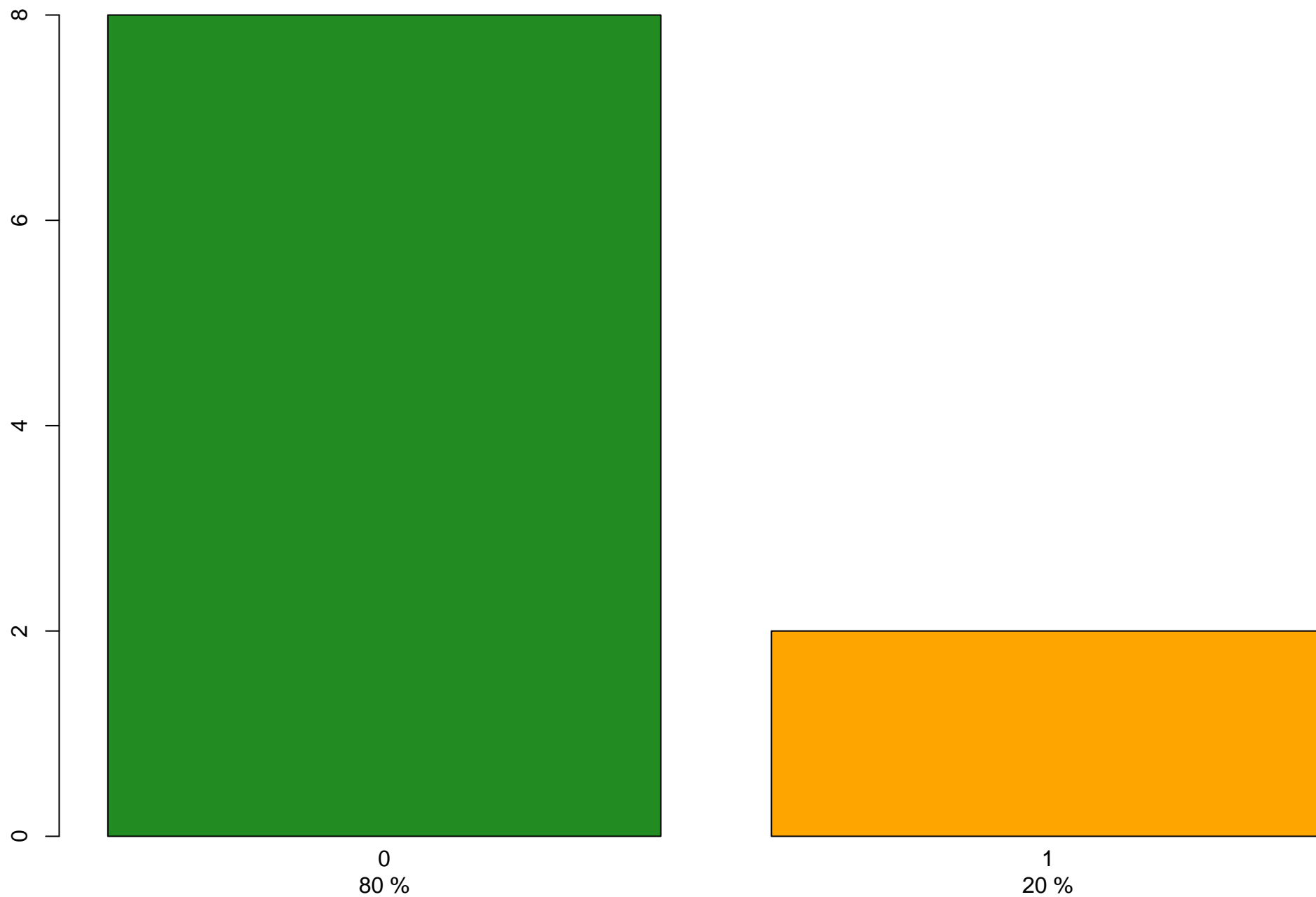
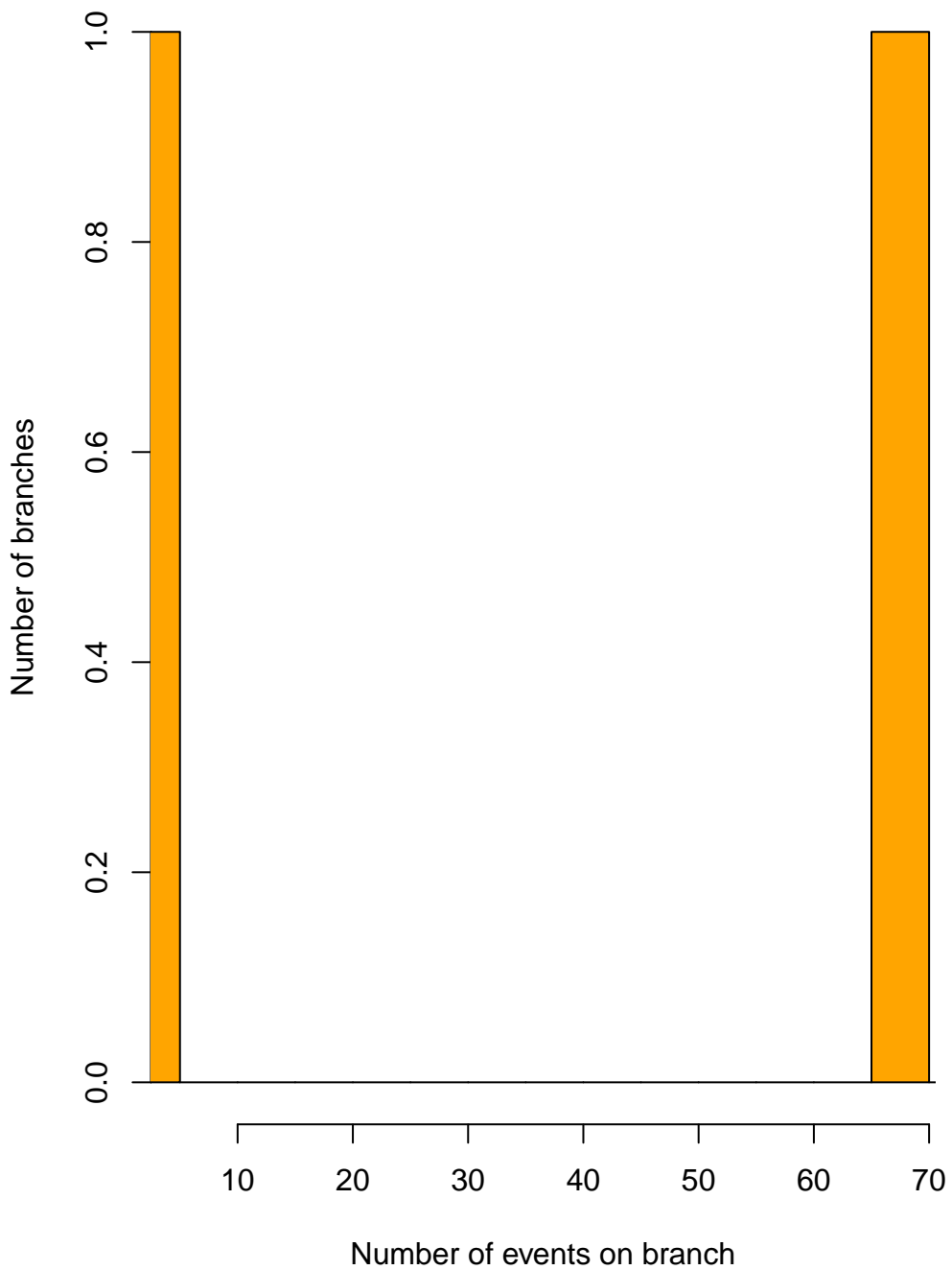


