# Supplementary tables

Table S1 TreeBASE DNA alignments and average log-likelihoods. In bold face are the highest log-likelihood found for each alignment.

| TreeBASE ID | #Taxa | #Sites | % Gaps / ambiguous characters | IQ-TREE with default stopping rule | RAxML | IQ-TREE restricted to RAxML time | PhyML | IQ-TREE restricted to PhyML time |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| M214 | 295 | 1836 | 13.32 | **-38,670.97** | -38,681.75 | -38,678.08 | -38,687.82 | -38,679.68 |
| M667 | 218 | 1002 | 4.67 | **-45,048.88** | -45,052.75 | -45,049.03 | -45,060.45 | **-45,048.88** |
| M980 | 249 | 1604 | 19.23 | **-19,611.37** | -19,619.88 | -19,614.52 | -19,629.07 | -19,613.97 |
| M1110 | 330 | 1711 | 10.14 | **-56,377.21** | -56,382.67 | -56,377.39 | -56,379.22 | **-56,377.21** |
| M1224 | 210 | 8235 | 40.95 | **-241,142.99** | -241,162.43 | -241,143.12 | -241,163.34 | -241,144.92 |
| M1838 | 228 | 1131 | 2.1 | **-76,967.34** | -77,073.62 | -76,971.09 | -77,041.43 | -76,972.60 |
| M2307 | 318 | 1434 | 3.87 | **-35,722.34** | -35,737.57 | -35,726.57 | -35,745.25 | -35,724.83 |
| M2534 | 207 | 976 | 10.23 | -23,626.38 | **-23,617.43** | -23,627.83 | -23,665.68 | -23,634.39 |
| M2902 | 220 | 1117 | 1.14 | -7,206.09 | -7,212.21 | -7,210.28 | **-7,204.67** | -7,207.63 |
| M2931 | 229 | 4722 | 23.7 | **-54,290.51** | -54,310.48 | -54,291.02 | -54,294.23 | -54,290.86 |
| M3031 | 276 | 1518 | 14.47 | **-20,237.53** | -20,249.97 | -20,243.53 | -20,266.95 | -20,245.69 |
| M3198 | 216 | 2578 | 11.09 | **-147,473.15** | -147,498.71 | -147,478.56 | -147,483.62 | -147,475.27 |
| M3514 | 217 | 3665 | 41.73 | **-141,010.38** | -141,030.79 | -141,037.88 | -141,063.13 | -141,044.94 |
| M3605 | 260 | 5315 | 34.05 | **-55,863.43** | -55,870.86 | -55,865.33 | -55,876.41 | -55,864.25 |
| M3777 | 363 | 1707 | 3.44 | -19,365.75 | -19,378.47 | -19,365.80 | **-19,364.62** | -19,365.76 |
| M4170 | 258 | 2559 | 5.51 | **-16,585.71** | -16,602.40 | -16,594.25 | -16,592.69 | -16,590.74 |
| M4324 | 206 | 4543 | 25.32 | **-117,989.19** | -118,026.61 | -118,003.45 | -118,098.31 | -117,992.93 |
| M4326 | 227 | 4055 | 9.73 | **-29,395.83** | -29,411.69 | -29,396.27 | -29,400.38 | -29,395.86 |
| M4399 | 205 | 8913 | 57.25 | **-59,907.83** | -59,915.50 | -59,915.65 | -59,918.08 | -59,912.89 |
| M4720 | 201 | 2899 | 30.81 | **-53,732.74** | -53,744.97 | **-53,732.74** | -53,734.79 | **-53,732.74** |
| M4727 | 350 | 6464 | 52.26 | **-206,129.75** | -206,208.32 | -206,132.97 | -206,150.81 | -206,130.16 |

| TreeBASE ID | #Taxa | #Sites | % Gaps / ambiguous characters | IQ-TREE with default stopping rule | RAxML | IQ-TREE restricted to RAxML time | PhyML | IQ-TREE restricted to PhyML time |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| M4794 | 204 | 12113 | 52.47 | **-148,388.80** | -148,434.07 | -148,453.76 | -148,669.35 | -148,413.50 |
