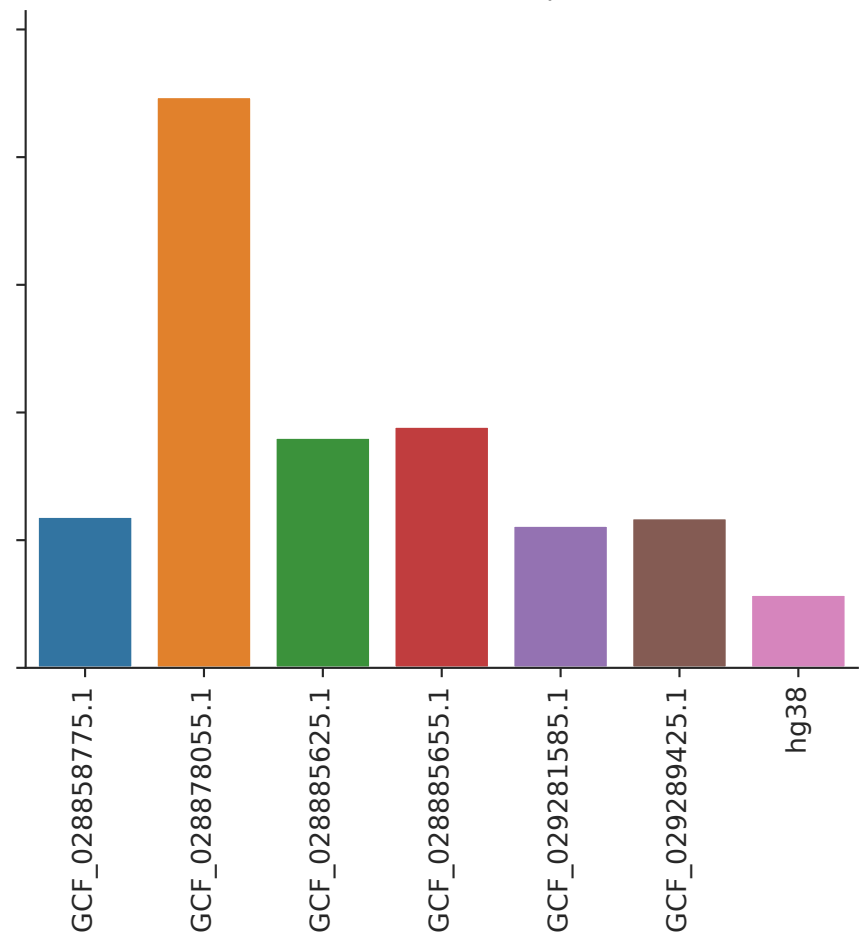
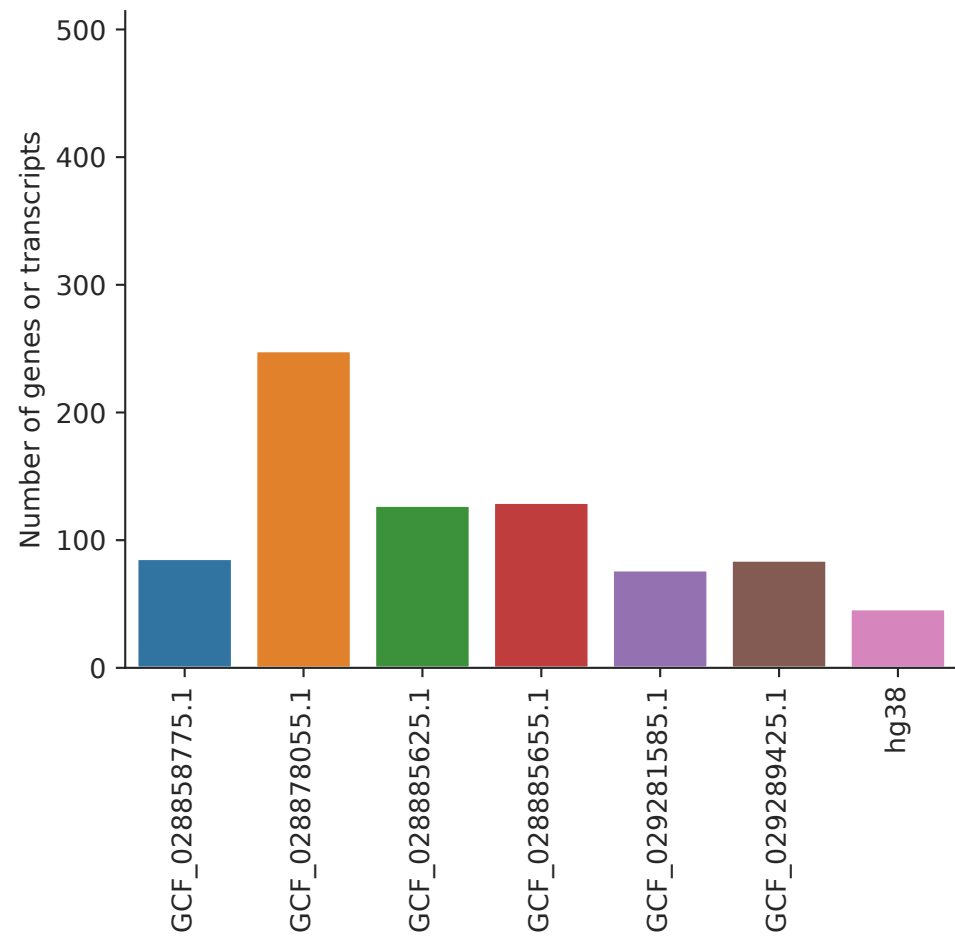


Number of missing orthologs in consensus set

variable = Genes

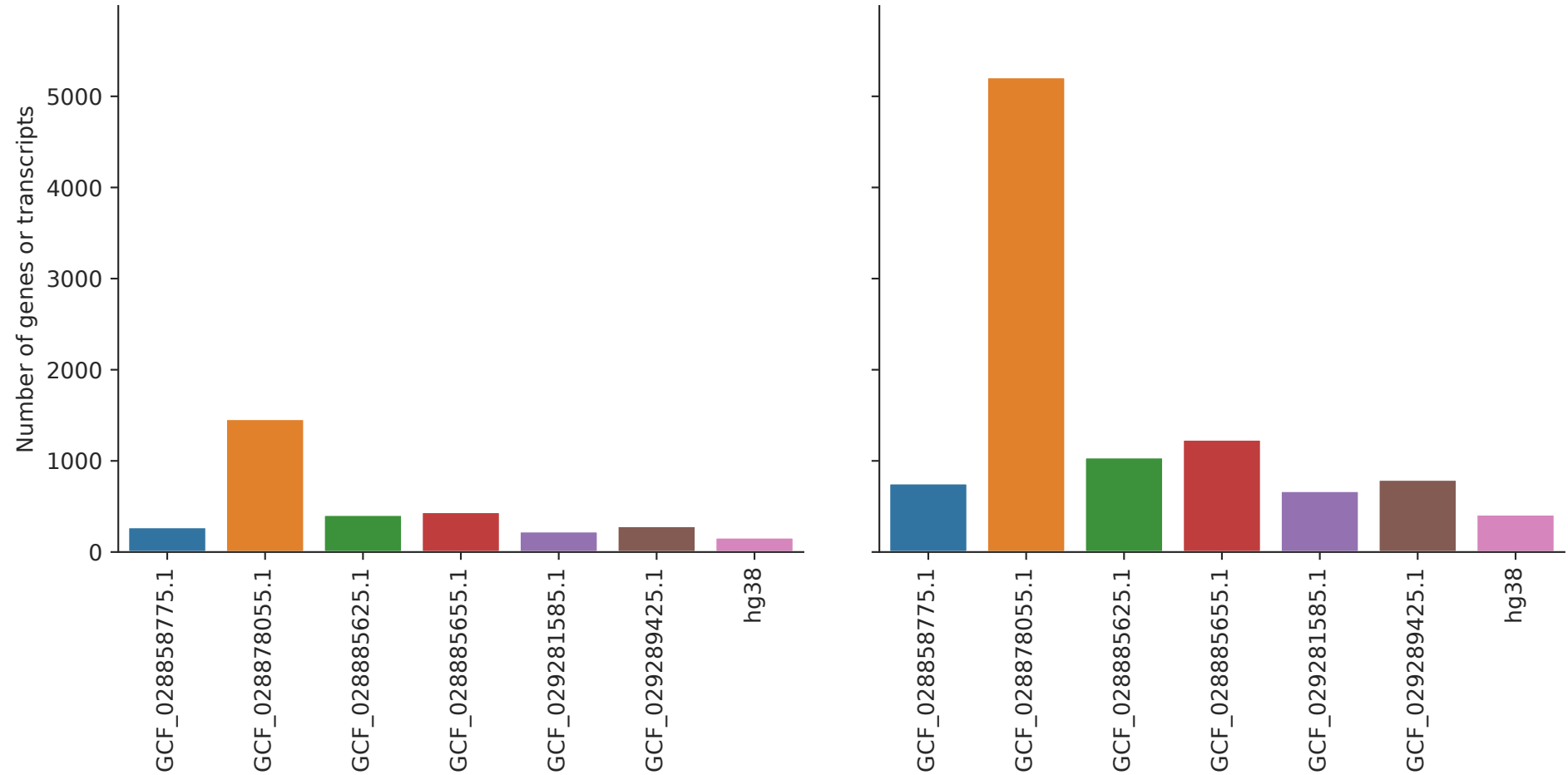
variable = Transcripts



Number of missing orthologs in consensus set for biotype protein_coding

variable = Genes

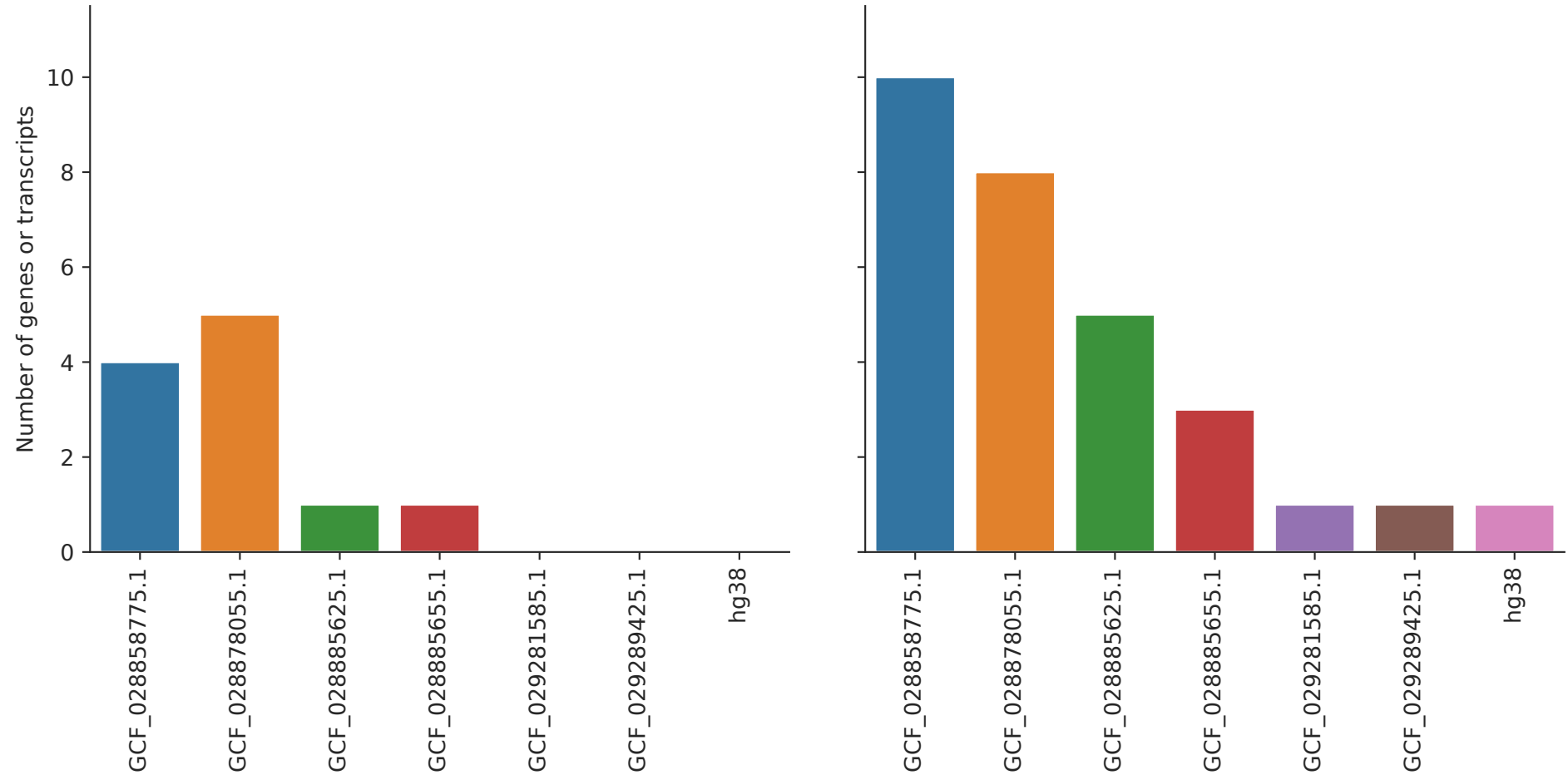
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_C_gene

variable = Genes

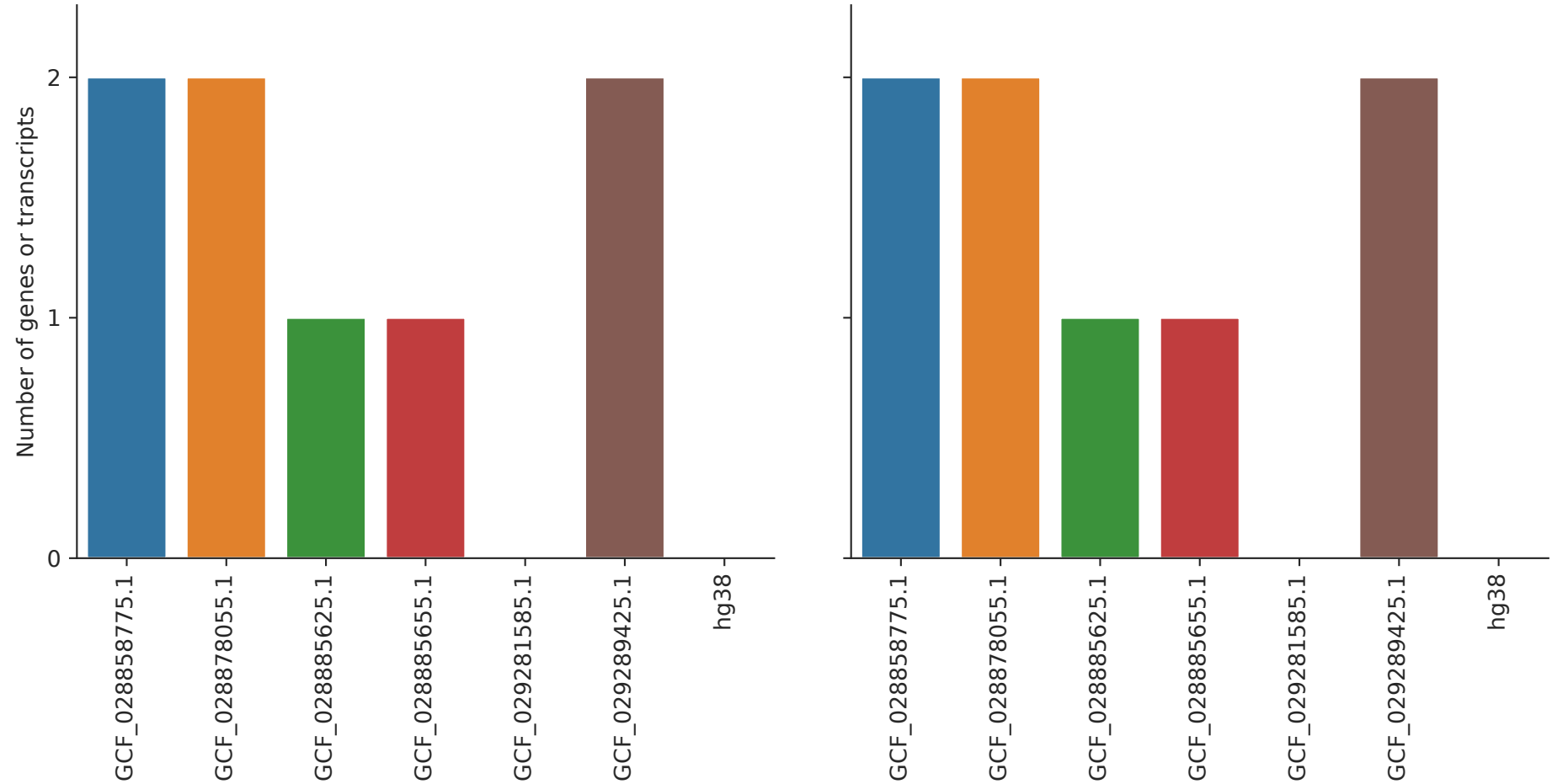
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_C_pseudogene

variable = Genes

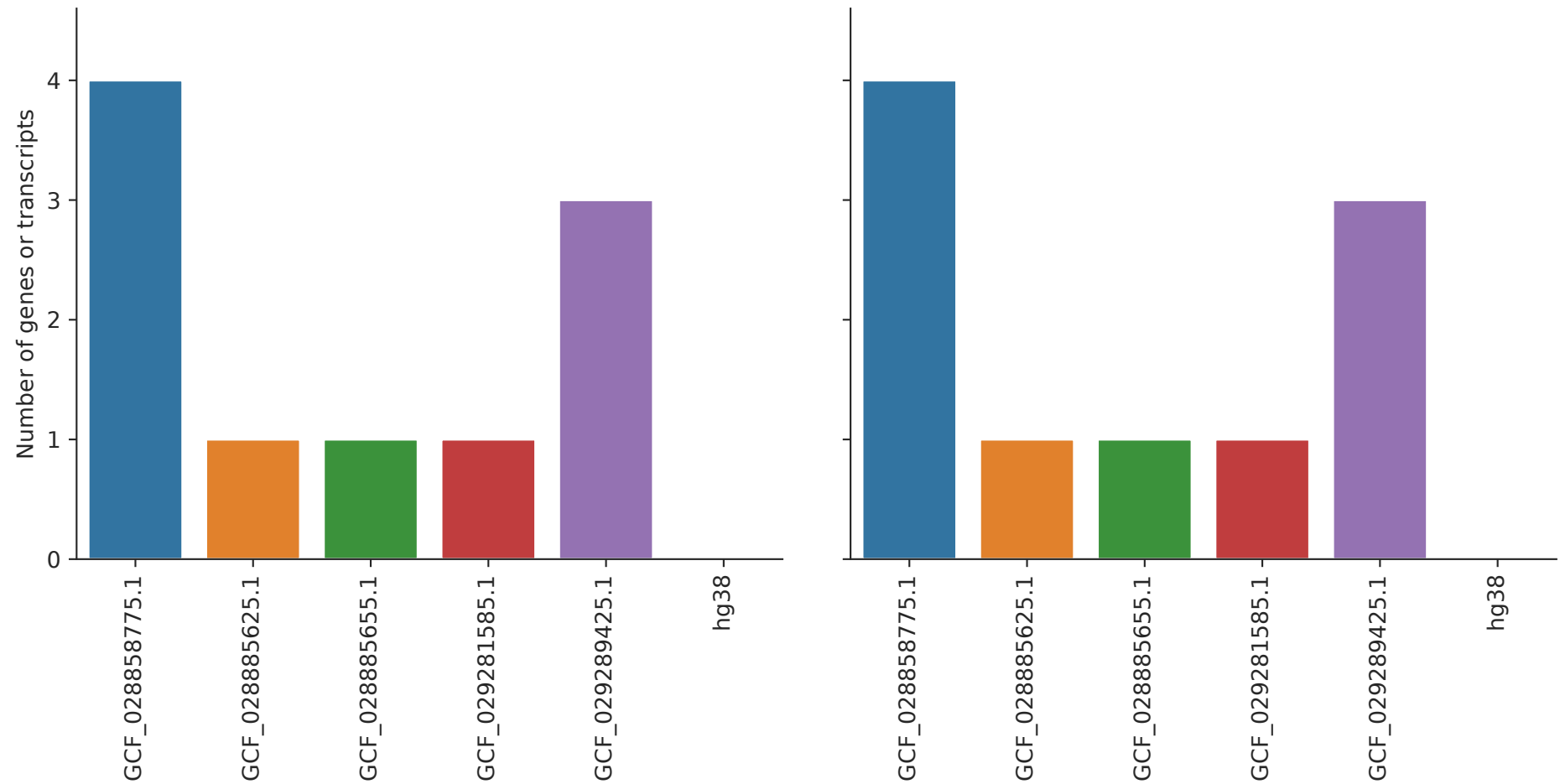
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_D_gene

variable = Genes

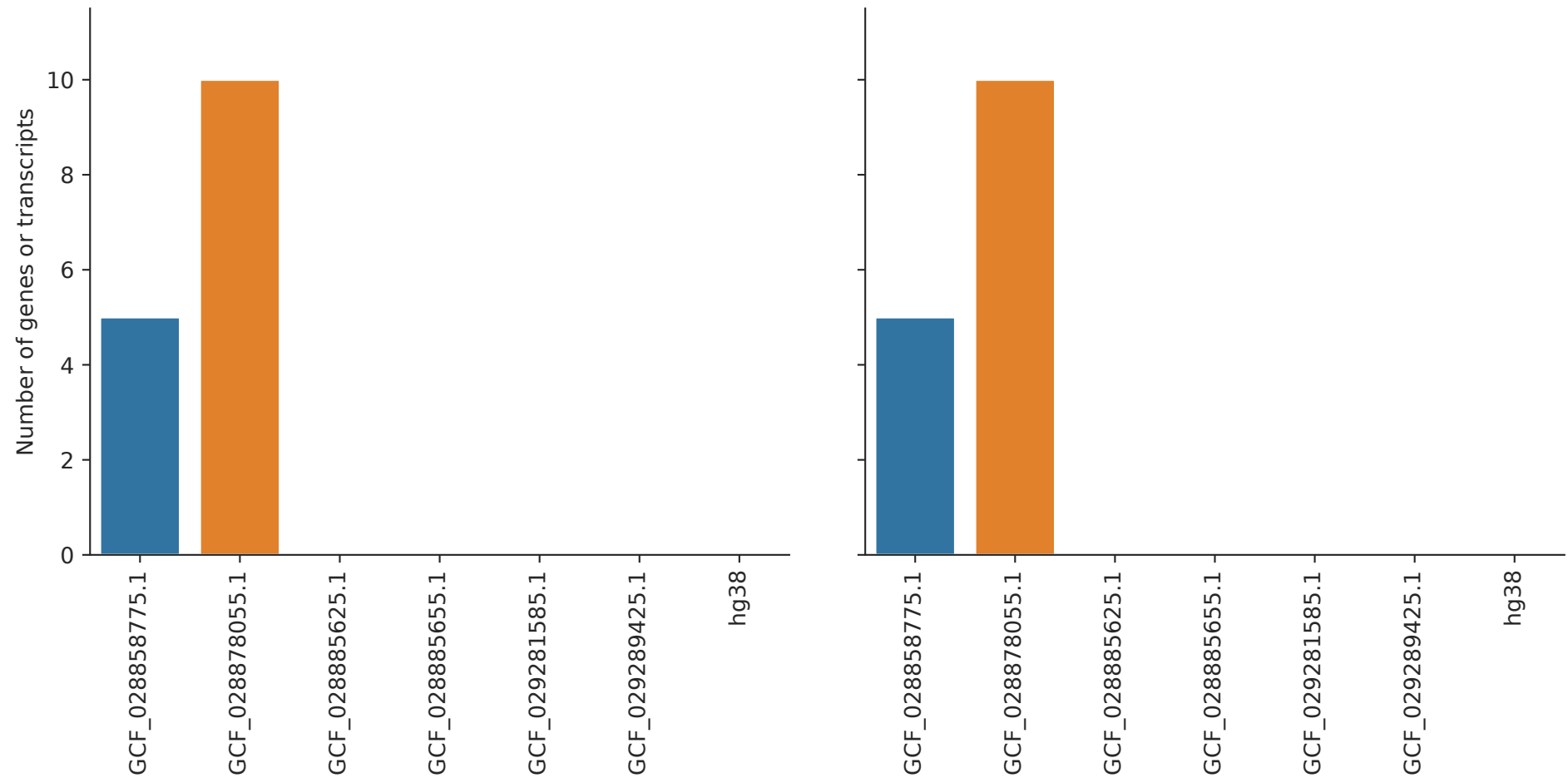
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_J_gene

