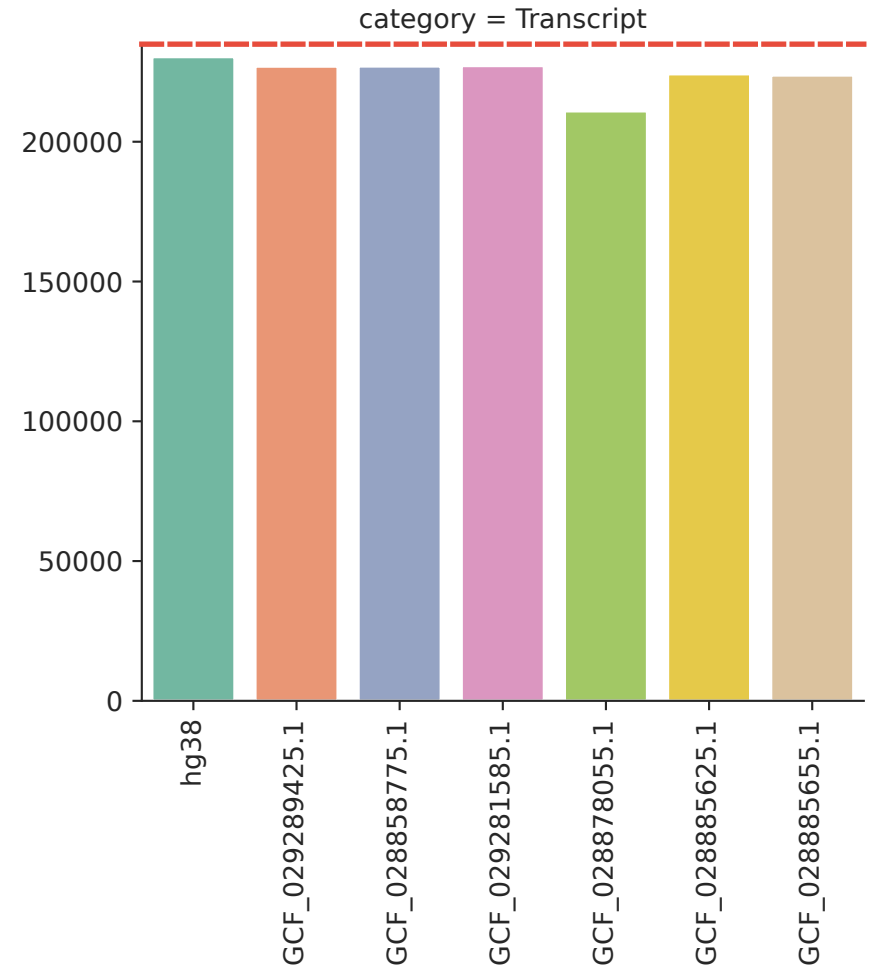
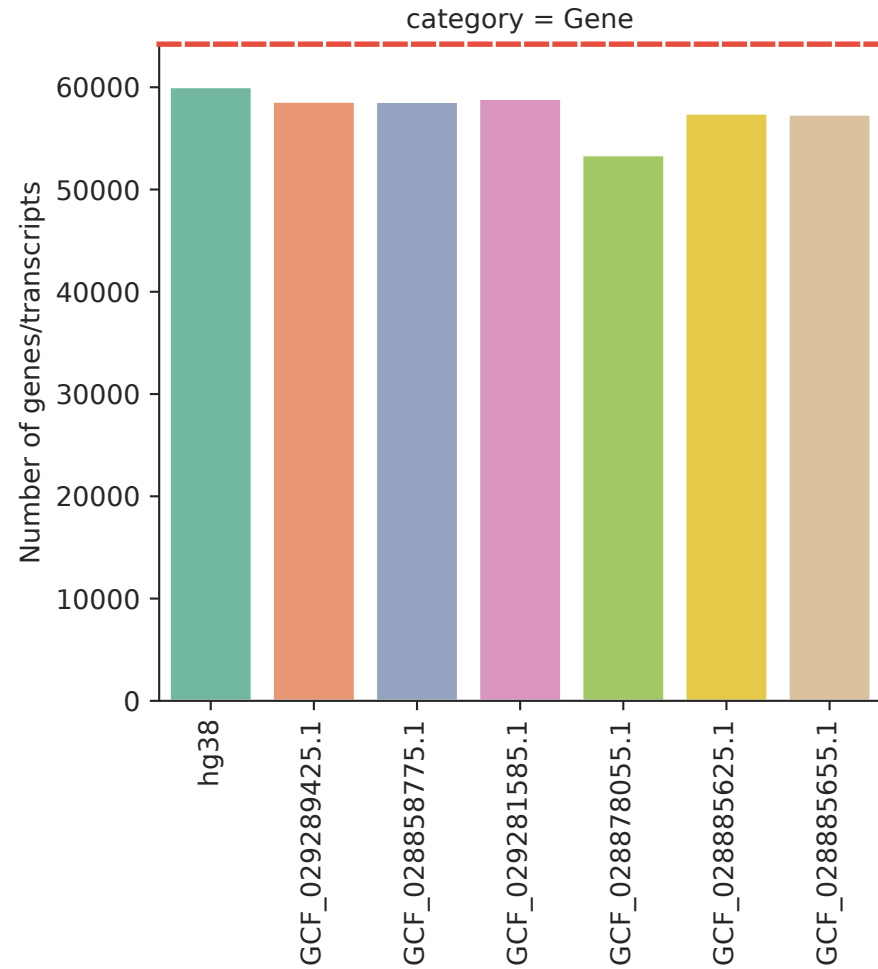
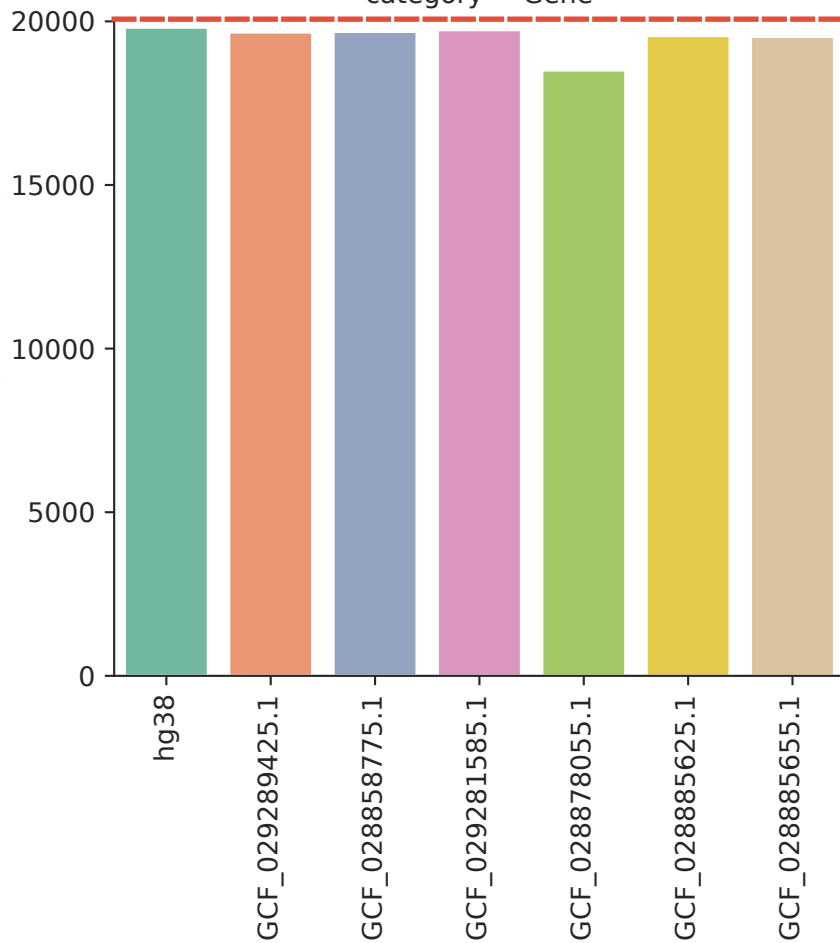


Number of comparative genes/transcripts present

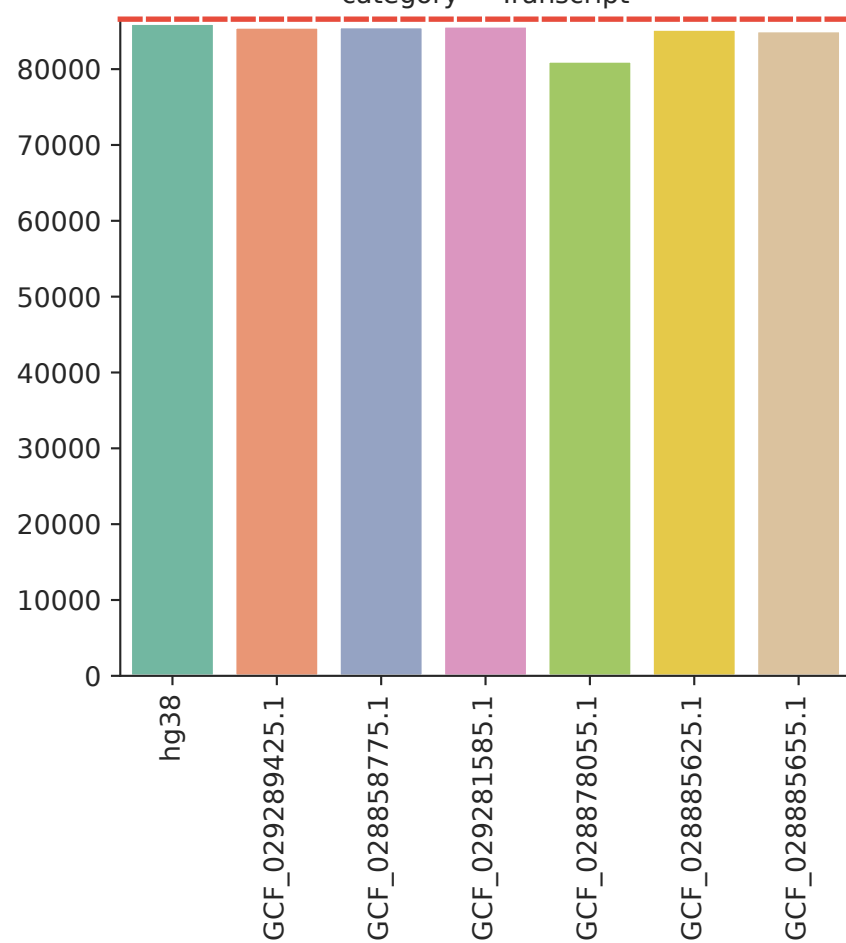


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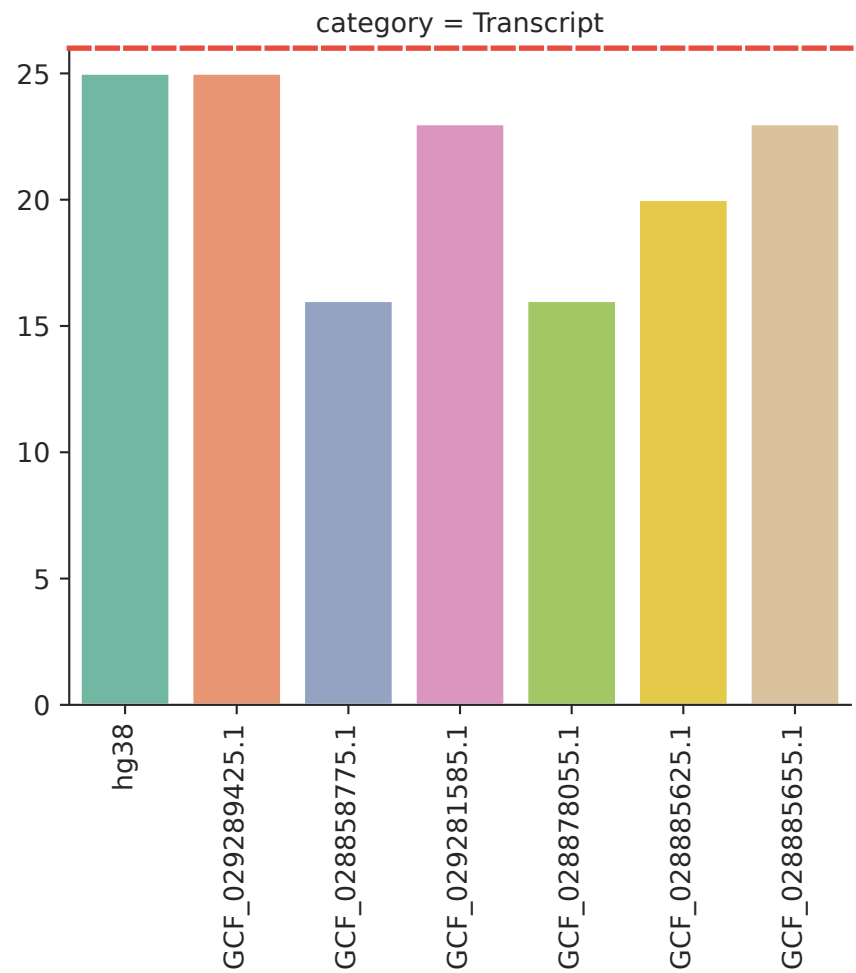
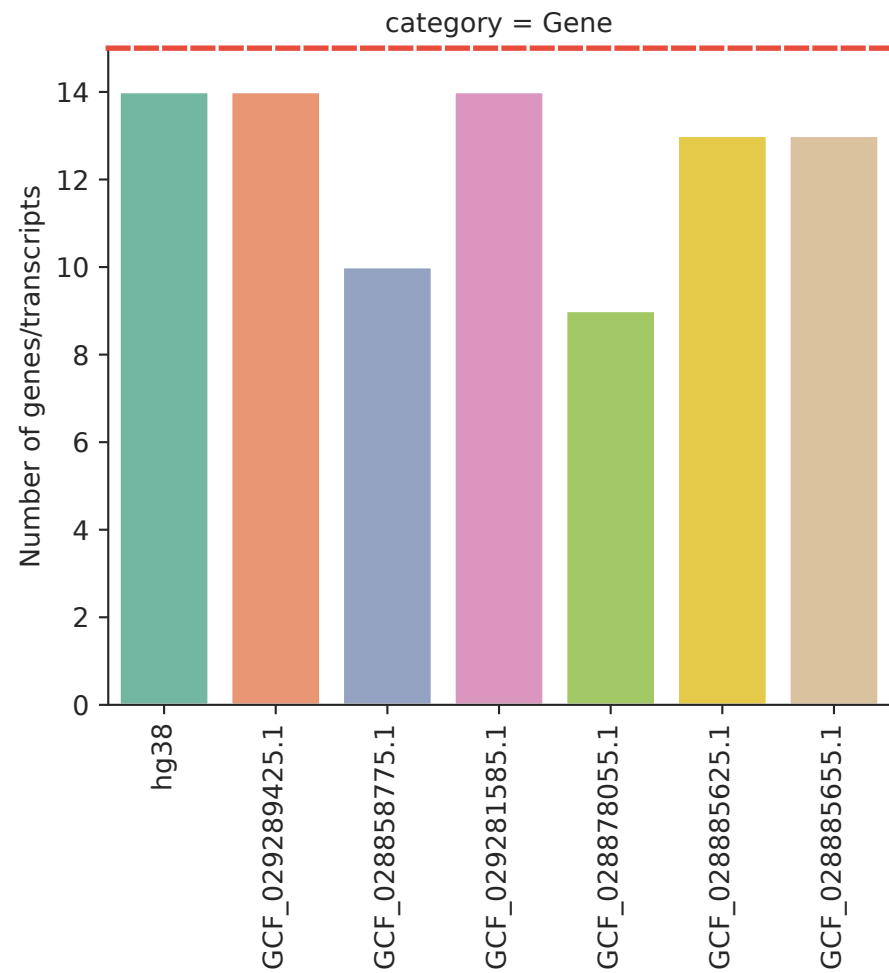
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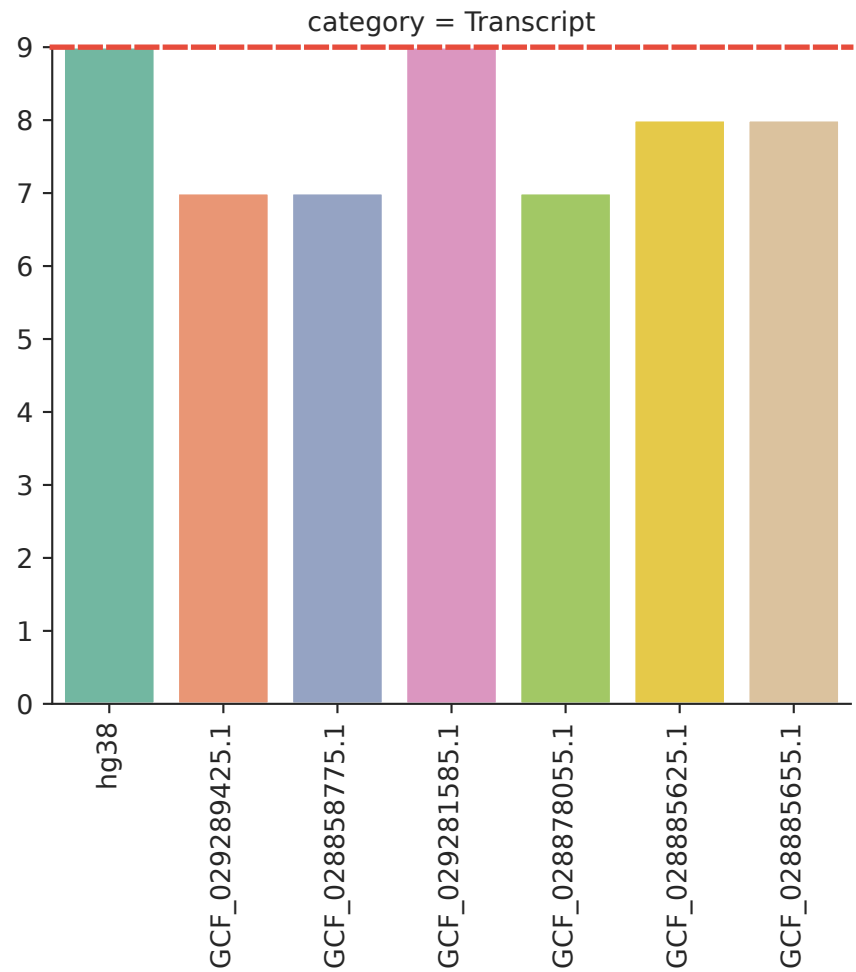
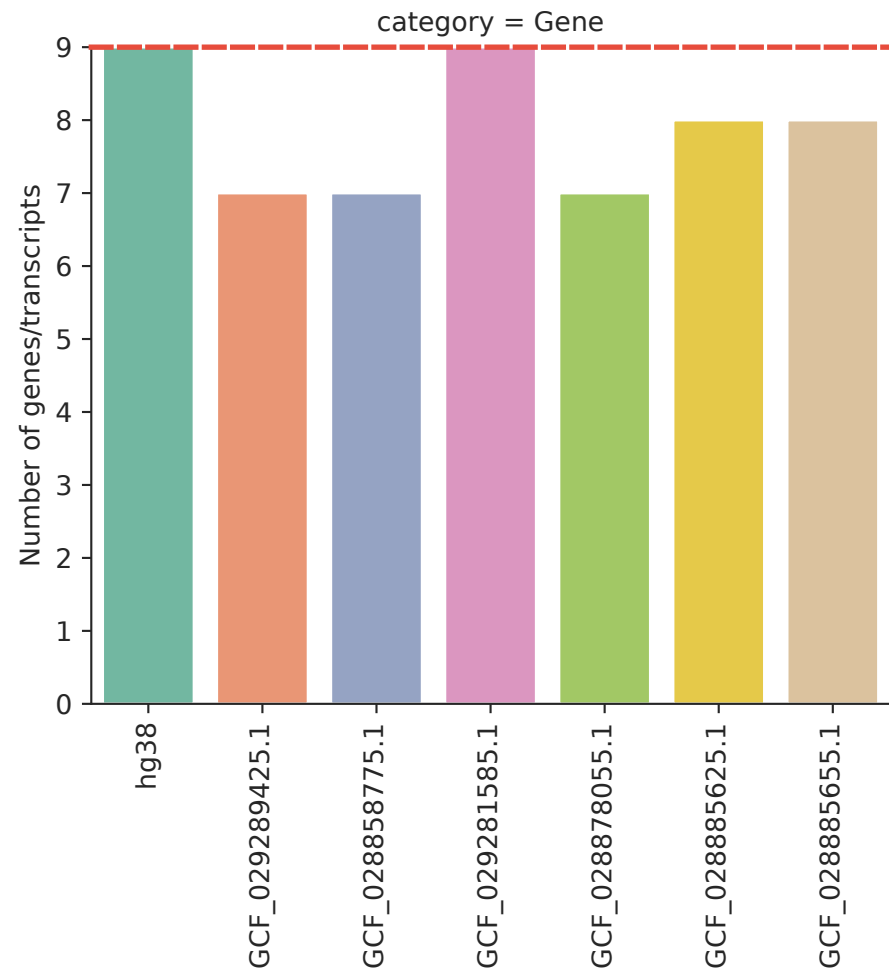
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Number of comparative genes/transcripts present for biotype IG_C_gene

