Surface Water Microbiome Response to Pyrogenic Carbon after a Wildland-Urban Interface Fire

Lyssa Morgan[1], Allison Tilzey[1], Maya El-Ajouz[1], Jialin Dong[1], Cameron Daley[1], Christopher I. Olivares[1,*]

*Corresponding Author: chris.olivares@uci.edu

[1]Civil & Environmental Engineering, University of California-Irvine, Irvine, CA 92697

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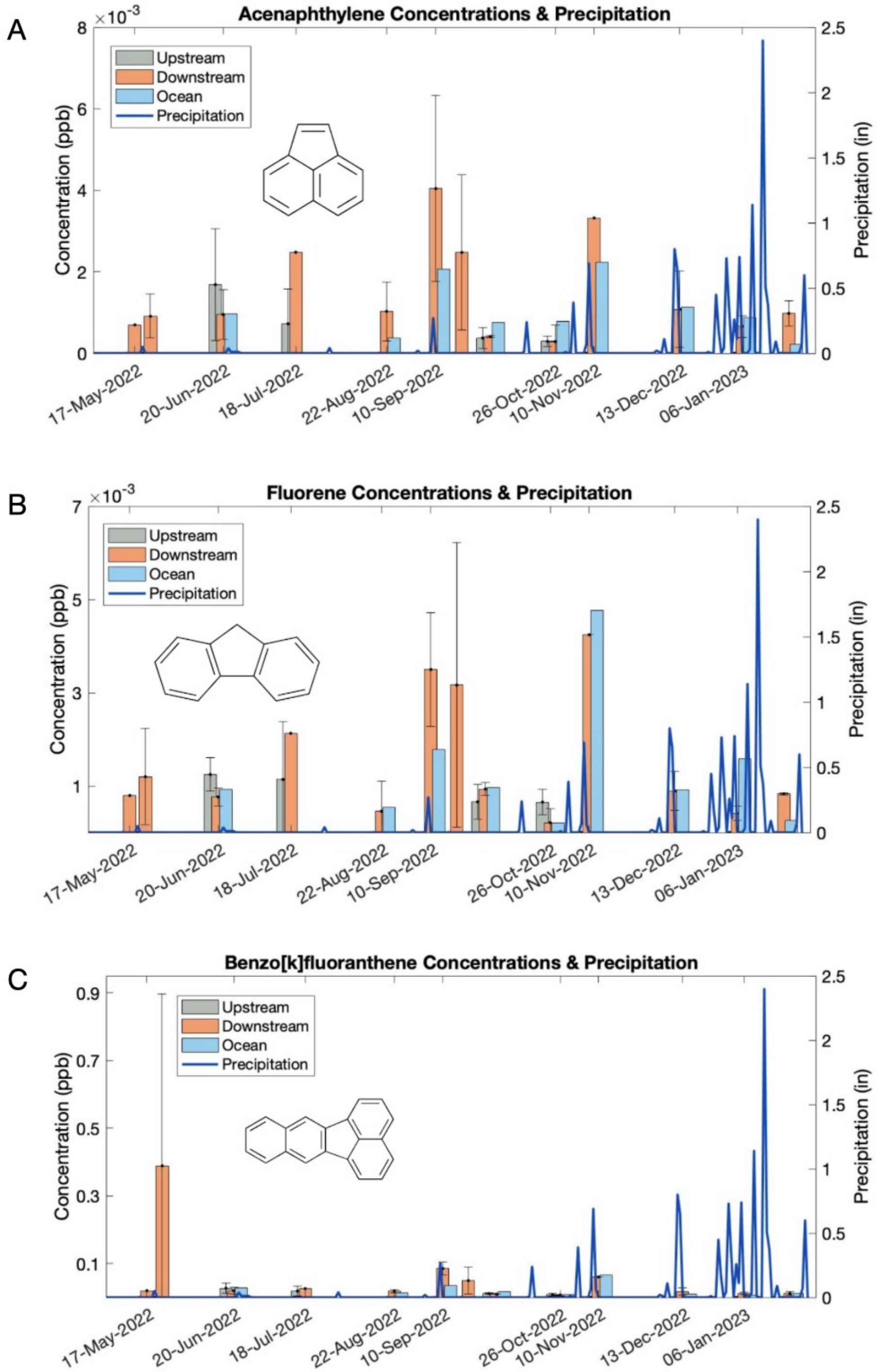

Figure S1. Concentration (ppb) of Acenaphthylene (A), Fluorene (B), and Benzo[k]fluoranthene (C), respectively, for sites downstream of burned area and creek ocean interface.

