

Supporting Information

Fig. S1 Comparative phylogenetic diversity of pond sediment samples (PS1 and PS2) according to LCA (Least Common Ancestor)-assignment algorithm computed by MEGAN (BLASTX, E-value = $1e-10$).

Fig. S2 Rarefaction plot of unique NCBI non-redundant protein database (<ftp://ftp.ncbi.nlm.nih.gov/blast/db/nr>, June, 2015) across pond sediment (PS1 and PS2) by using MEtaGenome ANalyzer (MEGAN 5.0) at default parameters.

Fig. S3 Heatmap showing metagenomic reassignment of pond sediment up to 1.02% as compared to 0.44% for all the metagenomes (1 Km, 5 Km, DS and SolexaDS). 61.43% of cellular organisms for pond sediment included bacteria [56.39 %], archaea [0.69 %] and eukarya [0.86 %].

Fig. S4 Detailed model for T6SS machinery present in a cell and its interaction with other microbes present in the pond sediment environment was determined by alignment searches against the KEGG GENES database. All-versus-all BLASTP (default parameters) followed by MCL clustering was used to determine clusters of homologs to validate the pathway.

Table S1 Phylogenetic reassignment of reads in PS1, PS2 and HCH gradient metagenomes (1 Km, 5 Km, DS, SolexaDS).

Table S2 Relative abundance of phyla present in pond sediment shown in the plot, with median values, variance, standard error, *P*-value and *Q*-value.

Table S3 Average of relative abundance of each bacterial genera (EGT analysis) unique to Pond Sediment is tabulated.

Table S4 The most abundant bacterial genera unique to Pond Sediment for computing genomic variation are represented.

Table S5 List of all essential single copy genes present in consensus with pond sediment and most abundant genomes present.

Table S6 Percentage of ORFs belonging to different subsystems (SEED) across HCH gradient (SolexaDS, 1 Km, 5 Km and DS) and Pond Sediment metagenomes (PS1 and PS2) respectively.

Table S7 List of enzymes present in pond sediment metagenome, which are involved in degradation of chlorocyclohexane and chlorobenzene (**ko00361**).

Table S8 List of various components of Type VI Secretory System and their effector proteins together with gene and KO (KEGG Orthology) names.

Fig. S1

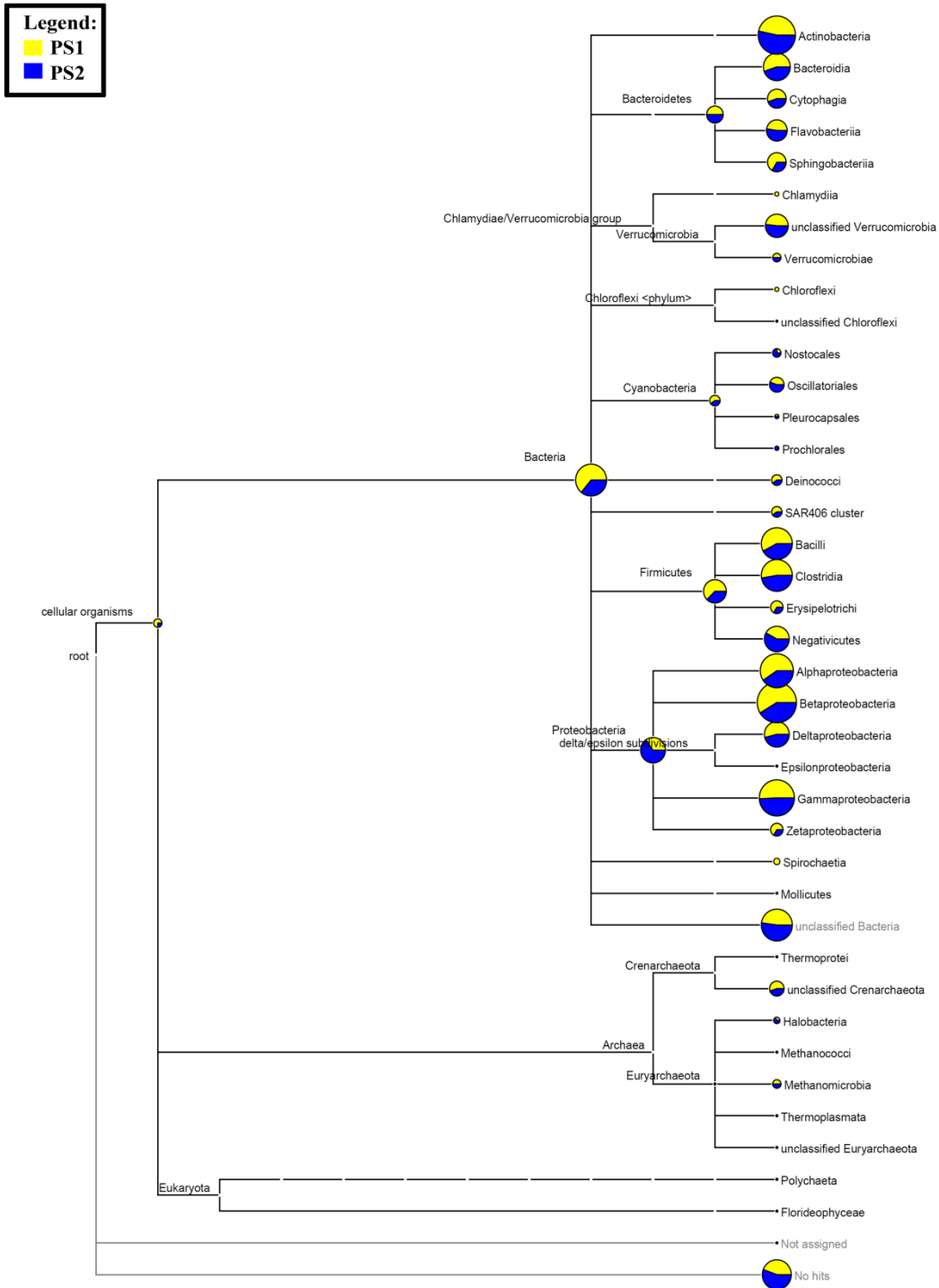


Fig. S1 Comparative phylogenetic diversity of pond sediment samples (PS1 and PS2) according to LCA (Least Common Ancestor)-assignment algorithm computed by MEGAN (BLASTX, E-value = $1e-10$).

