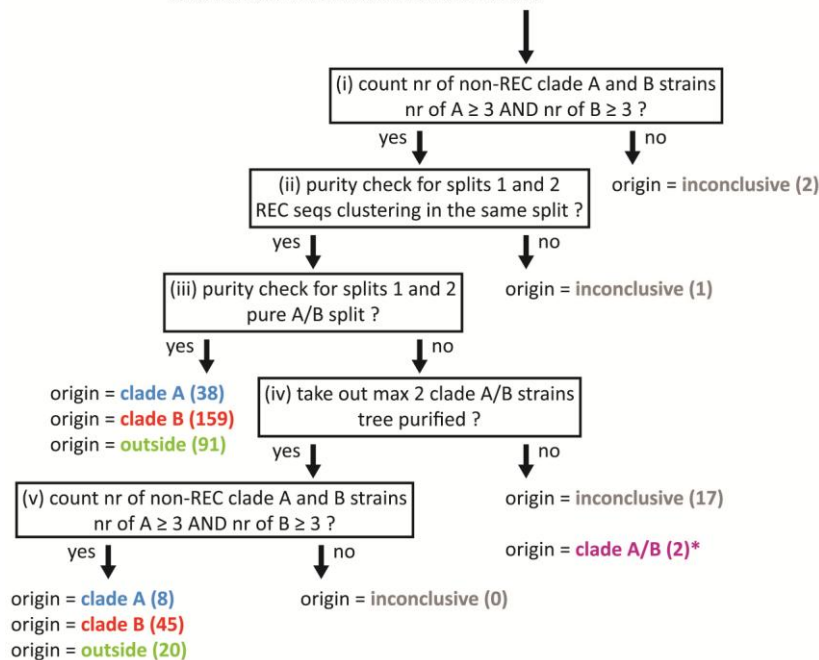


hypothetical 'recombination' sub-tree for recombination event X, where a recombinant sequence from a clade A strain "A (REC)" clusters with sequences from clade B strains

total number of recombination events: **383**



**Fig. S1.** Decision scheme for predicting recombinant sequence origins. For each recombination sub-tree, the topologies after the first major split were used to predict whether recombinant sequences originated from an (ancestral) clade A or clade B *E. faecium* strain, or from a species outside *E. faecium* when the recombinant sequences clustered separately from both clades. Inconclusive predictions are also indicated in the figure. \* In cases where recombinant sequences clustered with  $\geq 3$  clade A and  $\geq 3$  clade B strains in one split, the recombinant sequence origin was predicted to be *E. faecium* (i.e. unclear whether it was clade A or B). The number of times each origin was predicted is indicated between brackets.