Supporting information

**Materials and Methods**

**Site description and experimental design**

This study was carried out in a field site of the Duolun Restoration Ecology Experimentation and Demonstration Station (42°02’N, 116°17’E; 1324 m asl.) located in Inner Mongolia, China. This site is a typical temperate semiarid grassland with a temperate monsoon climate (Chen et al 2014). The mean annual precipitation is about 380 mm and the mean annual temperature is 2.1oC. The soil type is Haplic Calcisol (FAO) sandy loam with 71.9% sand, 15.6% silt and 12.5% clay. The grassland is dominated by a typical steppe vegetationincluding *Stipa krylovii*, *Agropyron cristatum*, *Artemisia frigida*, *Cleistogenes squarrosa* and *Potentilla acaulis.* Average plant heights are 20-40 cm, and plant coverages are 40-60%.

Here, we examine the effects of light-intensity lamb grazing under three conditions, alone or in combination with simulated aeolian soil erosion and deposition in a random block design (Figure S1a). In spring of 2010, five replicates for each of six conditions - no treatment control, soil erosion, soil deposition, lamb grazing, soil erosion plus lamb grazing, soil and deposition plus lamb grazing were set up. Each plot is a 4 m x 4 m square, with a 2.5 m buffer zone in between plots. PVC boards (10 cm aboveground) were placed around each plot to prevent movement of soil between plots. A background value survey showed that soil temperature, moisture, nutrient contents and plant properties were similar across plots at the time of experimental setup.

We conducted light grazing by enclosing a lamb into each grazed plot for 4 hours per month from June to September over a 3- year period from 2010 to 2012, based on current grazing intensity in the Xilinguole grassland. We carried out simulated wind erosion and soil deposition manipulations in early May 2010 and 2011, in consistency with this grassland’s erosion/ deposition patterns because the early growing season was prone to wind erosion when soil is not protected by snow or vegetation cover (Li et al 2004). Simulations were conducted by blowing a 1.5-3.0 cm layer of topsoil from soil eroded plots using a wind fire extinguisher (Taining Machinery Ltd. Co., Taizhou, Jiangsu, CN) (Figure S1c). We used a cloth bag to collect soils blown off from five replicates of eroded sites, evenly blended and divided them into five portions. Collected soils were then evenly distributed over the surfaces of the deposited plots using aseptic techniques. The eroded and deposited soil depths were estimated as modest yearly erosional and depositional intensities in Inner Mongolia grasslands (Zhao et al 2006).

**Sample collection and geochemical analyses**

To manifest the lasting effect of wind erosion and deposition on the grassland ecosystem, we collected soil samples in the middle of August, 2012, when the aboveground biomass was at the peak. At each plot, 4 soil cores of 0-10 cm depth were randomly taken using an auger (5 cm diameter) and mixed to obtain a composite sample. After passing through a 1 mm sieve and removing visible roots and stones, samples were stored on ice during transport to the laboratory. Sub-samples for microbial analysis were stored at -80oC and other sub-samples for geophysical and geochemical analyses were air-dried.

We examined 15 plant and soil variables, including plant species richness, plant coverage, soil temperature, water content, total organic carbon (TOC), total nitrogen (TN), ammonium (NH4+-N), nitrate (NO3--N), pH, dissolved organic carbon (DOC), sand percentage, silt percentage, clay percentage, microbial biomass carbon (MBC) and microbial biomass nitrogen (MBN).

To measure soil particle-size distribution, 1 g of soil was treated with 40% H2O2 before dispersal with sodium hexametaphosphate and sonication. The particle size distribution of soils samples was then determined using a laser particle size analyzer (LS13320, Beckman Coulter, Inc., Brea, CA, USA), which measured volume percent of particles classes from 0.04 to 2000 μm in diameter. Soil texture was assessed from the percentage of clay (<2 μm), silt (2–50 μm), and sand (50–2000 μm) following the taxonomy of the U.S.

Gravimetric soil moisture was measured after oven-drying at 105°C for 12 hrs. Soil temperature at a depth of 10 cm was determined using a thermocouple probe connected to an Automated Soil CO2 Flux System (LI-8100, Li-Cor, Lincoln, NE, USA) when sampling. Dissolved inorganic nitrogen (DIN), NH4+-N and NO3--N were extracted from 10 g of fresh soil with 50 ml of 2 M KCl, and measured with a Discrete Auto Analyzer (SmartChem 200, WestCo Scientific Instruments Inc., Italy). Soil pH was measured using a PB-10 basic pH meter (Sartorius AG, Göttingen, Germany) after mixing soil with water at the 1:2.5 ratio (w/v) and settling for 30 min. Total organic carbon (TOC) and total nitrogen (TN) were measured using a solid combustion method at the temperature of 960 oC in a combustion tube (Yeomans and Bremner 1991) with an elemental analyzer Elementar vario MACRO CUBE (Elementar Co., Hanau, Germany).

Microbial biomass carbon (MBC) and microbial biomass nitrogen (MBN) were measured by a fumigation-extraction method (Brookes et al 1985) with an Elementar vario Total Organic Carbon analyzer (Elementar Co., Hanau, Germany). The differences in extractable carbon and nitrogen contents between fumigated and unfumigated subsamples were calculated using conversion factors of 0.45 and 0.54, respectively. The organic carbon in unfumigated soil extracts was deemed as dissolved organic carbon (DOC).

A 1 m2 frame with 100 equally distributed grids was placed at the center of each plot of the permanent quadrat above the canopy to measure plant species richness and coverage. The plant species richness was the number of plant species identified in the quadrat. Plant coverage was visually estimated in the quadrat.

**Soil DNA preparation**

Genomic DNA of each soil microbial community was extracted from 5 g of soil sample by a freeze-grinding procedure as described previously (Zhou et al 1996). Then crude DNA was purified by phenol extraction and low melting agarose gel electrophoresis. DNA quality was determined by absorbance ratios of A260/280 nm and A260/230 nm using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies Inc., Wilmington, DE, USA). DNA quantity was determined by PicoGreen using a FLUOstar Optima plate reader (BMG Labtech, Jena, Germany).

**Illumina MiSeq sequencing and data processing**

High-throughput sequencing of 16S rRNA gene amplicons with an Illumina MiSeq (Illumina, San Diego, CA, USA) was used for bacterial taxonomy profiling. The V4 region of the 16S rRNA genes was amplified from 10 ng of DNA template with the primer pair 515F and 806R (5’-GTGCCAGCMGCCGCGGTAA-3’ and 5’-GGACTACHVGGGTWTCTAAT-3’). A sequential round of PCR was used to combine Illumina adapter sequences with barcodes to all amplified products. The MiSeq 500-cycles kit was used for 2 x 250 bp paired-end sequencing on a MiSeq instrument.

The raw sequences were processed on the Galaxy platform with a number of software tools. First, the quality of raw sequence data was evaluated with FastQC ([www.bioinformatics.babraham.ac.uk/projects/fastqc/](http://www.bioinformatics.babraham.ac.uk/projects/fastqc/)). Then, demultiplexing was carried out to remove PhiX sequences, and the sequences were sorted to the appropriate samples based on their barcodes, allowing for 1 or 2 mismatches. Quality trimming was performed with Btrim (Kong 2011). The paired-end reads were merged into full length sequences with FLASH (Magoč and Salzberg 2011). Sequences less than 200 bp or containing ambiguous bases were removed and chimeric sequences were discarded based on prediction by Uchime (Edgar et al 2011) using the reference database mode. A total of 880,912 good-quality sequences were acquired, ranging from 17,111 to 40,648 reads per sample. After removing singletons, 23,570 OTUs were generated by Uclust (Edgar 2010) at the 97% identity level from the resampling with 17,111 sequences per sample, with best hits to 474 genera. Taxonomic annotation of individual OTU was assigned according to representative sequences using RDP’s 16S Classifier (Wang et al 2007).

**GeoChip hybridization and data processing**

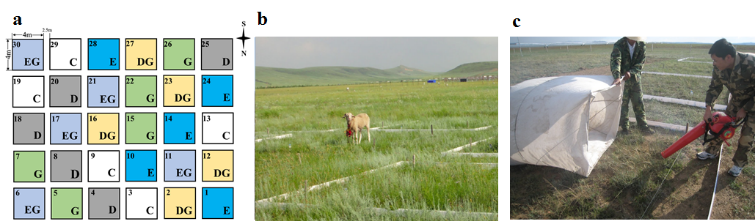
GeoChip 5.0 was used for functional gene profiling and carried out as previously described (Yang et al 2014). Briefly, 0.8 µg of DNA was labeled with Cy-3 dye by random priming and purified with a QIA quick purification kit (Qiagen, Valencia, CA, USA). After drying in a SpeedVac (ThermoSavant, Milford, MA, USA) for 45 min at 45 °C, labeled DNA was rehydrated with 27.5 µl of DI water and then hybridization solution was added. A total of 120 μl of hybridization solution was loaded onto the gasket slide and hybridized for 20-22 hrs at 67°C. GeoChip was imaged by a NimbleGen MS 200 microarray scanner (Roche, Pleasanton, CA, USA) as a Multi-TIFF. The signal intensity of each spot on the microarray was then quantified with the Agilent Feature Extraction program and loaded onto the GeoChip data analysis pipeline ([ieg.ou.edu/microarray/](file:///E:\1.内蒙数据\1风蚀和沉降\my%20paper\Erosion%20and%20deposition_supplemental%20materials_penultimate-jvn-mxy20150417.docx)) and used to indicate relative abundance of functional genes.

Data normalization and analyses of raw data were described previously(Yang et al 2014). The threshold of signal-to-noise ratio [SNR= (signal mean- background intensity) / background standard deviation)] of GeoChip was determined by thermophile probes, serving as negative controls for the grassland environment, in that less than 5% of all thermophile probes were detected. We also removed genes detected in no more than two out of five biological replicates and then logarithmically transformed the values, followed by normalization of the signal intensity of each spot by dividing by total abundance.

**Statistical analyses**

Differences of microbial taxonomic and functional compositions were examined by three dissimilarity tests of MRPP (Multiple response permutation procedure), anosim (analysis of similarities) and adonis (Permutational multivariate analysis of variance) based on the Bray–Curtis distance, using the GeoChip data analysis pipeline ([ieg.ou.edu/](http://ieg.ou.edu/)microarray/). The α-diversity was calculated by Shannon and Simpson indices. All comparisons were performed by LSD (Least significant difference) among different treatments (Bland and Altman 1995). The Principal Coordinate Analysis (PCoA) was used to examine microbial taxonomic and functional compositions, which was performed using functions in the Vegan and Picante package in R (v. 3.1.2.). All above statistical analyses were based on the resampled OTU table and the logarithmically transformed GeoChip data.

Figures and tables



**Figure S1.** (a) Site sketch of experimental sites. C, control; E, soil erosion; D, soil deposition; G, lamb grazing; EG, soil erosion plus lamb grazing; DG, soil deposition plus lamb grazing. (b) Picture of a lamb at the grazed sites. (c) Picture of wind erosion simulation.

**Table S1.** **Summary of soil and plant variable measurements**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Environmental variable | Control | Grazing | Erosion | Erosion  + Grazing | Deposition | Deposition  + Grazing |
| Soil T† (°C) | 18.9(0.8)‡ab§ | 19.2(0.6)ab | 19.7(0.4)a | 19.7(1.0)a | 18.4(0.4)b | 19.3(0.9)ab |
| Water content | 0.05(0.01)a | 0.05(0.01)a | 0.05(0.01)a | 0.05(0.01)a | 0.05(0.01)a | 0.05(0.01)a |
| TOC (%) | 1.58(0.19)a | 1.43(0.18)ab | 1.41(0.07)ab | 1.29(0.16)b | 1.52(0.16)a | 1.55(0.22)a |
| TN (%) | 0.17 (0.02)a | 0.16(0.02)a | 0.16(0.01)a | 0.15(0.02)a | 0.17(0.02)a | 0.18(0.03)a |
| NH4+ (mg/kg) | 6.00(1.45)a | 5.52 (1.37)a | 5.39(1.35)a | 5.04(1.03)a | 7.89(2.40)a | 6.25(2.71)a |
| NO3- (mg/kg) | 4.13(1.26)a | 4.47(0.85)a | 4.34(0.32)a | 4.55(0.74)a | 5.90(2.08)a | 4.42(0.60)a |
| pH | 7.10 (0.20)a | 7.20(0.09)a | 7.13(0.10)a | 7.16(0.27)a | 7.10(0.15)a | 7.17(0.13)a |
| DOC (mg/kg) | 74(7)b | 74(12)b | 65(13)b | 65(4)b | 123(41)a | 87(15)ab |
| Sand (%) | 71.20(3.00)a | 68.80(5.58)a | 72.50(2.19)a | 72.10(4.25)a | 72.00(5.65)a | 67.30(4.10)a |
| Silt (%) | 16.00(1.53)a | 17.60(3.57)a | 15.20(1.19)a | 15.40(2.48)a | 15.50(2.83)a | 18.10(2.67)a |
| Clay (%) | 12.80(1.51)a | 13.60(2.18)a | 12.30(1.06)a | 12.50(1.79)a | 12.50(2.82)a | 14.60(1.53)a |
| PSR | 160(74)a | 153(36)a | 177(38)a | 124(34)a | 129(29)a | 150(43)a |
| PC (%) | 53(17)a | 47(8)ab | 36(6)b | 37(9)b | 58(16)a | 53(10)a |
| MBC (mg/kg) | 227(91)a | 279(109)a | 289(99)a | 243(107)a | 263(103)a | 260(107)a |
| MBN (mg/kg) | 24(14)a | 35(18)a | 36(16)a | 31(17)a | 29(18)a | 30(17)a |

†Abbreviations: T- temperature; TOC -total organic carbon; DOC -dissolved organic carbon; TN-total nitrogen; PSR-Plant species richness; PC-Plant coverage; MBC-microbial biomass carbon; MBN-microbial biomass nitrogen.

‡All data are presented as mean (SD) calculated from five replicates.

§All comparisons were performed by LSD among different treatments and adjusted by Bonferroni method. Significant (*P*<0.05) differences among treatments are indicated by alphabetic letters.

**Table S2.** Diversity indices for microbial community

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Taxonomic diversity** | | **Functional diversity** | |
|  | Shannon Index | Simpson Index | Shannon Index | Simpson Index |
| Control | 7.84 (0.07) † a‡ | 895.42 (148.68) a | 9.71 (0.10) b | 16569.23 (1630.70) b |
| Grazing | 7.79 (0.06) a | 922.06 (85.90) a | 9.91 (0.12) ab | 20252.61 (2274.07) ab |
| Erosion | 7.79 (0.07) a | 850.35 (117.43) a | 9.96 (0.16) a | 21260.99 (3223.41) a |
| Erosion+Grazing | 7.75 (0.09) a | 810.08 (120.06) a | 9.75 (0.10) ab | 17132.91 (1556.02) ab |
| Deposition | 7.81 (0.03) a | 942.03 (76.65) a | 9.88 (0.09) ab | 19611.15 (1745.82) ab |
| Deposition+Grazing | 7.84 (0.07) a | 963.63 (81.92) a | 9.69 (0.11) b | 16192.18 (1777.04) b |

†All data are presented as mean (SD) calculated from 5 biological replicates. ‡Significant (*P*<0.05) differences among treatments are indicated by alphabetic letters above the bars by means of LSD.

