



Fig. S8. Incongruencies between gene family trees and AADgenome. Outliers from the 1:1 relationship between the minimum AADgenome across all genomes (x-axis) and the AADgenome computed among the three closest neighbors on the gene tree (y-axis) indicate potential LGT. This analysis was performed on 204 protein-coding genes that were found in the largest number of GORG-Tropics SAGs and had only one or very few copies per genome (median, mean, max copy number: 1, 1.04, 4). Multi-copies were treated separately. The P-values indicate statistically significant deviation from 1:1 line by a parametric test. Data points where the minimum AADgenome across the genomes equaled the AADgenome to the three closest neighbors (i.e., $x = y$) were excluded from the outlier detection analysis and are shown in grey.