

## Correction



# Correction: Microbial Community Profiling of Human Saliva Using Shotgun Metagenomic Sequencing

The *PLOS ONE* Staff

Figure 4 is an accidental duplication of Figure 3. Please see the correct Figure 4 here.

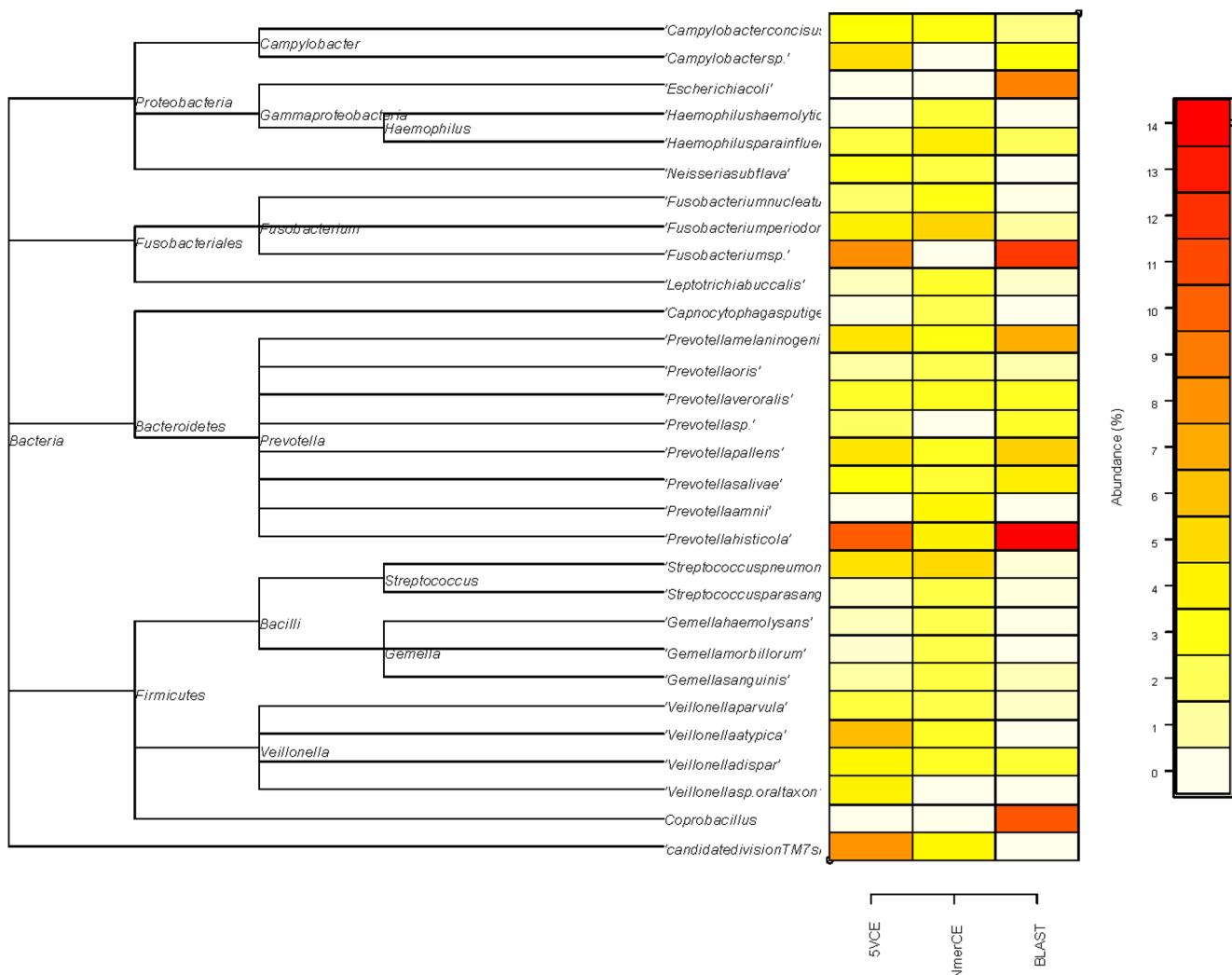
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## VFD12\_006 GAIIx Species Abundance (>2%)



**Figure 4. Relative abundance of species in VFD12-006 estimated by GAIIx sequencing and BLAST (microbial reference database), 5VCE, and NmerCE algorithms.**  
doi:10.1371/journal.pone.0097699.g004

## Reference

- Hasan NA, Young BA, Minard-Smith AT, Saeed K, Li H, et al. (2014) Microbial Community Profiling of Human Saliva Using Shotgun Metagenomic Sequencing. PLoS ONE 9(5): e97699. doi:10.1371/journal.pone.0097699