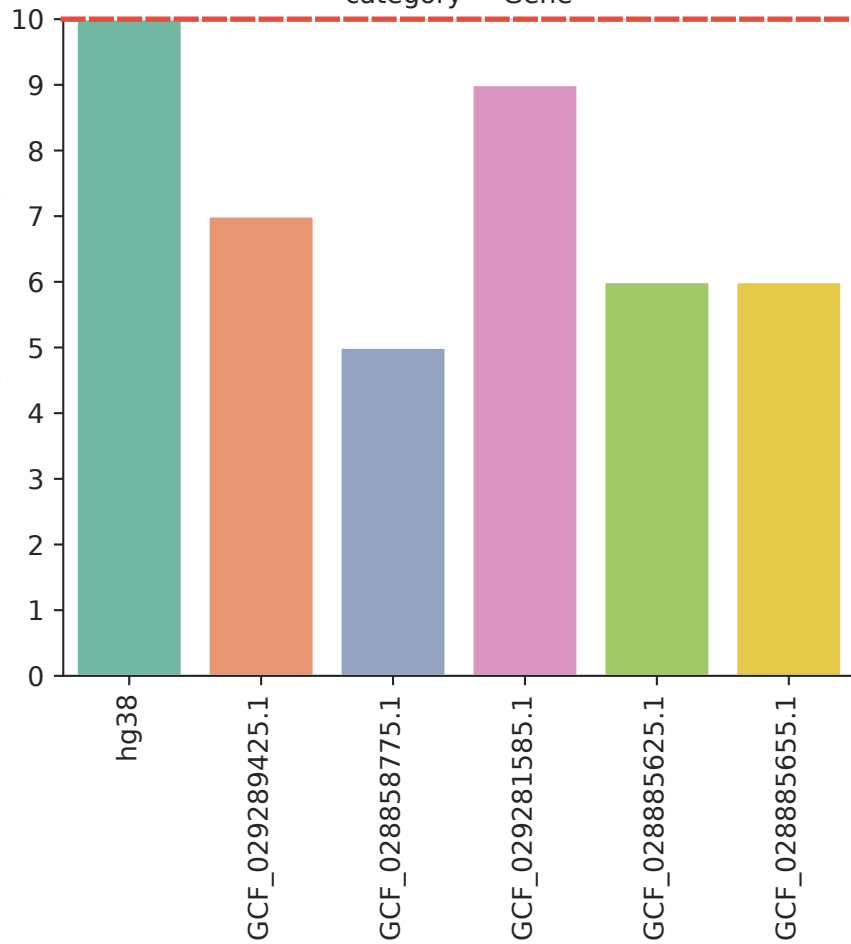


Number of comparative genes/transcripts present for biotype IG_C_pseudogene

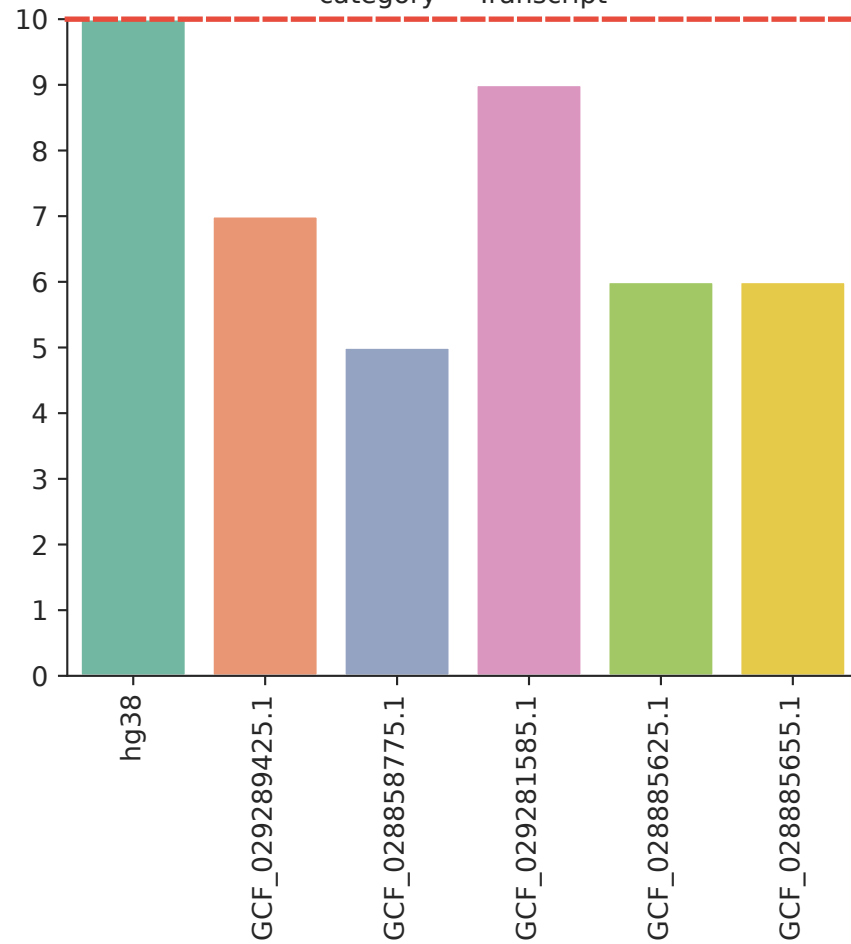


Number of comparative genes/transcripts present for biotype IG_D_gene

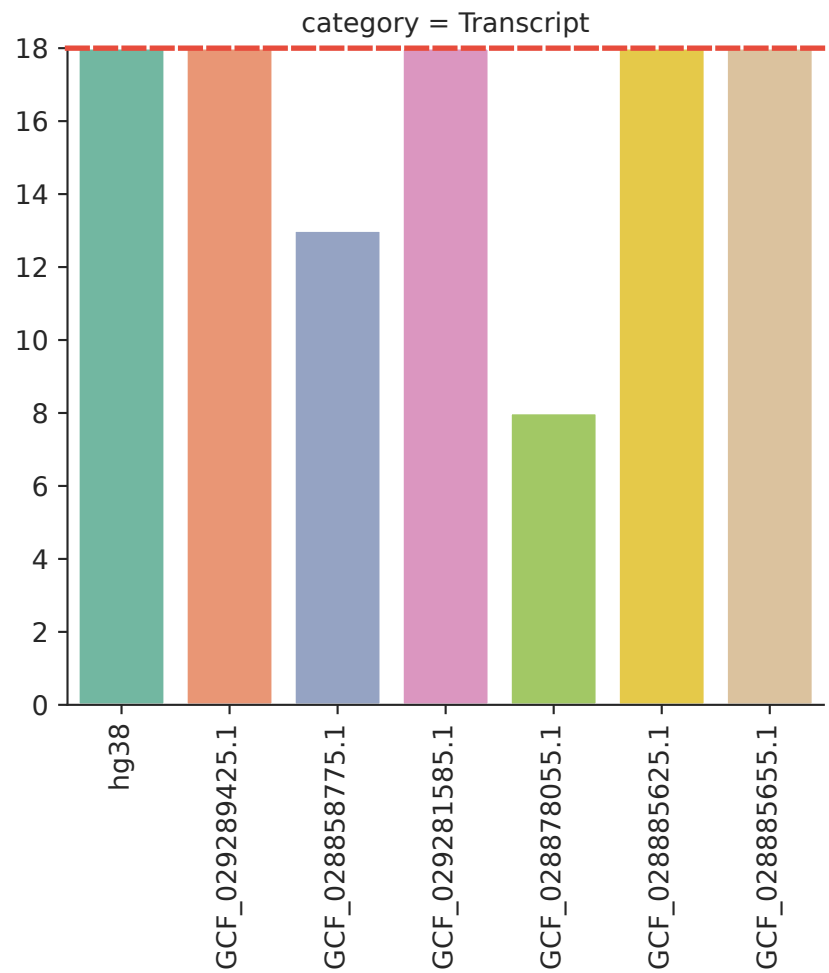
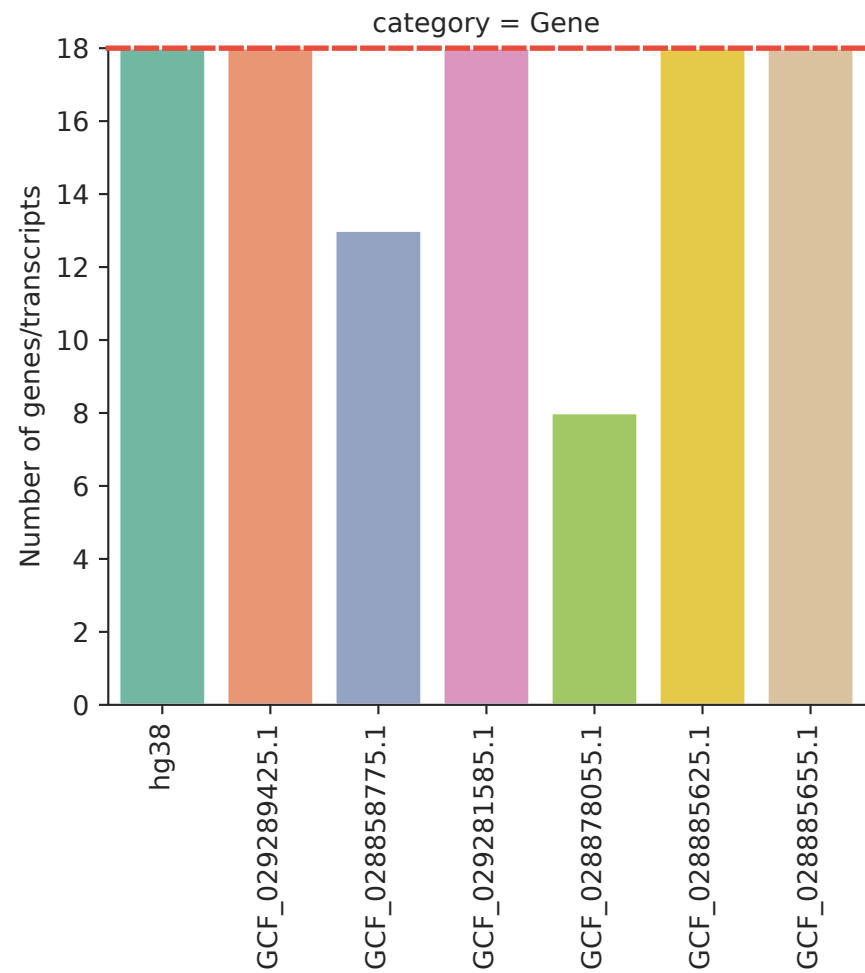
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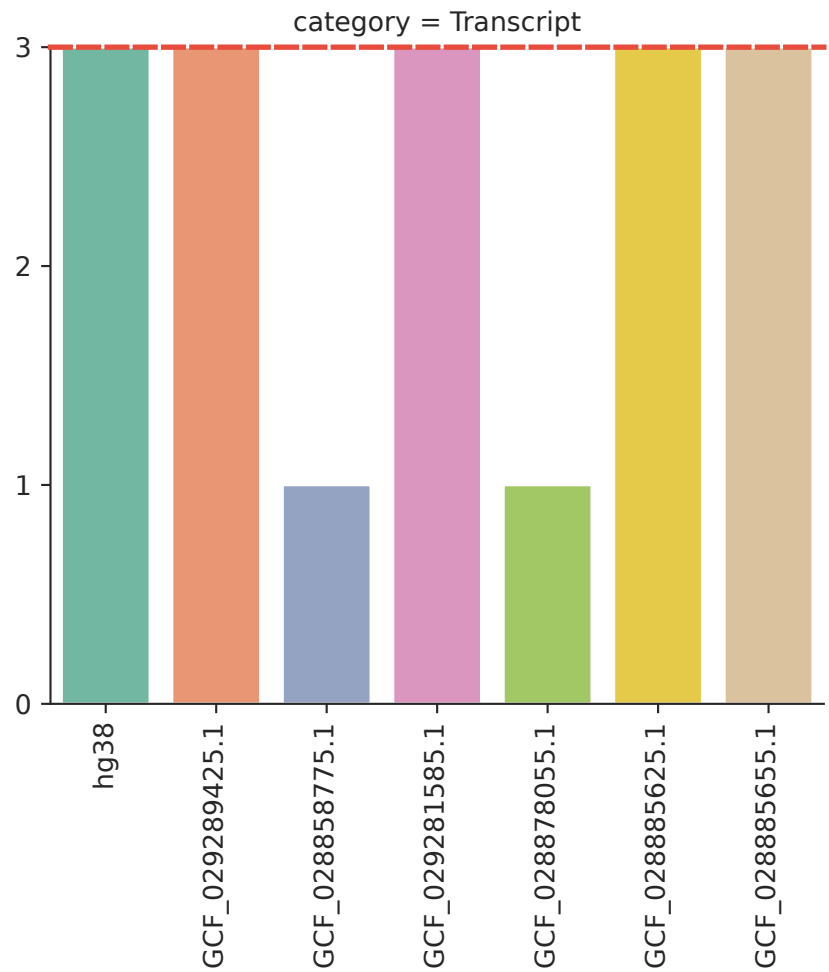
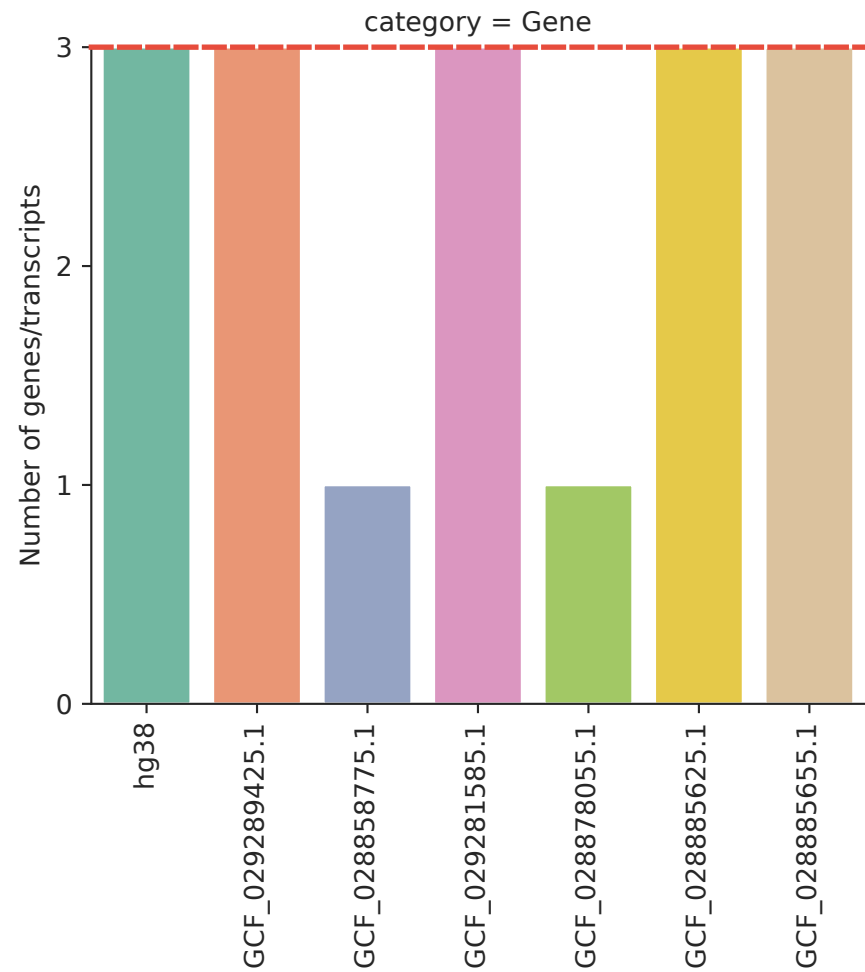
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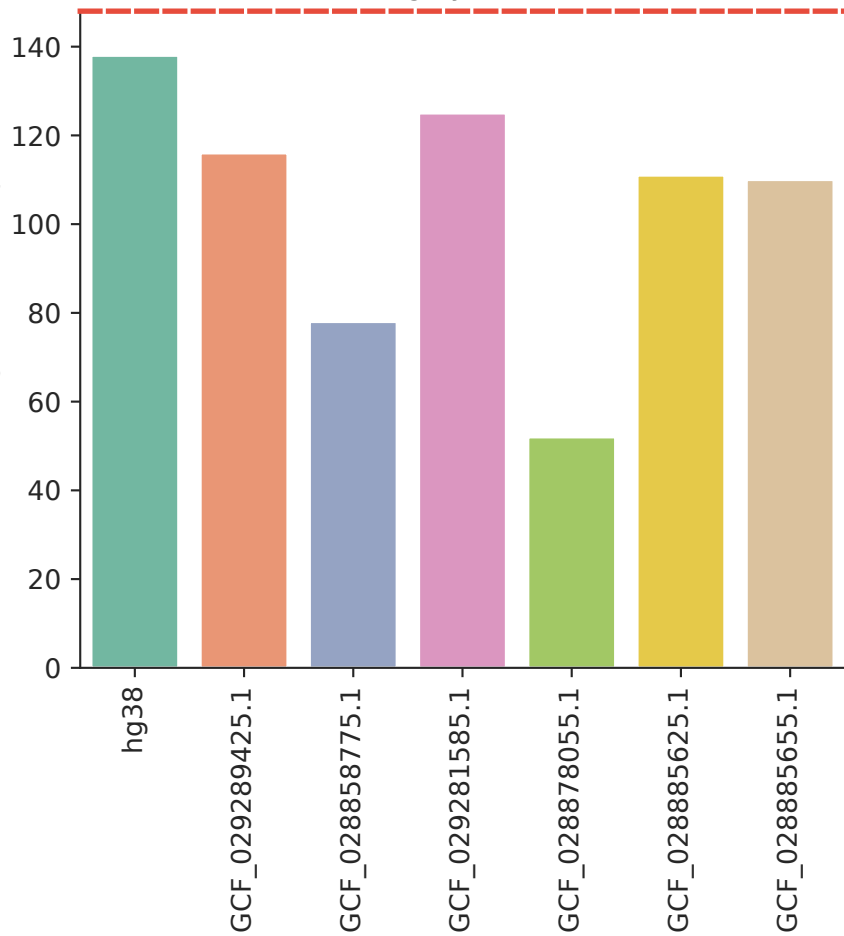


Number of comparative genes/transcripts present for biotype IG_J_pseudogene

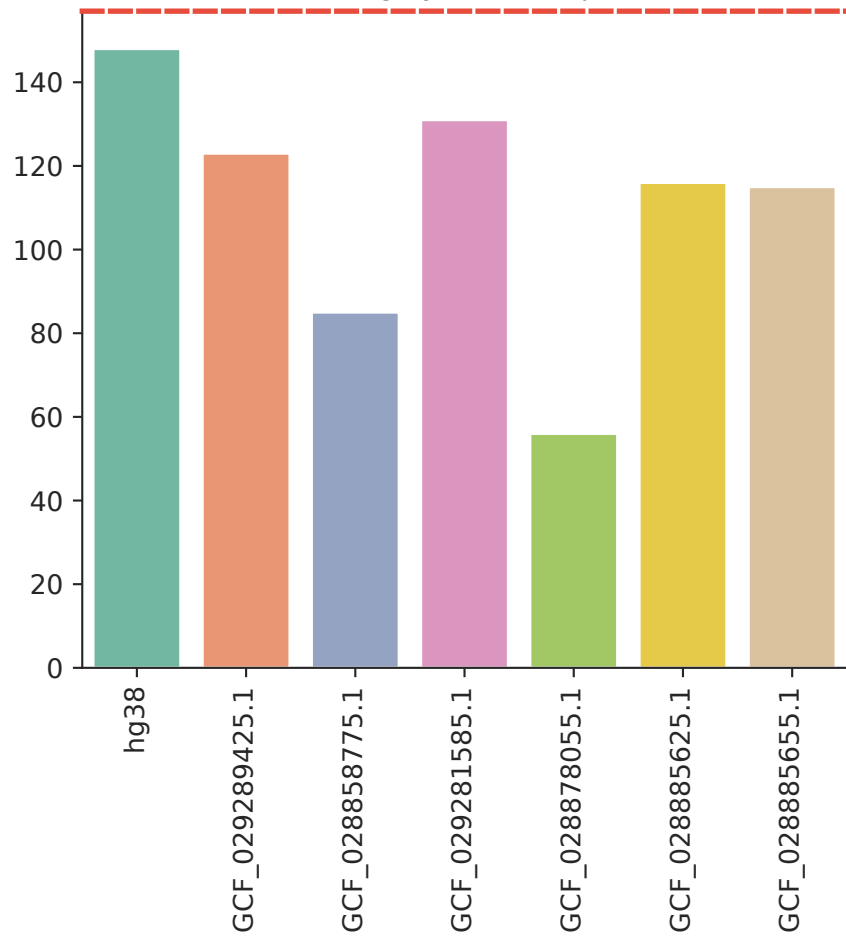


Number of comparative genes/transcripts present for biotype IG_V_gene

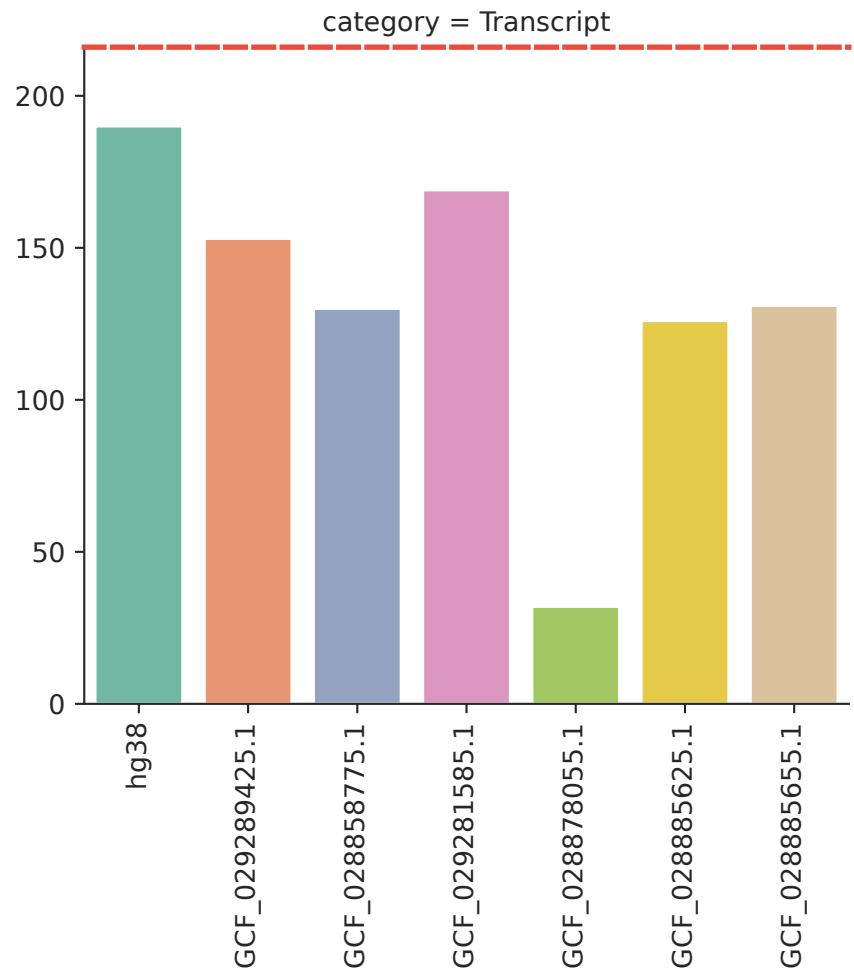
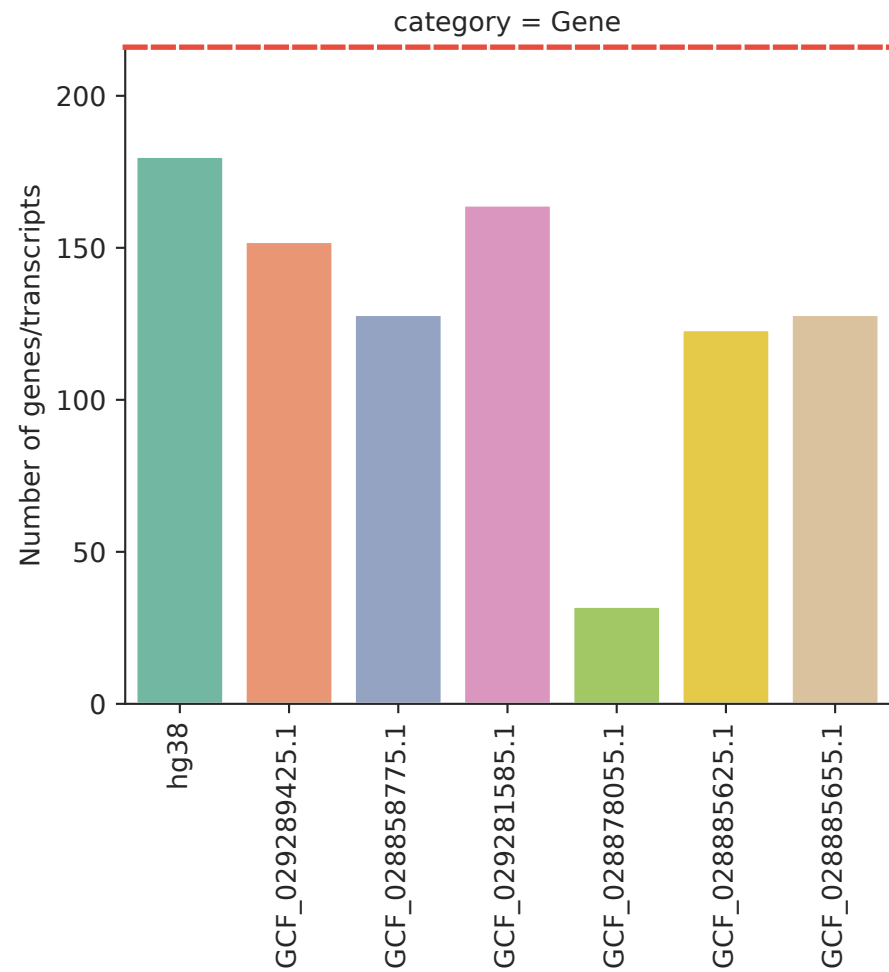
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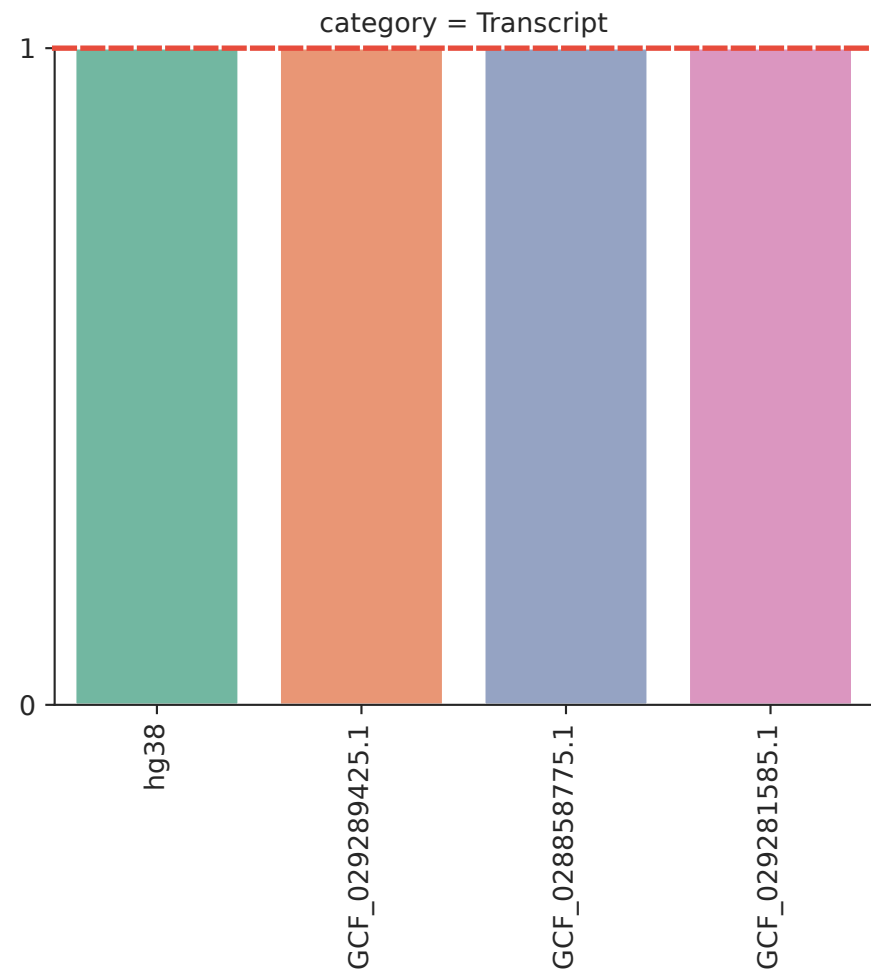
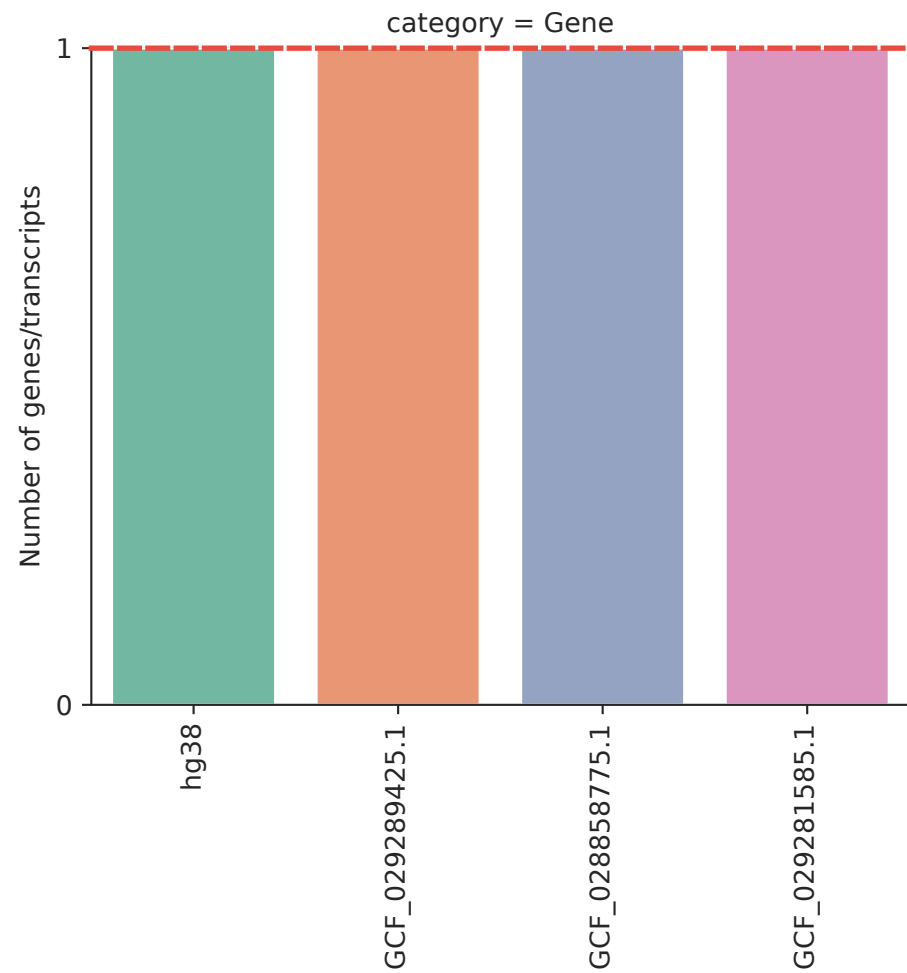
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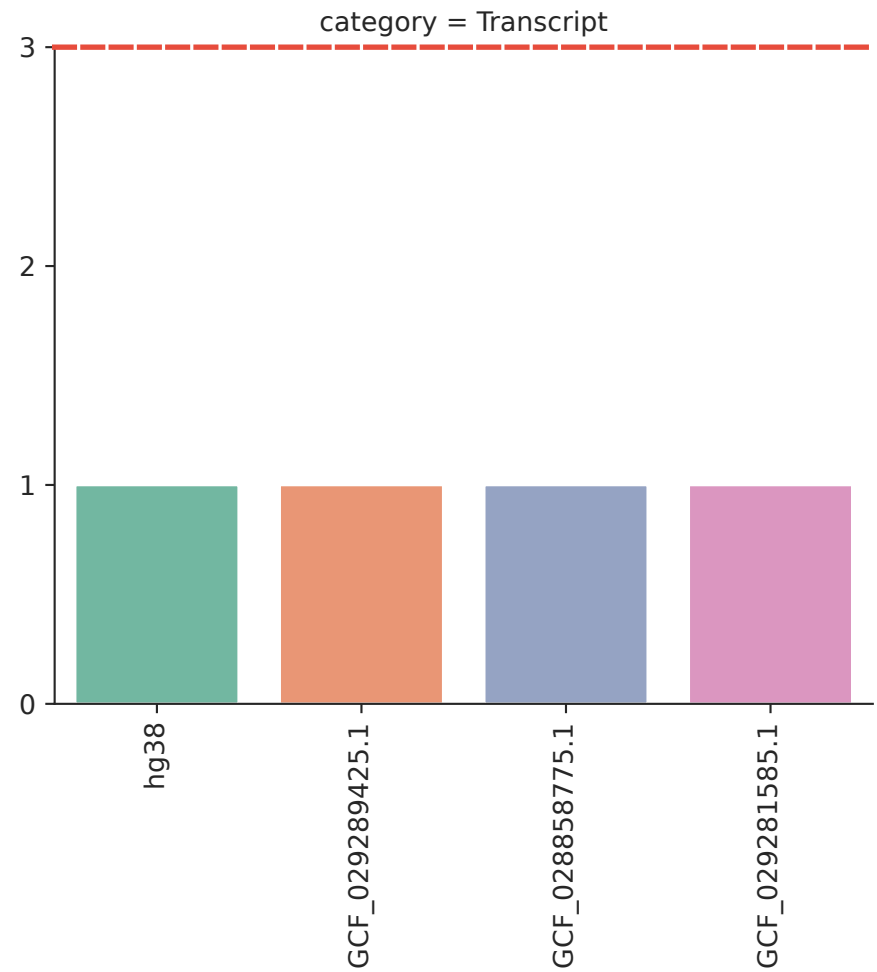
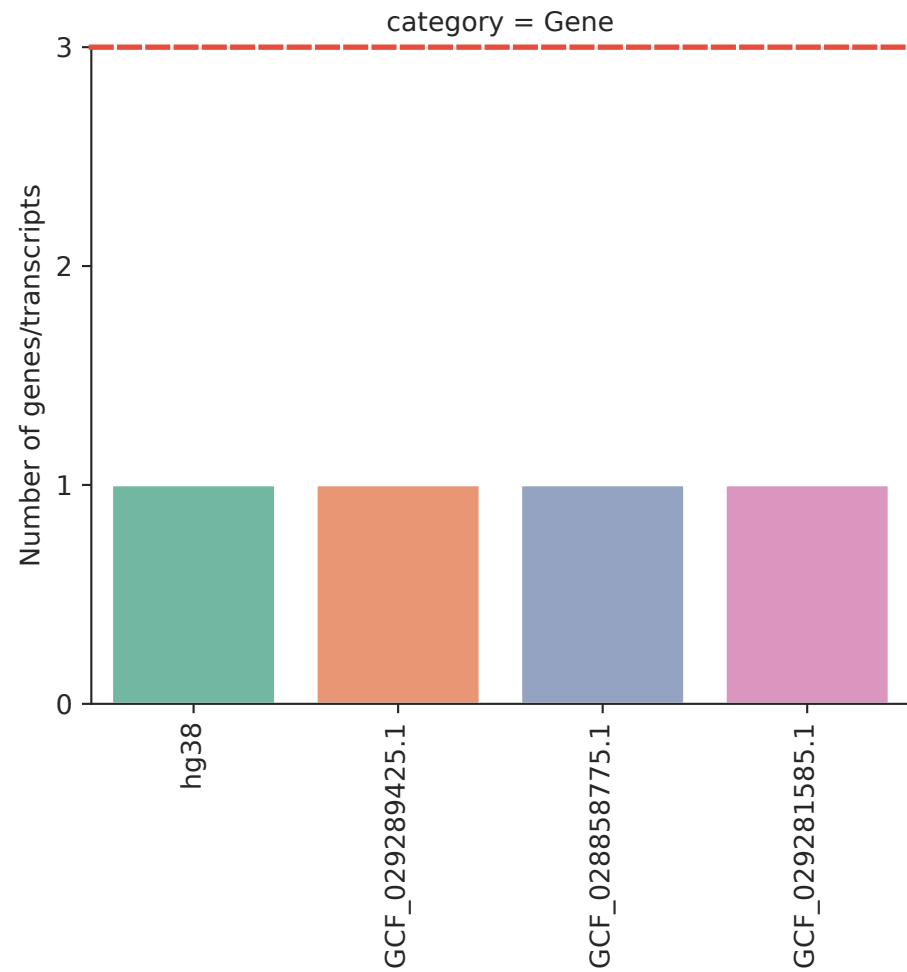
Number of comparative genes/transcripts present for biotype IG_V_pseudogene



