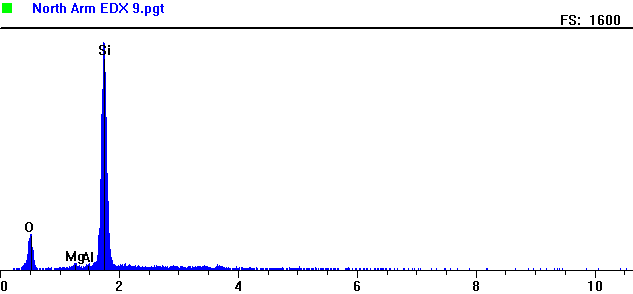


**Supp. Fig. 1**. **(A)** X-Ray Diffraction (XRD) analyses of the South Arm (SA) microbialite. **(B)** XRD analyses of the North Arm (NA) microbialite. Samples are both >95% aragonite (PDF 41-1474).

**Supp. Fig. 2.** Estimated abundances of elements in South Arm (SA) and North Arm (NA) microbialites. Data taken from multiple FEM elemental scans of a single sample for each arm.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | **Element** | **KRatio** | **Wt%** | **At%** | **Chi-Squared** | **Z Corr** | **A Corr** | **F Corr** | | O | 0.4697 | 58.77 | 71.19 | 29.57 | 0.973 | 2.240 | 0.999 | | Mg | 0.0178 | 1.70 | 1.35 | 34.07 | 1.026 | 1.637 | 0.989 | | Si | 0.4350 | 33.10 | 22.84 | 102.27 | 1.031 | 1.285 | 1.000 | | Al | 0.0775 | 6.43 | 4.62 | 93.56 | 1.059 | 1.385 | 0.983 | | **Total** | **1.0000** | **100.00** | **100.00** | **7.76** |  |  |  | |



**Supp. Fig. 3.** FEM Spot analysis shows the presence of a quartz grain within the NA microbialite. Crosshairs indicate location of spot analysis. Trace amounts of Mg and Al are also present.

**Supp. Table 1.** Genes identified in SA and NA microbialite responsible for variation in clustering   
along PCA axis 1. Genes with the abundance of >0.2 fold in either arms are shown here.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **# probe hits** | | **Annotation** | **Category** |
| **NA** | **SA** |
| *aceA* | 0 | 1 | Isocitrate lyase | Carbon Cycling |
| *aceB* | 2 | 2 | Malate synthase | Carbon Cycling |
| *amyA* | 6 | 3 | Pullulanase/amylase | Carbon Cycling |
| *ara* | 3 | 1 | Alpha-N-arabinofuranosidase | Carbon Cycling |
| *axe* | 1 | 0 | Carbohydrate esterase family 1 protein | Carbon Cycling |
| *bglB* | 1 | 0 | Beta-glucosidase | Carbon Cycling |
| *cbm1* | 1 | 0 | Putative expansin | Carbon Cycling |
| *ccmM* | 1 | 0 | Carbonate dehydratase | Carbon Cycling |
| *cda1* | 1 | 0 | Putative chitin deacetylase | Carbon Cycling |
| *chi* | 0 | 4 | Chitinase | Carbon Cycling |
| *fbp* | 2 | 1 | Fructose-1,6-bisphosphatase | Carbon Cycling |
| *fthfS* | 2 | 0 | Formate--tetrahydrofolate ligase | Carbon Cycling |
| *glx* | 1 | 0 | Glyoxal oxidase | Carbon Cycling |
| *lcc* | 0 | 2 | Laccase/phenoloxidase | Carbon Cycling |
| *man* | 0 | 1 | Mannanase/Mannan endo-1,4-beta-mannosidase | Carbon Cycling |
| *mcrA* | 1 | 0 | Methyl-coenzyme M reductase alpha subunit, partial | Carbon Cycling |
| *nplT* | 1 | 0 | Neopullulanase | Carbon Cycling |
| *pcc* | 1 | 0 | Propionyl-CoA carboxylase beta chain | Carbon Cycling |
| *pel* | 0 | 2 | Pectate lyase/pectinase | Carbon Cycling |
| *pgk* | 1 | 2 | Phosphoglycerate kinase | Carbon Cycling |
| *pme* | 1 | 0 | Unnamed protein product | Carbon Cycling |
| *pmoA* | 1 | 0 | Particulate methane monooxygenase alpha subunit | Carbon Cycling |
| *pnl3* | 1 | 0 | Pectin lyase, putative | Carbon Cycling |
| *rbcL* | 1 | 0 | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | Carbon Cycling |
| *rgaE* | 3 | 1 | Lipolytic protein G-D-S-L family | Carbon Cycling |
| *rgl* | 0 | 1 | FG-GAP repeat protein | Carbon Cycling |
| *tktA* | 1 | 1 | Transketolase | Carbon Cycling |
| *vanA* | 1 | 0 | Rieske (2Fe-2S) region | Carbon Cycling |
| *xyn* | 0 | 1 | Xylan 1,4-beta-xylosidase/xylanase | Carbon Cycling |
| *cccA* | 1 | 0 | Cytochrome | Electron transfer |
| *ccmC* | 1 | 0 | Cytochrome C | Electron transfer |
| *hynA* | 1 | 1 | NiFe hydrogenase large subunit | Electron transfer |
| *alr* | 0 | 2 | Aluminum resistance protein | Metal Homeostasis |
| *arsB* | 0 | 2 | Arsenical pump membrane protein | Metal Homeostasis |
| *arsC* | 2 | 0 | Glutaredoxin-dependent arsenate reductase | Metal Homeostasis |
| *bfr* | 0 | 1 | Putative bacterioferretin | Metal Homeostasis |
| *cadA* | 2 | 4 | Heavy metal translocating P-type ATPase | Metal Homeostasis |
| *cadBD* | 1 | 0 | Cadmium resistance transporter | Metal Homeostasis |
| *chrA* | 2 | 2 | Multidrug efflux transporter protein | Metal Homeostasis |
| *cirA* | 3 | 1 | TonB-dependent receptor | Metal Homeostasis |
| *copA* | 1 | 0 | Heavy metal translocating P-type ATPase | Metal Homeostasis |
| *corA* | 1 | 2 | Magnesium and cobalt transport protein CorA | Metal Homeostasis |
| *corC* | 1 | 0 | Magnesium and cobalt efflux protein | Metal Homeostasis |
| *cutA* | 0 | 1 | Divalent-cation tolerance protein CutA | Metal Homeostasis |
| *czcA* | 0 | 1 | Heavy metal efflux pump CzcA | Metal Homeostasis |
| *czcC* | 1 | 0 | Cobalt-zinc-cadmium resistance protein CzcC | Metal Homeostasis |
| *dps* | 1 | 0 | DNA protection during starvation protein | Metal Homeostasis |
| *fecA* | 2 | 1 | TonB-dependent outermembrane ferric citrate receptor | Metal Homeostasis |
| *feoB* | 1 | 3 | Ferrous iron transport protein B | Metal Homeostasis |
| *fepA* | 2 | 1 | Putative TonB-dependent receptor | Metal Homeostasis |
| *fhuE* | 1 | 0 | TonB-dependent siderophore receptor | Metal Homeostasis |
| *fiu* | 1 | 0 | TonB-dependent siderophore receptor | Metal Homeostasis |
| *fro* | 0 | 1 | Ferric reduction oxidase | Metal Homeostasis |
| *kefBC* | 0 | 1 | Glutathione-regulated potassium-efflux system protein | Metal Homeostasis |
| *mer* | 2 | 1 | Mercuric reductase | Metal Homeostasis |
| *merB* | 1 | 0 | Alkylmercury lyase | Metal Homeostasis |
| *mgtA* | 2 | 0 | Magnesium-transporting ATPase, P-type 1 | Metal Homeostasis |
| *mgtE* | 0 | 1 | Divalent cation transporter | Metal Homeostasis |
| *mntH* | 1 | 5 | Mn2+ and Fe2+ transporter | Metal Homeostasis |
| *mrpA* | 0 | 1 | Putative monovalent cation/H+ antiporter subunit A | Metal Homeostasis |
| *natB* | 1 | 0 | ABC-type Na+ efflux pump | Metal Homeostasis |
| *nhaA* | 2 | 0 | Na+/H+ antiporter NhaA | Metal Homeostasis |
| *nhaB* | 1 | 0 | Sodium/proton antiporter | Metal Homeostasis |
| *nhaP* | 3 | 3 | Sodium/hydrogen exchanger | Metal Homeostasis |
| *nikA* | 2 | 1 | Nickel ABC transporter | Metal Homeostasis |
| *psaA* | 0 | 1 | Manganese/iron ABC transporter substrate-binding protein | Metal Homeostasis |
| *rndA* | 1 | 1 | Heavy metal efflux pump, CzcA family | Metal Homeostasis |
| *silC* | 1 | 1 | RND efflux system, outer membrane lipoprotein, NodT | Metal Homeostasis |
| *silP* | 0 | 2 | Putative Cu-ATPase | Metal Homeostasis |
| *tehB* | 1 | 0 | Methyltransferase type 12 | Metal Homeostasis |
| *terc* | 0 | 2 | Predicted protein | Metal Homeostasis |
| *terD* | 0 | 1 | Putative export associated protein | Metal Homeostasis |
| *terZ* | 2 | 0 | Stress response protein | Metal Homeostasis |
| *terZD* | 1 | 2 | Tellurite resistance | Metal Homeostasis |
| *trkA* | 4 | 1 | Potassium/proton antiporter | Metal Homeostasis |
| *trkGH* | 1 | 2 | Potassium uptake protein, TrkH family | Metal Homeostasis |
| *zntA* | 1 | 0 | Heavy metal translocating P-type ATPase | Metal Homeostasis |
| *znuA* | 1 | 0 | Zinc ABC transporter substrate-binding protein | Metal Homeostasis |
| *znuC* | 1 | 2 | Manganese ABC transporter ATP-binding protein | Metal Homeostasis |
| *zupT* | 1 | 0 | Zinc transporter ZupT | Metal Homeostasis |
| *amt* | 1 | 1 | Ammonium transporter channel family | Nitrogen |
| *cnorB* | 1 | 0 | Nitric oxide reductase large subunit | Nitrogen |
