

Supplementary figure 9: CAZymes comparison in different habitats

The habitat annotation for each of the 355 *Streptomyces* genomes was downloaded from Genbank. Only genomes with habitat annotation were used in this analysis.

Visualization was achieved using the plotly graphics library.

Statistical significance was calculated using the Wilcoxon test (p-value < 0.05). P-values have been adjusted using multiple testing correction with FDR method

355 *Streptomyces* complete genomes with annotation (Land plants include rhizosphere, Marine plants include mangrove)

