**Table S1**

Chemical compounds detected in the common effluent treatment plant samples using GC/MS analysis (TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Predicted compounds  | TP01 | TP02 | TP03 | TP04 | TP05 | TP06  | TP07 | TP08 |
| **( peak area %)** |
| Diethyl, 1ethynylcyclohexyl ester  | 3.3 | ND# | ND | ND | ND | ND | ND | ND |
| 1,2-benzenedicarboxylic acid | 2.00 | 5.04 | 1.33 | ND | ND | 3.72 | ND | 7.48 |
| Phthalic acid | 5.47 | 4.14 | ND | 9.95 | 30.64 | 3.43 | ND | 17.84 |
| Oxalic acid, allyl octadecyl ester | 9.71 | ND | ND | 21.09 | ND | 10.89 | 12.31 | 28.59 |
| Benzenesulfonamide, 4-amino-n-ethyl | 28.54 | ND | ND | ND | ND | ND | ND | ND |
| 1-hexyl-2-nitrocyclohexane | 11.17 | 14.32 | ND | 22.98 | 7.57 | 8.34 | ND | 12.33 |
| Cyclopentane, (2-hexyloctyl)- | 5.85 | ND | ND | ND | ND | ND | ND | 15.8 |
| Bis(2-ethylhexyl) phthalate | 2.81 | ND | 0.33 | ND | ND | ND | 3.68 | ND |
| 2-methylhexacosane | 2.01 | ND | ND | ND | ND | ND | ND | ND |
| Decane, 3-ethyl-3-methyl | 2.05 | ND | ND | ND | ND | ND | ND | ND |
| Octatriacontane, 1,38-dibromo- | 1.33 | ND | ND | ND | ND | ND | ND | ND |
| 1-bromo-4-bromomethyldecane | ND | 25.04 | ND | ND | ND | ND | ND | ND |
| Phenol, 2,6-bis(1,1-dimethylethyl)- | ND | 7.17 | ND | ND | ND | ND | ND | ND |
| 4-tetradecene, | ND | 6.22 | ND | ND | ND | ND | ND | ND |
| Sulfurous acid, hexyl pentadecyl ester | ND | 2.04 | ND | ND | ND | ND | 5.71 | 11.31 |
| Octadecane, 3-ethyl-5-(2-ethylbutyl) | ND | 3.2 | ND | ND | ND | ND | ND | ND |
| Heptacosane | ND | 6.85 | ND | ND | ND | ND | ND | ND |
| Hydrazine, (2-methyl-1-propenyl) | ND | 1.14 | 10 | 14.77 | ND | ND | ND | ND |
| Dimethoxyamine | ND | 1.3 | ND | ND | ND | ND | ND | ND |
| 1-butanamine, n-(1-methylethyl | ND | ND | 0.61 | ND | ND | ND | ND | ND |
| Pentane, 2,2,4-trimethyl-4-nitro | ND | ND | 0.27 | ND | ND | ND | ND | ND |
| 2-cyano-2,3-dimethyl-, diethyl ester | ND | ND | 53.00 | ND | ND | ND | ND | ND |
| Benzenesulfonyl fluoride | ND  | ND | ND | 10.54 | ND | ND | 22.88 | ND |
| 4-ethyl-4-methyl-1-hexene | ND | ND | ND | 4.15 | ND | ND | ND | ND |
| 2-[(1,3-dioxobutyl)amino]ethyl ester | ND | ND | ND | ND | 14.1 | ND | ND | ND |
| 4-trifluoroacetoxyhexadecane | ND | ND | ND | ND | 22.41 | ND | ND | ND |
| 2-propenoic acid | ND | ND | ND | ND | 14.1 | ND | ND | ND  |
| 1-propanamine, n-nitro- | ND | ND | ND | ND | ND | 2.84 | ND | ND |
| 2-hexenal, 2-ethyl- | ND | ND | ND | ND | ND | 24.11 | ND | ND |
| 1,7-dimethyl-4-(1-methylethyl) cyclodecane | ND | ND | ND | ND | ND | 13.64 | ND | ND |
| 1,1'-biphenyl]-4,4'-diamine, 2,2'-dichloro | ND | ND | ND | ND | ND | 11.59 | ND | ND |
| 1,11-dibromoundecane | ND | ND | ND | ND | ND | ND | 6.7 | ND |
| Benzeneacetic acid, 2-tetradecyl ester | ND | ND | ND | ND | ND | ND | 3.28 | ND |
| 2-undecene, 5-methyl | ND | ND | ND | ND | ND | ND | 2.38 | ND |
| Dichloroacetic acid | ND | ND | ND | ND | ND | ND | 7.38 | ND |
| Cyclohexane, (2-decyldodecyl) | ND | ND | ND | ND | ND | ND | ND | 6.64 |
| Note: # ND: Not Detected  |  |  |  |  |  |  |  |  |