| *gdh* | 1 | 0 | NADP-specific glutamate dehydrogenase | Nitrogen |
| *hao* | 0 | 1 | Similar to hydroxylamine oxidoreductase hao | Nitrogen |
| *narB* | 2 | 0 | Assimilatory nitrate reductase | Nitrogen |
| *narG* | 1 | 1 | Nitrate reductase alpha subunit | Nitrogen |
| *nasA* | 1 | 0 | Periplasmic nitrate reductase, large subunit | Nitrogen |
| *nifH* | 0 | 3 | Nitrogenase iron protein | Nitrogen |
| *Nir* | 1 | 0 | Nitrite reductase | Nitrogen |
| *nirK* | 1 | 0 | Nitrite reductase | Nitrogen |
| *nirS* | 0 | 1 | Nitrite reductase | Nitrogen |
| *nosZ* | 2 | 1 | Nitrous oxide reductase | Nitrogen |
| *ureC* | 0 | 1 | Urease | Nitrogen |
| *atzA* | 0 | 1 | Amidohydrolase | Organic Remediation |
| *badH* | 0 | 1 | Alcohol dehydrogenase zinc-binding domain protein | Organic Remediation |
| *bcoA* | 1 | 0 | 2-hydroxyglutaryl-coa dehydratase, subunit alpha | Organic Remediation |
| *benA* | 2 | 1 | Benzoate 1,2-dioxygenase | Organic Remediation |
| *catA* | 0 | 2 | Catechol 2,3 dioxygenase/catechol\_b | Organic Remediation |
| *catB* | 2 | 1 | Muconate cycloisomerase I protein | Organic Remediation |
| *dehH* | 0 | 1 | Haloacid dehalogenase, type II | Organic Remediation |
| *dmsA* | 1 | 0 | Anaerobic dimethyl sulfoxide reductase chain A | Organic Remediation |
| *ebdA* | 1 | 0 | Ethylbenzene dehydrogenase, alpha subunit | Organic Remediation |
| *exaA* | 1 | 1 | Putative quinoprotein glucose dehydrogenase | Organic Remediation |
| *hcaE* | 0 | 1 | Phenylpropionate dioxygenase | Organic Remediation |
| *mdlA* | 0 | 1 | Muconate and chloromuconate cycloisomerases | Organic Remediation |
| *mhpA* | 1 | 0 | Putative hydroxylase | Organic Remediation |
| *msmA* | 1 | 0 | Methanesulfonate monooxygenase, hydroxylase alpha subunit | Organic Remediation |
| *nagG* | 1 | 0 | Putative salicylate 1-monooxygenase | Organic Remediation |
| *nfsA\_2* | 0 | 1 | Oxygen-insensitive NAD | Organic Remediation |
| *nfsB\_2* | 0 | 1 | NAD(P)H-flavin oxidoreductase | Organic Remediation |
| *nit* | 1 | 1 | Nitrilase | Organic Remediation |
| *oxoO* | 1 | 0 | Putative 2-oxo-1 2-dihydroquinoline 8-monooxygenase oxygenase subunit | Organic Remediation |
| *phn* | 2 | 0 | Phosphorous compounds metabolism-like protein | Organic Remediation |
| *proO* | 1 | 1 | Alpha-subunit of protocatechuate 4,5-dioxygenase | Organic Remediation |
| *tfdA* | 1 | 0 | Taurine dioxygenase | Organic Remediation |
| *tfdB* | 1 | 0 | 2,4-dichlorophenol 6-monooxygenase | Organic Remediation |
| *tftH* | 0 | 1 | Hydroxyquinol 1,2-dioxygenase/Catechol 1,2-dioxygenase | Organic Remediation |
| *cas1* | 0 | 1 | CRISPR-associated protein Cas1 | Other |
| *cas2* | 0 | 1 | CRISPR-associated protein Cas2 | Other |
| *cas3* | 0 | 1 | CRISPR-associated helicase Cas3 | Other |
| *cas6* | 1 | 0 | CRISPR-associated protein CT1974 | Other |
| *cas8* | 2 | 0 | CRISPR-associated protein\_ CT1133 | Other |
| *cmr5* | 0 | 1 | CRISPR-associated protein, Cmr5 family | Other |
| *cmr6* | 1 | 0 | CRISPR-associated RAMP protein, Cmr6 family | Other |
| *gyrB* | 5 | 2 | DNA gyrase, B subunit | Other |
| *hsp90* | 1 | 0 | 90 kDa heat-shock protein | Other |
| *ppk* | 1 | 3 | Polyphosphate kinase | Phosphorus |
| *ppk2* | 1 | 2 | Polyphosphate kinase | Phosphorus |
| *ppx* | 1 | 2 | Exopolyphosphatase | Phosphorus |
| *bciA* | 1 | 0 | Predicted protein | Secondary metabolism |
| *blh* | 1 | 0 | Bacteriorhodopsin related protein | Secondary metabolism |
| *cat* | 1 | 1 | Catalase | secondary metabolism |
| *chlL* | 0 | 1 | Magnesium chelatase | Secondary metabolism |
| *crtC* | 1 | 0 | Hydroxyneurosporene synthase | Secondary metabolism |
| *crtX* | 0 | 1 | Zeaxanthin glucosyl transferase | Secondary metabolism |
| *sod* | 1 | 0 | Superoxide dismutase | secondary metabolism |
| *speD* | 0 | 1 | Spermidine synthase | secondary metabolism |
| *ahpC* | 1 | 0 | Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen | Stress |
| *ahpF* | 0 | 1 | Alkyl hydroperoxide reductase subunit F | Stress |
| *clpP* | 2 | 1 | ATP-dependent Clp protease, proteolytic subunit ClpP | Stress |
| *cpxR* | 1 | 0 | Two component transcriptional regulator, winged helix family | Stress |
| *cspA* | 1 | 0 | Cold shock protein CspA | Stress |
| *cydB* | 1 | 1 | Cytochrome d ubiquinol oxidase, subunit II | Stress |
| *degP* | 1 | 0 | Periplasmic trypsin-like serine protease | Stress |
| *fnr* | 5 | 1 | Crp/FNR family transcriptional regulator | Stress |
| *katA* | 0 | 1 | Catalase | Stress |
| *katE* | 1 | 0 | Catalase | Stress |
| *kdpE* | 0 | 1 | Two component transcriptional regulator, winged helix family | Stress |
| *mtrB* | 1 | 0 | Two-component histidine kinase MtrB, partial | Stress |
| *narI* | 0 | 1 | Respiratory nitrate reductase, gamma subunit | Stress |
| *narJ* | 1 | 0 | Nitrate reductase maturase | Stress |
| *ntrB* | 2 | 0 | Nitrogen regulation protein NtrB | Stress |
| *ntrC* | 1 | 0 | Fis family two component sigma-54 specific transcriptional regulator | Stress |
| *obgE* | 0 | 2 | Possible GTP-binding protein | Stress |
| *ompR* | 1 | 1 | Response regulator (with CheY-like receiver domain and winged-helix DNA-binding domain) | Stress |
| *oxyR* | 1 | 0 | LysR family transcriptional regulator | Stress |
| *phoB* | 0 | 1 | DNA-binding response regulator PhoB | Stress |
| *pspA* | 0 | 1 | PspA/IM30 family protein | Stress |
| *pspC* | 1 | 0 | Phage shock protein C, PspC | Stress |
| *pspF* | 2 | 0 | Sigma-54 dependent transcriptional regulator | Stress |
| *pstA* | 1 | 0 | Phosphate-transport integral membrane ABC transporter, PstA | Stress |
| *pstS* | 1 | 0 | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS | Stress |
| *rpoD* | 1 | 2 | RNA polymerase sigma factor 70 (RpoD) | Stress |
| *rpoE* | 1 | 3 | RNA polymerase, sigma-24 subunit (RpoE), ECF subfamily | Stress |
| *rpoH* | 1 | 1 | RNA polymerase, sigma 32 subunit, RpoH | Stress |
| *rpoS* | 0 | 1 | RNA polymerase sigma factor 38 (RpoS) | Stress |
| *soxR* | 1 | 0 | Redox-sensitive transcriptional activator SoxR | Stress |
| *spoT* | 1 | 0 | Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase | Stress |
| *tps* | 1 | 0 | Trehalose-phosphatase | Stress |
| *apsA* | 0 | 1 | Adenosine-5'-phosphosulfate reductase alpha subunit, partial | Sulfur |
| *cysI* | 2 | 0 | Sulfite reductase beta | Sulfur |
| *cysJ* | 1 | 0 | Molybdopterin oxidoreductase | Sulfur |
| *dsrA* | 1 | 1 | Sulfite reductase alpha | Sulfur |
| *fccAB* | 0 | 1 | Sulfide dehydrogenase flavoprotein subunit | Sulfur |
| *soxA* | 1 | 0 | Putative cytochrome c | Sulfur |
| *soxB* | 1 | 0 | Sulfur oxidation protein SoxB | Sulfur |
| *soxY* | 0 | 2 | Probable sulfite oxidase molybdopterin subunit | Sulfur |
| *ampC* | 0 | 1 | Penicillin-binding protein, beta-lactamase class C | Virulence |
| *bclA* | 0 | 1 | Benzoate-CoA ligase | virulence |
| *bsaK* | 1 | 0 | Type III secretion system protein BsaK | virulence |
| *ccmA* | 1 | 3 | ABC transporter ATPase | Virulence |
| *hly* | 0 | 2 | Putative hemolysin III | virulence |
| *impH* | 1 | 0 | ImpH (secretion protein) | virulence |
| *iro* | 1 | 0 | TonB-dependent siderophore receptor | virulence |
| *mex* | 6 | 7 | RND family hydrophobe/amphiphile efflux pump | Virulence |
