## I. SUPPLEMENTARY MATERIAL

Supplementary material includes the XSL file with all organisms, their coordinates in codon space, statistical analysis of codon bias, information on respiration characteristics, etc. The XSL file with $1/2\ell_1$-distances between organisms is also available. These files can be found at `http://www.ihes.fr/~materials`, together with an interactive interface which allows the reader to explore online the space of organisms.

| | Organism | Acc Num |
|---|---|---|
| | **AQUIFICAE** | |
| 1 | *Aquifex aeolicus* | NC_000918 |
| | **CYANOBACTERIA** | |
| 2 | *Nostoc sp* | NC_003272 |
| 3 | *Synechocystis PCC6803* | NC_000911 |
| 4 | *Thermosynechococcus elongatus* | NC_004113 |
| | **ACTINOBACTERIA** | |
| 5 | *Bifidobacterium longum* | NC_004307 |
| 6 | *Corynebacterium efficiens YS-314* | BA000035 |
| 7 | *Corynebacterium glutamicum* | NC_003450 |
| 8 | *Mycobacterium leprae* | NC_002677 |
| 9 | *Mycobacterium tuberculosis CDC1551* | NC_002755 |
| 10 | *Mycobacterium tuberculosis H37Rv* | NC_000962 |
| 11 | *Streptomyces coelicolor* | NC_003888 |
| | **FIRMICUTES Bacillales** | |
| 12 | *Bacillus halodurans* | NC_002570 |
| 13 | *Bacillus subtilis* | NC_000964 |
| 14 | *Listeria innocua* | NC_003212 |
| 15 | *Listeria monocytogenes* | NC_003210 |
| 16 | *Oceanobacillus iheyensis* | NC_004193 |
| 17 | *Staphylococcus aureus Mu50* | NC_002758 |
| 18 | *Staphylococcus aureus MW2* | NC_003923 |
| 19 | *Staphylococcus aureus N315* | NC_002745 |
| | **FIRMICUTES Clostridia** | |
| 20 | *Clostridium acetobutylicum* | NC_003030 |
| 21 | *Clostridium perfringens* | NC_003366 |
| 22 | *Thermoanaerobacter tengcongensis* | NC_003869 |
| | **FIRMICUTES Lactobacillales** | |
| 23 | *Lactococcus lactis* | NC_002662 |
| 24 | *Streptococcus agalactiae 2603* | NC_004116 |
| 25 | *Streptococcus agalactiae NEM316* | NC_004368 |
| 26 | *Streptococcus mutans* | NC_004350 |
| 27 | *Streptococcus pneumoniae R6* | NC_003098 |
| 28 | *Streptococcus pneumoniae TIGR4* | NC_003028 |
| 29 | *Streptococcus pyogenes* | NC_002737 |
| 30 | *Streptococcus pyogenes MGAS315* | NC_004070 |
| 31 | *Streptococcus pyogenes MGAS8232* | NC_003485 |
| | **FIRMICUTES Mollicutes** | |
| 32 | *Mycoplasma genitalium* | NC_000908 |
| 33 | *Mycoplasma pneumoniae* | NC_000912 |
| 34 | *Mycoplasma pulmonis* | NC_002771 |
| 35 | *Ureaplasma urealyticum* | NC_002162 |
| | **FUSOBACTERIALES** | |
| 36 | *Fusobacterium nucleatum* | NC_003454 |
| | **SPIROCHAETALES** | |
| 37 | *Borrelia burgdorferi* | NC_001318 |
| 38 | *Treponema pallidum* | NC_000919 |
| 39 | *Leptospira interrogans* | NC_004342 NC_004343 |
| | **CHLAMYDIALES** | |
| 40 | *Chlamydia muridarum* | NC_002620 |
| 41 | *Chlamydia trachomatis* | NC_000117 |
| 42 | *Chlamydophila pneumoniae AR39* | NC_002179 |
| 43 | *Chlamydophila pneumoniae J138* | NC_002491 |
| | **PROTEOBACTERIA alpha** | |
| 44 | *Agrobacterium tumefaciens C58 Cereon* | NC_003062 NC_003063 |
