**Fig. S1. Population structure of a global collection of *Streptococcus suis* isolates.** (a) A core genome phylogeny of 962 isolates of *S. suis*. Individual disease (red) and carriage (blue) isolates are indicated in the inner strip. The more pathogenic clade is indicated by a red outer ring, and the less pathogenic clade by a blue outer ring. The locations of each strain in our two MA experiments are indicated on this strip (Table 1). (b) The proportion of isolates in each clade that are associated with disease (excluding isolates for which disease-association is unknown). (c) A box plot of genome sizes of isolates from each clade. (d) A box plot of the core genome GC-content of isolates from each clade.