GRIMM - Genome rearrangement algorithms

Multiple genome form	
Source genome: 1 2 3 18 4 5 6 103 102 101 100 99 98 97 96 95 94 93 92 91 90 21 22 23 24 80 79 78 77 75 74 73 72 71 70 69 68 67 66 65 64 63 42 52 41 62 59 58 57 54 56 55 50 48 47 46 60 61 45 44 51 40 43 49 53 39 38 37 36 35 34 76 33 32 31 30 29 28 27 26 25	
Destination genome: -26 -27 90 21 22 23 24 80 79 78 77 75 74 73 72 71 70 69 68 67 66 65 64 63 42 52 41 62 59 58 57 54 56 55 50 48 47 46 60 61 45 44 51 40 43 49 53 39 38 37 36 35 34 76 33 32 31 30 29 28 -91 -92 -93 25 81 82 83 84 85 86 87 88 89 20 19 17 16 15	
<u>Chromosomes:</u>	
Signs: signed unsigned	
run undo clear form Or, choose sample data ✓	
Formatting options	
Report Style: One line per genome One column Two column bef (chromosomes concatenated) (chromosomes separated) (chromosomes	
HorizontalVerticalYesShow all chromOnly affected company	
Show all possible initial steps of optimal scenarios ○	
Highlighting style: Should operations (reversal, translocation, fission, fusion) be highlighted, and when	?
○ before ○ after ● between/both ○ no highlighting	
Chromosome end onumeric (10) ● subscripts (C ₁₀) omit format:	
<u>Color coding:</u> Genes should be colored according to their chromosome in which genome:	
o source destination	
run undo clear form	
Click here or scroll up to enter new data or change options.	
106 genes Reversal Distance: 2	
One optimal reversal scenario	

Step Description

Reversal

2 Reversal

(Destination)

GRIMM 2.01 by Glenn Tesler University of California San D

GRIMM 2.01 by Glenn Tesler, University of California, San Diego.
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