**Supplementary materials**

**Table number: 6**

**Table S1.** Relative abundance of bacterial communities at various points along natural river channel A.

| #Taxonomy | A1 | A2 | A3 | A4 | A5 |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__unclassified_c__Deltaproteobacteria;f__unclassified_c__Deltaproteobacteria;g__unclassified_c__Deltaproteobacteria | 0.1019 | 0.0966 | 0.1040 | 0.1266 | 0.1091 |
| p__Acidobacteria;c__unclassified_p__Acidobacteria;o__unclassified_p__Acidobacteria;f__unclassified_p__Acidobacteria;g__unclassified_p__Acidobacteria | 0.0519 | 0.0458 | 0.0482 | 0.0459 | 0.0527 |
| p__Proteobacteria;c__Betaproteobacteria;o__unclassified_c__Betaproteobacteria;f__unclassified_c__Betaproteobacteria;g__unclassified_c__Betaproteobacteria | 0.0080 | 0.0053 | 0.0164 | 0.0414 | 0.0241 |
| p__Chloroflexi;c__unclassified_p__Chloroflexi;o__unclassified_p__Chloroflexi;f__unclassified_p__Chloroflexi;g__unclassified_p__Chloroflexi | 0.1059 | 0.1088 | 0.0730 | 0.0576 | 0.0637 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas | 0.0297 | 0.0270 | 0.0337 | 0.0552 | 0.0300 |
| p__Candidatus_Aminicenantes;c__unclassified_p__Candidatus_Aminicenantes;o__unclassified_p__Candidatus_Aminicenantes;f__unclassified_p__Candidatus_Aminicenantes;g__unclassified_p__Candidatus_Aminicenantes | 0.0450 | 0.0193 | 0.0210 | 0.0119 | 0.0914 |
| p__Proteobacteria;c__Gammaproteobacteria;o__unclassified_c__Gammaproteobacteria;f__unclassified_c__Gammaproteobacteria;g__unclassified_c__Gammaproteobacteria | 0.0036 | 0.0026 | 0.0043 | 0.0090 | 0.0107 |
| p__unclassified_d__Bacteria;c__unclassified_d__Bacteria;o__unclassified_d__Bacteria;f__unclassified_d__Bacteria;g__unclassified_d__Bacteria | 0.0304 | 0.0284 | 0.0288 | 0.0259 | 0.0275 |
| p__Planctomycetes;c__unclassified_p__Planctomycetes;o__unclassified_p__Planctomycetes;f__unclassified_p__Planctomycetes;g__unclassified_p__Planctomycetes | 0.0440 | 0.0480 | 0.0389 | 0.0216 | 0.0243 |
| p__Gemmatimonadetes_d__Bacteria;c__unclassified_p__Gemmatimonadetes_d__Bacteria;o__unclassified_p__Gemmatimonadetes_d__Bacteria;f__unclassified_p__Gemmatimonadetes_d__Bacteria;g__unclassified_p__Gemmatimonadetes_d__Bacteria | 0.0207 | 0.0404 | 0.0388 | 0.0140 | 0.0209 |
| p__Spirochaetes;c__unclassified_p__Spirochaetes;o__unclassified_p__Spirochaetes;f__unclassified_p__Spirochaetes;g__unclassified_p__Spirochaetes | 0.0293 | 0.0191 | 0.0249 | 0.0203 | 0.0214 |

| | | | | | |
|---|---|---|---|---|---|
| p__Actinobacteria;c__Actinobacteria;o__unclassified_c__Actinobacteria;f__unclassified_c__Actinobacteria;g__unclassified_c__Actinobacteria | 0.0062 | 0.0053 | 0.0068 | 0.0134 | 0.0100 |
| p__Chloroflexi;c__Anaerolineae;o__unclassified_c__Anaerolineae;f__unclassified_c__Anaerolineae;g__unclassified_c__Anaerolineae | 0.0352 | 0.0413 | 0.0175 | 0.0147 | 0.0180 |
| p__Candidatus_Rokubacteria;c__unclassified_p__Candidatus_Rokubacteria;o__unclassified_p__Candidatus_Rokubacteria;f__unclassified_p__Candidatus_Rokubacteria;g__unclassified_p__Candidatus_Rokubacteria | 0.0035 | 0.0031 | 0.0041 | 0.0082 | 0.0052 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bradyrhizobium | 0.0011 | 0.0009 | 0.0010 | 0.0024 | 0.0013 |
| p__Proteobacteria;c__Alphaproteobacteria;o__unclassified_c__Alphaproteobacteria;f__unclassified_c__Alphaproteobacteria;g__unclassified_c__Alphaproteobacteria | 0.0044 | 0.0030 | 0.0033 | 0.0046 | 0.0034 |
| p__Actinobacteria;c__unclassified_p__Actinobacteria;o__unclassified_p__Actinobacteria;f__unclassified_p__Actinobacteria;g__unclassified_p__Actinobacteria | 0.0074 | 0.0071 | 0.0134 | 0.0063 | 0.0094 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Anaeromyxobacteraceae;g__Anaeromyxobacter | 0.0024 | 0.0014 | 0.0044 | 0.0048 | 0.0047 |
| p__Nitrospirae;c__unclassified_p__Nitrospirae;o__unclassified_p__Nitrospirae;f__unclassified_p__Nitrospirae;g__unclassified_p__Nitrospirae | 0.0091 | 0.0066 | 0.0074 | 0.0059 | 0.0055 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira | 0.0005 | 0.0006 | 0.0007 | 0.0015 | 0.0008 |
| p__Proteobacteria;c__unclassified_p__Proteobacteria;o__unclassified_p__Proteobacteria;f__unclassified_p__Proteobacteria;g__unclassified_p__Proteobacteria | 0.0033 | 0.0029 | 0.0034 | 0.0039 | 0.0032 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__unclassified_f__Moraxellaceae | 0.0020 | 0.0018 | 0.0014 | 0.0033 | 0.0016 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unclassified_o__Rhizobiales;g__unclassified_o__Rhizobiales | 0.0079 | 0.0051 | 0.0050 | 0.0049 | 0.0044 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Azonexaceae;g__Dechloromonas | 0.0025 | 0.0002 | 0.0159 | 0.0158 | 0.0113 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__unclassified_o__Myxococcales;g__unclassified_o__Myxococcales | 0.0032 | 0.0044 | 0.0020 | 0.0027 | 0.0023 |

| | | | | | |
|---|---|---|---|---|---|
| p__Candidatus_Abyssubacteria;c__unclassified_p__Candidatus_Abyssubacteria;o__unclassified_p__Candidatus_Abyssubacteria;f__unclassified_p__Candidatus_Abyssubacteria;g__unclassified_p__Candidatus_Abyssubacteria | 0.0116 | 0.0271 | 0.0131 | 0.0150 | 0.0141 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobacteraceae;g__unclassified_f__Desulfobacteraceae | 0.0061 | 0.0044 | 0.0063 | 0.0115 | 0.0081 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__unclassified_f__Syntrophaceae | 0.0035 | 0.0032 | 0.0036 | 0.0059 | 0.0026 |
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__unclassified_o__Anaerolineales;g__unclassified_o__Anaerolineales | 0.0103 | 0.0100 | 0.0058 | 0.0038 | 0.0049 |
| p__Verrucomicrobia;c__unclassified_p__Verrucomicrobia;o__unclassified_p__Verrucomicrobia;f__unclassified_p__Verrucomicrobia;g__unclassified_p__Verrucomicrobia | 0.0048 | 0.0054 | 0.0041 | 0.0050 | 0.0043 |
| p__candidate_division_Zixibacteria;c__unclassified_p__candidate_division_Zixibacteria;o__unclassified_p__candidate_division_Zixibacteria;f__unclassified_p__candidate_division_Zixibacteria;g__unclassified_p__candidate_division_Zixibacteria | 0.0162 | 0.0121 | 0.0041 | 0.0103 | 0.0094 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__unclassified_o__Burkholderiales | 0.0007 | 0.0004 | 0.0011 | 0.0018 | 0.0013 |
| p__Candidatus_Eisenbacteria;c__unclassified_p__Candidatus_Eisenbacteria;o__unclassified_p__Candidatus_Eisenbacteria;f__unclassified_p__Candidatus_Eisenbacteria;g__unclassified_p__Candidatus_Eisenbacteria | 0.0015 | 0.0024 | 0.0012 | 0.0025 | 0.0020 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__unclassified_o__Gemmatimonadales;g__unclassified_o__Gemmatimonadales | 0.0028 | 0.0046 | 0.0044 | 0.0025 | 0.0031 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Desulfuromonadaceae;g__Desulfuromonas | 0.0006 | 0.0007 | 0.0010 | 0.0019 | 0.0013 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__unclassified_o__Syntrophobacterales;g__unclassified_o__Syntrophobacterales | 0.0015 | 0.0013 | 0.0016 | 0.0019 | 0.0014 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__unclassified_f__Rhodospirillaceae | 0.0005 | 0.0004 | 0.0006 | 0.0016 | 0.0009 |

