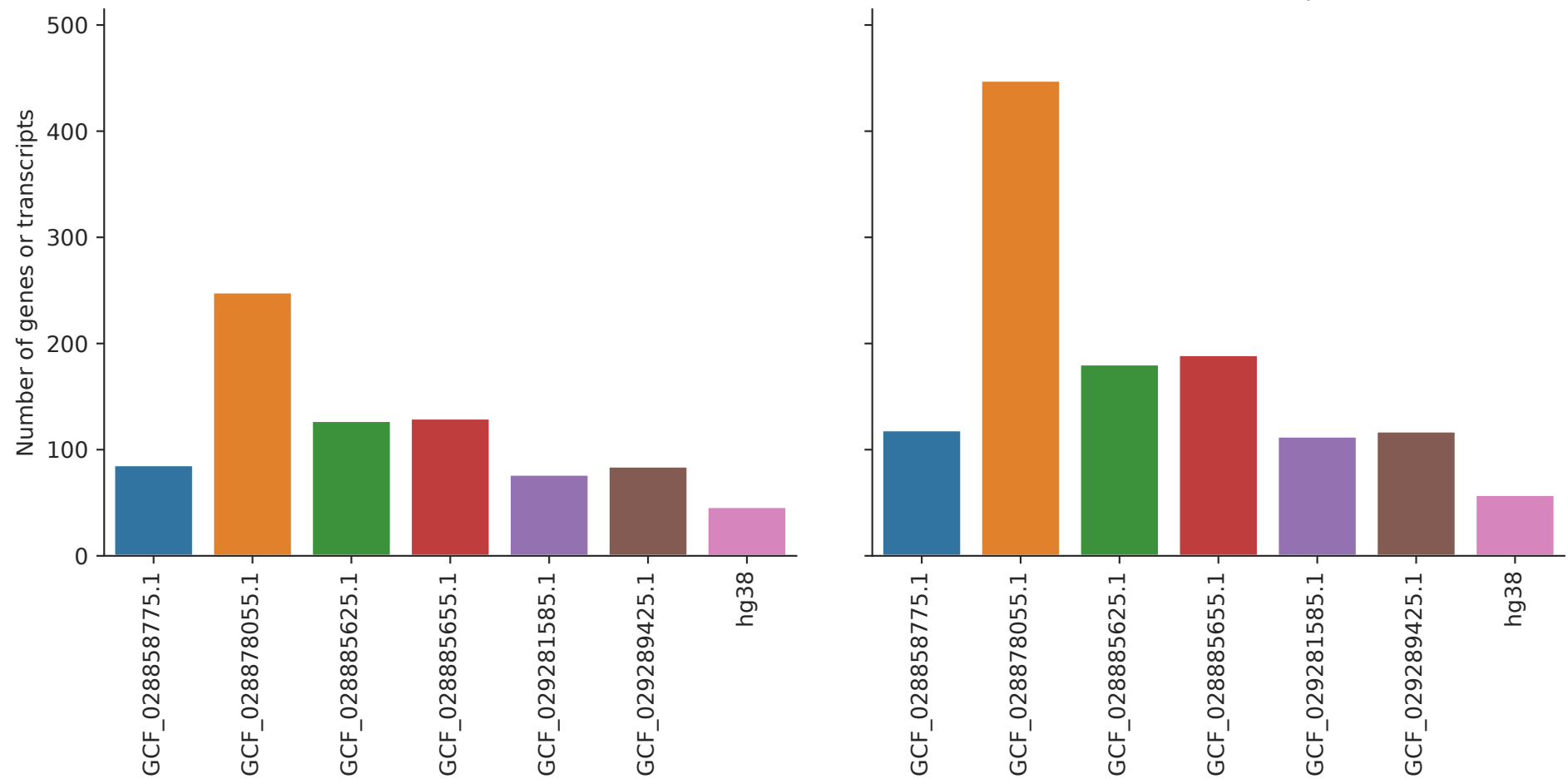


Number of missing orthologs in consensus set

variable = Genes

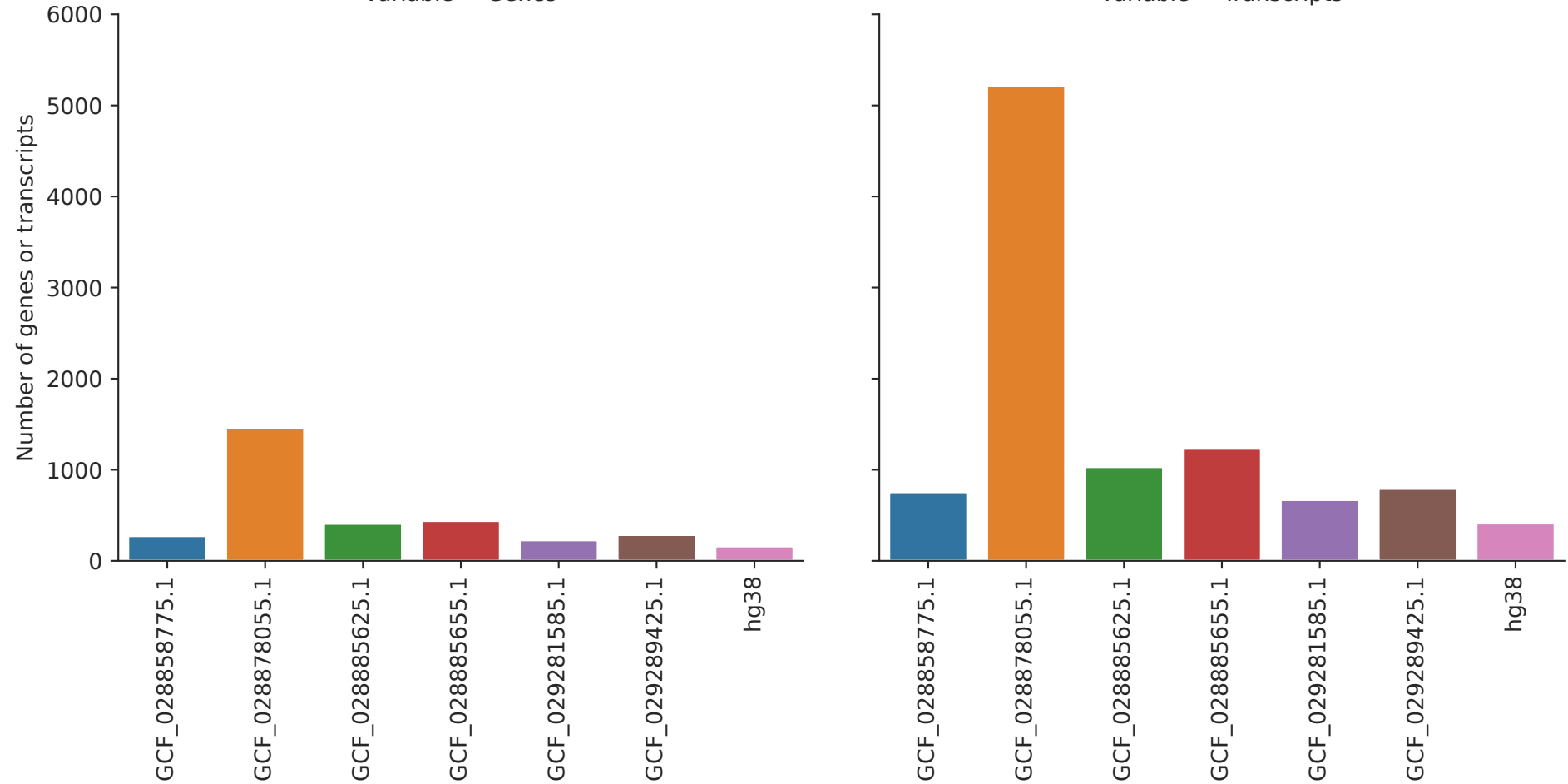
variable = Transcripts



Number of missing orthologs in consensus set for biotype protein_coding

variable = Genes

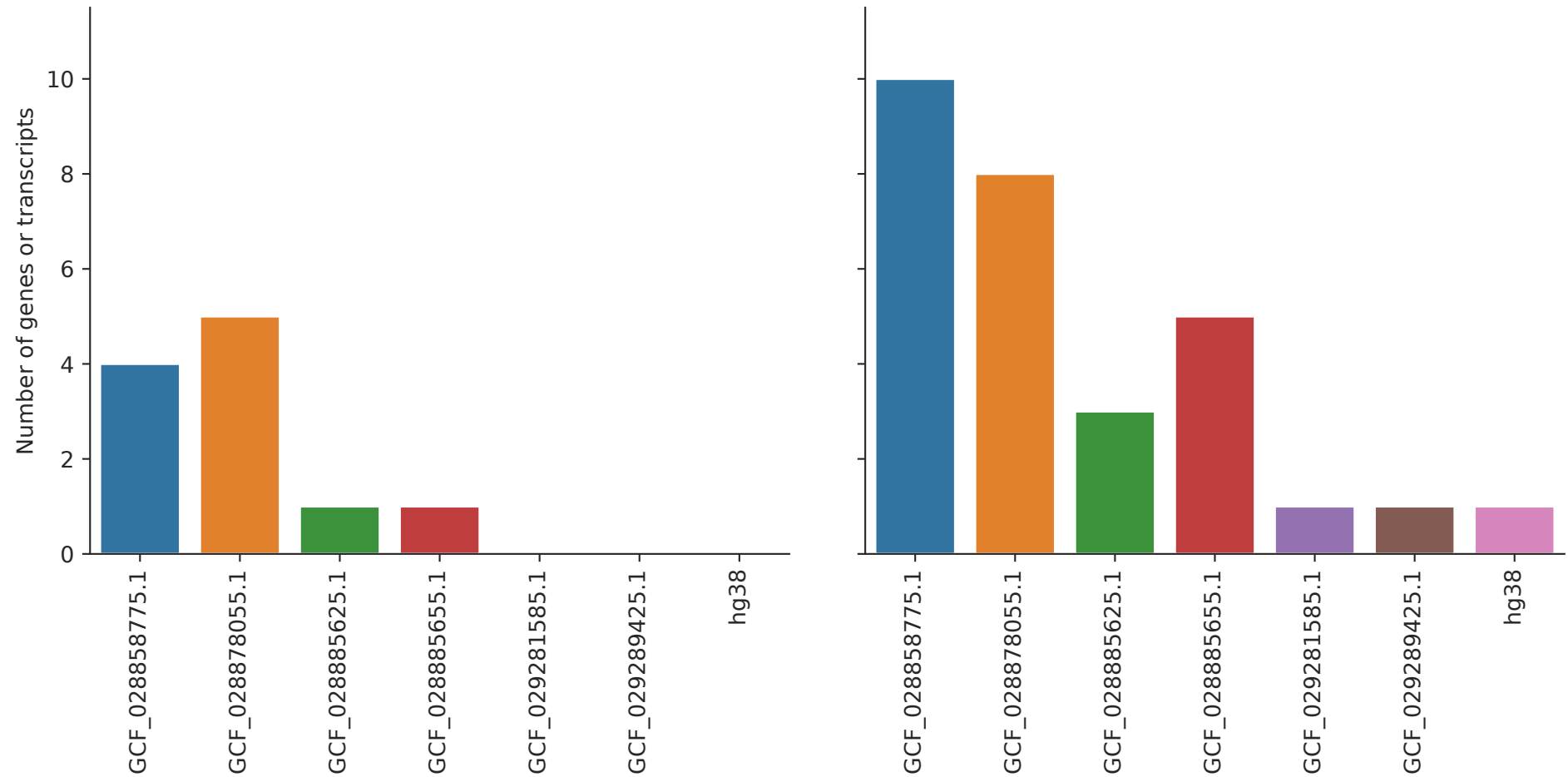
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_C_gene

variable = Genes

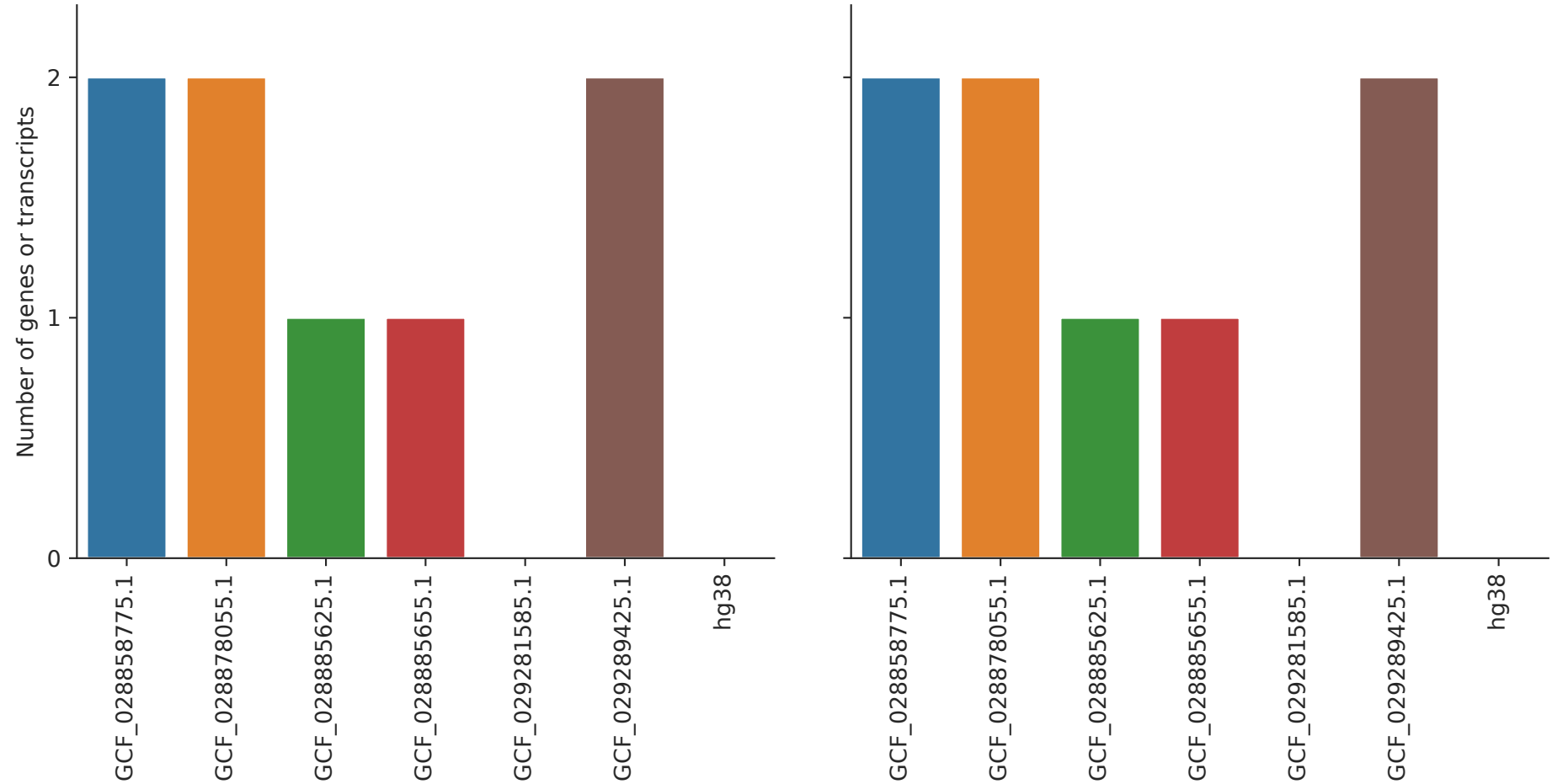
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_C_pseudogene

variable = Genes

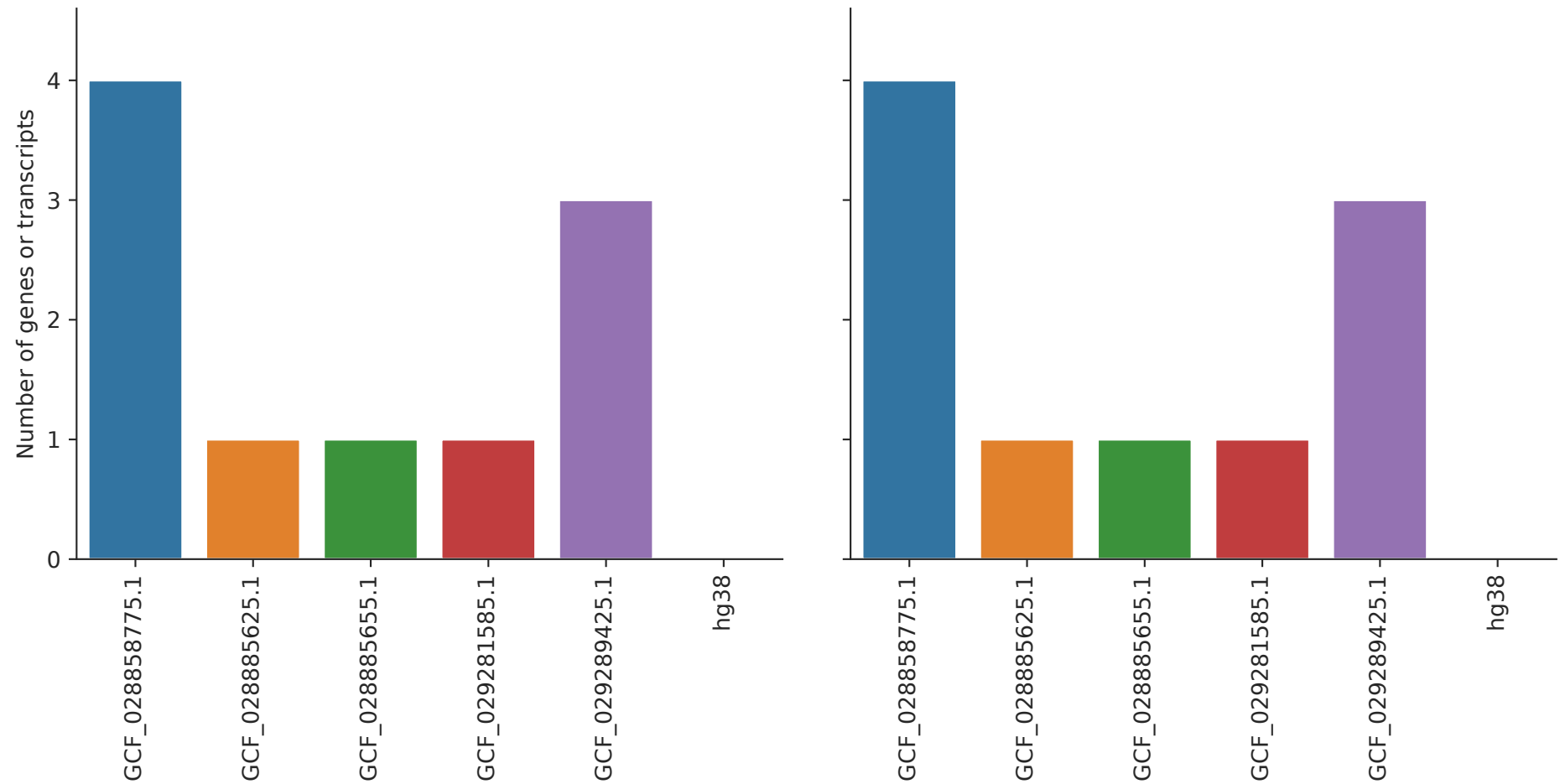
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_D_gene

variable = Genes

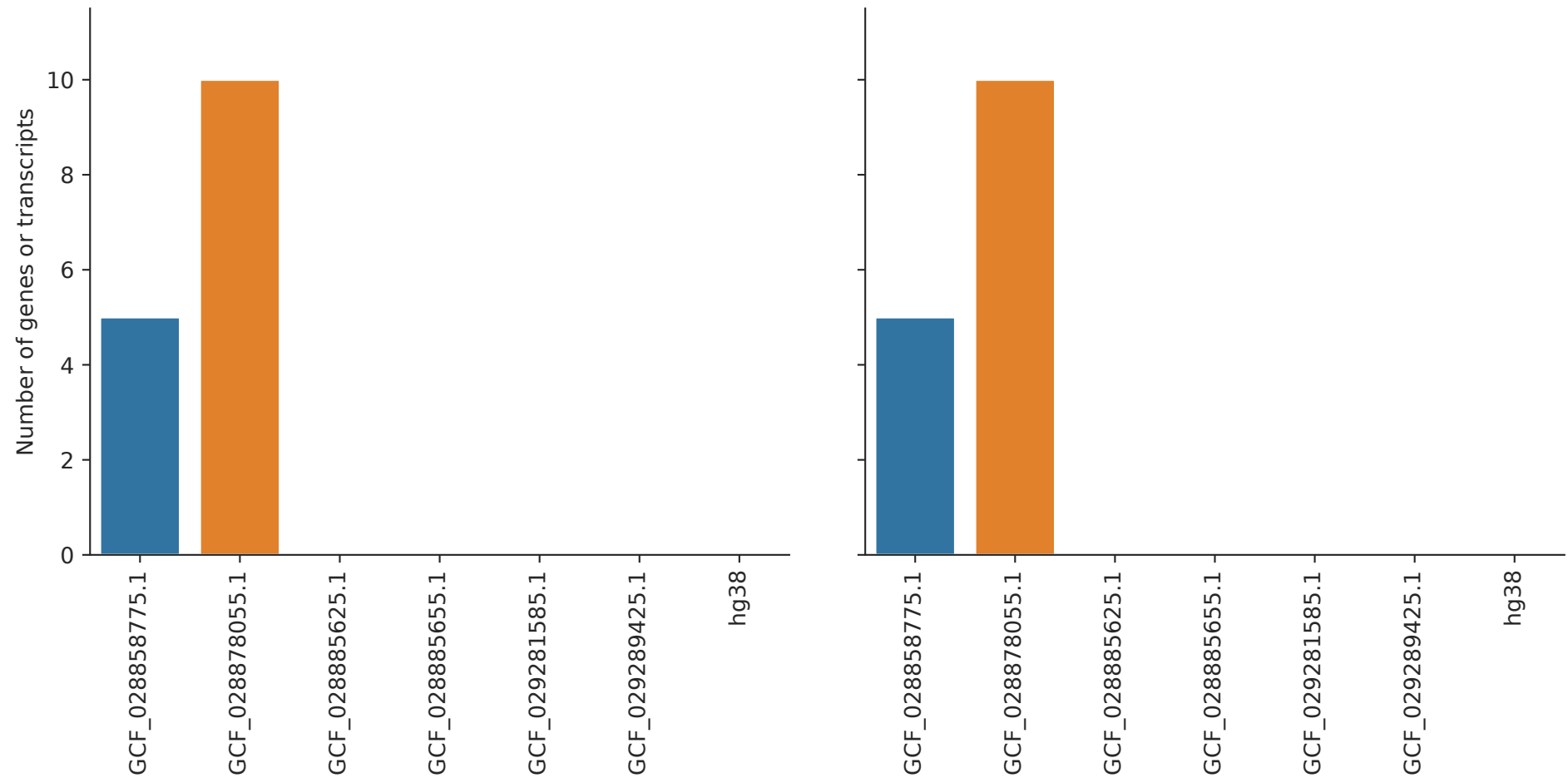
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_J_gene

