

Supplementary material

Time-resolved microbial guild responses to tidal cycling in a coastal acid-sulfate system

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Table S1. Soil sample list. (a) Duplicate sediment cores (I and II) were collected from three sites (A, B, and C) and four tidal stages (T1, T2, T3, and T4). (b) Duplicate subsamples (a and b) of three depths (2: 2–4 cm, 4: 6–8 cm, and 6: 12–14 cm) from core I were used for replicability evaluation. (c) Triplicate subsamples of each interval in core II were merged for microbial activity evaluation for RNA isolation and cDNA synthesis. (d) Samples across tidal stages were merged for DNA sample extraction. (e) Samples across seven depths were merged *DsrB* sample list from core II

(a)

	T1 (ebb tide) 13:45, 18 Sept 2013	T2 (low tide) 17:30, 18 Sept 2013	T3 (flood tide) 08:30, 19 Sept 2013	T4 (high tide) 11:30, 19 Sept 2013
Site A (supra-tidal)	Core I, Core II	Core I, Core II	Core I, Core II	Core I, Core II
Site B (inter-tidal)	Core I, Core II	Core I, Core II	Core I, Core II	Core I, Core II
Site C (sub-tidal)	Core I, Core II	Core I, Core II	Core I, Core II	Core I, Core II

(b)

Replicability evaluation samples												
Core I	T1 (ebb tide)			T2 (low tide)			T3 (flood tide)			T4 (high tide)		
Depth	Site A	Site B	Site C	Site A	Site B	Site C	Site A	Site B	Site C	Site A	Site B	Site C
2-4cm (2)	A_T1_2_a A_T1_2_b	B_T1_2_a B_T1_2_b	C_T1_2_a C_T1_2_b	A_T2_2_a A_T2_2_b	B_T2_2_a B_T2_2_b	C_T2_2_a C_T2_2_b	A_T3_2_a A_T3_2_b	B_T3_2_a B_T3_2_b	C_T3_2_a C_T3_2_b	A_T4_2_a A_T4_2_b	B_T4_2_a B_T4_2_b	C_T4_2_a C_T4_2_b
6-8cm (4)	A_T1_4_a A_T1_4_b	B_T1_4_a B_T1_4_b	C_T1_4_a C_T1_4_b	A_T2_4_a A_T2_4_b	B_T2_4_a B_T2_4_b	C_T2_4_a C_T2_4_b	A_T3_4_a A_T3_4_b	B_T3_4_a B_T3_4_b	C_T3_4_a C_T3_4_b	A_T4_4_a A_T4_4_b	B_T4_4_a B_T4_4_b	C_T4_4_a C_T4_4_b
12-14cm (6)	A_T1_6_a A_T1_6_b	B_T1_6_a B_T1_6_b	C_T1_6_a C_T1_6_b	A_T2_6_a A_T2_6_b	B_T2_6_a B_T2_6_b	C_T2_6_a C_T2_6_b	A_T3_6_a A_T3_6_b	B_T3_6_a B_T3_6_b	C_T3_6_a C_T3_6_b	A_T4_6_a A_T4_6_b	B_T4_6_a B_T4_6_b	C_T4_6_a C_T4_6_b

(c)

RNA (cDNA) samples												
Core II	T1 (ebb tide)			T2 (low tide)			T3 (flood tide)			T4 (high tide)		
Depth	Site A	Site B	Site C	Site A	Site B	Site C	Site A	Site B	Site C	Site A	Site B	Site C
0-2cm (1)	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1
2-4cm (2)	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2
4-6cm (3)	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3
6-8cm (4)	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4	A_T1_4
8-10cm (5)	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5	A_T1_5
12-14cm (6)	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6	A_T1_6
1	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7	A_T1_7

(d)

