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Supplementary Material

Sources of organic matter affect depth-related microbial community composition in sediments of Lake Erhai, Southwest China

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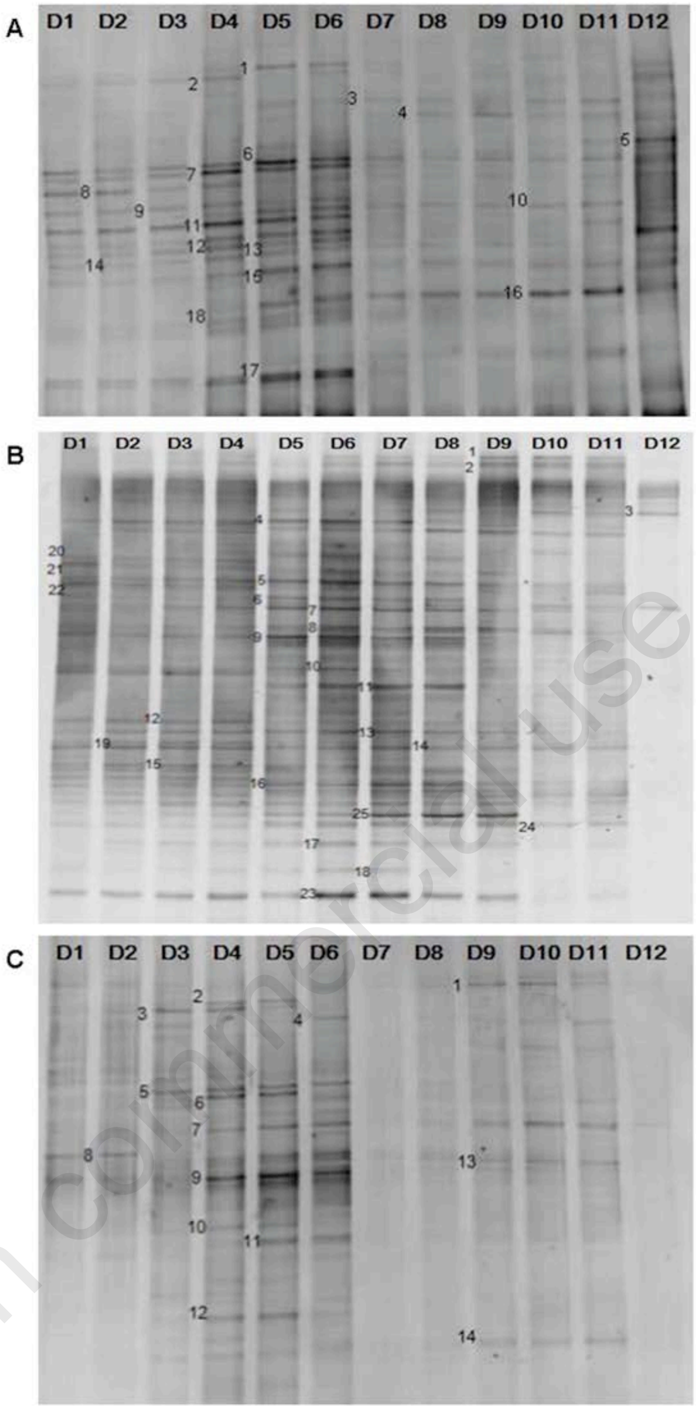
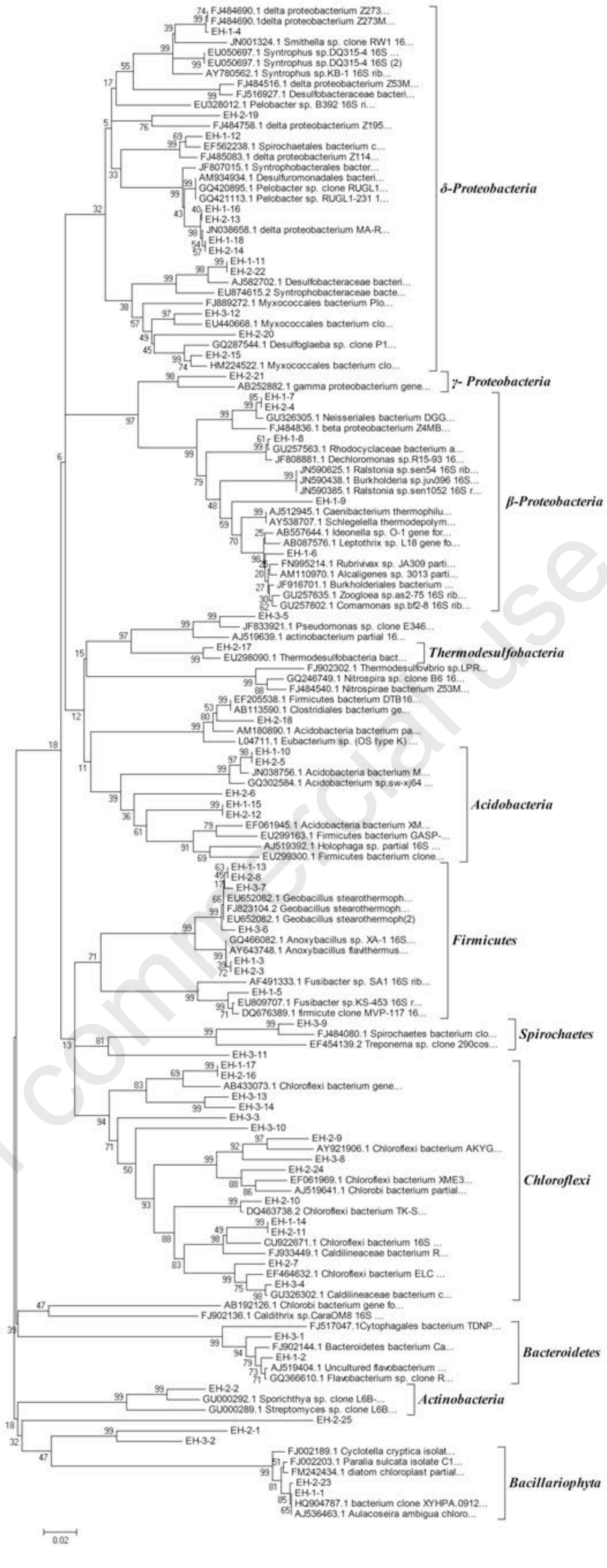


