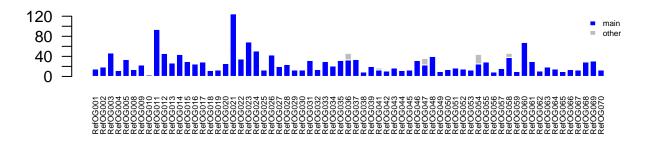


genes in best OG

n(best # 9.8 all) s fit (best 10)(5-0.995) n(best = all) = 59 (p=0.809 | r=0.997) n(best < all) = 8 (p=0.997 | r=0.771)

number of reference genes in main and other OGs



num OGs per refOG