Number of comparative genes/transcripts present for biotype IG_pseudogene

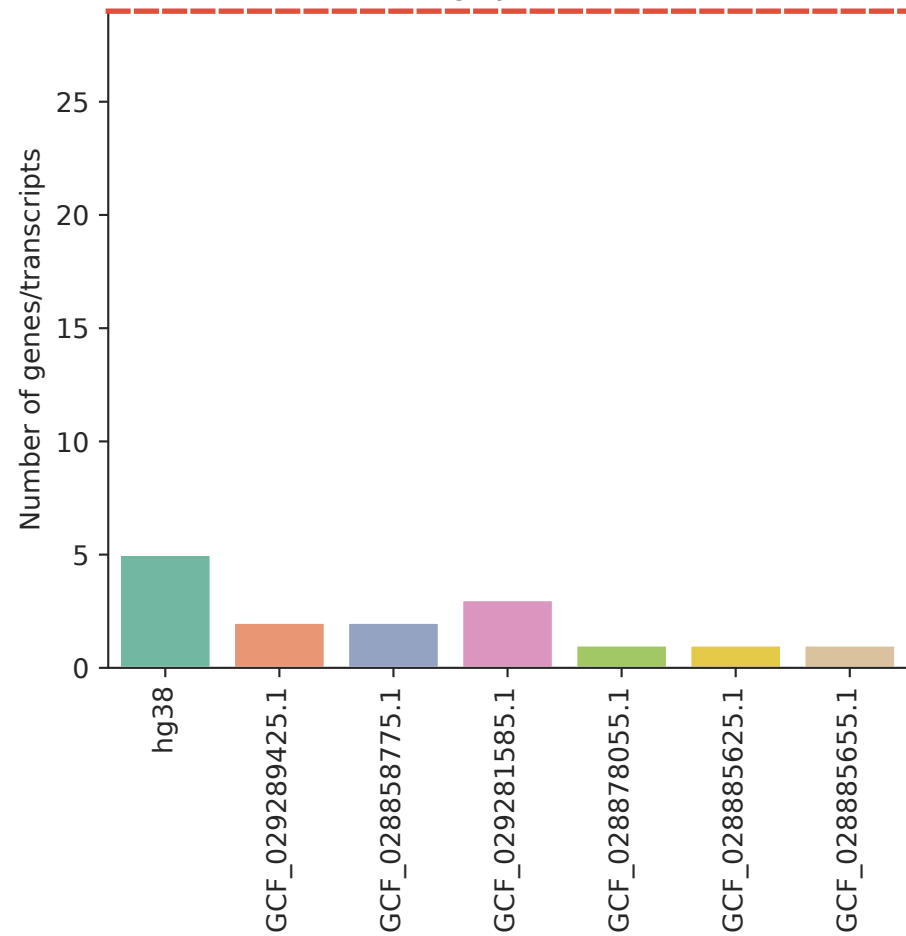


Number of comparative genes/transcripts present for biotype Mt_rRNA

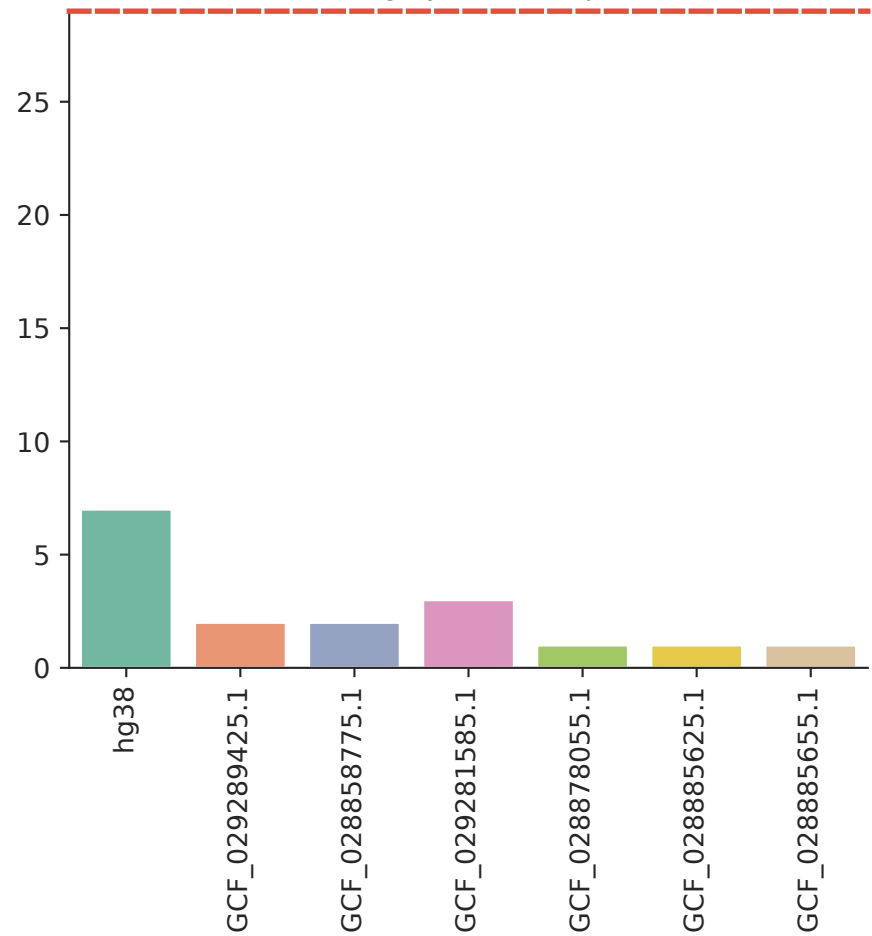


Number of comparative genes/transcripts present for biotype Mt_tRNA

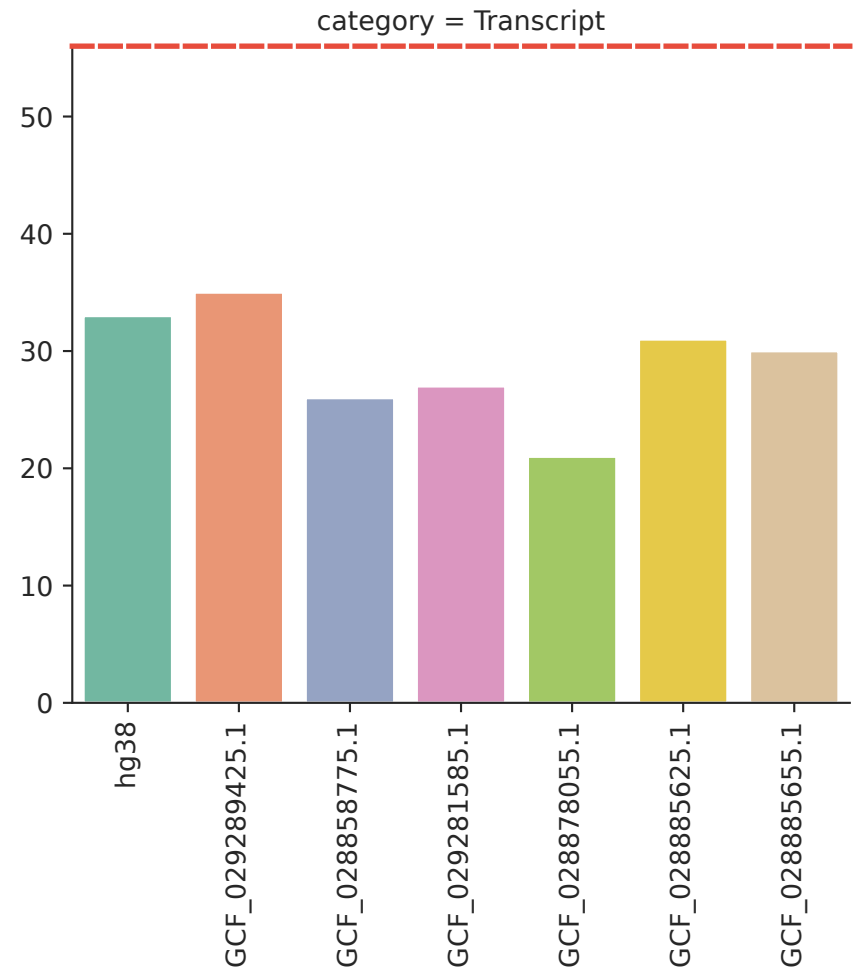
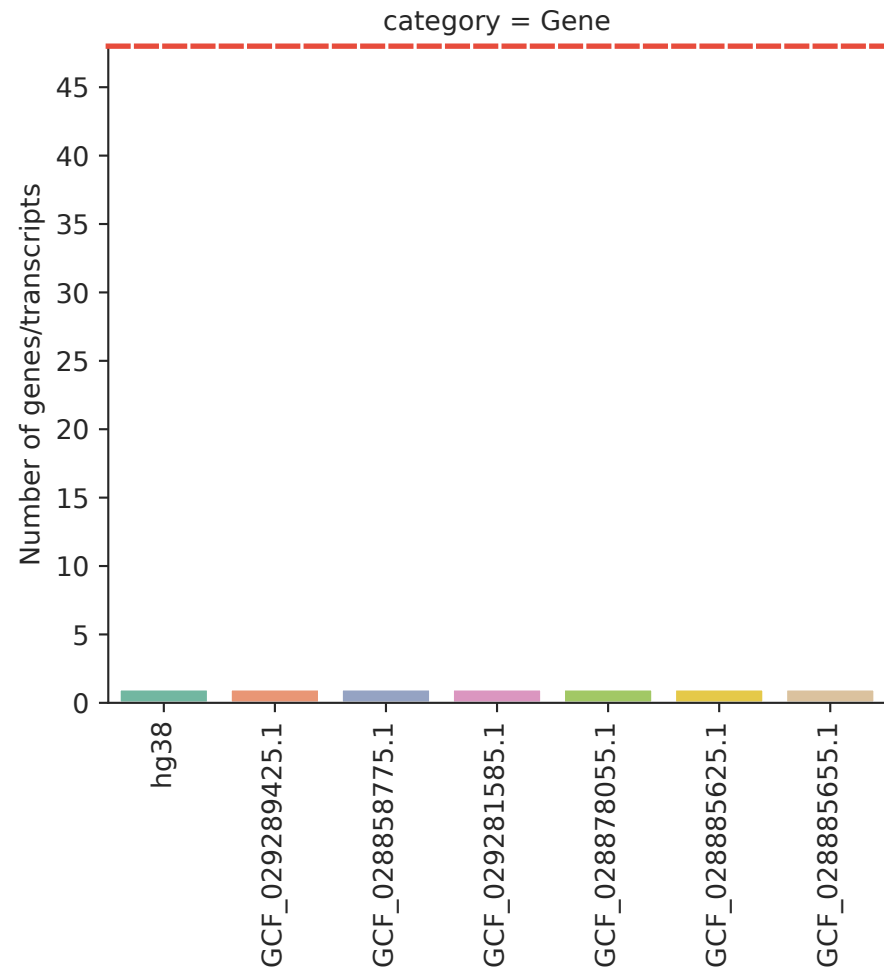
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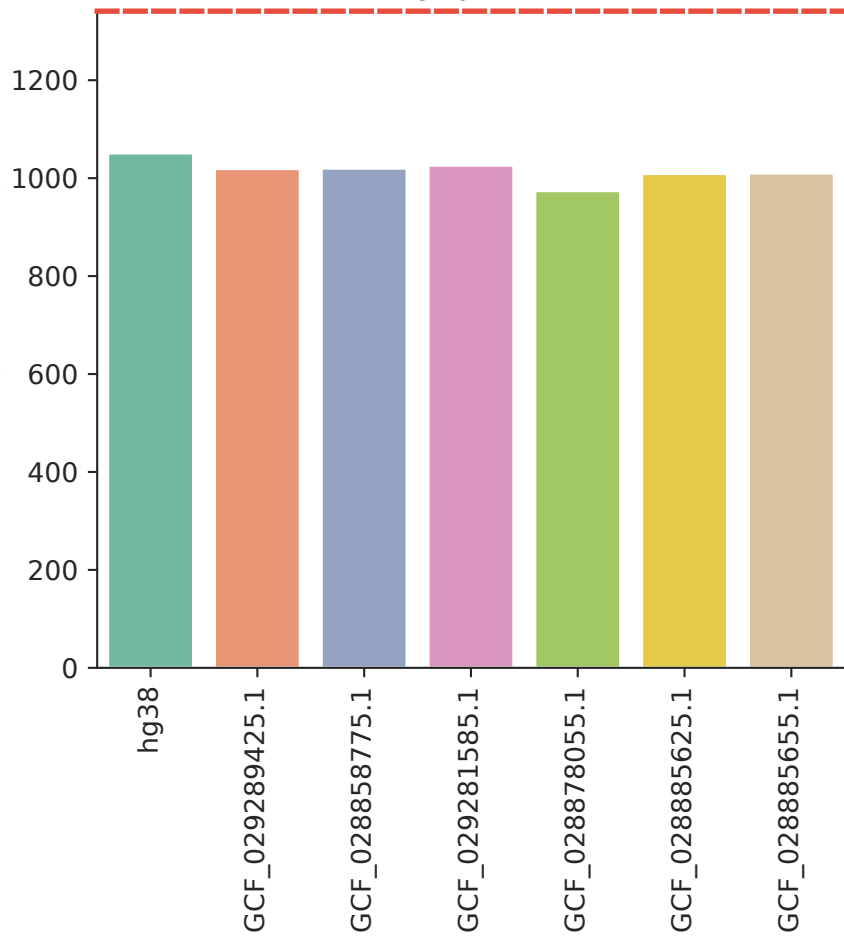


Number of comparative genes/transcripts present for biotype StringTie

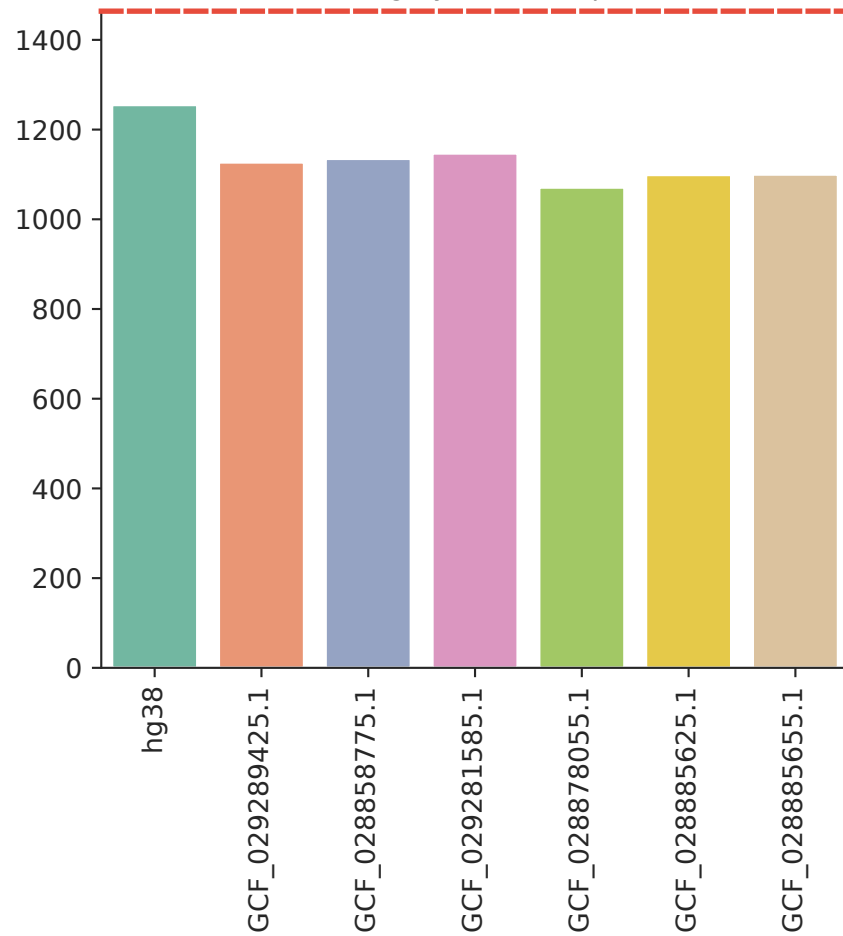


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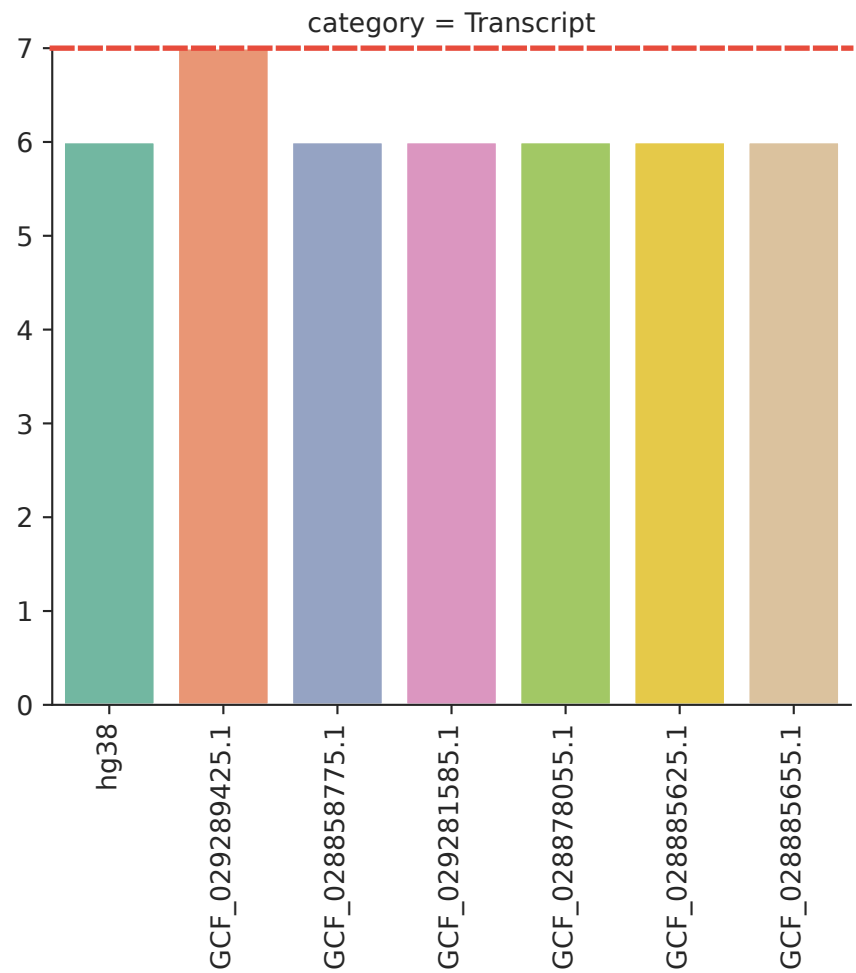
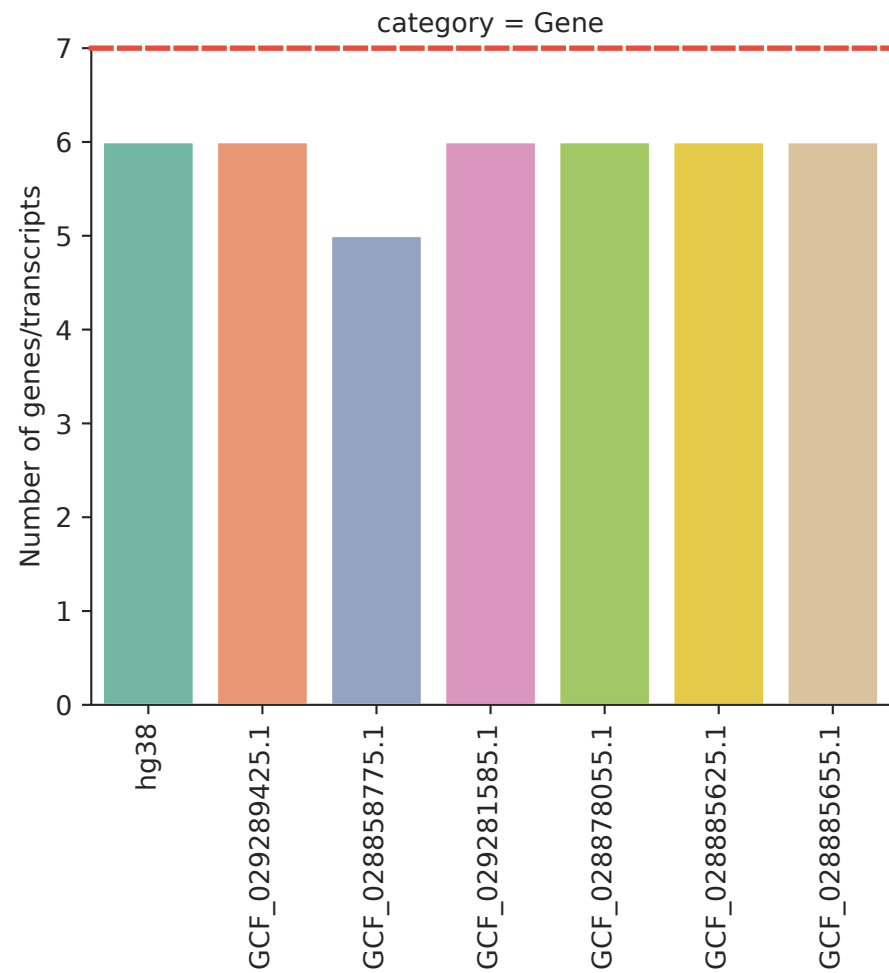
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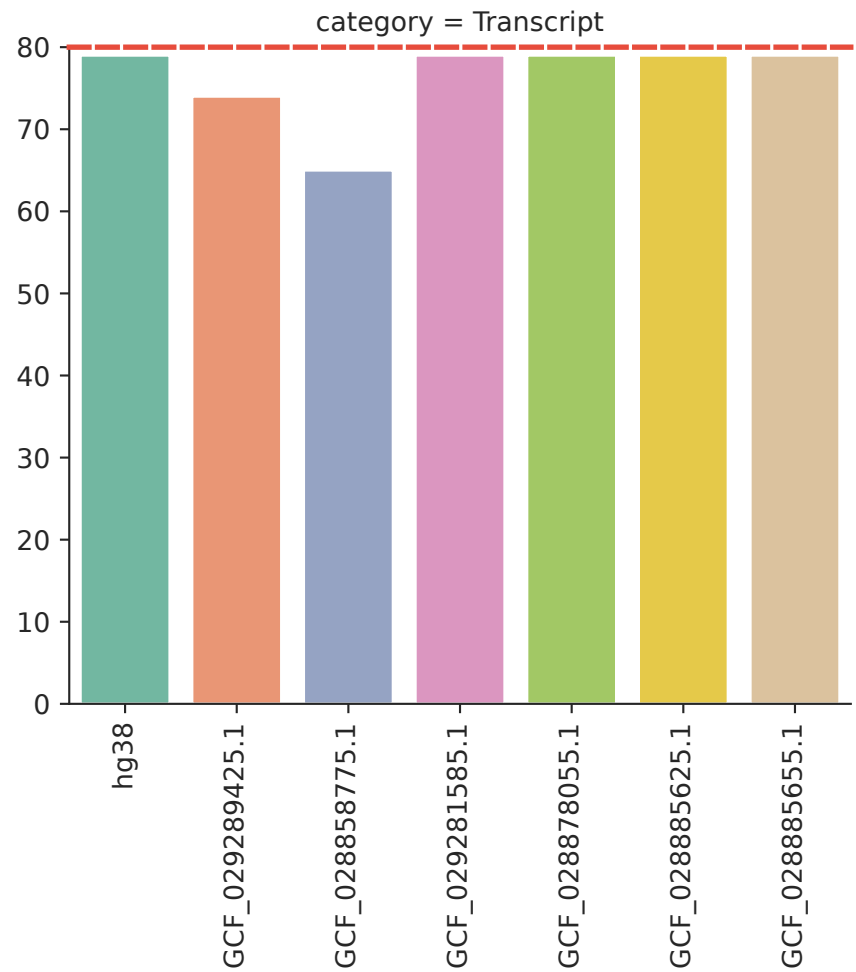
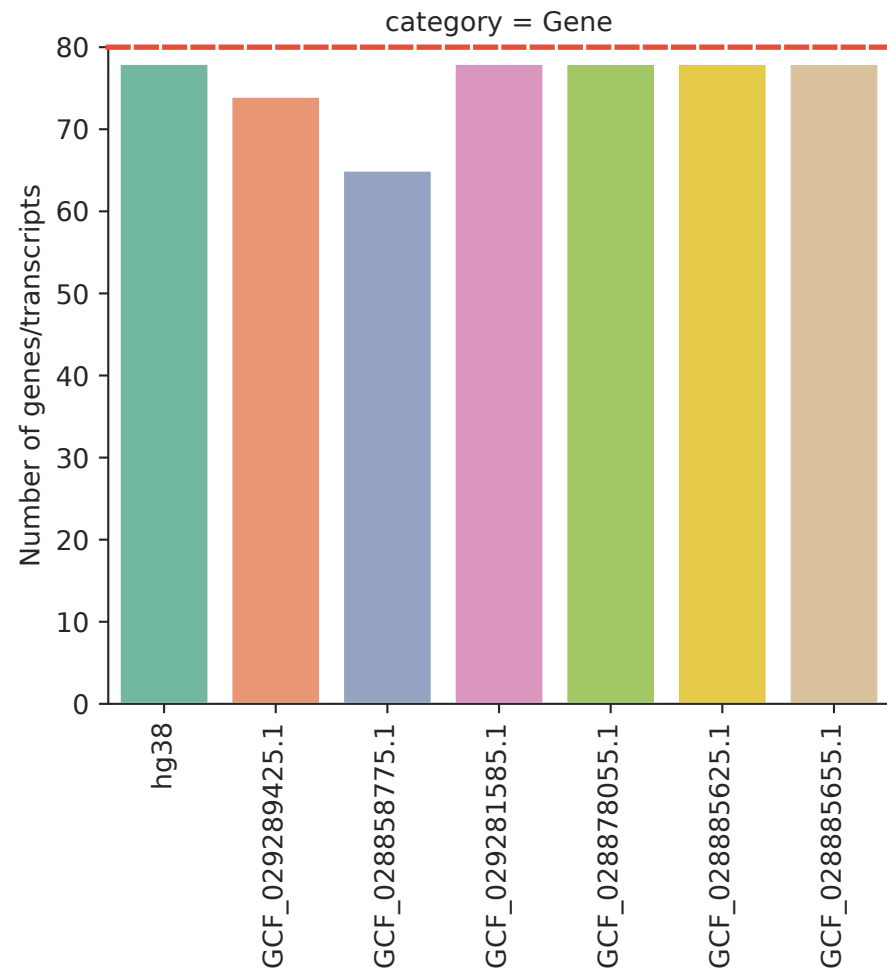
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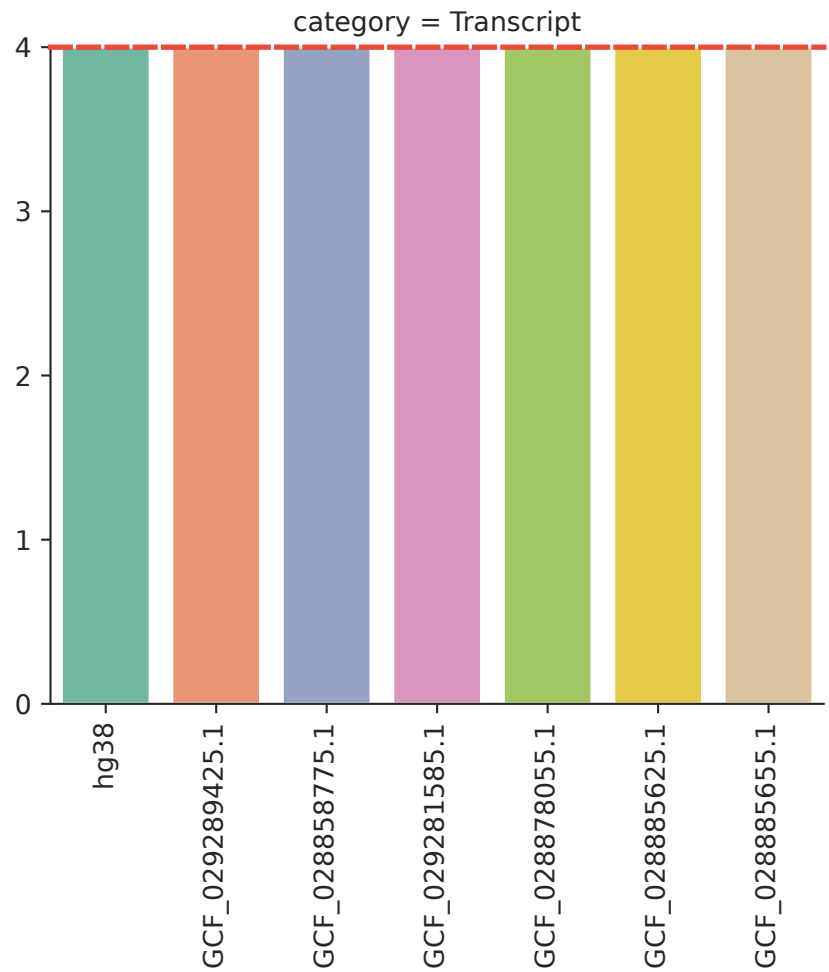
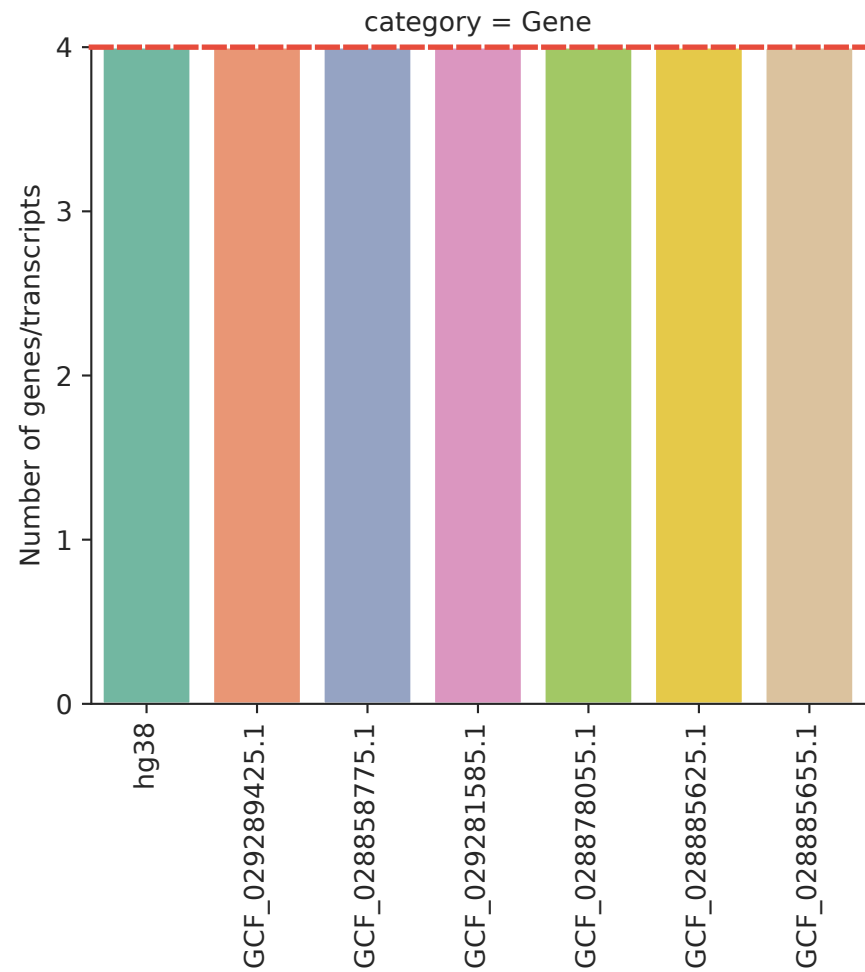
Number of comparative genes/transcripts present for biotype TR_C_gene



