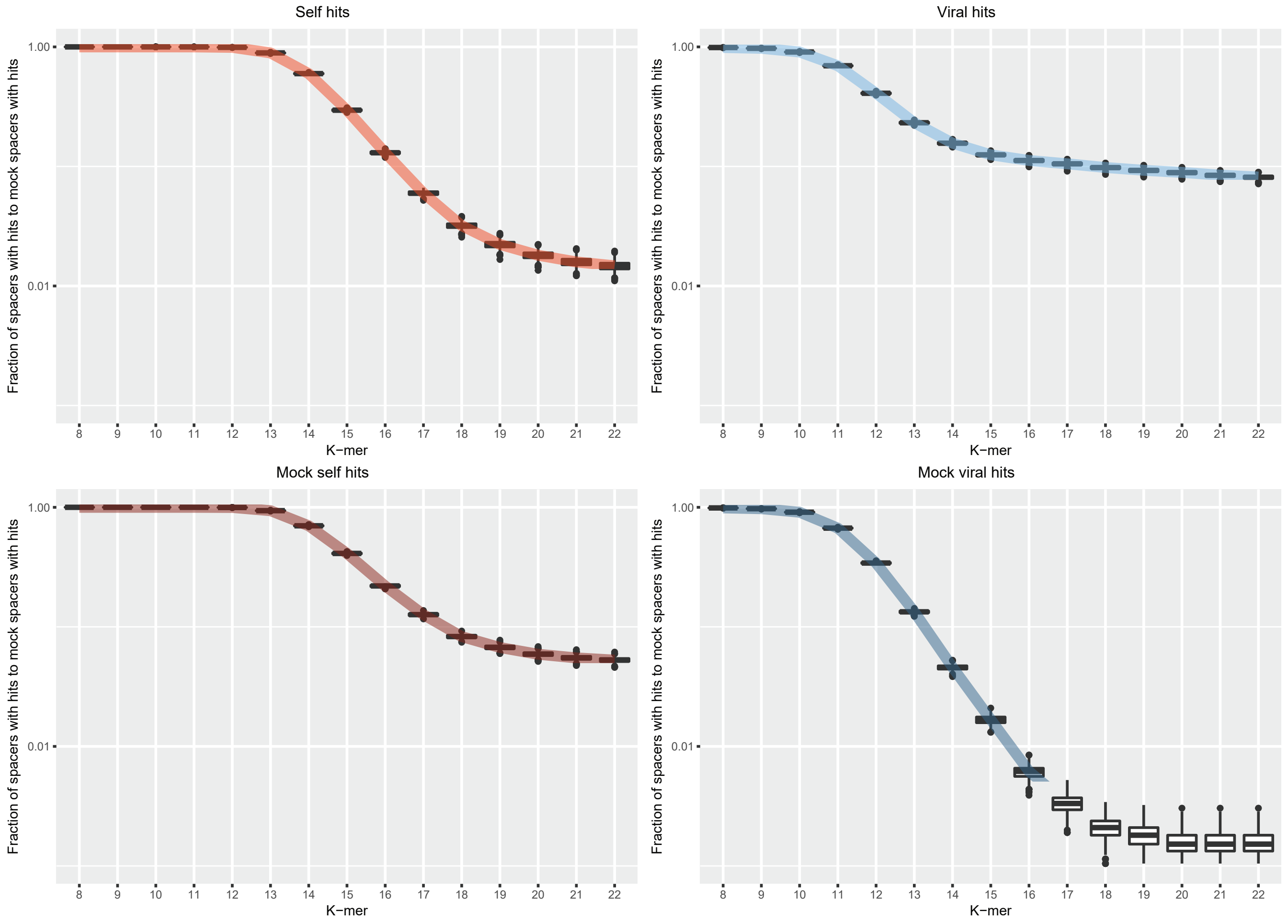
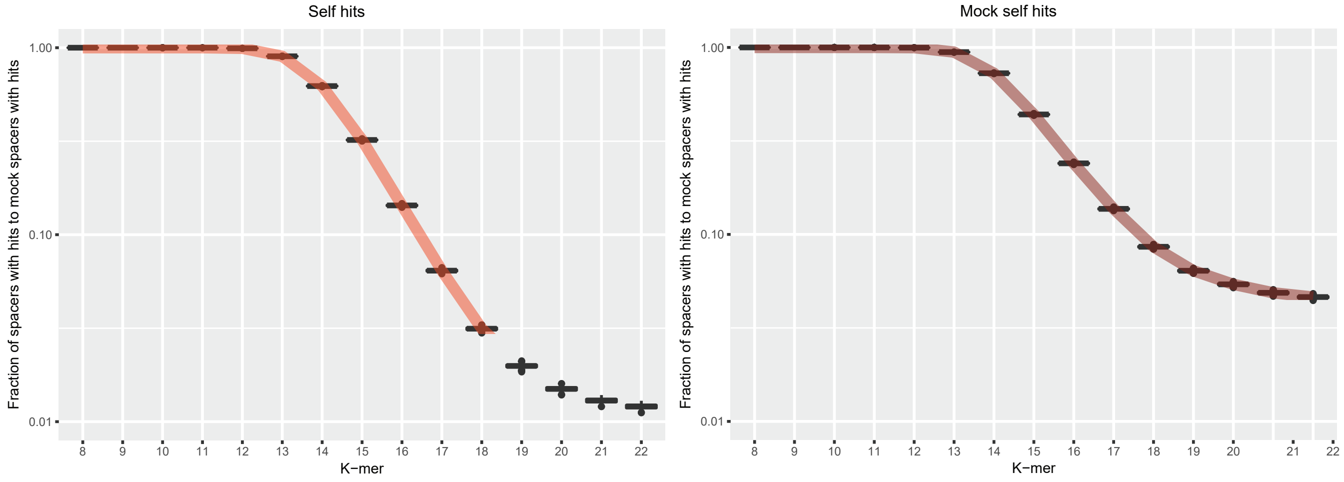
Supplementary figure 1