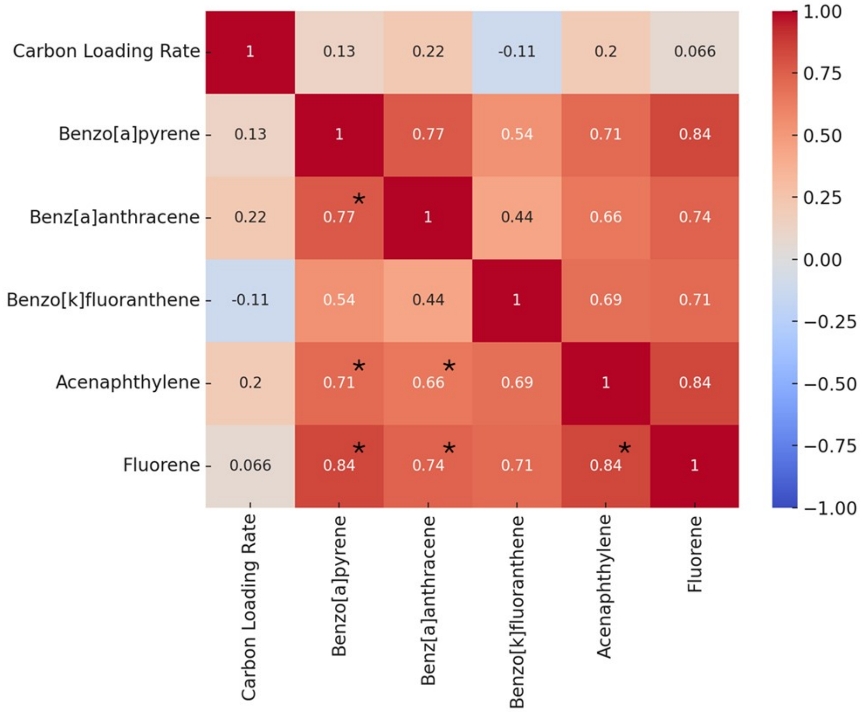

Figure S2. Heatmap of normalized Spearman rank correlation matrix with statistically significant correlations ($p < 0.05$, indicated with an asterisk *), of polycyclic aromatic hydrocarbons (PAHs) and carbon loading rate