| *mfs* | 11 | 10 | Major facilitator superfamily | Virulence |
| *nhABC1* | 0 | 1 | Pleiotropic drug resistance ABC transporter | virulence |
| *npp1* | 1 | 0 | Necrosis inducing protein | virulence |
| *pdr* | 2 | 0 | Pleiotropic drug resistance ABC transporter | virulence |
| *penP* | 0 | 1 | Penicillin-binding protein, beta-lactamase class A | Virulence |
| *ral* | 1 | 0 | Elicitin-like protein | virulence |
| *smr* | 3 | 0 | Small multidrug resistance protein | Virulence |
| *tet* | 1 | 1 | GTP-binding elongation factor protein, TetM/TetO family | Virulence |
| *vir* | 1 | 0 | Type IV secretion system protein B4, putative | virulence |
| *rdrp2* | 2 | 0 | RNA-dependent RNA polymerase | virus |
| *vp4* | 0 | 1 | Polyprotein | Virus |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Supp. Table 2.** Taxonomy and abundance ratios of genes identified that contributed to clustering of SA microbialites along PCA axis 1. | | | | |  |
| **Genbank** | **Organism** | **Gene** | **Abundance ratio (SA/NA)** | **Annotation** | **Category** | |
| 222440846 | Labrenzia alexandrii DFL-11 | *ppk2* | 1.22 | Polyphosphate kinase | Phosphorus | |
| 425481180 | Brevibacterium casei S18 | *ppk2* | 1.20 | Polyphosphate kinase | Phosphorus | |
| 395141258 | Propionibacterium propionicum F0230a | *ccmA* | 1.44 | ABC transporter ATPase | Virulence | |
| 229005897 | Bacillus mycoides Rock1-4 | *ccmA* | 1.20 | ABC transporter ATPase | Virulence | |
| 5918764 | Streptococcus mutans | *ccmA* | 1.20 | ABC transporter ATPase | Virulence | |
| 302885122 | Nectria haematococca mpVI 77-13-4 | *nhABC1* | 1.20 | Pleiotropic drug resistance ABC transporter | Virulence | |
| 350572275 | Neisseria wadsworthii 9715 | *aceA* | 1.34 | Isocitrate lyase | Carbon\_Cycling | |
| 98977496 | Sphingopyxis alaskensis RB2256 | *aceB* | 1.23 | Malate synthase | Carbon\_Cycling | |
| 333920797 | Amycolicicoccus subflavus DQS3-9A1 | *aceB* | 1.20 | Malate synthase | Carbon\_Cycling | |
| 167654708 | Anaerostipes caccae DSM 14662 | *ahpF* | 1.31 | Alkyl hydroperoxide reductase subunit F | Stress | |
| 10174981 | Bacillus halodurans C-125 | *alr* | 1.25 | Aluminum resistance protein | Metal\_Homeostasis | |
| 323141021 | Phascolarctobacterium succinatutens YIT 12067 | *alr* | 1.21 | Aluminum resistance protein | Metal\_Homeostasis | |
| 217410516 | Phaeodactylum tricornutum CCAP 1055/1 | *amt* | 1.22 | Ammonium transporter channel family | Nitrogen | |
| 289691664 | Mycobacterium tuberculosis T92 | *amyA* | 1.38 | Pullulanase/amylase | Carbon\_Cycling | |
| 377523082 | Gordonia otitidis NBRC 100426 | *amyA* | 1.26 | Pullulanase/amylase | Carbon\_Cycling | |
| 254262253 | Enterobacter helveticus | *amyA* | 1.26 | Pullulanase/amylase | Carbon\_Cycling | |
| 134298506 | Desulfotomaculum reducens MI-1 | *apsA* | 1.24 | Adenosine-5'-phosphosulfate reductase alpha subunit, partial | Sulfur | |
| 198270009 | Bacteroides plebeius DSM 17135 | *ara* | 1.23 | Alpha-N-arabinofuranosidase | Carbon\_Cycling | |
| 359772524 | Gordonia effusa NBRC 100432 | *arsB* | 1.28 | Arsenical pump membrane protein | Metal\_Homeostasis | |
| 385151748 | Bacillus sp. CH83 | *arsB* | 1.21 | Arsenical pump membrane protein | Metal\_Homeostasis | |
| 302325819 | Fibrobacter succinogenes subsp. succinogenes S85 | *atzA* | 1.22 | Amidohydrolase | Organic\_Remediation | |
| 190686677 | Cellvibrio japonicus Ueda107 | *penP* | 1.20 | Penicillin-binding protein, beta-lactamase class A | Virulence | |
| 254510297 | Rhodobacteraceae bacterium KLH11 | *ampC* | 1.29 | Penicillin-binding protein, beta-lactamase class C | Virulence | |
| 377832665 | Lactobacillus mucosae LM1 | *badH* | 1.24 | Alcohol dehydrogenase zinc-binding domain protein | Organic\_Remediation | |
| 375093907 | Saccharomonospora marina XMU15 | *benA* | 1.24 | Benzoate 1,2-dioxygenase | Virulence | |
| 348013219 | Neisseria shayeganii 871 | *bfr* | 1.23 | Putative bacterioferretin | Metal\_Homeostasis | |
| 84386611 | Vibrio splendidus 12B01 | *cadA* | 1.30 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 159892576 | Herpetosiphon aurantiacus ATCC 23779 | *cadA* | 1.23 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 118504792 | Pelobacter propionicus DSM 2379 | *cadA* | 1.22 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 384424192 | Vibrio cholerae LMA3984-4 | *cadA* | 1.21 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 219546464 | Methanosphaerula palustris E1-9c | *cas1* | 1.27 | CRISPR-associated protein Cas1 | Other | |
| 221156275 | Thermomicrobium roseum DSM 5159 | *cas2* | 1.22 | CRISPR-associated protein Cas2 | Other | |
| 296852183 | Meiothermus silvanus DSM 9946 | *cas3* | 1.25 | CRISPR-associated helicase Cas3 | Other | |
| 91796021 | Chromohalobacter salexigens DSM 3043 | *cat* | 1.21 | Catalase | Secondary\_metabolism | |
| 56798785 | uncultured bacterium | *catA* | 1.21 | Catechol 2,3 dioxygenase/catechol\_b | Organic\_Remediation | |
| 161339347 | uncultured bacterium | *catA* | 1.21 | Catechol 2,3 dioxygenase/catechol\_b | Organic\_Remediation | |
| 209535597 | Rhizobium leguminosarum bv. trifolii WSM2304 | *catA* | 1.21 | Catechol 2,3 dioxygenase/catechol\_b | Organic\_Remediation | |
| 161611272 | Ralstonia eutropha JMP134 | *catB* | 1.20 | Muconate cycloisomerase I protein | Organic\_Remediation | |
| 83632559 | Hahella chejuensis KCTC 2396 | *chi* | 1.32 | Chitinase | Carbon\_Cycling | |
| 155121777 | Paramecium bursaria chlorella virus MT325 | *chi* | 1.25 | Chitinase | Carbon\_Cycling | |
| 133778542 | uncultured bacterium | *chi* | 1.25 | Chitinase | Carbon\_Cycling | |
| 149279875 | Pedobacter sp. BAL39 | *chi* | 1.24 | Chitinase | Carbon\_Cycling | |
| 113890133 | Shewanella sp. MR-7 | *chrA* | 1.30 | Multidrug efflux transporter protein | Metal\_Homeostasis | |
| 91790708 | Polaromonas sp. JS666 | *chrA* | 1.23 | Multidrug efflux transporter protein | Metal\_Homeostasis | |
| 391858002 | Hydrocarboniphaga effusa AP103 | *cirA* | 1.23 | TonB-dependent receptor | Metal\_Homeostasis | |
| 410090223 | Pseudomonas viridiflava UASWS0038 | *clpP* | 1.27 | ATP-dependent Clp protease, proteolytic subunit ClpP | Stress | |
| 297145359 | Syntrophothermus lipocalidus DSM 12680 | *cmr5* | 1.21 | CRISPR-associated protein, Cmr5 family | Other | |
| 118469365 | Mycobacterium smegmatis str. MC2 155 | *corA* | 1.32 | Magnesium and cobalt transport protein CorA | Metal\_Homeostasis | |
| 345639289 | Streptomyces zinciresistens K42 | *corA* | 1.25 | Magnesium and cobalt transport protein CorA | Metal\_Homeostasis | |
| 383764493 | Caldilinea aerophila DSM 14535 = NBRC 104270 | *cutA* | 1.23 | Divalent-cation tolerance protein CutA | Metal\_Homeostasis | |
| 145297807 | Aeromonas salmonicida subsp. salmonicida A449 | *cydB* | 1.20 | Cytochrome d ubiquinol oxidase, subunit II | Stress | |
| 88858182 | Pseudoalteromonas tunicata D2 | *czcA* | 1.21 | Heavy metal efflux pump CzcA | Metal\_Homeostasis | |
| 78693202 | Bradyrhizobium sp. BTAi1 | *dehH* | 1.20 | Haloacid dehalogenase, type II | Organic\_Remediation | |
| 46519969 | uncultured sulfate-reducing bacterium | *dsrA* | 1.20 | Sulfite reductase alpha | Sulfur | |
| 389872731 | Advenella kashmirensis WT001 | *exaA* | 1.29 | Putative quinoprotein glucose dehydrogenase | Organic\_Remediation | |
