

Effects of sulfamethoxazole and copper on the natural microbial community from a fertilized soil

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Supplementary information (SI)

DNA extraction

The extraction of total prokaryotic DNA (0.25 g per replicate) from soil was performed using the DNeasy PowerSoil kit (Qiagen, Germantown Road Germantown, MD, USA) following the manufacturer's recommendations. The negative control (DNA-free water) was included during the entire workflow. The quantity and quality (280/260 and 260/230 absorbance ratio) of the DNA extracted were assessed with a spectrophotometry (Multiskan Sky Microplate Spectrophotometer, Thermo Fisher Scientific, MA, USA). After extraction, the DNA was stored at -20°C until use.

Quantification of antibiotic resistance genes, mobile genetic elements and bacterial 16S rRNA gene by qPCR analysis

The targeted qPCR assays used in this study were based on previously published methods (Barra Caracciolo et al., 2022; Visca et al., 2022), with some modifications. The genes investigated were sulfamethoxazole-resistance genes (*sul1* and *sul2*) and the class 1 integron-integrase gene (*intI1*). Moreover, the 16S rRNA gene copy numbers were determined to calculate the relative abundance of the resistance genes targeted in all samples collected. All qPCR assays were performed with the CFX96 real time PCR detection System (Bio-Rad, USA) using SYBR Green detection. For each reaction, a total volume of 20 µL containing 10 µL SsoAdvanced Universal SYBR Green Supermix (Bio-Rad, USA), 0.5 µL of each primer (10 µM) and 15 ng of DNA template was used. The thermal cycling conditions were as follows: 94°C for 3 min, 45 cycles at 94°C for 15 s, annealing temperature (T_m) specific for each gene and primer pair for 30 s. The fluorescence signal was read after each elongation step. At the end of each reaction, a melting curve starting at 55°C and increasing by 0.5°C up to 95°C was performed to verify amplicon specificity. Each assay was run in triplicate including the No Template Controls (NTC). To determine the presence of any possible qPCR inhibition, an inhibition test using samples diluted from 10 to 100-fold was conducted. The primer sequences are reported in Table S1.

Evaluation of microbial community composition by Next-Generation Sequence

Aliquots of the DNA extracted from three replicates for each condition were used for NGS. The V3-V4 region of 16S rRNA genes were amplified by Miseq Illumina with the Pro341F and Pro805R primers reported in Table S1. These primers were selected to ensure the simultaneous identification of *Bacteria* and *Archaea* (Takahashi et al., 2014). The raw sequences were imported and demultiplexed using QIIME2 next-generation microbiome bioinformatics platform v2019.11 (Bolyen et al., 2019) and denoised with the DADA2 plug-in described by Bokulich et al., (2018). The primers were removed using the “trim-left-f” (forward) and “trim-left-r” (reverse) functions of DADA2 (Mazzurco Miritana et al., 2020). These functions remove sequences from the beginning to a given location in the amplicon. The forward primers were 17 nucleotides long and the reverse primers were 21 nucleotides long. The amplicon sequencing variants (ASV) obtained were sorted using the Silva 132 database (<https://www.arb-silva.de>) with a naive Bayes classifier trained on the amplified regions with 80% confidence (Bokulich et al., 2018). The Evenness, Shannon and Chao1 indexes were estimated by QIIME2 in order to evaluate diversity of the prokaryotic community in the different conditions.

Supplementary tables and figures

Table S1 Primer names and sequences of antibiotic resistance genes, mobile genetic elements and bacterial 16S rRNA gene.

Primer name	Target gene	Primer sequence (5'→3')	Reference
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Sul1 fw	sul1	CGCACCGGAAACATCGCTGCAC	[1]
Sul1 rv		TGAAGTCCCGCCGAAGGCTCG	
Sul2 fw	sul2	GCGCTCAAGGCAGATGGCATT	[2]
Sul2 rv		GCGTTTGATACCGGCACCCGT	
IntI1 fw	intI1	TCGTGCGTCGCCATACA	[3]
IntI1 rv		GCTTGTTCTACGGCCGTTTGA	
16S fw	16S rRNA	CGGTGAATACGTTTCYCGG	[4]
16S rv		TACCTTGTTACGACTT	
341F	16S rRNA	CCTACGGGAGGCAGCAG	[5]
805RV		<i>GACTACHVGGGTATCTAATCC</i>	

[1] Vila-Costa M, Gioia R, Aceña J, et al (2017). Degradation of sulfonamides as a microbial resistance mechanism, Water Research 115, 309-317. <https://doi.org/10.1016/j.watres.2017.03.007>

[2] Kern MB, Klemmensen T, Espersen F (2002). Susceptibility of Danish *Escherichia coli* strains isolated from urinary tract infections and bacteraemia and distribution of sul genes conferring sulphonamide resistance 513-516. <https://doi.org/10.1093/jac/45.4.513>

[3] Byrne-Bailey KG, Gaze WH, Zhang L, et al (2011). Integron prevalence and diversity in manured soil, Applied and Environmental Microbiology 77, 684-687. <https://doi.org/10.1128/AEM.01425-10>

[4] McKinney CW, Dungan RS, Moore A, Leytem AB (2018). Occurrence and abundance of antibiotic resistance genes in agricultural soil receiving dairy manure (2018) 1-10. <https://doi.org/10.1093/femsec/fiy010>

[5] Baker GC, Smith JJ, Cowan DA (2003). Review and re-analysis of domain-specific 16S primers, Journal of Microbiological Methods 55, 541-555. <https://doi.org/10.1016/j.mimet.2003.08.009>

Table S2 Soil experimental condition characterization in terms of pH, OC %, C_H % and N%

Condition	pH			OC (%) C _H (%)		N (%)			
	3h	36d		3 h	36 d		3h	36 d	
		Soil	Rhizo		Soil	Rhizo		Soil	Rhizo
S	6.8±0.03	6.8±0.05	6.9±0.05	1.05±0.05 0.03±0.00	0.93±0.00 -	1.05±0.00 -	0.33±0.00	0.1±0.00	0.1±0.00
SC	6.6±0.03	6.8±0.02	6.8±0.03	1.05±0.05 0.03±0.00	-	-	0.3±0.00	-	-
SCA	6.6±0.03	6.8±0.03	6.9±0.03	1.00±0.00 0.02±0.00	-	-	0.29±0.00	-	-
Average S	6.7±0.00	6.8±0.02	6.9±0.02	1.03±0.00 0.03±0.00	0.93±0.00	1.05±0.00	0.3±0.00	0.1±0.00	0.1±0.00
SM	6.7±0.12	6.8±0.12	6.8±0.12	0.94±0.02 0.02±0.00	1.04±0.00 -	1.1±0.00 -	0.3±0.00	0.1±0.00	0.1±0.00
SCM	6.8±0.11	6.7±0.11	6.8±0.11	1.1±0.00 0.03±0.00	-	-	0.3±0.00	-	-
SMCA	6.7±0.01	6.5±0.01	6.7±0.01	1.13±0.03 0.03±0.00	-	-	0.31±0.00	-	-
Average SM	6.8±0.09	6.7±0.08	6.8±0.08	1.06±0.02 0.03±0.00	1.04±0.00	1.1±0.00	0.3±0.00	0.1±0.00	0.1±0.00
SD	6.7±0.01	7.1±0.02	6.7±0.02	1.1±0.00 0.03±0.00	1.26±0.03 -	1.15±0.00 -	0.3±0.00	0.36±0.00	0.29±0.00
SCD	6.8±0.02	7.4±0.02	6.9±0.02	1.2±0.00 0.03±0.00	-	-	0.3±0.00	-	-
SDCA	6.8±0.01	7.0±0.02	6.7±0.02	0.97±0.01 0.03±0.00	-	-	0.3±0.00	-	-
Average SD	6.8±0.01	7.2±0.01	6.8±0.01	1.09±0.02 0.03±0.00	1.26±0.03	1.15±0.00	0.3±0.00	0.36±0.00	0.29±0.00

Antibiotic or copper addition did not influence OC and N contents in the various soil conditions, consequently their values are reported as average values considering amended (SM, SCM, SMCA, and SD, SCD and SDCA) and un-amended soil (S, SC and SCA), (Table S2). Differently, with organic amendments, OC and N were introduced in the soil and this effect was particularly evident in the digestate-amended soil (without plants).

Table S3 Results of the PostHoc tests (Tukey test) of the ANOVA test considering live microbial abundances and experimental conditions.

PostHoc tests (wilcox test, method=BH)	diff	lwr	upr	p adj
S_3h-S_36d	332849.2	-27513235.17	28178933.57	1
S_P_36d-S_36d	20172575	-7673509.17	48018659.57	0.4932587
SC_36d-S_36d	6820577.2	-21025507.17	34666661.57	0.9999996
SC_3h-S_36d	1672795.5	-26173288.84	29518879.9	1
SC_P_36d-S_36d	3826133.5	-24019950.84	31672217.9	1
SCA_36d-S_36d	9470962.9	-18375121.5	37317047.24	0.9998228
SCA_3h-S_36d	-1786608.8	-29632693.17	26059475.57	1
SCA_P_36d-S_36d	20121999	-7724084.91	47968083.83	0.4982566
SCD_36d-S_36d	-9238170.1	-37084254.5	18607914.24	0.9998839
SCD_3h-S_36d	12030013	-15816071.17	39876097.57	0.9935787
SCD_P_36d-S_36d	-7756012.5	-35602096.84	20090071.9	0.9999952
SCM_36d-S_36d	-208641.47	-28054725.84	27637442.9	1
SCM_3h-S_36d	4720259.9	-23125824.5	32566344.24	1
SCM_P_36d-S_36d	23526949	-4319135.84	51373032.9	0.2150032
SD_36d-S_36d	28153536	307451.5	55999620.24	0.0444775
SD_3h-S_36d	13590447	-14255637.84	41436530.9	0.97219
SD_P_36d-S_36d	23668060	-4178024.17	51514144.57	0.2062864
SDCA_36d-S_36d	24223774	-3622310.17	52069858.57	0.1744636
SDCA_3h-S_36d	-3672487.1	-31518571.5	24173597.24	1
SDCA_P_36d-S_36d	26069801	-1776283.84	53915884.9	0.0952555
SM_36d-S_36d	4635880.5	-23210203.84	32481964.9	1
SM_3h-S_36d	3582541.2	-24263543.17	31428625.57	1
SM_P_36d-S_36d	23659652	-4186432.84	51505735.9	0.2067985
SMCA_36d-S_36d	8595679.5	-19250404.84	36441763.9	0.9999674
SMCA_3h-S_36d	3001866.2	-24844218.17	30847950.57	1
SMCA_P_36d-S_36d	37808301	9962216.5	65654385.24	0.0006341
S_P_36d-S_3h	19839726	-8006358.37	47685810.37	0.5263476
SC_36d-S_3h	6487728	-21358356.37	34333812.37	0.9999999
SC_3h-S_3h	1339946.3	-26506138.04	29186030.7	1
SC_P_36d-S_3h	3493284.3	-24352800.04	31339368.7	1
SCA_36d-S_3h	9138113.7	-18707970.7	36984198.04	0.9999037
SCA_3h-S_3h	-2119458	-29965542.37	25726626.37	1
SCA_P_36d-S_3h	19789150	-8056934.11	47635234.63	0.5314095
SCD_36d-S_3h	-9571019.3	-37417103.7	18275065.04	0.9997887
SCD_3h-S_3h	11697164	-16148920.37	39543248.37	0.9955812
SCD_P_36d-S_3h	-8088861.7	-35934946.04	19757222.7	0.9999894
SCM_36d-S_3h	-541490.67	-28387575.04	27304593.7	1
SCM_3h-S_3h	4387410.7	-23458673.7	32233495.04	1
SCM_P_36d-S_3h	23194099	-4651985.04	51040183.7	0.2365986
SD_36d-S_3h	27820687	-25397.7	55666771.04	0.0504823
SD_3h-S_3h	13257597	-14588487.04	41103681.7	0.9789111
SD_P_36d-S_3h	23335211	-4510873.37	51181295.37	0.2272654
SDCA_36d-S_3h	23890925	-3955159.37	51737009.37	0.1930474
SDCA_3h-S_3h	-4005336.3	-31851420.7	23840748.04	1
SDCA_P_36d-S_3h	25736951	-2109133.04	53583035.7	0.10679
SM_36d-S_3h	4303031.3	-23543053.04	32149115.7	1
SM_3h-S_3h	3249692	-24596392.37	31095776.37	1