| | | | | | |
|---|---|---|---|---|---|
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__unclassified_f__Anaerolineaceae | 0.0062 | 0.0070 | 0.0042 | 0.0036 | 0.0040 |
| p__Planctomycetes;c__Phycisphaerae;o__unclassified_c__Phycisphaerae;f__unclassified_c__Phycisphaerae;g__unclassified_c__Phycisphaerae | 0.0079 | 0.0086 | 0.0080 | 0.0046 | 0.0049 |
| p__Chloroflexi;c__Dehalococcoidia;o__unclassified_c__Dehalococcoidia;f__unclassified_c__Dehalococcoidia;g__unclassified_c__Dehalococcoidia | 0.0080 | 0.0060 | 0.0062 | 0.0029 | 0.0044 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__unclassified_f__Nitrospiraceae | 0.0015 | 0.0013 | 0.0014 | 0.0017 | 0.0014 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__unclassified_o__Nitrosomonadales;g__unclassified_o__Nitrosomonadales | 0.0002 | 0.0002 | 0.0004 | 0.0008 | 0.0011 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__unclassified_p__candidate_division_NC10 | 0.0030 | 0.0022 | 0.0022 | 0.0022 | 0.0021 |
| p__Acidobacteria;c__Thermoanaerobaculia;o__unclassified_c__Thermoanaerobaculia;f__unclassified_c__Thermoanaerobaculia;g__unclassified_c__Thermoanaerobaculia | 0.0006 | 0.0007 | 0.0006 | 0.0009 | 0.0010 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__Thiobacillaceae;g__Thiobacillus | 0.0004 | 0.0001 | 0.0023 | 0.0038 | 0.0123 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Aromatoleum | 0.0002 | 0.0002 | 0.0004 | 0.0009 | 0.0006 |
| p__Bacteroidetes;c__unclassified_p__Bacteroidetes;o__unclassified_p__Bacteroidetes;f__unclassified_p__Bacteroidetes;g__unclassified_p__Bacteroidetes | 0.0032 | 0.0032 | 0.0039 | 0.0046 | 0.0039 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__unclassified_f__Burkholderiaceae | 0.0004 | 0.0002 | 0.0005 | 0.0010 | 0.0007 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__unclassified_o__Xanthomonadales;g__unclassified_o__Xanthomonadales | 0.0006 | 0.0004 | 0.0008 | 0.0016 | 0.0011 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__unclassified_o__Desulfobacterales;g__unclassified_o__Desulfobacterales | 0.0047 | 0.0031 | 0.0053 | 0.0037 | 0.0036 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Syntrophus_f__Syntrophaceae | 0.0010 | 0.0011 | 0.0013 | 0.0014 | 0.0012 |

| | | | | | |
|---|---|---|---|---|---|
| p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__unclassified_o__Phycisphaerales;g__unclassified_o__Phycisphaerales | 0.0066 | 0.0069 | 0.0087 | 0.0032 | 0.0037 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__unclassified_f__Rhodocyclaceae | 0.0005 | 0.0002 | 0.0019 | 0.0027 | 0.0019 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas | 0.0032 | 0.0035 | 0.0033 | 0.0046 | 0.0036 |
| p__Acidobacteria;c__Vicinamibacteria;o__unclassified_c__Vicinamibacteria;f__Vicinamibacteraceae;g__Luteitalea | 0.0014 | 0.0015 | 0.0013 | 0.0015 | 0.0016 |
| p__Planctomycetes;c__Planctomycetia;o__Planctomycetales;f__Planctomycetaceae;g__unclassified_f__Planctomycetaceae | 0.0049 | 0.0054 | 0.0050 | 0.0030 | 0.0032 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae;g__Geobacter | 0.0014 | 0.0013 | 0.0019 | 0.0031 | 0.0023 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Acidiferrobacterales;f__Acidiferrobacteraceae;g__Sulfuricaulis | 0.0001 | 0.0000 | 0.0001 | 0.0004 | 0.0002 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys | 0.0003 | 0.0002 | 0.0006 | 0.0021 | 0.0010 |
| p__Acidobacteria;c__Holophagae;o__unclassified_c__Holophagae;f__unclassified_c__Holophagae;g__unclassified_c__Holophagae | 0.0025 | 0.0025 | 0.0016 | 0.0018 | 0.0021 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__Solibacteraceae;g__Candidatus_Solibacter | 0.0035 | 0.0035 | 0.0021 | 0.0020 | 0.0022 |
| p__Proteobacteria;c__Zetaproteobacteria;o__unclassified_c__Zetaproteobacteria;f__unclassified_c__Zetaproteobacteria;g__unclassified_c__Zetaproteobacteria | 0.0022 | 0.0013 | 0.0013 | 0.0012 | 0.0011 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium | 0.0001 | 0.0001 | 0.0002 | 0.0006 | 0.0002 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Rhodoplanes | 0.0002 | 0.0002 | 0.0003 | 0.0006 | 0.0004 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__unclassified_o__Rhodospirillales;g__unclassified_o__Rhodospirillales | 0.0003 | 0.0002 | 0.0003 | 0.0006 | 0.0004 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Piscinibacter | 0.0001 | 0.0000 | 0.0003 | 0.0006 | 0.0003 |
| p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobia_subdivision_3;g__unclassified_f__Verrucomicrobia_subdivision_3 | 0.0020 | 0.0023 | 0.0017 | 0.0017 | 0.0017 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Rubrivivax | 0.0002 | 0.0000 | 0.0004 | 0.0007 | 0.0004 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Ralstonia | 0.0031 | 0.0032 | 0.0032 | 0.0032 | 0.0034 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__unclassified_f__Comamonadaceae | 0.0002 | 0.0001 | 0.0003 | 0.0006 | 0.0004 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Ramlibacter | 0.0002 | 0.0002 | 0.0003 | 0.0006 | 0.0005 |
| p__Proteobacteria;c__Candidatus_Muproteobacteria;o__unclassified_c__Candidatus_Muproteobacteria;f__unclassified_c__Candidatus_Muproteobacteria;g__unclassified_c__Candidatus_Muproteobacteria | 0.0002 | 0.0001 | 0.0002 | 0.0004 | 0.0003 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Ideonella | 0.0001 | 0.0000 | 0.0003 | 0.0006 | 0.0004 |
| p__Firmicutes;c__unclassified_p__Firmicutes;o__unclassified_p__Firmicutes;f__unclassified_p__Firmicutes;g__unclassified_p__Firmicutes | 0.0033 | 0.0028 | 0.0030 | 0.0020 | 0.0022 |
| p__Candidatus_Omnitrophica;c__unclassified_p__Candidatus_Omnitrophica;o__unclassified_p__Candidatus_Omnitrophica;f__unclassified_p__Candidatus_Omnitrophica;g__unclassified_p__Candidatus_Omnitrophica | 0.0024 | 0.0041 | 0.0075 | 0.0013 | 0.0021 |
| p__Armatimonadetes;c__unclassified_p__Armatimonadetes;o__unclassified_p__Armatimonadetes;f__unclassified_p__Armatimonadetes;g__unclassified_p__Armatimonadetes | 0.0030 | 0.0030 | 0.0024 | 0.0016 | 0.0017 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__unclassified_f__Xanthobacteraceae | 0.0002 | 0.0001 | 0.0002 | 0.0005 | 0.0004 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Desulfobacca | 0.0034 | 0.0017 | 0.0017 | 0.0013 | 0.0015 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Nevskiales;f__Steroidobacteraceae;g__Steroidobacter | 0.0001 | 0.0001 | 0.0002 | 0.0004 | 0.0002 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Hydrogenophilalia;o__Hydrogenophilales;f__unclassified_o__Hydrogenophilales;g__unclassified_o__Hydrogenophilales | 0.0002 | 0.0001 | 0.0010 | 0.0018 | 0.0050 |
| p__Acidobacteria;c__Blastocatellia;o__unclassified_c__Blastocatellia;f__unclassified_c__Blastocatellia;g__unclassified_c__Blastocatellia | 0.0013 | 0.0013 | 0.0011 | 0.0009 | 0.0013 |
| p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__unclassified_o__Spirochaetales;g__unclassified_o__Spirochaetales | 0.0028 | 0.0020 | 0.0025 | 0.0023 | 0.0021 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thioploca | 0.0001 | 0.0001 | 0.0000 | 0.0001 | 0.0001 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax | 0.0002 | 0.0002 | 0.0003 | 0.0005 | 0.0004 |
| p__Elusimicrobia;c__unclassified_p__Elusimicrobia;o__unclassified_p__Elusimicrobia;f__unclassified_p__Elusimicrobia;g__unclassified_p__Elusimicrobia | 0.0016 | 0.0039 | 0.0019 | 0.0009 | 0.0013 |
| p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus_f__Nocardiaceae | 0.0019 | 0.0017 | 0.0013 | 0.0026 | 0.0022 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__Candidatus_Methylomirabilis | 0.0003 | 0.0003 | 0.0003 | 0.0002 | 0.0002 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__unclassified_o__Rhodocyclales;g__unclassified_o__Rhodocyclales | 0.0002 | 0.0001 | 0.0006 | 0.0007 | 0.0005 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas | 0.0002 | 0.0002 | 0.0002 | 0.0004 | 0.0003 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Brooklawnia | 0.0007 | 0.0000 | 0.0014 | 0.0105 | 0.0058 |
| p__Cyanobacteria;c__unclassified_p__Cyanobacteria;o__Oscillatoriales;f__Microcoleaceae;g__unclassified_f__Microcoleaceae | 0.0027 | 0.0001 | 0.0121 | 0.0015 | 0.0019 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__unclassified_o__Bryobacterales;g__unclassified_o__Bryobacterales | 0.0010 | 0.0010 | 0.0008 | 0.0008 | 0.0008 |
| p__Chrysiogenetes_d__Bacteria;c__Chrysiogenetes_p__Chrysiogenetes;o__Chrysiogenales;f__unclassified_o__Chrysiogenales;g__unclassified_o__Chrysiogenales | 0.0017 | 0.0009 | 0.0008 | 0.0014 | 0.0048 |