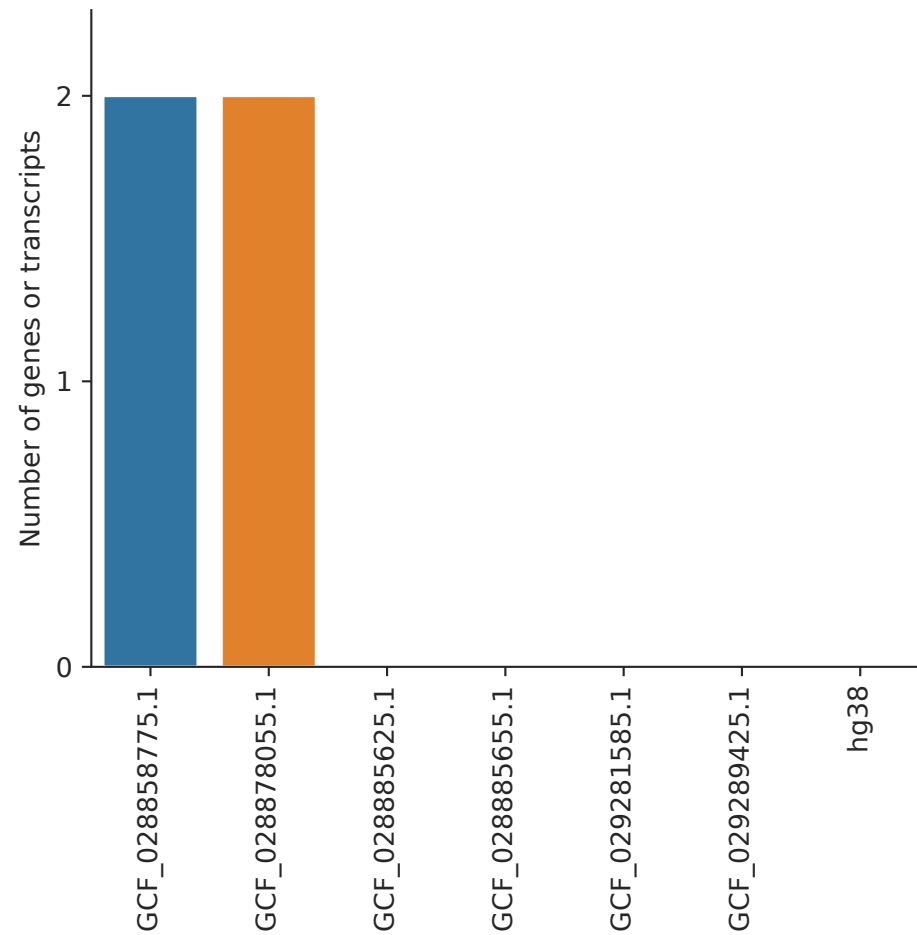
variable = Genes

variable = Transcripts

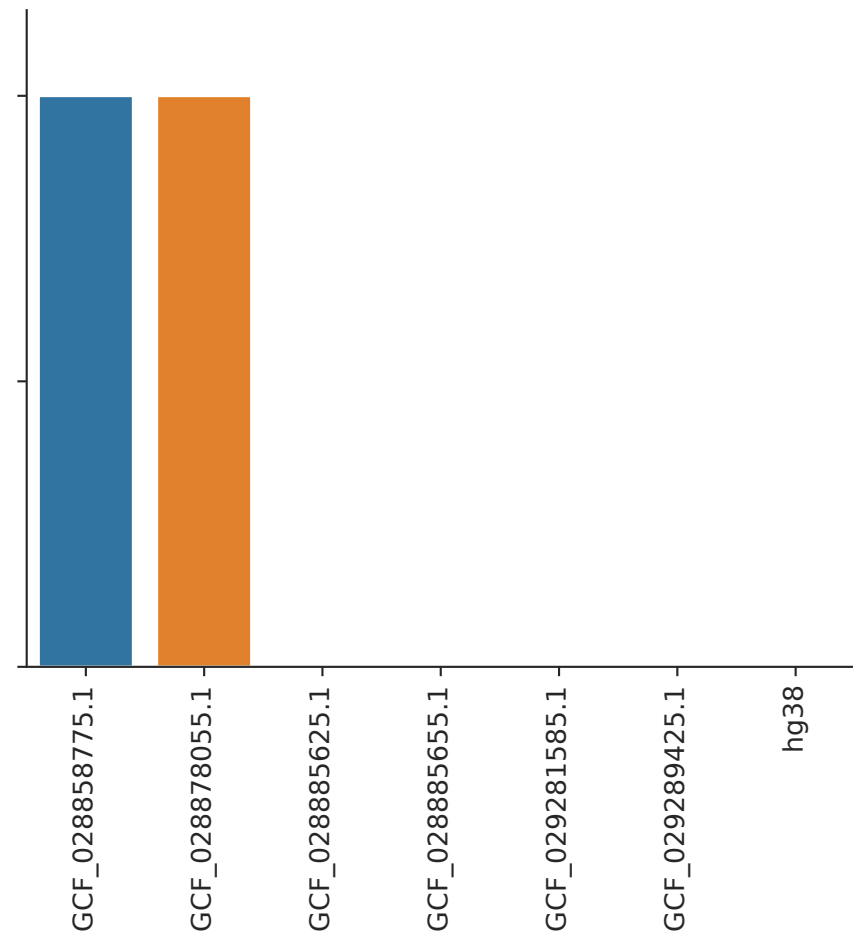


Number of missing orthologs in consensus set for biotype IG_J_pseudogene

variable = Genes



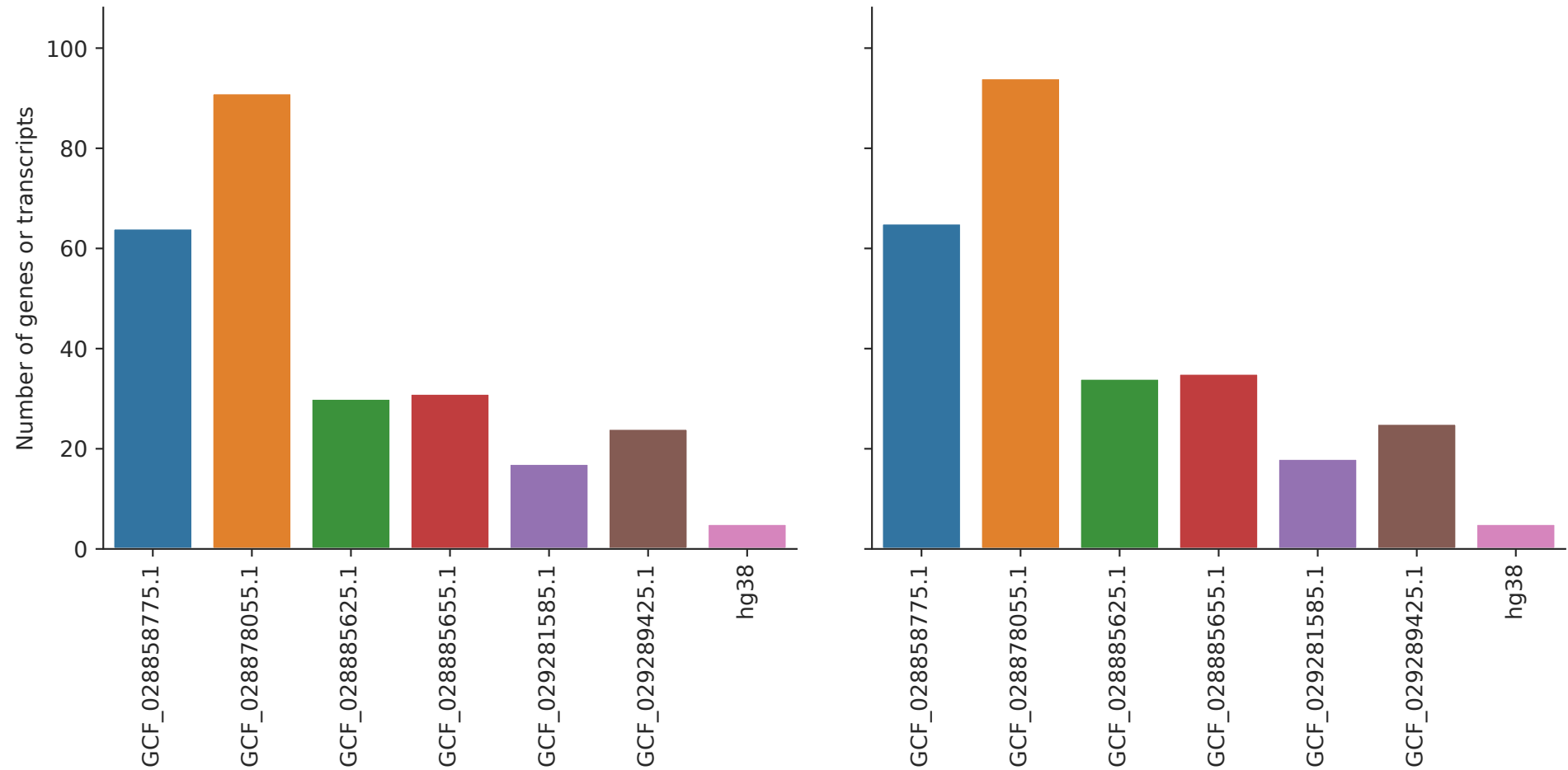
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_V_gene

variable = Genes

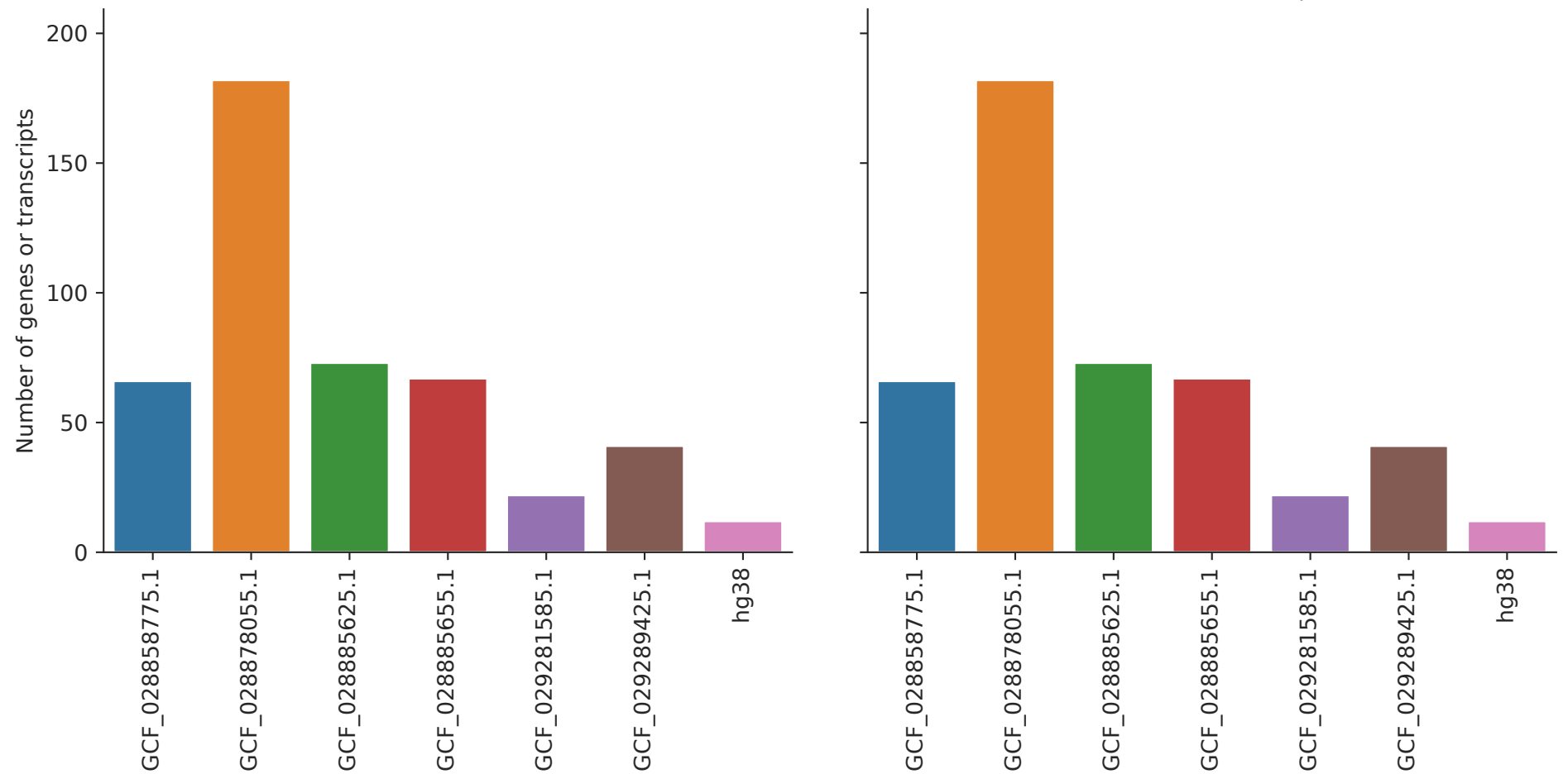
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_V_pseudogene