| 45 | *Agrobacterium tumefaciens C58 UWash* | NC_003304 NC_003305 |
| 46 | *Brucella melitensis* | NC_003317 NC_003318 |
| 47 | *Brucella suis 1330* | NC_004310 NC_004311 |
| 48 | *Caulobacter crescentus* | NC_002696 |
| 49 | *Mesorhizobium loti* | NC_002678 |
| 50 | *Rickettsia conorii* | NC_003103 |
| 51 | *Rickettsia prowazekii* | NC_000963 |
| 52 | *Sinorhizobium meliloti* | NC_003047 |
| | **PROTEOBACTERIA beta** | |
| 53 | *Neisseria meningitidis MC58* | NC_003112 |
| 54 | *Neisseria meningitidis Z2491* | NC_003116 |
| 55 | *Ralstonia solanacearum* | NC_003295 |
| | **PROTEOBACTERIA epsilon** | |
| 56 | *Campylobacter jejuni* | NC_002163 |
| 57 | *Helicobacter pylori 26695* | NC_000915 |
| 58 | *Helicobacter pylori J99* | NC_000921 |
| | **PROTEOBACTERIA gamma** | |
| 59 | *Buchnera aphidicola Sg* | NC_004061 |
| 60 | *Buchnera sp* | NC_002528 |
| 61 | *Escherichia coli K12* | NC_000913 |
| 62 | *Escherichia coli O157H7* | NC_002695 |
| 63 | *Escherichia coli O157H7 EDL933* | NC_002655 |
| 64 | *Haemophilus influenzae* | NC_000907 |
| 65 | *Pasteurella multocida* | NC_002663 |
| 66 | *Pseudomonas aeruginosa* | NC_002516 |
| 67 | *Salmonella typhi* | NC_003198 |
| 68 | *Salmonella typhimurium LT2* | NC_003197 |
| 69 | *Shewanella oneidensis* | NC_004347 |
| 70 | *Shigella flexneri 2a* | NC_004337 |
| 71 | *Wigglesworthia brevipalpis* | NC_004344 |
| 72 | *Vibrio cholerae* | NC_002505 NC_002506 |
| 73 | *Xanthomonas campestris* | NC_003902 |
| 74 | *Xanthomonas citri* | NC_003919 |
| 75 | *Xylella fastidiosa* | NC_002488 |
| 76 | *Yersinia pestis CO92* | NC_003143 |
| 77 | *Yersinia pestis KIM* | NC_004088 |
| | **CHLOROBIALES** | |
| 78 | *Chlorobium tepidum TLS* | NC_002932 |
| | **DEINOCOCCUS/THERMUS** | |
| 79 | *Deinococcus radiodurans* | NC_001263 NC_001264 |
| | **THERMOTOGALES** | |
| 80 | *Thermotoga maritima* | NC_000853 |
| | **ARCHEOGLOBALES** | |
| 81 | *Archaeoglobus fulgidus* | NC_000917 |
| | **METHANOBACTERIALES** | |
| 82 | *Methanobacterium thermoautotrophicum* | NC_000916 |
| | **METHANOPYRALES** | |
| 83 | *Methanopyrus kandleri* | NC_003551 |
| | **SULFOLOBALES** | |
| 84 | *Sulfolobus solfataricus* | NC_002754 |
| 85 | *Sulfolobus tokodaii* | NC_003106 |
| | **THERMOPLASMALES** | |
| 86 | *Thermoplasma acidophilum* | NC_002578 |
| 87 | *Thermoplasma volcanium* | NC_002689 |
| | **DESULFUROCOCCALES** | |
| 88 | *Aeropyrum pernix* | NC_000854 |
| | **HALOBACTERIALES** | |
| 89 | *Halobacterium sp* | NC_002607 |
| | **METHANOCOCCALES** | |
| 90 | *Methanococcus jannaschii* | NC_000909 |
| | **METHANOSARCINALES** | |
| 91 | *Methanosarcina acetivorans* | NC_003552 |
| 92 | *Methanosarcina mazei* | NC_003901 |
| | **THERMOCOCCALES** | |
| 93 | *Pyrococcus abyssi* | NC_000868 |
| 94 | *Pyrococcus furiosus* | NC_003413 |
| 95 | *Pyrococcus horikoshii* | NC_000961 |
| | **THERMOPROTEALES** | |
| 96 | *Pyrobaculum aerophilum* | NC_003364 |

TABLE I: Full list of genomes considered in the paper with their accession numbers in GeneBank FTP.