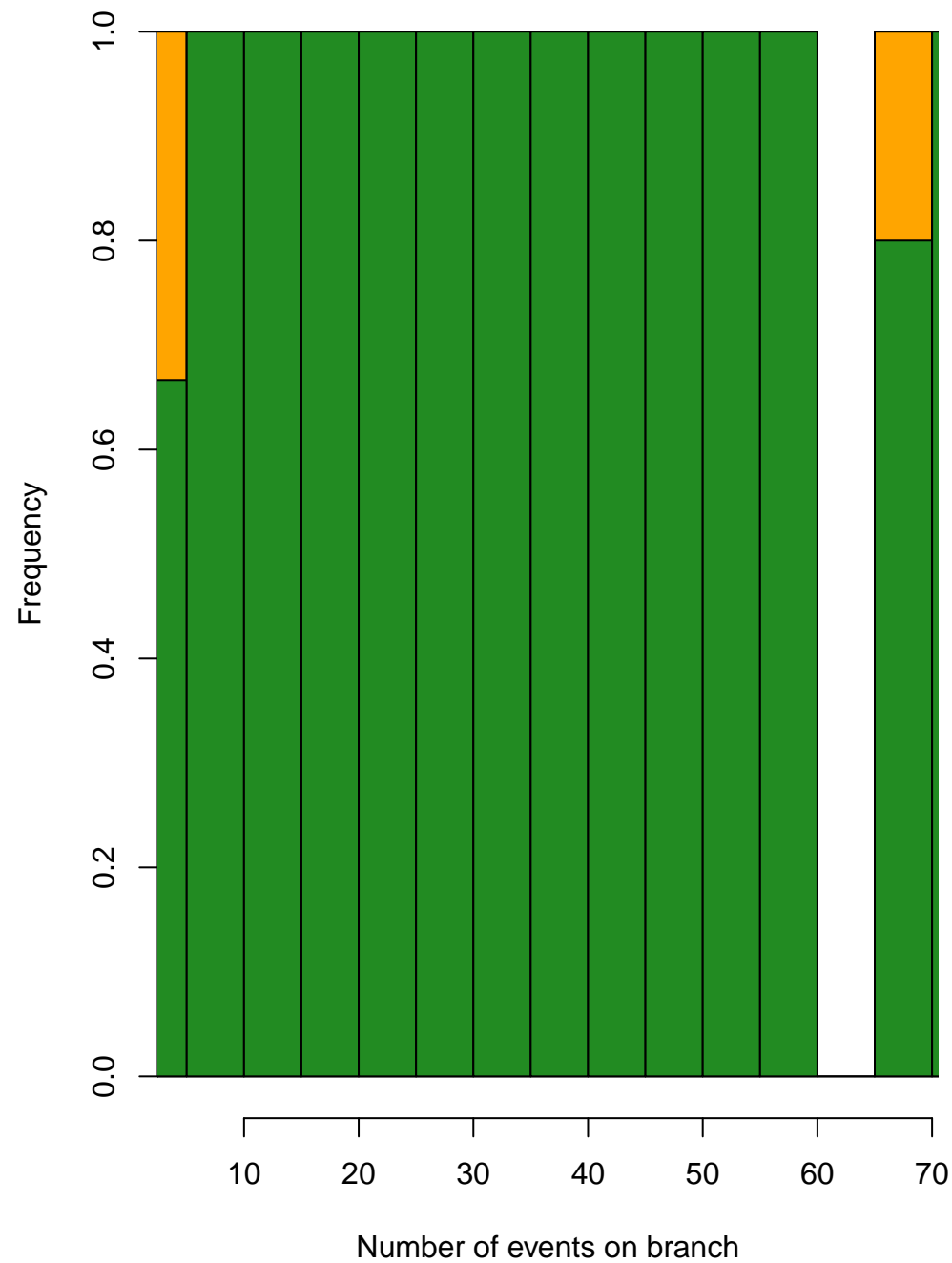
results_yeast1/ – Number of incorrect splits in 10 trees



