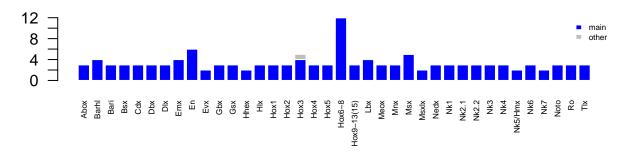


genes in best OG

n(best # 0.8 all) = 37 (best 0.651.000) n(best = all) = 37 (best 0.646 | r=1.000) n(best < all) = 1 (best 0.357 | r=1.000)

number of reference genes in main and other OGs



num OGs per refOG