variable = Genes

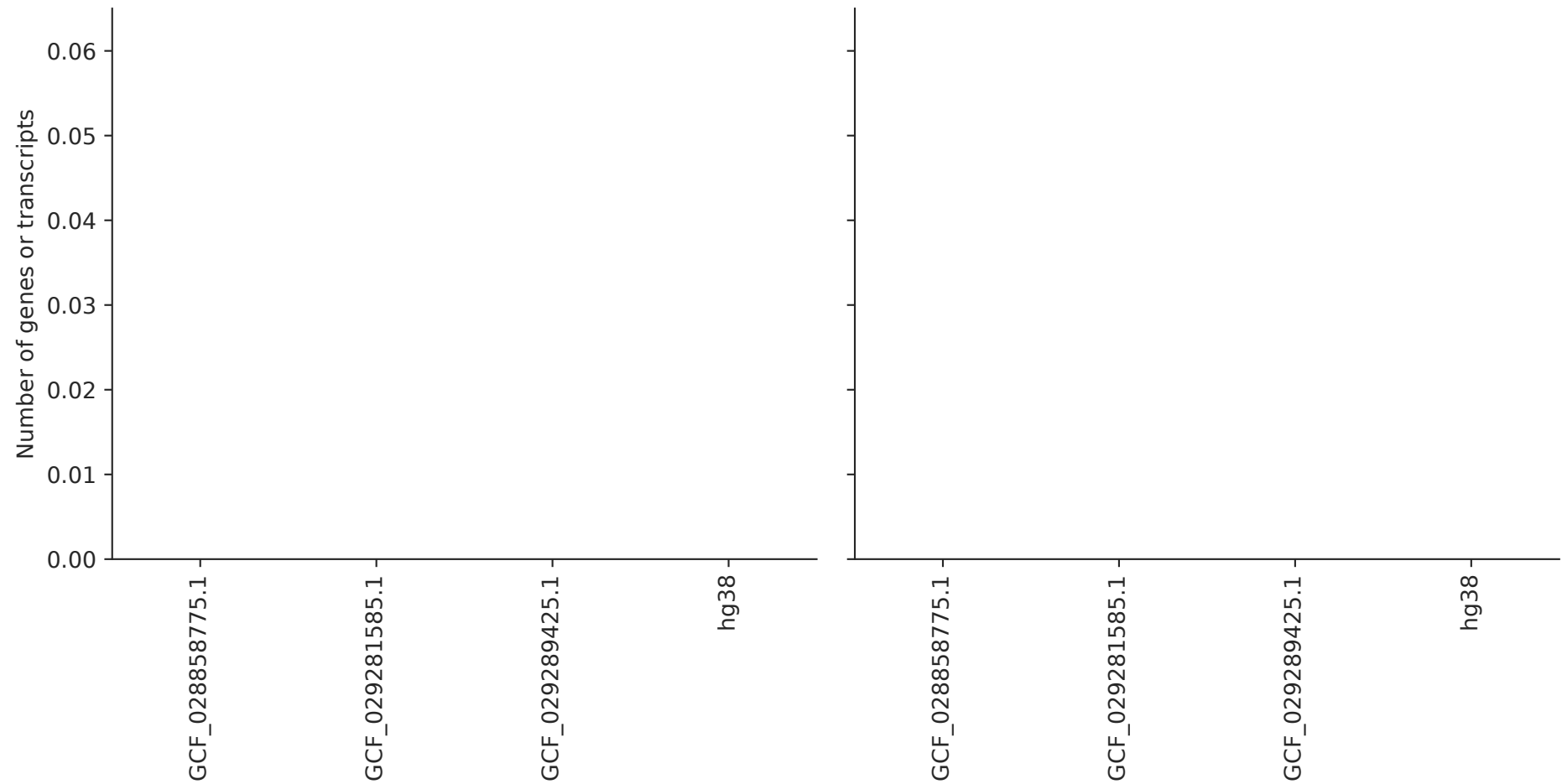
variable = Transcripts



Number of missing orthologs in consensus set for biotype IG_pseudogene

variable = Genes

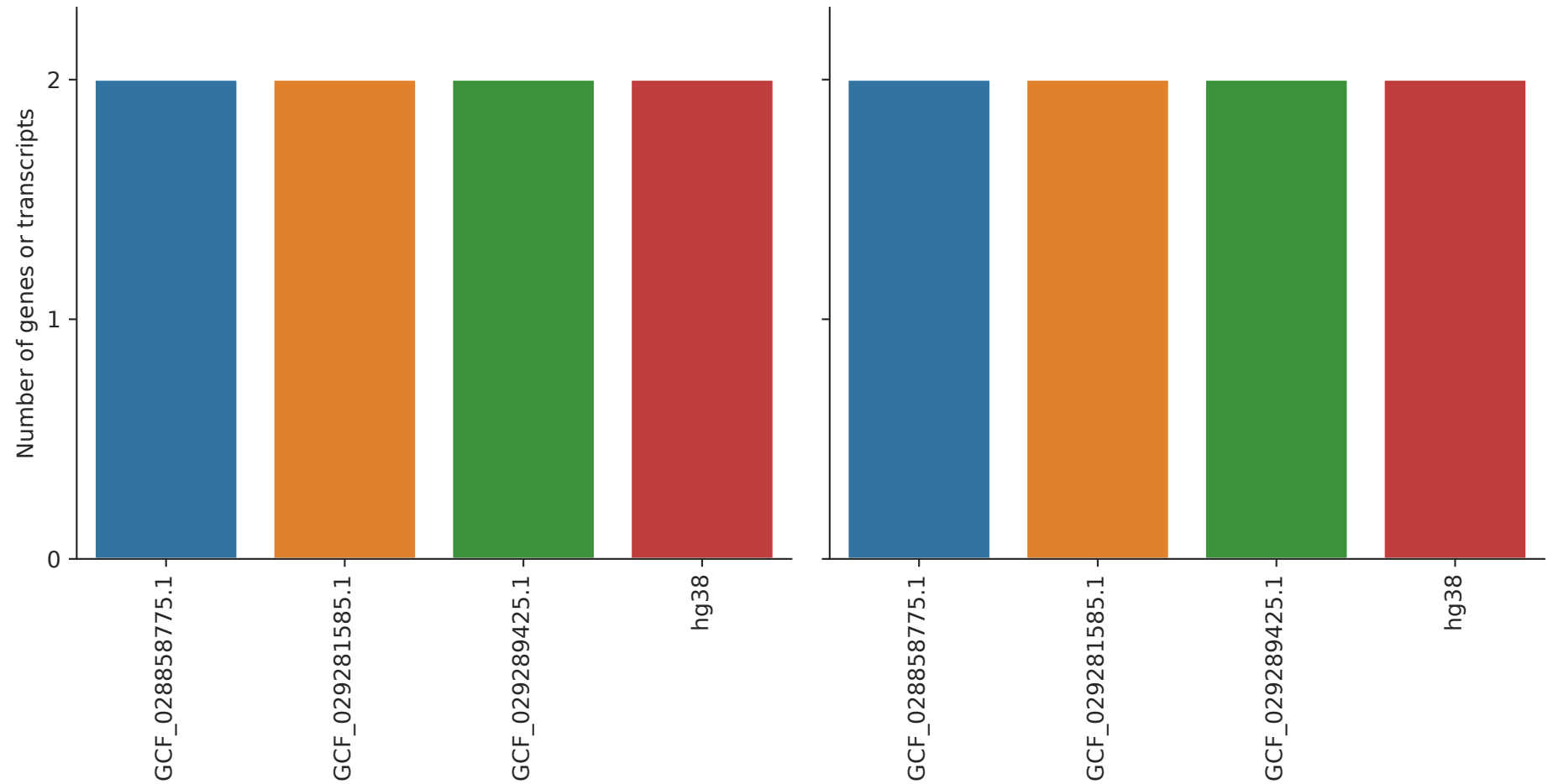
variable = Transcripts



Number of missing orthologs in consensus set for biotype Mt_rRNA

variable = Genes

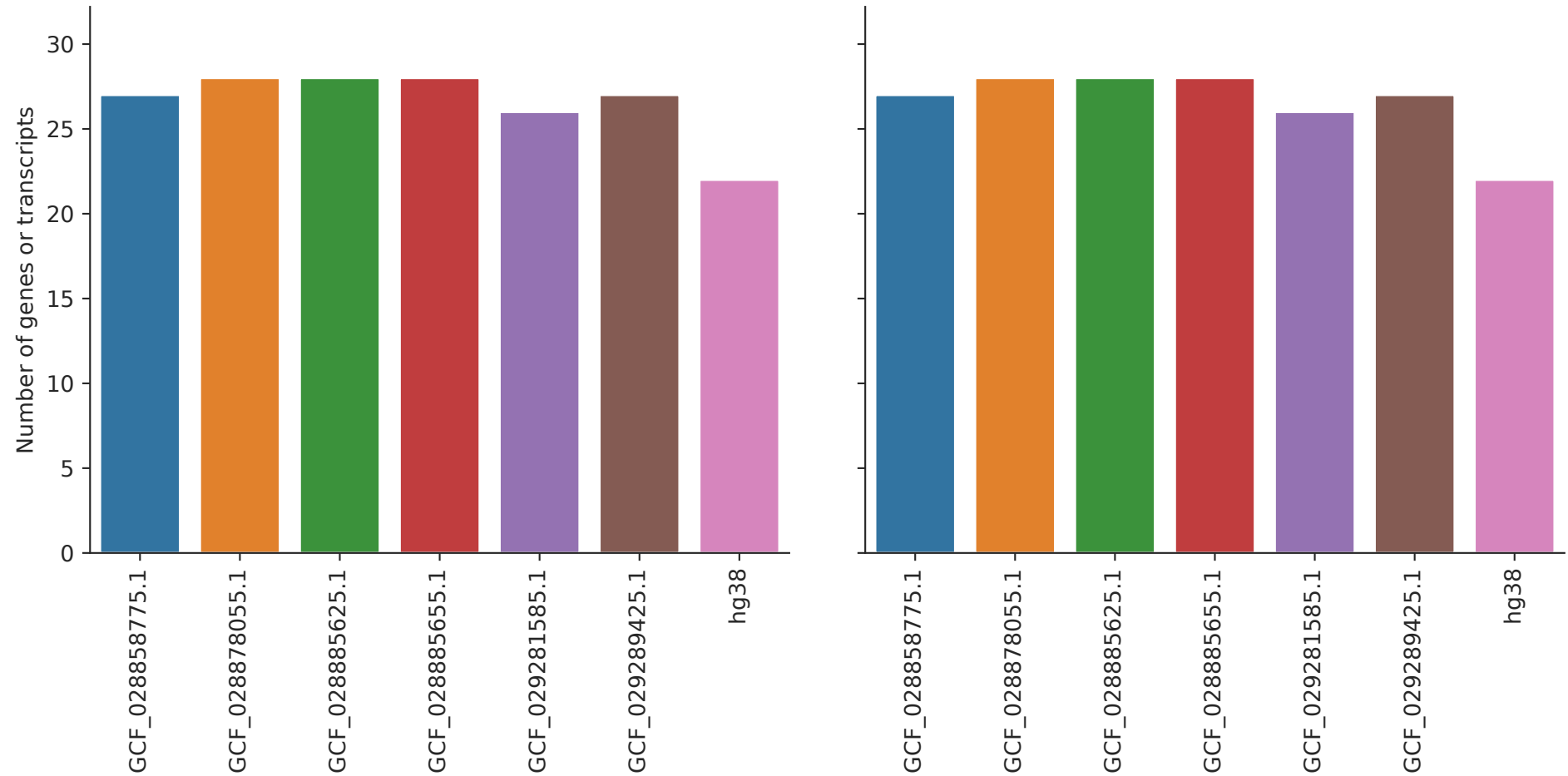
variable = Transcripts



Number of missing orthologs in consensus set for biotype Mt_tRNA

variable = Genes

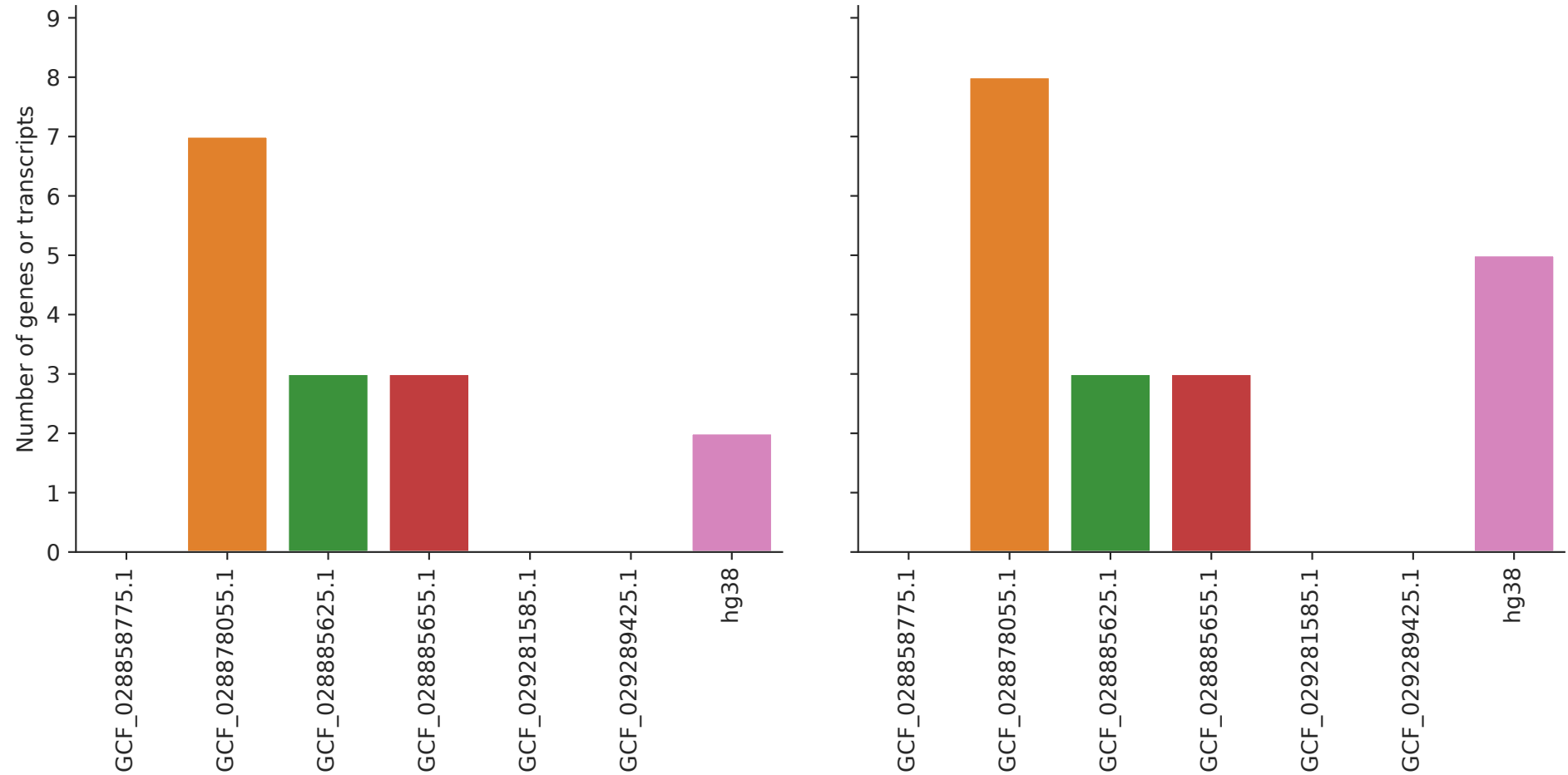
variable = Transcripts



Number of missing orthologs in consensus set for biotype StringTie

variable = Genes

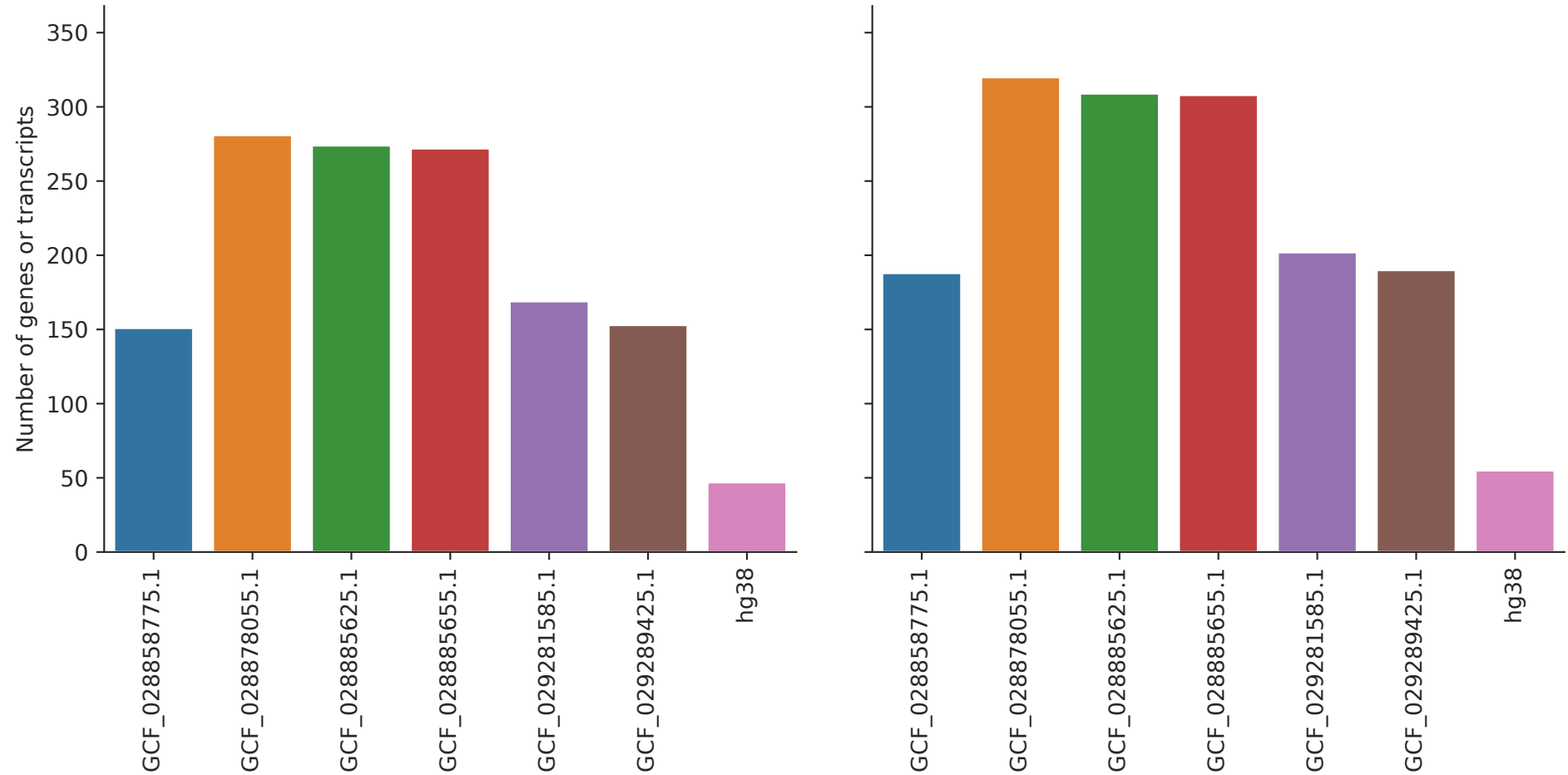
variable = Transcripts



Number of missing orthologs in consensus set for biotype TEC

variable = Genes

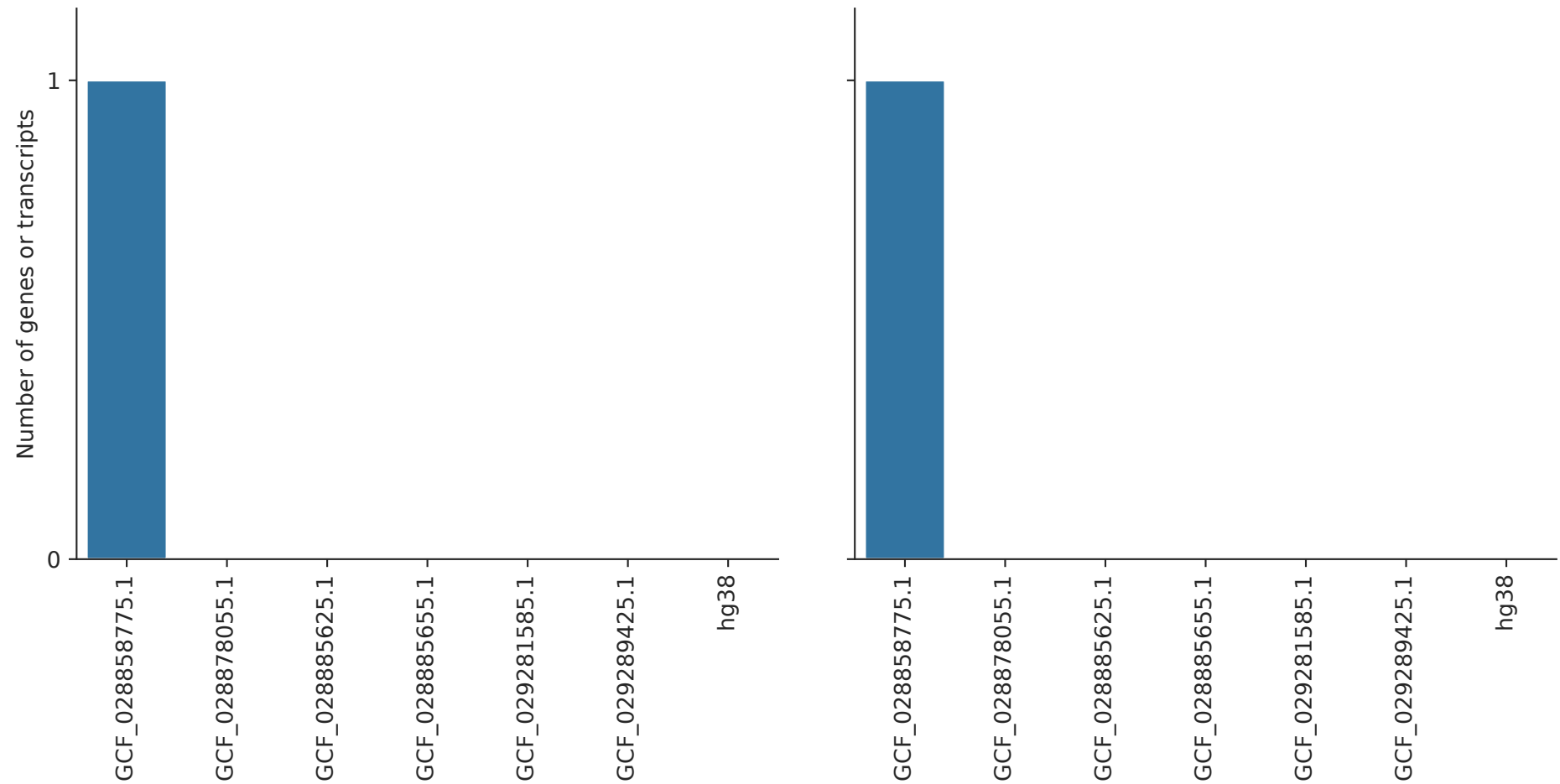
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_C_gene

variable = Genes

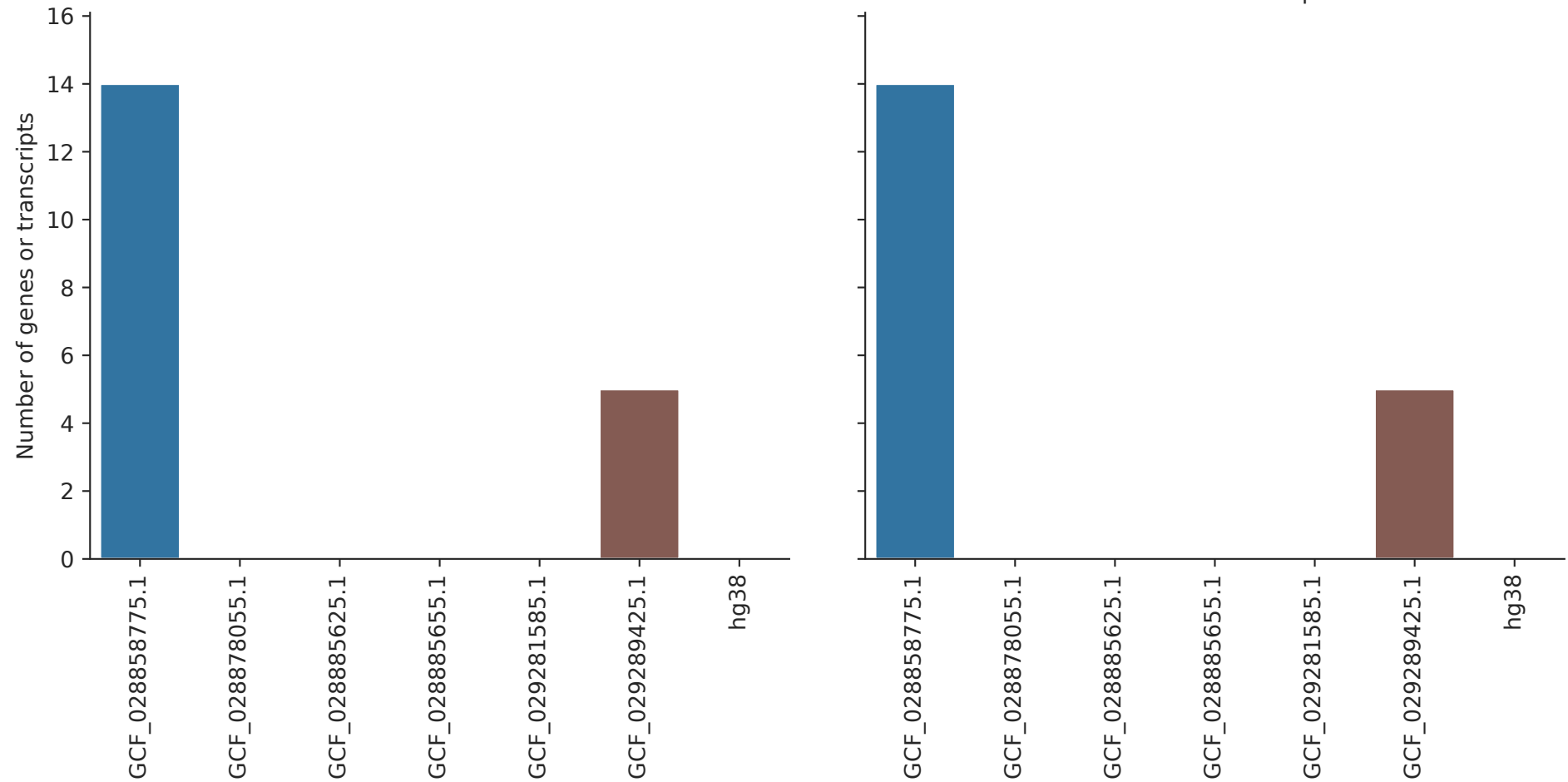
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_J_gene

variable = Genes

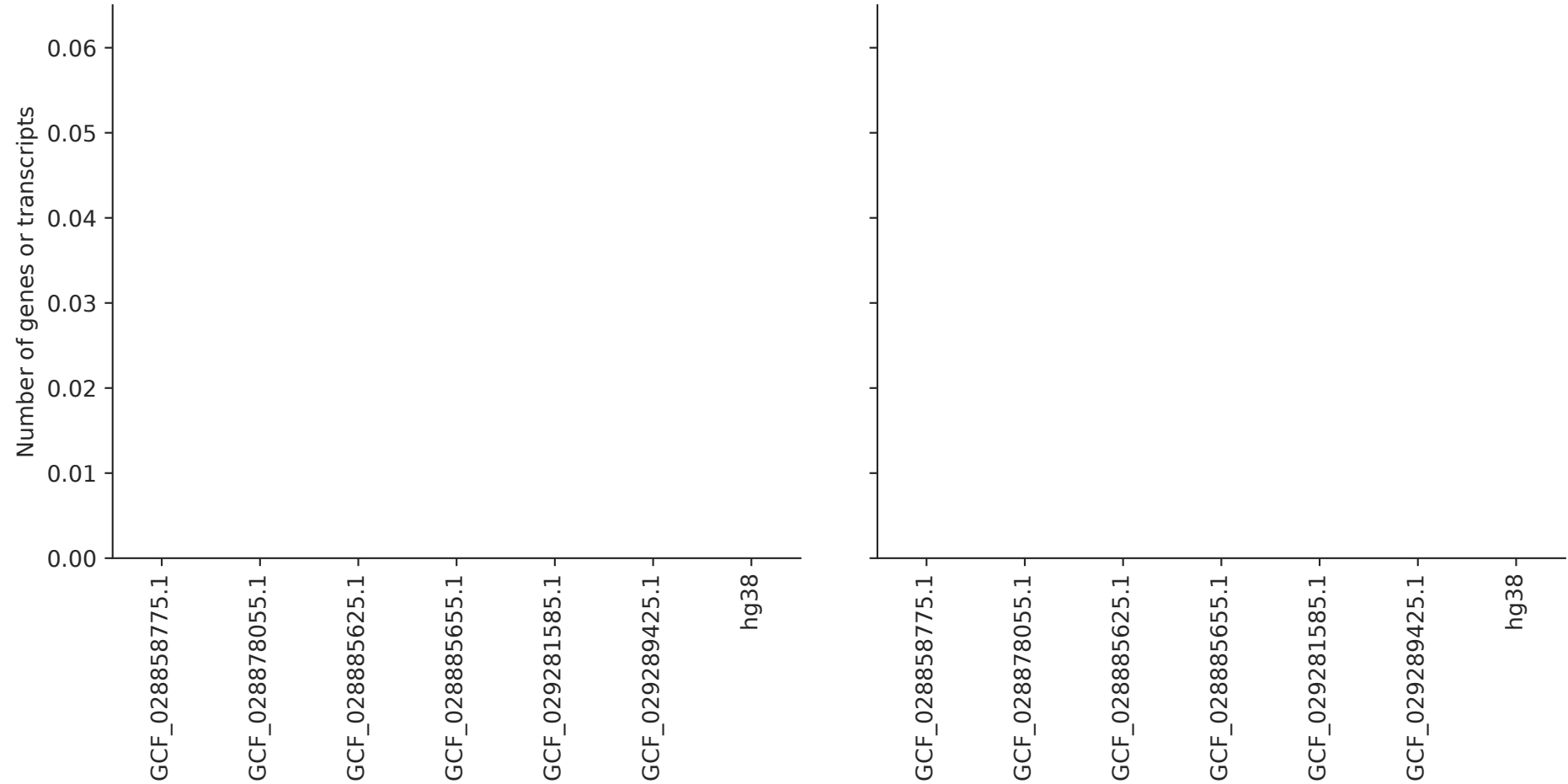
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_J_pseudogene