Supplementary Fig. 1 DGGE profiles (negative image) of 16S rRNA gene fragments, showing the depth-related sediment bacterial community at different sites. The capital letters A, B and C were used to distinguish the data of different Sites EH-1, EH-2 and EH-3, respectively. Lane D1, 0~2 cm; D2, 2~4 cm; D3, 4~6 cm; D4, 6~8 cm; D5, 8~10 cm; D6, 10~12 cm; D7, 12~16 cm; D8, 16~20 cm; D9, 20~26 cm; D10, 26~32 cm; D11, 32~38 cm; D12, 38~44 cm. The first band obtained from Site EH-1 was indicated by EH-1-1. The other bands were named in the same manner.



Supplementary Fig. 2. Phylogenetic tree.

Supplementary Tab. 1. Relationship of ribotypes sequenced to other sequences in the GenBank database.

Clone No.	Length of sequence (bp)	Closest match in GenBank database (accession no.)	Similarity	Accession No.
EH-1-1	566	*Aulacoseira granulata* var. *angustissima* isolate C104 16S ribosomal RNA gene, partial sequence; chloroplast (FJ002181.1)	99%	KC788751
EH-1-2	578	Uncultured *Flavobacterium* sp. clone RUGL6-349 (GQ366610.1)	99%	KC788752
EH-1-3	587	*Anoxybacillus flavithermus* strain C 16S ribosomal RNA gene (AY643748.1)	99%	KC788753
EH-1-4	587	Uncultured delta proteobacterium clone Z273MB57 (FJ484690.1)	98%	KC788754
EH-1-5	560	Uncultured Fusibacter sp. clone KS-453 (EU809707.1)	98%	KC788755
EH-1-6	585	Uncultured beta proteobacterium clone R12F 16S ribosomal RNA gene (EU499552.1)	98%	KC788756
EH-1-7	586	Uncultured Neisseriales bacterium clone DGGE gel band LVo-S30-2 (GU326305.1)	99%	KC788757
EH-1-8	587	Uncultured Betaproteobacteria bacterium 16S rRNA gene from clone QEDQ1BB01 (CU922947.1)	99%	KC788758
EH-1-9	585	Uncultured Betaproteobacteria bacterium 16S rRNA gene from clone QEDQ2BA07 (CU923553.1)	92%	KC788759
EH-1-10	587	Uncultured Acidobacteria bacterium clone LQH284 (JN868192.1)	99%	KC788760
EH-1-11	587	Uncultured delta proteobacterium clone CAR8MG07 (FJ902413.1)	95%	KC788761
EH-1-12	587	Uncultured delta proteobacterium clone Z195MB47 (FJ484762.1)	98%	KC788762
EH-1-13	588	Geobacillus stearothermophilus strain mt-11 16S ribosomal RNA gene (EU652082.1)	99%	KC788763
EH-1-14	564	Uncultured Caldilineaceae bacterium clone REV_R1PII_3F (FJ933449.1)	95%	KC788764
EH-1-15	584	Uncultured Acidobacteria bacterium clone XME61 (EF061945.1)	89%	KC788765
EH-1-16	587	Uncultured delta proteobacterium clone MA-R97 (JN038658.1)	99%	KC788766
EH-1-17	588	Uncultured Chloroflexi bacterium gene for 16S rRNA, partial sequence, clone: IODP1320B2.38 (AB433073.1)	92%	KC788767
EH-1-18	587	Uncultured delta proteobacterium clone LakeCentre43 (JQ726880.1)	99%	KC788768
EH-2-1	585	Uncultured bacterium gene for 16S rRNA, partial sequence, clone: ITKB-108 (AB198800.1)	92%	KC788769
EH-2-2	589	Uncultured *Sporichthya* sp. clone L6B-430 (GU000292.1)	95%	KC788770
EH-2-3	587	*Anoxybacillus flavithermus* strain C 16S ribosomal RNA gene (AY643748.1)	99%	KC788771
EH-2-4	586	Uncultured Neisseriales bacterium clone DGGE gel band LVo-S30-2 (GU326305.1)	99%	KC788772
EH-2-5	587	Uncultured Acidobacteria bacterium clone LQH284 (JN868192.1)	99%	KC788773
EH-2-6	588	Uncultured Acidobacteria bacterium clone M10Ba14 small subunit ribosomal RNA gene (AY360604.1)	93%	KC788774