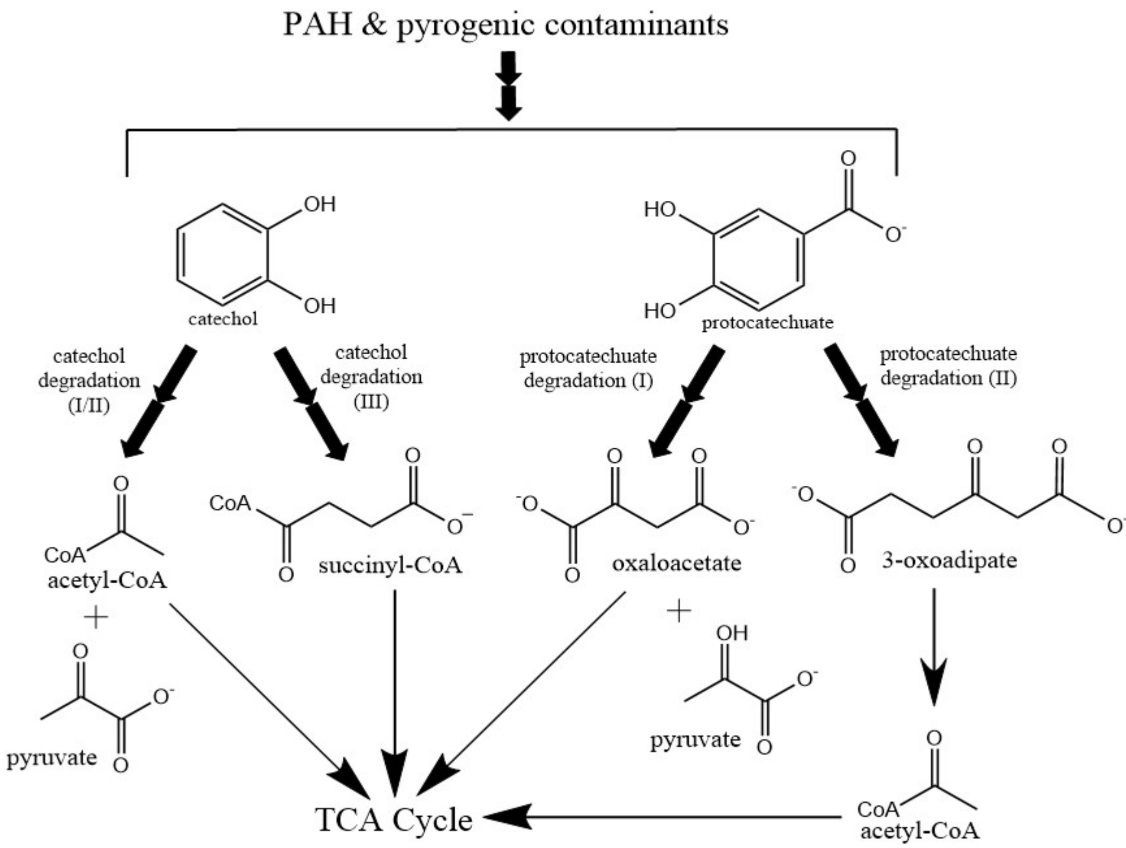

Figure S3. Catechol and protocatechuate degradation pathway intersections with the TCA cycle. Adapted from aerobic pathways reported EnviPath[1] and the University of

Minnesota biocatalysis/biodegradation database.[2]

