Supporting Text S1 Instructions for loading Supporting Data Sets into Artemis and ACT.

Correia elements annotations are stored in a genbank formatted feature table. These can be displayed on top of a genome annotation in ARTEMIS and ACT, which can be downloaded from the Wellcome Trust Sanger Centre web site (http://www.sanger.ac.uk/resources/software/artemis/).

For ARTEMIS, the procedure is as follow:

1 - Load an annotated genome sequence file (for example 'MC58.gbk') with the "File -> Open" menu.

2 - Load an additional GBK formatted Correia element annotation file (for example 'MC58 alpha right Y128T.gbk') with the "File -> Read an entry" menu. Any number of GBK or GFF file can be successively loaded and displayed in the main window.

The repeat density plot is loaded by using the "Graph -> Add user plot" menu and selecting the corresponding repeat density file (for example 'MC58 repeat density.'

Any desired two- or three-way whole-genome comparison can be made using ACT, as follows:

1 - "File -> Open" brings up the sequence selection window. For 'Sequence file 1' select a annotated genome sequence file (for example select 'Z2491.gbk').

2 - Repeat for 'Sequence file 2' selecting another annotated genome sequence file (for example select 'FAM18.gbk').

3 - In the 'Comparison file' window select the corresponding '.blstm' file. In this case it would be 'Z2491 Vs FAM18.blstm'.

Swapping the files in the Sequence file 1 and 2 windows will simply change whether the respective files appear above or below each other in the comparison window. Note, however, that one would have to select a different 'Comparison file' (in this example 'FAM18 Vs Z2491.blstm' instead of 'Z2491 Vs FAM18.blstm'). The Correia element annotations and the Repeat Density Plots can then be added in the same was as described above for Artemis. If a three-way

comparison is desired, add the appropriate files using the 'more files...' dialog. Warning messages should be ignored.