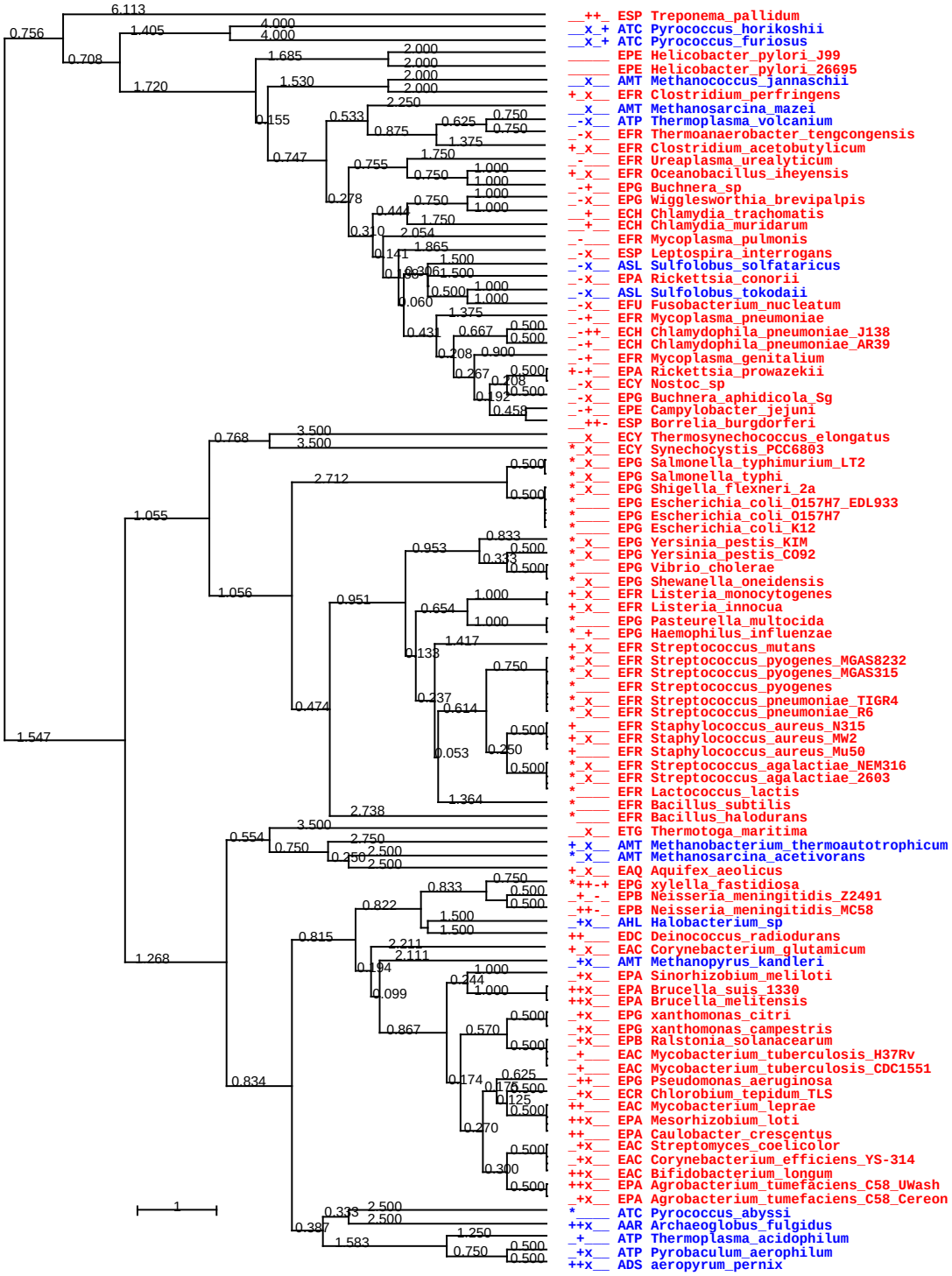


FIG. 1: Tree constructed from the binarized $\frac{1}{2}\ell_1$-distance matrix for the organisms in Table I.