| | | | | | |
|---|---|---|---|---|---|
| p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__unclassified_o__Bacteroidales;g__unclassified_o__Bacteroidales | 0.0010 | 0.0004 | 0.0014 | 0.0061 | 0.0026 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium | 0.0010 | 0.0006 | 0.0006 | 0.0008 | 0.0006 |
| p__Actinobacteria;c__Rubrobacteria;o__Gaiellales;f__Gaiellaceae;g__Gaiella | 0.0002 | 0.0001 | 0.0002 | 0.0007 | 0.0003 |
| p__Lentisphaerae;c__unclassified_p__Lentisphaerae;o__unclassified_p__Lentisphaerae;f__unclassified_p__Lentisphaerae;g__unclassified_p__Lentisphaerae | 0.0022 | 0.0020 | 0.0017 | 0.0013 | 0.0014 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Methylibium | 0.0001 | 0.0001 | 0.0002 | 0.0004 | 0.0002 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Curvibacter | 0.0001 | 0.0000 | 0.0002 | 0.0005 | 0.0016 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas | 0.0011 | 0.0019 | 0.0019 | 0.0008 | 0.0012 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides | 0.0006 | 0.0003 | 0.0003 | 0.0008 | 0.0006 |
| p__Candidatus_Latescibacteria;c__unclassified_p__Candidatus_Latescibacteria;o__unclassified_p__Candidatus_Latescibacteria;f__unclassified_p__Candidatus_Latescibacteria;g__unclassified_p__Candidatus_Latescibacteria | 0.0018 | 0.0017 | 0.0014 | 0.0011 | 0.0014 |
| p__Chloroflexi;c__Thermoflexia;o__unclassified_c__Thermoflexia;f__unclassified_c__Thermoflexia;g__unclassified_c__Thermoflexia | 0.0044 | 0.0053 | 0.0013 | 0.0012 | 0.0019 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Beggiatoa | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0001 |
| p__Candidatus_Woesebacteria;c__unclassified_p__Candidatus_Woesebacteria;o__unclassified_p__Candidatus_Woesebacteria;f__unclassified_p__Candidatus_Woesebacteria;g__unclassified_p__Candidatus_Woesebacteria | 0.0027 | 0.0009 | 0.0069 | 0.0005 | 0.0006 |
| p__Candidatus_Bipolaricaulota;c__unclassified_p__Candidatus_Bipolaricaulota;o__unclassified_p__Candidatus_Bipolaricaulota;f__unclassified_p__Candidatus_Bipolaricaulota;g__unclassified_p__Candidatus_Bipolaricaulota | 0.0037 | 0.0008 | 0.0029 | 0.0002 | 0.0005 |
| other | 0.2634 | 0.2982 | 0.3034 | 0.2990 | 0.2685 |

**Table S2.** Relative abundance of bacterial communities at various points along natural river channel B.

| #Taxonomy | B1 | B2 | B3 | B4 | B5 |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__unclassified_c__Deltaproteobacteria;f__unclassified_c__Deltaproteobacteria;g__unclassified_c__Deltaproteobacteria | 0.0873 | 0.0859 | 0.0693 | 0.0708 | 0.0549 |
| p__Acidobacteria;c__unclassified_p__Acidobacteria;o__unclassified_p__Acidobacteria;f__unclassified_p__Acidobacteria;g__unclassified_p__Acidobacteria | 0.1003 | 0.0989 | 0.1352 | 0.1409 | 0.1163 |
| p__Proteobacteria;c__Betaproteobacteria;o__unclassified_c__Betaproteobacteria;f__unclassified_c__Betaproteobacteria;g__unclassified_c__Betaproteobacteria | 0.0585 | 0.1132 | 0.1284 | 0.1340 | 0.0969 |
| p__Chloroflexi;c__unclassified_p__Chloroflexi;o__unclassified_p__Chloroflexi;f__unclassified_p__Chloroflexi;g__unclassified_p__Chloroflexi | 0.1031 | 0.0727 | 0.0481 | 0.0440 | 0.0367 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas | 0.0507 | 0.0282 | 0.0223 | 0.0147 | 0.0130 |
| p__Candidatus_Aminicenantes;c__unclassified_p__Candidatus_Aminicenantes;o__unclassified_p__Candidatus_Aminicenantes;f__unclassified_p__Candidatus_Aminicenantes;g__unclassified_p__Candidatus_Aminicenantes | 0.0497 | 0.0190 | 0.0030 | 0.0026 | 0.0022 |
| p__Proteobacteria;c__Gammaproteobacteria;o__unclassified_c__Gammaproteobacteria;f__unclassified_c__Gammaproteobacteria;g__unclassified_c__Gammaproteobacteria | 0.0105 | 0.0234 | 0.0394 | 0.0356 | 0.0383 |
| p__unclassified_d__Bacteria;c__unclassified_d__Bacteria;o__unclassified_d__Bacteria;f__unclassified_d__Bacteria;g__unclassified_d__Bacteria | 0.0288 | 0.0192 | 0.0112 | 0.0109 | 0.0110 |
| p__Planctomycetes;c__unclassified_p__Planctomycetes;o__unclassified_p__Planctomycetes;f__unclassified_p__Planctomycetes;g__unclassified_p__Planctomycetes | 0.0121 | 0.0105 | 0.0063 | 0.0066 | 0.0063 |
| p__Gemmatimonadetes_d__Bacteria;c__unclassified_p__Gemmatimonadetes_d__Bacteria;o__unclassified_p__Gemmatimonadetes_d__Bacteria;f__unclassified_p__Gemmatimonadetes_d__Bacteria;g__unclassified_p__Gemmatimonadetes_d__Bacteria | 0.0125 | 0.0156 | 0.0146 | 0.0150 | 0.0105 |
| p__Spirochaetes;c__unclassified_p__Spirochaetes;o__unclassified_p__Spirochaetes;f__unclassified_p__Spir | 0.0168 | 0.0117 | 0.0036 | 0.0035 | 0.0027 |

