

A

**otu\_b49400:** 3 sequences, all within 97% sequence identity.  
No named relatives. Likely phylum: JS1

**otu\_a800:** 4 sequences, all within 97% sequence identity.  
Next named relative: *Methanosalsum*, at 87% identity.

Lapham et al., hypersaline sediments, Gulf of Mexico  
Boetius et al., marine sediments, Gulf of Mexico  
Forney et al., deep-sea sediments, Mediterranean

otu_b49400	otu_a800
1	2
1	1
1	1

$p = 1.1 \cdot 10^{-7}$  (FDR; adjusted for multiple testing)

C

**otu\_b788:** 182 sequences, all within 90% sequence identity.  
Including 20 named isolates (*Acidithiobacillus*)

**otu\_b44:** 120 sequences, all within 90% sequence identity.  
Including 9 named isolates (*Leptospirillum*)

Abanto et al., acid water sample  
Aguilera et al., extreme acidic river  
Aguilera et al., acidic river  
Aguilera et al., filaments from acidic river  
Amano et al., Biogenic Fe-oxyhydroxide nodules  
Amils et al., extremely acidic environment  
Baker et al., acid mine drainage  
Chen et al., bioleaching heap  
Chen et al., low-grade copper bioleaching heap  
Dai et al., acid mine drainage  
Dai et al., acid mine drainage  
Gihring et al., subsurface water  
Hallberg et al., mine tailings  
Hallberg et al., mine water  
Hao et al., processed gold ore  
He et al., acid mine drainage  
Huo et al., acid mine drainage  
Ito et al., corroded concrete sample  
Liu et al., bioreactor  
Maier et al., mine tailings  
Qiu et al., bioleaching pulp

otu_b788	otu_b44
1	1
10	11
11	10
32	45
1	2
3	5
2	1
7	3
2	4
4	3
1	3
2	3
1	1
1	1
2	5
1	3
2	1
5	6
9	3
2	3

independent occurrences in 19 further samples

$p = 6.5 \cdot 10^{-36}$  (FDR; adjusted for multiple testing)

B

**otu\_b2012:** 158 sequences, all within 98% sequence identity.  
Includes 33 named isolates (*Stenotrophomonas*/*Xanthomonas*)

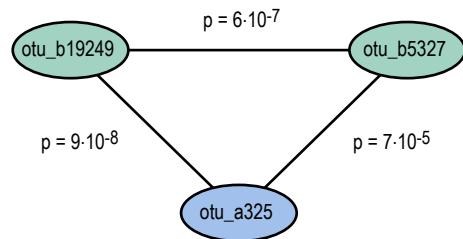
**otu\_b8:** 532 sequences, all within 98% sequence identity.  
Includes 22 named isolates (*Staphylococcus*)

otu_b2012	otu_b8
2	1
51	2
1	2
1	3
4	16
1	5
1	1
9	1
14	105
2	1

independent occurrences in 49 further samples

$p = 4.6 \cdot 10^{-10}$  (FDR; adjusted for multiple testing)

D



Delta-  
proteo-  
bacteria

Eury-  
archaeota

**otu\_b19249:** 22 sequences, all within 90% sequence identity.  
Next named relative: *Desulfovibulus*, at 88% identity.

**otu\_b5327:** 101 sequences, all within 90% sequence identity.  
Including one named isolate (*Endosymbiont of Olavius ilvae*)

**otu\_a325:** 74 sequences, all within 90% sequence identity.  
No named relative. Designation: *ANME-1*

Boetius et al., marine sediments  
Lapham et al., sediments  
Beal et al., methane seep sediments  
Boetius et al., hydrocarb. seep sediments  
Boetius et al., hydrocarb. seep sediments  
Forney et al., mud volcano  
Amann et al., sediment ab. hydrate ridge  
Boetius et al., marine sediments

independent occrs. in 47 further samples

otu_b19249	otu_b5327	otu_a325
5	2	8
2	3	5
1	2	-
1	-	1
-	1	1
2	2	1
1	5	-
5	5	30