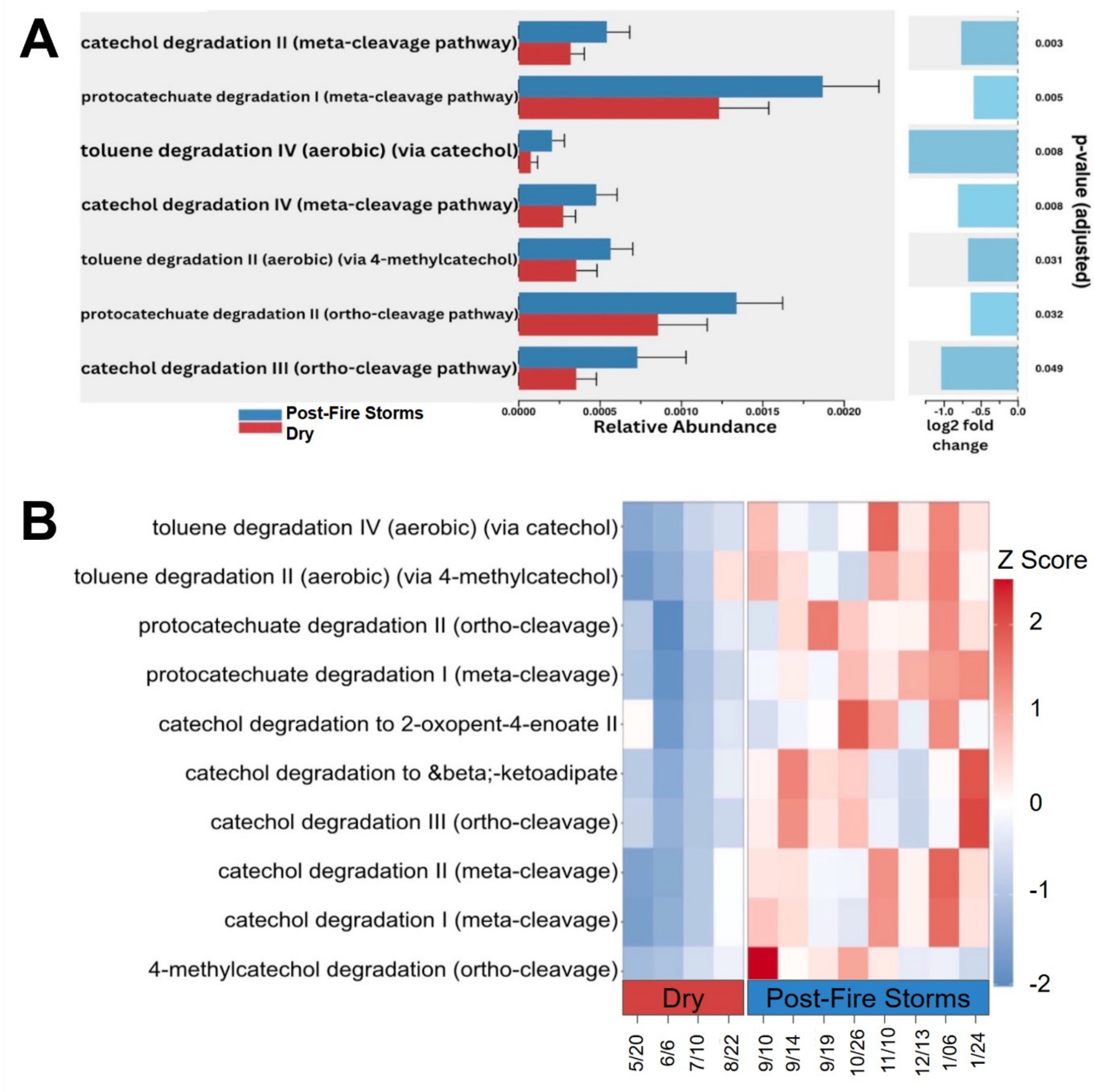

Figure S4 Panel A: Average relative abundances of predicted catechol and protocatechuate degradation pathways in dry and post-fire storms at the CCB site, directly downstream of the burned area. The log2 fold change compares dry vs. post-fire storm. Panel B: Timeline of Z-Scores of catechol and protocatechuate degradation pathways in the site directly downstream of the fire (CCB). Other downstream sites had similar patterns (SI, Figure S3)