| | | | | | |
|---|---|---|---|---|---|
| ochaetes;g__unclassified_p__Spirochaetes | | | | | |
| p__Actinobacteria;c__Actinobacteria;o__unclassified_c__Actinobacteria;f__unclassified_c__Actinobacteria;g__unclassified_c__Actinobacteria | 0.0177 | 0.0152 | 0.0196 | 0.0192 | 0.0202 |
| p__Chloroflexi;c__Anaerolineae;o__unclassified_c__Anaerolineae;f__unclassified_c__Anaerolineae;g__unclassified_c__Anaerolineae | 0.0199 | 0.0126 | 0.0051 | 0.0055 | 0.0051 |
| p__Candidatus_Rokubacteria;c__unclassified_p__Candidatus_Rokubacteria;o__unclassified_p__Candidatus_Rokubacteria;f__unclassified_p__Candidatus_Rokubacteria;g__unclassified_p__Candidatus_Rokubacteria | 0.0075 | 0.0181 | 0.0127 | 0.0111 | 0.0083 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bradyrhizobium | 0.0022 | 0.0048 | 0.0232 | 0.0167 | 0.0663 |
| p__Proteobacteria;c__Alphaproteobacteria;o__unclassified_c__Alphaproteobacteria;f__unclassified_c__Alphaproteobacteria;g__unclassified_c__Alphaproteobacteria | 0.0045 | 0.0100 | 0.0170 | 0.0171 | 0.0289 |
| p__Actinobacteria;c__unclassified_p__Actinobacteria;o__unclassified_p__Actinobacteria;f__unclassified_p__Actinobacteria;g__unclassified_p__Actinobacteria | 0.0191 | 0.0101 | 0.0058 | 0.0054 | 0.0045 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Anaeromyxobacteraceae;g__Anaeromyxobacter | 0.0032 | 0.0064 | 0.0215 | 0.0281 | 0.0329 |
| p__Nitrospirae;c__unclassified_p__Nitrospirae;o__unclassified_p__Nitrospirae;f__unclassified_p__Nitrospirae;g__unclassified_p__Nitrospirae | 0.0137 | 0.0133 | 0.0105 | 0.0105 | 0.0076 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira | 0.0011 | 0.0092 | 0.0150 | 0.0158 | 0.0102 |
| p__Proteobacteria;c__unclassified_p__Proteobacteria;o__unclassified_p__Proteobacteria;f__unclassified_p__Proteobacteria;g__unclassified_p__Proteobacteria | 0.0046 | 0.0069 | 0.0116 | 0.0099 | 0.0218 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__unclassified_f__Moraxellaceae | 0.0007 | 0.0010 | 0.0001 | 0.0000 | 0.0001 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unclassified_o__Rhizobiales;g__unclassified_o__Rhizobiales | 0.0049 | 0.0061 | 0.0106 | 0.0110 | 0.0093 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Azonexaceae;g__Dechloromonas | 0.0004 | 0.0008 | 0.0016 | 0.0017 | 0.0010 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__unclassified_o__Myxococcales;g__unclassified_o__Myxococcales | 0.0034 | 0.0078 | 0.0076 | 0.0087 | 0.0103 |
| p__Candidatus_Abyssubacteria;c__unclassified_p__Candidatus_Abyssubacteria;o__unclassified_p__Candidatus_Abyssubacteria;f__unclassified_p__Candidatus_Abyssubacteria;g__unclassified_p__Candidatus_Abyssubacteria | 0.0003 | 0.0003 | 0.0001 | 0.0001 | 0.0001 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobacteraceae;g__unclassified_f__Desulfobacteraceae | 0.0060 | 0.0042 | 0.0032 | 0.0030 | 0.0033 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__unclassified_f__Syntrophaceae | 0.0050 | 0.0035 | 0.0009 | 0.0008 | 0.0007 |
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__unclassified_o__Anaerolineales;g__unclassified_o__Anaerolineales | 0.0093 | 0.0059 | 0.0023 | 0.0023 | 0.0019 |
| p__Verrucomicrobia;c__unclassified_p__Verrucomicrobia;o__unclassified_p__Verrucomicrobia;f__unclassified_p__Verrucomicrobia;g__unclassified_p__Verrucomicrobia | 0.0036 | 0.0039 | 0.0031 | 0.0033 | 0.0033 |
| p__candidate_division_Zixibacteria;c__unclassified_p__candidate_division_Zixibacteria;o__unclassified_p__candidate_division_Zixibacteria;f__unclassified_p__candidate_division_Zixibacteria;g__unclassified_p__candidate_division_Zixibacteria | 0.0041 | 0.0024 | 0.0006 | 0.0007 | 0.0007 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__unclassified_o__Burkholderiales | 0.0051 | 0.0042 | 0.0040 | 0.0039 | 0.0036 |
| p__Candidatus_Eisenbacteria;c__unclassified_p__Candidatus_Eisenbacteria;o__unclassified_p__Candidatus_Eisenbacteria;f__unclassified_p__Candidatus_Eisenbacteria;g__unclassified_p__Candidatus_Eisenbacteria | 0.0045 | 0.0040 | 0.0046 | 0.0047 | 0.0035 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__unclassified_o__Gemmatimonadales;g__unclassified_o__Gemmatimonadales | 0.0029 | 0.0032 | 0.0037 | 0.0042 | 0.0032 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Desulfuromonadaceae;g__Desulfuromonas | 0.0012 | 0.0012 | 0.0009 | 0.0010 | 0.0006 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__unclassified_o__Syntrophobacterales; | 0.0025 | 0.0018 | 0.0015 | 0.0014 | 0.0014 |

| | | | | | |
|---|---|---|---|---|---|
| g__unclassified_o__Syntrophobacterales | | | | | |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__unclassified_f__Rhodospirillaceae | 0.0016 | 0.0055 | 0.0098 | 0.0069 | 0.0070 |
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__unclassified_f__Anaerolineaceae | 0.0056 | 0.0034 | 0.0010 | 0.0011 | 0.0011 |
| p__Planctomycetes;c__Phycisphaerae;o__unclassified_c__Phycisphaerae;f__unclassified_c__Phycisphaerae;g__unclassified_c__Phycisphaerae | 0.0027 | 0.0023 | 0.0013 | 0.0013 | 0.0019 |
| p__Chloroflexi;c__Dehalococcoidia;o__unclassified_c__Dehalococcoidia;f__unclassified_c__Dehalococcoidia;g__unclassified_c__Dehalococcoidia | 0.0071 | 0.0032 | 0.0014 | 0.0014 | 0.0012 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__unclassified_f__Nitrospiraceae | 0.0030 | 0.0055 | 0.0071 | 0.0076 | 0.0050 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__unclassified_o__Nitrosomonadales;g__unclassified_o__Nitrosomonadales | 0.0067 | 0.0187 | 0.0026 | 0.0033 | 0.0021 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__unclassified_p__candidate_division_NC10 | 0.0037 | 0.0034 | 0.0021 | 0.0023 | 0.0015 |
| p__Acidobacteria;c__Thermoanaerobaculia;o__unclassified_c__Thermoanaerobaculia;f__unclassified_c__Thermoanaerobaculia;g__unclassified_c__Thermoanaerobaculia | 0.0018 | 0.0036 | 0.0109 | 0.0083 | 0.0076 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__Thiobacillaceae;g__Thiobacillus | 0.0079 | 0.0023 | 0.0021 | 0.0021 | 0.0018 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Aromatoleum | 0.0024 | 0.0028 | 0.0043 | 0.0032 | 0.0032 |
| p__Bacteroidetes;c__unclassified_p__Bacteroidetes;o__unclassified_p__Bacteroidetes;f__unclassified_p__Bacteroidetes;g__unclassified_p__Bacteroidetes | 0.0041 | 0.0026 | 0.0017 | 0.0021 | 0.0019 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__unclassified_f__Burkholderiaceae | 0.0027 | 0.0059 | 0.0049 | 0.0048 | 0.0036 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__unclassified_o__Xanthomonadales;g__unclassified_o__Xanthomonadales | 0.0017 | 0.0023 | 0.0040 | 0.0040 | 0.0036 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__unclassified_o__Desulfobacterales;g__unclassified_o__Desulfobacterales | 0.0044 | 0.0027 | 0.0012 | 0.0011 | 0.0010 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Syntrophus_f__Syntrophaceae | 0.0015 | 0.0012 | 0.0005 | 0.0006 | 0.0005 |
| p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__unclassified_o__Phycisphaerales;g__unclassified_o__Phycisphaerales | 0.0011 | 0.0012 | 0.0004 | 0.0005 | 0.0005 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__unclassified_f__Rhodocyclaceae | 0.0010 | 0.0016 | 0.0018 | 0.0016 | 0.0013 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas | 0.0042 | 0.0019 | 0.0015 | 0.0010 | 0.0009 |
| p__Acidobacteria;c__Vicinamibacteria;o__unclassified_c__Vicinamibacteria;f__Vicinamibacteraceae;g__Luteitalea | 0.0035 | 0.0031 | 0.0038 | 0.0040 | 0.0033 |
| p__Planctomycetes;c__Planctomycetia;o__Planctomycetales;f__Planctomycetaceae;g__unclassified_f__Planctomycetaceae | 0.0020 | 0.0016 | 0.0010 | 0.0010 | 0.0010 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae;g__Geobacter | 0.0024 | 0.0015 | 0.0022 | 0.0041 | 0.0016 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Acidiferrobacterales;f__Acidiferrobacteraceae;g__Sulfuricaulis | 0.0032 | 0.0065 | 0.0072 | 0.0070 | 0.0061 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys | 0.0015 | 0.0026 | 0.0040 | 0.0039 | 0.0037 |
| p__Acidobacteria;c__Holophagae;o__unclassified_c__Holophagae;f__unclassified_c__Holophagae;g__unclassified_c__Holophagae | 0.0033 | 0.0022 | 0.0017 | 0.0015 | 0.0013 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__Solibacteraceae;g__Candidatus_Solibacter | 0.0028 | 0.0022 | 0.0013 | 0.0012 | 0.0011 |
| p__Proteobacteria;c__Zetaproteobacteria;o__unclassified_c__Zetaproteobacteria;f__unclassified_c__Zetaproteobacteria;g__unclassified_c__Zetaproteobacteria | 0.0028 | 0.0025 | 0.0014 | 0.0016 | 0.0011 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium | 0.0002 | 0.0004 | 0.0025 | 0.0009 | 0.0009 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Rhodoplanes | 0.0009 | 0.0019 | 0.0062 | 0.0060 | 0.0060 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__unclassified_o__Rhodospirillales;g__unclassified_o__Rhodospirillales | 0.0009 | 0.0128 | 0.0020 | 0.0020 | 0.0019 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Piscinibacter | 0.0009 | 0.0015 | 0.0035 | 0.0033 | 0.0029 |
| p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobia_subdivision_3;g__unclassified_f__Verrucomicrobia_subdivision_3 | 0.0014 | 0.0013 | 0.0010 | 0.0012 | 0.0011 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Rubrivivax | 0.0007 | 0.0012 | 0.0014 | 0.0013 | 0.0012 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Ralstonia | 0.0016 | 0.0007 | 0.0007 | 0.0007 | 0.0005 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__unclassified_f__Comamonadaceae | 0.0013 | 0.0014 | 0.0015 | 0.0013 | 0.0012 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Ramlibacter | 0.0015 | 0.0013 | 0.0012 | 0.0011 | 0.0009 |
| p__Proteobacteria;c__Candidatus_Muproteobacteria;o__unclassified_c__Candidatus_Muproteobacteria;f__unclassified_c__Candidatus_Muproteobacteria;g__unclassified_c__Candidatus_Muproteobacteria | 0.0017 | 0.0097 | 0.0040 | 0.0044 | 0.0034 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Ideonella | 0.0008 | 0.0014 | 0.0015 | 0.0014 | 0.0011 |
| p__Firmicutes;c__unclassified_p__Firmicutes;o__unclassified_p__Firmicutes;f__unclassified_p__Firmicutes;g__unclassified_p__Firmicutes | 0.0018 | 0.0013 | 0.0009 | 0.0008 | 0.0008 |
| p__Candidatus_Omnitrophica;c__unclassified_p__Candidatus_Omnitrophica;o__unclassified_p__Candidatus_Omnitrophica;f__unclassified_p__Candidatus_Omnitrophica;g__unclassified_p__Candidatus_Omnitrophica | 0.0008 | 0.0007 | 0.0004 | 0.0004 | 0.0003 |
| p__Armatimonadetes;c__unclassified_p__Armatimonadetes;o__unclassified_p__Armatimonadetes;f__unclassified_p__Armatimonadetes;g__unclassified_p__Armatimonadetes | 0.0018 | 0.0013 | 0.0009 | 0.0010 | 0.0010 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__unclassified_f__Xanth | 0.0008 | 0.0018 | 0.0052 | 0.0060 | 0.0039 |