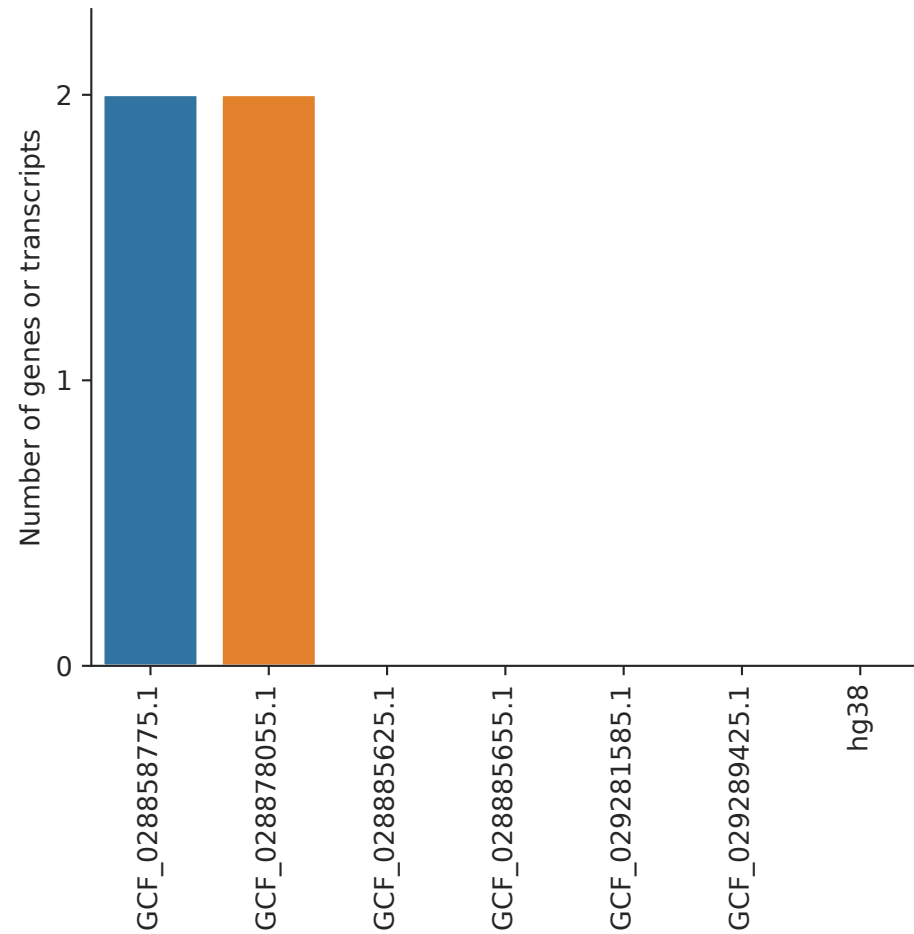
variable = Genes

variable = Transcripts

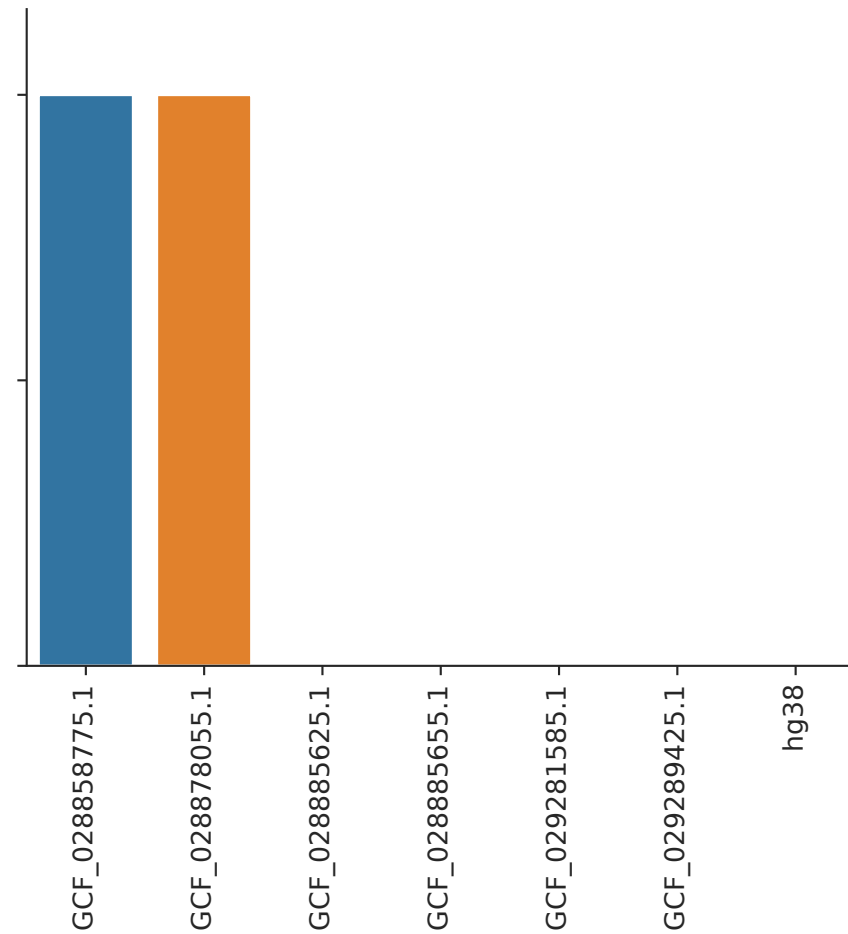


Number of missing orthologs in consensus set for biotype IG_J_pseudogene

variable = Genes



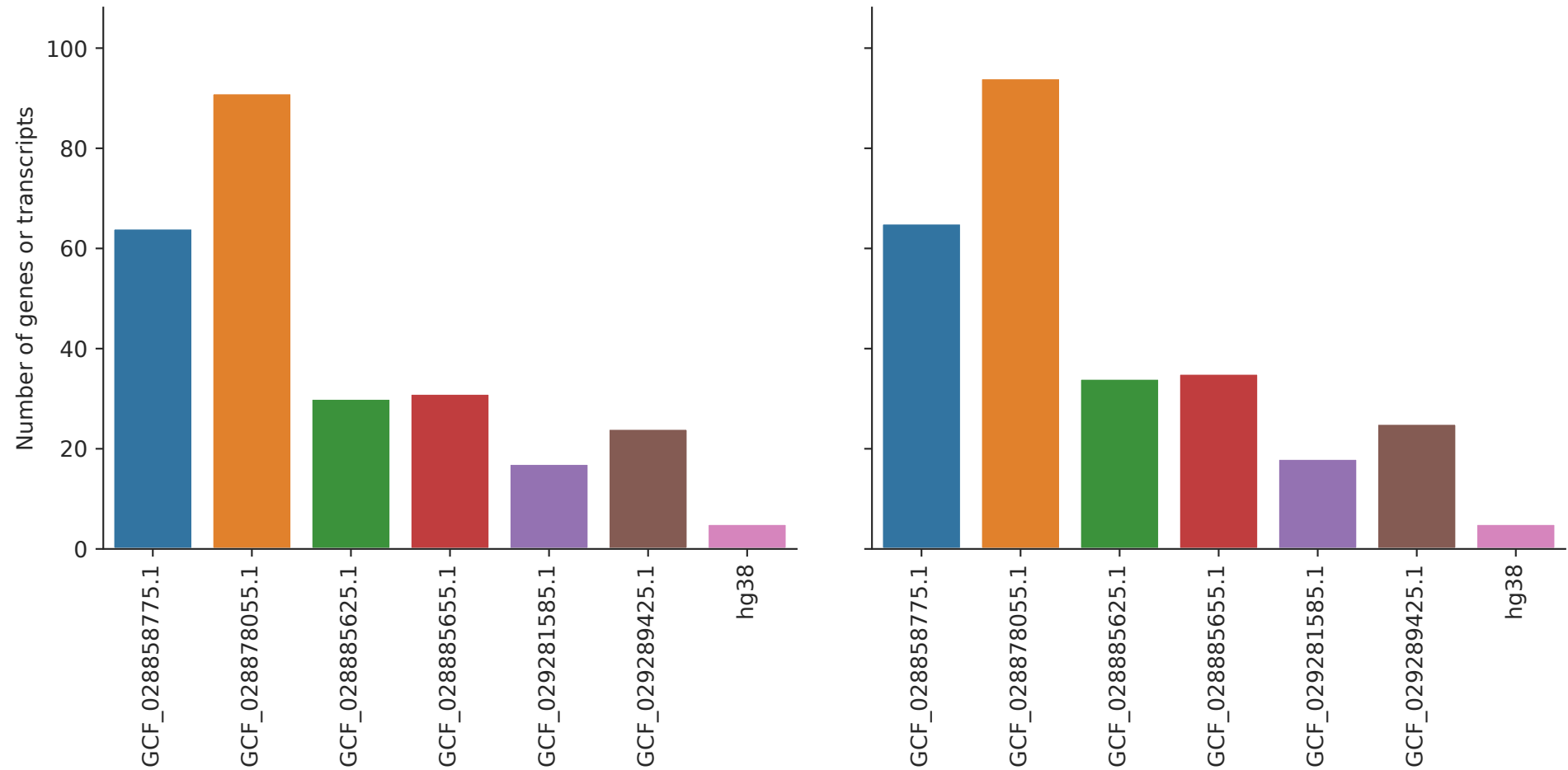
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_V_gene

variable = Genes

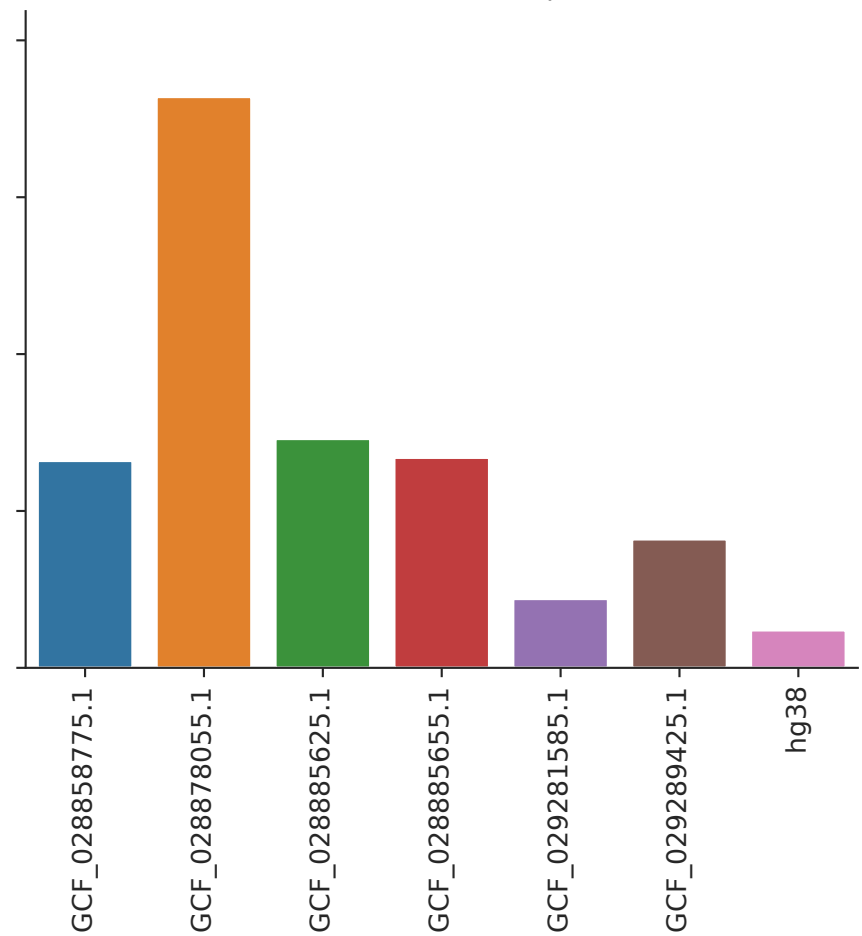
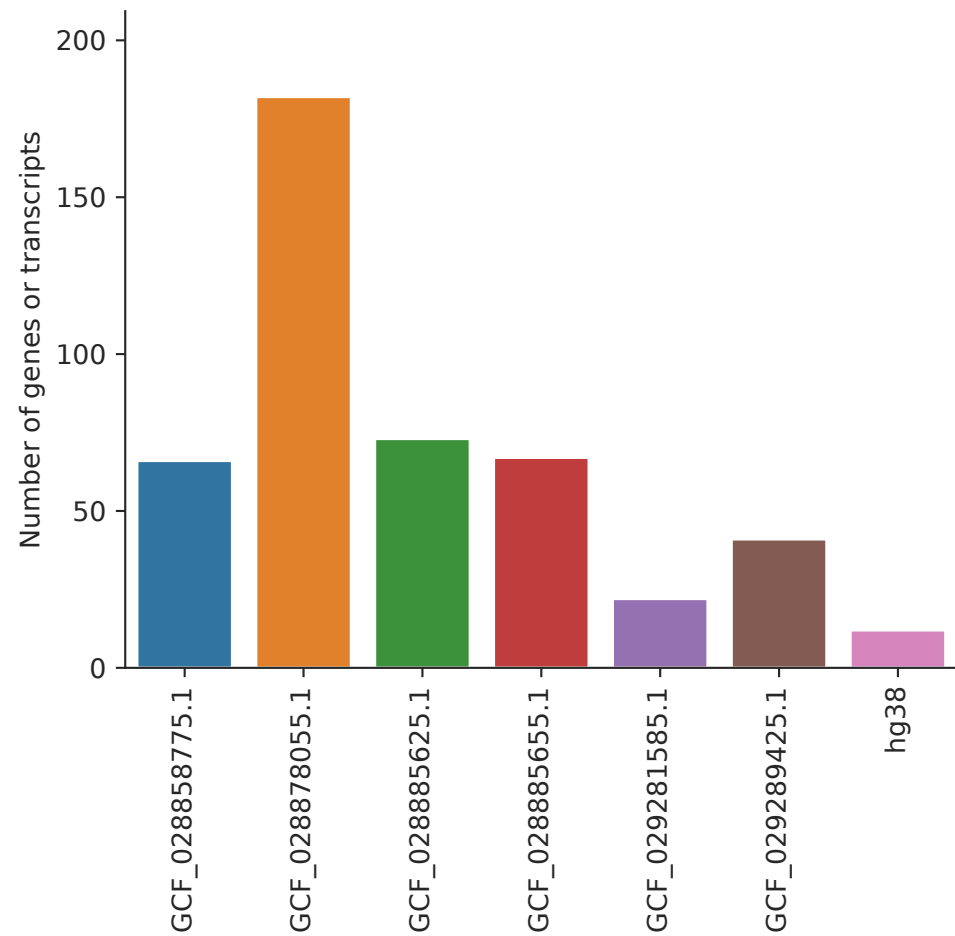
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_V_pseudogene

variable = Genes

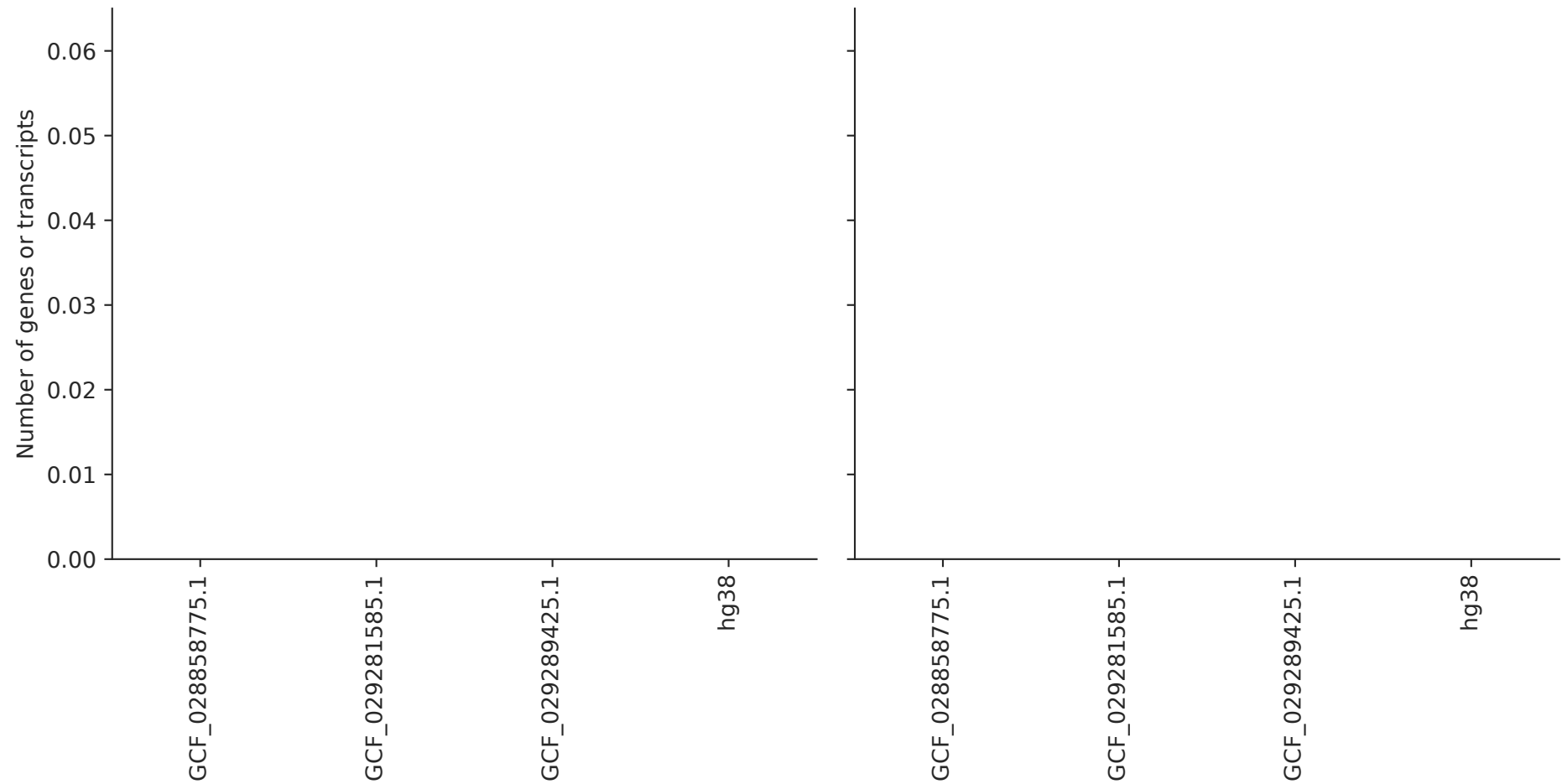
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_pseudogene