Number of comparative genes/transcripts present for biotype TR_J_gene

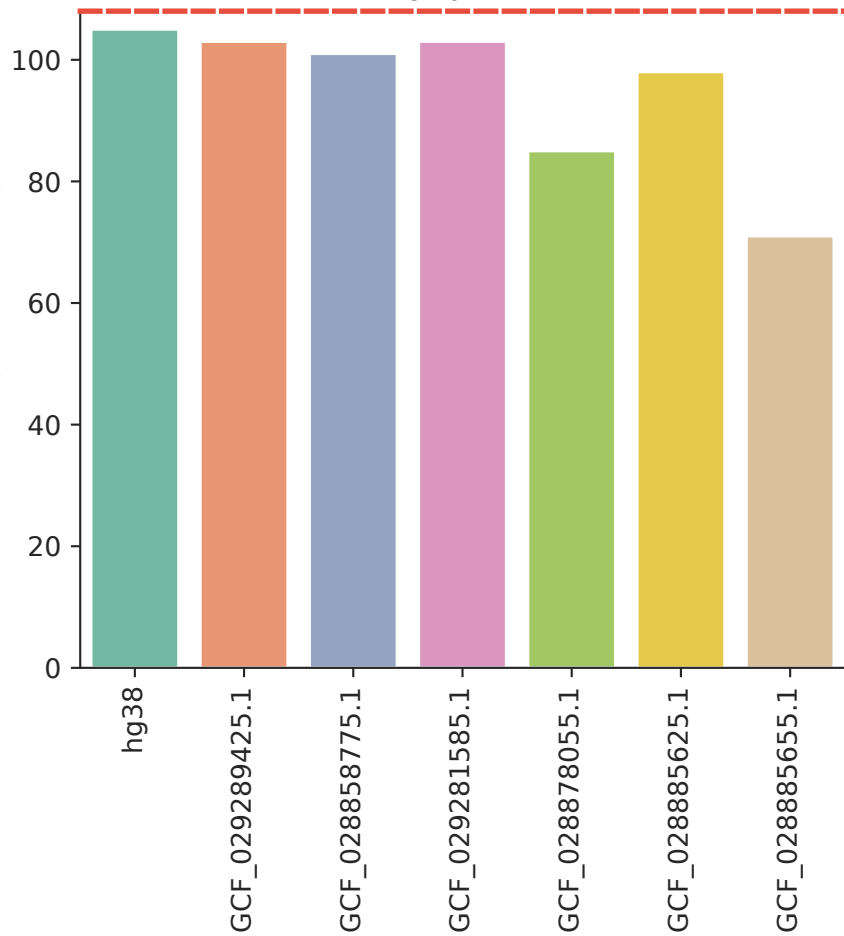


Number of comparative genes/transcripts present for biotype TR_J_pseudogene

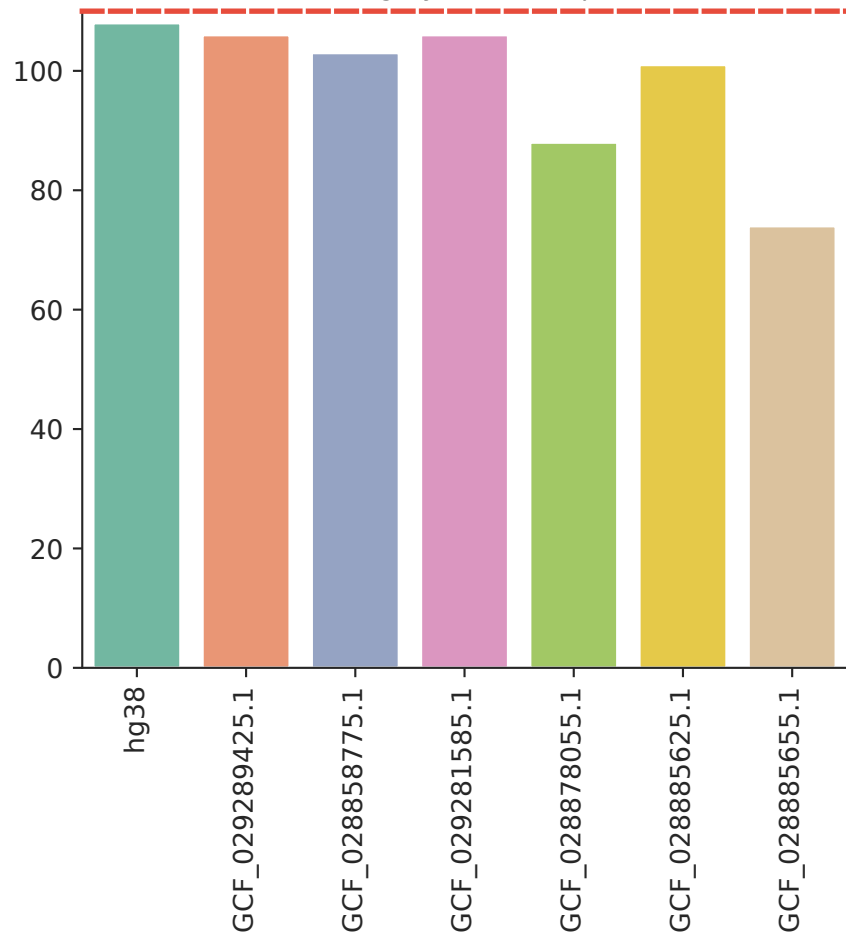


Number of comparative genes/transcripts present for biotype TR_V_gene

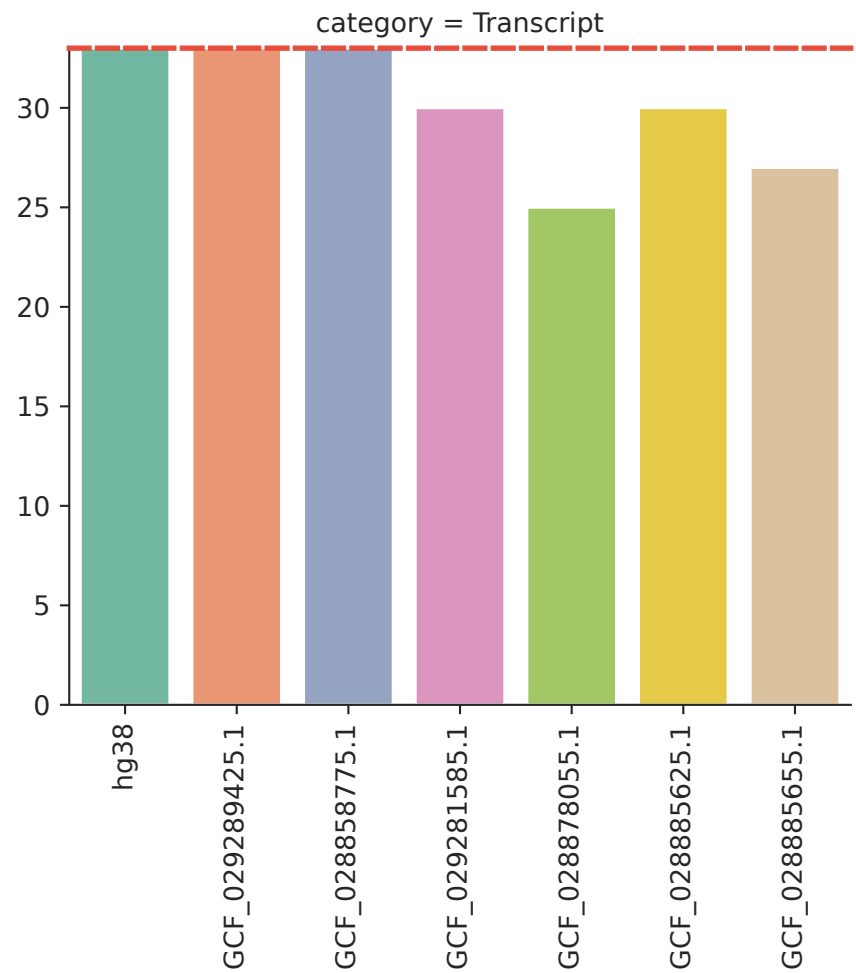
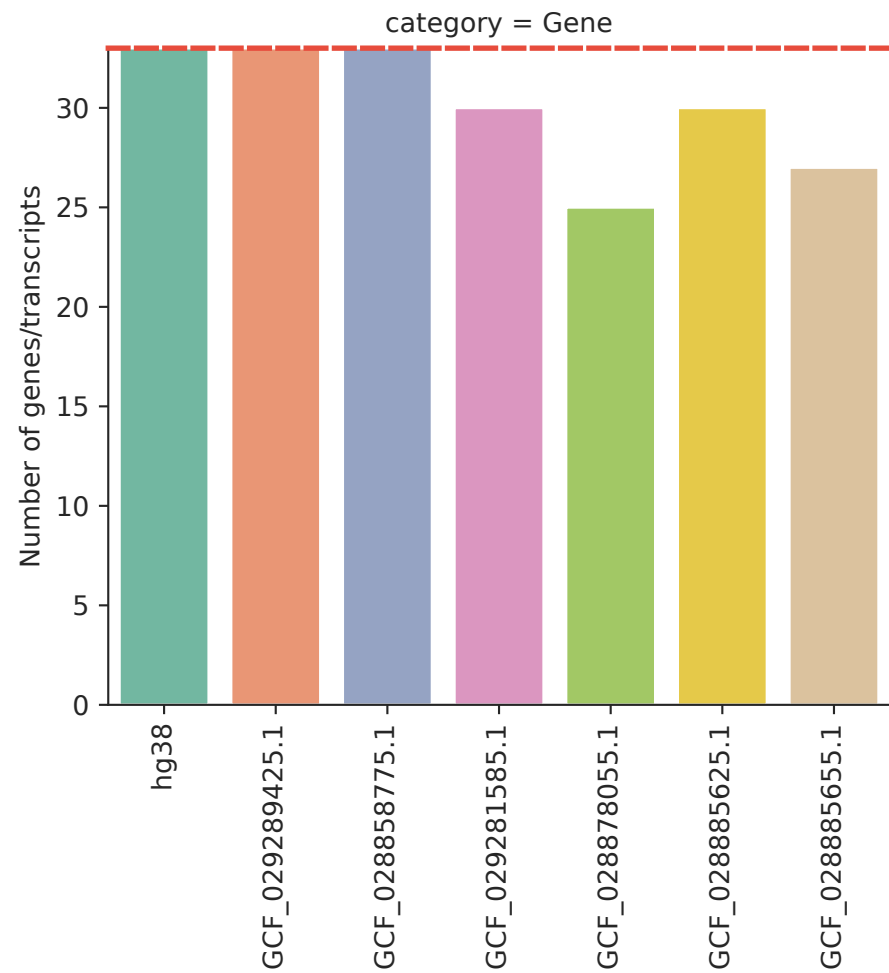
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category = Transcript

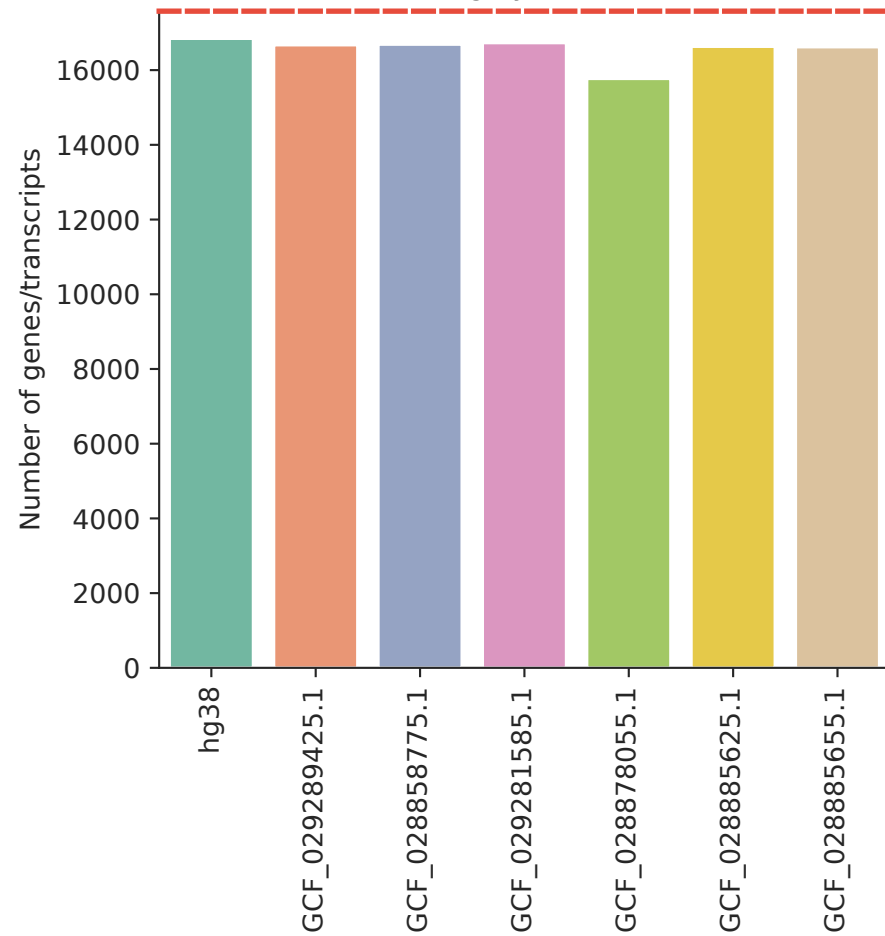


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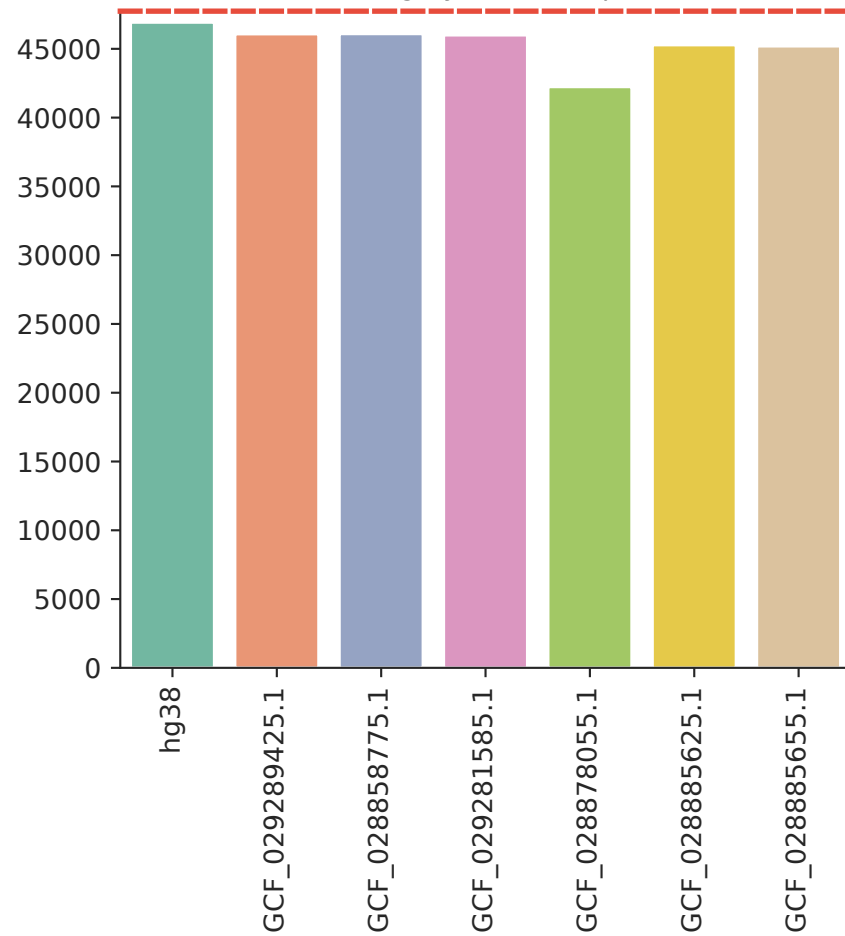


Number of comparative genes/transcripts present for biotype lncRNA

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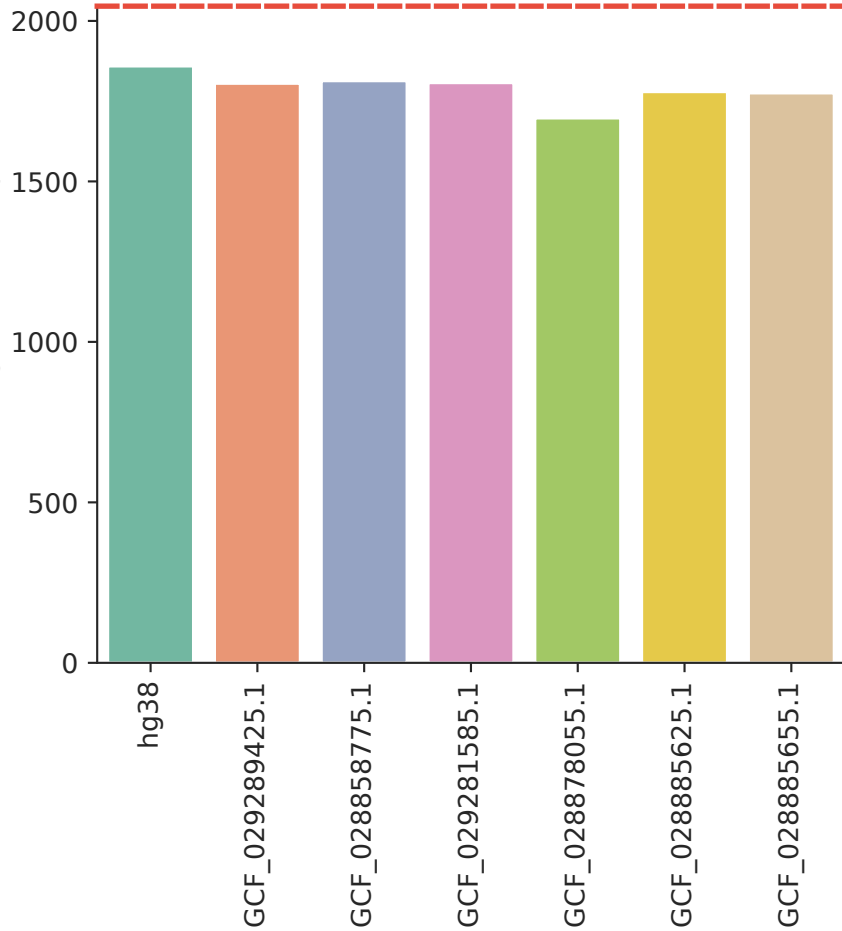


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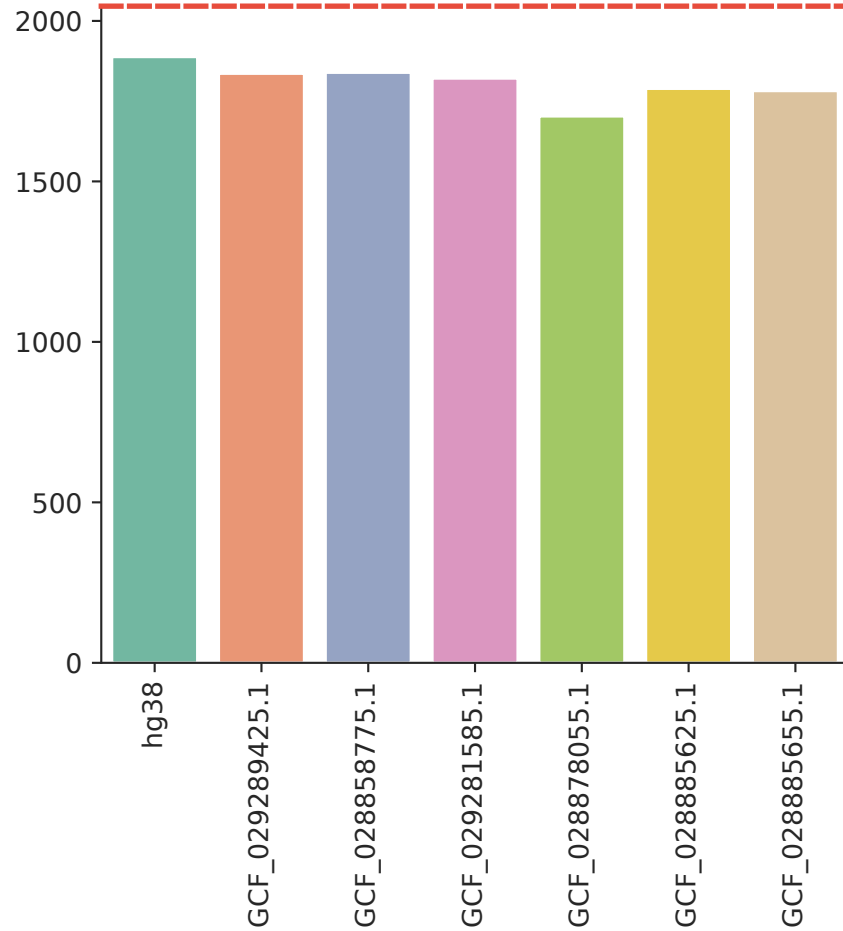


Number of comparative genes/transcripts present for biotype miRNA

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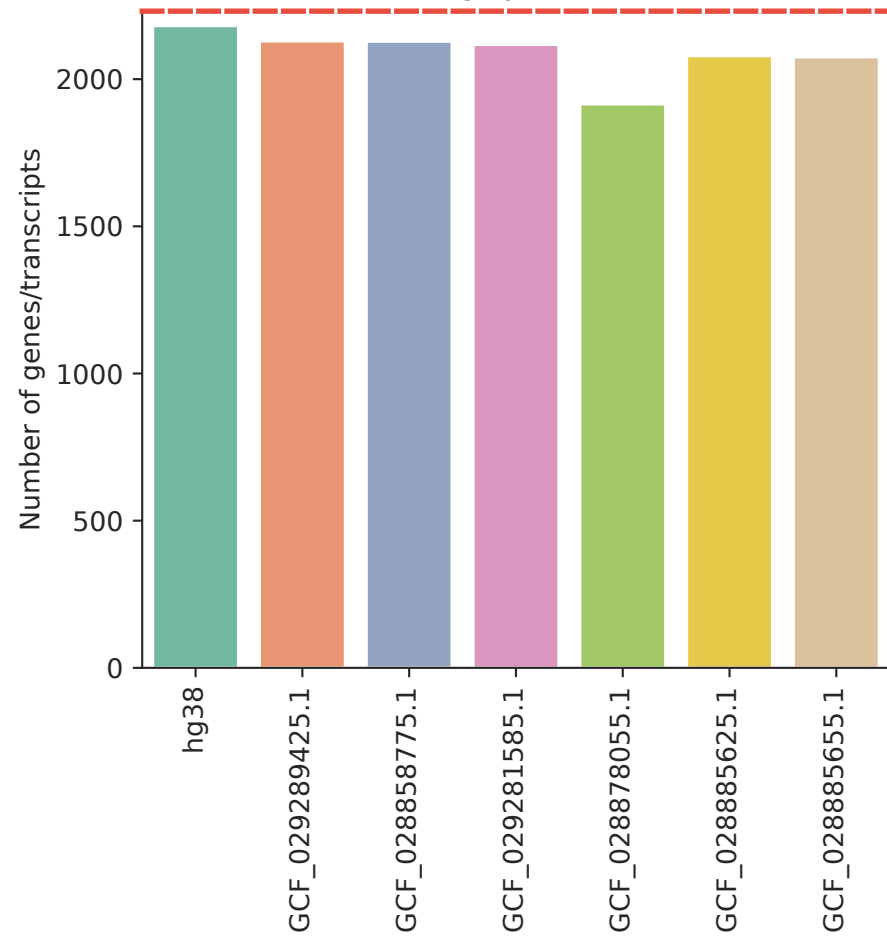


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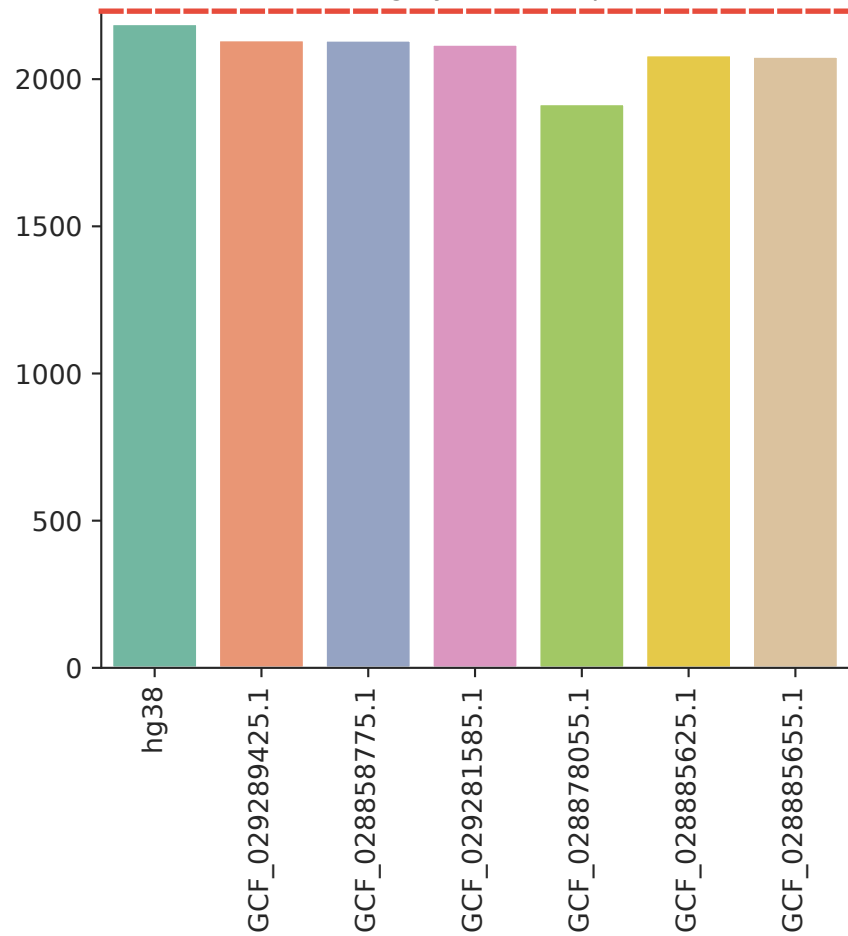


Number of comparative genes/transcripts present for biotype misc_RNA

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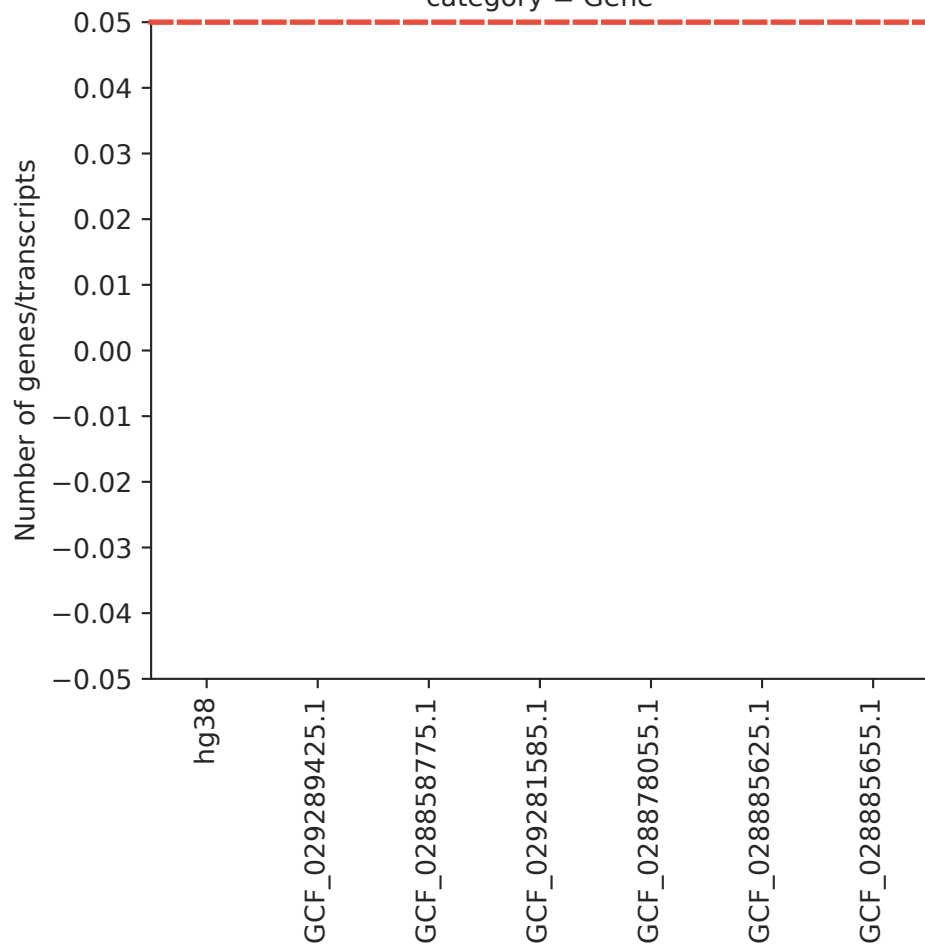