SM_P_36d-S_3h	23326802	-4519282.04	51172886.7	0.2278143
SMCA_36d-S_3h	8262830.3	-19583254.04	36108914.7	0.9999842
SMCA_3h-S_3h	2669017	-25177067.37	30515101.37	1
SMCA_P_36d-S_3h	37475452	9629367.3	65321536.04	0.0007441
SC_36d-S_P_36d	-13351998	-41198082.37	14494086.37	0.977148
SC_3h-S_P_36d	-18499780	-46345864.04	9346304.7	0.6604158
SC_P_36d-S_P_36d	-16346442	-44192526.04	11499642.7	0.8467807
SCA_36d-S_P_36d	-10701612	-38547696.7	17144472.04	0.9987601
SCA_3h-S_P_36d	-21959184	-49805268.37	5886900.37	0.3292865
SCA_P_36d-S_P_36d	-50575.737	-27896660.11	27795508.63	1
SCD_36d-S_P_36d	-29410745	-57256829.7	-1564660.96	0.027147
SCD_3h-S_P_36d	-8142562	-35988646.37	19703522.37	0.999988
SCD_P_36d-S_P_36d	-27928588	-55774672.04	-82503.3	0.0484613
SCM_36d-S_P_36d	-20381217	-48227301.04	7464867.7	0.4727809
SCM_3h-S_P_36d	-15452315	-43298399.7	12393769.04	0.9026367
SCM_P_36d-S_P_36d	3354373.3	-24491711.04	31200457.7	1
SD_36d-S_P_36d	7980960.7	-19865123.7	35827045.04	0.9999918
SD_3h-S_P_36d	-6582128.7	-34428213.04	21263955.7	0.9999998
SD_P_36d-S_P_36d	3495485	-24350599.37	31341569.37	1
SDCA_36d-S_P_36d	4051199	-23794885.37	31897283.37	1
SDCA_3h-S_P_36d	-23845062	-51691146.7	4001022.04	0.1957192
SDCA_P_36d-S_P_36d	5897225.3	-21948859.04	33743309.7	1
SM_36d-S_P_36d	-15536695	-43382779.04	12309389.7	0.8980083
SM_3h-S_P_36d	-16590034	-44436118.37	11256050.37	0.8290334
SM_P_36d-S_P_36d	3487076.3	-24359008.04	31333160.7	1
SMCA_36d-S_P_36d	-11576896	-39422980.04	16269188.7	0.9961623
SMCA_3h-S_P_36d	-17170709	-45016793.37	10675375.37	0.7827606
SMCA_P_36d-S_P_36d	17635726	-10210358.7	45481810.04	0.7421516
SC_3h-SC_36d	-5147781.7	-32993866.04	22698302.7	1
SC_P_36d-SC_36d	-2994443.7	-30840528.04	24851640.7	1
SCA_36d-SC_36d	2650385.7	-25195698.7	30496470.04	1
SCA_3h-SC_36d	-8607186	-36453270.37	19238898.37	0.9999666
SCA_P_36d-SC_36d	13301422	-14544662.11	41147506.63	0.9781062
SCD_36d-SC_36d	-16058747	-43904831.7	11787337.04	0.8663771
SCD_3h-SC_36d	5209436	-22636648.37	33055520.37	1
SCD_P_36d-SC_36d	-14576590	-42422674.04	13269494.7	0.9427985
SCM_36d-SC_36d	-7029218.7	-34875303.04	20816865.7	0.9999993
SCM_3h-SC_36d	-2100317.3	-29946401.7	25745767.04	1
SCM_P_36d-SC_36d	16706371	-11139713.04	44552455.7	0.8201977
SD_36d-SC_36d	21332959	-6513125.7	49179043.04	0.3833535
SD_3h-SC_36d	6769869.3	-21076215.04	34615953.7	0.9999997
SD_P_36d-SC_36d	16847483	-10998601.37	44693567.37	0.8091795
SDCA_36d-SC_36d	17403197	-10442887.37	45249281.37	0.7628145
SDCA_3h-SC_36d	-10493064	-38339148.7	17353020.04	0.9990798
SDCA_P_36d-SC_36d	19249223	-8596861.04	47095307.7	0.5857061
SM_36d-SC_36d	-2184696.7	-30030781.04	25661387.7	1
SM_3h-SC_36d	-3238036	-31084120.37	24608048.37	1
SM_P_36d-SC_36d	16839074	-11007010.04	44685158.7	0.8098451
SMCA_36d-SC_36d	1775102.3	-26070982.04	29621186.7	1

SMCA_3h-SC_36d	-3818711	-31664795.37	24027373.37	1
SMCA_P_36d-SC_36d	30987724	3141639.3	58833808.04	0.0141667
SC_P_36d-SC_3h	2153338	-25692746.37	29999422.37	1
SCA_36d-SC_3h	7798167.3	-20047917.04	35644251.7	0.9999947
SCA_3h-SC_3h	-3459404.3	-31305488.7	24386680.04	1
SCA_P_36d-SC_3h	18449204	-9396880.44	46295288.3	0.6653678
SCD_36d-SC_3h	-10910966	-38757050.04	16935118.7	0.9983468
SCD_3h-SC_3h	10357218	-17488866.7	38203302.04	0.9992472
SCD_P_36d-SC_3h	-9428808	-37274892.37	18417276.37	0.9998356
SCM_36d-SC_3h	-1881437	-29727521.37	25964647.37	1
SCM_3h-SC_3h	3047464.3	-24798620.04	30893548.7	1
SCM_P_36d-SC_3h	21854153	-5991931.37	49700237.37	0.3380462
SD_36d-SC_3h	26480740	-1365344.04	54326824.7	0.0824758
SD_3h-SC_3h	11917651	-15928433.37	39763735.37	0.9943248
SD_P_36d-SC_3h	21995265	-5850819.7	49841349.04	0.3263074
SDCA_36d-SC_3h	22550979	-5295105.7	50397063.04	0.2824389
SDCA_3h-SC_3h	-5345282.7	-33191367.04	22500801.7	1
SDCA_P_36d-SC_3h	24397005	-3449079.37	52243089.37	0.1653452
SM_36d-SC_3h	2963085	-24882999.37	30809169.37	1
SM_3h-SC_3h	1909745.7	-25936338.7	29755830.04	1
SM_P_36d-SC_3h	21986856	-5859228.37	49832940.37	0.3270003
SMCA_36d-SC_3h	6922884	-20923200.37	34768968.37	0.9999995
SMCA_3h-SC_3h	1329070.7	-26517013.7	29175155.04	1
SMCA_P_36d-SC_3h	36135505	8289420.96	63981589.7	0.0014067
SCA_36d-SC_P_36d	5644829.3	-22201255.04	33490913.7	1
SCA_3h-SC_P_36d	-5612742.3	-33458826.7	22233342.04	1
SCA_P_36d-SC_P_36d	16295866	-11550218.44	44141950.3	0.8503343
SCD_36d-SC_P_36d	-13064304	-40910388.04	14781780.7	0.9821914
SCD_3h-SC_P_36d	8203879.7	-19642204.7	36049964.04	0.9999862
SCD_P_36d-SC_P_36d	-11582146	-39428230.37	16263938.37	0.9961384
SCM_36d-SC_P_36d	-4034775	-31880859.37	23811309.37	1
SCM_3h-SC_P_36d	894126.33	-26951958.04	28740210.7	1
SCM_P_36d-SC_P_36d	19700815	-8145269.37	47546899.37	0.5402665
SD_36d-SC_P_36d	24327402	-3518682.04	52173486.7	0.168964
SD_3h-SC_P_36d	9764313	-18081771.37	37610397.37	0.9997059
SD_P_36d-SC_P_36d	19841927	-8004157.7	47688011.04	0.5261275
SDCA_36d-SC_P_36d	20397641	-7448443.7	48243725.04	0.4711795
SDCA_3h-SC_P_36d	-7498620.7	-35344705.04	20347463.7	0.9999975
SDCA_P_36d-SC_P_36d	22243667	-5602417.37	50089751.37	0.3062244
SM_36d-SC_P_36d	809747	-27036337.37	28655831.37	1
SM_3h-SC_P_36d	-243592.33	-28089676.7	27602492.04	1
SM_P_36d-SC_P_36d	19833518	-8012566.37	47679602.37	0.5269685
SMCA_36d-SC_P_36d	4769546	-23076538.37	32615630.37	1
SMCA_3h-SC_P_36d	-824267.33	-28670351.7	27021817.04	1
SMCA_P_36d-SC_P_36d	33982167	6136082.96	61828251.7	0.0038079
SCA_3h-SCA_36d	-11257572	-39103656.04	16588512.7	0.997403
SCA_P_36d-SCA_36d	10651037	-17195047.78	38497120.97	0.9988453
SCD_36d-SCA_36d	-18709133	-46555217.37	9136951.37	0.6397625
SCD_3h-SCA_36d	2559050.3	-25287034.04	30405134.7	1

SCD_P_36d-SCA_36d	-17226975	-45073059.7	10619109.04	0.7780025
SCM_36d-SCA_36d	-9679604.3	-37525688.7	18166480.04	0.9997452
SCM_3h-SCA_36d	-4750703	-32596787.37	23095381.37	1
SCM_P_36d-SCA_36d	14055986	-13790098.7	41902070.04	0.9602209
SD_36d-SCA_36d	18682573	-9163511.37	46528657.37	0.6423953
SD_3h-SCA_36d	4119483.7	-23726600.7	31965568.04	1
SD_P_36d-SCA_36d	14197097	-13648987.04	42043181.7	0.9559412
SDCA_36d-SCA_36d	14752811	-13093273.04	42598895.7	0.9358476
SDCA_3h-SCA_36d	-13143450	-40989534.37	14702634.37	0.9809003
SDCA_P_36d-SCA_36d	16598838	-11247246.7	44444922.04	0.8283728
SM_36d-SCA_36d	-4835082.3	-32681166.7	23011002.04	1
SM_3h-SCA_36d	-5888421.7	-33734506.04	21957662.7	1
SM_P_36d-SCA_36d	14188689	-13657395.7	42034773.04	0.9562051
SMCA_36d-SCA_36d	-875283.33	-28721367.7	26970801.04	1
SMCA_3h-SCA_36d	-6469096.7	-34315181.04	21376987.7	0.9999999
SMCA_P_36d-SCA_36d	28337338	491253.63	56183422.37	0.041442
SCA_P_36d-SCA_3h	21908608	-5937476.11	49754692.63	0.3334884
SCD_36d-SCA_3h	-7451561.3	-35297645.7	20394523.04	0.9999978
SCD_3h-SCA_3h	13816622	-14029462.37	41662706.37	0.9667724
SCD_P_36d-SCA_3h	-5969403.7	-33815488.04	21876680.7	1
SCM_36d-SCA_3h	1577967.3	-26268117.04	29424051.7	1
SCM_3h-SCA_3h	6506868.7	-21339215.7	34352953.04	0.9999999
SCM_P_36d-SCA_3h	25313557	-2532527.04	53159641.7	0.1231088
SD_36d-SCA_3h	29940145	2094060.3	57786229.04	0.0219018
SD_3h-SCA_3h	15377055	-12469029.04	43223139.7	0.9066509
SD_P_36d-SCA_3h	25454669	-2391415.37	53300753.37	0.1174577
SDCA_36d-SCA_3h	26010383	-1835701.37	53856467.37	0.0972345
SDCA_3h-SCA_3h	-1885878.3	-29731962.7	25960206.04	1
SDCA_P_36d-SCA_3h	27856409	10324.96	55702493.7	0.0498051
SM_36d-SCA_3h	6422489.3	-21423595.04	34268573.7	0.9999999
SM_3h-SCA_3h	5369150	-22476934.37	33215234.37	1
SM_P_36d-SCA_3h	25446260	-2399824.04	53292344.7	0.1177884
SMCA_36d-SCA_3h	10382288	-17463796.04	38228372.7	0.9992185
SMCA_3h-SCA_3h	4788475	-23057609.37	32634559.37	1
SMCA_P_36d-SCA_3h	39594910	11748825.3	67440994.04	0.0002658
SCD_36d-SCA_P_36d	-29360170	-57206253.97	-1514085.22	0.0277039
SCD_3h-SCA_P_36d	-8091986.3	-35938070.63	19754098.11	0.9999893
SCD_P_36d-SCA_P_36d	-27878012	-55724096.3	-31927.56	0.0493995
SCM_36d-SCA_P_36d	-20330641	-48176725.3	7515443.44	0.4777225
SCM_3h-SCA_P_36d	-15401740	-43247823.97	12444344.78	0.9053461
SCM_P_36d-SCA_P_36d	3404949.1	-24441135.3	31251033.44	1
SD_36d-SCA_P_36d	8031536.4	-19814547.97	35877620.78	0.9999907
SD_3h-SCA_P_36d	-6531552.9	-34377637.3	21314531.44	0.9999999
SD_P_36d-SCA_P_36d	3546060.7	-24300023.63	31392145.11	1
SDCA_36d-SCA_P_36d	4101774.7	-23744309.63	31947859.11	1
SDCA_3h-SCA_P_36d	-23794487	-51640570.97	4051597.78	0.1986972
SDCA_P_36d-SCA_P_36d	5947801.1	-21898283.3	33793885.44	1
SM_36d-SCA_P_36d	-15486119	-43332203.3	12359965.44	0.9007988
SM_3h-SCA_P_36d	-16539458	-44385542.63	11306626.11	0.832803