Core II	DNA samples		
Depth	Site A	Site B	Site C
0-2cm (1)	A_1	B_1	C_1
2-4cm (2)	A_2	B_2	C_2
4-6cm (3)	A_3	B_3	C_3
6-8cm (4)	A_4	B_4	C_4
8-10cm (5)	A_5	B_5	C_5
12-14cm (6)	A_6	B_6	C_6
18-20cm (7)	A_7	B_7	C_7

(e)

Core II	<i>dsrB</i> samples				
Extract from	cDNA	cDNA	cDNA	cDNA	DNA
Site	T1	T2	T3	T4	
Site A	A_T1_1	A_T1_1	A_T1_1	A_T1_1	A_T1_1
Site B	A_T1_2	A_T1_2	A_T1_2	A_T1_2	A_T1_2
Site C	A_T1_3	A_T1_3	A_T1_3	A_T1_3	A_T1_3

Table S2. OTUs that showed significant correlations with Fe and S parameters (Spearman's correlation coefficient >0.3 or <-0.3, $P < 0.05$)

Fe-, S-factors	Positive correlated OTUs	Negative correlated OTUs
AVS	14, 18, 24, 38, 41, 48, 50, 53, 54, 56, 66, 72, 74, 75, 76, 81, 86, 87, 95, 96, 106, 113, 120, 121, 123, 124, 126, 127, 134, 136, 137, 141, 142, 145, 146, 149, 150, 151, 152, 155, 157, 161, 162, 171, 175, 176, 177, 180, 182, 185, 186, 192, 193, 210, 218, 219, 220, 226, 229, 233, 237, 242, 244, 245, 246, 253, 291, 294, 309, 311, 313, 322, 328, 330, 359, 364, 379, 387, 390, 400, 417, 501	29, 34, 40, 49, 57, 69, 79, 82, 104, 131, 140, 153, 163, 181, 198, 263, 271
CRS	9, 14, 18, 24, 30, 32, 38, 39, 41, 44, 48, 50, 53, 54, 56, 65, 66, 71, 72, 74, 75, 76, 81, 84, 86, 87, 89, 91, 92, 93, 94, 95, 96, 103, 105, 106, 111, 113, 115, 120, 121, 123, 124, 126, 127, 129, 134, 135, 137, 139, 141, 142, 143, 145, 146, 147, 149, 150, 151, 152, 155, 157, 161, 162, 164, 166, 171, 173, 175, 176, 177, 178, 180, 182, 183, 185, 186, 190, 192, 193, 195, 197, 199, 202, 206, 210, 213, 219, 220, 222, 224, 226, 227, 229, 233, 237, 242, 244, 245, 246, 253, 254, 260, 264, 280, 281, 291, 293, 294, 306, 309, 311, 313, 319, 321, 322, 328, 330, 335, 342, 359, 364, 373, 379, 387, 390, 400, 417	10, 12, 13, 22, 26, 29, 45, 49, 51, 68, 78, 83, 90, 98, 104, 108, 109, 131, 156, 163, 169, 181, 191, 198, 203, 211, 230, 295, 308, 374, 392