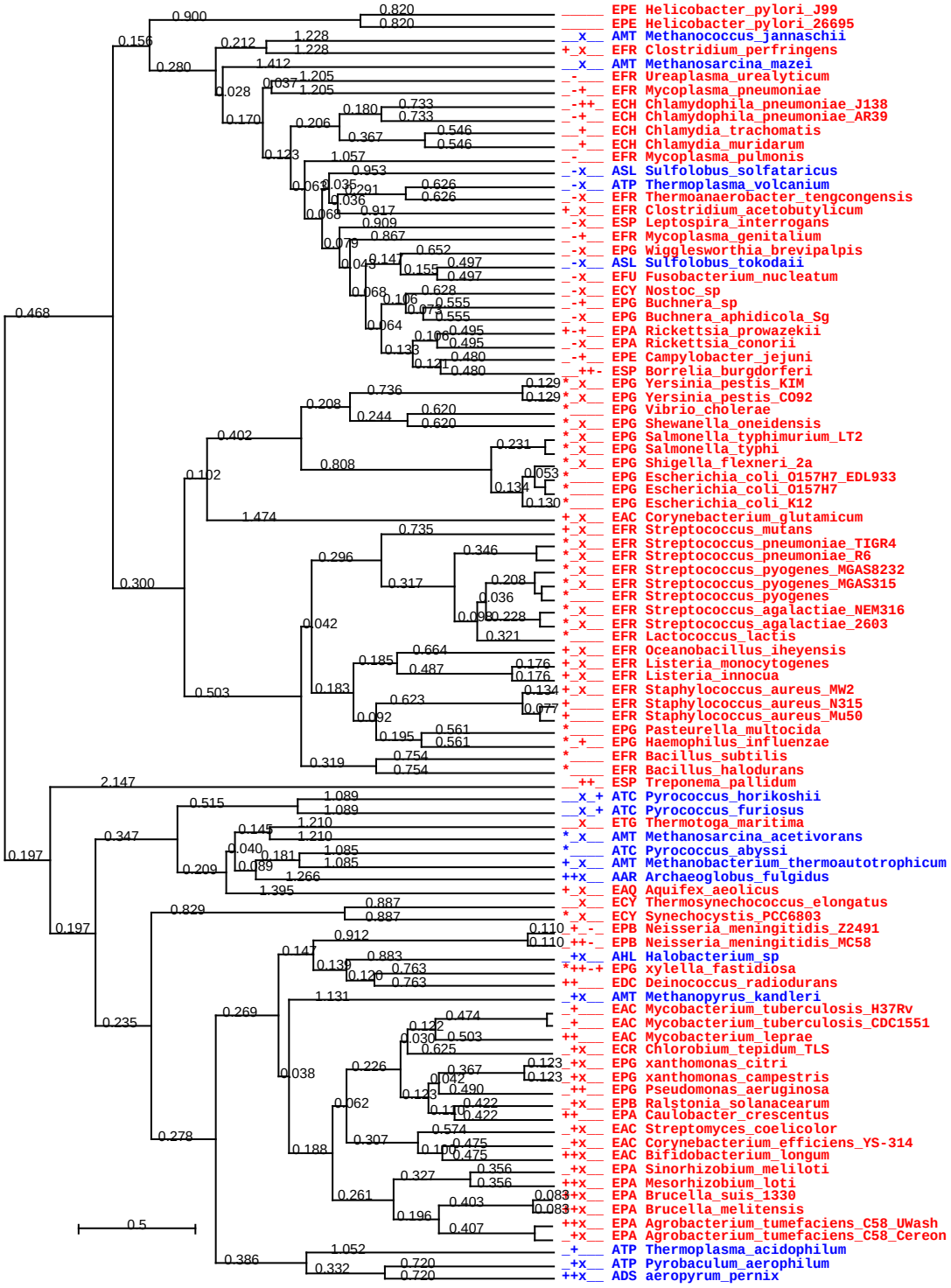


FIG. 2: Tree constructed from the Euclidean distance matrix for the organisms in Table I.