Clone No.	Length of sequence (bp)	Closest match in GenBank database (accession no.)	Similarity	Accession No.
EH-2-7	563	Uncultured Chloroflexi bacterium clone ELC_30_7_bac (EF464632.1)	97%	KC788775
EH-2-8	588	Geobacillus stearothermophilus strain mt-11 16S ribosomal RNA gene (EU652082.1)	99%	KC788776
EH-2-9	563	Uncultured Anaerolineaceae bacterium partial 16S rRNA gene, clone O:RM-E4 (HE974801.1)	95%	KC788777
EH-2-10	561	Uncultured Chloroflexi bacterium clone TK-SH18 (DQ463738.2)	99%	KC788778
EH-2-11	564	Uncultured Caldilineaceae bacterium clone REV_R1PII_3F (FJ933449.1)	95%	KC788779
EH-2-12	584	Uncultured Acidobacteria bacterium clone XME61 (EF061945.1)	89%	KC788780
EH-2-13	587	Uncultured delta proteobacterium clone MA-R97 (JN038658.1)	99%	KC788781
EH-2-14	587	Uncultured delta proteobacterium clone LakeCentre43 (JQ726880.1)	99%	KC788782
EH-2-15	587	Uncultured Syntrophobacteraceae bacterium clone D.an-116 (JX505183.1)	97%	KC788783
EH-2-16	588	Uncultured Chloroflexi bacterium gene for 16S rRNA, partial sequence, clone: IODP1320B2.38 (AB433073.1)	92%	KC788784
EH-2-17	587	Uncultured Thermodesulfobacteria bacterium clone GASP-KB2S2_B03 (EU298090.1)	97%	KC788785
EH-2-18	586	Uncultured Firmicutes bacterium clone DTB16 16S ribosomal RNA gene, partial sequence (EF205538.1)	97%	KC788786
EH-2-19	588	Uncultured delta proteobacterium clone Z195MB42 (FJ484758.1)	91%	KC788787
EH-2-20	586	Uncultured delta proteobacterium clone Z114MB41 (FJ485025.1)	94%	KC788788
EH-2-21	586	Uncultured gamma proteobacterium gene for 16S rRNA, partial sequence, clone: 478 (AB252882.1)	92%	KC788789
EH-2-22	587	Uncultured delta proteobacterium clone CAR8MG07 (FJ902413.1)	95%	KC788790
EH-2-23	567	Aulacoseira granulata var. angustissima isolate C104 16S ribosomal RNA gene, partial sequence; chloroplast (FJ002181.1)	99%	KC788791
EH-2-24	563	Uncultured Chlorobi bacterium partial 16S rRNA gene, clone Sh765B-TzT/AG-5 (AJ519641.1)	94%	KC788792
EH-2-25	606	Uncultured Chloroflexi bacterium gene for 16S rRNA, partial sequence, clone: IODP1324B2H2.78 (AB448857.1)	88%	KC788793
EH-3-1	578	Uncultured Flavobacterium sp. clone RUGL6-349 (GQ366610.1)	96%	KC788794
EH-3-2	585	Uncultured bacterium clone FL0428B_PF34 (FJ716470)	91%	KC788795
EH-3-3	564	Uncultured Chloroflexi bacterium partial 16S rRNA gene, clone CT2B224 (AM888232.1)	96%	KC788796
EH-3-4	562	Uncultured Caldilineaceae bacterium clone DGGE gel band LVo-S14-29 (GU326302.1)	99%	KC788797
EH-3-5	588	Uncultured Firmicutes bacterium clone GASP-MA2W3_D10 (EF663324.1)	97%	KC788798
EH-3-6	588	Geobacillus stearothermophilus partial 16S rRNA gene, strain CECT 48 (AJ554207.1)	99%	KC788799
EH-3-7	588	Geobacillus stearothermophilus strain L11 (FJ823104.1)	99%	KC788800

Clone No.	Length of sequence (bp)	Closest match in GenBank database (accession no.)	Similarity	Accession No.
EH-3-8	600	Uncultured Chloroflexi bacterium clone LMC83 16S ribosomal RNA gene (JN868246.1)	98%	KC788801
EH-3-9	587	Uncultured Spirochaetes bacterium clone Z100B88 (FJ484080.1)	97%	KC788802
EH-3-10	563	Uncultured Chloroflexi bacterium clone LPBBBM44 (FJ902026.1)	96%	KC788803
EH-3-11	563	Uncultured Coriobacteriaceae bacterium clone 5_28_E8_b (JQ087113.1)	86%	KC788804
EH-3-12	588	Uncultured delta proteobacterium clone A23YA03RM (FJ569286.1)	96%	KC788805
EH-3-13	562	Uncultured Chloroflexi bacterium clone MVS-19 (DQ676319.1)	94%	KC788806
EH-3-14	562	Uncultured Chloroflexi bacterium clone ES0303-B4 (FJ437712.1)	94%	KC788807