variable = Genes

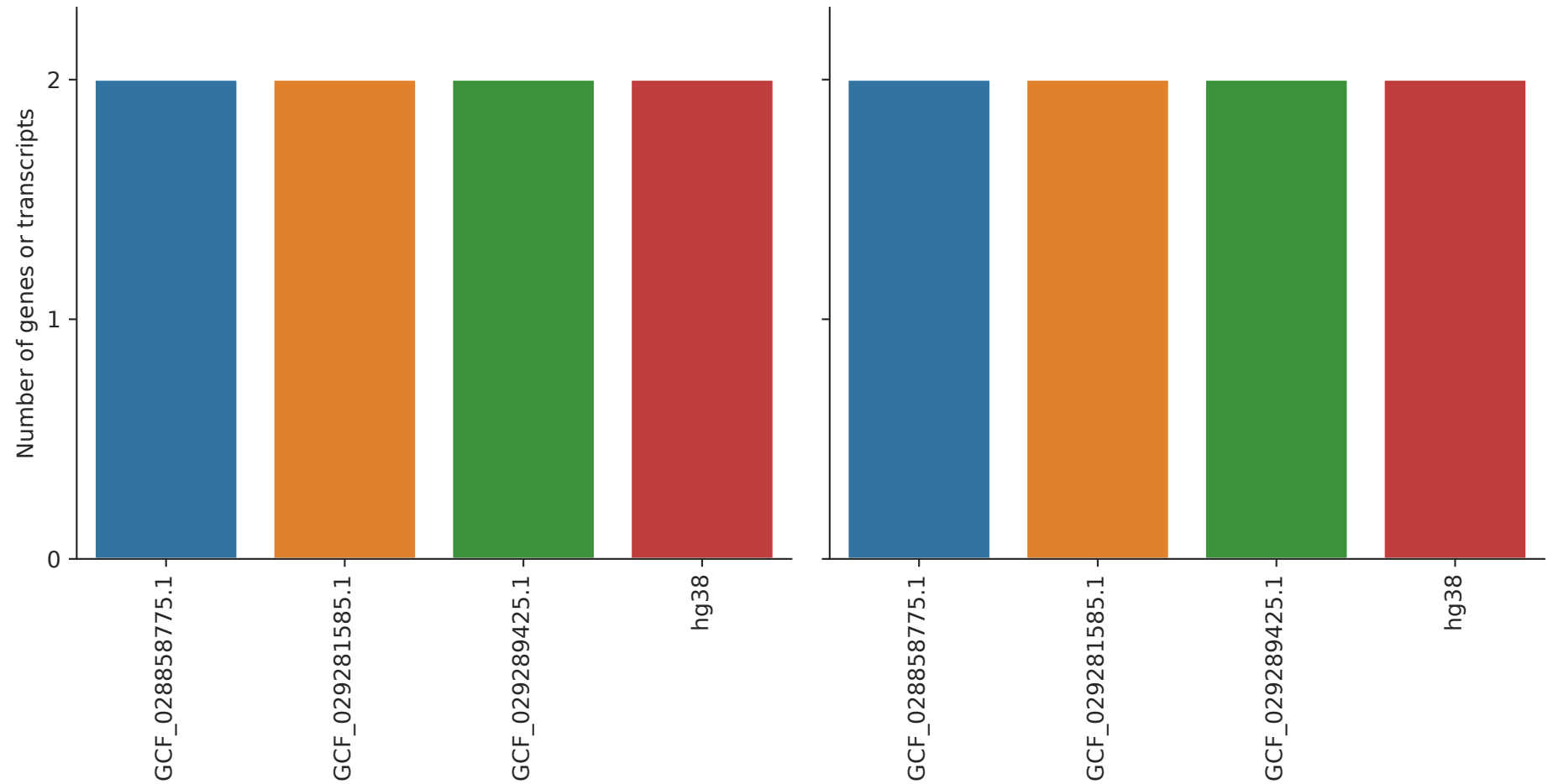
variable = Transcripts



Number of missing orthologs in consensus set for biotype Mt_rRNA

variable = Genes

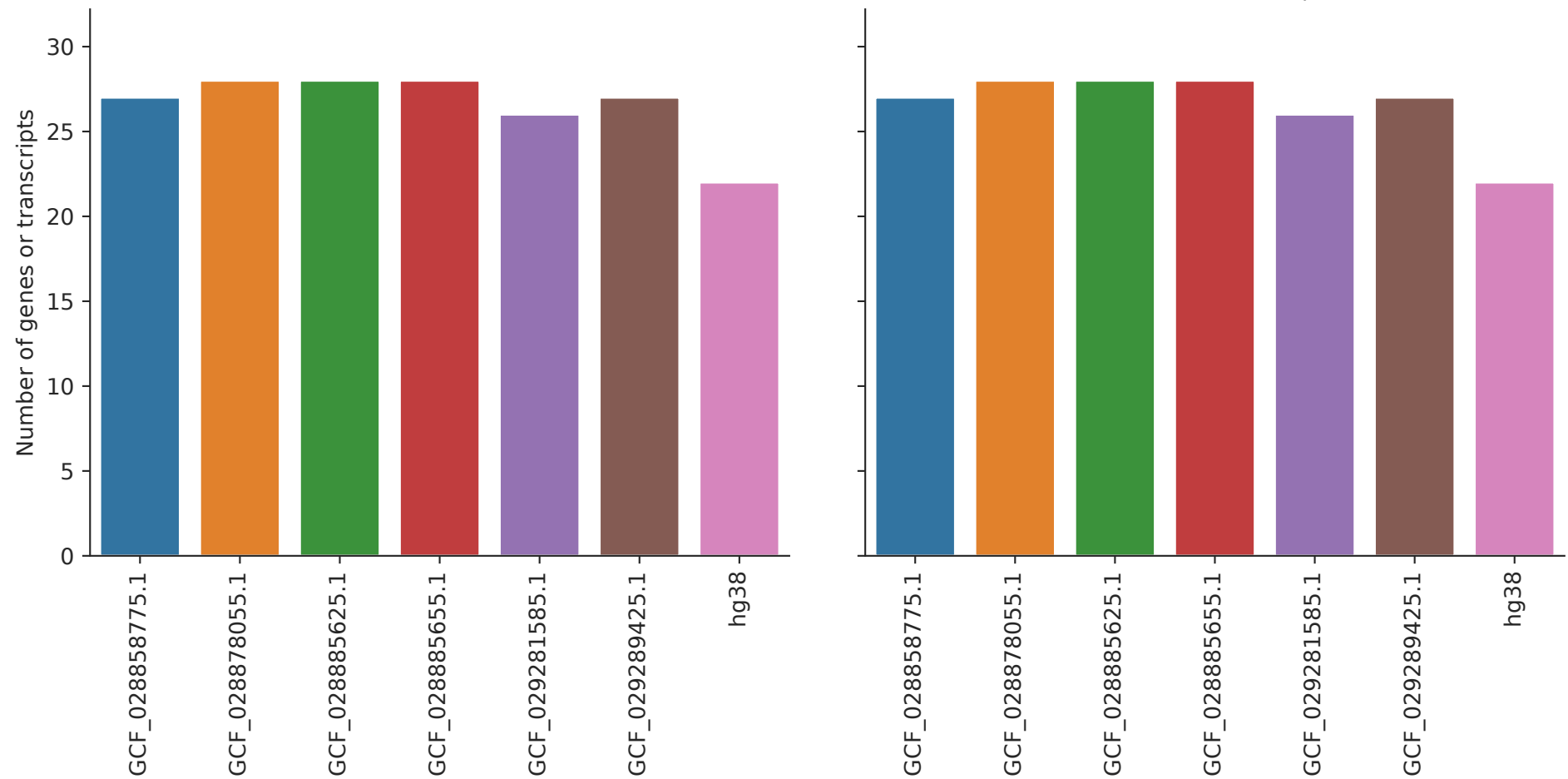
variable = Transcripts



Number of missing orthologs in consensus set for biotype Mt_tRNA

variable = Genes

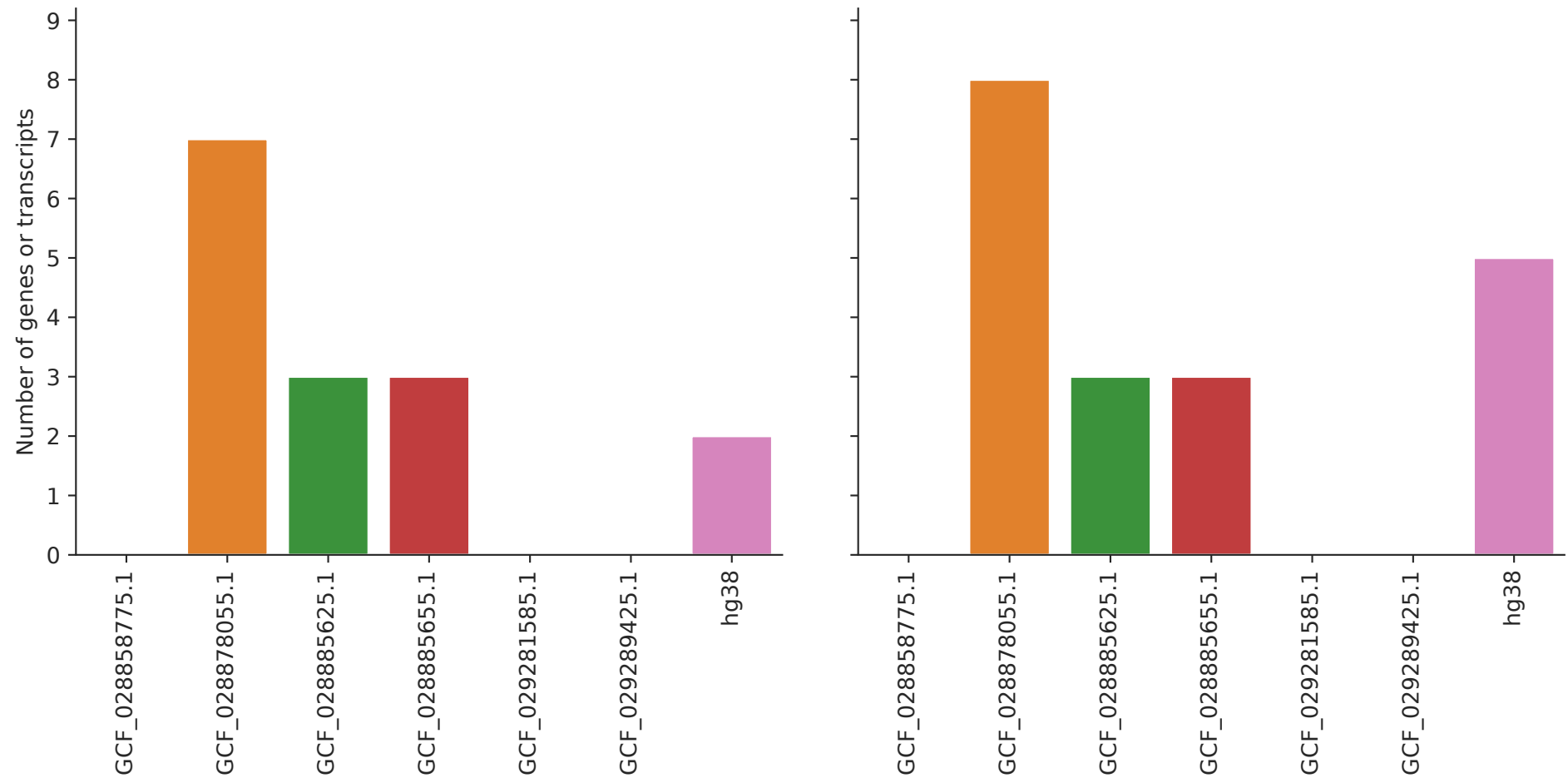
variable = Transcripts



Number of missing orthologs in consensus set for biotype StringTie

variable = Genes

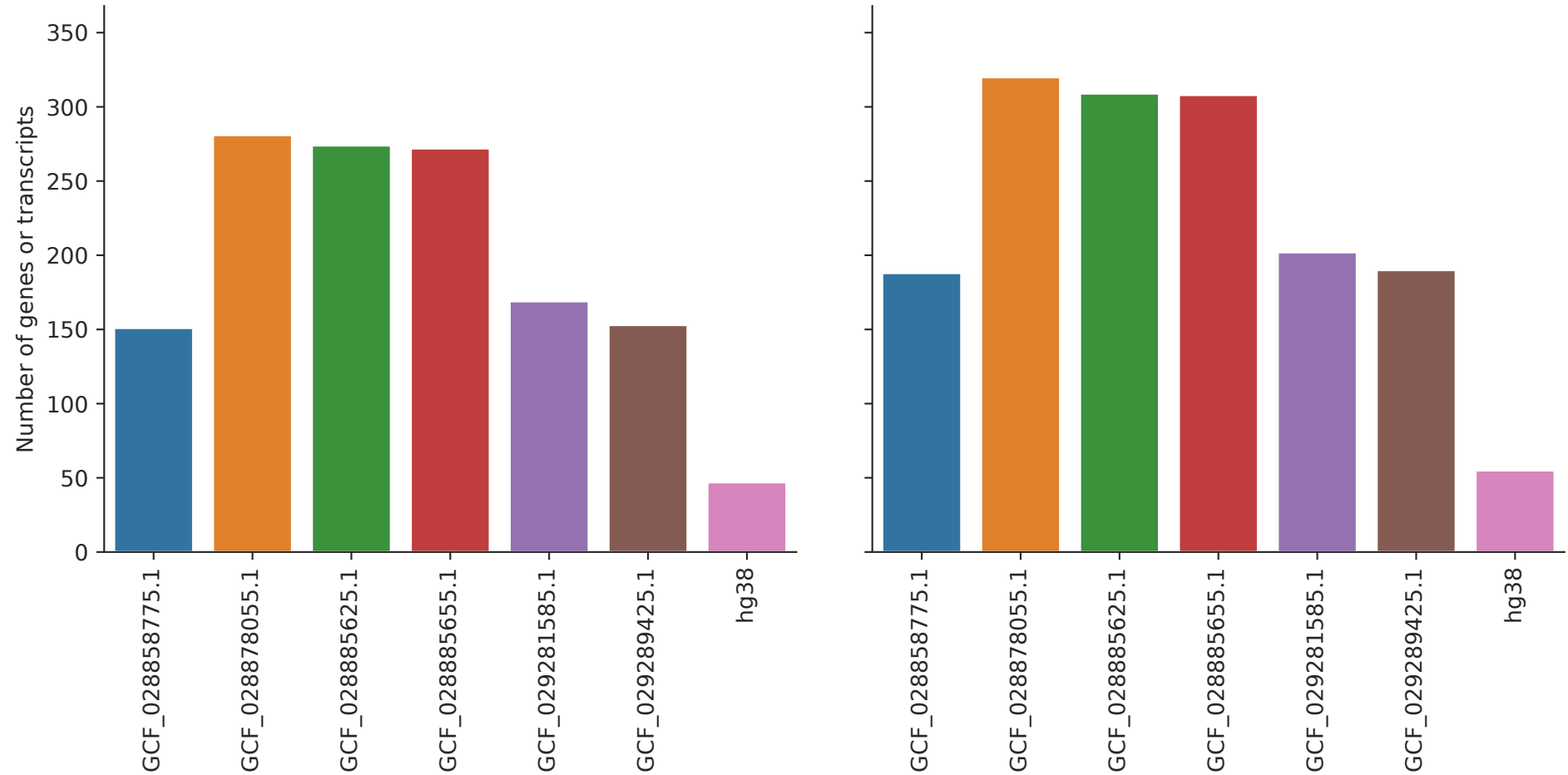
variable = Transcripts



Number of missing orthologs in consensus set for biotype TEC

variable = Genes

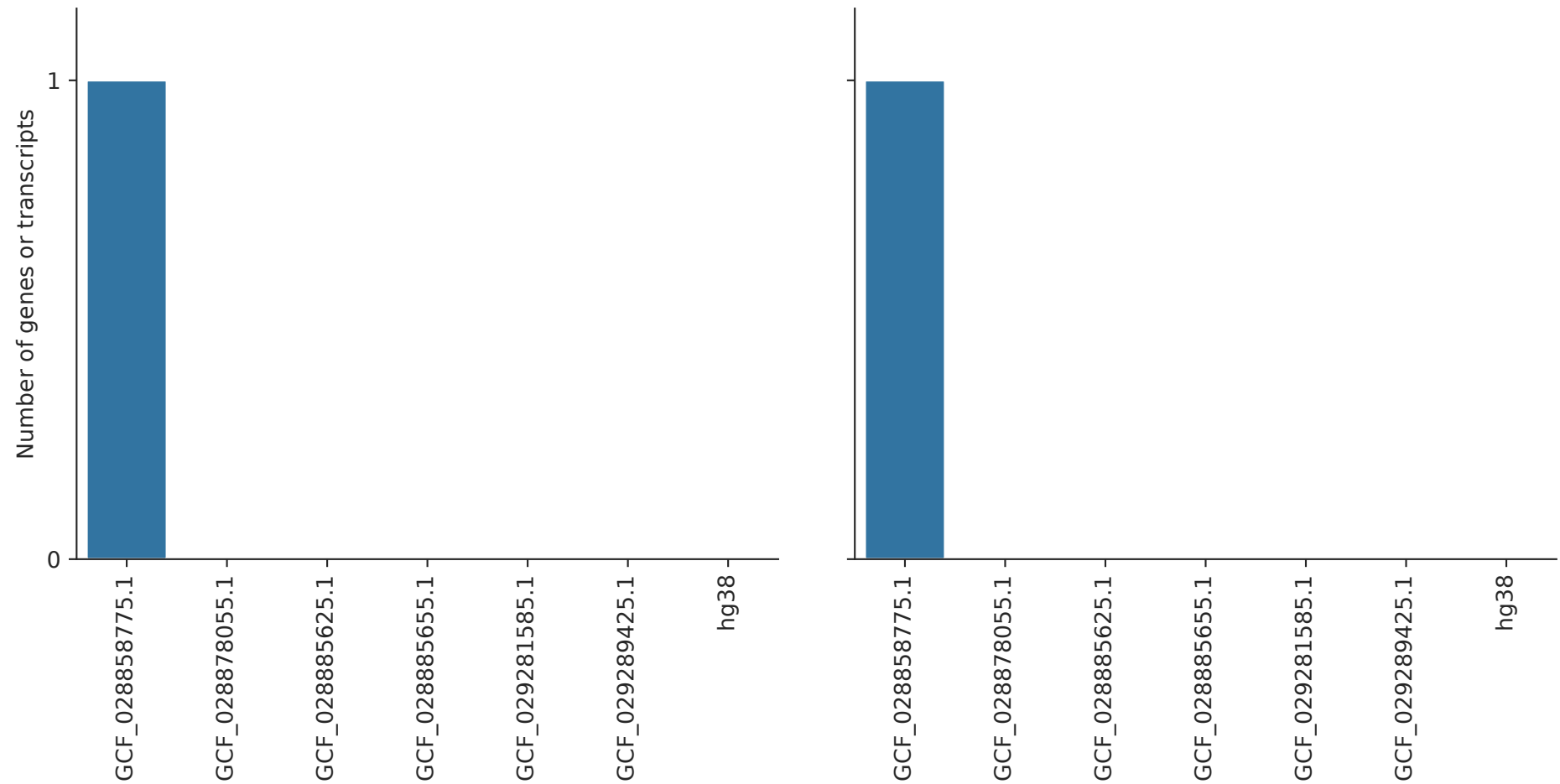
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_C_gene

variable = Genes

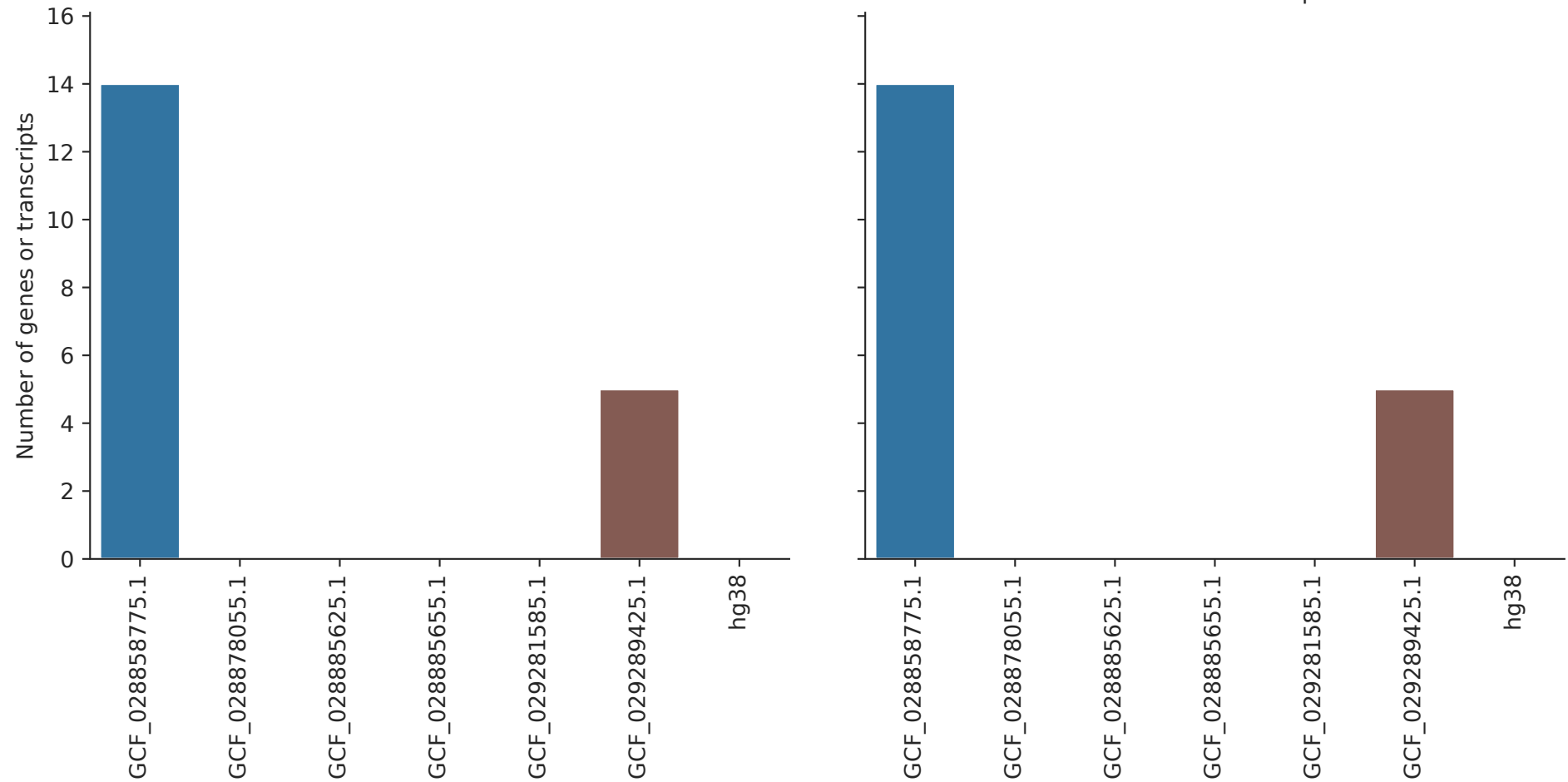
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_J_gene

variable = Genes

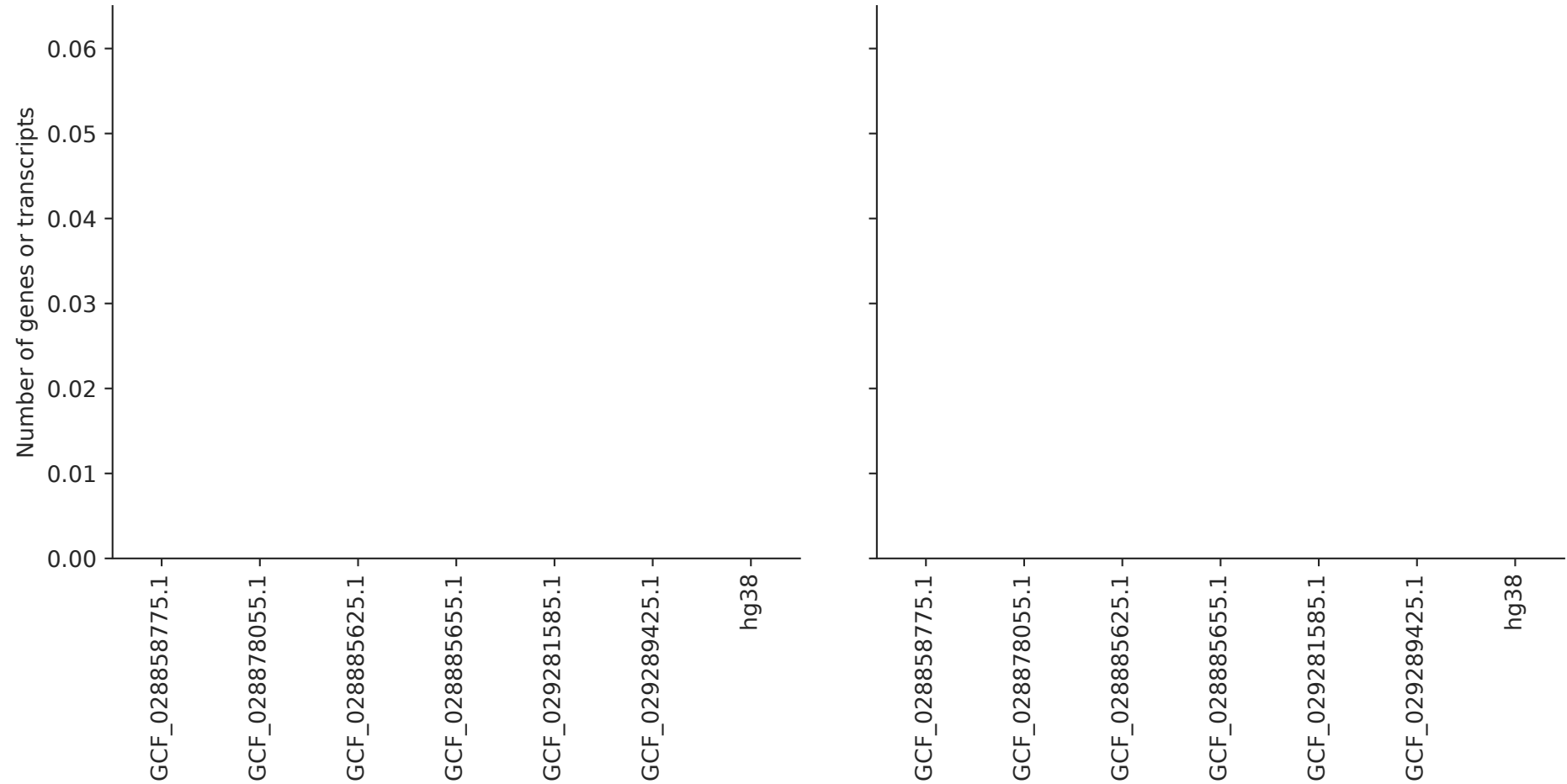
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_J_pseudogene

