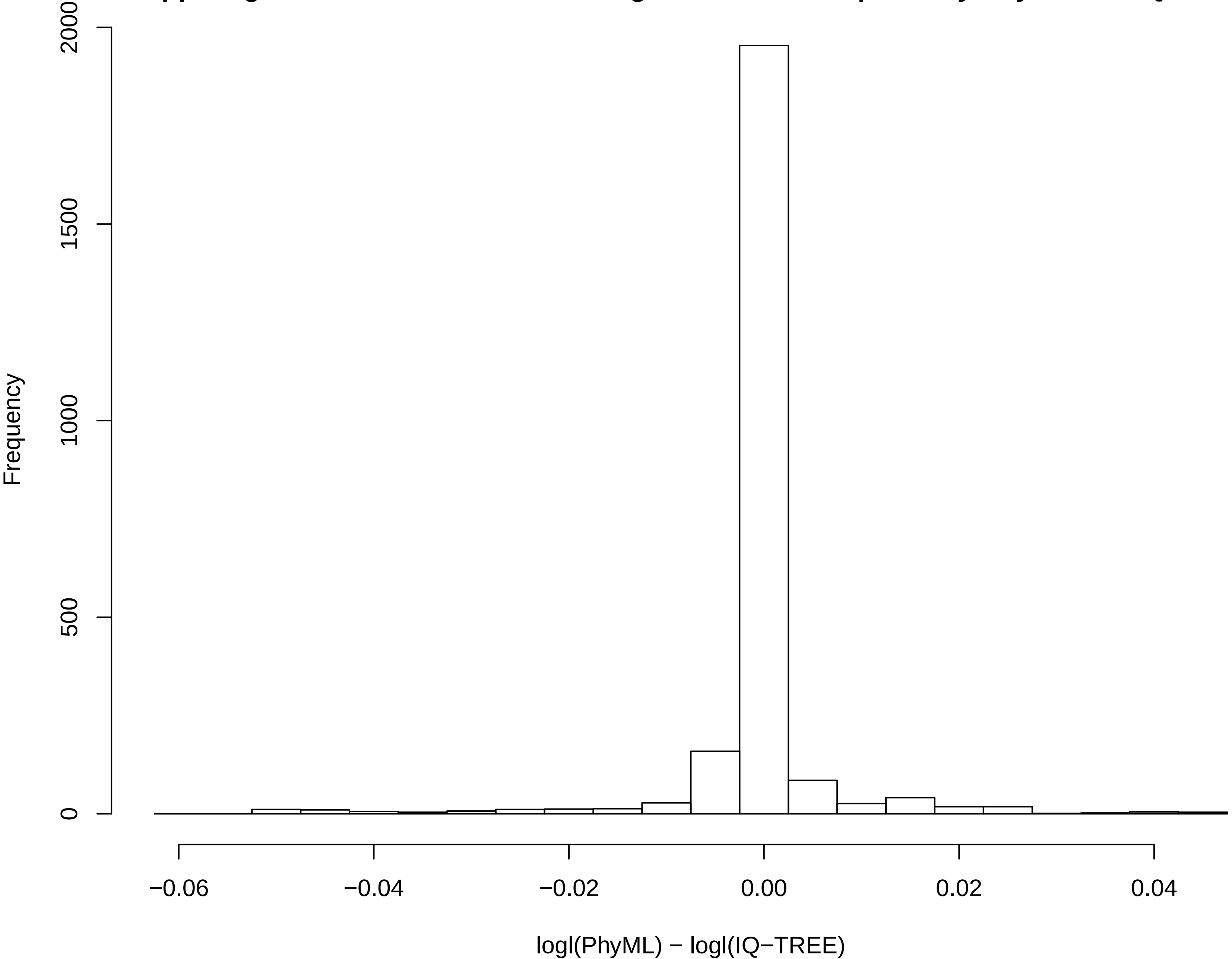
Supplementary figures

Supplementary Figure S0. Distribution of differences between log-likelihood computed by PhyML and IQ-TREE for the same tree and model parameters. Trees and model parameters are taken from results used in Figure 2.

Supplementary Figure S1. Log-likelihood differences for IQ-TREE with equal CPU times as RAxML times (a,b) or PhyML times (c,d): S1a, and S1b show the log-likelihood differences of IQ-TREE against RAxML using the 70 DNA (a) and 45 AA (b) alignments. S1c and S1d show the same against PhyML. The alignments are ordered by the average log-likelihood differences. The whiskers at each point show the standard errors of the differences. If the log-likelihood differences are smaller than 0.01 the results are regarded as being equal. S1a to S1d relate to the Subfigures 1a to 1d in the main text.

