

## CORRIGENDUM

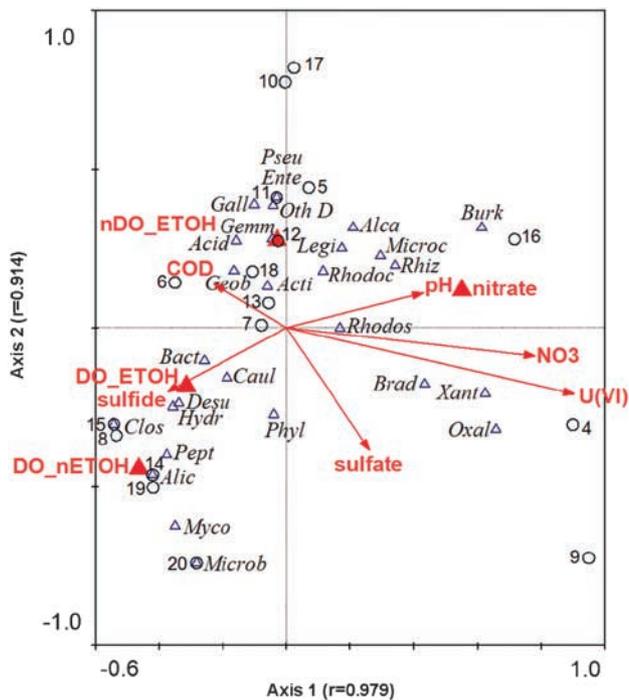
# Bacterial community succession during *in situ* uranium bioremediation: spatial similarities along controlled flow paths

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**Correction to:** The ISME Journal (2009) 3, 47–64; doi:10.1038/ismej.2008.77

The authors of the above noted an error in publication of this paper (AOP and in this issue) in the labeling of the dots in Figure 8. The corrected Figure 8 is shown below.



**Figure 8** Ordination diagram of axes 1 and 2 of the bacterial families from the wells of the bioreduction zone where engineering controls (nominal variables illustrated by triangles) and subsurface geochemistry (quantitative variables illustrated by arrows) were environmental variables and spatial locations were covariables. ‘Species’ are illustrated by open triangles and the abbreviations are as follows: Oxal: Oxalobacteraceae; Brad: Bradyrhizobiaceae; Xant: *Xanthomonas*; Rhodos: Rhodospirillaceae; Burk: Burkholderiaceae; Rhiz: Rhizobiaceae; Alca: Alcaligenaceae; Rhodoc: Rhodocyclaceae; Oth D: Other  $\delta$ -Proteobacteria; Geob: Geobacteraceae; Bact: Bacteroidetes; Micr: Microbacteraceae; Hydr: Hydrogenophilaceae; Clos: Clostridiaceae; Pept: Peptococcaceae; Caul: Caulobacteraceae; Myco: Mycobacteraceae; Desu: Desulfovibrionaceae; Alic: Alicyclobacillaceae; Phyl: Phyllobacteraceae; Microc: Micrococcaceae; Legi: Legionellaceae; Acti: Actinobacteria; Acid: Acidobacteria; Gall: Gallionellaceae; Ente: Enterobacteraceae; Pseu: Pseudomonadaceae. Only bacterial families with a cumulative fit  $\geq 5\%$  on the first two axes are shown. Samples are illustrated by open circles and the numbers correspond to the sample ID number in Table 2. The diagram accounts for approximately 63% of the variance in the species data ( $P = 0.018$ ).