| 133737732 | Herminiimonas arsenicoxydans | *fbp* | 1.21 | Fructose-1,6-bisphosphatase | Carbon\_Cycling | |
| 333984318 | Methylomonas methanica MC09 | *fccAB* | 1.22 | Sulfide dehydrogenase flavoprotein subunit | Sulfur | |
| 378949796 | Pseudomonas fluorescens F113 | *fecA* | 1.20 | TonB-dependent outermembrane ferric citrate receptor | Metal\_Homeostasis | |
| 228699379 | Bacillus cereus Rock3-44 | *feoB* | 1.28 | Ferrous iron transport protein B | Metal\_Homeostasis | |
| 329903455 | Oxalobacteraceae bacterium IMCC9480 | *feoB* | 1.21 | Ferrous iron transport protein B | Metal\_Homeostasis | |
| 226716885 | Laribacter hongkongensis HLHK9 | *feoB* | 1.21 | Ferrous iron transport protein B | Metal\_Homeostasis | |
| 386923529 | Escherichia blattae DSM 4481 | *fepA* | 1.21 | Putative TonB-dependent receptor | Metal\_Homeostasis | |
| 148553878 | Sphingomonas wittichii RW1 | *fnr* | 1.21 | Crp/FNR family transcriptional regulator | Stress | |
| 260942327 | Clavispora lusitaniae ATCC 42720 | *fro* | 1.24 | Ferric reduction oxidase | Metal\_Homeostasis | |
| 154154413 | Parvibaculum lavamentivorans DS-1 | *gyrB* | 1.26 | DNA gyrase, B subunit | Other | |
| 35210351 | Sulfobacillus thermosulfidooxidans | *gyrB* | 1.21 | DNA gyrase, B subunit | Other | |
| 222354086 | uncultured bacterium | *hao* | 1.23 | Similar to hydroxylamine oxidoreductase hao | Nitrogen | |
| 121609632 | Verminephrobacter eiseniae EF01-2 | *hcaE* | 1.25 | Phenylpropionate dioxygenase | Organic\_Remediation | |
| 224803011 | Opitutaceae bacterium TAV2 | *hly* | 1.24 | Putative hemolysin III | Virulence | |
| 226092209 | Gemmatimonas aurantiaca T-27 | *hly* | 1.21 | Putative hemolysin III | Virulence | |
| 239904916 | Desulfovibrio magneticus RS-1 | *hynA* | 1.23 | NiFe hydrogenase large subunit | Electron\_transfer | |
| 229592876 | Pseudomonas fluorescens SBW25 | *katA* | 1.24 | Catalase | Stress | |
| 167668707 | Anaerotruncus colihominis DSM 17241 | *kdpE* | 1.21 | Two component transcriptional regulator, winged helix family | Stress | |
| 170719413 | Pseudomonas putida W619 | *kefBC* | 1.24 | Glutathione-regulated potassium-efflux system protein | Metal\_Homeostasis | |
| 169848689 | Coprinopsis cinerea okayama7#130 | *lcc* | 1.23 | Laccase/phenoloxidase | Carbon\_Cycling | |
| 116507776 | Coprinopsis cinerea okayama7#130 | *lcc* | 1.23 | Laccase/phenoloxidase | Carbon\_Cycling | |
| 302418412 | Verticillium albo-atrum VaMs.102 | *man* | 1.30 | Mannanase/Mannan endo-1,4-beta-mannosidase | Carbon\_Cycling | |
| 110634296 | Mesorhizobium sp. BNC1 | *mdlA* | 1.20 | Muconate and chloromuconate cycloisomerases | Organic\_Remediation | |
| 214044173 | Roseobacter sp. GAI101 | *mer* | 1.21 | Mercuric reductase | Metal\_Homeostasis | |
| 311220562 | Rhodomicrobium vannielii ATCC 17100 | *mex* | 1.31 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 356676558 | SAR116 cluster alpha proteobacterium HIMB100 | *mex* | 1.23 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 295441357 | Burkholderia sp. CCGE1002 | *mex* | 1.23 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 398194172 | Pseudomonas sp. GM60 | *mex* | 1.23 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 395652730 | Pseudomonas extremaustralis 14-3 substr. 14-3b | *mex* | 1.21 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 56696409 | Ruegeria pomeroyi DSS-3 | *mex* | 1.20 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 379045420 | Frateuria aurantia DSM 6220 | *mex* | 1.20 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 398842837 | Pseudomonas sp. GM102 | *mfs* | 1.55 | Major facilitator superfamily | Virulence | |
| 296093999 | Thermobispora bispora DSM 43833 | *mfs* | 1.27 | Major facilitator superfamily | Virulence | |
| 170769757 | Escherichia albertii TW07627 | *mfs* | 1.27 | Major facilitator superfamily | Virulence | |
| 288915114 | Azospirillum sp. B510 | *mfs* | 1.25 | Major facilitator superfamily | Virulence | |
| 72121612 | Ralstonia eutropha JMP134 | *mfs* | 1.22 | Major facilitator superfamily | Virulence | |
| 261407632 | Paenibacillus sp. Y412MC10 | *mfs* | 1.21 | Major facilitator superfamily | Virulence | |
| 400291656 | Actinomyces naeslundii str. Howell 279 | *mfs* | 1.21 | Major facilitator superfamily | Virulence | |
| 296026497 | Tsukamurella paurometabola DSM 20162 | *mfs* | 1.21 | Major facilitator superfamily | Virulence | |
| 377557678 | Gordonia otitidis NBRC 100426 | *mfs* | 1.20 | Major facilitator superfamily | Virulence | |
| 377558031 | Gordonia otitidis NBRC 100426 | *mfs* | 1.20 | Major facilitator superfamily | Virulence | |
| 303278902 | Micromonas pusilla CCMP1545 | *chlL* | 1.20 | Magnesium chelatase | Secondary\_metabolism | |
| 332971182 | Psychrobacter sp. 1501(2011) | *mgtE* | 1.33 | Divalent cation transporter | Metal\_Homeostasis | |
| 77964244 | Burkholderia sp. 383 | *mntH* | 1.37 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 296393720 | Segniliparus rotundus DSM 44985 | *mntH* | 1.23 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 325572110 | Enterococcus casseliflavus ATCC 12755 | *mntH* | 1.23 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 325284842 | Deinococcus proteolyticus MRP | *mntH* | 1.21 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 396093726 | Enterobacter radicincitans DSM 16656 | *mntH* | 1.20 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 83840114 | Sulfitobacter sp. NAS-14.1 | *mrpA* | 1.25 | Putative monovalent cation/H+ antiporter subunit A | Metal\_Homeostasis | |
| 32307983 | uncultured bacterium | *narG* | 1.29 | Nitrate reductase alpha subunit | Nitrogen | |
| 336391801 | Lactobacillus coryniformis subsp. torquens KCTC 3535 | *narI* | 1.21 | Respiratory nitrate reductase, gamma subunit | Stress | |
| 225024493 | Eikenella corrodens ATCC 23834 | *nfsA\_2* | 1.26 | Oxygen-insensitive NAD | Organic\_Remediation | |
| 146310732 | Enterobacter sp. 638 | *nfsB\_2* | 1.29 | NAD(P)H-flavin oxidoreductase | Organic\_Remediation | |
| 390616613 | Mycobacterium chubuense NBB4 | *nhaP* | 1.25 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 68346366 | Pseudomonas fluorescens Pf-5 | *nhaP* | 1.23 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 157324475 | Serratia proteamaculans 568 | *nhaP* | 1.20 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 89512486 | uncultured nitrogen-fixing bacterium | *nifH* | 1.21 | Nitrogenase iron protein | Nitrogen | |
| 218759964 | Desulfatibacillum alkenivorans AK-01 | *nifH* | 1.21 | Nitrogenase iron protein | Nitrogen | |
| 290781797 | Megasphaera genomosp. type\_1 str. 28L | *nifH* | 1.21 | Nitrogenase iron protein | Nitrogen | |
| 300533676 | Corynebacterium genitalium ATCC 33030 | *nikA* | 1.32 | Peptide ABC transporter substrate-binding protein | Metal\_Homeostasis | |
| 68349021 | Pseudomonas sp. C10-2 | *nirS* | 1.21 | Nitrite reductase | Nitrogen | |
| 145577814 | Pseudomonas mendocina ymp | *nit* | 1.25 | Nitrilase | Organic\_Remediation | |
| 422314469 | uncultured bacterium | *nosZ* | 1.22 | Nitrous oxide reductase | Nitrogen | |
| 227949507 | Meiothermus ruber DSM 1279 | *obgE* | 1.22 | Possible GTP-binding protein | Stress | |
