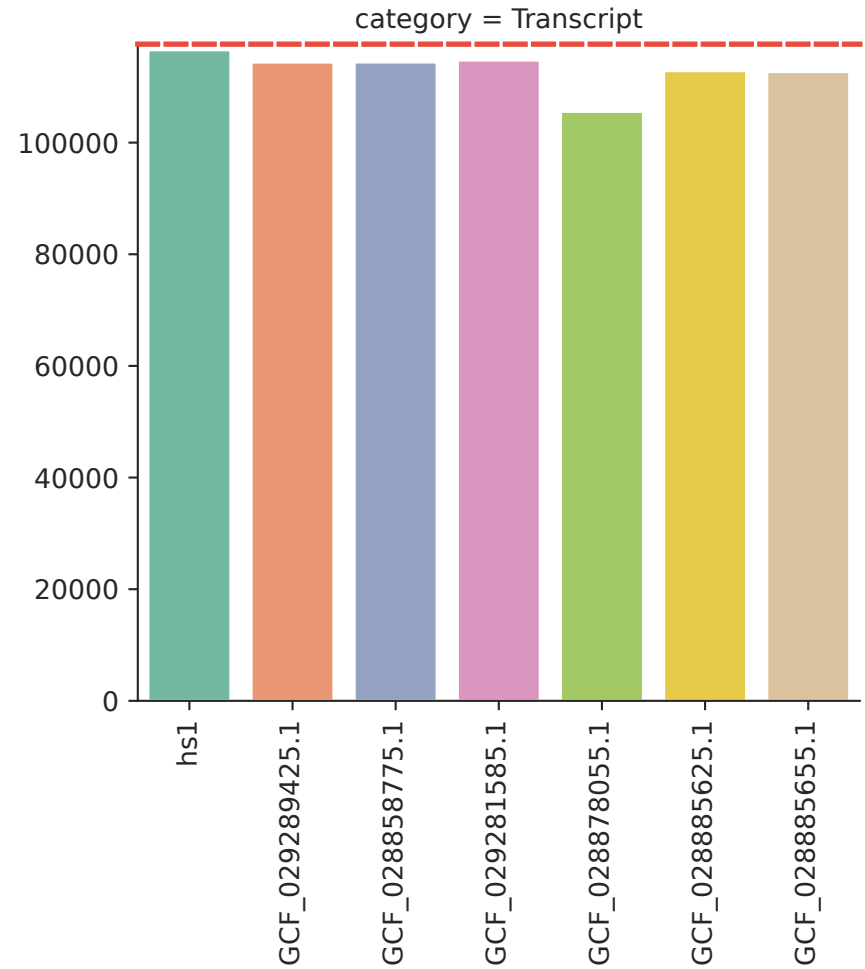
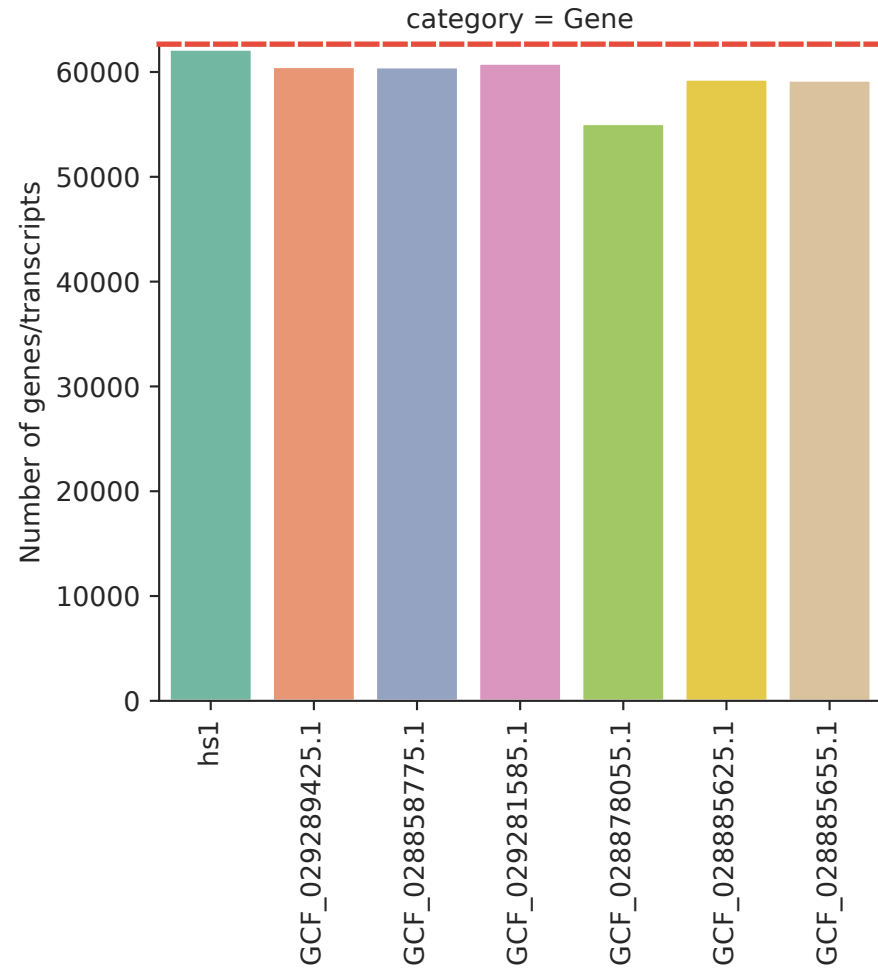
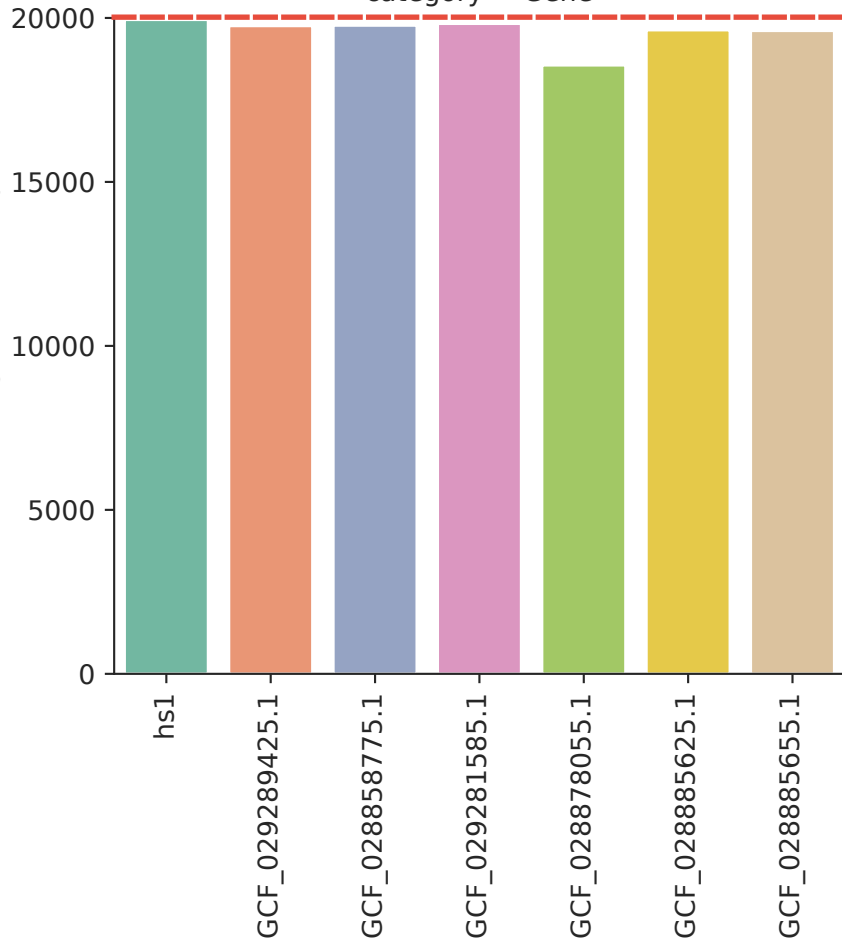


Number of comparative genes/transcripts present

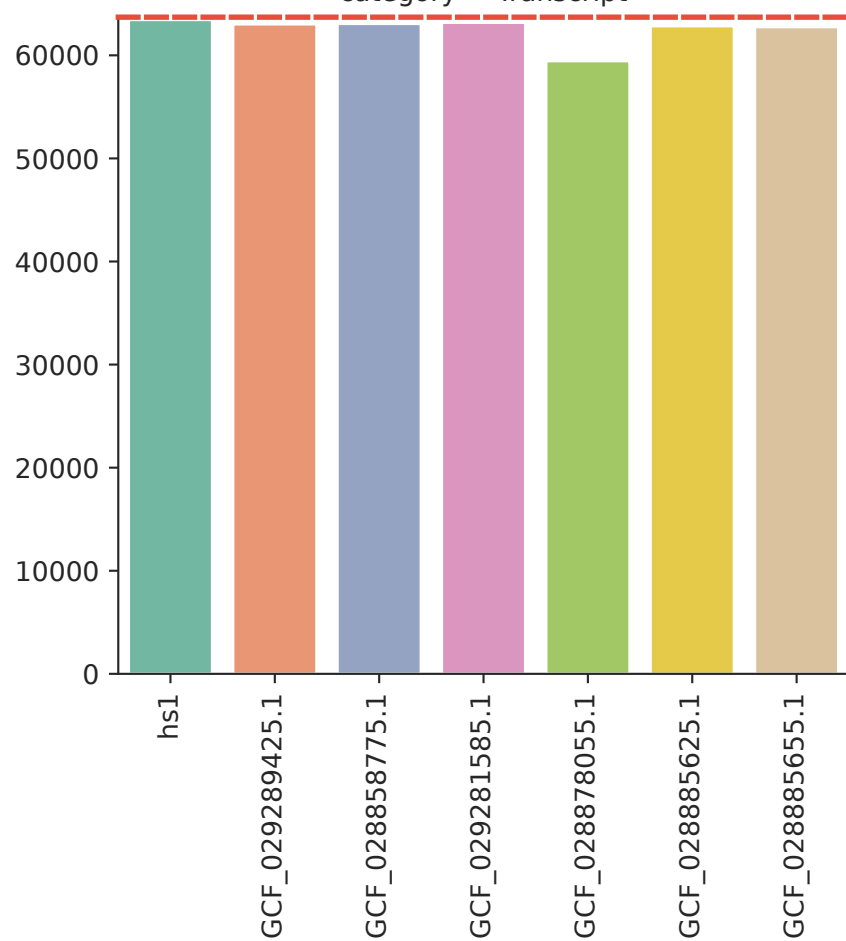


Number of comparative genes/transcripts present for biotype protein_coding

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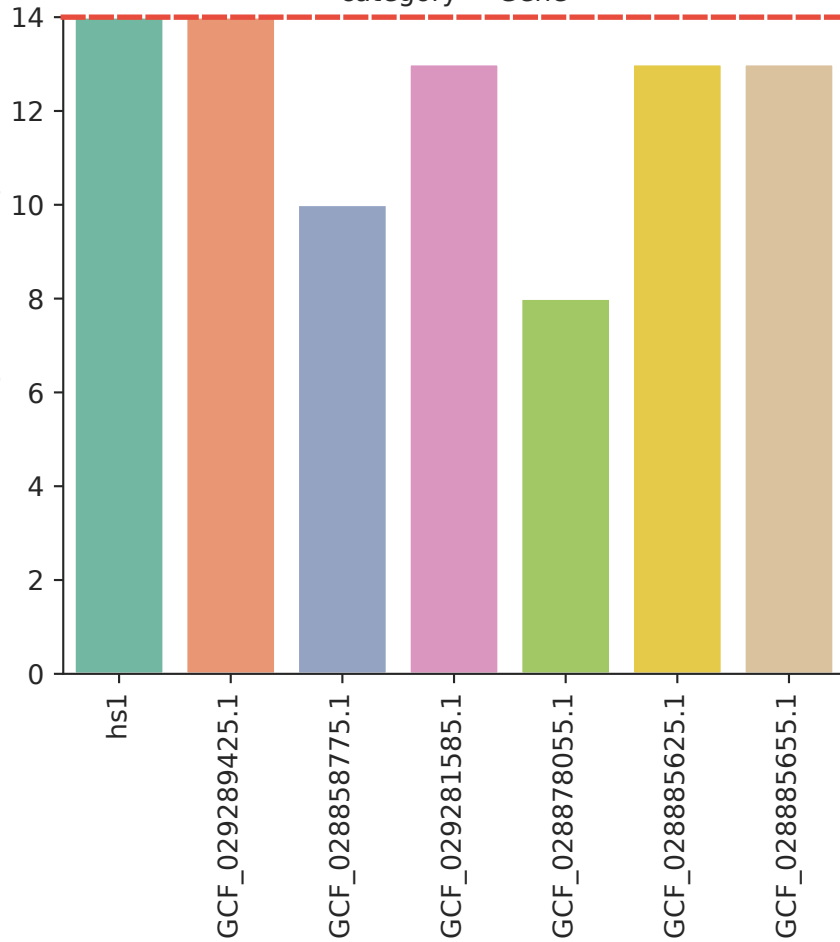


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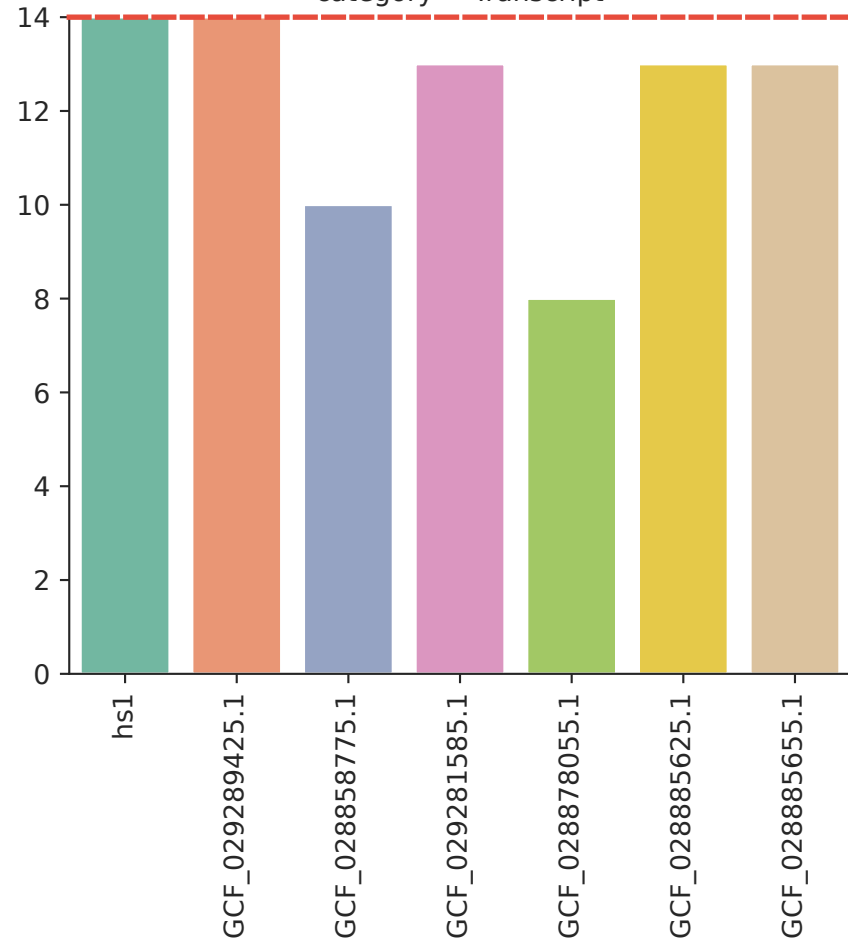


Number of comparative genes/transcripts present for biotype IG_C_gene

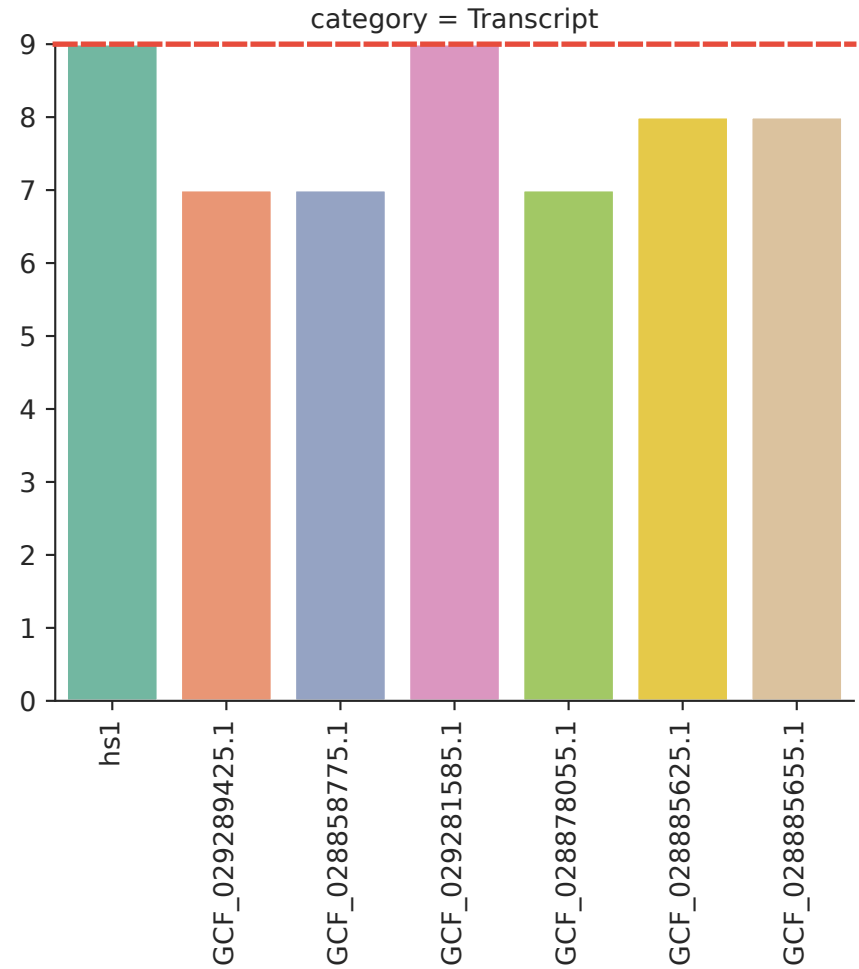
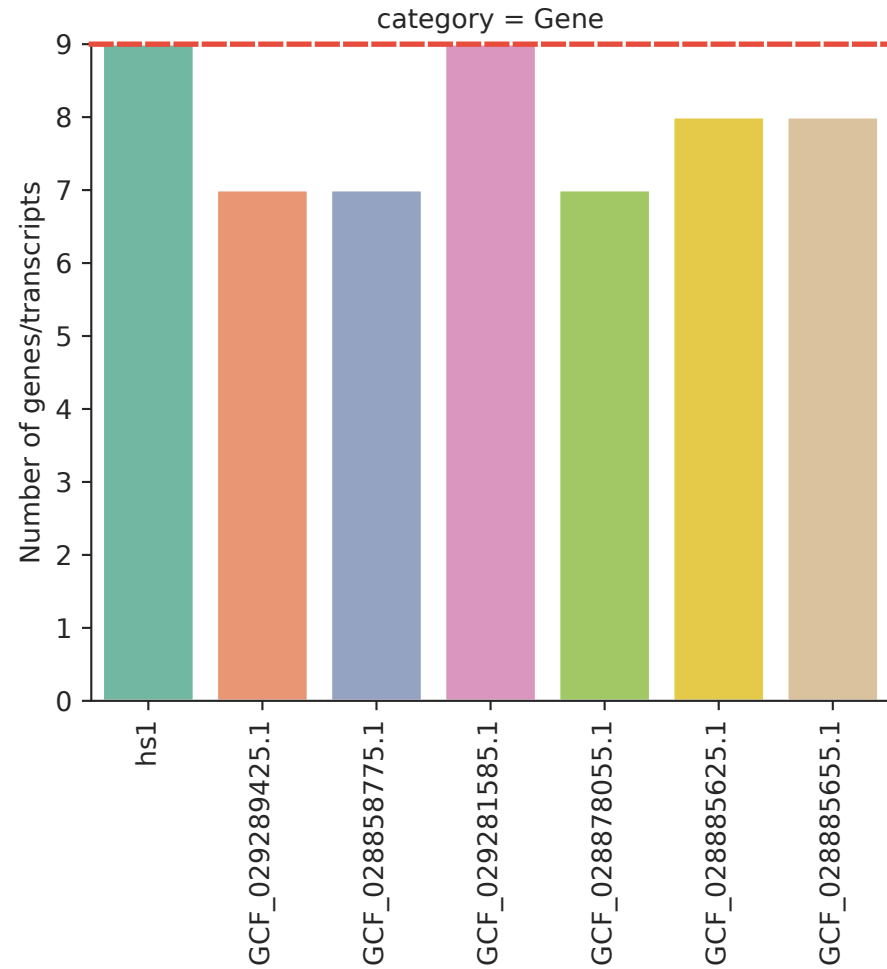
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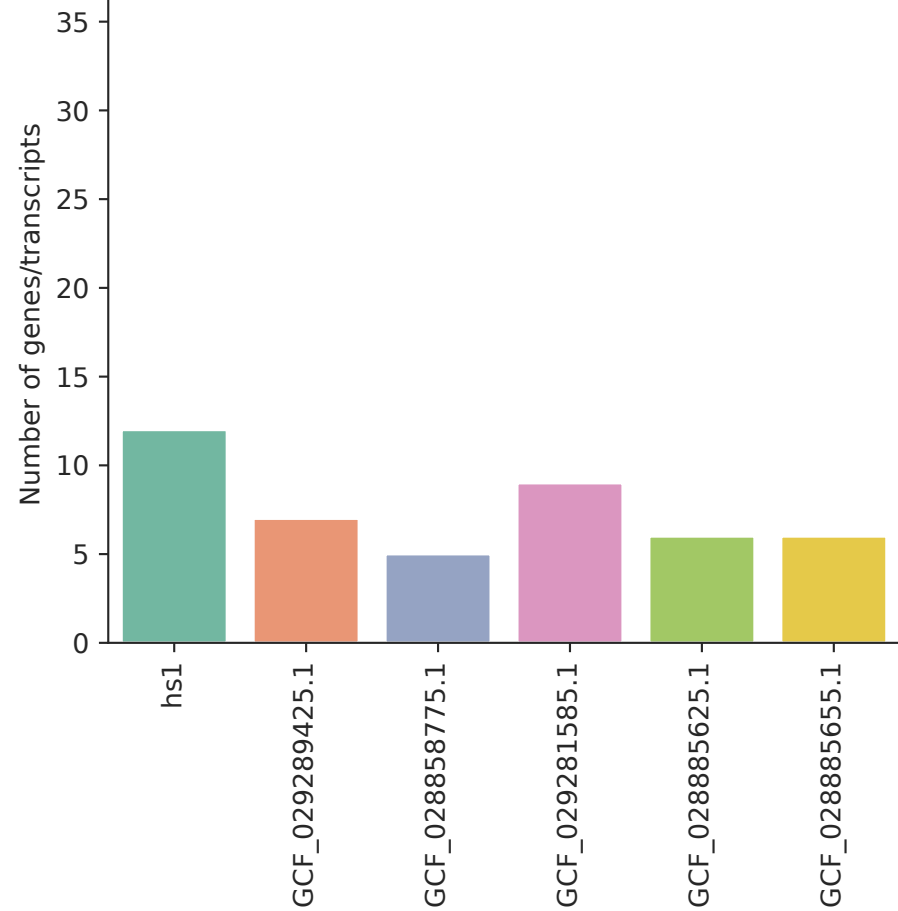