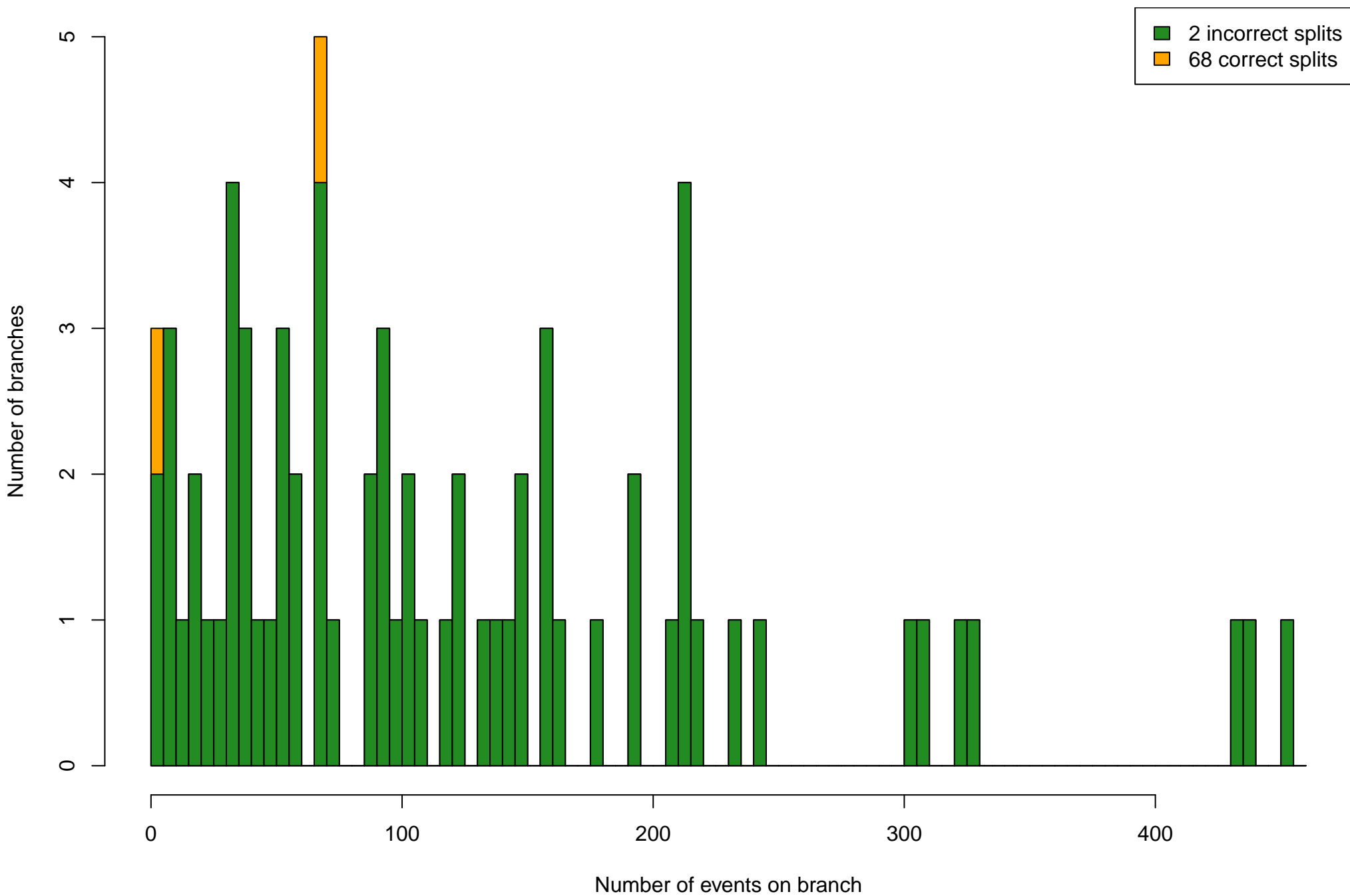
Incorrect edges lengths



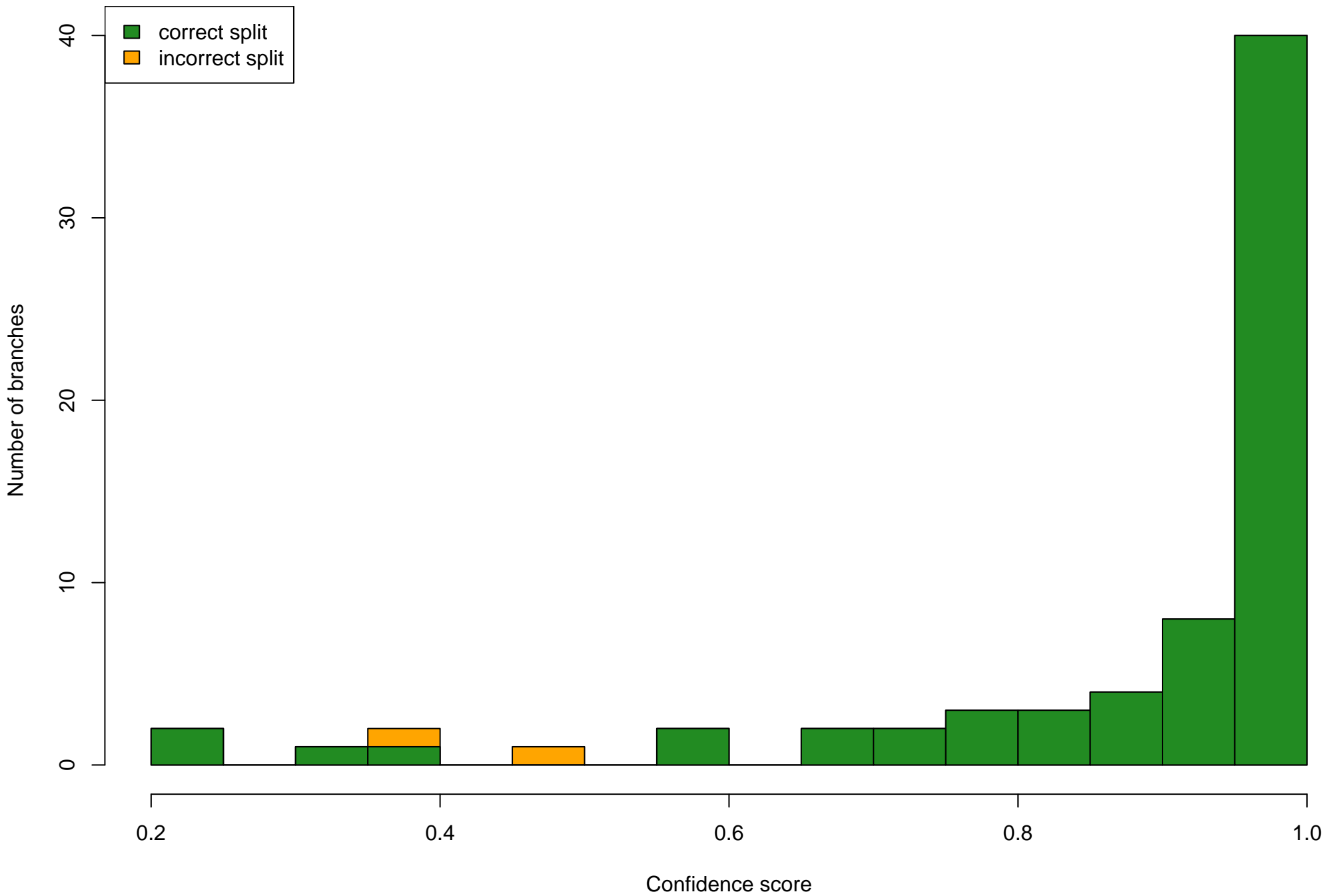
