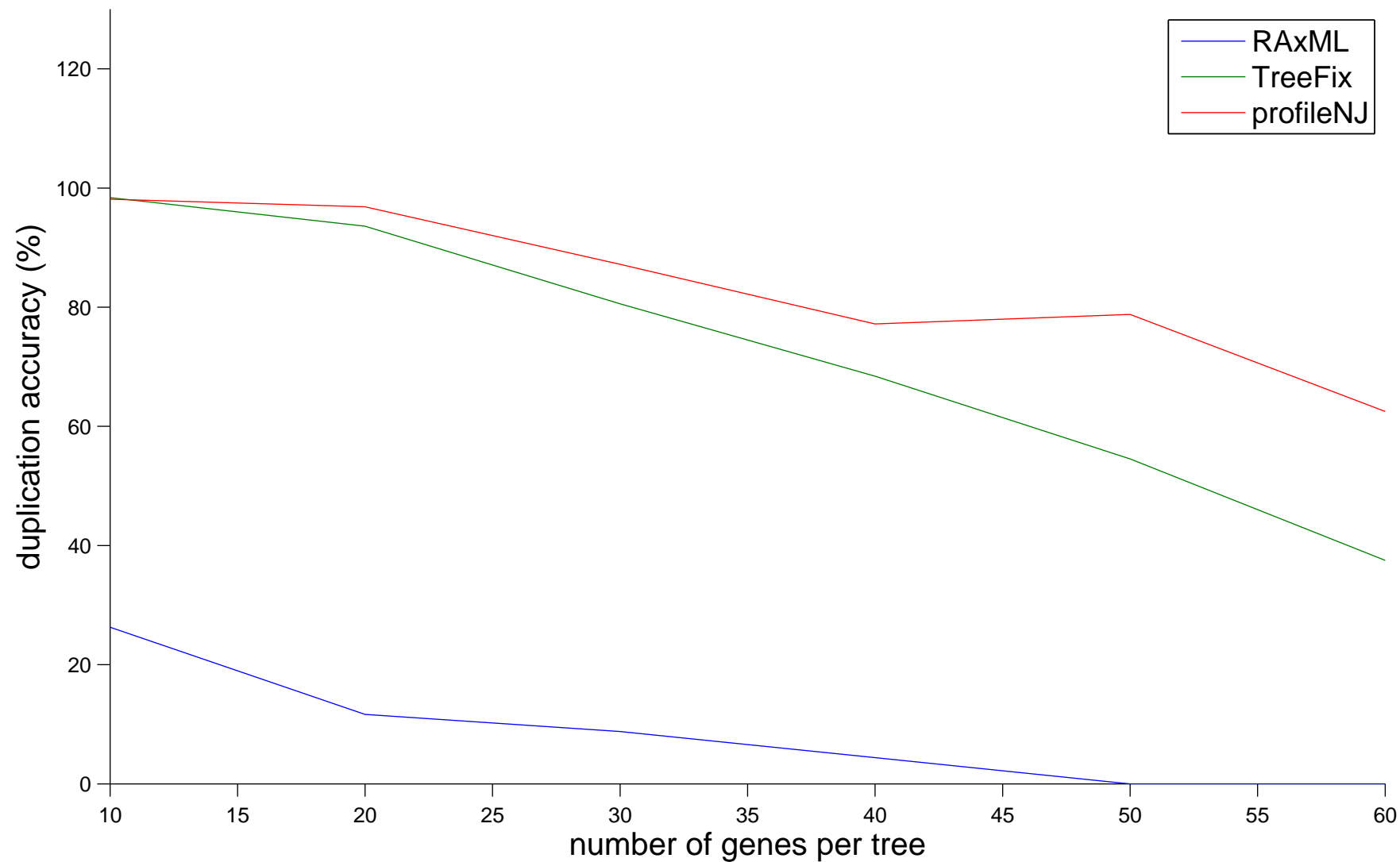
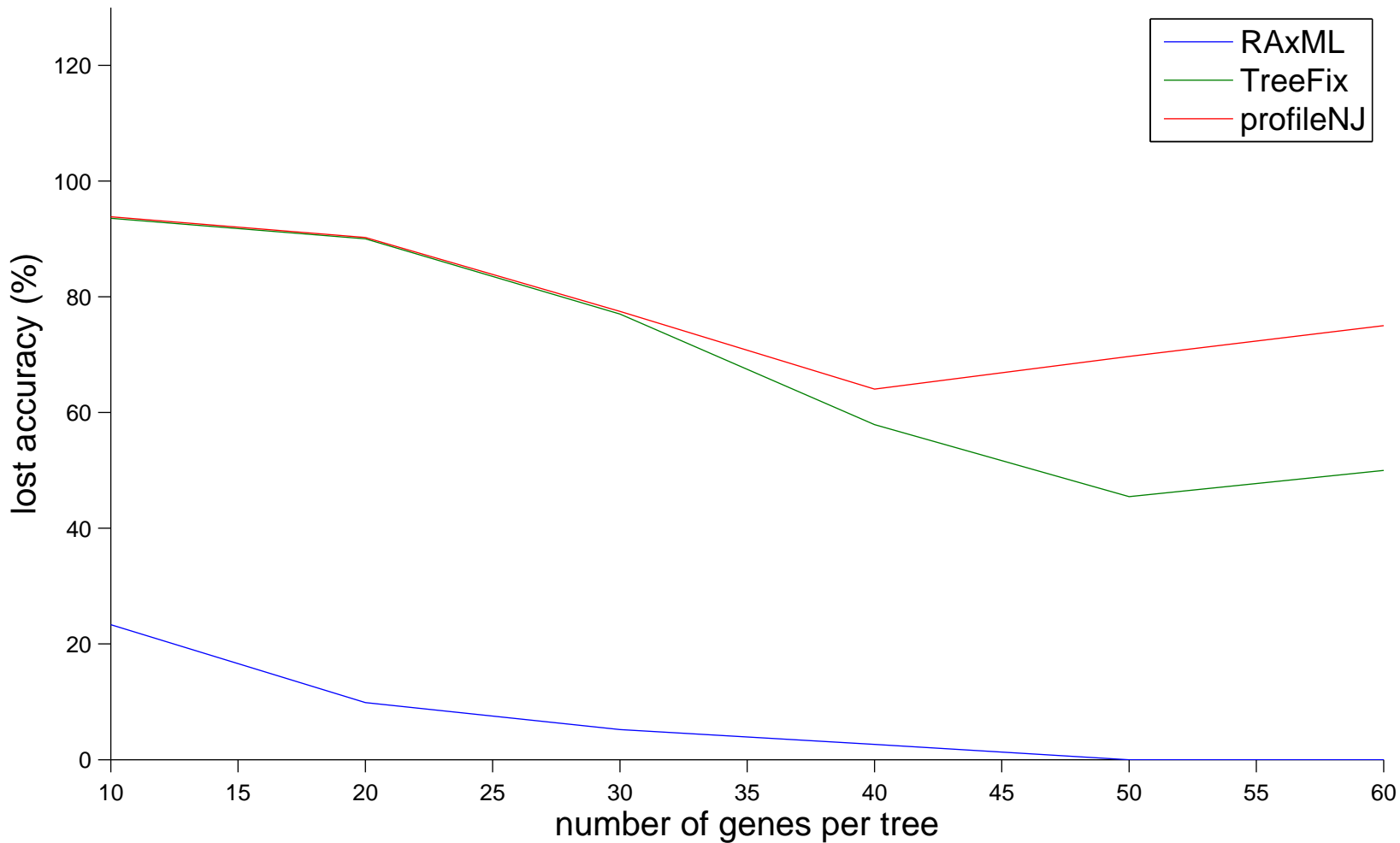


