Appendix
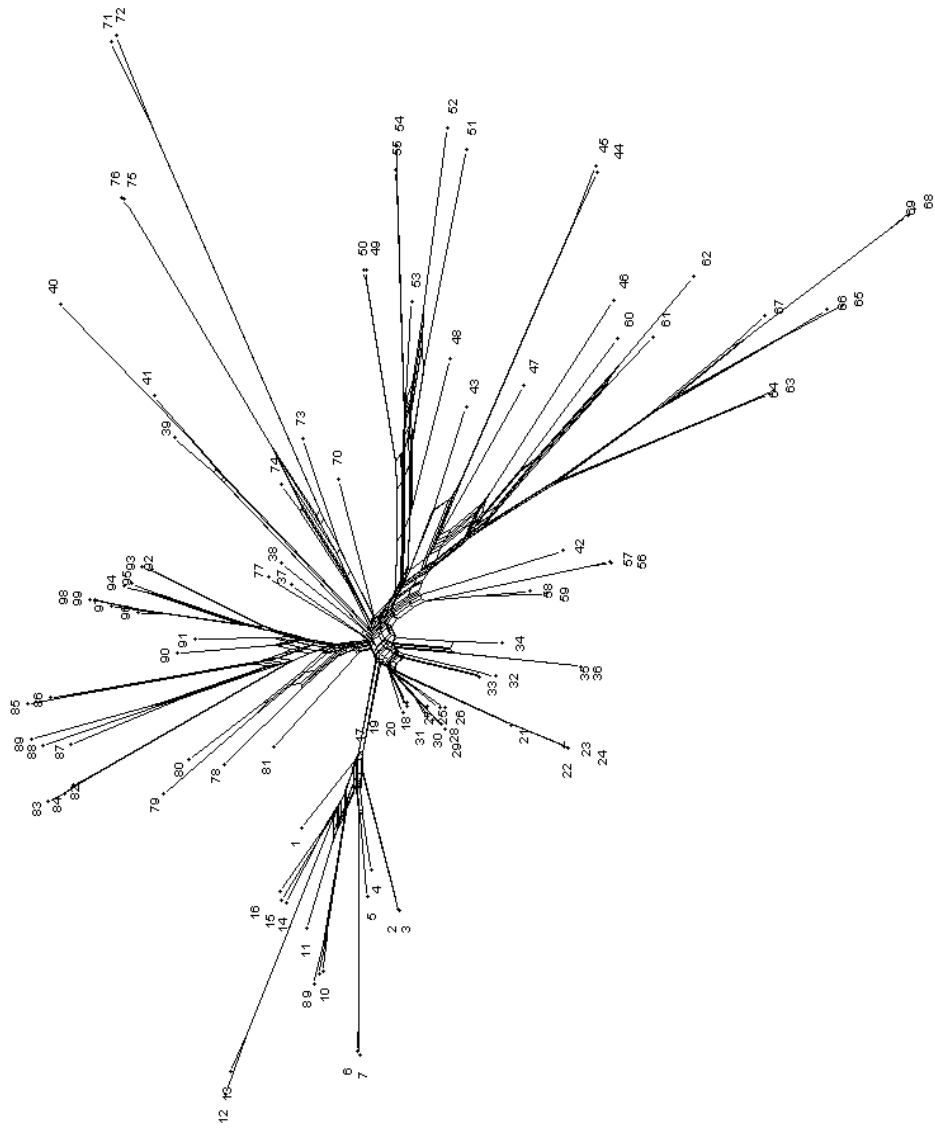
Genome sequences and accession numbers used in analyses:
1. *Halobacterium* sp. NC_002607
2. *Thermoplasma acidophilum* NC_002578
3. *Thermoplasma volcanicum* NC_002689
4. *Aeropyrum pernix* NC_000854
5. *Pyrobaculum aerophilum* NC_003364
6. *Sulfolobus solfataricus* NC_002754
7. *Solfolobus tokadei* NC_003106
8. *Pyrococcus furiosus* NC_003413
9. *Pyrococcus abyssi* NC_000868
10. *Pyrococcus horokoshii* NC_000961
11. *Archaeoglobus fulgidus* NC_000917
12. *Methanosarcina acetivorans* NC_003552
13. *Methanosarcina mazei* NC_003901
14. *Methanococcus jannaschii* NC_000909
15. *Methanobacterium thermoautotrophicum* NC_000916
16. *Methanopyrus kandleri* NC_003551
17. *Trophyerma whipplei* NC_004551
18. *Buchnera aphidicola* Bp NC_004545
19. *Buchnera aphidicola* Sg NC_004061
20. *Buchnera* sp. APS NC_002528
21. *Chlamydia trachomatis* NC_000117
22. *Chlamydia pneumoniae* NC_002620
23. *Chlamydophila pneumoniae* CWL029 NC_000922
24. *Chlamydophila pneumoniae* J138 NC_002491
25. *Borrelia burgdorferi* NC_001318
26. *Treponema pallidum* NC_000919
27. *Mycoplasma pulmonis* NC_002771
28. *Mycoplasma genitalium* NC_000908
29. *Mycoplasma pneumoniae* NC_000912
30. *Mycoplasma penetrans* NC_004432
31. *Ureaplasma urealyticum* NC_002162
32. *Rickettsia conorii* NC_003103
33. *Rickettsia prowazekei* NC_000963
34. *Campylobacter jejuni* NC_002163