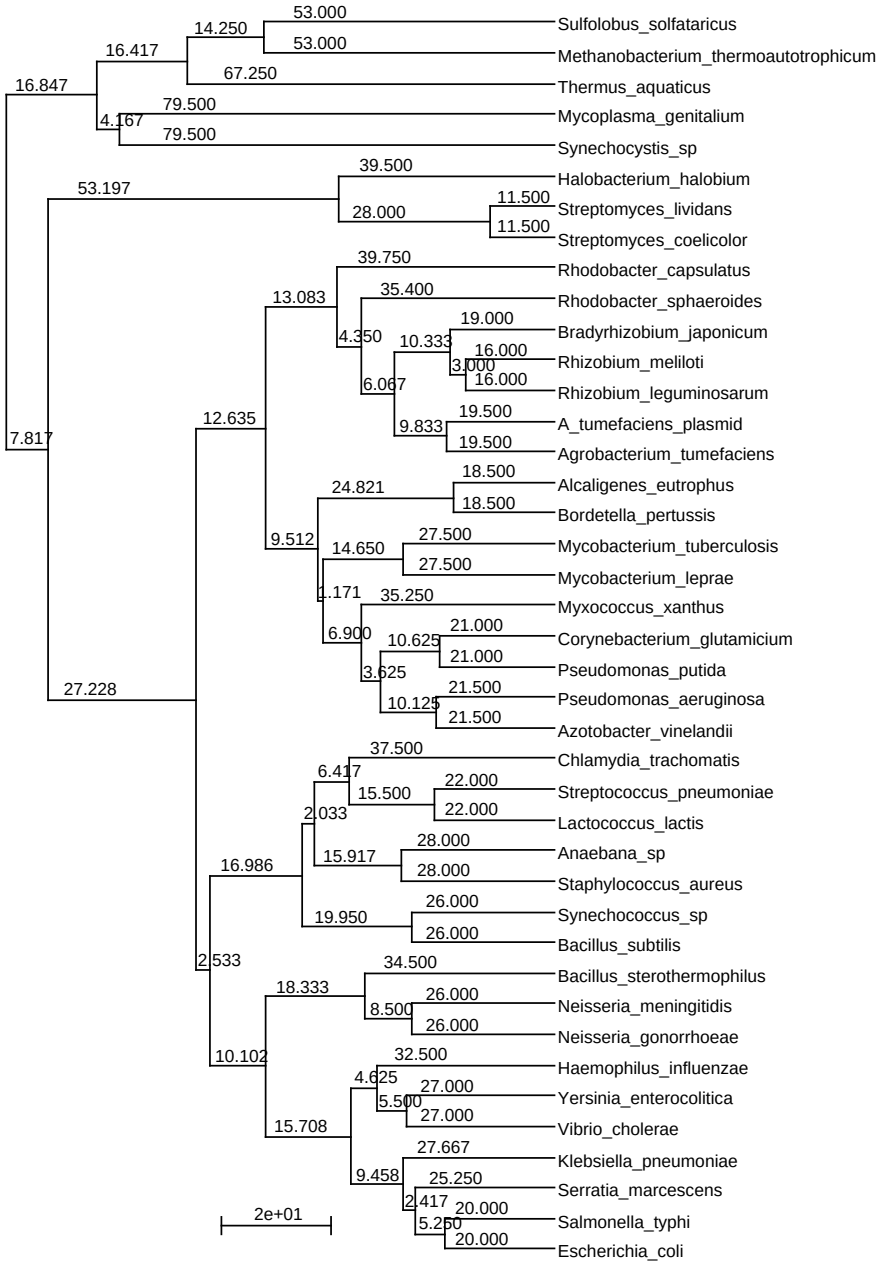


FIG. 3: Tree constructed from the $\delta^*$ distance matrix of Karlin et Mrázek data (Karlin, S. and Mrázek, J. (1998) Prokaryotic genome-wide comparisons and evolutionary implications, in *Bacterial genomes, physical structure and analysis*, edited by F. J. de Brujin, J.R. Lupski and G.M. Weinstock, Kluwer Academic Publishers, Boston).