Number of comparative genes/transcripts present for biotype IG_C_pseudogene

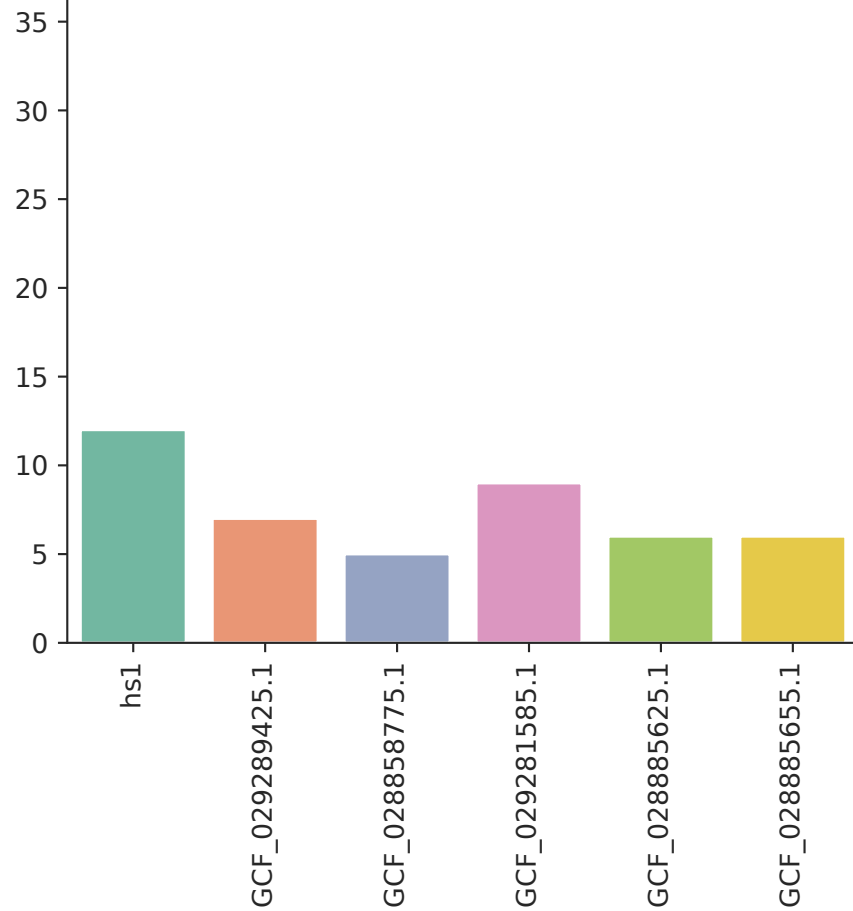


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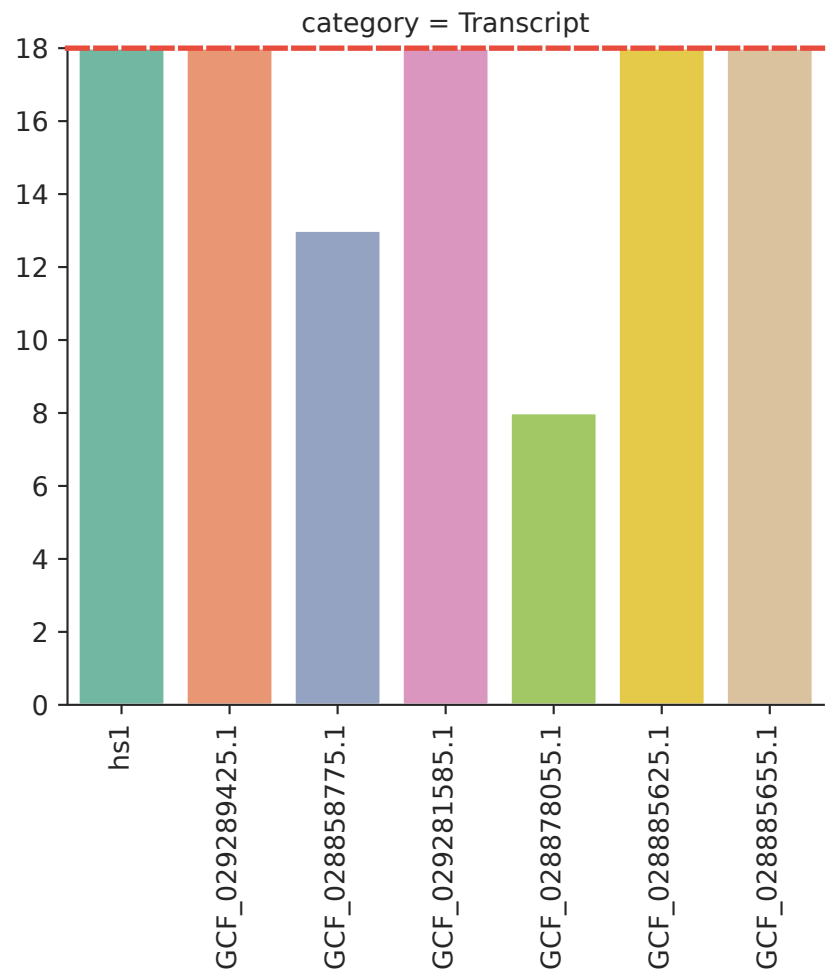
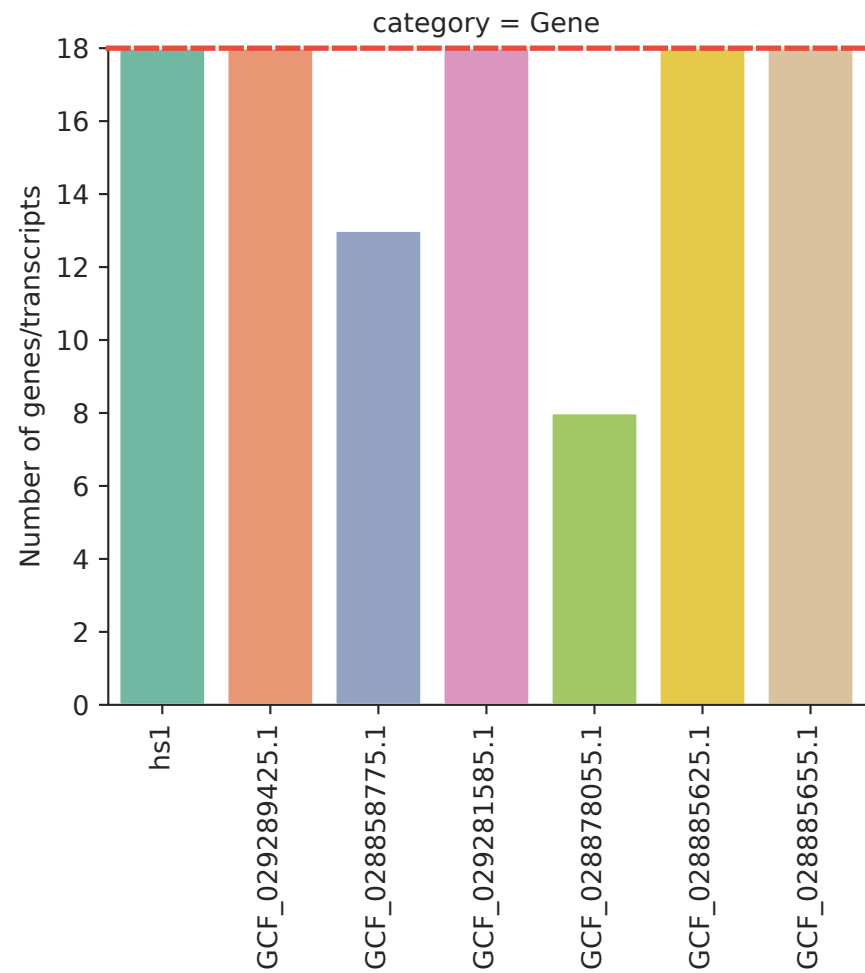
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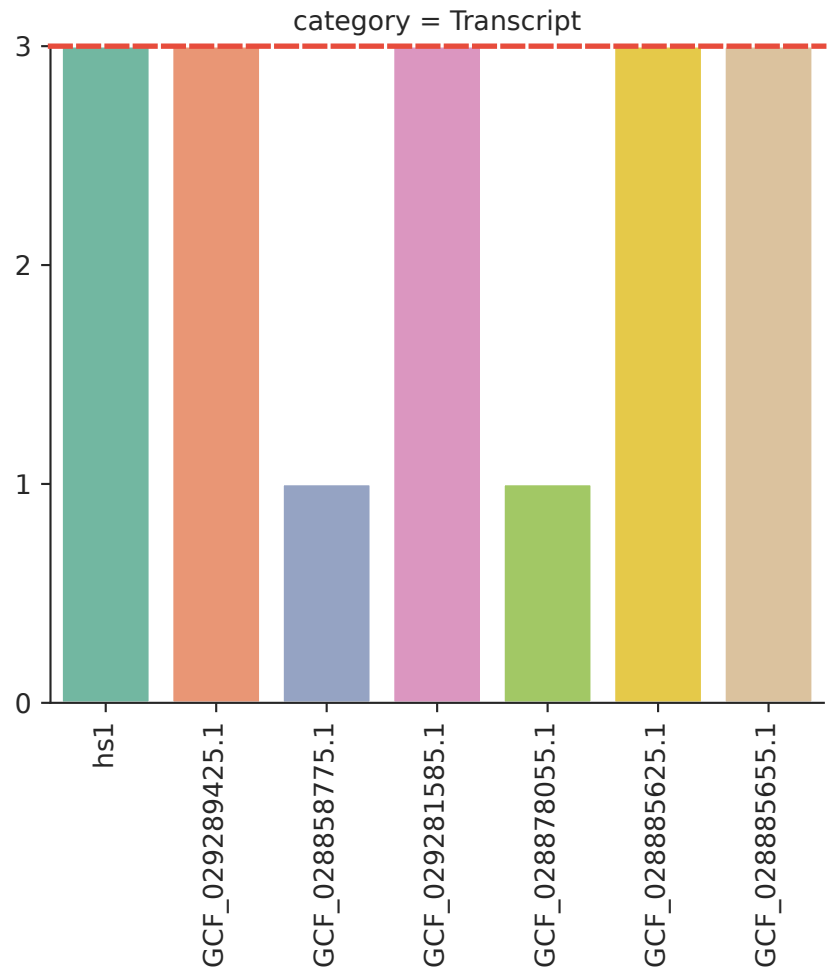
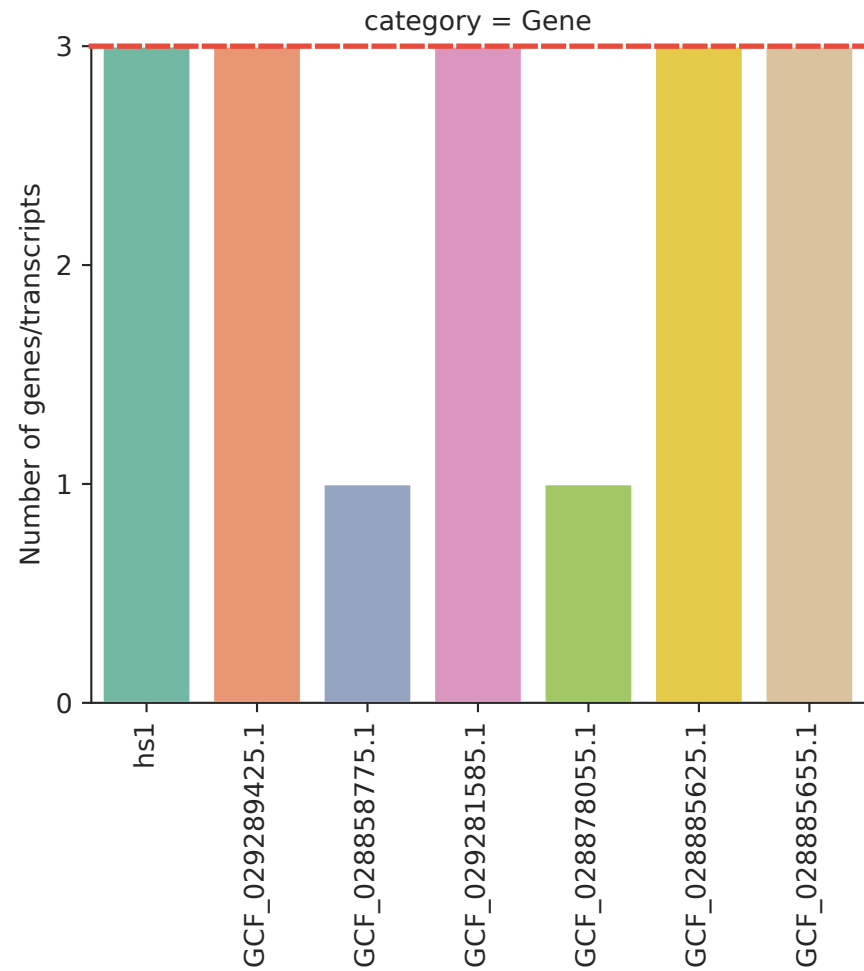
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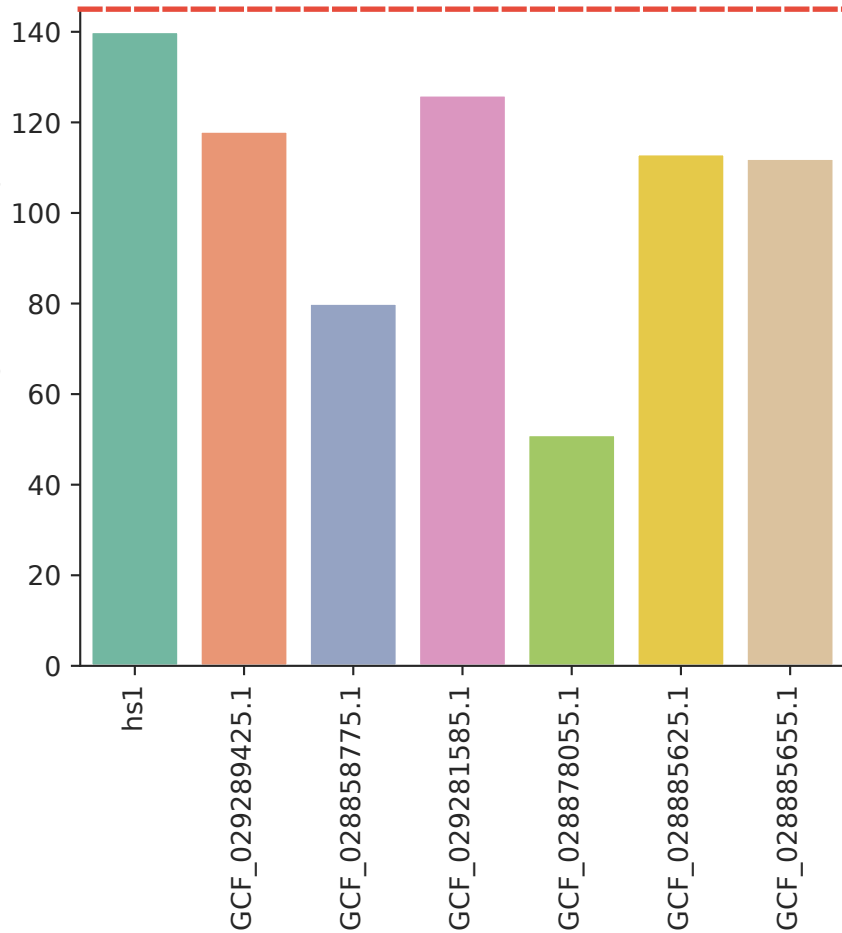


Number of comparative genes/transcripts present for biotype IG_J_pseudogene

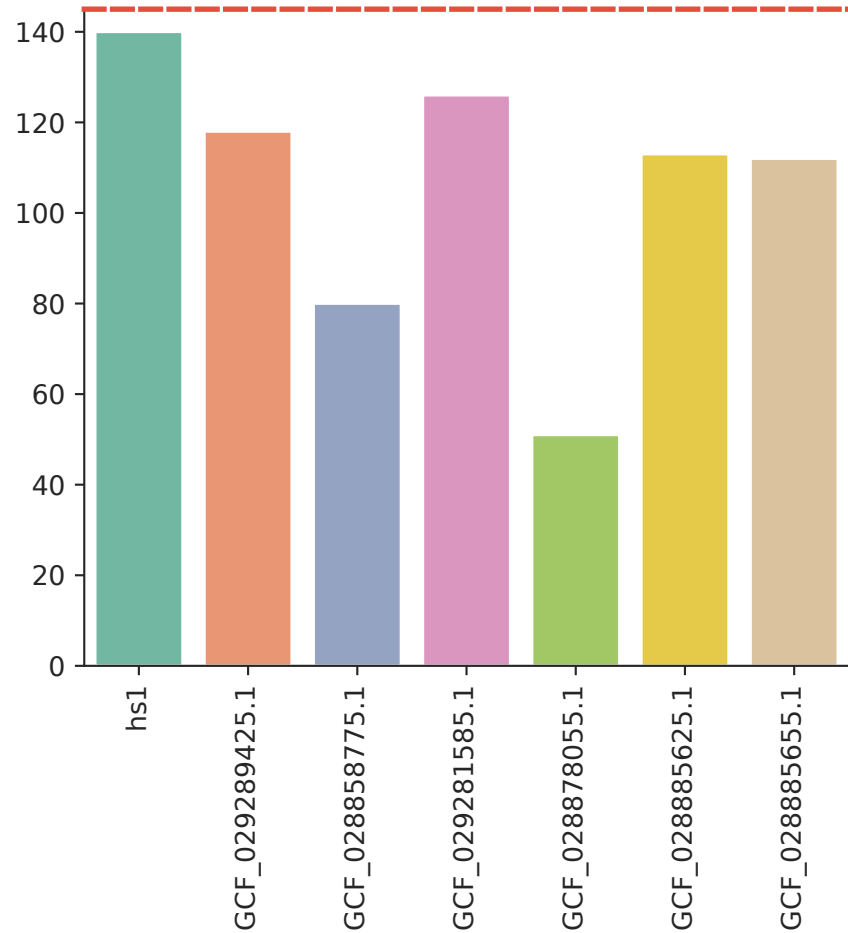


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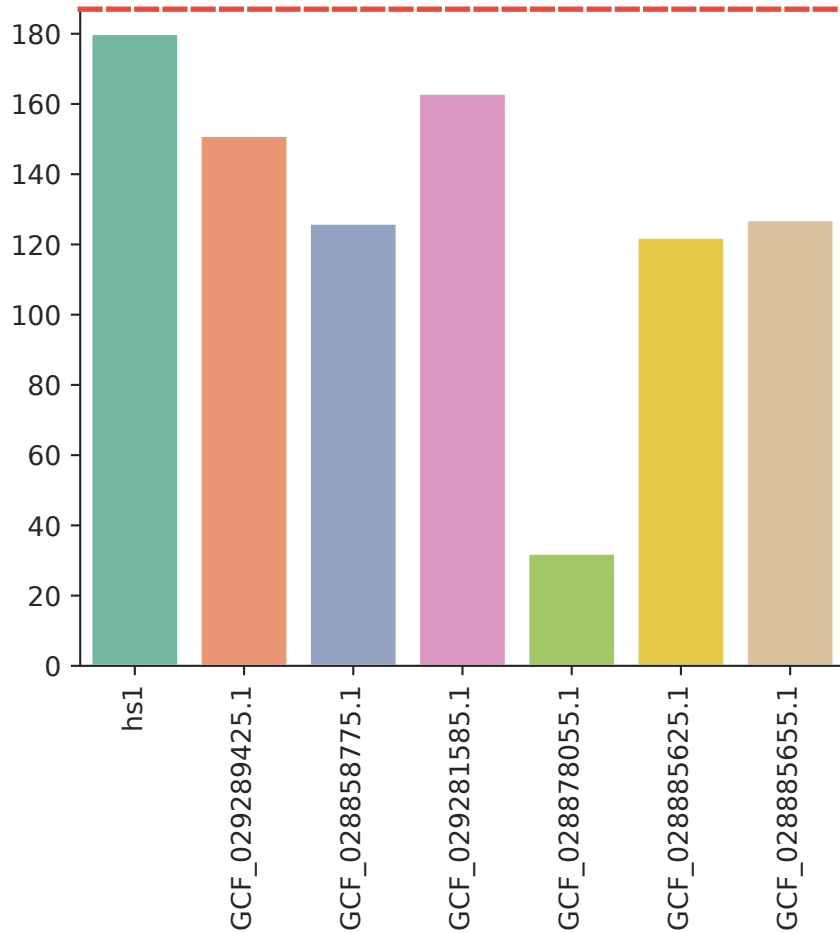


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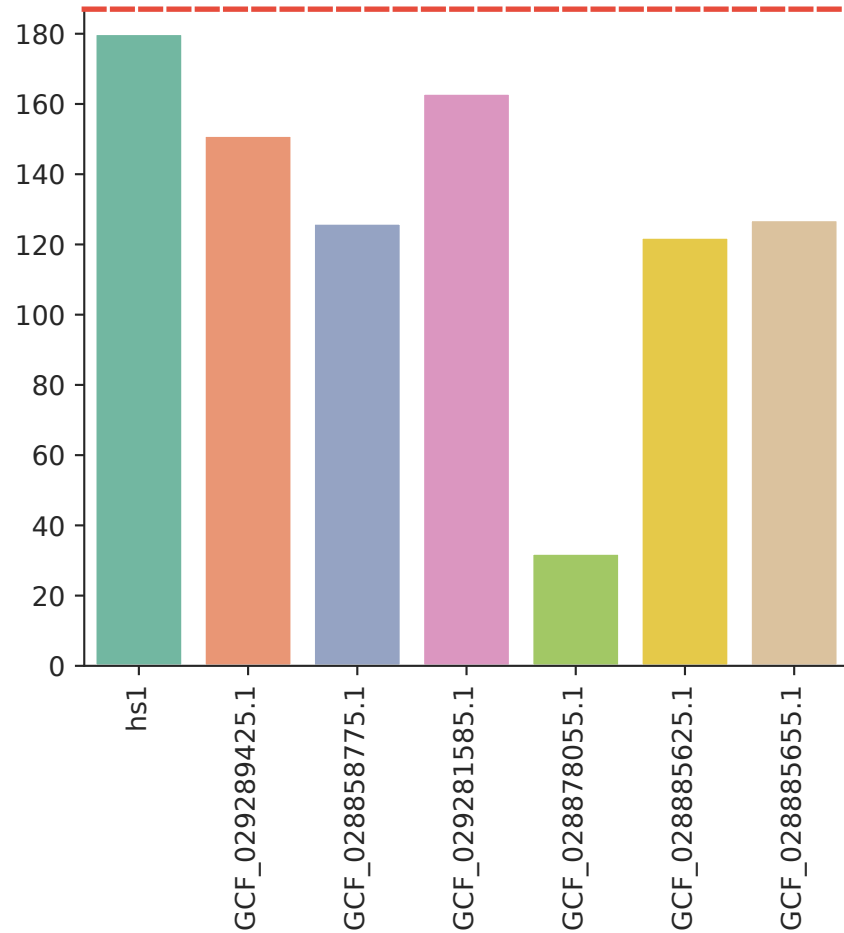


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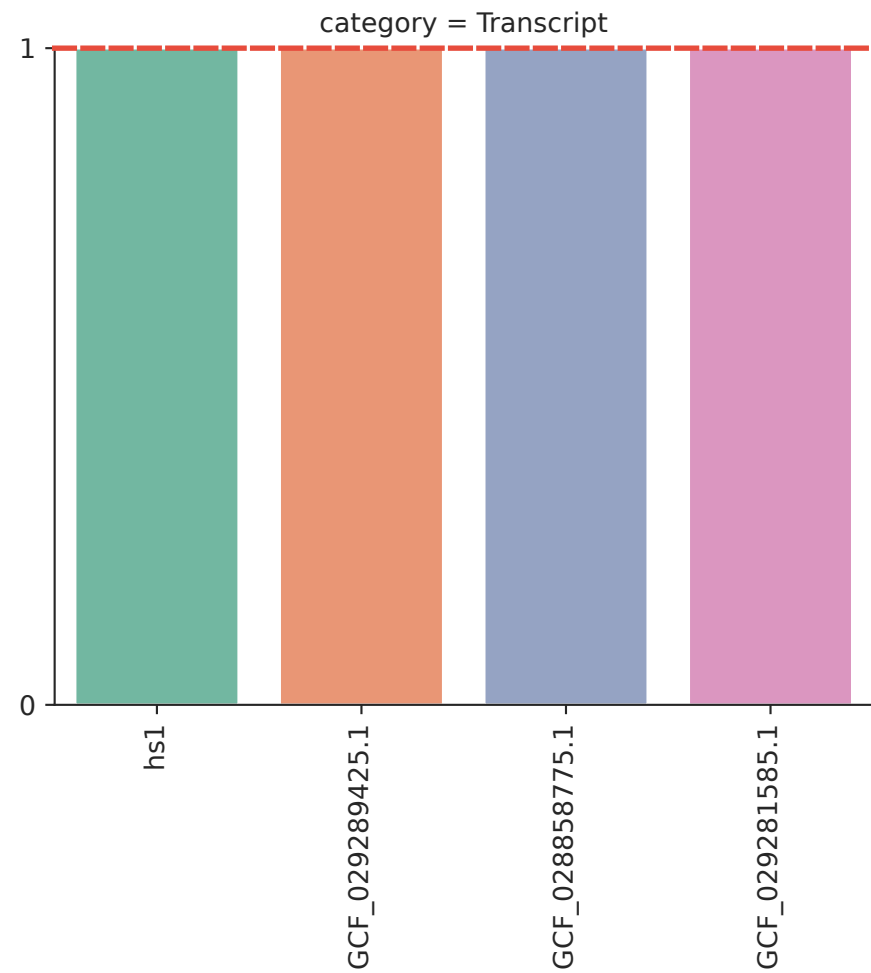
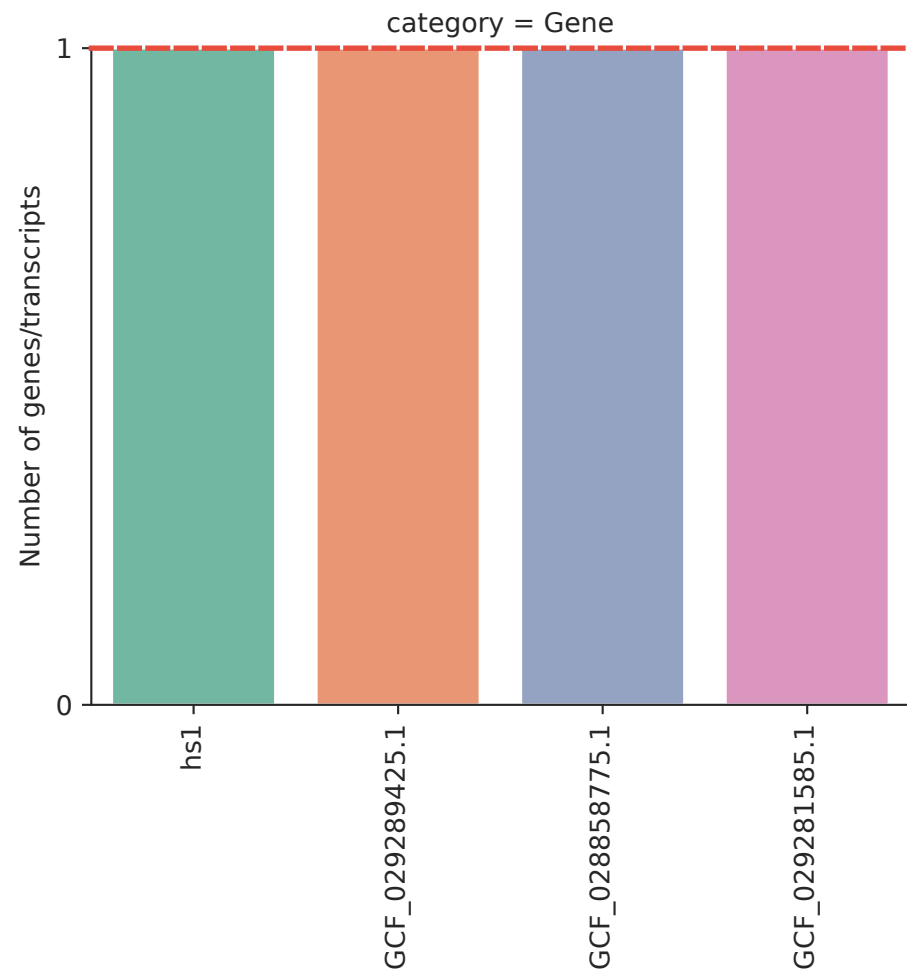
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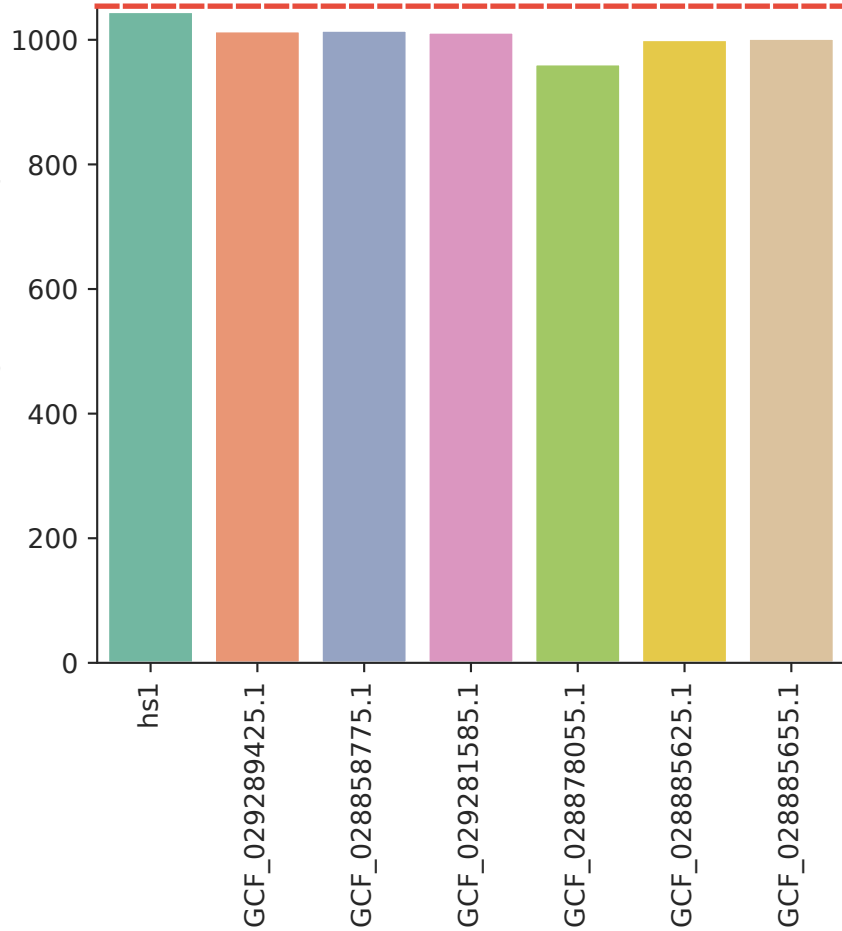


