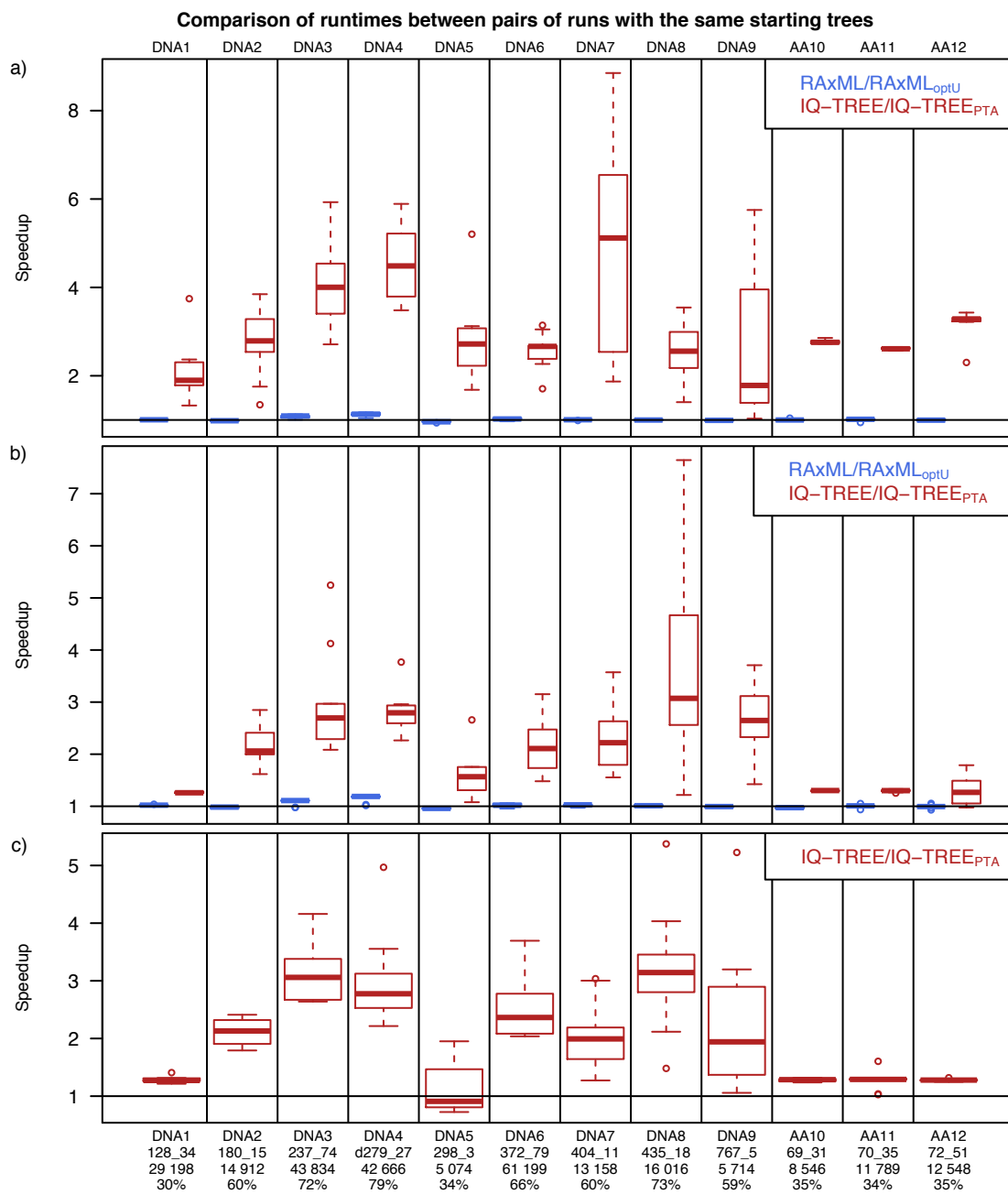


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Additional plots for a pairwise comparison of runs with the same starting trees.