1000-fold bootstrap resampling of the set of spacers from figure 2b (all completely sequenced genomes) and figure 2c (154 genomes with spacers matches in viruses). Lines represent original values: blue, real spacers matching viral genomes; dark blue, mock spacers matching viral genomes; red, real spacers matching the host genome; dark red, mock spacers matching the host genome. Box plots represent results of bootstrapping of these values.

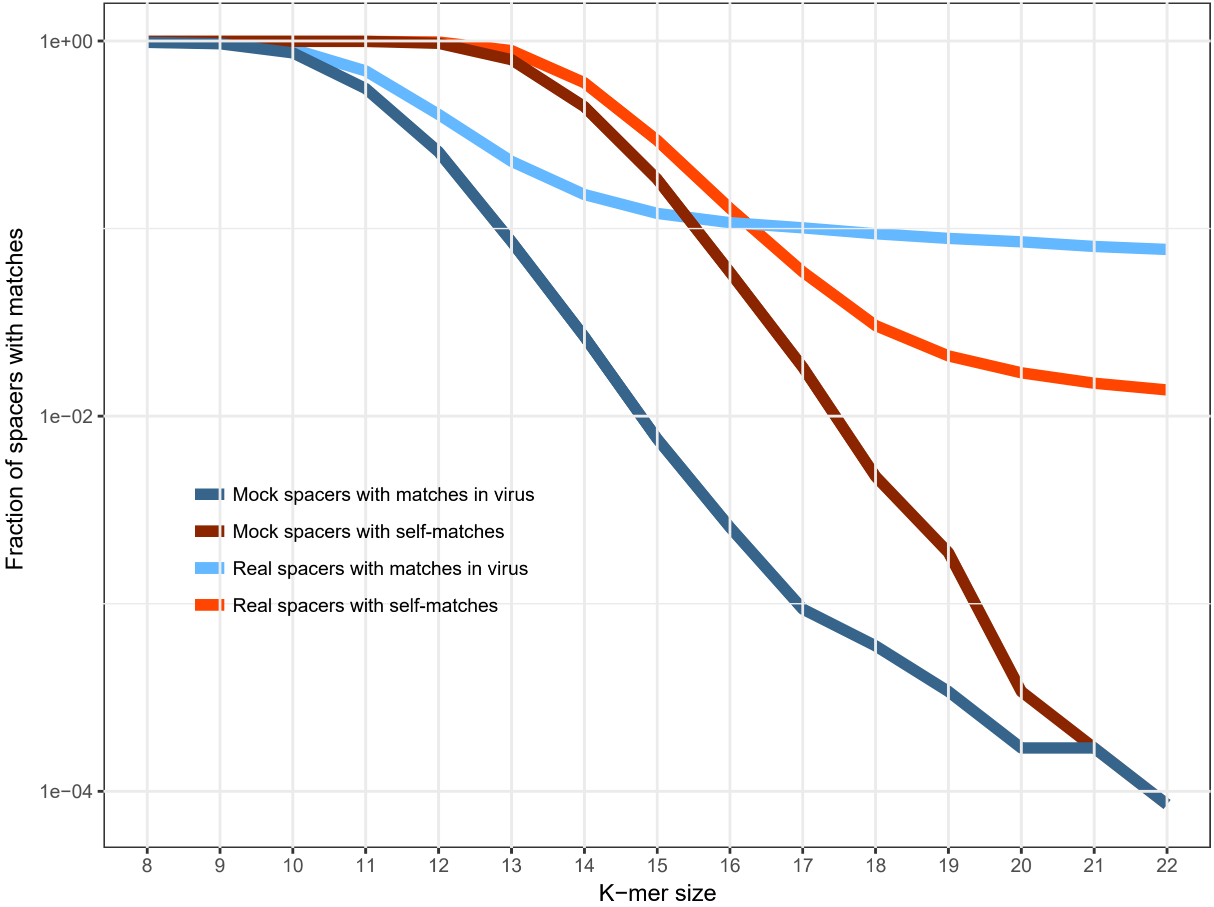