| 206685517 | Rhodobacterales bacterium Y4I | *obgE* | 1.21 | Possible GTP-binding protein | Stress | |
| 343917108 | Thiorhodococcus drewsii AZ1 | *ompR* | 1.34 | Response regulator(with CheY-like receiver domain and winged-helix DNA-binding domain) | Stress | |
| 358456673 | Frankia sp. CN3 | *pel* | 1.31 | Pectate lyase/pectinase | Carbon\_Cycling | |
| 59044731 | uncultured bacterium | *pel* | 1.23 | Pectate lyase/pectinase | Carbon\_Cycling | |
| 296114907 | Gluconacetobacter hansenii ATCC 23769 | *pgk* | 1.28 | Phosphoglycerate kinase | Carbon\_Cycling | |
| 294677245 | Rhodobacter capsulatus SB 1003 | *pgk* | 1.21 | Phosphoglycerate kinase | Carbon\_Cycling | |
| 224609817 | Thioalkalivibrio sp. K90mix | *phoB* | 1.24 | DNA-binding response regulator PhoB | Stress | |
| 319798783 | mine drainage metagenome | *ppk* | 1.31 | Polyphosphate kinase | Phosphorus | |
| 255319138 | Acinetobacter radioresistens SK82 | *ppk* | 1.24 | Polyphosphate kinase | Phosphorus | |
| 347580877 | Gluconacetobacter xylinus NBRC 3288 | *ppk* | 1.21 | Polyphosphate kinase | Phosphorus | |
| 357031000 | Gluconobacter morbifer G707 | *ppx* | 1.28 | Exopolyphosphatase | Phosphorus | |
| 71555864 | Pseudomonas syringae pv. phaseolicola 1448A | *ppx* | 1.24 | Exopolyphosphatase | Phosphorus | |
| 384083608 | gamma proteobacterium HIMB30 | *proO* | 1.24 | Alpha-subunit of protocatechuate 4,5-dioxygenase | Organic\_Remediation | |
| 389784279 | Rhodanobacter spathiphylli B39 | *pspA* | 1.22 | PspA/IM30 family protein | Stress | |
| 458299 | Human coxsackievirus A16 | *vp4* | 1.27 | Polyprotein | Virus | |
| 357203825 | Paenibacillus terrae HPL-003 | *rgaE* | 1.27 | Lipolytic protein G-D-S-L family | Carbon\_Cycling | |
| 291544608 | Ruminococcus sp. 18P13 | *rgl* | 1.24 | FG-GAP repeat protein | Carbon\_Cycling | |
| 372266776 | Alteromonas sp. S89 | *rndA* | 1.26 | Heavy metal efflux pump, CzcA family | Metal\_Homeostasis | |
| 418055861 | Hyphomicrobium denitrificans 1NES1 | *rpoE* | 1.25 | RNA polymerase, sigma-24 subunit (RpoE), ECF subfamily | Stress | |
| 156741641 | Roseiflexus castenholzii DSM 13941 | *rpoE* | 1.22 | RNA polymerase, sigma-24 subunit (RpoE), ECF subfamily | Stress | |
| 304407705 | Paenibacillus curdlanolyticus YK9 | *rpoE* | 1.22 | RNA polymerase, sigma-24 subunit (RpoE), ECF subfamily | Stress | |
| 324982175 | Kingella denitrificans ATCC 33394 | *rpoH* | 1.24 | RNA polymerase, sigma 32 subunit, RpoH | Stress | |
| 409121678 | Pseudomonas sp. Chol1 | *rpoS* | 1.21 | RNA polymerase sigma factor 38 (RpoS) | Stress | |
| 218297363 | Thermus aquaticus Y51MC23 | *rpoD* | 1.31 | RNA polymerase sigma factor 70 (RpoD) | Stress | |
| 167664305 | Clostridium scindens ATCC 35704 | *rpoD* | 1.25 | RNA polymerase sigma factor 70 (RpoD) | Stress | |
| 117986546 | Burkholderia phymatum STM815 | *silC* | 1.20 | RND efflux system, outer membrane lipoprotein, NodT | Metal\_Homeostasis | |
| 116062787 | Aeropyrum pernix K1 | *silP* | 1.29 | Putative Cu-ATPase | Metal\_Homeostasis | |
| 322694486 | Metarhizium acridum CQMa 102 | *silP* | 1.22 | Putative Cu-ATPase | Metal\_Homeostasis | |
| 170777897 | Leptothrix cholodnii SP-6 | *soxY* | 1.32 | Probable sulfite oxidase molybdopterin subunit | Sulfur | |
| 254474672 | Ruegeria sp. R11 | *soxY* | 1.23 | Probable sulfite oxidase molybdopterin subunit | Sulfur | |
| 149358352 | Marinobacter algicola DG893 | *speD* | 1.21 | Spermidine synthase | Secondary\_metabolism | |
| 291295379 | Meiothermus ruber DSM 1279 | *terc* | 1.26 | Predicted protein | Metal\_Homeostasis | |
| 259169713 | Lactobacillus antri DSM 16041 | *terc* | 1.20 | Predicted protein | Metal\_Homeostasis | |
| 78061122 | Burkholderia sp. 383 | *terD* | 1.23 | Putative export associated protein | Metal\_Homeostasis | |
| 391355192 | Desulfosporosinus acidiphilus SJ4 | *terZD* | 1.40 | Tellurite resistance | Metal\_Homeostasis | |
| 332187545 | Sphingomonas sp. S17 | *terZD* | 1.30 | Tellurite resistance | Metal\_Homeostasis | |
| 331083575 | Lachnospiraceae bacterium 6\_1\_63FAA | *tet* | 1.27 | GTP-binding elongation factor protein, TetM/TetO family | Virulence | |
| 194292157 | Cupriavidus taiwanensis LMG 19424 | *tftH* | 1.22 | Catechol 1,2-dioxygenase | Organic\_Remediation | |
| 375055287 | Rhizobium sp. PDO-076 | *tktA* | 1.20 | Transketolase | Carbon\_Cycling | |
| 336315180 | Rheinheimera sp. A13L | *trkA* | 1.25 | Potassium/proton antiporter | Metal\_Homeostasis | |
| 89099428 | Bacillus sp. NRRL B-14911 | *trkGH* | 1.22 | Potassium uptake protein, TrkH family | Metal\_Homeostasis | |
| 217990143 | Bacteroides] pectinophilus ATCC 43243 | *trkGH* | 1.20 | Potassium uptake protein, TrkH family | Metal\_Homeostasis | |
| 389871545 | Advenella kashmirensis WT001 | *ureC* | 1.24 | Urease | Nitrogen | |
| 283472098 | Xanthomonas albilineans GPE PC73 | *xyn* | 1.23 | Xylan 1,4-beta-xylosidase/xylanase | Carbon\_Cycling | |
| 333900581 | Pseudomonas fulva 12-X | *crtX* | 1.26 | Zeaxanthin glucosyl transferase | Secondary\_metabolism | |
| 350561554 | Thioalkalivibrio thiocyanoxidans ARh 4 | *znuC* | 1.22 | Manganese ABC transporter ATP-binding protein | Metal\_Homeostasis | |
| 88798730 | Reinekea sp. MED297 | *znuC* | 1.21 | Manganese ABC transporter ATP-binding protein | Metal\_Homeostasis | |

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| **Supp. Table 3.** Taxonomy and abundance ratios of genes identified that contributed to clustering of NA microbialites along PCA axis 1. | | | | |  |
| **Genbank** | **Organism** | **Gene** | **Abundance Ratio (NA/SA)** | **Annotation** | **Category** | |
| 146188565 | uncultured sulfate-reducing bacterium | *dsrA* | 1.52 | Sulfite reductase alpha | Sulfur | |
| 332372314 | uncultured bacterium | *rbcL* | 1.46 | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | Carbon\_Cycling | |
| 343798237 | Thiocapsa marina 5811 | *rndA* | 1.46 | Heavy metal efflux pump, CzcA family | Metal\_Homeostasis | |
| 157780232 | Savillea micropora | *hsp90* | 1.45 | 90 kDa heat-shock protein | Other | |
| 269212765 | Actinomyces sp. oral taxon 848 str. F0332 | *gyrB* | 1.42 | DNA gyrase, B subunit | Other | |
| 398353894 | Sinorhizobium fredii USDA 257 | *mfs* | 1.39 | Membrane transporter | Virulence | |
| 118765785 | Bifidobacterium adolescentis ATCC 15703 | *cas8* | 1.38 | CRISPR-associated protein\_ CT1133 | Other | |
| 307774532 | Roseibium sp. TrichSKD4 | *ntrB* | 1.38 | Nitrogen regulation protein NtrB | Stress | |
| 379059290 | Serinicoccus profundi MCCC 1A05965 | *amyA* | 1.37 | Pullulanase/amylase | Carbon\_Cycling | |
| 76883226 | Nitrosococcus oceani ATCC 19707 | *rndA* | 1.37 | Heavy metal efflux pump, CzcA family | Metal\_Homeostasis | |
| 374367281 | Cupriavidus basilensis OR16 | *catB* | 1.36 | Muconate cycloisomerase I protein | Organic\_Remediation | |
| 350531930 | Vibrio rotiferianus DAT722 | *nhaB* | 1.35 | Sodium/proton antiporter | Metal\_Homeostasis | |
| 219950047 | Methylobacterium nodulans ORS 2060 | *fnr* | 1.35 | Crp/FNR family transcriptional regulator | Stress | |
| 390565739 | Nitrolancetus hollandicus Lb | *gyrB* | 1.35 | DNA gyrase, B subunit | Other | |