Fig. S2

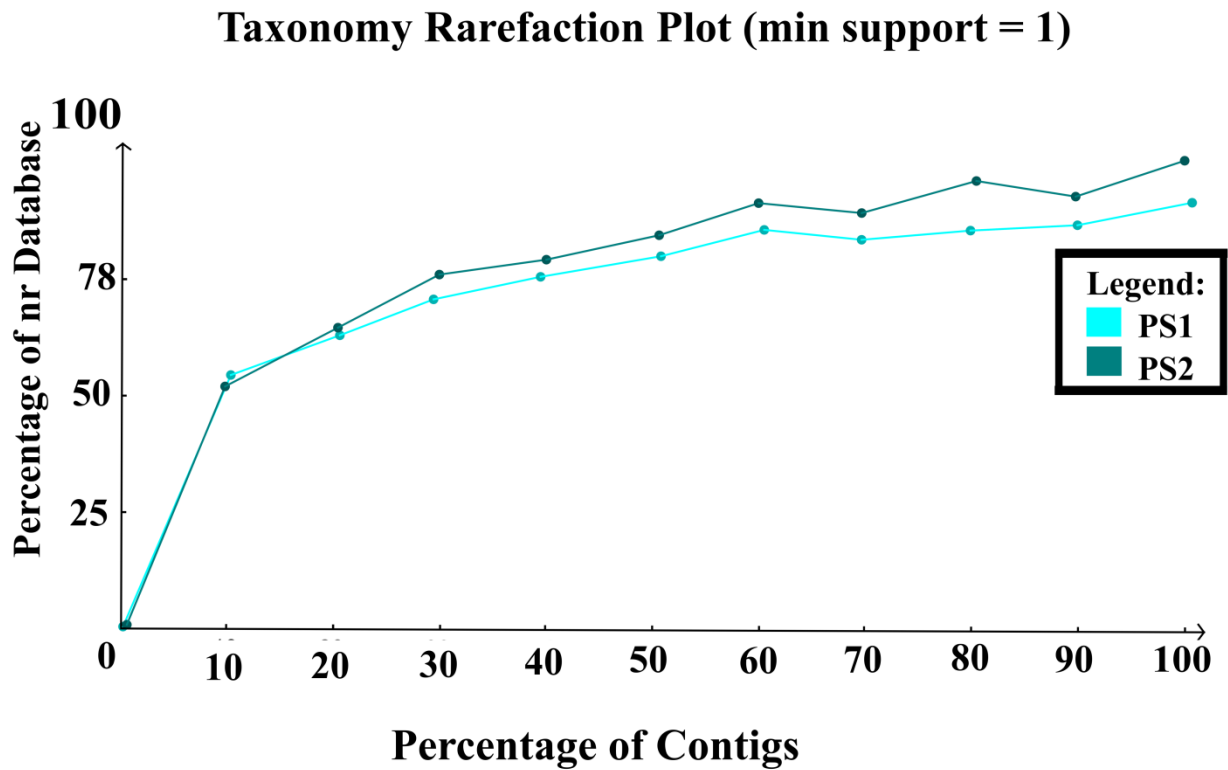


Fig. S2 Rarefaction plot of unique NCBI non-redundant protein database (<ftp://ftp.ncbi.nlm.nih.gov/blast/db/nr>, June, 2015) across pond sediment (PS1 and PS2) by using MEtaGenome ANalyzer (MEGAN 5.0) at default parameters.