SM_P_36d-SCA_P_36d	3537652.1	-24308432.3	31383736.44	1
SMCA_36d-SCA_P_36d	-11526320	-39372404.3	16319764.44	0.9963868
SMCA_3h-SCA_P_36d	-17120133	-44966217.63	10725951.11	0.7869985
SMCA_P_36d-SCA_P_36d	17686301	-10159782.97	45532385.78	0.7375701
SCD_3h-SCD_36d	21268183	-6577901.04	49114267.7	0.3891859
SCD_P_36d-SCD_36d	1482157.7	-26363926.7	29328242.04	1
SCM_36d-SCD_36d	9029528.7	-18816555.7	36875613.04	0.9999218
SCM_3h-SCD_36d	13958430	-13887654.37	41804514.37	0.9629963
SCM_P_36d-SCD_36d	32765119	4919034.3	60611203.04	0.0065678
SD_36d-SCD_36d	37391706	9545621.63	65237790.37	0.0007745
SD_3h-SCD_36d	22828617	-5017467.7	50674701.04	0.261988
SD_P_36d-SCD_36d	32906230	5060145.96	60752314.7	0.00617
SDCA_36d-SCD_36d	33461944	5615859.96	61308028.7	0.0048152
SDCA_3h-SCD_36d	5565683	-22280401.37	33411767.37	1
SDCA_P_36d-SCD_36d	35307971	7461886.3	63154055.04	0.0020715
SM_36d-SCD_36d	13874051	-13972033.7	41720135.04	0.9652794
SM_3h-SCD_36d	12820711	-15025373.04	40666795.7	0.9857408
SM_P_36d-SCD_36d	32897822	5051737.3	60743906.04	0.0061931
SMCA_36d-SCD_36d	17833850	-10012234.7	45679934.04	0.7240389
SMCA_3h-SCD_36d	12240036	-15606048.04	40086120.7	0.9919677
SMCA_P_36d-SCD_36d	47046471	19200386.63	74892555.37	0.0000062
SCD_P_36d-SCD_3h	-19786026	-47632110.04	8060058.7	0.5317225
SCM_36d-SCD_3h	-12238655	-40084739.04	15607429.7	0.9919792
SCM_3h-SCD_3h	-7309753.3	-35155837.7	20536331.04	0.9999985
SCM_P_36d-SCD_3h	11496935	-16349149.04	39343019.7	0.9965121
SD_36d-SCD_3h	16123523	-11722561.7	43969607.04	0.8620967
SD_3h-SCD_3h	1560433.3	-26285651.04	29406517.7	1
SD_P_36d-SCD_3h	11638047	-16208037.37	39484131.37	0.9958754
SDCA_36d-SCD_3h	12193761	-15652323.37	40039845.37	0.9923483
SDCA_3h-SCD_3h	-15702500	-43548584.7	12143584.04	0.8885195
SDCA_P_36d-SCD_3h	14039787	-13806297.04	41885871.7	0.9606919
SM_36d-SCD_3h	-7394132.7	-35240217.04	20451951.7	0.9999981
SM_3h-SCD_3h	-8447472	-36293556.37	19398612.37	0.9999763
SM_P_36d-SCD_3h	11629638	-16216446.04	39475722.7	0.9959159
SMCA_36d-SCD_3h	-3434333.7	-31280418.04	24411750.7	1
SMCA_3h-SCD_3h	-9028147	-36874231.37	18817937.37	0.999922
SMCA_P_36d-SCD_3h	25778288	-2067796.7	53624372.04	0.1052973
SCM_36d-SCD_P_36d	7547371	-20298713.37	35393455.37	0.9999972
SCM_3h-SCD_P_36d	12476272	-15369812.04	40322356.7	0.9897761
SCM_P_36d-SCD_P_36d	31282961	3436876.63	59129045.37	0.0124992
SD_36d-SCD_P_36d	35909548	8063463.96	63755632.7	0.0015643
SD_3h-SCD_P_36d	21346459	-6499625.37	49192543.37	0.3821432
SD_P_36d-SCD_P_36d	31424073	3577988.3	59270157.04	0.0117687
SDCA_36d-SCD_P_36d	31979787	4133702.3	59825871.04	0.0092637
SDCA_3h-SCD_P_36d	4083525.3	-23762559.04	31929609.7	1
SDCA_P_36d-SCD_P_36d	33825813	5979728.63	61671897.37	0.0040873
SM_36d-SCD_P_36d	12391893	-15454191.37	40237977.37	0.9906084
SM_3h-SCD_P_36d	11338554	-16507530.7	39184638.04	0.9971261
SM_P_36d-SCD_P_36d	31415664	3569579.63	59261748.37	0.0118111

SMCA_36d-SCD_P_36d	16351692	-11494392.37	44197776.37	0.8464091
SMCA_3h-SCD_P_36d	10757879	-17088205.7	38603963.04	0.9986589
SMCA_P_36d-SCD_P_36d	45564313	17718228.96	73410397.7	0.0000132
SCM_3h-SCM_36d	4928901.3	-22917183.04	32774985.7	1
SCM_P_36d-SCM_36d	23735590	-4110494.37	51581674.37	0.2022068
SD_36d-SCM_36d	28362177	516092.96	56208261.7	0.0410463
SD_3h-SCM_36d	13799088	-14046996.37	41645172.37	0.9672185
SD_P_36d-SCM_36d	23876702	-3969382.7	51722786.04	0.1938731
SDCA_36d-SCM_36d	24432416	-3413668.7	52278500.04	0.1635272
SDCA_3h-SCM_36d	-3463845.7	-31309930.04	24382238.7	1
SDCA_P_36d-SCM_36d	26278442	-1567642.37	54124526.37	0.0885725
SM_36d-SCM_36d	4844522	-23001562.37	32690606.37	1
SM_3h-SCM_36d	3791182.7	-24054901.7	31637267.04	1
SM_P_36d-SCM_36d	23868293	-3977791.37	51714377.37	0.1943625
SMCA_36d-SCM_36d	8804321	-19041763.37	36650405.37	0.9999499
SMCA_3h-SCM_36d	3210507.7	-24635576.7	31056592.04	1
SMCA_P_36d-SCM_36d	38016942	10170857.96	65863026.7	0.0005734
SCM_P_36d-SCM_3h	18806689	-9039395.7	46652773.04	0.6300657
SD_36d-SCM_3h	23433276	-4412808.37	51279360.37	0.2209336
SD_3h-SCM_3h	8870186.7	-18975897.7	36716271.04	0.9999428
SD_P_36d-SCM_3h	18947800	-8898284.04	46793884.7	0.6159751
SDCA_36d-SCM_3h	19503514	-8342570.04	47349598.7	0.5601014
SDCA_3h-SCM_3h	-8392747	-36238831.37	19453337.37	0.9999789
SDCA_P_36d-SCM_3h	21349541	-6496543.7	49195625.04	0.3818672
SM_36d-SCM_3h	-84379.333	-27930463.7	27761705.04	1
SM_3h-SCM_3h	-1137718.7	-28983803.04	26708365.7	1
SM_P_36d-SCM_3h	18939392	-8906692.7	46785476.04	0.6168166
SMCA_36d-SCM_3h	3875419.7	-23970664.7	31721504.04	1
SMCA_3h-SCM_3h	-1718393.7	-29564478.04	26127690.7	1
SMCA_P_36d-SCM_3h	33088041	5241956.63	60934125.37	0.0056912
SD_36d-SCM_P_36d	4626587.3	-23219497.04	32472671.7	1
SD_3h-SCM_P_36d	-9936502	-37782586.37	17909582.37	0.9996093
SD_P_36d-SCM_P_36d	141111.67	-27704972.7	27987196.04	1
SDCA_36d-SCM_P_36d	696825.67	-27149258.7	28542910.04	1
SDCA_3h-SCM_P_36d	-27199436	-55045520.04	646648.7	0.063631
SDCA_P_36d-SCM_P_36d	2542852	-25303232.37	30388936.37	1
SM_36d-SCM_P_36d	-18891068	-46737152.37	8955016.37	0.6216482
SM_3h-SCM_P_36d	-19944407	-47790491.7	7901677.04	0.5158953
SM_P_36d-SCM_P_36d	132703	-27713381.37	27978787.37	1
SMCA_36d-SCM_P_36d	-14931269	-42777353.37	12914815.37	0.9282385
SMCA_3h-SCM_P_36d	-20525082	-48371166.7	7321002.04	0.4588109
SMCA_P_36d-SCM_P_36d	14281352	-13564732.04	42127436.7	0.9532323
SD_3h-SD_36d	-14563089	-42409173.7	13282995.04	0.9433083
SD_P_36d-SD_36d	-4485475.7	-32331560.04	23360608.7	1
SDCA_36d-SD_36d	-3929761.7	-31775846.04	23916322.7	1
SDCA_3h-SD_36d	-31826023	-59672107.37	-3979938.63	0.0099014
SDCA_P_36d-SD_36d	-2083735.3	-29929819.7	25762349.04	1
SM_36d-SD_36d	-23517655	-51363739.7	4328429.04	0.2155864
SM_3h-SD_36d	-24570995	-52417079.04	3275089.7	0.1565607