| 44996041 | Chlamydomonas reinhardtii | *amt* | 1.35 | Ammonium transporter channel family | Nitrogen | |
| 334130353 | Methyloversatilis universalis FAM5 | *ompR* | 1.34 | Response regulator (with CheY-like receiver domain and winged-helix DNA-binding domain) | Stress | |
| 126458901 | Pyrobaculum calidifontis JCM 11548 | *cmr6* | 1.34 | CRISPR-associated RAMP protein, Cmr6 family | Other | |
| 359775571 | Arthrobacter globiformis NBRC 12137 | *nhaP* | 1.34 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 301094546 | Phytophthora infestans T30-4 | *npp1* | 1.34 | Necrosis inducing protein | Virulence | |
| 334130996 | Methyloversatilis universalis FAM5 | *msmA* | 1.33 | Methanesulfonate monooxygenase, hydroxylase alpha subunit | Organic\_Remediation | |
| 116200458 | Chaetomium globosum CBS 148.51 | *axe* | 1.33 | Carbohydrate esterase family 1 protein | Carbon\_Cycling | |
| 319751308 | Isosphaera pallida ATCC 43644 | *trkA* | 1.33 | Potassium/proton antiporter | Metal\_Homeostasis | |
| 149808847 | Moritella sp. PE36 | *iro* | 1.33 | TonB-dependent siderophore receptor | Virulence | |
| 301111093 | Phytophthora infestans T30-4 | *pnl3* | 1.33 | Pectin lyase, putative | Carbon\_Cycling | |
| 373871225 | Gillisia limnaea DSM 15749 | *nhaP* | 1.32 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 239816104 | Variovorax paradoxus S110 | *fnr* | 1.32 | Crp/FNR family transcriptional regulator | Stress | |
| 222105548 | Streptomyces toxytricini | *pcc* | 1.32 | Propionyl-CoA carboxylase beta chain | Carbon\_Cycling | |
| 343784642 | Haloarcula hispanica ATCC 33960 | *narB* | 1.31 | Assimilatory nitrate reductase | Nitrogen | |
| 332172179 | Glaciecola sp. 4H-3-7+YE-5 | *mer* | 1.31 | Mercuric Reductase | Metal\_Homeostasis | |
| 209958041 | Rhodospirillum centenum SW | *fnr* | 1.31 | Crp/FNR family transcriptional regulator | Stress | |
| 357422714 | Azospirillum lipoferum 4B | *chrA* | 1.31 | Multidrug efflux transporter protein | Metal\_Homeostasis | |
| 154253808 | Parvibaculum lavamentivorans DS-1 | *czcC* | 1.31 | Cobalt-zinc-cadmium resistance protein CzcC | Metal\_Homeostasis | |
| 320138283 | Selenomonas artemidis F0399 | *mfs* | 1.30 | Membrane transporter | Virulence | |
| 83859811 | Oceanicaulis alexandrii HTCC2633 | *tktA* | 1.30 | Transketolase | Carbon\_Cycling | |
| 258512154 | Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446 | *mntH* | 1.30 | Mn2+ and Fe2+ transporter | Metal\_Homeostasis | |
| 393759946 | Alcaligenes faecalis subsp. faecalis NCIB 8687 | *ccmC* | 1.30 | Cytochrome C | Electron\_transfer | |
| 118501813 | Pelobacter propionicus DSM 2379 | *rpoH* | 1.30 | RNA polymerase, sigma 32 subunit, RpoH | Stress | |
| 166367532 | Microcystis aeruginosa NIES-843 | *ccmM* | 1.29 | Carbonate dehydratase | Carbon\_Cycling | |
| 170749958 | Methylobacterium radiotolerans JCM 2831 | *fbp* | 1.29 | Fructose-1,6-bisphosphatase | Carbon\_Cycling | |
| 33152878 | Haemophilus ducreyi 35000HP | *smr* | 1.29 | Small multidrug resistance protein | Virulence | |
| 154155295 | Parvibaculum lavamentivorans DS-1 | *cysI* | 1.29 | Sulfite reductase beta | Sulfur | |
| 299749935 | Coprinopsis cinerea okayama7#130 | *cda1* | 1.29 | Putative chitin deacetylase | Carbon\_Cycling | |
| 169851646 | Coprinopsis cinerea okayama7#130 | *cbm1* | 1.28 | Putative expansin | Carbon\_Cycling | |
| 359343670 | Pseudovibrio sp. FO-BEG1 | *znuA* | 1.28 | Zinc ABC transporter substrate-binding protein | Metal\_Homeostasis | |
| 329119978 | Neisseria bacilliformis ATCC BAA-1200 | *gdh* | 1.28 | NADP-specific glutamate dehydrogenase | Nitrogen | |
| 145297733 | Aeromonas salmonicida subsp. salmonicida A449 | *corC* | 1.28 | Magnesium and cobalt efflux protein | Metal\_Homeostasis | |
| 83757573 | Salinibacter ruber DSM 13855 | *mer* | 1.28 | Mercuric Reductase | Metal\_Homeostasis | |
| 312167743 | Burkholderia rhizoxinica HKI 454 | *spoT* | 1.28 | Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase | Stress | |
| 308801086 | Ostreococcus tauri | *nhaA* | 1.27 | Na+/H+ antiporter NhaA | Metal\_Homeostasis | |
| 72163439 | Thermobifida fusca YX | *mgtA* | 1.27 | Magnesium-transporting ATPase, P-type 1 | Metal\_Homeostasis | |
| 169885375 | Synechococcus sp. PCC 7002 | *trkA* | 1.27 | Potassium/proton antiporter | Metal\_Homeostasis | |
| 126617761 | Cyanothece sp. CCY0110 | *pstA* | 1.27 | Phosphate-transport integral membrane ABC transporter, PstA | Stress | |
| 373941035 | Ectothiorhodospira sp. PHS-1 | *pspF* | 1.27 | Sigma-54 dependent transcriptional regulator | Stress | |
| 227348699 | Corynebacterium pseudogenitalium ATCC 33035 | *cspA* | 1.27 | Cold shock protein CspA | Stress | |
| 478733300 | uncultured bacterium | *cnorB* | 1.27 | Nitric oxide reductase large subunit | Nitrogen | |
| 62468078 | uncultured bacterium | *bcoA* | 1.26 | 2-hydroxyglutaryl-coa dehydratase, subunit alpha | Organic\_Remediation | |
| 21646002 | Chlorobium tepidum TLS | *mfs* | 1.26 | Membrane transporter | Virulence | |
| 343784933 | Haloarcula hispanica ATCC 33960 | *trkGH* | 1.26 | Potassium uptake protein, TrkH family | Metal\_Homeostasis | |
| 374620194 | gamma proteobacterium HIMB55 | *arsC* | 1.26 | Glutaredoxin-dependent arsenate reductase | Metal\_Homeostasis | |
| 358753816 | Granulicella mallensis MP5ACTX8 | *ara* | 1.26 | Alpha-N-arabinofuranosidase | Carbon\_Cycling | |
| 88864229 | Jannaschia sp. CCS1 | *sod* | 1.26 | Superoxide dismutase | Secondary\_metabolism | |
| 86283192 | Rhizobium etli CFN 42 | *pgk* | 1.26 | Phosphoglycerate kinase | Carbon\_Cycling | |
| 56314767 | Azoarcus sp. EbN1 | *ebdA* | 1.26 | Ethylbenzene dehydrogenase, alpha subunit | Organic\_Remediation | |
| 241204268 | Rhizobium leguminosarum bv. trifolii WSM1325 | *dps* | 1.26 | DNA protection during starvation protein | Metal\_Homeostasis | |
| 289531688 | Natrialba magadii ATCC 43099 | *trkA* | 1.26 | Potassium/proton antiporter | Metal\_Homeostasis | |
| 55376485 | Haloarcula marismortui ATCC 43049 | *zntA* | 1.26 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 283799601 | uncultured bacterium | *pmoA* | 1.26 | Particulate methane monooxygenase alpha subunit | Carbon\_Cycling | |
| 349685703 | Gluconacetobacter oboediens 174Bp2 | *clpP* | 1.26 | ATP-dependent Clp protease, proteolytic subunit ClpP | Stress | |
| 365856662 | Acetobacteraceae bacterium AT-5844 | *nikA* | 1.26 | Nickel ABC transporter | Metal\_Homeostasis | |
| 350530045 | Vibrio rotiferianus DAT722 | *fbp* | 1.25 | Fructose-1,6-bisphosphatase | Carbon\_Cycling | |
| 377558716 | Gordonia otitidis NBRC 100426 | *bglB* | 1.25 | Beta-glucosidase | Carbon\_Cycling | |
| 297164831 | Truepera radiovictrix DSM 17093 | *amyA* | 1.25 | Pullulanase/amylase | Carbon\_Cycling | |
| 161380716 | Oceanibulbus indolifex HEL-45 | *ppx* | 1.25 | Exopolyphosphatase | Phosphorus | |
| 409395438 | Pseudomonas sp. Chol1 | *oxoO* | 1.25 | Putative 2-oxo-1 2-dihydroquinoline 8-monooxygenase oxygenase subunit | Organic\_Remediation | |
| 85693125 | Idiomarina baltica OS145 | *degP* | 1.25 | Periplasmic trypsin-like serine protease | Stress | |
| 71849260 | Dechloromonas aromatica RCB | *fepA* | 1.25 | Putative TonB-denpendent receptor | Metal\_Homeostasis | |