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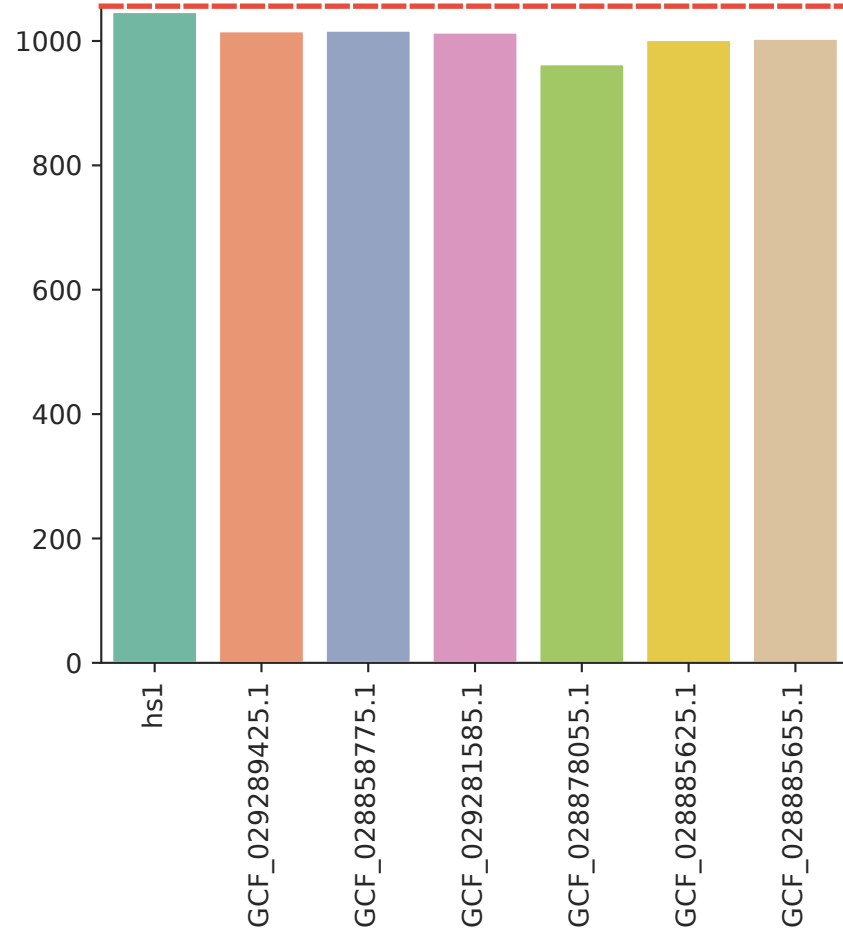


Number of comparative genes/transcripts present for biotype TEC

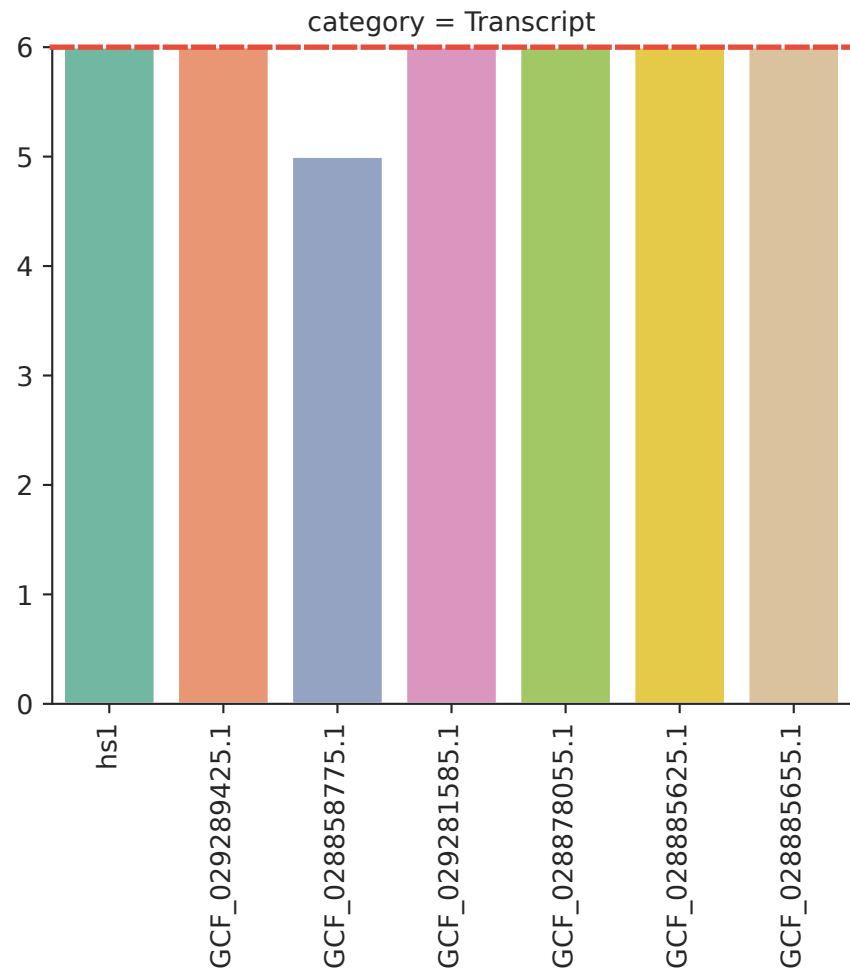
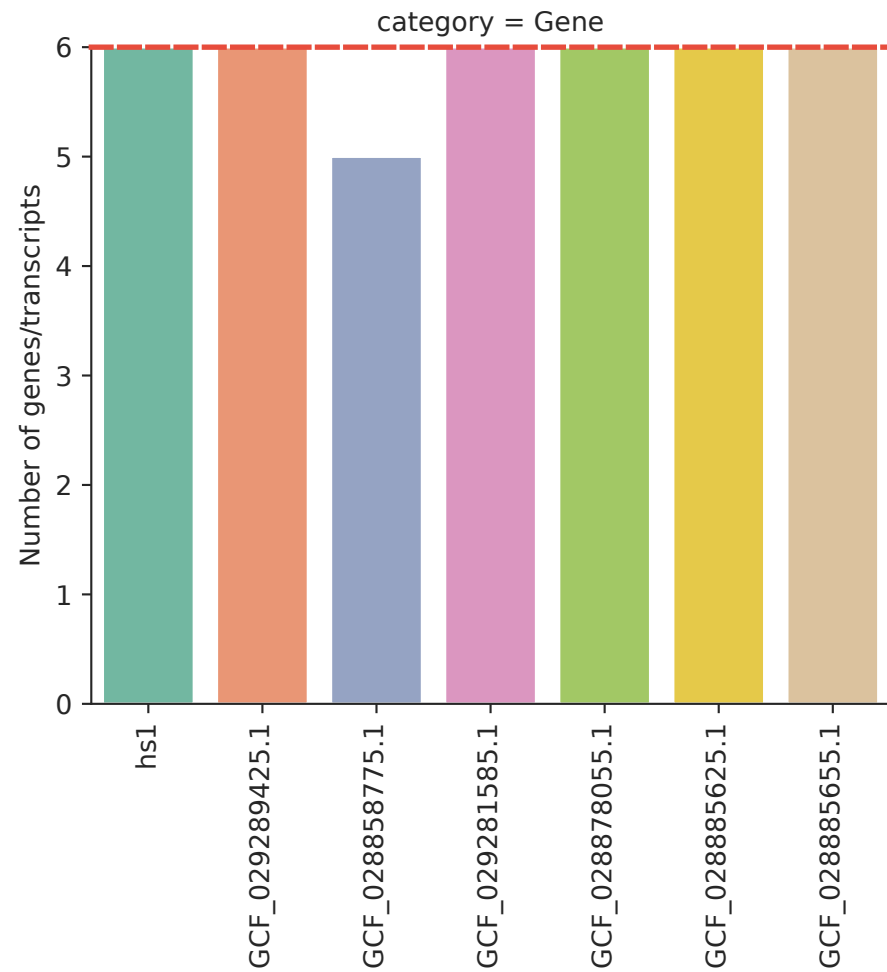
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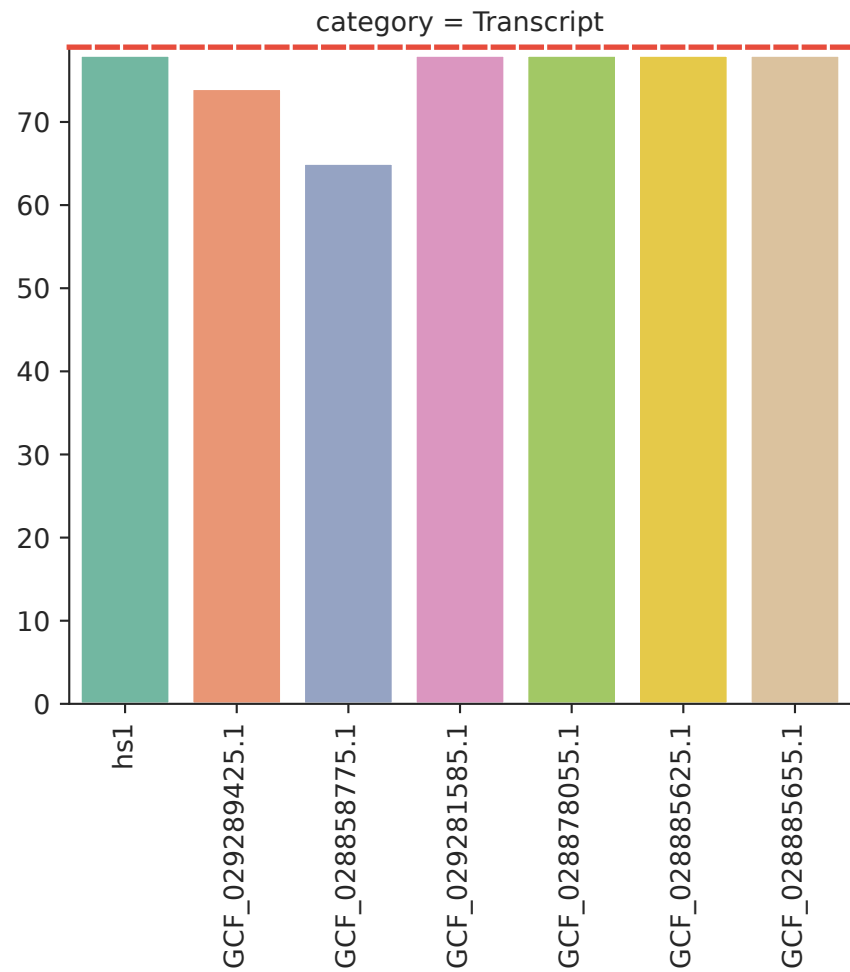
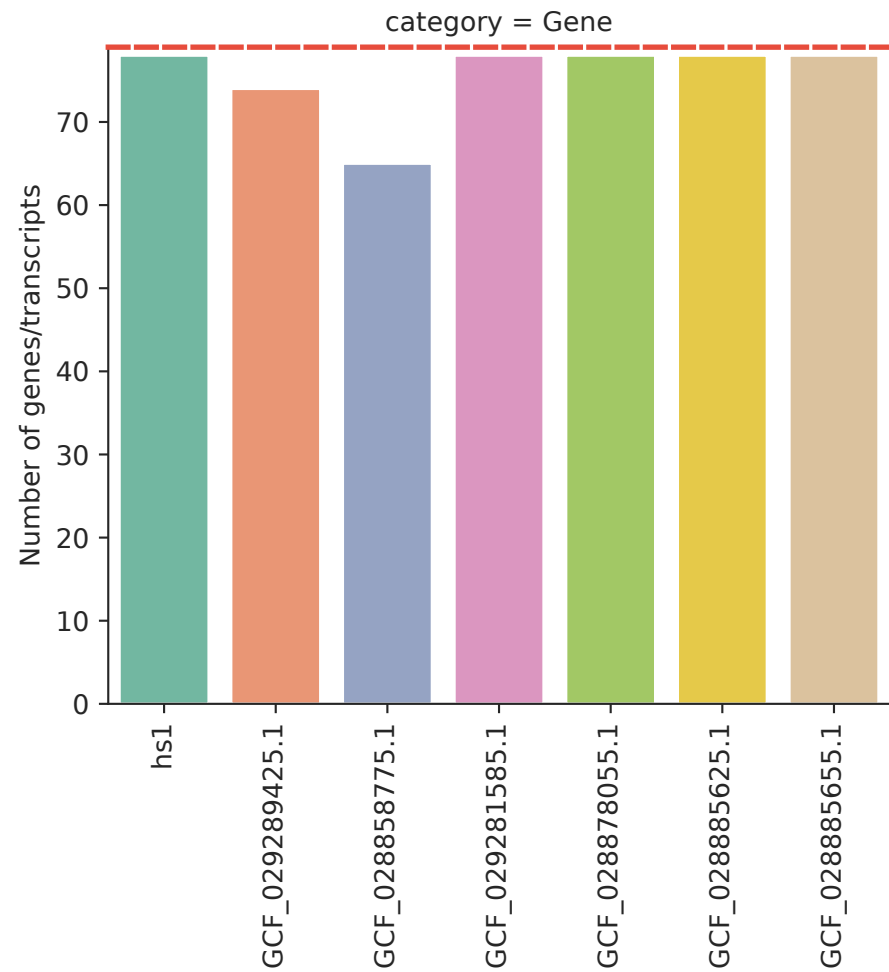
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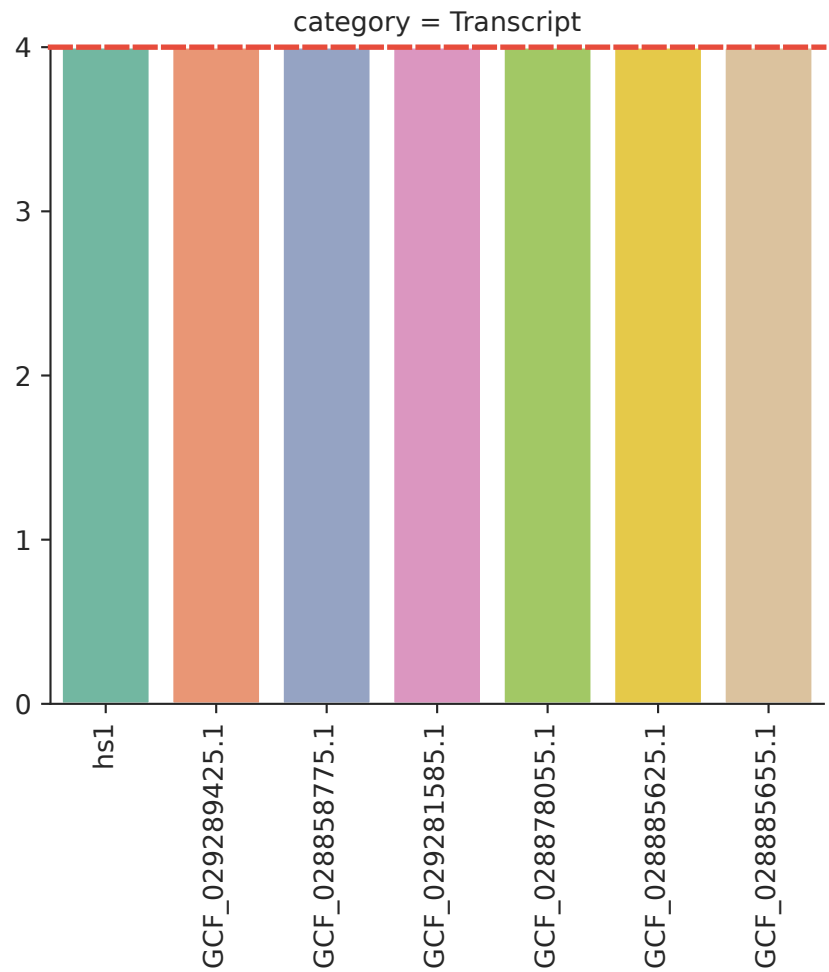
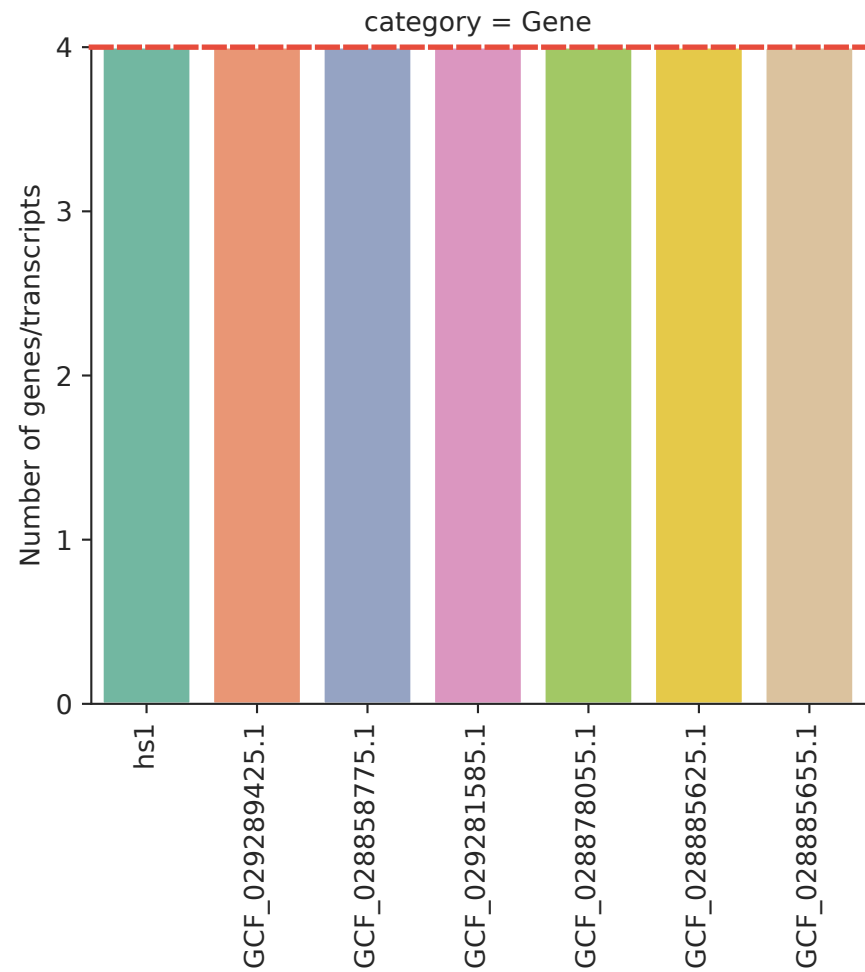
Number of comparative genes/transcripts present for biotype TR_C_gene



Number of comparative genes/transcripts present for biotype TR_J_gene

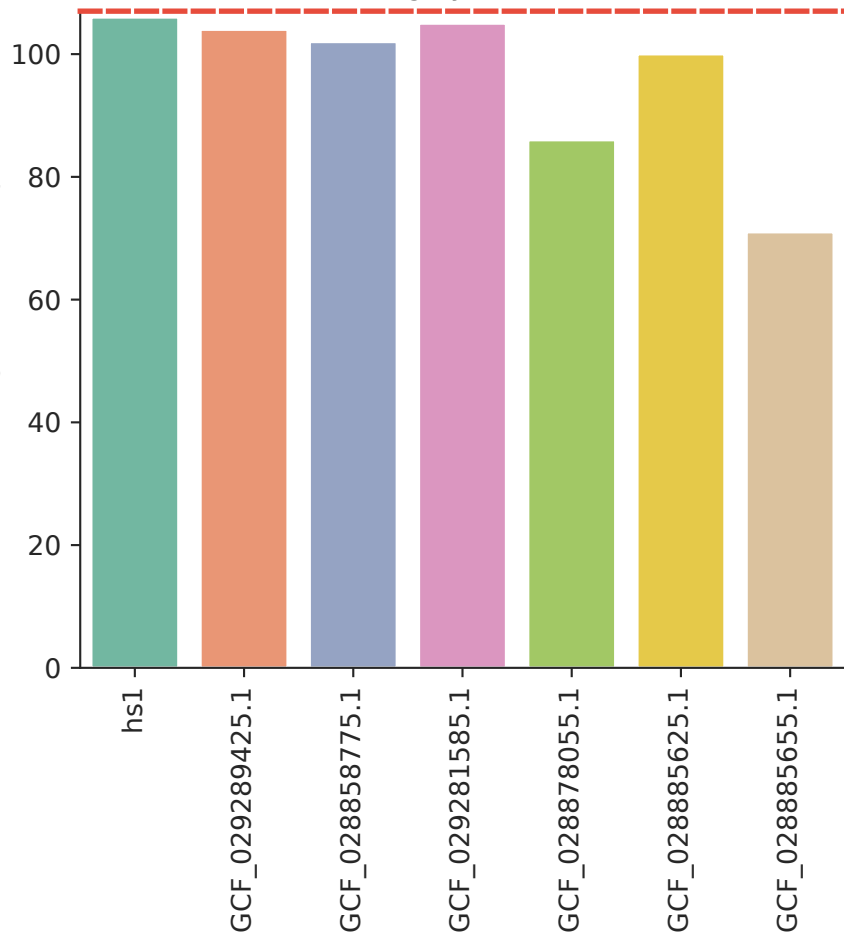


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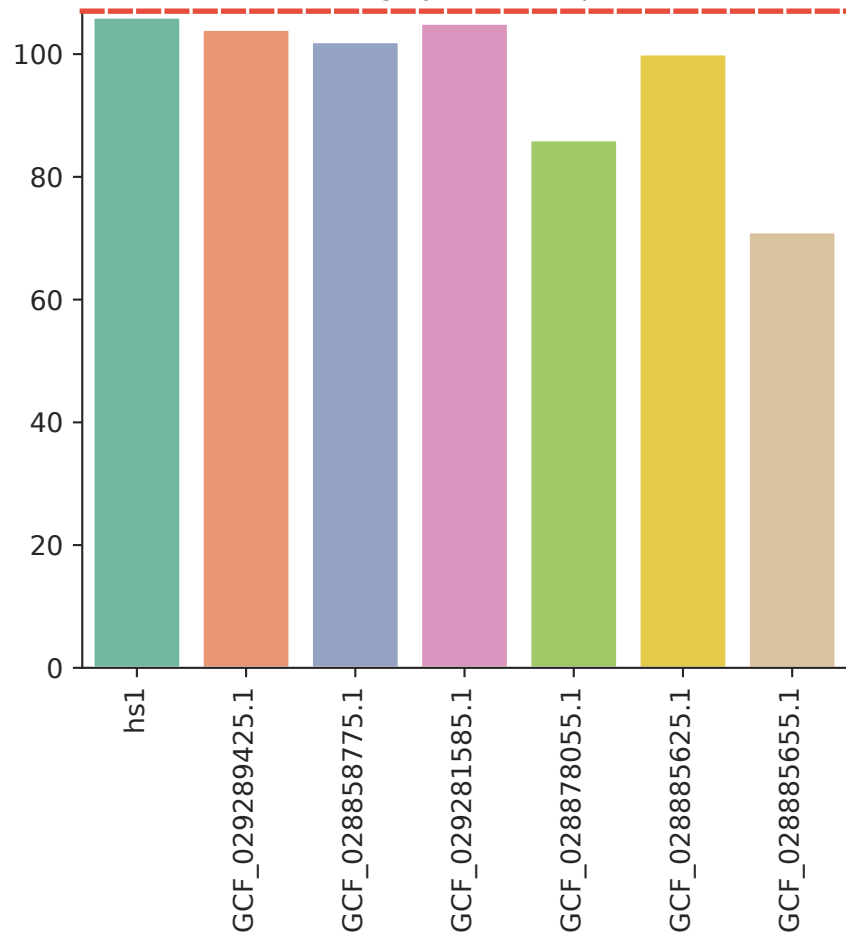