SM_P_36d-SD_36d	-4493884.3	-32339968.7	23352200.04	1
SMCA_36d-SD_36d	-19557856	-47403940.7	8288228.04	0.554633
SMCA_3h-SD_36d	-25151670	-52997754.04	2694414.7	0.1298617
SMCA_P_36d-SD_36d	9654765	-18191319.37	37500849.37	0.9997558
SD_P_36d-SD_3h	10077614	-17768470.7	37923698.04	0.9995103
SDCA_36d-SD_3h	10633328	-17212756.7	38479412.04	0.998874
SDCA_3h-SD_3h	-17262934	-45109018.04	10583150.7	0.7749381
SDCA_P_36d-SD_3h	12479354	-15366730.37	40325438.37	0.9897446
SM_36d-SD_3h	-8954566	-36800650.37	18891518.37	0.9999324
SM_3h-SD_3h	-10007905	-37853989.7	17838179.04	0.9995617
SM_P_36d-SD_3h	10069205	-17776879.37	37915289.37	0.9995168
SMCA_36d-SD_3h	-4994767	-32840851.37	22851317.37	1
SMCA_3h-SD_3h	-10588580	-38434664.7	17257504.04	0.9989436
SMCA_P_36d-SD_3h	24217854	-3628230.04	52063938.7	0.1747819
SDCA_36d-SD_P_36d	555714	-27290370.37	28401798.37	1
SDCA_3h-SD_P_36d	-27340547	-55186631.7	505537.04	0.0604065
SDCA_P_36d-SD_P_36d	2401740.3	-25444344.04	30247824.7	1
SM_36d-SD_P_36d	-19032180	-46878264.04	8813904.7	0.6075204
SM_3h-SD_P_36d	-20085519	-47931603.37	7760565.37	0.5018691
SM_P_36d-SD_P_36d	-8408.667	-27854493.04	27837675.7	1
SMCA_36d-SD_P_36d	-15072381	-42918465.04	12773703.7	0.9218074
SMCA_3h-SD_P_36d	-20666194	-48512278.37	7179890.37	0.4452443
SMCA_P_36d-SD_P_36d	14140241	-13705843.7	41986325.04	0.9577038
SDCA_3h-SDCA_36d	-27896261	-55742345.7	-50176.96	0.0490591
SDCA_P_36d-SDCA_36d	1846026.3	-26000058.04	29692110.7	1
SM_36d-SDCA_36d	-19587894	-47433978.04	8258190.7	0.5516118
SM_3h-SDCA_36d	-20641233	-48487317.37	7204851.37	0.4476336
SM_P_36d-SDCA_36d	-564122.67	-28410207.04	27281961.7	1
SMCA_36d-SDCA_36d	-15628095	-43474179.04	12217989.7	0.8928422
SMCA_3h-SDCA_36d	-21221908	-49067992.37	6624176.37	0.3933781
SMCA_P_36d-SDCA_36d	13584527	-14261557.7	41430611.04	0.9723222
SDCA_P_36d-SDCA_3h	29742288	1896203.3	57588372.04	0.0237423
SM_36d-SDCA_3h	8308367.7	-19537716.7	36154452.04	0.9999825
SM_3h-SDCA_3h	7255028.3	-20591056.04	35101112.7	0.9999987
SM_P_36d-SDCA_3h	27332139	-513945.7	55178223.04	0.0605945
SMCA_36d-SDCA_3h	12268167	-15577917.7	40114251.04	0.9917288
SMCA_3h-SDCA_3h	6674353.3	-21171731.04	34520437.7	0.9999998
SMCA_P_36d-SDCA_3h	41480788	13634703.63	69326872.37	0.0001044
SM_36d-SDCA_P_36d	-21433920	-49280004.37	6412164.37	0.374348
SM_3h-SDCA_P_36d	-22487259	-50333343.7	5358825.04	0.2872725
SM_P_36d-SDCA_P_36d	-2410149	-30256233.37	25435935.37	1
SMCA_36d-SDCA_P_36d	-17474121	-45320205.37	10371963.37	0.7565843
SMCA_3h-SDCA_P_36d	-23067934	-50914018.7	4778150.04	0.245165
SMCA_P_36d-SDCA_P_36d	11738500	-16107584.04	39584584.7	0.9953652
SM_3h-SM_36d	-1053339.3	-28899423.7	26792745.04	1
SM_P_36d-SM_36d	19023771	-8822313.37	46869855.37	0.6083638
SMCA_36d-SM_36d	3959799	-23886285.37	31805883.37	1
SMCA_3h-SM_36d	-1634014.3	-29480098.7	26212070.04	1
SMCA_P_36d-SM_36d	33172420	5326335.96	61018504.7	0.0054812

SM_P_36d-SM_3h	20077110	-7768974.04	47923194.7	0.5027026
SMCA_36d-SM_3h	5013138.3	-22832946.04	32859222.7	1
SMCA_3h-SM_3h	-580675	-28426759.37	27265409.37	1
SMCA_P_36d-SM_3h	34225760	6379675.3	62071844.04	0.0034087
SMCA_36d-SM_P_36d	-15063972	-42910056.37	12782112.37	0.922201
SMCA_3h-SM_P_36d	-20657785	-48503869.7	7188299.04	0.4460487
SMCA_P_36d-SM_P_36d	14148649	-13697435.04	41994733.7	0.9574464
SMCA_3h-SMCA_36d	-5593813.3	-33439897.7	22252271.04	1
SMCA_P_36d-SMCA_36d	29212621	1366536.96	57058705.7	0.0293888
SMCA_P_36d-SMCA_3h	34806435	6960350.3	62652519.04	0.0026124

Table S4 Results of the PostHoc tests (Tukey test) of the ANOVA test considering microbial dehydrogenase activity and conditions.

	diff	lwr	upr	p adj
S_3h-S_36d	23.79207	2.285862	45.29828	0.015295
S_P_36d-S_36d	16.46559	-5.04062	37.97179	0.38456
SC_36d-S_36d	17.17477	-4.33144	38.68098	0.306692
SC_3h-S_36d	17.11811	-4.3881	38.62432	0.312551
SC_P_36d-S_36d	15.60732	-5.89888	37.11353	0.489741
SCA_36d-S_36d	20.34865	-1.15756	41.85486	0.086456
SCA_3h-S_36d	33.2076	11.70139	54.71381	4.88E-05
SCA_P_36d-S_36d	26.59106	5.08485	48.09726	0.003105
SCD_36d-S_36d	22.315	0.808793	43.82121	0.033359
SCD_3h-S_36d	31.6905	10.18429	53.19671	0.000131
SCD_P_36d-S_36d	41.17358	19.66737	62.67979	2E-07
SCM_36d-S_36d	35.21578	13.70957	56.72199	0.000013
SCM_3h-S_36d	65.21027	43.70407	86.71648	0
SCM_P_36d-S_36d	35.08578	13.57958	56.59199	1.42E-05
SD_36d-S_36d	13.28488	-8.22132	34.79109	0.78019
SD_3h-S_36d	27.30317	5.796965	48.80938	0.00203
SD_P_36d-S_36d	48.88047	27.37427	70.38668	0
SDCA_36d-S_36d	18.9224	-2.5838	40.42861	0.16007
SDCA_3h-S_36d	37.55615	16.04994	59.06236	2.7E-06
SDCA_P_36d-S_36d	36.05894	14.55274	57.56515	7.4E-06
SM_36d-S_36d	30.11086	8.60465	51.61706	0.000358
SM_3h-S_36d	41.30084	19.79463	62.80705	2E-07
SM_P_36d-S_36d	47.17022	25.66401	68.67642	0
SMCA_36d-S_36d	25.52704	4.020832	47.03325	0.005783
SMCA_3h-S_36d	23.09762	1.59141	44.60382	0.022204
SMCA_P_36d-S_36d	25.18874	3.682533	46.69495	0.00702
S_P_36d-S_3h	-7.32648	-28.8327	14.17972	0.999818
SC_36d-S_3h	-6.6173	-28.1235	14.88891	0.999969
SC_3h-S_3h	-6.67396	-28.1802	14.83225	0.999964
SC_P_36d-S_3h	-8.18475	-29.691	13.32146	0.99893
SCA_36d-S_3h	-3.44342	-24.9496	18.06279	1
SCA_3h-S_3h	9.41553	-12.0907	30.92174	0.992369
SCA_P_36d-S_3h	2.798988	-18.7072	24.3052	1
SCD_36d-S_3h	-1.47707	-22.9833	20.02914	1
SCD_3h-S_3h	7.89843	-13.6078	29.40464	0.999382

SCD_P_36d-S_3h	17.38151	-4.1247	38.88772	0.285887
SCM_36d-S_3h	11.42371	-10.0825	32.92992	0.934254
SCM_3h-S_3h	41.41821	19.912	62.92441	2E-07
SCM_P_36d-S_3h	11.29372	-10.2125	32.79992	0.941021
SD_36d-S_3h	-10.5072	-32.0134	10.99902	0.971871
SD_3h-S_3h	3.511103	-17.9951	25.01731	1
SD_P_36d-S_3h	25.0884	3.582196	46.59461	0.007433
SDCA_36d-S_3h	-4.86967	-26.3759	16.63654	1
SDCA_3h-S_3h	13.76408	-7.74213	35.27029	0.725168
SDCA_P_36d-S_3h	12.26687	-9.23933	33.77308	0.877595
SM_36d-S_3h	6.318788	-15.1874	27.825	0.999987
SM_3h-S_3h	17.50877	-3.99743	39.01498	0.273532
SM_P_36d-S_3h	23.37815	1.871939	44.88435	0.019124
SMCA_36d-S_3h	1.73497	-19.7712	23.24118	1
SMCA_3h-S_3h	-0.69445	-22.2007	20.81175	1
SMCA_P_36d-S_3h	1.396672	-20.1095	22.90288	1
SC_36d-S_P_36d	0.709185	-20.797	22.21539	1
SC_3h-S_P_36d	0.652524	-20.8537	22.15873	1
SC_P_36d-S_P_36d	-0.85826	-22.3645	20.64794	1
SCA_36d-S_P_36d	3.883064	-17.6231	25.38927	1
SCA_3h-S_P_36d	16.74201	-4.76419	38.24822	0.353072
SCA_P_36d-S_P_36d	10.12547	-11.3807	31.63168	0.981448
SCD_36d-S_P_36d	5.849414	-15.6568	27.35562	0.999997
SCD_3h-S_P_36d	15.22491	-6.28129	36.73112	0.539033
SCD_P_36d-S_P_36d	24.70799	3.201786	46.2142	0.009216
SCM_36d-S_P_36d	18.75019	-2.75601	40.2564	0.171589
SCM_3h-S_P_36d	48.74469	27.23848	70.2509	0
SCM_P_36d-S_P_36d	18.6202	-2.88601	40.1264	0.180696
SD_36d-S_P_36d	-3.1807	-24.6869	18.32551	1
SD_3h-S_P_36d	10.83759	-10.6686	32.34379	0.960905
SD_P_36d-S_P_36d	32.41489	10.90868	53.92109	8.17E-05
SDCA_36d-S_P_36d	2.456818	-19.0494	23.96302	1
SDCA_3h-S_P_36d	21.09056	-0.41564	42.59677	0.061139
SDCA_P_36d-S_P_36d	19.59336	-1.91285	41.09956	0.120849
SM_36d-S_P_36d	13.64527	-7.86094	35.15148	0.73925
SM_3h-S_P_36d	24.83526	3.329048	46.34146	0.008579
SM_P_36d-S_P_36d	30.70463	9.198422	52.21084	0.000246
SMCA_36d-S_P_36d	9.061453	-12.4448	30.56766	0.995396
SMCA_3h-S_P_36d	6.63203	-14.8742	28.13824	0.999968
SMCA_P_36d-S_P_36d	8.723154	-12.7831	30.22936	0.997279
SC_3h-SC_36d	-0.05666	-21.5629	21.44955	1
SC_P_36d-SC_36d	-1.56745	-23.0737	19.93876	1
SCA_36d-SC_36d	3.173879	-18.3323	24.68009	1
SCA_3h-SC_36d	16.03283	-5.47338	37.53904	0.436384
SCA_P_36d-SC_36d	9.416286	-12.0899	30.92249	0.992361
SCD_36d-SC_36d	5.140229	-16.366	26.64644	1
SCD_3h-SC_36d	14.51573	-6.99048	36.02194	0.631243
SCD_P_36d-SC_36d	23.99881	2.492602	45.50502	0.013662
SCM_36d-SC_36d	18.04101	-3.4652	39.54721	0.225694