35. *Helicobacter pylori* 26695 NC_000915
36. *Helicobacter pylori* J99 NC_000921
37. *Aquifex aeolicus* NC_000918
38. *Chlorobium tepidum* NC_002932
39. *Thermosynechoccus elongatus* NC_004113
40. *Nostoc* sp. NC_003272
41. *Synechocystis* sp. BA000022
42. *Nitrosomonas europaea* NC_004757
43. *Xylella fastidiosa* NC_002488
44. *Xanthomonas campestris* NC_003902
45. *Xanthomonas axonopodis* NC_003919
46. *Pseudomonas aeruginosa* NC_002516
47. *Ralstonia solanacearum* NC_003295
48. *Caulobacter crescentus* NC_002696
49. *Brucella melitensis* NC_003317
50. *Brucella suis* NC_004310
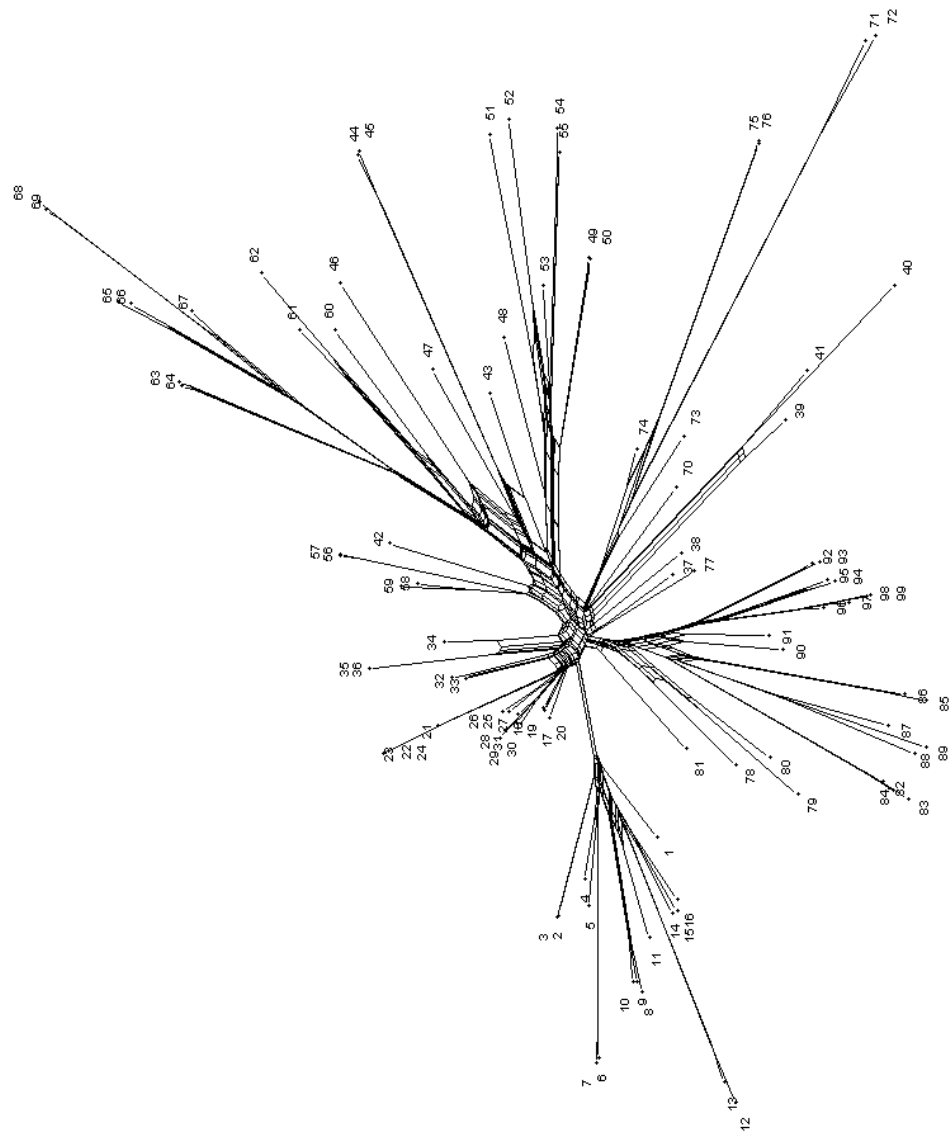51. *Bradyrhizobium japonicum* NC_004463
52. *Mesorhizobium loti* NC_002678

53. *Sinorhizobium meliloti* NC_003047
54. *Agrobacterium tumefaciens* C58 NC_003062
55. *Agrobacterium tumefaciens* C58 UW NC_003304
56. *Neisseria meningitidis* MC58 NC_003112
57. *Neisseria meningitidis* Z2491 NC_003116
58. *Haemophilus influenzae* NC_000907
59. *Pasteurella multilocida* NC_002663
60. *Shewanella oneidensis* NC_004347
61. *Vibrio cholerae NC_002505*
62. *Vibrio parahaemolyticus* NC_004603
63. *Yersinia pestis* C092 NC_003143
64. *Yersinia pestis* KIM NC_004088
65. *Salmonella enterica* NC_003198
66. *Salmonella typhimurium* NC_003197
67. *Escherichia coli* K12 NC_000913
68. *Escherichia coli* O157H7 NC_002695
69. *Escherichia coli* O157H7 EDL933 NC_002655
70. *Deinococcus radiodurans* NC_001263
