

Supplementary Information

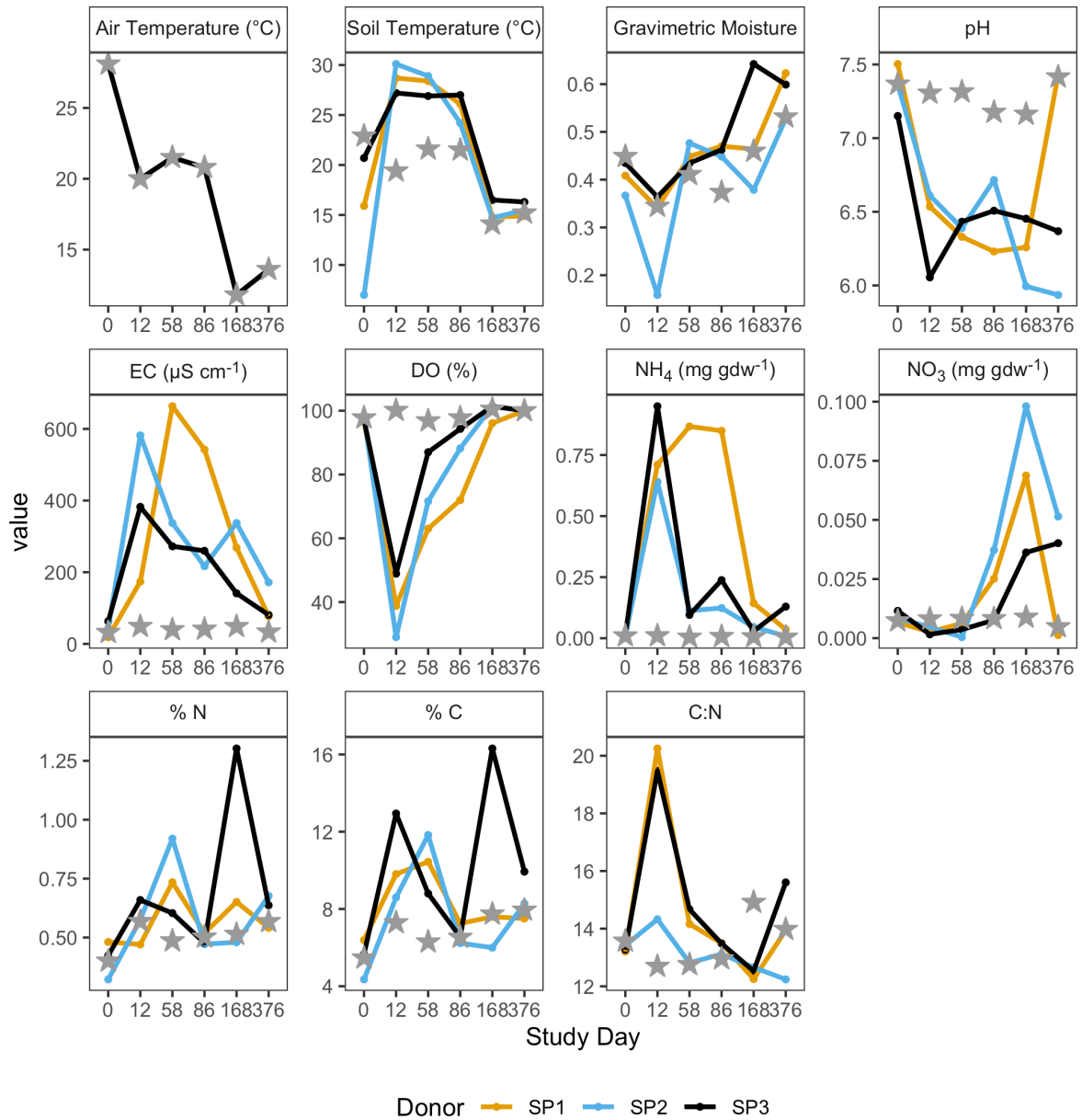


Figure S1. Soil physiochemical parameters in decomposition soils during the one-year study. Data is shown for each individual donor: SP1 (gold), SP2 (blue), and SP2 (black). Values for the full 16 cm core samples were estimated by summing values interface (0-1 cm) and core (0-16 cm) reported by Taylor et al. (2024) in 1:16 and 15:16 ratios, respectively. Controls reported here are means of three experimental controls that were unimpacted by decomposition and are represented by stars.

