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.

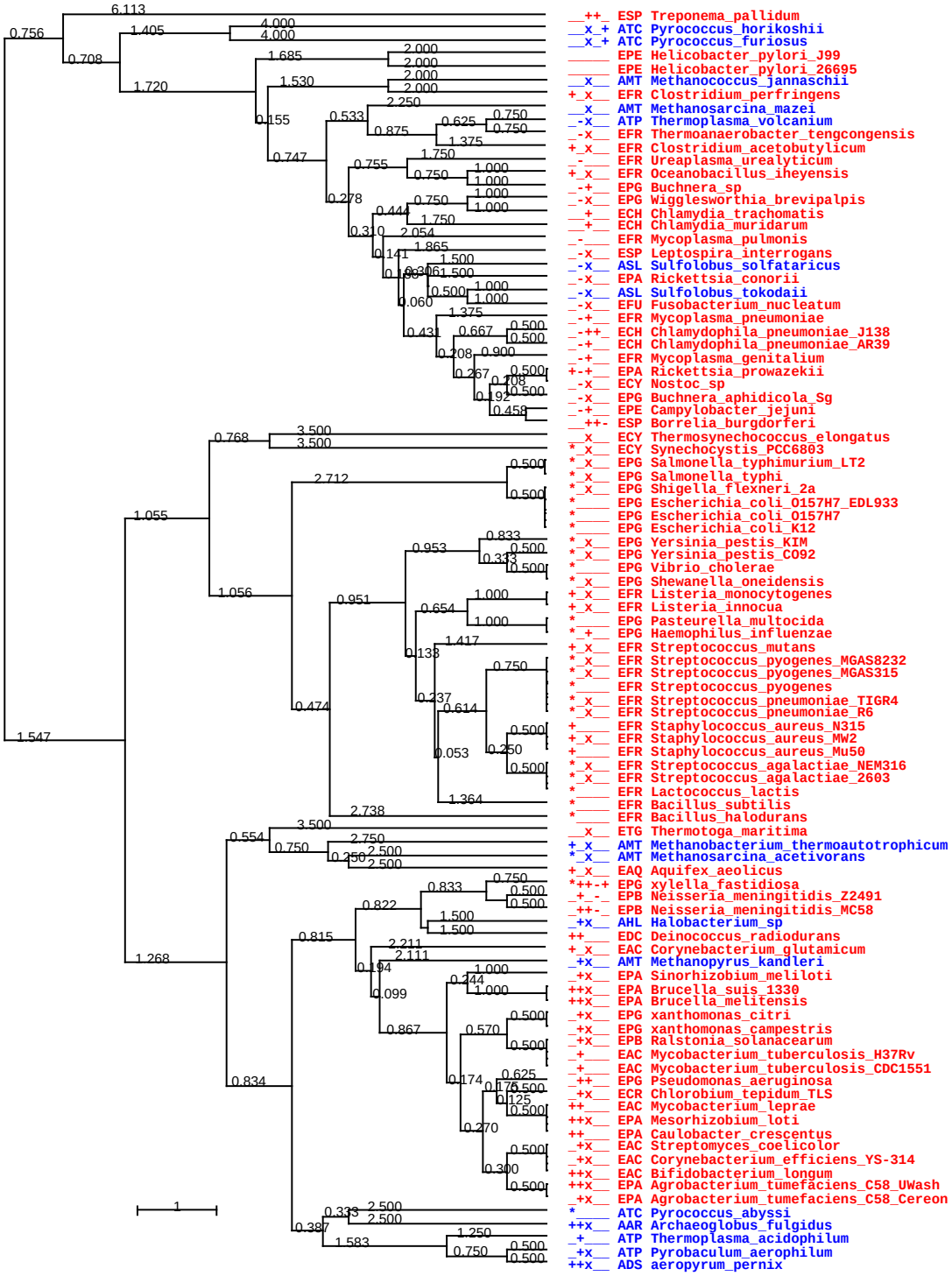

FIG. 1: Tree constructed from the binarized $\frac{1}{2}\ell_1$-distance matrix for the organisms in Table I.

