Supplementary Materials:

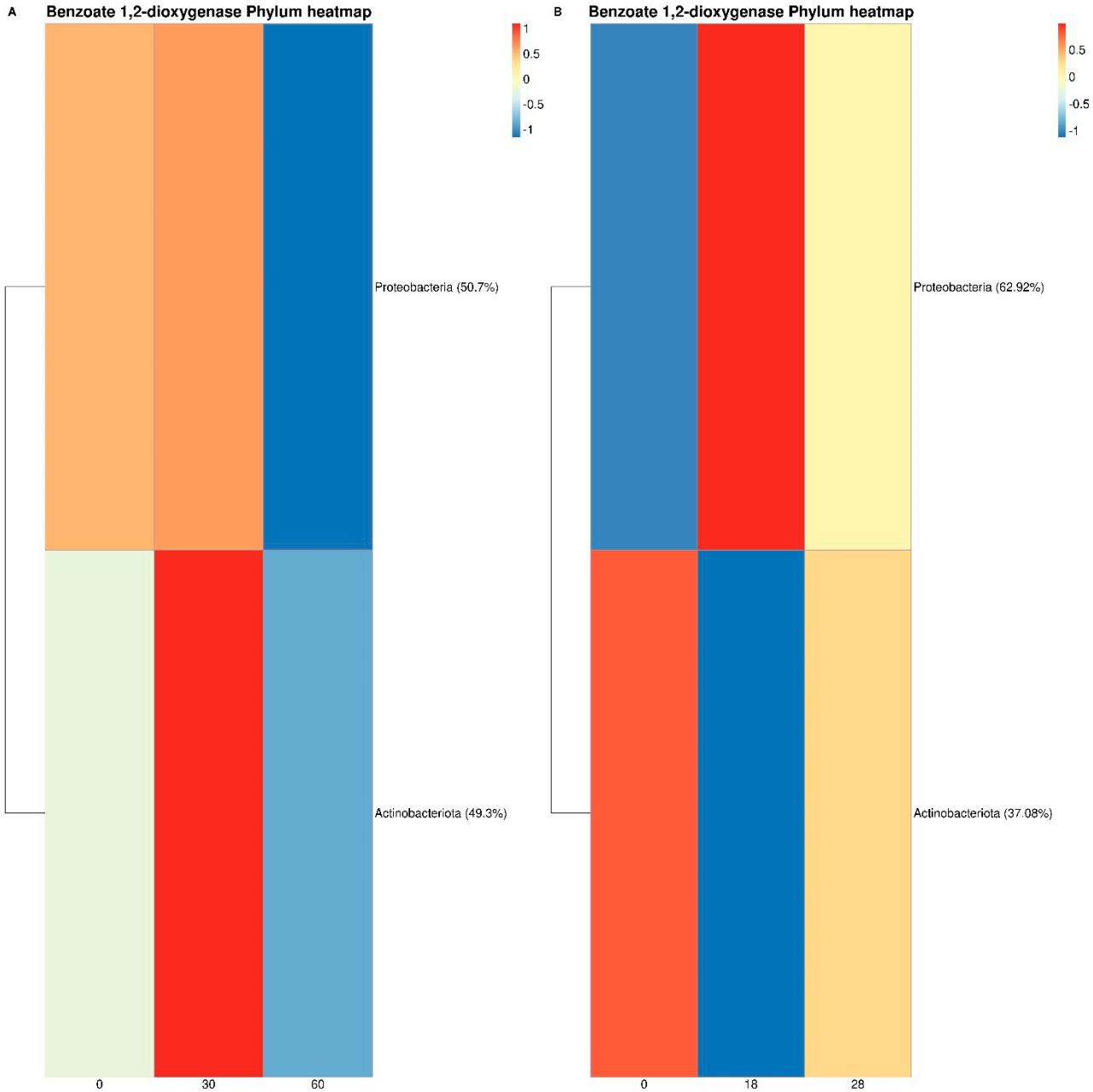

Figure S1. Functional Heatmap for Benzoate 1,2- dioxygenase at Genus level. Functional Heatmap showing SMS community (panel **A**) and *Lambertella* sp. MUT 5852 community (panel **B**), phylum contribution to Benzoate 1,2- dioxygenase (EC:1.14.12.10). Percentages reported near genus names represent the relative abundance of the sum of contribution of that genus per sample, against total sum of contributions: a cut-off value of 0.005% was chosen. Hierarchical clustering was performed on rows by Pearson correlation, based on Euclidean distance. In order to evidence variation, a colour scheme that represents row-wise Z-scores of per genus contributions per sample, was chosen. For this colour scheme, a Z value of 0 matches the reported percentage near the genus contributor.