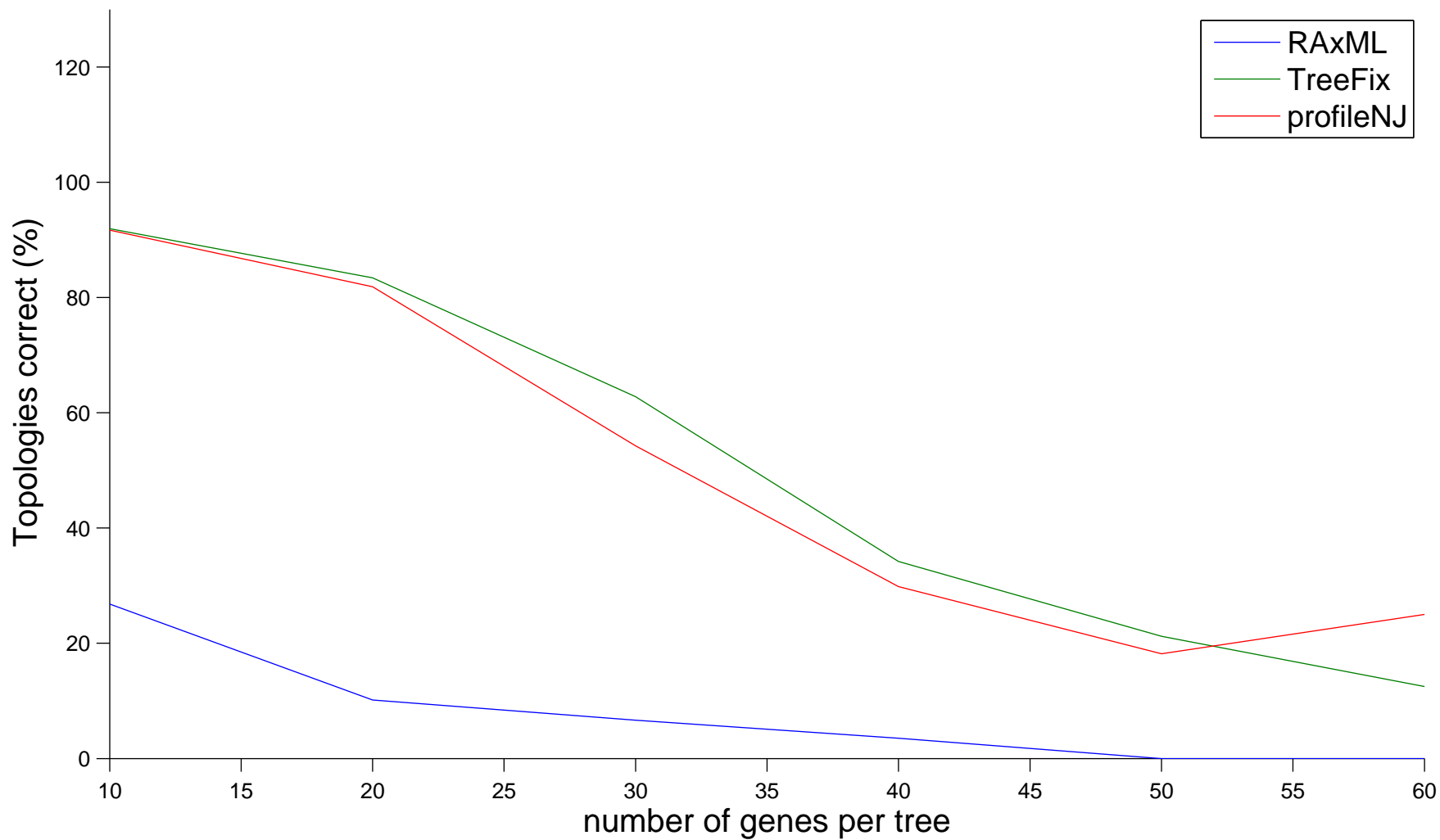
Accuracy of inferred duplication for gene trees of increasing size for simulated fungi dataset



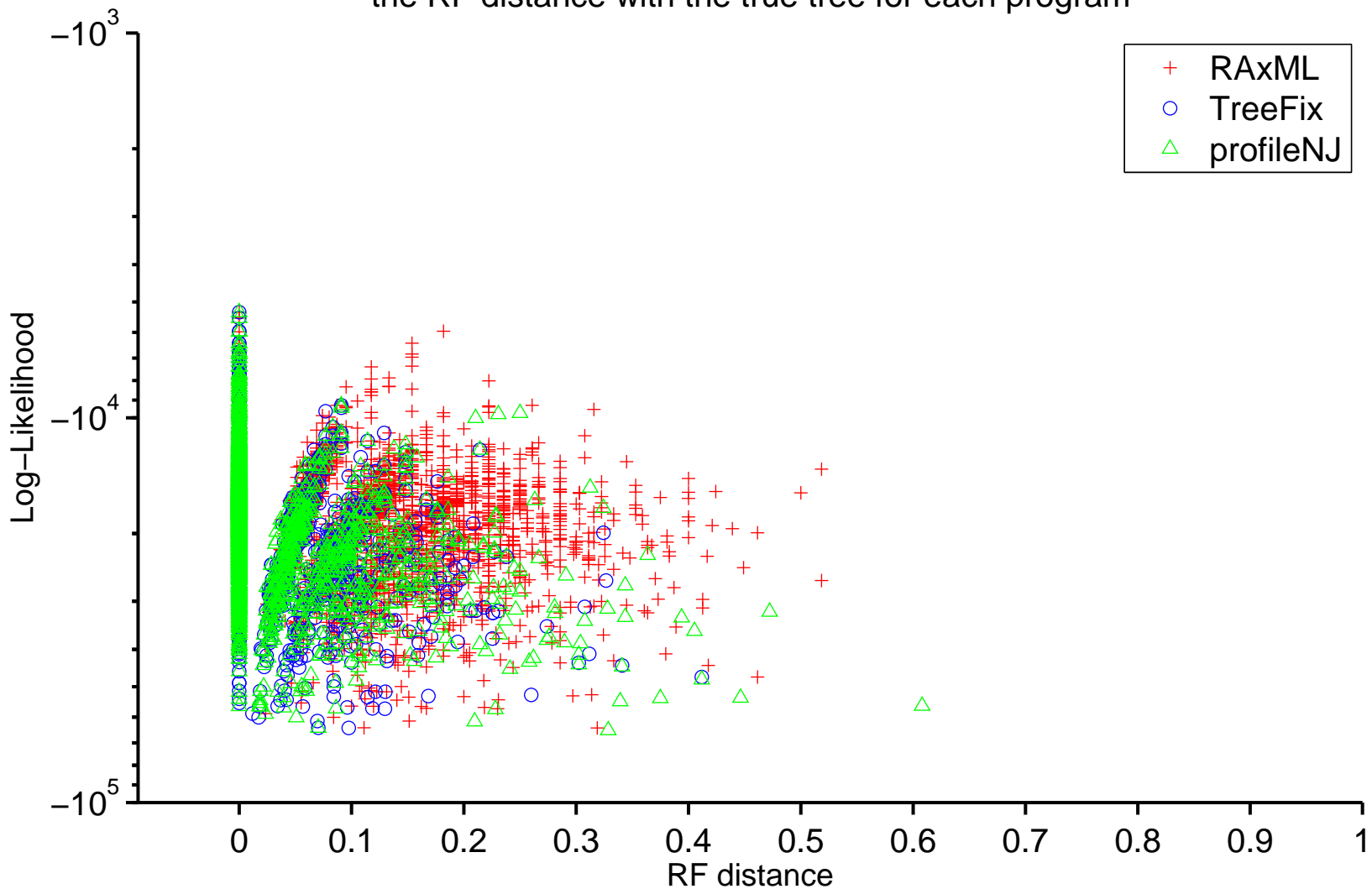
Accuracy of inferred lost for gene trees of increasing size for simulated fungi dataset



