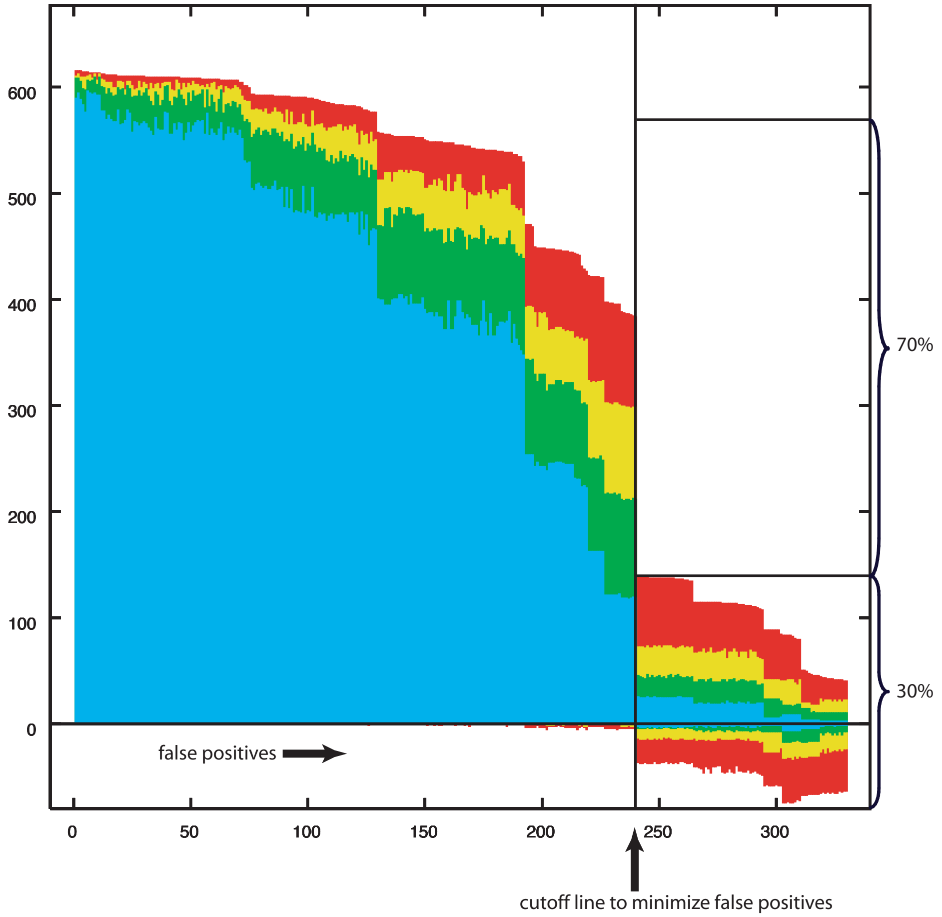
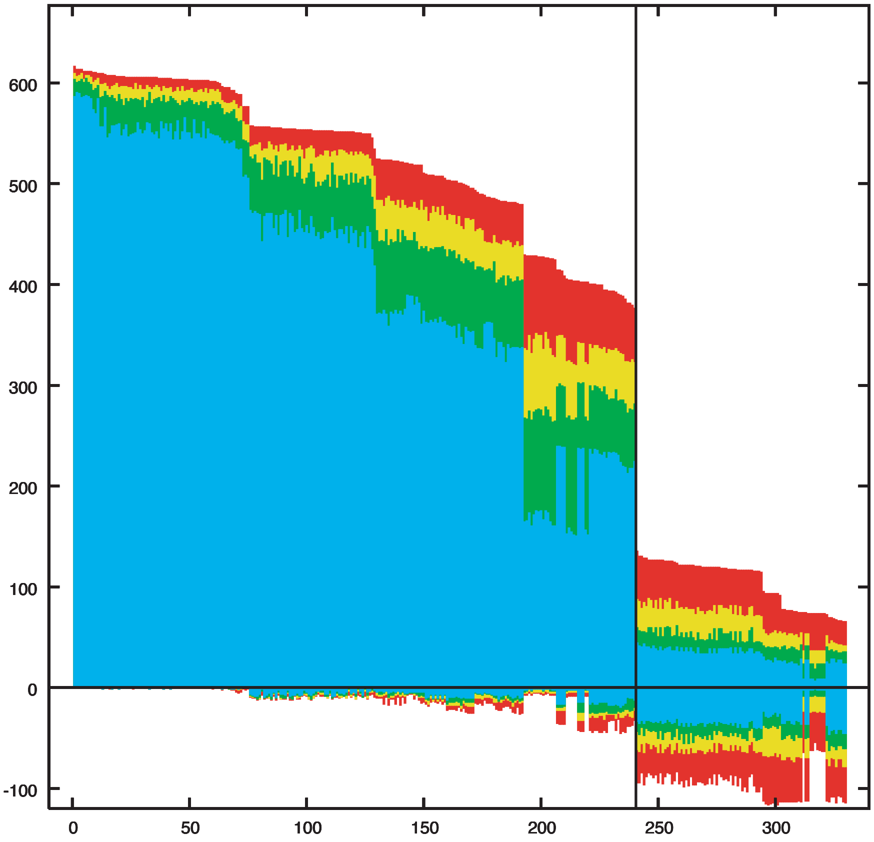
RESULTS OF SIMULATIONS (see Figure 2 legend in the main text for figure notations)



Quartet decomposition analyses of simulated genomes (no gene gain/loss, no HGT). The analyses were performed on 620 core genes. 277 datasets of orthologous genes had at least one quartet conflicting with plurality (false positives). Majority of this conflicts were reported for quartets that are not resolved by the majority of the datasets. Excluding quartets to the right of vertical black line reduces the number of false positives to 31 datasets. This exclusion correspond to the value of X=30%.



Quartet decomposition analyses of simulated genomes II (no gene gain/loss, but with HGT). 11-13 % genes in each simulated genome have at least one transfer event in their evolutionary history. The analyses were performed on 623 core genes. 60 datasets were reported as false positives for transfer, and transfers in 141 datasets were not detected (false negatives). With application of a cutoff X=30%, the number of false positives went down to 3, while the number of false negatives went up to 358. By minimizing false positives, we also exclude legitimate transfer events, therefore underestimating total number of conflicts.