variable = Genes

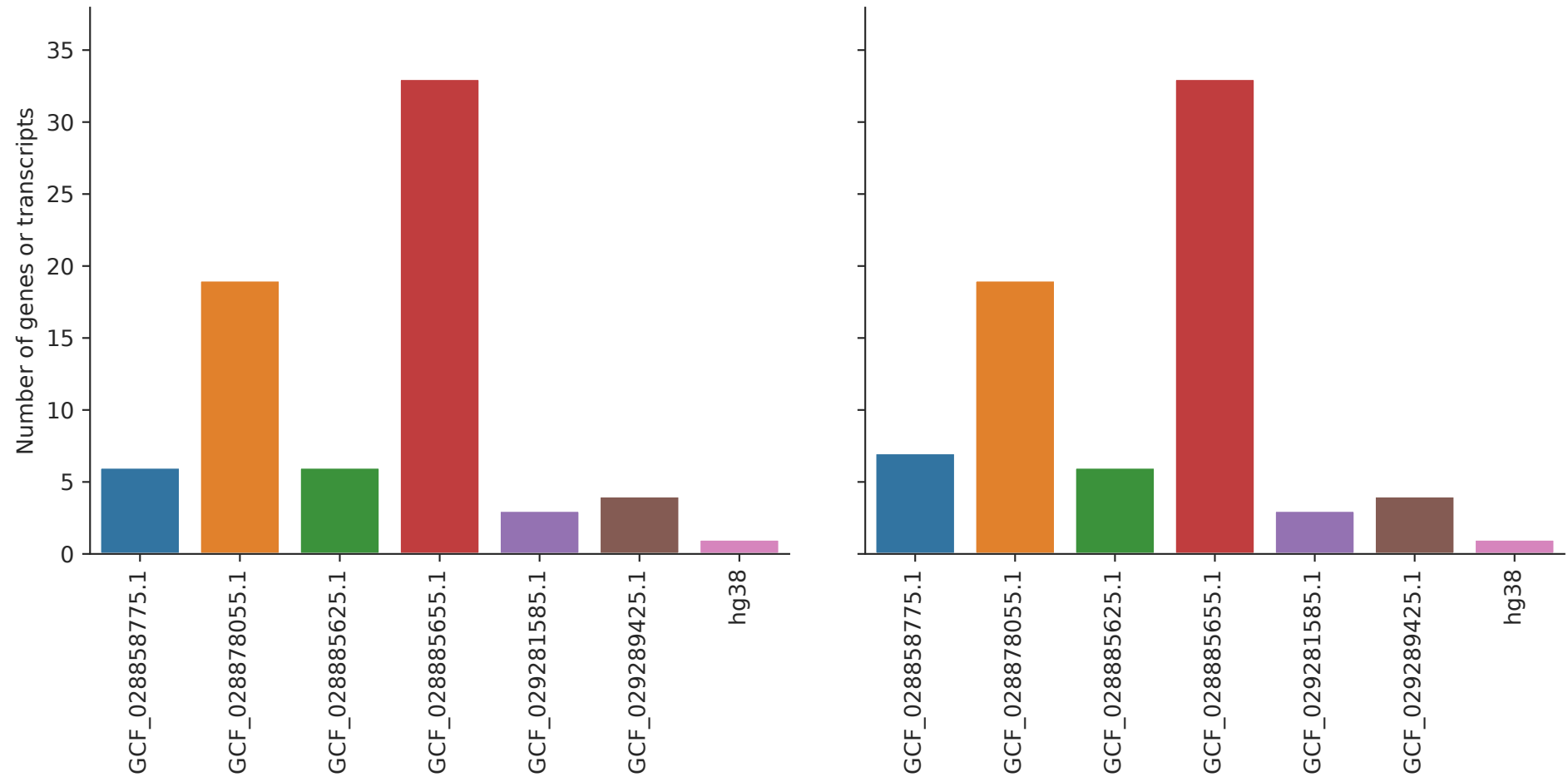
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_V_gene

variable = Genes

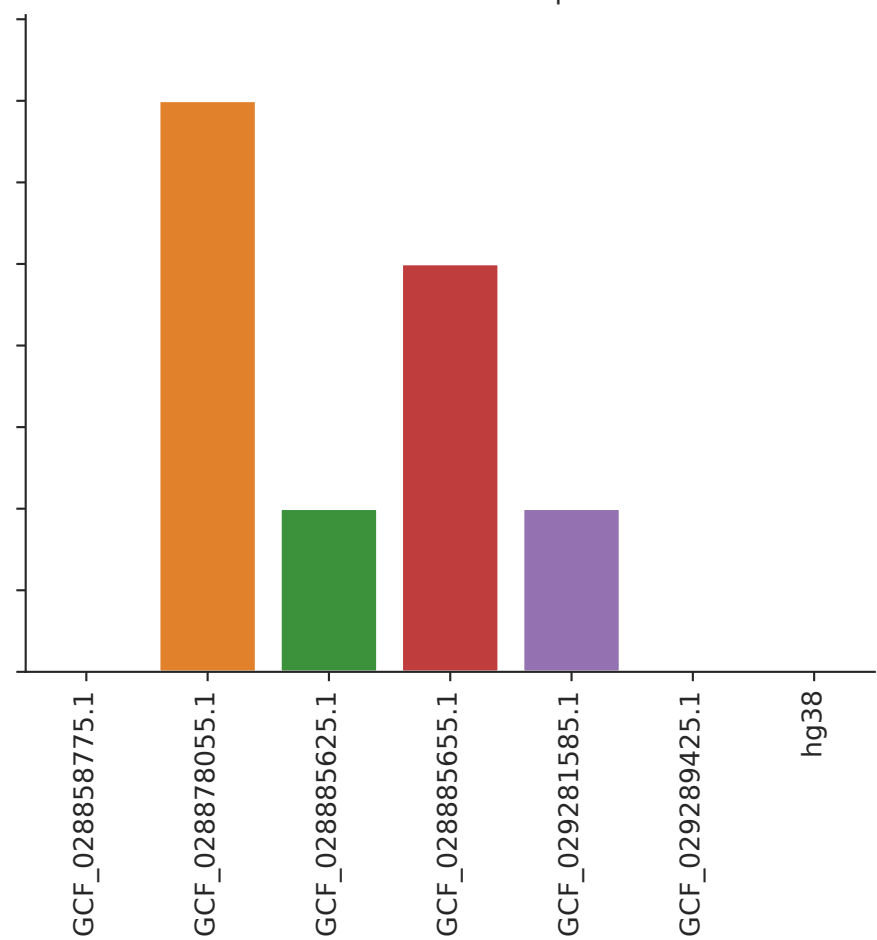
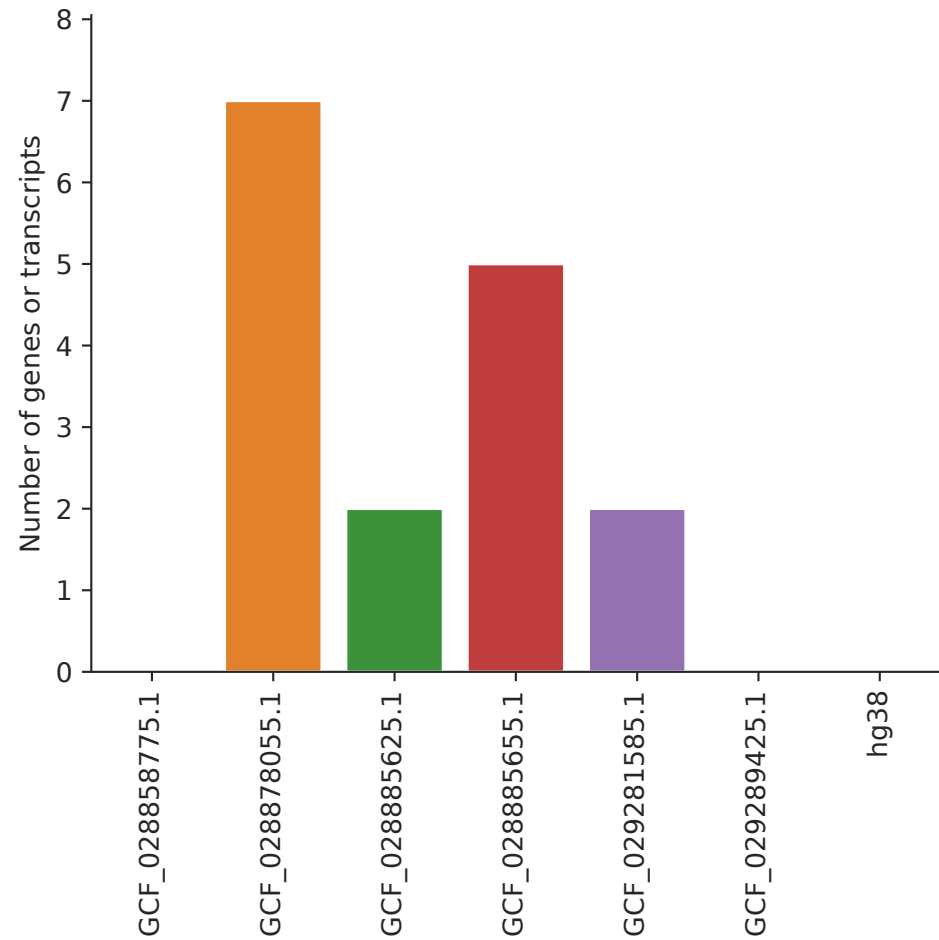
variable = Transcripts



Number of missing orthologs in consensus set for biotype TR_V_pseudogene

variable = Genes

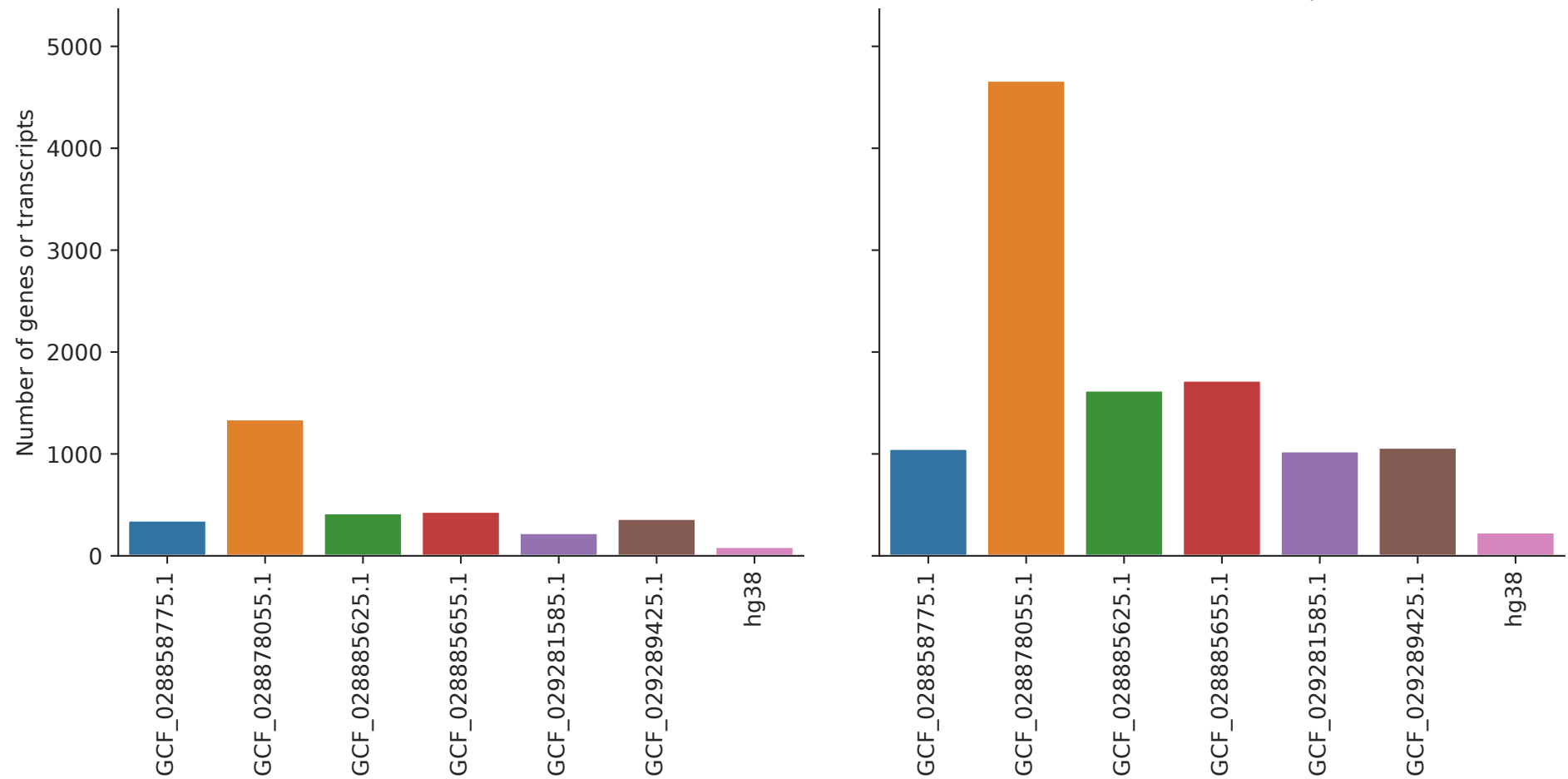
variable = Transcripts



Number of missing orthologs in consensus set for biotype lncRNA

variable = Genes

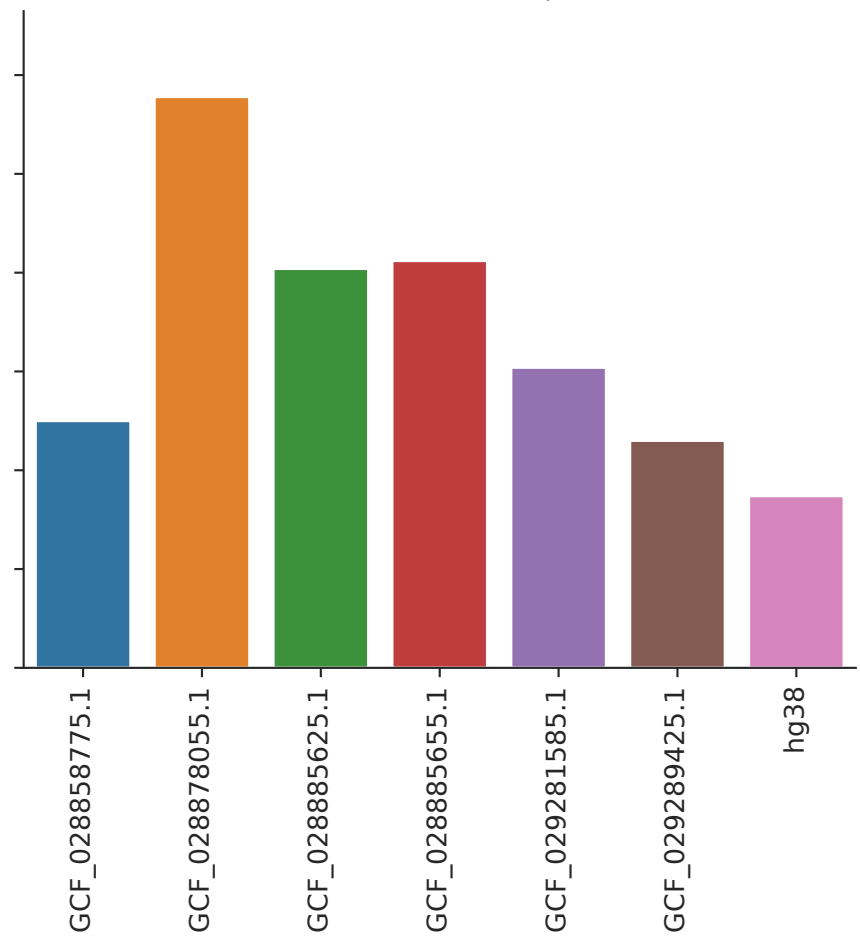
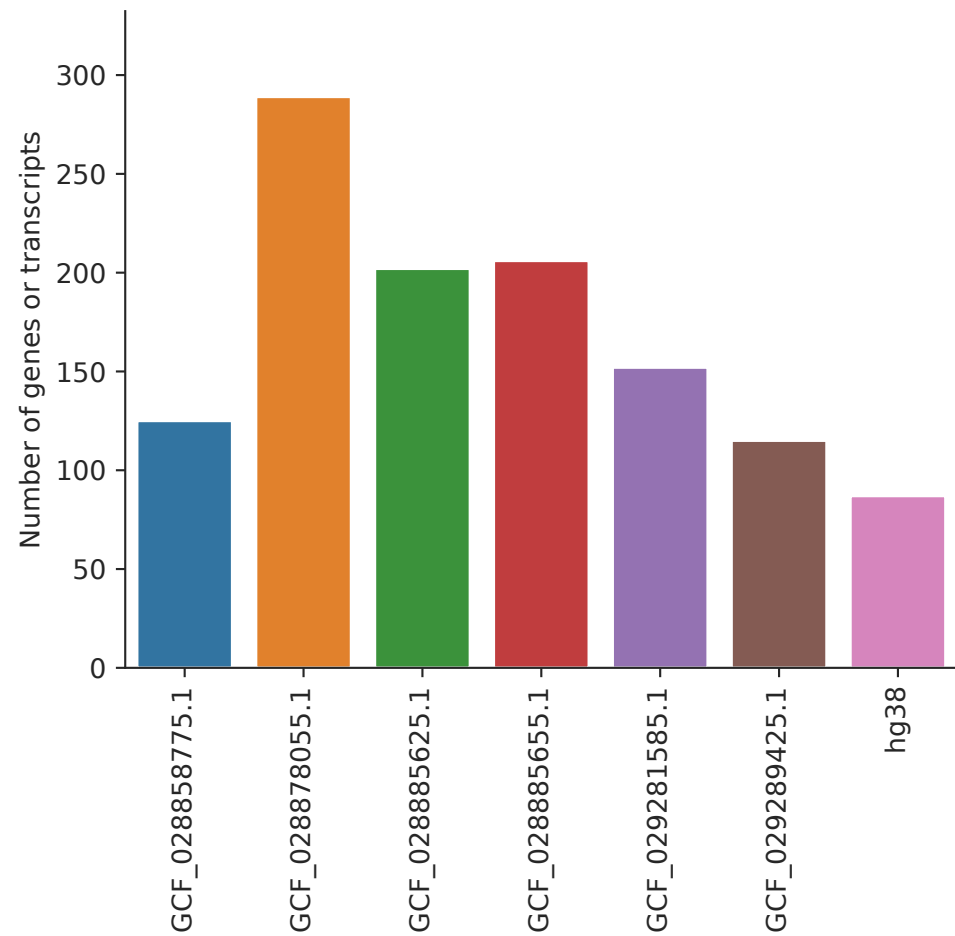
variable = Transcripts