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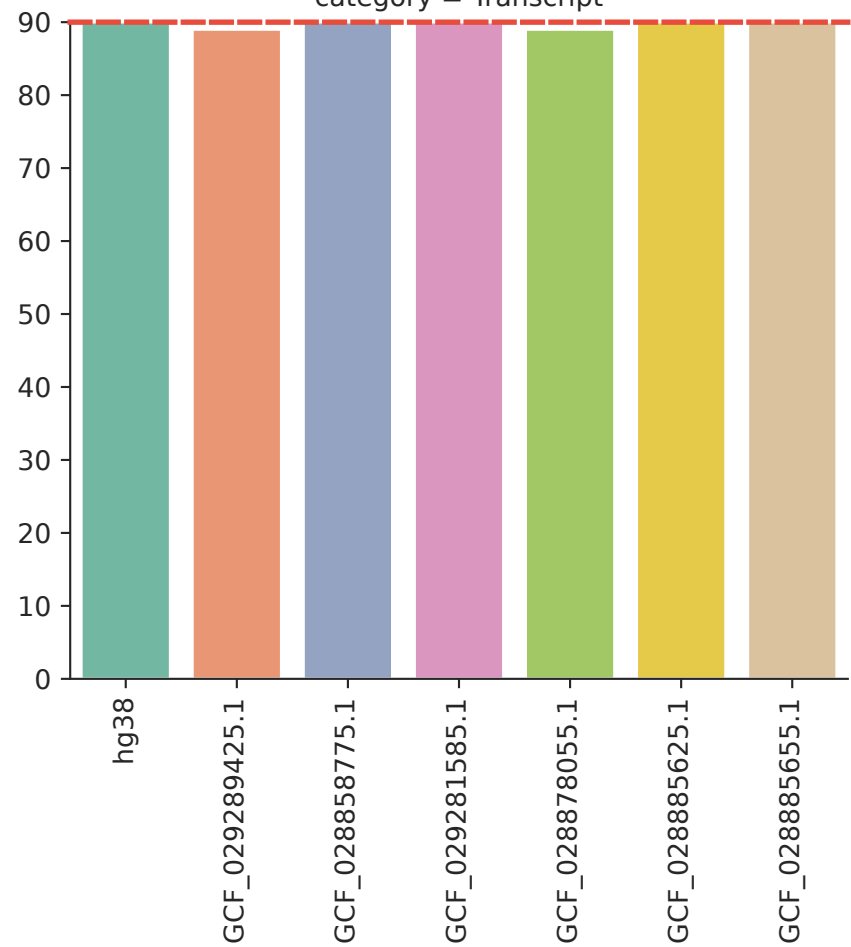


Number of comparative genes/transcripts present for biotype non_stop_decay

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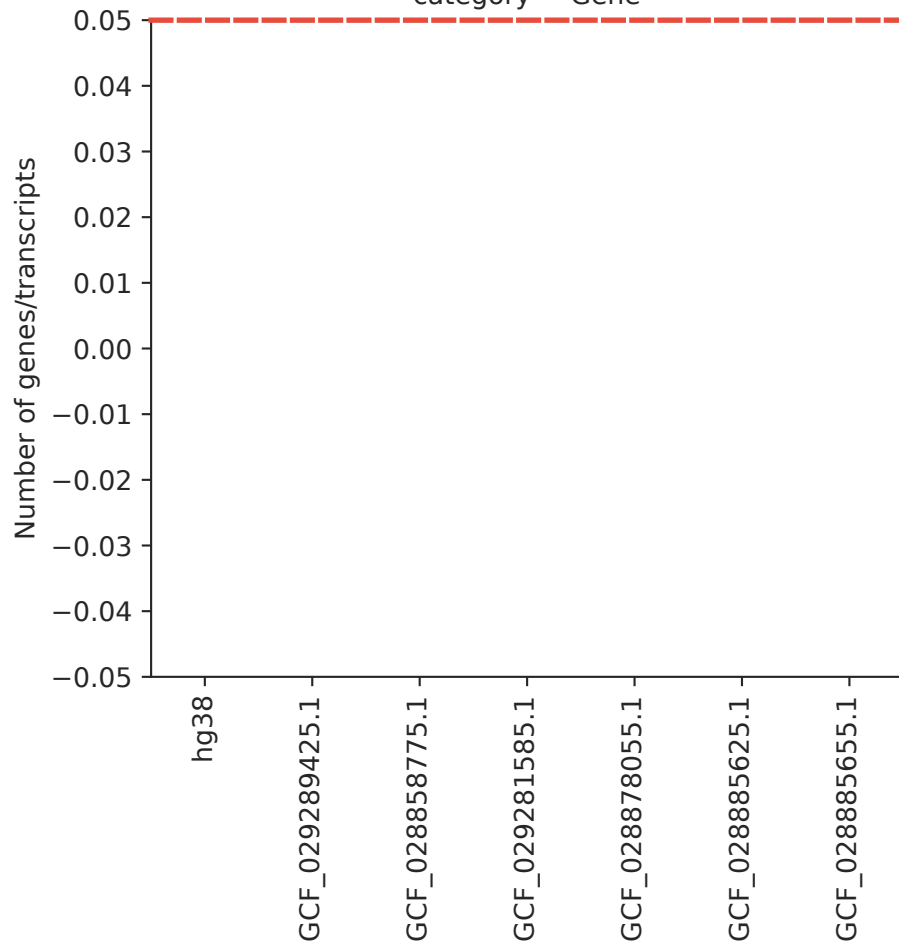


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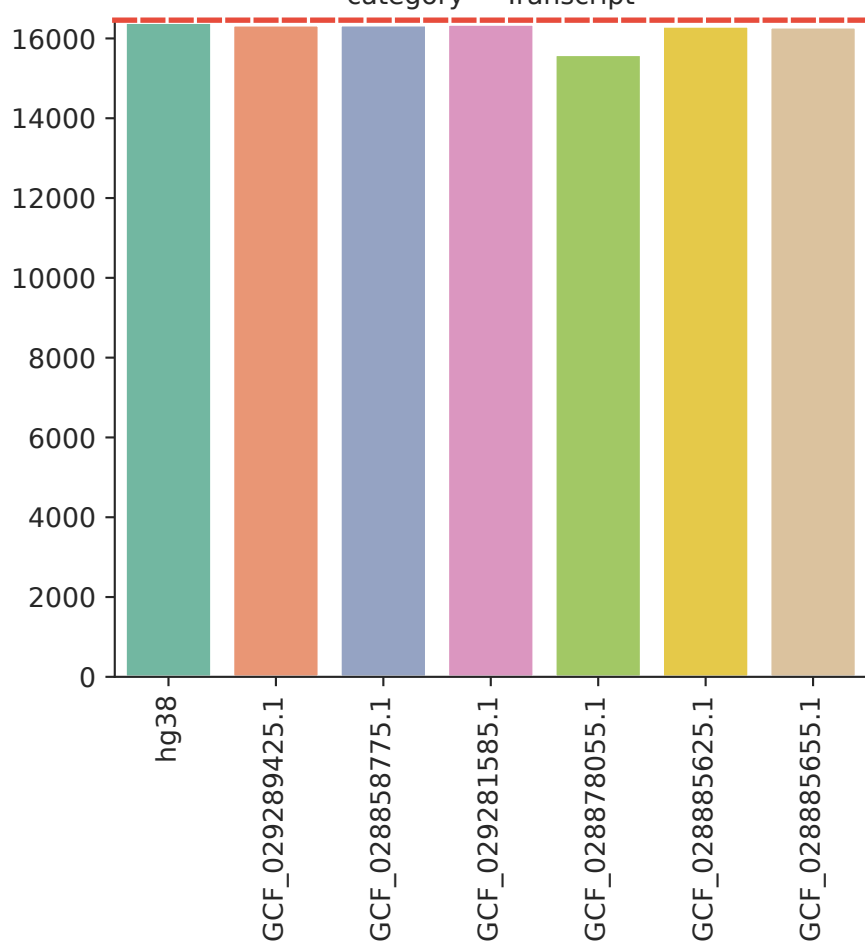


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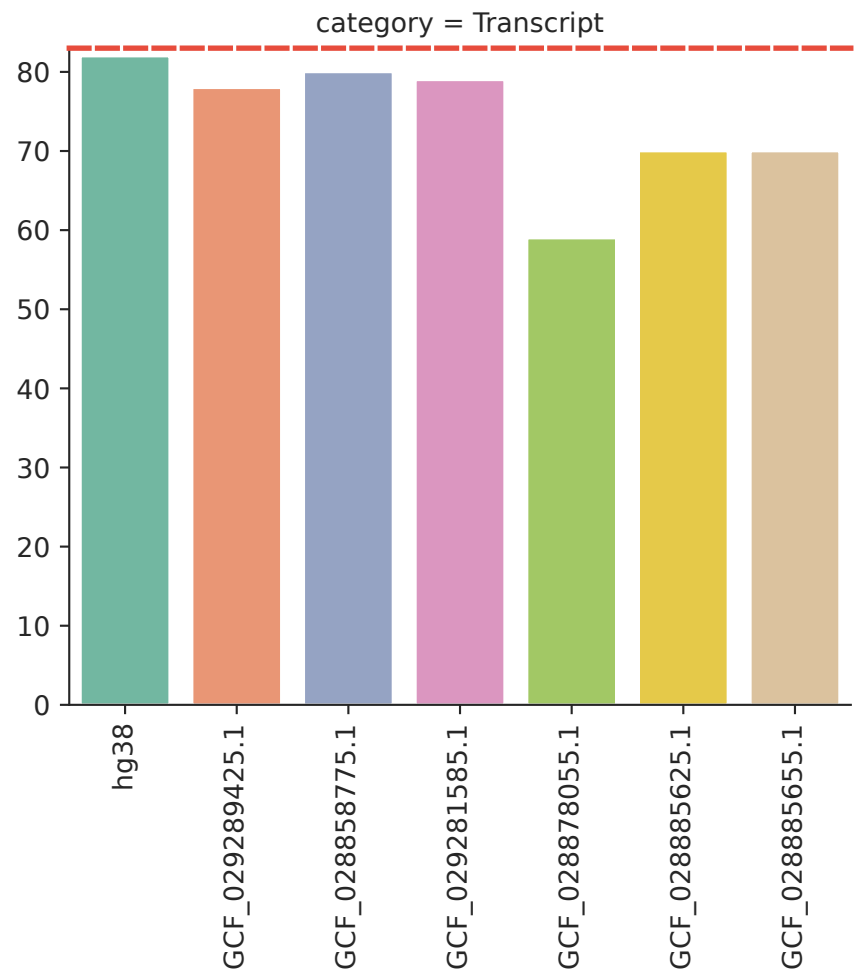
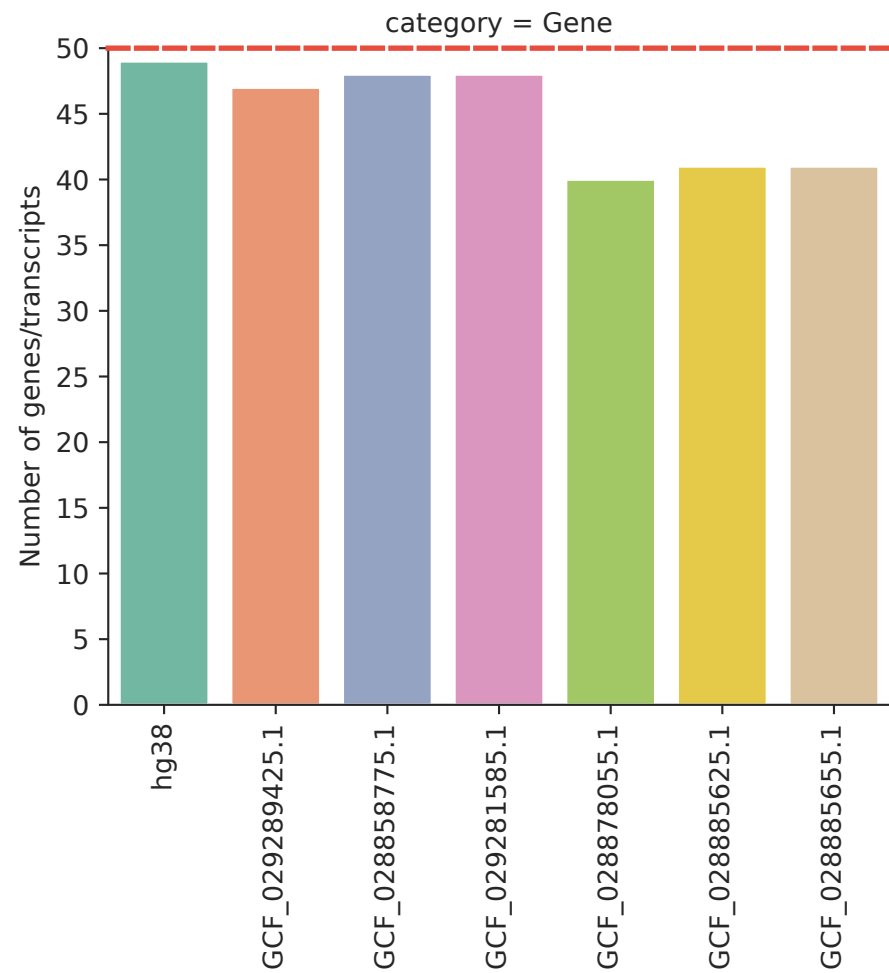
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category = Transcript

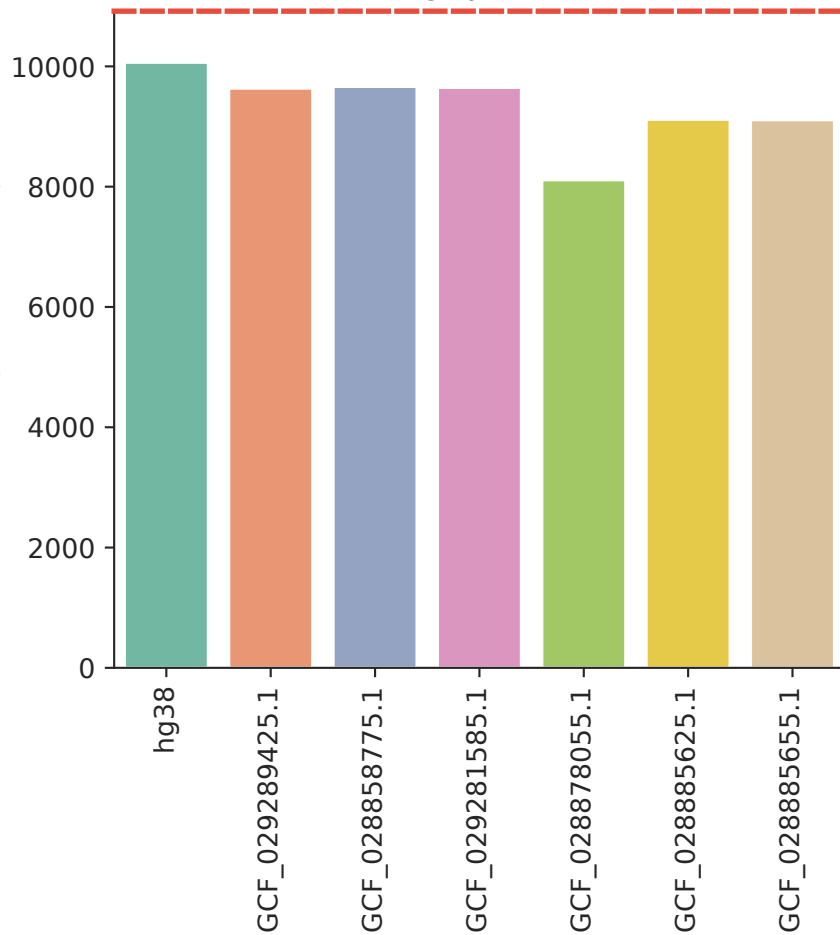


Number of comparative genes/transcripts present for biotype polymorphic_pseudogene

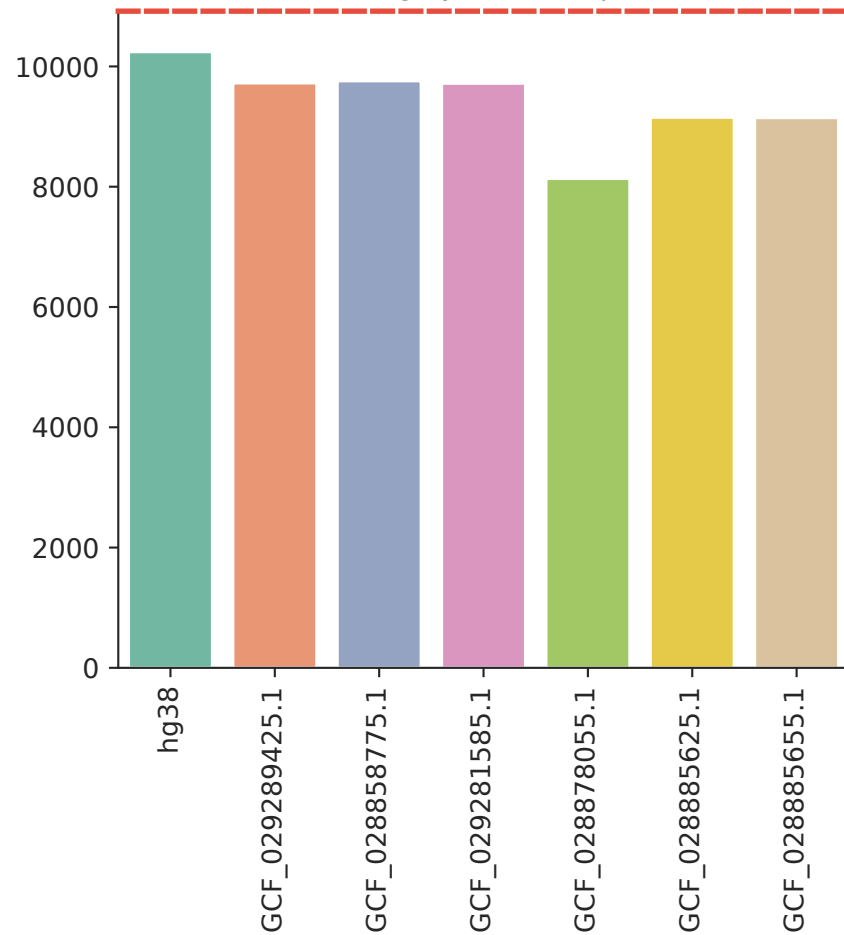


Number of comparative genes/transcripts present for biotype processed_pseudogene

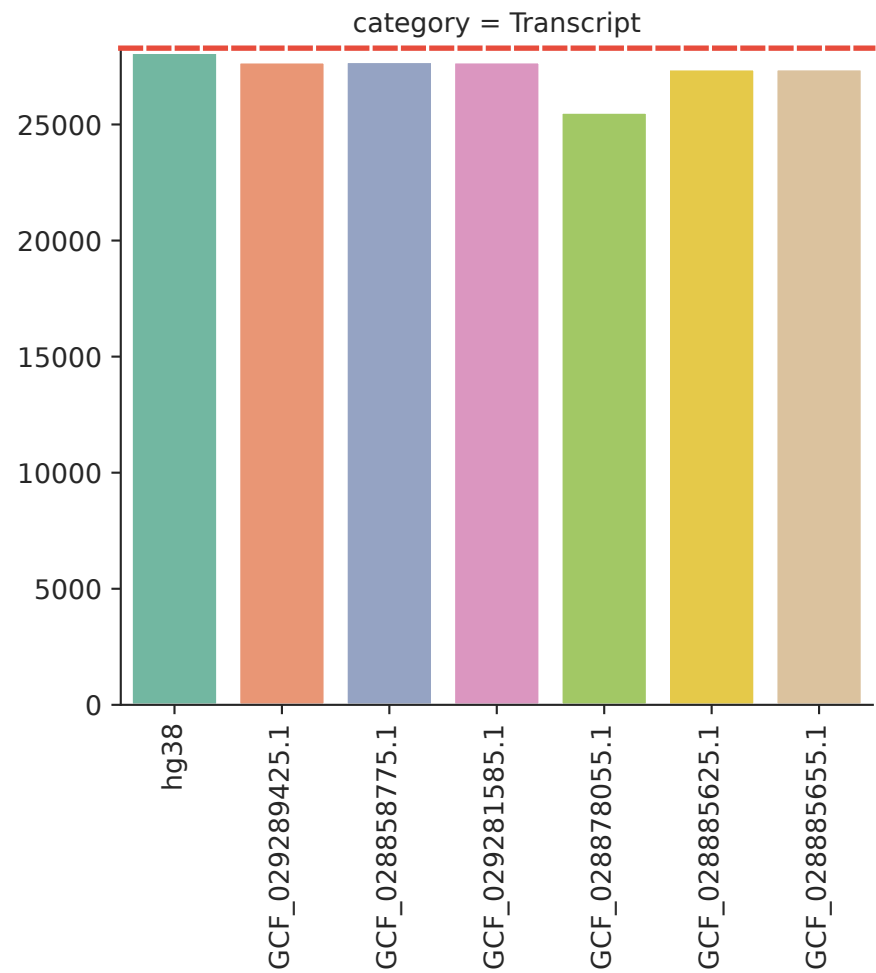
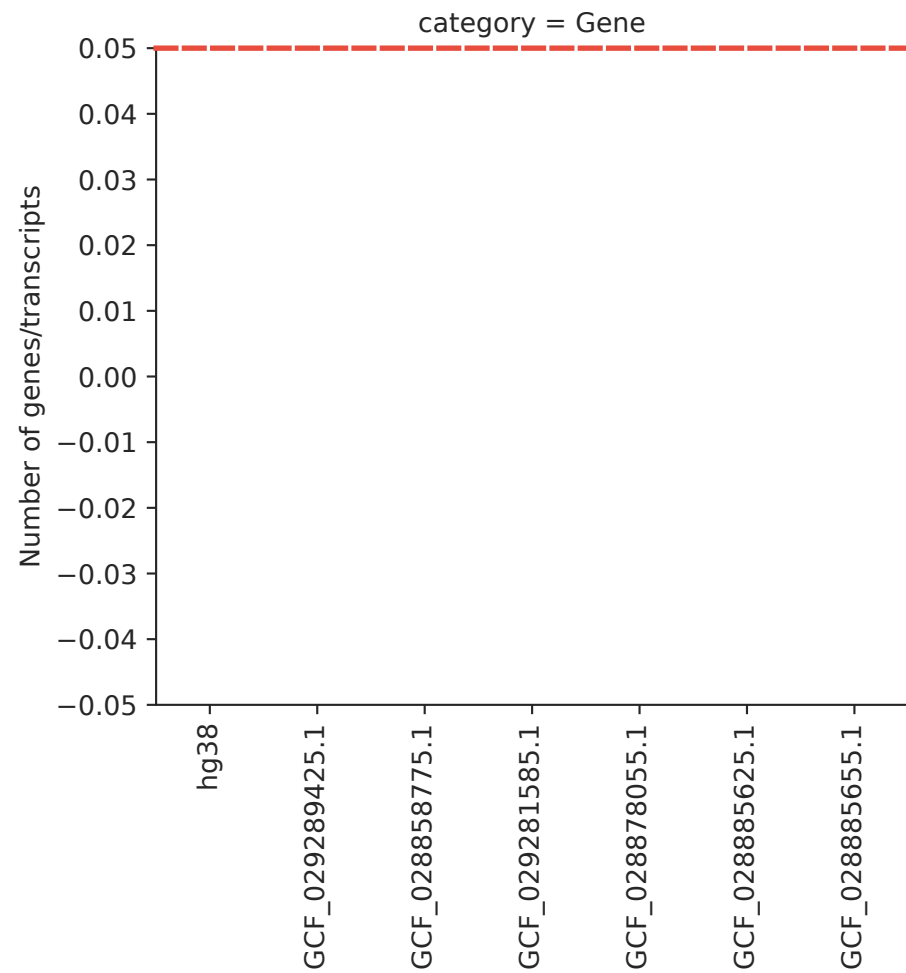
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category = Transcript

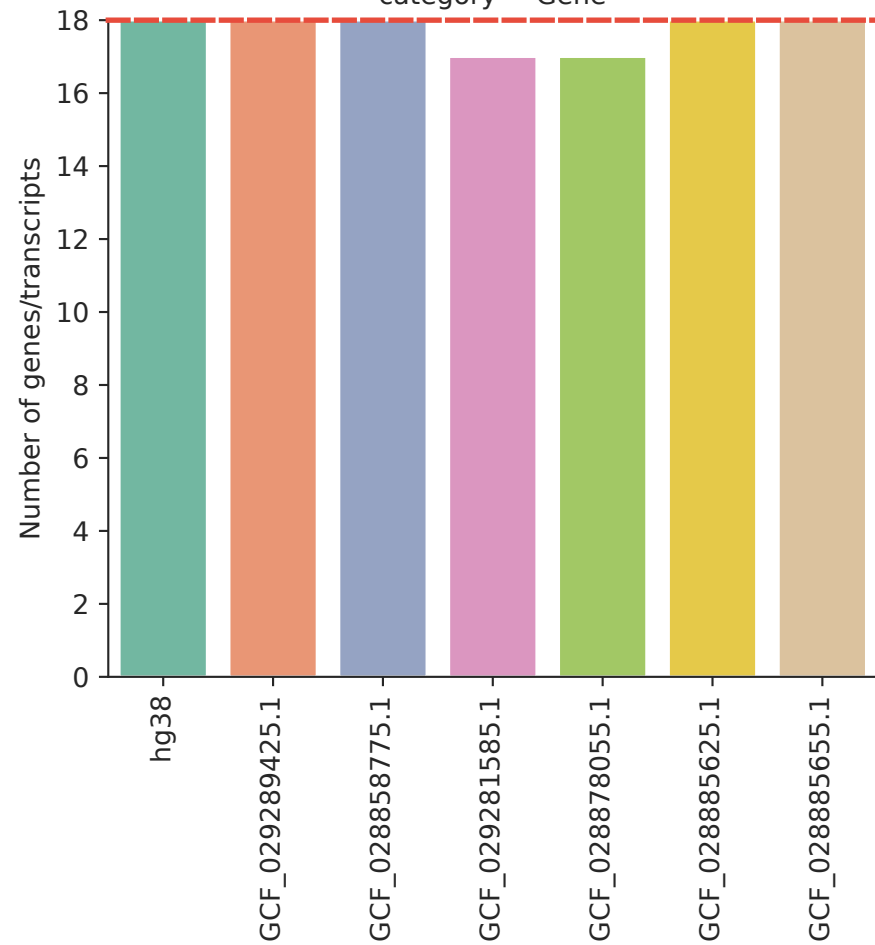


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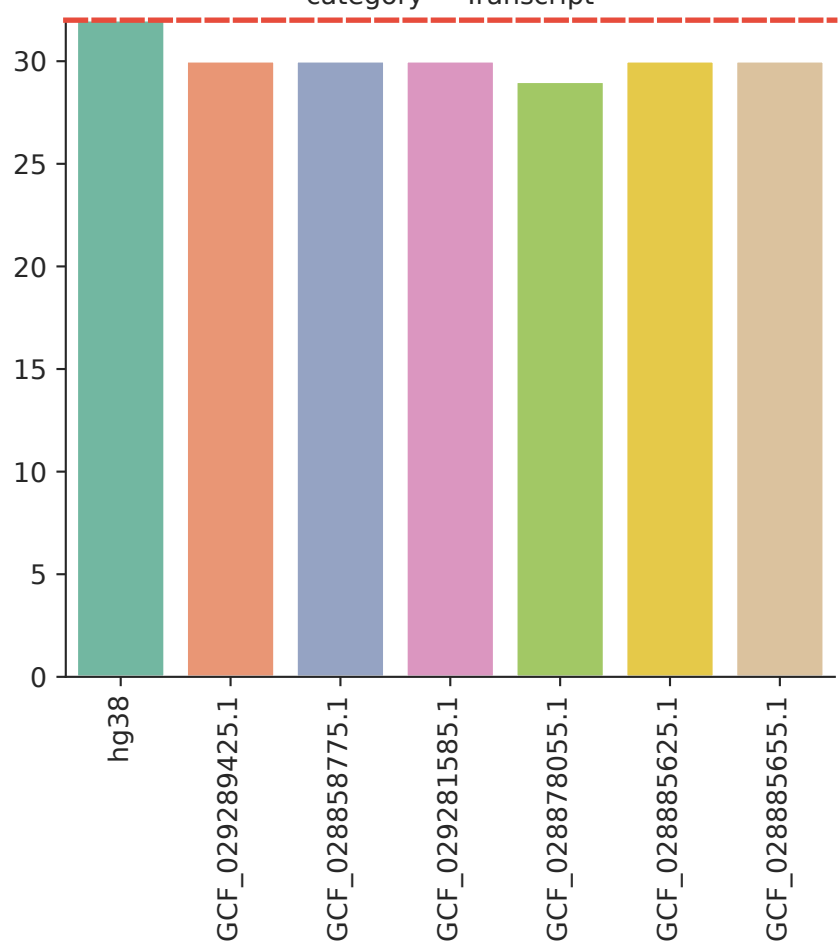