| | | | | | |
|---|---|---|---|---|---|
| obacteraceae | | | | | |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Desulfobacca | 0.0035 | 0.0019 | 0.0014 | 0.0013 | 0.0011 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Nevskiales;f__Steroidobacteraceae;g__Steroidobacter | 0.0003 | 0.0006 | 0.0053 | 0.0015 | 0.0087 |
| p__Proteobacteria;c__Hydrogenophilalia;o__Hydrogenophilales;f__unclassified_o__Hydrogenophilales;g__unclassified_o__Hydrogenophilales | 0.0034 | 0.0015 | 0.0014 | 0.0013 | 0.0011 |
| p__Acidobacteria;c__Blastocatellia;o__unclassified_c__Blastocatellia;f__unclassified_c__Blastocatellia;g__unclassified_c__Blastocatellia | 0.0018 | 0.0017 | 0.0021 | 0.0021 | 0.0018 |
| p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__unclassified_o__Spirochaetales;g__unclassified_o__Spirochaetales | 0.0014 | 0.0010 | 0.0002 | 0.0003 | 0.0002 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thioploca | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax | 0.0011 | 0.0014 | 0.0016 | 0.0015 | 0.0016 |
| p__Elusimicrobia;c__unclassified_p__Elusimicrobia;o__unclassified_p__Elusimicrobia;f__unclassified_p__Elusimicrobia;g__unclassified_p__Elusimicrobia | 0.0008 | 0.0007 | 0.0005 | 0.0006 | 0.0006 |
| p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus_f__Nocardiaceae | 0.0026 | 0.0010 | 0.0015 | 0.0013 | 0.0009 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__Candidatus_Methylomirabilis | 0.0003 | 0.0003 | 0.0004 | 0.0004 | 0.0003 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__unclassified_o__Rhodocyclales;g__unclassified_o__Rhodocyclales | 0.0007 | 0.0010 | 0.0010 | 0.0010 | 0.0007 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas | 0.0003 | 0.0006 | 0.0015 | 0.0009 | 0.0018 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Brooklawnia | 0.0000 | 0.0001 | 0.0001 | 0.0002 | 0.0002 |
| p__Cyanobacteria;c__unclassified_p__Cyanobacteria;o__Oscillatoriales;f__Microcoleaceae;g__unclassified_f__Microcoleaceae | 0.0000 | 0.0000 | 0.0006 | 0.0000 | 0.0001 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__unclassified_o__Bryobacterales;g__unclassified_ | 0.0019 | 0.0014 | 0.0011 | 0.0010 | 0.0009 |

| | | | | | |
|---|---|---|---|---|---|
| o__Bryobacterales | | | | | |
| p__Chrysiogenetes_d__Bacteria;c__Chrysiogenetes_p__Chrysiogenetes;o__Chrysiogenales;f__unclassified_o__Chrysiogenales;g__unclassified_o__Chrysiogenales | 0.0022 | 0.0013 | 0.0001 | 0.0001 | 0.0001 |
| p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__unclassified_o__Bacteroidales;g__unclassified_o__Bacteroidales | 0.0017 | 0.0007 | 0.0002 | 0.0005 | 0.0003 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium | 0.0006 | 0.0010 | 0.0021 | 0.0022 | 0.0019 |
| p__Actinobacteria;c__Rubrobacteria;o__Gaiellales;f__Gaiellaceae;g__Gaiella | 0.0008 | 0.0014 | 0.0033 | 0.0038 | 0.0025 |
| p__Lentisphaerae;c__unclassified_p__Lentisphaerae;o__unclassified_p__Lentisphaerae;f__unclassified_p__Lentisphaerae;g__unclassified_p__Lentisphaerae | 0.0012 | 0.0007 | 0.0004 | 0.0004 | 0.0005 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Methylibium | 0.0006 | 0.0010 | 0.0013 | 0.0011 | 0.0010 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Curvibacter | 0.0059 | 0.0019 | 0.0007 | 0.0005 | 0.0004 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas | 0.0010 | 0.0011 | 0.0011 | 0.0011 | 0.0009 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides | 0.0007 | 0.0006 | 0.0010 | 0.0009 | 0.0008 |
| p__Candidatus_Latescibacteria;c__unclassified_p__Candidatus_Latescibacteria;o__unclassified_p__Candidatus_Latescibacteria;f__unclassified_p__Candidatus_Latescibacteria;g__unclassified_p__Candidatus_Latescibacteria | 0.0019 | 0.0011 | 0.0008 | 0.0008 | 0.0007 |
| p__Chloroflexi;c__Thermoflexia;o__unclassified_c__Thermoflexia;f__unclassified_c__Thermoflexia;g__unclassified_c__Thermoflexia | 0.0006 | 0.0005 | 0.0001 | 0.0001 | 0.0001 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Beggiatoa | 0.0000 | 0.0001 | 0.0001 | 0.0000 | 0.0001 |
| p__Candidatus_Woesebacteria;c__unclassified_p__Candidatus_Woesebacteria;o__unclassified_p__Candidatus_Woesebacteria;f__unclassified_p__Candidatus_Woesebacteria;g__unclassified_p__Candidatus_Woesebacteria | 0.0007 | 0.0020 | 0.0001 | 0.0000 | 0.0000 |
| p__Candidatus_Bipolaricaulota;c__unclassified_p__Candidatus_Bipolaricaulota;o__unclassified_p__Candi | 0.0031 | 0.0007 | 0.0001 | 0.0001 | 0.0001 |

| | | | | | |
|---|---|---|---|---|---|
| datus_Bipolaricaulota;f__unclassified_p__Candidatus_Bipolaricaulota;g__unclassified_p__Candidatus_Bipolaricaulota | | | | | |
| other | 0.1815 | 0.1862 | 0.1877 | 0.2006 | 0.2409 |

**Table S3.** Relative abundance of bacterial communities at various points along natural river channel C.

| #Taxonomy | C1 | C2 | C3 | C4 | C5 |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__unclassified_c__Deltaproteobacteria;f__unclassified_c__Deltaproteobacteria;g__unclassified_c__Deltaproteobacteria | 0.1029 | 0.1144 | 0.0933 | 0.0973 | 0.0985 |
| p__Acidobacteria;c__unclassified_p__Acidobacteria;o__unclassified_p__Acidobacteria;f__unclassified_p__Acidobacteria;g__unclassified_p__Acidobacteria | 0.0619 | 0.0666 | 0.0682 | 0.0672 | 0.0663 |
| p__Proteobacteria;c__Betaproteobacteria;o__unclassified_c__Betaproteobacteria;f__unclassified_c__Betaproteobacteria;g__unclassified_c__Betaproteobacteria | 0.1034 | 0.1086 | 0.1014 | 0.0973 | 0.1010 |
| p__Chloroflexi;c__unclassified_p__Chloroflexi;o__unclassified_p__Chloroflexi;f__unclassified_p__Chloroflexi;g__unclassified_p__Chloroflexi | 0.0588 | 0.0600 | 0.0565 | 0.0624 | 0.0698 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas | 0.0237 | 0.0215 | 0.0211 | 0.0223 | 0.0222 |
| p__Candidatus_Aminicenantes;c__unclassified_p__Candidatus_Aminicenantes;o__unclassified_p__Candidatus_Aminicenantes;f__unclassified_p__Candidatus_Aminicenantes;g__unclassified_p__Candidatus_Aminicenantes | 0.0098 | 0.0099 | 0.0126 | 0.0137 | 0.0109 |
| p__Proteobacteria;c__Gammaproteobacteria;o__unclassified_c__Gammaproteobacteria;f__unclassified_c__Gammaproteobacteria;g__unclassified_c__Gammaproteobacteria | 0.0256 | 0.0266 | 0.0278 | 0.0252 | 0.0312 |
| p__unclassified_d__Bacteria;c__unclassified_d__Bacteria;o__unclassified_d__Bacteria;f__unclassified_d__Bacteria;g__unclassified_d__Bacteria | 0.0154 | 0.0152 | 0.0158 | 0.0159 | 0.0144 |
| p__Planctomycetes;c__unclassified_p__Planctomycetes;o__unclassified_p__Planctomycetes;f__unclassified_p__Planctomycetes;g__unclassified_p__Planctomycetes | 0.0123 | 0.0129 | 0.0125 | 0.0118 | 0.0096 |