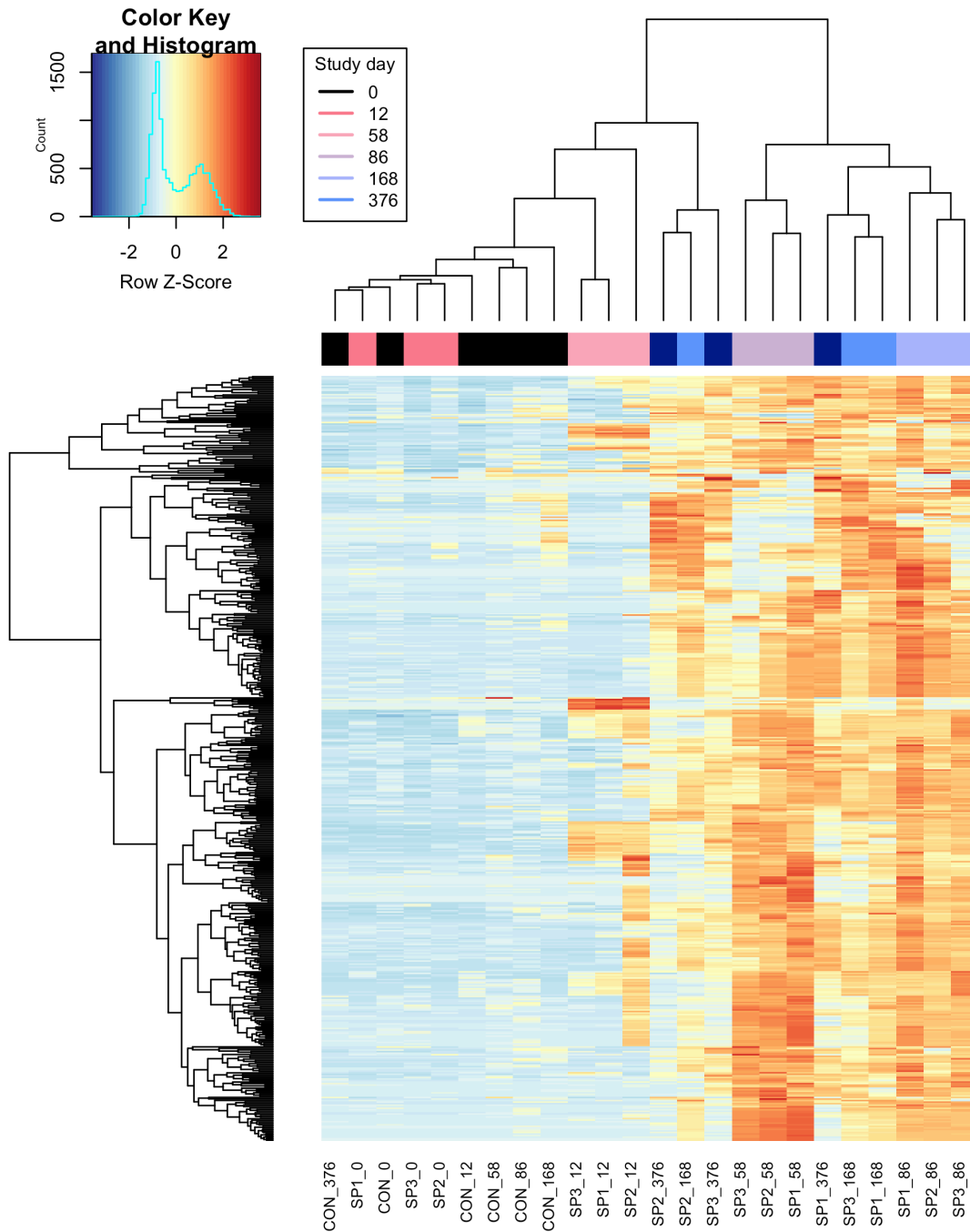


Figure S2. Hierarchical clustering heatmap showing the log counts per million (CPM) of the top 500 most variable genes across samples. Variable genes were determined by selecting genes with the highest variance in gene expression. Samples are clustered along the x-axis using Euclidean distances between samples and colored by study day. Sample names denote

donor (SP1, SP2, SP3) and sample day.

Table S1. Permutational analysis of variance (PERMANOVA) results identifying significant environmental parameters which explain some of the variation in soil gene expression profiles. Environmental parameter data is from Taylor et al. (2024). Variables with $p < 0.05$ are indicated in bold.

	Df	SumOfSqs	MeanSqs	F Value	R ²	Pr(>F)
ADH _A	1	0.287	0.287	3.061	0.082	0.047
ADH_I	1	0.536	0.536	5.712	0.152	0.001
ADH _S	1	0.154	0.154	1.640	0.044	0.158
T _A	1	0.185	0.185	1.970	0.053	0.123
T_S	1	0.258	0.258	2.749	0.073	0.039
GWC	1	0.117	0.117	1.245	0.033	0.285
pH	1	0.258	0.258	2.751	0.073	0.033
EC	1	0.294	0.294	3.139	0.084	0.031
DO	1	0.086	0.086	0.920	0.025	0.483
CO ₂	1	0.131	0.131	1.399	0.037	0.240
NH ₄	1	0.127	0.127	1.352	0.036	0.205
NO ₃	1	0.081	0.081	0.861	0.023	0.479
N %	1	0.101	0.101	1.072	0.029	0.332
C %	1	0.092	0.092	0.980	0.026	0.403
C:N	1	0.059	0.059	0.630	0.017	0.727
Residuals	8	0.751	0.094	NA	0.213	NA
Total	23	3.517	NA	NA	1.000	NA

