83 species with 2 or more strains

(1) species selection

(2) Intra-species pairwise comparisons

704 pairwise MAUVE alignments

(3) LCB analysis

rearranged genomes

colinear genomes

(4) segmentation integration

MAUVE pairwise and maximal alignments

MGA pairwise and maximal alignments

MOSAIC database

Annotations

Backbones

Variable segments

(5) annotation integration