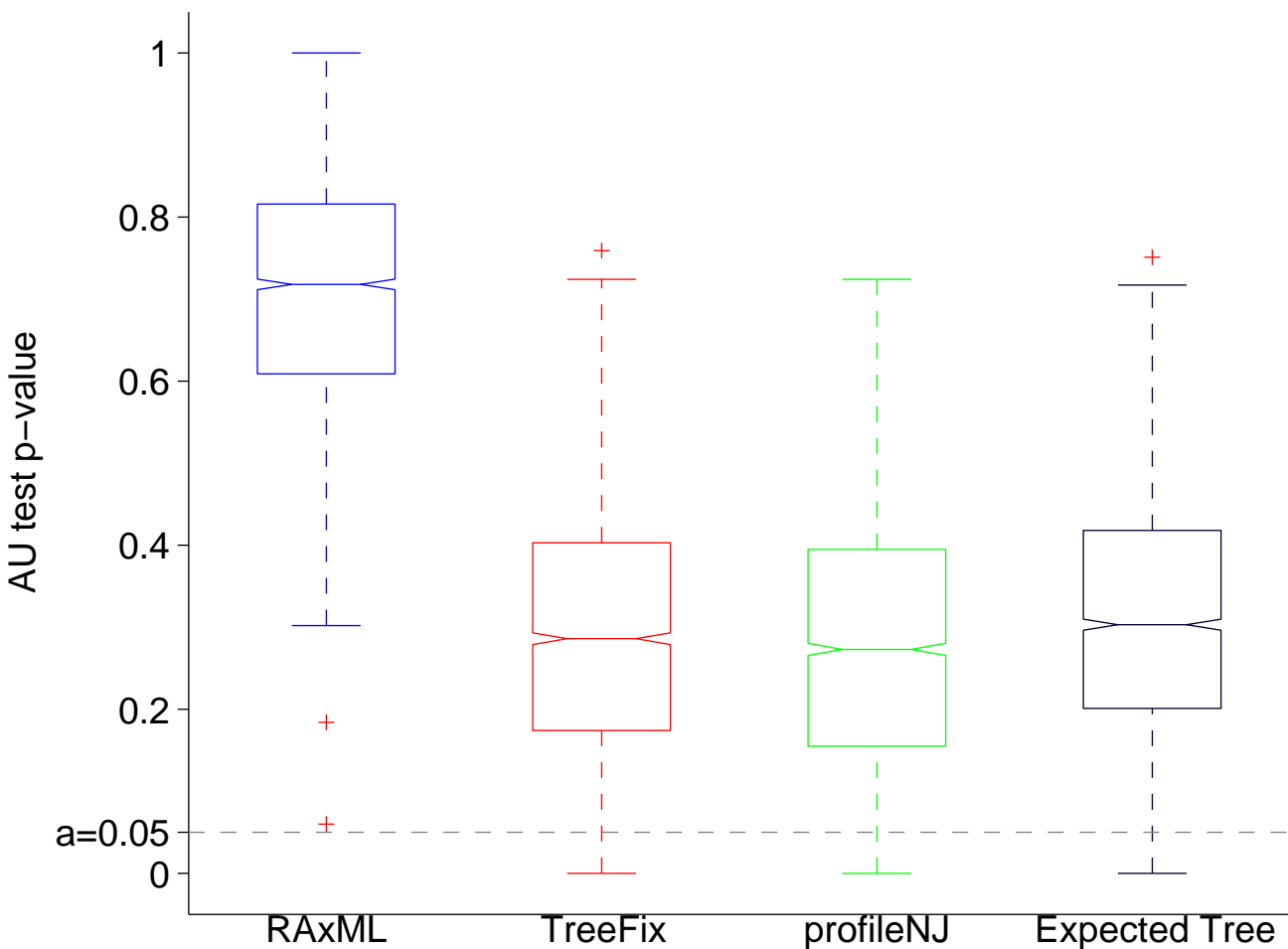
Accuracy of the inferred topology for gene trees of increasing size for simulated fungi dataset



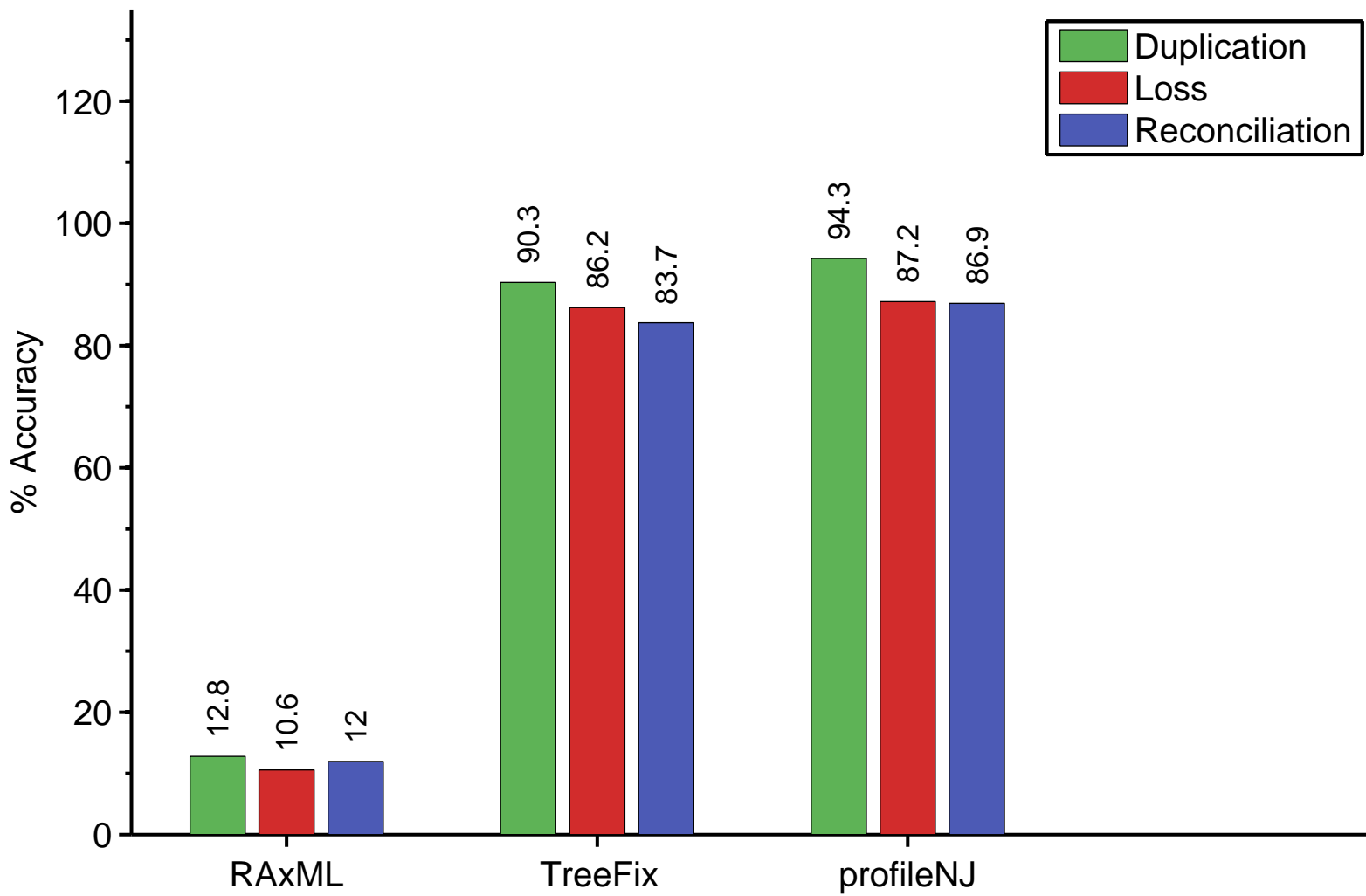
Tree likelihood according to
the RF distance with the true tree for each program