ES	2, 3, 52, 53, 58, 62, 66, 72, 76, 81, 95, 113, 121, 123, 124, 136, 137, 141, 145, 146, 159, 171, 175, 176, 177, 182, 184, 185, 219, 226, 229, 237, 245, 291, 309, 322, 328, 359, 364, 379, 387, 390, 400, 417, 501	11, 33, 34, 40, 82, 90, 104, 108, 118, 131, 140, 144, 153, 154, 158, 163, 188, 189, 209, 225, 232, 238, 247, 252, 259, 263, 271, 275, 282, 289, 337, 338, 341, 479
Fe(II)-MgCl₂	25, 58, 72, 76, 136, 182, 185, 215, 235, 390, 412, 490	4, 5, 7, 11, 31, 33, 34, 40, 57, 67, 69, 79, 82, 88, 118, 119, 122, 131, 138, 140, 144, 153, 154, 158, 164, 174, 188, 189, 207, 228, 232, 238, 247, 255, 259, 263, 264, 269, 271, 273, 275, 282, 289, 297, 310, 314, 317, 321, 323, 325, 337, 338, 397, 409, 479
Fe(III)-MgCl₂	134, 229	51, 57, 101, 271, 275, 310, 338, 397
Fe(II)-HCl	14, 18, 38, 53, 56, 66, 72, 74, 75, 76, 81, 86, 87, 95, 103, 113, 120, 121, 123, 124, 127, 129, 134, 136, 137, 141, 142, 145, 146, 149, 150, 151, 152, 155, 157, 161, 162, 175, 176, 177, 180, 182, 185, 186, 192, 193, 210, 219, 220, 226, 229, 233, 237, 242, 245, 246, 291, 294, 309, 322, 328, 330, 359, 364, 379, 387, 390, 400, 417, 501	11, 22, 26, 29, 33, 34, 35, 40, 49, 51, 57, 69, 79, 82, 90, 104, 108, 131, 140, 153, 154, 158, 163, 189, 207, 225, 238, 239, 247, 249, 255, 258, 259, 263, 271, 282, 289, 337, 341, 346, 479
Fe(III)-HCl	4, 5, 7, 9, 18, 19, 20, 24, 30, 31, 32, 38, 39, 41, 44, 48, 50, 53, 56, 65, 66, 71, 74, 75, 84, 86, 87, 88, 89, 91, 92, 93, 94, 95, 96, 103, 105, 106, 113, 115, 120, 121, 123, 124, 126, 127, 128, 129, 132, 134, 135, 137, 139, 141, 142, 143, 144, 145, 146, 147, 149, 152, 155, 157, 161, 162, 164, 166, 175, 176, 177, 178, 180, 183, 186, 188, 190, 192, 193, 195, 199, 202, 205, 206, 210, 213, 219, 220, 222, 226, 227, 229, 233, 236, 237, 240, 242, 244, 245, 246, 253, 254, 260, 267, 280, 281, 288, 291, 293, 294, 297, 309, 311, 313, 318, 319, 321, 323, 330, 333, 335, 338, 342, 351, 356, 364, 373, 379, 387	10, 12, 13, 15, 17, 22, 25, 26, 28, 29, 36, 37, 45, 46, 49, 51, 60, 68, 70, 73, 77, 78, 83, 85, 90, 98, 101, 104, 107, 108, 109, 117, 156, 163, 169, 181, 191, 196, 198, 203, 204, 211, 215, 230, 241, 251, 295, 308, 312, 374, 380, 392, 416, 464, 490