| 398378818 | Rhizobium sp. AP16 | *tet* | 1.25 | GTP-binding elongation factor protein, TetM/TetO family | Virulence | |
| 124874701 | Burkholderia cenocepacia PC184 | *nagG* | 1.25 | Putative salicylate 1-monooxygenase | Organic\_Remediation | |
| 163262915 | Bordetella petrii | *aceB* | 1.25 | Malate synthase | Carbon\_Cycling | |
| 337758208 | Hyphomicrobium sp. MC1 | *exaA* | 1.25 | Putative quinoprotein glucose dehydrogenase, subunit A | Organic\_Remediation | |
| 14023174 | Mesorhizobium loti MAFF303099 | *soxR* | 1.25 | Redox-sensitive transcriptional activator SoxR | Stress | |
| 383759238 | Rubrivivax gelatinosus IL144 | *ppk* | 1.25 | Polyphosphate kinase | Phosphorus | |
| 2983678 | Aquifex aeolicus VF5 | *dmsA* | 1.25 | Anaerobic dimethyl sulfoxide reductase chain A | Organic\_Remediation | |
| 54015074 | Nocardia farcinica IFM 10152 | *terZD* | 1.25 | Tellurite resistance | Metal\_Homeostasis | |
| 52425291 | Mannheimia succiniciproducens MBEL55E | *amyA* | 1.25 | Pullulanase/amylase | Carbon\_Cycling | |
| 28805042 | Vibrio parahaemolyticus RIMD 2210633 | *smr* | 1.25 | Small multidrug resistance protein | Virulence | |
| 111220093 | Frankia alni ACN14a | *terZ* | 1.24 | Stress response protein | Metal\_Homeostasis | |
| 170721316 | Pseudomonas putida W619 | *cccA* | 1.24 | Cytochrome | Electron\_transfer | |
| 78065954 | Burkholderia sp. 383 | *mhpA* | 1.24 | Putative hydroxylase | Organic\_Remediation | |
| 115389832 | Aspergillus terreus NIH2624 | *pdr* | 1.24 | Pleiotropic drug resistance ABC transporter | Virulence | |
| 239519263 | Clostridiales bacterium 1\_7\_47FAA | *nplT* | 1.24 | Neopullulanase | Carbon\_Cycling | |
| 55231357 | Haloarcula marismortui ATCC 43049 | *blh* | 1.24 | Bacteriorhodopsin related protein | Secondary\_metabolism | |
| 88702651 | uncultured soil bacterium | *nosZ* | 1.24 | Nitrous oxide reductase | Nitrogen | |
| 291345499 | Streptomyces ghanaensis ATCC 14672 | *mfs* | 1.24 | Membrane transporter | Virulence | |
| 378550722 | Citricoccus sp. CH26A | *amyA* | 1.24 | Pullulanase/amylase | Carbon\_Cycling | |
| 309311742 | Puccinia graminis f. sp. tritici CRL 75-36-700-3 | *glx* | 1.24 | Glyoxal oxidase | Carbon\_Cycling | |
| 73541946 | Ralstonia eutropha JMP134 | *rpoE* | 1.24 | RNA polymerase, sigma-24 subunit (RpoE), ECF subfamily | Stress | |
| 336025688 | Mesorhizobium opportunistum WSM2075 | *cydB* | 1.24 | Cytochrome d ubiquinol oxidase, subunit II | Stress | |
| 184192696 | Burkholderia phymatum STM815 | *ntrC* | 1.24 | Fis family two component sigma-54 specific transcriptional regulator | Stress | |
| 377536719 | Mobilicoccus pelagius NBRC 104925 | *zupT* | 1.23 | Zinc transporter ZupT | Metal\_Homeostasis | |
| 29607727 | Streptomyces avermitilis MA-4680 | *pstS* | 1.23 | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS | Stress | |
| 161784474 | Gluconacetobacter diazotrophicus PAl 5 | *cas8* | 1.23 | CRISPR-associated protein\_ CT1133 | Other | |
| 225376384 | Roseburia inulinivorans DSM 16841 | *pme* | 1.23 | Unnamed protein product | Carbon\_Cycling | |
| 32445804 | Rhodopirellula baltica SH 1 | *ahpC* | 1.23 | Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen | Stress | |
| 91784277 | Burkholderia xenovorans LB400 | *ntrB* | 1.23 | Nitrogen regulation protein NtrB | Stress | |
| 289624496 | Pseudomonas syringae pv. aesculi str. NCPPB3681 | *impH* | 1.23 | ImpH (secretion protein) | Virulence | |
| 55229837 | Haloarcula marismortui ATCC 43049 | *mfs* | 1.23 | Membrane transporter | Virulence | |
| 284033275 | Kribbella flavida DSM 17836 | *corA* | 1.23 | Magnesium and cobalt transport protein CorA | Metal\_Homeostasis | |
| 218763834 | Desulfatibacillum alkenivorans AK-01 | *feoB* | 1.23 | Ferrous iron transport protein B | Metal\_Homeostasis | |
| 340777020 | Acetobacter aceti NBRC 14818 | *nit* | 1.23 | NAD+ synthetase | Organic\_Remediation | |
| 170698157 | Burkholderia ambifaria IOP40-10 | *bsaK* | 1.23 | Type III secretion system protein BsaK | Virulence | |
| 284989771 | Geodermatophilus obscurus DSM 43160 | *amyA* | 1.23 | Pullulanase/amylase | Carbon\_Cycling | |
| 269793931 | Sanguibacter keddieii DSM 10542 | *nikA* | 1.23 | Nickel ABC transporter | Metal\_Homeostasis | |
| 383814038 | Serratia sp. M24T3 | *pspC* | 1.23 | Phage shock protein C, PspC | Stress | |
| 344211518 | Haloarcula hispanica ATCC 33960 | *nosZ* | 1.23 | Nitrous oxide reductase | Nitrogen | |
| 70730635 | Pseudomonas protegens Pf-5 | *mex* | 1.23 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 328542839 | Polymorphum gilvum SL003B-26A1 | *mex* | 1.23 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 254510664 | Rhodobacteraceae bacterium KLH11 | *fnr* | 1.23 | Crp/FNR family transcriptional regulator | Stress | |
| 148503104 | Sphingomonas wittichii RW1 | *katE* | 1.22 | Catalase | Stress | |
| 388469804 | Pseudomonas synxantha BG33R | *fecA* | 1.22 | TonB-dependent outermembrane ferric citrate receptor | Metal\_Homeostasis | |
| 145011716 | Magnaporthe grisea 70-15 | *ara* | 1.22 | Alpha-N-arabinofuranosidase | Carbon\_Cycling | |
| 225352717 | Bifidobacterium pseudocatenulatum DSM 20438 = JCM 1200 | *amyA* | 1.22 | Pullulanase/amylase | Carbon\_Cycling | |
| 453381689 | Gordonia paraffinivorans NBRC 108238 | *ppk2* | 1.22 | Polyphosphate kinase | Phosphorus | |
| 338783015 | Achromobacter xylosoxidans AXX-A | *fhuE* | 1.22 | TonB-dependent siderophore receptor | Metal\_Homeostasis | |
| 149239777 | Lodderomyces elongisporus NRRL YB-4239 | *tps* | 1.22 | Trehalose-phosphatase | Stress | |
| 168195744 | Methylobacterium sp. 4-46 | *oxyR* | 1.22 | LysR family transcriptional regulator | Stress | |
| 358458441 | Frankia sp. CN3 | *proO* | 1.22 | Alpha-subunit of protocatechuate 4,5-dioxygenase | Organic\_Remediation | |
| 315604695 | Actinomyces sp. oral taxon 180 str. F0310 | *clpP* | 1.22 | ATP-dependent Clp protease, proteolytic subunit ClpP | Stress | |
| 283810631 | Kribbella flavida DSM 17836 | *rpoD* | 1.22 | RNA polymerase sigma factor 70 (RpoD) | Stress | |
| 359425175 | Gordonia amarae NBRC 15530 | *mtrB* | 1.22 | Two-component histidine kinase MtrB, partial | Stress | |
| 283572367 | Desulfovibrio sp. FW1012B | *catB* | 1.22 | Muconate cycloisomerase I protein | Secondary\_metabolism | |
| 358069571 | Burkholderia cenocepacia H111 | *silC* | 1.22 | RND efflux system, outer membrane lipoprotein, NodT | Metal\_Homeostasis | |
| 357596852 | Novosphingobium pentaromativorans US6-1 | *cirA* | 1.22 | TonB-dependent receptor | Metal\_Homeostasis | |
| 308226331 | Oscillochloris trichoides DG6 | *phn* | 1.22 | Phosphorous compounds metabolism-like protein | Organic\_Remediation | |
| 325050893 | Acidiphilium multivorum AIU301 | *crtC* | 1.22 | Hydroxyneurosporene synthase | Secondary\_metabolism | |
| 209504514 | Burkholderia sp. H160 | *ara* | 1.22 | Alpha-N-arabinofuranosidase | Carbon\_Cycling | |
| 345639544 | Streptomyces zinciresistens K42 | *cadA* | 1.22 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 116625174 | Candidatus Solibacter usitatus Ellin6076 | *cirA* | 1.22 | TonB-dependent receptor | Metal\_Homeostasis | |
| 356892785 | alpha proteobacterium CECT 7668 | *gyrB* | 1.22 | DNA gyrase, B subunit | Other | |