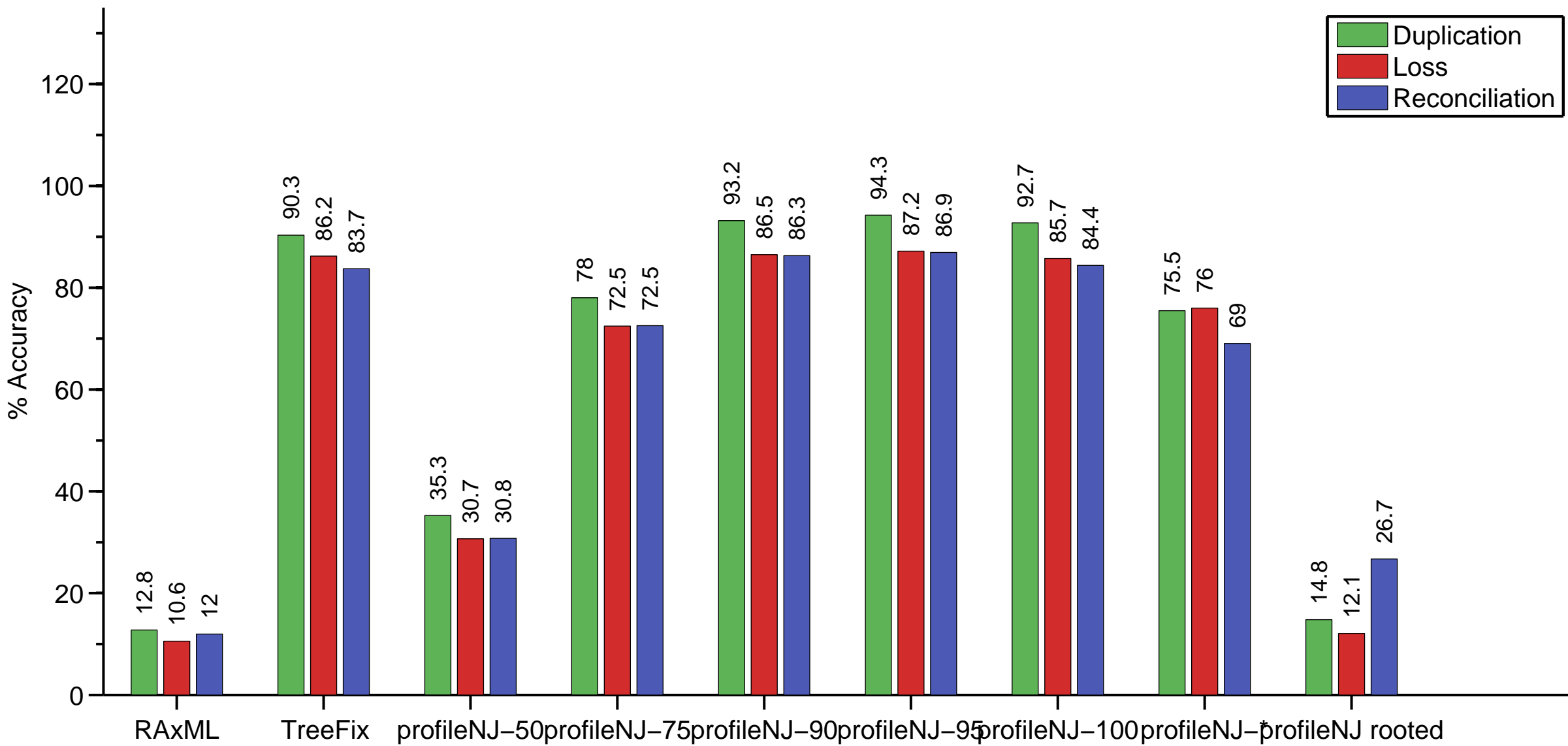
Comparison of AU test p-value between the true tree and tree returned by RAxML, profileNJ and TreeFix



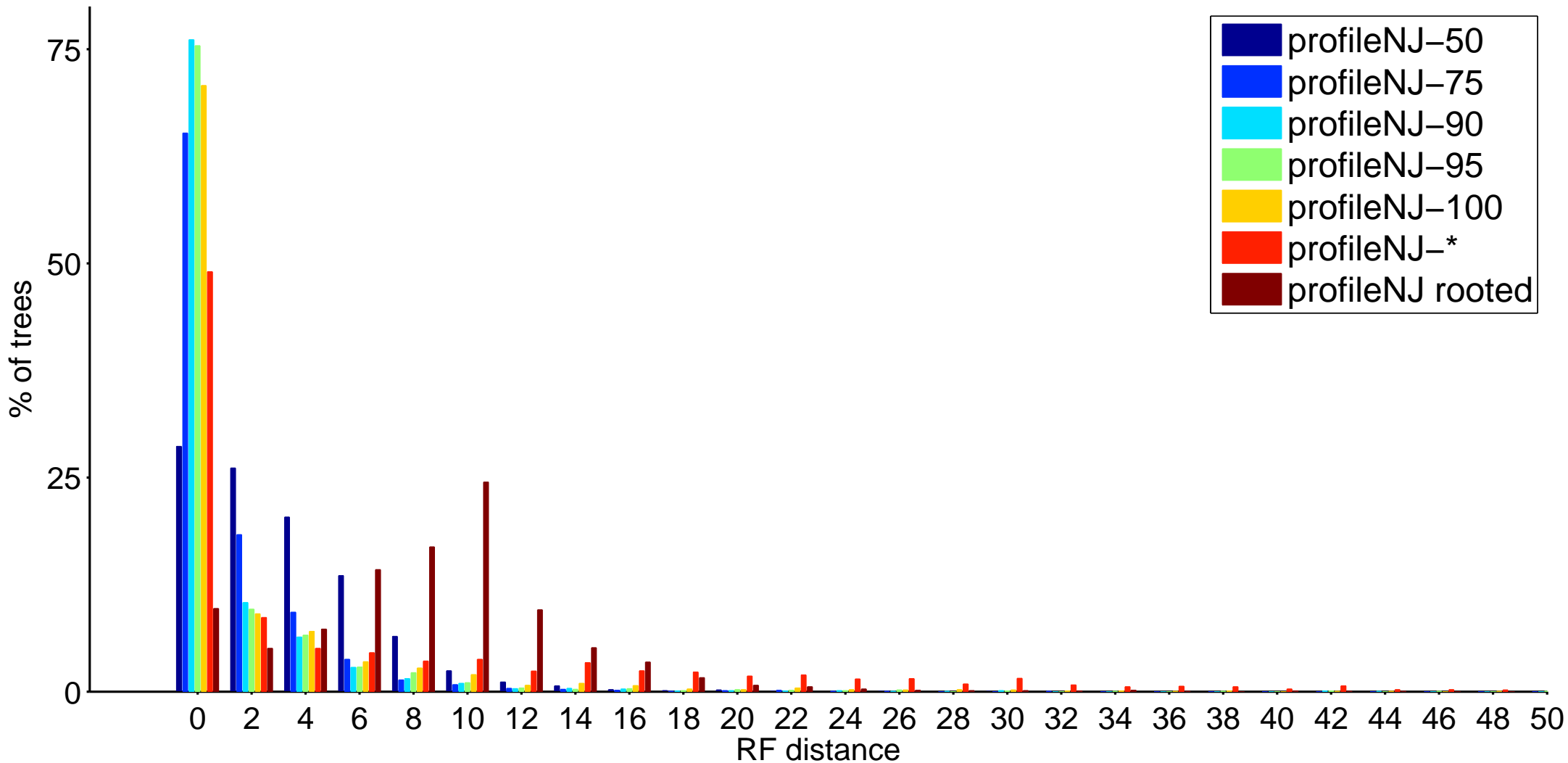
Duplication, Loss and Reconciliation accuracy for each program