Fe(CDB)	9, 18, 24, 38, 41, 44, 50, 53, 56, 65, 66, 72, 74, 75, 76, 81, 84, 86, 87, 89, 91, 93, 94, 95, 96, 106, 113, 120, 121, 123, 124, 126, 127, 134, 135, 137, 141, 142, 145, 146, 147, 149, 152, 155, 157, 161, 162, 164, 166, 173, 175, 176, 177, 180, 182, 183, 185, 186, 192, 193, 197, 202, 210, 219, 220, 224, 226, 229, 233, 237, 242, 244, 245, 246, 253, 264, 291, 293, 294, 309, 311, 313, 319, 328, 330, 342, 364, 379, 387, 417	12, 13, 22, 26, 29, 45, 49, 51, 68, 78, 83, 90, 97, 98, 104, 108, 109, 114, 131, 156, 163, 181, 191, 198, 203, 211, 251, 374
DOP	3, 53, 81, 136, 151, 182, 185, 322, 359, 390, 400	116
DOS	3, 23, 25, 36, 53, 76, 81, 100, 101, 136, 151, 182, 185, 212, 215, 218, 322, 359, 390, 391, 400, 501	79, 116

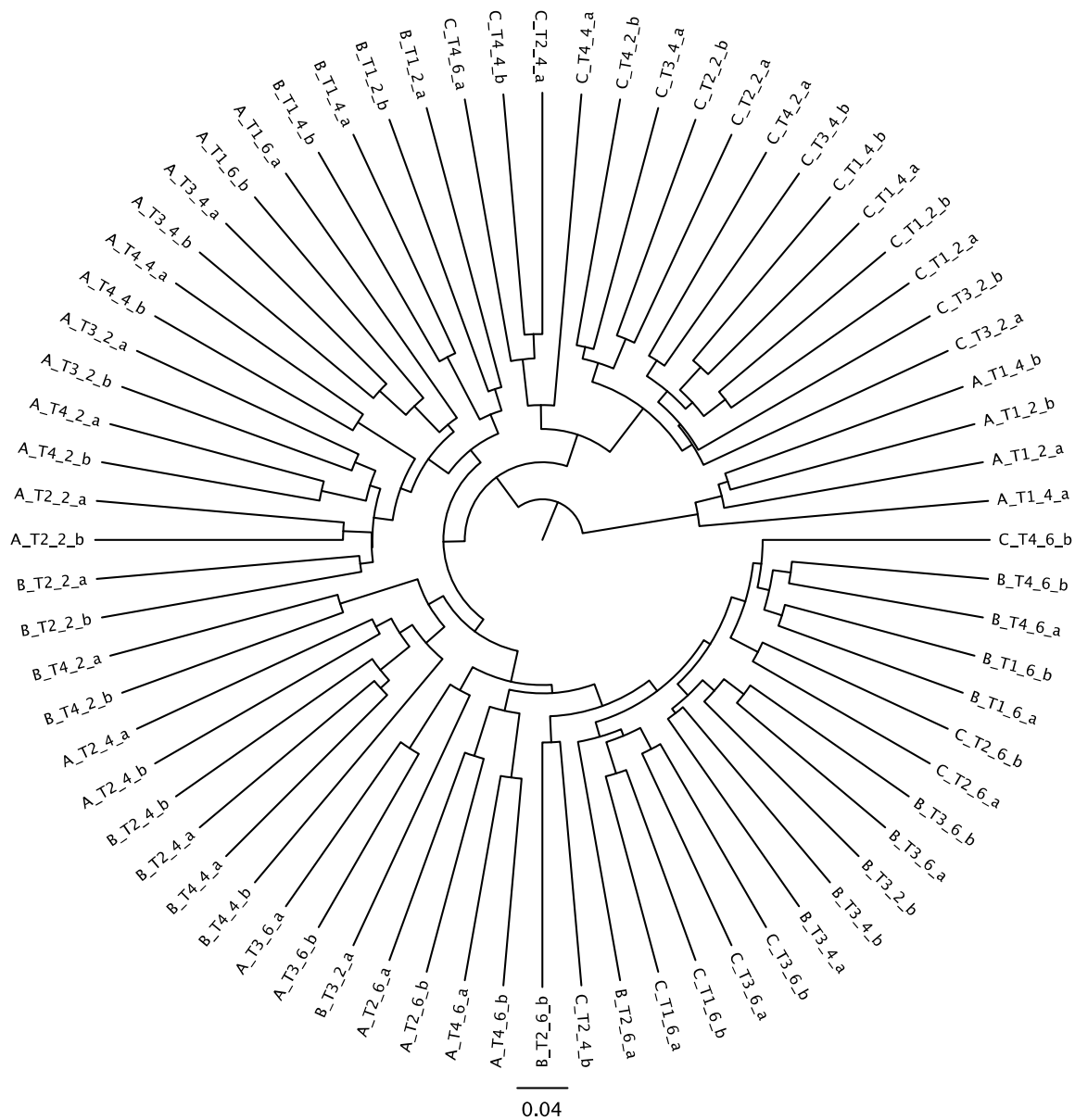


Fig. S1. A Newick-formatted tree shows the similarity of the samples that were collected from duplicated subsediments (a and b) of three depth intervals (2: 2–4 cm, 4: 6–8 cm, 6: 12–14 cm), three sites (A, B and C), and four tidal stages (T1: ebb tide, T2, low tide, T3, flood tide, T4: high tide) using Yue and Clayton index.