| | | | | | |
|---|---|---|---|---|---|
| p__Gemmatimonadetes_d__Bacteria;c__unclassified_p__Gemmatimonadetes_d__Bacteria;o__unclassified_p__Gemmatimonadetes_d__Bacteria;f__unclassified_p__Gemmatimonadetes_d__Bacteria;g__unclassified_p__Gemmatimonadetes_d__Bacteria | 0.0127 | 0.0129 | 0.0128 | 0.0121 | 0.0117 |
| p__Spirochaetes;c__unclassified_p__Spirochaetes;o__unclassified_p__Spirochaetes;f__unclassified_p__Spirochaetes;g__unclassified_p__Spirochaetes | 0.0132 | 0.0142 | 0.0174 | 0.0160 | 0.0115 |
| p__Actinobacteria;c__Actinobacteria;o__unclassified_c__Actinobacteria;f__unclassified_c__Actinobacteria;g__unclassified_c__Actinobacteria | 0.0168 | 0.0203 | 0.0165 | 0.0180 | 0.0175 |
| p__Chloroflexi;c__Anaerolineae;o__unclassified_c__Anaerolineae;f__unclassified_c__Anaerolineae;g__unclassified_c__Anaerolineae | 0.0087 | 0.0076 | 0.0085 | 0.0098 | 0.0090 |
| p__Candidatus_Rokubacteria;c__unclassified_p__Candidatus_Rokubacteria;o__unclassified_p__Candidatus_Rokubacteria;f__unclassified_p__Candidatus_Rokubacteria;g__unclassified_p__Candidatus_Rokubacteria | 0.0224 | 0.0261 | 0.0232 | 0.0238 | 0.0208 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae;g__Bradyrhizobium | 0.0088 | 0.0080 | 0.0090 | 0.0086 | 0.0081 |
| p__Proteobacteria;c__Alphaproteobacteria;o__unclassified_c__Alphaproteobacteria;f__unclassified_c__Alphaproteobacteria;g__unclassified_c__Alphaproteobacteria | 0.0089 | 0.0087 | 0.0082 | 0.0087 | 0.0082 |
| p__Actinobacteria;c__unclassified_p__Actinobacteria;o__unclassified_p__Actinobacteria;f__unclassified_p__Actinobacteria;g__unclassified_p__Actinobacteria | 0.0076 | 0.0089 | 0.0092 | 0.0101 | 0.0102 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Anaeromyxobacteraceae;g__Anaeromyxobacter | 0.0036 | 0.0033 | 0.0036 | 0.0035 | 0.0032 |
| p__Nitrospirae;c__unclassified_p__Nitrospirae;o__unclassified_p__Nitrospirae;f__unclassified_p__Nitrospirae;g__unclassified_p__Nitrospirae | 0.0072 | 0.0068 | 0.0071 | 0.0076 | 0.0071 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira | 0.0114 | 0.0088 | 0.0095 | 0.0094 | 0.0103 |
| p__Proteobacteria;c__unclassified_p__Proteobacteria;o__unclassified_p__Proteobacteria;f__unclassified_p__Proteobacteria;g__unclassified_p__Proteobacteria | 0.0058 | 0.0059 | 0.0071 | 0.0063 | 0.0074 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__unclassified_f__Moraxellaceae | 0.0227 | 0.0235 | 0.0187 | 0.0166 | 0.0100 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__unclassified_o__Rhizobiales;g__unclassified_o__Rhizobiales | 0.0064 | 0.0072 | 0.0062 | 0.0073 | 0.0068 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Azonexaceae;g__Dechloromonas | 0.0077 | 0.0088 | 0.0092 | 0.0086 | 0.0058 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__unclassified_o__Myxococcales;g__unclassified_o__Myxococcales | 0.0058 | 0.0064 | 0.0068 | 0.0061 | 0.0061 |
| p__Candidatus_Abyssubacteria;c__unclassified_p__Candidatus_Abyssubacteria;o__unclassified_p__Candidatus_Abyssubacteria;f__unclassified_p__Candidatus_Abyssubacteria;g__unclassified_p__Candidatus_Abyssubacteria | 0.0002 | 0.0002 | 0.0002 | 0.0002 | 0.0002 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobacteraceae;g__unclassified_f__Desulfobacteraceae | 0.0038 | 0.0034 | 0.0054 | 0.0063 | 0.0055 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__unclassified_f__Syntrophaceae | 0.0090 | 0.0093 | 0.0102 | 0.0105 | 0.0074 |
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__unclassified_o__Anaerolineales;g__unclassified_o__Anaerolineales | 0.0033 | 0.0030 | 0.0033 | 0.0037 | 0.0036 |
| p__Verrucomicrobia;c__unclassified_p__Verrucomicrobia;o__unclassified_p__Verrucomicrobia;f__unclassified_p__Verrucomicrobia;g__unclassified_p__Verrucomicrobia | 0.0062 | 0.0057 | 0.0068 | 0.0068 | 0.0053 |
| p__candidate_division_Zixibacteria;c__unclassified_p__candidate_division_Zixibacteria;o__unclassified_p__candidate_division_Zixibacteria;f__unclassified_p__candidate_division_Zixibacteria;g__unclassified_p__candidate_division_Zixibacteria | 0.0008 | 0.0007 | 0.0009 | 0.0009 | 0.0008 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__unclassified_o__Burkholderiales | 0.0074 | 0.0076 | 0.0076 | 0.0067 | 0.0064 |
| p__Candidatus_Eisenbacteria;c__unclassified_p__Candidatus_Eisenbacteria;o__unclassified_p__Candidatus_Eisenbacteria;f__unclassified_p__Candidatus_Eisenbacteria;g__unclassified_p__Candidatus_Eisenbacteria | 0.0059 | 0.0061 | 0.0064 | 0.0061 | 0.0052 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__unclassified_o__Gemmatimonadales;g__unclassified_o__Gemmatimonadales | 0.0045 | 0.0048 | 0.0046 | 0.0043 | 0.0041 |

| | | | | | |
|---|---|---|---|---|---|
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Desulfuromonadaceae;g__Desulfuromonas | 0.0085 | 0.0078 | 0.0112 | 0.0113 | 0.0076 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__unclassified_o__Syntrophobacterales;g__unclassified_o__Syntrophobacterales | 0.0074 | 0.0077 | 0.0087 | 0.0095 | 0.0073 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__unclassified_f__Rhodospirillaceae | 0.0049 | 0.0043 | 0.0043 | 0.0041 | 0.0038 |
| p__Chloroflexi;c__Anaerolineae;o__Anaerolineales;f__Anaerolineaceae;g__unclassified_f__Anaerolineaceae | 0.0032 | 0.0029 | 0.0037 | 0.0039 | 0.0036 |
| p__Planctomycetes;c__Phycisphaerae;o__unclassified_c__Phycisphaerae;f__unclassified_c__Phycisphaerae;g__unclassified_c__Phycisphaerae | 0.0023 | 0.0022 | 0.0023 | 0.0022 | 0.0017 |
| p__Chloroflexi;c__Dehalococcoidia;o__unclassified_c__Dehalococcoidia;f__unclassified_c__Dehalococcoidia;g__unclassified_c__Dehalococcoidia | 0.0015 | 0.0015 | 0.0015 | 0.0016 | 0.0018 |
| p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__unclassified_f__Nitrospiraceae | 0.0027 | 0.0026 | 0.0027 | 0.0030 | 0.0028 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__unclassified_o__Nitrosomonadales;g__unclassified_o__Nitrosomonadales | 0.0027 | 0.0024 | 0.0021 | 0.0019 | 0.0029 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__unclassified_p__candidate_division_NC10 | 0.0043 | 0.0043 | 0.0049 | 0.0046 | 0.0050 |
| p__Acidobacteria;c__Thermoanaerobaculia;o__unclassified_c__Thermoanaerobaculia;f__unclassified_c__Thermoanaerobaculia;g__unclassified_c__Thermoanaerobaculia | 0.0020 | 0.0026 | 0.0020 | 0.0020 | 0.0024 |
| p__Proteobacteria;c__Betaproteobacteria;o__Nitrosomonadales;f__Thiobacillaceae;g__Thiobacillus | 0.0016 | 0.0017 | 0.0019 | 0.0018 | 0.0019 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__Aromatoleum | 0.0048 | 0.0054 | 0.0049 | 0.0048 | 0.0054 |
| p__Bacteroidetes;c__unclassified_p__Bacteroidetes;o__unclassified_p__Bacteroidetes;f__unclassified_p__Bacteroidetes;g__unclassified_p__Bacteroidetes | 0.0026 | 0.0017 | 0.0024 | 0.0027 | 0.0019 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__unclassified_f__Burk | 0.0034 | 0.0035 | 0.0038 | 0.0034 | 0.0031 |