Number of missing orthologs in consensus set for biotype miRNA

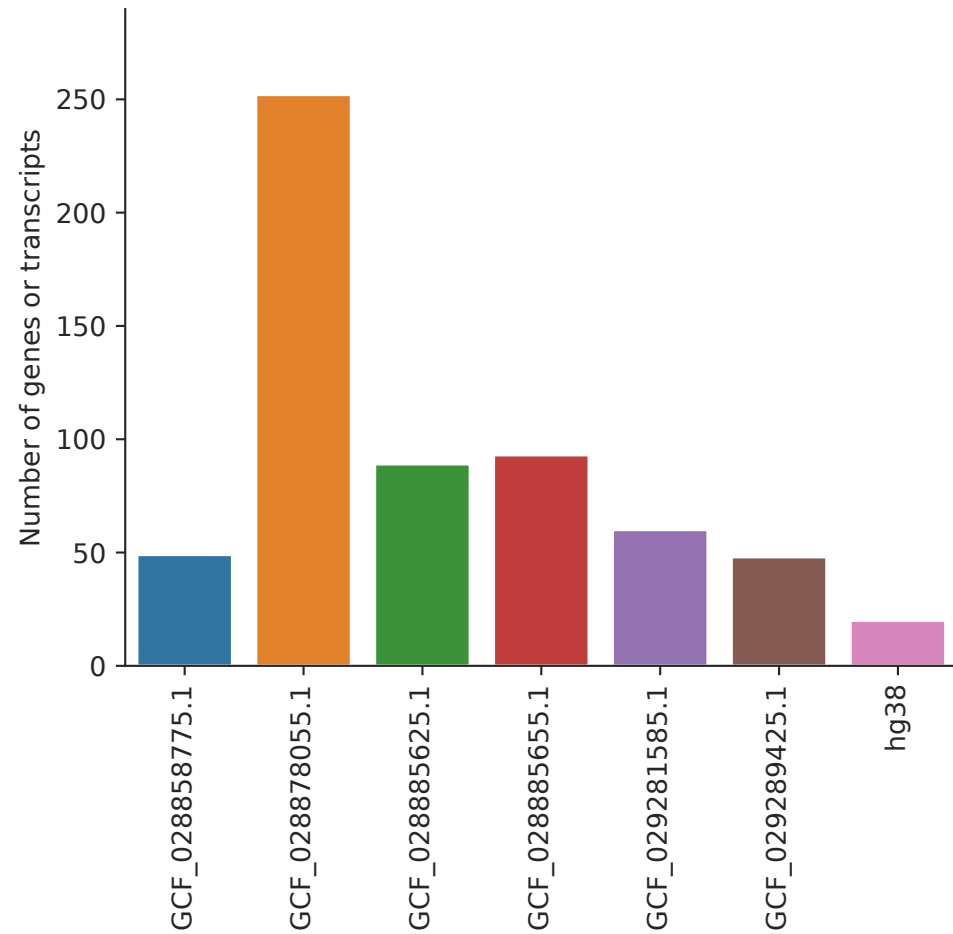
variable = Genes

variable = Transcripts

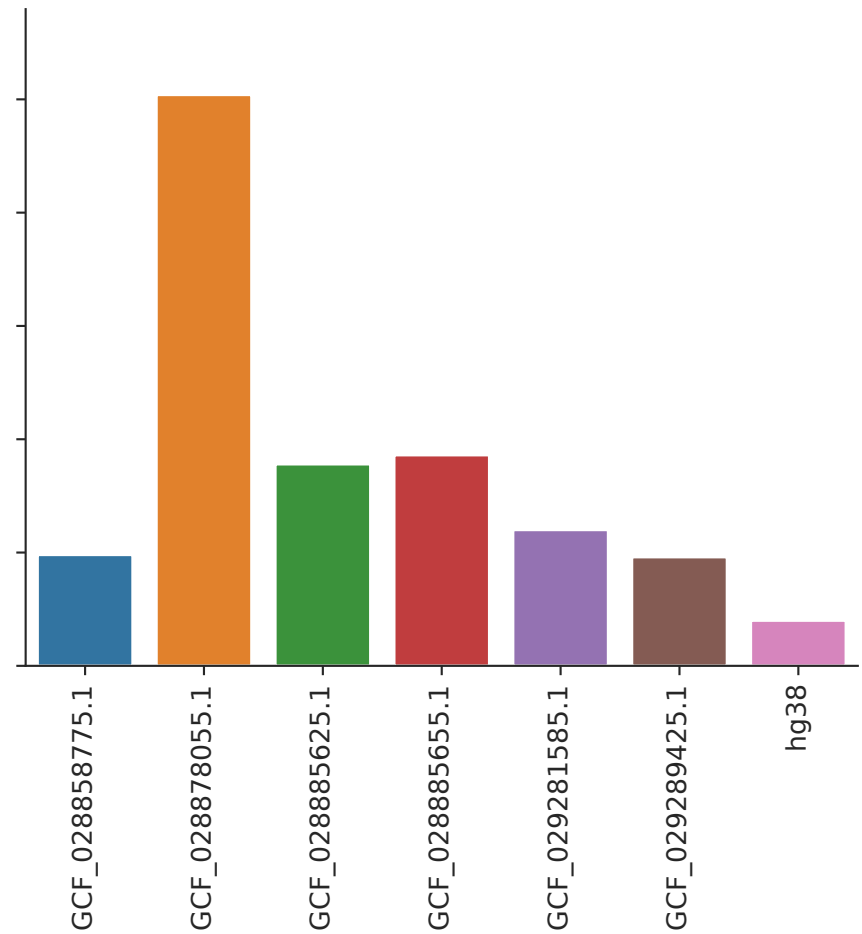


Number of missing orthologs in consensus set for biotype misc_RNA

variable = Genes



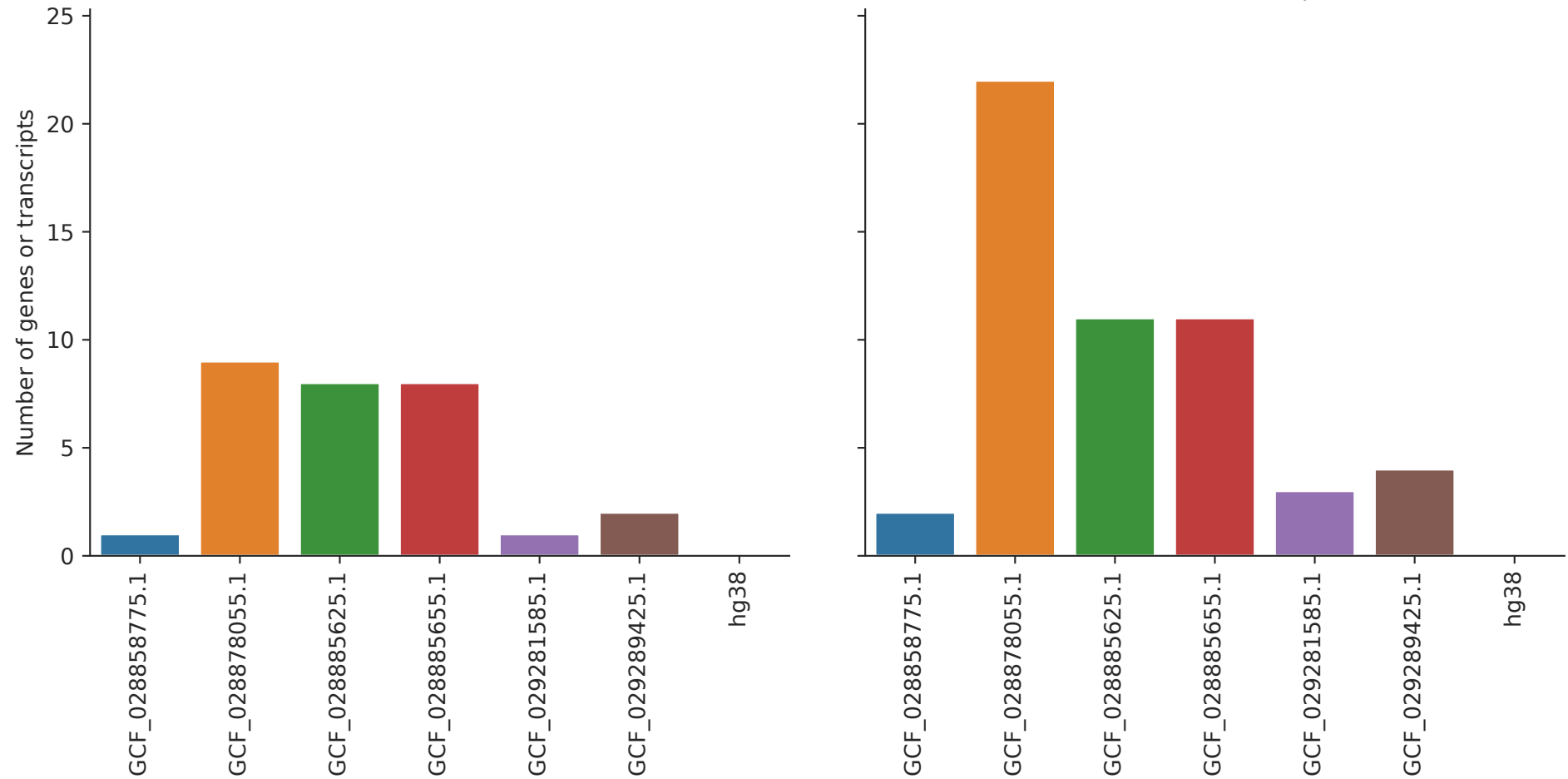
variable = Transcripts



Number of missing orthologs in consensus set for biotype polymorphic_pseudogene

variable = Genes

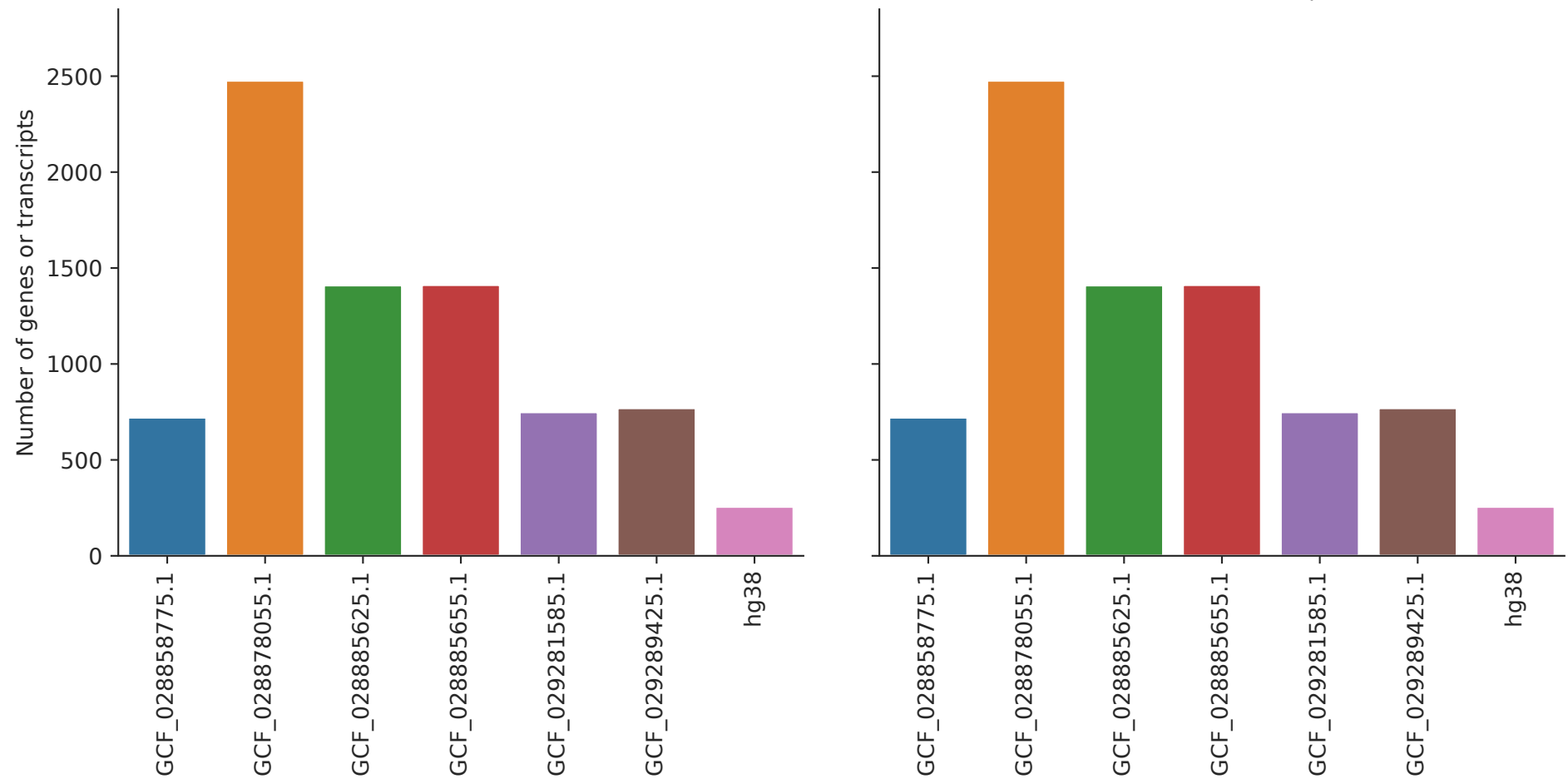
variable = Transcripts



Number of missing orthologs in consensus set for biotype processed_pseudogene

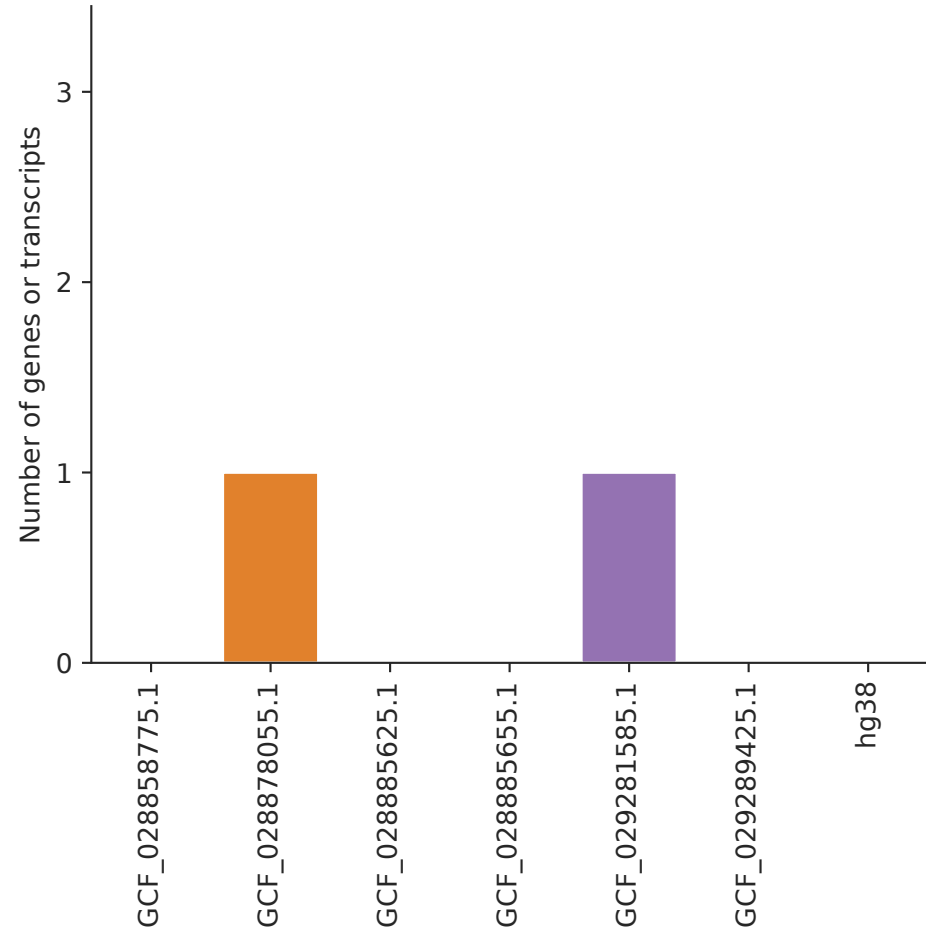
variable = Genes

variable = Transcripts

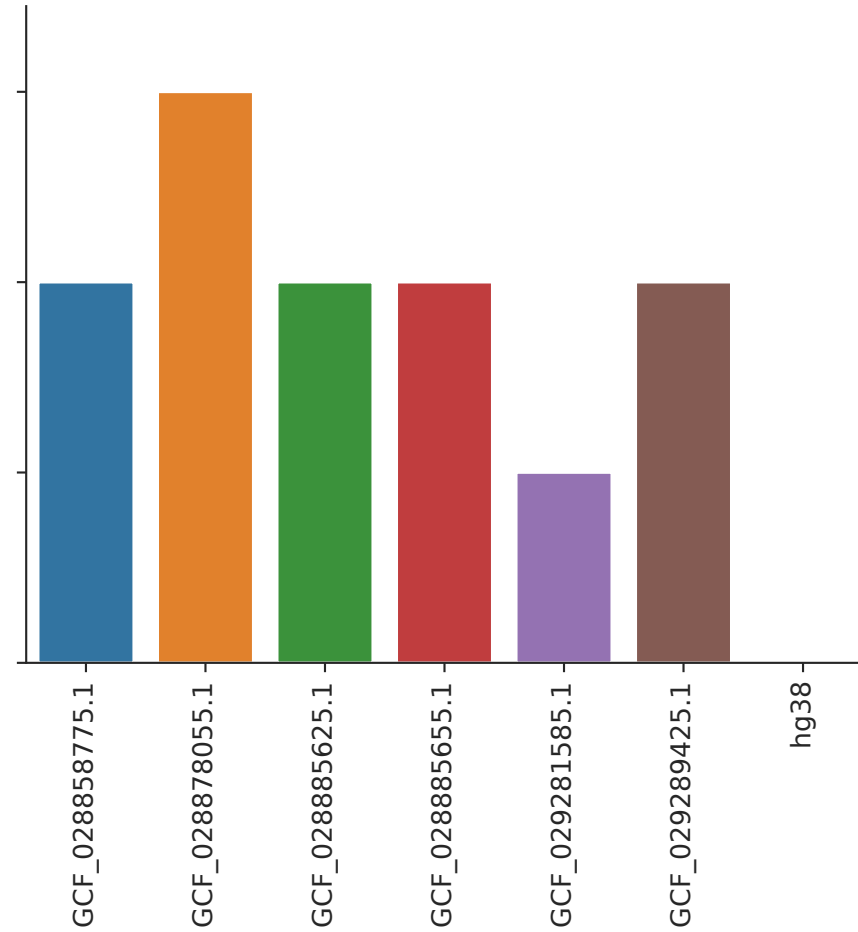


Number of missing orthologs in consensus set for biotype pseudogene

variable = Genes



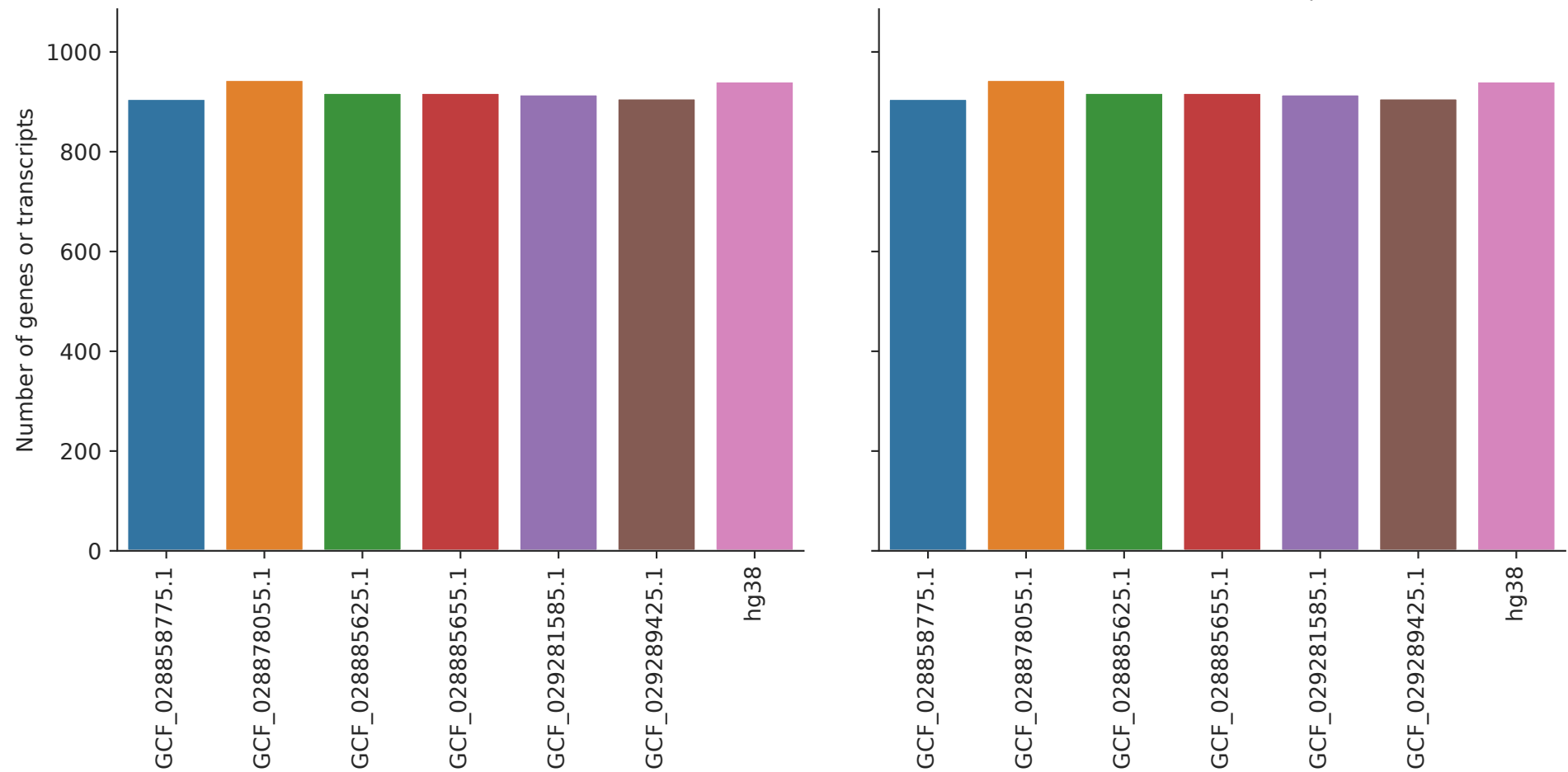
variable = Transcripts



Number of missing orthologs in consensus set for biotype rRNA