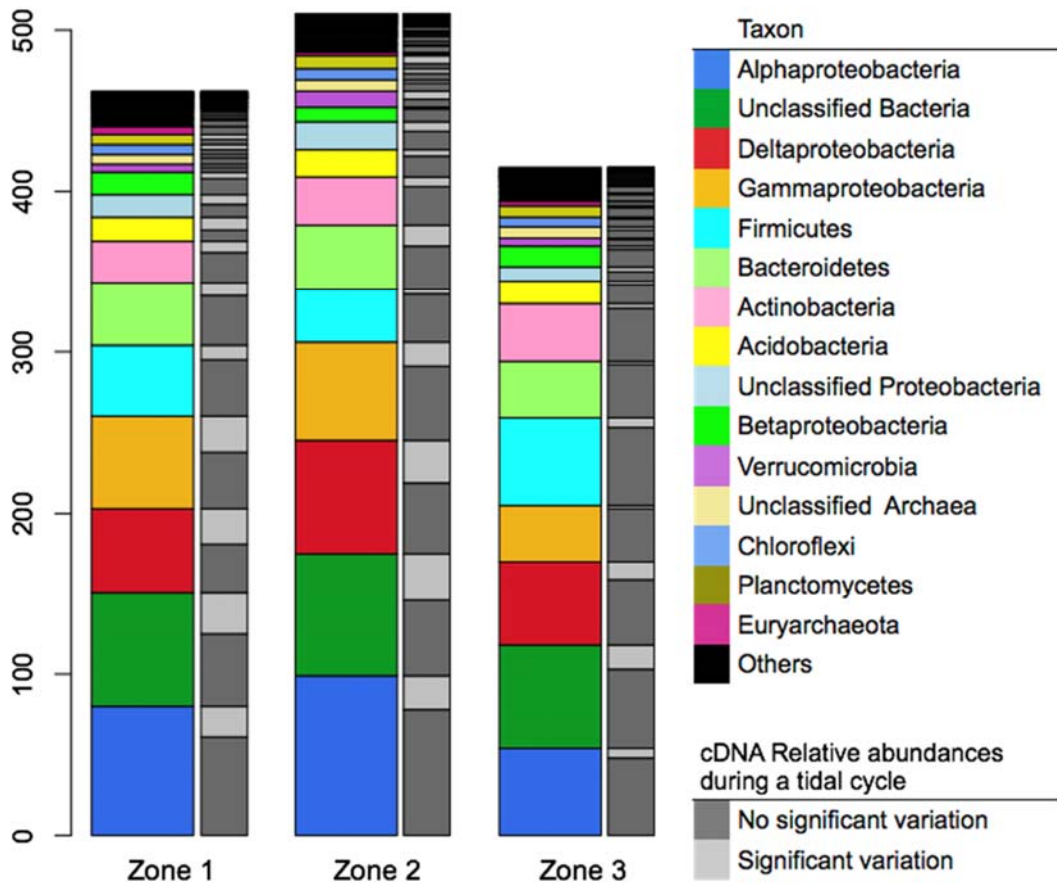


Fig. S2. Microbial structures of cDNA (coloured bars) in three geographical zones in OTU number, and the OTU fractions of two groups: cDNA showing or not showing significant variations across a tidal cycle (grey scale bars).