results_yeast1/



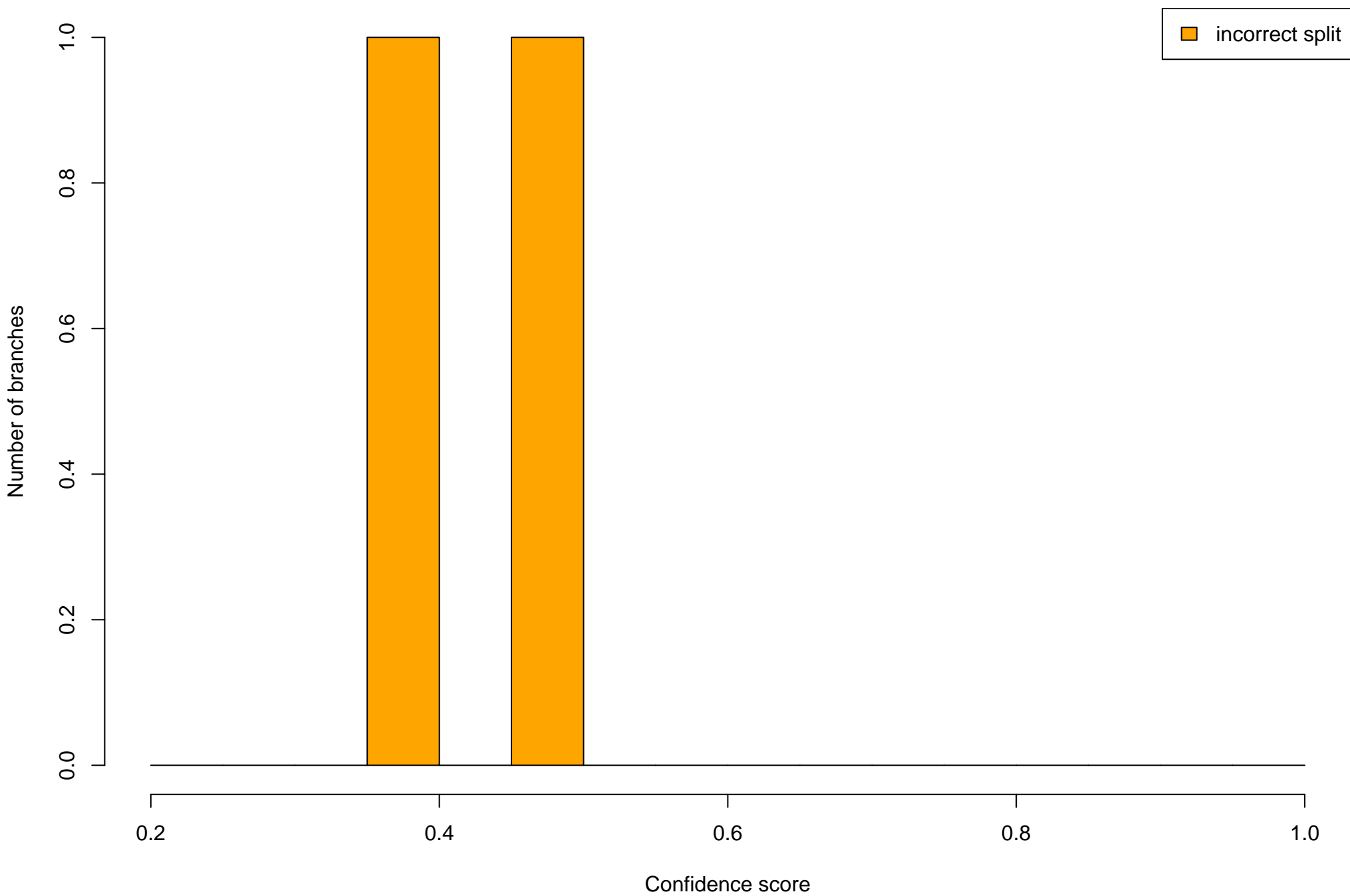
results_yeast1/ – Branch lengths



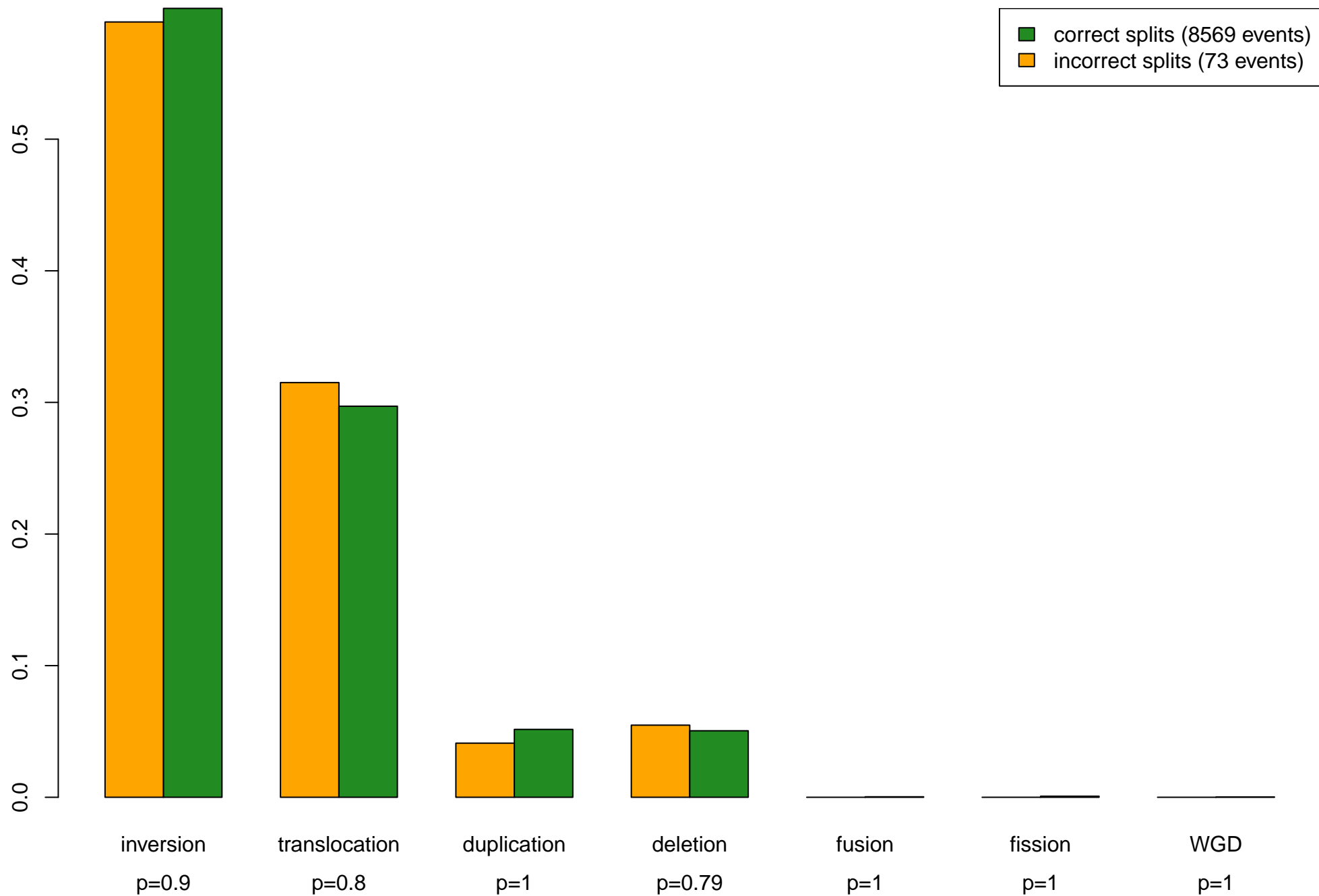
results_yeast1/ – PhyChro tree – branch confidence scores



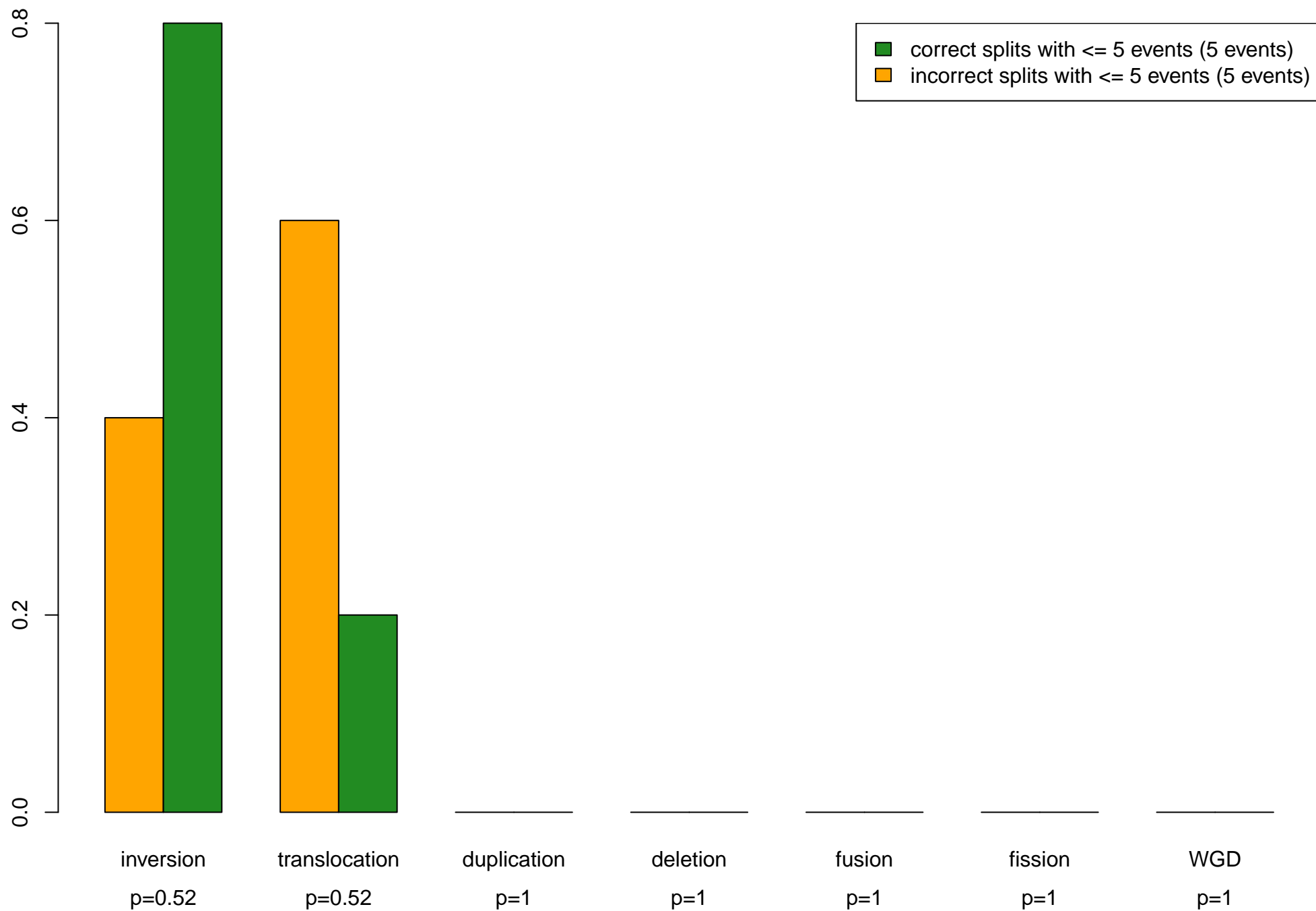
results_yeast1/ – PhyChro