**Table S3.** Two-way ANOVA for microbial taxonomic and functional compositions

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | Taxonomic compositions | | Functional compositions | |
|  |  | Shannon Index | Simpson Index | Shannon  Index | Simpson  Index |
| Grazing | F | 1.27 | 0.02 | 0.01 | 0.05 |
| *P* | 0.28 | 0.90 | 0.91 | 0.83 |
| Erosion | F | 1.87 | 2.14 | 0.55 | 0.60 |
| *P* | 0.19 | 0.16 | 0.47 | 0.45 |
| Grazing×Erosion | F | 0.00 | 0.39 | 14.35 | 14.78 |
| *P* | 0.95 | 0.54 | <0.01\*\*† | <0.01\*\* |
| Grazing | F | 0.09 | 0.28 | 0.00 | 0.02 |
| *P* | 0.77 | 0.61 | 0.97 | 0.88 |
| Deposition | F | 0.20 | 0.92 | 0.34 | 0.37 |
| *P* | 0.66 | 0.35 | 0.57 | 0.55 |
| Grazing×Deposition | F | 1.44 | 0.00 | 16.63 | 17.97 |
| *P* | 0.25 | 0.96 | <0.001\*\*\* | <0.001\*\*\* |

†Asterisk indicates significant differences. \*\*\*, *P*<0.001; \*\*, *P*<0.01; \*, *P*<0.05

**Table S4.** The differences of individual functional genes composition between ungrazed and grazed sites under control, eroded and deposited conditions based on the dissimilarity test of Adonis