| | | | | | |
|---|---|---|---|---|---|
| holderiaceae | | | | | |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__unclassified_o__Xanthomonadales;g__unclassified_o__Xanthomonadales | 0.0044 | 0.0040 | 0.0043 | 0.0042 | 0.0044 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__unclassified_o__Desulfobacterales;g__unclassified_o__Desulfobacterales | 0.0016 | 0.0015 | 0.0022 | 0.0028 | 0.0022 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Syntrophus_f__Syntrophaceae | 0.0061 | 0.0063 | 0.0057 | 0.0062 | 0.0050 |
| p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__unclassified_o__Phycisphaerales;g__unclassified_o__Phycisphaerales | 0.0013 | 0.0013 | 0.0013 | 0.0013 | 0.0011 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae;g__unclassified_f__Rhodocyclaceae | 0.0048 | 0.0053 | 0.0051 | 0.0049 | 0.0042 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas | 0.0019 | 0.0020 | 0.0018 | 0.0018 | 0.0018 |
| p__Acidobacteria;c__Vicinamibacteria;o__unclassified_c__Vicinamibacteria;f__Vicinamibacteraceae;g__Luteitalea | 0.0024 | 0.0025 | 0.0023 | 0.0025 | 0.0024 |
| p__Planctomycetes;c__Planctomycetia;o__Planctomycetales;f__Planctomycetaceae;g__unclassified_f__Planctomycetaceae | 0.0017 | 0.0017 | 0.0017 | 0.0017 | 0.0014 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae;g__Geobacter | 0.0025 | 0.0023 | 0.0027 | 0.0028 | 0.0020 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Acidiferrobacterales;f__Acidiferrobacteraceae;g__Sulfuricaulis | 0.0004 | 0.0004 | 0.0004 | 0.0005 | 0.0004 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Pseudolabrys | 0.0027 | 0.0027 | 0.0023 | 0.0026 | 0.0026 |
| p__Acidobacteria;c__Holophagae;o__unclassified_c__Holophagae;f__unclassified_c__Holophagae;g__unclassified_c__Holophagae | 0.0019 | 0.0021 | 0.0025 | 0.0026 | 0.0027 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__Solibacteraceae;g__Candidatus_Solibacter | 0.0019 | 0.0017 | 0.0018 | 0.0017 | 0.0017 |
| p__Proteobacteria;c__Zetaproteobacteria;o__unclassified_c__Zetaproteobacteria;f__unclassified_c__Zetapr | 0.0023 | 0.0023 | 0.0029 | 0.0029 | 0.0024 |

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|---|---|---|---|---|---|
| oteobacteria;g__unclassified_c__Zetaproteobacteria | | | | | |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium | 0.0055 | 0.0053 | 0.0046 | 0.0044 | 0.0034 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Rhodoplanes | 0.0013 | 0.0013 | 0.0012 | 0.0013 | 0.0011 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__unclassified_o__Rhodospirillales;g__unclassified_o__Rhodospirillales | 0.0016 | 0.0016 | 0.0014 | 0.0015 | 0.0013 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Piscinibacter | 0.0032 | 0.0028 | 0.0032 | 0.0027 | 0.0026 |
| p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobia_subdivision_3;g__unclassified_f__Verrucomicrobia_subdivision_3 | 0.0024 | 0.0021 | 0.0029 | 0.0027 | 0.0022 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Rubrivivax | 0.0043 | 0.0044 | 0.0043 | 0.0036 | 0.0033 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Ralstonia | 0.0015 | 0.0018 | 0.0012 | 0.0015 | 0.0012 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__unclassified_f__Comamonadaceae | 0.0043 | 0.0039 | 0.0038 | 0.0033 | 0.0030 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Ramlibacter | 0.0047 | 0.0042 | 0.0037 | 0.0032 | 0.0030 |
| p__Proteobacteria;c__Candidatus_Muproteobacteria;o__unclassified_c__Candidatus_Muproteobacteria;f__unclassified_c__Candidatus_Muproteobacteria;g__unclassified_c__Candidatus_Muproteobacteria | 0.0004 | 0.0004 | 0.0004 | 0.0004 | 0.0005 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Ideonella | 0.0039 | 0.0038 | 0.0038 | 0.0033 | 0.0031 |
| p__Firmicutes;c__unclassified_p__Firmicutes;o__unclassified_p__Firmicutes;f__unclassified_p__Firmicutes;g__unclassified_p__Firmicutes | 0.0012 | 0.0012 | 0.0014 | 0.0012 | 0.0012 |
| p__Candidatus_Omnitrophica;c__unclassified_p__Candidatus_Omnitrophica;o__unclassified_p__Candidatus_Omnitrophica;f__unclassified_p__Candidatus_Omnitrophica;g__unclassified_p__Candidatus_Omnitrophica | 0.0011 | 0.0009 | 0.0010 | 0.0011 | 0.0007 |

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|---|---|---|---|---|---|
| p__Armatimonadetes;c__unclassified_p__Armatimonadetes;o__unclassified_p__Armatimonadetes;f__unclassified_p__Armatimonadetes;g__unclassified_p__Armatimonadetes | 0.0014 | 0.0013 | 0.0013 | 0.0013 | 0.0013 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__unclassified_f__Xanthobacteraceae | 0.0010 | 0.0010 | 0.0008 | 0.0010 | 0.0008 |
| p__Proteobacteria;c__Deltaproteobacteria;o__Syntrophobacterales;f__Syntrophaceae;g__Desulfobacca | 0.0005 | 0.0006 | 0.0009 | 0.0014 | 0.0012 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Nevskiales;f__Steroidobacteraceae;g__Steroidobacter | 0.0011 | 0.0010 | 0.0013 | 0.0009 | 0.0016 |
| p__Proteobacteria;c__Hydrogenophilalia;o__Hydrogenophilales;f__unclassified_o__Hydrogenophilales;g__unclassified_o__Hydrogenophilales | 0.0011 | 0.0011 | 0.0011 | 0.0011 | 0.0011 |
| p__Acidobacteria;c__Blastocatellia;o__unclassified_c__Blastocatellia;f__unclassified_c__Blastocatellia;g__unclassified_c__Blastocatellia | 0.0013 | 0.0012 | 0.0013 | 0.0013 | 0.0013 |
| p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__unclassified_o__Spirochaetales;g__unclassified_o__Spirochaetales | 0.0012 | 0.0012 | 0.0016 | 0.0015 | 0.0010 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thioploca | 0.0016 | 0.0013 | 0.0038 | 0.0035 | 0.0107 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Variovorax | 0.0026 | 0.0024 | 0.0025 | 0.0021 | 0.0020 |
| p__Elusimicrobia;c__unclassified_p__Elusimicrobia;o__unclassified_p__Elusimicrobia;f__unclassified_p__Elusimicrobia;g__unclassified_p__Elusimicrobia | 0.0017 | 0.0015 | 0.0015 | 0.0016 | 0.0010 |
| p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus_f__Nocardiaceae | 0.0006 | 0.0006 | 0.0005 | 0.0008 | 0.0007 |
| p__candidate_division_NC10;c__unclassified_p__candidate_division_NC10;o__unclassified_p__candidate_division_NC10;f__unclassified_p__candidate_division_NC10;g__Candidatus_Methylomirabilis | 0.0013 | 0.0009 | 0.0015 | 0.0011 | 0.0120 |
| p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__unclassified_o__Rhodocyclales;g__unclassified_o__Rhodocyclales | 0.0026 | 0.0028 | 0.0027 | 0.0026 | 0.0024 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas | 0.0039 | 0.0026 | 0.0022 | 0.0021 | 0.0022 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Brooklawnia | 0.0000 | 0.0001 | 0.0001 | 0.0001 | 0.0001 |