**Table S2**

Gene abundance with in each metagenome dataset for Benzoate degradation

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| KEGG ID | Genes | Enzymes | TP01 | TP02 | TP03 | TP04 | TP05 | TP06 | TP07 | TP08 |
| K14333 | DHBD | 2,3-dihydroxybenzoate decarboxylase [EC:4.1.1.46] | 3 | 1 | 4 | 4 | 7 | 7 | 6 | 7 |
| K00446 | dmpB, xylE | catechol 2,3-dioxygenase [EC:1.13.11.2] | 16 | 4 | 17 | 19 | 25 | 17 | 13 | 29 |
| K07104 | catE | catechol 2,3-dioxygenase [EC:1.13.11.2] | 15 | 21 | 22 | 24 | 9 | 5 | 27 | 9 |
| K10621 | cmtC, dhbA | 2,3-dihydroxy-p-cumate/2,3-dihydroxybenzoate 3,4-dioxygenase [EC:1.13.11.- 1.13.11.14] | 1 | 0 | 1 | 1 | 2 | 2 | 1 | 2 |
| K10622 | cmtD, dhbB | HCOMODA/2-hydroxy-3-carboxy-muconic semialdehyde decarboxylase [EC:4.1.1.-] | 1 | 0 | 1 | 2 | 2 | 1 | 2 | 0 |
| K10216 | dmpD, xylF | 2-hydroxymuconate-semialdehyde hydrolase [EC:3.7.1.9] | 10 | 5 | 10 | 10 | 16 | 10 | 13 | 11 |
| K02554 | mhpD | 2-keto-4-pentenoate hydratase [EC:4.2.1.80] | 5 | 5 | 11 | 7 | 12 | 6 | 10 | 8 |
| K18364 | bphH, xylJ, tesE | 2-oxopent-4-enoate/cis-2-oxohex-4-enoate hydratase [EC:4.2.1.80 4.2.1.132] | 5 | 4 | 9 | 12 | 11 | 4 | 12 | 10 |
| K01666 | mhpE | 4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39] | 17 | 8 | 18 | 17 | 18 | 11 | 23 | 15 |
| K18365 | bphI, xylK, nahM, tesG | 4-hydroxy-2-oxovalerate/4-hydroxy-2-oxohexanoate aldolase [EC:4.1.3.39 4.1.3.43] | 12 | 5 | 11 | 15 | 10 | 5 | 9 | 11 |
| K10217 | dmpC, xylG, praB | aminomuconate-semialdehyde/2-hydroxymuconate-6-semialdehyde dehydrogenase [EC:1.2.1.32 1.2.1.85] | 10 | 4 | 15 | 18 | 25 | 14 | 18 | 23 |
| K01617 | dmpH, xylI, nahK | 2-oxo-3-hexenedioate decarboxylase [EC:4.1.1.77] | 10 | 1 | 7 | 11 | 16 | 9 | 5 | 7 |
| K01821 | praC, xylH | 4-oxalocrotonate tautomerase [EC:5.3.2.6] | 31 | 14 | 31 | 30 | 25 | 10 | 32 | 24 |
| K04116 | aliA | cyclohexanecarboxylate-CoA ligase [EC:6.2.1.-] | 1 | 0 | 0 | 2 | 6 | 2 | 1 | 4 |
| K04117 | aliB | cyclohexanecarboxyl-CoA dehydrogenase [EC:1.3.99.-] | 3 | 0 | 5 | 4 | 5 | 3 | 6 | 6 |
| K07535 | badH | 2-hydroxycyclohexanecarboxyl-CoA dehydrogenase [EC:1.1.1.-] | 8 | 4 | 7 | 6 | 10 | 4 | 8 | 10 |
| K07536 | badI | 2-ketocyclohexanecarboxyl-CoA hydrolase [EC:3.1.2.-] | 3 | 0 | 1 | 1 | 4 | 2 | 0 | 5 |
| K04118 | - | pimeloyl-CoA dehydrogenase [EC:1.3.1.62] | 7 | 2 | 5 | 7 | 19 | 11 | 12 | 10 |
| K04112 | bcrC, badD | benzoyl-CoA reductase subunit C [EC:1.3.7.8] | 0 | 0 | 0 | 0 | 1 | 3 | 3 | 4 |
| K19515 | bamB | benzoyl-CoA reductase subunit BamB [EC:1.3.-.-] | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| K15511 | boxA | benzoyl-CoA 2,3-epoxidase subunit A [EC:1.14.13.208] | 2 | 2 | 1 | 2 | 8 | 6 | 4 | 10 |