variable = Genes

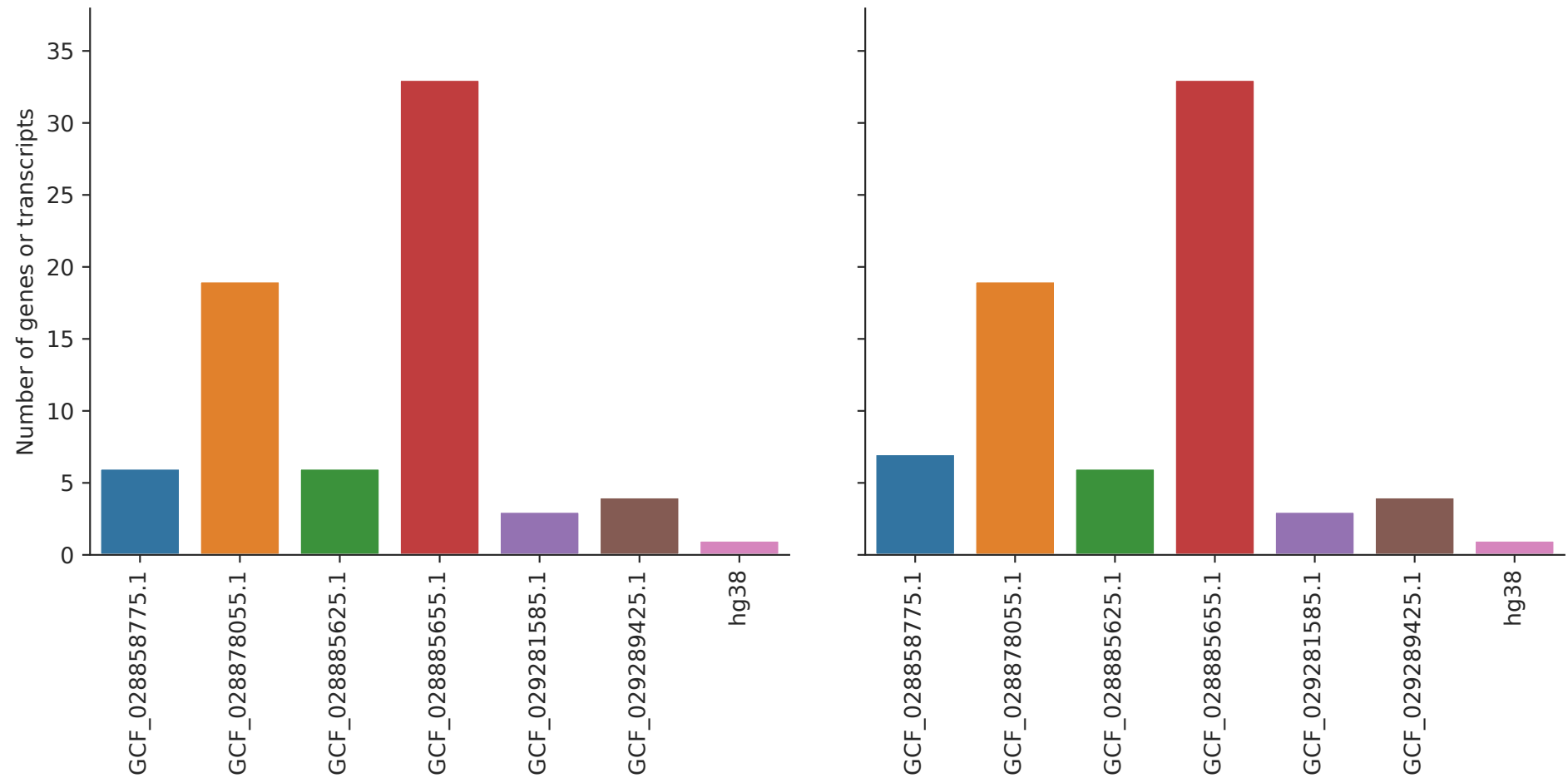
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_V_gene

variable = Genes

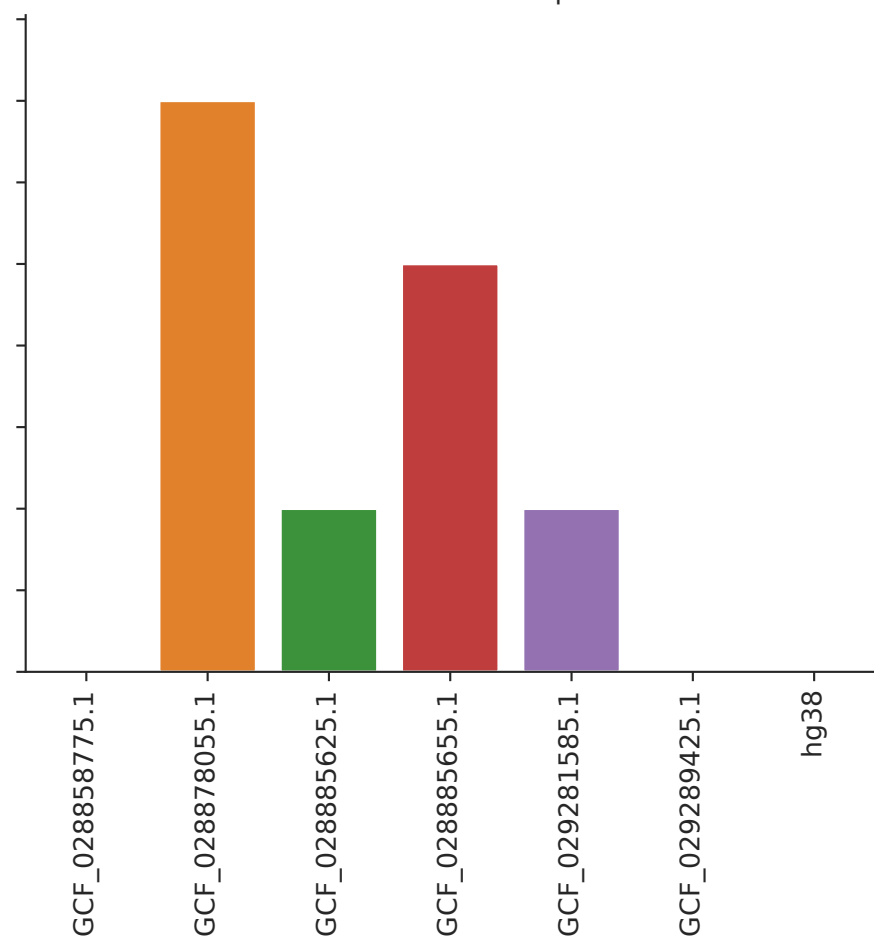
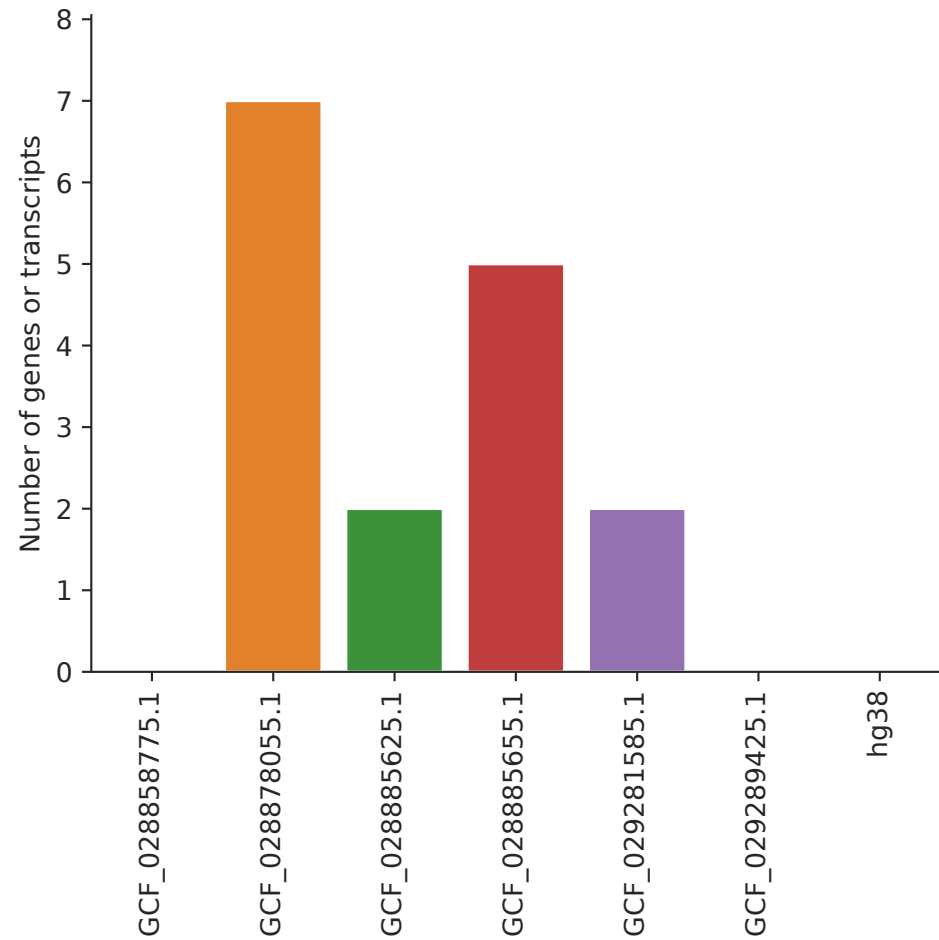
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_V_pseudogene

variable = Genes

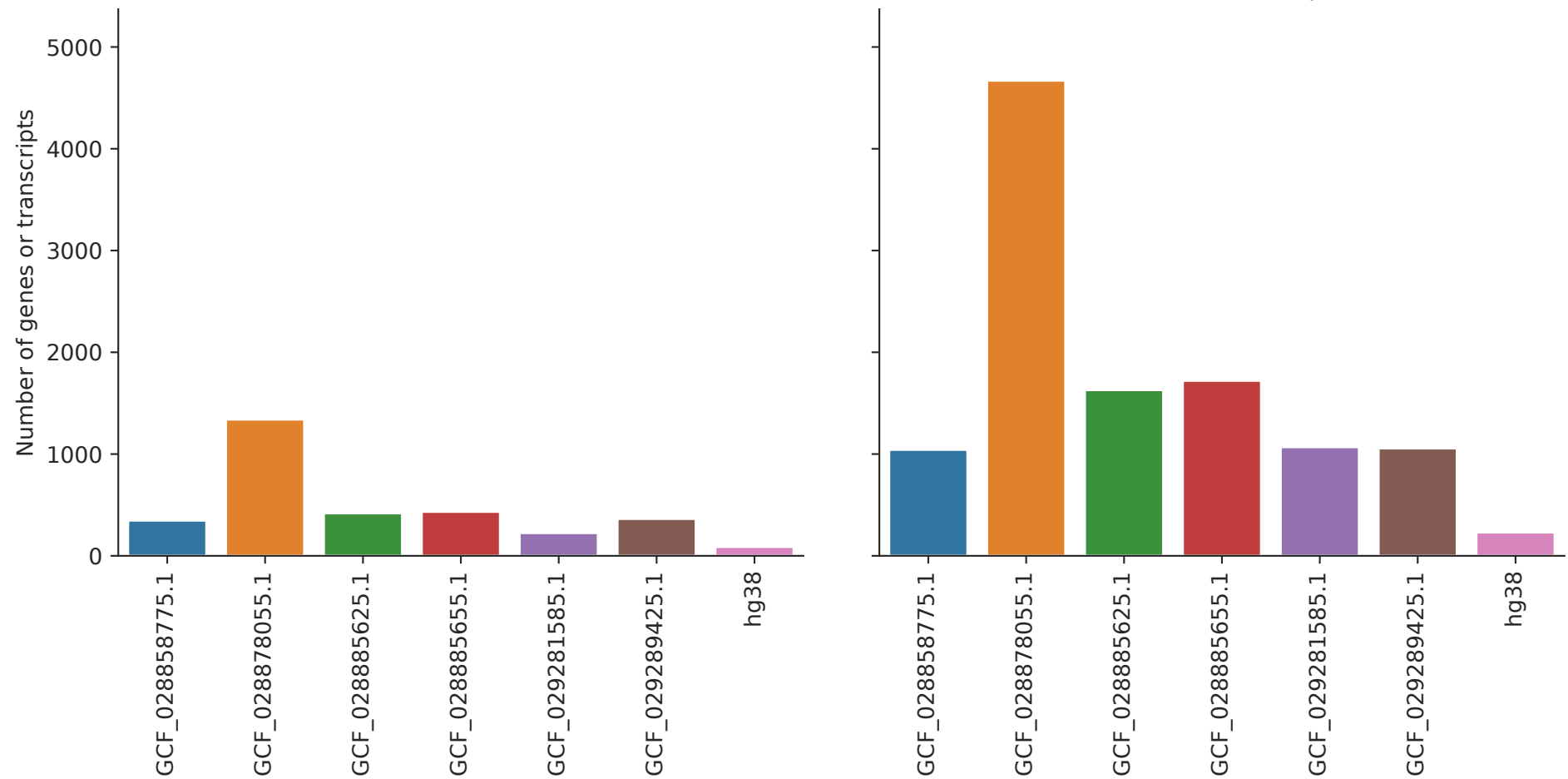
variable = Transcripts



Number of missing orthologs in consensus set for biotype lncRNA

variable = Genes

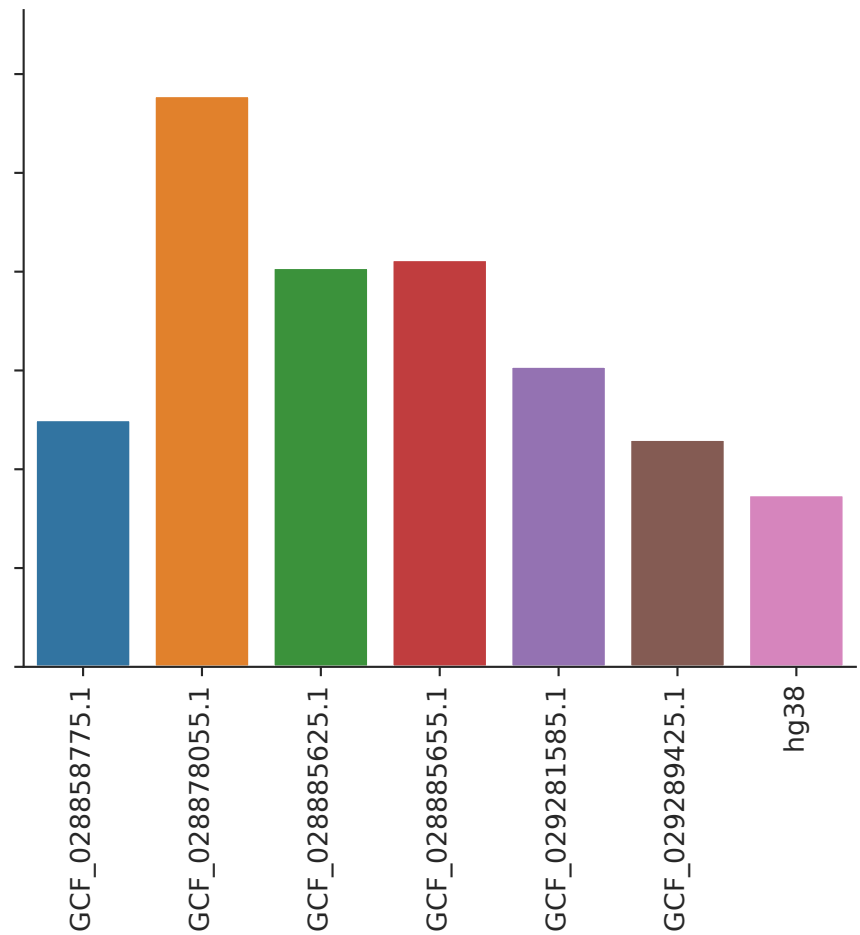
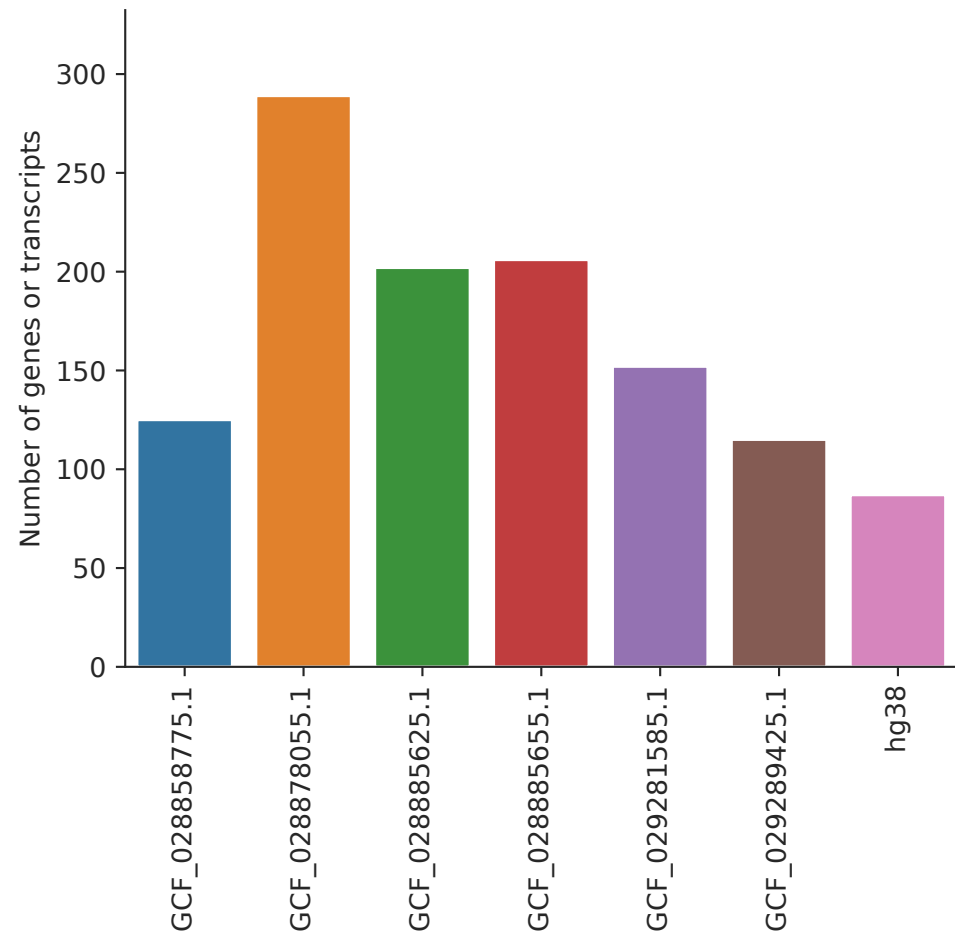
variable = Transcripts