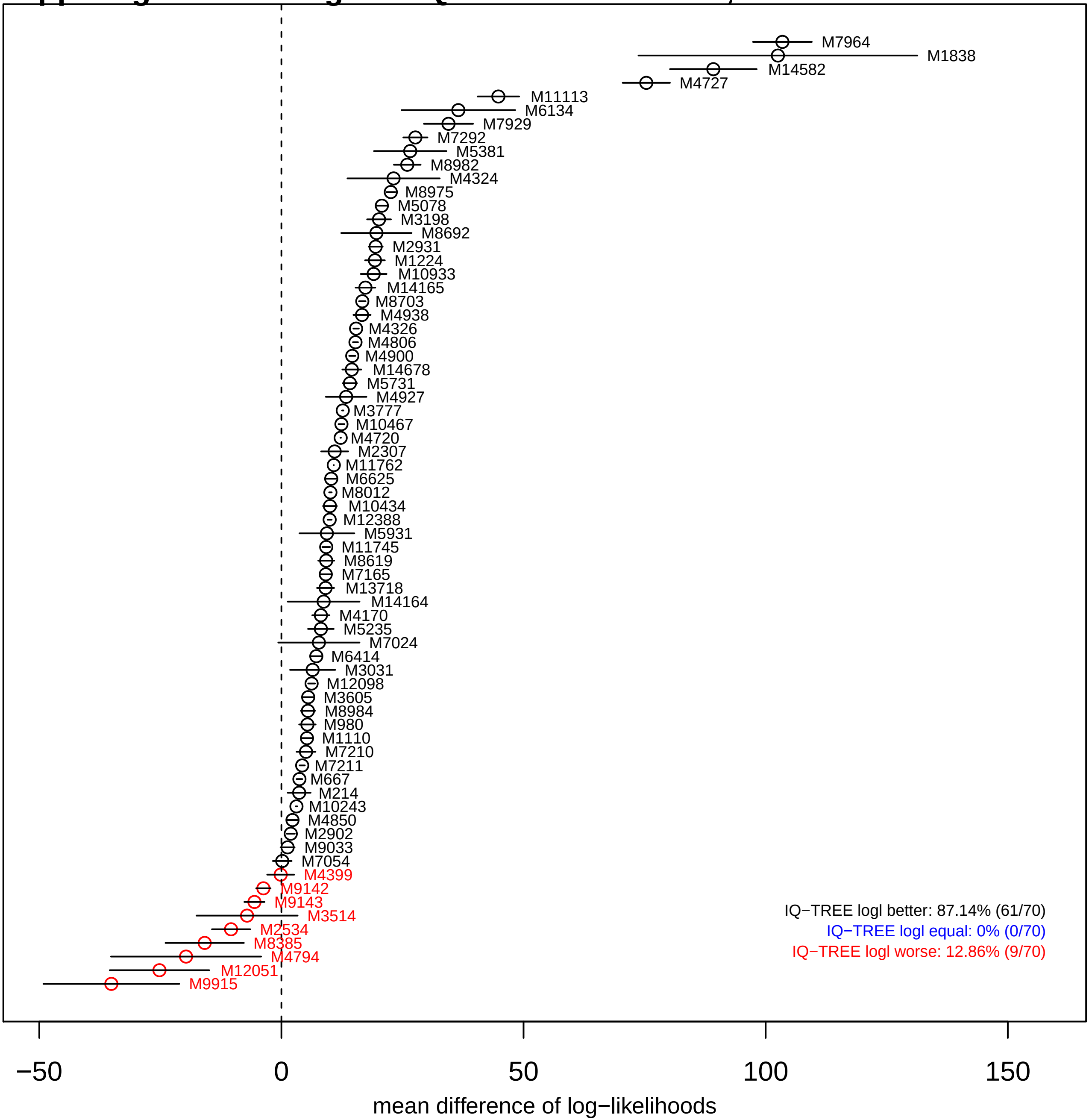
Supplementary Figure S2. Log-likelihood differences for IQ-TREE with CPU times determined by its stopping rule: S2a, and S2b show the log-likelihood differences of IQ-TREE against RAxML using the 70 DNA (a) and 45 AA (b) alignments. S2c and S2d show the same against PhyML. The alignments are ordered by the average log-likelihood differences. The whiskers at each point show the standard errors of the differences. If the log-likelihood differences are smaller than 0.01 the results are regarded as being equal. S2a to S2d relate to the Subfigures 2a to 2d in the main text.

Supplementary Figure S3. Performance of IQ-TREE versus PhyML with random starting trees for 70 DNA (a) and 45 AA (b) alignments. Each dot in the main diagrams represents for one alignment the mean differences of the CPU times (y-axis) and of the mean differences of log-likelihoods (x-axis) of the reconstructed trees by the programs compared. The whiskers at each point show the standard errors of the differences. The histograms at the top and the side present the marginal frequencies. Dots to the right of the vertical dashed line represent alignments where IQ-TREE found a higher likelihood. If a dot is below the horizontal dashed line the reconstruction by IQ-TREE was faster. Percentages in the quadrants of histograms denote the fraction of alignments in that region. Percentages on the dashed line reflect the number of alignments where log-likelihood differences are smaller than 0.01. To allow this analysis (--rand_start --n_rand_start=1 --s spr) the source code of PhyML had to be fixed to perform and output a proper tree search from a random starting tree.

