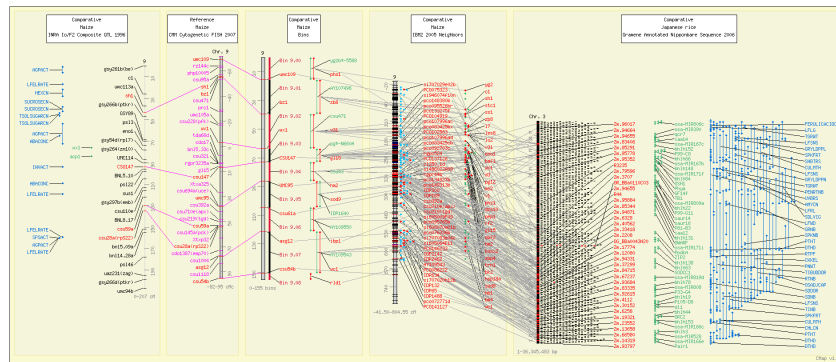# Genome Visualization and Comparison Using CMap[1] and Circos[2]


CMap is a generic and extensible comparative map viewer that runs in standard web browsers and aims to assist biological researchers seeking to extrapolate known map data into unknown areas. A user can compare an unlimited number of maps, view pair-wise comparisons of known correspondences, and search for maps or for features by name, species, type and accession.
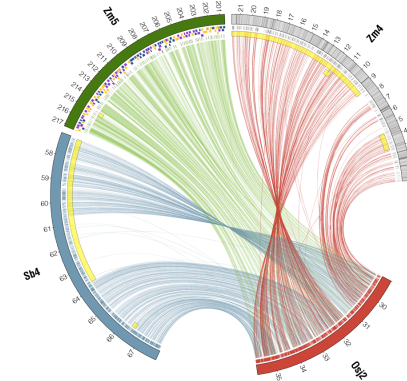
Circos is a program that employs a circular layout to display relationships between genomes as scatter, line and histogram plots, heat maps, tiles, connectors and text.
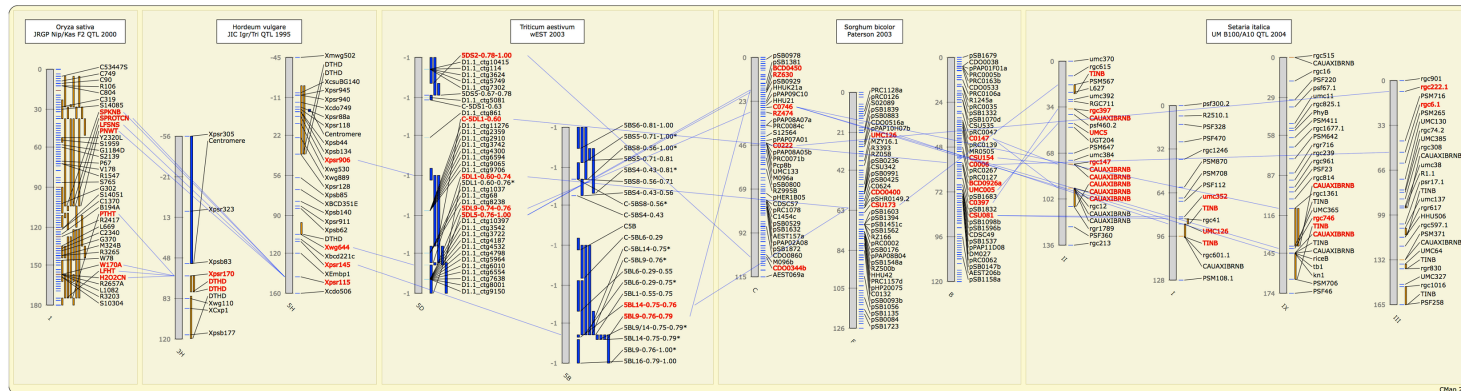
Version 2 of CMap currently in development will integrate the Circos circular genome visualization program to directly create novel views of existing CMap data.
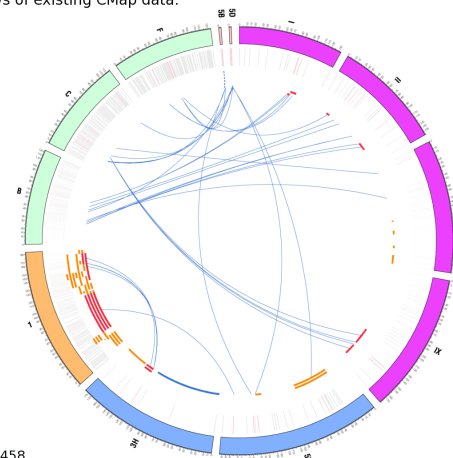
[1] Youens-Clark, K., et al. CMap 1.01: A comparative mapping application for the Internet. Bioinformatics (2009) doi:10.1093/bioinformatics/btp458.
[2] Krzywinski, M. et al. Circos: an Information Aesthetic for Comparative Genomics. Genome Res (2009) 19:1639-1645.