Fig. S3

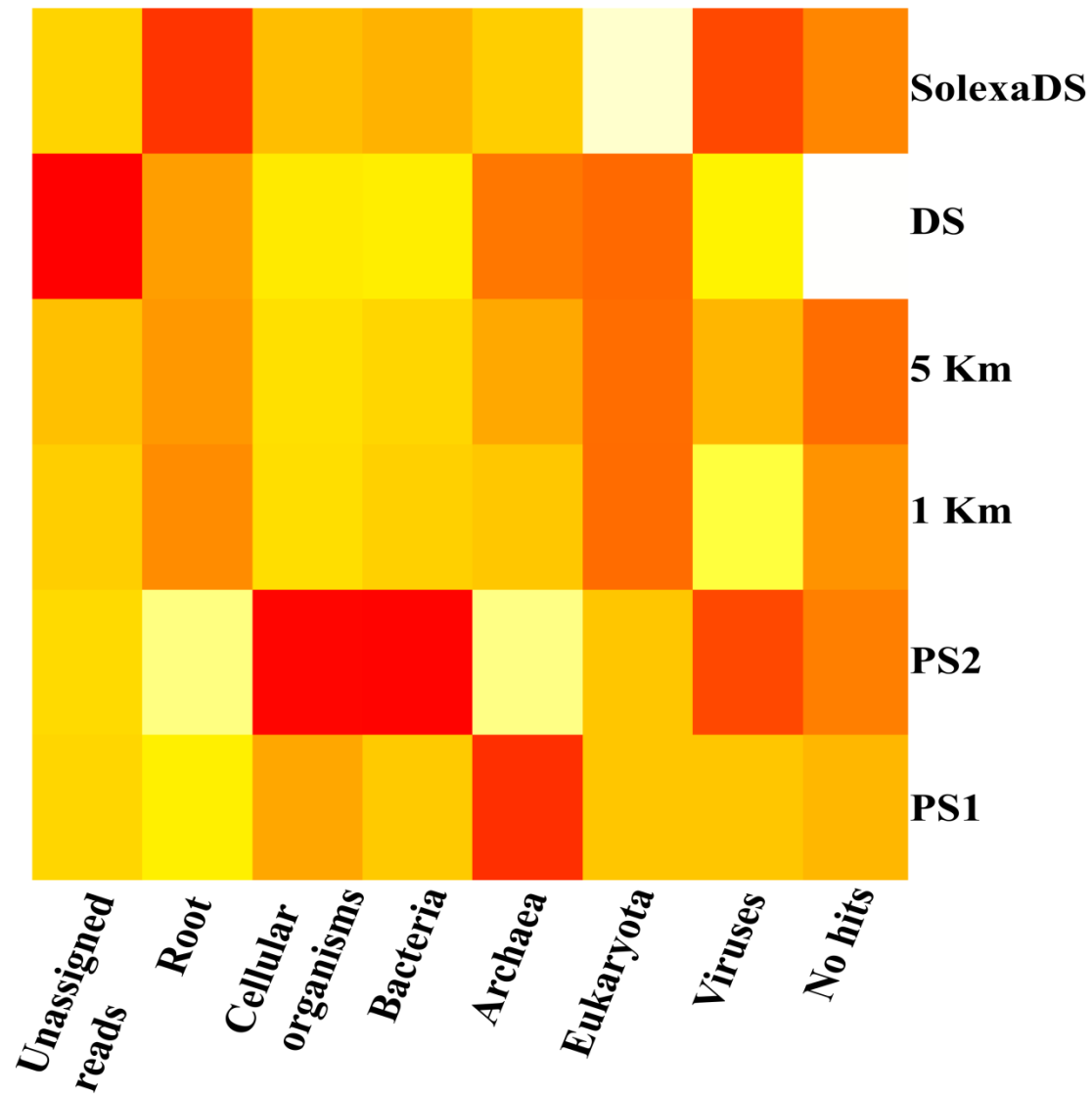


Fig. S3 Heatmap showing metagenomic reassignment of PS up to 1.02% as compared to 0.44% for all the metagenomes (1 Km, 5 Km, DS and SolexaDS). 61.43% of cellular organisms for PS included bacteria [56.39 %], archaea [0.69 %] and eukarya [0.86 %].

Fig. S4

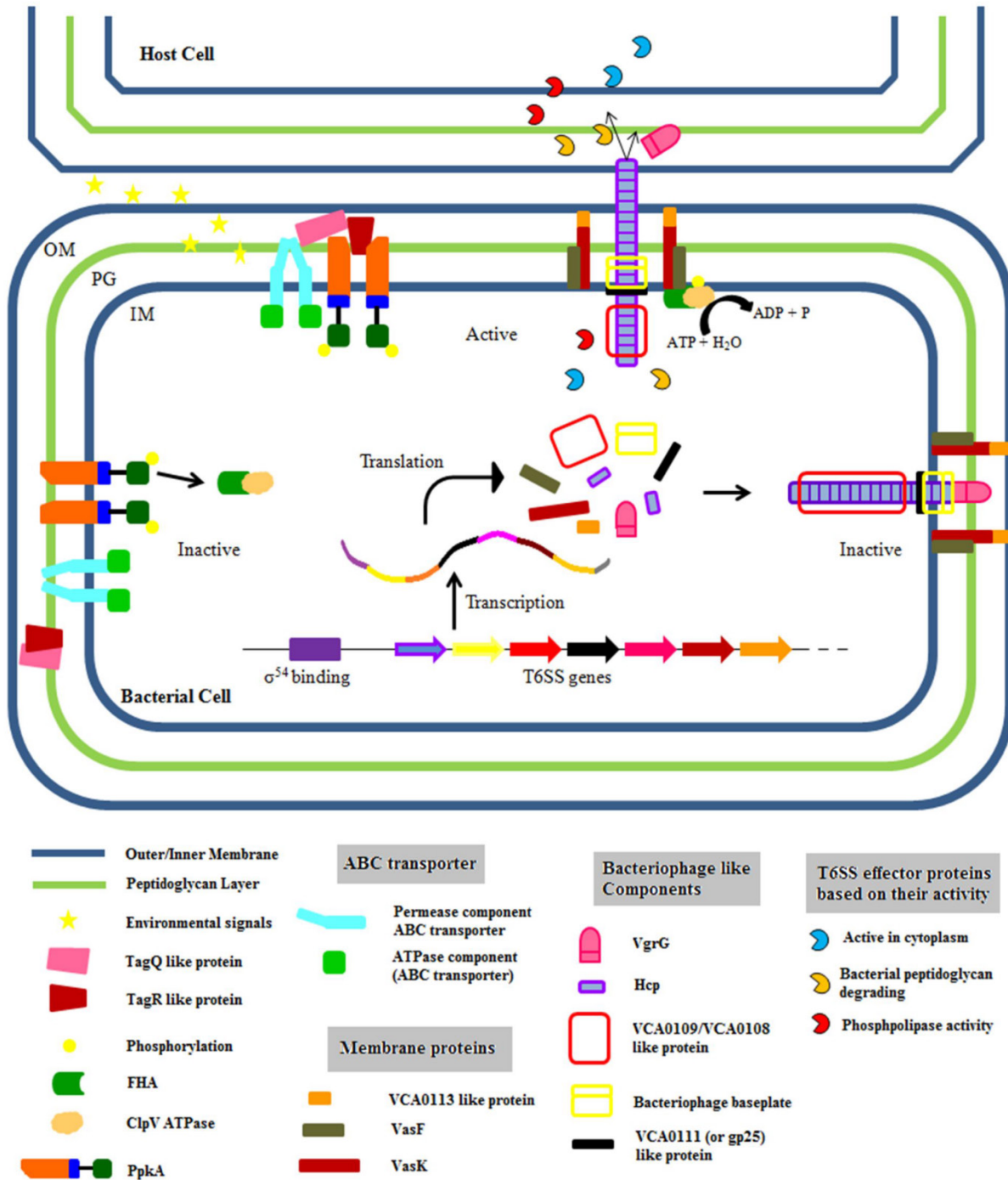


Fig. S4 Detailed model for T6SS machinery present in a cell and its interaction with other microbes present in the pond sediment environment was determined by alignment searches against the KEGG GENES database. All-versus-all BLASTP (default parameters) followed by MCL clustering was used to determine clusters of homolog's to validate the pathway.