Bootstrap for values shown on figure 2b (all completely sequenced genomes)



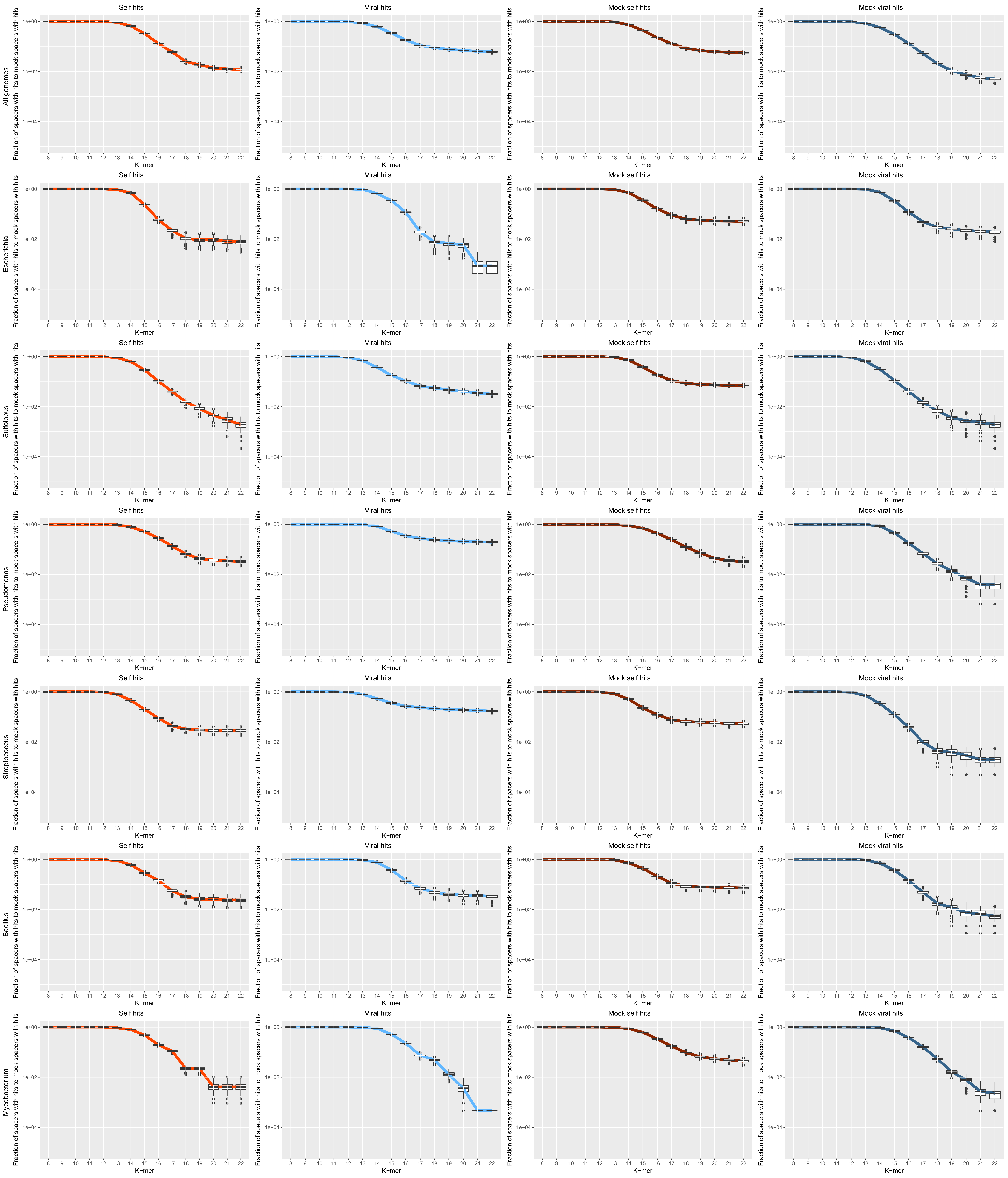
Supplementary figure 2

Fractions of virus-matching and self-matching spacers (of the total number of spacers) for the scrambled spacers set for 154 genomes containing CRISPRs with identifiable protospacers in viruses. Line colors: blue, real spacers matching viral genomes; dark blue, mock spacers matching viral genomes; red, real spacers matching the host genome; dark red, mock spacers matching the host genome.



