Electronic Supplementary Material (ESI) for Environmental Science: Water Research & Technology.

Electronic supplementary information (ESI) for the article: “EMA-amplicon-based taxonomic characterisation of the viable bacterial community present in untreated and SODIS treated roof-harvested rainwater”.

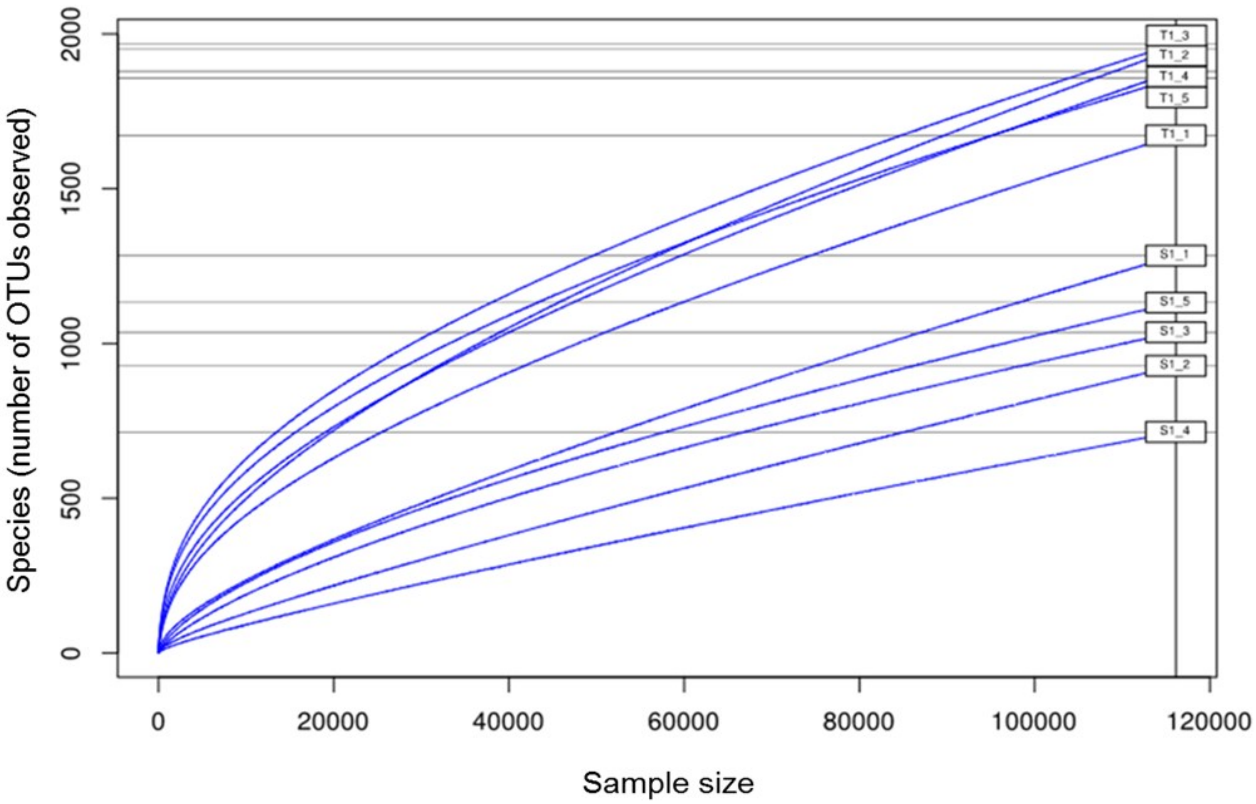

Fig. S1 Rarefaction curves indicating the species richness (OTUs observed) for each sample collected from Tank 1 (T1_1, 2, 3, 4 and 5) and SODIS-CPC-1 (S1_1, 2, 3, 4 and 5).