SCM_3h-SC_36d	48.0355	26.5293	69.54171	0
SCM_P_36d-SC_36d	17.91101	-3.59519	39.41722	0.236803
SD_36d-SC_36d	-3.88989	-25.3961	17.61632	1
SD_3h-SC_36d	10.1284	-11.3778	31.63461	0.981386
SD_P_36d-SC_36d	31.7057	10.19949	53.21191	0.000129
SDCA_36d-SC_36d	1.747633	-19.7586	23.25384	1
SDCA_3h-SC_36d	20.38138	-1.12483	41.88759	0.085175
SDCA_P_36d-SC_36d	18.88417	-2.62204	40.39038	0.162575
SM_36d-SC_36d	12.93609	-8.57012	34.44229	0.816861
SM_3h-SC_36d	24.12607	2.619864	45.63228	0.012739
SM_P_36d-SC_36d	29.99544	8.489237	51.50165	0.000385
SMCA_36d-SC_36d	8.352268	-13.1539	29.85848	0.99855
SMCA_3h-SC_36d	5.922846	-15.5834	27.42905	0.999996
SMCA_P_36d-SC_36d	8.01397	-13.4922	29.52018	0.999225
SC_P_36d-SC_3h	-1.51079	-23.017	19.99542	1
SCA_36d-SC_3h	3.23054	-18.2757	24.73675	1
SCA_3h-SC_3h	16.08949	-5.41672	37.5957	0.429442
SCA_P_36d-SC_3h	9.472947	-12.0333	30.97915	0.991752
SCD_36d-SC_3h	5.19689	-16.3093	26.7031	1
SCD_3h-SC_3h	14.57239	-6.93382	36.0786	0.623929
SCD_P_36d-SC_3h	24.05547	2.549263	45.56168	0.013244
SCM_36d-SC_3h	18.09767	-3.40854	39.60388	0.220968
SCM_3h-SC_3h	48.09217	26.58596	69.59837	0
SCM_P_36d-SC_3h	17.96767	-3.53853	39.47388	0.231915
SD_36d-SC_3h	-3.83323	-25.3394	17.67298	1
SD_3h-SC_3h	10.18506	-11.3211	31.69127	0.98015
SD_P_36d-SC_3h	31.76236	10.25616	53.26857	0.000125
SDCA_36d-SC_3h	1.804294	-19.7019	23.3105	1
SDCA_3h-SC_3h	20.43804	-1.06817	41.94425	0.082995
SDCA_P_36d-SC_3h	18.94083	-2.56537	40.44704	0.158874
SM_36d-SC_3h	12.99275	-8.51346	34.49895	0.811121
SM_3h-SC_3h	24.18273	2.676525	45.68894	0.012347
SM_P_36d-SC_3h	30.05211	8.545898	51.55831	0.000372
SMCA_36d-SC_3h	8.408929	-13.0973	29.91514	0.998398
SMCA_3h-SC_3h	5.979507	-15.5267	27.48571	0.999995
SMCA_P_36d-SC_3h	8.070631	-13.4356	29.57684	0.999136
SCA_36d-SC_P_36d	4.741328	-16.7649	26.24754	1
SCA_3h-SC_P_36d	17.60028	-3.90593	39.10648	0.264866
SCA_P_36d-SC_P_36d	10.98374	-10.5225	32.48994	0.955163
SCD_36d-SC_P_36d	6.707678	-14.7985	28.21389	0.999961
SCD_3h-SC_P_36d	16.08318	-5.42303	37.58938	0.430213
SCD_P_36d-SC_P_36d	25.56626	4.06005	47.07246	0.005653
SCM_36d-SC_P_36d	19.60846	-1.89775	41.11466	0.120065
SCM_3h-SC_P_36d	49.60295	28.09675	71.10916	0
SCM_P_36d-SC_P_36d	19.47846	-2.02775	40.98467	0.126952
SD_36d-SC_P_36d	-2.32244	-23.8286	19.18377	1
SD_3h-SC_P_36d	11.69585	-9.81036	33.20206	0.918416
SD_P_36d-SC_P_36d	33.27315	11.76694	54.77936	4.67E-05
SDCA_36d-SC_P_36d	3.315082	-18.1911	24.82129	1

SDCA_3h-SC_P_36d	21.94883	0.442621	43.45504	0.040151
SDCA_P_36d-SC_P_36d	20.45162	-1.05459	41.95783	0.08248
SM_36d-SC_P_36d	14.50354	-7.00267	36.00974	0.632815
SM_3h-SC_P_36d	25.69352	4.187312	47.19973	0.005253
SM_P_36d-SC_P_36d	31.56289	10.05669	53.0691	0.000142
SMCA_36d-SC_P_36d	9.919717	-11.5865	31.42592	0.985428
SMCA_3h-SC_P_36d	7.490294	-14.0159	28.9965	0.999737
SMCA_P_36d-SC_P_36d	9.581418	-11.9248	31.08763	0.990474
SCA_3h-SCA_36d	12.85895	-8.64726	34.36516	0.824532
SCA_P_36d-SCA_36d	6.242407	-15.2638	27.74861	0.99999
SCD_36d-SCA_36d	1.96635	-19.5399	23.47256	1
SCD_3h-SCA_36d	11.34185	-10.1644	32.84806	0.938574
SCD_P_36d-SCA_36d	20.82493	-0.68128	42.33114	0.069346
SCM_36d-SCA_36d	14.86713	-6.63908	36.37334	0.585643
SCM_3h-SCA_36d	44.86162	23.35542	66.36783	0
SCM_P_36d-SCA_36d	14.73713	-6.76907	36.24334	0.602567
SD_36d-SCA_36d	-7.06377	-28.57	14.44244	0.999902
SD_3h-SCA_36d	6.954522	-14.5517	28.46073	0.999926
SD_P_36d-SCA_36d	28.53182	7.025615	50.03803	0.00096
SDCA_36d-SCA_36d	-1.42625	-22.9325	20.07996	1
SDCA_3h-SCA_36d	17.2075	-4.29871	38.71371	0.303339
SDCA_P_36d-SCA_36d	15.71029	-5.79591	37.2165	0.476653
SM_36d-SCA_36d	9.762207	-11.744	31.26841	0.987991
SM_3h-SCA_36d	20.95219	-0.55402	42.4584	0.065302
SM_P_36d-SCA_36d	26.82157	5.315358	48.32777	0.002708
SMCA_36d-SCA_36d	5.178389	-16.3278	26.6846	1
SMCA_3h-SCA_36d	2.748966	-18.7572	24.25517	1
SMCA_P_36d-SCA_36d	4.84009	-16.6661	26.3463	1
SCA_P_36d-SCA_3h	-6.61654	-28.1227	14.88967	0.999969
SCD_36d-SCA_3h	-10.8926	-32.3988	10.61361	0.958811
SCD_3h-SCA_3h	-1.5171	-23.0233	19.98911	1
SCD_P_36d-SCA_3h	7.965981	-13.5402	29.47219	0.999294
SCM_36d-SCA_3h	2.008179	-19.498	23.51439	1
SCM_3h-SCA_3h	32.00268	10.49647	53.50888	0.000107
SCM_P_36d-SCA_3h	1.878185	-19.628	23.38439	1
SD_36d-SCA_3h	-19.9227	-41.4289	1.583492	0.104671
SD_3h-SCA_3h	-5.90443	-27.4106	15.60178	0.999996
SD_P_36d-SCA_3h	15.67287	-5.83333	37.17908	0.481398
SDCA_36d-SCA_3h	-14.2852	-35.7914	7.221012	0.66075
SDCA_3h-SCA_3h	4.348551	-17.1577	25.85476	1
SDCA_P_36d-SCA_3h	2.851343	-18.6549	24.35755	1
SM_36d-SCA_3h	-3.09674	-24.6029	18.40947	1
SM_3h-SCA_3h	8.093242	-13.413	29.59945	0.999098
SM_P_36d-SCA_3h	13.96262	-7.54359	35.46882	0.701087
SMCA_36d-SCA_3h	-7.68056	-29.1868	13.82565	0.999604
SMCA_3h-SCA_3h	-10.11	-31.6162	11.39622	0.981775
SMCA_P_36d-SCA_3h	-8.01886	-29.5251	13.48735	0.999218
SCD_36d-SCA_P_36d	-4.27606	-25.7823	17.23015	1
SCD_3h-SCA_P_36d	5.099442	-16.4068	26.60565	1

SCD_P_36d-SCA_P_36d	14.58252	-6.92368	36.08873	0.622619
SCM_36d-SCA_P_36d	8.624721	-12.8815	30.13093	0.997685
SCM_3h-SCA_P_36d	38.61922	17.11301	60.12542	1.3E-06
SCM_P_36d-SCA_P_36d	8.494727	-13.0115	30.00093	0.998141
SD_36d-SCA_P_36d	-13.3062	-34.8124	8.200034	0.777853
SD_3h-SCA_P_36d	0.712115	-20.7941	22.21832	1
SD_P_36d-SCA_P_36d	22.28942	0.783208	43.79562	0.033797
SDCA_36d-SCA_P_36d	-7.66865	-29.1749	13.83755	0.999614
SDCA_3h-SCA_P_36d	10.96509	-10.5411	32.4713	0.955928
SDCA_P_36d-SCA_P_36d	9.467885	-12.0383	30.97409	0.991808
SM_36d-SCA_P_36d	3.5198	-17.9864	25.02601	1
SM_3h-SCA_P_36d	14.70978	-6.79642	36.21599	0.606121
SM_P_36d-SCA_P_36d	20.57916	-0.92705	42.08537	0.077771
SMCA_36d-SCA_P_36d	-1.06402	-22.5702	20.44219	1
SMCA_3h-SCA_P_36d	-3.49344	-24.9996	18.01277	1
SMCA_P_36d-SCA_P_36d	-1.40232	-22.9085	20.10389	1
SCD_3h-SCD_36d	9.375499	-12.1307	30.88171	0.992777
SCD_P_36d-SCD_36d	18.85858	-2.64763	40.36479	0.164268
SCM_36d-SCD_36d	12.90078	-8.60543	34.40699	0.820393
SCM_3h-SCD_36d	42.89527	21.38907	64.40148	1E-07
SCM_P_36d-SCD_36d	12.77078	-8.73542	34.27699	0.833095
SD_36d-SCD_36d	-9.03012	-30.5363	12.47609	0.995607
SD_3h-SCD_36d	4.988172	-16.518	26.49438	1
SD_P_36d-SCD_36d	26.56547	5.059265	48.07168	0.003153
SDCA_36d-SCD_36d	-3.3926	-24.8988	18.11361	1
SDCA_3h-SCD_36d	15.24115	-6.26506	36.74736	0.536924
SDCA_P_36d-SCD_36d	13.74394	-7.76227	35.25015	0.727573
SM_36d-SCD_36d	7.795857	-13.7103	29.30206	0.999498
SM_3h-SCD_36d	18.98584	-2.52037	40.49205	0.155981
SM_P_36d-SCD_36d	24.85522	3.349008	46.36142	0.008483
SMCA_36d-SCD_36d	3.212039	-18.2942	24.71825	1
SMCA_3h-SCD_36d	0.782616	-20.7236	22.28882	1
SMCA_P_36d-SCD_36d	2.87374	-18.6325	24.37995	1
SCD_P_36d-SCD_3h	9.483081	-12.0231	30.98929	0.991639
SCM_36d-SCD_3h	3.525279	-17.9809	25.03149	1
SCM_3h-SCD_3h	33.51978	12.01357	55.02598	3.98E-05
SCM_P_36d-SCD_3h	3.395285	-18.1109	24.90149	1
SD_36d-SCD_3h	-18.4056	-39.9118	3.100593	0.196517
SD_3h-SCD_3h	-4.38733	-25.8935	17.11888	1
SD_P_36d-SCD_3h	17.18997	-4.31623	38.69618	0.305132
SDCA_36d-SCD_3h	-12.7681	-34.2743	8.738112	0.833352
SDCA_3h-SCD_3h	5.865651	-15.6406	27.37186	0.999997
SDCA_P_36d-SCD_3h	4.368443	-17.1378	25.87465	1
SM_36d-SCD_3h	-1.57964	-23.0858	19.92657	1
SM_3h-SCD_3h	9.610343	-11.8959	31.11655	0.990107
SM_P_36d-SCD_3h	15.47972	-6.02649	36.98592	0.506084
SMCA_36d-SCD_3h	-6.16346	-27.6697	15.34275	0.999992
SMCA_3h-SCD_3h	-8.59288	-30.0991	12.91332	0.997805
SMCA_P_36d-SCD_3h	-6.50176	-28.008	15.00445	0.999978