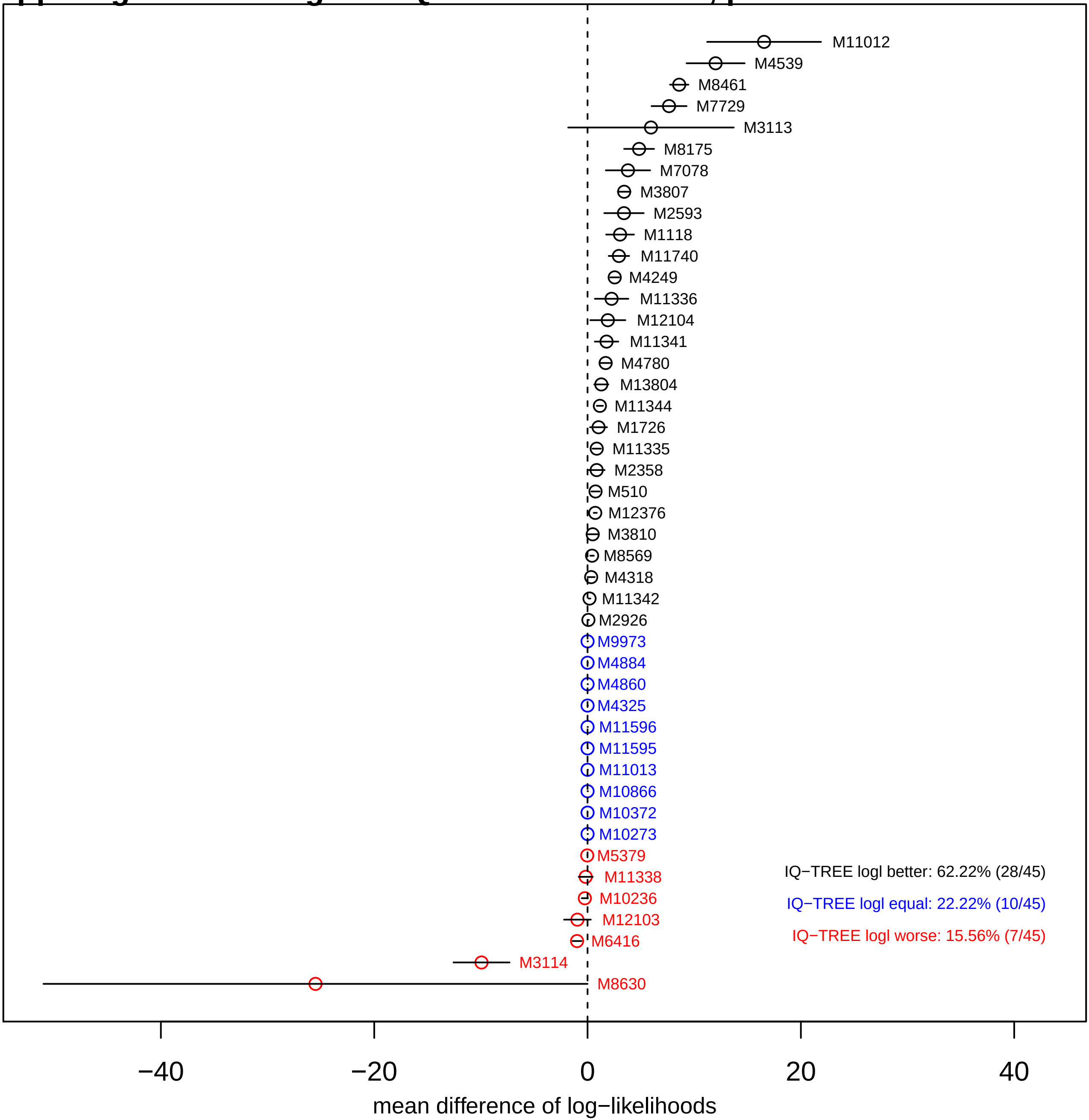


Suppl. Fig. S0: Differences between log−likelihood computed by PhyML and IQ−TREE

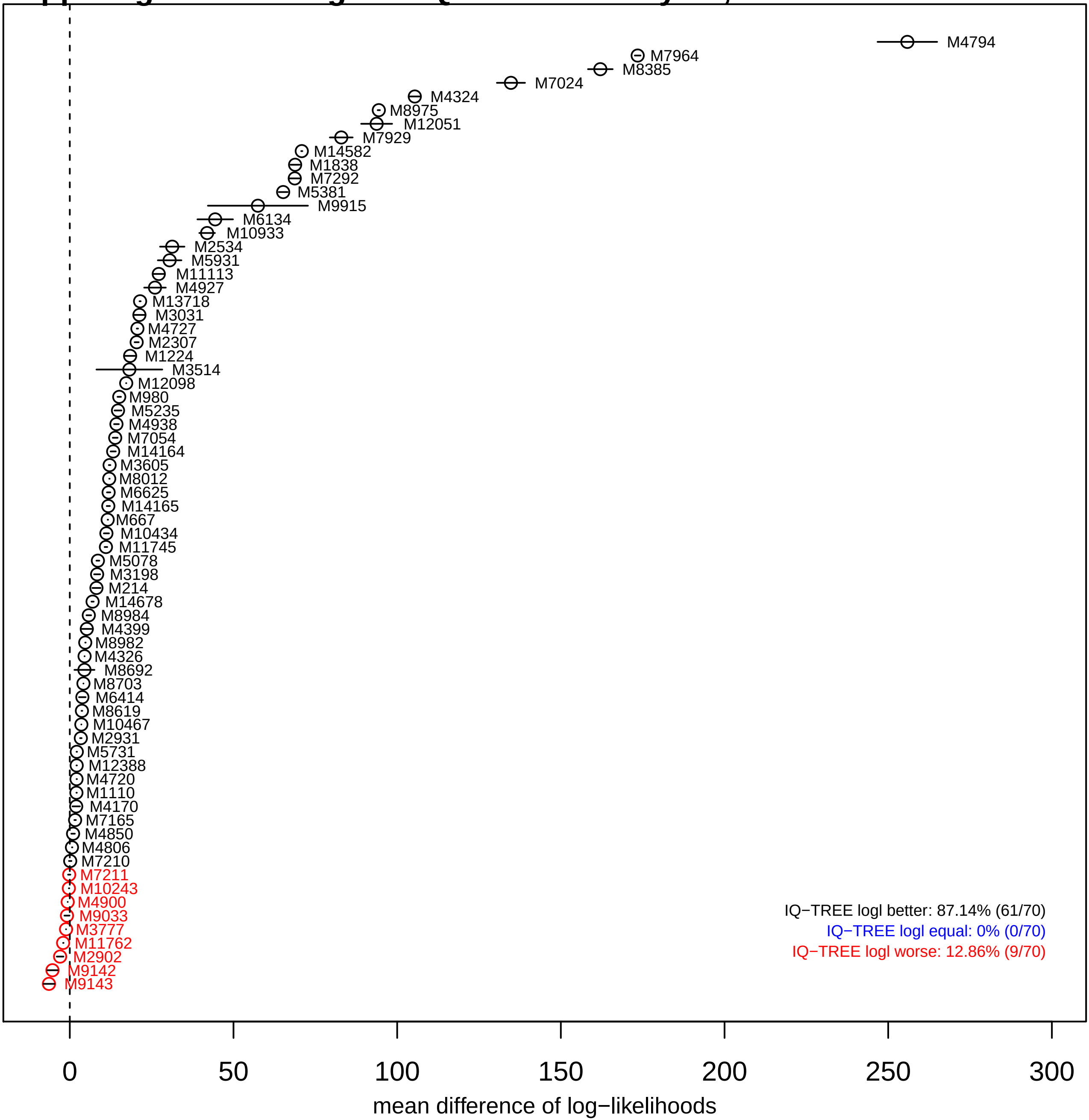