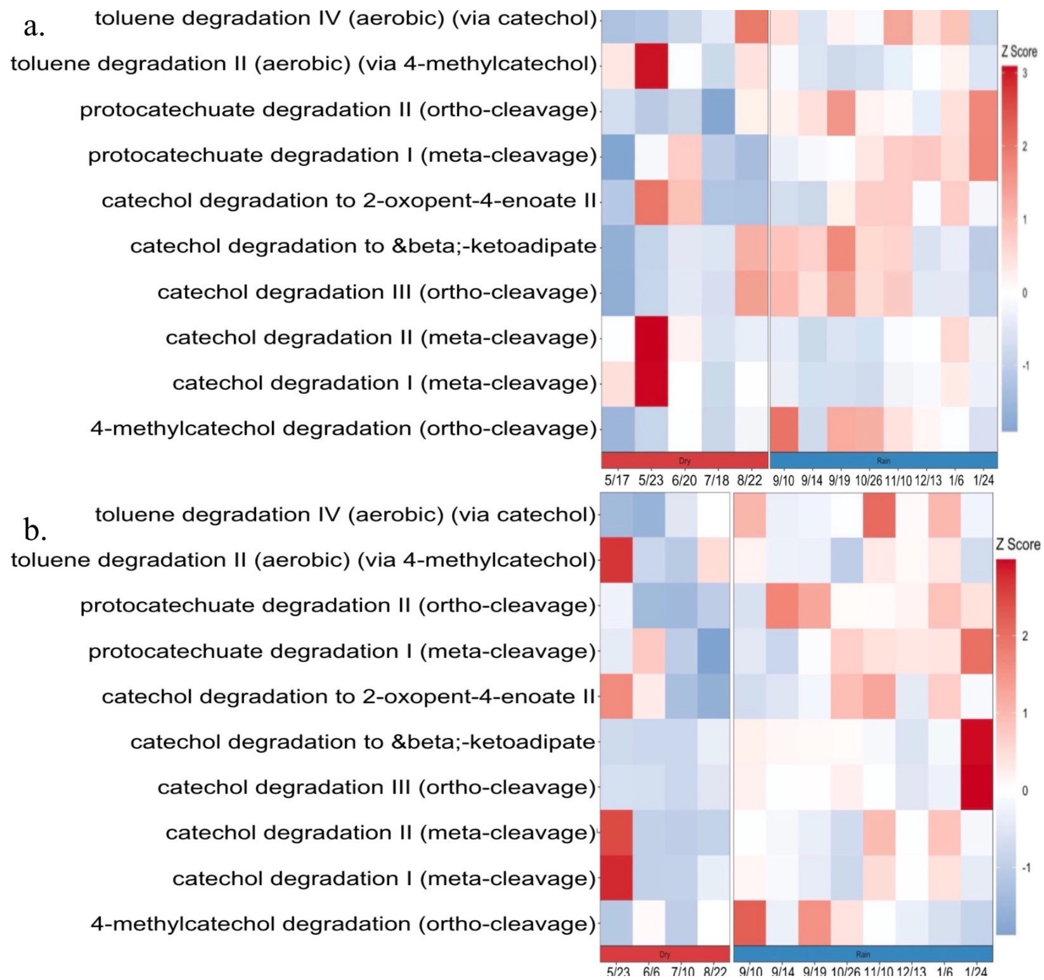

Figure S5. Z-Scores of predicted catechol and protocatechuate degradation pathways at further downstream sites of the fire Pacific Coast Highway (Panel A) and the ocean interface (Panel B). The red section above the dates denotes the dry period after the fire, the blue section above the dates indicates post-fire storms.