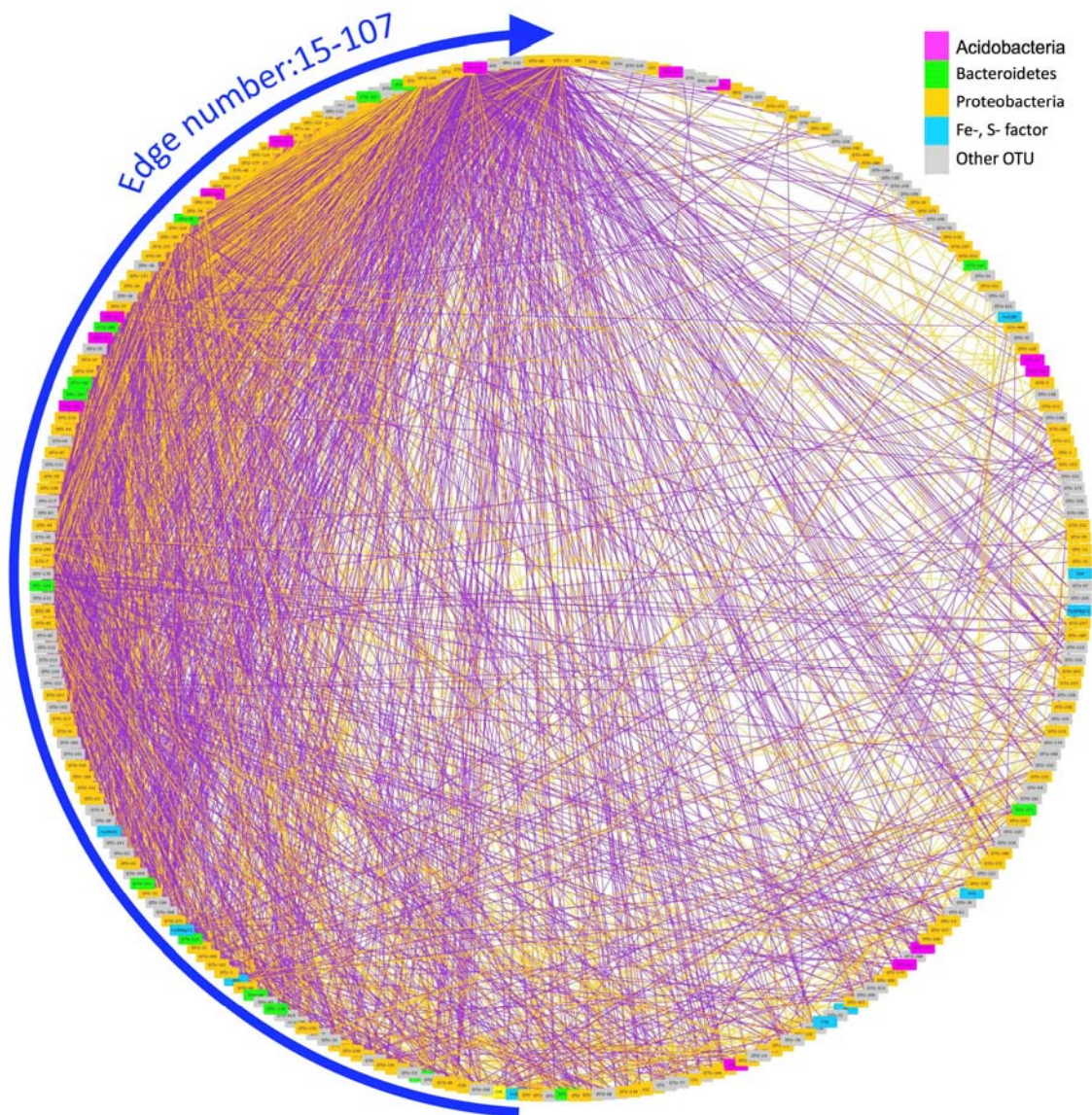


Fig. S3. Microbial Fe and S co-occurrence networks. Coloured OTUs at phylum level listed around the outer rings showed significant correlations with blue Fe and S parameters (Spearman's correlation coefficient >0.3 or <-0.3 , $P < 0.05$), as represented by the yellow and purple lines, which represent positive and negative correlations respectively. OTUs that had more than 14 edges were selected and are displayed in Fig. 8.