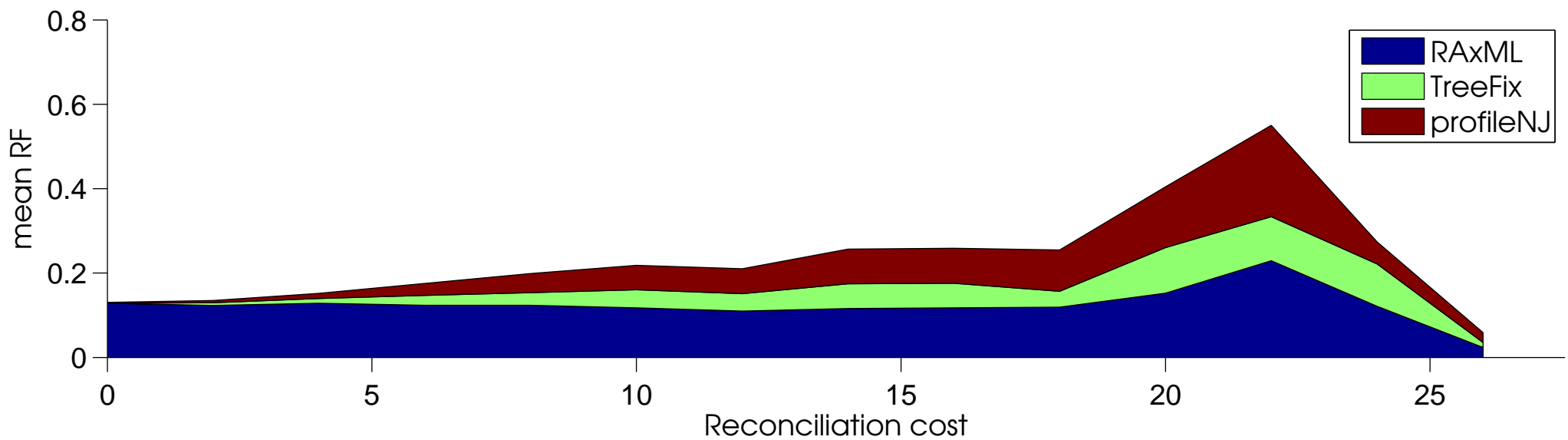
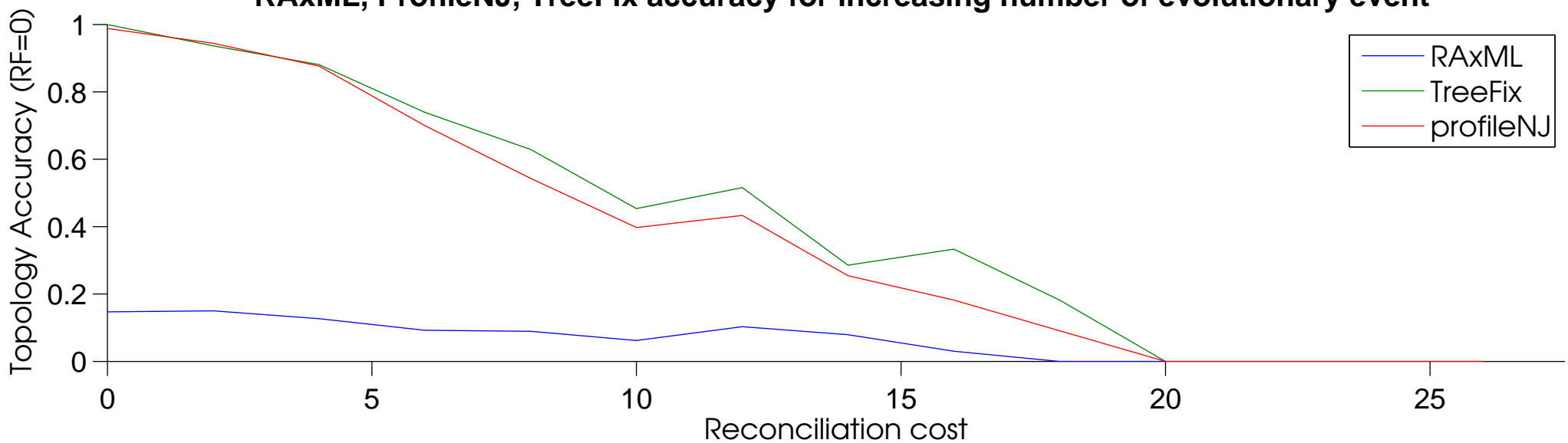
Duplication, Loss and Reconciliation accuracy for each program