| K15513 | boxC | benzoyl-CoA-dihydrodiol lyase [EC:4.1.2.44] | 3 |  | 3 | 6 | 13 | 8 | 3 | 11 |
| K07538 | had | 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase [EC:1.1.1.368] | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| K07539 | oah | 6-oxocyclohex-1-ene-carbonyl-CoA hydrolase [EC:3.7.1.21] | 1 | 0 | 0 | 0 | 1 | 2 | 0 | 3 |
| K15514 | boxD | 3,4-dehydroadipyl-CoA semialdehyde dehydrogenase [EC:1.2.1.77] | 2 | 0 | 1 | 3 | 4 | 3 | 2 | 2 |
| K01782 | fadJ | enoyl-CoA hydratase [EC:1.1.1.35] | 43 | 14 | 38 | 41 | 51 | 33 | 50 | 56 |
| K00632 | fadA, fadI | acetyl-CoA acyltransferase [EC:2.3.1.16] | 67 | 26 | 73 | 68 | 82 | 49 | 104 | 74 |
| K16173 | acd | glutaryl-CoA dehydrogenase (non-decarboxylating) [EC:1.3.99.32] | 0 | 0 | 0 | 1 | 2 | 2 | 0 | 2 |
| K00252 | GCDH, gcdH | glutaryl-CoA dehydrogenase [EC:1.3.8.6] | 43 | 22 | 50 | 45 | 84 | 45 | 62 | 62 |
| K01615 | gcdA | glutaconyl-CoA decarboxylase [EC:4.1.1.70] | 2 | 4 | 3 | 2 |  | 1 | 4 | 1 |
| K01692 | paaF, echA | enoyl-CoA hydratase [EC:4.2.1.17] | 77 | 26 | 60 | 81 | 141 | 70 | 89 | 130 |
| K00074 | paaH, hbd, fadB, mmgB | 3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157] | 64 | 43 | 77 | 89 | 97 | 56 | 103 | 93 |
| K00626 | atoB | acetyl-CoA C-acetyltransferase [EC:2.3.1.9] | 141 | 86 | 168 | 185 | 245 | 128 | 228 | 218 |
| K04108 | hcrA, hbaC | 4-hydroxybenzoyl-CoA reductase subunit alpha [EC:1.3.7.9] | 0 | 1 | 0 | 0 | 3 | 2 | 0 | 3 |
| K04107 | hcrC, hbaB | 4-hydroxybenzoyl-CoA reductase subunit alpha [EC:1.3.7.9] | 0 | 0 | 0 | 0 | 1 | 0 | 2 | 0 |
| K04110 | badA | benzoate-CoA ligase [EC:6.2.1.25] | 1 |  | 1 | 3 | 5 | 2 | 2 | 6 |
| K01075 | - | 4-hydroxybenzoyl-CoA thioesterase [EC:3.1.2.23] | 10 | 7 | 12 | 14 | 11 | 4 | 15 | 13 |
| K04105 | hbaA | 4-hydroxybenzoate-CoA ligase [EC:6.2.1.27 6.2.1.25] | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| K07824 | CYP53A1 | benzoate 4-monooxygenase [EC:1.14.14.92] | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| K00481 | pobA | p-hydroxybenzoate 3-monooxygenase [EC:1.14.13.2] | 8 | 1 | 8 | 10 | 16 | 10 | 10 | 16 |
| K16268 | todC2, bedC2, tcbAb | benzene/toluene/chlorobenzene dioxygenase subunit beta [EC:1.14.12.3 1.14.12.11 1.14.12.26] | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 0 |
| K05549 | benA-xylX | benzoate/toluate 1,2-dioxygenase subunit alpha [EC:1.14.12.10 1.14.12.-] | 23 | 7 | 31 | 27 | 44 | 28 | 27 | 31 |
| K05550 | benB-xylY | benzoate/toluate 1,2-dioxygenase subunit beta [EC:1.14.12.10 1.14.12.-] | 11 | 3 | 13 | 11 | 11 | 10 | 7 | 11 |
