

Supplementary information to:

Genome investigations show host adaptation and transmission of LA-MRSA CC398 from pigs into Danish healthcare institutions

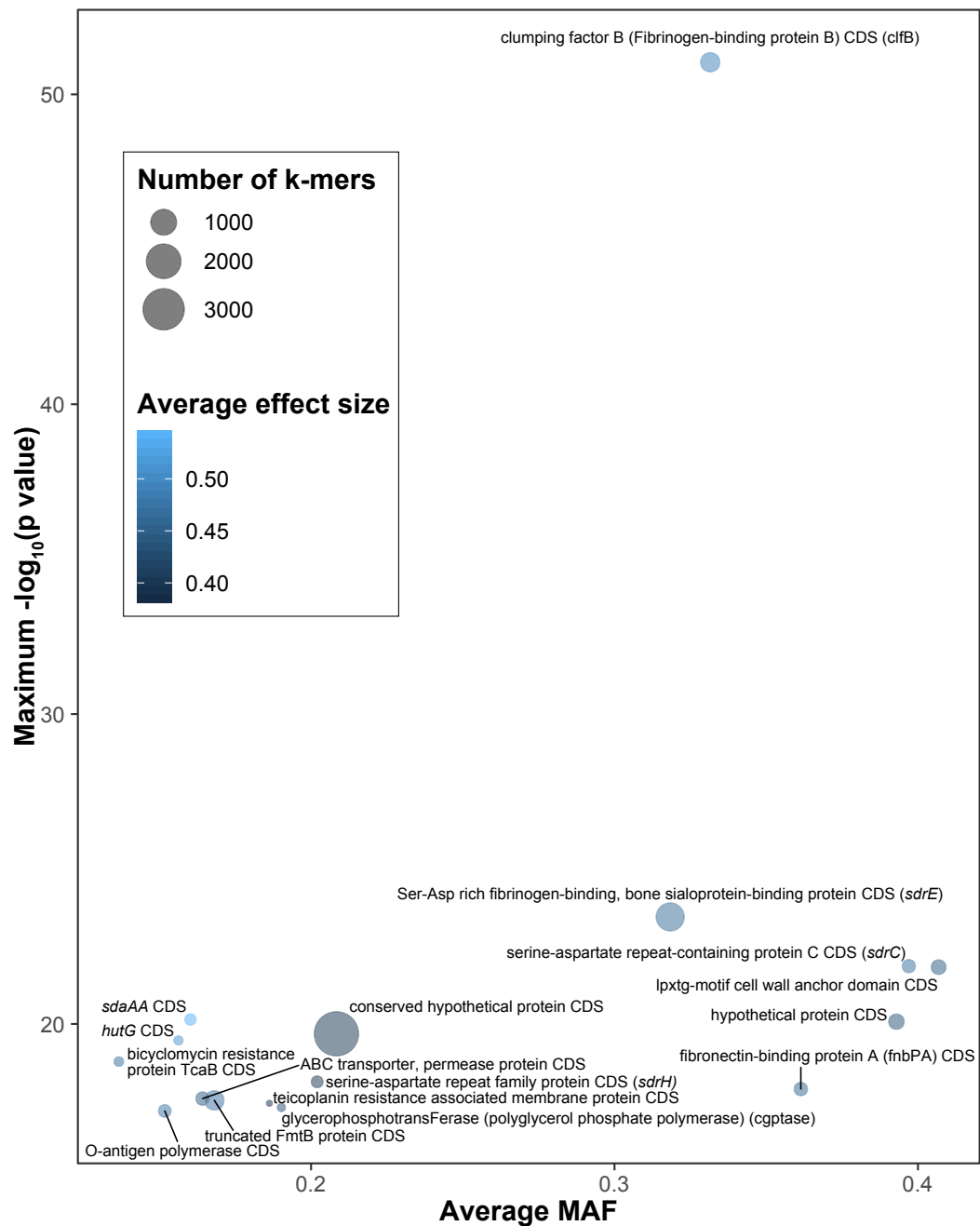
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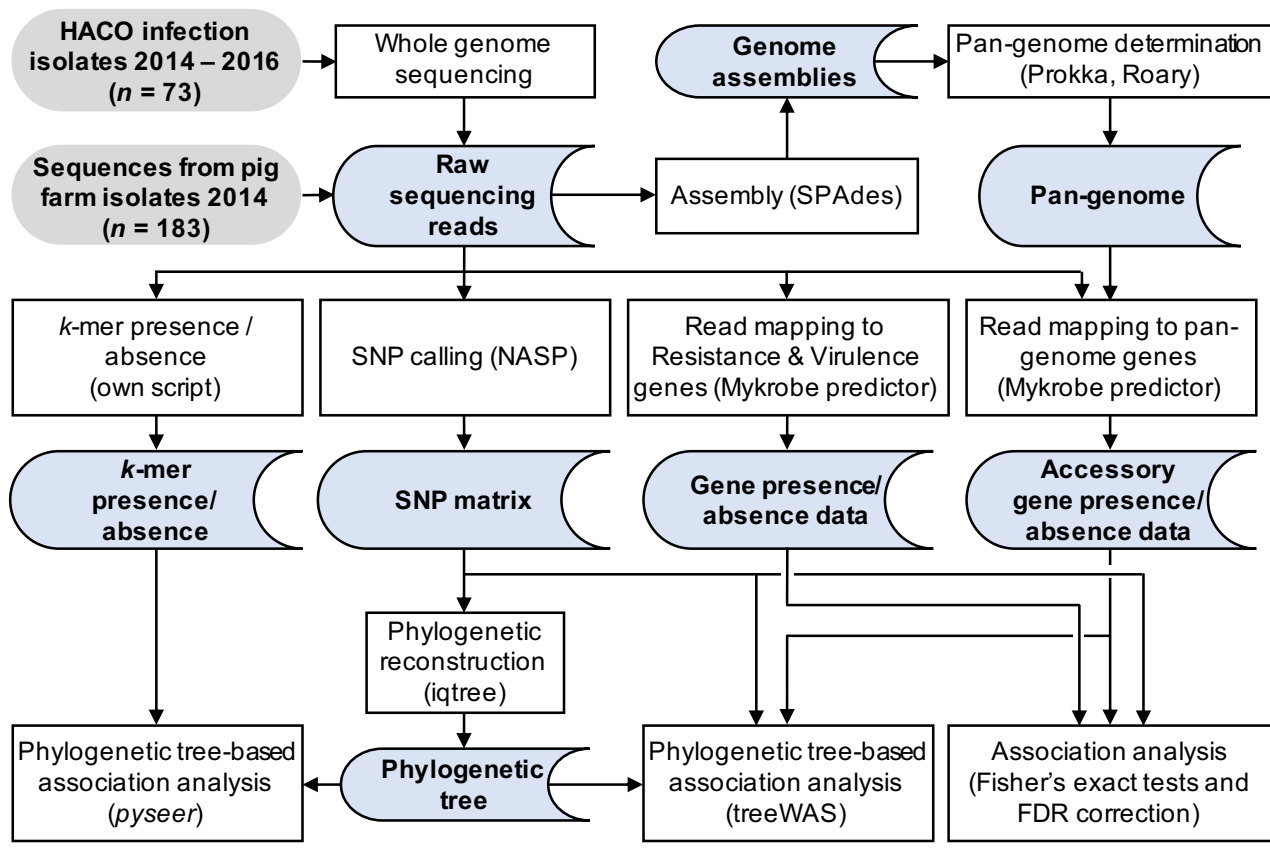
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Supplementary Figure S1



Supplementary Figure S1: Genomic regions with human host associations. The figure shows k -mer hits as obtained in *pyseer* and their mapping to sequence annotations in the ST398 S0385 reference genome. Only hits with a p value $\leq 10^{-17}$ are shown. Gene hits are shown as circles placed according to the lowest p value of any k -mer with a hit in a gene (y-axis) and the average minor allele frequency (MAF) indicating the commonness of the hits (x-axis). The circles are sized according to the number of k -mer hits mapped to the region and colored according to the effect size indicating the distribution among the phenotypes.

Supplementary Figure S2



Supplementary Figure S2: Study overview. Initial datasets (grey boxes), analyses (white boxes) and intermediate datasets/results (blue boxes) are connected according to their use in the study.