Number of missing orthologs in consensus set for biotype miRNA

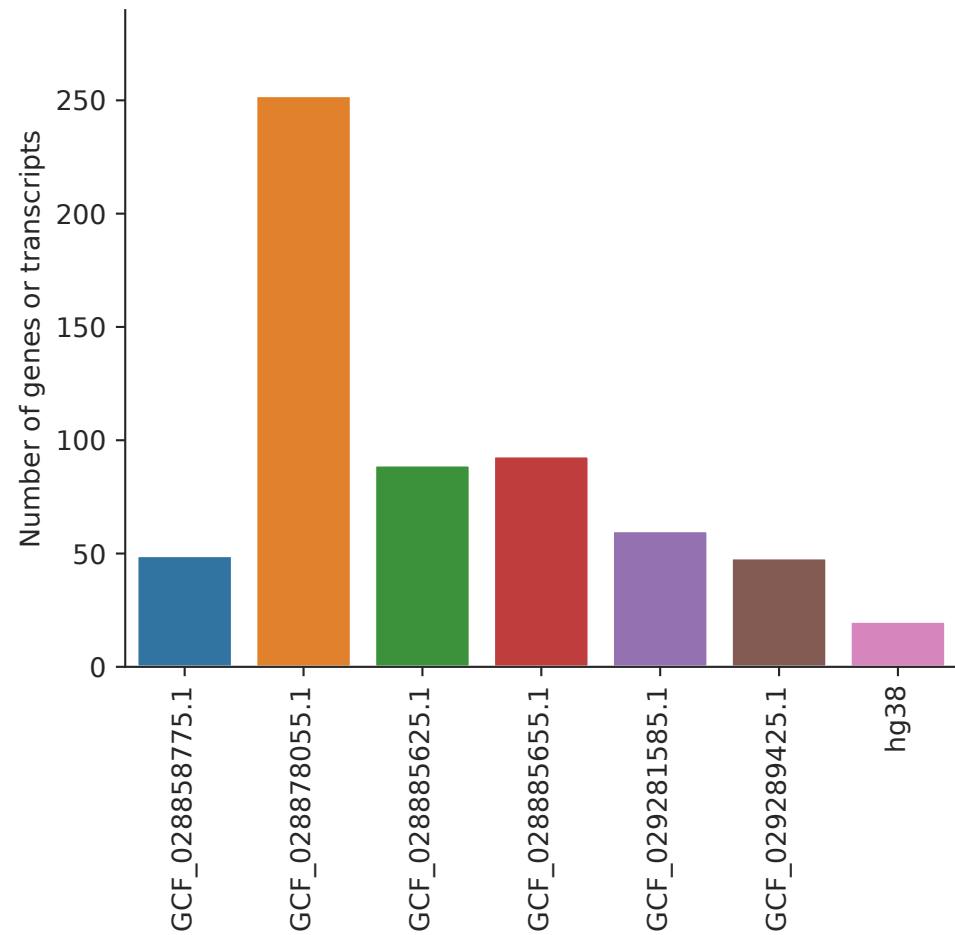
variable = Genes

variable = Transcripts

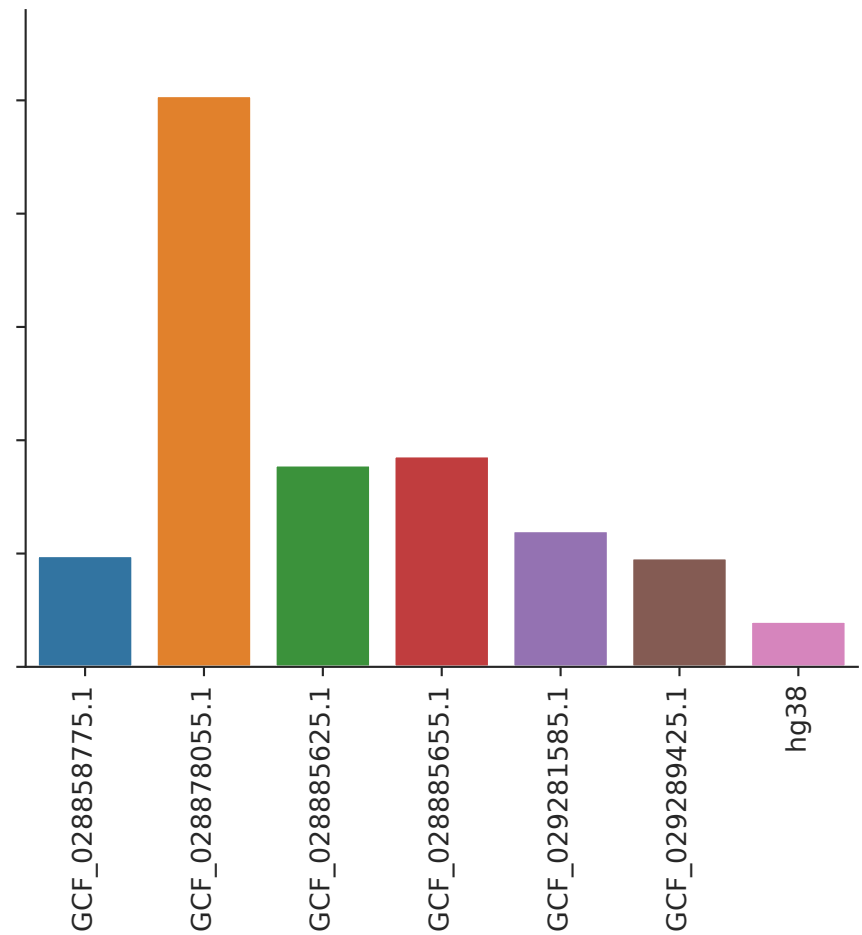


Number of missing orthologs in consensus set for biotype misc_RNA

variable = Genes



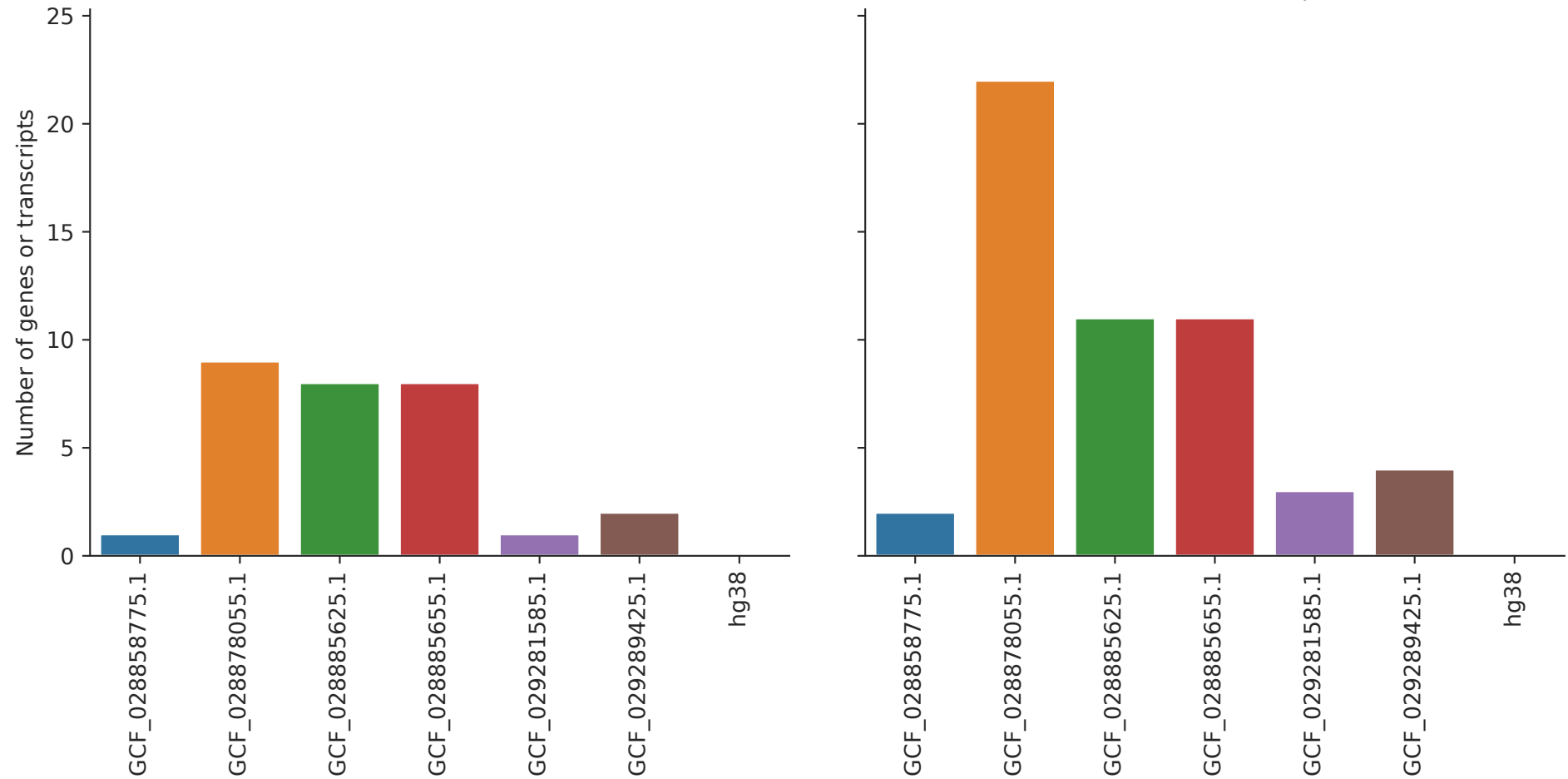
variable = Transcripts



Number of missing orthologs in consensus set for biotype polymorphic_pseudogene

variable = Genes

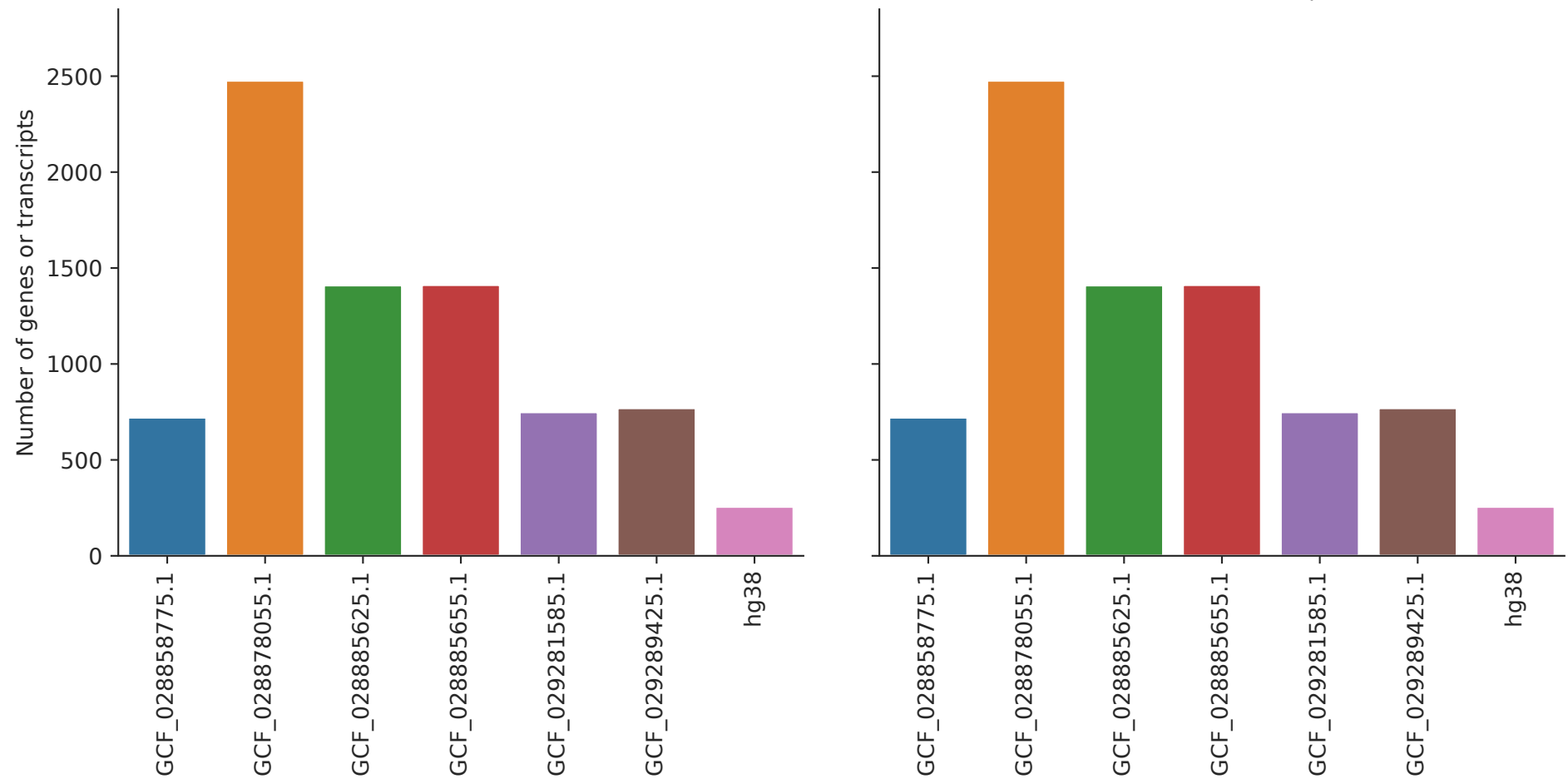
variable = Transcripts



Number of missing orthologs in consensus set for biotype processed_pseudogene

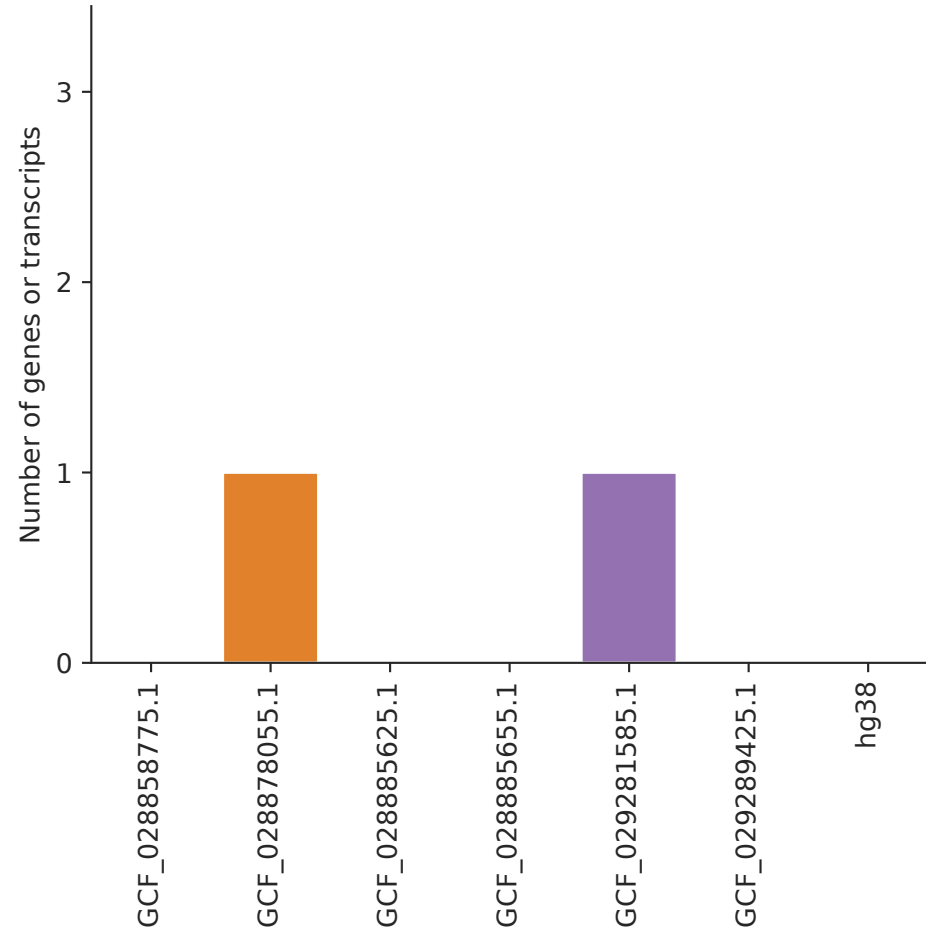
variable = Genes

variable = Transcripts

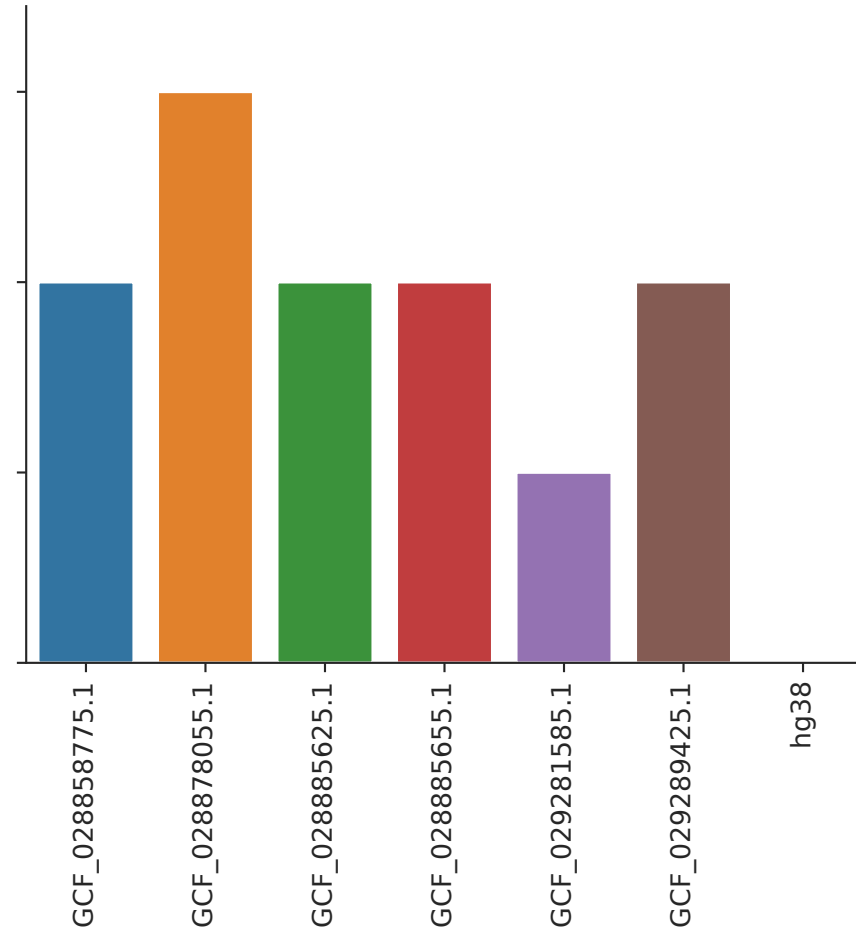


Number of missing orthologs in consensus set for biotype pseudogene

variable = Genes



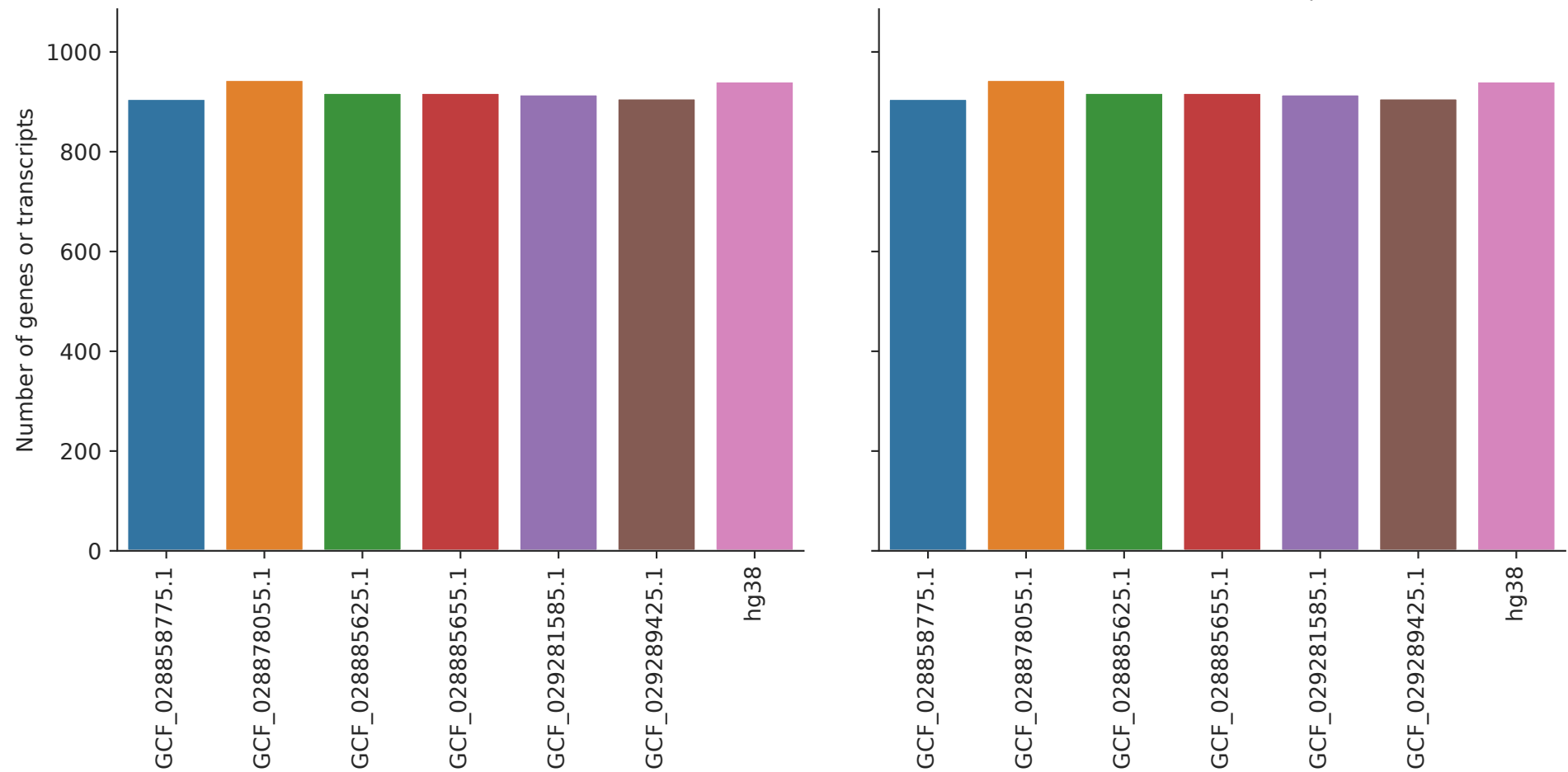
variable = Transcripts



Number of missing orthologs in consensus set for biotype rRNA