Suppl. Fig. S1a: for Fig. 1a: IQ−TREE vs. RAxML, DNA/restricted runtime



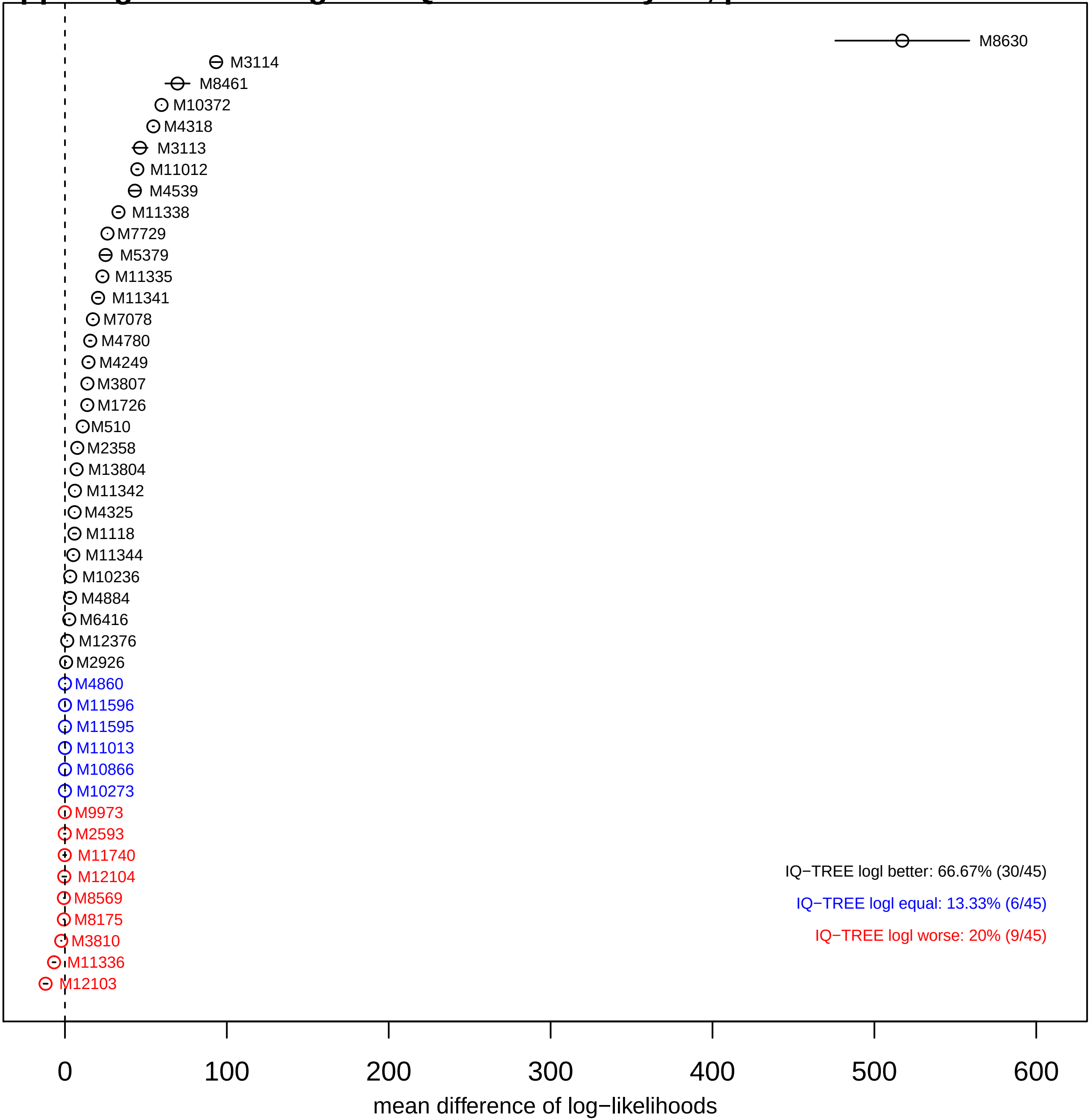
Suppl. Fig. S1b: for Fig. 1b: IQ−TREE vs. RAxML, protein/restricted runtime