|  |  |  | **Control** | | **Eroded** | | **Deposited** | |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Carbon cycling** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| amyA | Carbon degradation | Starch | 0.44 | ***0.01*** | 0.40 | ***<0.01*** | 0.39 | ***<0.01*** | 6258.04 |
| chitinase | Carbon degradation | Chitin | 0.44 | ***0.01*** | 0.37 | ***0.02*** | 0.39 | ***<0.01*** | 2119.22 |
| acetylglucosaminidase | Carbon degradation | Chitin | 0.46 | ***0.01*** | 0.38 | ***0.01*** | 0.34 | ***0.01*** | 1421.19 |
| cellobiase | Carbon degradation | Cellulose | 0.43 | ***0.01*** | 0.43 | ***0.01*** | 0.39 | ***<0.01*** | 1360.04 |
| ara | Carbon degradation | Hemicellulose | 0.46 | ***<0.01*** | 0.42 | ***<0.01*** | 0.34 | ***<0.01*** | 1004.22 |
| AceB | Carbon degradation | Glyoxylate cycle | 0.43 | ***0.02*** | 0.39 | ***<0.01*** | 0.42 | ***<0.01*** | 954.04 |
| tktA | Carbon fixation | Calvin cycle | 0.42 | ***0.02*** | 0.38 | ***<0.01*** | 0.39 | ***<0.01*** | 915.81 |
| pcc | Carbon fixation | multiple systems | 0.48 | ***<0.01*** | 0.39 | ***<0.01*** | 0.38 | ***<0.01*** | 906.95 |
| phenol\_oxidase | Carbon degradation | Lignin | 0.45 | ***<0.01*** | 0.38 | ***<0.01*** | 0.38 | ***<0.01*** | 875.07 |
| FTHFS | Carbon fixation | Reductive acetyl–CoA pathway | 0.43 | ***0.02*** | 0.44 | ***<0.01*** | 0.38 | ***<0.01*** | 823.96 |
| endochitinase | Carbon degradation | Chitin | 0.43 | ***0.02*** | 0.42 | ***<0.01*** | 0.37 | ***<0.01*** | 741.67 |
| AceA | Carbon degradation | Glyoxylate cycle | 0.42 | ***0.03*** | 0.38 | ***<0.01*** | 0.39 | ***<0.01*** | 654.26 |
| CsoS1\_CcmK | Carbon fixation | Bacterial Microcompartments | 0.42 | ***0.03*** | 0.37 | ***0.02*** | 0.39 | ***<0.01*** | 652.06 |
| pectate\_lyase | Carbon degradation | Pectin | 0.44 | ***0.01*** | 0.37 | ***<0.01*** | 0.36 | ***<0.01*** | 638.51 |
| cda | Carbon degradation | Starch | 0.40 | ***0.03*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 620.47 |
| GAPDH\_Calvin | Carbon fixation | Calvin cycle | 0.42 | ***0.01*** | 0.41 | ***<0.01*** | 0.36 | ***<0.01*** | 581.60 |
| endoglucanase | Carbon degradation | Cellulose | 0.42 | ***0.02*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 578.21 |
| mannanase | Carbon degradation | Hemicellulose | 0.48 | ***<0.01*** | 0.38 | ***<0.01*** | 0.43 | ***<0.01*** | 566.87 |
| TIM | Carbon fixation | Calvin cycle | 0.42 | ***0.04*** | 0.36 | ***<0.01*** | 0.32 | ***<0.01*** | 534.13 |
| vanA | Carbon degradation | Vanillin/Lignin | 0.46 | ***<0.01*** | 0.39 | ***<0.01*** | 0.36 | ***<0.01*** | 499.56 |
| rubisco | Carbon fixation | Calvin cycle | 0.46 | ***<0.01*** | 0.46 | ***<0.01*** | 0.42 | ***<0.01*** | 491.20 |
| RgaE | Carbon degradation | Pectin | 0.45 | ***0.02*** | 0.39 | ***<0.01*** | 0.35 | ***<0.01*** | 484.55 |
| CODH | Carbon fixation | Reductive acetyl–CoA pathway | 0.44 | ***<0.01*** | 0.48 | ***<0.01*** | 0.37 | ***<0.01*** | 458.07 |
| pulA | Carbon degradation | Starch | 0.46 | ***0.01*** | 0.42 | ***<0.01*** | 0.34 | ***<0.01*** | 438.50 |
| cutinase | Carbon degradation | Cutin | 0.42 | ***0.03*** | 0.43 | ***<0.01*** | 0.33 | ***<0.01*** | 437.82 |
| PRI | Carbon fixation | Calvin cycle | 0.41 | ***0.02*** | 0.44 | ***<0.01*** | 0.38 | ***<0.01*** | 437.34 |
| xylA | Carbon degradation | Hemicellulose | 0.45 | ***<0.01*** | 0.38 | ***<0.01*** | 0.40 | ***<0.01*** | 397.47 |
| FBPase | Carbon fixation | Calvin cycle | 0.43 | ***0.02*** | 0.41 | ***<0.01*** | 0.39 | ***<0.01*** | 390.02 |
| glucoamylase | Carbon degradation | Starch | 0.44 | ***0.02*** | 0.42 | ***<0.01*** | 0.37 | ***0.01*** | 387.40 |
| pme | Carbon degradation | Pectin | 0.37 | ***0.03*** | 0.45 | ***<0.01*** | 0.41 | ***<0.01*** | 384.48 |
| rgl | Carbon degradation | Pectin | 0.42 | ***0.02*** | 0.39 | ***<0.01*** | 0.30 | ***0.02*** | 379.82 |
| ccmL | Carbon fixation | Bacterial Microcompartments | 0.49 | ***0.01*** | 0.44 | ***<0.01*** | 0.37 | ***<0.01*** | 373.97 |
| pgk | Carbon fixation | Calvin cycle | 0.46 | ***0.00*** | 0.42 | ***<0.01*** | 0.39 | ***<0.01*** | 348.75 |
| alginase | Carbon degradation | Alginate | 0.40 | ***0.01*** | 0.49 | ***<0.01*** | 0.42 | ***<0.01*** | 251.06 |
| FBP\_aldolase | Carbon fixation | Calvin cycle | 0.44 | ***0.01*** | 0.37 | ***<0.01*** | 0.34 | ***0.01*** | 215.90 |
| PRK | Carbon fixation | Calvin cycle | 0.50 | ***0.01*** | 0.39 | ***<0.01*** | 0.46 | ***<0.01*** | 208.87 |
| CDH\_2\_carveol\_dehydrogenase | Carbon degradation | Cellulose | 0.39 | ***0.03*** | 0.29 | 0.05 | 0.40 | ***<0.01*** | 189.34 |
| exoglucanase | Carbon degradation | Cellulose | 0.42 | ***<0.01*** | 0.35 | ***0.01*** | 0.37 | ***<0.01*** | 189.05 |
| nplT | Carbon degradation | Starch | 0.36 | ***0.02*** | 0.34 | ***0.03*** | 0.30 | ***<0.01*** | 182.14 |
| mcrA | Methane | Methanogenesis | 0.46 | ***<0.01*** | 0.34 | ***<0.01*** | 0.35 | ***<0.01*** | 168.31 |
| glx | Carbon degradation | Lignin | 0.39 | ***0.02*** | 0.31 | ***0.04*** | 0.38 | ***<0.01*** | 159.77 |
| limEH | Carbon degradation | Terpenes | 0.46 | ***<0.01*** | 0.44 | ***<0.01*** | 0.27 | ***0.01*** | 150.78 |
| xylanase | Carbon degradation | Hemicellulose | 0.39 | ***0.02*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 150.18 |
| vdh | Carbon degradation | Vanillin/Lignin | 0.33 | ***0.03*** | 0.35 | ***<0.01*** | 0.22 | 0.06 | 142.76 |
| rgh | Carbon degradation | Pectin | 0.46 | ***0.02*** | 0.29 | 0.06 | 0.39 | ***<0.01*** | 126.69 |
| pmoA | Methane | Methane oxidation | 0.44 | ***<0.01*** | 0.39 | ***0.01*** | 0.51 | ***<0.01*** | 109.43 |
| exochitinase | Carbon degradation | Chitin | 0.43 | ***0.02*** | 0.38 | ***<0.01*** | 0.25 | 0.05 | 101.90 |
| CsoS2 | Carbon fixation | Bacterial Microcompartments | 0.32 | ***0.04*** | 0.35 | ***<0.01*** | 0.31 | ***0.01*** | 97.70 |
| frdA\_rTCA | Carbon fixation | Reductive tricarboxylic acid cycle | 0.29 | ***0.02*** | 0.39 | ***<0.01*** | 0.29 | ***<0.01*** | 97.06 |
| CDH | Carbon degradation | Terpenes | 0.43 | ***0.01*** | 0.26 | 0.07 | 0.41 | ***<0.01*** | 87.01 |
| AcnA | Carbon fixation | Reductive tricarboxylic acid cycle | 0.44 | ***<0.01*** | 0.35 | ***<0.01*** | 0.43 | ***<0.01*** | 84.13 |
| aclB | Carbon fixation | Reductive tricarboxylic acid cycle | 0.24 | 0.09 | 0.37 | ***<0.01*** | 0.38 | ***<0.01*** | 84.01 |
| beta\_agarase | Carbon degradation | Agar | 0.46 | ***0.01*** | 0.47 | ***<0.01*** | 0.32 | ***0.01*** | 81.68 |
| hyaluronidase | Carbon degradation | hyaluronic acid | 0.30 | ***0.05*** | 0.44 | ***<0.01*** | 0.44 | ***<0.01*** | 75.49 |
| mnp | Carbon degradation | Lignin | 0.42 | ***0.04*** | 0.38 | ***<0.01*** | 0.31 | ***0.04*** | 75.45 |
| pec\_CDeg | Carbon degradation | Pectin | 0.31 | 0.06 | 0.38 | ***<0.01*** | 0.60 | ***<0.01*** | 74.22 |
| CsoSCA | Carbon fixation | Bacterial Microcompartments | 0.32 | 0.05 | 0.36 | ***<0.01*** | 0.23 | 0.09 | 65.56 |
| lip | antiphagocytosis |  | 0.43 | ***0.01*** | 0.39 | ***<0.01*** | 0.39 | ***<0.01*** | 62.94 |
| phospholipase\_D | Carbon degradation | Phospholipids | 0.42 | ***0.02*** | 0.16 | 0.17 | 0.42 | ***<0.01*** | 62.01 |
| protease\_serine | Carbon degradation | protein | 0.37 | ***<0.01*** | 0.38 | ***<0.01*** | 0.23 | ***0.05*** | 61.63 |
| Cyanide\_hydratase | Carbon degradation | Cyanide | 0.47 | ***<0.01*** | 0.38 | ***0.02*** | 0.32 | ***<0.01*** | 61.31 |
| exopolygalacturonase | Carbon degradation | Pectin | 0.28 | ***0.03*** | 0.53 | ***<0.01*** | 0.43 | ***<0.01*** | 59.79 |
| metalloprotease | Carbon degradation | protein | 0.20 | 0.14 | 0.25 | 0.09 | 0.16 | 0.22 | 53.73 |
| pme\_CDeg | Carbon degradation | Pectin | 0.32 | ***0.04*** | 0.39 | ***0.03*** | 0.22 | ***0.04*** | 48.04 |
| PEPC | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.41 | ***0.02*** | 0.24 | 0.09 | 0.32 | ***<0.01*** | 46.29 |
| Heparinase | Carbon degradation | Heparin | 0.26 | ***0.04*** | 0.49 | ***<0.01*** | 0.26 | ***0.02*** | 45.03 |
| phospholipase\_C | Carbon degradation | Phospholipids | 0.40 | ***0.03*** | 0.44 | ***<0.01*** | 0.52 | ***<0.01*** | 44.00 |
| oorA | Carbon fixation | Reductive tricarboxylic acid cycle | 0.33 | ***0.04*** | 0.31 | 0.05 | 0.42 | ***<0.01*** | 39.01 |
| sucD | Carbon fixation | Reductive tricarboxylic acid cycle | 0.38 | ***0.01*** | 0.68 | ***<0.01*** | 0.26 | ***0.03*** | 38.87 |
| mmoX | Methane | Methane oxidation | 0.22 | 0.10 | 0.39 | ***<0.01*** | 0.26 | ***0.02*** | 38.22 |
| AACT\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.56 | ***0.01*** | 0.55 | ***<0.01*** | 0.47 | ***<0.01*** | 37.70 |
| pectinase | Carbon degradation | Pectin | 0.46 | ***<0.01*** | 0.39 | ***0.02*** | 0.43 | ***<0.01*** | 36.12 |
| ccmM | Carbon fixation | Bacterial Microcompartments | 0.44 | ***<0.01*** | 0.45 | ***<0.01*** | 0.34 | ***<0.01*** | 33.33 |
| mdh | Carbon fixation | Reductive tricarboxylic acid cycle | 0.32 | ***0.03*** | 0.37 | ***0.03*** | 0.31 | ***0.03*** | 31.83 |
| phospholipase\_A2 | Carbon degradation | Phospholipids | 0.30 | ***0.02*** | 0.37 | ***0.02*** | 0.31 | ***0.03*** | 30.84 |
| lactase | Carbon degradation | Lactose | 0.42 | ***0.01*** | 0.30 | ***0.01*** | 0.31 | ***0.01*** | 30.52 |
| fumarase\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.27 | ***0.04*** | 0.45 | ***<0.01*** | 0.43 | ***<0.01*** | 30.21 |
| por\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.40 | ***0.01*** | 0.46 | ***<0.01*** | 0.38 | ***<0.01*** | 29.48 |
| protease\_aspartate | Carbon degradation | protein | 0.47 | ***0.02*** | 0.56 | ***<0.01*** | 0.27 | 0.06 | 29.19 |
| inulinase | Carbon degradation | Inulin | 0.39 | ***0.04*** | 0.47 | ***0.01*** | 0.55 | ***<0.01*** | 28.76 |
| Pg\_Oomycetes | Carbon degradation | Pectin | 0.20 | 0.10 | 0.34 | ***0.03*** | 0.21 | 0.10 | 28.12 |
| MCM | Carbon fixation | 3-hydroxypropionate bicycle | 0.28 | 0.07 | 0.51 | ***0.01*** | 0.35 | ***0.02*** | 27.56 |
| alpha\_galactosidase | Carbon degradation | Other | 0.59 | ***0.01*** | 0.26 | 0.08 | 0.29 | ***0.01*** | 27.55 |
| endopolygalacturonase | Carbon degradation | Pectin | 0.43 | ***0.01*** | 0.50 | ***0.01*** | 0.34 | ***0.01*** | 26.13 |
| hdrB | Methane | Methanogenesis | 0.46 | ***0.01*** | 0.67 | ***<0.01*** | 0.37 | ***0.02*** | 24.53 |
| camDCBA | Carbon degradation | Camphor | 0.45 | ***0.01*** | 0.40 | ***0.01*** | 0.34 | ***0.02*** | 24.39 |
| pel\_CDeg | Carbon degradation | Pectin | 0.33 | 0.06 | 0.23 | 0.11 | 0.28 | 0.06 | 22.67 |
| LMO | Carbon degradation | Terpenes | 0.41 | ***0.01*** | 0.16 | 0.24 | 0.28 | ***0.02*** | 20.44 |
| pectin\_lyase\_Oomycetes | Carbon degradation | Pectin | 0.34 | ***0.04*** | 0.61 | ***<0.01*** | 0.43 | ***<0.01*** | 20.33 |
| PEP\_synthase | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.48 | ***0.01*** | 0.57 | ***<0.01*** | 0.15 | 0.31 | 19.72 |
| ccmN | Carbon fixation | Bacterial Microcompartments | 0.38 | ***0.03*** | 0.60 | ***<0.01*** | 0.64 | ***<0.01*** | 18.62 |
| C\_CoA\_hydratase\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.23 | 0.12 | 0.27 | 0.07 | 0.34 | ***0.02*** | 18.46 |
| pectate\_lyase\_Oomycetes | Carbon degradation | Pectin | 0.42 | ***0.01*** | 0.53 | ***<0.01*** | 0.08 | 0.42 | 17.81 |
| AssA | Other Hydrocarbons |  | 0.33 | ***0.03*** | 0.30 | 0.05 | 0.25 | 0.11 | 17.30 |
| frdA | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.19 | 0.15 | 0.28 | 0.09 | 0.50 | ***0.03*** | 14.39 |
| Glucose\_oxidase | Carbon degradation | glucose | 0.21 | 0.20 | 0.27 | 0.15 | 0.40 | ***0.03*** | 13.64 |
| mdh\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.51 | ***<0.01*** | 0.17 | 0.20 | 0.25 | 0.12 | 12.78 |
| IcfA | Carbon fixation | Bacterial Microcompartments | 0.37 | ***0.02*** | 0.38 | ***0.01*** | 0.45 | ***<0.01*** | 12.29 |
| Ligninase | Carbon degradation | Lignin | 0.17 | 0.19 | 0.45 | ***0.00*** | 0.30 | ***0.04*** | 11.31 |
| pcc\_3HP | Carbon fixation | 3-hydroxypropionate bicycle | 0.55 | ***0.03*** | 0.48 | ***0.03*** | 0.18 | 0.11 | 10.50 |
| ccl | Carbon fixation | Reductive tricarboxylic acid cycle | 0.57 | ***0.02*** | 0.30 | ***0.04*** | 0.28 | ***0.05*** | 10.32 |
| Sulfhydryl\_oxidase | Carbon degradation | Other | 0.45 | ***0.01*** | 0.36 | ***<0.01*** | 0.20 | 0.31 | 10.29 |