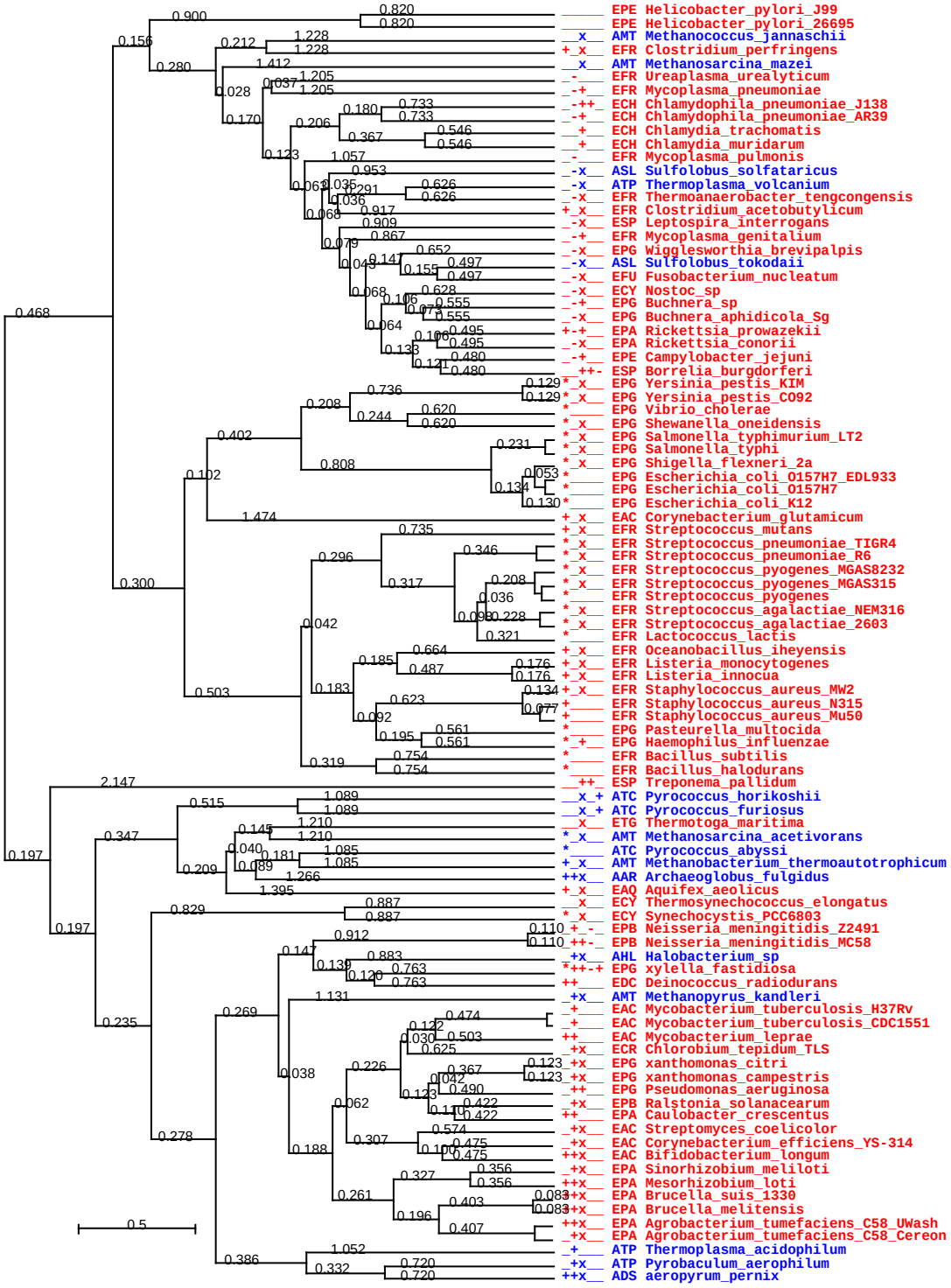

FIG. 2: Tree constructed from the Euclidean distance matrix for the organisms in Table I.