| K05783 | benD-xylL | dihydroxycyclohexadiene carboxylate dehydrogenase [EC:1.3.1.25 1.3.1.-] | 3 | 2 | 7 | 4 | 3 | 2 | 5 | 1 |
| K04100 | ligA | protocatechuate 4,5-dioxygenase, alpha chain [EC:1.13.11.8] | 6 | 1 | 4 | 4 | 13 | 6 | 7 | 11 |
| K04101 | ligB | protocatechuate 4,5-dioxygenase, beta chain [EC:1.13.11.8] | 6 | 1 | 7 | 12 | 34 | 12 | 9 | 25 |
| K10216 | dmpD, xylF | 2-hydroxymuconate-semialdehyde hydrolase [EC:3.7.1.9] | 10 | 5 | 10 | 10 | 16 | 10 | 13 | 11 |
| K10218 | ligK, galC | 4-hydroxy-4-methyl-2-oxoglutarate aldolase [EC:4.1.3.17] | 14 | 12 | 18 | 18 | 12 | 5 | 23 | 13 |
| K10220 | ligJ | 4-oxalmesaconate hydratase [EC:4.2.1.83] | 7 | 3 | 5 | 6 | 19 | 9 | 5 | 15 |
| K16515 | galB | 4-oxalomesaconate hydratase [EC:4.2.1.83] | 4 | 0 | 4 | 3 | 8 | 5 | 3 | 6 |
| K16514 | galD | 4-oxalomesaconate tautomerase [EC:5.3.2.8] | 5 | 1 | 7 | 4 | 7 | 3 | 12 | 9 |
| K10221 | ligI | 2-pyrone-4,6-dicarboxylate lactonase [EC:3.1.1.57] | 12 | 7 | 8 | 5 | 14 | 9 | 17 | 10 |
| K10219 | ligC | 2-hydroxy-4-carboxymuconate semialdehyde hemiacetal dehydrogenase [EC:1.1.1.312] | 6 | 1 | 4 | 7 | 13 | 8 | 11 | 12 |
| K20941 | graF | gamma-resorcylate decarboxylase [EC:4.1.1.103] | 0 | 0 | 2 | 0 | 3 | 0 | 1 | 4 |
| K20943 | - | resorcinol 4-hydroxylase (NADPH) [EC:1.14.13.219] | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| K20942 | graA | resorcinol 4-hydroxylase (FADH2) [EC:1.14.14.27] | 1 | 0 | 2 | 0 | 0 | 0 | 1 | 2 |
| K04098 | chqB | hydroxyquinol 1,2-dioxygenase [EC:1.13.11.37] | 2 | 2 | 1 | 5 | 15 | 8 | 6 | 12 |
| K00217 | - | maleylacetate reductase [EC:1.3.1.32] | 15 | 4 | 17 | 17 | 16 | 10 | 17 | 19 |
| K00448 | pcaG | protocatechuate 3,4-dioxygenase, alpha subunit [EC:1.13.11.3] | 8 | 2 | 12 | 11 | 16 | 10 | 12 | 16 |
| K00449 | pcaH | protocatechuate 3,4-dioxygenase, beta subunit [EC:1.13.11.3] | 9 | 6 | 12 | 8 | 15 | 9 | 17 | 14 |
| K01607 | pcaC | 4-carboxymuconolactone decarboxylase [EC:4.1.1.44] | 41 | 27 | 42 | 55 | 49 | 28 | 58 | 48 |
| K03381 | catA | catechol 1,2-dioxygenase [EC:1.13.11.1] | 14 | 7 | 19 | 17 | 15 | 7 | 17 | 12 |
| K01857 | pcaB | 3-carboxy-cis,cis-muconate cycloisomerase [EC:5.5.1.2] | 10 | 3 | 7 | 9 | 15 | 7 | 13 | 14 |
| K03464 | catC | muconolactone D-isomerase [EC:5.3.3.4] | 5 | 2 | 7 | 9 | 2 | 1 | 8 | 2 |
| K01055 | pcaD | 3-oxoadipate enol-lactonase [EC:3.1.1.24] | 17 | 7 | 27 | 36 | 34 | 17 | 32 | 31 |
| K01031 | pcaI | 3-oxoadipate CoA-transferase, alpha subunit [EC:2.8.3.6] | 5 | 9 | 10 | 9 | 16 | 10 | 9 | 17 |
| K01032 | pcaJ | 3-oxoadipate CoA-transferase, beta subunit [EC:2.8.3.6] | 5 | 9 | 10 | 10 | 12 | 6 | 7 | 10 |
| K07823 | pcaF | 3-oxoadipyl-CoA thiolase [EC:2.3.1.174] | 3 | 1 | 5 | 4 | 3 | 3 | 5 | 4 |