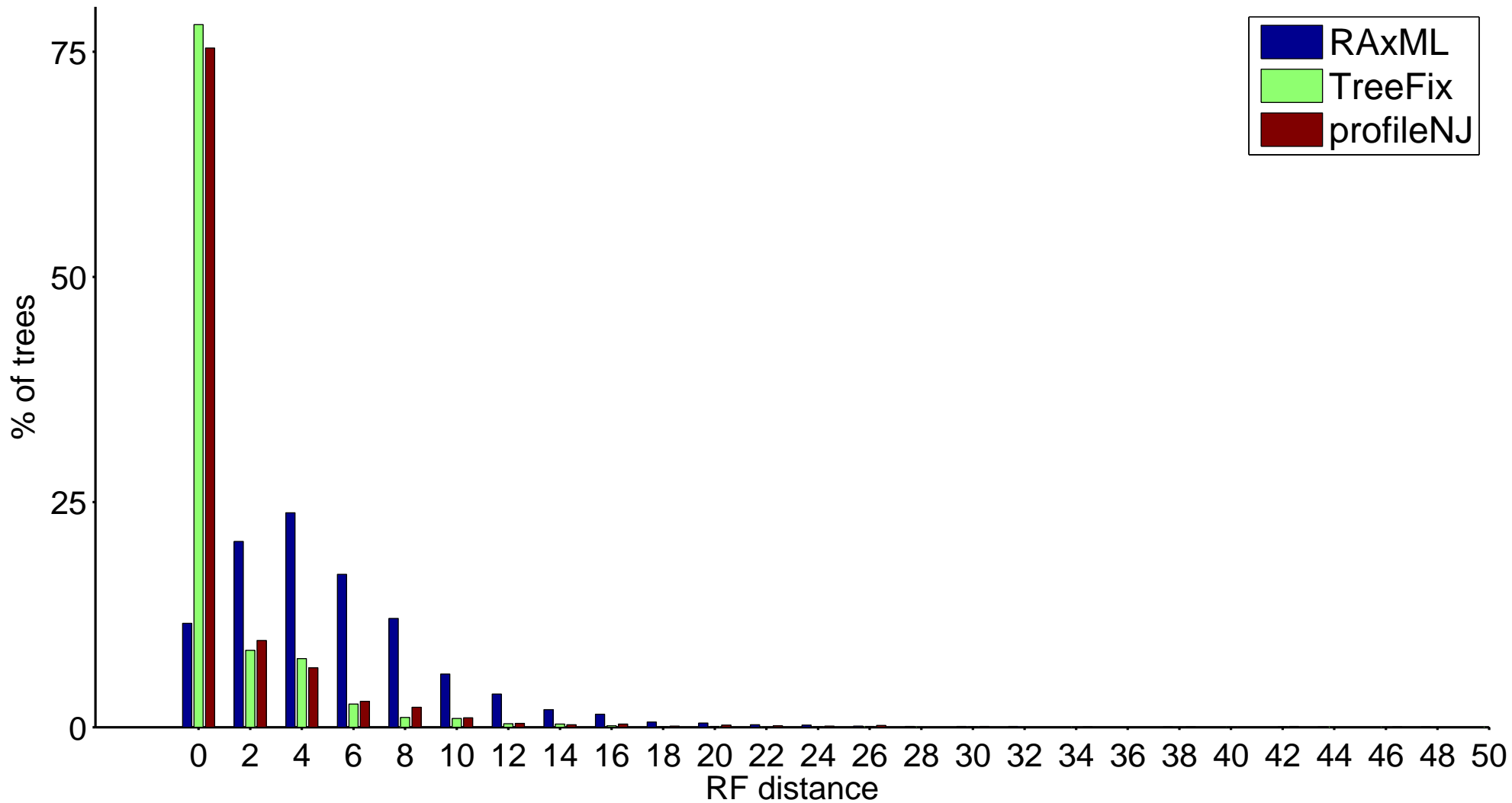
RF comparision between TreeSolver, TreeFix and RAxML method



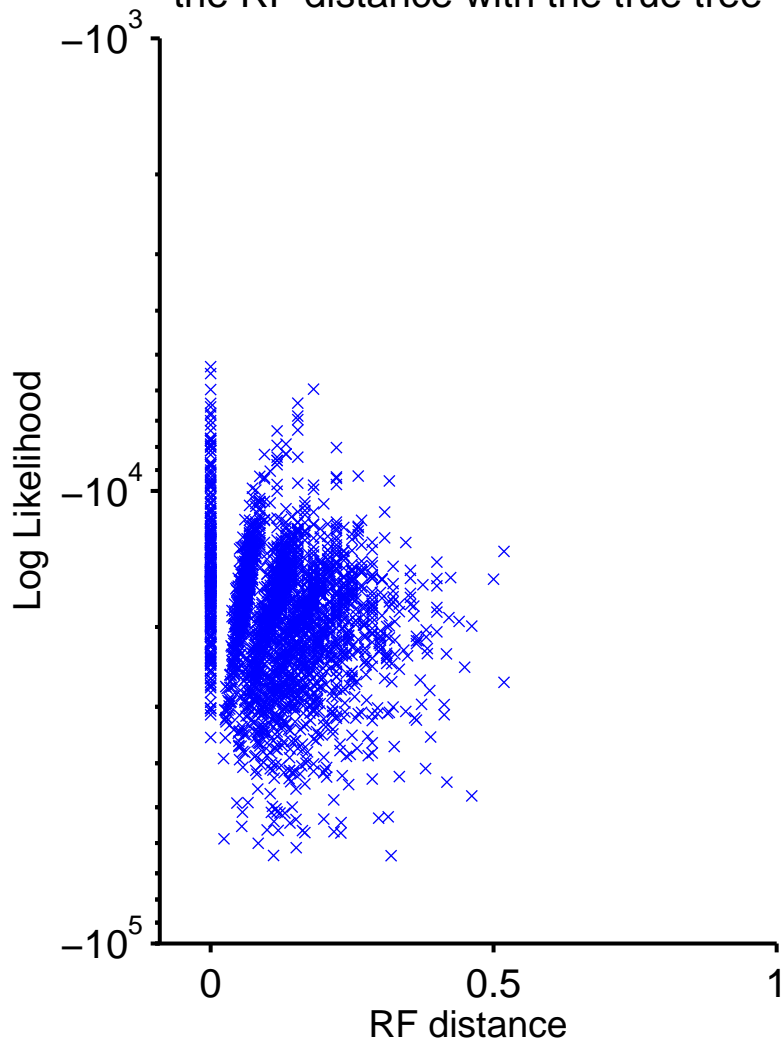
RAXML, ProfileNJ, TreeFix accuracy for increasing number of evolutionary event



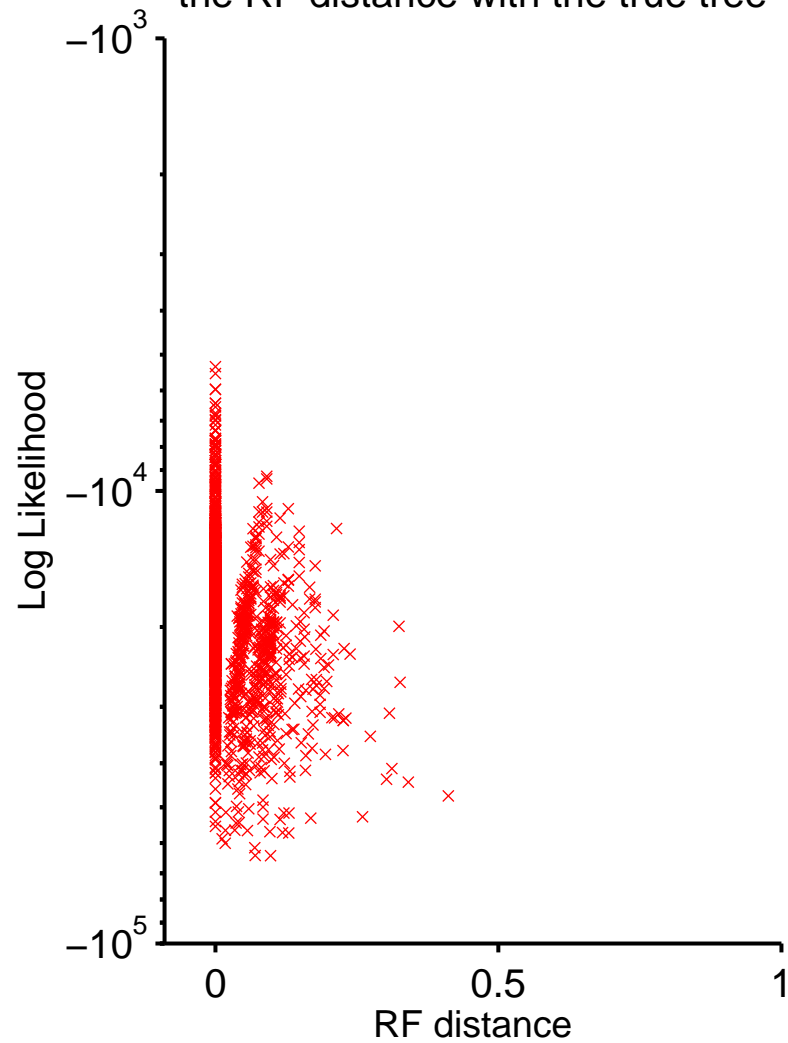
RF comparision between TreeSolver, TreeFix and RAxML method