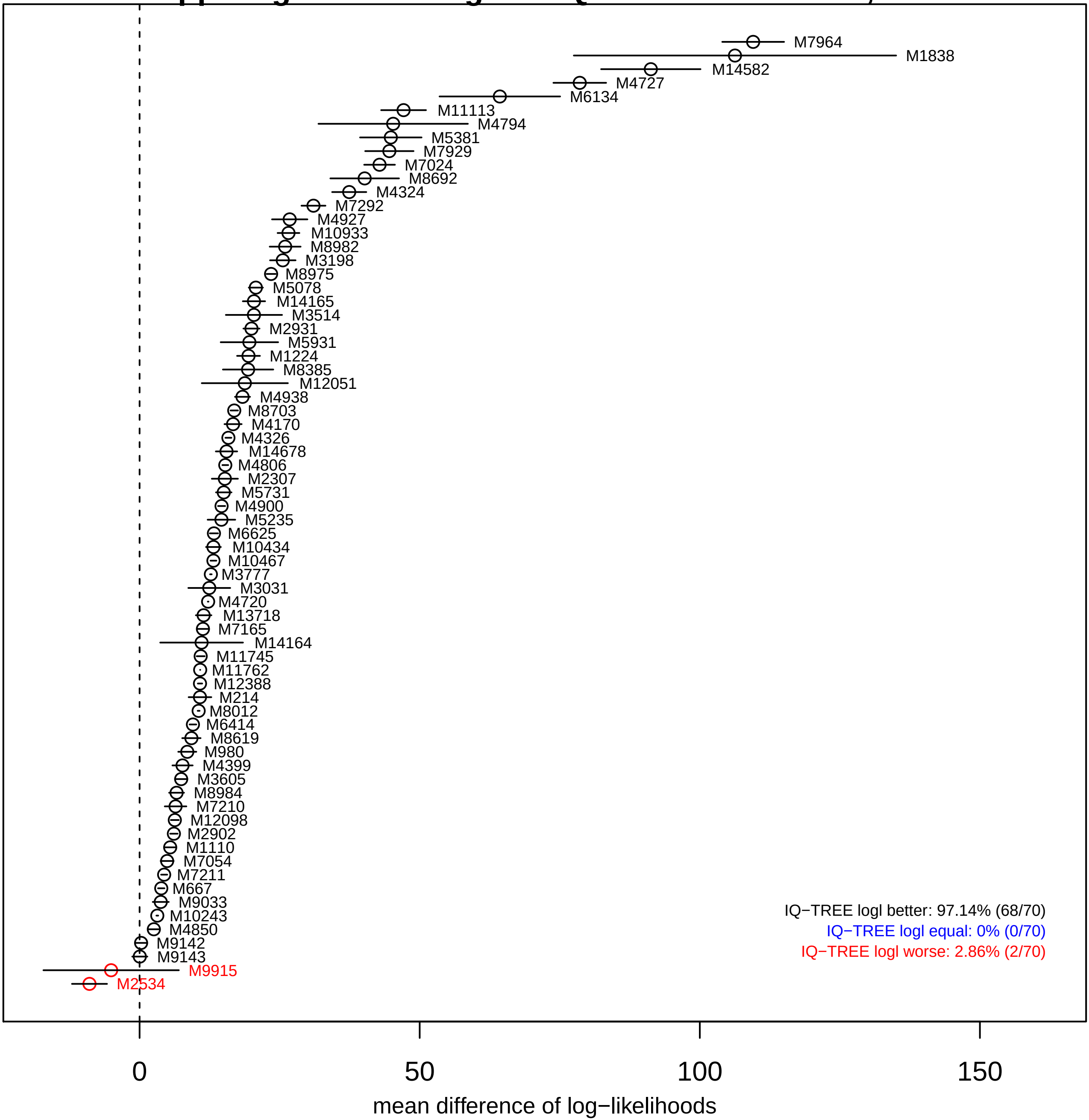
Suppl. Fig. S1c: for Fig. 1c: IQ−TREE vs. PhyML, DNA/restricted runtime