Number of comparative genes/transcripts present for biotype pseudogene

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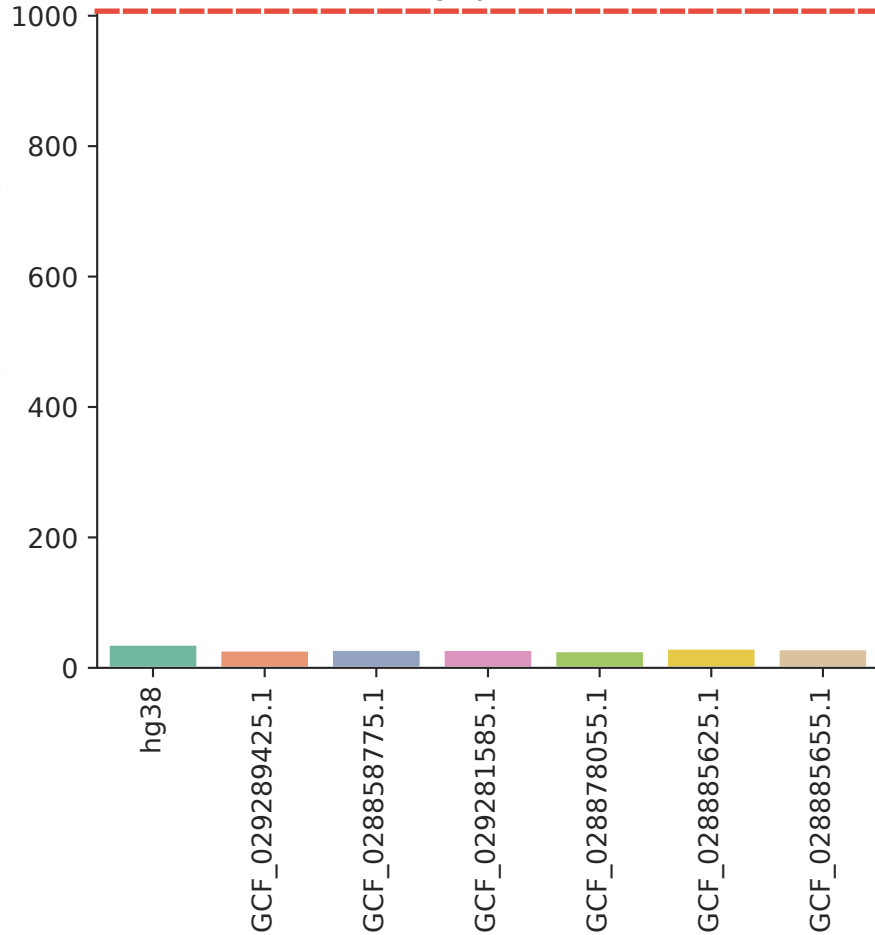


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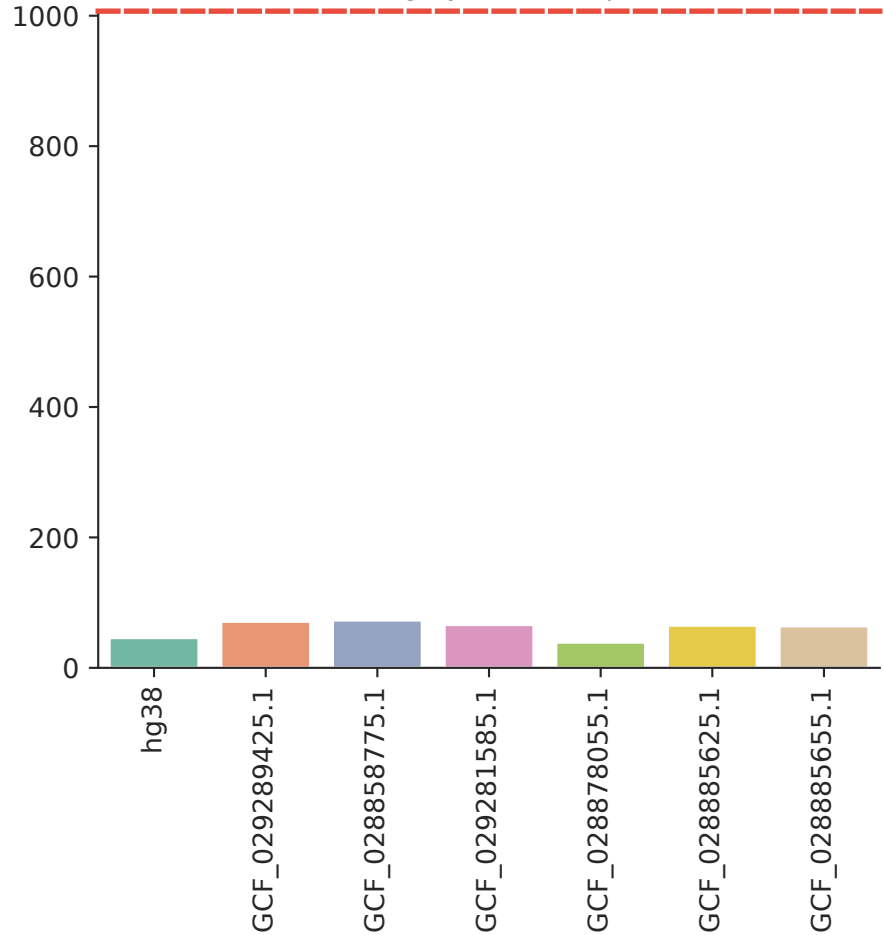


Number of comparative genes/transcripts present for biotype rRNA

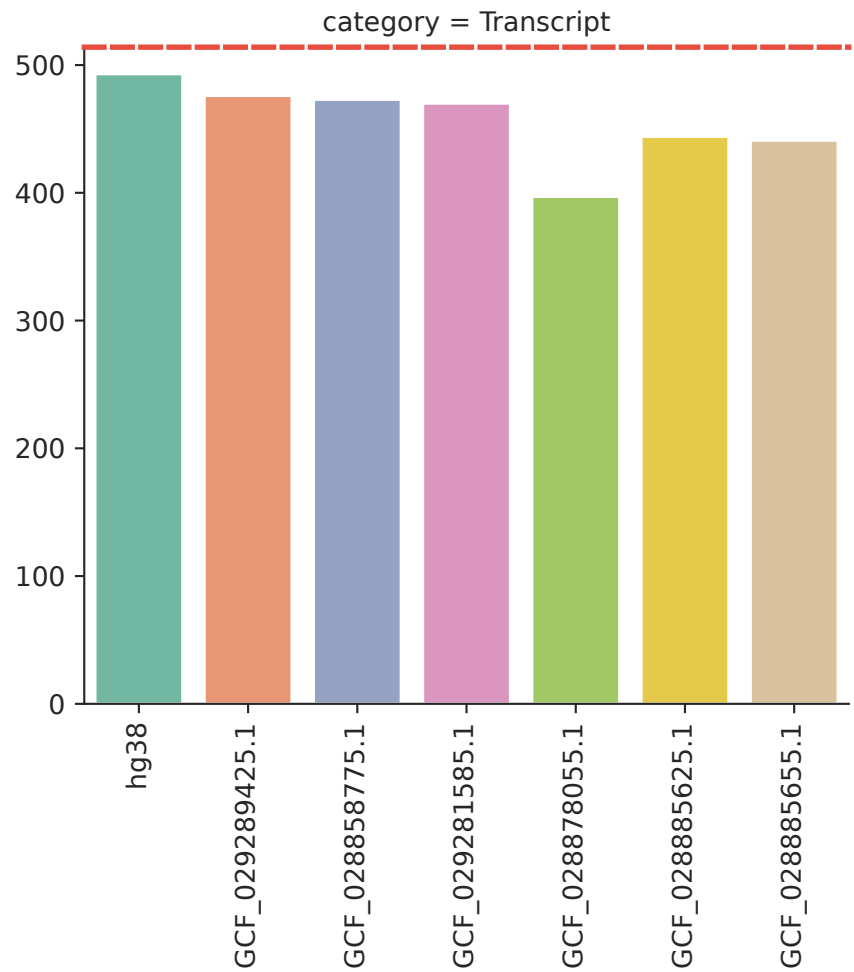
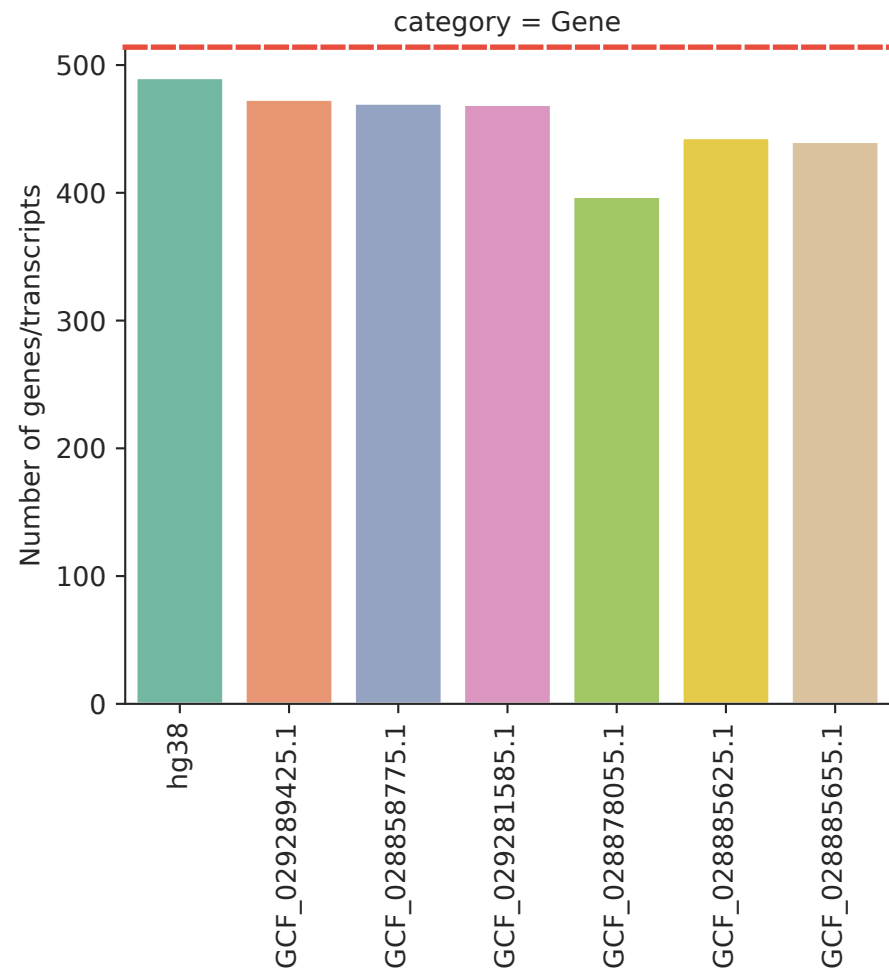
category = Gene



category = Transcript

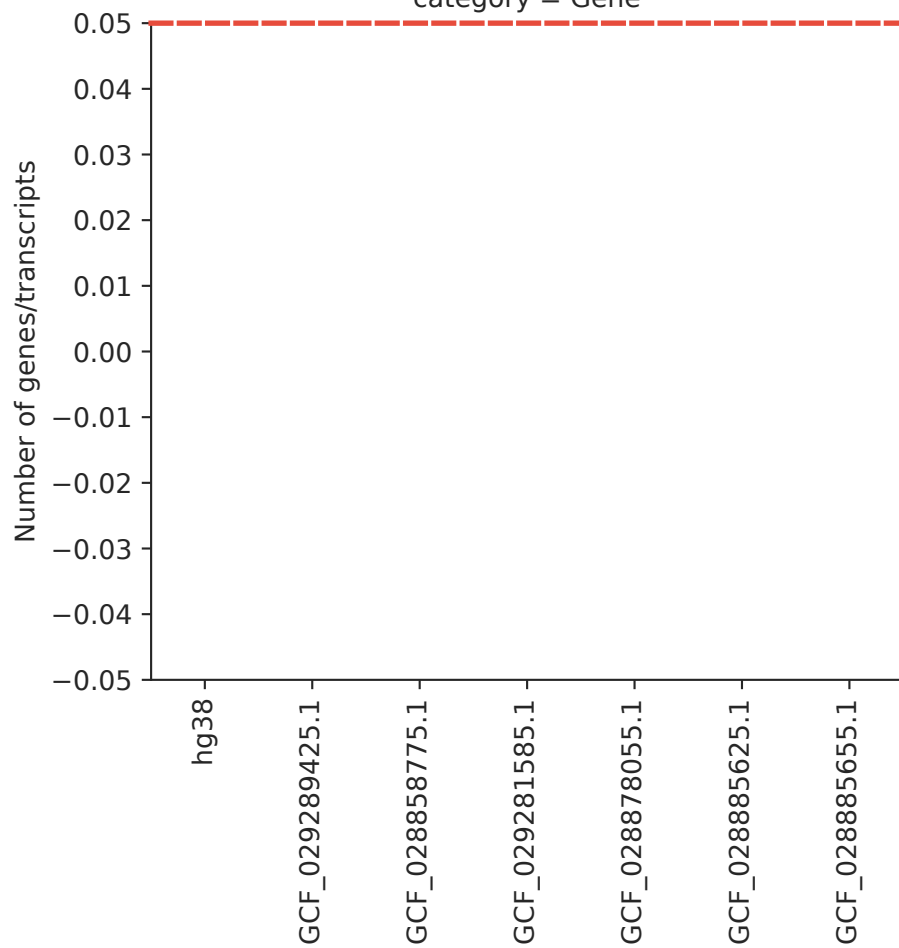


Number of comparative genes/transcripts present for biotype rRNA_pseudogene

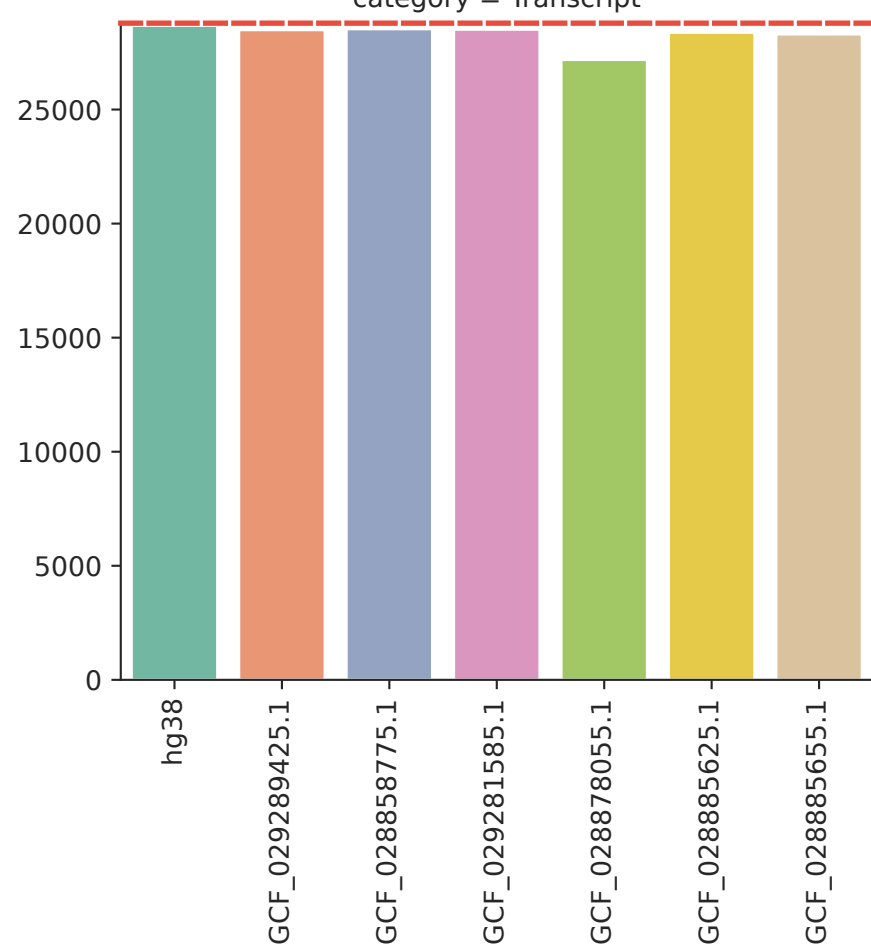


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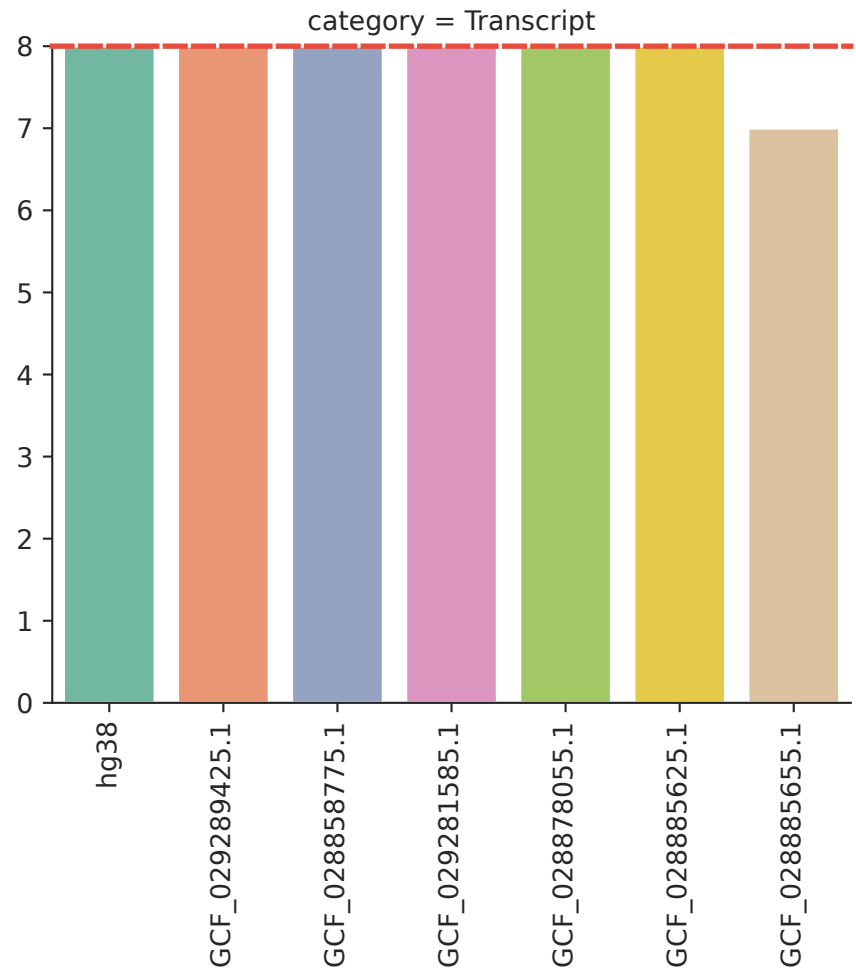
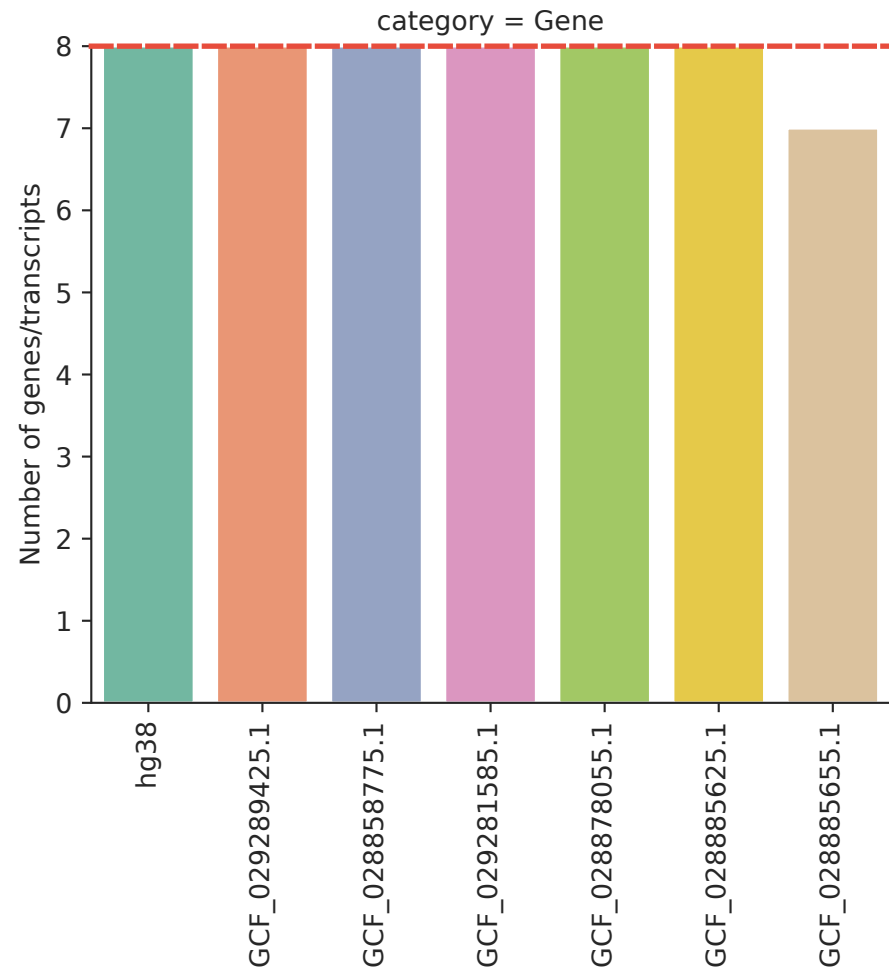
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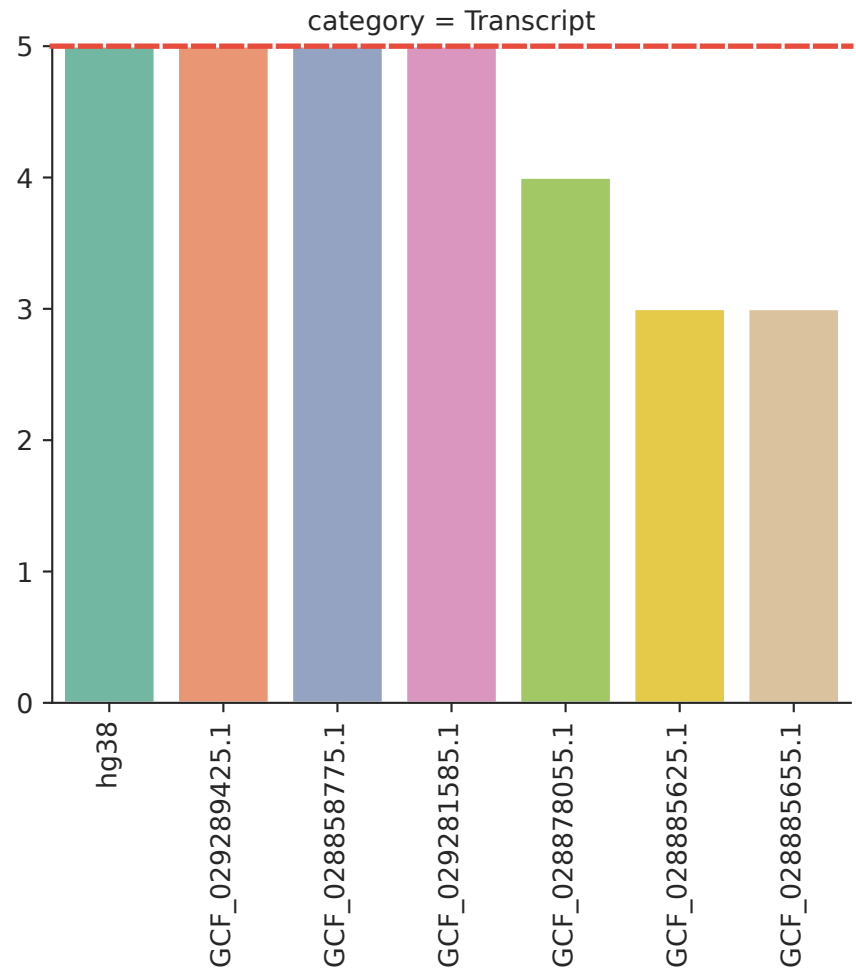
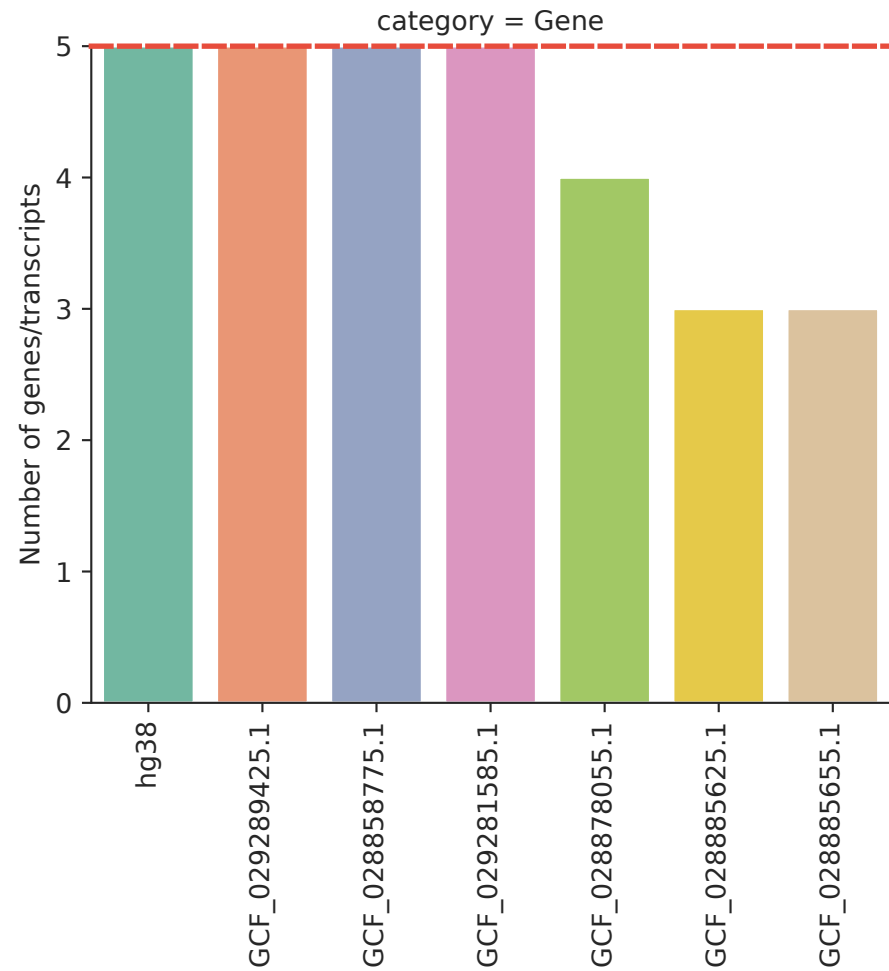
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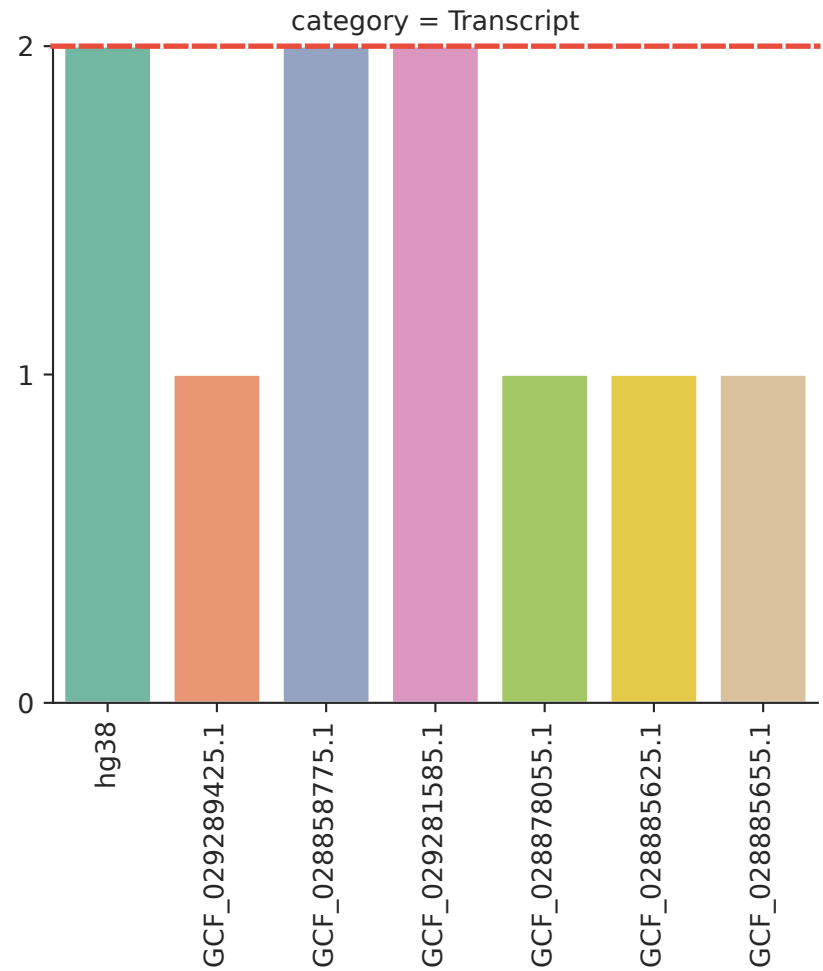
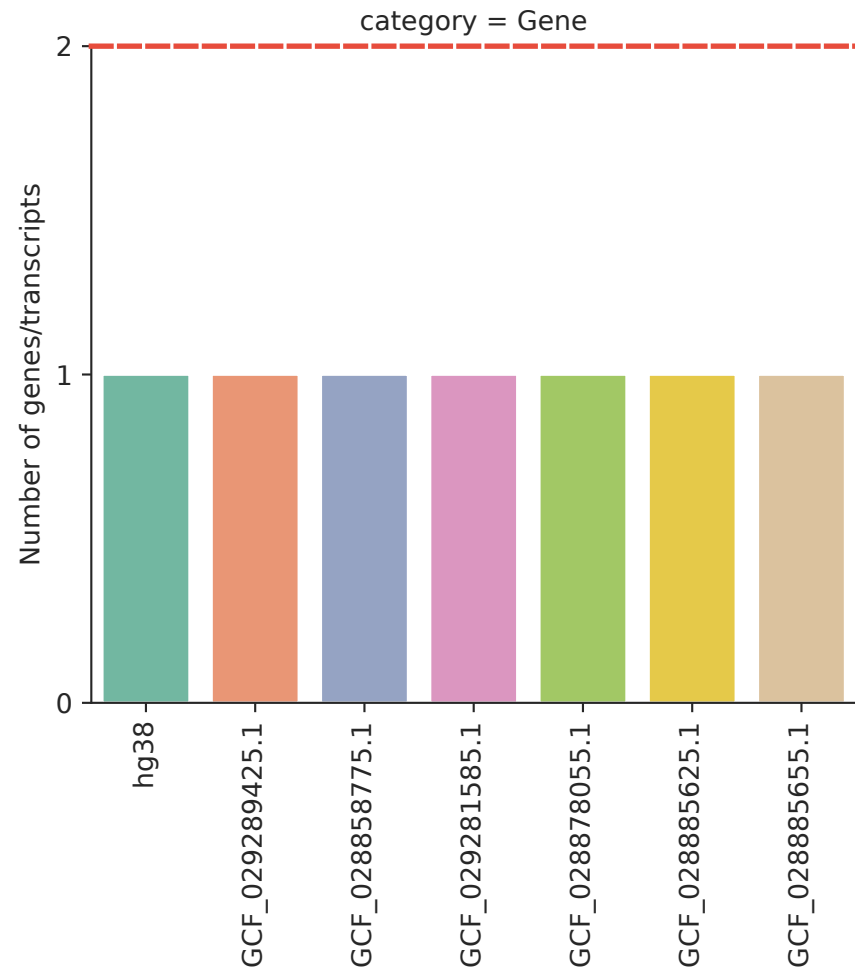
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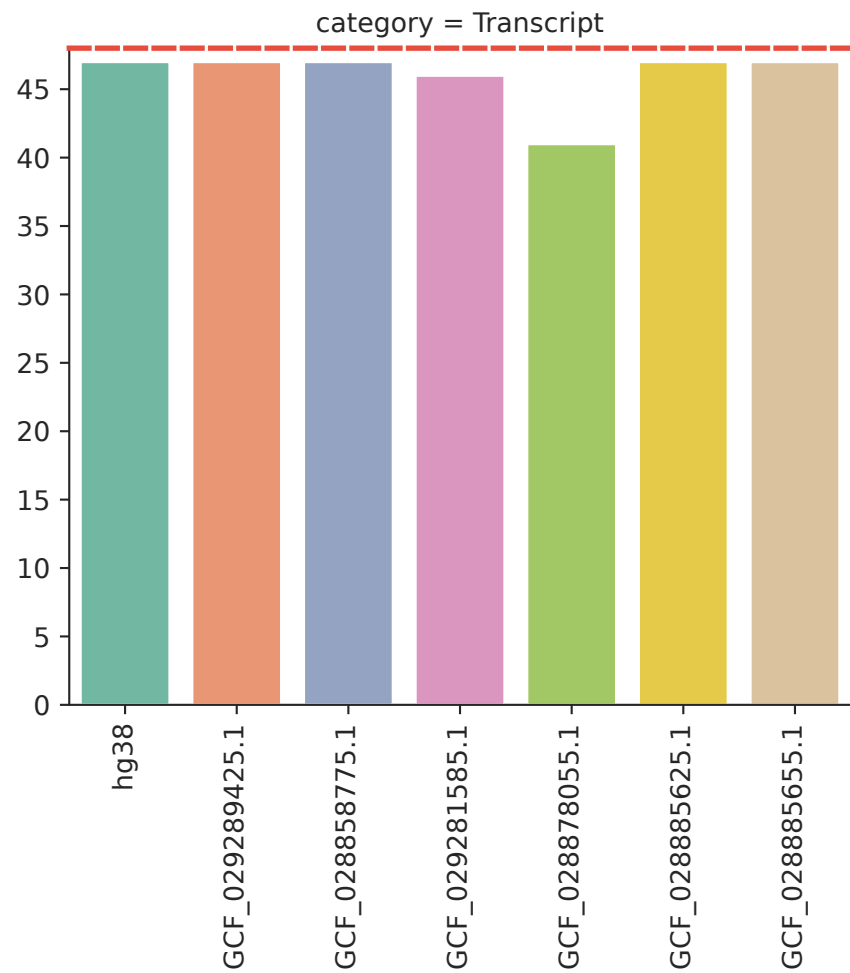
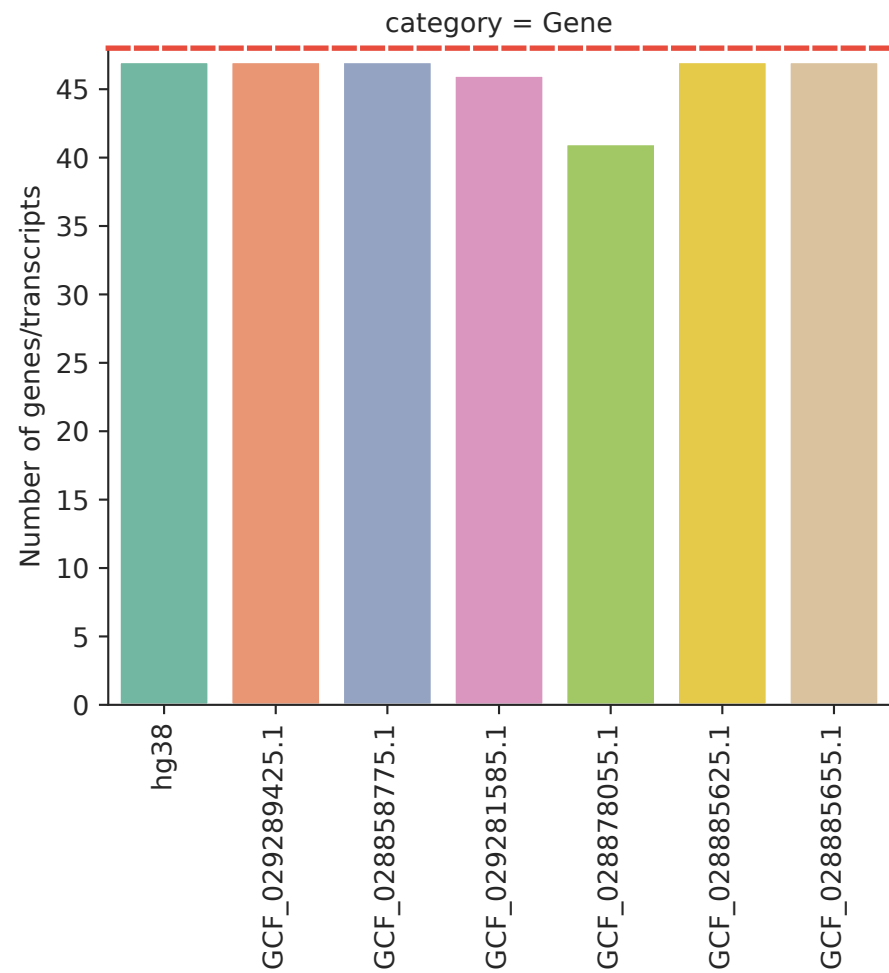
Number of comparative genes/transcripts present for biotype sRNA