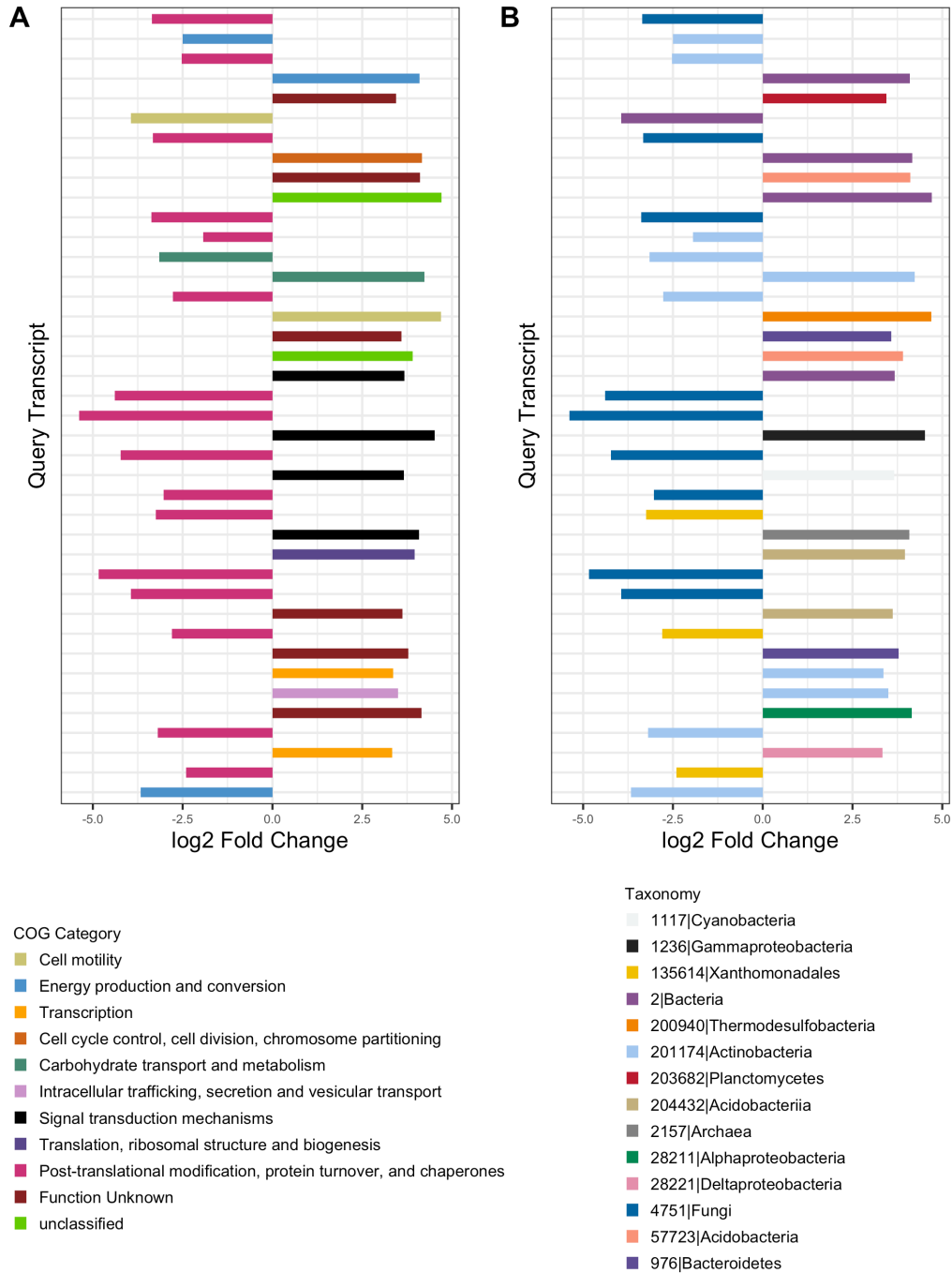


Figure S3. Top 40 up- and down-regulated genes in controls relative to decomposition soils across all study days, colored by COG functional category (A) and taxonomic annotation (B). Positive values denote higher expression in controls, while negative values are higher in decomposition soils.

Table S2. Top 20 most significant up- and down-regulated gene queries, determined by log2 fold change and adjusted p-values, in control relative to decomposition soils. Positive log2 fold change values represent genes whose expression was higher in control soils, while negative log2 fold change values were higher in decomposition soils. Taxonomic annotation, COG categories, gene description, gene names, and EC were assigned via eggNOG-mapper.

