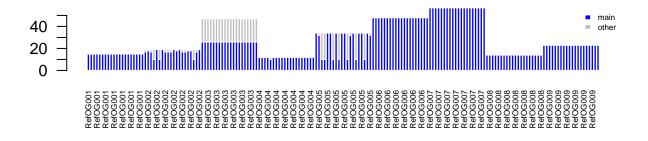


genes in best OG

number of reference genes in main and other OGs



num OGs per refOG