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Figure S1. Runtime ratios for RAxML/RAxML_{optU} and IQ-TREE/IQ-TREE_{PTA} for the same

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starting tree and same set of 100 starting trees respectively under (a) EUL, (b) EL-equal and (c) EL-

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proportional partition models. Each boxplot shows the result of 10 ratios for each program. Ratios

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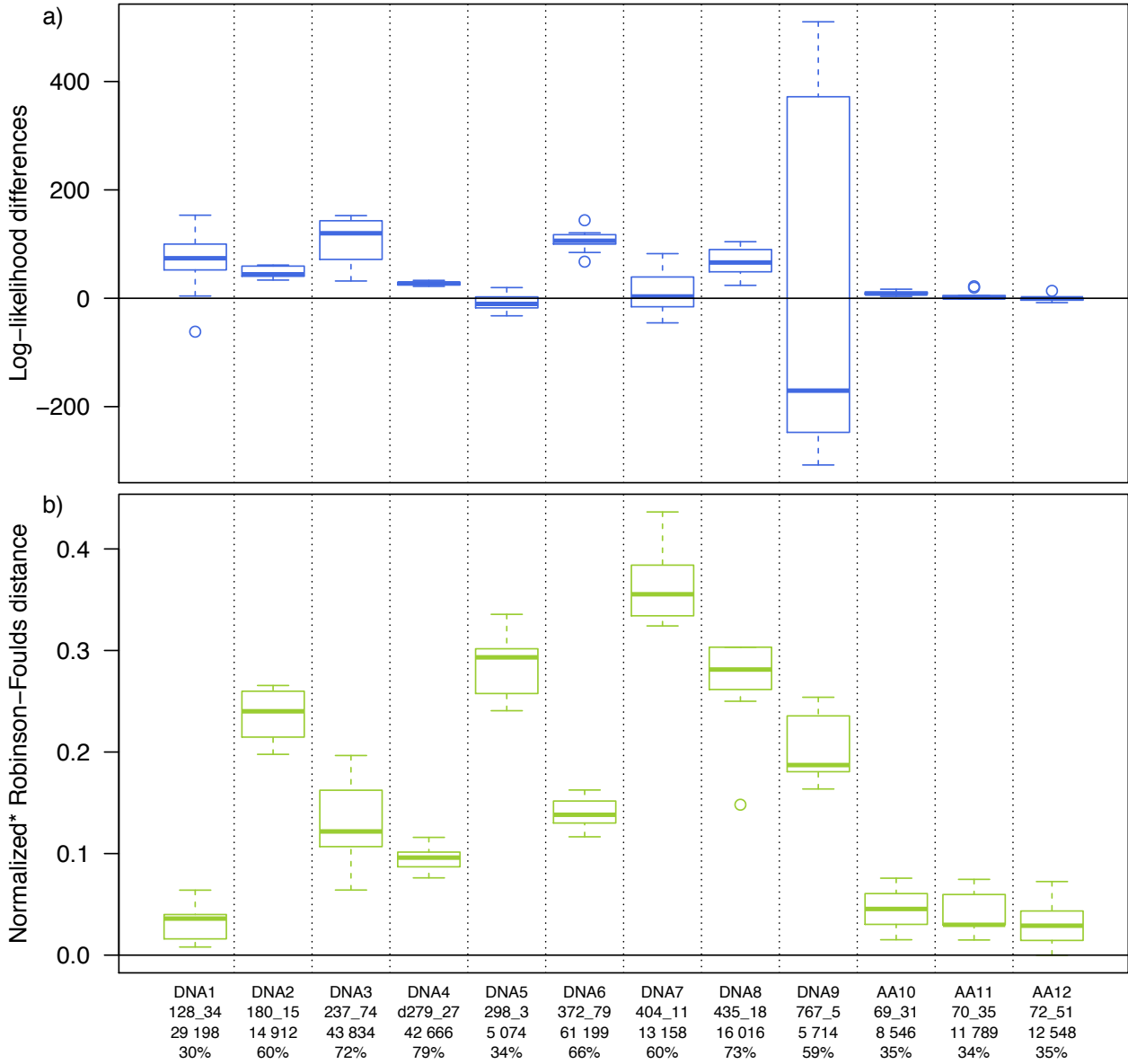
larger than 1 indicate instances where RAxML and IQ-TREE are slower than RAxML_{optU} and IQ-

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TREE_{PTA} respectively.

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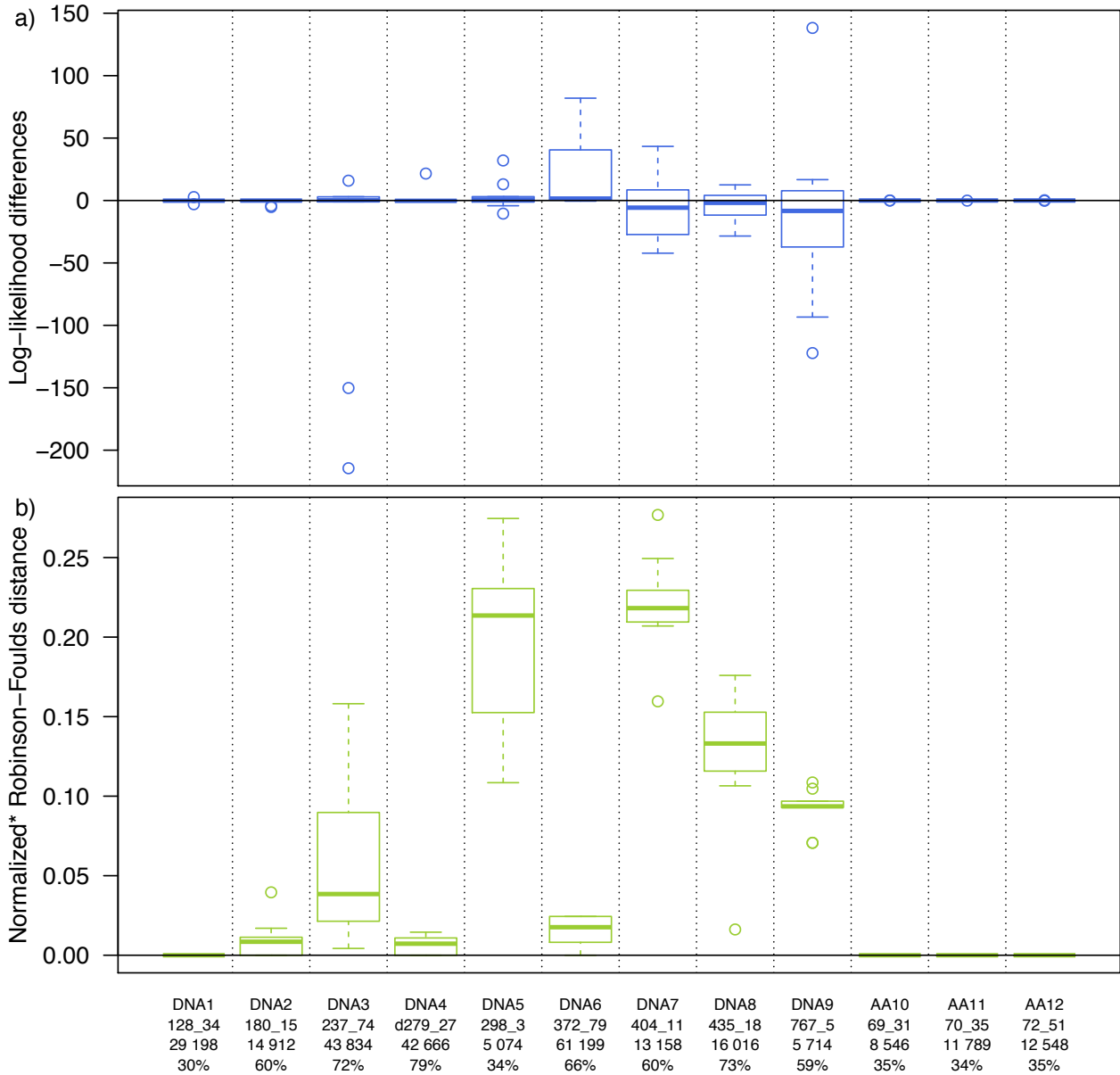
Comparison of IQ-TREE and IQ-TREE_{PTA} runs under the EUL model



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 11 **Figure S2. (a)** Log-likelihood differences for IQ-TREE and IQ-TREE_{PTA} for the same set of 100
 12 starting trees under the EUL model. Each boxplot shows the result of 10 log-likelihood differences.
 13 Differences larger than 0 indicate instances where IQ-TREE_{PTA} has higher log-likelihood. **(b)**
 14 Robinson-Foulds distances for IQ-TREE and IQ-TREE_{PTA} ML trees, normalized by $2(n - 3)$,
 15 where n is the number of taxa of each alignment.

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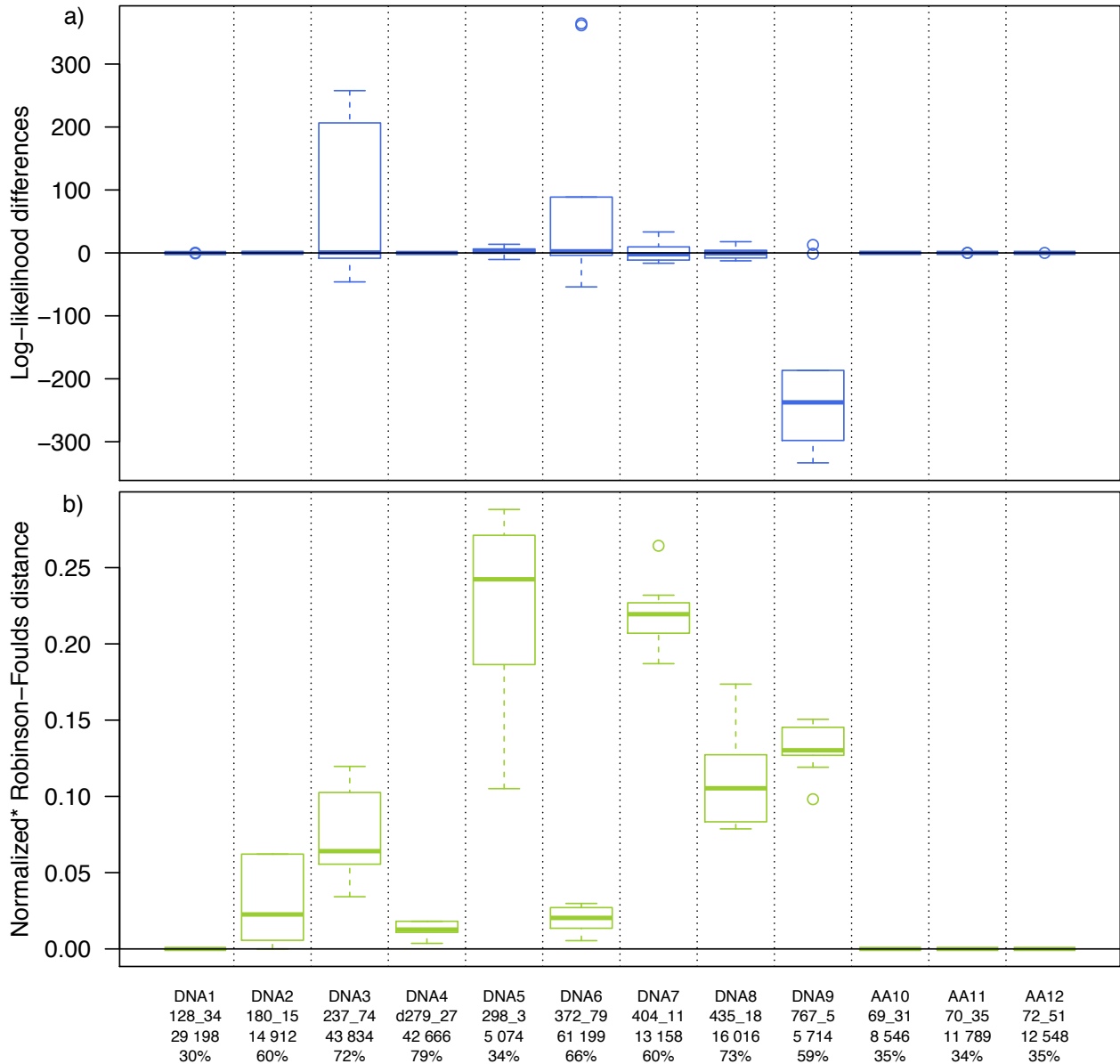
Comparison of IQ-TREE and IQ-TREE_{PTA} runs under the EL-equal model



17

18 **Figure S3. (a)** Log-likelihood differences for IQ-TREE and IQ-TREE_{PTA} for the same set of 100
 19 starting trees under the EL-equal model. Each boxplot shows the result of 10 log-likelihood
 20 differences. Differences larger than 0 indicate instances where IQ-TREE_{PTA} has higher log-
 21 likelihood. **(b)** Robinson-Foulds distances for IQ-TREE and IQ-TREE_{PTA} ML trees, normalized by
 22 $2(n - 3)$, where n is the number of taxa of each alignment.

Comparison of IQ-TREE and IQ-TREE_{PTA} runs under the EL-proportional model



23

24 **Figure S4. (a)** Log-likelihood differences for IQ-TREE and IQ-TREE_{PTA} for the same set of 100
 25 starting trees under the EL-proportional model. Each boxplot shows the result of 10 log-likelihood
 26 differences. Differences larger than 0 indicate instances where IQ-TREE_{PTA} has higher log-
 27 likelihood. **(b)** Robinson-Foulds distances for IQ-TREE and IQ-TREE_{PTA} ML trees, normalized by
 28 $2(n - 3)$, where n is the number of taxa of each alignment.