**Table S2**

Metabolic pathways for phenylalanine degradation and gene abundance in each metagenome datasets

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| KEGG ID | Genes | Enzymes  | Enzyme commission number | TP01 | TP02 | TP03 | TP04 | TP05 | TP06 | TP07 | TP08 |
| K02618 | paaZ | oxepin-CoA hydrolase / 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase  | EC:3.3.2.12 1.2.1.91 | 16 | 16 | 22 | 22 | 41 | 31 | 23 | 42 |
| K02609 | paaA | ring-1,2-phenylacetyl-CoA epoxidase subunit PaaA | EC:1.14.13.149 | 8 | 3 | 9 | 11 | 21 | 13 | 12 | 19 |
| K02610 | paaB | ring-1,2-phenylacetyl-CoA epoxidase subunit PaaB | - | 7 | 4 | 5 | 7 | 8 | 5 | 10 | 8 |
| K02611 | paaC | ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC | EC:1.14.13.149 | 8 | 2 | 7 | 10 | 16 | 8 | 11 | 12 |
| K02612 | paaD | ring-1,2-phenylacetyl-CoA epoxidase subunit PaaD | - | 10 | 10 | 9 | 15 | 9 | 9 | 15 | 8 |
| K02613 | paaE | ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE | - | 13 | 5 | 17 | 24 | 20 | 14 | 14 | 23 |
| K01692 | paaF, echA | enoyl-CoA hydratase  | EC:4.2.1.17 | 77 | 26 | 60 | 81 | 141 | 70 | 89 | 130 |
| K15866 | paaG | 2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase  | EC:5.3.3.18 | 42 | 14 | 39 | 43 | 87 | 44 | 46 | 77 |
| K00074 | paaH, hbd, fadB, mmgB | 3-hydroxybutyryl-CoA dehydrogenase  | EC:1.1.1.157 | 64 | 43 | 77 | 89 | 97 | 56 | 103 | 93 |
| K02615 | paaJ | 3-oxo-5,6-didehydrosuberyl-CoA/3-oxoadipyl-CoA thiolase | EC:2.3.1.223 2.3.1.174 | 2 | 1 | 5 | 5 | 2 | 2 | 5 | 2 |
| K01912 | paaK | phenylacetate-CoA ligase  | EC:6.2.1.30 | 97 | 90 | 119 | 131 | 81 | 43 | 189 | 77 |
| K02616 | paaX | phenylacetic acid degradation operon negative regulatory protein | - | 8 | 0 | 5 | 5 | 3 | 0 | 9 | 5 |
| K02617 | paaY | phenylacetic acid degradation protein |  - | 36 | 27 | 50 | 42 | 36 | 29 | 52 | 34 |

(TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal)

**Table S3**

Metabolic pathways and abundance of gene in metagenome dataset for degradation of 1,2 Dichloromethane

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| KEGG ID | Genes | Enzymes and Enzyme commission number | TP01 | TP02 | TP03 | TP04 | TP05 | TP06 | TP07 | TP08 |
| K01563 | dhaA | haloalkane dehalogenase [EC:3.8.1.5] | 5 | 0 | 3 | 4 | 18 | 10 | 6 | 13 |
| K14028 | mdh1, mxaF | methanol dehydrogenase (cytochrome c) subunit 1 [EC:1.1.2.7] | 5 | 0 | 3 | 3 | 5 | 2 | 8 | 4 |
| K01561 | dehH | haloacetate dehalogenase [EC:3.8.1.3] | 5 | 1 | 8 | 7 | 15 | 9 | 11 | 19 |
| K01560 | - | 2-haloacid dehalogenase [EC:3.8.1.2] | 33 | 21 | 36 | 38 | 34 | 21 | 48 | 31 |
| K00128 | ALDH | aldehyde dehydrogenase (NAD+) [EC:1.2.1.3] | 66 | 38 | 76 | 82 | 162 | 111 | 99 | 158 |

(TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal)

**Table S4**

Metabolic pathways for Benzoate degradation and gene abundance of in study dataset

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| KEGG ID | Gene Name  | Enzyme Name  | Enzyme commission number | *Bacillus licheniformis* | *Pseudomonas aeruginosa* |
| K00446 | dmpB, xylE | Catechol 2,3-dioxygenase |  EC:1.13.11.2 | 1 | 0 |
| K07104 | catE | Catechol 2,3-dioxygenase  | EC:1.13.11.2 | 1 | 0 |
| K00632 | fadA, fadI | Acetyl-CoA acyltransferase  | EC:2.3.1.16 | 7 | 6 |
| K00074 | paaH, hbd, fadB, mmgB | 3-hydroxybutyryl-CoA dehydrogenase  | EC:1.1.1.157 | 4 | 3 |
| K00626 | atoB | Acetyl-CoA C-acetyltransferase  | EC:2.3.1.9 | 6 | 5 |
| K00481 | pobA | p-hydroxybenzoate 3-monooxygenase  | EC:1.14.13.2 | 0 | 1 |
| K00448 | pcaG | Protocatechuate 3,4-dioxygenase, alpha subunit  | EC:1.13.11.3 | 0 | 2 |
| K00449 | pcaH | Protocatechuate 3,4-dioxygenase, beta subunit | EC:1.13.11.3 | 0 | 1 |
| K01607 | pcaC | 4-carboxymuconolactone decarboxylase  | EC:4.1.1.44 | 0 | 1 |
| K03381 | catA | Catechol 1,2-dioxygenase  | EC:1.13.11.1 | 0 | 2 |
| K01857 | pcaB | 3-carboxy-cis,cis-muconate cycloisomerase  | EC:5.5.1.2 | 0 | 1 |
| K03464 | catC | Muconolactone D-isomerase  | EC:5.3.3.4 | 0 | 1 |
| K01055 | pcaD | 3-oxoadipate enol-lactonase  | EC:3.1.1.24 | 0 | 3 |
| K01031 | pcaI | 3-oxoadipate CoA-transferase, alpha subunit  | EC:2.8.3.6 | 0 | 3 |
| K05783 | benD-xylL | dihydroxycyclohexadiene carboxylate dehydrogenase  | EC:1.3.1.25  | 0 | 1 |
| K05549 | benA-xylX | benzoate/toluate 1,2-dioxygenase subunit alpha  | EC:1.14.12.10 |  0 | 1 |

**Table S5**

Metabolic pathways for Phenylalanine degradation and abundance of each gene in study dataset

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| KEGG ID  | Gene Name  | Enzymes  | Enzyme commission number | *Bacillus licheniformis* | *Pseudomonas aeruginosa* |
| K01692 | paaF, echA | enoyl-CoA hydratase  | EC:4.2.1.17 | 2 | 11 |
| K00074 | paaH, hbd, fadB, mmgB | 3-hydroxybutyryl-CoA dehydrogenase  | EC:1.1.1.157 | 2 | 3 |

**Table S6**

Metabolic pathways for 1,2 Dichloromethane degradation and abundance of each gene in study dataset

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| KEGG ID | Gene Name | Enzyme Name | Enzyme commission number | *Bacillus licheniformis* | *Pseudomonas aeruginosa* |
| K00128 | ALDH | aldehyde dehydrogenase (NAD+)  | EC:1.2.1.3 | 3 | 3 |

**Fig. S1**: Rarefaction curve analysis of the stages of CETP- Vatva metagenome sequences

**Fig. S2:** COG based mapping of metagenomics derived ORFs at level 1 ((TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air Flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal).



**Fig. S3:** Heatmap representing the clustering of distance measure using Euclidean and clustering algorithm at COG level 2 ((TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air Flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal).

**Fig. S4** KEGG based mapping of metagenomics derived ORFs at level 1(TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air Flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal).



**Fig. S5**: Clustering result shown as heatmap (distance measure using euclidean and clustering algorithm using at KEGG level 2((TP01: CETP collection tank; TP02: Textile industry effluent; TP03: Clariflocculator tank outlet; TP04: Dissolved air Flotation tank outlet; TP05: Aeration tank; TP06: Final outlet of effluent; TP07: Sludge disposal; TP08: Final sludge disposal).