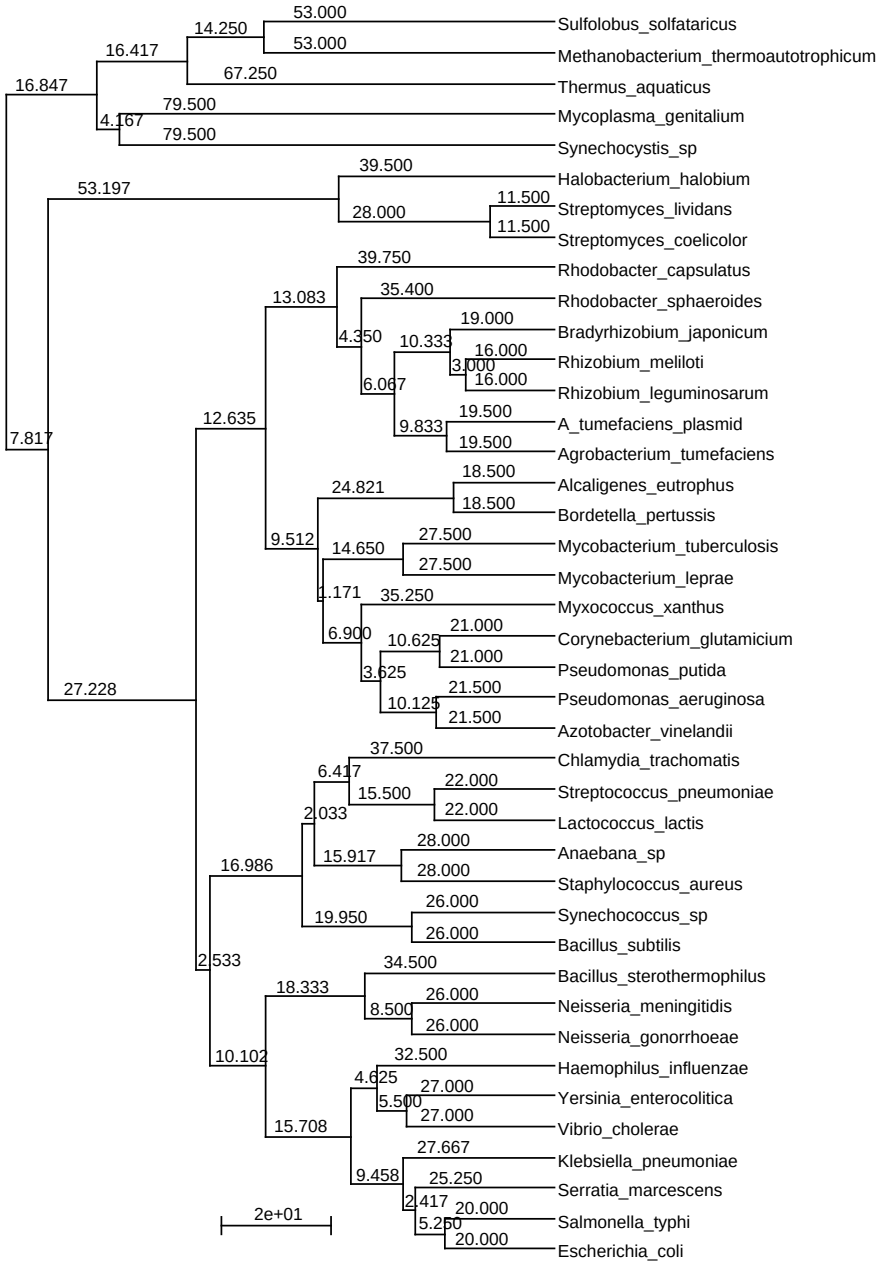

FIG. 3: Tree constructed from the δ^* distance matrix of Karlin et Mrázek data (Karlin, S. and Mrázek, J. (1998) Prokaryotic genome-wide comparisons and evolutionary implications, in *Bacterial genomes, physical structure and analysis*, edited by F. J. de Brujin, J.R. Lupski and G.M. Weinstock, Kluwer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