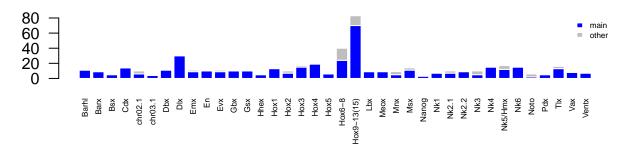


# genes in best OG

## number of reference genes in main and other OGs



## num OGs per refOG