Table S1 Phylogenetic reassignment of reads in PS1, PS2 and HCH gradient metagenomes (1 Km, 5 Km, DS, SolexaDS).

| | PS1 | PS2 | 1 Km | 5 Km | DS | SolexaDS |
|--|--------|--------|--------|--------|--------|----------|
| r.m.r from Proteobacteria | 0.695 | 0.7424 | 1.8109 | 0.9326 | 0.5948 | 0.5428 |
| r.m.r from Actinobacteria | 1.1189 | 0.8451 | 1.0104 | 0.7413 | 1.8444 | 0.9483 |
| r.m.r from Chloroflexi | 1.2422 | 0.7524 | 0.6637 | 0.5392 | 0.5526 | 0.9569 |
| r.m.r from Bacteroidetes | 1.3185 | 0.5787 | 1.0256 | 0.3604 | 0.6374 | 0.899 |
| r.m.r from Acidobacteria | 1.2946 | 0.7471 | 0.6517 | 0.5088 | 0.9655 | 0.9882 |
| r.m.r from Planctomycetes | 1.2031 | 0.7407 | 0.4659 | 0.5342 | 1.4762 | 0.939 |
| r.m.r from Verrucomicrobia | 1.0000 | 0.6667 | 0.9444 | 0.5532 | 2.8065 | 0.7849 |
| r.m.r from Firmicutes | 1.3676 | 0.9125 | 0.5636 | 0.6795 | 0.5088 | 1.1341 |
| r.m.r from Cyanobacteria | 1.1481 | 0.8615 | 0.4255 | 0.5942 | 1.6000 | 1.0000 |
| r.m.r from Gemmatimonadetes | 1.3214 | 0.7568 | 1.1000 | 0.5135 | 0.8182 | 1.0000 |
| r.m.r from Thaumarchaeota | 1.0370 | 0.8065 | 0.4074 | 0.6571 | 1.3333 | 1.0000 |
| r.m.r from Euryarchaeota | 1.0000 | 1.0000 | 2.6250 | 0.8750 | 0.6000 | 1.1667 |
| r.m.r from Deinococcus-Thermus | 1.0000 | 0.8000 | 0.5714 | 0.7778 | 2.7500 | 0.8182 |
| r.m.r from Nitrospirae | 1.1111 | 0.9000 | 0.4444 | 0.8000 | 0.7500 | 1.0000 |
| r.m.r from Armatimonadetes | 1.5714 | 0000 | 0000 | 0.2727 | 0000 | 1.0000 |
| r.m.r from Spirochaetes | 1.5714 | 0.2727 | 0.7500 | 0.3333 | 1.3333 | 1.0000 |
| r.m.r from Candidatus Saccharibacteria | 1.0000 | 1.0000 | 5.5000 | 1.0000 | 0.2500 | 1.0000 |
| r.m.r from Chlorobi | 1.0000 | 1.0000 | 0.0000 | 0.0000 | 1.3333 | 1.0000 |
| r.m.r from Poribacteria | 1.6667 | 0000 | 0000 | 0.4000 | 0000 | 1.0000 |
| r.m.r from Aminicenantes | 1.5000 | 0000 | 1.0000 | 0.6667 | 0000 | 1.0000 |
| r.m.r from Ignavibacteriae | 1.3333 | 0000 | 0000 | 0.5000 | 0000 | 1.0000 |

Table S2 Relative abundance of phyla present in pond sediment shown in the plot, with median values, variance, standard error, *P*-value and *Q*-value.

| Name | mean(PS1) | variance(PS1) | std.err(PS1) | average | mean(PS2) | variance(PS2) | std.err(PS2) | p-value | q-value |
|---------------------|-----------|---------------|--------------|----------|-----------|---------------|--------------|----------|----------|
| Acidobacteria | 0.010111 | 4.28E-08 | 0.000207 | 0.010486 | 0.01086 | 5.42E-08 | 0.000233 | 0.016577 | 0.032467 |
| Actinobacteria | 0.259609 | 8.21E-07 | 0.000906 | 0.26683 | 0.27405 | 1.00E-06 | 0.001002 | 1.02E-26 | 7.04E-26 |
| Chlamydiae | 0.002 | 8.53E-09 | 9.24E-05 | 0.002054 | 0.002108 | 1.06E-08 | 0.000103 | 0.45E-24 | 0.31E-24 |
| Chlorobi | 0.011599 | 4.90E-08 | 0.000221 | 0.011991 | 0.012383 | 6.17E-08 | 0.000248 | 0.018736 | 0.032467 |
| Chloroflexi | 0.025821 | 1.08E-07 | 0.000328 | 0.023854 | 0.021886 | 1.08E-07 | 0.000329 | 4.11E-17 | 1.90E-16 |
| Cyanobacteria | 0.009569 | 4.05E-08 | 0.000201 | 0.009869 | 0.010169 | 5.08E-08 | 0.000225 | 0.048117 | 0.046703 |
| Deinococcus-Thermus | 0.007787 | 3.30E-08 | 0.000182 | 0.00757 | 0.007354 | 3.68E-08 | 0.000192 | 0.10E-16 | 0.13E-16 |
| Euryarchaeota | 0.035116 | 1.45E-07 | 0.000381 | 0.035866 | 0.036615 | 1.78E-07 | 0.000422 | 0.00843 | 0.023374 |
| Firmicutes | 0.062284 | 2.50E-07 | 0.0005 | 0.061739 | 0.061195 | 2.90E-07 | 0.000538 | 0.14E-16 | 0.13E-16 |
| Fusobacteria | 0.000479 | 2.04E-09 | 4.52E-05 | 0.000474 | 0.000469 | 2.37E-09 | 4.86E-05 | 0.94E-13 | 0.42E-13 |
| Nitrospirae | 0.000137 | 5.84E-10 | 2.42E-05 | 0.000149 | 0.000161 | 8.14E-10 | 2.85E-05 | 0.59E-13 | 0.32E-13 |
| Planctomycete | 0.0137 | 5.79E-08 | 0.0002 | 0.014 | 0.0145 | 7.21E-08 | 0.0002 | 0.031 | 0.047 |