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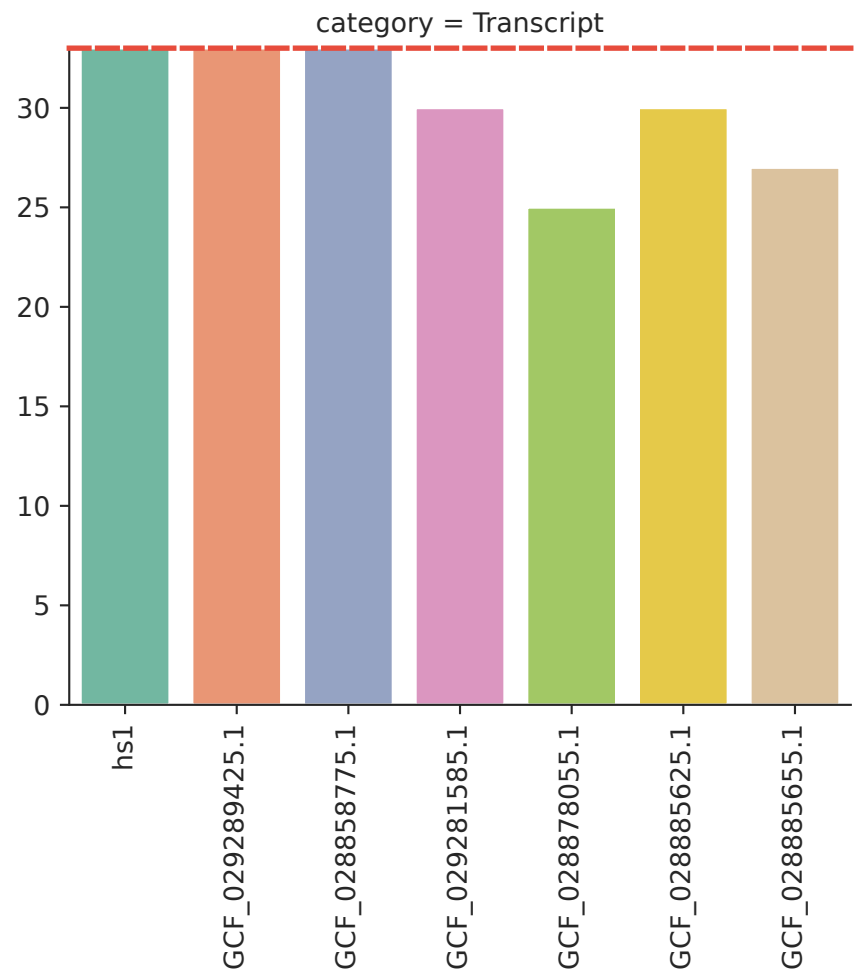
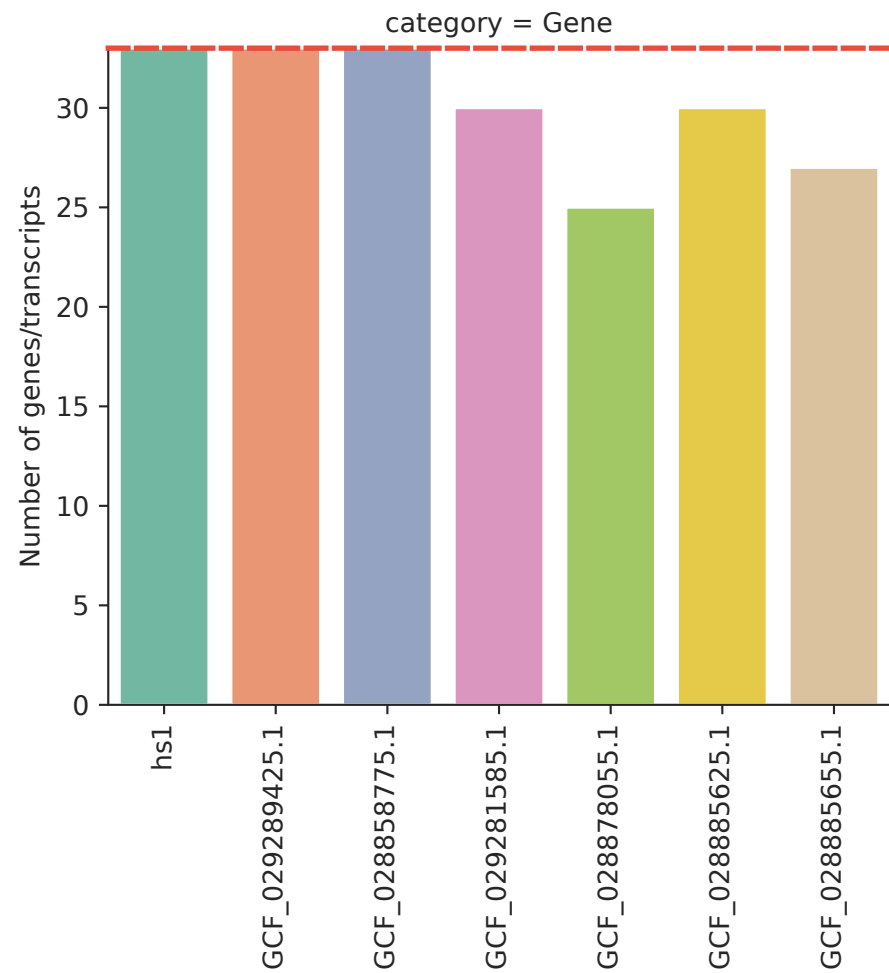
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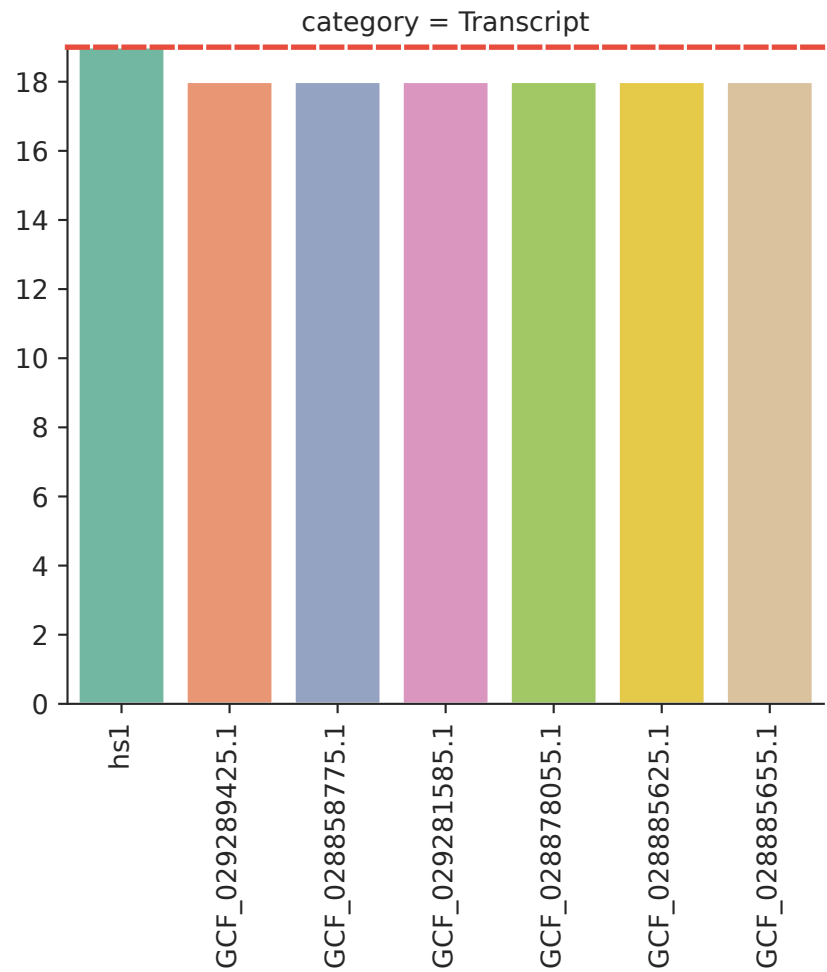
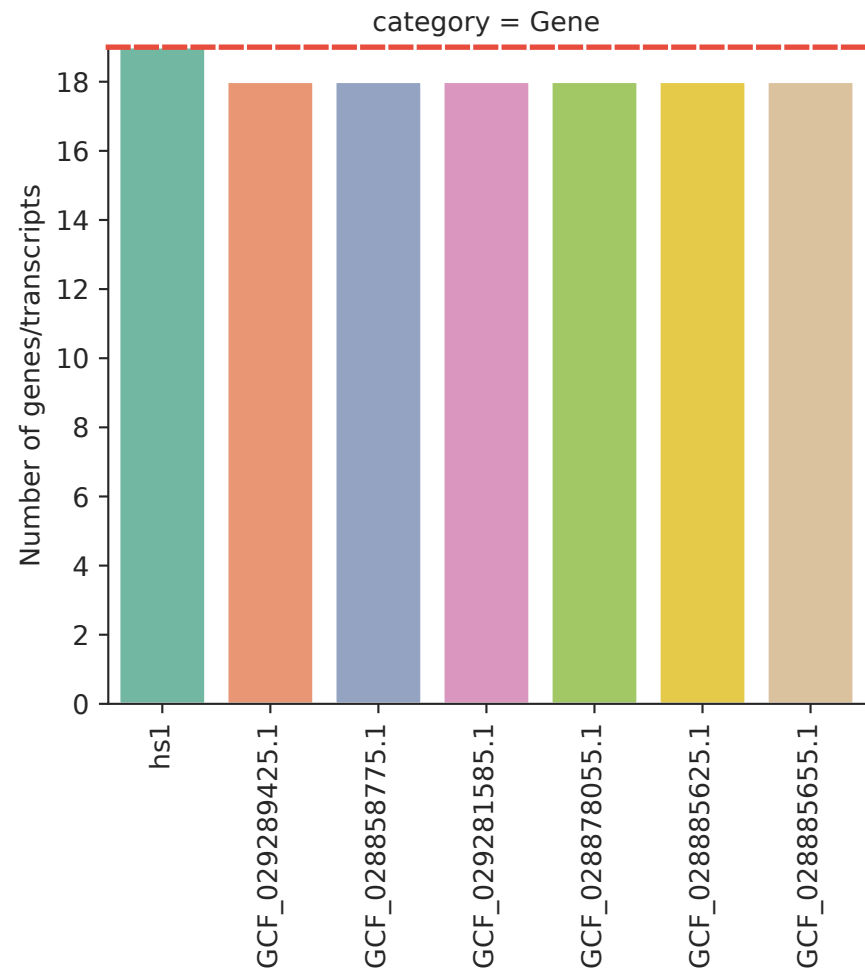
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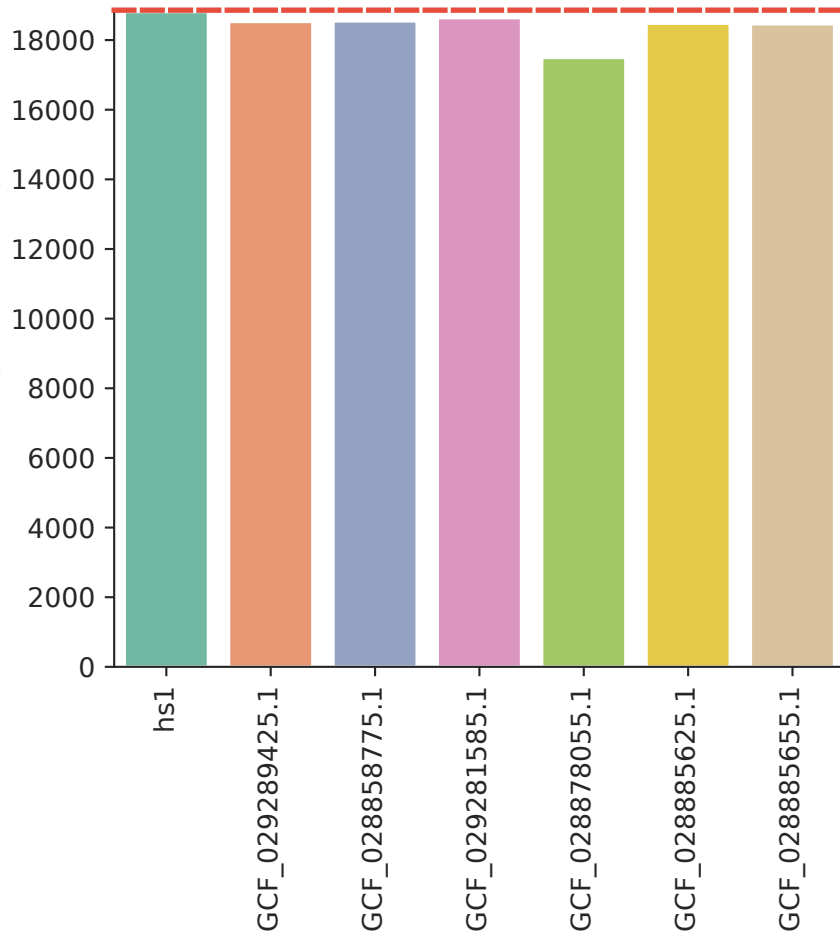


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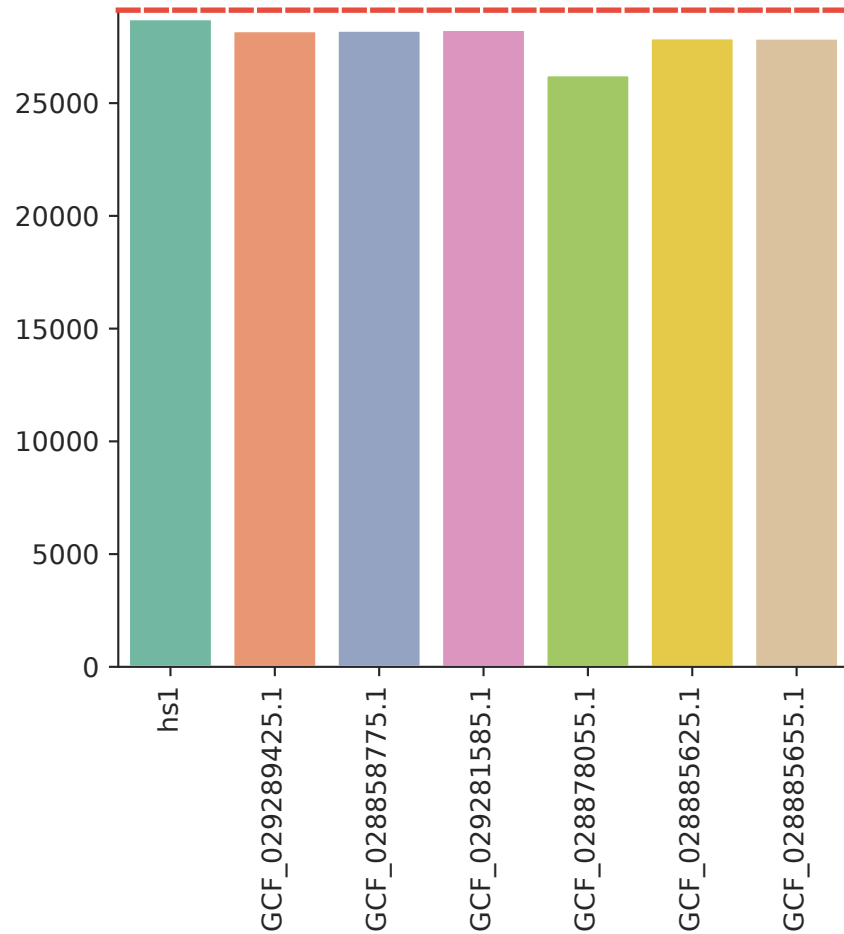


Number of comparative genes/transcripts present for biotype lncRNA

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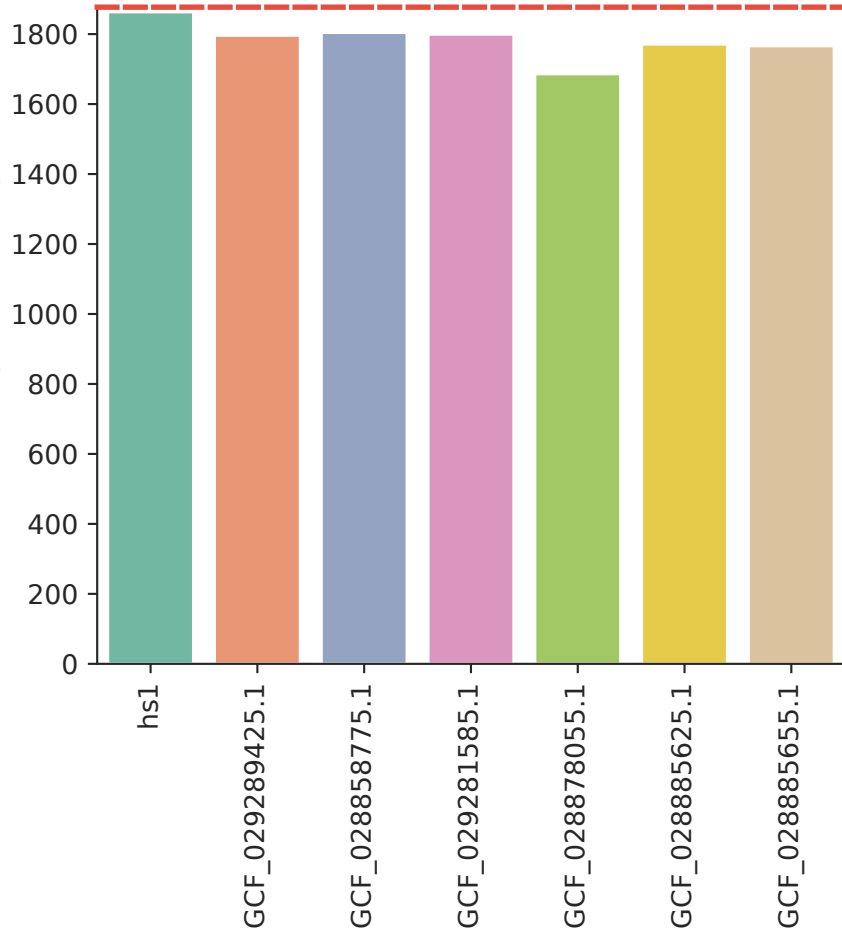


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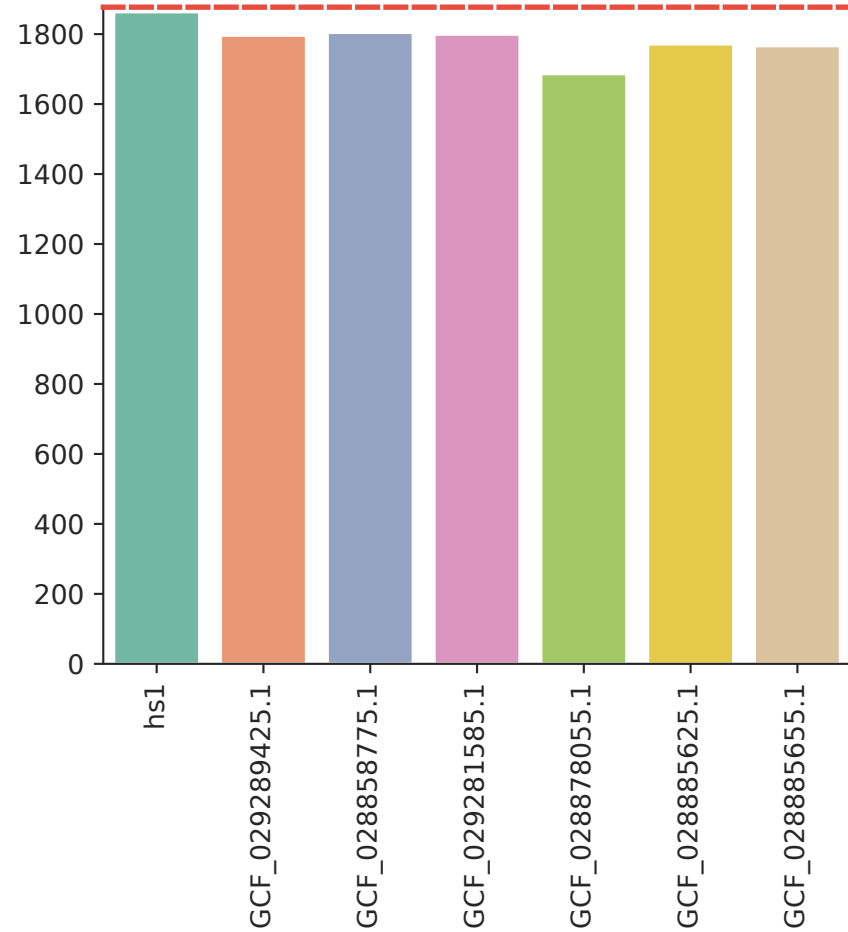


Number of comparative genes/transcripts present for biotype miRNA

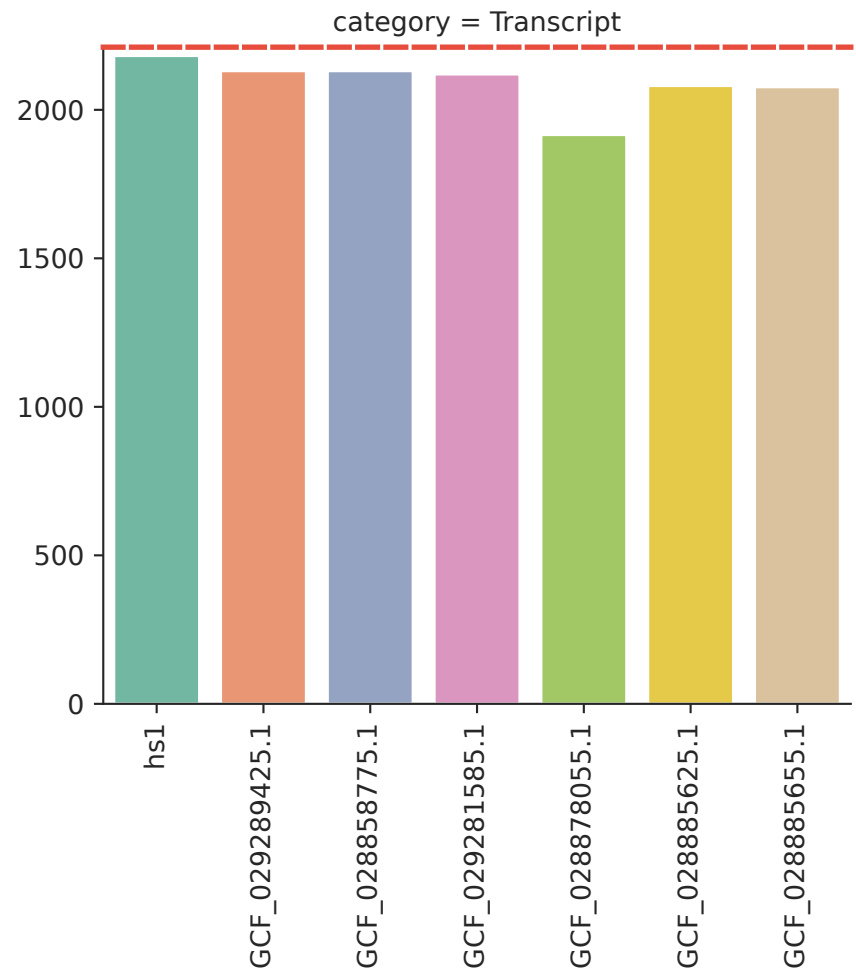
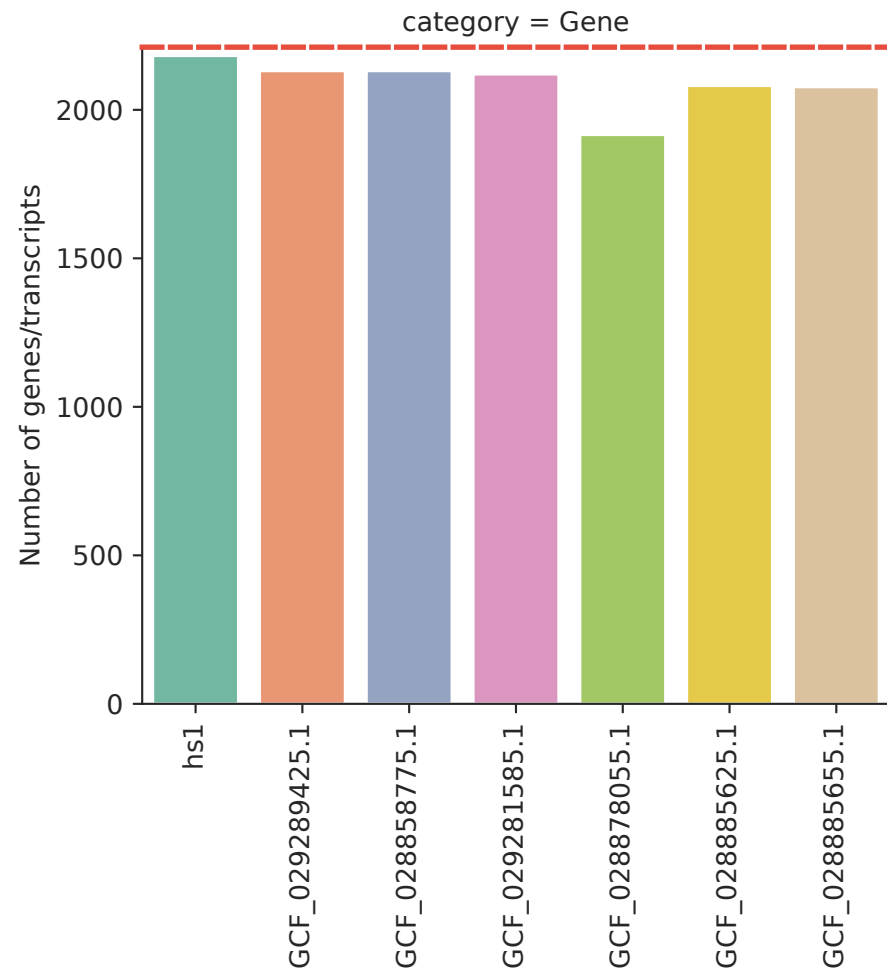
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category = Transcript

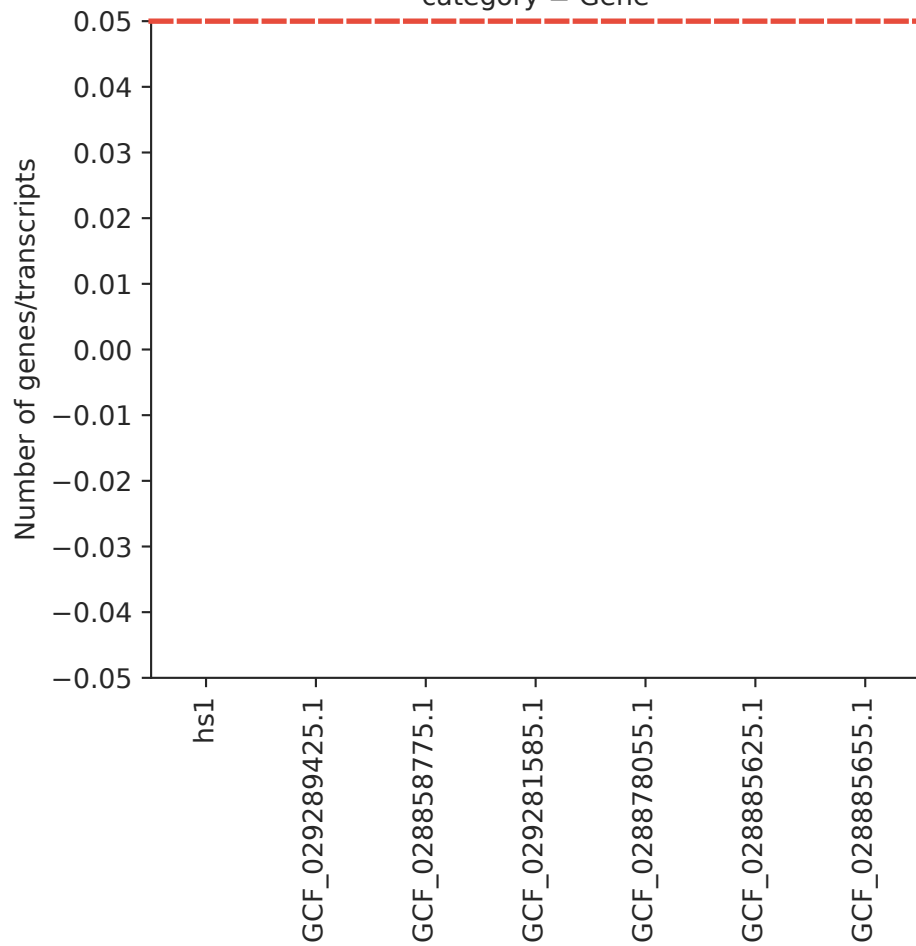


Number of comparative genes/transcripts present for biotype misc_RNA

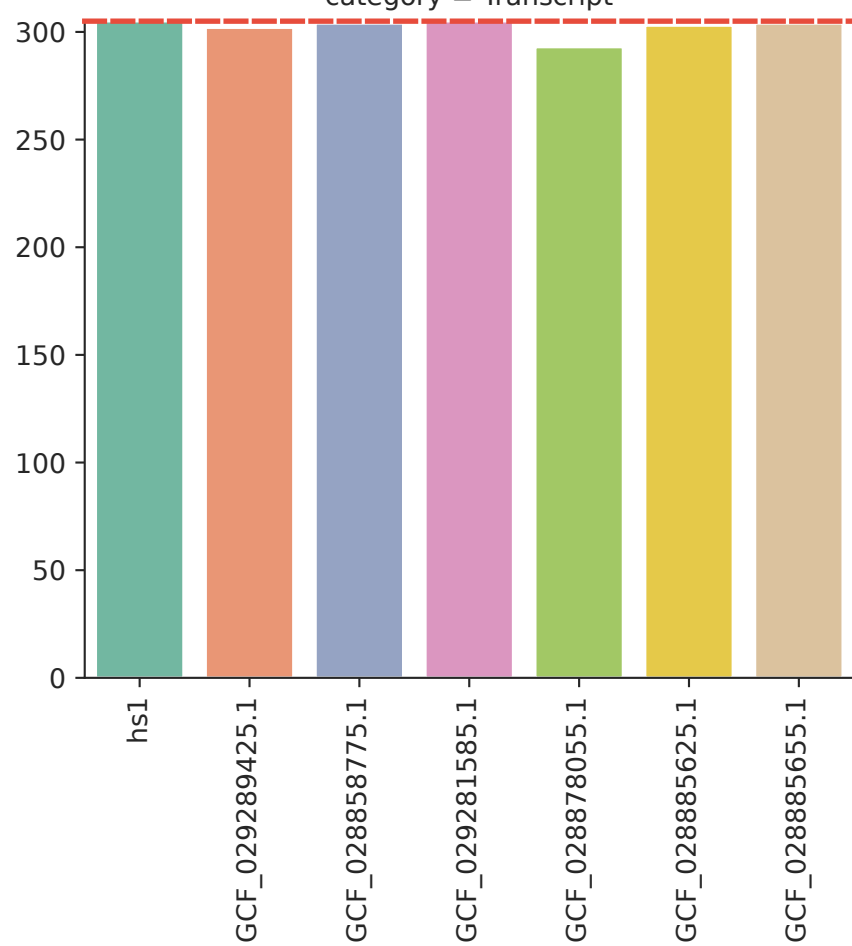


Number of comparative genes/transcripts present for biotype nonsense_mediated_decay

