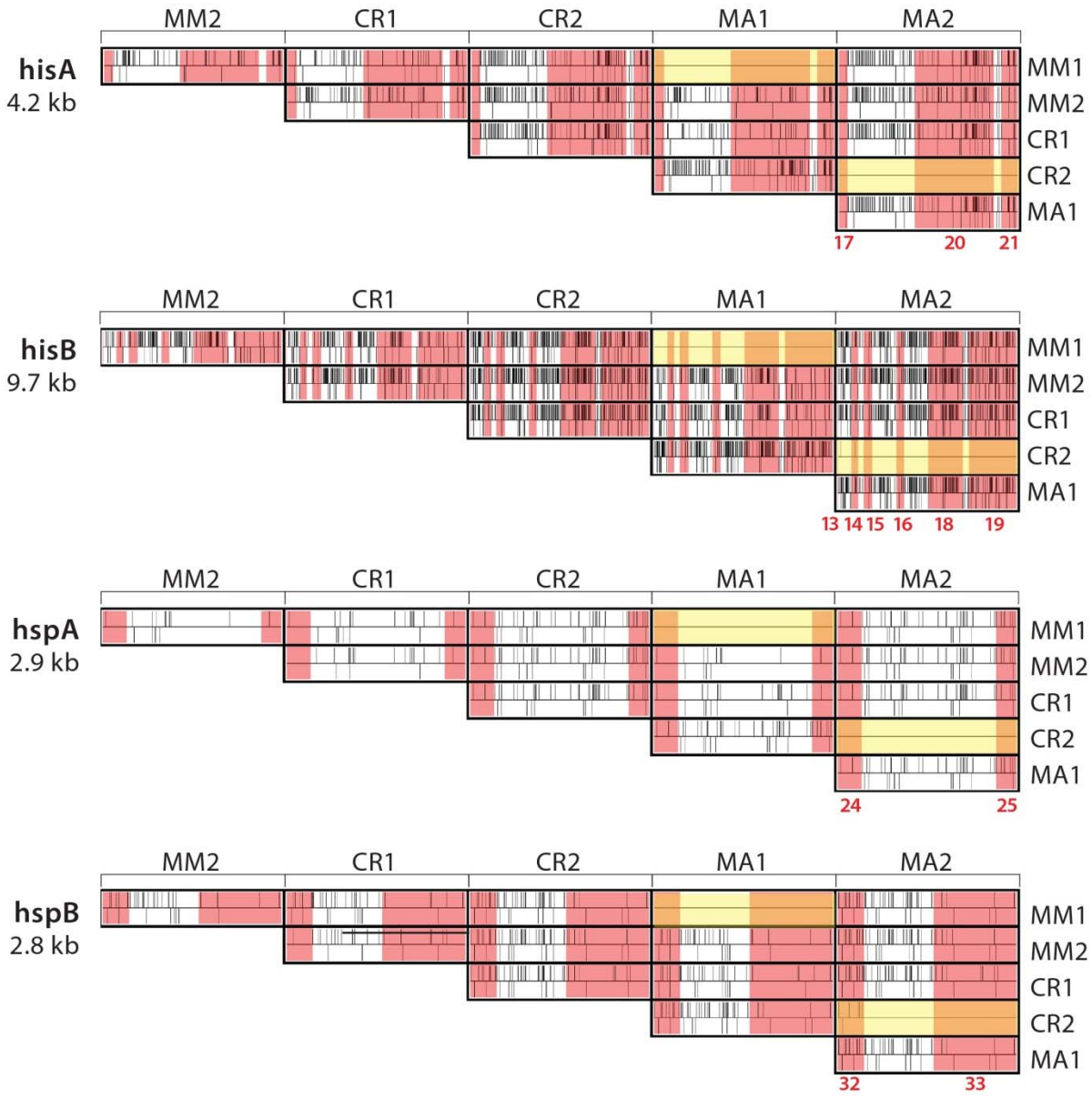

Figure S2 Pairwise differences between sequences of isolates MA, MM and CR in each of the four regions examined. Substitutions are indicated by thin vertical lines above, indels by lines below. Genes are shaded in red. In each region one of the sequences of MA is identical to one of the sequences of MM and the other sequence of MA is either identical or nearly identical to a sequence of CR, as shown in cells with yellow background. The sequences of MA2 and CR2 differ by two substitutions in the hisB region, one between genes 13 and 14 and the other in an intron of gene 14. The sequences of MA2 and CR2 in the hspB region differ by 5 substitutions in exons and one indel in an intron, all in gene 32. In each region, all other pairwise differences are spread throughout the region. There are no indels or stop codons in any exon of any annotated gene except for three 14-28 aa deletions in an exon of gene 18, a poorly supported putative osteopetrosis-associated gene, and a truncation of 6 amino acids at the C-terminus of the H2Av gene (gene 17) in the hisA region. Gene numbers and annotation are from Hur *et al.* 2009.