SCM_36d-SCD_P_36d	-5.9578	-27.464	15.54841	0.999996
SCM_3h-SCD_P_36d	24.0367	2.530488	45.5429	0.013381
SCM_P_36d-SCD_P_36d	-6.0878	-27.594	15.41841	0.999994
SD_36d-SCD_P_36d	-27.8887	-49.3949	-6.38249	0.001424
SD_3h-SCD_P_36d	-13.8704	-35.3766	7.6358	0.712352
SD_P_36d-SCD_P_36d	7.706893	-13.7993	29.2131	0.999582
SDCA_36d-SCD_P_36d	-22.2512	-43.7574	-0.74497	0.034462
SDCA_3h-SCD_P_36d	-3.61743	-25.1236	17.88878	1
SDCA_P_36d-SCD_P_36d	-5.11464	-26.6208	16.39157	1
SM_36d-SCD_P_36d	-11.0627	-32.5689	10.44348	0.951819
SM_3h-SCD_P_36d	0.127262	-21.3789	21.63347	1
SM_P_36d-SCD_P_36d	5.996636	-15.5096	27.50284	0.999995
SMCA_36d-SCD_P_36d	-15.6465	-37.1527	5.859666	0.484745
SMCA_3h-SCD_P_36d	-18.076	-39.5822	3.430244	0.22277
SMCA_P_36d-SCD_P_36d	-15.9848	-37.491	5.521368	0.442296
SCM_3h-SCM_36d	29.9945	8.488289	51.5007	0.000385
SCM_P_36d-SCM_36d	-0.12999	-21.6362	21.37621	1
SD_36d-SCM_36d	-21.9309	-43.4371	-0.42469	0.040514
SD_3h-SCM_36d	-7.91261	-29.4188	13.5936	0.999365
SD_P_36d-SCM_36d	13.66469	-7.84151	35.1709	0.736966
SDCA_36d-SCM_36d	-16.2934	-37.7996	5.212833	0.404839
SDCA_3h-SCM_36d	2.340372	-19.1658	23.84658	1
SDCA_P_36d-SCM_36d	0.843164	-20.663	22.34937	1
SM_36d-SCM_36d	-5.10492	-26.6111	16.40129	1
SM_3h-SCM_36d	6.085063	-15.4211	27.59127	0.999994
SM_P_36d-SCM_36d	11.95444	-9.55177	33.46064	0.901214
SMCA_36d-SCM_36d	-9.68874	-31.1949	11.81747	0.989056
SMCA_3h-SCM_36d	-12.1182	-33.6244	9.388045	0.889223
SMCA_P_36d-SCM_36d	-10.027	-31.5332	11.47917	0.983447
SCM_P_36d-SCM_3h	-30.1245	-51.6307	-8.61828	0.000355
SD_36d-SCM_3h	-51.9254	-73.4316	-30.4192	0
SD_3h-SCM_3h	-37.9071	-59.4133	-16.4009	2.2E-06
SD_P_36d-SCM_3h	-16.3298	-37.836	5.176405	0.400509
SDCA_36d-SCM_3h	-46.2879	-67.7941	-24.7817	0
SDCA_3h-SCM_3h	-27.6541	-49.1603	-6.14792	0.001642
SDCA_P_36d-SCM_3h	-29.1513	-50.6575	-7.64513	0.000654
SM_36d-SCM_3h	-35.0994	-56.6056	-13.5932	0.000014
SM_3h-SCM_3h	-23.9094	-45.4156	-2.40323	0.014347
SM_P_36d-SCM_3h	-18.0401	-39.5463	3.466147	0.225774
SMCA_36d-SCM_3h	-39.6832	-61.1894	-18.177	7E-07
SMCA_3h-SCM_3h	-42.1127	-63.6189	-20.6065	1E-07
SMCA_P_36d-SCM_3h	-40.0215	-61.5277	-18.5153	5E-07
SD_36d-SCM_P_36d	-21.8009	-43.3071	-0.29469	0.04323
SD_3h-SCM_P_36d	-7.78261	-29.2888	13.7236	0.999511
SD_P_36d-SCM_P_36d	13.79469	-7.71152	35.3009	0.721499
SDCA_36d-SCM_P_36d	-16.1634	-37.6696	5.342827	0.420455
SDCA_3h-SCM_P_36d	2.470366	-19.0358	23.97657	1
SDCA_P_36d-SCM_P_36d	0.973158	-20.533	22.47937	1
SM_36d-SCM_P_36d	-4.97493	-26.4811	16.53128	1

SM_3h-SCM_P_36d	6.215058	-15.2911	27.72126	0.99999
SM_P_36d-SCM_P_36d	12.08443	-9.42178	33.59064	0.891763
SMCA_36d-SCM_P_36d	-9.55875	-31.065	11.94746	0.990753
SMCA_3h-SCM_P_36d	-11.9882	-33.4944	9.51804	0.898813
SMCA_P_36d-SCM_P_36d	-9.89704	-31.4033	11.60916	0.985822
SD_3h-SD_36d	14.01829	-7.48792	35.5245	0.694224
SD_P_36d-SD_36d	35.59559	14.08938	57.1018	1.01E-05
SDCA_36d-SD_36d	5.637519	-15.8687	27.14373	0.999999
SDCA_3h-SD_36d	24.27127	2.765059	45.77747	0.011758
SDCA_P_36d-SD_36d	22.77406	1.267851	44.28026	0.026319
SM_36d-SD_36d	16.82597	-4.68023	38.33218	0.343786
SM_3h-SD_36d	28.01596	6.50975	49.52216	0.001317
SM_P_36d-SD_36d	33.88533	12.37912	55.39154	3.13E-05
SMCA_36d-SD_36d	12.24215	-9.26405	33.74836	0.879576
SMCA_3h-SD_36d	9.812732	-11.6935	31.31894	0.987212
SMCA_P_36d-SD_36d	11.90386	-9.60235	33.41006	0.904746
SD_P_36d-SD_3h	21.5773	0.071093	43.08351	0.048286
SDCA_36d-SD_3h	-8.38077	-29.887	13.12544	0.998475
SDCA_3h-SD_3h	10.25298	-11.2532	31.75919	0.978585
SDCA_P_36d-SD_3h	8.75577	-12.7504	30.26198	0.997132
SM_36d-SD_3h	2.807685	-18.6985	24.31389	1
SM_3h-SD_3h	13.99767	-7.50854	35.50388	0.696771
SM_P_36d-SD_3h	19.86704	-1.63916	41.37325	0.107272
SMCA_36d-SD_3h	-1.77613	-23.2823	19.73007	1
SMCA_3h-SD_3h	-4.20556	-25.7118	17.30065	1
SMCA_P_36d-SD_3h	-2.11443	-23.6206	19.39178	1
SDCA_36d-SD_P_36d	-29.9581	-51.4643	-8.45186	0.000394
SDCA_3h-SD_P_36d	-11.3243	-32.8305	10.18189	0.939473
SDCA_P_36d-SD_P_36d	-12.8215	-34.3277	8.684677	0.828193
SM_36d-SD_P_36d	-18.7696	-40.2758	2.736592	0.170259
SM_3h-SD_P_36d	-7.57963	-29.0858	13.92658	0.999681
SM_P_36d-SD_P_36d	-1.71026	-23.2165	19.79595	1
SMCA_36d-SD_P_36d	-23.3534	-44.8596	-1.84723	0.019379
SMCA_3h-SD_P_36d	-25.7829	-47.2891	-4.27665	0.004988
SMCA_P_36d-SD_P_36d	-23.6917	-45.1979	-2.18552	0.016152
SDCA_3h-SDCA_36d	18.63375	-2.87246	40.13995	0.17973
SDCA_P_36d-SDCA_36d	17.13654	-4.36967	38.64275	0.310638
SM_36d-SDCA_36d	11.18845	-10.3178	32.69466	0.946132
SM_3h-SDCA_36d	22.37844	0.872231	43.88464	0.032294
SM_P_36d-SDCA_36d	28.24781	6.741604	49.75402	0.001143
SMCA_36d-SDCA_36d	6.604635	-14.9016	28.11084	0.99997
SMCA_3h-SDCA_36d	4.175213	-17.331	25.68142	1
SMCA_P_36d-SDCA_36d	6.266337	-15.2399	27.77254	0.999989
SDCA_P_36d-SDCA_3h	-1.49721	-23.0034	20.009	1
SM_36d-SDCA_3h	-7.44529	-28.9515	14.06091	0.999762
SM_3h-SDCA_3h	3.744691	-17.7615	25.2509	1
SM_P_36d-SDCA_3h	9.614065	-11.8921	31.12027	0.990059
SMCA_36d-SDCA_3h	-12.0291	-33.5353	9.477096	0.895851
SMCA_3h-SDCA_3h	-14.4585	-35.9647	7.047673	0.638604

SMCA_P_36d-SDCA_3h	-12.3674	-33.8736	9.138797	0.869338
SM_36d-SDCA_P_36d	-5.94808	-27.4543	15.55812	0.999996
SM_3h-SDCA_P_36d	5.241899	-16.2643	26.74811	1
SM_P_36d-SDCA_P_36d	11.11127	-10.3949	32.61748	0.949676
SMCA_36d-SDCA_P_36d	-10.5319	-32.0381	10.9743	0.971142
SMCA_3h-SDCA_P_36d	-12.9613	-34.4675	8.544882	0.814315
SMCA_P_36d-SDCA_P_36d	-10.8702	-32.3764	10.63601	0.959673
SM_3h-SM_36d	11.18998	-10.3162	32.69619	0.94606
SM_P_36d-SM_36d	17.05936	-4.44685	38.56557	0.318695
SMCA_36d-SM_36d	-4.58382	-26.09	16.92239	1
SMCA_3h-SM_36d	-7.01324	-28.5194	14.49297	0.999914
SMCA_P_36d-SM_36d	-4.92212	-26.4283	16.58409	1
SM_P_36d-SM_3h	5.869374	-15.6368	27.37558	0.999997
SMCA_36d-SM_3h	-15.7738	-37.28	5.732404	0.468631
SMCA_3h-SM_3h	-18.2032	-39.7094	3.302982	0.212353
SMCA_P_36d-SM_3h	-16.1121	-37.6183	5.394106	0.426683
SMCA_36d-SM_P_36d	-21.6432	-43.1494	-0.13697	0.046745
SMCA_3h-SM_P_36d	-24.0726	-45.5788	-2.56639	0.01312
SMCA_P_36d-SM_P_36d	-21.9815	-43.4877	-0.47527	0.039499
SMCA_3h-SMCA_36d	-2.42942	-23.9356	19.07678	1
SMCA_P_36d-SMCA_36d	-0.3383	-21.8445	21.16791	1
SMCA_P_36d-SMCA_3h	2.091124	-19.4151	23.59733	1

Table S5 PostHoc test (wilcox test, method=BH) performed on Kruskal-Wallis test considering ARG abundances and conditions.