Number of comparative genes/transcripts present for biotype scRNA

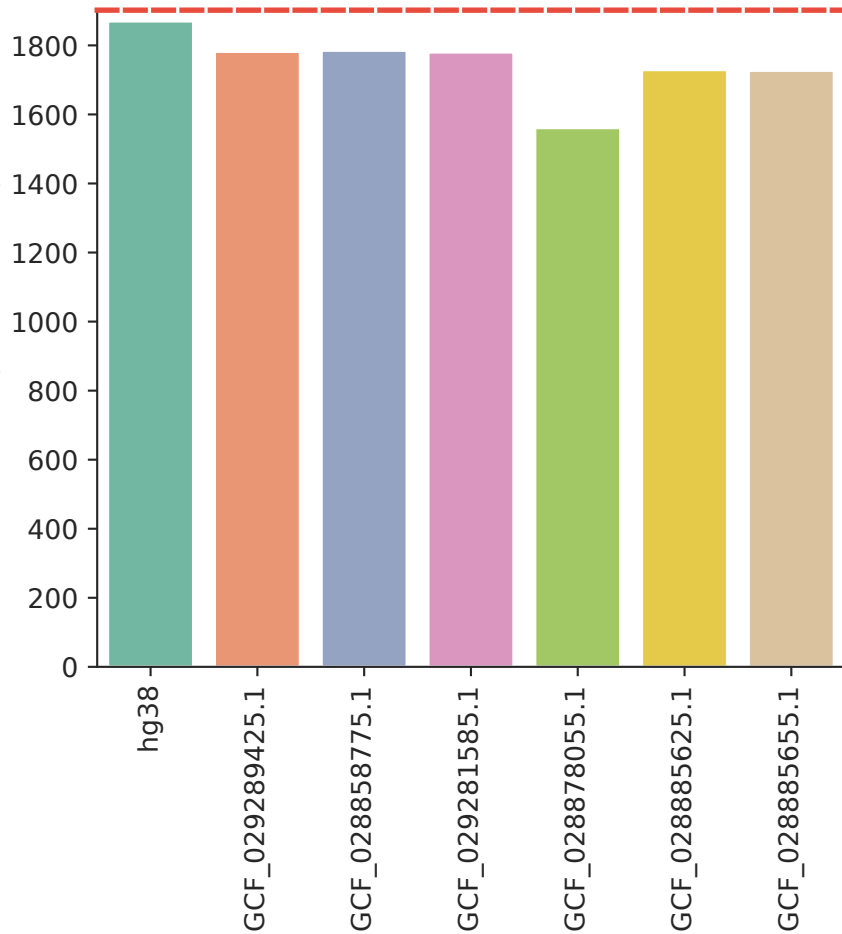


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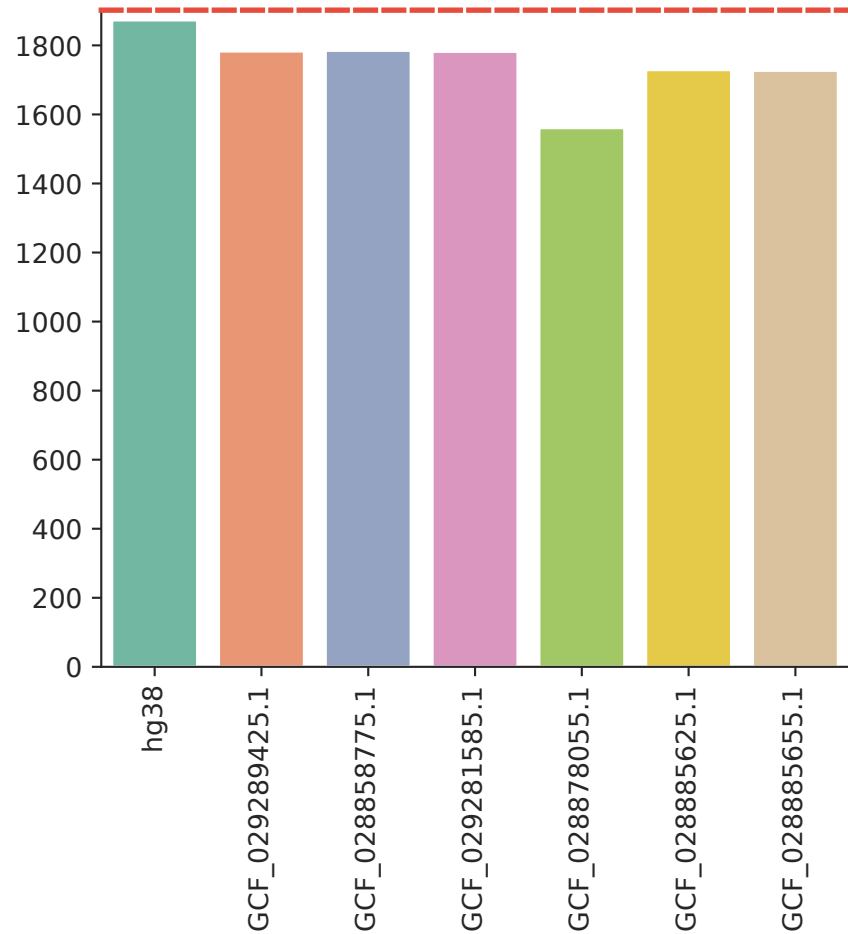


Number of comparative genes/transcripts present for biotype snRNA

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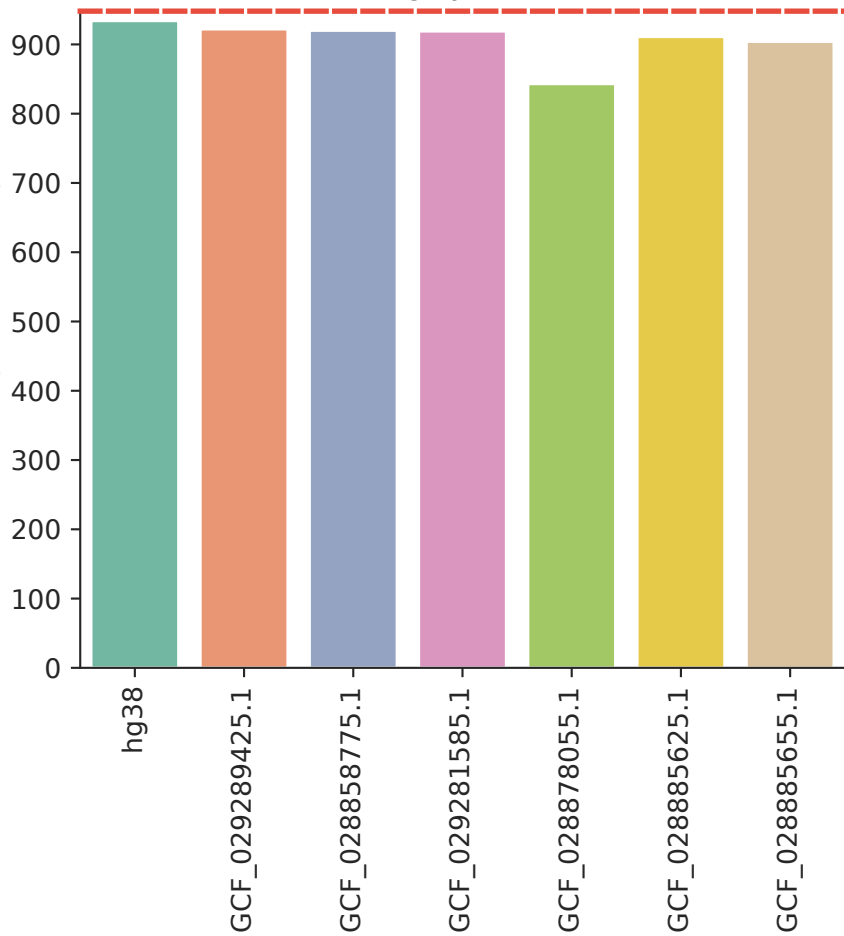


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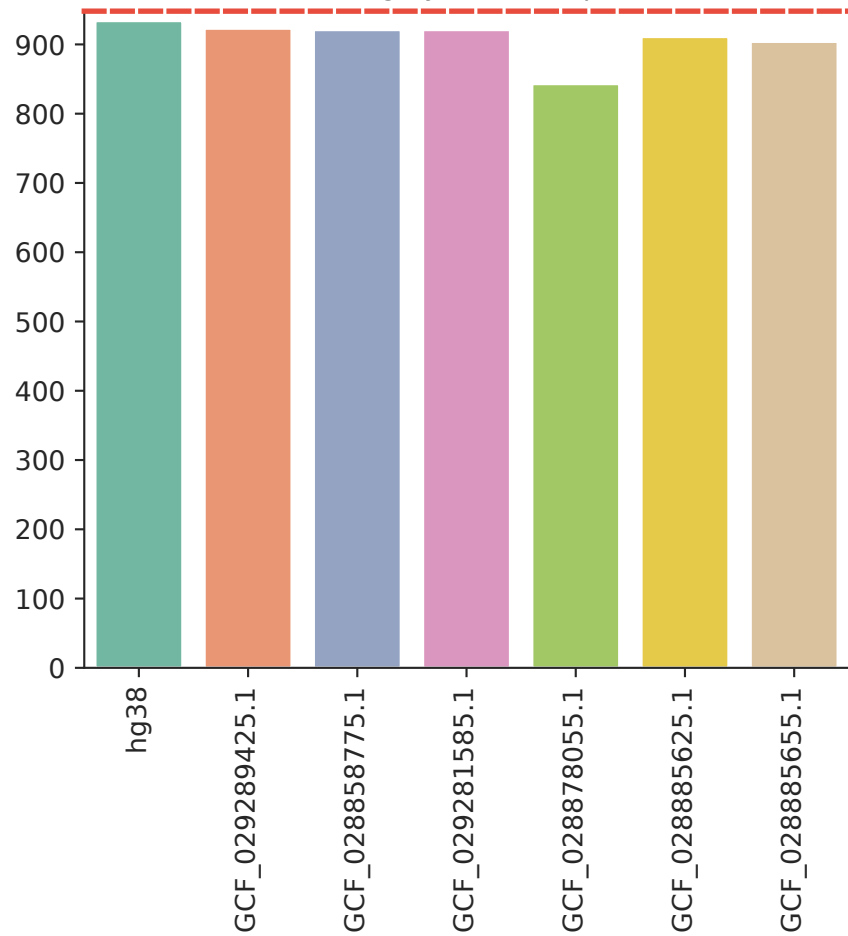


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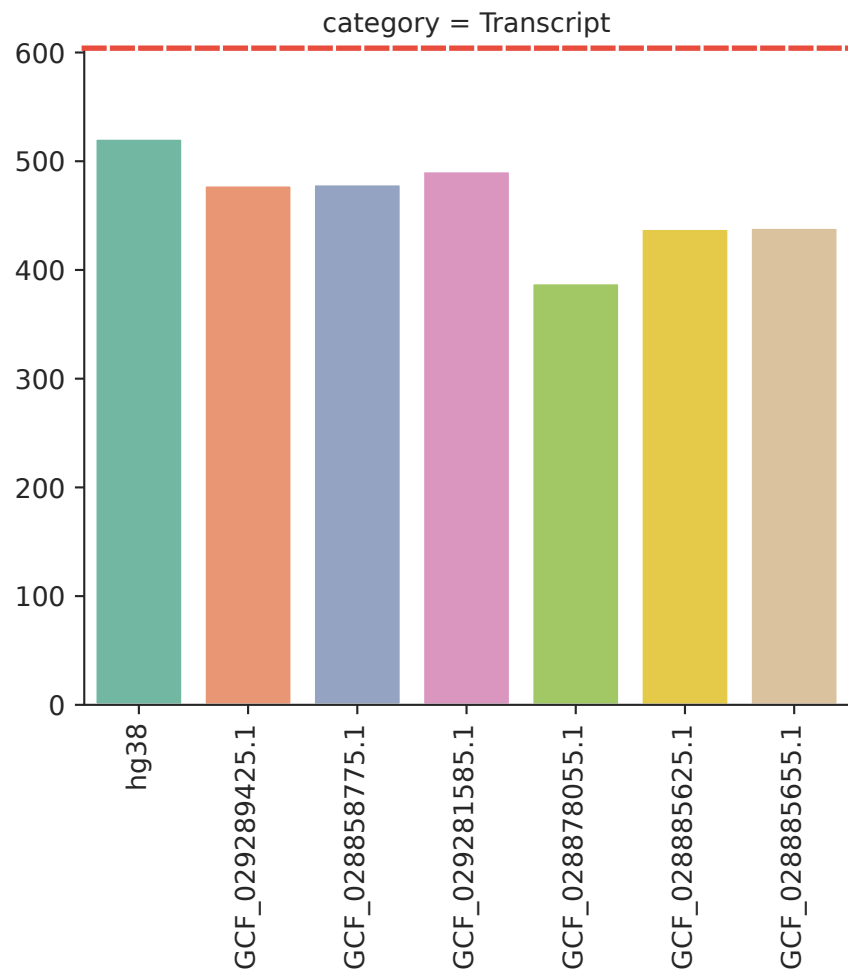
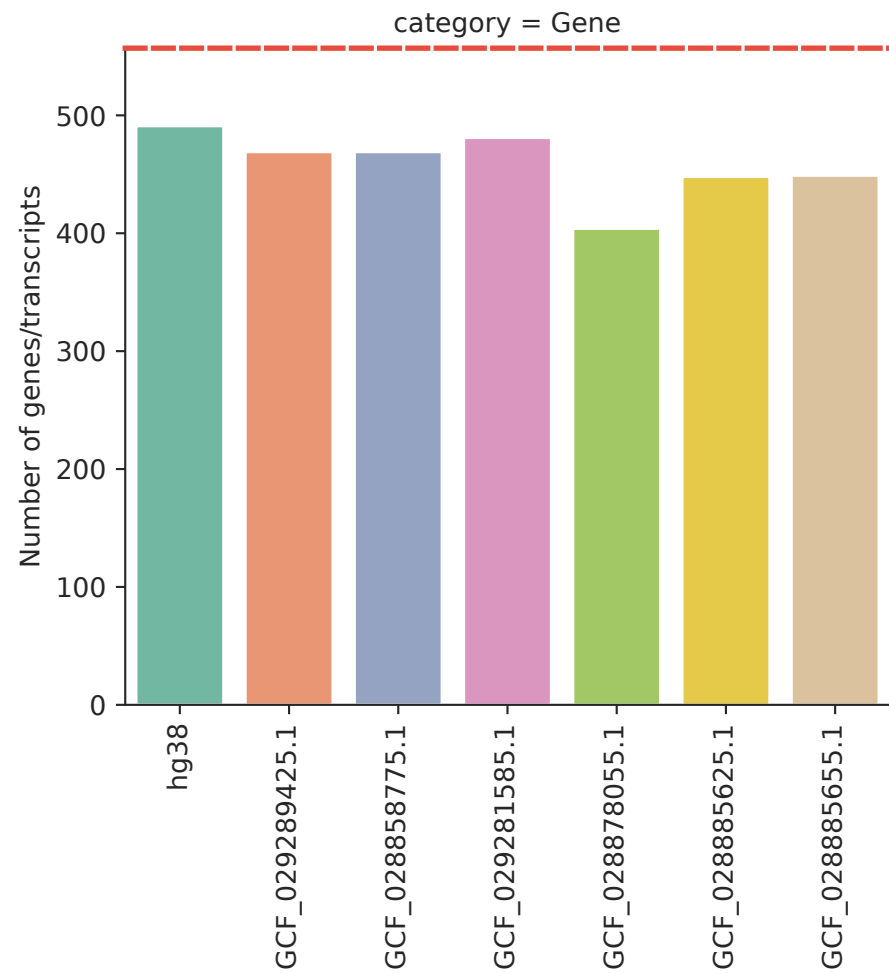
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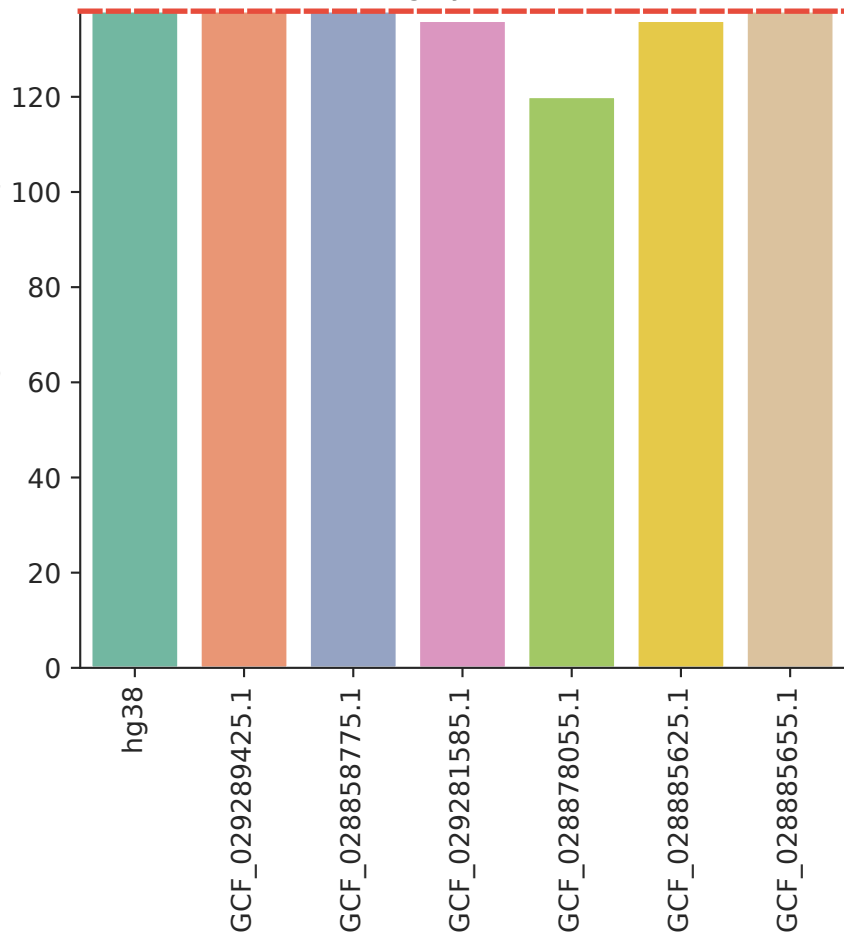


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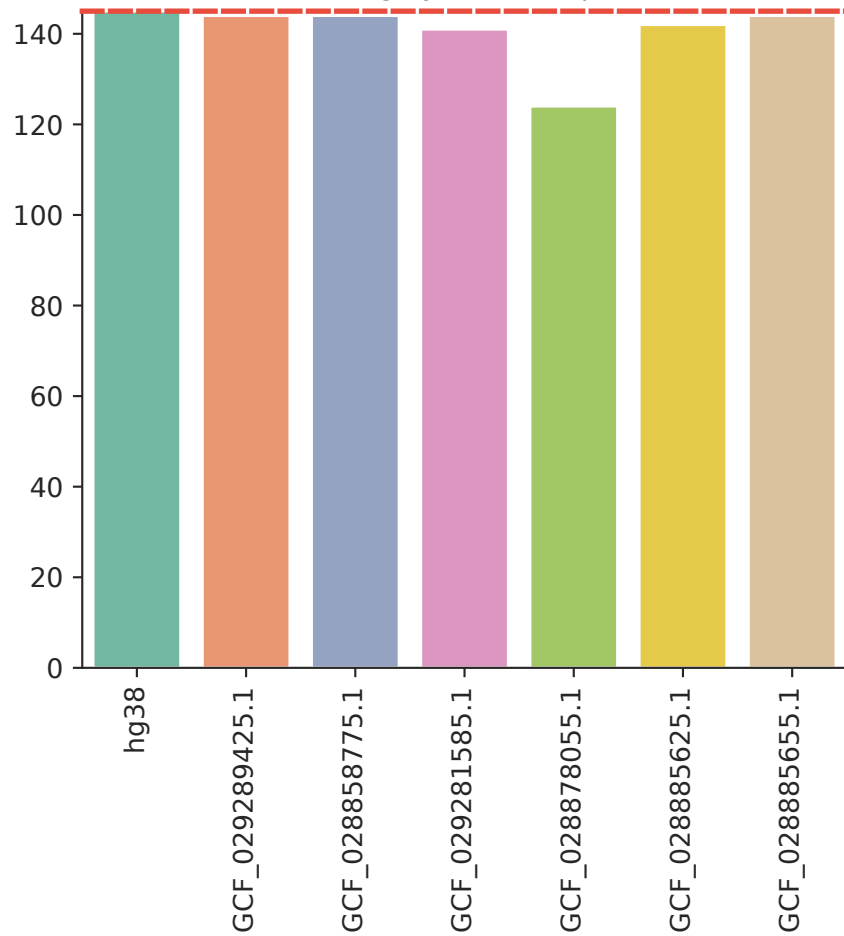


Number of comparative genes/transcripts present for biotype transcribed_unitary_pseudogene