variable = Genes

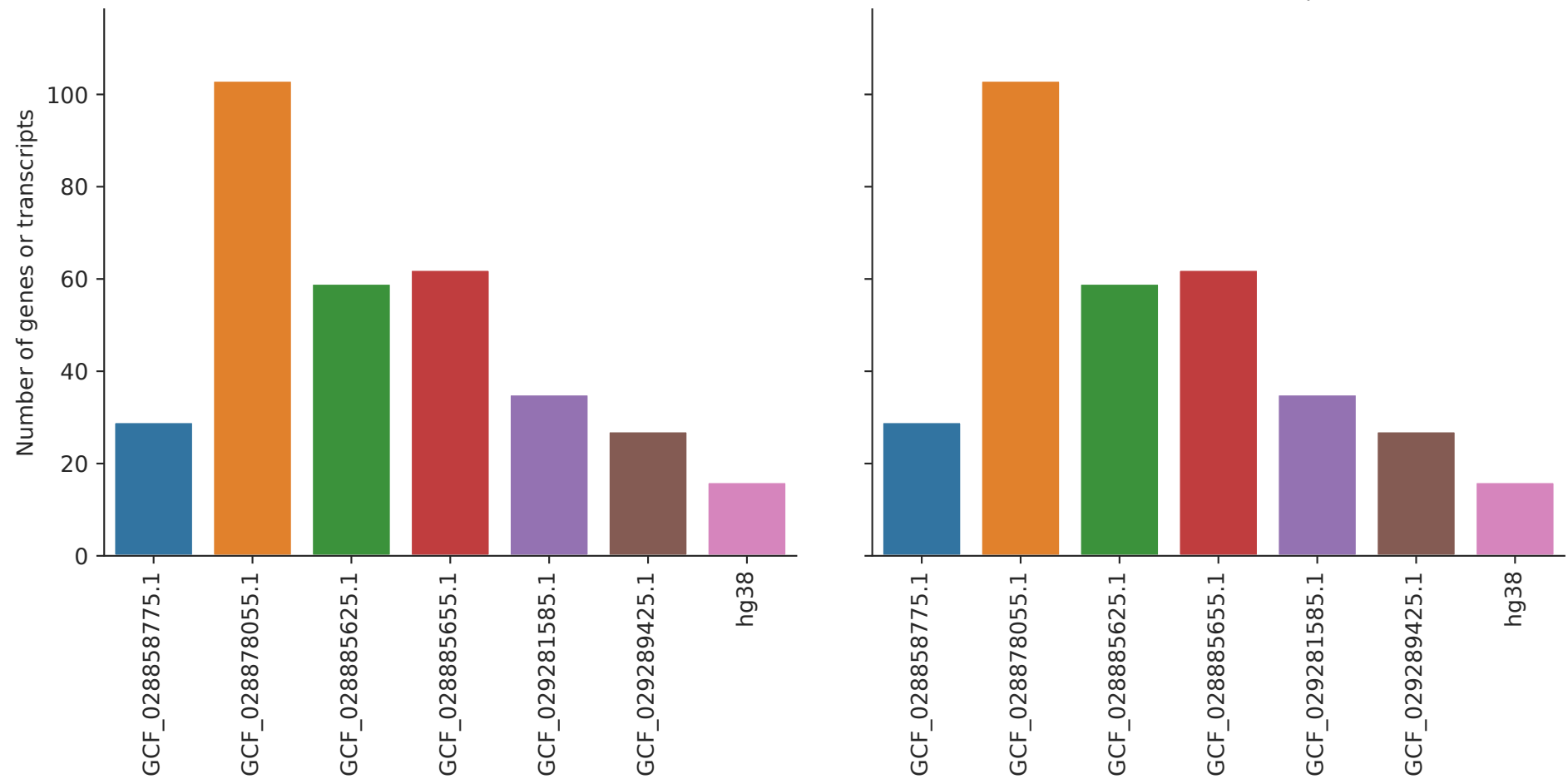
variable = Transcripts



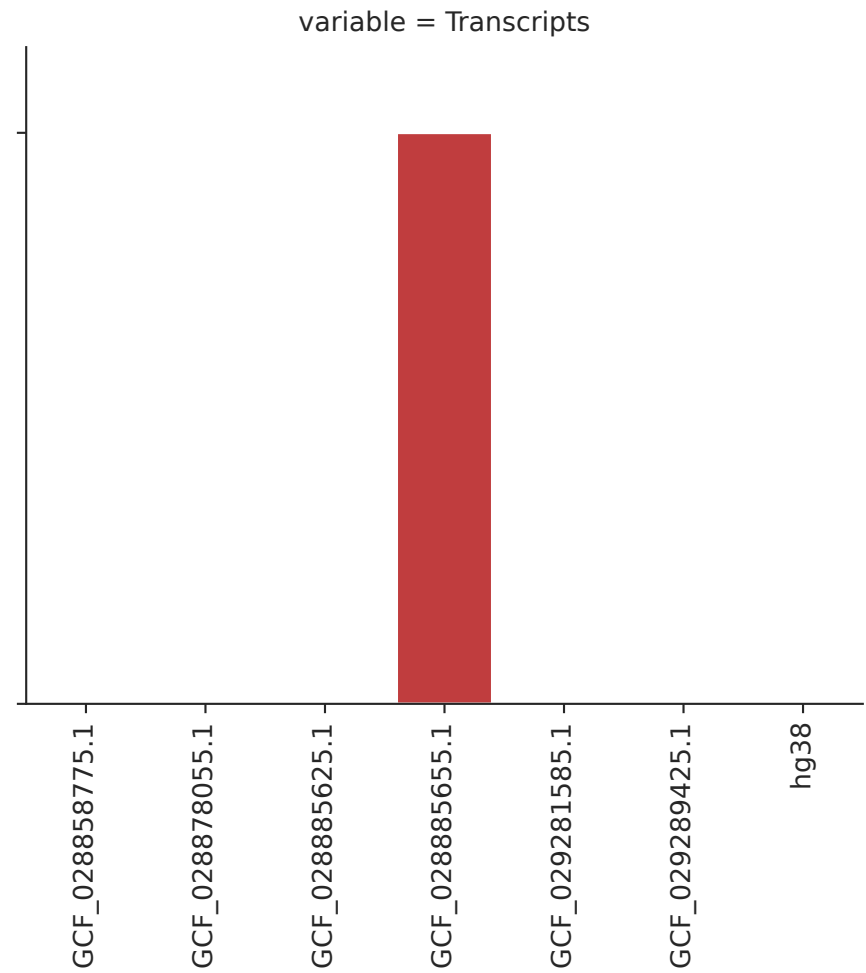
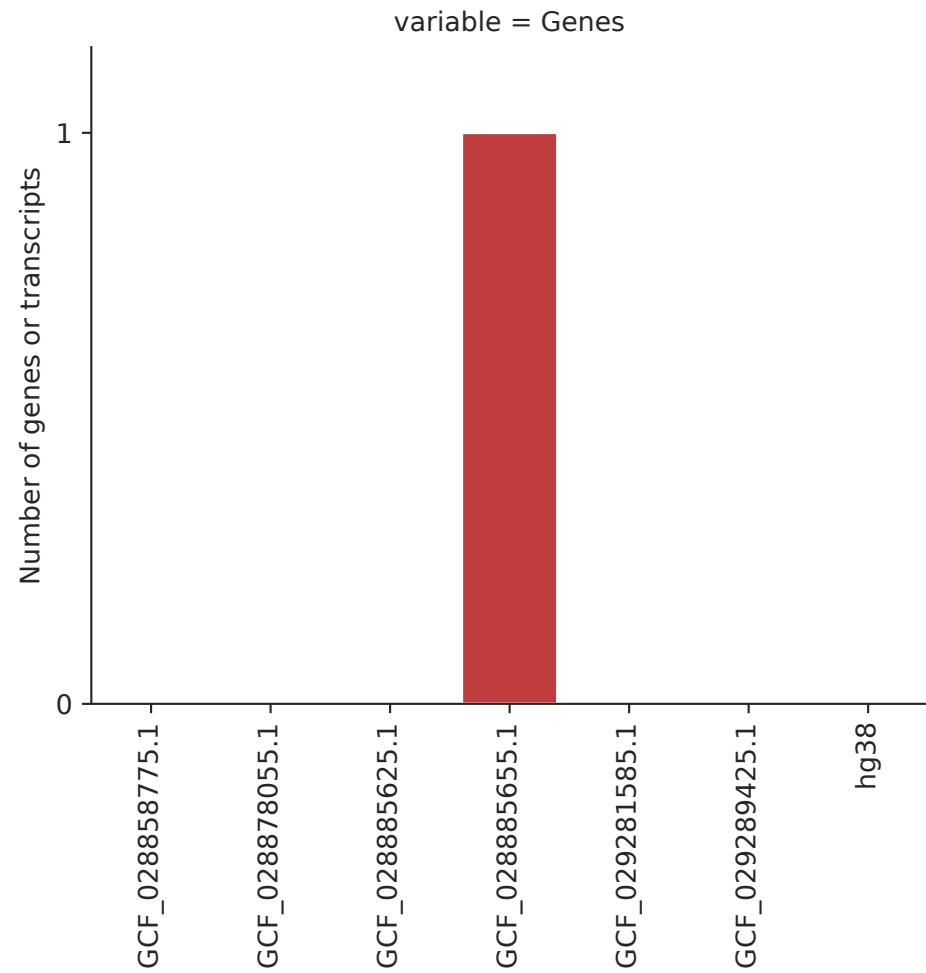
Number of missing orthologs in consensus set for biotype rRNA_pseudogene

variable = Genes

variable = Transcripts



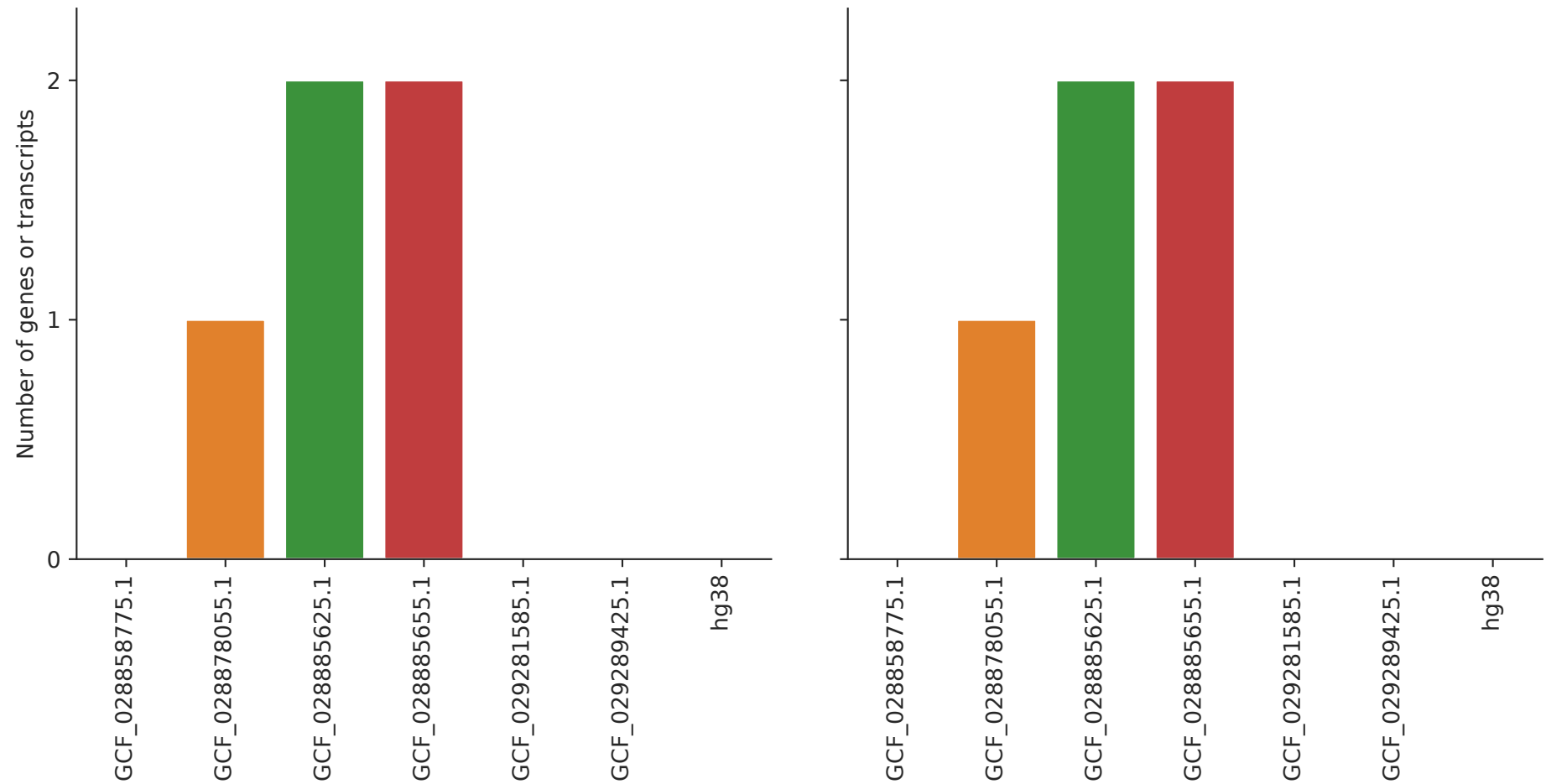
Number of missing orthologs in consensus set for biotype ribozyme



Number of missing orthologs in consensus set for biotype sRNA

variable = Genes

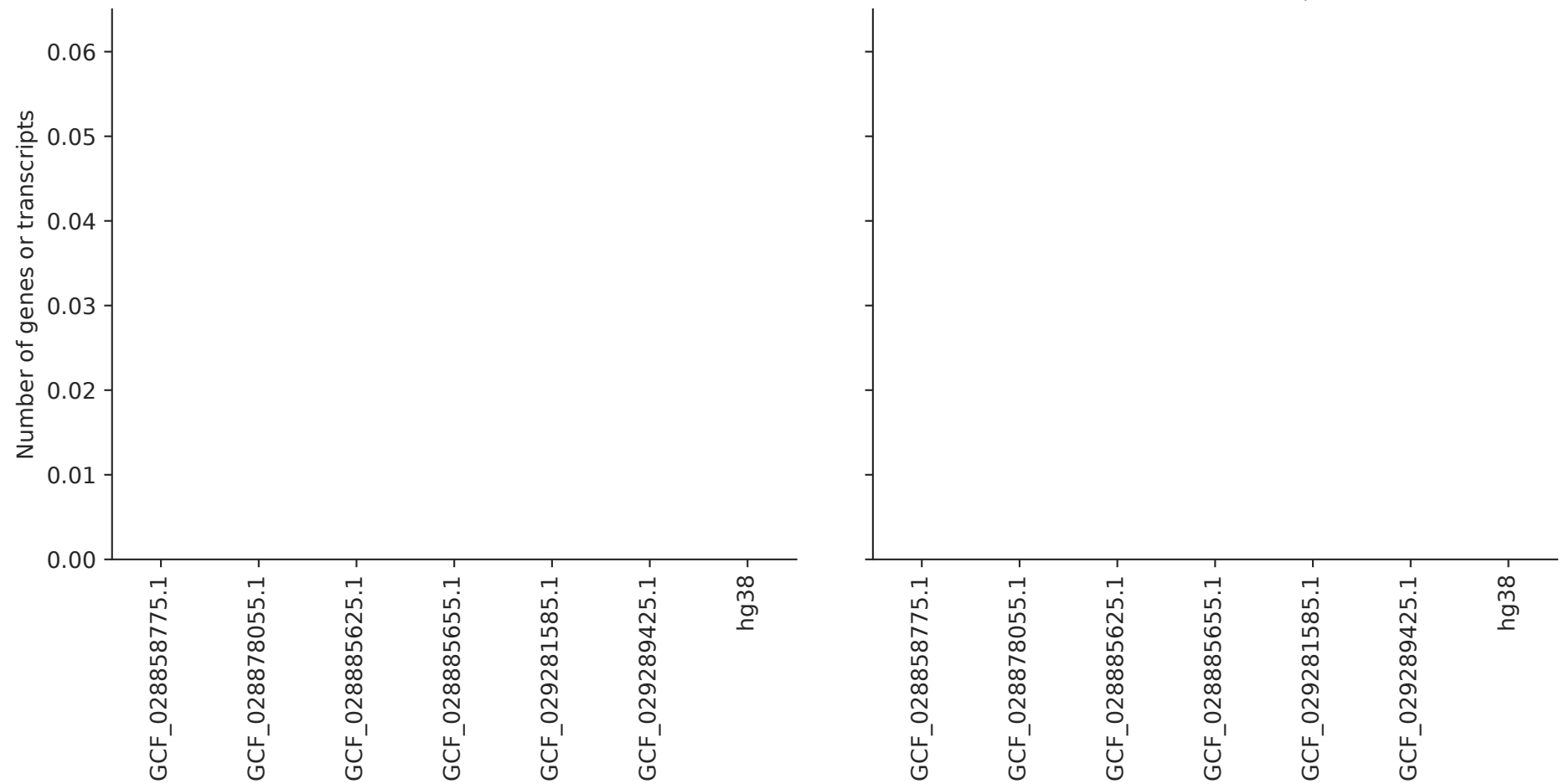
variable = Transcripts



Number of missing orthologs in consensus set for biotype scRNA

variable = Genes

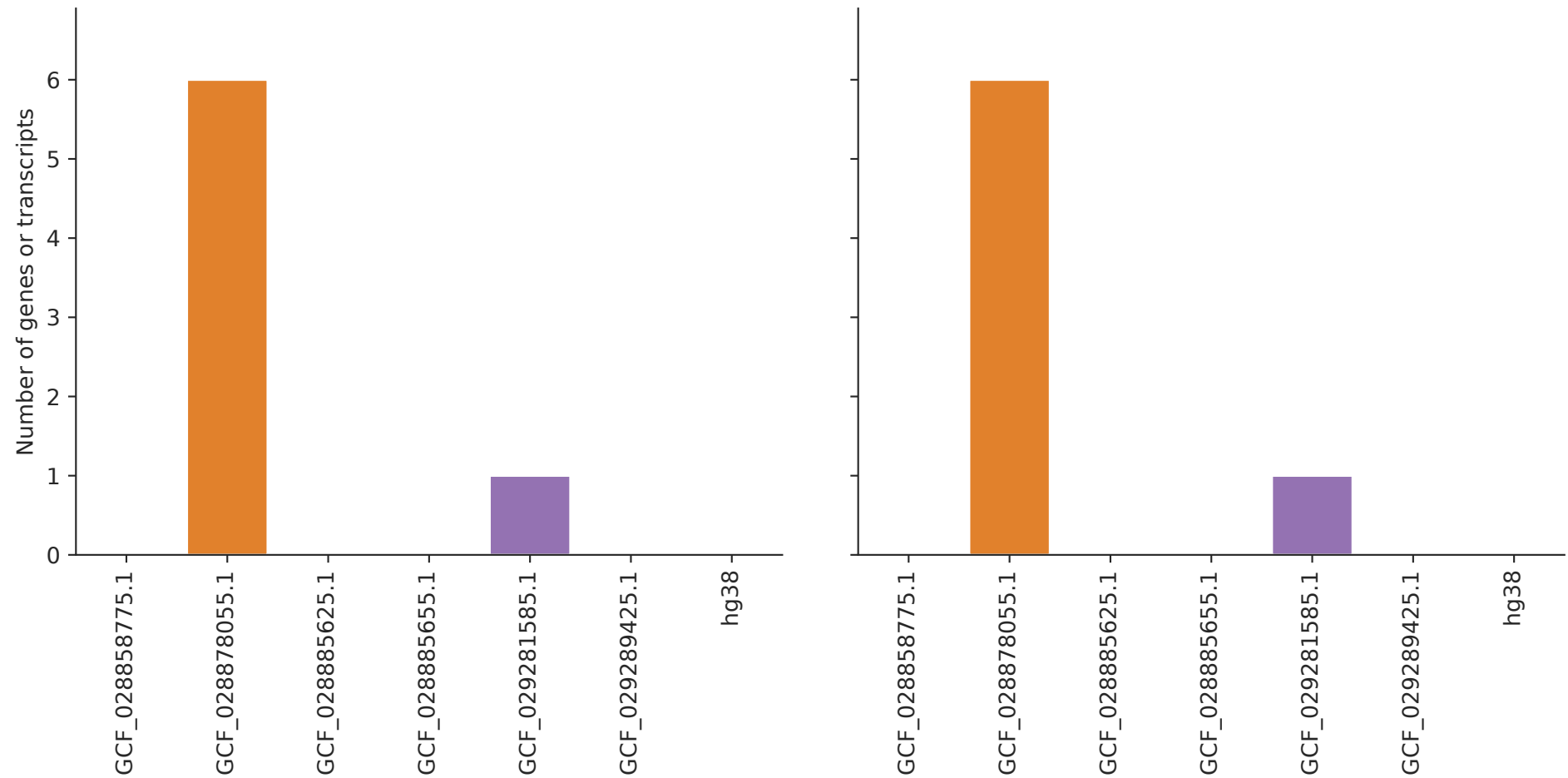
variable = Transcripts



Number of missing orthologs in consensus set for biotype scaRNA

variable = Genes

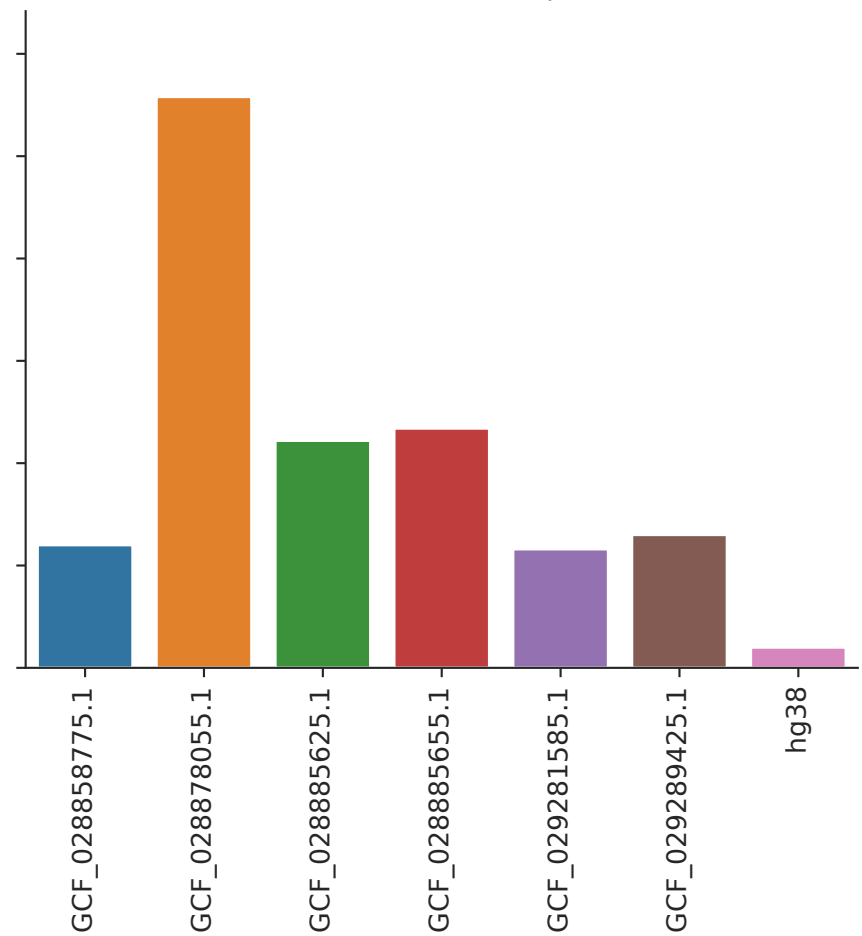
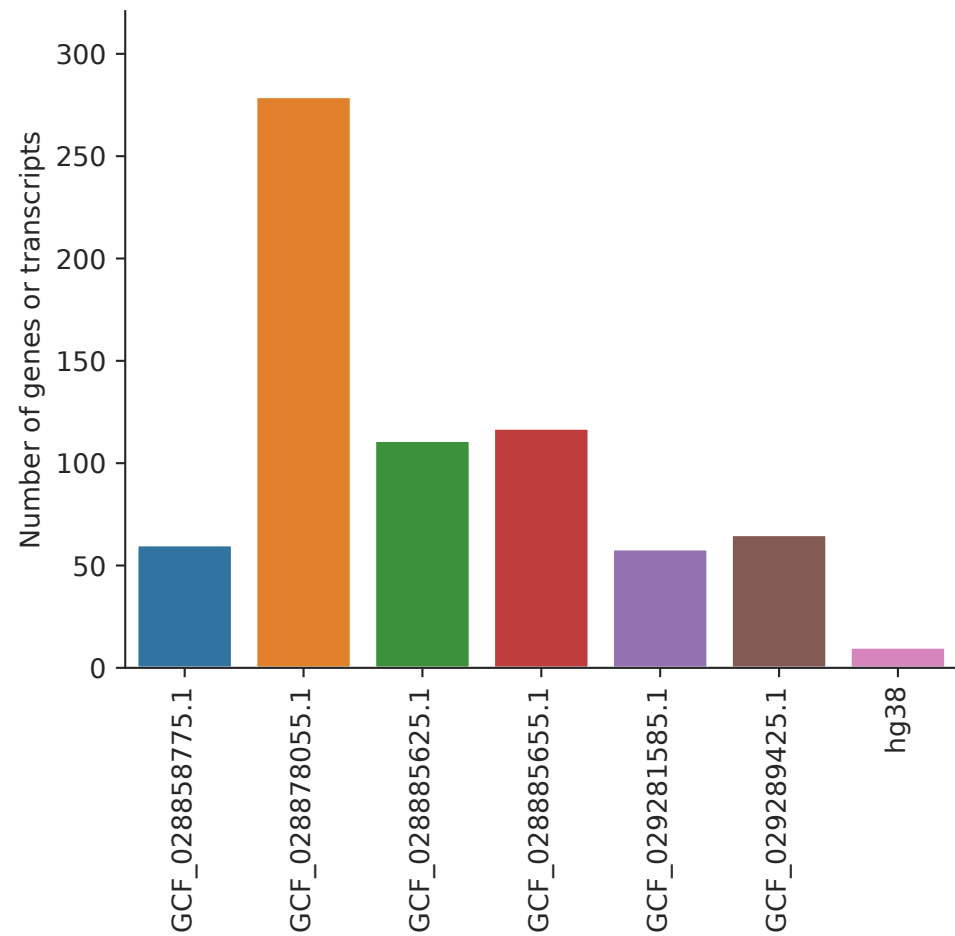
variable = Transcripts



