



### **16S phylogenetic tree.**

This tree has been reconstructed with complete 16S rRNA sequences from major Prokaryotic taxa which were retrieved directly from the Ribosomal Database Project web site (<http://rdp.cme.msu.edu>) (Cole J.R. *et al.*, Nucleic Acids Research, 22:4673-4680, 1994). One sequence was retained for each bacterial class or for phylum (if the latter was too large); in the case of gamma proteobacteria, we selected the sequences from the most common species. This led to a total dataset of 53 members. Sequences were then aligned with the ClustalW software (Thompson, J.D. *et al.*, Nucleic Acids Research, 22:4673-4680, 1994) using default parameters. Finally, we used the Mega2 software to perform the phylogenetic tree reconstruction (<http://www.megasoftware.net>) (Kumar S. *et al.*, Bioinformatics, 17:1244-1245, 2001). We chose the Neighbour-Joining method with p-distance to reconstruct the tree and gaps were deleted pairwise. The robustness of the tree topology was assessed by a standard bootstrap analysis with 500 replications.

This 16S phylogenetic tree shows evidence for HGT emerges from patterns of conservation of a chromosomal segment depicted in the Fig. 3 of the main manuscript. Bacteria with genomes sharing the region are depicted in red if the region is complete, in green if all of the genes of the region except hutT (coding a histidase) are present, and in blue if the region is only partially syntenic.