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3586165_1	4.699	0	Thermodesulfobacteria	NU	Type II secretion system (T2SS), protein E, N-terminal domain	-	-
k123_5240316_1	3.444	0	Planctomycetes	S	TIGRFAM type VI secretion protein, VC_A0111 family	-	-
k123_4233415_1	4.708	0	Bacteria	-	-	-	-
k123_5247798_1	4.101	0	Bacteria	CO	amine dehydrogenase activity	-	-
k123_1022852_1	3.340	0	Deltaproteobacteria	K	ROS/MUCR transcriptional regulator protein	-	-
k123_4454813_1	4.159	0	Bacteria	D	protein conserved in cyanobacteria	-	-
k123_3793442_4	4.229	0	Actinobacteria	G	pfkB family carbohydrate kinase	kdgK	2.7.1.45
k123_3567914_2	3.910	0	Acidobacteria	-	-	-	-
k123_3575243_1	3.586	0	Bacteroidetes	S	Protein of unknown function (DUF1501)	-	-

(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1456133_1	3.496	0	Actinobacteria	U	TadE-like protein	-	-
k123_1678879_1	3.364	0	Actinobacteria	K	DNA binding	-	-
k123_1448646_1	4.154	0	Alphaproteobacteria	S	Type VI secretion system effector, Hcp	-	-
k123_2582928_1	3.665	0	Cyanobacteria	T	Signal Transduction Histidine Kinase	-	-
k123_4454279_1	4.115	0	Acidobacteria	S	Type VI secretion system effector, Hcp	-	-
k123_2804786_1	4.518	0	Gammaproteobacteria	T	Domain present in phytochromes and cGMP-specific phosphodiesterases.	-	-
k123_1682627_1	3.786	0	Bacteroidetes	S	Protein of unknown function (DUF1800)	-	-
k123_3238410_1	3.678	0	Bacteria	T	phosphoprotein phosphatase activity	-	6.5.1.3

(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_2360350_2	3.954	0	Acidobacteriia	J	One of the early assembly proteins it binds 23S rRNA. One of the proteins that surrounds the polypeptide exit tunnel on the outside of the ribosome. Forms the main docking site for trigger factor binding to the ribosome	rplW	-
k123_244719_2	4.077	0	Archaea	T	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	-	2.7.7.65
k123_1904408_4	3.615	0	Acidobacteriia	S	ASPIC and UnbV	-	-
k123_4681706_1	-3.333	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_2129273_1	-3.939	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_2784358_1	-4.226	0	Fungi	O	Heat shock protein	HSP82	-

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(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_2453574_1	-3.251	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_2580989_1	-3.034	0	Fungi	O	MreB/Mbl protein	SSA2	-
k123_784972_1	-3.361	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-
k123_5131902_2	-3.945	0	Bacteria	N	domain, Protein	-	3.2.1.81,3.2.1.97

(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1897324_1	-2.804	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_1007534_1	-3.669	0	Actinobacteria	C	Ferredoxin	fdxA	-
k123_1119824_1	-3.191	0	Actinobacteria	O	Heat shock 70 kDa protein	dnaK	-
k123_3696373_1	-2.768	0	Actinobacteria	O	Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions	groL2	-
k123_3023451_1	-5.388	0	Fungi	O	Hsp90 protein	HSP82	-

(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1018246_1	-2.400	0	Xanthomonadales	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-
k123_4142344_1	-3.376	0	Fungi	O	Hsp90 protein	HSP82	-
k123_3914888_1	-3.146	0	Actinobacteria	G	Phosphoketolase	-	4.1.2.22,4.1.2.9
k123_3122150_1	-4.387	0	Fungi	O	Heat shock protein	HSP82	-
k123_4027381_1	-1.934	0	Actinobacteria	O	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE	clpB	-

(continued)

Query	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_572232_1	-2.504	0	Actinobacteria	C	4Fe-4S dicluster domain	fadF	-
k123_559972_1	-2.527	0	Actinobacteria	O	Heat shock 70 kDa protein	dnaK	-
k123_2243380_1	-4.837	0	Fungi	O	Belongs to the heat shock protein 70 family	SSA2	-

Table S3. Top 10 most significant up- and down-regulated transcripts, determined by log2 fold change and adjusted p-values, for each sequential timepoint comparison. Positive log2 fold change values represent genes whose expression was higher in the later decomposition timepoint soils, while negative log2 fold change values are higher in earlier decomposition timepoint soils. Taxonomic annotation, COG categories, gene names, and EC were assigned via eggNOG-mapper. The comparison column distinguishes each timepoint comparison.