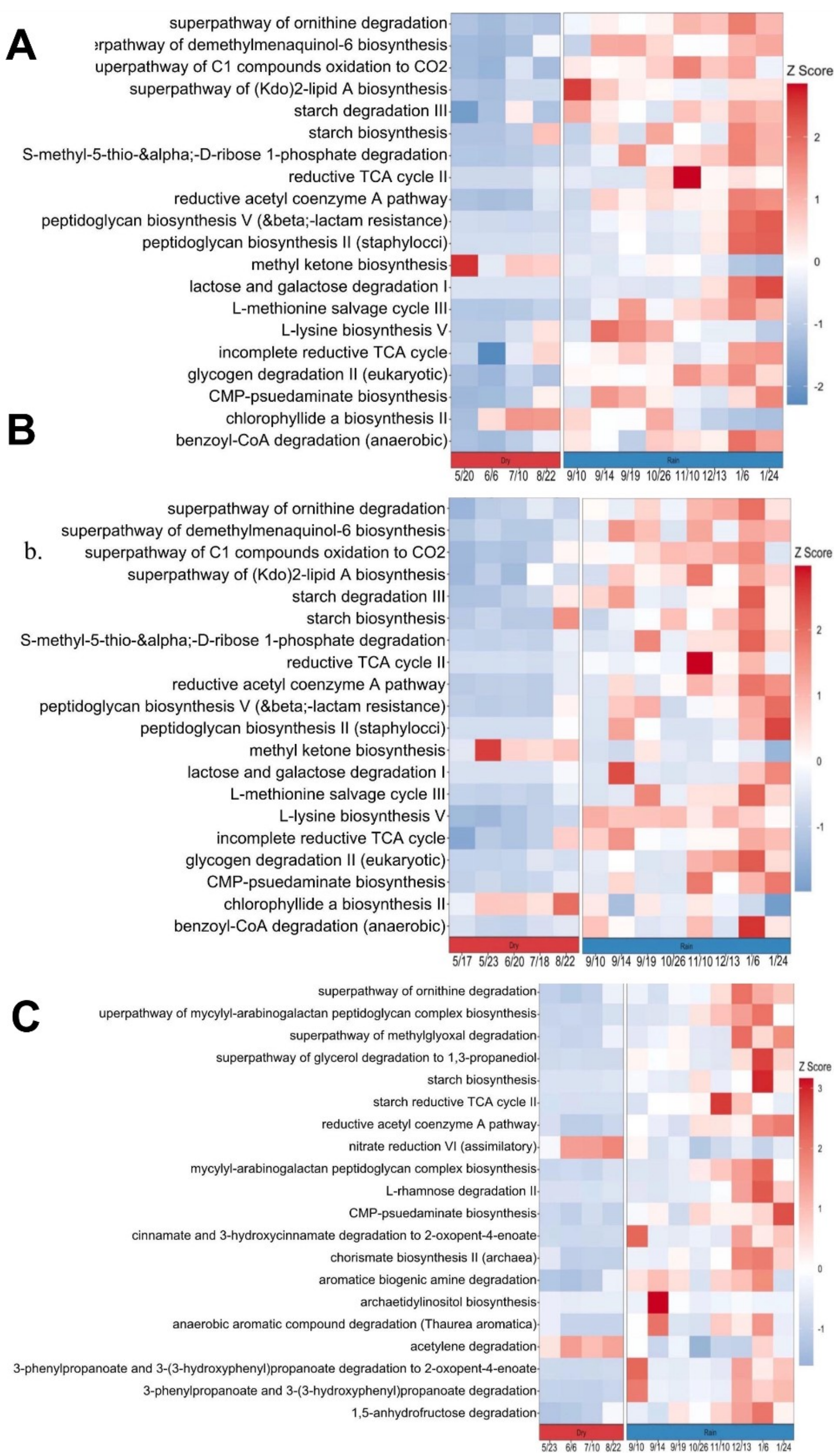

Figure S6. Timeline showing changes in relative abundance of general predicted metabolism for sites CCB (Panel A), ACB (Panel B), and OC (Panel C) with the 20 lowest p-values. Horizontal bands above dates: dry (red), post-fire storms (blue).