	S_3h	S_P_36d	S_36d	SC_3h	SC_P_36d	SC_36d	SCA_3h	SCA_P_36d
S_P_36d	0.33857	-	-	-	-	-	-	-
S_36d	0.25362	0.90481	-	-	-	-	-	-
SC_3h	0.33719	0.48678	0.57249	-	-	-	-	-
SC_P_36d	0.21185	0.73582	0.92785	0.61733	-	-	-	-
SC_36d	0.89158	0.09876	0.01014	0.12355	0.02033	-	-	-
SCA_3h	0.20533	1	0.49791	0.73582	0.73384	0.12355	-	-
SCA_P_36d	0.73384	0.70434	0.62287	0.38224	0.50973	0.38914	0.83581	-
SCA_36d	0.96727	0.18638	0.07187	0.12355	0.06855	1	0.33857	0.48184
SCD_3h	0.57729	0.40685	0.38914	0.24117	0.38914	0.57249	0.47677	0.51675
SCD_P_36d	0.81406	0.0526	0.01431	0.0588	0.01431	0.77699	0.09876	0.34808
SCD_36d	0.62287	0.0093	0.00106	0.02591	0.00255	0.62287	0.07155	0.07187
SDCA_3h	0.83242	0.48678	0.38914	0.27449	0.38914	0.81406	0.47677	0.83581
SDCA_P_36d	0.27449	0.01156	0.00623	0.01331	0.00337	0.3546	0.06378	0.0424
SDCA_36d	0.49791	0.0174	0.00529	0.02367	0.00623	0.49791	0.08013	0.09876
SCM_3h	0.57729	0.42773	0.38914	0.24117	0.38914	0.58984	0.47677	0.51675
SCM_P_36d	0.93706	0.11733	0.01908	0.09876	0.02033	0.71571	0.25362	0.37474
SCM_36d	0.54415	0.02318	0.00678	0.02591	0.01156	0.73384	0.13697	0.1743
SCMA_3h	0.8733	0.47677	0.38914	0.3546	0.40685	0.81406	0.47677	0.73384
SCMA_P_36d	0.62287	0.90481	0.96727	0.38224	0.62287	0.38279	1	0.73582
SCMA_36d	0.3546	0.02367	0.02318	0.02242	0.01431	0.42103	0.09876	0.13031
SD_3h	0.47677	0.38914	0.38914	0.20533	0.38914	0.45177	0.47677	0.45177
SD_P_36d	0.31782	0.77903	0.99892	0.54415	0.98796	0.0174	0.61733	0.68775
SD_36d	0.20034	0.73177	0.40435	0.49791	0.4798	0.12671	0.99405	0.6574

SM_3h	0.70679	0.48678	0.40685	0.31695	0.42773	0.62287	0.47677	0.54415
SM_P_36d	0.09876	0.3546	0.38914	0.86253	0.49172	0.00255	0.23565	0.27449
SM_36d	0.78758	0.51675	0.3546	0.38914	0.38224	0.49791	0.73384	0.85632
	SCA_36d	SCD_3h	SCD_P_36d	SCD_P_36d	SDCA_3h	SDCA_P_36d	SDCA_36d	
S_P_36d	-	-	-	-	-	-	-	-
S_36d	-	-	-	-	-	-	-	-
SC_3h	-	-	-	-	-	-	-	-
SC_P_36d	-	-	-	-	-	-	-	-
SC_36d	-	-	-	-	-	-	-	-
SCA_3h	-	-	-	-	-	-	-	-
SCA_P_36d	-	-	-	-	-	-	-	-
SCA_36d	-	-	-	-	-	-	-	-
SCD_3h	0.61733	-	-	-	-	-	-	-
SCD_P_36d	0.90481	0.51675	-	-	-	-	-	-
SCD_36d	0.53817	0.62287	0.6574	-	-	-	-	-
SDCA_3h	0.90481	0.44611	0.78758	0.81406	-	-	-	-
SDCA_P_36d	0.33719	0.96727	0.23565	0.62287	0.3546	-	-	-
SDCA_36d	0.39459	0.7883	0.50537	0.75738	0.57249	0.90481	-	-
SCM_3h	0.62287	0.90481	0.45177	0.71571	0.47677	0.99405	0.90481	-
SCM_P_36d	0.86985	0.51675	0.7883	0.38914	0.81406	0.25389	0.38914	-
SCM_36d	0.82775	0.62287	0.60883	0.75738	0.86253	0.38914	0.53817	-
SCMA_3h	0.86253	0.49791	0.89158	0.99405	0.90481	0.6574	0.71571	-
SCMA_P_36d	0.30911	0.48678	0.38224	0.02596	0.62287	0.01156	0.03889	-
SCMA_36d	0.48184	0.81406	0.39205	0.90481	0.51675	0.70434	0.90481	-
SD_3h	0.42773	0.73582	0.38914	0.48678	0.20533	0.71571	0.7883	-
SD_P_36d	0.06855	0.38914	0.02367	0.00317	0.38914	0.00623	0.00623	-
SD_36d	0.40435	0.38914	0.02596	0.0174	0.38914	0.01536	0.02596	-
SM_3h	0.69082	0.83242	0.62287	0.73384	0.49791	0.90481	0.86253	-
SM_P_36d	0.01265	0.38914	0.00724	0.00089	0.38914	0.00106	0.00119	-
SM_36d	0.73177	0.58316	0.456	0.33719	0.99405	0.11508	0.27449	-
	SCM_3h	SCM_P_36d	SCM_36d	SCMA_3h	SCMA_P_36d	SCMA_36d	SD_3h	
S_P_36d	-	-	-	-	-	-	-	-
S_36d	-	-	-	-	-	-	-	-
SC_3h	-	-	-	-	-	-	-	-
SC_P_36d	-	-	-	-	-	-	-	-
SC_36d	-	-	-	-	-	-	-	-
SCA_3h	-	-	-	-	-	-	-	-
SCA_P_36d	-	-	-	-	-	-	-	-
SCA_36d	-	-	-	-	-	-	-	-
SCD_3h	-	-	-	-	-	-	-	-
SCD_P_36d	-	-	-	-	-	-	-	-
SCD_36d	-	-	-	-	-	-	-	-
SDCA_3h	-	-	-	-	-	-	-	-
SDCA_P_36d	-	-	-	-	-	-	-	-
SDCA_36d	-	-	-	-	-	-	-	-
SCM_3h	-	-	-	-	-	-	-	-
SCM_P_36d	0.51675	-	-	-	-	-	-	-
SCM_36d	0.62287	0.6131	-	-	-	-	-	-
SCMA_3h	0.57729	0.73384	0.96727	-	-	-	-	-

SCMA_P_36d	0.45177	0.16284	0.02538	0.6574	-	-	-
SCMA_36d	0.89158	0.42103	0.62287	0.69082	0.02538	-	-
SD_3h	0.57729	0.45177	0.38914	0.38472	0.38914	0.58984	-
SD_P_36d	0.38914	0.02367	0.01331	0.42773	0.83581	0.02318	0.38914
SD_36d	0.38914	0.25389	0.06083	0.42738	1	0.04418	0.38914
SM_3h	0.83242	0.57249	0.71571	0.57729	0.49791	0.86253	0.90481
SM_P_36d	0.38914	0.00255	0.00255	0.38914	0.30911	0.00529	0.38914
SM_36d	0.58316	0.54415	0.38914	0.83581	0.60883	0.27449	0.49791
	SD_P_36d	SD_36d	SM_3h	SM_P_36d			
S_P_36d	-	-	-	-			
S_36d	-	-	-	-			
SC_3h	-	-	-	-			
SC_P_36d	-	-	-	-			
SC_36d	-	-	-	-			
SCA_3h	-	-	-	-			
SCA_P_36d	-	-	-	-			
SCA_36d	-	-	-	-			
SCD_3h	-	-	-	-			
SCD_P_36d	-	-	-	-			
SCD_36d	-	-	-	-			
SDCA_3h	-	-	-	-			
SDCA_P_36d	-	-	-	-			
SDCA_36d	-	-	-	-			
SCM_3h	-	-	-	-			
SCM_P_36d	-	-	-	-			
SCM_36d	-	-	-	-			
SCMA_3h	-	-	-	-			
SCMA_P_36d	-	-	-	-			
SCMA_36d	-	-	-	-			
SD_3h	-	-	-	-			
SD_P_36d	-	-	-	-			
SD_36d	0.62287	-	-	-			
SM_3h	0.38914	0.49791	-	-			
SM_P_36d	0.49791	0.27449	0.38914	-			
SM_36d	0.40435	0.54415	0.58316	0.09876			

Table S6 PERMANOVA performed considering ASV, amendment presence and sampling time.

	Df	Sum0fSqs	R2	F	p-value
Amendment	1	0.5158	0.03227	2.9275	0.001***
Time	1	1.6958	0.10608	9.6242	0.001***
Amendment:time	1	0.3825	0.02393	2.1710	0.003**
Residual	76	13.3917	0.83772		
Total	79	15.9859	1.00000		

Table S7 PERMANOVA performed considering ASV and plant presence.

	Df	Sum0fSqs	R2	F	p-value
Plant	1	0.9817	0.06141	5.1036	0.001***
Residual	78	15.0042	0.93859		
Total	79	15.9859	1.00000		

Table S8 Main microbial classes found in 3h experimental conditions and their relative abundances

Experimental conditions at 3h	Class and Relative Abundances (%)			
S	Actinobacteria (32.4%)	Gammaproteobacteria (14.01%)	Alphaproteobacteria (11.5%)	Bacteroidia (6.6%)
SC	Actinobacteria (23.9%)	Gammaproteobacteria (12.9%)	Bacteroidia (12.2%)	Bacilli (11.6%)
SCA	Actinobacteria (28.8%)	Gammaproteobacteria (12.9%)	Bacteroidia (11.3%)	Anaerolineae (1.5%)
SM	Actinobacteria (22.1%)	Gammaproteobacteria (8.9%)	Alphaproteobacteria (8.8%)	Bacteroidia (15.8%)
SCM	Actinobacteria (21.2%)	Gammaproteobacteria (11.3%)	Bacteroidia (12.1%)	Bacilli (13.3%)
SMCA	Actinobacteria (17.8%)	Gammaproteobacteria (10.7%)	Bacteroidia (19%)	Bacilli (13.8%)
SD	Actinobacteria (24.3%)	Gammaproteobacteria (13.3%)	Alphaproteobacteria (11.2%)	Bacteroidia (14.6%)
SCD	Actinobacteria (25.7%)	Gammaproteobacteria (14.7%)	Alphaproteobacteria (13.2%)	Bacteroidia (13.3%)
SDCA	Actinobacteria (22.1%)	Gammaproteobacteria (15.2%)	Alphaproteobacteria (12.8%)	Bacteroidia (15.5%)

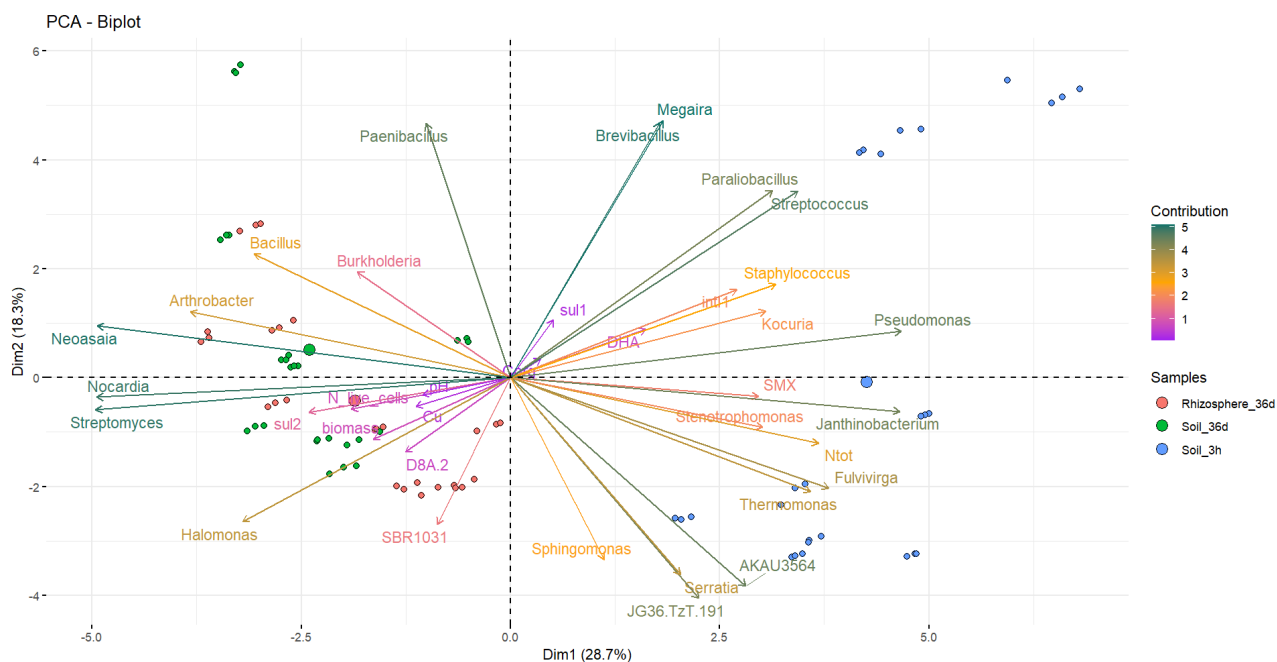


Figure S1 Principal Component Analysis (PCA) performed on the following variables: antibiotic concentrations (SMX), MGE and ARG relative abundances (intI1, sul1, sul2), Cu concentration (Cu), organic C (%) and total N (%), pH, live cell abundance, DHA, main microbial genera. The blue dots represent samples at 3 hours, the green dots samples of soil at 36 days and red ones, samples of rhizosphere at 36 days. The gradient contribution represents the contribution of the variables to each dimension (from purple: weak to green: strong).