| | | | | | | | | | |
|---------------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| s | 27 | 08 | 41 | 117 | 07 | 08 | 69 | 136 | 959 |
| Proteobacteria | 0.4573 79 | 1.06E- 06 | 0.0010 3 | 0.453 623 | 0.4498 67 | 1.25E- 06 | 0.0011 17 | 7.81E -07 | 2.71E -06 |
| Spirochaetes | 0.0088 93 | 3.77E- 08 | 0.0001 94 | 0.008 865 | 0.0088 37 | 4.42E- 08 | 0.0002 1 | 0.85E -17 | 0.40E -17 |
| Tenericutes | 0.0006 58 | 2.81E- 09 | 5.30E- 05 | 0.000 74 | 0.0008 22 | 4.14E- 09 | 6.44E- 05 | 0.053 747 | 0.047 334 |
| Thaumarchaeo ta | 0.0002 95 | 1.26E- 09 | 3.55E- 05 | 0.000 258 | 0.0002 22 | 1.12E- 09 | 3.35E- 05 | 0.16E -16 | 0.14E -15 |
| Thermotogae | 0.0022 65 | 9.66E- 09 | 9.83E- 05 | 0.002 409 | 0.0025 52 | 1.28E- 08 | 0.0001 13 | 0.038 286 | 0.027 334 |
| Verrucomicrobi a | 0.0151 37 | 6.37E- 08 | 0.0002 52 | 0.014 696 | 0.0142 55 | 7.09E- 08 | 0.0002 66 | 0.016 981 | 0.032 467 |
| unknown phylum | 0.0338 73 | 1.40E- 07 | 0.0003 74 | 0.030 785 | 0.0276 97 | 1.36E- 07 | 0.0003 69 | 2.12E -31 | 2.94E -30 |

Table S3 Average of relative abundance of each bacterial genera (EGT analysis) unique to Pond Sediment is tabulated.

| Genera Name | PS1 | PS2 |
|-------------------------|------------|------------|
| <i>Bacillus</i> | 1.095556 | 1.093299 |
| <i>Sphingomonas</i> | 0.528266 | 0.453674 |
| <i>Novosphingobium</i> | 0.8062 | 0.822214 |
| <i>Chloroflexus</i> | 0.658666 | 0.659788 |
| <i>Mycobacterium</i> | 2.58517 | 2.698521 |
| <i>Corynebacterium</i> | 2.397659 | 2.681718 |
| <i>Rhodococcus</i> | 2.625147 | 2.653713 |
| <i>Bradyrhizobium</i> | 2.590881 | 2.610026 |
| <i>Sorangium</i> | 2.71557 | 2.517051 |
| <i>Thauera</i> | 2.787909 | 2.653713 |
| <i>Methylibium</i> | 3.140087 | 2.807179 |
| <i>Candidatus</i> | 7.236762 | 5.811509 |
| <i>Anaeromyxobacter</i> | 7.579421 | 7.022427 |
| <i>Streptomyces</i> | 8.921501 | 11.23207 |
| <i>Burkholderia</i> | 10.76044 | 10.74367 |
| <i>Sphingobium</i> | 0.911853 | 0.887185 |

Table S4 The most abundant bacterial genera unique to Pond Sediment for computing genomic variation are represented.

| Complete Genomes | Accession No. |
|--|----------------------|
| <i>Anaeromyxobacter</i> sp. Fw109–5 chromosome, complete genome | NC_009675 |
| <i>Streptomyces venezuelae</i> ATCC 10712, complete genome | NC_018750 |
| <i>Rubrivivax gelatinosus</i> IL144, complete genome | NC_017075 |
| <i>Anaeromyxobacter dehalogenans</i> 2CP-C chromosome, complete genome | NC_007760 |
| <i>Streptomyces coelicolor</i> A3(2) chromosome, complete genome | NC_003888 |
| <i>Conexibacter woesei</i> DSM 14684 chromosome, complete genome | NC_013739 |
| <i>Methylibium petroleiphilum</i> PM1 chromosome, complete genome | NC_008825 |
| <i>Anaeromyxobacter</i> sp. K chromosome, complete genome | NC_011145 |
| <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB 382 chromosome, complete genome | NC_009480 |
| <i>Leptothrix cholodnii</i> SP–6 chromosome, complete genome | NC_010524 |
| <i>Anaeromyxobacter dehalogenans</i> 2CP–1 chromosome, complete genome | NC_011891 |
| <i>Streptomyces hygrosopicus</i> subsp. <i>jinggangensis</i> 5008 chromosome, complete genome | NC_017765 |
| <i>Kitasatospora setae</i> KM–6054, complete genome | NC_016109 |
| <i>Isoptericola variabilis</i> 225 chromosome, complete genome | NC_015588 |
| <i>Thermobispora bispora</i> DSM 43833 chromosome, complete genome | NC_014165 |
| <i>Brachybacterium faecium</i> DSM 4810 chromosome, complete genome | NC_013172 |
| <i>Kineococcus radiotolerans</i> SRS 30216 chromosome, complete genome | NC_009664 |
| <i>Nocardioides</i> sp. JS614 chromosome, complete genome | NC_008699 |
| <i>Ramlibacter tataouinensis</i> TTB310 chromosome, complete genome | NC_015677 |
| <i>Sorangium cellulosum</i> 'So ce 56' chromosome, complete genome | NC_010162 |
| <i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i> chromosome, complete genome | NC_010407 |