| suc\_CoA\_red\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.49 | ***0.04*** | 0.12 | 0.46 | 0.53 | ***0.01*** | 9.79 |
| chitin\_deacetylase | Carbon degradation | Chitin | 0.20 | 0.12 | 0.08 | 0.50 | 0.00 | 1.00 | 9.48 |
| isopullulanase | Carbon degradation | Starch | 0.28 | ***0.03*** | 0.26 | 0.06 | 0.05 | 0.56 | 8.79 |
| apu | Carbon degradation | Starch | 0.24 | ***0.04*** | 0.21 | 0.12 | 0.04 | 0.73 | 8.50 |
| sucA\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.35 | ***0.01*** | 0.50 | ***0.03*** | 0.66 | ***<0.01*** | 8.26 |
| adhC | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.43 | ***<0.01*** | 0.23 | 0.08 | 0.09 | 0.43 | 7.79 |
| invertase | Carbon degradation | sucrose | 0.41 | ***0.03*** | 0.20 | 0.15 | 0.00 | 1.00 | 7.49 |
| icd | Carbon fixation | Reductive tricarboxylic acid cycle | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 7.15 |
| amyX | Carbon degradation | Starch | 0.00 | 1.00 | 0.10 | 0.47 | 0.00 | 1.00 | 7.11 |
| MMCE\_3HP4HB | Carbon fixation | 3-hydroxypropionate/4-hydroxybutyrate cycle | 0.09 | 0.61 | 0.00 | 1.00 | 0.08 | 0.53 | 7.00 |
| mct | Carbon fixation | 3-hydroxypropionate bicycle | 0.00 | 1.00 | 0.00 | 0.88 | 0.27 | ***<0.01*** | 6.81 |
| fumarase\_3HP4HB | Carbon fixation | 3-hydroxypropionate/4-hydroxybutyrate cycle | 0.00 | 1.00 | 0.00 | 1.00 | 0.20 | ***0.05*** | 6.10 |
| mcr | Carbon fixation | 3-hydroxypropionate bicycle | NA† | NA | 0.00 | 1.00 | 0.00 | 1.00 | 5.55 |
| 4HBCD | Carbon fixation | 3-hydroxypropionate/4-hydroxybutyrate cycle | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.54 |
| lipase | Carbon degradation | Lipids | 0.51 | ***0.03*** | 0.38 | ***0.01*** | 0.12 | 0.22 | 5.53 |
| MCM\_3HP4HB | Carbon fixation | 3-hydroxypropionate/4-hydroxybutyrate cycle | 0.60 | ***0.02*** | 0.41 | 0.06 | 0.65 | ***<0.01*** | 5.37 |
| accD | Carbon fixation | 3-hydroxypropionate bicycle | 0.39 | 0.07 | 0.00 | 1.00 | 0.39 | 0.06 | 4.95 |
| 4HBCD\_DiC4HB | Carbon fixation | Dicarboxylate/4-hydroxybutyrate cycle | 0.39 | 0.06 | 0.38 | 0.08 | 0.40 | 0.05 | 4.95 |
| pcs | Carbon fixation | 3-hydroxypropionate bicycle | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.76 |
| MMCE | Carbon fixation | 3-hydroxypropionate bicycle | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.70 |
| dextranase | Carbon degradation | sucrose | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.22 |
| mcl | Carbon fixation | 3-hydroxypropionate bicycle | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.08 |
| chitinase\_Oomycetes | Carbon degradation | Chitin | NA | NA | 0.00 | 1.00 | NA | NA | 3.78 |
| **Nitrogen** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| narG | Denitrification |  | 0.39 | ***0.03*** | 0.44 | ***<0.01*** | 0.38 | ***<0.01*** | 1593.24 |
| nifH | Nitrogen fixation |  | 0.46 | ***<0.01*** | 0.41 | ***<0.01*** | 0.36 | ***<0.01*** | 1359.99 |
| ureC | Ammonification |  | 0.42 | ***0.02*** | 0.42 | ***<0.01*** | 0.37 | ***<0.01*** | 1218.54 |
| amoA | Nitrification |  | 0.42 | ***0.02*** | 0.42 | ***<0.01*** | 0.40 | ***<0.01*** | 955.76 |
| AOA | Nitrification |  | 0.43 | ***0.03*** | 0.47 | ***0.01*** | 0.43 | ***0.01*** | 172.26 |
| AOB | Nitrification |  | 0.41 | ***0.03*** | 0.41 | ***0.01*** | 0.39 | ***0.01*** | 783.50 |
| nosZ | Denitrification |  | 0.42 | ***0.02*** | 0.45 | ***<0.01*** | 0.39 | ***<0.01*** | 647.64 |
| nirS | Denitrification |  | 0.45 | ***<0.01*** | 0.45 | ***<0.01*** | 0.37 | ***0.01*** | 588.35 |
| gdh | Ammonification |  | 0.36 | ***0.03*** | 0.47 | ***<0.01*** | 0.34 | ***<0.01*** | 411.31 |
| nrfA | Dissimilatory N reduction |  | 0.45 | ***0.01*** | 0.32 | ***0.01*** | 0.37 | ***<0.01*** | 342.91 |
| napA | Dissimilatory N reduction |  | 0.42 | ***<0.01*** | 0.39 | ***0.01*** | 0.38 | ***<0.01*** | 208.24 |
| nasA | Assimilatory N reduction |  | 0.45 | ***<0.01*** | 0.50 | ***<0.01*** | 0.36 | ***<0.01*** | 200.07 |
| nirB | Assimilatory N reduction |  | 0.38 | ***0.01*** | 0.48 | ***<0.01*** | 0.36 | ***<0.01*** | 181.60 |
| norB | Denitrification |  | 0.47 | ***<0.01*** | 0.45 | ***<0.01*** | 0.39 | ***<0.01*** | 148.78 |
| NiR | Assimilatory N reduction |  | 0.36 | ***0.03*** | 0.39 | ***<0.01*** | 0.33 | ***0.01*** | 139.82 |
| nirA | Assimilatory N reduction |  | 0.46 | ***0.01*** | 0.46 | ***<0.01*** | 0.42 | ***0.01*** | 114.46 |
| hao | Nitrification |  | 0.47 | ***<0.01*** | 0.45 | ***0.01*** | 0.40 | ***<0.01*** | 50.47 |
| hzo | Anammox |  | 0.44 | ***<0.01*** | 0.40 | ***<0.01*** | 0.20 | ***0.05*** | 20.29 |
| nirK | Denitrification |  | 0.52 | ***0.01*** | 0.41 | ***<0.01*** | 0.43 | ***<0.01*** | 10.07 |
| **Sulphur** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| dsrA | sulfite reduction |  | 0.43 | ***0.02*** | 0.42 | ***<0.01*** | 0.37 | ***<0.01*** | 1055.64 |
| dsrB | sulfite reduction |  | 0.44 | ***<0.01*** | 0.43 | ***<0.01*** | 0.44 | ***<0.01*** | 638.44 |
| sox | Sulfur Oxidation |  | 0.46 | ***0.01*** | 0.40 | ***<0.01*** | 0.35 | ***<0.01*** | 506.65 |
| CysJ | Reduction |  | 0.40 | ***0.03*** | 0.43 | ***<0.01*** | 0.32 | ***<0.01*** | 504.29 |
| sir | sulfite reduction |  | 0.45 | ***<0.01*** | 0.42 | ***<0.01*** | 0.35 | ***<0.01*** | 286.59 |
| fccAB | Sulfide Oxidation |  | 0.42 | ***0.02*** | 0.38 | ***<0.01*** | 0.37 | ***<0.01*** | 202.26 |
| APS\_AprA | adenylylsulfate reductase |  | 0.45 | ***<0.01*** | 0.39 | ***<0.01*** | 0.31 | ***0.01*** | 183.44 |
| sqr | Sulfide Oxidation |  | 0.46 | ***<0.01*** | 0.49 | ***<0.01*** | 0.34 | ***<0.01*** | 173.80 |
| soxY | Sulfur Oxidation |  | 0.49 | ***<0.01*** | 0.41 | ***<0.01*** | 0.46 | ***<0.01*** | 158.41 |
| soxC | Sulphur oxidation |  | 0.38 | ***0.03*** | 0.38 | ***<0.01*** | 0.46 | ***<0.01*** | 140.30 |
| dmdA | DMSP degradation |  | 0.49 | ***0.01*** | 0.45 | ***<0.01*** | 0.40 | ***<0.01*** | 131.34 |
| AprA | adenylylsulfate reductase |  | 0.33 | ***0.03*** | 0.45 | ***<0.01*** | 0.43 | ***<0.01*** | 119.02 |
| soxB | Sulphur oxidation |  | 0.46 | ***0.03*** | 0.49 | ***<0.01*** | 0.37 | ***0.02*** | 115.57 |
| CysI | Other |  | 0.53 | ***0.01*** | 0.56 | ***<0.01*** | 0.39 | ***<0.01*** | 104.46 |
| soxA | Sulphur oxidation |  | 0.35 | ***0.04*** | 0.58 | ***<0.01*** | 0.36 | ***<0.01*** | 87.70 |
| APS\_AprB | adenylylsulfate reductase |  | 0.43 | ***<0.01*** | 0.34 | ***<0.01*** | 0.31 | ***<0.01*** | 87.60 |
| soxV | Sulphur oxidation |  | 0.34 | ***0.02*** | 0.39 | ***0.02*** | 0.47 | ***<0.01*** | 68.04 |
| **Phosphorus** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| ppx | Polyphosphate degradation |  | 0.42 | ***0.01*** | 0.44 | ***<0.01*** | 0.33 | ***<0.01*** | 2226.72 |
| ppk | Polyphosphate synthesis |  | 0.41 | ***0.01*** | 0.39 | ***<0.01*** | 0.38 | ***<0.01*** | 648.80 |
| phytase | Phytic acid hydrolysis |  | 0.43 | ***0.02*** | 0.35 | ***0.02*** | 0.36 | ***<0.01*** | 348.55 |
| **Stress** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| sigma\_24 | sigma factor |  | 0.47 | ***<0.01*** | 0.41 | ***<0.01*** | 0.38 | ***<0.01*** | 864.28 |
| pstB | Phosphate limitation |  | 0.44 | ***0.01*** | 0.41 | ***<0.01*** | 0.40 | ***<0.01*** | 785.96 |
| fnr | Oxygen limitation |  | 0.39 | ***0.01*** | 0.45 | ***<0.01*** | 0.41 | ***<0.01*** | 579.08 |
| obgE | Stringent response |  | 0.43 | ***<0.01*** | 0.44 | ***<0.01*** | 0.36 | ***<0.01*** | 480.48 |
| sigma\_70 | sigma factor |  | 0.47 | ***<0.01*** | 0.44 | ***<0.01*** | 0.42 | ***<0.01*** | 451.23 |
| glnA | Nitrogen limitation |  | 0.52 | ***0.01*** | 0.44 | ***<0.01*** | 0.45 | ***<0.01*** | 413.46 |
| katE | Heat shock |  | 0.44 | ***0.01*** | 0.40 | ***<0.01*** | 0.43 | ***<0.01*** | 374.30 |
| hrcA | Heat shock |  | 0.40 | ***0.03*** | 0.44 | ***<0.01*** | 0.36 | ***<0.01*** | 287.89 |
| pstC | Phosphate limitation |  | 0.41 | ***0.02*** | 0.44 | ***<0.01*** | 0.48 | ***<0.01*** | 257.71 |
| ahpC | Oxidative stress |  | 0.57 | ***<0.01*** | 0.46 | ***<0.01*** | 0.41 | ***<0.01*** | 240.24 |
| pstA | Phosphate limitation |  | 0.46 | ***<0.01*** | 0.47 | ***<0.01*** | 0.33 | ***0.01*** | 223.75 |
| phoB | Phosphate limitation |  | 0.51 | ***<0.01*** | 0.45 | ***<0.01*** | 0.34 | ***<0.01*** | 188.72 |
| oxyR | Oxidative stress |  | 0.41 | ***<0.01*** | 0.45 | ***<0.01*** | 0.39 | ***<0.01*** | 170.60 |
| grpE | Heat shock |  | 0.48 | ***0.01*** | 0.39 | ***<0.01*** | 0.51 | ***<0.01*** | 167.95 |
| sigma\_32 | sigma factor |  | 0.40 | ***0.01*** | 0.54 | ***<0.01*** | 0.38 | ***<0.01*** | 159.53 |
| narI | Oxygen limitation |  | 0.45 | ***<0.01*** | 0.45 | ***<0.01*** | 0.54 | ***<0.01*** | 148.06 |
| clpC | Protein stress |  | 0.43 | ***0.01*** | 0.55 | ***<0.01*** | 0.48 | ***<0.01*** | 125.69 |
| proV | Osmotic stress |  | 0.50 | ***<0.01*** | 0.44 | ***<0.01*** | 0.43 | ***<0.01*** | 124.71 |
| ahpF | Oxidative stress |  | 0.33 | ***0.03*** | 0.38 | ***0.01*** | 0.33 | ***<0.01*** | 105.42 |
| pstS | Phosphate limitation |  | 0.34 | ***0.02*** | 0.31 | ***0.04*** | 0.38 | ***<0.01*** | 99.05 |
| sigma\_38 | sigma factor |  | 0.40 | ***<0.01*** | 0.39 | ***0.01*** | 0.35 | ***<0.01*** | 89.97 |
| dnaK | Heat shock |  | 0.42 | ***0.01*** | 0.43 | ***<0.01*** | 0.36 | ***0.01*** | 74.37 |
| narH | Oxygen limitation |  | 0.33 | ***0.02*** | 0.48 | ***<0.01*** | 0.39 | ***<0.01*** | 68.64 |
| phoA | Phosphate limitation |  | 0.54 | ***<0.01*** | 0.34 | ***0.01*** | 0.43 | ***<0.01*** | 67.11 |
| groEL | Heat shock |  | 0.48 | ***0.01*** | 0.19 | 0.16 | 0.45 | ***<0.01*** | 46.05 |
| cydB | Oxygen limitation |  | 0.45 | ***<0.01*** | 0.58 | ***<0.01*** | 0.37 | ***<0.01*** | 44.29 |
| ctsR | Protein stress |  | 0.52 | ***0.01*** | 0.35 | ***0.05*** | 0.54 | ***<0.01*** | 35.25 |
| narJ | Oxygen limitation |  | 0.53 | ***0.02*** | 0.42 | ***0.01*** | 0.38 | ***0.01*** | 32.34 |
| glnR | Nitrogen limitation |  | 0.40 | ***<0.01*** | 0.35 | ***0.01*** | 0.24 | 0.10 | 30.00 |
| katA | Oxidative stress |  | 0.35 | ***<0.01*** | 0.27 | 0.08 | 0.21 | 0.09 | 28.90 |
| cydA | Oxygen limitation |  | 0.58 | ***<0.01*** | 0.63 | ***<0.01*** | 0.28 | ***0.04*** | 28.30 |
| cspB | Cold shock |  | 0.17 | 0.23 | 0.32 | ***0.03*** | 0.19 | 0.19 | 16.19 |
| bglP | Glucose limitation |  | 0.56 | ***<0.01*** | 0.02 | 0.73 | 0.21 | ***0.01*** | 16.14 |
| bglH | Glucose limitation |  | 0.23 | 0.08 | 0.40 | 0.06 | 0.30 | 0.08 | 16.02 |
| arcB | Oxygen limitation |  | 0.13 | 0.38 | 0.50 | ***0.02*** | 0.21 | 0.18 | 15.93 |
| proX | Osmotic stress |  | 0.20 | 0.09 | 0.36 | ***<0.01*** | 0.56 | ***<0.01*** | 15.16 |
| cspA | Cold shock |  | 0.21 | 0.09 | 0.33 | ***0.05*** | 0.13 | 0.43 | 13.37 |
| opuE | Osmotic stress |  | 0.49 | ***0.02*** | 0.19 | 0.16 | 0.96 | ***<0.01*** | 10.86 |
| arcA | Oxygen limitation |  | 0.13 | 0.49 | 0.11 | 0.50 | 0.52 | ***0.01*** | 8.77 |
| proW | Osmotic stress |  | 0.11 | 0.18 | 0.14 | ***0.04*** | 0.23 | ***0.03*** | 7.47 |
| GroES | Heat shock |  | 0.23 | 0.07 | 0.36 | ***0.03*** | 0.00 | 1.00 | 5.66 |
| tnrA | Nitrogen limitation |  | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 5.35 |
| desR | Cold shock |  | 0.00 | 1.00 | NA | NA | NA | NA | 4.70 |
| perR | Oxidative stress |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 4.24 |
| **Antibiotic resistance** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| SMR\_antibiotics | Antibiotic resistance | transporter | 0.49 | ***<0.01*** | 0.41 | ***<0.01*** | 0.43 | ***<0.01*** | 374.75 |
| MFS\_antibiotic | Antibiotic resistance | transporter | 0.39 | ***0.02*** | 0.47 | ***<0.01*** | 0.35 | ***<0.01*** | 257.56 |
| B\_lactamase\_C | Antibiotic resistance | Degradation | 0.46 | ***0.02*** | 0.50 | ***<0.01*** | 0.45 | ***<0.01*** | 233.58 |
| Tet | Antibiotic resistance | transporter | 0.35 | ***0.02*** | 0.30 | 0.05 | 0.41 | ***<0.01*** | 144.08 |
| B\_lactamase\_A | Antibiotic resistance | Degradation | 0.43 | ***<0.01*** | 0.47 | ***<0.01*** | 0.34 | ***<0.01*** | 119.61 |
| ABC\_antibiotic\_transporter | Antibiotic resistance | transporter | 0.36 | ***0.03*** | 0.37 | ***<0.01*** | 0.20 | 0.12 | 71.88 |
| MATE\_antibiotic | Antibiotic resistance | transporter | 0.30 | ***0.04*** | 0.34 | ***0.01*** | 0.37 | ***<0.01*** | 63.34 |
| Mex | Antibiotic resistance | transporter | 0.42 | ***<0.01*** | 0.40 | ***0.01*** | 0.35 | ***<0.01*** | 37.97 |
