



**Supplementary Figure 1.** Representation of predicted homologously-recombined regions. The left panel represents the ML phylogeny of *S. equi*, with BAPs cluster and MLST type shown in columns adjacent to the tree, as in Figure 1. The right panel represents regions identified as exhibiting significantly raised SNP density, indicative of import of variation en masse via homologous recombination or regions under high selective pressures. Above the panel is a representation of the genome annotation of *S. equi* Se4047.