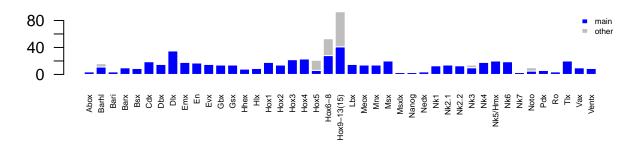


# genes in best OG

n(best # 9.8 all) s 37 (best 0.997) n(best = all) = 35 (p=0.943 | r=1.000) n(best < all) = 8 (p=1.000 | r=0.633)

## number of reference genes in main and other OGs



## num OGs per refOG

