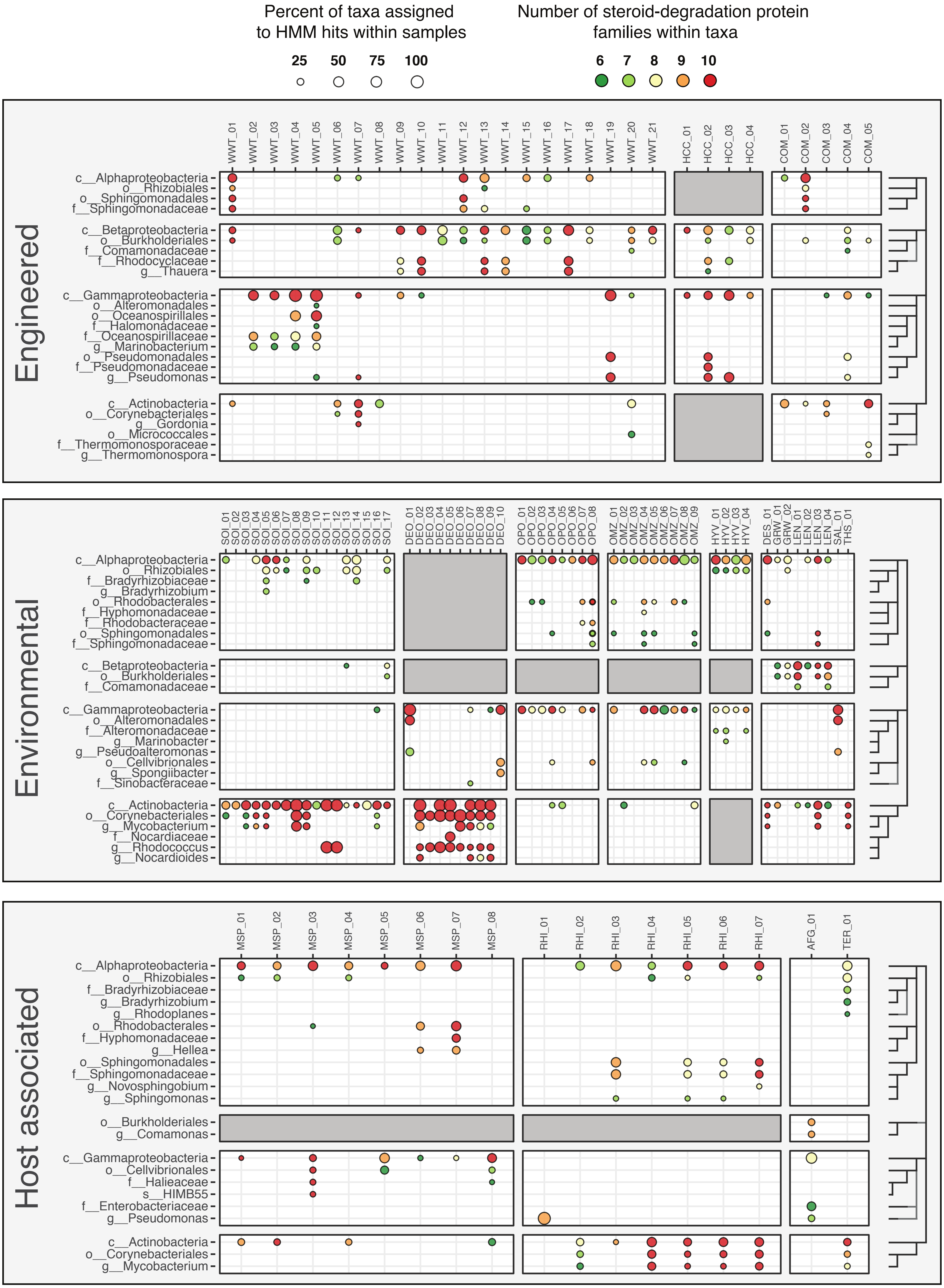

Fig. S3: Lowest common ancestor analysis of steroid-degradation HMM hits. Only taxa are shown that were assigned to more than 10% of HMM hits within a metagenome sample and to more than five out of ten steroid-degradation protein families. Percent of HMM hits within a metagenome sample are represented by circle size and the number of steroid-degradation protein families per taxa are colour coded. Only the lowest taxonomic rank is shown in cases where higher ranks had identical percentage and pathway completeness values.