| B\_lactamase | Antibiotic resistance | Degradation | 0.59 | ***<0.01*** | 0.55 | ***<0.01*** | 0.22 | 0.17 | 16.89 |
| Van | Antibiotic resistance | subunit modification | 0.23 | 0.22 | 0.42 | ***0.03*** | 0.45 | ***0.02*** | 8.57 |
| B\_lactamase\_B | Antibiotic resistance | Degradation | 0.11 | 0.30 | 0.08 | 0.53 | 0.17 | 0.13 | 7.97 |
| **Bacteria phage** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| RNA\_dependent\_\_RNA\_polymerase | Prokaryotic | REPLICATION | 0.42 | ***0.02*** | 0.43 | ***0.01*** | 0.30 | ***0.02*** | 26.92 |
| DNA\_polymerase\_type\_I | Prokaryotic | REPLICATION | 0.21 | 0.21 | 0.33 | 0.06 | 0.44 | ***<0.01*** | 22.67 |
| helicase\_P4alpha\_type | Prokaryotic | REPLICATION | 0.28 | 0.08 | 0.26 | 0.19 | 0.20 | 0.23 | 19.87 |
| helicase\_family\_4 | Prokaryotic | REPLICATION | 0.46 | ***<0.01*** | 0.56 | ***0.01*** | 0.45 | ***0.03*** | 10.95 |
| major\_capsid\_protein | Prokaryotic | STRUCTURAL | 0.45 | ***0.02*** | -0.02 | 0.90 | 0.20 | 0.31 | 10.92 |
| helicase\_family\_4\_DnaB\_like | Prokaryotic | REPLICATION | 0.57 | ***0.02*** | -0.01 | 0.71 | 0.05 | 0.56 | 10.81 |
| integrase\_tyrosine | Prokaryotic | REPLICATION | 0.07 | 0.48 | 0.42 | ***0.04*** | 0.13 | 0.57 | 10.77 |
| contractile\_tail\_sheath\_protein | Prokaryotic | STRUCTURAL | 0.15 | 0.29 | 0.27 | ***0.04*** | 0.17 | 0.20 | 10.57 |
| terminase\_large\_subunit | Prokaryotic | REPLICATION | 0.38 | ***0.03*** | 0.59 | ***0.04*** | 0.27 | 0.14 | 9.08 |
| T4\_recomb\_endonuclease | Prokaryotic | REPLICATION | 0.06 | 0.62 | 0.19 | 0.10 | 0.06 | 0.36 | 8.82 |
| primase | Prokaryotic | REPLICATION | 0.43 | ***0.05*** | 0.13 | 0.50 | 0.26 | ***0.02*** | 8.78 |
| lysin | Prokaryotic | LYSIS | 0.65 | ***0.00*** | 0.56 | ***0.01*** | 0.14 | 0.40 | 8.29 |
| Host\_recognition\_T4\_type | Prokaryotic | HOST RECOGNITION/STRUCTURAL | 0.26 | 0.16 | 0.47 | ***<0.01*** | 0.17 | 0.18 | 8.09 |
| endolysin\_transglycosylase | Prokaryotic | LYSIS | 0.20 | 0.06 | 0.00 | 1.00 | 0.00 | 1.00 | 6.83 |
| holin\_type1 | Prokaryotic | LYSIS | 0.07 | 0.37 | 0.31 | ***<0.01*** | 0.49 | ***0.02*** | 6.78 |
| single\_strand\_annealing\_protein | Prokaryotic | REPLICATION | 0.22 | 0.17 | 0.16 | 0.12 | 0.57 | ***0.02*** | 6.46 |
| ssb | Prokaryotic | REPLICATION | 0.00 | 1.00 | 0.06 | 0.40 | 0.00 | 1.00 | 6.01 |
| terminase\_small\_subunit | Prokaryotic | REPLICATION | 0.37 | ***0.02*** | 0.07 | 0.43 | 0.12 | 0.07 | 5.57 |
| Host\_recognition\_T2\_type | Prokaryotic | HOST RECOGNITION/STRUCTURAL | 0.18 | 0.07 | 0.42 | 0.08 | 0.39 | ***<0.01*** | 5.54 |
| tape\_measure\_protein | Prokaryotic | STRUCTURAL | 0.13 | ***0.04*** | 0.40 | 0.07 | 0.12 | 0.06 | 5.41 |
| holin\_type\_2 | LYSIS |  | 0.00 | 1.00 | 0.45 | ***0.01*** | 0.00 | 1.00 | 5.11 |
| DNA\_ligase | Prokaryotic | REPLICATION | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 5.00 |
| contractile\_central\_tail\_tube\_protein | Prokaryotic | STRUCTURAL | 0.00 | 1.00 | 0.00 | 1.00 | 0.13 | ***<0.01*** | 4.94 |
| helicase\_family\_1\_Dda\_like | Prokaryotic | REPLICATION | NA | NA | 0.00 | 1.00 | NA | NA | 4.84 |
| integrase\_serine | Prokaryotic | REPLICATION | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.77 |
| scaffold | Prokaryotic | STRUCTURAL | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 4.62 |
| non\_contractile\_major\_tail\_protein | Prokaryotic | STRUCTURAL | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.56 |
| UvsW | Prokaryotic | REPLICATION | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.39 |
| sliding\_clamp\_T4 | Prokaryotic | REPLICATION | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.01 |
| mycobacterium\_LysB\_lipase | Prokaryotic | LYSIS | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 3.74 |
| endolysin\_glycosidase | Prokaryotic | LYSIS | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 3.68 |
| **Bioleaching** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| ferredoxin\_oxidoreductase | Electron transport |  | 0.40 | ***0.01*** | 0.22 | 0.12 | 0.26 | 0.09 | 47.94 |
| glycosyl\_transferase\_EPS | EPS |  | 0.46 | ***0.01*** | 0.52 | ***<0.01*** | 0.27 | ***0.05*** | 44.37 |
| cytochrome\_c | Electron transport |  | 0.41 | ***0.02*** | 0.39 | ***<0.01*** | 0.47 | ***<0.01*** | 22.49 |
| NADH\_ubiquinone\_oxidoreductase | Electron transport |  | 0.31 | ***0.03*** | 0.41 | ***0.01*** | 0.25 | ***0.05*** | 20.37 |
| heat\_shock\_protein | other category |  | 0.35 | ***0.02*** | 0.46 | ***0.01*** | 0.01 | 0.82 | 19.59 |
| cbb | Carbon fixation |  | 0.69 | ***<0.01*** | 0.37 | ***<0.01*** | 0.26 | 0.13 | 18.71 |
| biotin\_carboxylase | Carbon fixation |  | 0.32 | ***0.01*** | 0.12 | 0.39 | 0.09 | 0.71 | 17.24 |
| 4Fe\_4S\_ferredoxin | Electron transport |  | 0.16 | 0.24 | 0.34 | 0.05 | 0.53 | ***<0.01*** | 15.92 |
| NADH\_quinone\_oxidoreductase | Electron transport |  | 0.37 | ***0.05*** | 0.34 | ***0.03*** | 0.23 | 0.17 | 15.07 |
| Fe\_S\_cluster\_binding\_protein | Electron transport |  | 0.47 | ***<0.01*** | 0.45 | ***0.01*** | 0.25 | 0.15 | 10.57 |
| mercury\_resistant\_gene | Metal Resistance |  | 0.15 | 0.16 | 0.41 | ***0.02*** | 0.12 | 0.08 | 9.78 |
| ABC\_transporter\_I | other category |  | 0.16 | 0.28 | 0.18 | ***0.05*** | 0.00 | 1.00 | 9.19 |
| nitrogen\_fixation\_genes | Nitrogen |  | 0.16 | 0.43 | 0.10 | 0.56 | 0.16 | 0.46 | 8.69 |
| formate\_hydrogenlyase\_complex | Carbon fixation |  | 0.30 | ***0.03*** | 0.11 | 0.56 | 0.28 | ***0.02*** | 8.62 |
| antioxidant | Metal Resistance |  | 0.36 | ***0.01*** | 0.17 | ***0.04*** | 0.00 | 1.00 | 8.59 |
| capsular\_polysaccharide\_biosynthesis\_protein\_EPS | EPS |  | 0.91 | ***<0.01*** | 0.21 | 0.07 | 0.27 | 0.08 | 8.36 |
| related\_thiosulfate\_gene | Sulphur |  | 0.11 | 0.38 | 0.19 | 0.09 | 0.15 | 0.22 | 8.22 |
| NDEDFP\_EPS | EPS |  | 0.62 | ***0.04*** | 0.38 | ***0.02*** | 0.51 | ***0.02*** | 7.91 |
| thioredoxin | Sulphur |  | 0.36 | ***0.03*** | 0.92 | ***<0.01*** | 0.07 | 0.56 | 7.82 |
| ferrochelatase | Iron oxidation |  | 0.26 | 0.16 | 0.68 | ***0.01*** | 0.60 | ***0.01*** | 7.77 |
| chromium\_resistance | Metal Resistance |  | 0.10 | 0.40 | 0.85 | ***<0.01*** | 0.00 | 1.00 | 7.02 |
| GAPDH | Carbon fixation |  | 0.62 | ***<0.01*** | 0.41 | ***0.01*** | 0.22 | 0.28 | 6.94 |
| ABC\_transporter\_II | other category |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 6.74 |
| polysaccharide\_biosynthesis\_protein\_EPS | EPS |  | 0.65 | ***0.01*** | 0.42 | 0.08 | 0.10 | 0.51 | 6.54 |
| ATP\_synthase\_F1\_or\_F0 | other category |  | 0.12 | 0.17 | 0.22 | ***0.01*** | 0.52 | ***0.02*** | 6.47 |
| nif\_II | Nitrogen |  | 0.58 | ***0.03*** | 0.50 | ***0.04*** | 0.93 | ***0.01*** | 6.40 |
| formate\_dehydrogenase\_family\_accessory\_protein | other category |  | 0.45 | ***0.02*** | 0.23 | 0.13 | 0.58 | ***0.02*** | 6.36 |
| arsenic\_resistance\_gene | Metal Resistance |  | 0.12 | ***0.04*** | 0.42 | 0.07 | 0.47 | ***<0.01*** | 5.81 |
| pyruvate\_carboxylase | Carbon fixation |  | 0.50 | ***0.03*** | 0.51 | ***0.03*** | 0.53 | ***<0.01*** | 5.67 |
| universal\_stress\_Family\_protein\_III | other category |  | 0.42 | ***0.01*** | 0.12 | 0.13 | 0.56 | ***0.01*** | 5.23 |
| copper\_resistance\_gene | Metal Resistance |  | 0.00 | 1.00 | 0.13 | 0.07 | 0.14 | ***0.05*** | 5.15 |
| Fe\_S\_oxidoreductase | Electron transport |  | 0.37 | 0.05 | 0.12 | 0.13 | 0.36 | 0.06 | 5.12 |
| acpA\_III | other category |  | 0.47 | ***0.04*** | 0.42 | 0.09 | 0.47 | ***0.04*** | 5.09 |
| ferredoxin\_I | Electron transport |  | 0.38 | 0.06 | 0.35 | 0.10 | 0.38 | 0.06 | 4.96 |
| ADP\_heptose\_synthase\_EPS | EPS |  | 0.36 | 0.06 | 0.13 | 0.12 | 0.32 | 0.08 | 4.94 |
| ABC\_transporter\_III | other category |  | 0.55 | ***0.02*** | 0.51 | ***0.03*** | 0.54 | ***0.01*** | 4.93 |
| terminal\_quinol\_oxidase | Bioleaching | Electron transport | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 4.92 |
| GDP\_EPS | EPS |  | 0.45 | ***0.03*** | 0.12 | 0.09 | 0.49 | ***0.02*** | 4.89 |
| PGK\_bioleaching |  |  | 0.00 | 1.00 | 0.13 | 0.06 | 0.43 | ***0.03*** | 4.89 |
| tyrosine\_protein\_kinase\_EPS | EPS |  | 0.46 | ***0.04*** | 0.44 | ***0.04*** | 0.48 | ***0.02*** | 4.88 |
| aa3\_type\_cytochrome\_oxidase | Electron transport |  | 0.12 | 0.06 | 0.35 | 0.09 | 0.53 | ***0.01*** | 4.82 |
| cytochrome\_bd | Electron transport |  | 0.12 | 0.09 | 0.00 | 1.00 | 0.00 | 1.00 | 4.82 |
| heavy\_metal | Metal Resistance |  | 0.35 | 0.07 | 0.41 | 0.07 | 0.12 | 0.13 | 4.80 |
| LpxB | other category |  | 0.40 | ***0.04*** | 0.40 | 0.07 | 0.40 | ***0.04*** | 4.78 |
| UDS\_EPS | EPS |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.76 |
| nitrogenase\_iron\_protein | Nitrogen |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.76 |
| cytochrome\_b | Electron transport |  | 0.53 | ***0.02*** | 0.40 | 0.07 | 0.00 | 1.00 | 4.76 |
| cadmium\_resistance\_gene | Metal Resistance |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.12 | 0.11 | 4.73 |
| UHGNAS\_EPS | EPS |  | 0.12 | ***0.03*** | 0.12 | 0.08 | 0.13 | ***<0.01*** | 4.72 |
| sulfur\_reductase | Sulphur |  | 0.00 | 1.00 | 0.41 | 0.08 | 0.13 | ***0.01*** | 4.69 |
| UTP\_glucose\_1\_phosphate\_uridylyltransferase\_EPS | EPS |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.68 |
| peroxiredoxin | Metal Resistance |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.14 | ***0.03*** | 4.64 |
| NAD\_dependent\_epimerase\_dehydratase\_family\_protein\_EPS | EPS |  | NA | NA | 0.00 | 1.00 | NA | NA | 4.62 |
| acetyl\_CoA\_carboxylase | Carbon fixation |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.54 |
| terminal\_oxidase | Electron transport |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.54 |
| Adaptations\_to\_atypical\_conditionsIII | other category |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.12 | ***0.04*** | 4.50 |
| rusticyanin | Iron | oxidation | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.47 |
| sulfite\_dehydrogenase | Sulphur |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.42 |
| LPS\_heptosyltransferase\_EPS | EPS |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.17 |
| cyc4 | Electron transport |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.02 |
| ATP\_binding\_protein\_related\_resistance | Antibiotic Resistance |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 3.87 |
| **Energy process** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| cytochrome | Energy process |  | 0.44 | ***0.01*** | 0.44 | ***<0.01*** | 0.33 | ***<0.01*** | 348.43 |
| hydrogenase | Energy process |  | 0.49 | ***<0.01*** | 0.32 | ***0.04*** | 0.42 | ***<0.01*** | 83.69 |
| P450 | Energy process |  | 0.29 | 0.05 | 0.25 | 0.14 | 0.46 | ***<0.01*** | 19.59 |
| Ni\_Fe\_hydrogenase | Energy process |  | 0.15 | 0.21 | 0.51 | ***0.04*** | 0.28 | 0.06 | 7.96 |
| **Fungi function** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| ABC\_multidrug\_fungi | antibiotic resistance | transporter | 0.56 | ***<0.01*** | 0.52 | ***<0.01*** | 0.43 | ***<0.01*** | 241.36 |
| chitin\_synthase | major biomolecule | Chitin synthesis | 0.38 | ***0.03*** | 0.27 | 0.09 | 0.39 | ***<0.01*** | 151.01 |
| trk\_fungi | Potassium | Transport | 0.44 | ***<0.01*** | 0.34 | ***0.03*** | 0.37 | ***<0.01*** | 124.41 |
| p450aro | Aromatics | polycyclic aromatics | 0.34 | ***0.02*** | 0.24 | 0.10 | 0.30 | ***0.01*** | 65.84 |
| ferroxidase\_high\_affinity | iron | Transport | 0.44 | ***0.02*** | 0.38 | ***<0.01*** | 0.33 | ***0.01*** | 61.31 |
| nitrate\_reductase\_fungi | N Assimilation |  | 0.29 | ***0.04*** | 0.30 | 0.06 | 0.40 | ***<0.01*** | 51.31 |
| phospholipase\_B\_fungi | degradation |  | 0.37 | ***0.01*** | 0.46 | ***<0.01*** | 0.34 | ***<0.01*** | 34.76 |
| sulfate\_transporter | Assimilation |  | 0.40 | ***0.04*** | 0.67 | ***<0.01*** | 0.45 | ***<0.01*** | 33.27 |
| NRPS | iron |  | 0.40 | ***0.02*** | 0.18 | 0.31 | 0.51 | ***<0.01*** | 26.83 |
| catalase\_KatG\_fungi | virulence |  | 0.51 | ***<0.01*** | 0.48 | ***<0.01*** | 0.28 | 0.07 | 25.00 |
| dmaW\_ergot | Toxin | ergot | 0.32 | 0.05 | 0.51 | ***0.01*** | 0.23 | 0.15 | 24.41 |
| hmgC\_fungi | Aromatics | Aromatic carboxylic acid | 0.35 | ***0.03*** | 0.12 | 0.34 | 0.59 | ***<0.01*** | 23.32 |
| vacuolar\_iron\_transport | iron | Transport | 0.36 | ***0.04*** | 0.37 | ***0.01*** | 0.57 | ***<0.01*** | 22.83 |
