

Total 2,307 *H. pylori* genomes

NCBI Refseq: 2,293 genomes
This study: 14 newly assembled genomes



Pairwise genome comparison

Pairwise ANI of 2,307 Hp genomes using
FastANI



Visualization and clustering

Heatmap: Euclidean distance and average
linkage
cutree, $k = 5$



Group 4 and 5

Closest reference genome assignment

331 Hp genomes within the same clade as
the 14 study genomes



cgSNP analysis

345 ingroup genomes + 1 CC33C outgroup
Snippy/Gubbins: 3,832 SNVs
RAxML-NG: 4 subgroups (SNP1–SNP4)