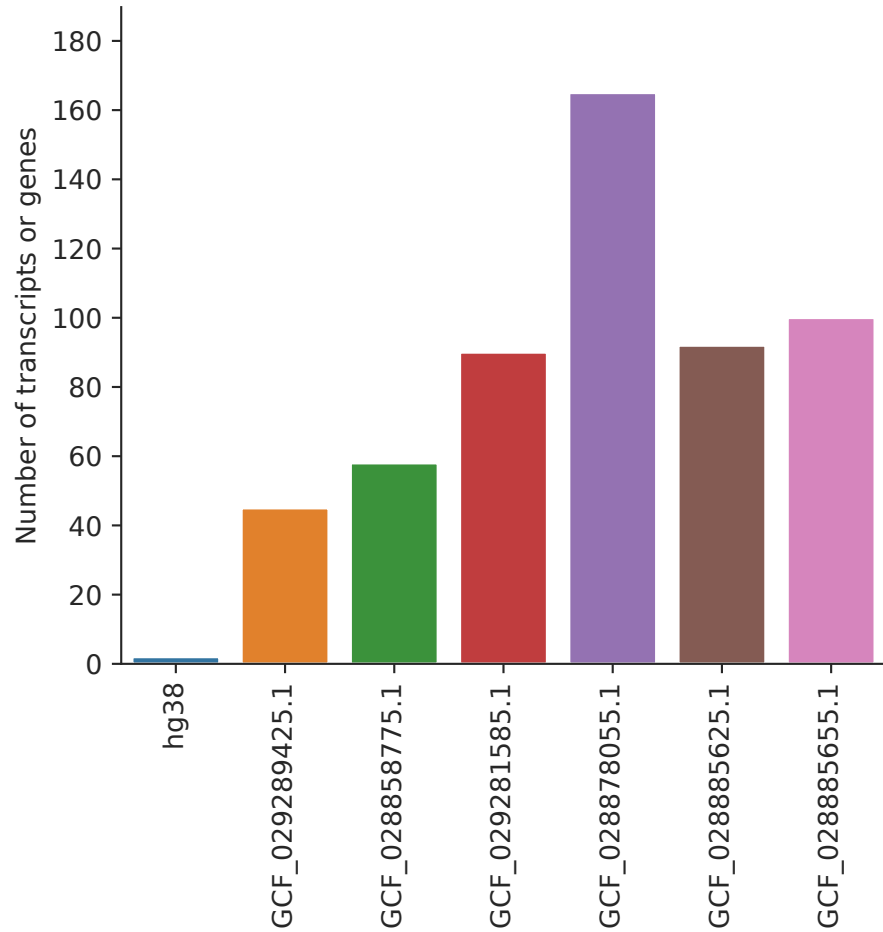


# Split genes

category = Number of contig split genes



category = Number of intra-contig split genes