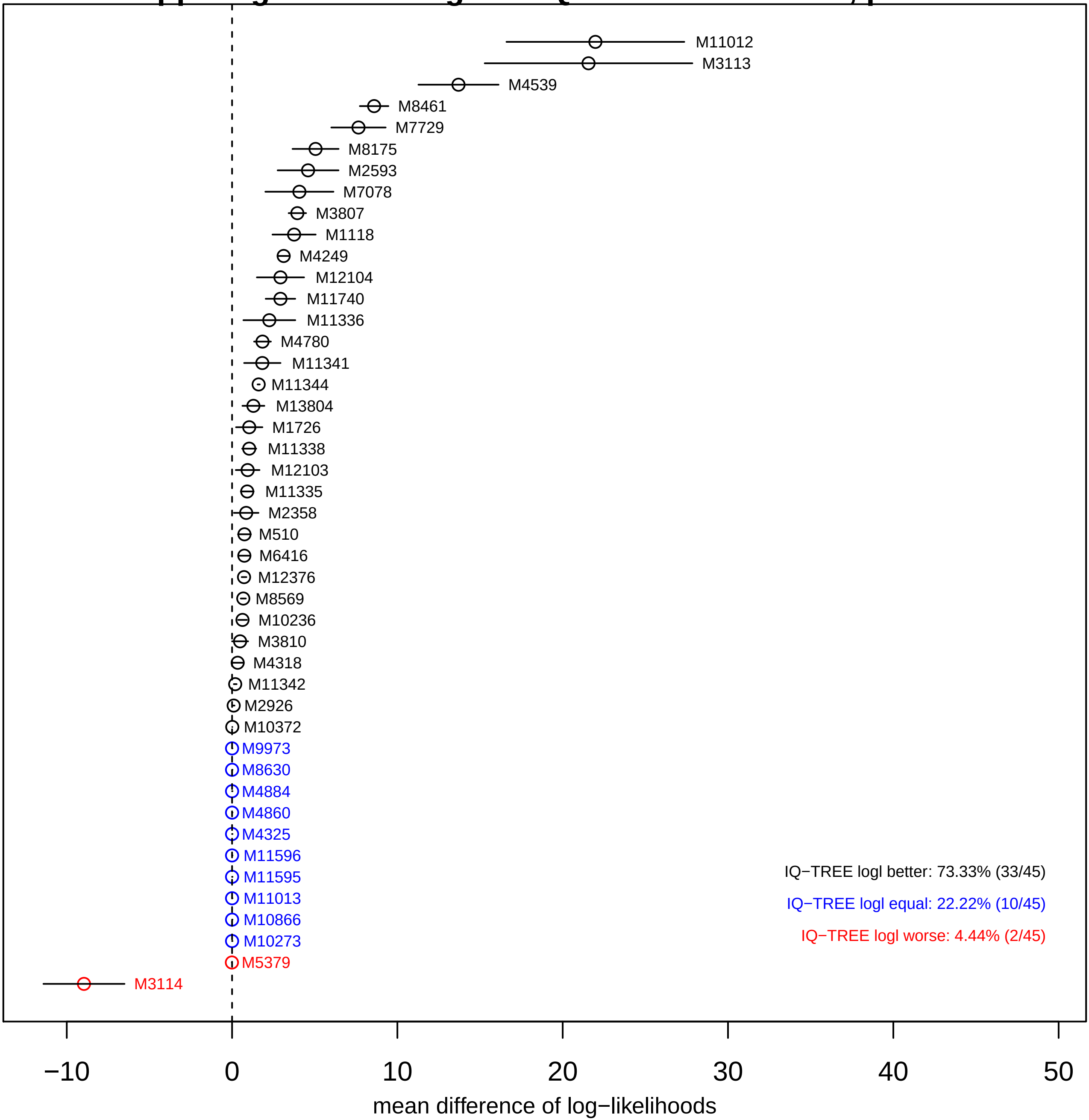
Suppl. Fig. S1d: for Fig. 1d: IQ−TREE vs. PhyML, protein/restricted runtime