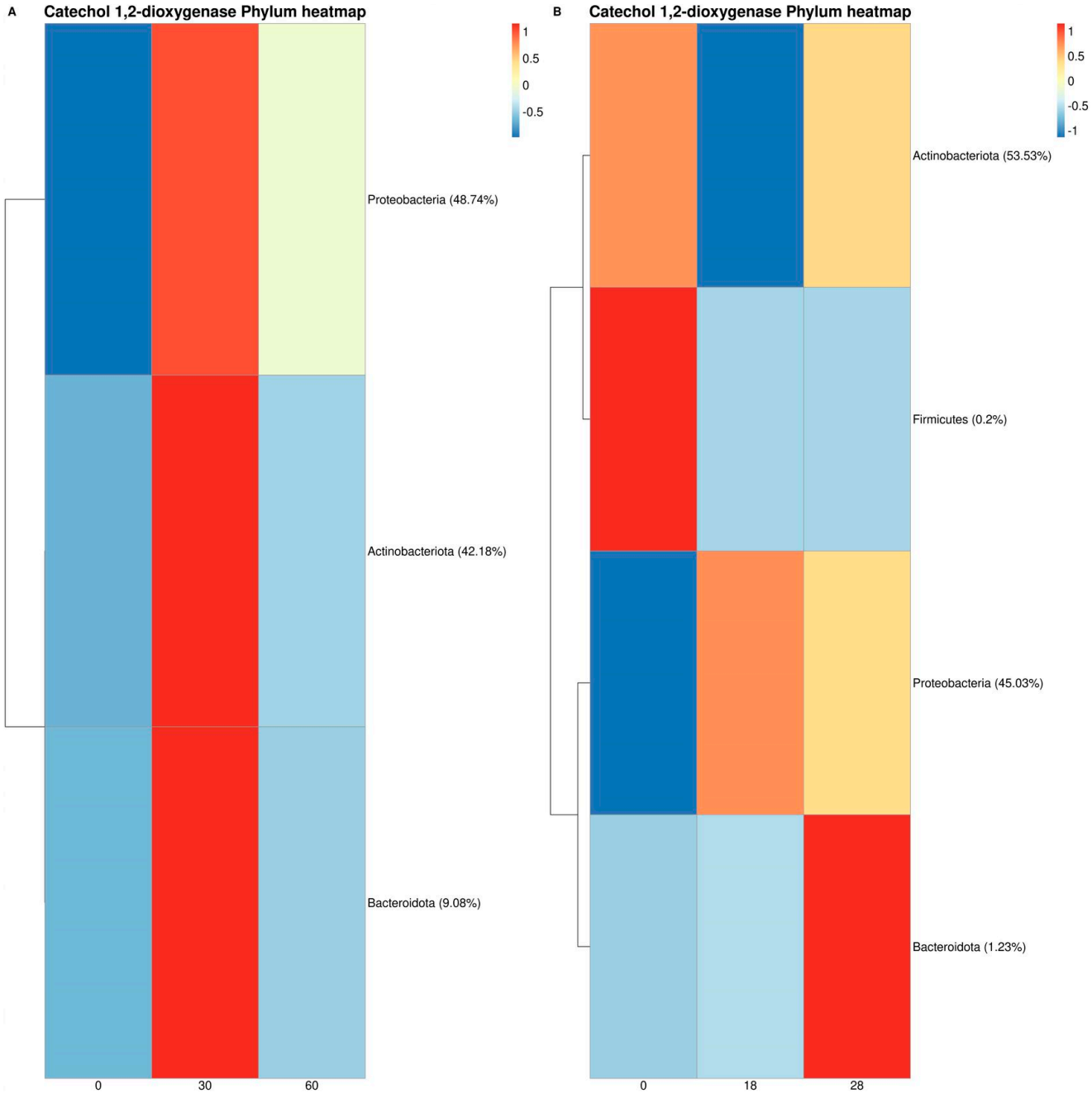

Figure S2. Functional Heatmap for Catechol 1,2- dioxygenase at Genus level. Functional Heatmap showing SMS community (panel **A**) and *Lambertella* sp. MUT 5852 community (panel **B**), phylum contribution to Catechol 1,2- dioxygenase (EC:1.13.11.1). Percentages reported near genus names represent the relative abundance of the sum of contribution of that genus per sample, against total sum of contributions: a cut-off value of 0.005% was chosen. Hierarchical clustering was performed on rows by Pearson correlation, based on Euclidean distance. In order to evidence variation, a colour scheme that represents row-wise Z-scores of per genus contributions per sample, was chosen. For this colour scheme, a Z value of 0 matches the reported percentage near the genus contributor.