| | | | | | |
|---|---|---|---|---|---|
| p__Cyanobacteria;c__unclassified_p__Cyanobacteria;o__Oscillatoriales;f__Microcoleaceae;g__unclassified_f__Microcoleaceae | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0001 |
| p__Acidobacteria;c__Acidobacteriia;o__Bryobacterales;f__unclassified_o__Bryobacterales;g__unclassified_o__Bryobacterales | 0.0017 | 0.0015 | 0.0018 | 0.0017 | 0.0016 |
| p__Chrysiogenetes_d__Bacteria;c__Chrysiogenetes_p__Chrysiogenetes;o__Chrysiogenales;f__unclassified_o__Chrysiogenales;g__unclassified_o__Chrysiogenales | 0.0009 | 0.0007 | 0.0012 | 0.0013 | 0.0012 |
| p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__unclassified_o__Bacteroidales;g__unclassified_o__Bacteroidales | 0.0008 | 0.0004 | 0.0008 | 0.0009 | 0.0006 |
| p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium | 0.0014 | 0.0016 | 0.0012 | 0.0016 | 0.0014 |
| p__Actinobacteria;c__Rubrobacteria;o__Gaiellales;f__Gaiellaceae;g__Gaiella | 0.0009 | 0.0009 | 0.0007 | 0.0008 | 0.0010 |
| p__Lentisphaerae;c__unclassified_p__Lentisphaerae;o__unclassified_p__Lentisphaerae;f__unclassified_p__Lentisphaerae;g__unclassified_p__Lentisphaerae | 0.0011 | 0.0010 | 0.0012 | 0.0011 | 0.0009 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__unclassified_o__Burkholderiales;g__Methylibium | 0.0024 | 0.0024 | 0.0023 | 0.0022 | 0.0019 |
| p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;g__Curvibacter | 0.0010 | 0.0010 | 0.0010 | 0.0010 | 0.0009 |
| p__Gemmatimonadetes_d__Bacteria;c__Gemmatimonadetes_p__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__Gemmatimonas | 0.0010 | 0.0010 | 0.0009 | 0.0008 | 0.0008 |
| p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides | 0.0061 | 0.0011 | 0.0009 | 0.0010 | 0.0011 |
| p__Candidatus_Latescibacteria;c__unclassified_p__Candidatus_Latescibacteria;o__unclassified_p__Candidatus_Latescibacteria;f__unclassified_p__Candidatus_Latescibacteria;g__unclassified_p__Candidatus_Latescibacteria | 0.0006 | 0.0008 | 0.0008 | 0.0008 | 0.0007 |
| p__Chloroflexi;c__Thermoflexia;o__unclassified_c__Thermoflexia;f__unclassified_c__Thermoflexia;g__unclassified_c__Thermoflexia | 0.0001 | 0.0001 | 0.0001 | 0.0002 | 0.0001 |
| p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Beggiatoa | 0.0012 | 0.0009 | 0.0027 | 0.0026 | 0.0078 |
| p__Candidatus_Woesebacteria;c__unclassified_p__Candidatus_Woesebacteria;o__unclassified_p__Candid | 0.0003 | 0.0002 | 0.0002 | 0.0002 | 0.0001 |

| | | | | | |
|---|---|---|---|---|---|
| atus_Woesebacteria;f__unclassified_p__Candidatus_Woesebacteria;g__unclassified_p__Candidatus_Woesebacteria | | | | | |
| p__Candidatus_Bipolaricaulota;c__unclassified_p__Candidatus_Bipolaricaulota;o__unclassified_p__Candidatus_Bipolaricaulota;f__unclassified_p__Candidatus_Bipolaricaulota;g__unclassified_p__Candidatus_Bipolaricaulota | 0.0004 | 0.0006 | 0.0007 | 0.0007 | 0.0006 |
| other | 0.2105 | 0.1917 | 0.2070 | 0.2039 | 0.2116 |

**Table S4.** Relative abundance of secondary functions at various points along natural river channel A.

| Secondary function | A1 | A2 | A3 | A4 | A5 | Primary function |
|---|---|---|---|---|---|---|
| global and overview maps | 27.46% | 27.85% | 27.57% | 27.36% | 27.52% | L1 |
| carbohydrate metabolism | 9.76% | 9.71% | 9.43% | 9.18% | 9.28% | L1 |
| amino acid metabolism | 7.83% | 7.97% | 8.04% | 8.30% | 8.05% | L1 |
| energy metabolism | 7.44% | 7.49% | 7.52% | 7.58% | 7.53% | L1 |
| metabolism of cofactors and vitamins | 4.68% | 4.83% | 4.81% | 4.82% | 4.85% | L1 |
| membrane transport | 4.31% | 4.11% | 4.16% | 4.26% | 4.15% | L3 |
| cellular community – prokaryotes | 3.89% | 3.87% | 3.88% | 3.98% | 3.86% | L4 |
| signal transduction | 3.28% | 3.28% | 3.32% | 3.51% | 3.51% | L3 |
| translation | 3.53% | 3.60% | 3.69% | 3.50% | 3.46% | L2 |
| nucleotide metabolism | 2.89% | 2.86% | 2.98% | 2.90% | 2.92% | L1 |
| replication and repair | 2.64% | 2.58% | 2.67% | 2.58% | 2.60% | L2 |
| lipid metabolism | 2.31% | 2.31% | 2.28% | 2.27% | 2.26% | L1 |
| metabolism of other amino acids | 2.08% | 2.09% | 2.05% | 2.09% | 2.06% | L1 |
| folding, sorting, and degradation | 1.99% | 1.96% | 2.02% | 2.05% | 2.05% | L2 |
| xenobiotics biodegradation and metabolism | 1.56% | 1.48% | 1.52% | 1.68% | 1.59% | L1 |
| glycan biosynthesis and metabolism | 1.96% | 1.93% | 1.85% | 1.60% | 1.82% | L1 |
| biosynthesis of other secondary metabolites | 1.61% | 1.71% | 1.64% | 1.58% | 1.63% | L1 |

**Table S5.** Relative abundance of secondary functions at various points along natural river channel B.

| Secondary function | B1 | B2 | B3 | B4 | B5 | Primary function |
|---|---|---|---|---|---|---|
| global and overview maps | 27.27% | 27.18% | 27.18% | 27.23% | 26.98% | L1 |
| carbohydrate metabolism | 9.32% | 8.93% | 8.90% | 8.95% | 8.84% | L1 |
| amino acid metabolism | 8.12% | 8.38% | 8.82% | 8.70% | 8.70% | L1 |
| energy metabolism | 7.48% | 7.35% | 7.30% | 7.37% | 6.98% | L1 |
| metabolism of cofactors and vitamins | 4.60% | 4.73% | 4.57% | 4.56% | 4.55% | L1 |
| membrane transport | 4.44% | 4.39% | 4.33% | 4.27% | 4.39% | L3 |
| cellular community – prokaryotes | 3.97% | 4.00% | 3.91% | 3.82% | 3.91% | L4 |
| signal transduction | 3.57% | 3.67% | 3.69% | 3.66% | 3.94% | L3 |
| translation | 3.11% | 2.98% | 2.81% | 2.83% | 2.69% | L2 |
| nucleotide metabolism | 2.91% | 2.84% | 2.81% | 2.79% | 2.76% | L1 |
| replication and repair | 2.50% | 2.46% | 2.28% | 2.30% | 2.27% | L2 |
| lipid metabolism | 2.41% | 2.39% | 2.45% | 2.49% | 2.49% | L1 |
| metabolism of other amino acids | 2.23% | 2.32% | 2.50% | 2.47% | 2.52% | L1 |
| folding, sorting, and degradation | 1.98% | 1.98% | 1.93% | 1.97% | 1.86% | L2 |
| xenobiotics biodegradation and metabolism | 1.75% | 1.93% | 2.20% | 2.17% | 2.26% | L1 |
| glycan biosynthesis and metabolism | 1.79% | 1.68% | 1.53% | 1.58% | 1.55% | L1 |
| biosynthesis of other secondary metabolites | 1.57% | 1.52% | 1.58% | 1.56% | 1.58% | L1 |

**Table S6.** Relative abundance of secondary functions at various points along natural river channel C.

| Secondary function | C1 | C2 | C3 | C4 | C5 | Primary function |
|---|---|---|---|---|---|---|
| global and overview maps | 26.90% | 26.95% | 26.85% | 26.97% | 26.95% | L1 |
| carbohydrate metabolism | 9.10% | 8.99% | 9.10% | 9.14% | 9.06% | L1 |
| amino acid metabolism | 8.70% | 8.75% | 8.63% | 8.65% | 8.57% | L1 |

| Secondary function | C1 | C2 | C3 | C4 | C5 | Primary function |
|---|---|---|---|---|---|---|
| energy metabolism | 7.88% | 7.79% | 7.84% | 7.87% | 7.89% | L1 |
| metabolism of cofactors and vitamins | 4.40% | 4.47% | 4.36% | 4.43% | 4.53% | L1 |
| membrane transport | 4.31% | 4.37% | 4.31% | 4.36% | 4.35% | L3 |
| cellular community – prokaryotes | 3.89% | 3.93% | 3.90% | 3.95% | 3.92% | L4 |
| signal transduction | 3.44% | 3.40% | 3.45% | 3.37% | 3.40% | L3 |
| translation | 3.23% | 3.22% | 3.24% | 3.22% | 3.21% | L2 |
| nucleotide metabolism | 2.93% | 2.91% | 2.93% | 2.91% | 2.90% | L1 |
| replication and repair | 2.43% | 2.43% | 2.44% | 2.42% | 2.50% | L2 |
| lipid metabolism | 2.38% | 2.41% | 2.35% | 2.34% | 2.34% | L1 |
| metabolism of other amino acids | 2.25% | 2.26% | 2.29% | 2.25% | 2.23% | L1 |
| folding, sorting, and degradation | 2.18% | 2.12% | 2.15% | 2.17% | 2.19% | L2 |
| xenobiotics biodegradation and metabolism | 2.00% | 2.01% | 2.00% | 1.97% | 1.91% | L1 |
| glycan biosynthesis and metabolism | 1.36% | 1.37% | 1.41% | 1.38% | 1.42% | L1 |
| biosynthesis of other secondary metabolites | 1.40% | 1.43% | 1.41% | 1.45% | 1.40% | L1 |