| iron\_permease\_high\_affinity | iron | Transport | 0.27 | ***0.03*** | 0.23 | 0.11 | 0.27 | ***0.03*** | 20.50 |
| glnA\_fungi | Ammonificcation |  | 0.29 | ***0.02*** | 0.57 | ***<0.01*** | 0.09 | 0.55 | 19.88 |
| nbaC\_fungi | Aromatics | Nitoaromatics | 0.21 | 0.06 | 0.14 | 0.28 | 0.41 | ***<0.01*** | 16.70 |
| hmgB\_fungi | Aromatics | Aromatic carboxylic acid | 0.64 | ***0.01*** | 0.29 | ***0.02*** | 0.35 | ***0.02*** | 14.87 |
| ATP\_sulphurylase | Assimilation |  | 0.26 | 0.12 | 0.36 | ***0.02*** | 0.47 | ***<0.01*** | 12.18 |
| PAPS\_reductase | Assimilation |  | 0.50 | ***<0.01*** | 0.18 | 0.17 | 0.49 | ***0.02*** | 12.11 |
| aflatoxin\_aflM | toxin | Versicolorin reductase | 0.49 | ***<0.01*** | 0.43 | ***0.02*** | -0.04 | 0.98 | 11.72 |
| sidA | iron | transport | 0.42 | ***<0.01*** | 0.08 | 0.77 | 0.48 | ***<0.01*** | 11.67 |
| nirK | Denitrification |  | 0.52 | ***0.01*** | 0.41 | ***<0.01*** | 0.43 | ***<0.01*** | 10.07 |
| siderophore\_transporter | iron | transport | 0.35 | ***0.01*** | 0.16 | 0.21 | 0.32 | ***0.01*** | 9.02 |
| MFS\_fungi | drug resistance |  | 0.60 | ***<0.01*** | 0.31 | 0.15 | 0.38 | ***0.04*** | 8.21 |
| aflatoxin\_aflQ | toxin | O-methylsterigmatocystin oxidoreductase | 0.67 | ***0.01*** | 0.26 | 0.18 | 0.09 | 0.45 | 7.89 |
| superoxide\_dismutase\_fungi | virulence |  | 0.36 | ***0.02*** | 0.44 | ***<0.01*** | 0.00 | 1.00 | 7.21 |
| aromatic\_peroxygenase | Aromatics | Other | 0.24 | 0.10 | 0.20 | 0.16 | 0.95 | ***<0.01*** | 7.08 |
| ppx\_fungi | Polyphosphate degradation |  | 0.00 | 1.00 | 0.09 | 0.61 | 0.00 | 1.00 | 6.92 |
| ferric\_reductase\_transporter | iron | Transport | 0.63 | ***<0.01*** | 0.62 | ***<0.01*** | 0.16 | 0.10 | 6.87 |
| arsA\_fungi | Arsenic | Transport | 0.19 | 0.09 | 0.00 | 1.00 | 0.00 | 1.00 | 6.78 |
| phytase\_fungi | Phytic acid hydrolysis |  | 0.28 | 0.10 | 0.23 | 0.11 | 0.52 | ***<0.01*** | 6.70 |
| calcineurin\_A\_fungi | virulence |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 6.51 |
| Dyp | halogenated compounds |  | 0.33 | ***<0.01*** | 0.03 | 0.58 | 0.41 | ***0.04*** | 6.17 |
| Al | Aluminum | Transport | 0.35 | ***0.01*** | 0.58 | ***<0.01*** | 0.49 | ***<0.01*** | 5.39 |
| patulin\_6MSAS | toxin |  | 0.12 | 0.15 | 0.35 | 0.08 | 0.35 | 0.05 | 4.99 |
| sidC | iron | transport | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.94 |
| p450nor | respiration |  | NA | NA | NA | NA | 0.00 | 1.00 | 4.85 |
| metallothionein | Multiple metals | Sequestration | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.46 |
| conidial\_laccase | Pigments |  | 0.12 | 0.09 | 0.00 | 1.00 | 0.00 | 1.00 | 4.30 |
| Cl\_peroxidase\_fungi | Aromatics | Other aromatics | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 4.05 |
| sdsA\_fungi | Others |  | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.04 |
| aflatoxin\_aflN | toxin |  | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 4.02 |
| cah\_fungi | Others |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 3.98 |
| aflatoxin\_aflL | toxin |  | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 3.73 |
| alkK | Others |  | 0.48 | ***<0.01*** | 0.45 | ***<0.01*** | 0.61 | ***<0.01*** | 3.44 |
| **Metal Resistance** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| trkGH | Potassium | Transport | 0.40 | ***0.03*** | 0.37 | ***0.02*** | 0.33 | ***0.01*** | 2111.67 |
| trkA | Potassium | Transport | 0.45 | ***0.01*** | 0.34 | ***0.02*** | 0.36 | ***<0.01*** | 2061.18 |
| feoB | Iron | Transport | 0.36 | ***0.02*** | 0.40 | ***<0.01*** | 0.38 | ***<0.01*** | 1755.50 |
| kefBC | Potassium | Transport | 0.34 | ***0.03*** | 0.38 | ***0.02*** | 0.34 | ***<0.01*** | 674.66 |
| CopA | Copper | Transport | 0.47 | ***<0.01*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 659.89 |
| fepA\_iron | Iron | Transport | 0.44 | ***0.01*** | 0.43 | ***<0.01*** | 0.36 | ***<0.01*** | 642.37 |
| kdpA | Potassium | Transport | 0.36 | ***0.03*** | 0.44 | ***<0.01*** | 0.35 | ***<0.01*** | 573.73 |
| ChrA | Chromium | Transport | 0.43 | ***<0.01*** | 0.47 | ***<0.01*** | 0.41 | ***<0.01*** | 517.53 |
| kup | Potassium | Transport | 0.39 | ***0.02*** | 0.44 | ***<0.01*** | 0.34 | ***<0.01*** | 418.45 |
| fhuE | Iron | Transport | 0.39 | ***0.01*** | 0.35 | ***<0.01*** | 0.33 | ***<0.01*** | 362.02 |
| mer | Mercury | Detoxification | 0.43 | ***<0.01*** | 0.37 | ***0.01*** | 0.42 | ***<0.01*** | 349.05 |
| czcA | Cadmium,Cobalt,Zinc | Transport | 0.53 | ***<0.01*** | 0.44 | ***<0.01*** | 0.46 | ***<0.01*** | 331.10 |
| CadA | Cadmium | Transport | 0.48 | ***0.01*** | 0.50 | ***<0.01*** | 0.38 | ***<0.01*** | 316.50 |
| fecA | Iron | Transport | 0.44 | ***0.03*** | 0.43 | ***<0.01*** | 0.34 | ***0.02*** | 307.69 |
| bfr | Iron | storage | 0.42 | ***<0.01*** | 0.40 | ***0.01*** | 0.40 | ***<0.01*** | 297.53 |
| ArsC | Arsenic | Detoxification | 0.51 | ***<0.01*** | 0.49 | ***<0.01*** | 0.35 | ***<0.01*** | 263.65 |
| ZntA | Zinc | Transport | 0.51 | ***<0.01*** | 0.48 | ***<0.01*** | 0.40 | ***<0.01*** | 246.04 |
| czcD | Cadmium,Cobalt,Zinc | Transport | 0.41 | ***0.01*** | 0.44 | ***<0.01*** | 0.43 | ***<0.01*** | 202.75 |
| TerD | Tellurium | Transport | 0.39 | ***0.01*** | 0.39 | ***<0.01*** | 0.37 | ***<0.01*** | 161.53 |
| ktrBD | Potassium | Transport | 0.37 | ***0.03*** | 0.34 | ***0.04*** | 0.50 | ***<0.01*** | 159.98 |
| TerC | Tellurium | Detoxification | 0.42 | ***0.04*** | 0.46 | ***<0.01*** | 0.42 | ***<0.01*** | 159.51 |
| silC | Silver | Transport | 0.47 | ***<0.01*** | 0.41 | ***<0.01*** | 0.46 | ***<0.01*** | 153.28 |
| fhuA | Iron | Transport | 0.28 | ***0.03*** | 0.41 | ***<0.01*** | 0.33 | ***0.01*** | 117.33 |
| aoxB | Arsenic | Detoxification | 0.32 | ***<0.01*** | 0.32 | ***<0.01*** | 0.30 | ***<0.01*** | 94.82 |
| TehB | Tellurium | Detoxification | 0.50 | ***0.01*** | 0.33 | ***0.01*** | 0.30 | ***<0.01*** | 70.82 |
| TerZ | Tellurium | Transport | 0.53 | ***<0.01*** | 0.52 | ***<0.01*** | 0.45 | ***<0.01*** | 56.04 |
| entB | Iron | Transport | 0.36 | ***0.02*** | 0.45 | ***<0.01*** | 0.33 | ***0.03*** | 54.95 |
| arsB | Arsenic | Transport | 0.32 | ***0.02*** | 0.38 | ***<0.01*** | 0.38 | ***<0.01*** | 41.92 |
| merP | Mercury | Transport | 0.56 | ***0.01*** | 0.36 | ***0.04*** | 0.30 | ***<0.01*** | 37.54 |
| merB | Mercury | Detoxification | 0.36 | ***0.01*** | 0.24 | 0.14 | 0.40 | ***<0.01*** | 24.19 |
| pbrA | Lead | Transport | 0.58 | ***<0.01*** | 0.57 | ***<0.01*** | 0.74 | ***<0.01*** | 21.95 |
| SilA | Silver | Transport | 0.32 | 0.05 | 0.52 | ***<0.01*** | 0.22 | 0.13 | 21.86 |
| arsM | Arsenic | Detoxification | 0.52 | ***0.01*** | 0.18 | 0.10 | 0.30 | ***0.04*** | 21.26 |
| ZitB | Zinc | Transport | 0.26 | 0.12 | 0.36 | 0.09 | 0.39 | ***<0.01*** | 20.79 |
| cadBD | Cadmium | Transport | 0.35 | 0.12 | 0.63 | ***<0.01*** | 0.35 | ***0.02*** | 17.53 |
| ArsA | Arsenic | Transport | 0.59 | ***0.01*** | 0.37 | ***<0.01*** | 0.41 | ***<0.01*** | 16.79 |
| merT | Mercury | Transport | 0.46 | ***<0.01*** | 0.07 | 0.59 | 0.33 | ***<0.01*** | 16.49 |
| czcC | Cadmium,Cobalt,Zinc | Transport | 0.38 | ***0.03*** | 0.61 | ***<0.01*** | 0.27 | ***0.02*** | 15.99 |
| nreB | Nickel | Transport | 0.49 | ***<0.01*** | 0.17 | 0.25 | 0.50 | ***<0.01*** | 15.57 |
| CusA | Copper | Transport | 0.09 | 0.48 | 0.33 | ***0.03*** | 0.54 | ***<0.01*** | 12.56 |
| silP | Silver | Transport | 0.16 | 0.32 | 0.17 | 0.22 | 0.11 | 0.48 | 12.34 |
| metC | Mercury | Detoxification | 0.30 | ***0.03*** | 0.42 | ***0.03*** | 0.09 | 0.53 | 9.75 |
| CusF | Copper | Transport | 0.29 | 0.23 | 0.42 | ***0.01*** | 0.13 | 0.19 | 8.92 |
| cnrC | Cobalt,Nickel | Transport | 0.10 | 0.30 | 0.44 | ***0.05*** | 0.04 | 0.60 | 7.88 |
| CorC | Cobalt | Transport | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 7.07 |
| SmtA | Multiple metals | Sequester | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 6.17 |
| rcnA | Cobalt,Nickel | Transport | 0.14 | 0.06 | 0.49 | ***0.01*** | 0.42 | ***0.01*** | 5.82 |
| Al | Aluminum | Transport | 0.35 | ***0.01*** | 0.58 | ***<0.01*** | 0.49 | ***<0.01*** | 5.39 |
| CueO | Copper | Detoxification | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.13 |
| SilE | Silver | Transport | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.11 |
| pbrT | Lead | Transport | 0.00 | 1.00 | 0.18 | 0.07 | 0.62 | ***<0.01*** | 5.01 |
| merF | Mercury | Transport | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.85 |
| CusC | Copper | Transport | NA | NA | 0.00 | 1.00 | NA | NA | 4.36 |
| cnrA | Cobalt,Nickel | Transport | NA | NA | 0.00 | 1.00 | NA | NA | 3.26 |
| **Organic Remediation** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| pimF | Aromatics | Aromatic carboxylic acid | 0.40 | ***0.03*** | 0.41 | ***<0.01*** | 0.38 | ***<0.01*** | 1333.20 |
| nagG | Aromatics | Aromatic carboxylic acid | 0.49 | ***<0.01*** | 0.43 | ***<0.01*** | 0.34 | ***<0.01*** | 384.41 |
| Catechol | Aromatics | Other aromatics | 0.45 | ***0.01*** | 0.47 | ***<0.01*** | 0.41 | ***<0.01*** | 312.55 |
| nahA | Aromatics | Polycyclic aromatics | 0.43 | ***0.01*** | 0.46 | ***<0.01*** | 0.40 | ***<0.01*** | 258.02 |
| pobA | Aromatics | Aromatic carboxylic acid | 0.42 | ***0.03*** | 0.32 | ***<0.01*** | 0.38 | ***<0.01*** | 219.54 |
| nmoA | Aromatics | Nitoaromatics | 0.31 | ***0.04*** | 0.43 | ***<0.01*** | 0.41 | ***<0.01*** | 213.36 |
| pcaG | Aromatics | Other aromatics | 0.40 | ***0.02*** | 0.44 | ***<0.01*** | 0.41 | ***<0.01*** | 201.43 |
| GCoADH | Aromatics | Aromatic carboxylic acid | 0.44 | ***0.01*** | 0.33 | ***<0.01*** | 0.38 | ***<0.01*** | 201.10 |
| phn | Herbicides related compound |  | 0.55 | ***<0.01*** | 0.48 | ***<0.01*** | 0.39 | ***<0.01*** | 196.76 |
| pheA | Aromatics | Other aromatics | 0.43 | ***<0.01*** | 0.36 | ***0.01*** | 0.42 | ***<0.01*** | 196.16 |
| tfdA | Aromatics | Chlorinated aromatics | 0.48 | ***0.01*** | 0.51 | ***<0.01*** | 0.47 | ***<0.01*** | 165.56 |
| linB | Pesticides related compound |  | 0.37 | ***0.01*** | 0.47 | ***<0.01*** | 0.46 | ***<0.01*** | 161.56 |
| nitA | Aromatics | Other aromatics | 0.45 | ***<0.01*** | 0.50 | ***<0.01*** | 0.41 | ***<0.01*** | 160.19 |
| bphA | Aromatics | Polycyclic aromatics | 0.46 | ***<0.01*** | 0.40 | ***0.01*** | 0.37 | ***<0.01*** | 157.47 |
| hmgC | Aromatics | Aromatic carboxylic acid | 0.36 | ***0.01*** | 0.49 | ***<0.01*** | 0.33 | ***<0.01*** | 156.52 |
| alkB | Other Hydrocarbons |  | 0.37 | ***0.02*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 151.15 |
| nhh | Aromatics | Nitoaromatics | 0.40 | ***0.02*** | 0.33 | ***<0.01*** | 0.33 | ***<0.01*** | 150.56 |
| mdlC | Aromatics | Aromatic carboxylic acid | 0.50 | ***<0.01*** | 0.35 | ***<0.01*** | 0.38 | ***<0.01*** | 149.00 |
| mdlA | Aromatics | Aromatic alpha hydroxy acid | 0.40 | ***<0.01*** | 0.44 | ***<0.01*** | 0.43 | ***<0.01*** | 146.48 |
| catB | Aromatics | BTEX and related aromatics | 0.49 | ***<0.01*** | 0.36 | ***0.01*** | 0.41 | ***<0.01*** | 133.39 |
| hmgB | Aromatics | Aromatic carboxylic acid | 0.41 | ***<0.01*** | 0.39 | ***<0.01*** | 0.28 | ***<0.01*** | 132.10 |
| PhaB | Aromatics | Aromatic carboxylic acid | 0.61 | ***<0.01*** | 0.55 | ***<0.01*** | 0.57 | ***<0.01*** | 126.81 |
| Arylest | Aromatics | Other aromatics | 0.44 | ***0.01*** | 0.46 | ***<0.01*** | 0.44 | ***<0.01*** | 121.76 |
| proO | Aromatics | Other aromatics | 0.39 | ***0.01*** | 0.40 | ***0.01*** | 0.31 | ***0.03*** | 116.81 |
| exaA | Chlorinated solvents |  | 0.42 | ***0.03*** | 0.42 | ***<0.01*** | 0.41 | ***<0.01*** | 116.13 |
| akbF | Aromatics | BTEX and related aromatics | 0.51 | ***<0.01*** | 0.48 | ***<0.01*** | 0.36 | ***<0.01*** | 111.99 |
| hmgA | Aromatics | Aromatic carboxylic acid | 0.51 | ***<0.01*** | 0.41 | ***<0.01*** | 0.32 | ***<0.01*** | 109.79 |
| catechol\_B | Aromatics | Other aromatics | 0.45 | ***<0.01*** | 0.32 | ***0.01*** | 0.42 | ***<0.01*** | 107.32 |
| phtA | Aromatics | Aromatic carboxylic acid | 0.45 | ***<0.01*** | 0.33 | ***<0.01*** | 0.34 | ***0.04*** | 103.39 |
| chnB | Other Hydrocarbons |  | 0.36 | ***<0.01*** | 0.45 | ***<0.01*** | 0.41 | ***<0.01*** | 102.96 |
| cbdA | Aromatics | Chlorinated aromatics | 0.39 | ***0.02*** | 0.50 | ***<0.01*** | 0.29 | ***0.02*** | 102.37 |
| atzB | Herbicides related compound |  | 0.40 | ***0.01*** | 0.35 | ***<0.01*** | 0.35 | ***0.03*** | 97.46 |
