



Figure S1: Phylogenetic tree of 729 aromatic amino acid hydroxylases. Branches of eukaryotes and prokaryotes are distinguishable by color, black and gray respectively. Stripes around the tree designate the type of hydroxylase which corresponds to each specie. Duplication events are marked within each clade. Tree was inferred using the Neighbor-Joining method. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Evolutionary distances were computed using Poisson correction method. All positions with less than 2% site coverage were eliminate, a total of 495 positions were in the final dataset. Evolutionary analysis was conducted in MEGA9.