Table S1. Differentially abundant genera with carbon loading correlations

Family/Genus	Carbon Loading Rate Correlation	P value	Significant	Differentially Abundant
f__Microbacteriaceae;g__SV1-3	-0.3635942782	0.0102	Yes	Dry
f__Microbacteriaceae;g__Rhodoluna	-0.3427809474	0.0159	Yes	Dry
f__Microbacteriaceae;g__Candidatus_Planktoluna	-0.1666111286	0.2525	No	Dry
f__Alteromonadaceae;g__Paraglaciecola	-0.1078184644	0.4609	No	Dry
f__Flavobacteriaceae;__	-0.145086151	0.3199	No	Dry
f__Nitrincolaceae;g__Marinobacterium	-0.1587421492	0.276	No	Dry
f__Flavobacteriaceae;g__Polaribacter	-0.1757967006	0.227	No	Dry
f__Sphingomonadaceae;__	0.5965674592	0	Yes	Rain
f__Moraxellaceae;g__Acinetobacter	0.1391146997	0.3404	No	Rain
f__Sulfurimonadaceae;g__Sulfuricurvum	0.2618370997	0.0692	No	Rain
f__Oxalobacteraceae;g__Massilia	0.7945192026	0	Yes	Rain
f__Methylophilaceae;g__Candidatus_Methylopumilus	0.776291707	0	Yes	Rain
f__Alcaligenaceae;g__GKS98_freshwater_group	0.5882500239	0	Yes	Rain
f__Prevotellaceae;g__Prevotella	-0.2364904896	0.1018	No	Dry
Unassigned;__;__;__;__;__	0.07091932613	0.6282	No	Dry
f__Sphingomonadaceae;g__Sphingomonas	0.7738651767	0	Yes	Rain
f__Spirosomaceae;g__Arcicella	0.607299212	0	Yes	Rain
f__Diplorickettsiaceae;g__Rickettsiella	0.7526666693	0	Yes	Rain
f__Sphingobacteriaceae;g__Pedobacter	0.7344794179	0	Yes	Rain
f__Cryomorphaceae;g__Phaeocystidibacter	-0.1773061378	0.2229	No	Dry
f__Bacillaceae;g__Bacillus	0.6137989701	0	Yes	Rain
f__Lachnospiraceae;g__Agathobacter	-0.2153164753	0.1373	No	Dry
f__Ruminococcaceae;g__Faecalibacterium	-0.2051245667	0.1574	No	Dry
f__Sphingomonadaceae;g__Sphingobium	0.6548258437	0	Yes	Rain
f__Cyclobacteriaceae;g__uncultured	-0.3070822579	0.0319	Yes	Dry
f__Litoricolaceae;g__Litoricola	-0.2479929348	0.0858	No	Dry
f__Moraxellaceae;g__Alkanindiges	0.6772403128	0	Yes	Rain
f__67-14;g__67-14	0.1640338342	0.2601	No	Rain
f__Streptomycetaceae;g__Streptomyces	0.749689986	0	Yes	Rain
f__Rhodocyclaceae;g__Ferribacterium	0.4409999889	0.0015	Yes	Rain
f__Chitinophagaceae;g__Chitinophagaceae	0.3562535815	0.012	Yes	Rain
f__Micrococcaceae;__	0.684177831	0	Yes	Rain
f__Diplorickettsiaceae;__	0.7936965527	0	Yes	Rain
f__uncultured;g__uncultured	0.6509000934	0	Yes	Rain
f__Paenibacillaceae;g__Paenibacillus	0.6069368552	0	Yes	Rain

f__Nitrosomonadaceae;g__MND1	0.6384911676	0	Yes	Rain
f__Rhodocyclaceae;g__C39	0.1708604108	0.2405	No	Rain
f__Sphingobacteriaceae;g__Mucilaginibacter	0.6899341049	0	Yes	Rain
f__Azospirillaceae;g__Skermanella	0.6997489486	0	Yes	Rain
f__Lachnospiraceae;g__Lachnospira	-0.1646954872	0.2581	No	Dry
f__Diplorickettsiaceae;g__Aquicella	0.6248478339	0	Yes	Rain
f__Beijerinckiaceae;g__Methylobacterium-Methylorubrum	0.7709336479	0	Yes	Rain
f__Lachnospiraceae;g__Dorea	-0.1507646598	0.3011	No	Dry
f__Moraxellaceae;g__uncultured	0.5442054515	0.0001	Yes	Rain
f__Sporichthyaceae;g__Candidatus_Planktophila	-0.1471519208	0.313	No	Dry
f__Lachnospiraceae;g__Coprococcus	-0.1806837767	0.2141	No	Dry
f__Rhodobacteraceae;g__Marivita	-0.1997103474	0.1689	No	Dry
f__Lachnospiraceae;g__[Eubacterium]_hallii_group	-0.2294799224	0.1127	No	Dry
f__Lachnospiraceae;g__Lachnospiraceae_ND3007_group	-0.2030248027	0.1618	No	Dry

References

(1) Wicker, J.; Lorsbach, T.; Gütlein, M.; Schmid, E.; Latino, D.; Kramer, S.; Fenner, K. EnviPath--The Environmental Contaminant Biotransformation Pathway Resource. *Nucleic Acids Res.* **2016**, *44* (D1), D502-8.

(2) Gao, J.; Ellis, L. B. M.; Wackett, L. P. The University of Minnesota Biocatalysis/Biodegradation Database: Improving Public Access. *Nucleic Acids Res.* **2010**, *38* (Database issue), D488-91.