

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.

	otu_b49400	otu_a800
Lapham et al., hypersaline sediments, Gulf of Mexico	1	2
Boetius et al., marine sediments, Gulf of Mexico	1	1
Forney et al., deep-sea sediments, Mediterranean	1	1

$p = 1.1 \cdot 10^{-07}$  (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
Blakesley et al., ear punch biopsy	2	1
Chen et al., clean-room air	51	2
Cho et al., plant leaf	1	2
Dekas et al., clean-room air	1	3
Nevalainen et al., indoor dust	4	16
Dekas et al., aircraft cabin air	1	5
Andersen et al., endotracheal aspirate	1	1
Chen et al., clean-room air	9	1
Blakesley et al., inner elbow skin	14	105
Cho et al., plant root	2	1
independent occurrences in 49 further samples		

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

C

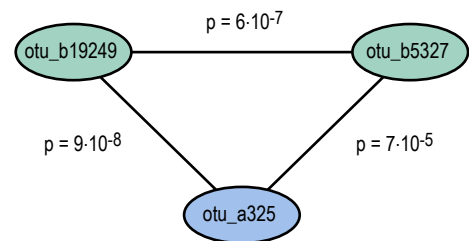
**otu\_b788:** 182 sequences, all within 90% sequence identity.  
Including 20 named isolates (*Acidithiobacillus*)

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

	otu_b788	otu_b44
Abanto et al., acid water sample	1	1
Aguilera et al., extreme acidic river	10	11
Aguilera et al., acidic river	11	10
Aguilera et al., filaments from acidic river	32	45
Amano et al., Biogenic Fe-oxyhydroxide nodules	1	2
Amils et al., extremely acidic environment	3	5
Baker et al., acid mine drainage	2	1
Chen et al., bioleaching heap	7	3
Chen et al., low-grade copper bioleaching heap	2	4
Dai et al., acid mine drainage	4	3
Gihring et al., subsurface water	1	3
Hallberg et al., mine tailings	2	3
Hallberg et al., mine water	1	1
Hao et al., processed gold ore	1	1
He et al., acid mine drainage	2	5
Huo et al., acid mine drainage	1	3
Ito et al., corroded concrete sample	2	1
Liu et al., bioreactor	5	6
Maier et al., mine tailings	9	3
Qiu et al., bioleaching pulp	2	3
independent occurrences in 19 further samples		

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

D



Delta-  
proteo-  
bacteria

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

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

Eury-  
archaeota

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

	otu_b19249	otu_b5327	otu_a325
Boetius et al., marine sediments	5	2	8
Lapham et al., sediments	2	3	5
Beal et al., methane seep sediments	1	2	-
Boetius et al., hydrocarb. seep sediments	1	-	1
Boetius et al., hydrocarb. seep sediments	-	1	1
Forney et al., mud volcano	2	2	1
Amann et al., sediment ab. hydrate ridge	1	5	-
Boetius et al., marine sediments	5	5	30
independent occrs. in 47 further samples			