71. *Streptomyces avertimilis* NC_003155
72. *Streptomyces coelicolor* NC_003888
73. *Cornyebacterim efficiens* NC_004369
74. *Mycobacterium leprae* NC_002677
75. *Mycobacterium tuberculosis* CDC1551 NC_002755
76. *Mycobacterium tuberculosis* H37Rv NC_000962
77. *Thermotoga maritima* NC_000853
78. *Thermoanaerobacter tencongensis* NC_003869
79. *Clostridium acetobulyticum* NC_003030
80. *Clostridium perfringens* NC_003366
81. *Fusobacterium nucleatum* NC_003454
82. *Staphylococcus aureus* MW2 NC_003923
83. *Staphylococcus aureus* Mu50 NC_002758
84. *Staphylococcus aureus* N315 NC_002745
85. *Listeria innocua* NC_003212
86. *Listeria monocytogenes* NC-003210
87. *Oceanobacillus iheyensis* NC_004193
88. *Bacillus halodurans* NC_002570
89. *Bacillus subtilis* NC_000964
90. *Lactobacillus plantarum* NC_004567
91. *Lactococcus lactis* NC_002662
92. *Streptococcus pneumoniae* R6 NC_003098
93. *Streptococcus pneumoniae* NC_003028
94. *Streptococcus agalactiae* 2603VR NC_004116
95. *Streptococcus agalactiae* NEM316 NC_004368
96. *Streptococcus pyogenes* NC_002737
97. *Streptococcus pyogenes* MGAS8232 NC_003485
98. *Streptococcus pyogenes* MGAS315 NC_004070
99. *Streptococcus pyog pyogenes* SSI1 NC_004606

Overleaf. NeighborNet output for data sets derived from the homology criteria *10/30*, *20/40*, *30/50*, *40/60*, *50/70*, and *60/80*. Genomes are indicated by numbers, which correspond to sequences indicated above.