| M4806 | 222 | 3995 | 26.7 | **-73,850.56** | -73,865.86 | **-73,850.56** | -73,851.22 | **-73,850.56** |
| M4850 | 328 | 2166 | 6.15 | -23,425.32 | -23,427.86 | -23,425.57 | -23,426.00 | **-23,425.01** |
| M4900 | 206 | 3074 | 31.27 | -62,389.10 | -62,403.73 | -62,389.11 | **-62,388.47** | -62,389.10 |
| M4927 | 268 | 1275 | 37.89 | **-15,275.77** | -15,302.56 | -15,289.19 | -15,314.22 | -15,288.21 |
| M4938 | 213 | 1250 | 8.13 | **-36,243.38** | -36,261.75 | -36,245.11 | -36,258.73 | -36,244.48 |
| M5078 | 265 | 9768 | 14.48 | **-317,361.67** | -317,382.43 | -317,361.69 | -317,370.73 | -317,362.15 |
| M5235 | 298 | 11596 | 67.51 | **-66,573.65** | -66,588.26 | -66,580.11 | -66,592.51 | -66,577.79 |
| M5381 | 413 | 3632 | 10.42 | **-224,667.49** | -224,712.33 | -224,685.74 | -224,733.80 | -224,668.63 |
| M5731 | 242 | 9626 | 62.94 | **-79,593.92** | -79,608.95 | -79,594.80 | -79,596.64 | -79,594.50 |
| M5931 | 298 | 4948 | 47.67 | **-71,241.57** | -71,261.17 | -71,251.78 | -71,281.02 | -71,250.53 |
| M6134 | 219 | 5158 | 28.53 | **-30,201.02** | -30,265.32 | -30,228.78 | -30,266.62 | -30,222.20 |
| M6414 | 209 | 2000 | 29.9 | **-36,707.55** | -36,717.07 | -36,709.87 | -36,713.05 | -36,709.22 |
| M6625 | 247 | 1812 | 32.17 | **-17,190.07** | -17,203.34 | -17,193.05 | -17,205.32 | -17,193.46 |
| M7024 | 767 | 5814 | 66.73 | **-381,126.07** | -381,168.90 | -381,161.16 | -381,269.87 | -381,135.11 |
| M7054 | 222 | 6237 | 35.63 | **-79,139.05** | -79,143.97 | -79,143.80 | -79,155.57 | -79,141.71 |
| M7165 | 357 | 4475 | 17.65 | **-76,166.48** | -76,177.78 | -76,168.62 | -76,168.94 | -76,167.32 |
| M7210 | 204 | 1701 | 64.48 | **-14,803.61** | -14,810.03 | -14,804.95 | -14,804.61 | -14,804.49 |
| M7211 | 201 | 1519 | 50.61 | **-16,465.75** | -16,470.14 | -16,465.85 | -16,466.11 | -16,466.29 |
| M7292 | 213 | 7572 | 44.14 | **-192,598.51** | -192,629.55 | -192,601.89 | -192,673.02 | -192,604.30 |
| M7929 | 428 | 15016 | 57.7 | **-410,939.26** | -410,983.84 | -410,949.34 | -411,028.18 | -410,945.26 |
| M7964 | 640 | 25260 | 41.43 | -1,327,204.51 | -1,327,314.04 | -1,327,210.58 | -1,327,375.92 | **-1,327,202.44** |
| M8012 | 213 | 2333 | 5.76 | **-67,060.36** | -67,070.90 | -67,060.78 | -67,072.40 | **-67,060.36** |
| M8385 | 212 | 19972 | 63.57 | **-347,340.89** | -347,360.26 | -347,376.10 | -347,515.64 | -347,353.57 |
| M8619 | 246 | 11829 | 65.9 | **-93,597.01** | -93,606.25 | **-93,597.01** | -93,600.99 | -93,597.29 |
| M8692 | 395 | 3583 | 14.73 | **-24,993.81** | -25,033.99 | -25,014.37 | -25,014.32 | -25,009.85 |