variable = Genes

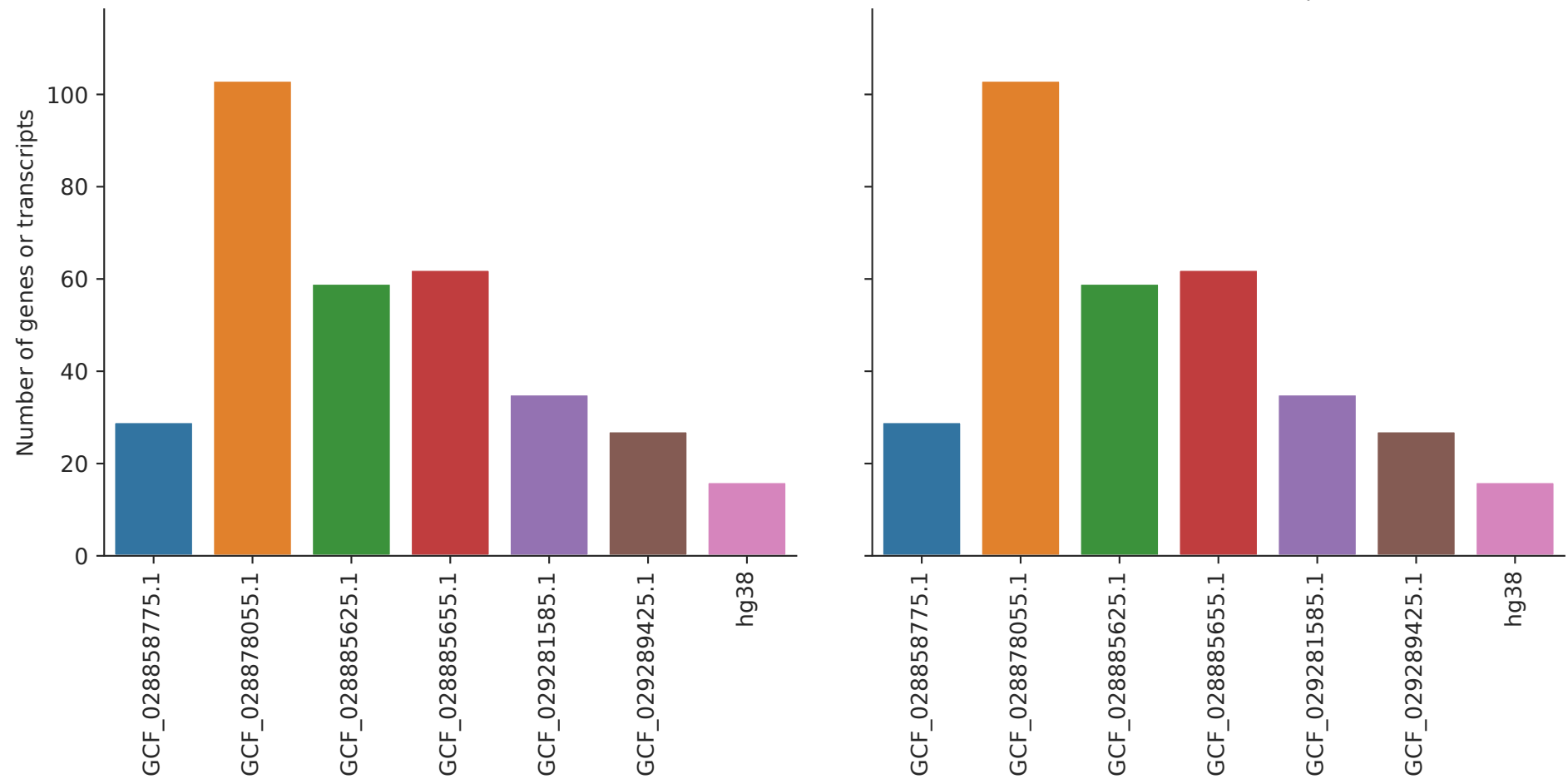
variable = Transcripts



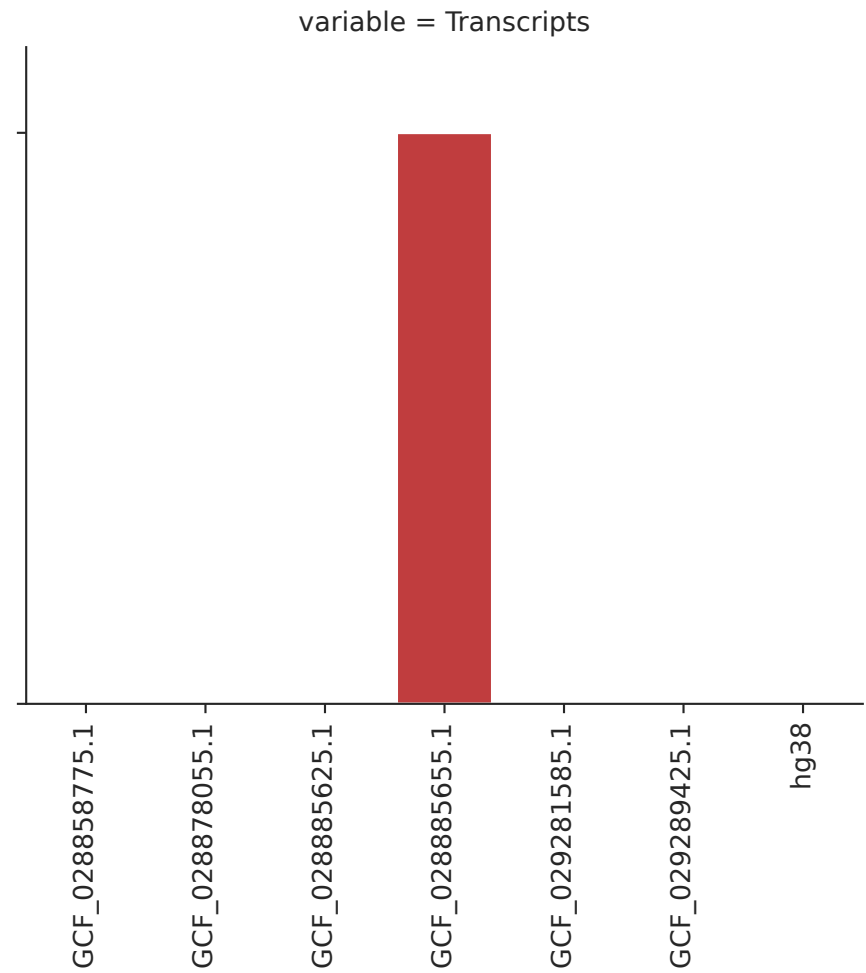
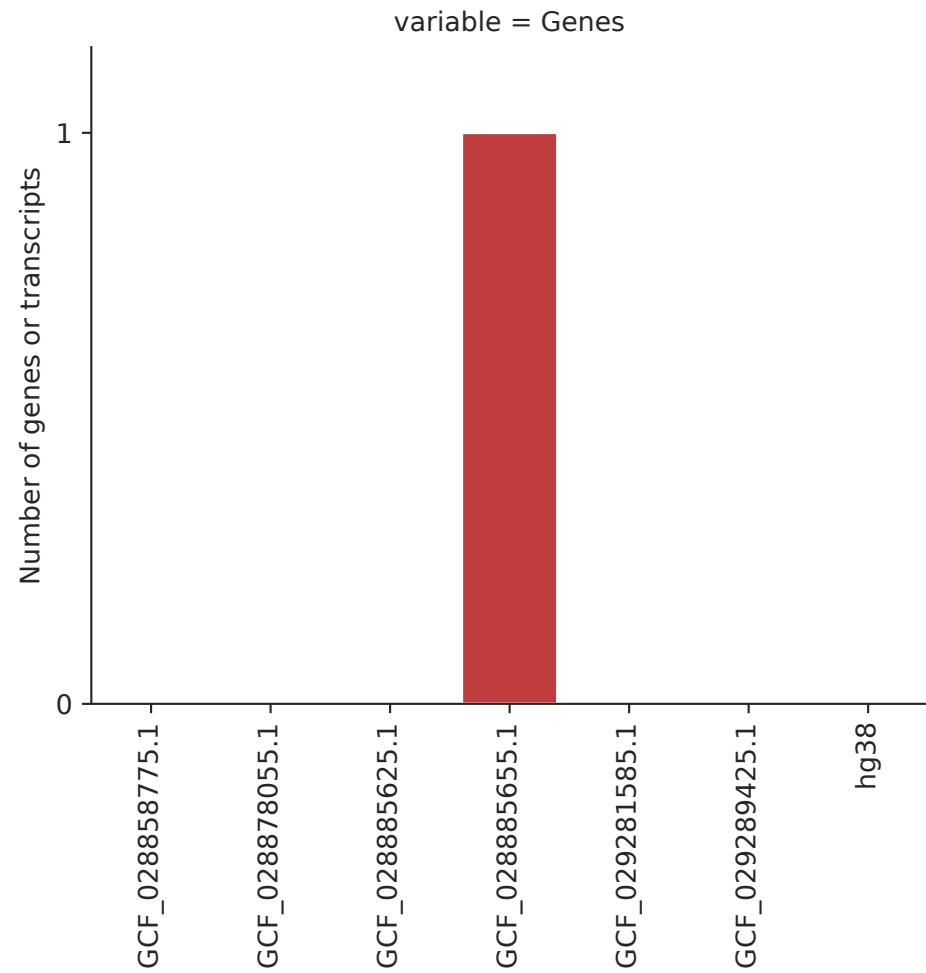
Number of missing orthologs in consensus set for biotype rRNA_pseudogene

variable = Genes

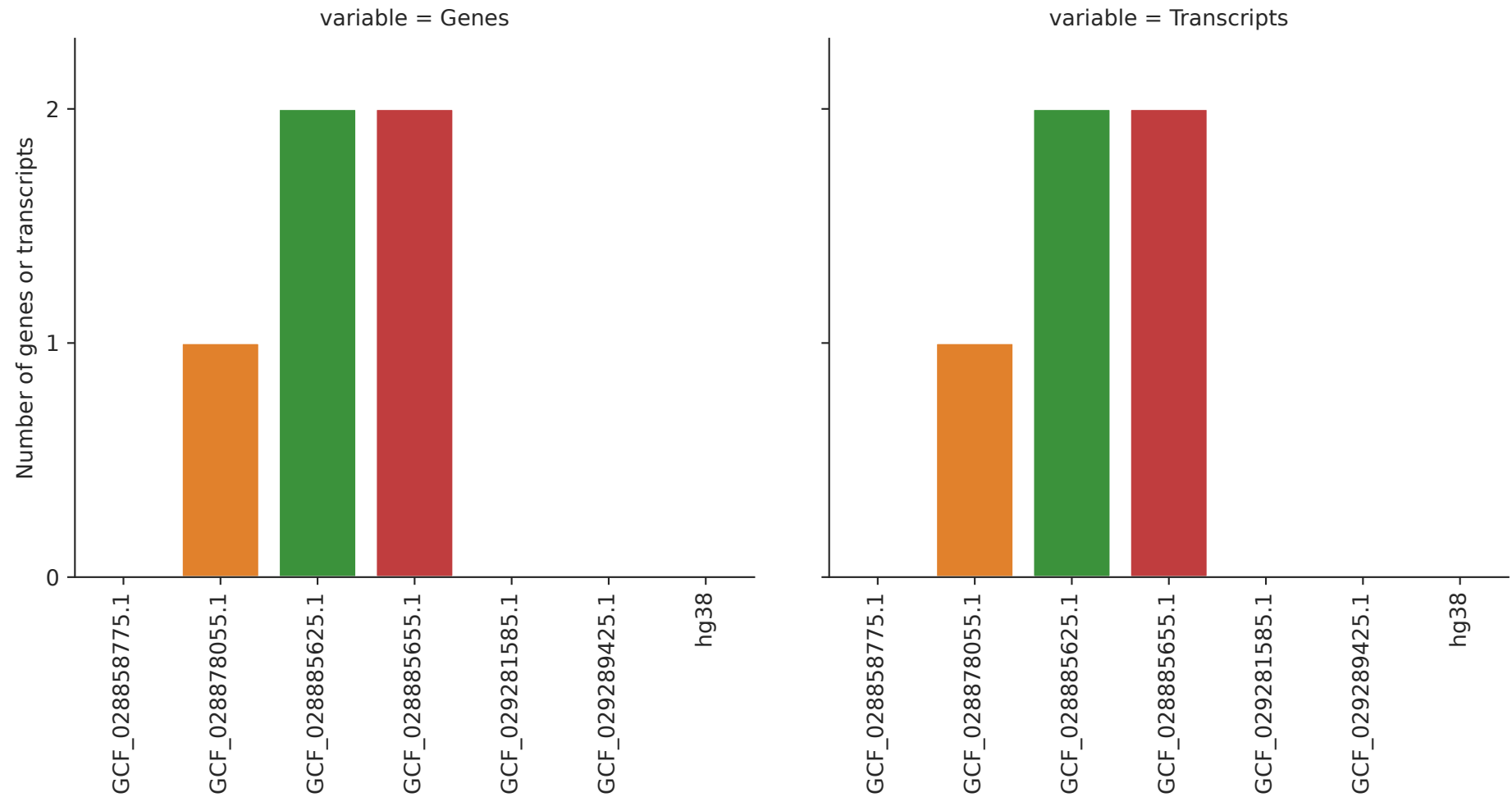
variable = Transcripts



Number of missing orthologs in consensus set for biotype ribozyme



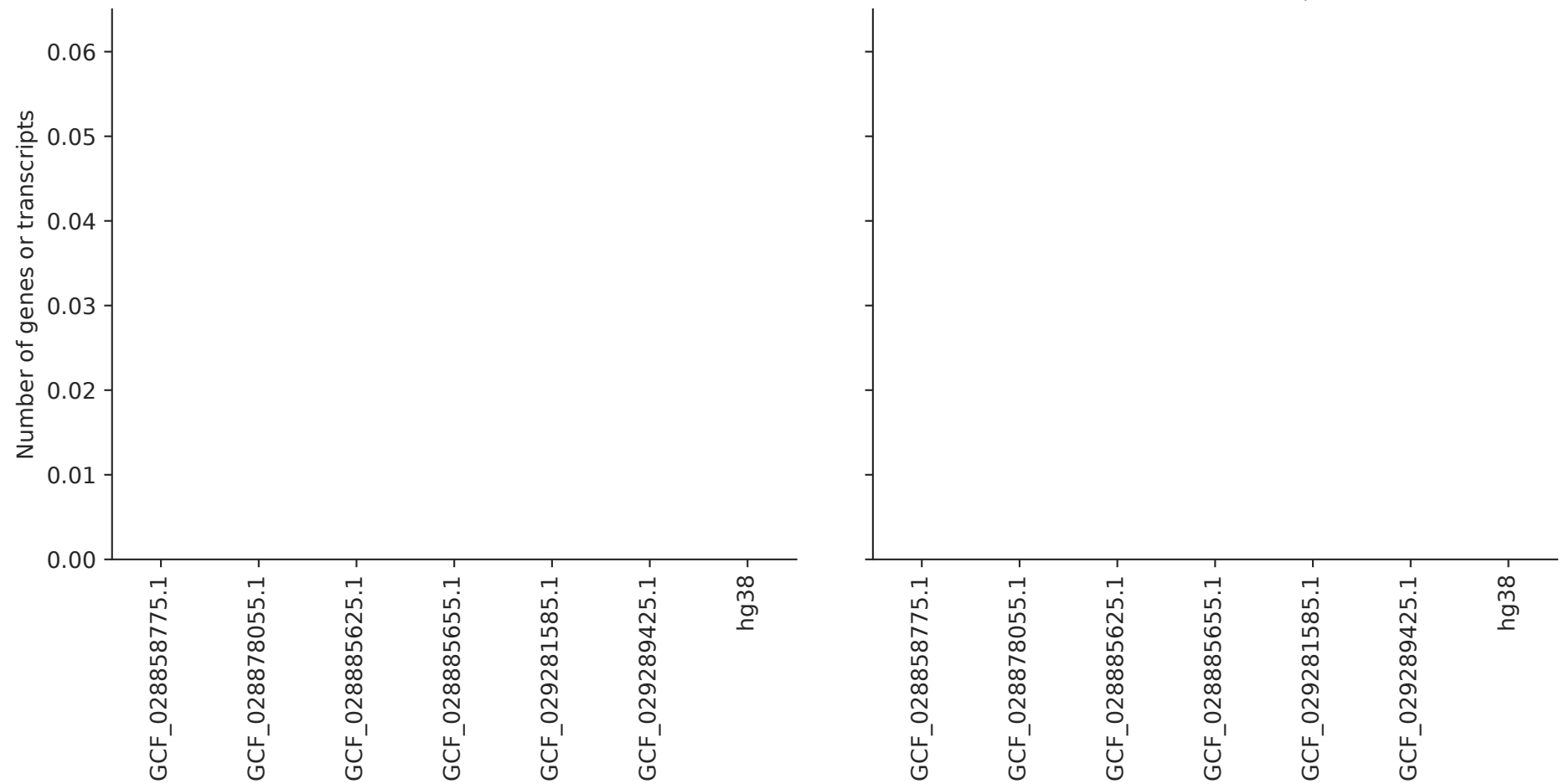
Number of missing orthologs in consensus set for biotype sRNA



Number of missing orthologs in consensus set for biotype scRNA

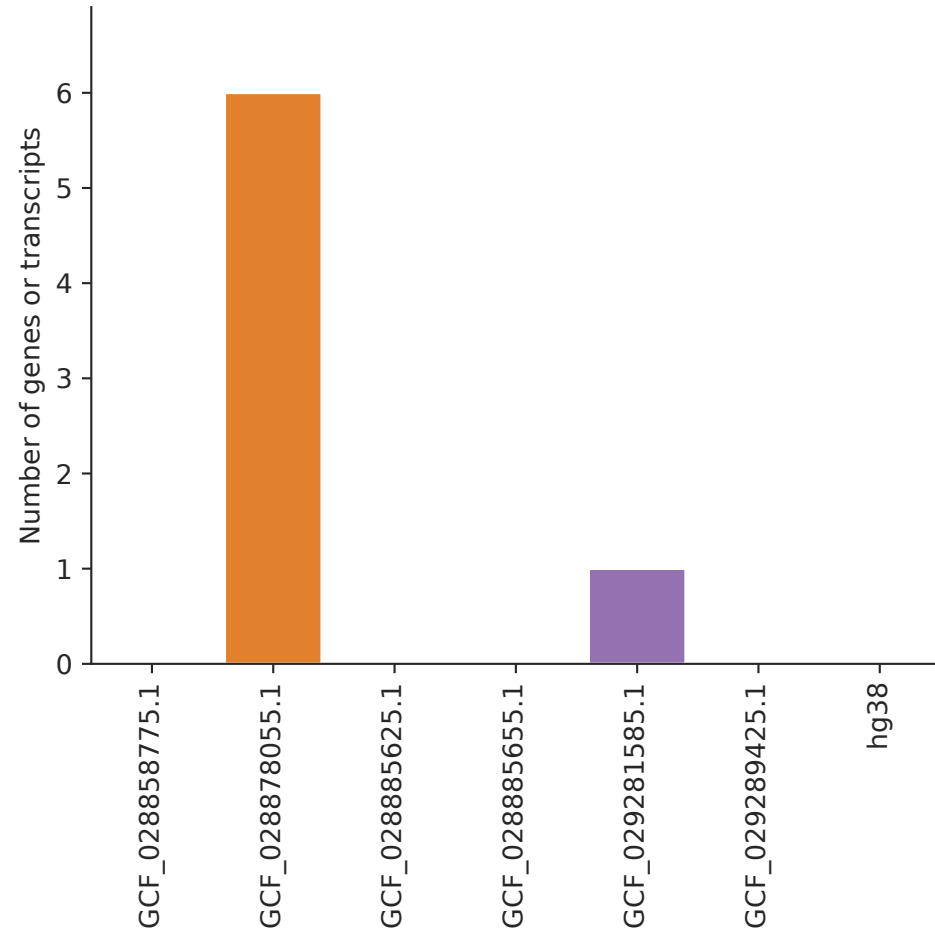
variable = Genes

variable = Transcripts

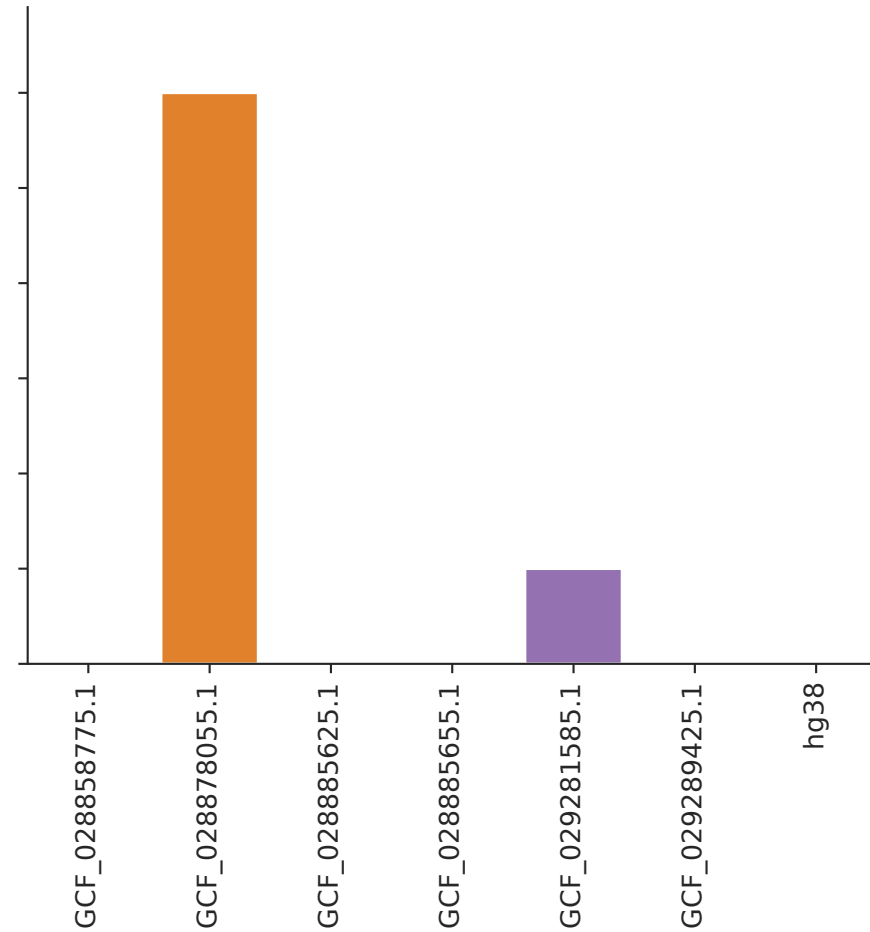


Number of missing orthologs in consensus set for biotype scaRNA

variable = Genes



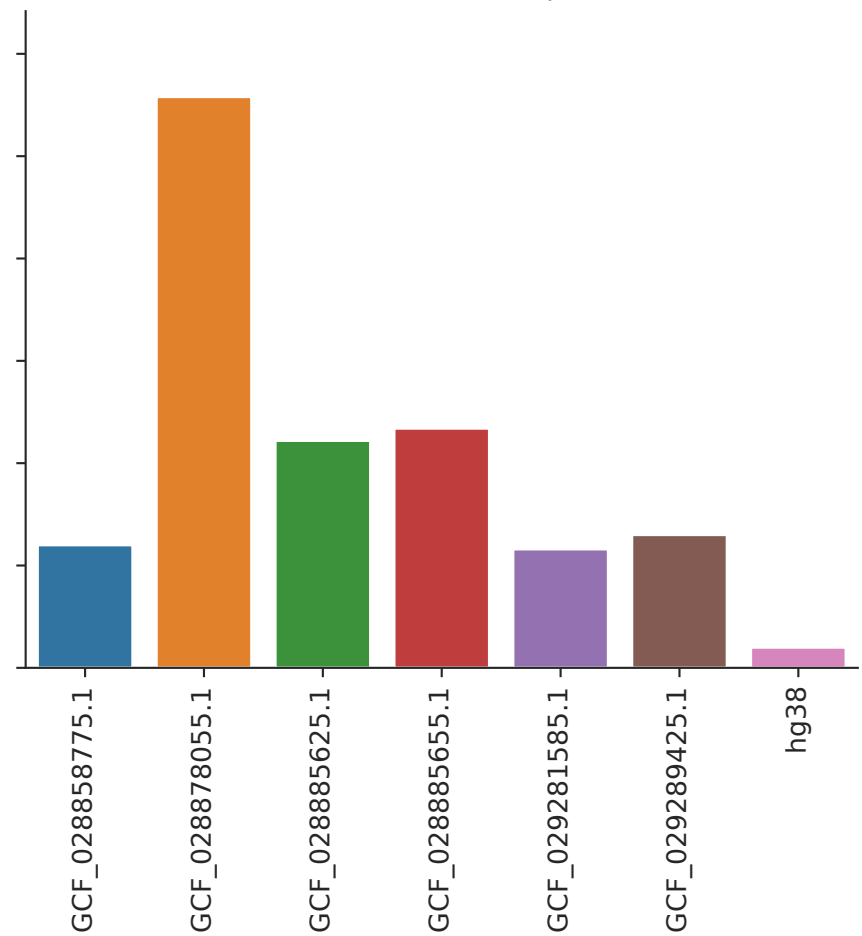
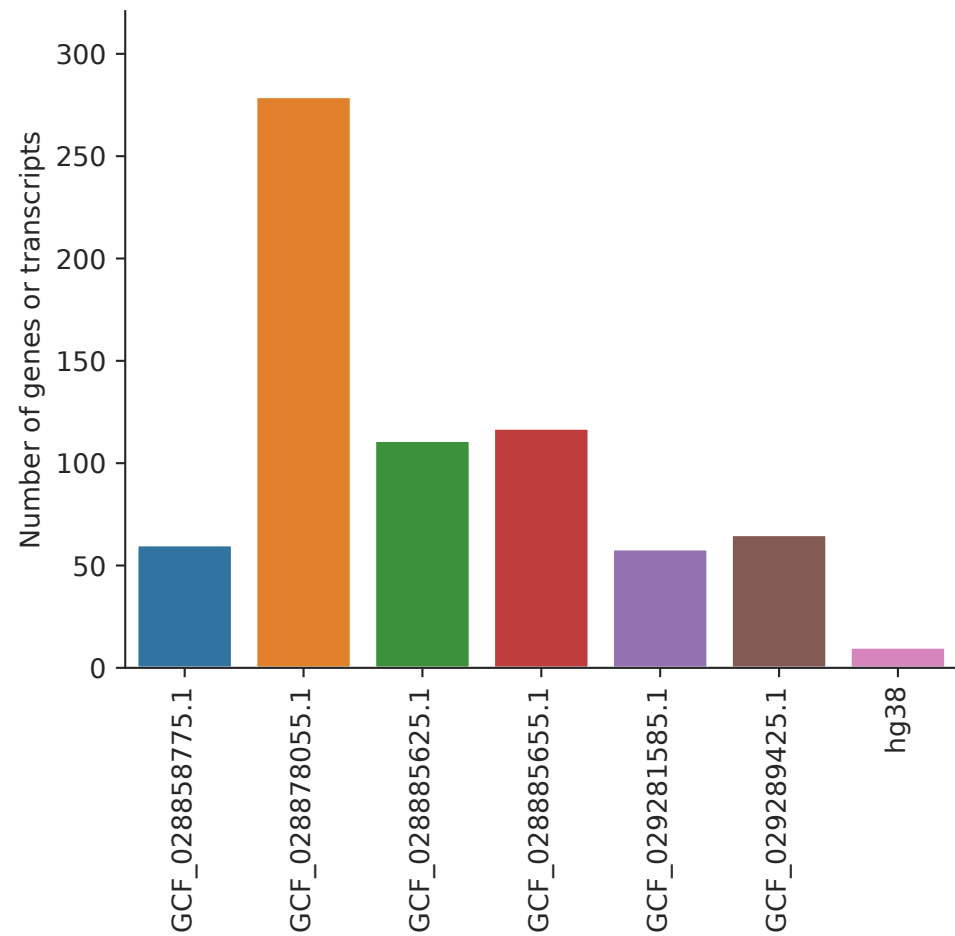
variable = Transcripts