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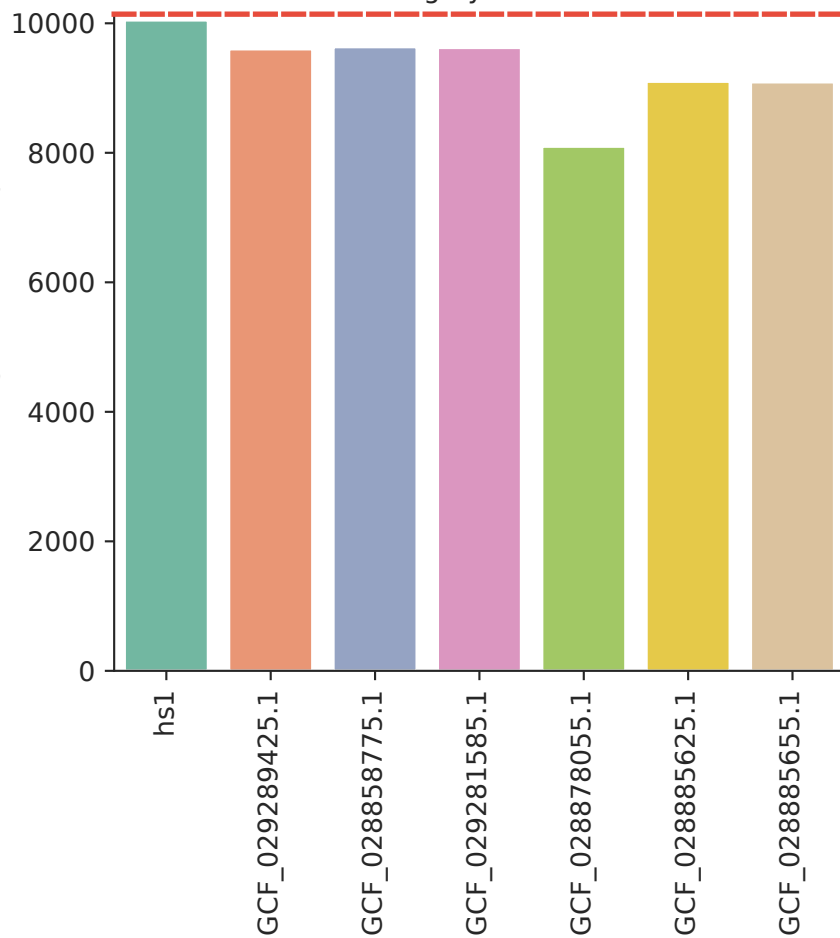


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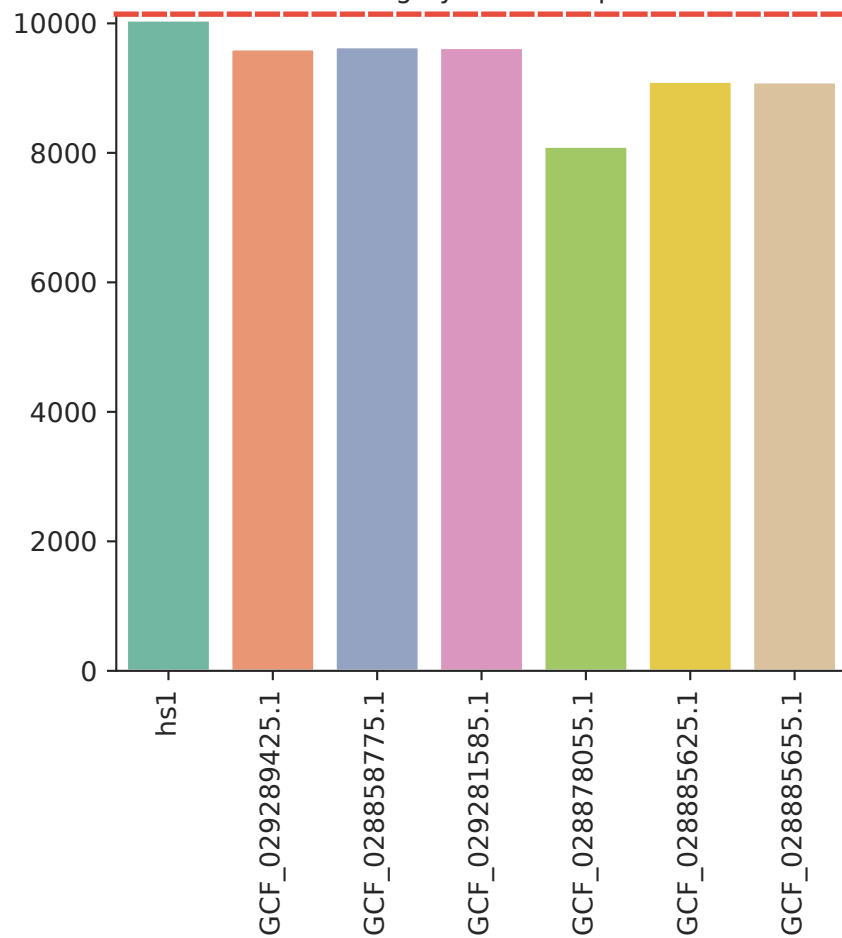


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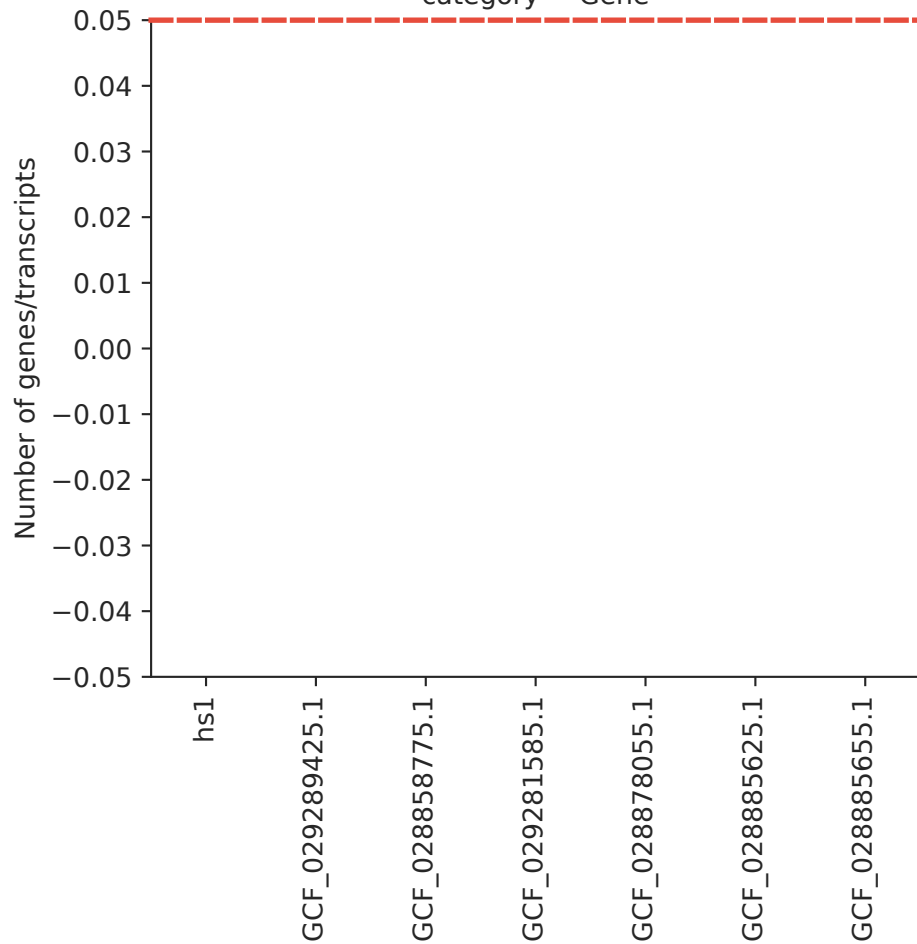


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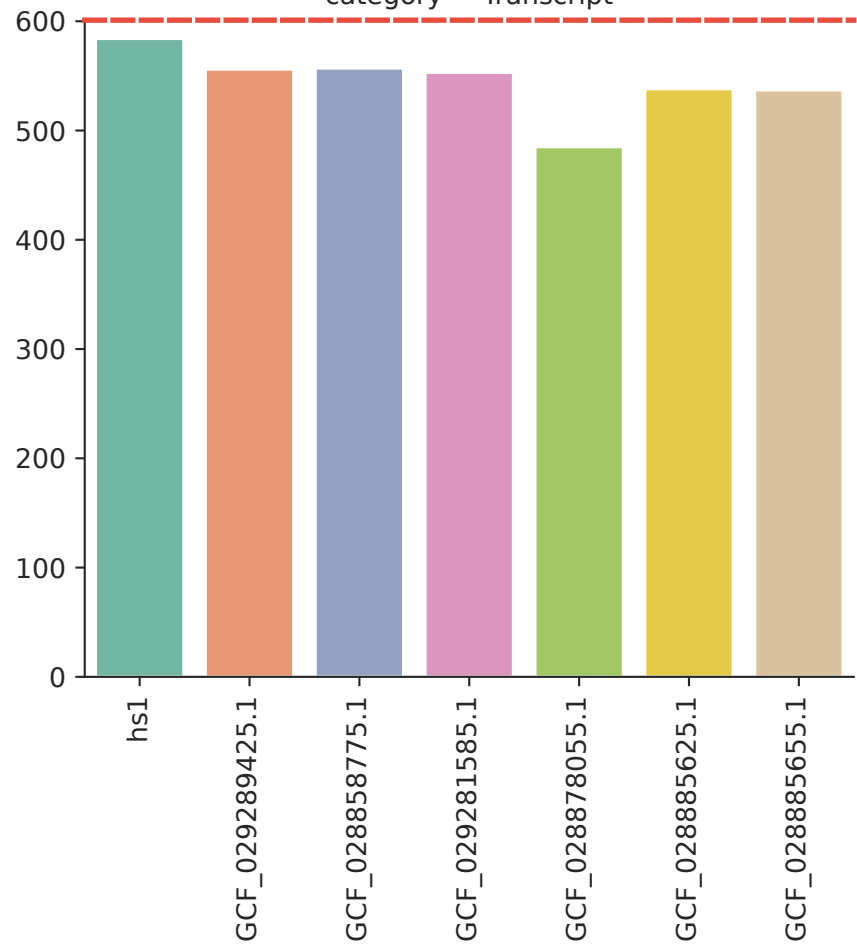


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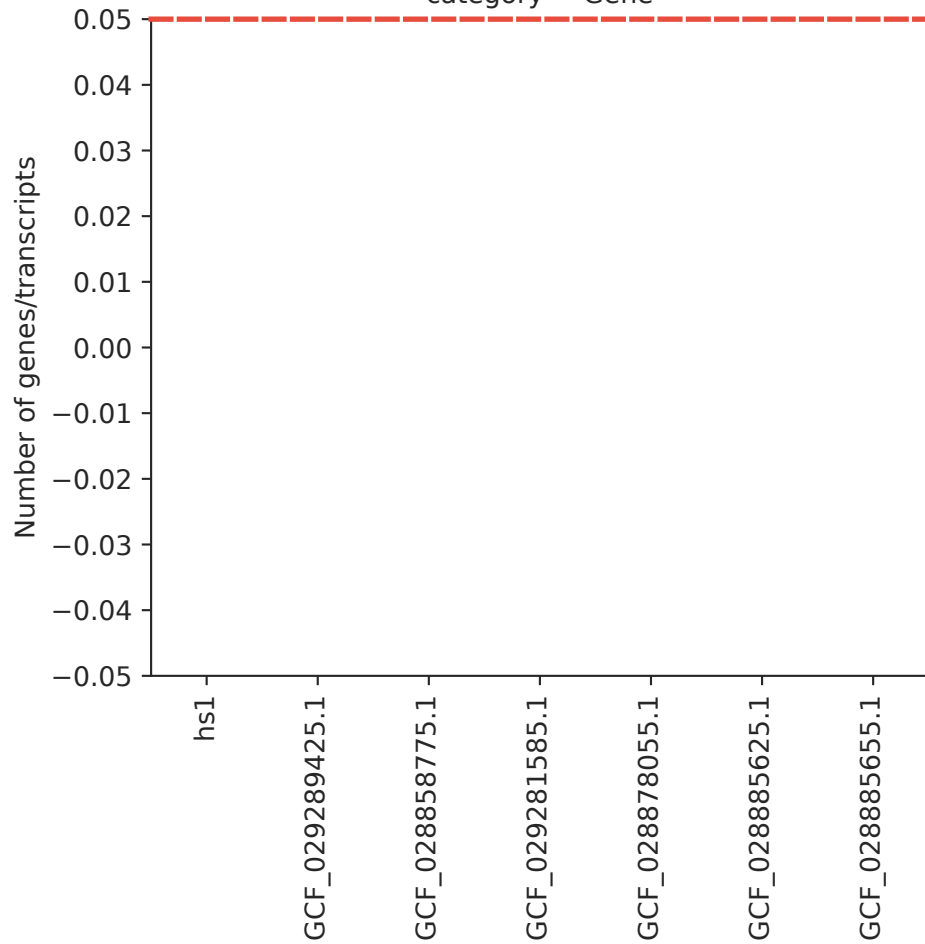


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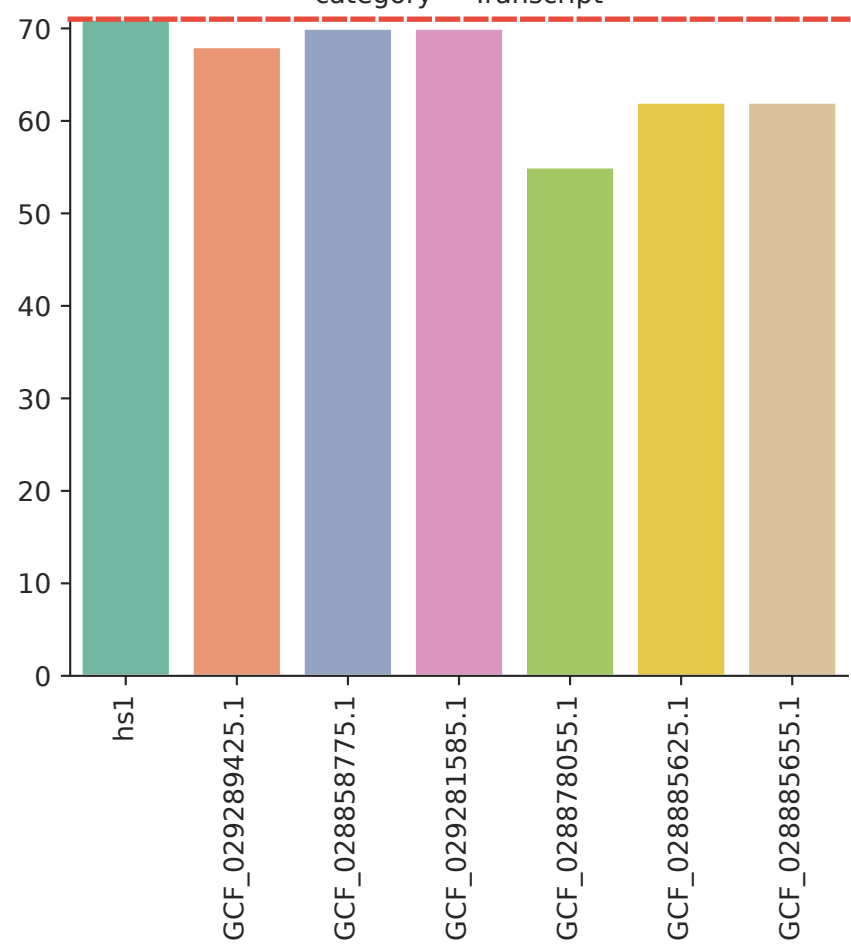


Number of comparative genes/transcripts present for biotype protein_coding_LoF

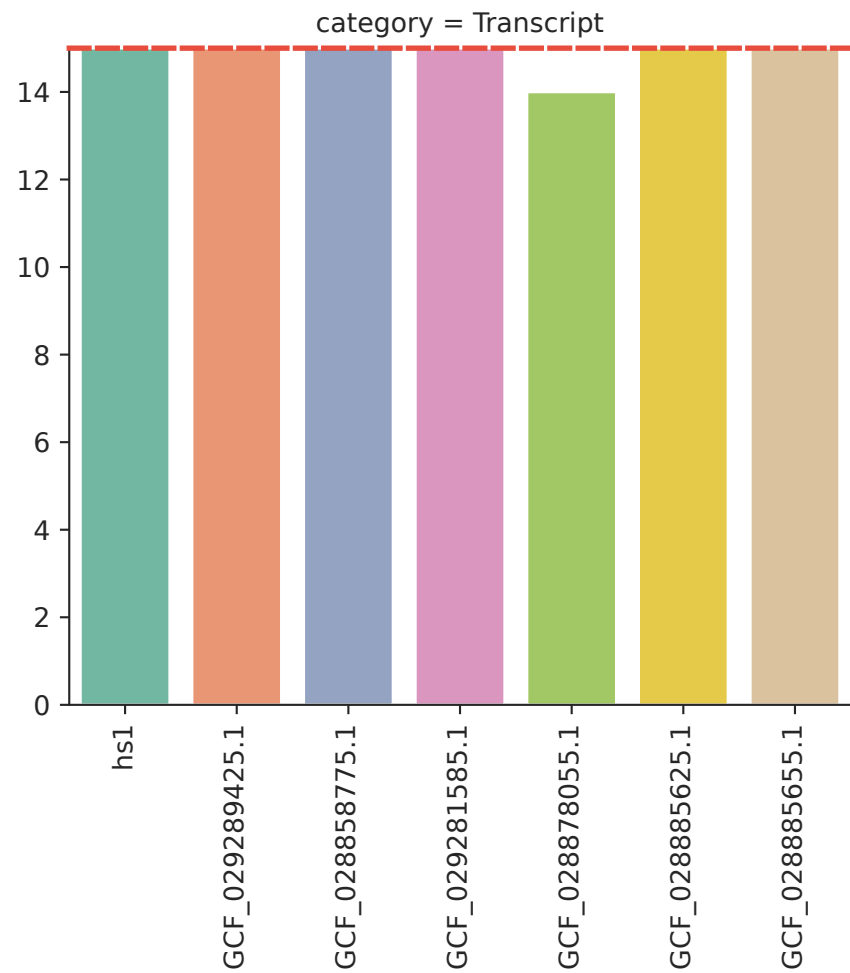
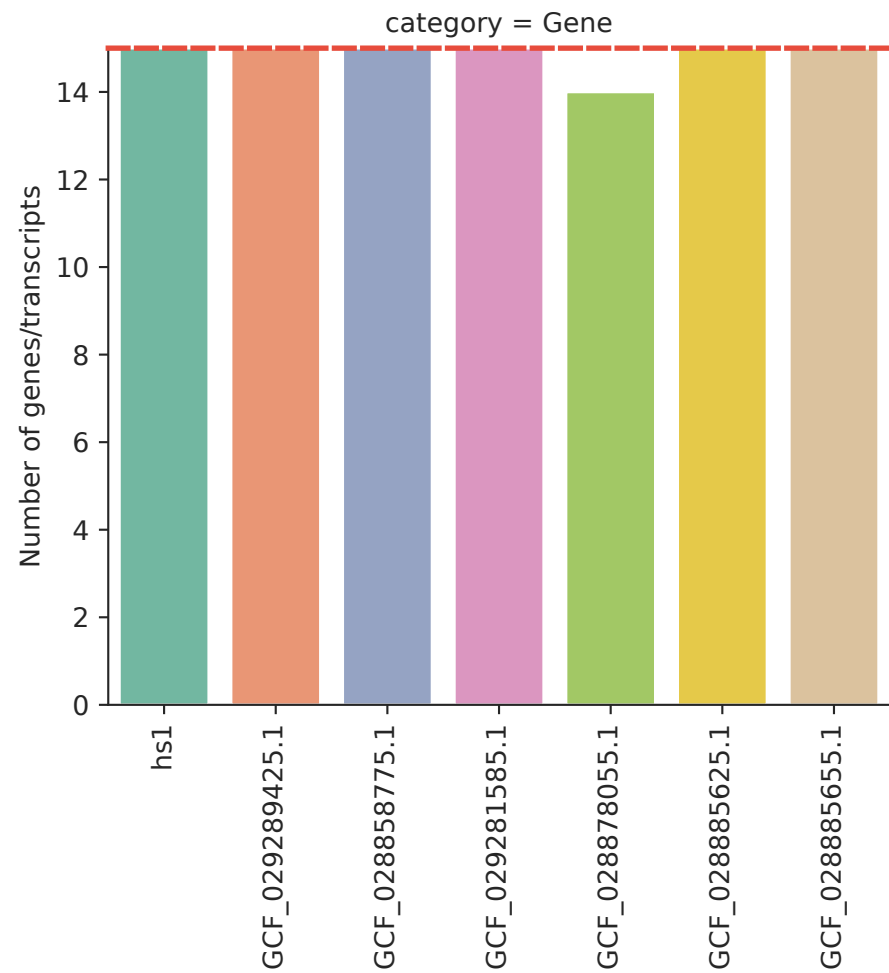
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category = Transcript

