



Fig. S3. Results of recombination analysis on the 1.2 Mbp core genome of 34 *E. faecium* strains using BratNextGen. On the left, a ‘Proportion of Shared Ancestry’ (PSA) tree is shown, which clusters strains together on the basis of shared recombination events. The tree is cut at the threshold level 0.22 to obtain three clusters of strains (a singleton cluster in the middle and the upper and lower clusters colored by green and red branches, respectively). In the middle, colored bars show predicted recombination events (note that the coloring scheme is partially arbitrary and intended for visualization purposes only). Strains are shown on the right.