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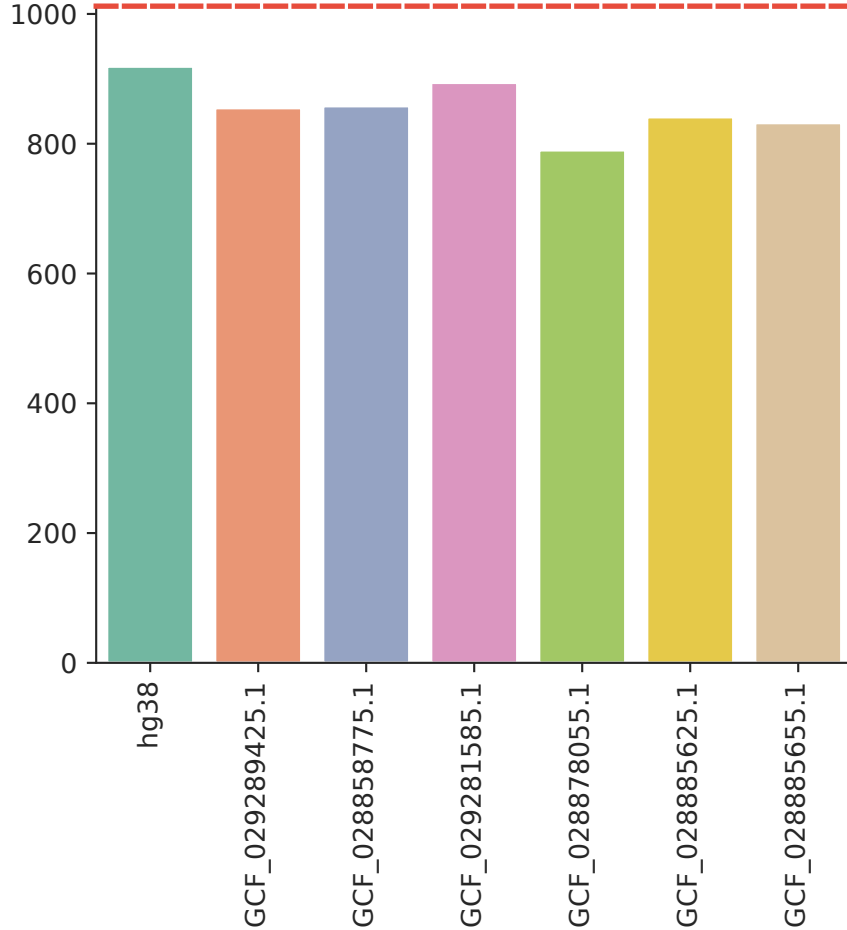


category = Transcript

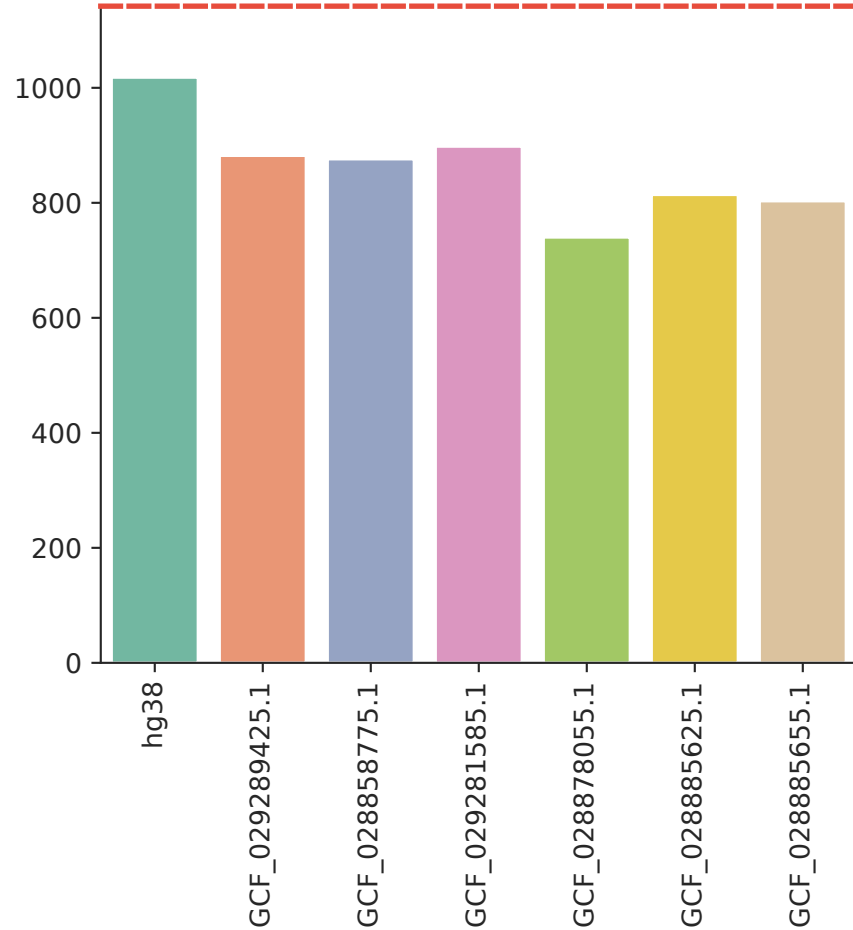


Number of comparative genes/transcripts present for biotype transcribed_unprocessed_pseudogene

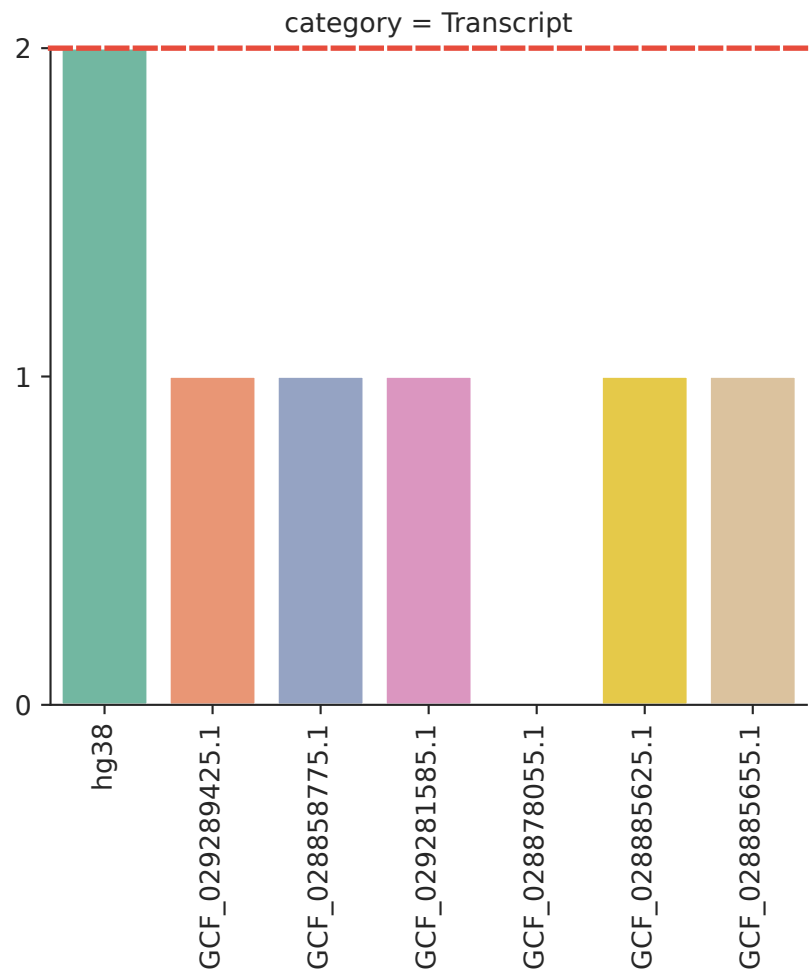
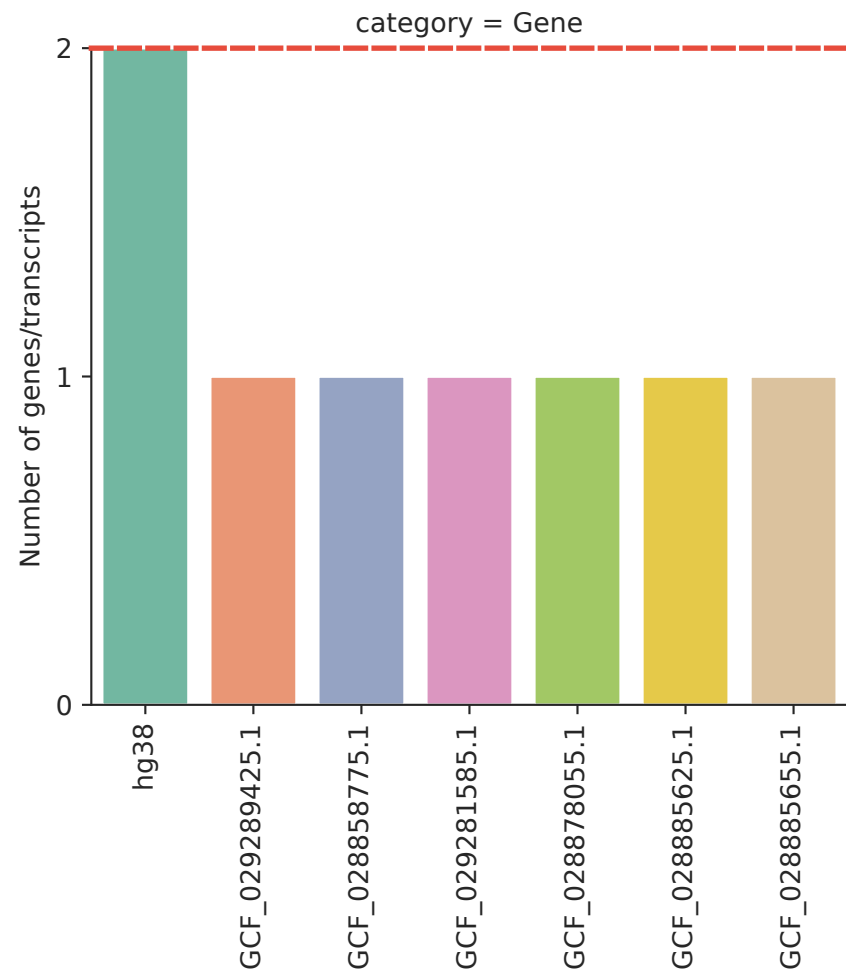
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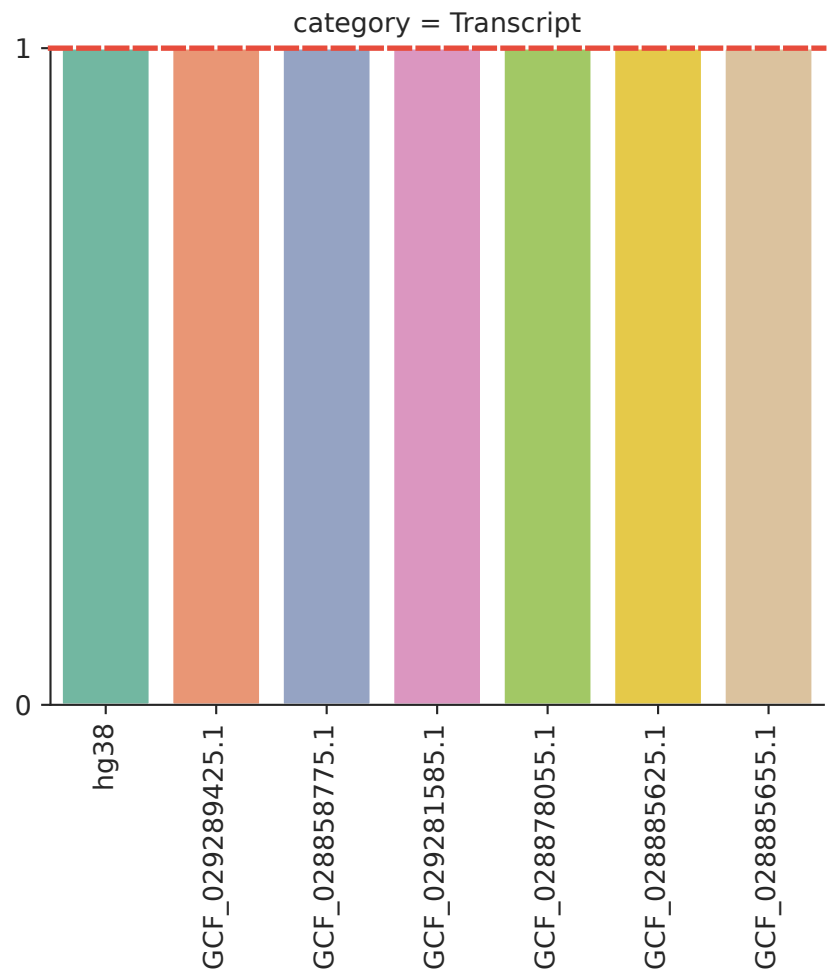
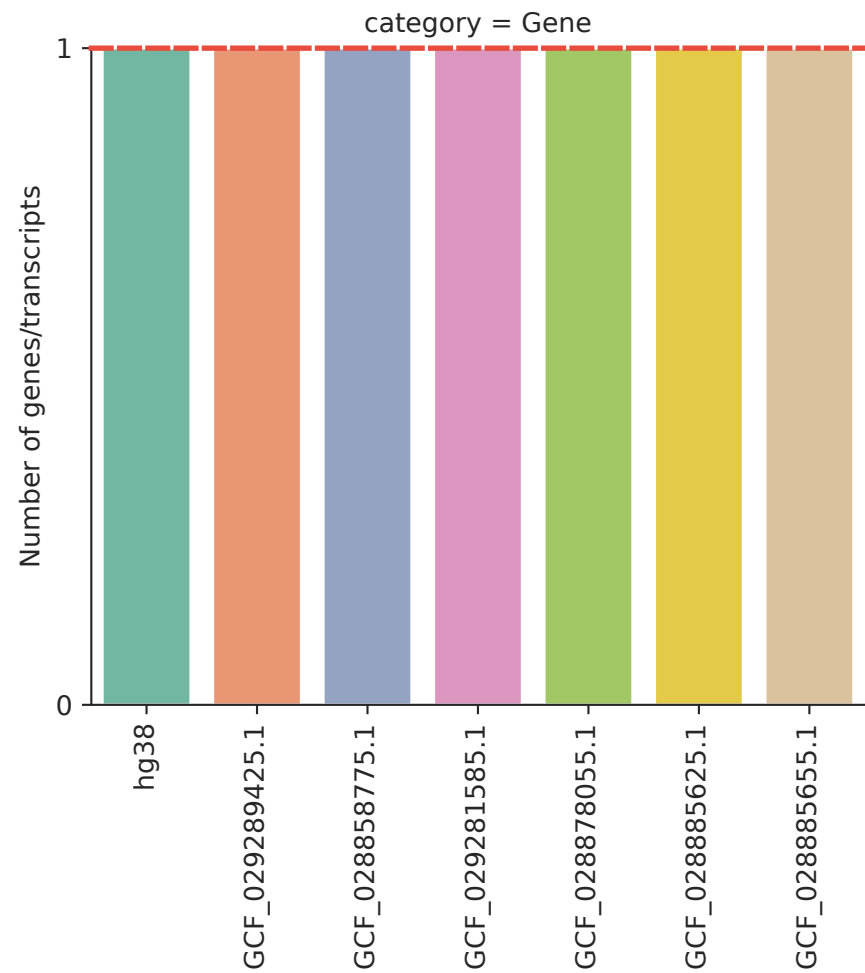
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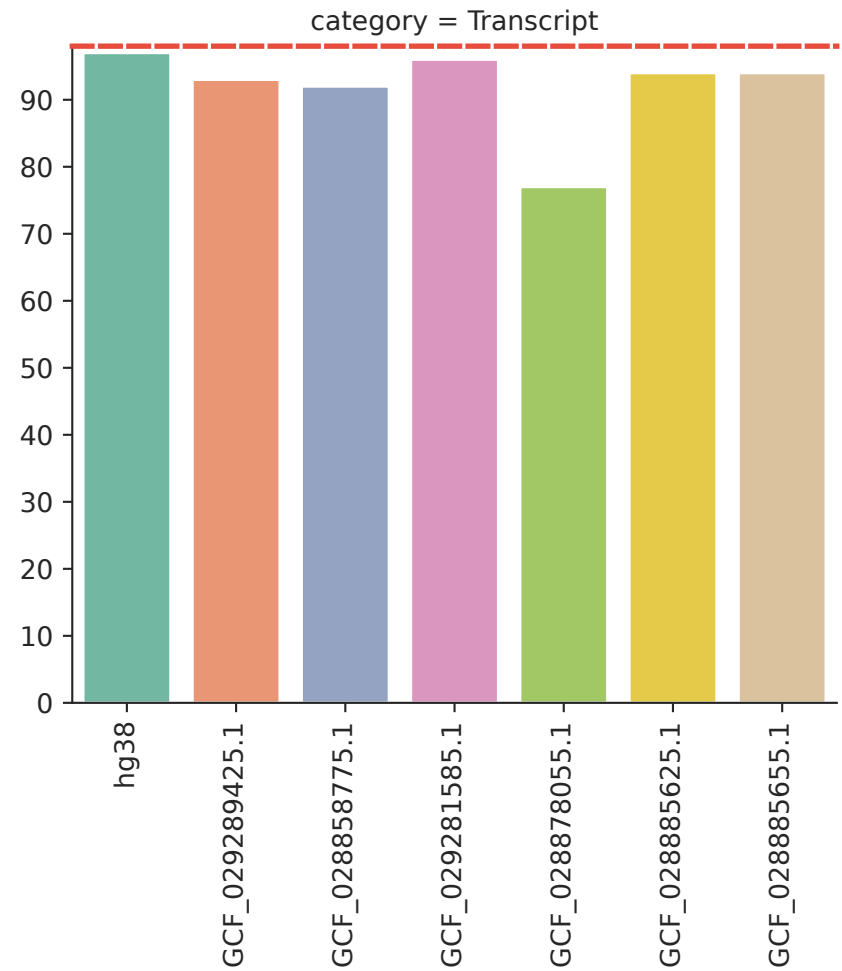
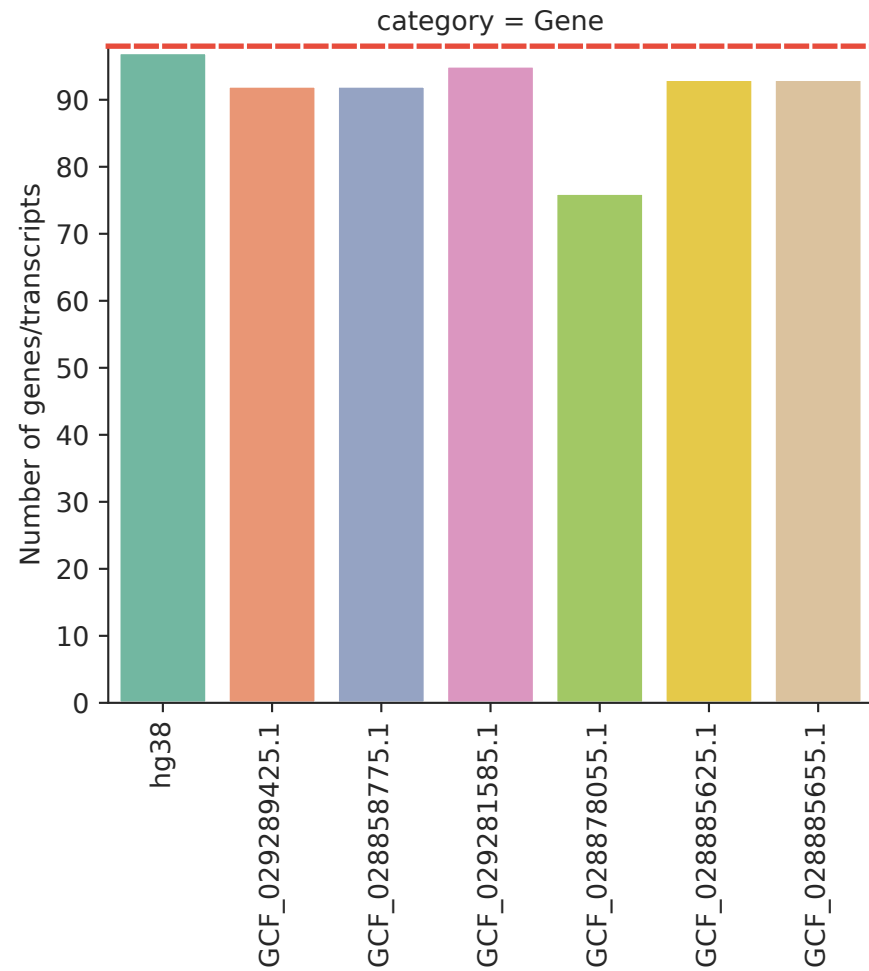
Number of comparative genes/transcripts present for biotype translated_pseudogene



Number of comparative genes/transcripts present for biotype translated_unprocessed_pseudogene

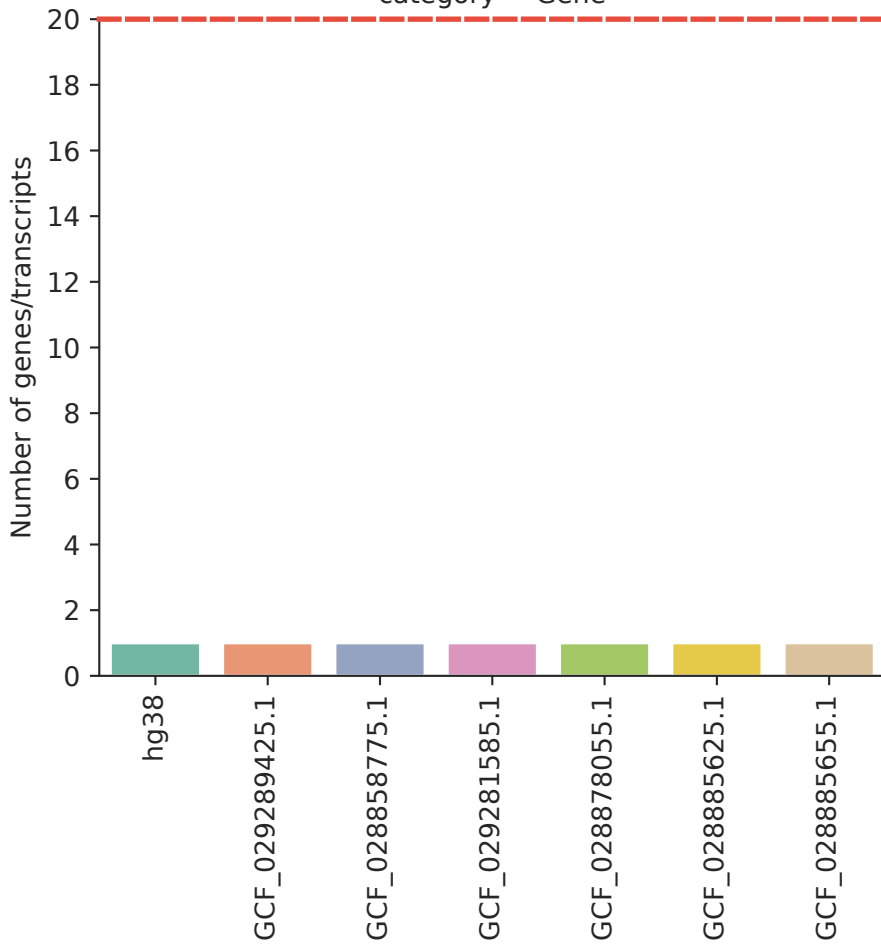


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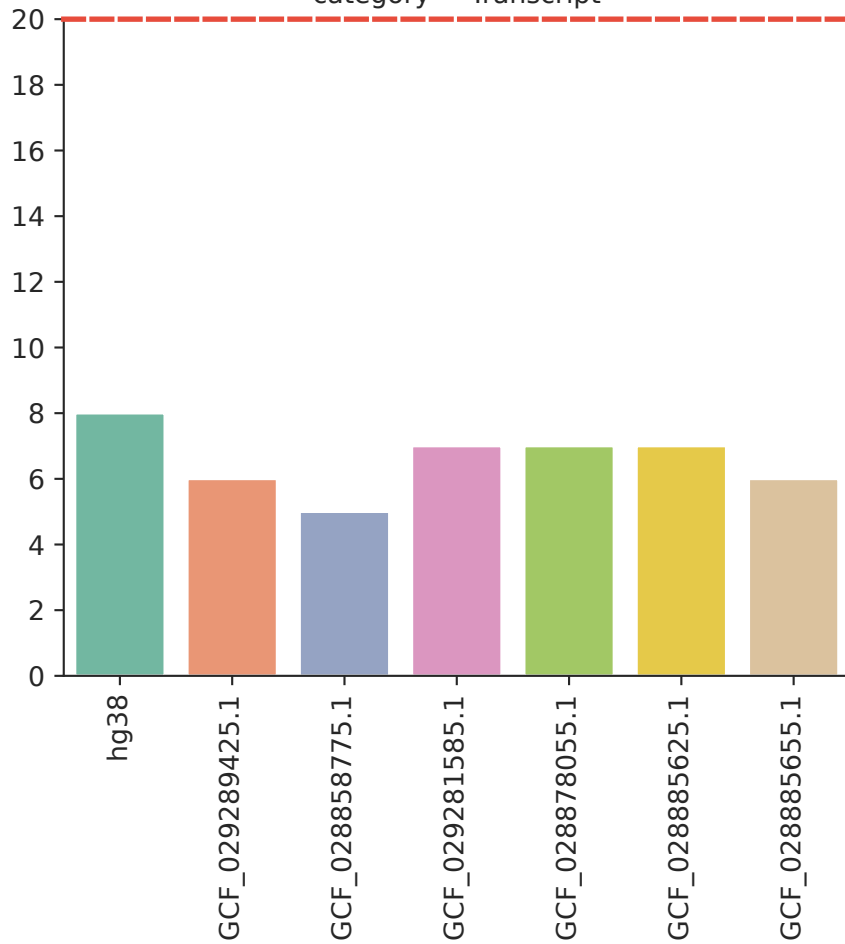


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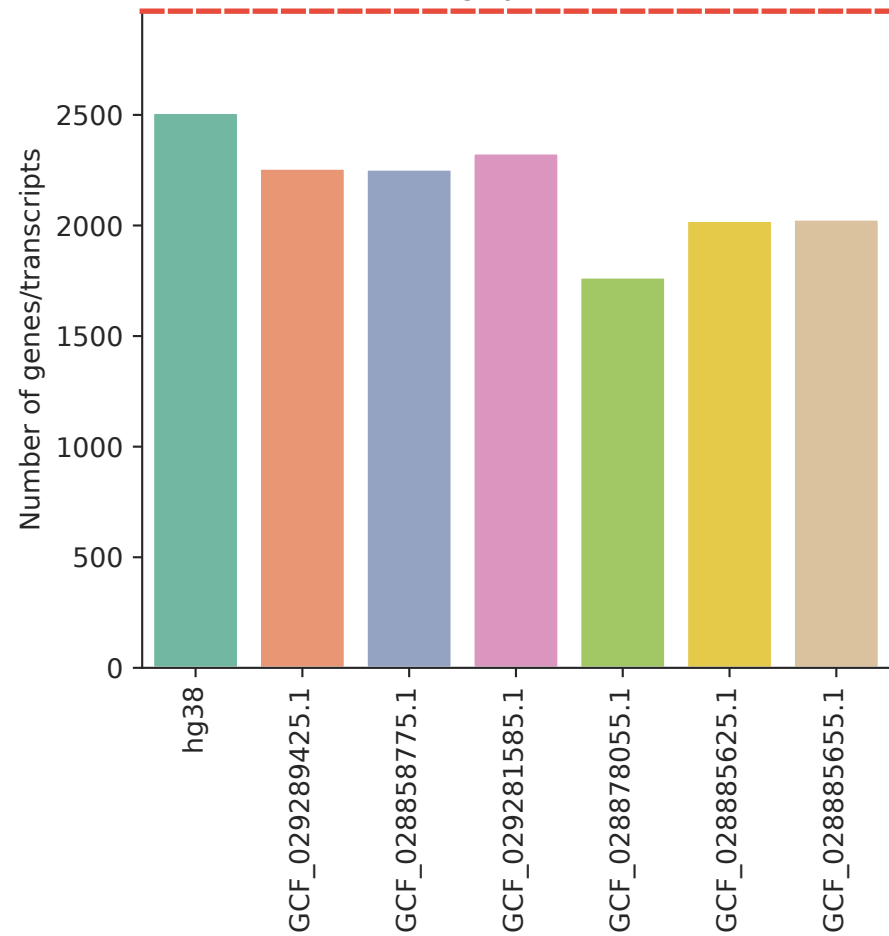


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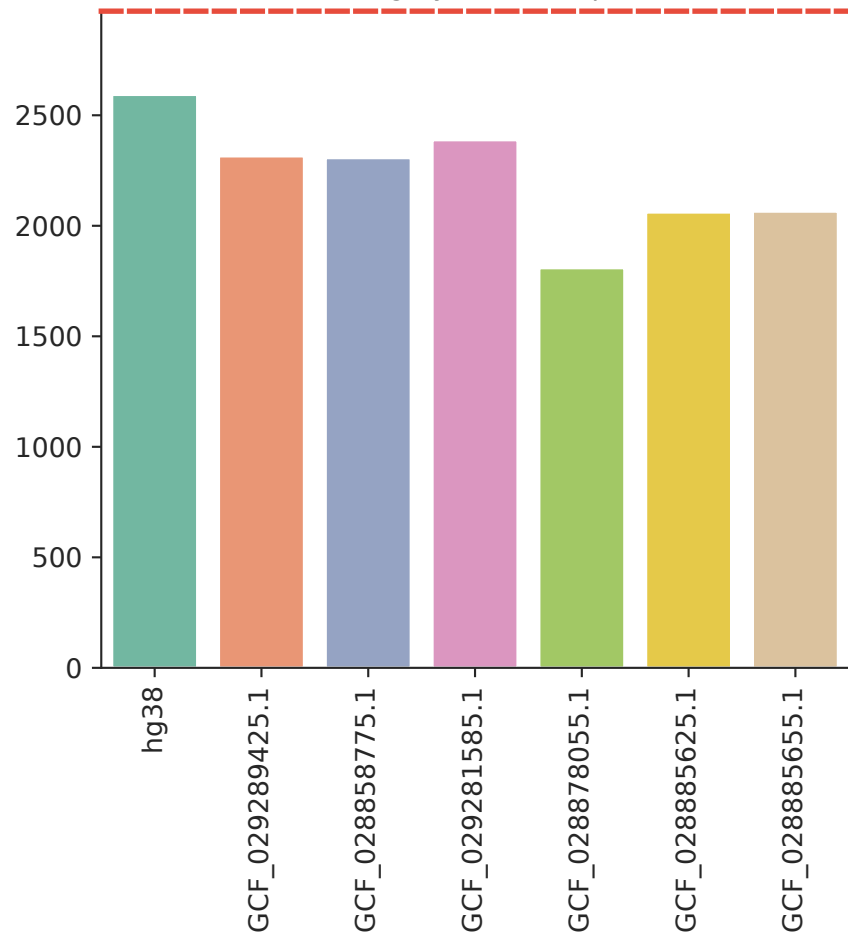


Number of comparative genes/transcripts present for biotype unprocessed_pseudogene

category = Gene



category = Transcript



Number of comparative genes/transcripts present for biotype vault_RNA