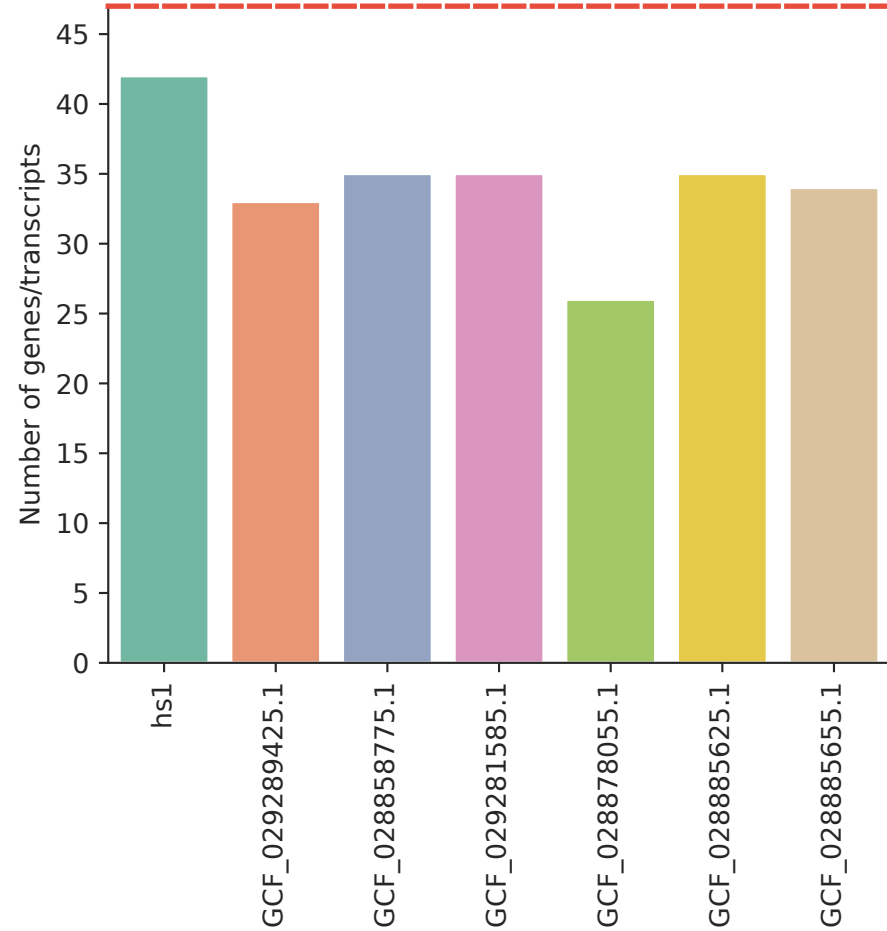


Number of comparative genes/transcripts present for biotype pseudogene

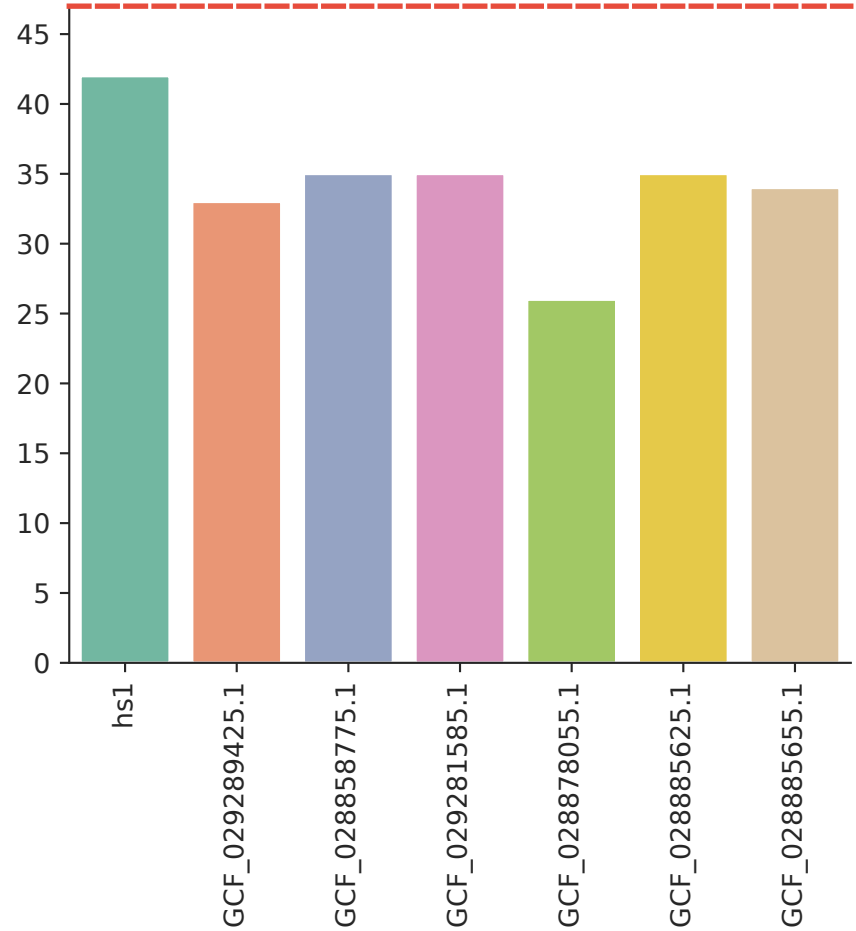


Number of comparative genes/transcripts present for biotype rRNA

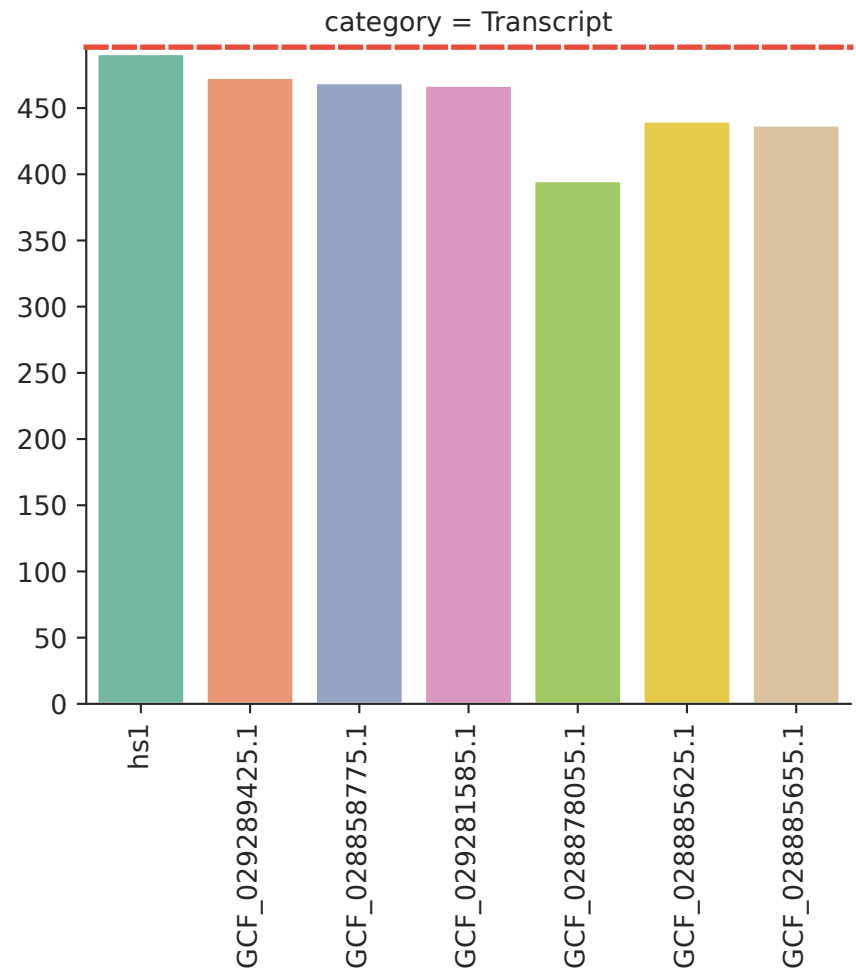
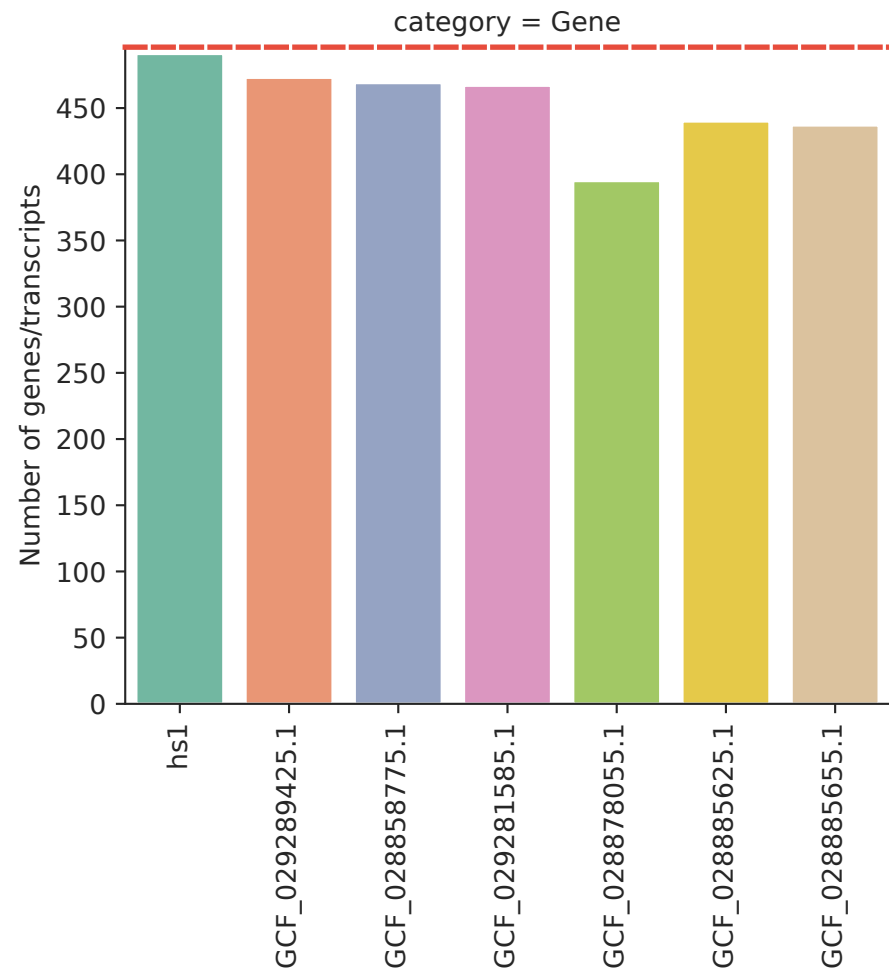
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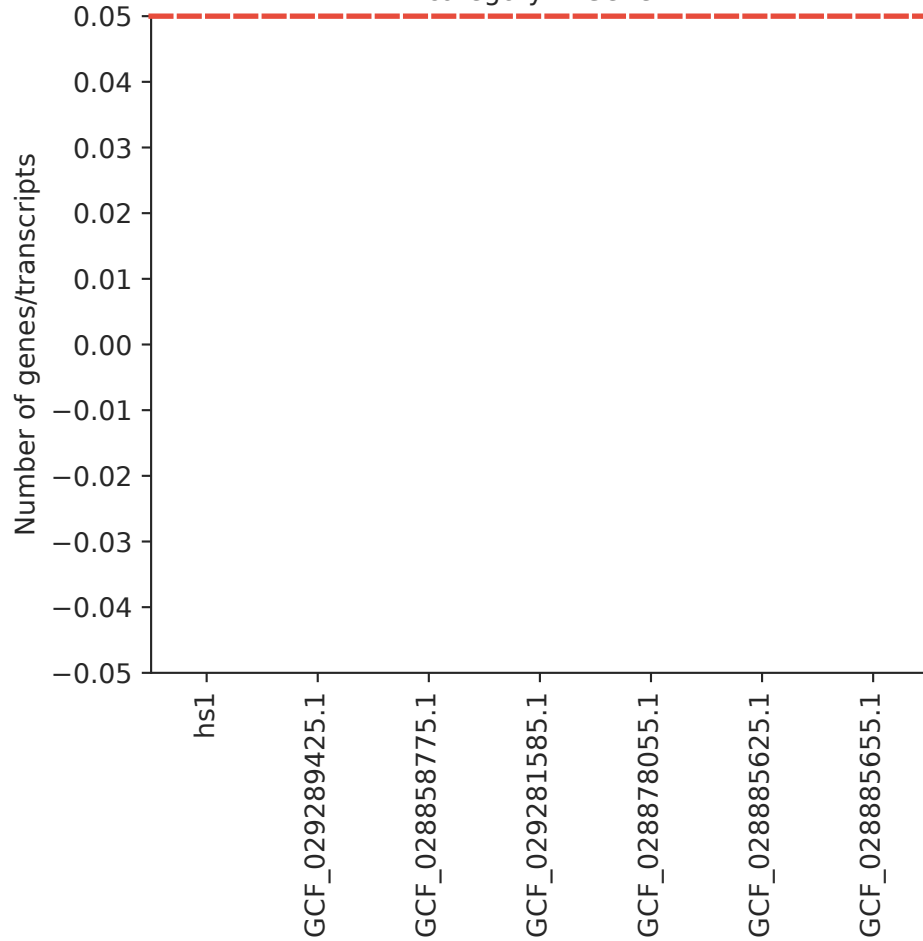


Number of comparative genes/transcripts present for biotype rRNA_pseudogene

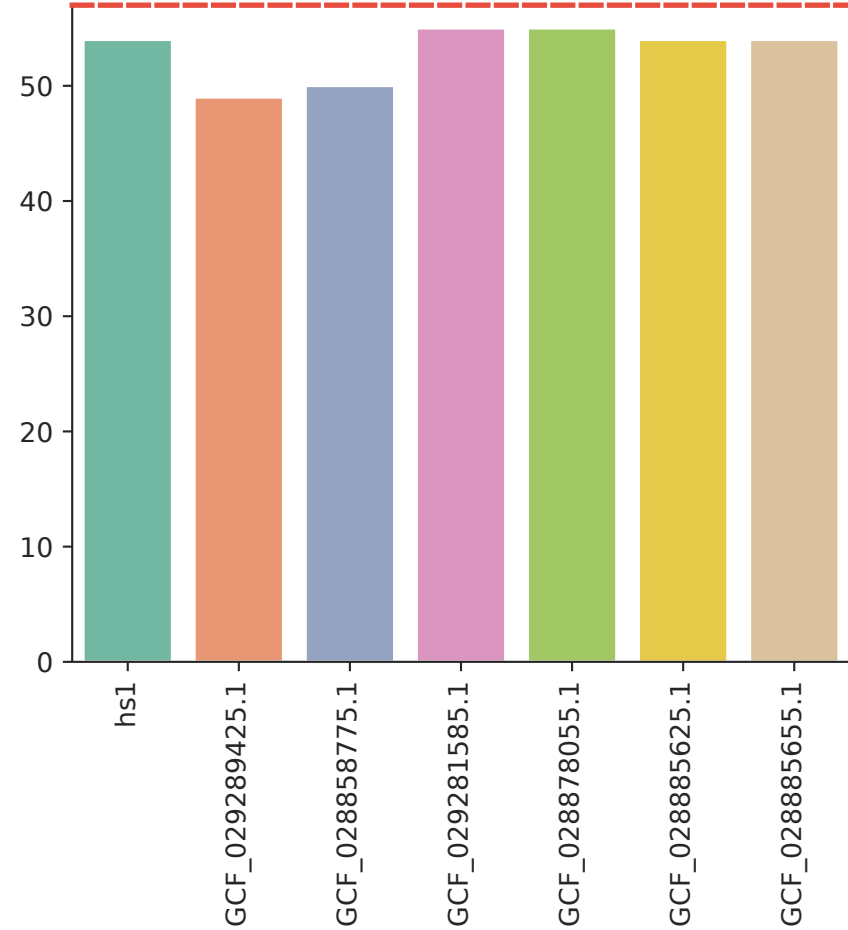


Number of comparative genes/transcripts present for biotype retained_intron

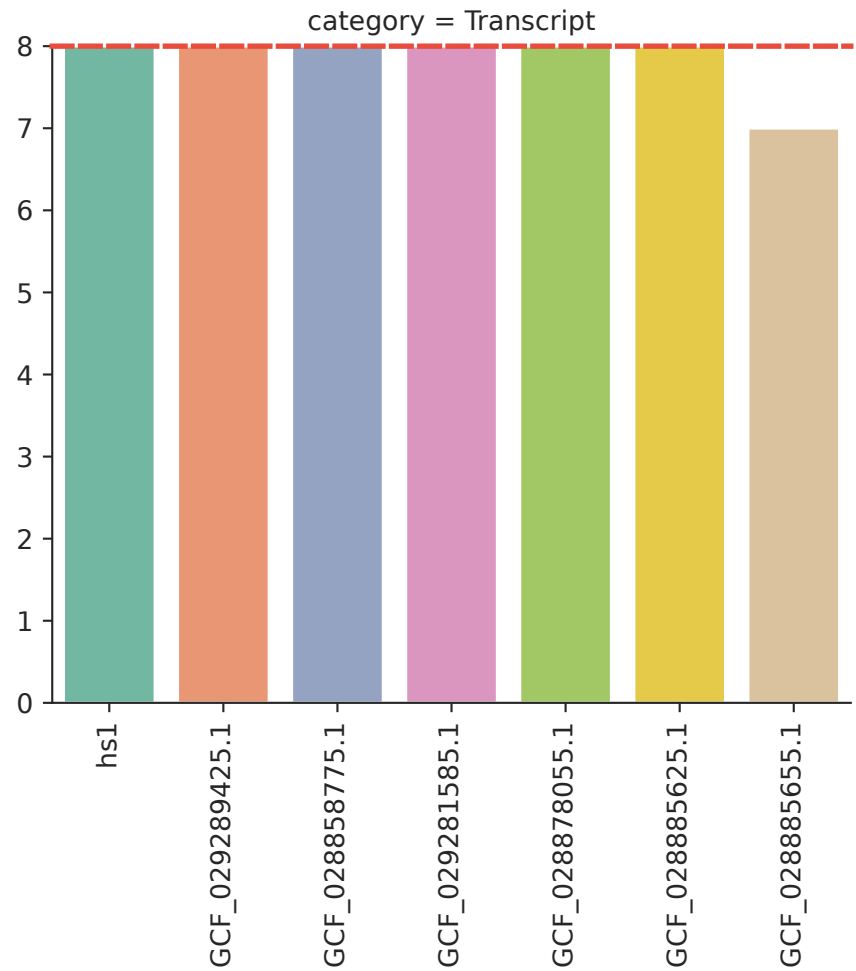
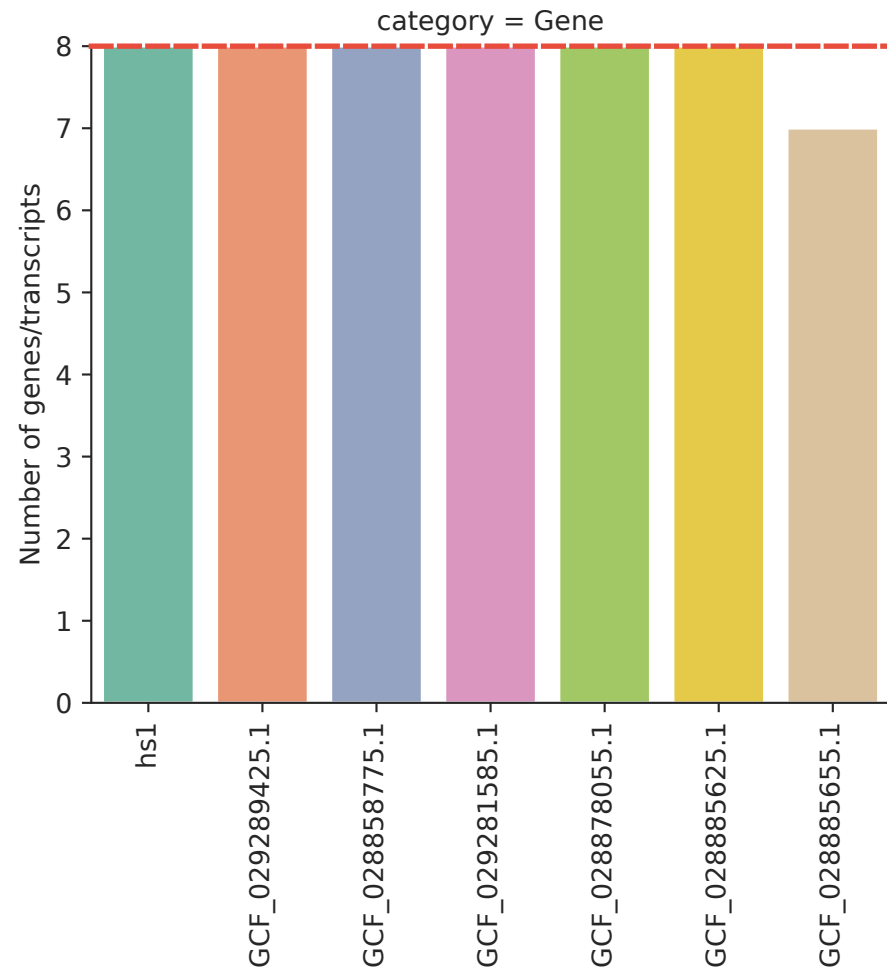
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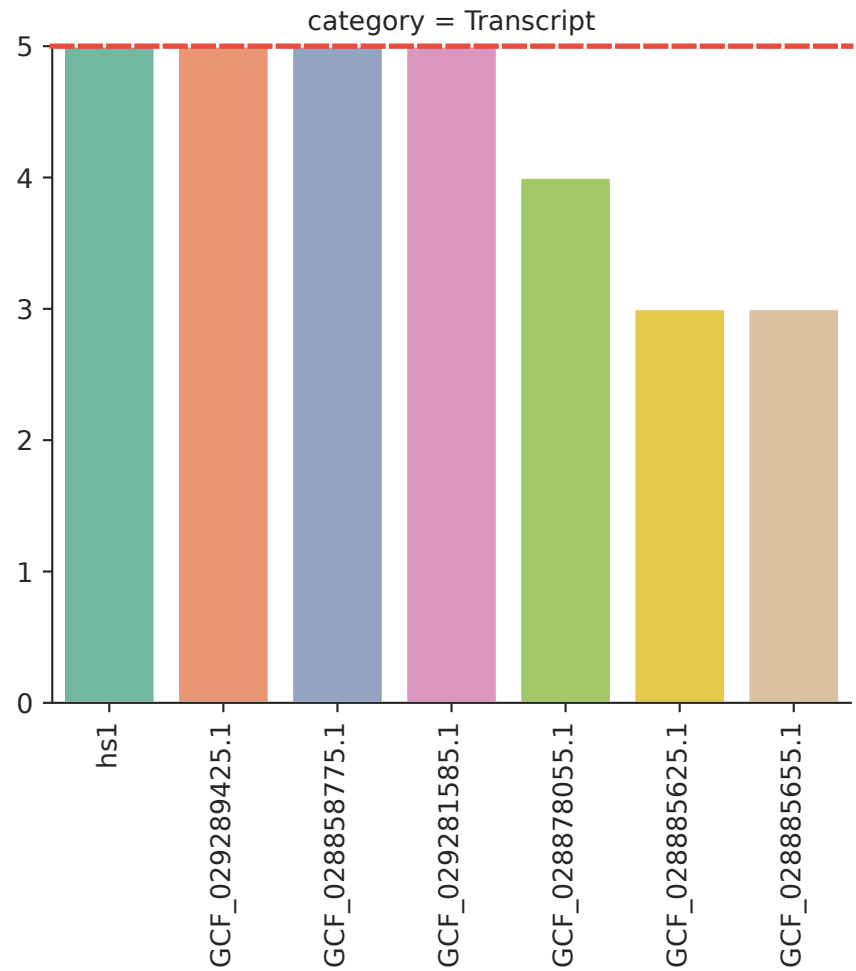
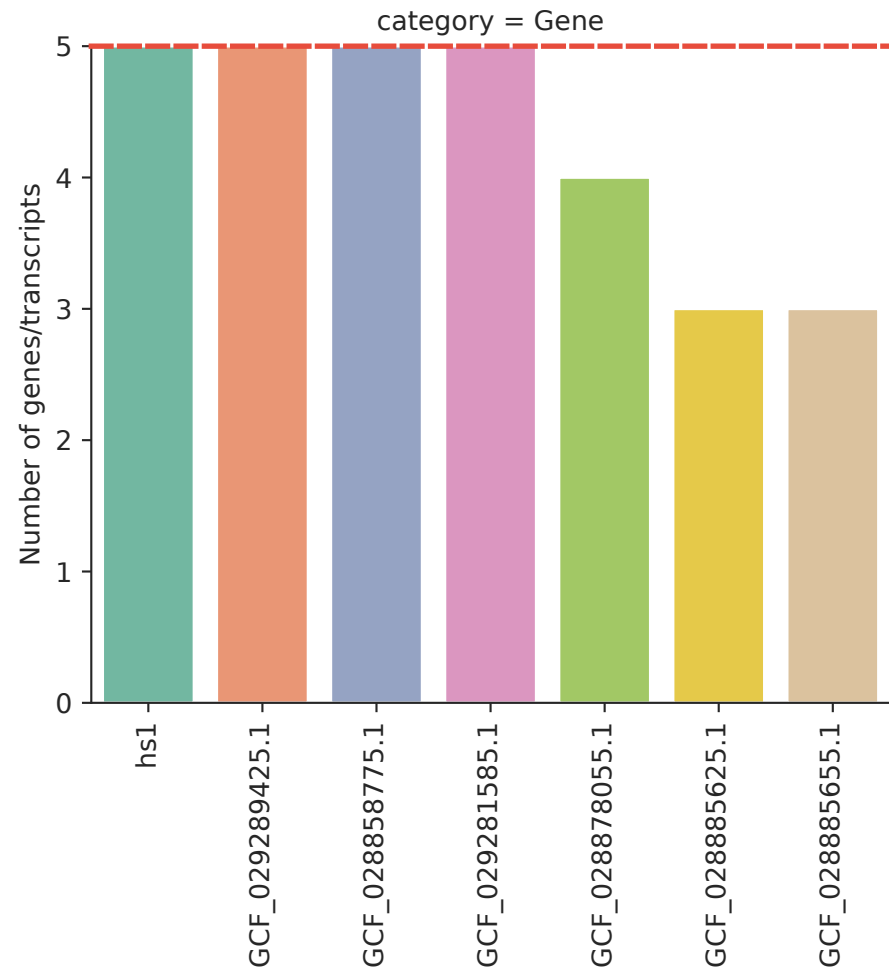
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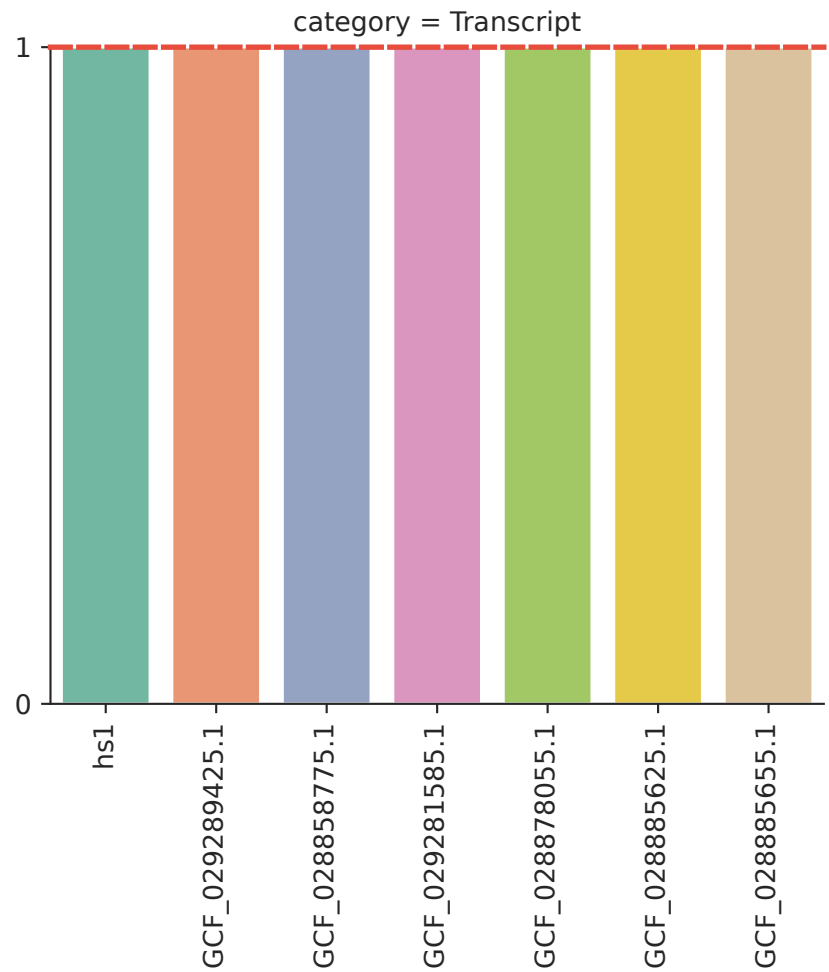
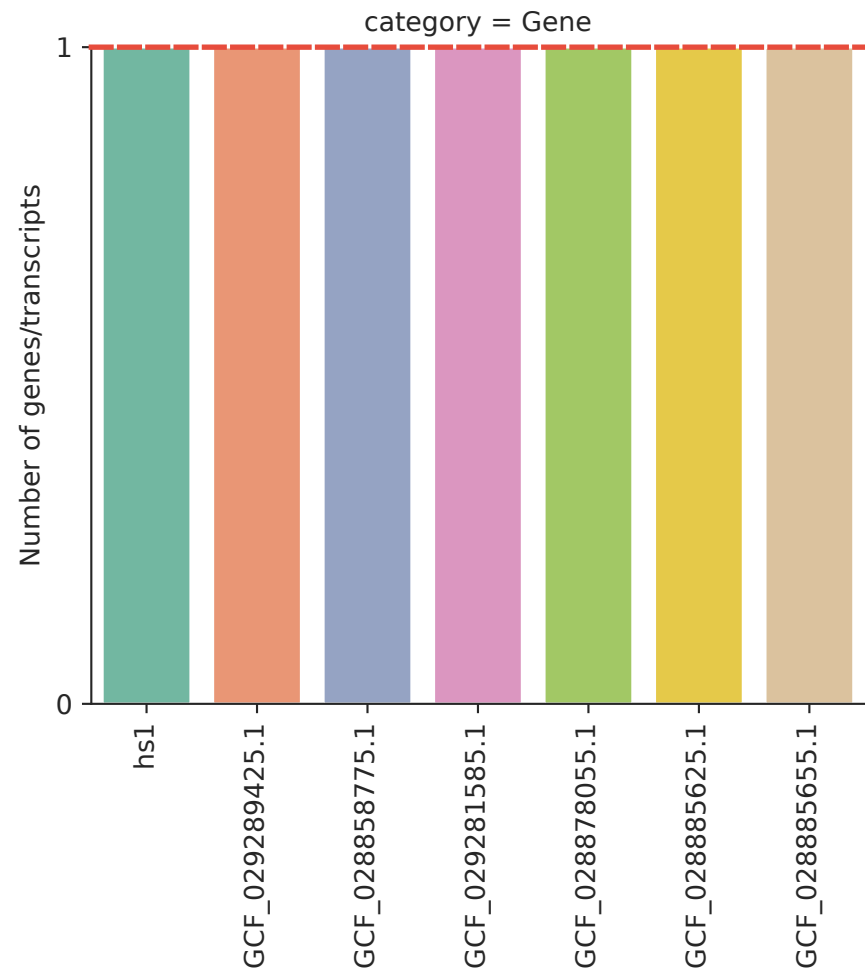
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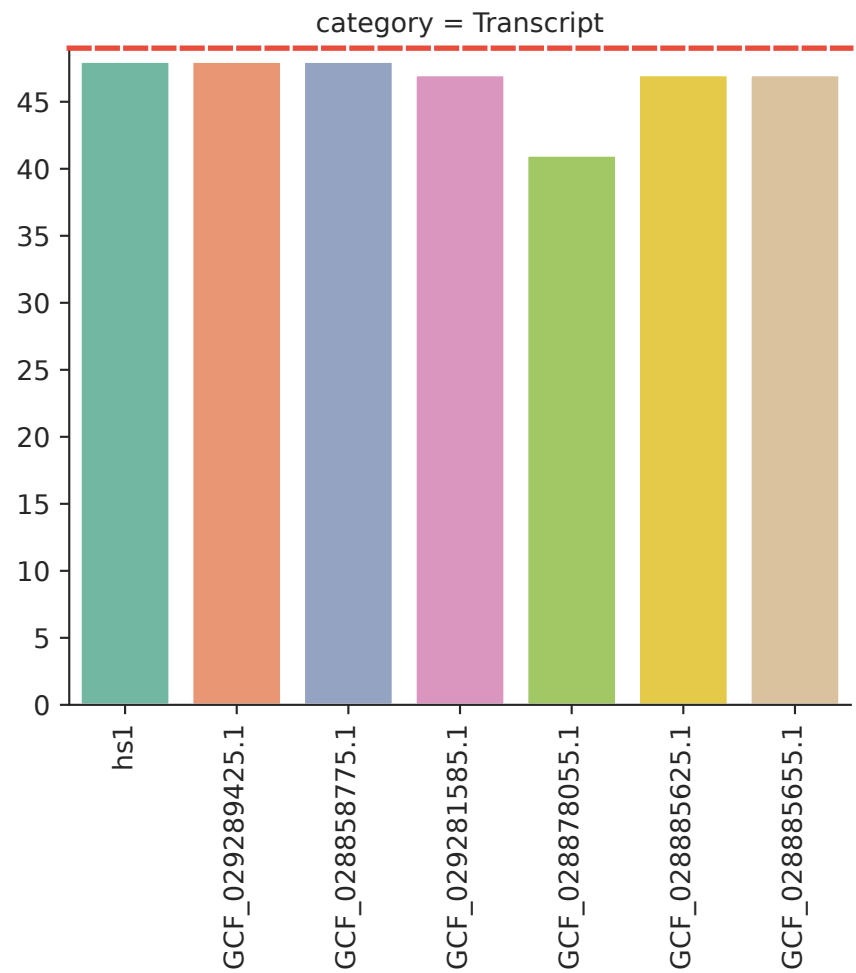
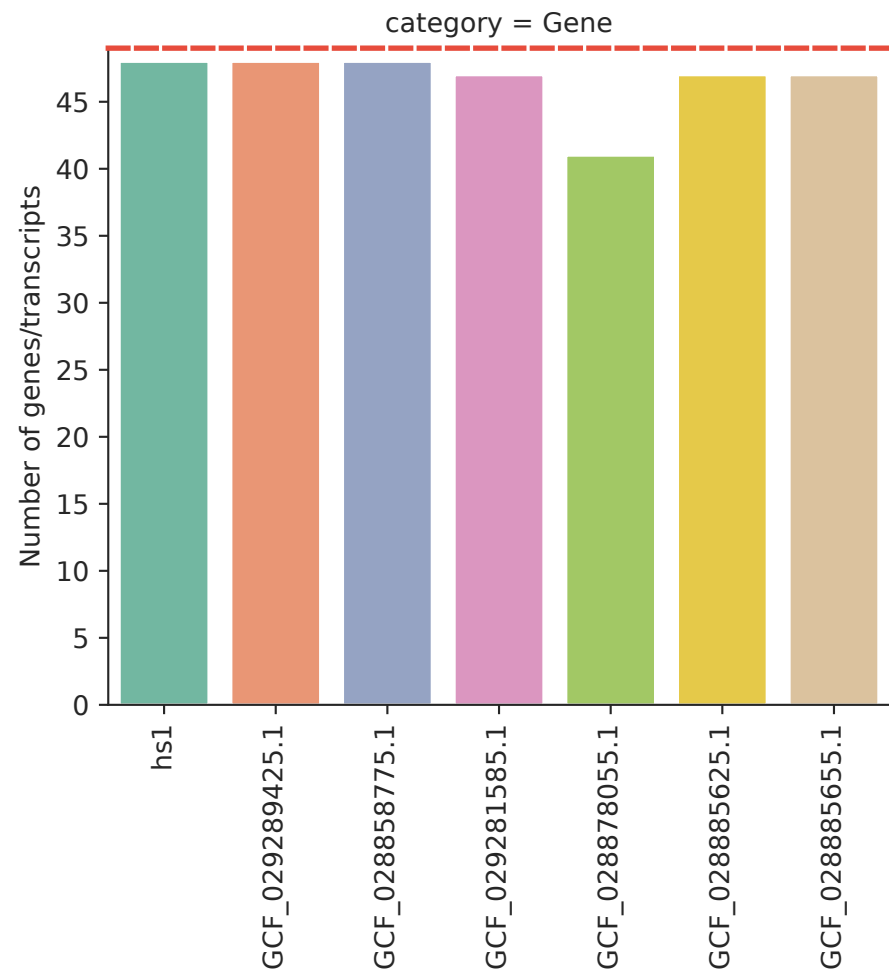
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Number of comparative genes/transcripts present for biotype scRNA