Number of missing orthologs in consensus set for biotype snRNA

variable = Genes

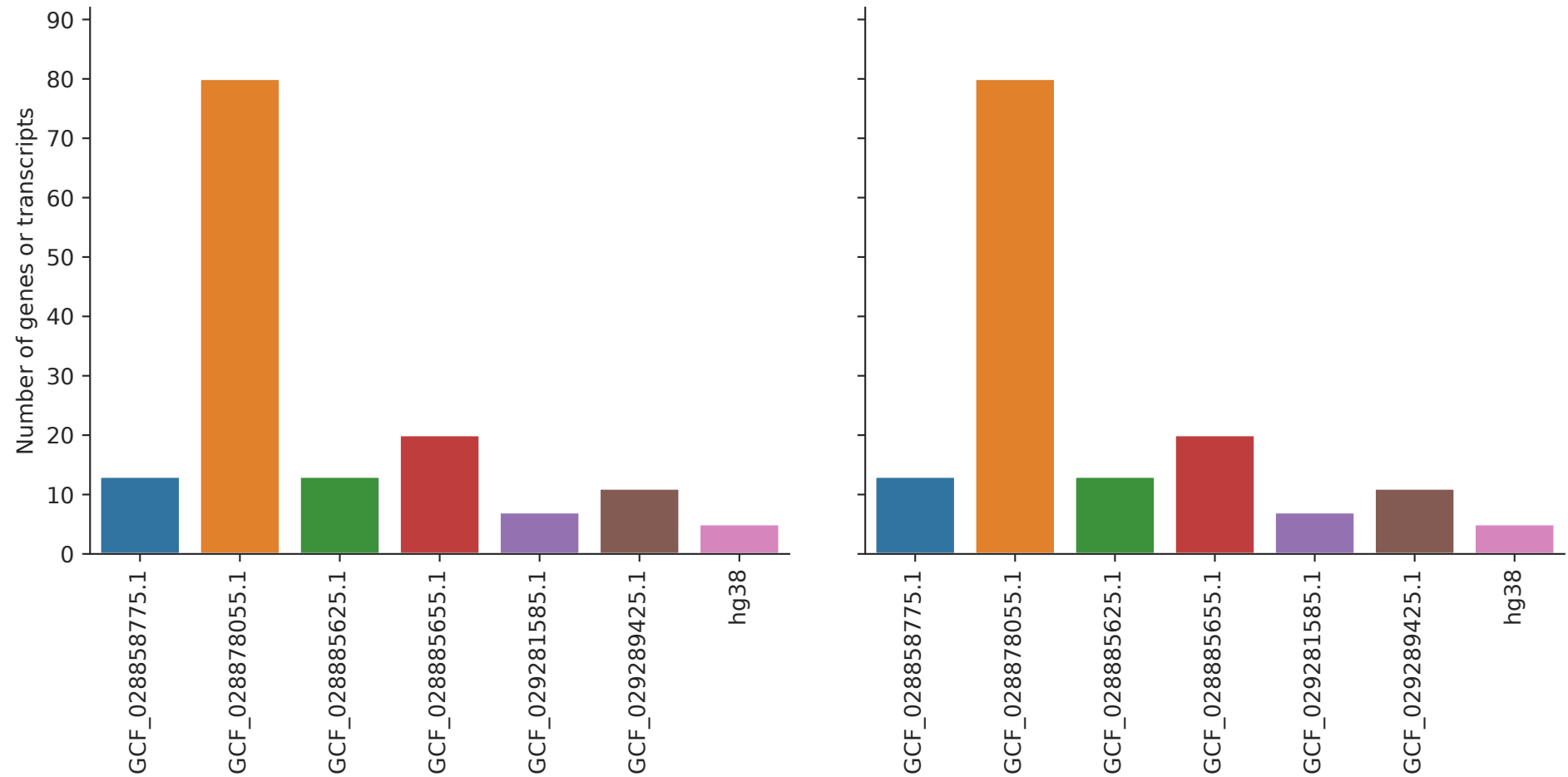
variable = Transcripts



Number of missing orthologs in consensus set for biotype snoRNA

variable = Genes

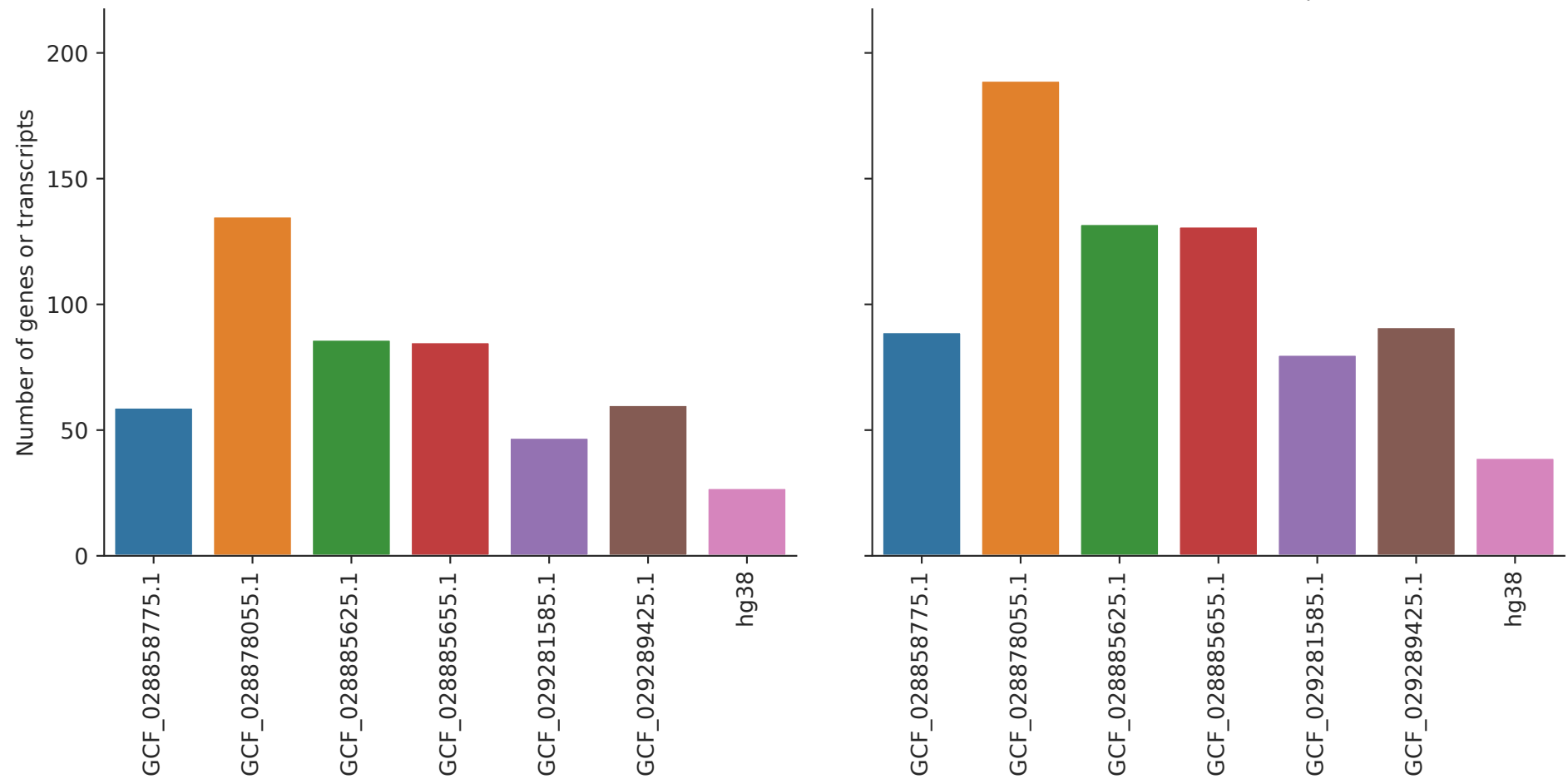
variable = Transcripts



Number of missing orthologs in consensus set for biotype transcribed_processed_pseudogene

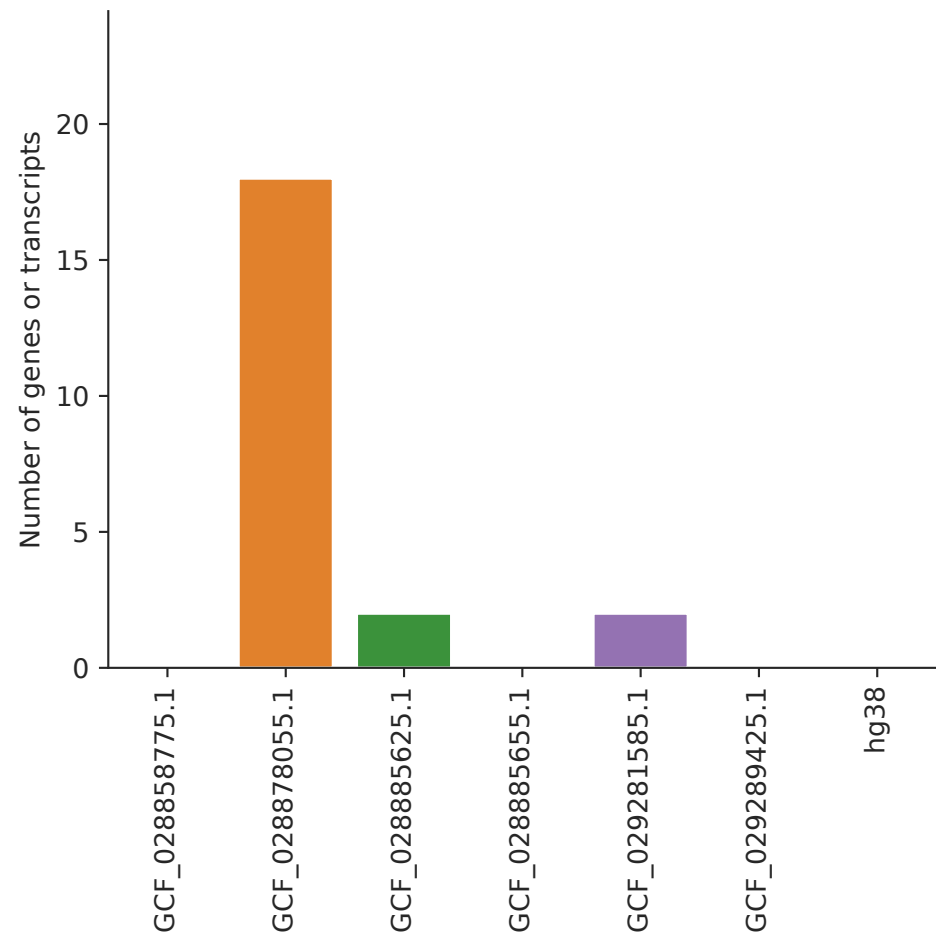
variable = Genes

variable = Transcripts

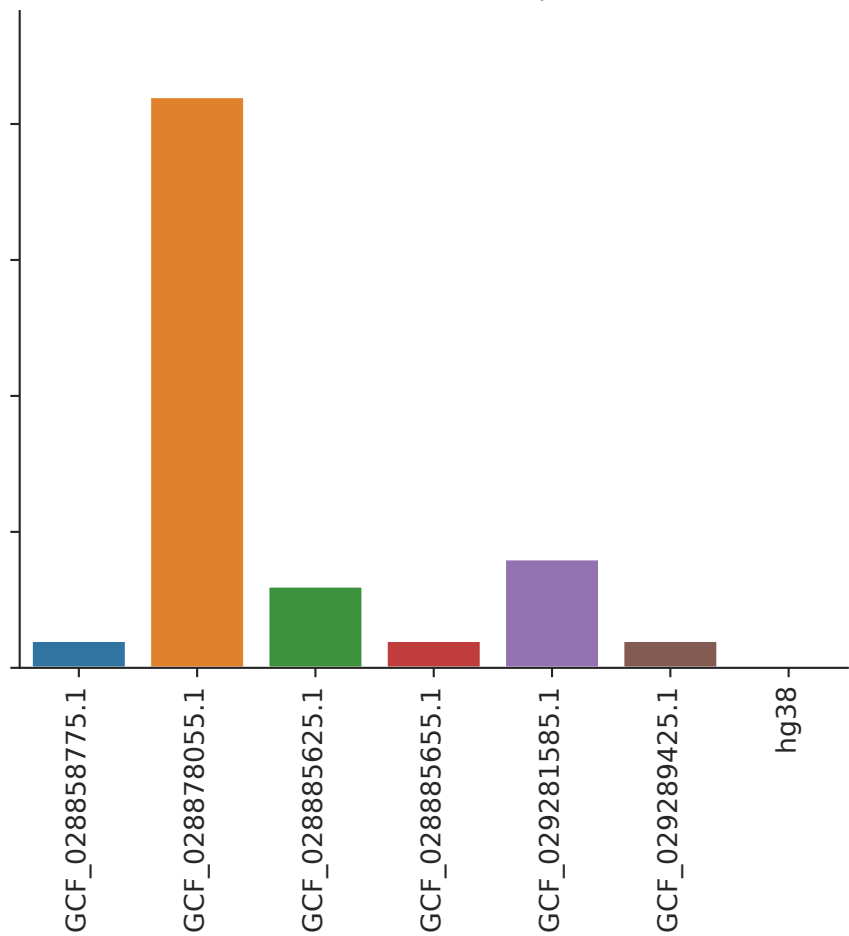


Number of missing orthologs in consensus set for biotype transcribed_unitary_pseudogene

variable = Genes



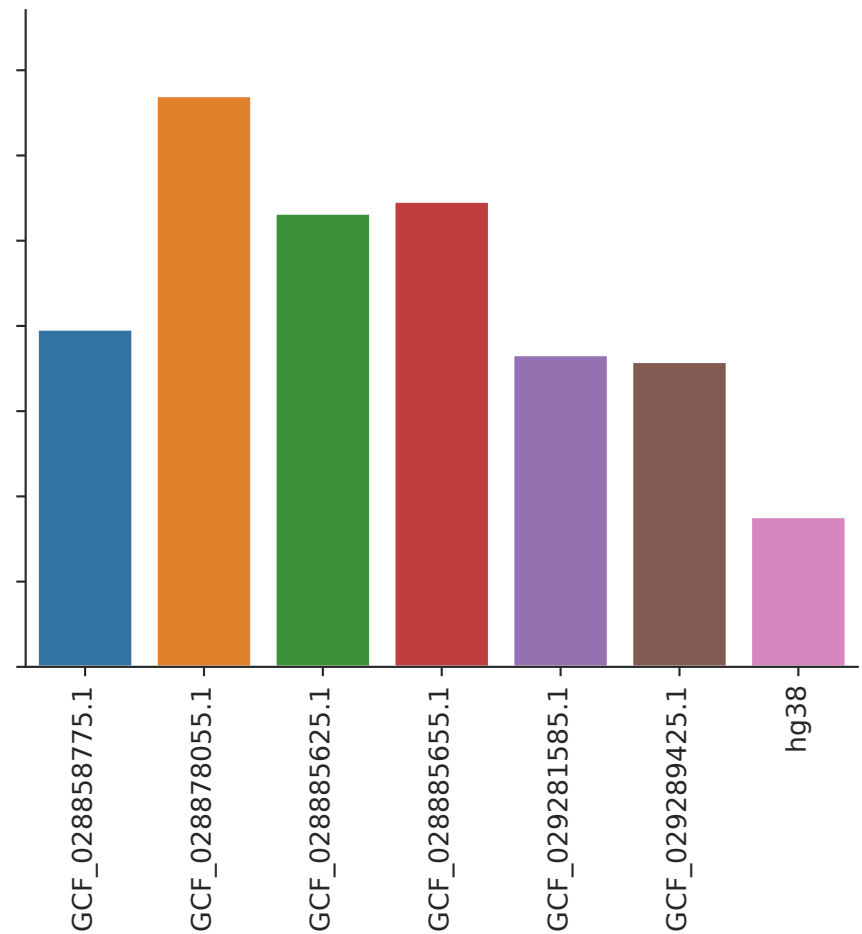
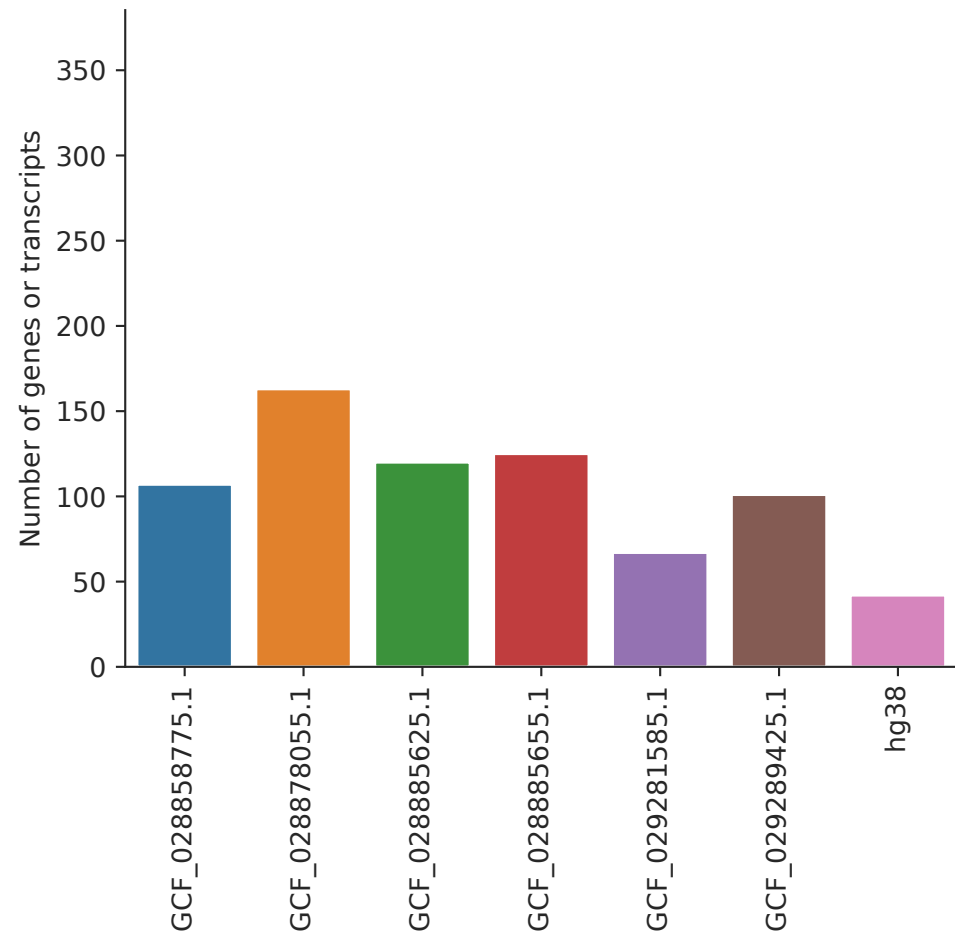
variable = Transcripts