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3351426_1	0-12	11.410	< 0.001	Clostridia	S	Flavin reductase like domain	-	-
k123_3689959_6	0-12	12.863	< 0.001	Bacilli	GM	NmrA-like family	-	-
k123_1682409_1	0-12	12.514	< 0.001	Bacilli	C	Oxidoreductase required for the transfer of electrons from pyruvate to flavodoxin	nifJ	1.2.7.1
k123_4131385_2	0-12	11.768	< 0.001	Bacilli	M	Domain of unknown function (DUF5011)	-	-
k123_3474748_6	0-12	11.248	< 0.001	Bacilli	E	ABC transporter substrate-binding protein	oppA	-
k123_2018420_1	0-12	11.126	< 0.001	Bacilli	G	PTS fructose transporter subunit IIC	fruA	2.7.1.202
k123_4134106_1	0-12	10.776	< 0.001	Bacilli	C	e3 binding domain	pdhC	2.3.1.12
k123_2451258_1	0-12	12.572	< 0.001	Clostridia	M	S-layer homology domain	-	-
k123_3683359_3	0-12	12.858	< 0.001	Bacilli	P	P-type ATPase	copA	3.6.3.54
k123_2018420_3	0-12	9.998	< 0.001	Bacilli	GKT	Transcriptional antiterminator	manR	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_4030449_2	0-12	-7.201	< 0.001	Gammaproteobacteria	C	PFAM blue (type 1) copper domain protein	-	-
k123_1903136_2	0-12	-6.769	< 0.001	Actinobacteria	Q	Taurine catabolism dioxygenase TauD, TfdA family	-	1.14.11.17
k123_4017556_1	0-12	-6.740	< 0.001	Betaproteobacteria	Q	Taurine dioxygenase	-	1.14.11.17
k123_2470867_1	0-12	-6.354	< 0.001	Actinobacteria	Q	taurine catabolism dioxygenase	tauD	1.14.11.17
k123_2231885_1	0-12	-5.426	< 0.001	Actinobacteria	E	ABC-type branched-chain amino acid transport	-	-
k123_1903136_1	0-12	-5.513	< 0.001	Actinobacteria	K	Bacterial regulatory proteins, tetR family	-	-
k123_3697194_1	0-12	-5.446	< 0.001	Actinobacteria	Q	Taurine catabolism dioxygenase TauD, TfdA family	tauD	1.14.11.17

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_4238273_1	0-12	-6.106	< 0.001	Deltaproteobacteria	S	Part of the outer membrane protein assembly complex, which is involved in assembly and insertion of beta-barrel proteins into the outer membrane	-	-
k123_2680211_1	0-12	-5.155	< 0.001	Proteobacteria	Q	Multicopper oxidase	-	1.16.3.3
k123_4688925_2	0-12	-6.014	< 0.001	Betaproteobacteria	C	D-arabinono-1,4-lactone oxidase	-	-
k123_785677_1	12-58	12.106	< 0.001	Betaproteobacteria	J	One of the primary rRNA binding proteins, it binds directly near the 3'-end of the 23S rRNA, where it nucleates assembly of the 50S subunit	rplC	-
k123_2456034_2	12-58	11.226	< 0.001	Betaproteobacteria	J	Forms part of the polypeptide exit tunnel	rplD	-
k123_3024550_1	12-58	10.815	< 0.001	Betaproteobacteria	J	This is one of the proteins that binds to the 5S RNA in the ribosome where it forms part of the central protuberance	ctc	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1916443_2	12-58	11.317	< 0.001	Betaproteobacteria	J	Binds directly to 23S ribosomal RNA and is necessary for the in vitro assembly process of the 50S ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit	rplT	-
k123_794397_5	12-58	12.046	< 0.001	Betaproteobacteria	J	Ribosomal protein L17	rplQ	-
k123_1010408_1	12-58	11.827	< 0.001	Betaproteobacteria	J	This is 1 of the proteins that binds and probably mediates the attachment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance. In the 70S ribosome it contacts protein S13 of the 30S subunit (bridge B1b), connecting the 2 subunits	rplE	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1115623_7	12-58	10.795	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-
k123_3802697_1	12-58	10.705	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-
k123_5130820_1	12-58	11.586	< 0.001	Betaproteobacteria	JKL	Belongs to the DEAD box helicase family	rhIE1	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_2572977_1	12-58	11.374	< 0.001	Betaproteobacteria	U	The central subunit of the protein translocation channel SecYEG. Consists of two halves formed by TMs 1-5 and 6-10. These two domains form a lateral gate at the front which open onto the bilayer between TMs 2 and 7, and are clamped together by SecE at the back. The channel is closed by both a pore ring composed of hydrophobic SecY residues and a short helix (helix 2A) on the extracellular side of the membrane which forms a plug. The plug probably moves laterally to allow the channel to open. The ring and the pore may move independently	secY	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3351426_1	12-58	-10.845	< 0.001	Clostridia	S	Flavin reductase like domain	-	-
k123_3689959_6	12-58	-12.298	< 0.001	Bacilli	GM	NmrA-like family	-	-
k123_4131385_2	12-58	-11.203	< 0.001	Bacilli	M	Domain of unknown function (DUF5011)	-	-
k123_1682409_1	12-58	-11.434	< 0.001	Bacilli	C	Oxidoreductase required for the transfer of electrons from pyruvate to flavodoxin	nifJ	1.2.7.1
k123_3028891_1	12-58	-10.738	< 0.001	Clostridia	K	PFAM flavin reductase	-	-
k123_2018420_3	12-58	-9.433	< 0.001	Bacilli	GKT	Transcriptional antiterminator	manR	-
k123_3469192_2	12-58	-9.634	< 0.001	Clostridia	T	S-layer homology domain	-	-
k123_3683359_3	12-58	-11.778	< 0.001	Bacilli	P	P-type ATPase	copA	3.6.3.54
k123_335030_2	12-58	-11.417	< 0.001	Bacilli	C	Iron-containing alcohol dehydrogenase	adhB	1.1.1.1,1.1.1.202
k123_3012292_1	12-58	-9.296	< 0.001	Bacilli	S	Putative neutral zinc metalloproteinase	yugP	-
k123_3581297_1	58-86	8.049	< 0.001	Fungi	-	-	-	-
k123_133381_1	58-86	8.362	< 0.001	Betaproteobacteria	C	anaerobic respiration	-	1.7.2.6
k123_3681927_1	58-86	8.474	< 0.001	Betaproteobacteria	C	Cytochrome C oxidase subunit II, periplasmic domain	-	1.9.3.1