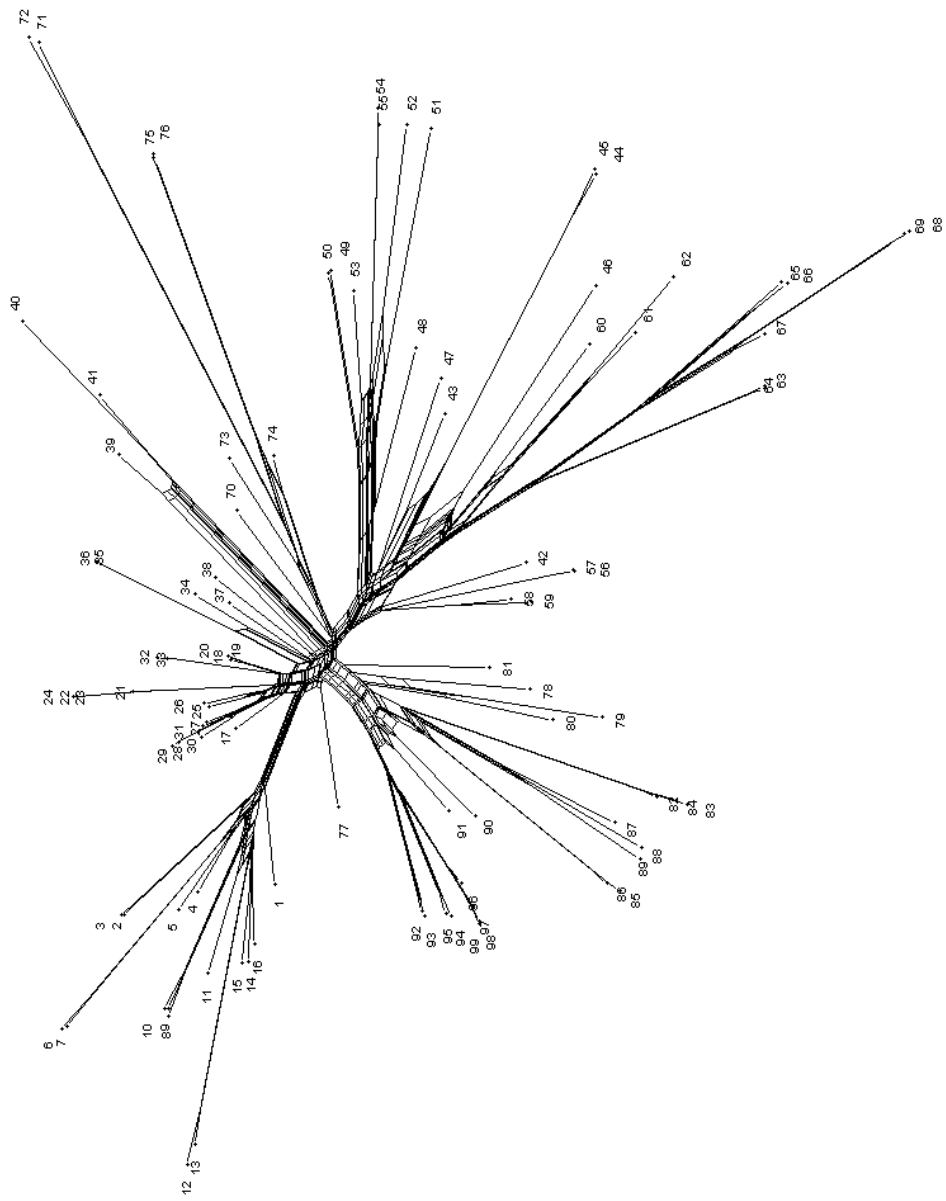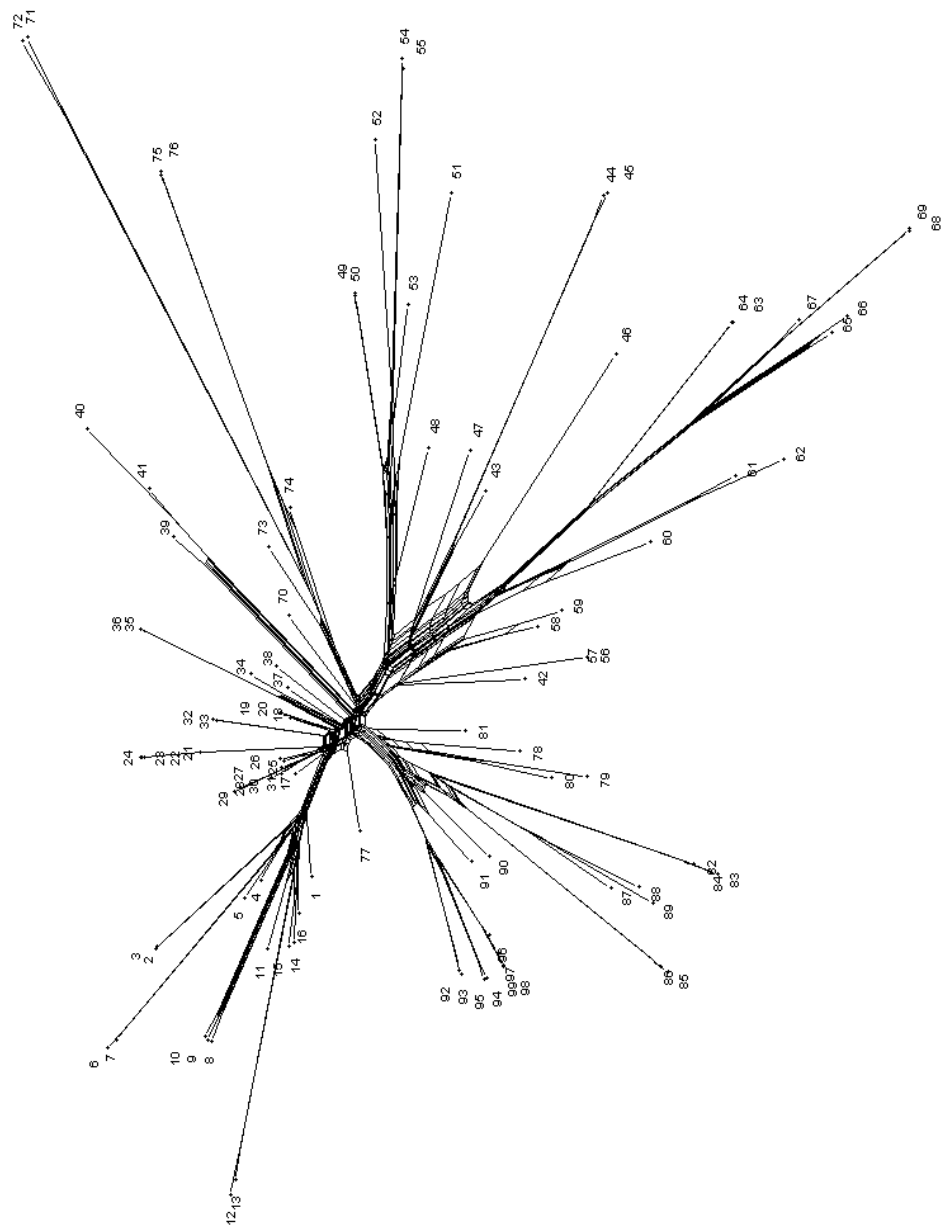