Number of missing orthologs in consensus set for biotype transcribed_unprocessed_pseudogene

variable = Genes

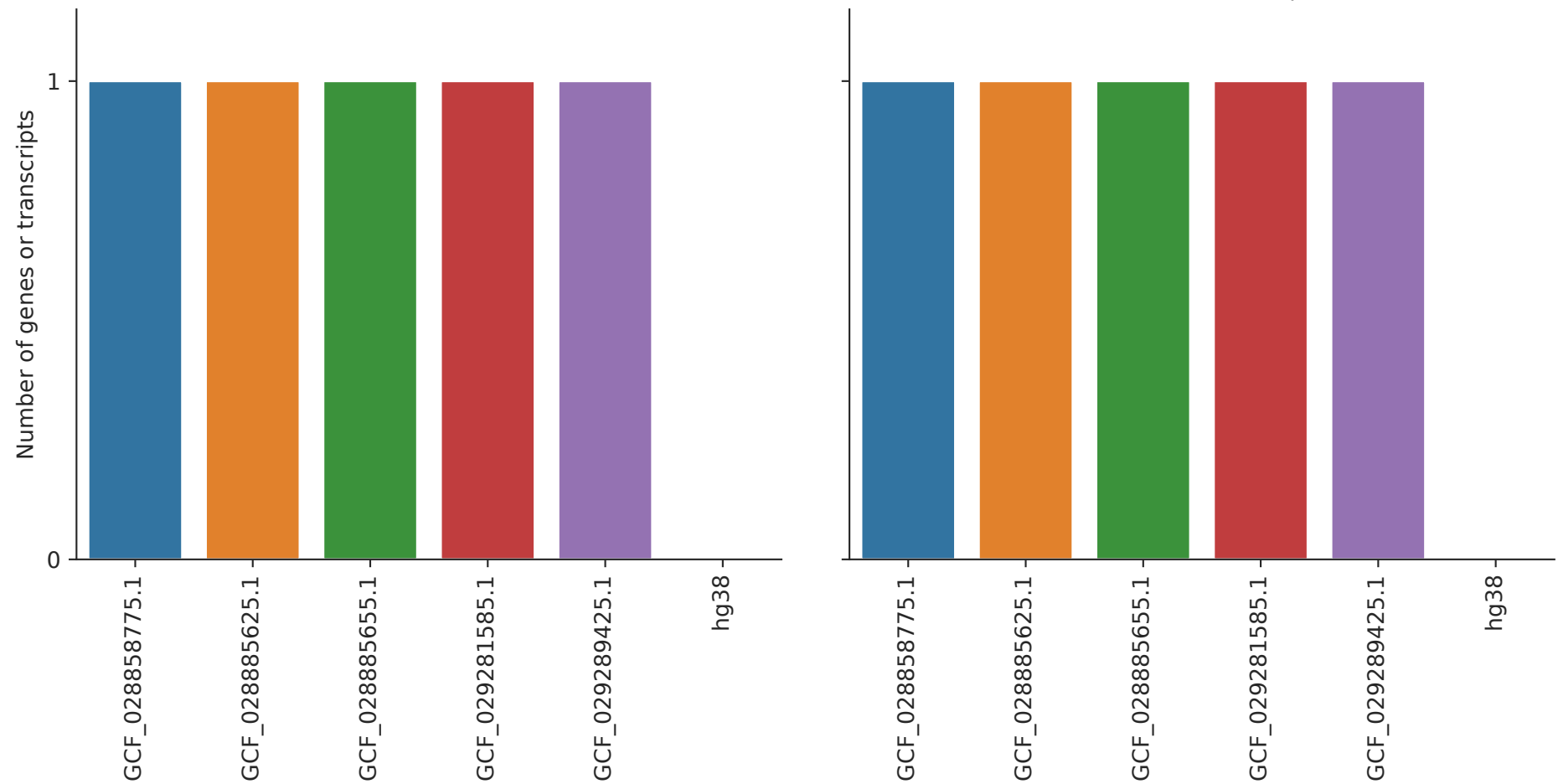
variable = Transcripts



Number of missing orthologs in consensus set for biotype translated_pseudogene

variable = Genes

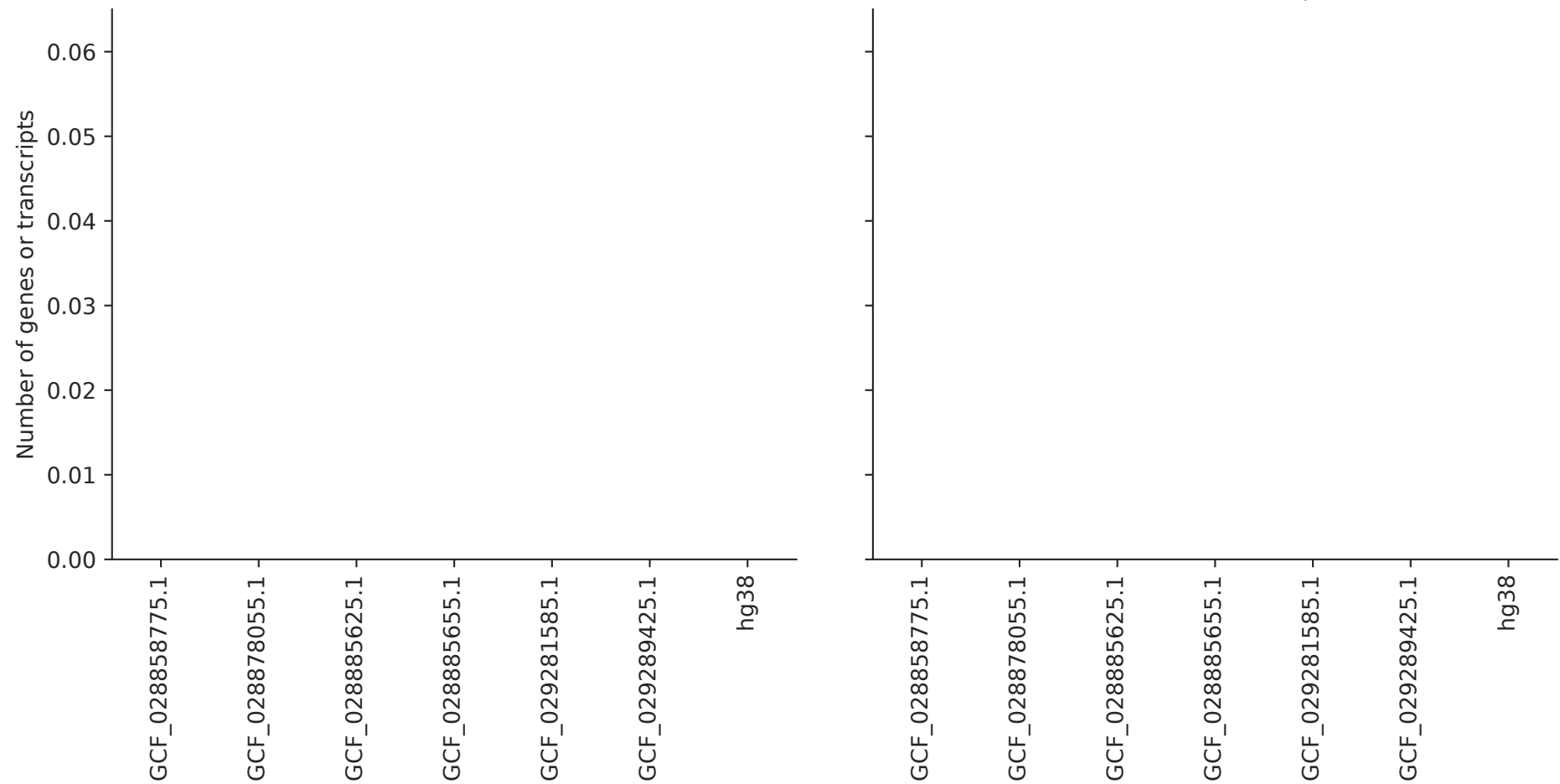
variable = Transcripts



Number of missing orthologs in consensus set for biotype translated_unprocessed_pseudogene

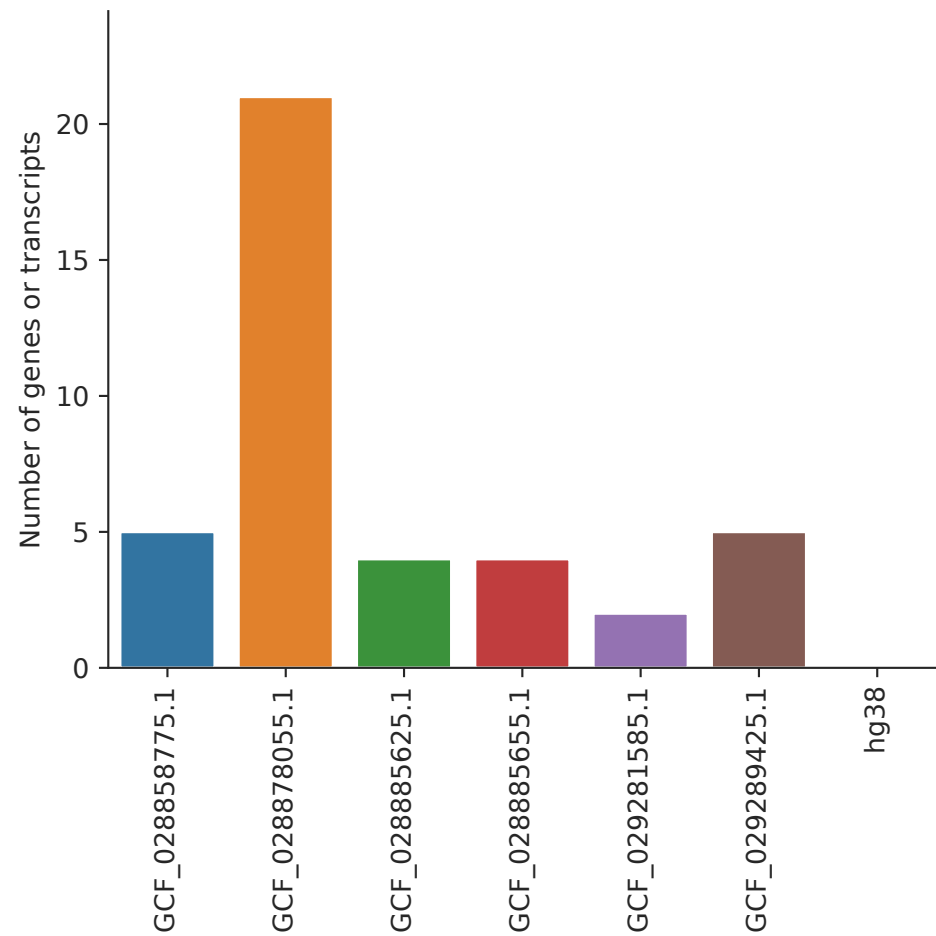
variable = Genes

variable = Transcripts

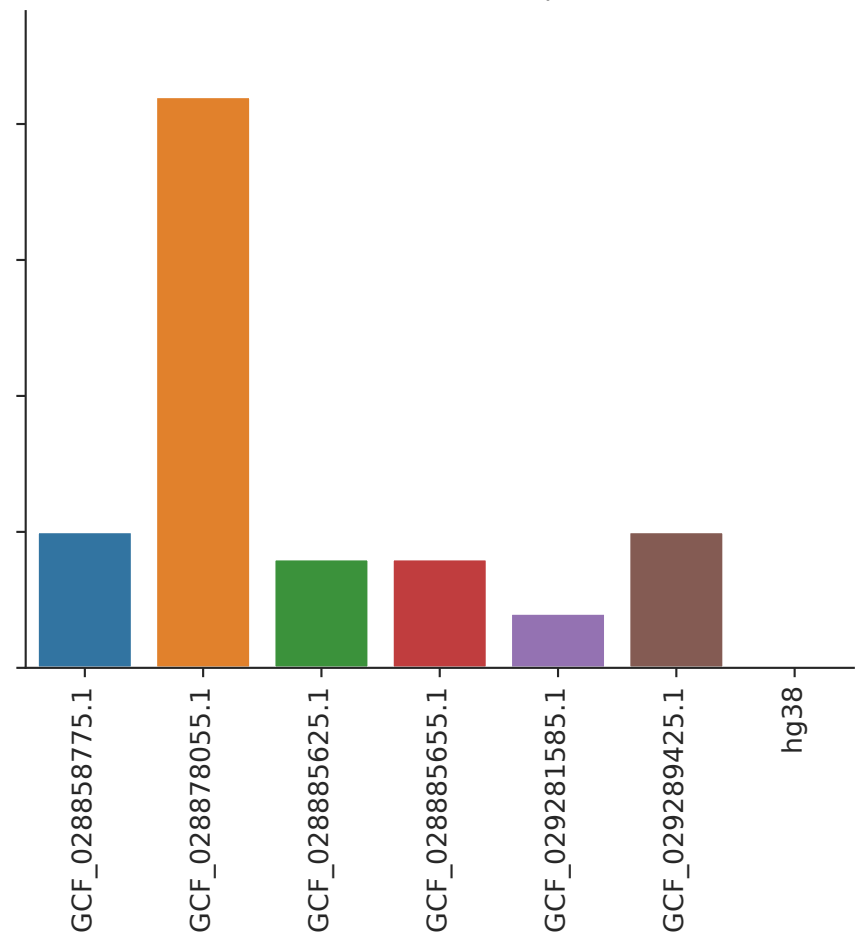


Number of missing orthologs in consensus set for biotype unitary_pseudogene

variable = Genes



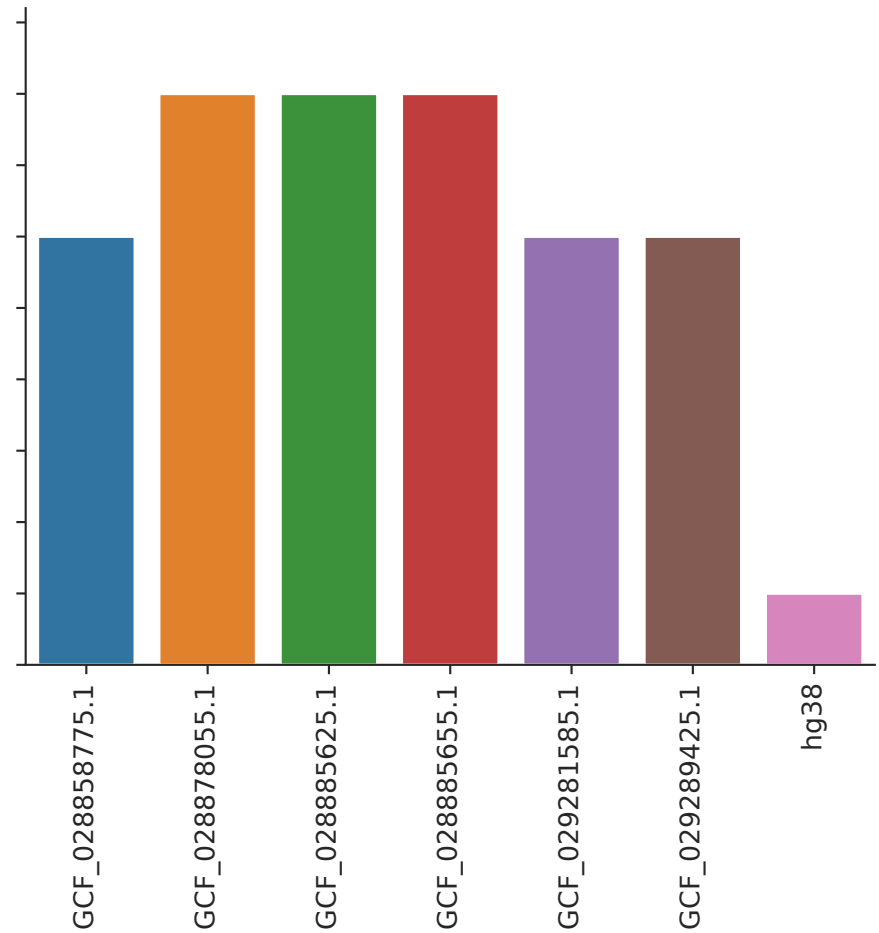
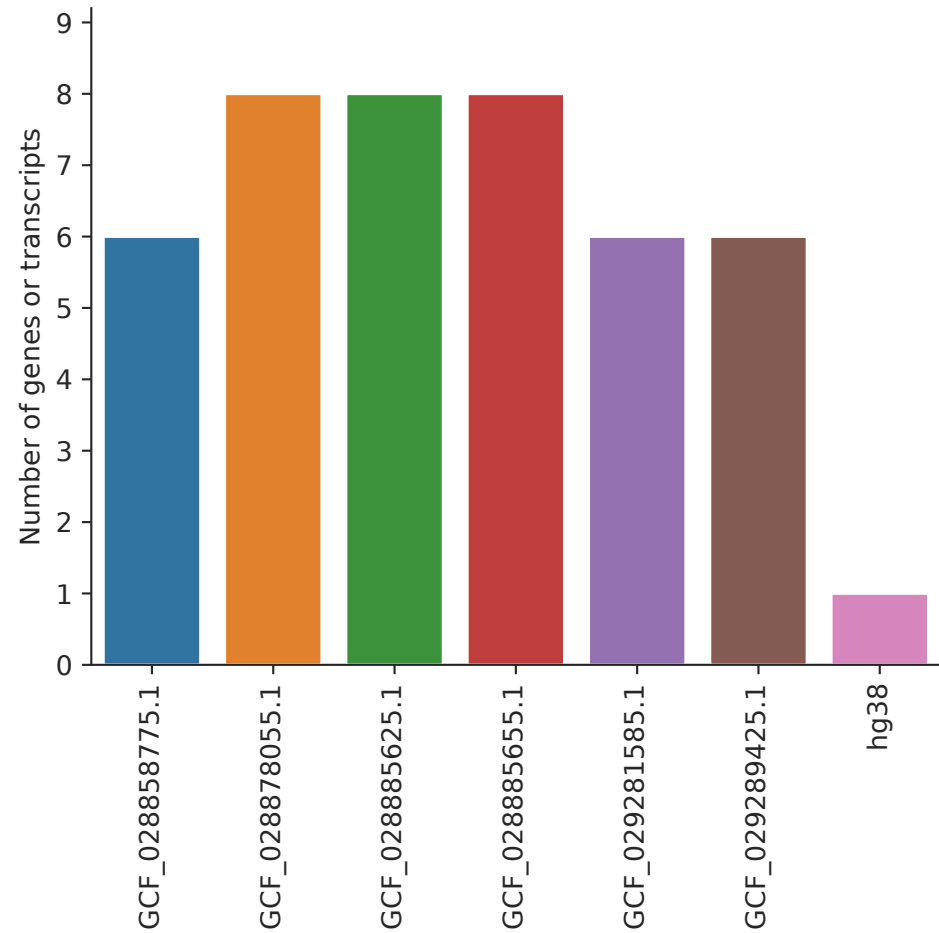
variable = Transcripts



Number of missing orthologs in consensus set for biotype unknown_likely_coding

variable = Genes

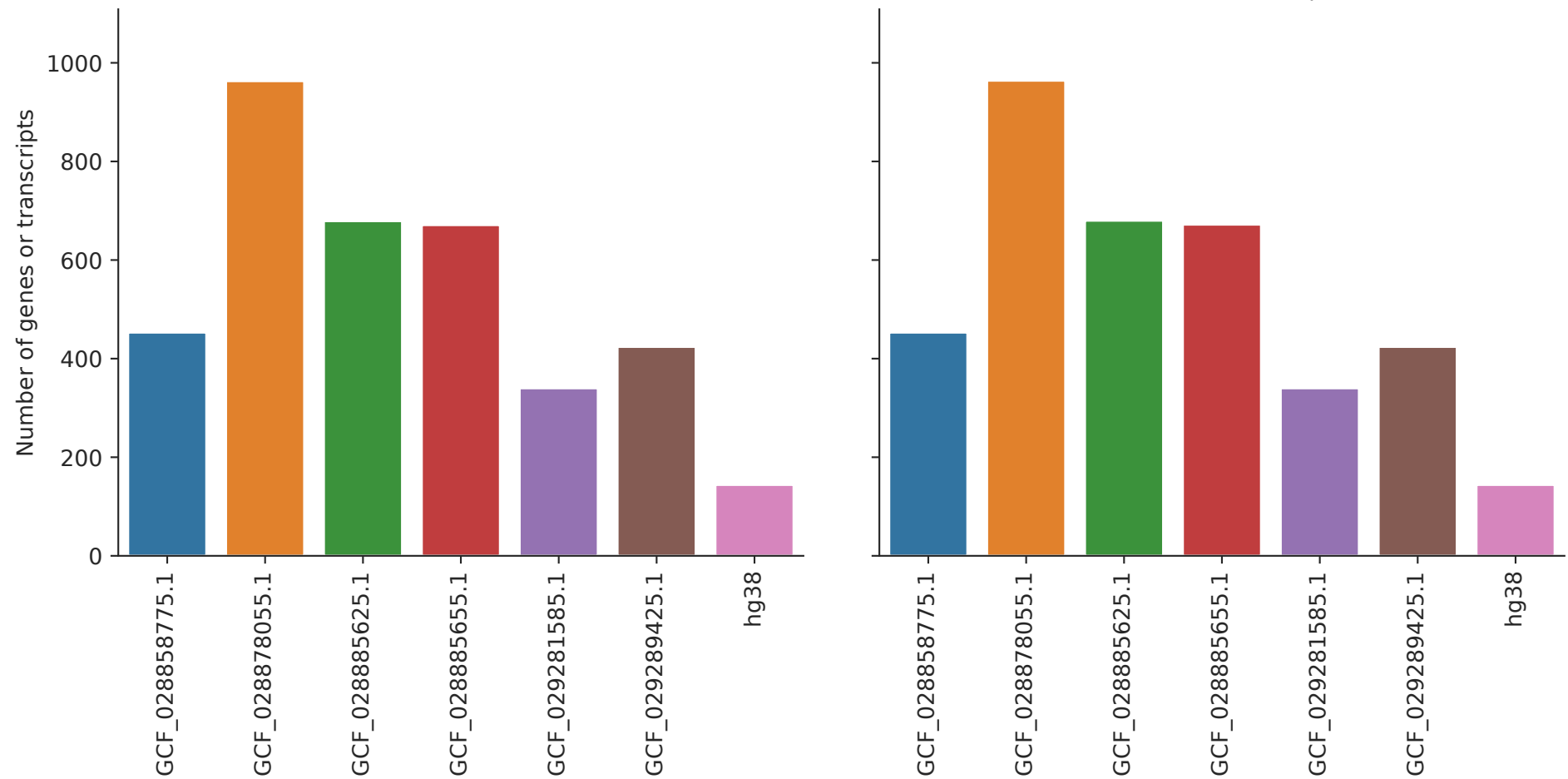
variable = Transcripts



Number of missing orthologs in consensus set for biotype unprocessed_pseudogene

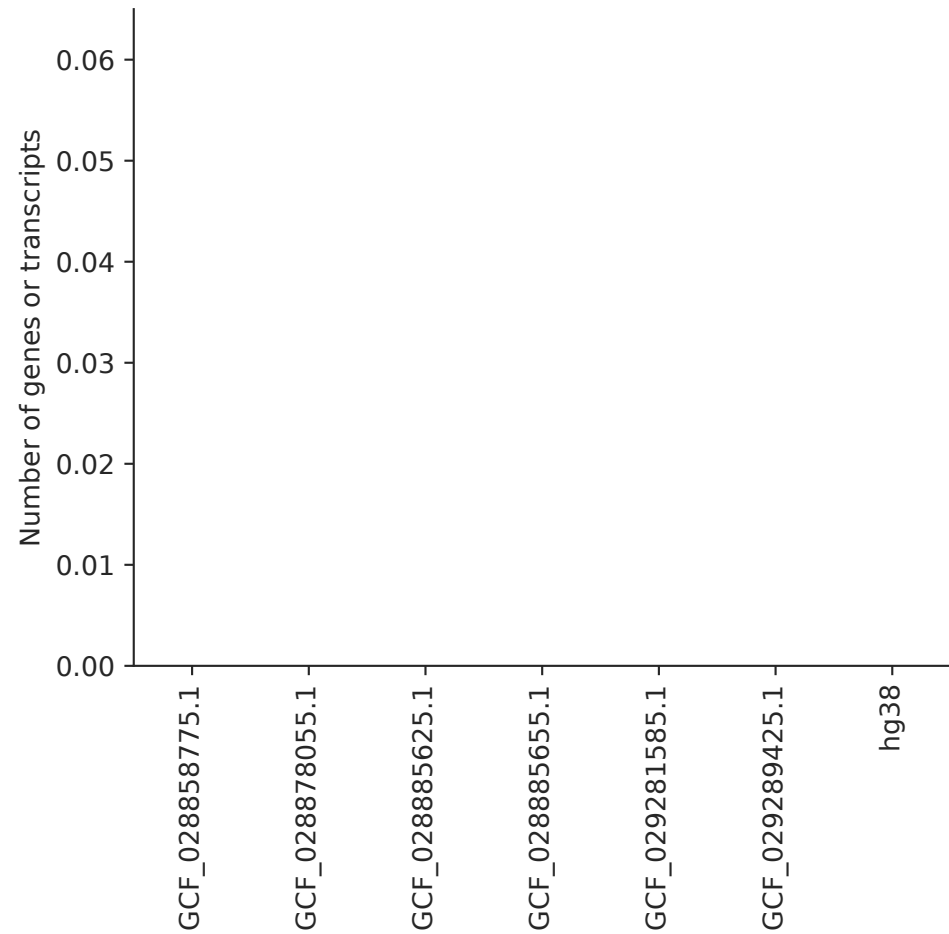
variable = Genes

variable = Transcripts



Number of missing orthologs in consensus set for biotype vault_RNA

variable = Genes



variable = Transcripts