Table S1 Nomenclature of the Tank 1 and SODIC-CPC-1 samples as presented on Figures 1 and 2

Sampling event	Tank 1	SODIS-CPC-1
1	T1_1	S1_1
2	T1_2	S1_2
3	T1_3	S1_3
4	T1_4	S1_4
5	T1_5	S1_5

Table S2 Relative abundance percentages of the primary families detected in the before (Tank 1: T1_1, 2, 3, 4 and 5) and after SODIS treated (SODIS-CPC-1: S1_1, 2, 3, 4 and 5) rainwater samples used for Figure 1. Sequences with a homology ≥80% were used

Family	T1_1	T1_2	T1_3	T1_4	T1_5	Mean Tank 1	S1_1	S1_2	S1_3	S1_4	S1_5	Mean SODIS 1
Unclassified	29.873	33.175	70.809	43.699	58.350	47.181	14.189	10.486	12.790	10.125	13.638	12.246
Nocardiaceae	57.854	17.873	0.925	4.619	1.066	16.468	59.474	75.760	0.763	83.580	0.594	44.034
Pseudomonadaceae	0.048	37.307	0.207	6.430	0.471	8.893	0.015	0.012	0.009	0.012	0.015	0.013
Sphingomonadaceae	3.143	0.473	1.101	22.126	2.978	5.964	0.278	0.017	0.025	0.003	0.125	0.090
Planctomycetaceae	2.104	2.794	8.694	2.069	5.539	4.240	0.272	0.062	0.313	0.036	0.305	0.197
Chitinophagaceae	1.555	3.165	4.435	3.351	3.163	3.134	2.366	0.030	0.304	0.044	1.930	0.935
Oxalobacteraceae	0.337	0.050	0.618	2.175	11.507	2.938	6.174	4.273	0.005	0.084	14.252	4.957
Less abundant families	1.476	1.154	3.537	1.575	3.160	2.180	0.805	1.256	0.324	0.997	0.213	0.719
Parachlamydiaceae	0.578	1.202	1.135	3.339	0.660	1.383	0.266	0.013	0.046	0.006	0.044	0.075
Acetobacteraceae	0.351	0.258	3.327	0.502	1.987	1.285	0.498	0.022	0.154	0.024	0.217	0.183
Sinobacteraceae	0.301	0.545	0.262	2.159	2.375	1.128	0.001	0.002	0.003	0.002	0.007	0.003
Opitutaceae	0.595	0.540	0.823	1.136	0.975	0.814	0.112	0.007	0.028	0.004	0.087	0.048
Mycobacteriaceae	0.351	0.401	1.723	0.247	1.167	0.778	0.030	0.000	0.006	0.000	0.011	0.009
Comamonadaceae	0.378	0.288	0.556	1.595	0.750	0.713	0.320	0.030	0.022	0.005	0.010	0.078
Enterobacteriaceae	0.036	0.014	0.246	2.947	0.130	0.675	0.008	0.001	0.004	0.000	0.005	0.004
Rhodocyclaceae	0.331	0.169	0.061	1.348	1.078	0.598	0.008	0.002	0.001	0.001	0.009	0.004
Caulobacteraceae	0.197	0.048	0.171	0.211	1.137	0.353	0.486	0.782	0.011	0.011	0.693	0.396
Methylophilaceae	0.012	0.094	0.023	0.067	1.506	0.341	0.000	0.001	0.002	0.000	0.005	0.002
Bradyrhizobiaceae	0.259	0.273	0.612	0.128	0.358	0.326	1.191	0.004	0.002	0.001	0.003	0.240
Legionellaceae	0.055	0.017	0.159	0.040	1.328	0.320	0.006	0.000	0.003	0.000	0.003	0.002
Methylobacteriaceae	0.012	0.009	0.398	0.013	0.101	0.107	1.222	0.002	0.057	0.002	0.187	0.294
Rhizobiaceae	0.055	0.081	0.141	0.072	0.123	0.094	3.061	3.117	0.003	0.000	0.036	1.243
Micrococcaceae	0.026	0.028	0.027	0.145	0.075	0.060	0.096	1.534	84.296	5.037	67.596	31.712
Microbacteriaceae	0.054	0.039	0.007	0.002	0.008	0.022	0.243	2.586	0.002	0.002	0.012	0.569
Xanthomonadaceae	0.021	0.002	0.002	0.004	0.006	0.007	8.879	0.002	0.828	0.026	0.002	1.947