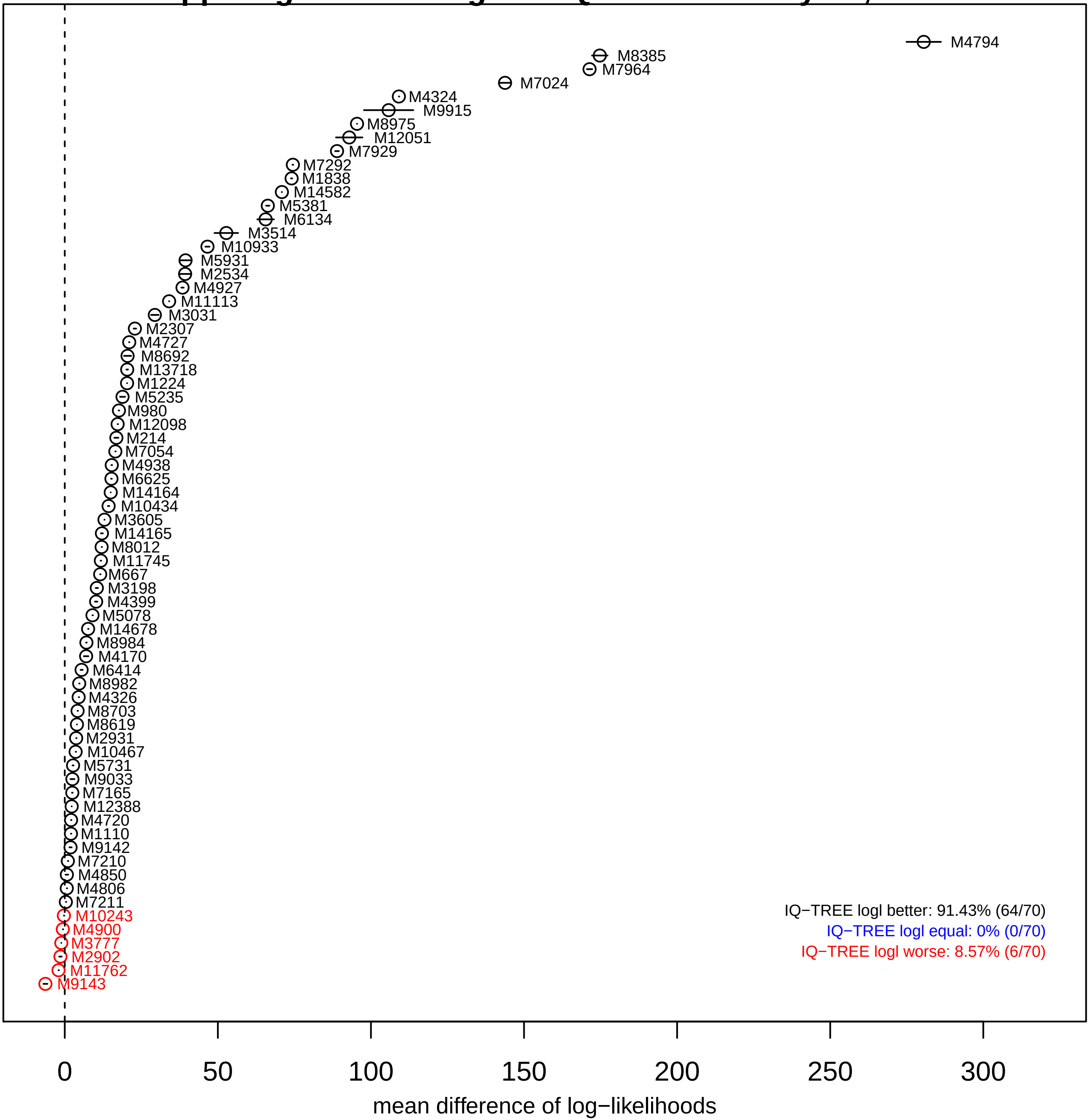
Suppl. Fig. S2a: for Fig. 2a: IQ−TREE vs. RAxML, DNA



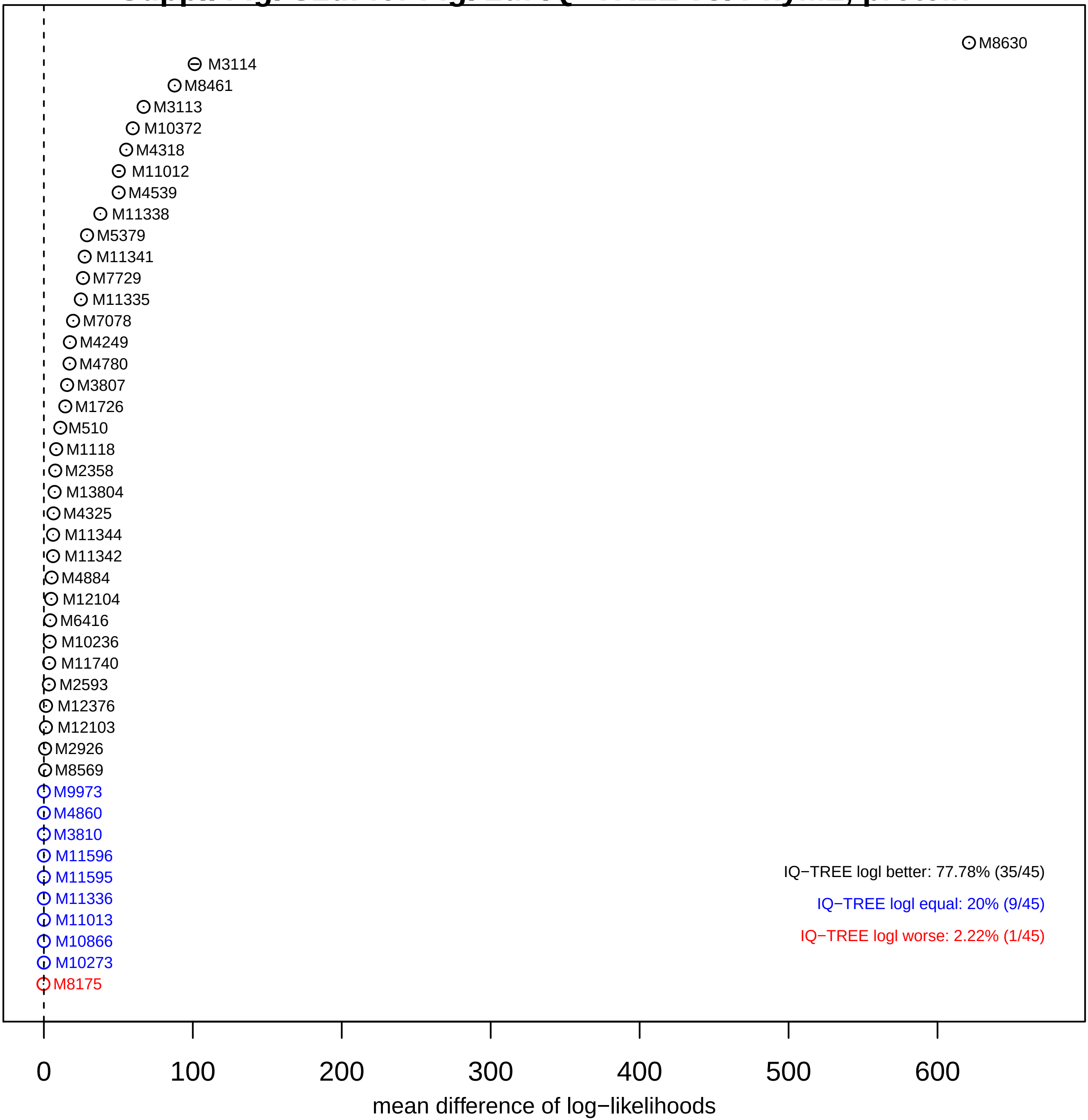
Suppl. Fig. S2b: for Fig. 2b: IQ−TREE vs. RAxML, protein