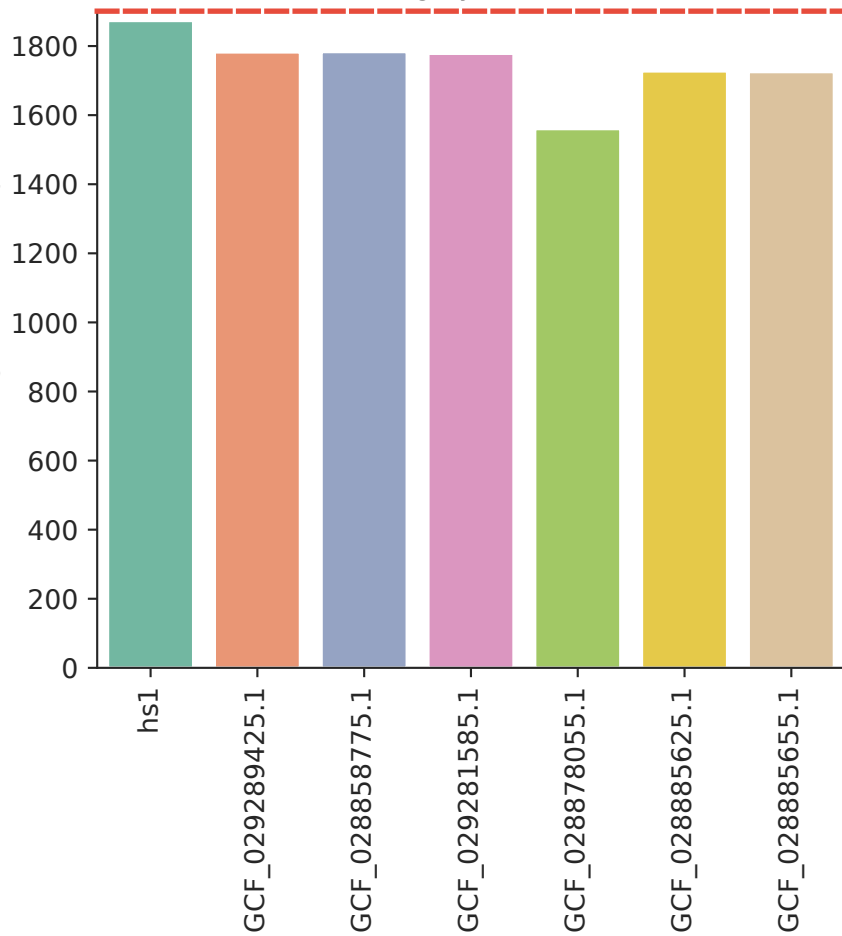


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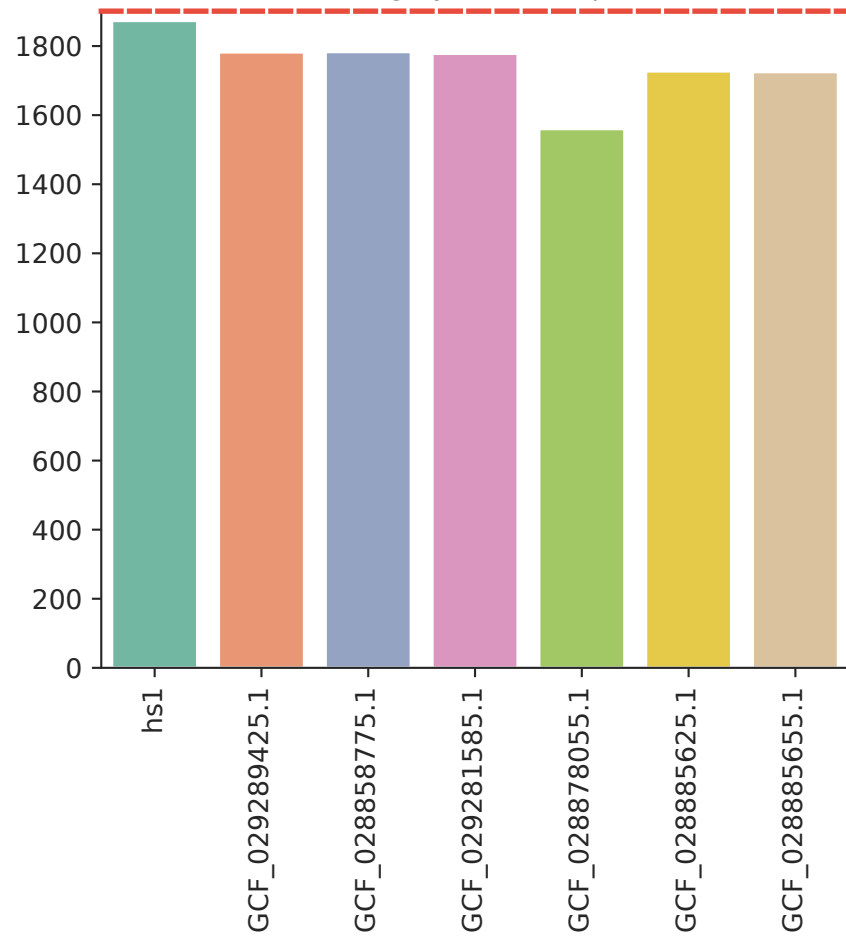


Number of comparative genes/transcripts present for biotype snRNA

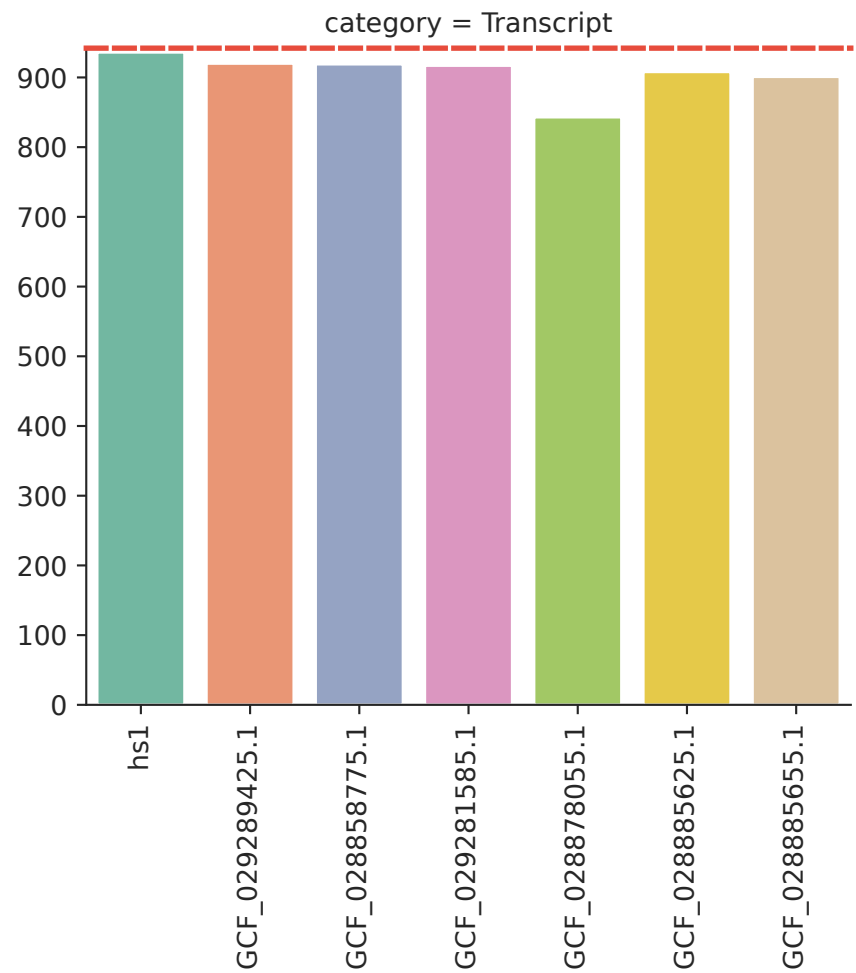
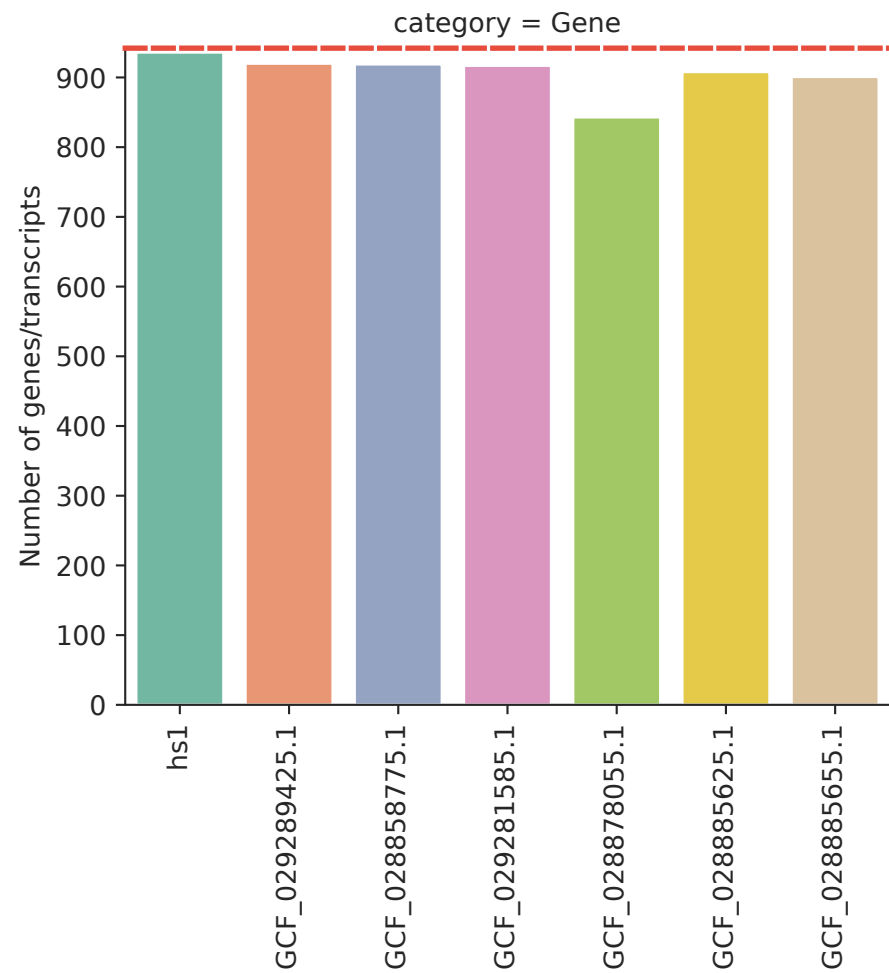
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category = Transcript

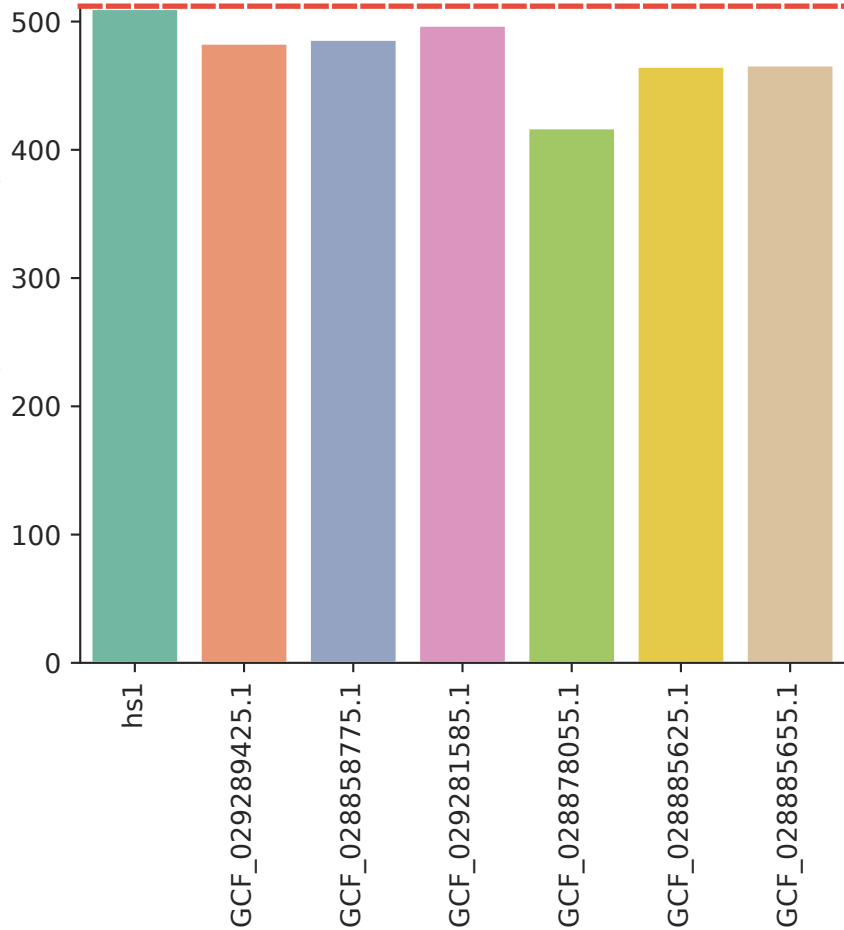


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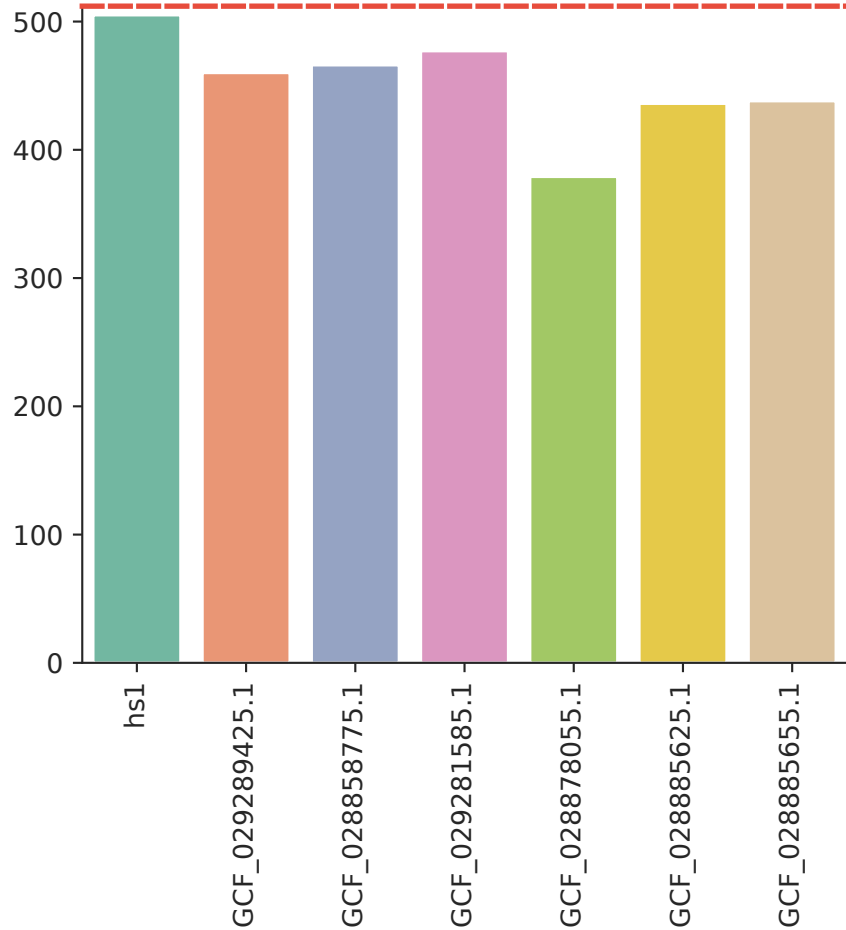


Number of comparative genes/transcripts present for biotype transcribed_processed_pseudogene

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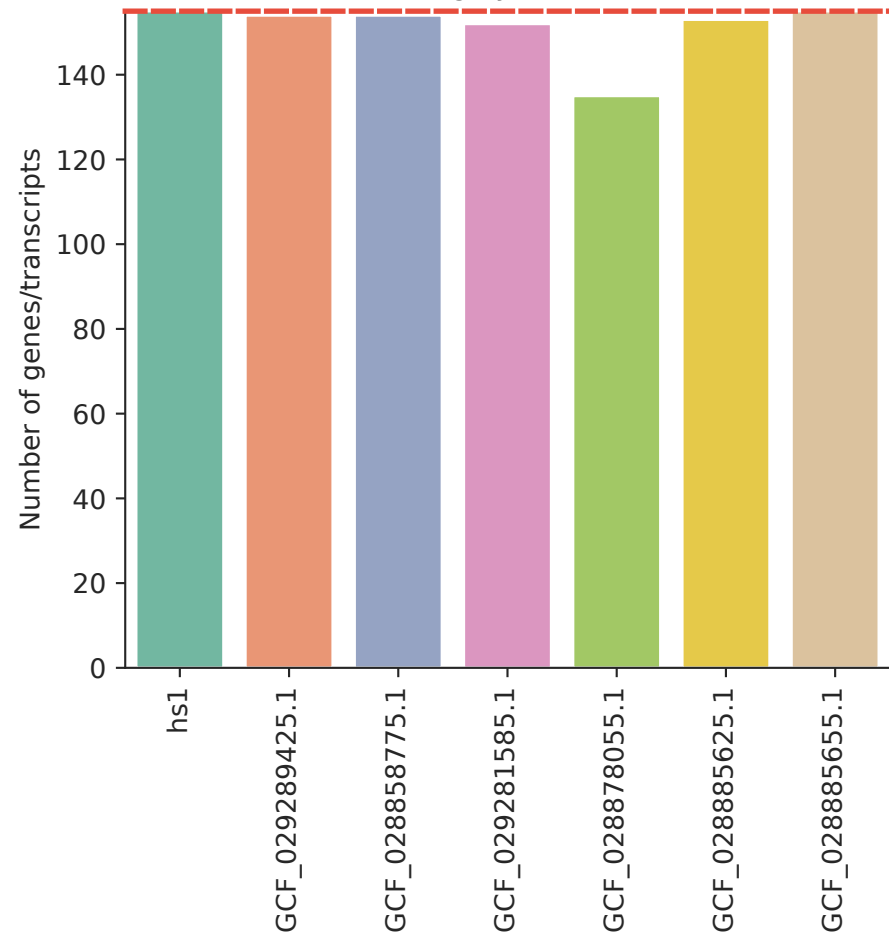


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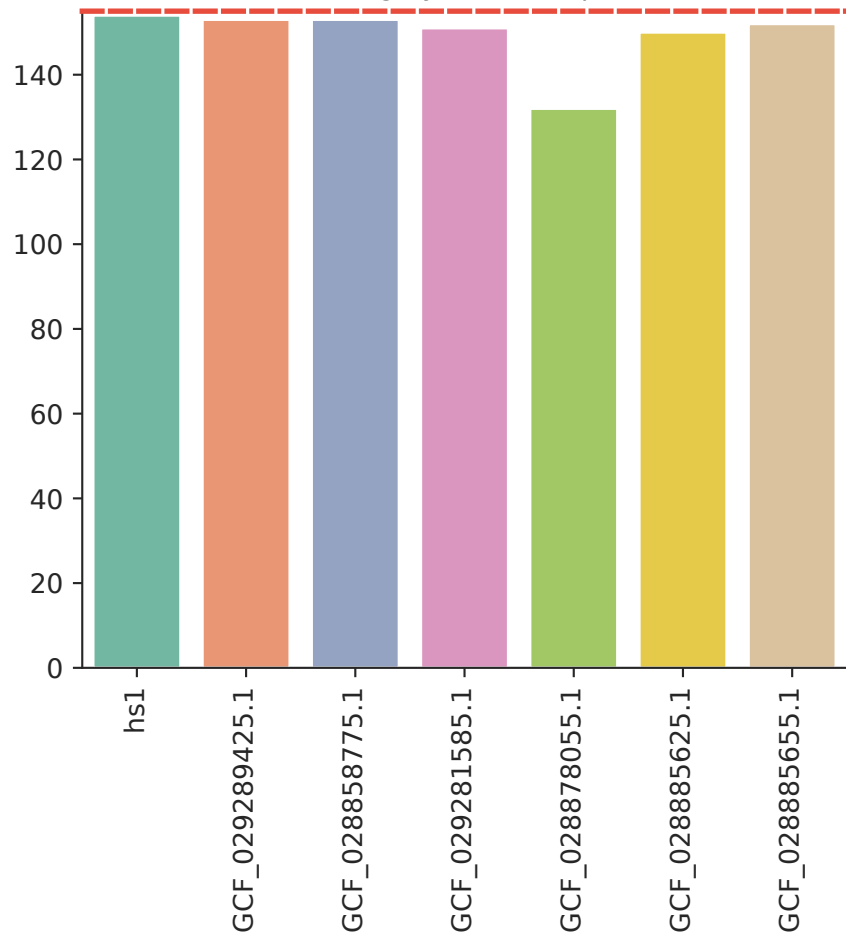