Table S9 Results of correlations between variables and Dimension 1 of PCA

Variables	Dimension 1	
	r correlation	p.value
<i>Pseudomonas</i>	0.8554163	2.79E-24
<i>Janthinobacterium</i>	0.8523903	5.95E-24
<i>Fulvivirga</i>	0.6973664	4.73E-13
Ntot	0.6742548	5.20E-12
<i>Thermomonas</i>	0.6579316	2.50E-11
<i>Streptococcus</i>	0.6297807	3.01E-10
<i>Staphylococcus</i>	0.5813749	1.26E-08
<i>Paraliobacillus</i>	0.5741176	2.10E-08
<i>Kocuria</i>	0.5586354	5.98E-08
<i>Stenotrophomonas</i>	0.5521541	9.11E-08
SMX	0.5436262	1.57E-07
<i>AKAU3564</i>	0.515531	8.43E-07

intI1	0.4958559	2.51E-06
<i>JG36.TzT.191</i>	0.4120386	1.32E-04
<i>Serratia</i>	0.3721833	6.23E-04
<i>Megaira</i>	0.3349793	2.24E-03
<i>Brevibacillus</i>	0.3268918	2.90E-03
DHA	0.29689	7.11E-03
<i>D8A.2</i>	-0.2303121	3.86E-02
biomass	-0.3007699	6.37E-03
<i>Burkholderia</i>	-0.3354633	2.20E-03
N_live_cells	-0.3484853	1.43E-03
sul2	-0.4412199	3.74E-05
<i>Bacillus</i>	-0.5614525	4.96E-08
<i>Halomonas</i>	-0.5873464	8.23E-09
<i>Arthrobacter</i>	-0.7014673	3.02E-13
<i>Neosasaia</i>	-0.9056367	3.63E-31
<i>Nocardia</i>	-0.906278	2.81E-31
<i>Streptomyces</i>	-0.909008	9.22E-32

Table S10 Results of correlations between variables and Dimension 2 of PCA

Variables	Dimension 2	
	r correlation	p.value
<i>Megaira</i>	0.864402	2.65E-25
<i>Brevibacillus</i>	0.858453	1.28E-24
<i>Paenibacillus</i>	0.8559058	2.47E-24
<i>Paraliobacillus</i>	0.6302262	2.90E-10
<i>Streptococcus</i>	0.6276452	3.59E-10
<i>Bacillus</i>	0.415685	1.14E-04
<i>Burkholderia</i>	0.3559346	1.11E-03
<i>Staphylococcus</i>	0.315261	4.15E-03
intI1	0.2954277	7.42E-03
<i>Kocuria</i>	0.2247916	4.36E-02
<i>Arthrobacter</i>	0.2212381	4.72E-02
Ntot	-0.2212986	4.71E-02
<i>D8A.2</i>	-0.2509385	2.38E-02
<i>Fulvivirga</i>	-0.3718846	6.30E-04
<i>Thermomonas</i>	-0.3842295	3.98E-04
<i>Halomonas</i>	-0.483962	4.71E-06
<i>SBR1031</i>	-0.4945618	2.69E-06
<i>Sphingomonas</i>	-0.612721	1.21E-09
<i>Serratia</i>	-0.662927	1.56E-11
<i>AKAU3564</i>	-0.7012606	3.09E-13
<i>JG36.TzT.191</i>	-0.7432858	1.92E-15

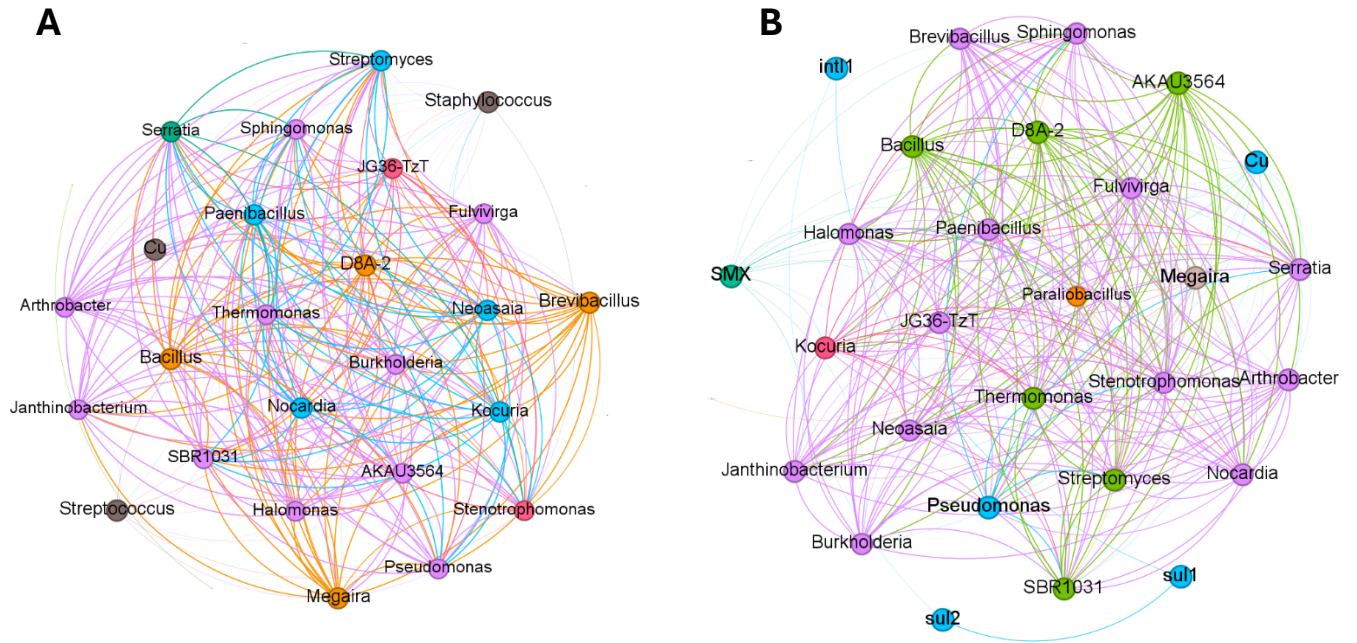


Figure S2 Network analysis revealing the co-occurrence patterns among ARGs, MGE, AB, Cu and microbial genera analyzed in manure (A: on the left) and digestate (B: on the right) amended conditions at 36 days.

Table S11 Results of the PostHoc tests (Tukey test) of the ANOVA test considering plant biomass (dry weight) at 36 days and conditions.

	diff	lwr	upr	p adj
SC_P_36d-S_P_36d	-0.191983505	-0.56571726	0.18175025	0.7248146
SCA_P_36d-S_P_36d	-0.259688862	-0.63342262	0.11404489	0.3557913
SCD_P_36d-S_P_36d	0.402115169	0.02838142	0.77584892	0.0278691
SCM_P_36d-S_P_36d	-0.116882657	-0.49061641	0.2568511	0.9763414
SD_P_36d-S_P_36d	0.595939945	0.22220619	0.9696737	0.000341
SDCA_P_36d-S_P_36d	0.573947956	0.2002142	0.94768171	0.0005709
SM_P_36d-S_P_36d	0.103316873	-0.27041688	0.47705063	0.9889839
SMCA_P_36d-S_P_36d	-0.107945877	-0.48167963	0.26578788	0.9854684
SCA_P_36d-SC_P_36d	-0.067705357	-0.44143911	0.3060284	0.9993962
SCD_P_36d-SC_P_36d	0.594098674	0.22036492	0.96783243	0.000356
SCM_P_36d-SC_P_36d	0.075100847	-0.29863291	0.4488346	0.9987291
SD_P_36d-SC_P_36d	0.78792345	0.4141897	1.1616572	0.0000041
SDCA_P_36d-SC_P_36d	0.76593146	0.39219771	1.13966521	0.0000067
SM_P_36d-SC_P_36d	0.295300378	-0.07843338	0.66903413	0.2097247
SMCA_P_36d-SC_P_36d	0.084037628	-0.28969613	0.45777138	0.9972097
SCD_P_36d-SCA_P_36d	0.661804031	0.28807028	1.03553779	0.0000731
SCM_P_36d-SCA_P_36d	0.142806205	-0.23092755	0.51653996	0.927058
SD_P_36d-SCA_P_36d	0.855628807	0.48189505	1.22936256	0.0000009
SDCA_P_36d-SCA_P_36d	0.833636818	0.45990306	1.20737057	0.0000015
SM_P_36d-SCA_P_36d	0.363005735	-0.01072802	0.73673949	0.0618918
SMCA_P_36d-SCA_P_36d	0.151742985	-0.22199077	0.52547674	0.900748
SCM_P_36d-SCD_P_36d	-0.518997827	-0.89273158	-0.14526407	0.0020544
SD_P_36d-SCD_P_36d	0.193824776	-0.17990898	0.56755853	0.7150001
SDCA_P_36d-SCD_P_36d	0.171832786	-0.20190097	0.54556654	0.8235517
SM_P_36d-SCD_P_36d	-0.298798296	-0.67253205	0.07493546	0.1981625
SMCA_P_36d-SCD_P_36d	-0.510061046	-0.8837948	-0.13632729	0.0025256
SD_P_36d-SCM_P_36d	0.712822603	0.33908885	1.08655636	0.0000224
SDCA_P_36d-SCM_P_36d	0.690830613	0.31709686	1.06456437	0.0000372
SM_P_36d-SCM_P_36d	0.220199531	-0.15353422	0.59393328	0.5672895
SMCA_P_36d-SCM_P_36d	0.008936781	-0.36479697	0.38267053	1
SDCA_P_36d-SD_P_36d	-0.02199199	-0.39572574	0.35174176	0.9999999

SM_P_36d-SD_P_36d	-0.492623072	-0.86635683	-0.11888932	0.00377
SMCA_P_36d-SD_P_36d	-0.703885822	-1.07761958	-0.33015207	0.0000275
SM_P_36d-SDCA_P_36d	-0.470631082	-0.84436484	-0.09689733	0.0062156
SMCA_P_36d-SDCA_P_36d	-0.681893832	-1.05562759	-0.30816008	0.0000458
SMCA_P_36d-SM_P_36d	-0.21126275	-0.5849965	0.162471	0.6181861
SCM_P_36d-SCD_P_36d	-0.518997827	-0.89273158	-0.14526407	0.0020544
SD_P_36d-SCD_P_36d	0.193824776	-0.17990898	0.56755853	0.7150001
SDCA_P_36d-SCD_P_36d	0.171832786	-0.20190097	0.54556654	0.8235517
SM_P_36d-SCD_P_36d	-0.298798296	-0.67253205	0.07493546	0.1981625
SMCA_P_36d-SCD_P_36d	-0.510061046	-0.8837948	-0.13632729	0.0025256
SD_P_36d-SCM_P_36d	0.712822603	0.33908885	1.08655636	0.0000224
SDCA_P_36d-SCM_P_36d	0.690830613	0.31709686	1.06456437	0.0000372
SM_P_36d-SCM_P_36d	0.220199531	-0.15353422	0.59393328	0.5672895
SMCA_P_36d-SCM_P_36d	0.008936781	-0.36479697	0.38267053	1
SDCA_P_36d-SD_P_36d	-0.02199199	-0.39572574	0.35174176	0.9999999
SM_P_36d-SD_P_36d	-0.492623072	-0.86635683	-0.11888932	0.00377
SMCA_P_36d-SD_P_36d	-0.703885822	-1.07761958	-0.33015207	0.0000275
SM_P_36d-SDCA_P_36d	-0.470631082	-0.84436484	-0.09689733	0.0062156
SMCA_P_36d-SDCA_P_36d	-0.681893832	-1.05562759	-0.30816008	0.0000458
SMCA_P_36d-SM_P_36d	-0.21126275	-0.5849965	0.162471	0.6181861