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_4461993_6	58-86	10.379	< 0.001	Bacteroidetes	S	Tetratricopeptide repeat protein	-	-
k123_1691746_1	58-86	8.748	< 0.001	Rhodospirillales	C	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient. This subunit may bind ubiquinone	nuoH	1.6.5.3

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_1674520_1	58-86	8.655	< 0.001	Alphaproteobacteria	C	Produces ATP from ADP in the presence of a proton gradient across the membrane. The alpha chain is a regulatory subunit	atpA	3.6.3.14
k123_4907595_1	58-86	8.469	< 0.001	Oceanospirillales	J	Belongs to the universal ribosomal protein uS2 family	rpsB	-
k123_788629_1	58-86	8.018	< 0.001	Bacteroidetes	PT	COGs COG3712 Fe2 -dicitrate sensor membrane component	-	-
k123_784141_1	58-86	6.602	< 0.001	Bacteroidetes	-	-	-	-
k123_2678388_2	58-86	7.966	< 0.001	Betaproteobacteria	C	Subunits I and II form the functional core of the enzyme complex. Electrons originating in cytochrome c are transferred via heme a and Cu(A) to the binuclear center formed by heme a3 and Cu(B)	coxB	1.9.3.1

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_903075_1	58-86	-7.906	< 0.001	Bacteroidetes	-	-	-	-
k123_2460567_2	58-86	-7.060	< 0.001	Bacteroidetes	S	Functions as a peptidoglycan terminase that cleaves nascent peptidoglycan strands endolytically to terminate their elongation	mltG	-
k123_680086_2	58-86	-6.939	< 0.001	Bacteria	-	-	-	-
k123_3353720_2	58-86	-7.036	< 0.001	Bacteroidetes	U	Preprotein translocase SecG subunit	secG	-
k123_4342821_1	58-86	-6.571	< 0.001	Bacteroidetes	CO	Redoxin	-	-
k123_680086_6	58-86	-6.695	< 0.001	Bacteroidetes	G	Sad1 / UNC-like C-terminal	-	-
k123_3687116_4	58-86	-6.677	< 0.001	Bacteroidetes	S	Belongs to the pirin family	yhhW	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_349053_1	58-86	-6.992	< 0.001	Bacteroidetes	F	Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine 5'-phosphate (XMP), the first committed and rate-limiting step in the de novo synthesis of guanine nucleotides, and therefore plays an important role in the regulation of cell growth	guaB	1.1.1.205
k123_2348950_2	58-86	-6.358	< 0.001	Bacteroidetes	O	Heat shock protein	-	-
k123_1004837_2	58-86	-7.162	< 0.001	Bacteroidetes	S	Fimbrillin-like	-	-
k123_465331_1	86-168	6.832	< 0.001	Bacteroidetes	M	Pkd domain containing protein	-	-
k123_1247591_2	86-168	6.662	< 0.001	Xanthomonadales	-	-	-	-
k123_356907_3	86-168	7.008	< 0.001	Actinobacteria	I	Fatty acid desaturase	desA3_2	-
k123_1802620_3	86-168	6.775	< 0.001	Actinobacteria	S	Protein of unknown function (DUF1360)	-	-
k123_4137171_1	86-168	7.254	< 0.001	Actinobacteria	U	WD40-like Beta Propeller Repeat	-	-
k123_1449660_1	86-168	7.112	< 0.001	Actinobacteria	S	LVIVD repeat	-	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_3015796_1	86-168	6.131	< 0.001	Actinobacteria	S	Tetratricopeptide repeat	-	-
k123_4469568_1	86-168	8.516	< 0.001	Gammaproteobacteria	NU	Pilin (bacterial filament)	pilA	-
k123_4013561_1	86-168	6.723	< 0.001	Xanthomonadales	N	Required for morphogenesis and for the elongation of the flagellar filament by facilitating polymerization of the flagellin monomers at the tip of growing filament. Forms a capping structure, which prevents flagellin subunits (transported through the central channel of the flagellum) from leaking out without polymerization at the distal end	fliD	-