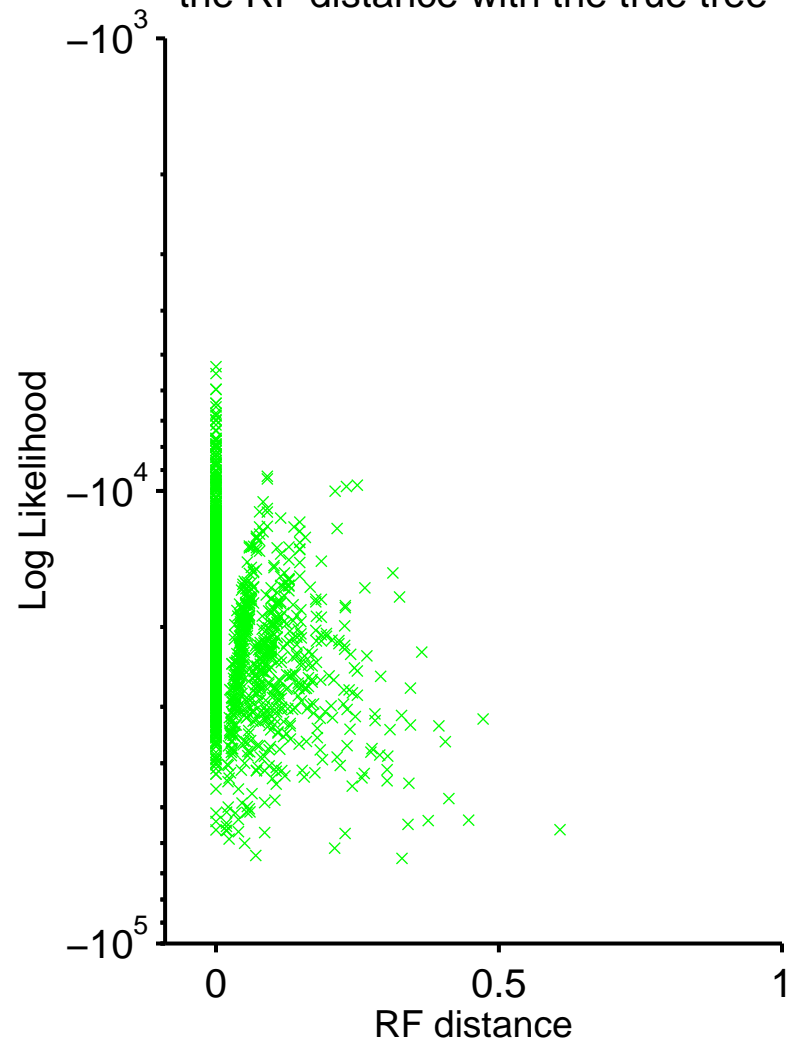
Likelihood of RAXML trees according to the RF distance with the true tree



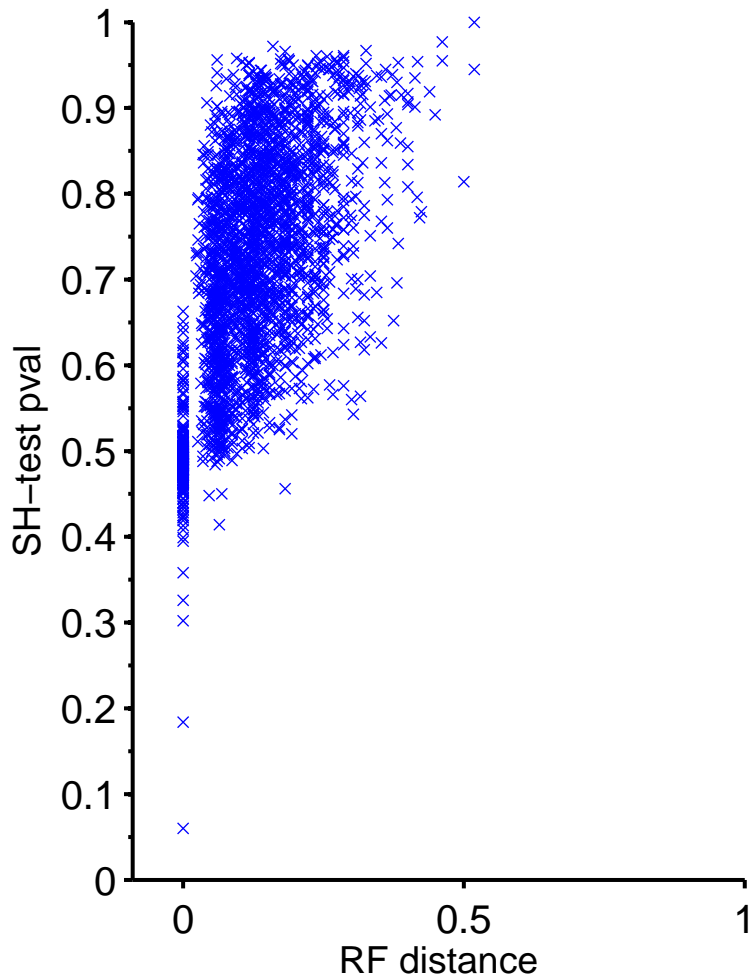
Likelihood of TreeFix trees according to the RF distance with the true tree



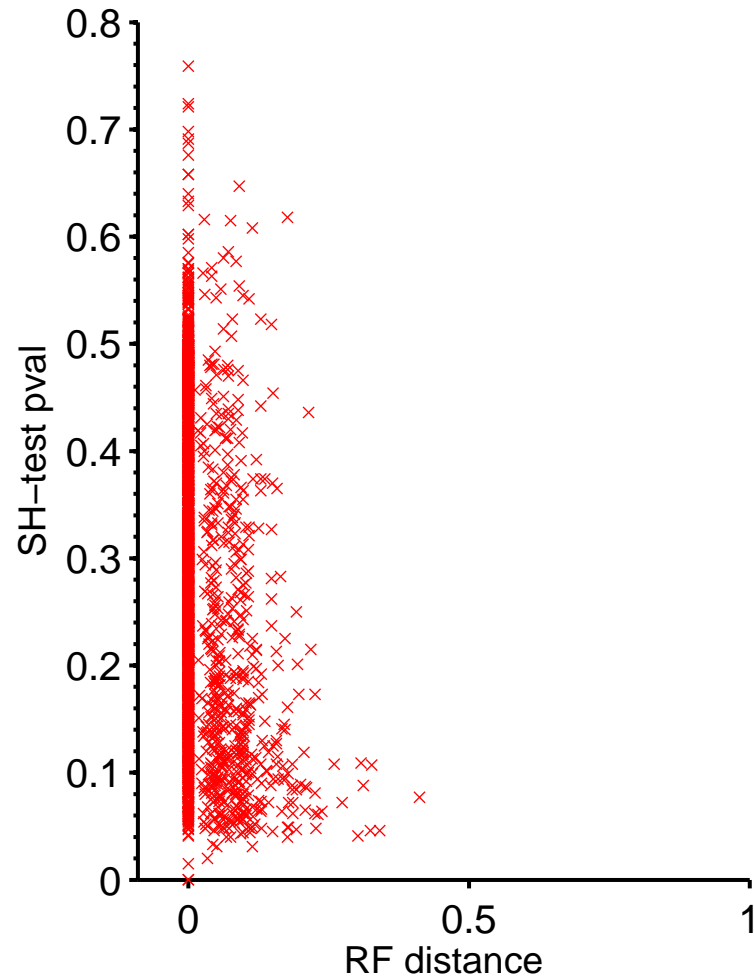
Likelihood of profileNJ trees according to the RF distance with the true tree