| 317401731 | Achromobacter xylosoxidans C54 | *mfs* | 1.22 | Membrane transporter | Virulence | |
| 227832731 | Corynebacterium aurimucosum ATCC 700975 | *cas6* | 1.22 | CRISPR-associated protein CT1974 | Other | |
| 260645984 | Streptomyces scabiei 87.22 | *rgaE* | 1.22 | Lipolytic protein G-D-S-L family | Carbon\_Cycling | |
| 334135132 | Paenibacillus sp. HGF7 | *smr* | 1.22 | Small multidrug resistance protein | Virulence | |
| 377571305 | Gordonia terrae NBRC 100016 | *mfs* | 1.21 | Membrane transporter | Virulence | |
| 312196143 | Frankia sp. EuI1c | *mfs* | 1.21 | Membrane transporter | Virulence | |
| 349797344 | Neisseria wadsworthii 9715 | *cysI* | 1.21 | Sulfite reductase beta | Sulfur | |
| 327177872 | uncultured bacterium | *fthfS* | 1.21 | Formate--tetrahydrofolate ligase | Carbon\_Cycling | |
| 89352997 | Xanthobacter autotrophicus Py2 | *benA* | 1.21 | Benzoate 1,2-dioxygenase | Organic\_Remediation | |
| 383935401 | Rheinheimera nanhaiensis E407-8 | *chrA* | 1.21 | Multidrug efflux transporter protein | Metal\_Homeostasis | |
| 56459841 | Idiomarina loihiensis L2TR | *pspF* | 1.21 | Sigma-54 dependent transcriptional regulator | Stress | |
| 149817772 | Plesiocystis pacifica SIR-1 | *vanA* | 1.21 | Rieske (2Fe-2S) region | Carbon\_Cycling | |
| 330817113 | Burkholderia gladioli BSR3 | *mex* | 1.21 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 110632493 | Chelativorans sp. BNC1 | *natB* | 1.21 | ABC-type Na+ efflux pump | Metal\_Homeostasis | |
| 338778012 | Achromobacter xylosoxidans AXX-A | *mfs* | 1.21 | Membrane transporter | Virulence | |
| 222451844 | Halorubrum lacusprofundi ATCC 49239 | *arsC* | 1.21 | Glutaredoxin-dependent arsenate reductase | Metal\_Homeostasis | |
| 298708002 | Ectocarpus siliculosus | *bciA* | 1.21 | Predicted protein | Secondary\_metabolism | |
| 84381416 | Janibacter sp. HTCC2649 | *mfs* | 1.21 | Membrane transporter | Virulence | |
| 296128216 | Cellulomonas flavigena DSM 20109 | *cadBD* | 1.21 | Cadmium resistance transporter | Metal\_Homeostasis | |
| 350599898 | Halomonas sp. HAL1 | *mex* | 1.21 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 121590112 | Halorhodospira halophila SL1 | *fepA* | 1.21 | Putative TonB-denpendent receptor | Metal\_Homeostasis | |
| 352104634 | Halomonas sp. HAL1 | *copA* | 1.21 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 69286520 | Kineococcus radiotolerans SRS30216 | *terZ* | 1.21 | Stress response protein | Metal\_Homeostasis | |
| 344210197 | Haloarcula hispanica ATCC 33960 | *tehB* | 1.21 | Methyltransferase type 12 | Metal\_Homeostasis | |
| 83757114 | Salinibacter ruber DSM 13855 | *gyrB* | 1.21 | DNA gyrase, B subunit | Other | |
| 212554474 | Shewanella piezotolerans WP3 | *fecA* | 1.21 | TonB-dependent outermembrane ferric citrate receptor | Metal\_Homeostasis | |
| 83943925 | Sulfitobacter sp. EE-36 | *fthfS* | 1.21 | Formate--tetrahydrofolate ligase | Carbon\_Cycling | |
| 269848493 | Anaplasma centrale str. Israel | *vir* | 1.21 | Type IV secretion system protein B4, putative | Virulence | |
| 178925573 | uncultured bacterium | *narB* | 1.20 | Assimilatory nitrate reductase | Nitrogen | |
| 222082120 | Agrobacterium radiobacter K84 | *mfs* | 1.20 | Membrane transporter | Virulence | |
| 71848364 | Dechloromonas aromatica RCB | *soxA* | 1.20 | Putative cytochrome c | Sulfur | |
| 389862872 | Modestobacter marinus | *ccmA* | 1.20 | Nodulation ABC transporter NodI | Virulence | |
| 163794540 | alpha proteobacterium BAL199 | *merB* | 1.20 | Alkylmercury lyase | Metal\_Homeostasis | |
| 404441825 | Mycobacterium vaccae ATCC 25954 | *tfdA* | 1.20 | Taurine dioxygenase | Organic\_Remediation | |
| 267850475 | Alternanthera mosaic virus | *rdrp2* | 1.20 | RNA-dependent RNA polymerase | Virus | |
| 170746771 | Methylobacterium radiotolerans JCM 2831 | *fnr* | 1.20 | Crp/FNR family transcriptional regulator | Stress | |
| 334687655 | Microlunatus phosphovorus NM-1 | *ccmA* | 1.20 | Nodulation ABC transporter NodI | Virulence | |
| 374349028 | uncultured bacterium | *nirK* | 1.20 | Nitrite reductase | Nitrogen | |
| 169793464 | uncultured bacterium | *narG* | 1.20 | Nitrate reductase alpha subunit | Nitrogen | |
| 300115098 | Nitrosococcus watsonii C-113 | *nhaP* | 1.20 | Sodium/hydrogen exchanger | Metal\_Homeostasis | |
| 239796540 | Desulfovibrio magneticus RS-1 | *hynA* | 1.20 | NiFe hydrogenase large subunit | Electron\_transfer | |
| 83949540 | Roseovarius nubinhibens ISM | *nhaA* | 1.20 | Na+/H+ antiporter NhaA | Metal\_Homeostasis | |
| 291371367 | Haloferax volcanii DS2 | *znuC* | 1.20 | Manganese ABC transporter ATP-binding protein | Metal\_Homeostasis | |
| 337279018 | Ramlibacter tataouinensis TTB310 | *soxB* | 1.20 | Sulfur oxidation protein SoxB | Sulfur | |
| 389875521 | Tistrella mobilis KA081020-065 | *mex* | 1.20 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 388431560 | Rhodanobacter sp. 115 | *fiu* | 1.20 | TonB-dependent siderophore receptor | Metal\_Homeostasis | |
| 193225844 | Cupriavidus taiwanensis | *phn* | 1.20 | Phosphorous compounds metabolism-like protein | Organic\_Remediation | |
| 78518946 | Bradyrhizobium sp. BTAi1 | *nasA* | 1.20 | Periplasmic nitrate reductase, large subunit | Nitrogen | |
| 121307272 | Thermosinus carboxydivorans Nor1 | *trkA* | 1.20 | Potassium/proton antiporter | Metal\_Homeostasis | |
| 116613035 | Arthrobacter sp. FB24 | *cadA* | 1.20 | Heavy metal translocating P-type ATPase | Metal\_Homeostasis | |
| 227069619 | uncultured archaeon | *Nir* | 1.20 | Nitrite reductase | Nitrogen | |
| 395433146 | Flavobacterium sp. F52 | *rndA* | 1.20 | Heavy metal efflux pump, CzcA family | Metal\_Homeostasis | |
| 29838402 | Phytophthora brassicae | *ral* | 1.20 | Elicitin-like protein | Virulence | |
| 116248770 | Rhizobium leguminosarum bv. viciae 3841 | *tfdB* | 1.20 | 2,4-dichlorophenol 6-monooxygenase | Organic\_Remediation | |
| 154496040 | Bacteroides capillosus ATCC 29799 | *mgtA* | 1.20 | Magnesium-transporting ATPase, P-type 1 | Metal\_Homeostasis | |
| 380704262 | Aeromonas caviae | *gyrB* | 1.20 | DNA gyrase, B subunit | Other | |
| 410370810 | Klebsiella oxytoca M5al | *catB* | 1.20 | Muconate cycloisomerase I protein | Organic\_Remediation | |
| 256036267 | Chitinophaga pinensis DSM 2588 | *cirA* | 1.20 | TonB-dependent receptor | Metal\_Homeostasis | |
| 118703608 | Sphingomonas wittichii RW1 | *benA* | 1.20 | Benzoate 1,2-dioxygenase | Organic\_Remediation | |
| 355536823 | Agrobacterium tumefaciens CCNWGS0286 | *mex* | 1.20 | RND family hydrophobe/amphiphile efflux pump | Virulence | |
| 260222065 | Curvibacter putative symbiont of Hydra magnipapillata | *aceB* | 1.20 | Malate synthase | Carbon\_Cycling | |
| 283481909 | uncultured methanogenic archaeon | *mcrA* | 1.20 | Methyl-coenzyme M reductase alpha subunit, partial | Carbon\_Cycling | |
| 95111891 | Pseudomonas entomophila L48 | *cpxR* | 1.20 | Two component transcriptional regulator, winged helix family | Stress | |
| 83650206 | Burkholderia thailandensis E264 | *cysJ* | 1.20 | Molybdopterin oxidoreductase | Sulfur | |
| 297203252 | Streptomyces sviceus ATCC 29083 | *rgaE* | 1.20 | Lipolytic protein G-D-S-L family | Carbon\_Cycling | |