k123_4136401_2	86-168	6.097	< 0.001	Actinobacteria	O	FKBP-type peptidyl-prolyl cis-trans isomerase	fkfB	5.2.1.8
k123_2576445_1	86-168	-7.806	< 0.001	Xanthomonadales	M	Belongs to the ompA family	mopB	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_2013370_2	86-168	-7.409	< 0.001	Gammaproteobacteria	S	Protein of unknown function (DUF1471)	-	-
k123_1784040_1	86-168	-7.539	< 0.001	Clostridia	L	PFAM Reverse transcriptase (RNA-dependent DNA polymerase)	-	-
k123_2784492_8	86-168	-7.104	< 0.001	Actinobacteria	Q	Amidohydrolase family	-	-
k123_1671881_1	86-168	-7.712	< 0.001	Bacteroidetes	P	von Willebrand factor, type A	-	-
k123_115662_2	86-168	-8.927	< 0.001	Bacilli	C	succinate dehydrogenase	sdhA	1.3.5.1,1.3.5.4
k123_2013542_1	86-168	-7.286	< 0.001	Betaproteobacteria	S	Domain of unknown function (DUF4148)	-	-
k123_784141_1	86-168	-6.401	< 0.001	Bacteroidetes	-	-	-	-
k123_126934_1	86-168	-8.876	< 0.001	Bacteroidetes	M	Belongs to the membrane fusion protein (MFP) (TC 8.A.1) family	-	-
k123_3912958_2	86-168	-7.098	< 0.001	Bacteroidetes	C	cytochrome c oxidase	ccoG	-
k123_4347668_1	168-376	7.985	< 0.001	Archaea	-	-	-	-
k123_2010423_2	168-376	8.457	< 0.001	Acidobacteria	J	Forms part of the ribosomal stalk, playing a central role in the interaction of the ribosome with GTP-bound translation factors	rplJ	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_4021403_1	168-376	6.597	< 0.001	Acidobacteria	O	Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions	groL	-
k123_2899693_1	168-376	6.546	< 0.001	Acidobacteria	O	Belongs to the ClpA ClpB family	-	-
k123_461276_1	168-376	9.975	< 0.001	Bacteria	N	domain, Protein	-	-
k123_13363_1	168-376	6.773	< 0.001	Acidobacteria	O	Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions	groL	-
k123_3585893_1	168-376	6.944	< 0.001	Acidobacteria	K	DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates	rpoC	2.7.7.6
k123_3020221_1	168-376	7.640	< 0.001	Xanthomonadales	-	-	-	-
k123_4015238_2	168-376	8.717	< 0.001	Acidobacteria	U	MotA TolQ ExbB proton channel	-	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_4017681_1	168-376	8.220	< 0.001	Acidobacteria	J	Binds the lower part of the 30S subunit head. Binds mRNA in the 70S ribosome, positioning it for translation	rpsC	-
k123_465331_1	168-376	-7.066	< 0.001	Bacteroidetes	M	Pkd domain containing protein	-	-
k123_4458935_1	168-376	-7.201	< 0.001	Epsilonproteobacteria	Q	calcium- and calmodulin-responsive adenylate cyclase activity	-	-
k123_5025476_3	168-376	-8.470	< 0.001	Actinobacteria	G	phosphocarrier protein hpr	ptsH	-
k123_1114482_1	168-376	-6.397	< 0.001	Bacteroidetes	MU	Outer membrane efflux protein	-	-
k123_4360823_3	168-376	-6.013	< 0.001	Gammaproteobacteria	IQ	KR domain	-	1.1.1.159
k123_3135574_1	168-376	-7.251	< 0.001	Actinobacteria	K	transcriptional regulator (DeoR family)	fruR	-
k123_3354064_4	168-376	-6.628	< 0.001	Actinobacteria	G	Bacterial extracellular solute-binding protein	-	-
k123_2683111_1	168-376	-6.487	< 0.001	Actinobacteria	G	L-arabinose isomerase	-	5.3.1.4
k123_4463835_2	168-376	-6.188	< 0.001	Actinobacteria	K	DNA-templated transcription, initiation	-	-

(continued)

Query	Comparison	Coefficient	p-Value	Taxonomic Annotation	COG Category	Description	Gene Name	EC
k123_2915236_1	168-376	-7.060	< 0.001	Actinobacteria	M	probably involved in cell wall	-	-