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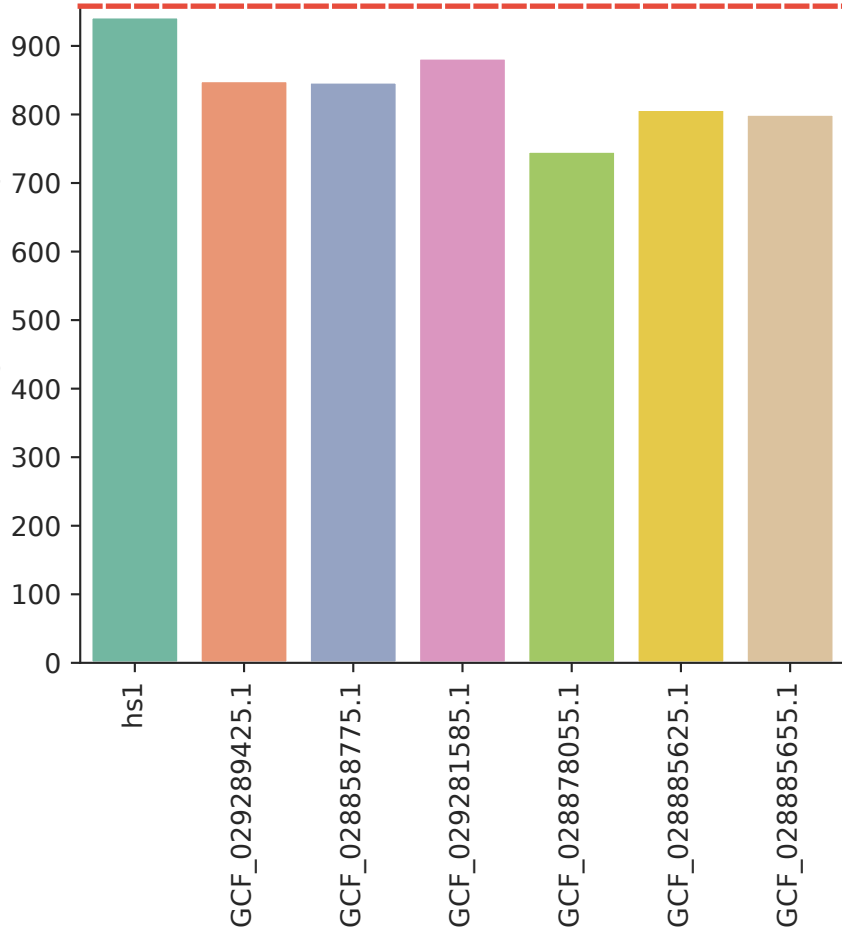


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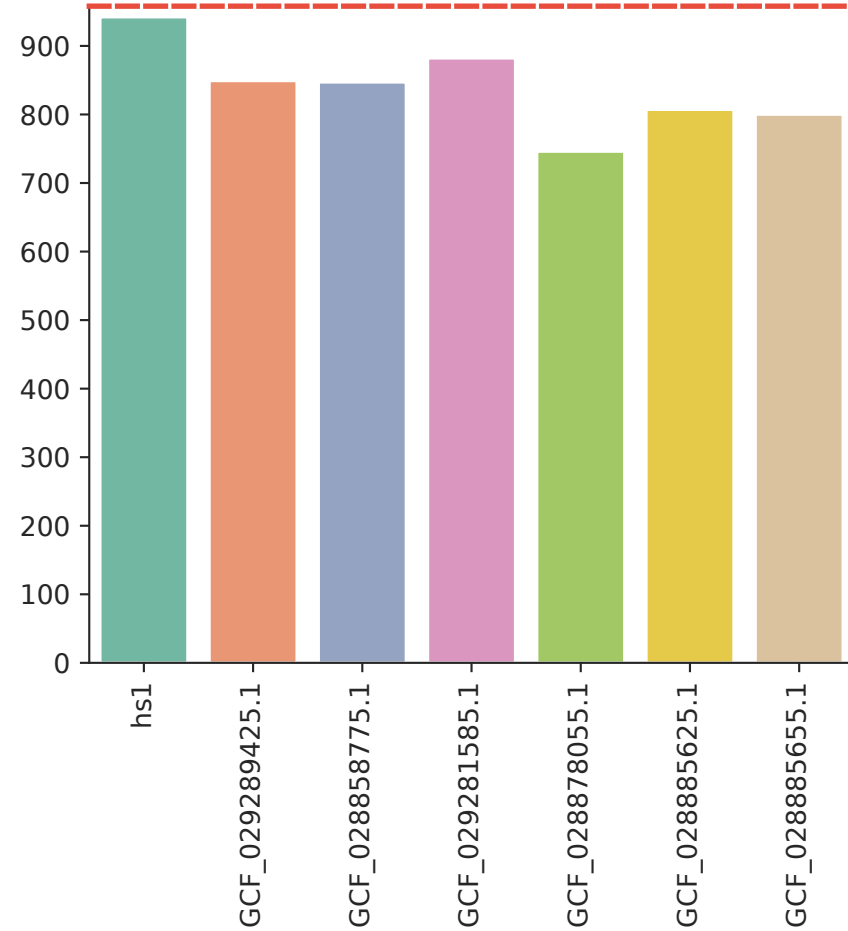


Number of comparative genes/transcripts present for biotype transcribed_unprocessed_pseudogene

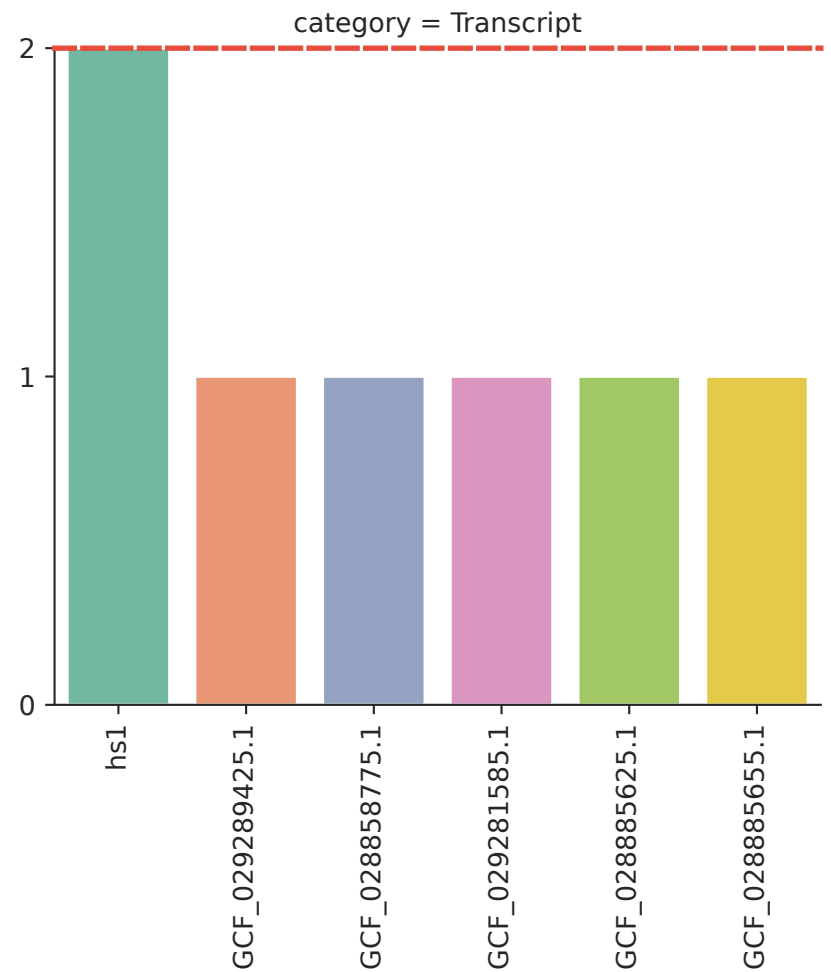
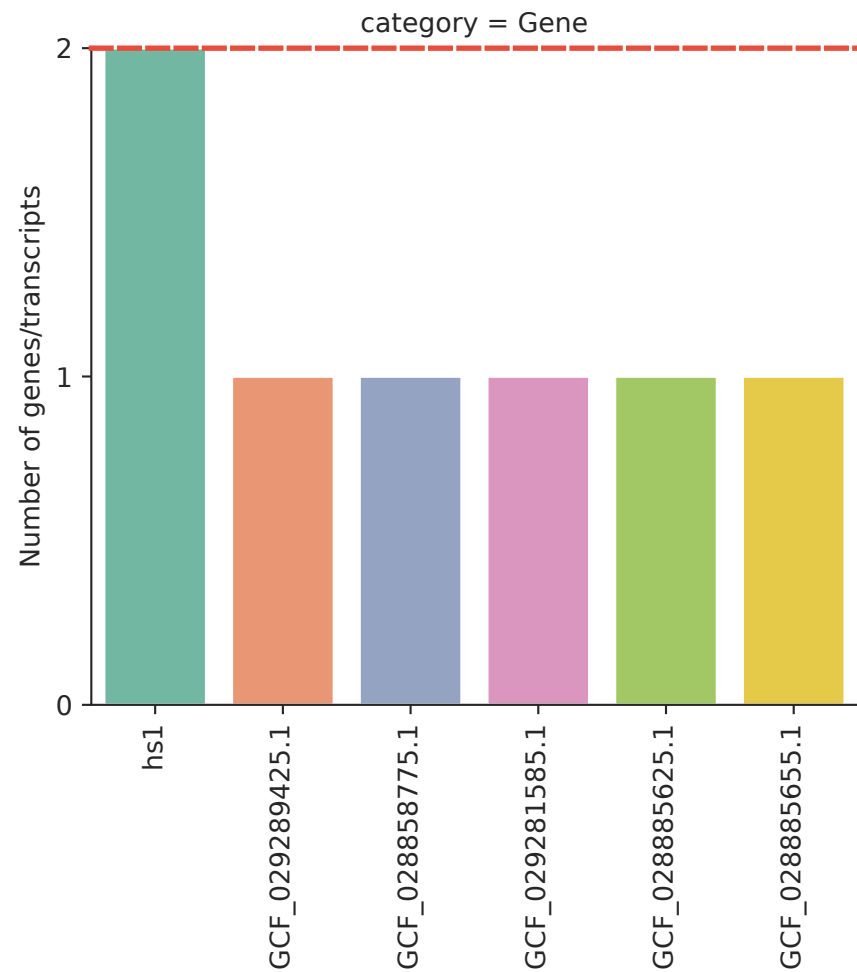
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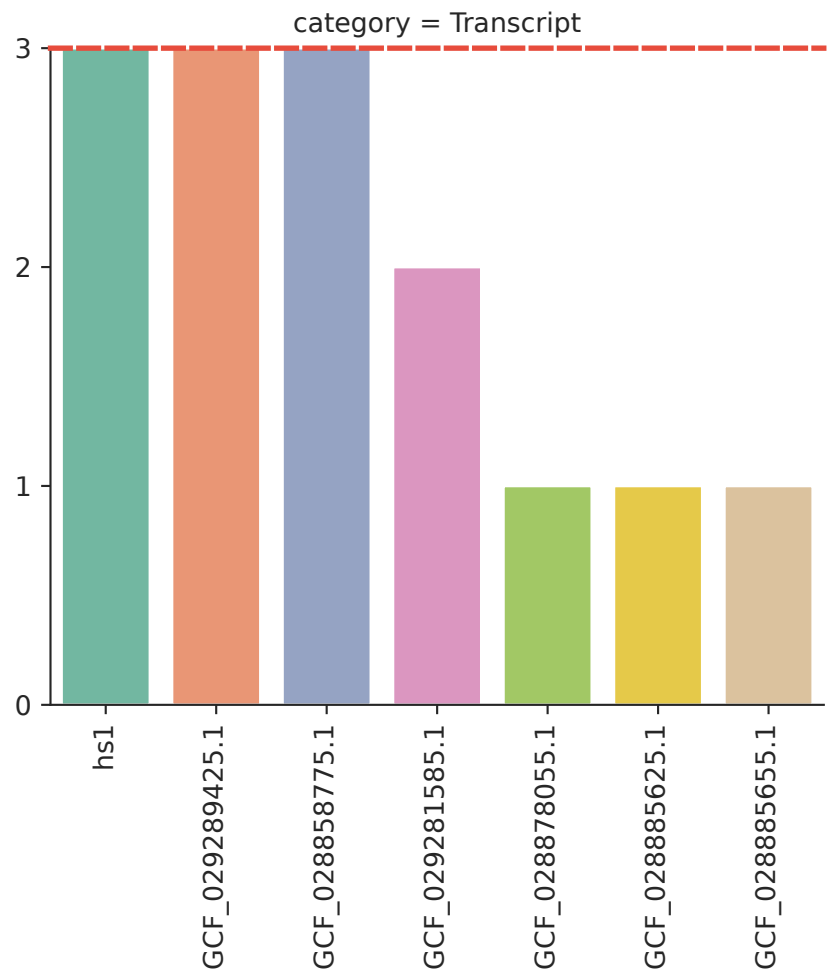
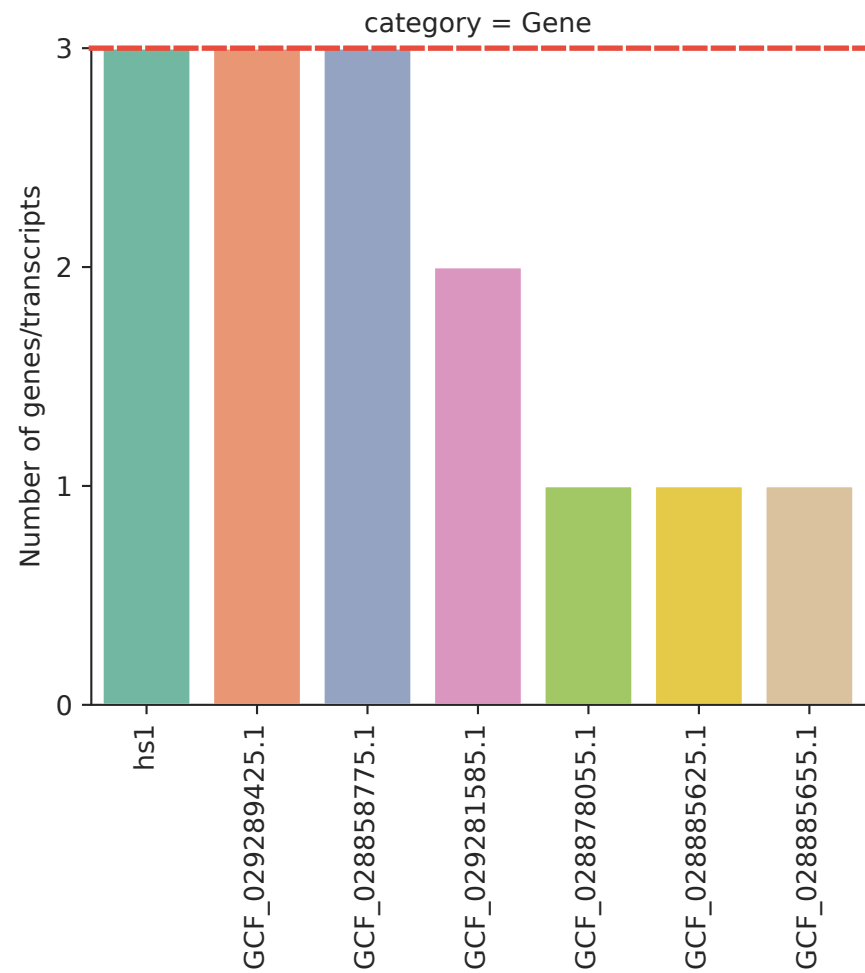
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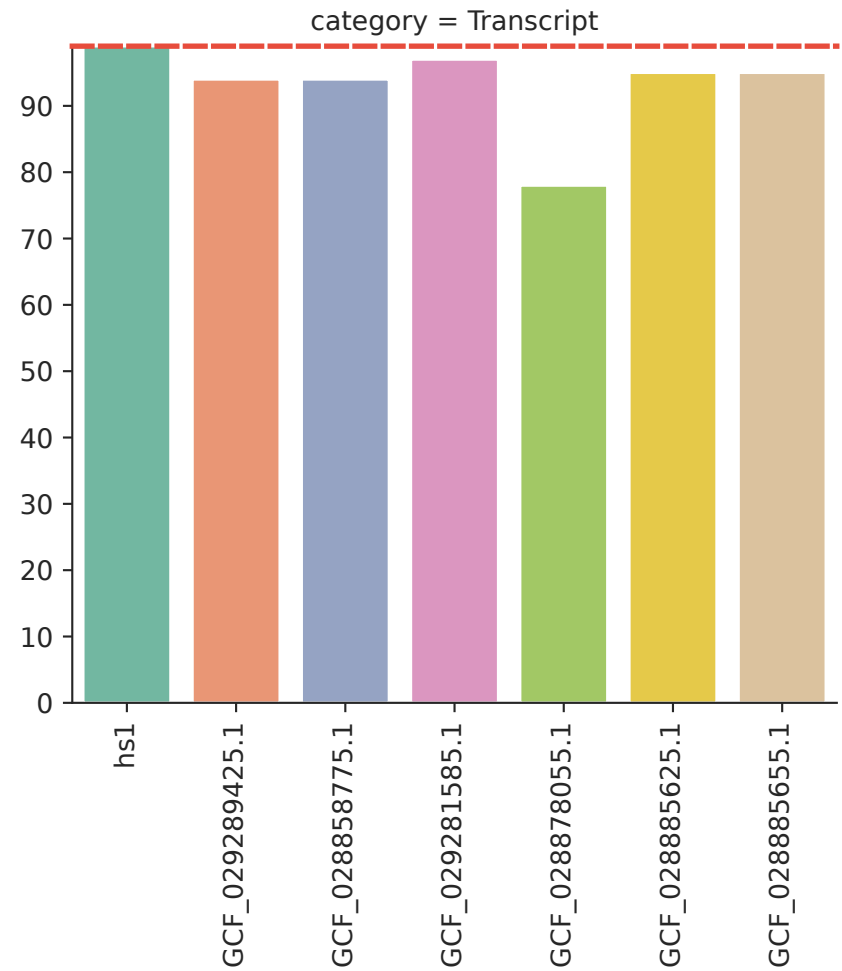
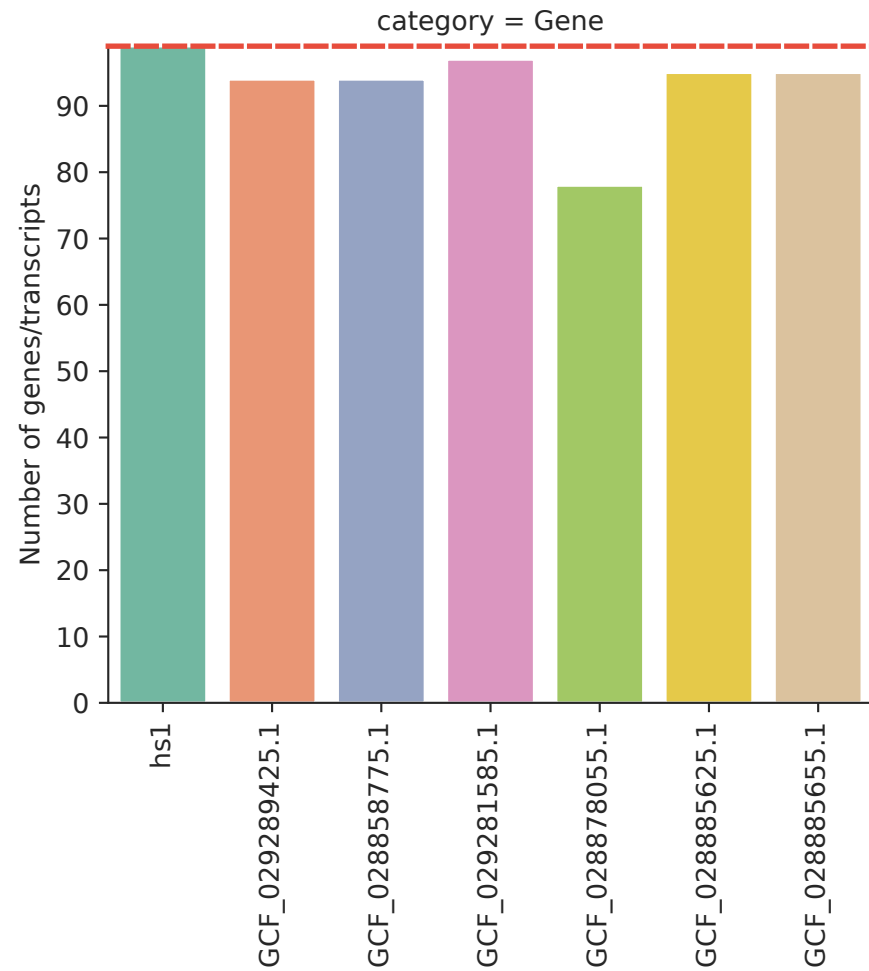
Number of comparative genes/transcripts present for biotype translated_pseudogene



Number of comparative genes/transcripts present for biotype translated_unprocessed_pseudogene

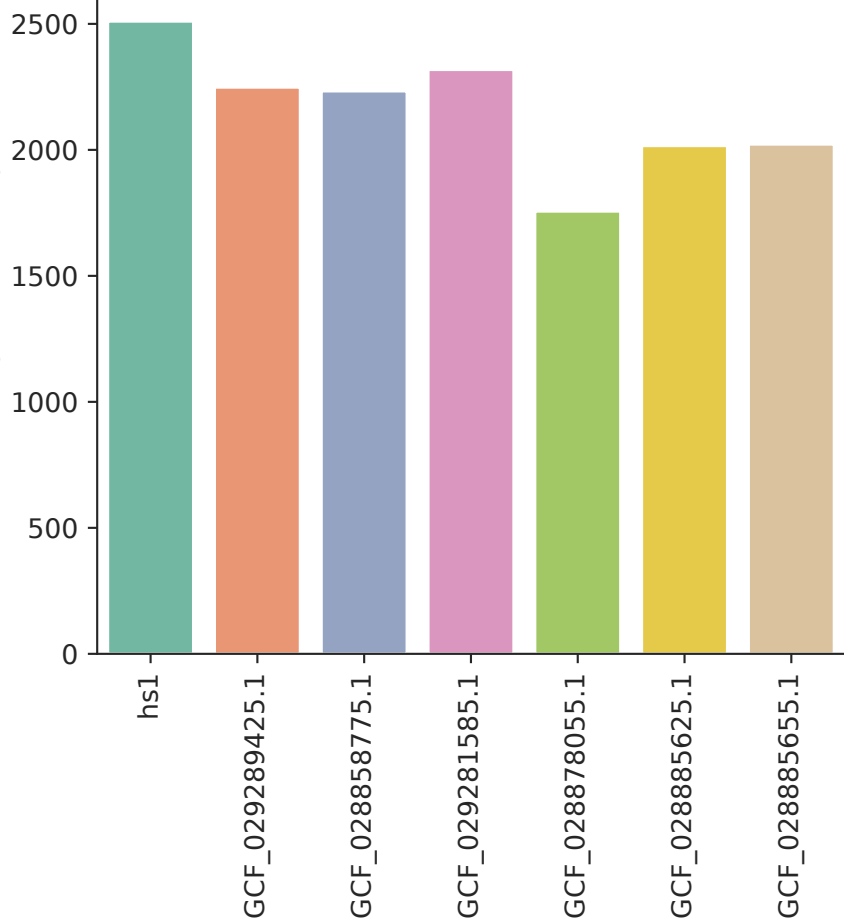


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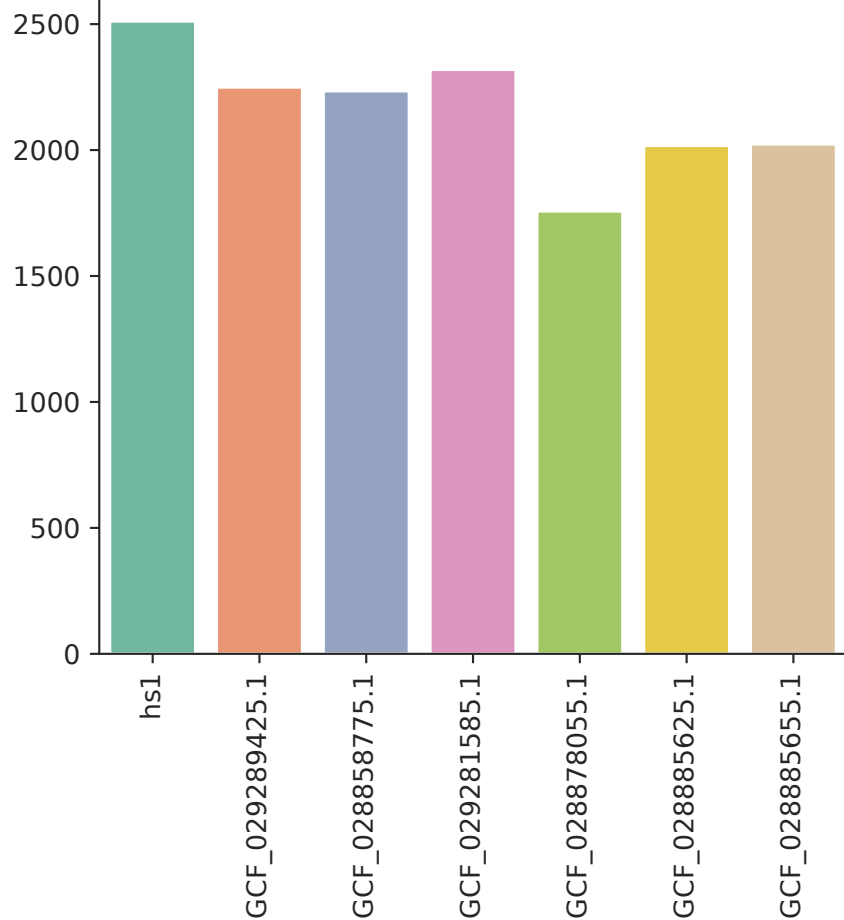


Number of comparative genes/transcripts present for biotype unprocessed_pseudogene

category = Gene



category = Transcript



Number of comparative genes/transcripts present for biotype vault_RNA