tree – branch confidence scores



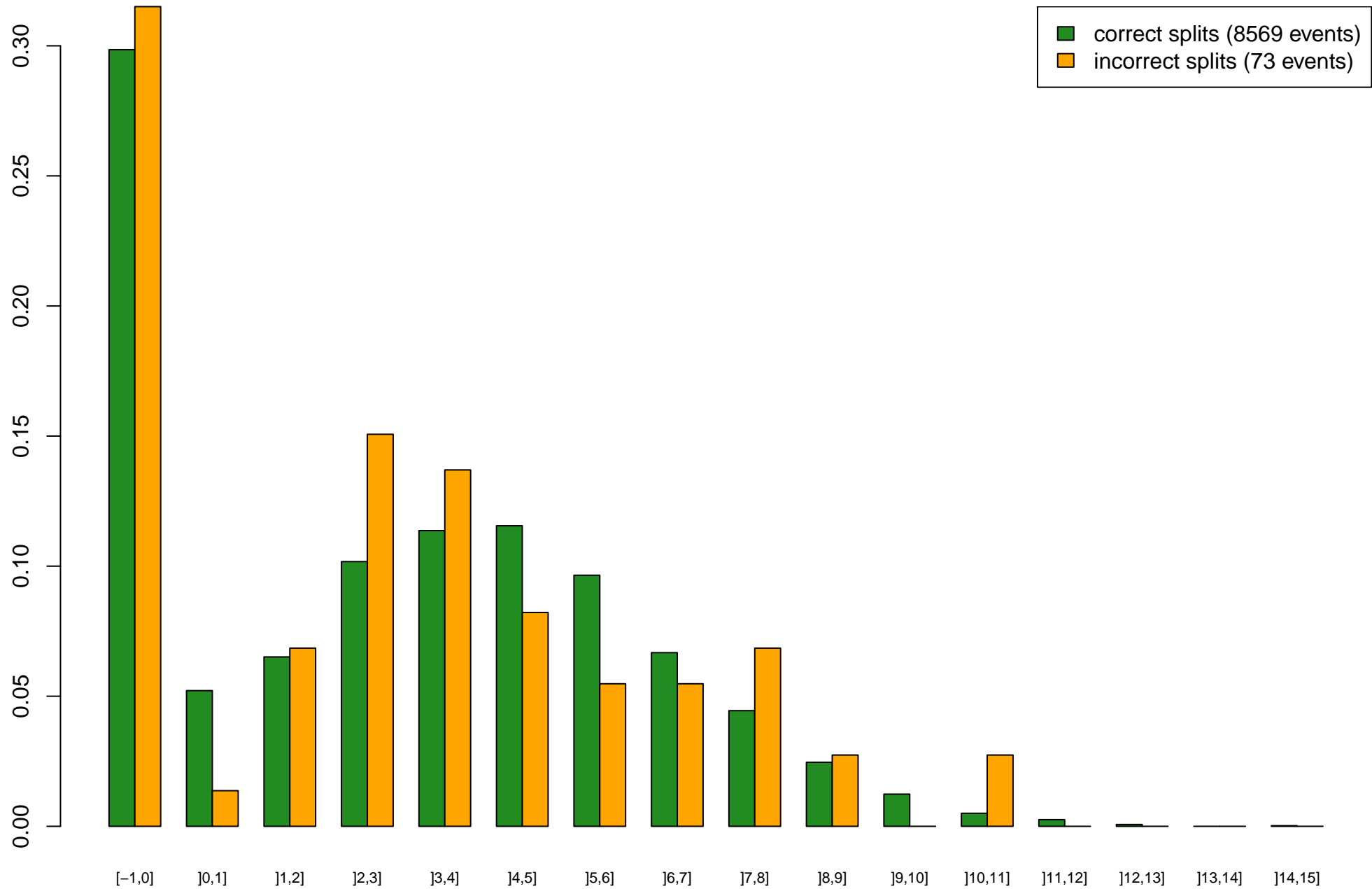
Event types



Event types



Event lengths (in number of genes)



Event lengths (in number of genes)