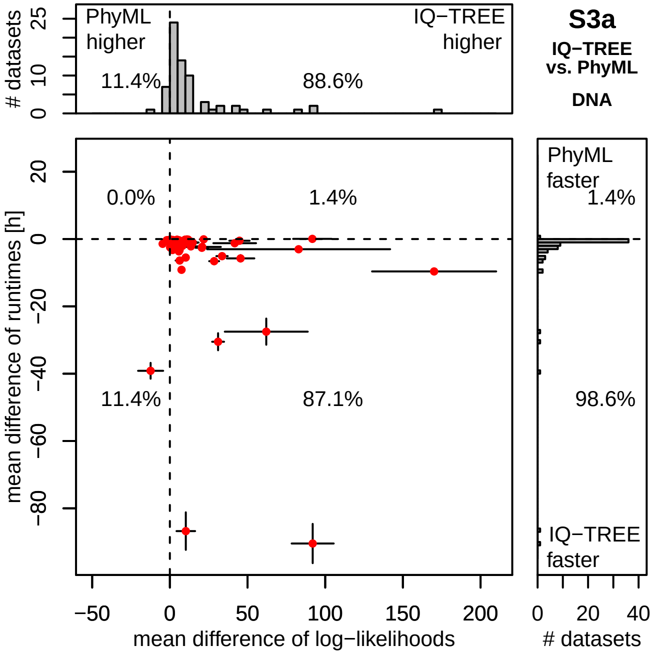


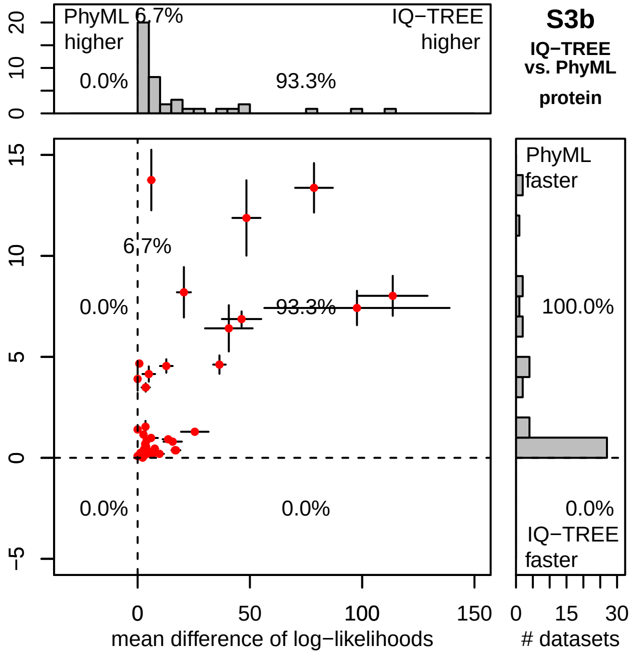
Suppl. Fig. S2c: for Fig. 2c: IQ−TREE vs. PhyML, DNA



Suppl. Fig. S2d: for Fig. 2d: IQ−TREE vs. PhyML, protein




S3a
IQ−TREE
vs. PhyML
DNA
PhyML
higher
IQ−TREE
higher
11.4%
88.6%
datasets
0
10
25
0.0%
1.4%
11.4%
87.1%
mean difference of runtimes [h]
20
0
−20
−40
−60
−80
−50
0
50
100
150
200
mean difference of log−likelihoods
PhyML
faster
1.4%
98.6%
IQ−TREE
faster
0
20
40
datasets


S3b
IQ−TREE
vs. PhyML
protein
PhyML
higher
6.7%
IQ−TREE
higher
0.0%
93.3%
0
10
20
6.7%
0.0%
93.3%
0.0%
0.0%
15
10
5
0
−5
0
50
100
150
mean difference of log−likelihoods
PhyML
faster
100.0%
0.0%
IQ−TREE
faster
0
15
30
datasets