Number of missing orthologs in consensus set for biotype snRNA

variable = Genes

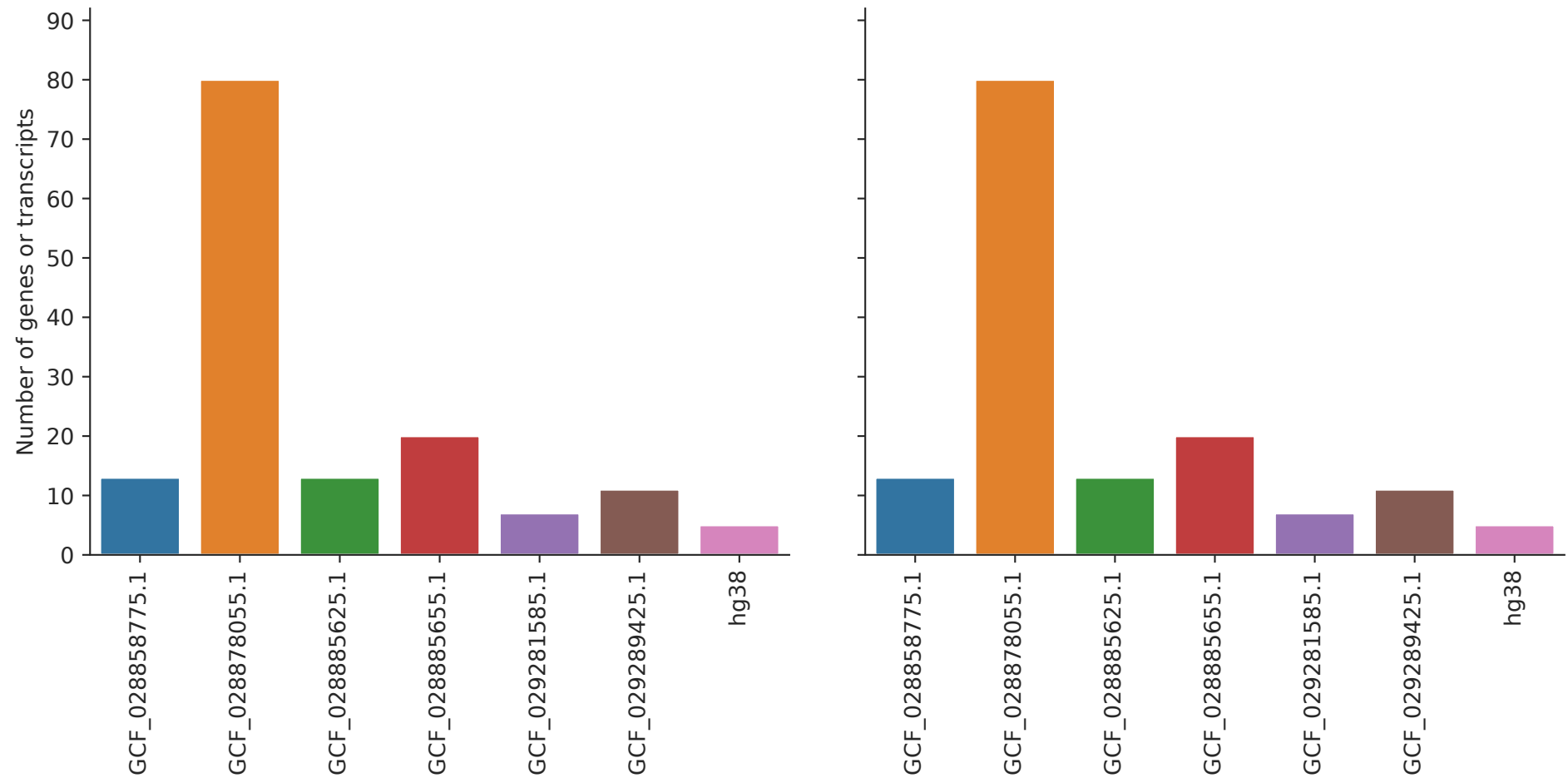
variable = Transcripts



Number of missing orthologs in consensus set for biotype snoRNA

variable = Genes

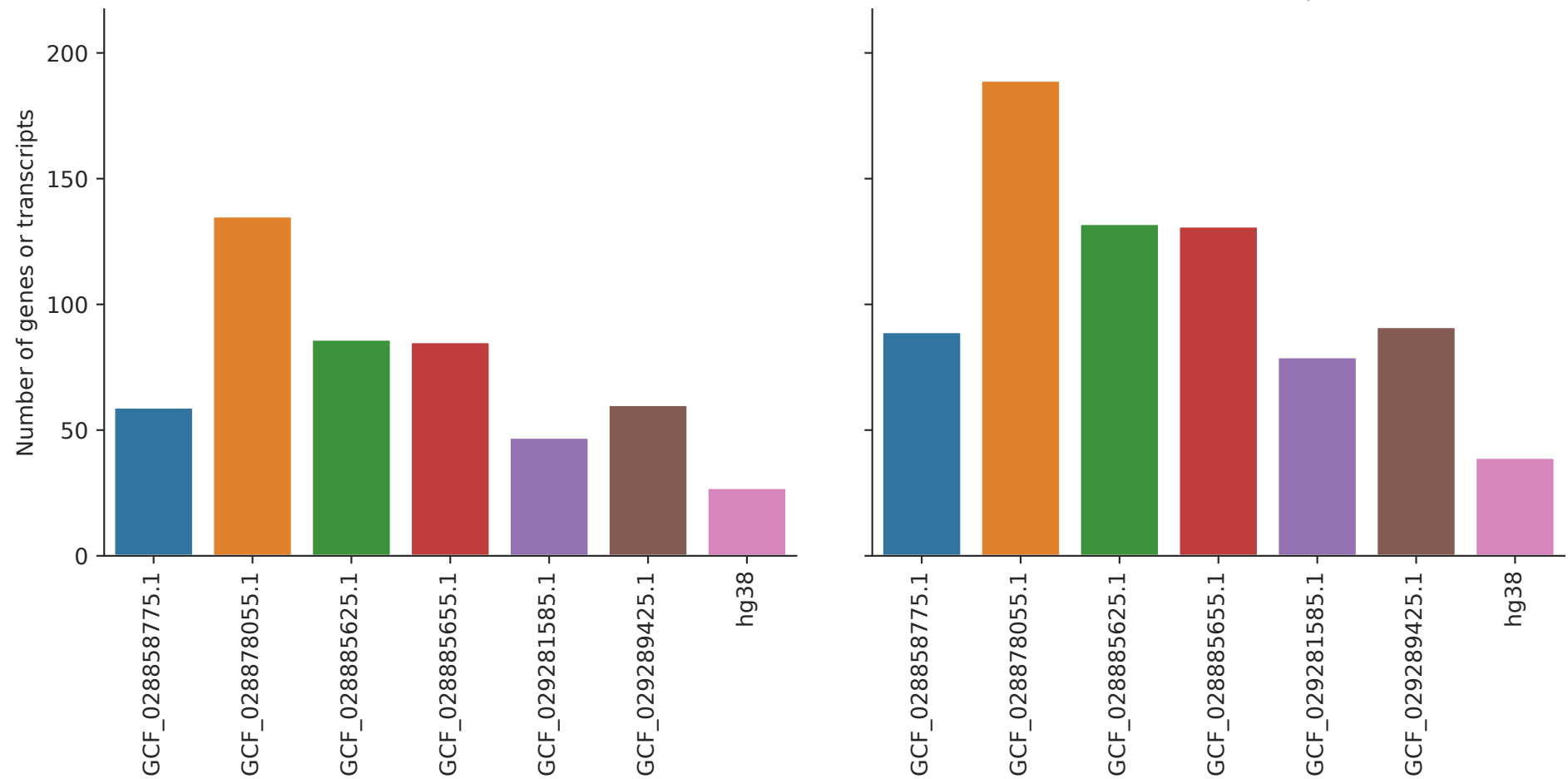
variable = Transcripts



Number of missing orthologs in consensus set for biotype transcribed_processed_pseudogene

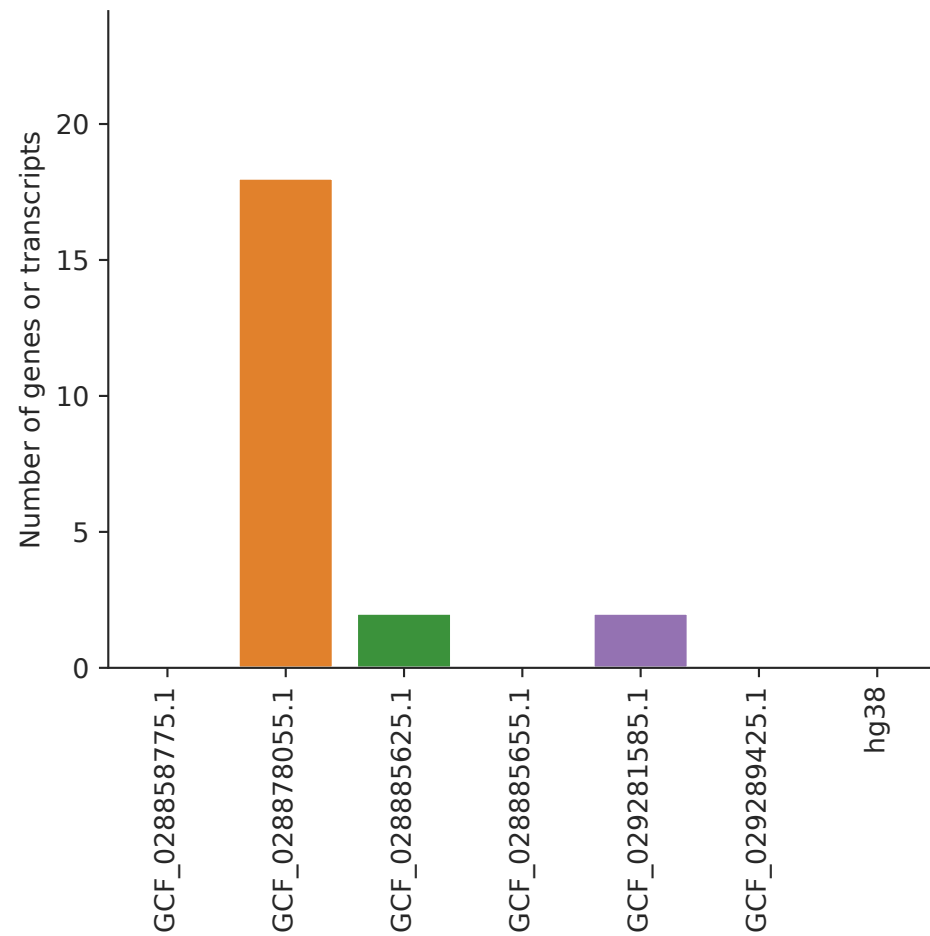
variable = Genes

variable = Transcripts

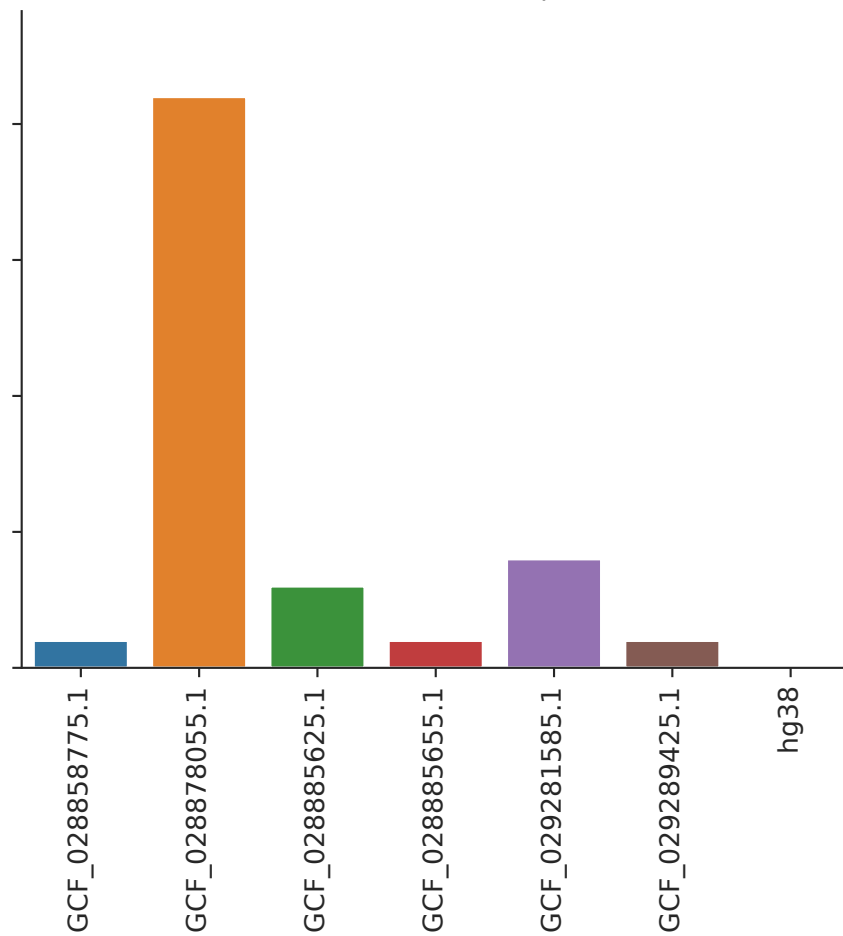


Number of missing orthologs in consensus set for biotype transcribed_unitary_pseudogene

variable = Genes



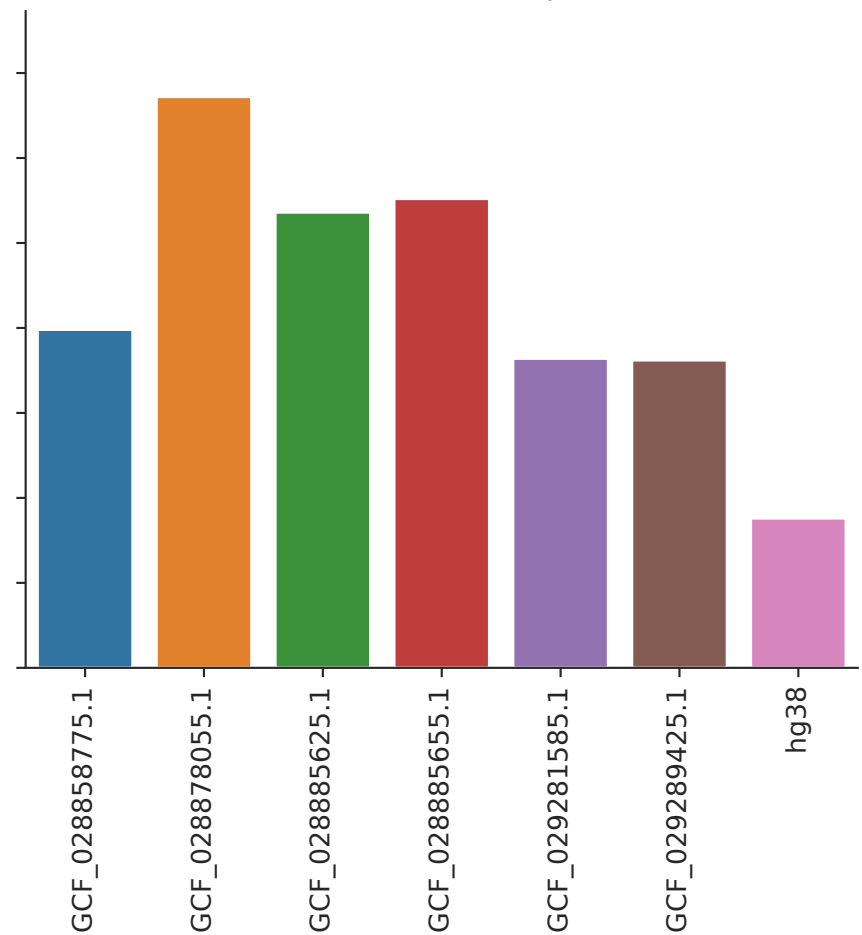
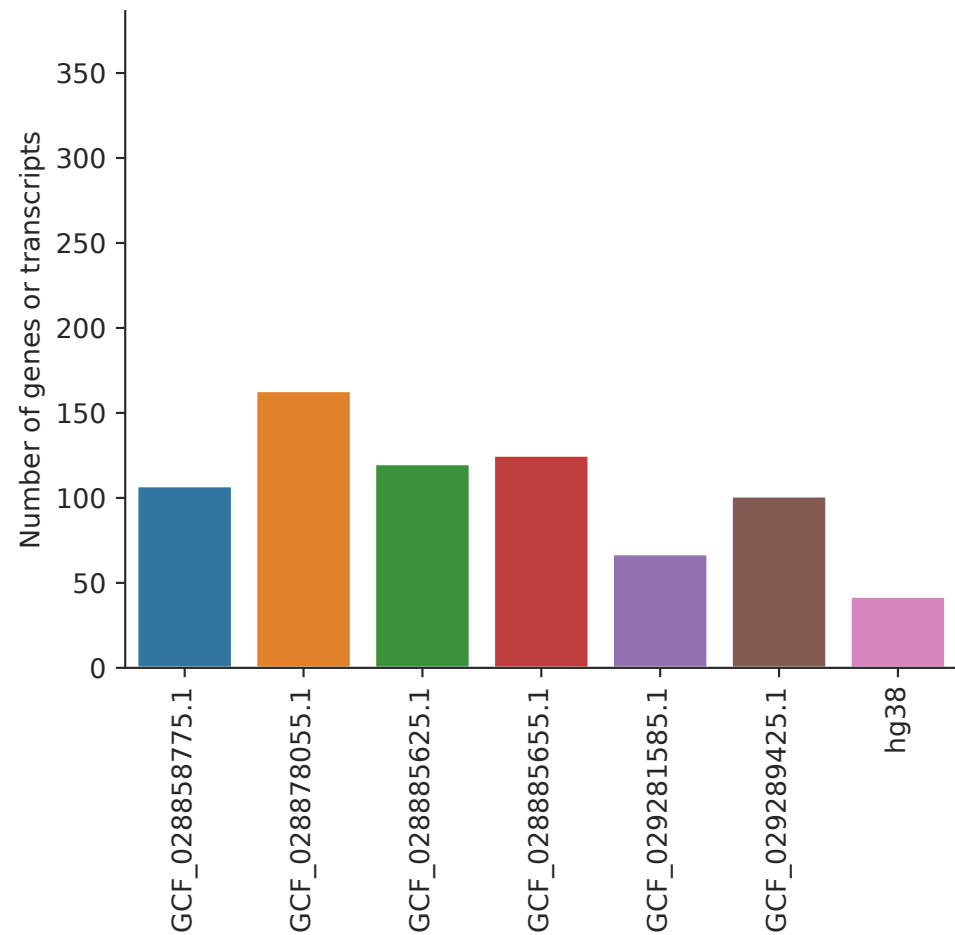
variable = Transcripts