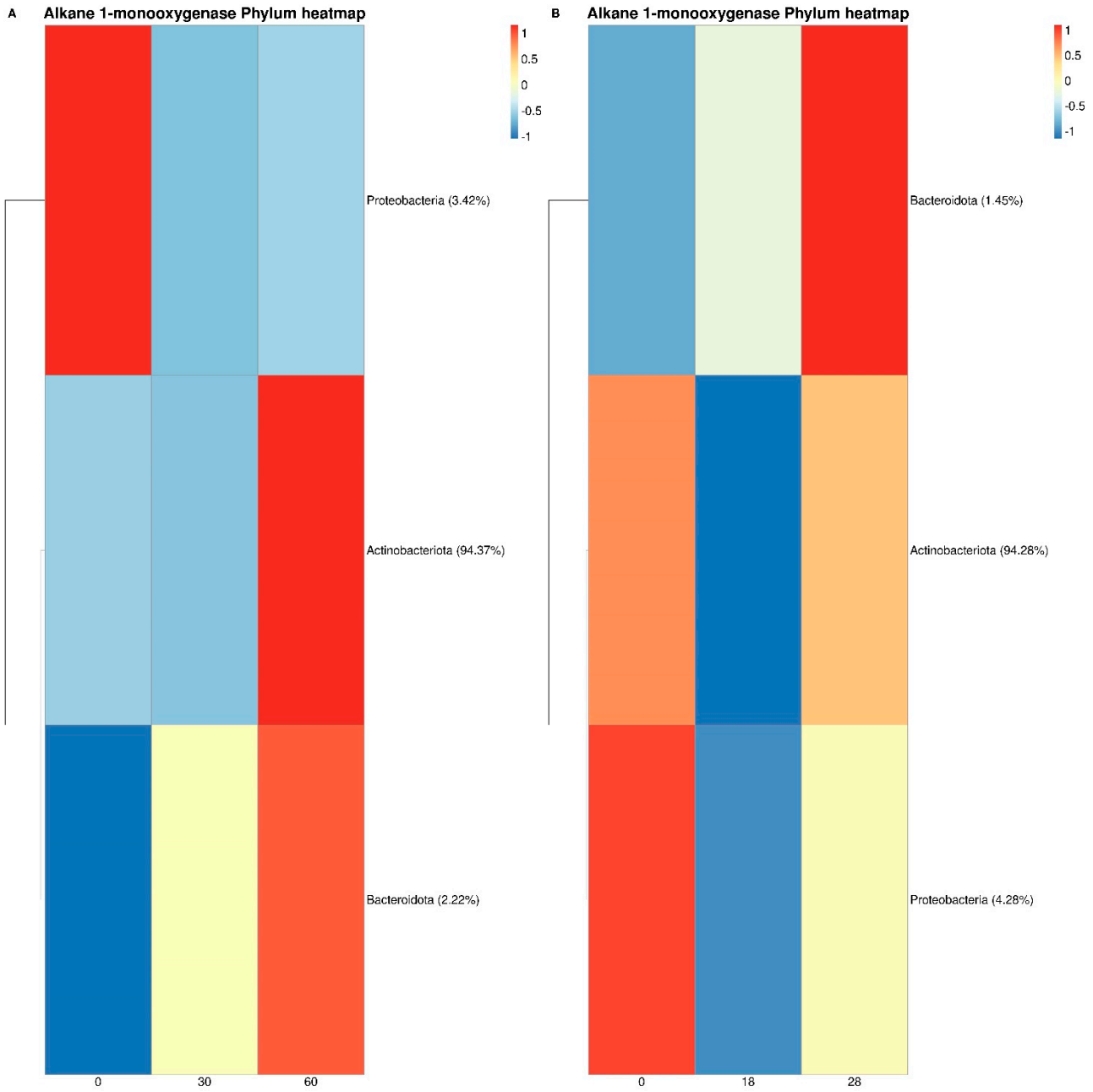

Figure S3. Functional Heatmap for Alkane 1-monooxygenase at Genus level. Functional Heatmap showing SMS community (panel **A**) and *Lambertella* sp. MUT 5852 community (panel **B**), phylum contribution to Alkane 1-monooxygenase (EC:1.14.15.3). Percentages reported near genus names represent the relative abundance of the sum of contribution of that genus per sample, against total sum of contributions: a cut-off value of 0.005% was chosen. Hierarchical clustering was performed on rows by Pearson correlation, based on Euclidean distance. In order to evidence variation, a colour scheme that represents row-wise Z-scores of per genus contributions per sample, was chosen. For this colour scheme, a Z value of 0 matches the reported percentage near the genus contributor.