| atzA | Herbicides related compound |  | 0.39 | ***0.02*** | 0.27 | ***0.04*** | 0.38 | ***<0.01*** | 91.98 |
| bphC | Aromatics | Polycyclic aromatics | 0.39 | ***0.02*** | 0.39 | ***0.01*** | 0.42 | ***<0.01*** | 88.02 |
| nagI | Aromatics | Aromatic carboxylic acid | 0.41 | ***0.02*** | 0.27 | ***0.04*** | 0.36 | ***<0.01*** | 82.83 |
| tftH | Aromatics | Chlorinated aromatics | 0.57 | ***0.01*** | 0.34 | ***0.03*** | 0.47 | ***<0.01*** | 81.27 |
| linC | Pesticides related compound |  | 0.32 | 0.06 | 0.53 | ***<0.01*** | 0.33 | ***<0.01*** | 80.68 |
| rd | Chlorinated solvents |  | 0.45 | ***0.01*** | 0.43 | ***<0.01*** | 0.38 | ***<0.01*** | 75.55 |
| trzN | Herbicides related compound |  | 0.39 | ***0.03*** | 0.29 | ***0.02*** | 0.49 | ***<0.01*** | 74.31 |
| tutFDG | Aromatics | BTEX and related aromatics | 0.39 | ***0.02*** | 0.49 | ***<0.01*** | 0.45 | ***<0.01*** | 73.08 |
| bclA | Aromatics | Aromatic carboxylic acid | 0.40 | ***<0.01*** | 0.34 | ***0.03*** | 0.38 | ***<0.01*** | 72.96 |
| pnbA | Aromatics | Nitoaromatics | 0.35 | ***0.03*** | 0.31 | ***0.02*** | 0.50 | ***<0.01*** | 71.53 |
| bco | Aromatics | Aromatic carboxylic acid | 0.47 | ***0.01*** | 0.34 | ***0.03*** | 0.41 | ***0.01*** | 71.04 |
| BADH | Aromatics | Other aromatics | 0.40 | ***<0.01*** | 0.51 | ***<0.01*** | 0.31 | ***0.01*** | 64.96 |
| arhA | Aromatics | Heterocyclic aromatics | 0.48 | ***0.01*** | 0.39 | ***0.01*** | 0.25 | 0.05 | 62.21 |
| dmsA | Others |  | 0.13 | 0.33 | 0.47 | ***<0.01*** | 0.46 | ***<0.01*** | 57.29 |
| mauAB | Herbicides related compound |  | 0.47 | ***<0.01*** | 0.22 | 0.12 | 0.17 | 0.18 | 53.56 |
| pcpE | Herbicides related compound |  | 0.37 | ***0.01*** | 0.26 | ***0.04*** | 0.36 | ***<0.01*** | 52.49 |
| xylF | Aromatics | BTEX and related aromatics | 0.53 | ***<0.01*** | 0.47 | ***<0.01*** | 0.23 | ***0.03*** | 49.20 |
| atzC | Herbicides related compound |  | 0.44 | ***<0.01*** | 0.55 | ***<0.01*** | 0.38 | ***<0.01*** | 47.28 |
| benD | Aromatics | Aromatic carboxylic acid | 0.39 | ***0.02*** | 0.28 | ***0.01*** | 0.33 | ***0.04*** | 46.92 |
| HcaB | Aromatics | Aromatic carboxylic acid | 0.34 | ***0.01*** | 0.23 | 0.21 | 0.27 | ***0.03*** | 46.74 |
| pcpB | Herbicides related compound |  | 0.42 | ***0.01*** | 0.43 | ***<0.01*** | 0.25 | 0.06 | 41.35 |
| xylG | Aromatics | Aromatic carboxylic acid | 0.36 | ***0.02*** | 0.14 | 0.27 | 0.29 | 0.07 | 35.82 |
| ohbAB | Aromatics | Aromatic carboxylic acid | 0.51 | ***<0.01*** | 0.16 | 0.17 | 0.40 | ***<0.01*** | 35.67 |
| mhpA | Aromatics | Aromatic carboxylic acid | 0.27 | ***<0.01*** | 0.57 | ***<0.01*** | 0.44 | ***<0.01*** | 35.55 |
| BpH | Aromatics | Aromatic carboxylic acid | 0.40 | ***0.01*** | 0.48 | ***<0.01*** | 0.55 | ***<0.01*** | 35.44 |
| alkH | Other Hydrocarbons |  | 0.43 | ***<0.01*** | 0.48 | ***0.01*** | 0.49 | ***0.01*** | 35.11 |
| GcdB | Aromatics | Aromatic carboxylic acid | 0.55 | ***<0.01*** | 0.62 | ***0.01*** | 0.11 | 0.41 | 33.75 |
| dehH | Chlorinated solvents |  | 0.62 | ***0.01*** | 0.49 | ***<0.01*** | 0.46 | ***<0.01*** | 33.00 |
| dehH109 | Chlorinated solvents |  | 0.29 | 0.08 | 0.36 | ***<0.01*** | 0.34 | ***0.03*** | 32.92 |
| nagK | Aromatics | Aromatic carboxylic acid | 0.32 | ***0.05*** | 0.39 | ***0.01*** | 0.69 | ***<0.01*** | 32.61 |
| benAB | Aromatics | Aromatic carboxylic acid | 0.42 | ***0.03*** | 0.29 | ***0.04*** | 0.55 | ***<0.01*** | 30.44 |
| tfdB | Aromatics | Chlorinated aromatics | 0.22 | 0.16 | 0.44 | ***<0.01*** | 0.26 | 0.07 | 30.31 |
| Xamo | Other Hydrocarbons |  | 0.29 | 0.06 | 0.13 | 0.35 | 0.31 | ***0.02*** | 30.24 |
| xylC | Aromatics | BTEX and related aromatics | 0.44 | ***<0.01*** | 0.47 | ***<0.01*** | 0.38 | ***0.01*** | 28.72 |
| nagL | Aromatics | Aromatic carboxylic acid | 0.48 | ***0.03*** | 0.10 | 0.53 | 0.51 | ***0.01*** | 28.50 |
| todC | Aromatics | BTEX and related aromatics | 0.41 | ***0.04*** | 0.30 | ***0.02*** | 0.39 | ***<0.01*** | 28.12 |
| hdnO | Aromatics | Heterocyclic aromatics | 0.38 | ***0.01*** | 0.54 | ***<0.01*** | 0.43 | ***<0.01*** | 27.47 |
| alkJ | Other Hydrocarbons |  | 0.41 | ***<0.01*** | 0.38 | ***0.01*** | 0.34 | ***0.02*** | 27.38 |
| cumA | Aromatics | Other aromatics | 0.73 | ***<0.01*** | 0.42 | ***<0.01*** | 0.53 | ***<0.01*** | 26.90 |
| cmuA | Chlorinated solvents |  | 0.12 | 0.41 | 0.13 | 0.29 | 0.36 | ***0.01*** | 26.41 |
| atzD | Herbicides related compound |  | 0.38 | ***0.01*** | 0.38 | ***<0.01*** | 0.22 | 0.17 | 26.09 |
| mdlB | Aromatics | Aromatic carboxylic acid | 0.55 | ***0.01*** | 0.50 | ***0.02*** | 0.52 | ***<0.01*** | 25.73 |
| nahF | Aromatics | Polycyclic aromatics | 0.24 | 0.11 | 0.43 | ***<0.01*** | 0.28 | 0.07 | 24.94 |
| bphD | Aromatics | Polycyclic aromatics | 0.47 | ***<0.01*** | 0.44 | ***<0.01*** | 0.40 | ***0.01*** | 24.72 |
| xylJ | Aromatics | BTEX and related aromatics | 0.23 | 0.08 | 0.55 | ***<0.01*** | 0.48 | ***<0.01*** | 24.10 |
| AmiE | Aromatics | Other aromatics | 0.13 | 0.42 | 0.52 | ***<0.01*** | 0.13 | 0.44 | 23.80 |
| nbaC | Aromatics | Nitoaromatics | 0.34 | ***0.02*** | 0.39 | ***0.02*** | 0.37 | ***<0.01*** | 23.20 |
| phdCI | Aromatics | Polycyclic aromatics | 0.34 | ***0.03*** | 0.43 | ***<0.01*** | 0.23 | 0.07 | 23.09 |
| cpnA | Other Hydrocarbons |  | 0.21 | 0.17 | 0.56 | ***<0.01*** | 0.12 | 0.36 | 21.97 |
| mdlD | Aromatics | Other aromatics | 0.21 | 0.17 | 0.53 | ***<0.01*** | 0.41 | ***<0.01*** | 21.53 |
| ALN | Others |  | 0.20 | ***0.05*** | 0.11 | 0.46 | 0.46 | ***0.01*** | 21.42 |
| nitro | Others |  | 0.33 | ***0.03*** | 0.37 | ***<0.01*** | 0.33 | ***0.01*** | 20.01 |
| xlnD | Aromatics | Other aromatics | 0.42 | ***<0.01*** | 0.37 | ***0.01*** | 0.11 | 0.44 | 18.64 |
| oxdB | Aromatics | Nitoaromatics | 0.46 | ***0.01*** | 0.41 | ***0.01*** | 0.26 | 0.05 | 15.79 |
| adpB | Pesticides related compound |  | 0.44 | ***0.03*** | 0.44 | ***0.01*** | 0.29 | 0.09 | 14.93 |
| bphB | Aromatics | Polycyclic aromatics | 0.37 | ***0.02*** | 0.67 | ***<0.01*** | 0.60 | ***<0.01*** | 13.50 |
| ophC | Aromatics | Aromatic carboxylic acid | 0.66 | ***<0.01*** | 0.37 | ***0.01*** | 0.58 | ***<0.01*** | 13.38 |
| PceA | Others |  | 0.55 | ***0.01*** | 0.45 | ***0.02*** | 0.25 | 0.10 | 12.84 |
| dxnA | Aromatics | Heterocyclic aromatics | 0.37 | ***0.01*** | 0.27 | 0.07 | 0.59 | ***<0.01*** | 12.35 |
| pchCF | Aromatics | BTEX and related aromatics | 0.20 | ***0.05*** | 0.47 | ***<0.01*** | 0.00 | 1.00 | 12.21 |
| mhpB | Aromatics | Aromatic carboxylic acid | 0.01 | 0.58 | 0.15 | 0.11 | -0.01 | 0.55 | 12.11 |
| carA | Aromatics | Heterocyclic aromatics | 0.40 | ***0.01*** | 0.73 | ***<0.01*** | 0.34 | ***0.05*** | 11.86 |
| ChnE | Other Hydrocarbons |  | 0.48 | ***0.03*** | 0.36 | ***0.03*** | 0.47 | ***0.03*** | 10.44 |
| qorL | Aromatics | Polycyclic aromatics | 0.32 | 0.09 | 0.34 | 0.06 | 0.35 | ***<0.01*** | 10.37 |
| phdI | Aromatics | Polycyclic aromatics | 0.24 | ***0.02*** | 0.39 | ***0.05*** | 0.54 | ***0.01*** | 9.83 |
| cymA | Aromatics | Other aromatics | 0.45 | ***0.03*** | 0.41 | 0.08 | 0.21 | ***0.05*** | 9.45 |
| fcbA | Aromatics | Chlorinated aromatics | 0.47 | ***0.03*** | 0.42 | ***0.05*** | 0.37 | ***0.03*** | 9.39 |
| phdJ | Aromatics | Polycyclic aromatics | 0.38 | ***<0.01*** | 0.00 | 0.88 | 0.43 | ***0.03*** | 8.64 |
| scnABC | Others |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 8.48 |
| tomA | Aromatics | BTEX and related aromatics | 0.22 | ***0.03*** | 0.07 | 0.45 | -0.09 | 0.84 | 8.33 |
| ChnA | Other Hydrocarbons |  | 0.31 | ***0.02*** | 0.00 | 1.00 | 0.00 | 1.00 | 8.30 |
| BMO | Other Hydrocarbons |  | 0.00 | 1.00 | 0.29 | ***0.02*** | 0.00 | 1.00 | 8.24 |
| tdnB | Aromatics | Other aromatics | 0.12 | 0.49 | 0.46 | ***0.01*** | 0.68 | ***<0.01*** | 8.02 |
| chnC | Other Hydrocarbons |  | 0.35 | ***0.03*** | 0.07 | 0.38 | 0.23 | ***0.03*** | 7.86 |
| trzE | Herbicides related compound |  | 0.27 | ***0.02*** | 0.21 | 0.08 | 0.00 | 1.00 | 7.62 |
| mhpC | Aromatics | Aromatic carboxylic acid | 0.67 | ***<0.01*** | 0.32 | ***0.01*** | 0.15 | 0.13 | 7.21 |
| nicdehydr | Aromatics | Heterocyclic aromatics | 0.59 | ***0.02*** | 0.26 | 0.06 | 0.00 | 1.00 | 7.09 |
| phdA | Aromatics | Polycyclic aromatics | 0.24 | 0.15 | 0.42 | 0.07 | 0.68 | ***<0.01*** | 6.93 |
| MSAD | Others |  | 0.48 | ***0.01*** | 0.17 | 0.15 | 0.09 | 0.57 | 6.86 |
| pcpA | Aromatics | Chlorinated aromatics | -0.02 | 0.67 | -0.05 | 0.89 | 0.00 | 1.00 | 6.80 |
| CMCI | Aromatics | Other aromatics | 0.00 | 1.00 | 0.19 | 0.06 | 0.00 | 1.00 | 6.78 |
| nbzC | Aromatics | Nitoaromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 6.62 |
| nidA | Aromatics | Polycyclic aromatics | 0.20 | ***0.05*** | 0.06 | 0.38 | 0.48 | ***<0.01*** | 6.57 |
| cpnB | Other Hydrocarbons |  | NA | NA | 0.00 | 1.00 | NA | NA | 6.16 |
| xylL | Aromatics | Aromatic carboxylic acid | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 6.13 |
| mhqA | Aromatics | Nitoaromatics | 0.53 | ***0.02*** | 0.71 | ***<0.01*** | 0.43 | ***0.03*** | 6.10 |
| cpnC | Other Hydrocarbons |  | 0.14 | 0.40 | 0.29 | 0.08 | 0.54 | ***0.01*** | 5.90 |
| cah | Others |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.76 |
| pchA | Aromatics | BTEX and related aromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.69 |
| cumC | Aromatics | Other aromatics | 0.00 | 1.00 | 0.21 | ***0.04*** | 0.12 | ***0.02*** | 5.61 |
| HcaACD | Aromatics | Aromatic carboxylic acid | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.58 |
| phtB | Aromatics | Aromatic carboxylic acid | 0.42 | ***<0.01*** | 0.37 | 0.09 | 0.49 | ***0.03*** | 5.49 |
| Apc | Aromatics | BTEX and related aromatics | 0.48 | ***0.03*** | 0.42 | 0.09 | 0.48 | ***0.04*** | 5.41 |
| trzA | Herbicides related compound |  | 0.00 | 1.00 | 0.24 | ***0.04*** | 0.00 | 1.00 | 5.10 |
| nahB | Aromatics | Polycyclic aromatics | 0.45 | ***0.03*** | 0.41 | 0.06 | 0.12 | ***0.03*** | 4.96 |
| phdK | Polycyclic aromatics |  | 0.00 | 1.00 | 0.13 | 0.10 | 0.00 | 1.00 | 4.93 |
| xylXY | Aromatics | Aromatic carboxylic acid | 0.41 | ***0.02*** | 0.43 | 0.05 | 0.39 | ***0.04*** | 4.90 |
| nbz | Aromatics | Nitoaromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.87 |
| bbs | Aromatics | BTEX and related aromatics | 0.54 | ***0.04*** | 0.12 | 0.09 | 0.72 | ***<0.01*** | 4.85 |
| ebdABC | Aromatics | BTEX and related aromatics | 0.43 | ***0.04*** | 0.43 | 0.07 | 0.50 | ***0.02*** | 4.84 |
| cymC | Aromatics | Other aromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.72 |
| nbzB | Aromatics | Nitoaromatics | 0.00 | 1.00 | NA | NA | NA | NA | 4.72 |
| nphA | Aromatics | Nitoaromatics | 0.13 | ***0.05*** | 0.12 | 0.16 | 0.00 | 1.00 | 4.72 |
| cpnE | Other Hydrocarbons |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.65 |
| dfbA |  |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.63 |
| cbaA | Aromatics | Chlorinated aromatics | NA | NA | NA | NA | 0.00 | 1.00 | 4.62 |
| dbdC | Aromatics | Heterocyclic aromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.12 | ***0.01*** | 4.57 |
| bbsG | Aromatics | BTEX and related aromatics | 0.13 | ***0.03*** | 0.00 | 1.00 | 0.00 | 1.00 | 4.49 |
| tphA | Aromatics | Aromatic carboxylic acid | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.48 |
| linD | Pesticides related compound |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.12 | ***0.02*** | 4.46 |
| fcbC | Aromatics | Chlorinated aromatics | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.43 |
| xylM | Aromatics | BTEX and related aromatics | 0.00 | 1.00 | NA | NA | 0.12 | ***0.02*** | 4.33 |
| fcbB | Aromatics | Chlorinated aromatics | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.28 |
| Quinoline | Aromatics | Polycyclic aromatics | 0.00 | 1.00 | 0.13 | 0.07 | 0.00 | 1.00 | 4.23 |
| thmAB | Others |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.16 |
| Onr | Others |  | NA | NA | 0.00 | 1.00 | NA | NA | 4.13 |
| cbeA | Aromatics | Chlorinated aromatics | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.10 |
| dbdD | Aromatics | Heterocyclic aromatics | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.02 |
| badK | Aromatics | Aromatic carboxylic acid | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 3.87 |