| M8703 | 215 | 1038 | 0.31 | **-17,399.39** | -17,416.29 | -17,399.58 | -17,403.57 | -17,399.41 |

| TreeBASE ID | #Taxa | #Sites | % Gaps / ambiguous characters | IQ-TREE with default stopping rule | RAxML | IQ-TREE restricted to RAxML time | PhyML | IQ-TREE restricted to PhyML time |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| M8975 | 405 | 3027 | 1.78 | **-92,430.53** | -92,454.00 | -92,431.41 | -92,525.99 | -92,431.59 |
| M8982 | 297 | 6954 | 42.72 | **-141,323.67** | -141,349.66 | **-141,323.67** | -141,328.39 | **-141,323.67** |
| M8984 | 201 | 3931 | 29.43 | **-21,997.97** | -22,004.58 | -21,999.10 | -22,005.05 | -21,999.24 |
| M9033 | 300 | 1394 | 7.1 | **-23,867.40** | -23,871.18 | -23,869.91 | -23,869.90 | -23,870.76 |
| M9142 | 235 | 1854 | 9.07 | **-18,985.30** | -18,985.57 | -18,989.29 | -18,987.18 | -18,992.48 |
| M9143 | 228 | 1223 | 11.52 | -8,917.67 | -8,917.71 | -8,923.28 | **-8,911.35** | -8,917.71 |
| M9915 | 504 | 2757 | 54.26 | -483,690.03 | **-483,684.95** | -483,720.07 | -483,795.81 | -483,738.35 |
| M10243 | 203 | 1771 | 0.4 | -16,344.85 | -16,348.02 | -16,344.91 | **-16,344.57** | -16,344.86 |
| M10434 | 544 | 5681 | 7.2 | **-139,349.11** | -139,362.30 | -139,352.27 | -139,363.43 | -139,352.25 |
| M10467 | 202 | 4074 | 45.87 | **-91,948.98** | -91,962.16 | -91,949.77 | -91,952.53 | -91,949.00 |
| M10933 | 229 | 2696 | 22.58 | **-94,316.14** | -94,342.72 | -94,323.67 | -94,362.75 | -94,320.81 |
| M11113 | 344 | 9778 | 15.7 | **-487,985.38** | -488,032.50 | -487,987.70 | -488,019.47 | -487,992.29 |
| M11745 | 316 | 1494 | 49.58 | **-19,004.08** | -19,014.98 | -19,005.73 | -19,015.87 | -19,004.84 |
| M11762 | 208 | 2468 | 0.06 | -20,050.65 | -20,061.46 | -20,050.65 | **-20,048.61** | -20,050.65 |
| M12051 | 699 | 6914 | 40.96 | -384,988.31 | -385,007.09 | -385,032.28 | -385,081.21 | **-384,987.48** |
| M12098 | 231 | 4108 | 38.01 | **-129,824.04** | -129,830.33 | -129,824.09 | -129,841.30 | -129,824.07 |
| M12388 | 324 | 1405 | 42.11 | **-9,609.98** | -9,620.77 | -9,610.81 | -9,612.25 | -9,610.15 |
| M13718 | 235 | 2309 | 37.25 | -100,203.82 | -100,215.25 | -100,206.13 | -100,224.21 | **-100,202.73** |
| M14164 | 204 | 5549 | 59.37 | **-40,356.16** | -40,367.22 | -40,358.50 | -40,371.17 | -40,357.91 |
| M14165 | 204 | 5611 | 41.84 | **-144,455.80** | -144,476.21 | -144,458.86 | -144,467.93 | -144,456.17 |
| M14582 | 372 | 61199 | 68.64 | **-656,241.64** | -656,332.90 | -656,243.70 | -656,312.55 | -656,241.69 |
| M14678 | 225 | 2673 | 25.51 | **-47,166.74** | -47,182.26 | -47,167.72 | -47,174.37 | -47,167.41 |

Table S2 TreeBASE protein alignments and average log-likelihoods. In bold face are the highest log-likelihood found for each alignment.