Number of missing orthologs in consensus set for biotype transcribed_unprocessed_pseudogene

variable = Genes

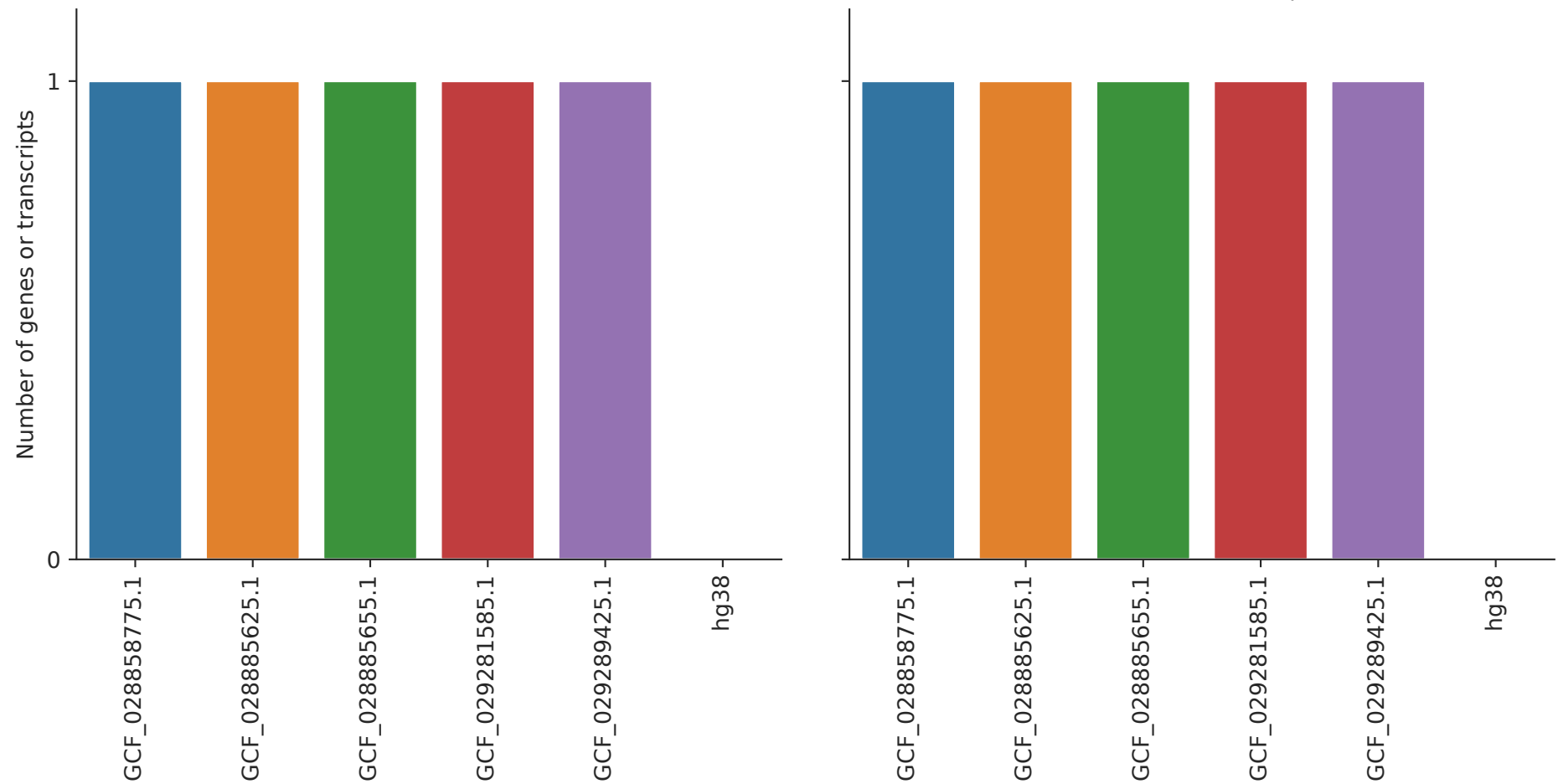
variable = Transcripts



Number of missing orthologs in consensus set for biotype translated_processed_pseudogene

variable = Genes

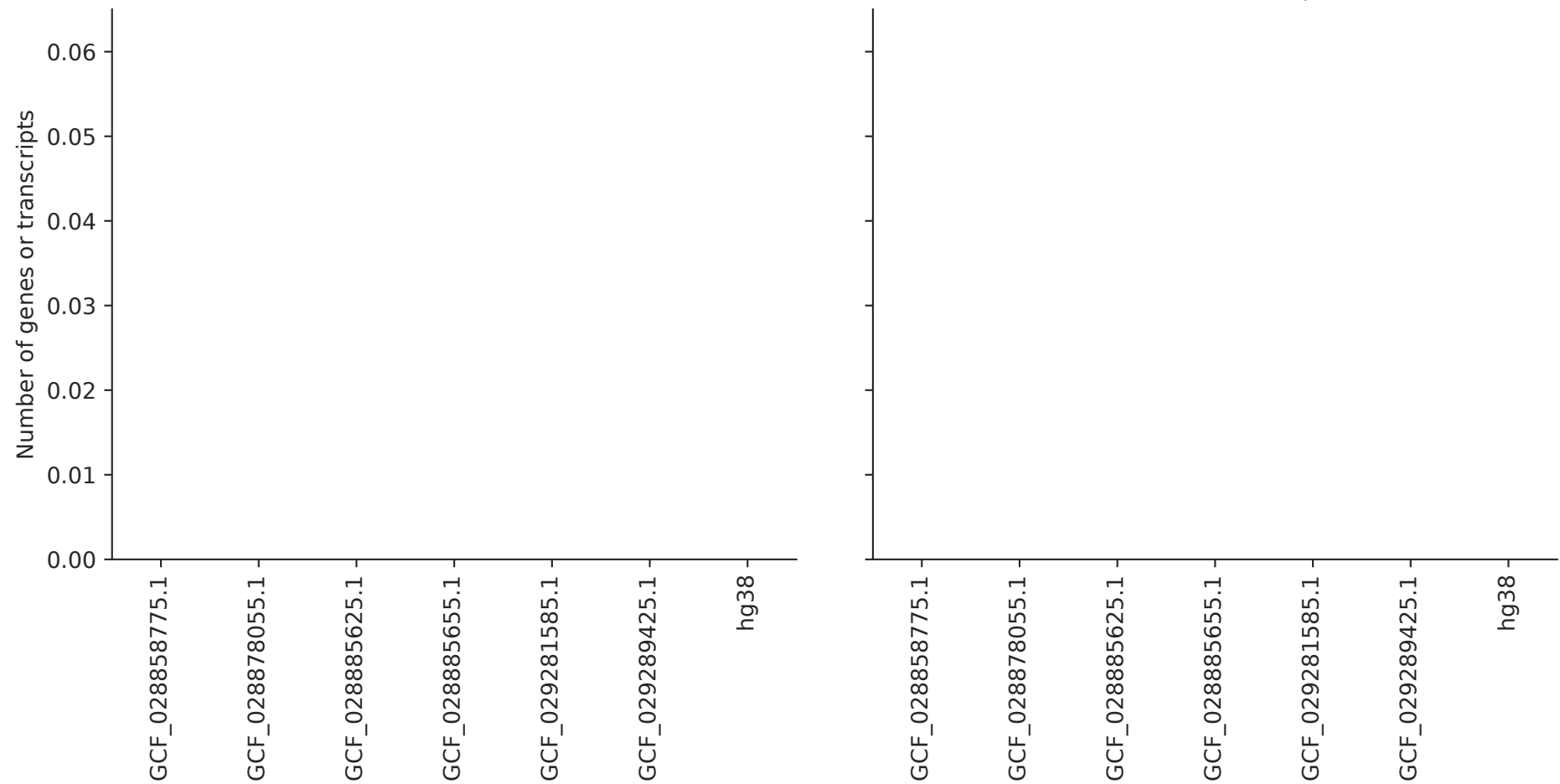
variable = Transcripts



Number of missing orthologs in consensus set for biotype translated_unprocessed_pseudogene

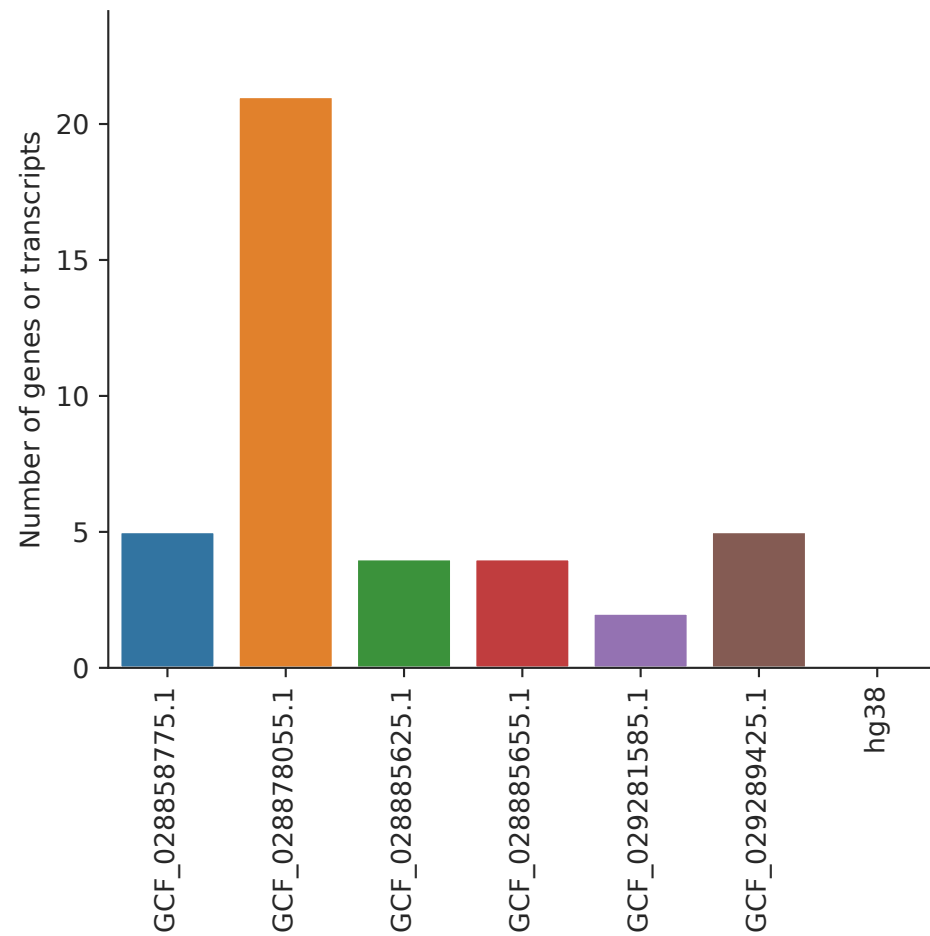
variable = Genes

variable = Transcripts

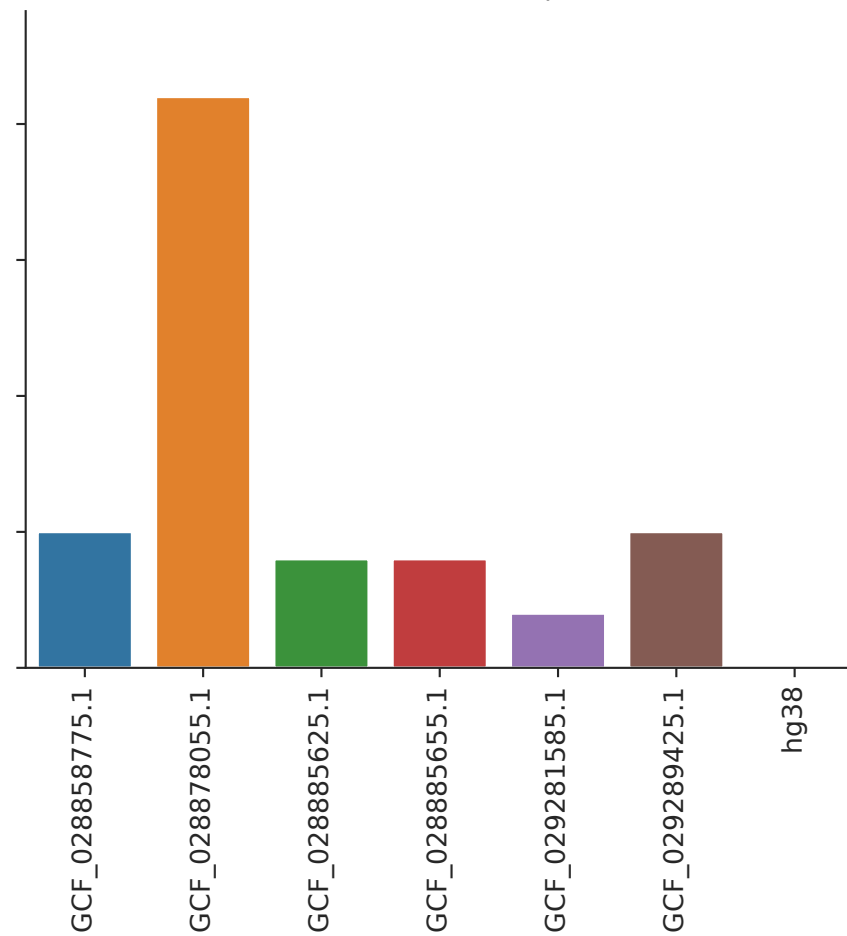


Number of missing orthologs in consensus set for biotype unitary_pseudogene

variable = Genes



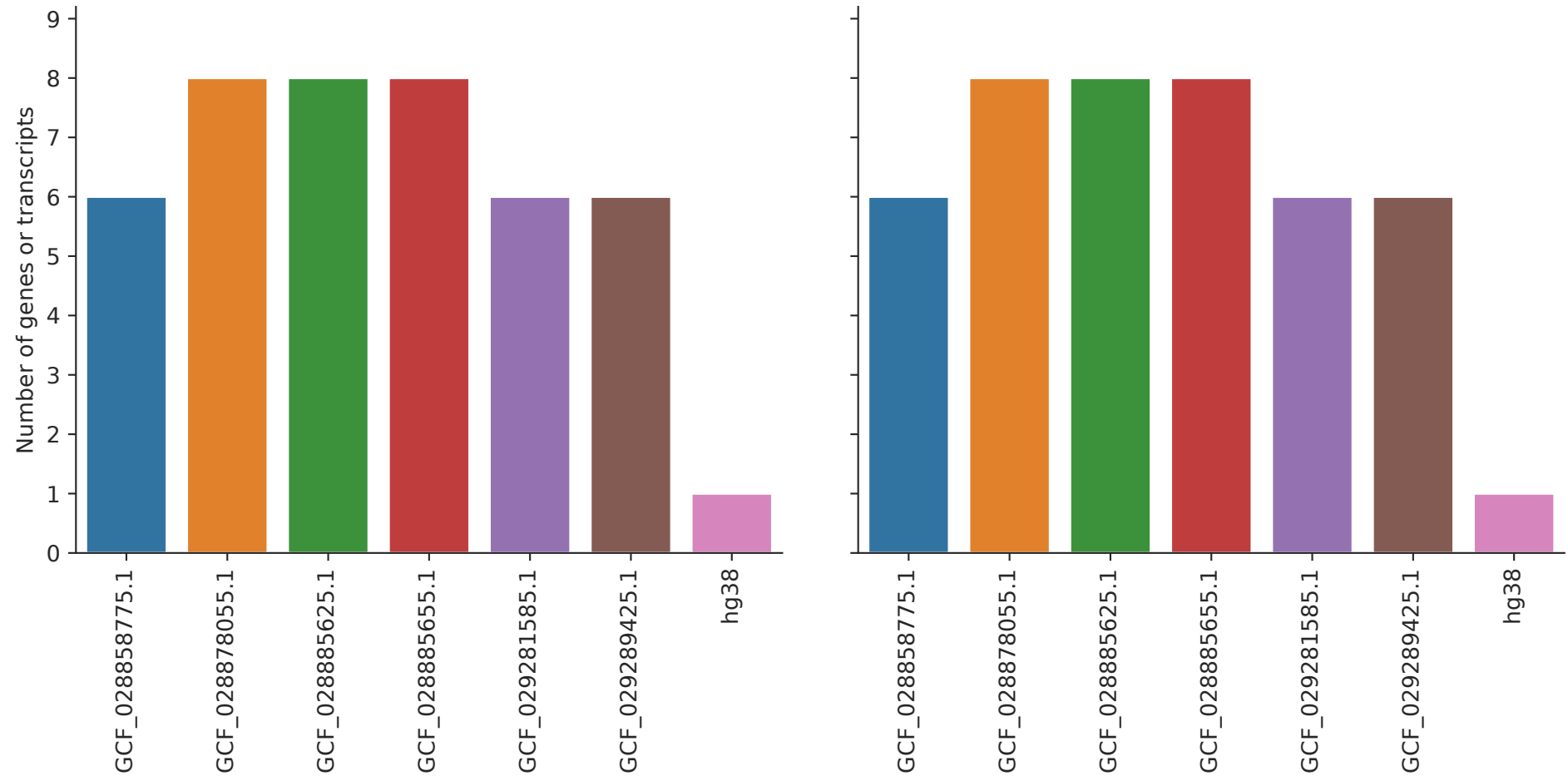
variable = Transcripts



Number of missing orthologs in consensus set for biotype unknown_likely_coding

variable = Genes

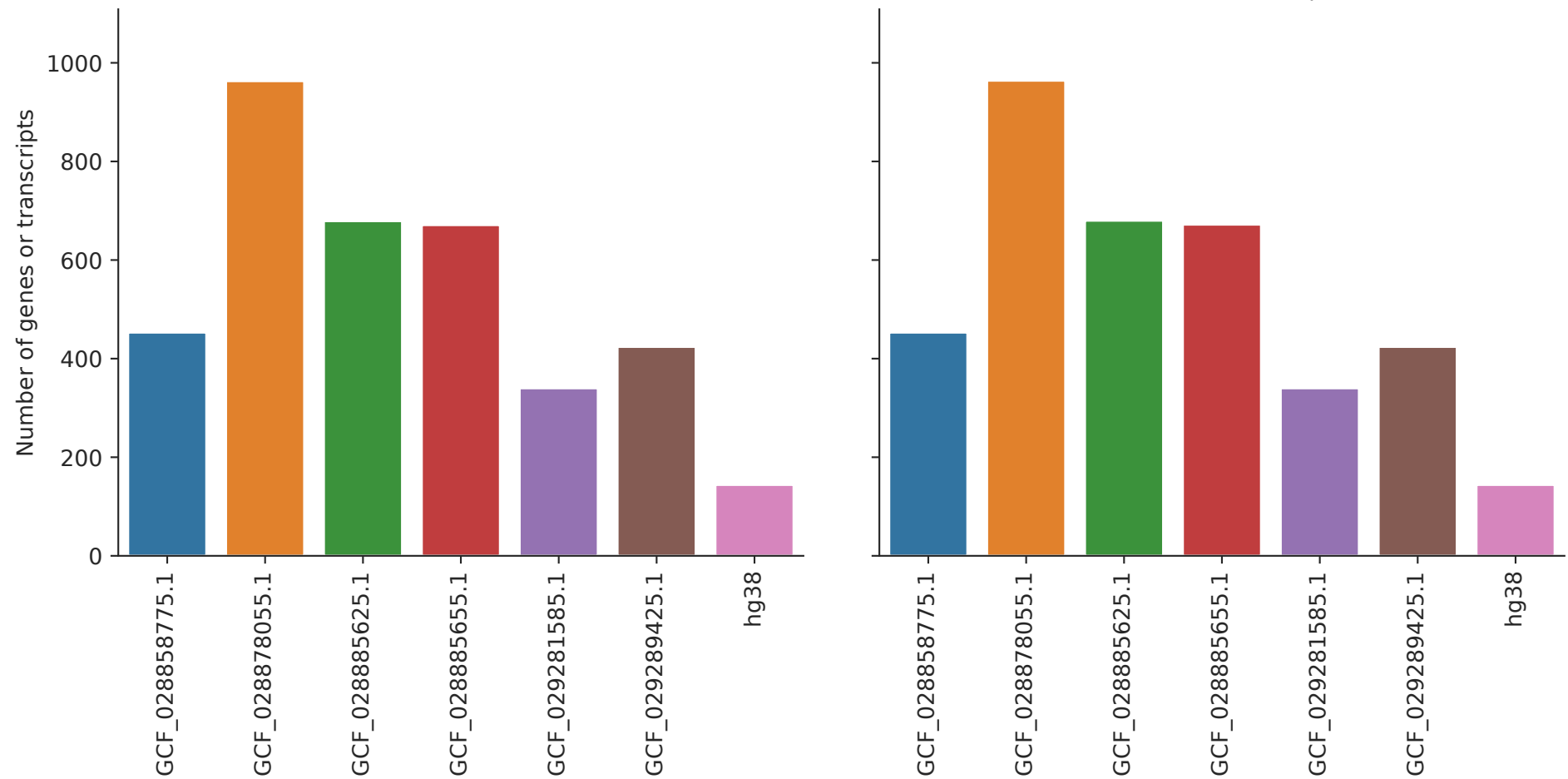
variable = Transcripts



Number of missing orthologs in consensus set for biotype unprocessed_pseudogene

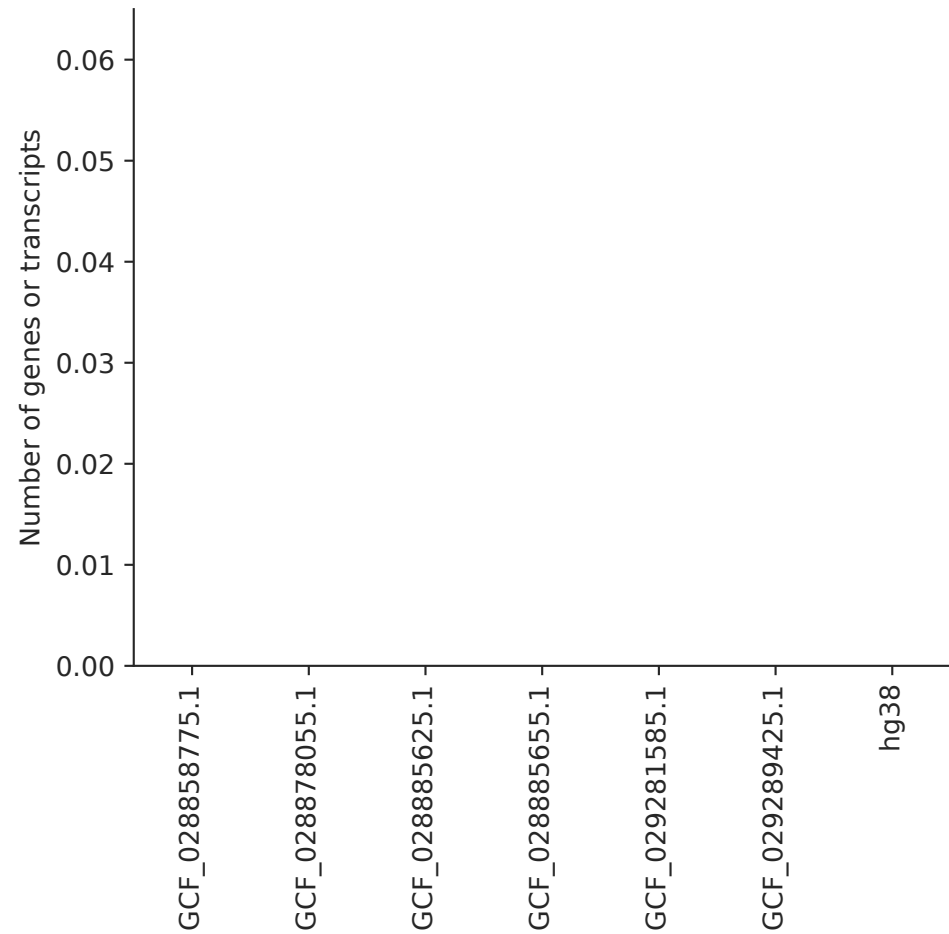
variable = Genes

variable = Transcripts



Number of missing orthologs in consensus set for biotype vault_RNA

variable = Genes



variable = Transcripts