Table S3 Relative abundance percentages of the primary genera detected in the before (Tank 1: T1_1, 2, 3, 4 and 5) and after SODIS treated (SODIS-CPC-1: S1_1, 2, 3, 4 and 5) rainwater samples used for Figure 2. Sequences with a homology ≥80% were used

Genus	T1_1	T1_2	T1_3	T1_4	T1_5	Mean Tank 1	S1_1	S1_2	S1_3	S1_4	S1_5	Mean SODIS 1
Arthrobacter	0.025	0.031	0.019	0.143	0.069	0.057	0.099	1.690	94.151	5.518	74.689	35.229
Bosea	0.000	0.001	0.000	0.000	0.002	0.001	1.133	0.003	0.000	0.000	0.000	0.227
Caulobacter	0.099	0.021	0.113	0.164	1.020	0.283	0.018	0.007	0.009	0.011	0.763	0.162
Gemmata	0.210	0.454	1.082	0.260	0.628	0.527	0.075	0.047	0.158	0.012	0.045	0.068
Kaistia	0.057	0.087	0.119	0.075	0.116	0.091	3.150	3.447	0.003	0.000	0.038	1.328
Legionella	0.057	0.019	0.137	0.041	1.267	0.304	0.006	0.000	0.003	0.000	0.003	0.003
Methylobacterium	0.011	0.010	0.343	0.014	0.096	0.095	1.284	0.002	0.055	0.002	0.207	0.310
Mycobacterium	0.318	0.408	1.469	0.253	1.106	0.711	0.030	0.000	0.007	0.000	0.011	0.010
Neochlamydia	0.107	1.008	0.524	3.265	0.329	1.047	0.065	0.007	0.016	0.000	0.020	0.021
Nevskia	0.312	0.589	0.220	2.224	2.249	1.119	0.001	0.003	0.002	0.000	0.003	0.002
Novosphingobium	0.265	0.041	0.613	0.583	1.975	0.695	0.009	0.003	0.006	0.003	0.027	0.009
Oxalicibacterium	0.177	0.046	0.282	0.516	0.530	0.310	5.966	4.610	0.003	0.088	15.657	5.265
Pseudomonas	0.010	40.105	0.006	5.995	0.090	9.241	0.004	0.004	0.004	0.010	0.005	0.006
Rhodococcus	60.152	19.367	0.621	4.589	0.685	17.083	62.355	83.622	0.841	92.374	0.599	47.958
Sediminibacterium	0.385	0.612	2.113	2.170	1.678	1.392	2.392	0.028	0.303	0.047	2.081	0.970
Sphingobium	2.774	0.377	0.010	19.056	0.670	4.577	0.003	0.003	0.003	0.000	0.002	0.002
Sphingomonas	0.087	0.034	0.065	1.829	0.092	0.422	0.005	0.002	0.003	0.000	0.001	0.002
Stenotrophomonas	0.022	0.002	0.001	0.003	0.000	0.006	9.261	0.001	0.000	0.001	0.002	1.853
Undibacterium	0.144	0.001	0.222	1.591	10.349	2.461	0.001	0.003	0.002	0.001	0.006	0.003
Yersinia	0.009	0.009	0.193	3.013	0.115	0.668	0.000	0.001	0.003	0.000	0.006	0.002
Less abundant genera	2.782	2.567	5.598	5.114	5.663	4.345	1.928	2.341	1.598	1.058	0.824	1.550
Unclassified	31.998	34.211	86.249	49.102	71.271	54.566	12.214	4.177	2.828	0.876	5.013	5.021