| TreeBASE ID | #Taxa | #Sites | % Gaps / ambiguous characters | IQ-TREE with default stopping rule | RAxML | IQ-TREE restricted to RAxML time | PhyML | IQ-TREE restricted to PhyML time |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| M510 | 57 | 430 | 9.38 | **-8,164.14** | -8,165.75 | **-8,164.14** | -8,175.26 | -8,164.17 |
| M1118 | 137 | 348 | 26.31 | **-12,837.91** | -12,840.76 | -12,838.72 | -12,845.97 | -12,839.32 |
| M1726 | 50 | 1000 | 37.18 | **-68,153.56** | -68,154.33 | -68,153.61 | -68,167.93 | -68,154.15 |
| M2358 | 55 | 714 | 20.72 | **-14,670.25** | -14,670.31 | **-14,670.25** | -14,677.96 | **-14,670.25** |
| M2593 | 56 | 386 | 2.98 | **-8,945.24** | -8,948.11 | -8,945.25 | -8,948.04 | -8,948.29 |
| M2926 | 105 | 899 | 43.08 | **-85,026.88** | -85,026.90 | -85,026.90 | -85,027.77 | -85,026.94 |
| M3113 | 77 | 9918 | 55.33 | **-361,280.00** | -361,297.06 | -361,281.64 | -361,347.19 | -361,294.78 |
| M3114 | 77 | 11234 | 55.77 | -434,506.92 | **-434,504.13** | -434,519.03 | -434,614.68 | -434,525.05 |
| M3807 | 82 | 591 | 41.38 | **-38,706.56** | -38,709.34 | -38,706.87 | -38,722.00 | -38,707.97 |
| M3810 | 55 | 271 | 21.31 | **-11,061.54** | -11,061.76 | **-11,061.54** | -11,061.55 | -11,063.98 |
| M4249 | 153 | 455 | 45.47 | **-57,701.68** | -57,704.83 | -57,702.29 | -57,718.75 | -57,703.21 |
| M4318 | 78 | 2295 | 3.97 | **-185,004.73** | **-185,004.73** | **-185,004.73** | -185,058.96 | -185,005.08 |
| M4325 | 73 | 230 | 1.05 | **-21,106.15** | **-21,106.15** | -21,106.15 | -21,112.61 | -21,106.55 |
| M4539 | 59 | 12428 | 19.66 | **-473,611.99** | -473,622.19 | **-473,611.99** | -473,662.13 | -473,622.59 |
| M4780 | 90 | 583 | 45.96 | **-45,725.34** | -45,726.37 | -45,725.36 | -45,742.72 | -45,726.26 |
| M4860 | 62 | 11544 | 18.61 | **-426,418.62** | **-426,418.62** | **-426,418.62** | -426,418.65 | **-426,418.62** |
| M4884 | 50 | 11827 | 34.80 | **-242,169.69** | **-242,169.69** | **-242,169.69** | -242,174.90 | -242,173.32 |
| M5379 | 60 | 7776 | 13.91 | -279,270.38 | **-279,270.36** | -279,270.39 | -279,299.37 | -279,282.01 |
| M6416 | 57 | 126 | 7.10 | **-5,181.98** | -5,182.79 | -5,182.93 | -5,186.26 | -5,184.03 |
| M7078 | 77 | 12457 | 13.04 | **-379,457.82** | -379,463.94 | -379,458.13 | -379,477.72 | -379,459.36 |
| M7729 | 62 | 2973 | 29.31 | **-110,353.19** | -110,361.23 | -110,353.19 | -110,379.37 | -110,353.20 |
| M8175 | 194 | 665 | 29.40 | -26,504.23 | -26,506.99 | -26,504.27 | **-26,503.94** | -26,504.89 |
| M8461 | 89 | 5699 | 29.89 | **-307,038.70** | -307,047.10 | -307,040.16 | -307,126.42 | -307,056.90 |
