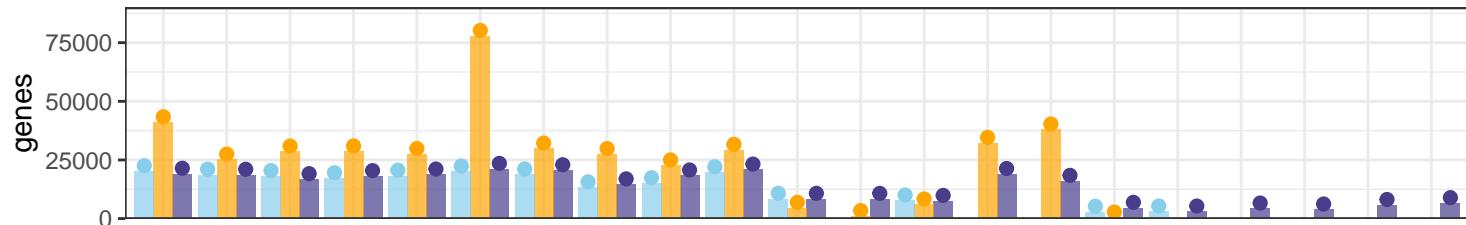


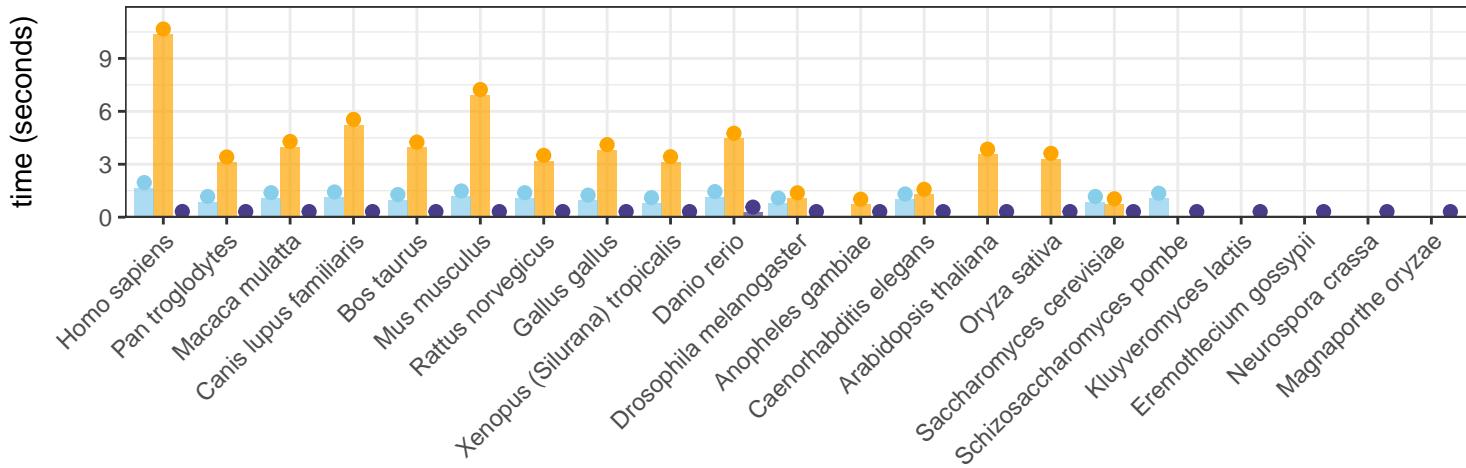
a

all_genes() : genes retrieved



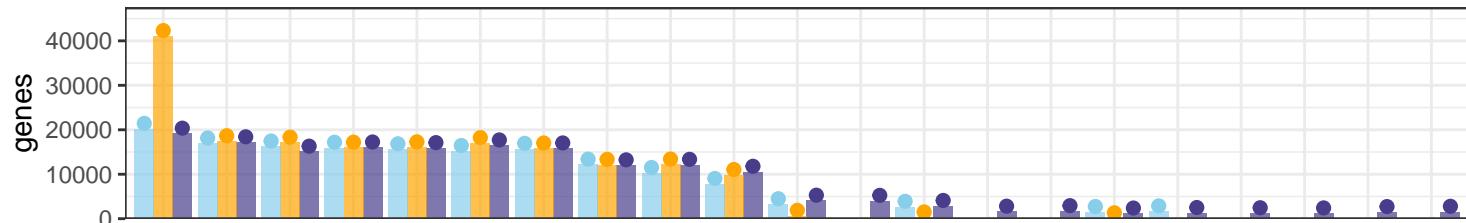
b

all_genes() : time elapsed



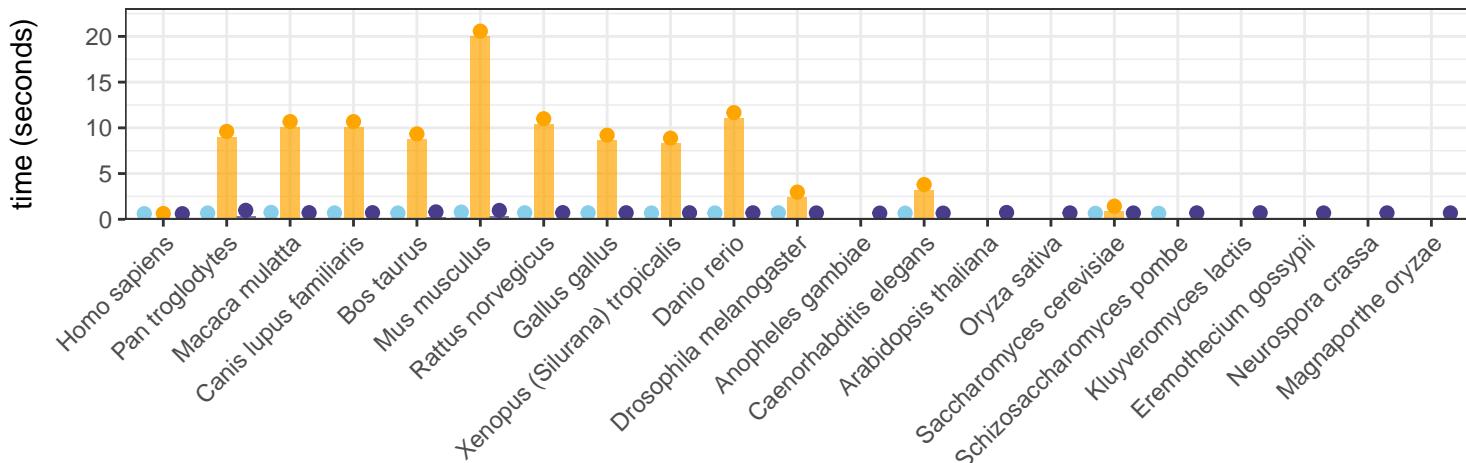
c

convert_orthologs() : genes retrieved



d

convert_orthologs() : time elapsed



method babelgene gprofiler homologene