

Supplementary figure 8: Comparison of percentages of smBGCs, CAZymes and TTA-bearing proteins between *Streptomyces* and Actinobacteria

The boxplots on the left of the phylogenomic tree represent the percentage of smBGCs, CAZymes and TTA-bearing proteins in *Streptomyces* (213 genomes) and Actinobacteria (192 genomes). Statistical significance was calculated using the Wilcoxon test (p-value < 0.05).

The horizontal bars next to the tree represent the number of chromosomally encoded proteins, the percentage of smBGCs, the percentage of CAZymes and the percentage of TTA-bearing proteins in the Actinobacterial genomes.

The red vertical dotted bars indicate the *Streptomyces* +- 2Z-scores interval for that specific feature.

The black vertical dotted bar indicates the value of *Streptomyces coelicolor* reference genome for that specific feature.