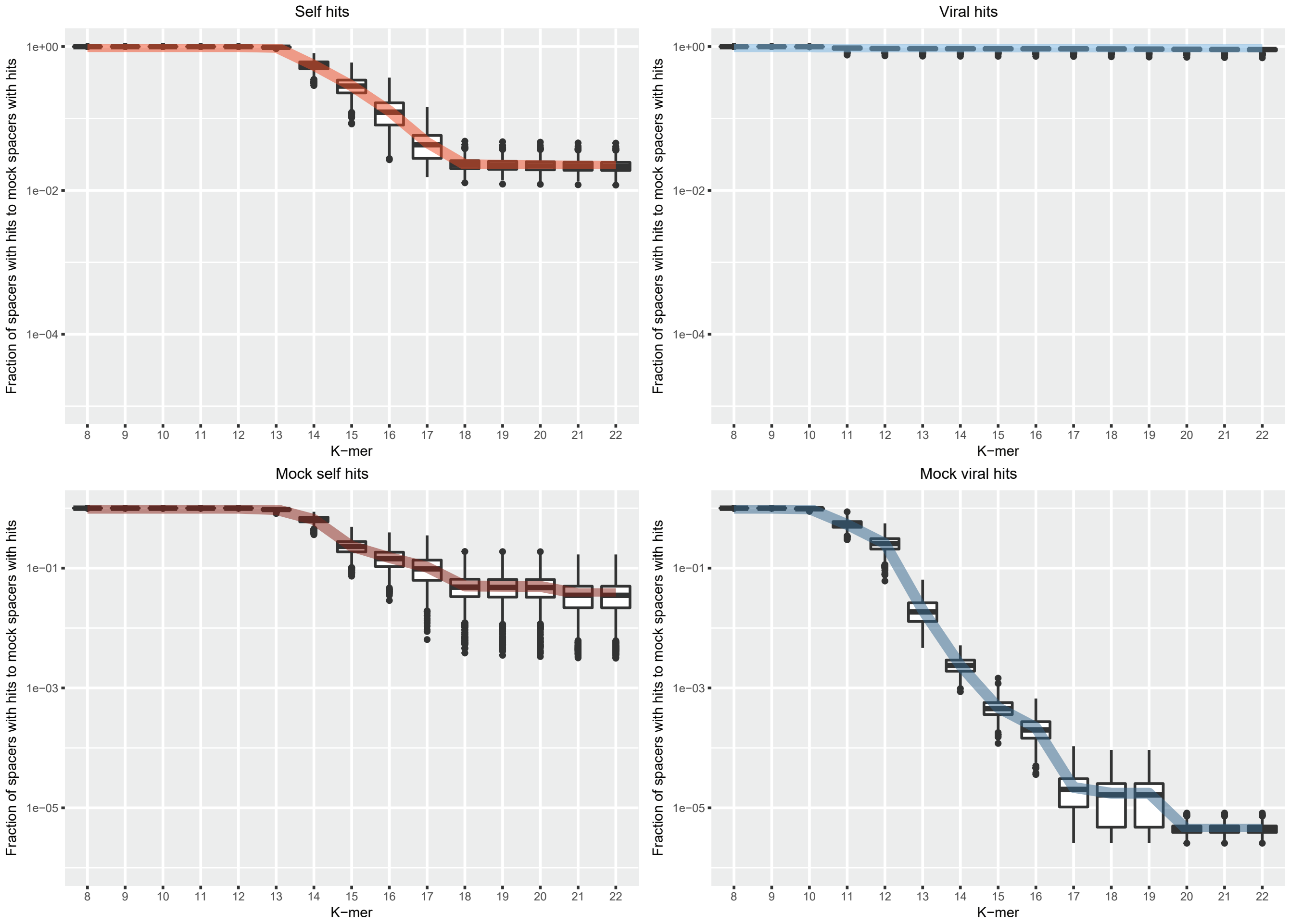
Supplementary figure 3

1000-fold bootstrap resampling of the set of spacers from figure 3 (genomes with well sampled viromes).



Supplementary figure 4

1000-fold bootstrap resampling of the set of spacers from figure 4
(data from adaptation experiments).



Bootstrap for values shown on figure 4 for lambda phage