| | |
|--|-----------|
| <i>Phenylobacterium zucineum</i> HLK1 chromosome, complete genome | NC_011144 |
| <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350 chromosome, complete genome | NC_010572 |
| <i>Burkholderia</i> sp. KJ006 chromosome 1, complete sequence | NC_017920 |
| <i>Micrococcus luteus</i> NCTC 2665 chromosome, complete genome | NC_012803 |
| <i>Actinosynnema mirum</i> DSM 43827 chromosome, complete genome | NC_013093 |
| <i>Beutenbergia cavernae</i> DSM 12333 chromosome, complete genome | NC_012669 |
| <i>Modestobacter marinus</i> , complete genome | NC_017955 |
| <i>Phycisphaera mikurensis</i> NBRC 102666, complete genome | NC_017080 |
| <i>Starkeya novella</i> DSM 506 chromosome, complete genome | NC_014217 |
| <i>Variovorax paradoxus</i> S110 chromosome 1, complete sequence | NC_012791 |
| <i>Streptomyces</i> sp. SirexAA-E chromosome, complete genome | NC_015953 |
| <i>Oceanithermus profundus</i> DSM 14977 chromosome, complete genome | NC_014761 |
| <i>Pseudoxanthomonas suwonensis</i> 11-1 chromosome, complete genome | NC_014924 |
| <i>Sphingomonas wittichii</i> RW1 chromosome, complete genome | NC_009511 |
| <i>Cellvibrio gilvus</i> ATCC 13127 chromosome, complete genome | NC_015671 |
| <i>Haliangium ochraceum</i> DSM 14365 chromosome, complete genome | NC_013440 |
| <i>Streptomyces scabiei</i> 87.22 chromosome, complete genome | NC_013929 |
| <i>Methylobacterium radiotolerans</i> JCM 2831 chromosome, complete genome | NC_010505 |
| <i>Microbacterium testaceum</i> StLB037, complete genome | NC_015125 |
| <i>Burkholderia glumae</i> BGR1 chromosome 1, complete sequence | NC_012724 |
| <i>Streptomyces flavogriseus</i> ATCC 33331 chromosome, complete genome | NC_016114 |
| <i>Geodermatophilus obscurus</i> DSM 43160 chromosome, complete genome | NC_013757 |
| <i>Saccharothrix espanaensis</i> DSM 44229 complete genome | NC_019673 |
| <i>Thiobacillus denitrificans</i> ATCC 25259 chromosome, complete genome | NC_007404 |
| <i>Cellulomonas fimi</i> ATCC 484 chromosome, complete genome | NC_015514 |

| | |
|--|-------------|
| <i>Micromonospora</i> sp. L5 chromosome, complete genome | NC_014815 |
| <i>Azoarcus</i> sp. BH72 chromosome, complete genome | NC_008702 |
| <i>Pseudonocardia dioxanivorans</i> CB1190 chromosome, complete genome | NC_015312 |
| <i>Kribbella flavida</i> DSM 17836 chromosome, complete genome | NC_013729 |
| <i>Blastococcus saxobsidens</i> DD2, complete genome | NC_016943 |
| <i>Burkholderia multivorans</i> ATCC 17616 chromosome 1, complete sequence | NC_010084 |
| <i>Burkholderia cepacia</i> GG4 chromosome 1, complete sequence | NC_018513 |
| <i>Kytococcus sedentarius</i> DSM 20547 chromosome, complete genome | NC_013169 |
| <i>Rubrobacter xylanophilus</i> DSM 9941 chromosome, complete genome | NC_008148 |
| <i>Xylanimonas cellulosilytica</i> DSM 15894 chromosome, complete genome | NC_013530 |
| <i>Cellulomonas flavigena</i> DSM 20109 chromosome, complete genome | NC_014151 |
| <i>Micromonospora aurantiaca</i> ATCC 27029 chromosome, complete genome | NC_014391 |
| <i>Sanguibacter keddieii</i> DSM 10542 chromosome, complete genome | NC_013521 |
| <i>Burkholderia gladioli</i> BSR3 chromosome 1, complete sequence | NC_015381 |
| <i>Streptomyces cattleya</i> NRRL 8057, complete genome | NC_016111 |
| <i>Streptomyces cattleya</i> NRRL 8057 = DSM 46488 chromosome, complete genome | NC_017586 |
| <i>Streptomyces avermitilis</i> MA-4680, complete genome | NC_003155 |
| <i>Amycolatopsis mediterranei</i> S699 chromosome, complete genome | NC_018266 |
| <i>Rhodopseudomonas palustris</i> HaA2 chromosome, complete genome | NC_007778 |
| <i>Variovorax paradoxus</i> EPS chromosome, complete genome | NC_014931 |
| <i>Sphingobium indicum</i> B90A, whole genome sequence | AJXQ0100000 |
| <i>Sphingobium lactosutens</i> DS20, whole genome sequence | ATDP0100000 |
| <i>Sphingobium lucknowense</i> F2, whole genome sequence | JANF0200000 |
| <i>Sphingobium</i> sp. HDIP04, whole genome sequence | ATDO0100000 |
| <i>Sphingobium chinhatense</i> IP26, whole genome sequence | AUDA0100000 |

| | |
|--|-------------|
| <i>Novosphingobium lindaniclasticum</i> LE124, whole genome sequence | ATHL0100000 |
| <i>Sphingobium quisquiliarum</i> P25, whole genome sequence | ATHO0100000 |
| <i>Sphingobium ummariense</i> RL-3, whole genome sequence | AUWY0100000 |

Table S5 List of all essential single copy genes present in consensus with pond sediment and most abundant genomes present.