| M8569* | 164 | 383 | 44.67 | **-40,594.84** | -40,595.64 | -40,595.27 | -40,595.81 | -40,596.53 |

| TreeBASE ID | #Taxa | #Sites | % Gaps / ambiguous characters | IQ-TREE with default stopping rule | RAxML | IQ-TREE restricted to RAxML time | PhyML | IQ-TREE restricted to PhyML time |
|---:|---:|---:|---:|---:|---:|---:|---:|---:|
| M8630 | 50 | 21154 | 0.22 | **-588,675.92** | -588,675.92 | **-588,675.92** | -589,298.44 | -588,831.51 |
| M9973 | 60 | 327 | 3.42 | **-13,077.17** | -13,077.98 | -13,077.19 | -13,077.18 | -13,077.26 |
| M10236 | 59 | 164 | 62.23 | **-5,113.01** | -5,113.90 | -5,113.93 | -5,117.14 | -5,114.20 |
| M10273 | 169 | 11009 | 17.16 | **-650,541.12** | **-650,541.12** | **-650,541.12** | -650,541.14 | **-650,541.12** |
| M10372 | 169 | 22426 | 15.93 | **-1,359,736.89** | -1,359,736.90 | **-1,359,736.89** | -1,359,796.74 | -1,359,736.90 |
| M10866 | 88 | 3329 | 3.26 | -150,463.11 | **-150,463.11** | -150,463.11 | -150,463.12 | -150,463.11 |
| M11012 | 55 | 11500 | 19.55 | **-495,773.15** | -495,787.73 | -495,778.73 | -495,824.51 | -495,778.26 |
| M11013 | 55 | 8741 | 19.14 | **-251,347.86** | **-251,347.86** | **-251,347.86** | -251,347.87 | **-251,347.86** |
| M11335 | 99 | 696 | 27.19 | **-41,474.35** | -41,475.04 | -41,474.41 | -41,499.34 | -41,476.80 |
| M11336 | 95 | 268 | 0.00 | **-14,847.24** | -14,849.76 | **-14,847.24** | -14,847.24 | -14,853.97 |
| M11338 | 100 | 567 | 48.18 | **-32,213.69** | -32,217.12 | -32,215.33 | -32,251.85 | -32,217.06 |
| M11341 | 100 | 699 | 26.36 | **-53,103.85** | -53,105.13 | -53,104.67 | -53,131.42 | -53,113.88 |
| M11342 | 91 | 323 | 0.00 | **-24,050.26** | -24,050.42 | **-24,050.26** | -24,056.54 | **-24,050.26** |
| M11344 | 84 | 691 | 50.36 | **-42,681.83** | -42,683.91 | -42,681.85 | -42,687.96 | -42,683.34 |
| M11595 | 66 | 463 | 12.87 | **-27,727.92** | -27,727.92 | **-27,727.92** | **-27,727.92** | **-27,727.92** |
| M11596 | 62 | 439 | 17.46 | **-34,244.66** | **-34,244.66** | **-34,244.66** | -34,244.66 | **-34,244.66** |
| M11740 | 138 | 4427 | 2.62 | -376,122.31 | -376,125.26 | **-376,121.96** | -376,125.96 | -376,128.09 |
| M12103 | 97 | 199 | 0.00 | **-17,447.60** | -17,448.40 | -17,449.18 | -17,448.93 | -17,459.79 |
| M12104 | 93 | 349 | 0.00 | **-16,139.84** | -16,144.58 | -16,140.05 | -16,144.77 | -16,145.06 |
| M12376 | 116 | 327 | 37.23 | **-20,453.87** | -20,454.54 | -20,453.88 | -20,455.30 | -20,453.91 |
| M13804 | 78 | 1889 | 16.89 | **-113,431.86** | -113,433.54 | **-113,431.86** | -113,439.18 | **-113,431.86** |

* We removed the sequence *Homo_sapiens_GSTA3* from the original multiple sequence alignment because it was obviously unaligned.