| tcpA | Herbicides related compound |  | 0.00 | 1.00 | NA | NA | NA | NA | 3.84 |
| phdG | Aromatics | Polycyclic aromatics | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 3.80 |
| msmABCD | Others |  | NA | NA | 0.00 | 1.00 | NA | NA | 3.55 |
| alkK | Others |  | 0.48 | ***<0.01*** | 0.45 | ***<0.01*** | 0.61 | ***<0.01*** | 3.44 |
| **soil\_benifit** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| cat\_bac | antioxidant enzyme |  | 0.45 | ***<0.01*** | 0.49 | ***<0.01*** | 0.51 | ***<0.01*** | 222.13 |
| tre\_fun | drought tolerance |  | 0.56 | ***<0.01*** | 0.51 | ***<0.01*** | 0.42 | ***<0.01*** | 156.63 |
| phzF | antibiotic |  | 0.54 | ***<0.01*** | 0.42 | ***<0.01*** | 0.44 | ***<0.01*** | 144.03 |
| per\_fun | antioxidant enzyme |  | 0.46 | ***<0.01*** | 0.27 | ***0.04*** | 0.45 | ***<0.01*** | 136.09 |
| sped\_bac | plant hormone |  | 0.47 | ***0.01*** | 0.47 | ***<0.01*** | 0.56 | ***<0.01*** | 128.03 |
| pcbC | antibiotic |  | 0.43 | ***0.01*** | 0.43 | ***<0.01*** | 0.43 | ***<0.01*** | 113.92 |
| acc | other |  | 0.37 | ***<0.01*** | 0.29 | ***<0.01*** | 0.38 | ***<0.01*** | 106.45 |
| spe | plant hormone |  | 0.54 | ***<0.01*** | 0.47 | ***<0.01*** | 0.19 | 0.10 | 91.36 |
| sid\_fun | anti-pathogen |  | 0.30 | ***0.03*** | 0.53 | ***<0.01*** | 0.46 | ***<0.01*** | 63.25 |
| sod\_CuZn | antioxidant enzyme |  | 0.41 | ***<0.01*** | 0.42 | ***<0.01*** | 0.31 | ***<0.01*** | 54.92 |
| cat\_fun | antioxidant enzyme |  | 0.39 | ***0.01*** | 0.30 | 0.05 | 0.49 | ***<0.01*** | 49.96 |
| sid\_bac | anti-pathogen |  | 0.47 | ***<0.01*** | 0.37 | ***<0.01*** | 0.56 | ***<0.01*** | 34.86 |
| per\_bac | antioxidant enzyme |  | 0.27 | 0.08 | 0.22 | 0.12 | 0.44 | ***<0.01*** | 34.17 |
| sped\_fungi | plant hormone |  | 0.30 | ***0.02*** | 0.61 | ***<0.01*** | 0.32 | ***0.01*** | 16.44 |
| bacA | antibiotic |  | 0.25 | 0.13 | 0.31 | 0.08 | 0.34 | ***<0.01*** | 10.30 |
| cat\_arc | antioxidant enzyme |  | 0.16 | 0.45 | 0.35 | ***<0.01*** | 0.25 | 0.11 | 8.43 |
| lgrD | antibiotic |  | 0.45 | ***<0.01*** | 0.27 | 0.08 | 0.09 | 0.55 | 8.41 |
| pabA | antibiotic |  | 0.59 | ***0.04*** | 0.46 | ***0.03*** | 0.39 | ***0.01*** | 8.26 |
| spaR | antibiotic |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.06 | 0.63 | 7.11 |
| sid\_arc | anti-pathogen |  | 0.22 | ***0.04*** | 0.21 | ***0.04*** | 0.46 | ***0.01*** | 6.14 |
| strR | antibiotic |  | 0.43 | ***0.04*** | 0.43 | 0.07 | 0.40 | ***0.04*** | 5.78 |
| sped\_ara | plant hormone |  | 0.21 | 0.08 | 0.23 | 0.06 | 0.00 | 1.00 | 5.28 |
| sod\_nickel | antioxidant enzyme |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.18 |
| per\_arc | antioxidant enzyme |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 5.04 |
| nep | plant hormone |  | 0.12 | ***0.05*** | 0.13 | 0.10 | 0.20 | 0.08 | 4.95 |
| lipo |  |  | 0.00 | 1.00 | 0.40 | 0.09 | 0.53 | ***0.02*** | 4.80 |
| lmbA | antibiotic |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.73 |
| pec | other |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.70 |
| prnB | antibiotic |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.13 | ***0.04*** | 4.64 |
| cks | plant hormone |  | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 4.01 |
| **soil\_borne\_pathogen** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| INF1\_elicitin\_Oomycetes | elicitor | oomycete | 0.29 | ***0.04*** | 0.45 | ***<0.01*** | 0.38 | ***0.01*** | 53.80 |
| papC | adherence |  | 0.52 | ***0.01*** | 0.51 | ***<0.01*** | 0.48 | ***0.01*** | 49.88 |
| scytalone\_dehydratase\_Fungi | Pigments | Melanin | 0.35 | ***0.03*** | 0.48 | ***0.02*** | 0.38 | ***0.02*** | 29.64 |
| coat\_Nepovirus | Eukaryotic | structural | 0.41 | ***0.02*** | 0.30 | ***0.04*** | 0.10 | 0.45 | 27.16 |
| necrosis\_Oomycetes | oomycete | virulence | 0.28 | ***0.03*** | 0.32 | ***<0.01*** | 0.16 | 0.08 | 23.54 |
| RdRp\_Nepovirus | Eukaryotic | replication | 0.21 | 0.09 | 0.31 | ***0.03*** | 0.15 | 0.28 | 19.20 |
| coat\_Tombusvirus | Eukaryotic | structural | 0.17 | 0.26 | 0.54 | ***<0.01*** | 0.19 | 0.31 | 18.49 |
| serine\_protease\_inhibitor\_Oomycetes | oomycete | virulence | 0.22 | 0.19 | 0.27 | ***0.03*** | 0.25 | ***0.03*** | 18.35 |
| igaA | regulation |  | 0.40 | ***0.05*** | 0.36 | ***0.04*** | 0.63 | ***<0.01*** | 17.06 |
| mgtB | magnesium uptake |  | 0.17 | 0.28 | 0.46 | ***0.04*** | 0.09 | 0.46 | 16.10 |
| yopD | type III secretion system |  | 0.14 | 0.46 | 0.32 | 0.06 | 0.60 | ***<0.01*** | 13.54 |
| replicase\_Tombusvirus | Eukaryotic | replication | 0.18 | 0.32 | 0.64 | ***<0.01*** | 0.31 | ***0.02*** | 13.43 |
| replicase\_Carmovirus | Eukaryotic | replication | 0.48 | ***0.04*** | 0.52 | ***0.03*** | 0.21 | ***0.02*** | 10.38 |
| hrpP | type III secretion system |  | 0.42 | ***0.03*** | 0.07 | 0.48 | 0.39 | ***<0.01*** | 9.38 |
| coat\_Tobravirus | Eukaryotic | structural | 0.18 | 0.11 | 0.40 | 0.11 | 0.20 | 0.28 | 9.14 |
| vir | type IV secretion system |  | 0.32 | 0.07 | 0.43 | ***0.03*** | 0.11 | 0.34 | 9.08 |
| coat\_Aureusvirus | Eukaryotic | structural | 0.27 | ***0.03*** | -0.04 | 0.64 | 0.25 | ***0.02*** | 8.92 |
| RdRp\_Dianthovirus | Eukaryotic | replication | 0.15 | 0.21 | 0.44 | 0.07 | 0.13 | 0.49 | 8.39 |
| AVR1b\_Oomycetes | effector protein | oomycete | 0.43 | ***<0.01*** | 0.42 | ***0.01*** | 0.26 | ***0.01*** | 8.35 |
| CRN\_Oomycetes | effector protein | oomycete | 0.19 | ***0.03*** | 0.35 | ***0.03*** | 0.18 | 0.18 | 8.20 |
| hrpB2 | type III secretion system |  | 0.07 | 0.45 | 0.33 | ***<0.01*** | 0.00 | 1.00 | 7.62 |
| hrcU | type III secretion system |  | 0.52 | ***0.02*** | 0.45 | ***0.01*** | 0.45 | ***0.01*** | 7.57 |
| movement\_Furovirus | Eukaryotic | movement protein | 0.12 | 0.45 | 0.13 | 0.23 | 0.66 | ***0.01*** | 7.56 |
| pat1 | protease |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.03 | 0.76 | 7.42 |
| acsD | iron uptake |  | 0.26 | ***0.05*** | 0.25 | 0.06 | 0.61 | ***<0.01*** | 6.89 |
| txtA | toxin |  | 0.11 | 0.28 | 0.17 | 0.09 | 0.42 | 0.06 | 6.80 |
| coat\_Tritimovirus | Eukaryotic | structural | 0.36 | ***0.02*** | 0.21 | 0.06 | 0.35 | 0.08 | 6.80 |
| acsC | iron uptake |  | 0.60 | ***<0.01*** | 0.23 | ***0.04*** | 0.08 | 0.51 | 6.67 |
| actin\_\_Cercozoa | Phylogenetic |  | 0.35 | ***0.02*** | 0.00 | 1.00 | -0.03 | 0.73 | 6.36 |
| yscX | type III secretion system |  | 0.46 | ***0.02*** | 0.43 | 0.08 | 0.17 | ***0.04*** | 5.84 |
| hopAF1 | type III secretion system |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.82 |
| AVR1\_Oomycetes | effector protein | oomycete | 0.19 | 0.07 | 0.38 | ***0.02*** | 0.55 | ***0.01*** | 5.77 |
| impH | type VI secretion system |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.56 |
| hrpG | regulation |  | 0.37 | ***0.03*** | 0.00 | 1.00 | 0.23 | ***0.02*** | 5.55 |
| avrA | type III secretion system |  | 0.00 | 1.00 | 0.34 | ***<0.01*** | 0.02 | 0.71 | 5.50 |
| glucanase\_inhibitor\_Oomycetes | oomycete | virulence | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.44 |
| ATR13\_Oomycetes | effector protein | oomycete | 0.00 | 1.00 | NA | NA | NA | NA | 5.36 |
| coat\_Carmovirus | Eukaryotic | structural | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.33 |
| CBEL\_Oomycetes | effector protein | oomycete | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.30 |
| yopT | type III secretion system |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 5.16 |
| coat\_Benyvirus | Eukaryotic | structural | 0.13 | ***0.05*** | 0.00 | 1.00 | 0.00 | 1.00 | 5.14 |
| PcF\_Oomycetes | toxin | oomycete | 0.24 | 0.07 | 0.00 | 1.00 | 0.00 | 1.00 | 5.06 |
| replicase\_Tobravirus | Eukaryotic | replication | 0.00 | 1.00 | 0.00 | 1.00 | 0.12 | 0.14 | 5.05 |
| mip | intracellular survival |  | 0.44 | ***0.03*** | 0.12 | 0.13 | 0.38 | ***0.05*** | 5.03 |
| avrBs3 | type III secretion system |  | 0.56 | ***0.02*** | 0.12 | 0.06 | 0.65 | ***<0.01*** | 4.95 |
| xopD | type III secretion system | immune evasion | NA | NA | 0.00 | 1.00 | NA | NA | 4.93 |
| hasA | iron uptake |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.93 |
| replicase\_Benyvirus | Eukaryotic | replication | 0.45 | ***0.04*** | 0.37 | 0.08 | 0.41 | 0.05 | 4.91 |
| hrpY2 | type III secretion system |  | 0.12 | 0.10 | 0.00 | 1.00 | 0.00 | 1.00 | 4.77 |
| coat\_Dianthovirus | Eukaryotic | structural | 0.00 | 1.00 | 0.12 | 0.09 | 0.13 | ***<0.01*** | 4.75 |
| avrBs1 | type III secretion system |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.13 | 0.06 | 4.68 |
| tom | immune evasion | resistance to antimicrobial molecules | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.65 |
| replicase\_Cheravirus | Eukaryotic | replication | 0.13 | 0.06 | 0.12 | 0.13 | 0.12 | 0.06 | 4.64 |
| dspE | type III secretion system |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 4.45 |
| trehalose\_synthase\_Cercozoa | cercozoa | virulence | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.43 |
| virE2 | nuclear uptake |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.42 |
| coat\_furovirus | Eukaryotic | structural | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.42 |
| pch | iron uptake |  | 0.00 | 1.00 | NA | NA | NA | NA | 4.37 |
| fyuA | iron uptake |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 4.33 |
| coat\_Necrovirus | Eukaryotic | structural | 0.00 | 1.00 | 0.00 | 1.00 | NA | NA | 4.19 |
| xcpZ | type II secretion system |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 3.95 |
| esaT6 | ESX-1 secretion system |  | NA | NA | 0.00 | 1.00 | 0.00 | 1.00 | 3.91 |
| hrpX | type III secretion system |  | 0.00 | 1.00 | 0.00 | 1.00 | 0.00 | 1.00 | 3.88 |
| xcpY | type II secretion system |  | NA | NA | 0.00 | 1.00 | NA | NA | 3.59 |
| pinF1 | unclassified |  | NA | NA | 0.00 | 1.00 | NA | NA | 3.32 |
| **virulence** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| pilin | adherence |  | 0.43 | ***0.01*** | 0.50 | ***<0.01*** | 0.46 | ***<0.01*** | 269.73 |
| iro | iron uptake |  | 0.47 | ***0.01*** | 0.46 | ***<0.01*** | 0.33 | ***<0.01*** | 239.41 |
| hly | toxin | hemolysin | 0.43 | ***0.01*** | 0.57 | ***<0.01*** | 0.32 | ***0.01*** | 170.02 |
| type\_III\_secretion | type III secretion system |  | 0.48 | ***<0.01*** | 0.47 | ***<0.01*** | 0.39 | ***<0.01*** | 151.08 |
| cap | antiphagocytosis | adherence | 0.42 | ***0.02*** | 0.41 | ***<0.01*** | 0.40 | ***<0.01*** | 134.33 |
| pap | adherence |  | 0.56 | ***<0.01*** | 0.33 | ***0.03*** | 0.30 | ***0.03*** | 47.17 |
| srt | adherence | colonization | 0.20 | 0.18 | 0.31 | ***0.05*** | 0.45 | ***<0.01*** | 38.38 |
| iuc | iron uptake |  | 0.67 | ***<0.01*** | 0.35 | ***0.02*** | 0.34 | ***0.01*** | 28.91 |
| inv | invasion |  | 0.26 | ***0.03*** | 0.28 | 0.10 | 0.08 | 0.64 | 20.24 |
| vip | virulence protein |  | 0.54 | ***<0.01*** | 0.57 | ***0.02*** | 0.09 | 0.60 | 14.66 |
| toxin | toxin |  | 0.16 | 0.19 | 0.21 | 0.17 | 0.59 | ***<0.01*** | 13.82 |
| fimbriae | adherence |  | 0.00 | 1.00 | NA | NA | 0.00 | 1.00 | 4.29 |
| **other category** |  |  |  |  |  |  |  |  |  |
| **Gene Name** | Sub-category1 | Sub-category2 | R2 | *P* | R2 | *P* | R2 | *P* | Average Abundance |
| BchY | Pigments | Bacteriochlorophyll | 0.39 | ***0.02*** | 0.24 | 0.08 | 0.38 | ***<0.01*** | 69.36 |
| gyrB | Phylogenetic |  | 0.44 | ***<0.01*** | 0.43 | ***<0.01*** | 0.43 | ***<0.01*** | 11.97 |

†NA - not applicable for calculation.

**Table S5**. The difference of *amoA* gene composition between ungrazed and grazed sites at different taxonomic resolutions

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Statistic level | Species | | Genus | | Family | | Order | | Class | | Phylum | |
|  | R2 | *P* | R2 | *P* | R2 | *P* | R2 | *P* | R2 | *P* | R2 | *P* |
| C vs G | 0.412 | 0.023 \*† | 0.361 | 0.032 \* | 0.355 | 0.015\* | 0.317 | 0.047 \* | 0.383 | 0.024 \* | 0.451 | 0.008 \*\* |
| E vs EG | 0.421 | 0.007 \*\* | 0.351 | 0.0156 \* | 0.381 | 0.008 \*\* | 0.372 | 0.006 \*\* | 0.390 | 0.008 \*\* | 0.495 | 0.008 \*\* |
| D vs DG | 0.331 | 0.016 \* | 0.323 | 0.007 \*\* | 0.287 | 0.018 \* | 0.292 | 0.017 \* | 0.347 | 0.015 \* | 0.429 | 0.008 \*\* |

†Asterisk indicates significant differences based on dissimilarity test of Adonis. \*\*, *P*<0.010; \*, *P*<0.05.

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