| Gene Symbol | Accession No | Description |
|--------------------|---------------------|---|
| cgtA | TIGR02729 | Obg family GTPase CgtA |
| coaE | TIGR00152 | dephospho-CoA kinase |
| dnaK | TIGR02350 | chaperone protein DnaK |
| dnaN | TIGR00663 | DNA polymerase III, beta subunit |
| dnaX | TIGR02397 | DNA polymerase III, subunits gamma and tau |
| engA | TIGR03594 | ribosome-associated GTPase EngA |
| frr | TIGR00496 | ribosome recycling factor |
| grpE | PF01025 | co-chaperone GrpE |
| infB | TIGR00487 | translation initiation factor IF-2 |
| infC | TIGR00168 | translation initiation factor IF-3 |
| mnmA | TIGR00420 | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase |

| | | |
|-------------|------------------|--|
| mraW | PF01795 | MraW methylase family |
| nusG | TIGR00922 | transcription termination/antitermination factor NusG |
| pgk | PF00162 | phosphoglycerate kinase |
| pheS | TIGR00468 | phenylalanyl-tRNA synthetase, alpha subunit |
| rfaA | TIGR00082 | ribosome-binding factor A |
| rplA | TIGR01169 | ribosomal protein L1 |
| rplB | TIGR01171 | ribosomal protein L2 |
| rplC | PF00297 | ribosomal protein L3 |
| rplD | PF00573 | ribosomal protein L4 |
| rplE | PF00281 | ribosomal protein L5 |
| rplF | PF00347 | ribosomal protein L6 |
| rplK | TIGR01632 | ribosomal protein L11 |
| rplM | TIGR01066 | ribosomal protein L13 |
| rplN | TIGR01067 | ribosomal protein L14 |
| rplO | TIGR01071 | ribosomal protein L15 |
| rplP | TIGR01164 | ribosomal protein L16 |
| rplQ | TIGR00059 | ribosomal protein L17 |
| rplR | TIGR00060 | ribosomal protein L18 |

| | | |
|-------------|------------------|---|
| rplS | TIGR01024 | ribosomal protein L19 |
| rplT | TIGR01032 | ribosomal protein L20 |
| rplU | TIGR00061 | ribosomal protein L21 |
| rplV | TIGR01044 | ribosomal protein L22 |
| rplW | PF00276 | ribosomal protein L23 |
| rplX | TIGR01079 | ribosomal protein L24 |
| rpmA | TIGR00062 | ribosomal protein L27 |
| rpmC | TIGR00012 | ribosomal protein L29 |
| rpoA | TIGR02027 | DNA-directed RNA polymerase, alpha subunit |
| rpoB | TIGR02013 | DNA-directed RNA polymerase, beta subunit |
| rpsB | TIGR01011 | ribosomal protein S2 |
| rpsC | TIGR01009 | ribosomal protein S3 |
| rpsD | TIGR01017 | ribosomal protein S4 |
| rpsG | TIGR01029 | ribosomal protein S7 |
| rpsH | PF00410 | ribosomal protein S8 |
| rpsI | PF00380 | ribosomal protein S9 |
| rpsJ | TIGR01049 | ribosomal protein S10 |
| rpsK | PF00411 | ribosomal protein S11 |

| | | |
|-------------|------------------|---|
| rpsL | TIGR00981 | ribosomal protein S12 |
| rpsM | PF00416 | ribosomal protein S13 |
| rpsO | TIGR00952 | ribosomal protein S15 |
| rpsP | TIGR00002 | ribosomal protein S16 |
| rpsQ | PF00366 | ribosomal protein S17 |
| rpsS | TIGR01050 | ribosomal protein S19 |
| secE | TIGR00964 | preprotein translocase, SecE subunit |
| secY | TIGR00967 | preprotein translocase, SecY subunit |
| smpB | TIGR00086 | SmpB protein |
| Tig | TIGR00115 | trigger factor |
| tilS | TIGR02432 | tRNA(Ile)-lysidine synthetase |
| Tsf | TIGR00116 | translation elongation factor Ts |
| tyrS | TIGR00234 | tyrosyl-tRNA synthetase |

Table S6 Percentage of ORFs belonging to different subsystems (SEED) across HCH gradient (Solexa DS, 1 Km, 5 Km and DS) and Pond Sediment metagenomes (PS1 and PS2) respectively.

| Subsystems | PS1 | PS2 | Solexa DS | 1 Km | 5 Km | DS |
|---|------------|------------|------------------|-------------|-------------|-----------|
| Amino Acids and Derivatives | 15.51 | 15.38 | 14.98 | 2.53 | 15.07 | 15.23 |
| Carbohydrates | 9.97 | 9.94 | 9.85 | 1.69 | 11.58 | 10.21 |
| Cell Division and Cell Cycle | 8.24 | 8.10 | 8.98 | 1.44 | 8.61 | 8.67 |
| Cell Wall and Capsule | 7.82 | 7.88 | 7.89 | 1.36 | 8.87 | 8.23 |
| Clustering-based subsystems | 8.01 | 7.99 | 7.44 | 1.26 | 7.39 | 7.57 |
| Cofactors, Vitamins, Prosthetic Groups, Pigments | 6.51 | 6.61 | 6.40 | 1.06 | 6.10 | 6.42 |
| DNA Metabolism | 3.89 | 4.00 | 3.93 | 0.67 | 3.94 | 4.04 |
| Dormancy and Sporulation | 3.57 | 3.49 | 4.06 | 0.67 | 3.77 | 4.04 |
| Fatty Acids, Lipids, and Isoprenoids | 3.50 | 3.45 | 3.98 | 0.67 | 3.72 | 4.02 |
| Iron acquisition and metabolism | 4.24 | 4.36 | 3.63 | 0.62 | 1.62 | 3.75 |
| Membrane Transport | 3.70 | 3.76 | 3.13 | 0.51 | 3.42 | 3.08 |
| Metabolism of Aromatic Compounds | 3.53 | 3.70 | 3.30 | 0.53 | 2.82 | 3.21 |
| Miscellaneous | 3.12 | 3.14 | 3.22 | 0.52 | 2.76 | 3.12 |
| Motility and Chemotaxis | 2.74 | 2.70 | 2.89 | 0.46 | 2.85 | 2.76 |
| Nitrogen Metabolism | 2.60 | 2.64 | 2.60 | 0.47 | 2.79 | 2.81 |
| Nucleosides and Nucleotides | 1.76 | 1.74 | 1.50 | 0.23 | 4.10 | 1.37 |
| Phages, Prophages, Transposable elements, Plasmids | 2.01 | 2.00 | 2.10 | 0.31 | 1.54 | 1.85 |
| Phosphorus Metabolism | 1.25 | 1.19 | 1.97 | 0.31 | 1.56 | 1.84 |
| Photosynthesis | 1.54 | 1.56 | 1.49 | 0.24 | 1.36 | 1.45 |
| Potassium metabolism | 1.27 | 1.30 | 1.39 | 0.23 | 1.38 | 1.41 |