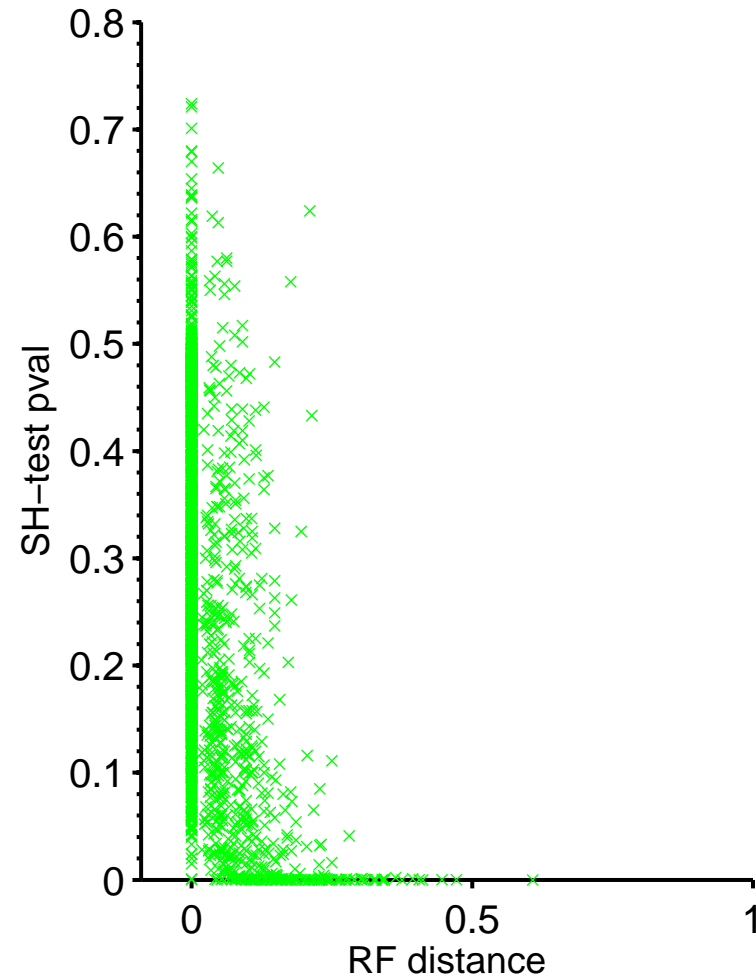
SH-test p-val of RAxML trees according to the RF distance with the true tree



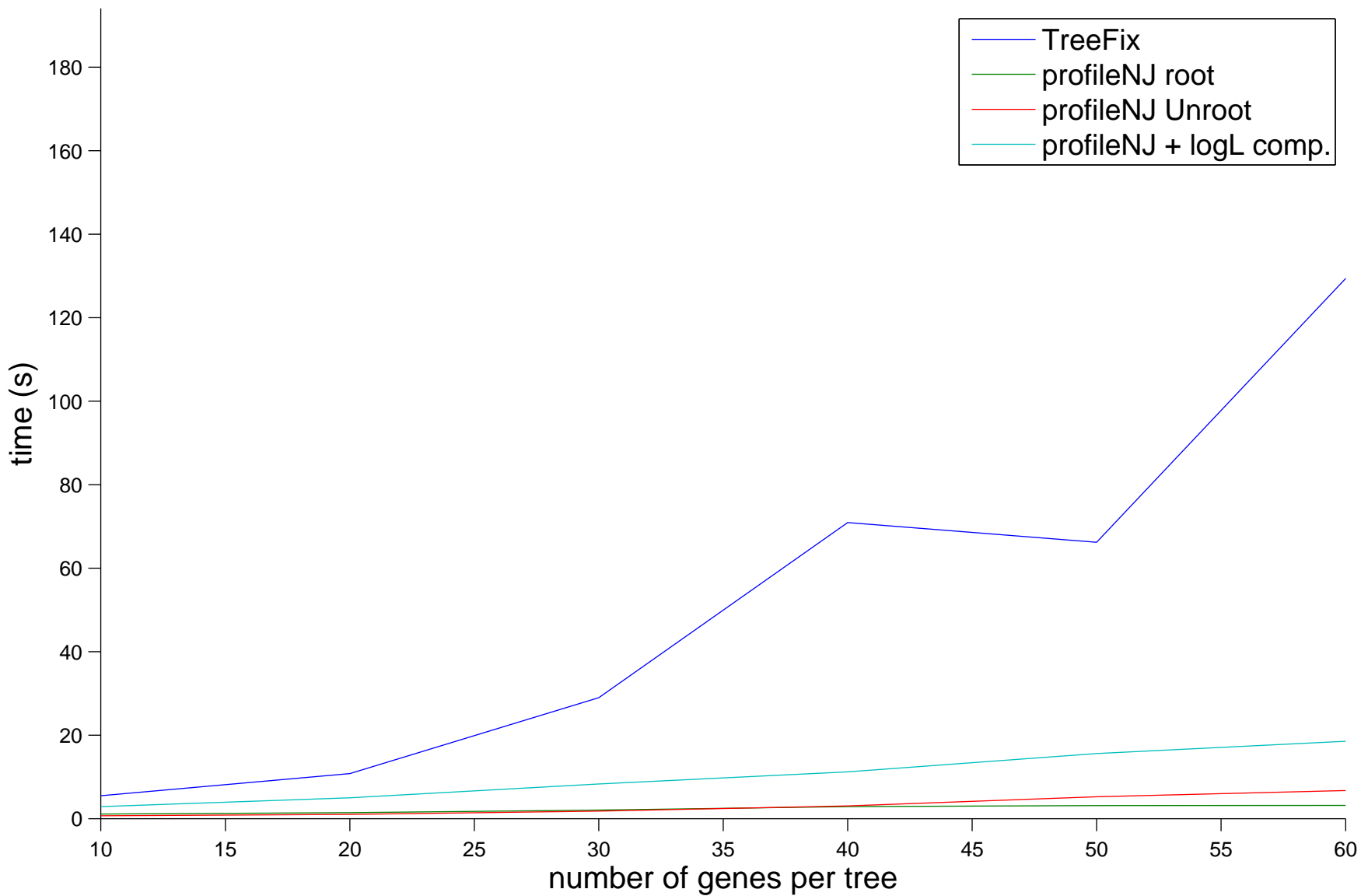
SH-test p-val of TreeFix trees according to the RF distance with the true tree



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



profileNJ execution time as a function of the number of solutions