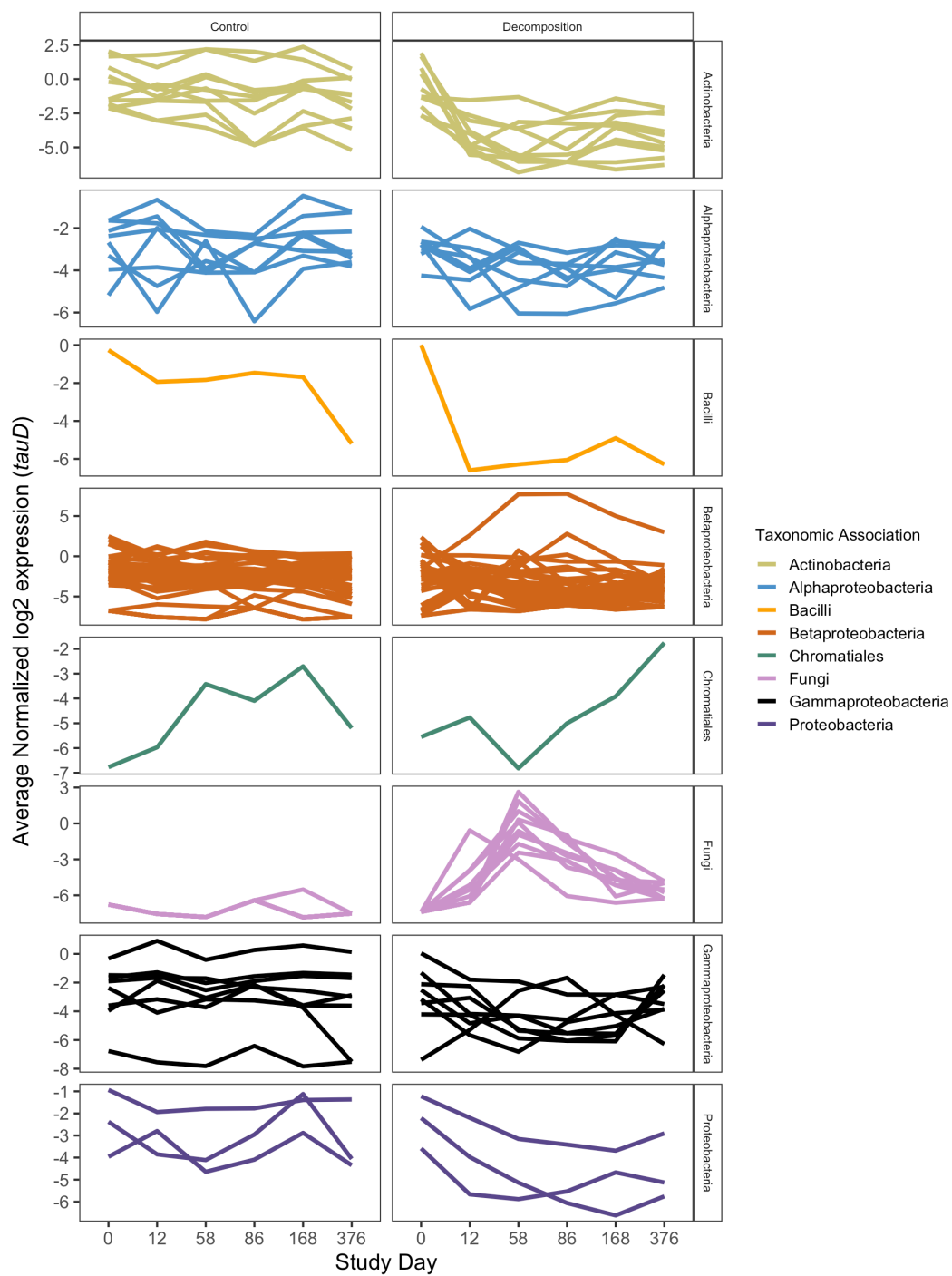


Figure S4. Mean normalized log₂ expression of *tauD* genes by taxonomic association (color) in control and decomposition soils at each study day. Each line represents one *tauD* gene query, while color denotes taxonomic association as determined by eggNOG-mapper.

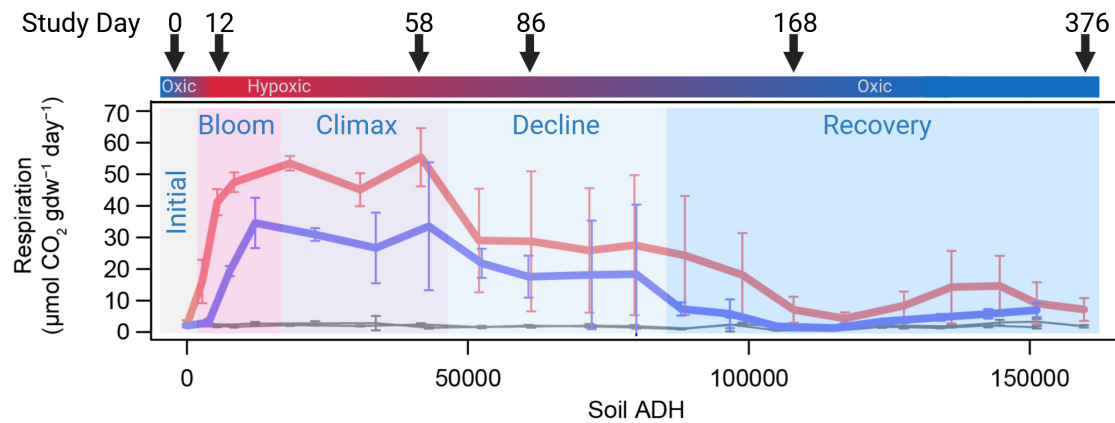


Figure S5. Sampling timepoints chosen for this study based key phases of microbial activity. Lines show respiration reference data from Taylor et al. (2024) for both warm season (red) and cool season (blue) decomposition trials, along with control soils (black) as a function of soil accumulated degree hours (ADH). Oxic/hypoxic status is based on soil oxygen data from Taylor et al. (2024). Samples selected from the warm season trial for the metatranscriptomic analysis in this present study are indicated by black arrows; study day indicates days since decomposition initiated.