxAssemblyCoverage' value '0'

setParameter

Parameter 'CoverageType' value '1'

setGenomeParam

Parameter 'GenomeLength' value '25000000'

assemble

RealignContigs

saveProject

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file : "/Users/UIUC/Desktop/454 Crepidula Files/Crepidula 454data/FullAss454.sqd"

Time to Preassemble 0:0:6

Scanned against repeated sequences: