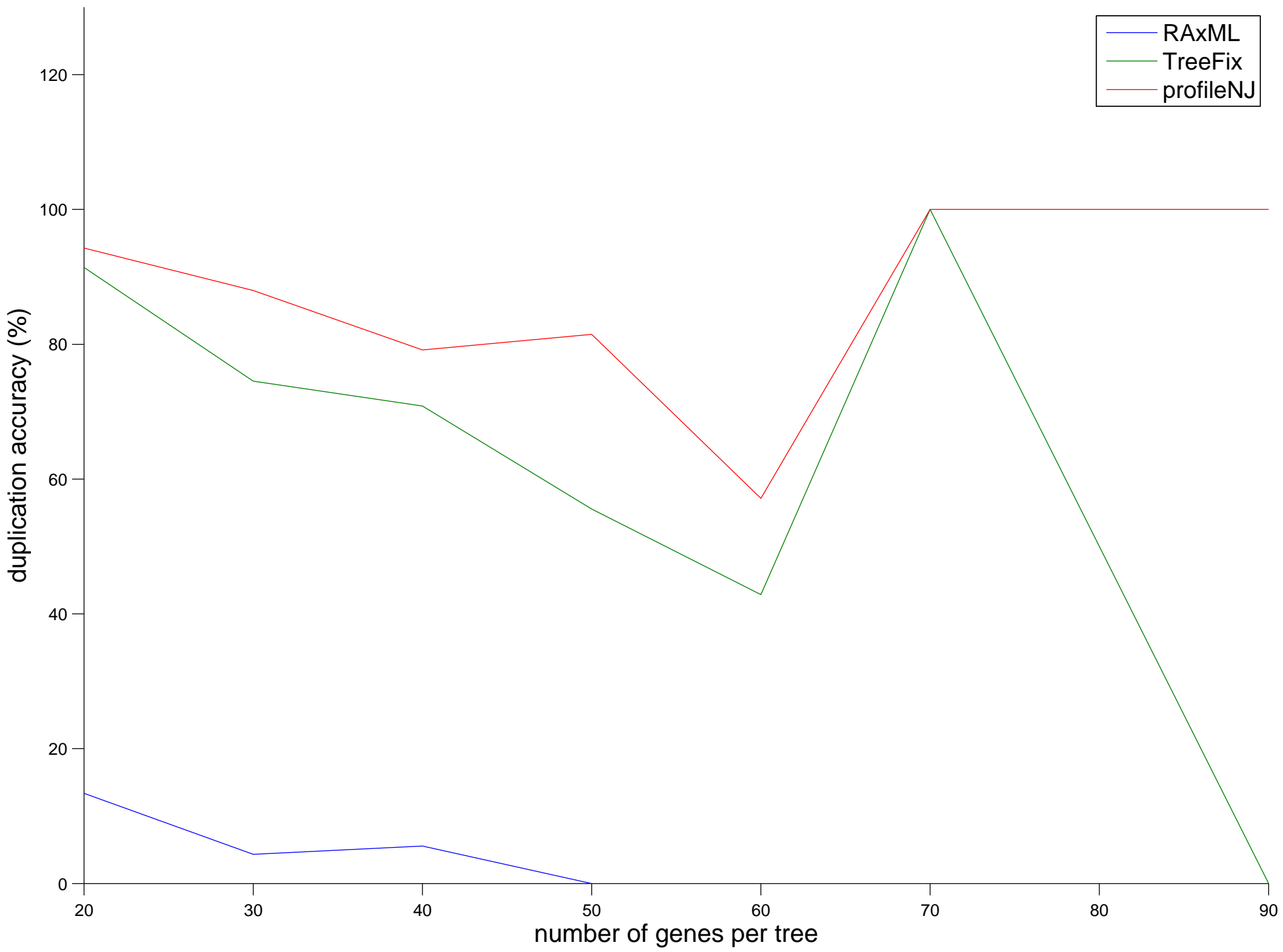
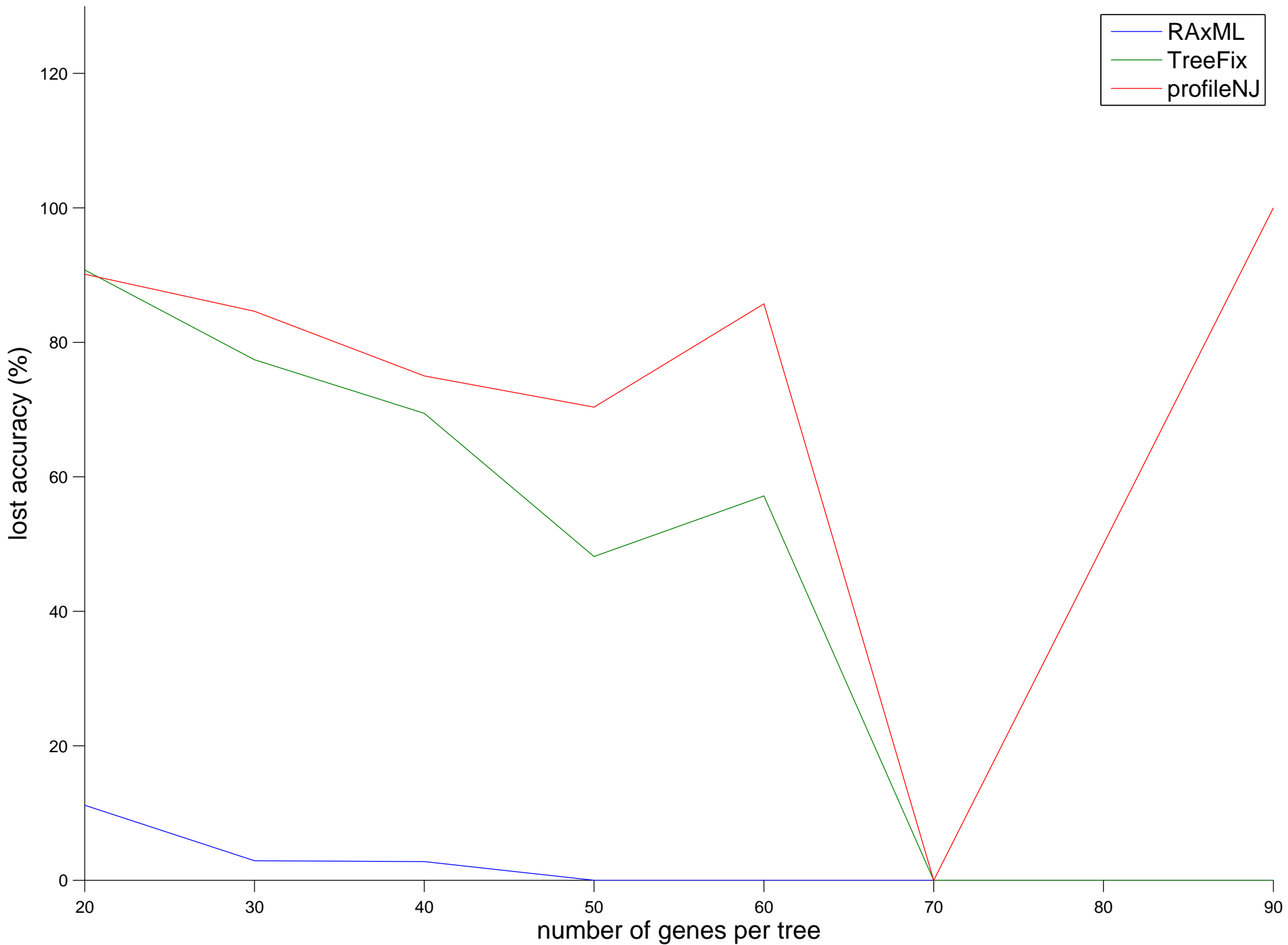


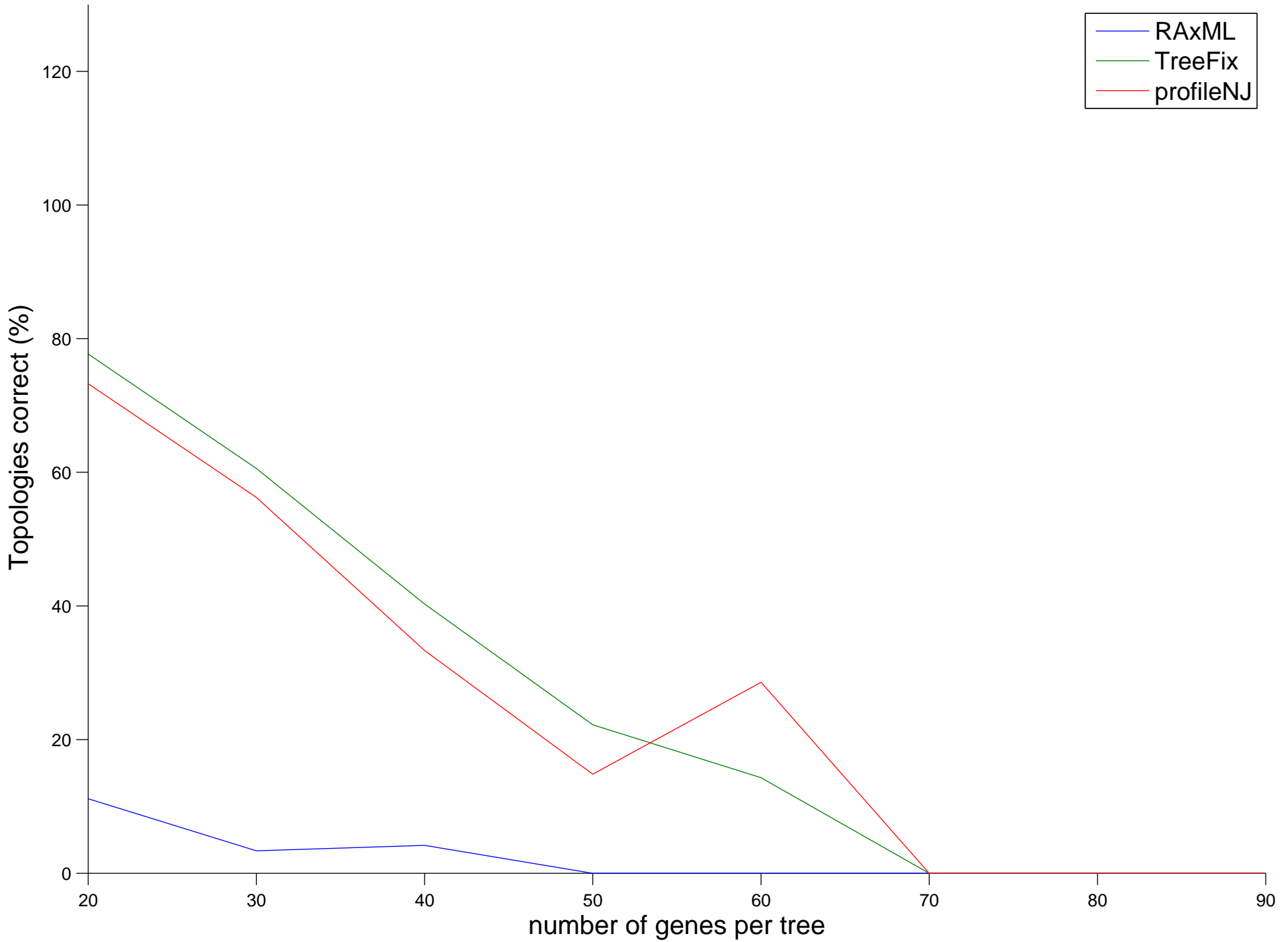
Accuracy of inferred duplication for gene trees of increasing size for simulated fungi dataset



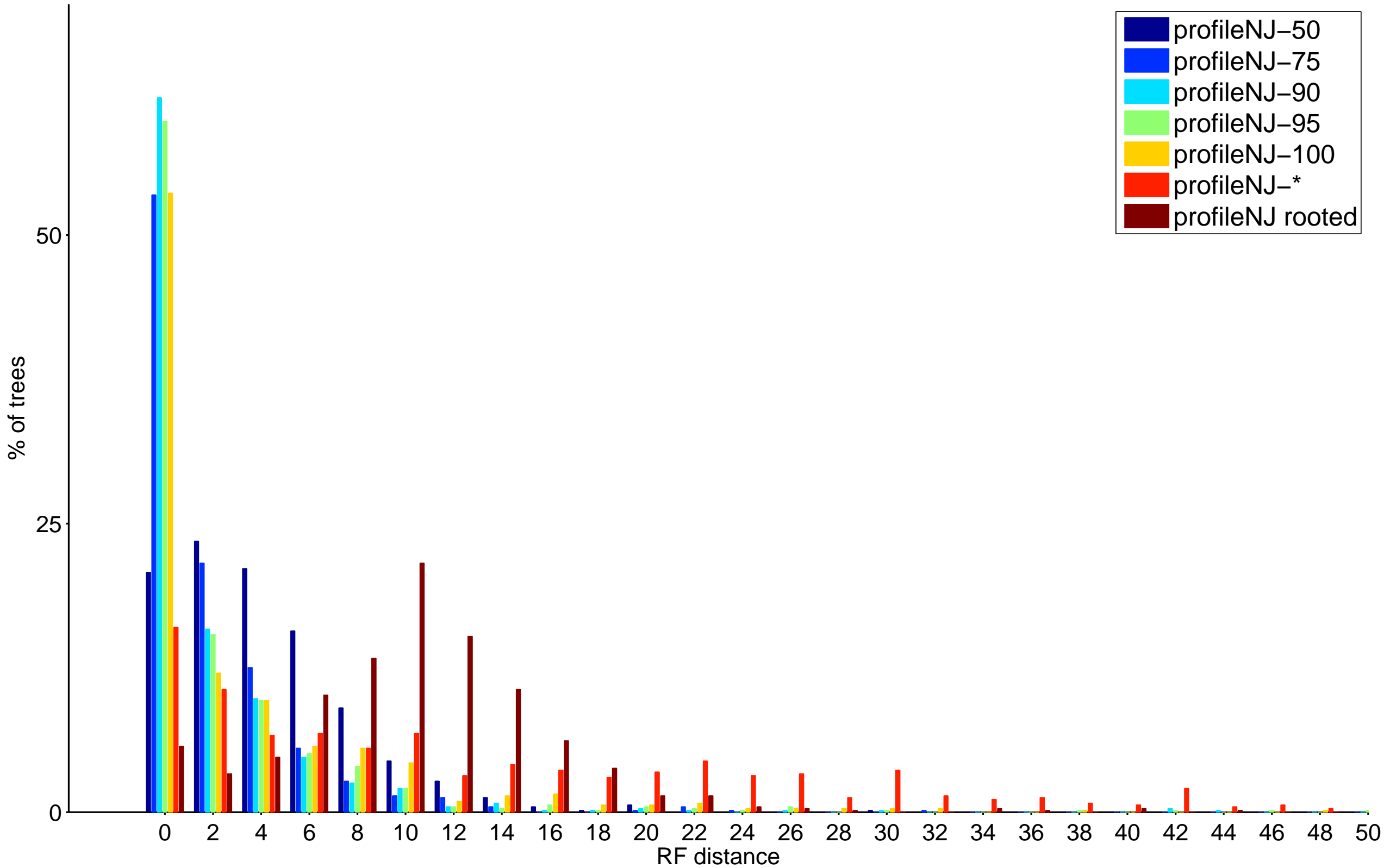
Accuracy of inferred lost for gene trees of increasing size for simulated fungi dataset



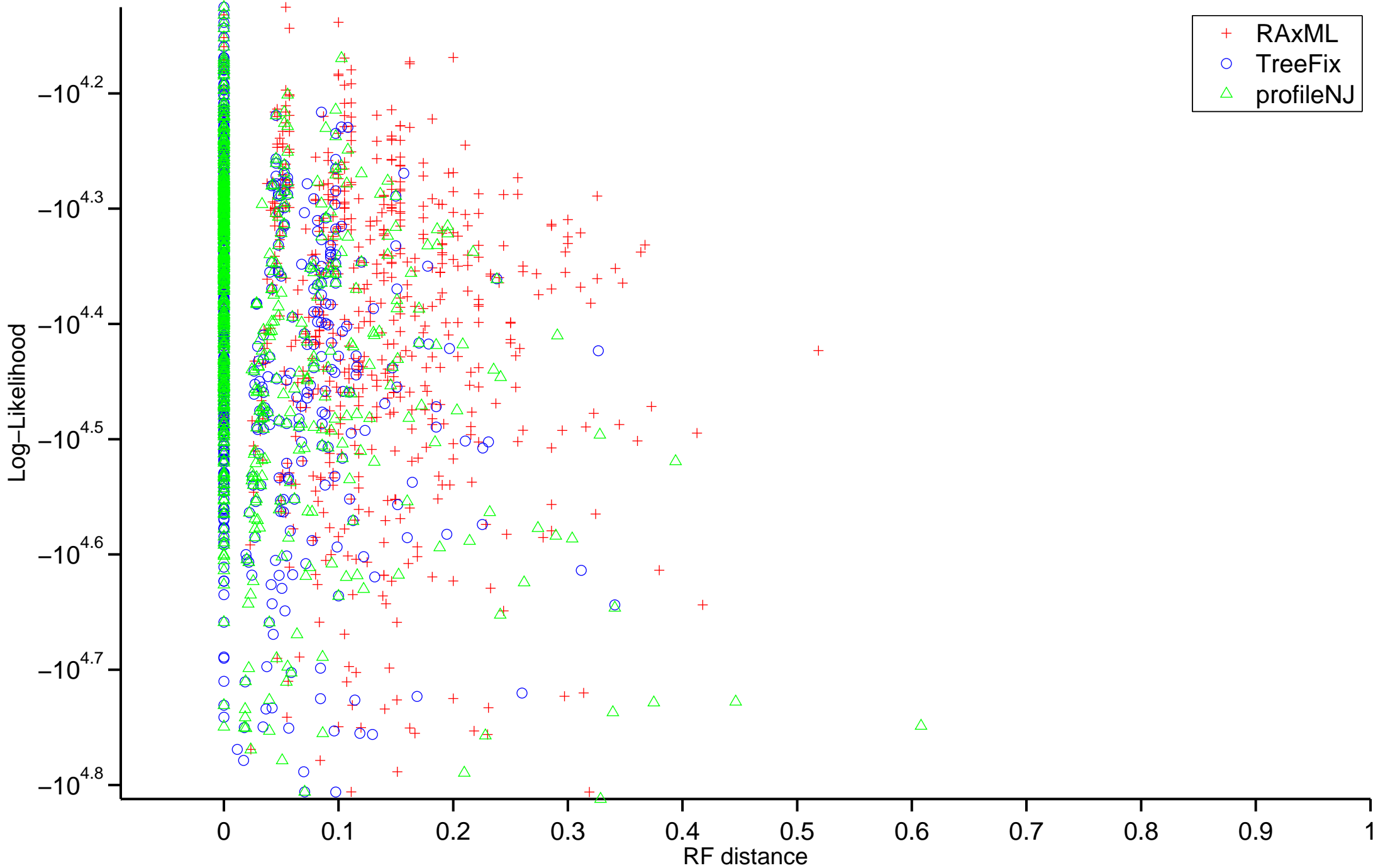
Accuracy of the inferred topology for gene trees of increasing size for simulated fungi dataset



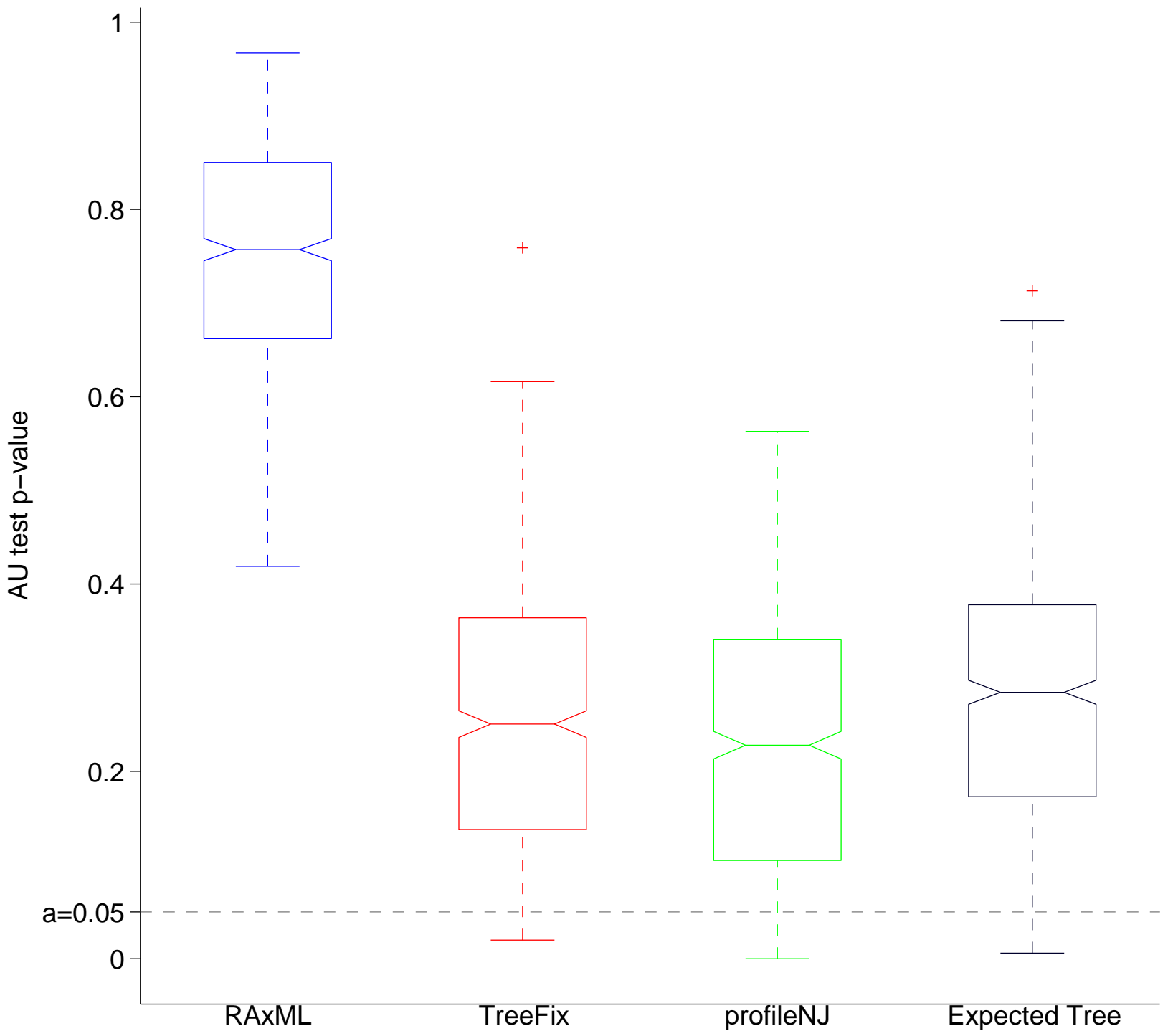
RF comparision between TreeSolver, TreeFix and RAxML method



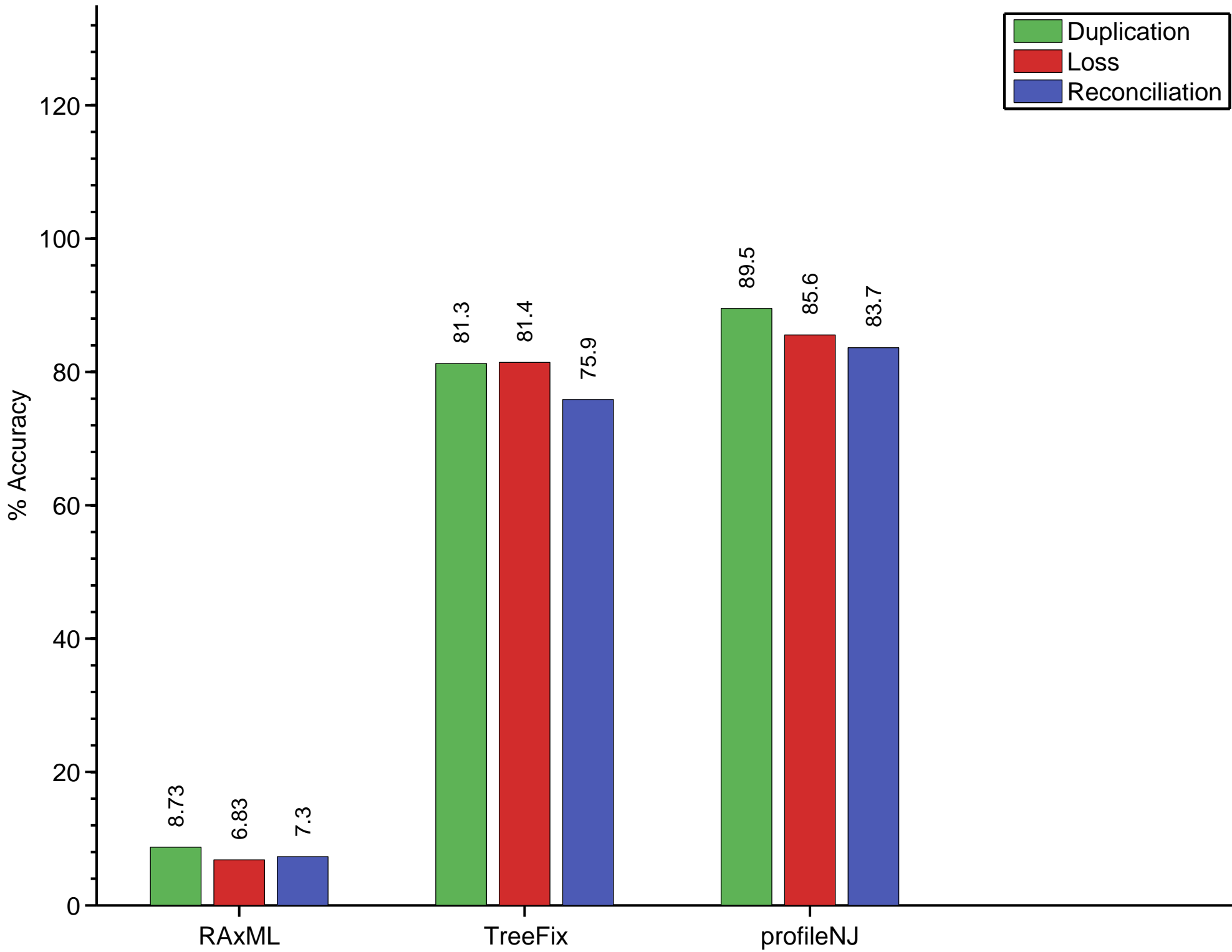
Tree likelihood according to
the RF distance with the true tree for each program



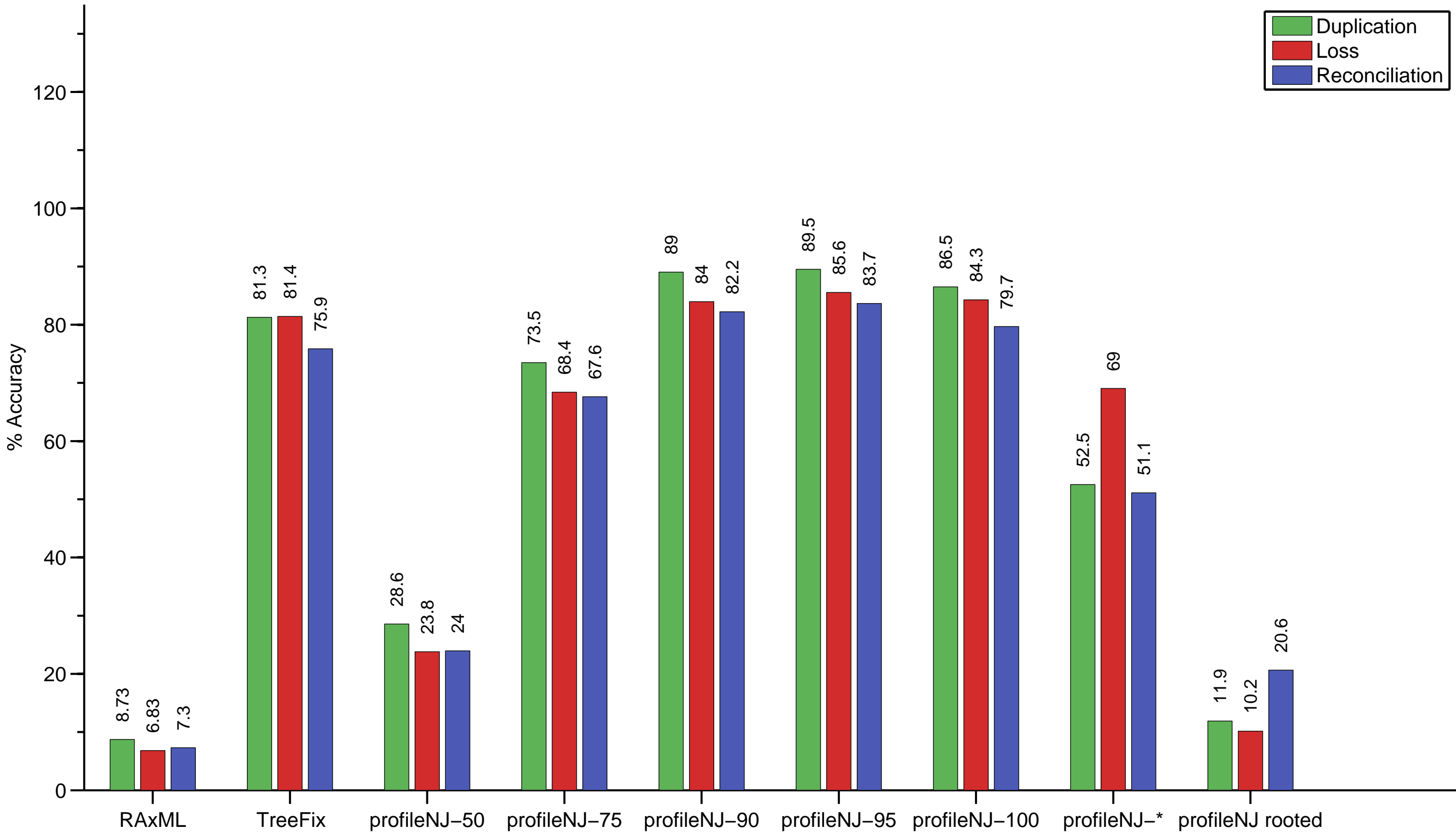
**Comparison of AU test p-value between the true tree
and tree returned by RAxML, profileNJ and TreeFix**



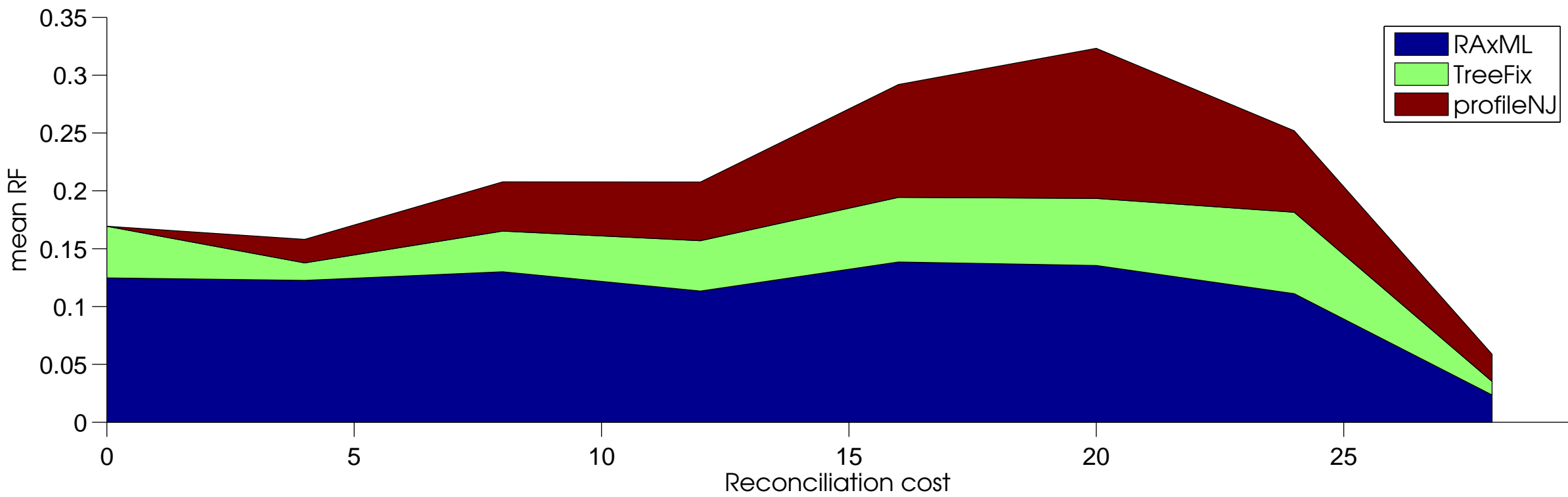
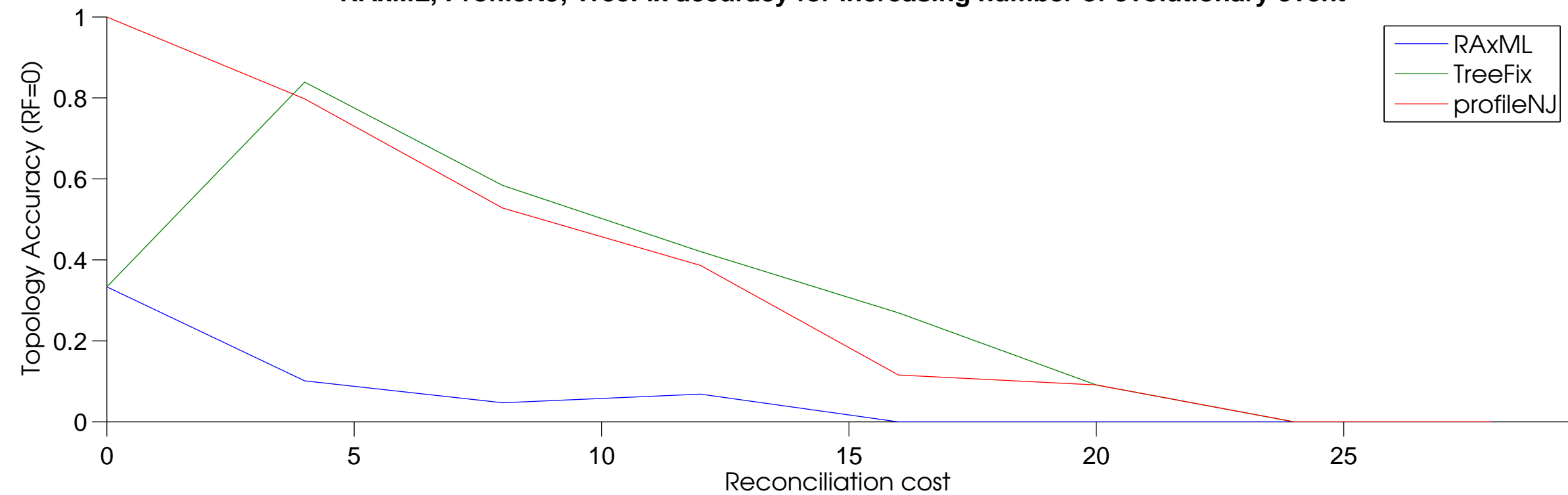
Duplication, Loss and Reconciliation accuracy for each program



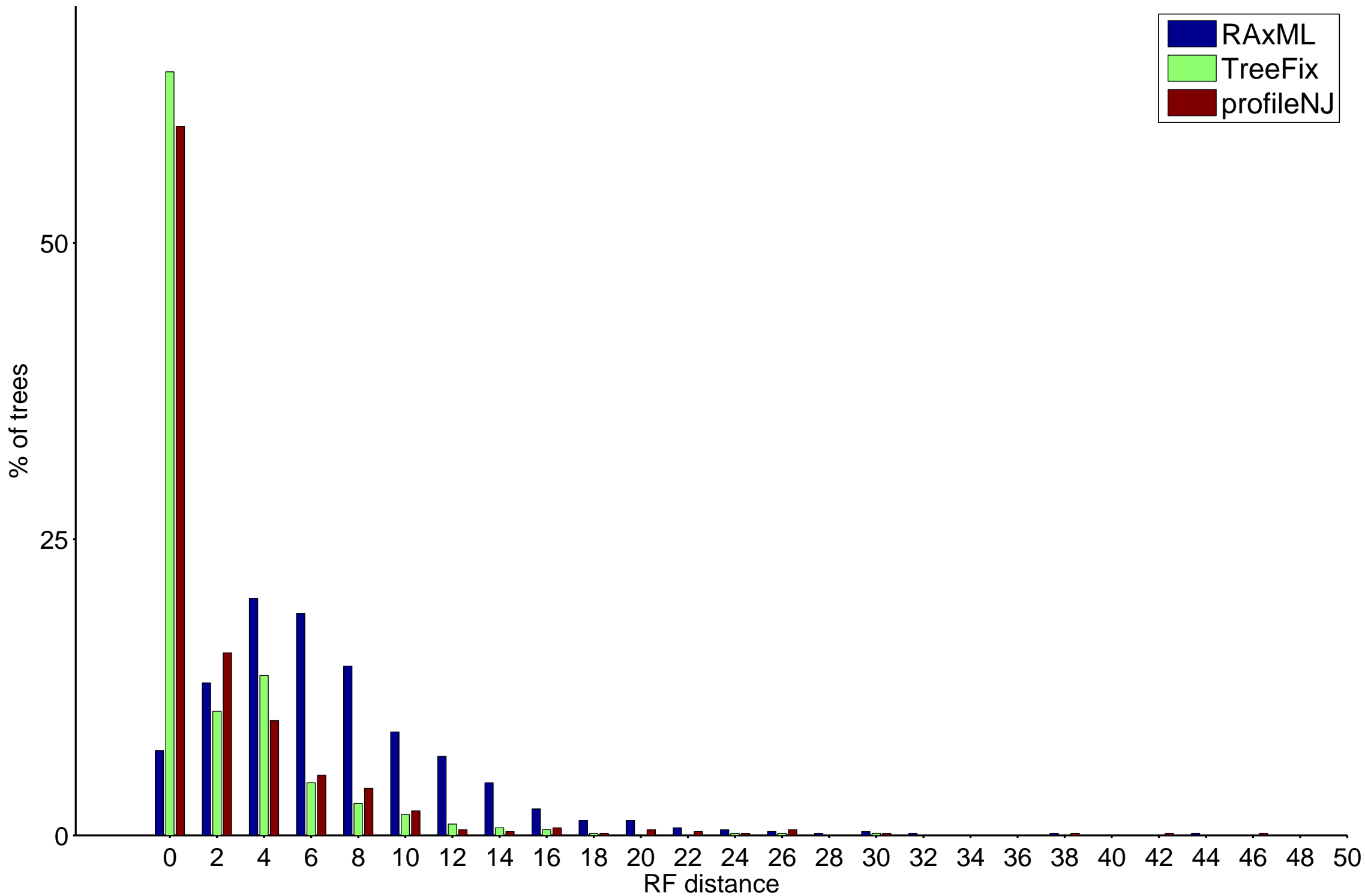
Duplication, Loss and Reconciliation accuracy for each program



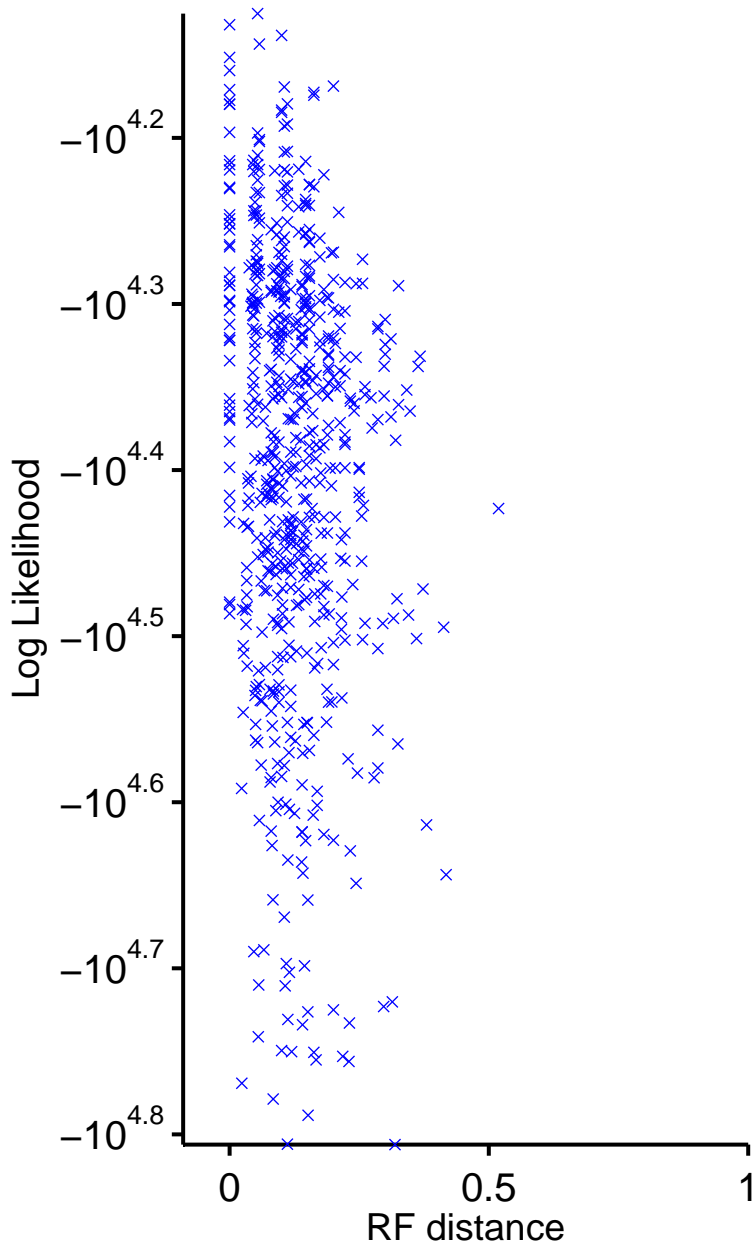
RAXML, ProfileNJ, TreeFix accuracy for increasing number of evolutionary event



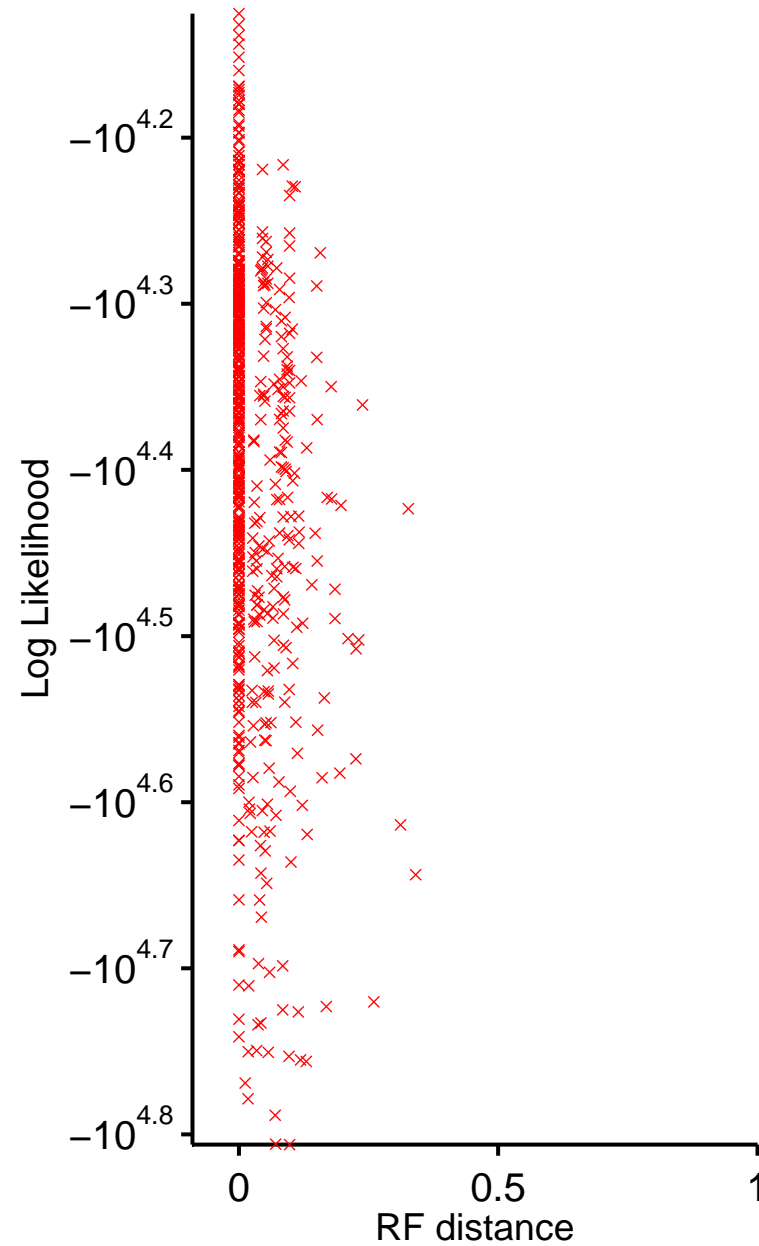
RF comparision between TreeSolver, TreeFix and RAxML method



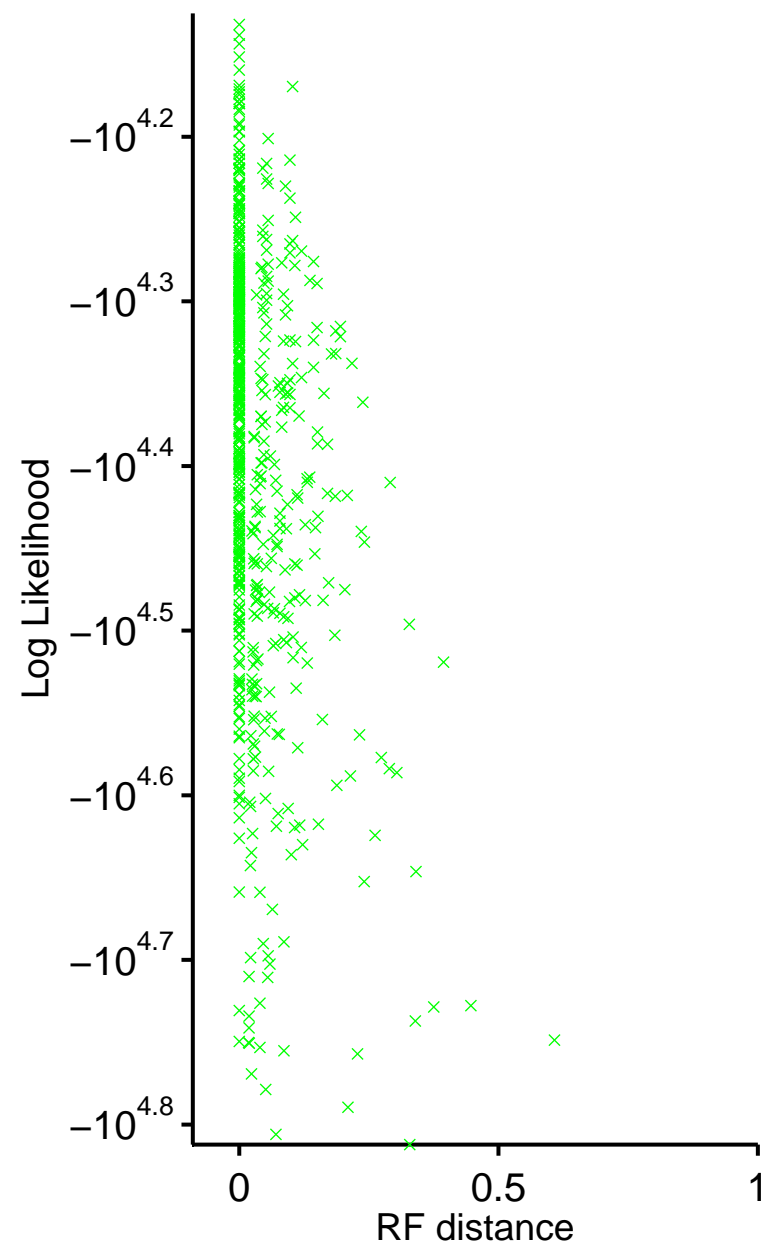
Likelihood of RAxML trees according to the RF distance with the true tree



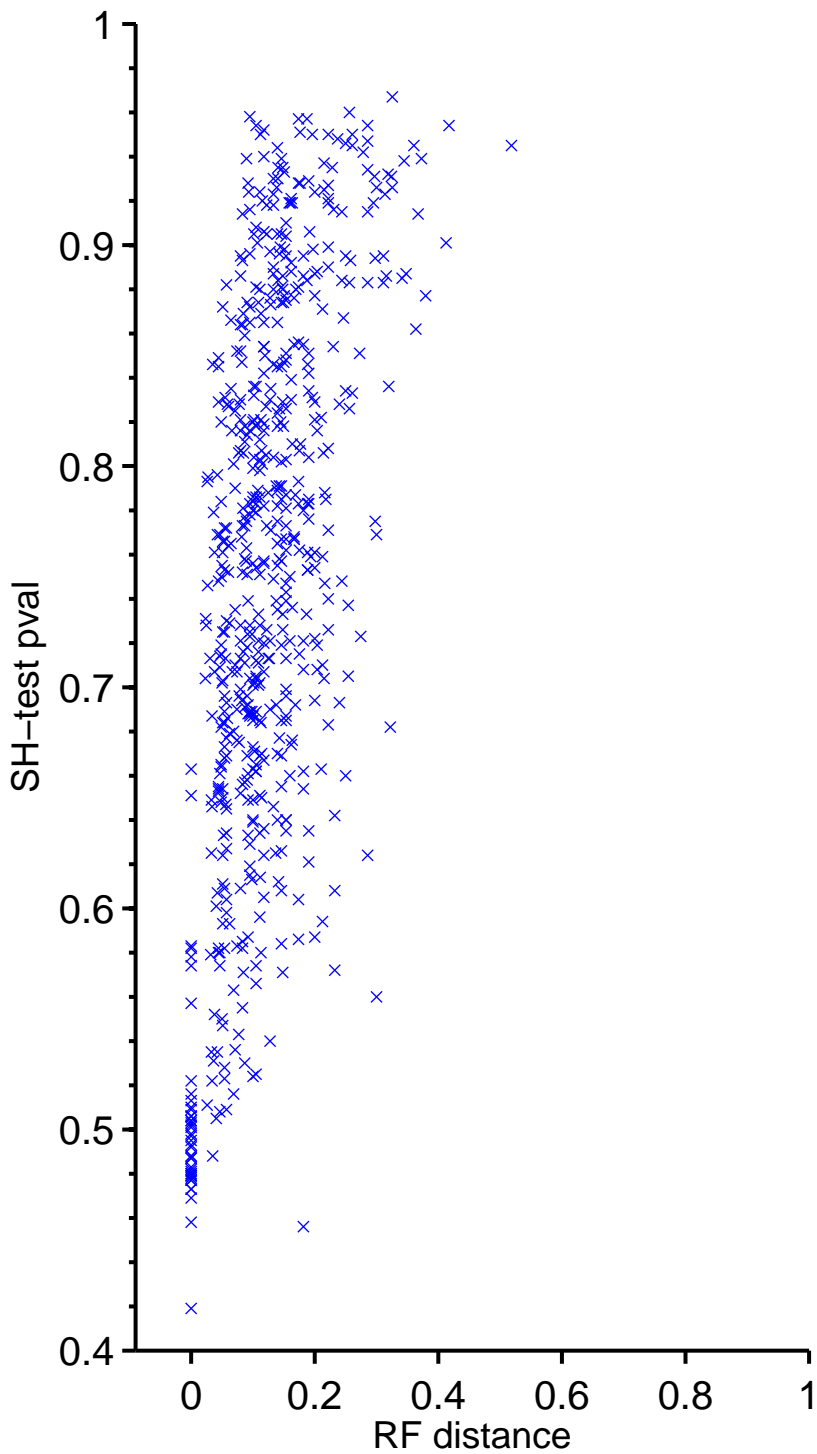
Likelihood of TreeFix trees according to the RF distance with the true tree



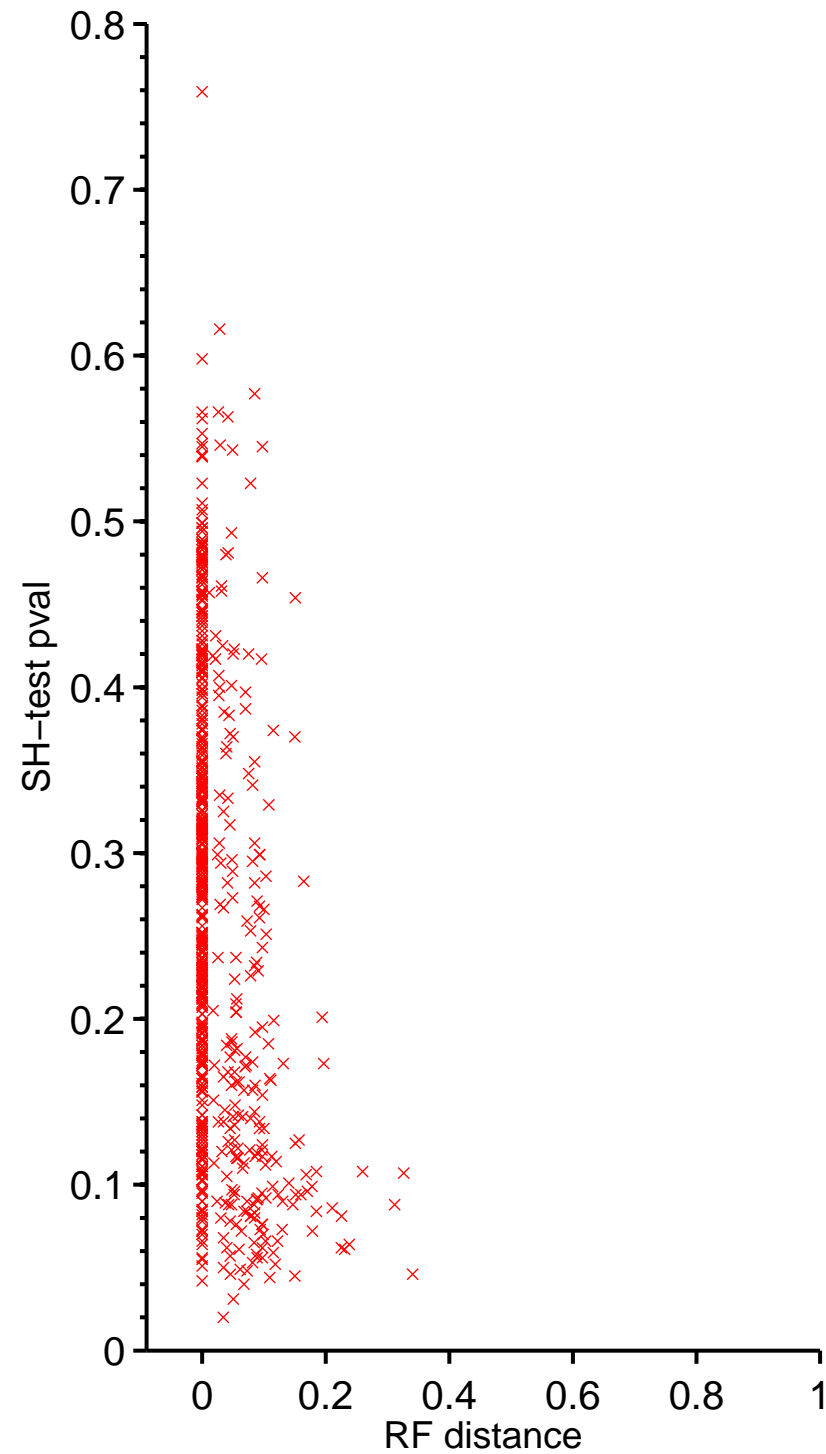
Likelihood of profileNJ trees according to the RF distance with the true tree



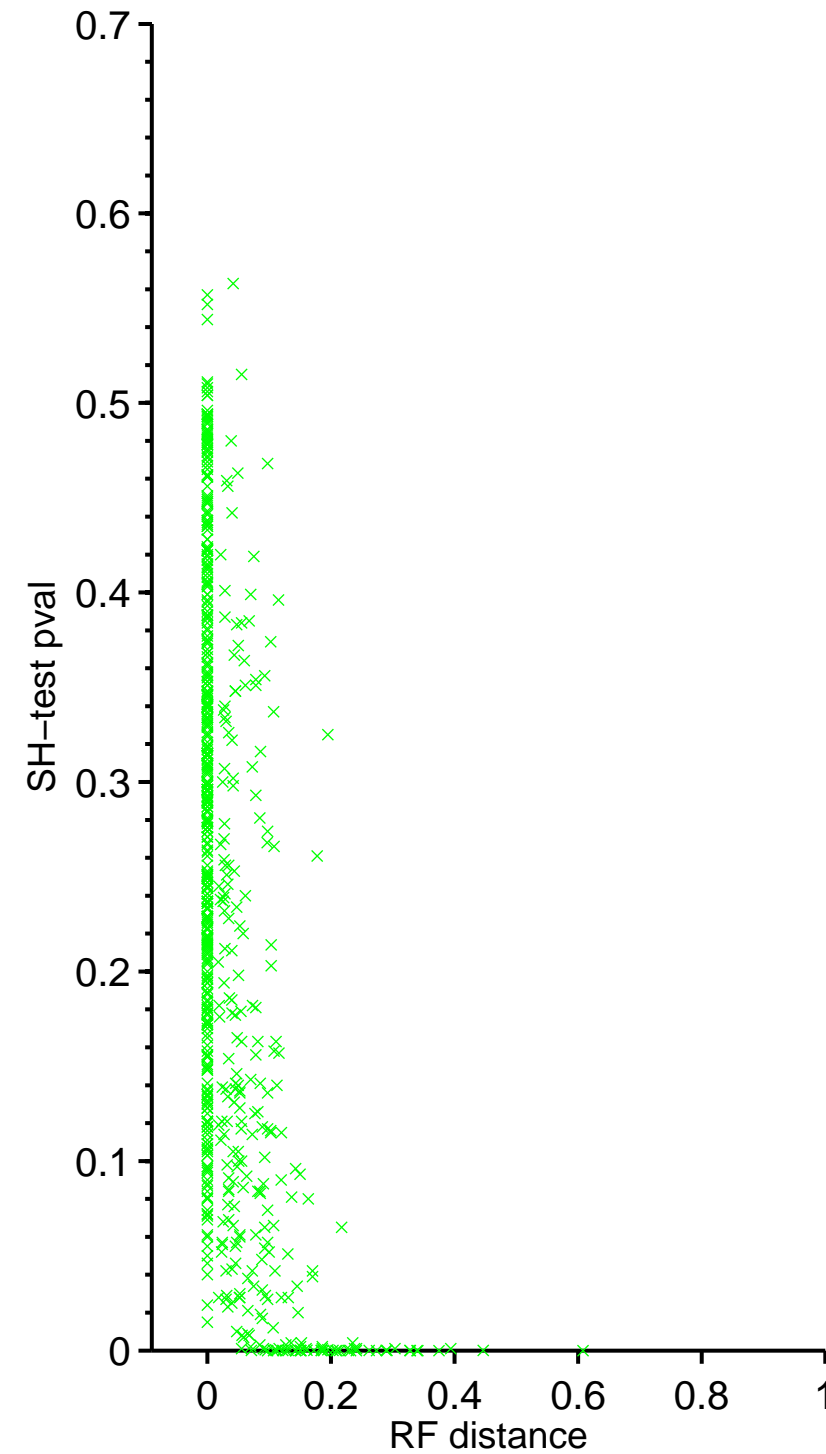
SH-test p-val of RAxML trees according to the RF distance with the true tree



SH-test p-val of TreeFix trees according to the RF distance with the true tree



SH-test p-val of profileNJ trees according to the RF distance with the true tree



Runtime for gene trees of increasing size for simulated fungi dataset