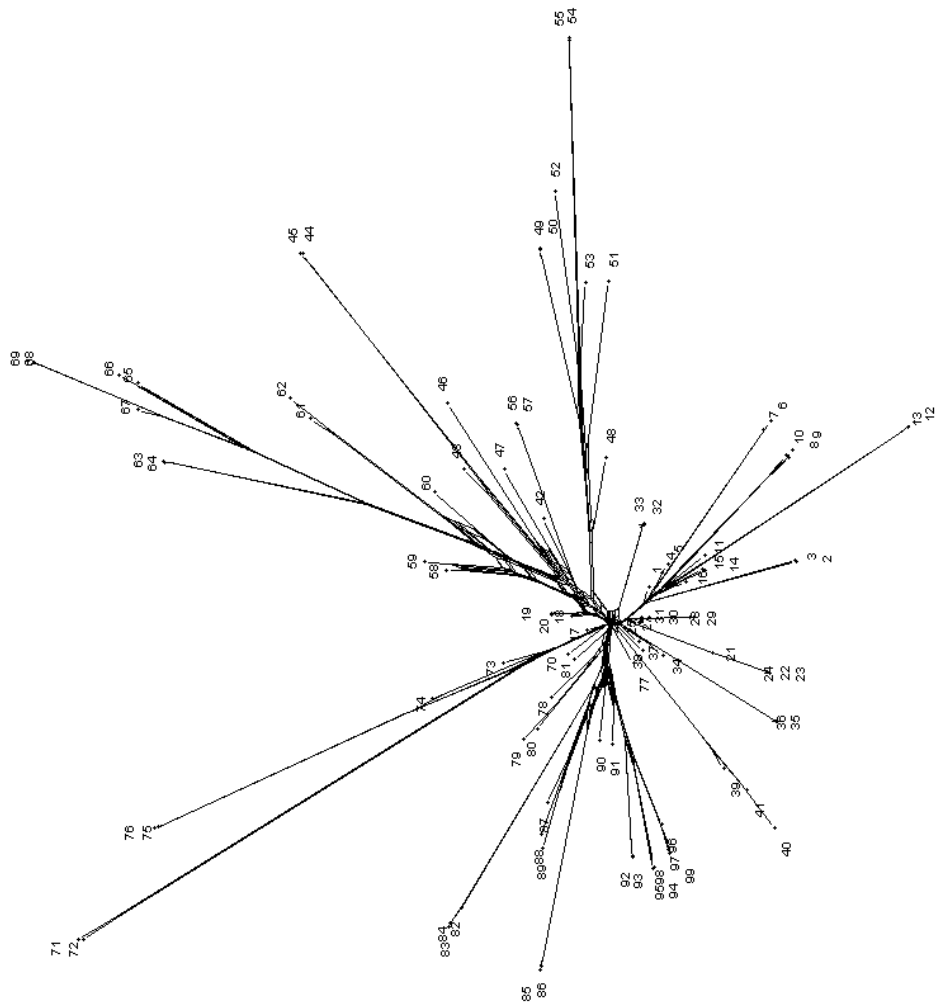
0.01

Computed by SplitsTree4

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