| | | | | | | |
|---------------------------------------|------|------|------|------|------|------|
| Protein Metabolism | 1.28 | 1.25 | 1.13 | 0.17 | 1.10 | 1.02 |
| Regulation and Cell signaling | 1.09 | 1.02 | 1.11 | 0.17 | 0.94 | 1.05 |
| Respiration | 0.94 | 0.93 | 0.87 | 0.16 | 0.92 | 0.95 |
| RNA Metabolism | 0.73 | 0.73 | 1.08 | 0.14 | 0.63 | 0.86 |
| Secondary Metabolism | 0.42 | 0.39 | 0.37 | 0.06 | 0.49 | 0.36 |
| Stress Response | 0.44 | 0.45 | 0.38 | 0.06 | 0.37 | 0.36 |
| Sulfur Metabolism | 0.17 | 0.20 | 0.22 | 0.03 | 0.19 | 0.20 |
| Virulence, Disease and Defense | 0.14 | 0.11 | 0.11 | 0.02 | 0.12 | 0.12 |

Table S7 List of enzymes present in pond sediment metagenome which are involved in degradation of chlorocyclohexane and chlorobenzene (**ko00361**).

| S. no. | EC Number | Enzyme Name | Enzyme Class | Predicted Role |
|--------|---|---|----------------------|---|
| 1 | EC 3.1.1.45 | Carboxymethylenebutenolidase | Hydrolases | Act on carboxylic ester bonds in carbon-halide compounds |
| 2 | EC 3.8.1.2, EC 3.8.1.3 | 2-haloacid dehalogenase, haloacetate dehalogenase | „ | Act on halide bonds in carbon-halide compounds |
| 3 | EC 1.3.1.1.32, EC 1.13.11.37, EC 1.13.11.39 and EC 1.14.13.50 | Maleylacetate reductase, Hydroxyquinol 1,2-dioxygenase, Biphenyl-2,3-dioL-1,2-dioxygenase and Pentachlorophenol 4-monooxygenase | Oxidoreduc tase | Act on CH-CH group of the donor and on single donors with O ₂ as oxidant for the rest |
| 4 | EC 5.5.1.7 | Chloromuconate cycloisomerase | Isomerases | It acts on 2-chloro-2,5-dihydro-5-oxofuran-2-acetate and gives one product 3-chloro-cis,cis-muconate |
| 5 | EC 4.5.1.- | (LinA) γ -hexachlorocyclohexane dehydrochlorinase | Carbon-halide lyases | Catalyzes the conversion of γ -HCH to to 1,3,4,6-tetrachloro-1,4-cyclohexadiene (1,4-TCDN). Many copies of <i>linA</i> (AY903217.1, AY331258.1, AJ871378.1, AJ871379.1, AJ871381.1, AJ871382.1, AJ871383.1, AJ871385.1, D90355.2, AY690622.3 and AB601887.1) (Evalue > 1e-5) |

| | | | | |
|---|------------|-------------------------|------------|--|
| 6 | EC 3.8.1.5 | Haloalkane dehalogenase | Hydrolases | Acts on halide bonds. Many copies of <i>linB</i> (AB278602.1, AB304076.1, AB304077.1, AB304078.1, AB304079.1, AB304080.1, AB304081.1, AY903216.1, DQ767899.1, HQ385918.1, HQ385917.1, HQ385916.1, HQ385915.1, GQ915275.1, FJ966198.1, FJ966199.1, FJ966200.1, FJ966201.1, FJ966202.1 and GQ915275.1) (Evalue > 1e-5) |
|---|------------|-------------------------|------------|--|

Table S8 List of various components of Type VI Secretory System and their effector proteins together with gene and KO (KEGG Orthology) names.

| KO id | Gene name | <i>Vibrio cholera</i> (AE003853) | <i>Burkholderia mallei</i> ATCC 23344 (CP000011) | <i>Pseudomonas aeruginosa</i> PAO1 (AE004091) |
|-----------------------------|------------------|----------------------------------|--|---|
| Tailed Bacteriophage | | | | |
| K11903 | <i>Hcp</i> | - | BMAA0742 | PA0085 |
| K11904 | <i>vgrG</i> | VC_A0123 | BMAA0737 | PA0091, PA0095 |
| K11904 | <i>tssB</i> | VC_A0108 | BMAA0743 | PA0084 |
| K11895 | <i>tssE/gp25</i> | VC_A0111 | BMAA0739 | PA0089 |
| Membrane Associated | | | | |
| K11892 | <i>tssL/vasF</i> | VC_A0115 | BMAA0731 | PA0078 |
| K11906 | <i>tssJ</i> | VC_A0113 | BMAA0733 | PA0080 |
| K11896 | <i>vasA</i> | VC_A0110 | BMAA0740 | PA0088 |

| | | | | |
|------------------------|--------------|----------|----------|--------|
| K11894 | - | VC_A0112 | - | PA0081 |
| K11910 | - | VC_A0119 | BMAA0747 | PA0082 |
| K11893 | <i>tssK</i> | VC_A0114 | BMAA0732 | PA0079 |
| K11907 | <i>clpVI</i> | VC_A0116 | BMAA0738 | PA0090 |
| | | | | |
| Accessory Genes | | | | |
| K11908 | <i>vasH</i> | VC_A0117 | - | - |
| K02557 | - | VC0893 | - | - |
| K11898 | <i>sciE</i> | - | - | PA0086 |
| - | Tle2 | VC1418 | - | |
| K01115 | Tle5 | - | - | PA3487 |
| K01296 | Tae3 | - | - | - |
| K02919 | Tae4 | - | - | - |
| K08309 | Tge1(Tse3) | - | - | - |
| K01185 | Tge3 | - | - | - |