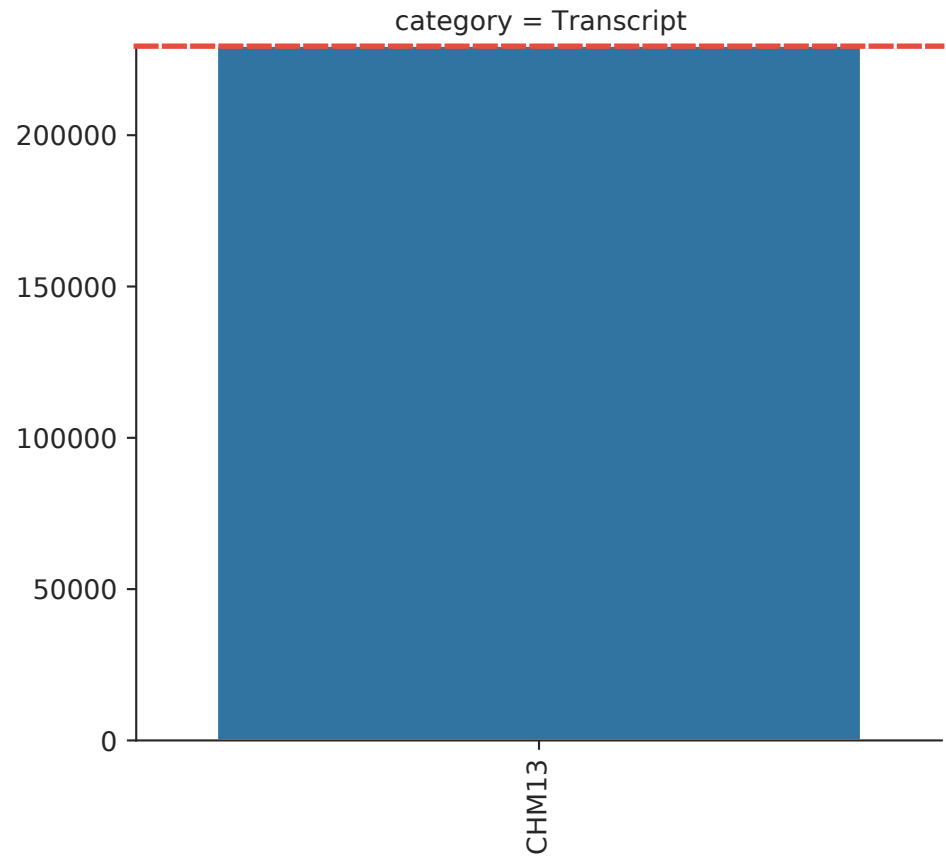
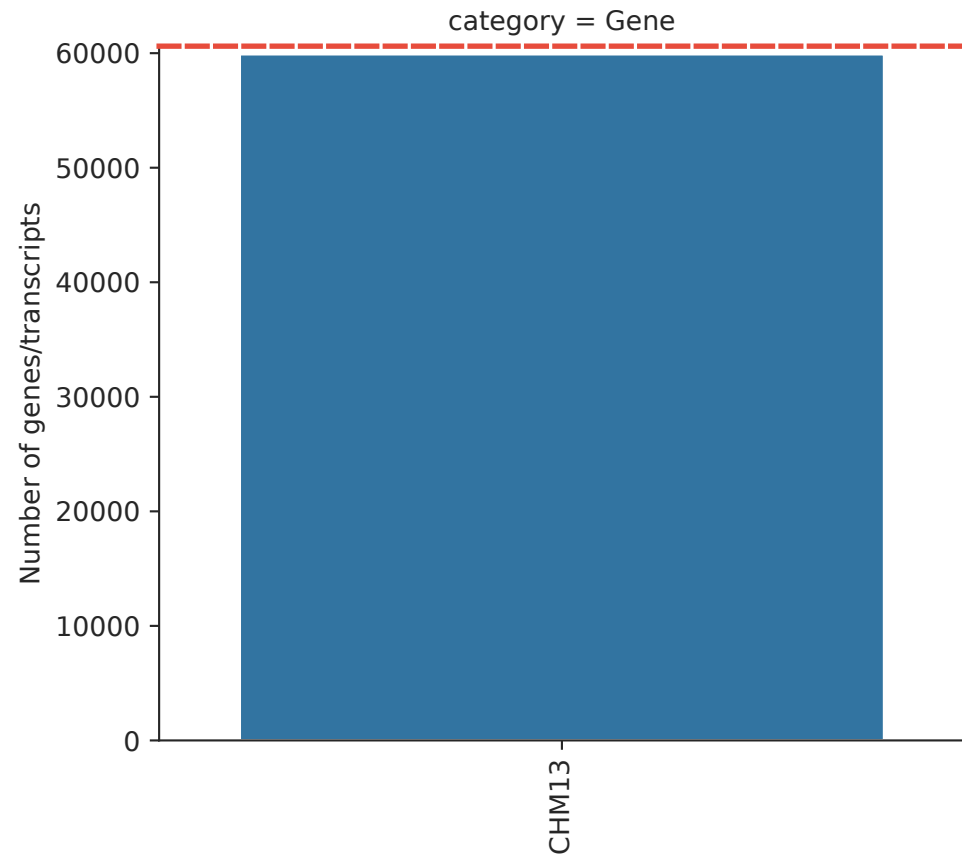
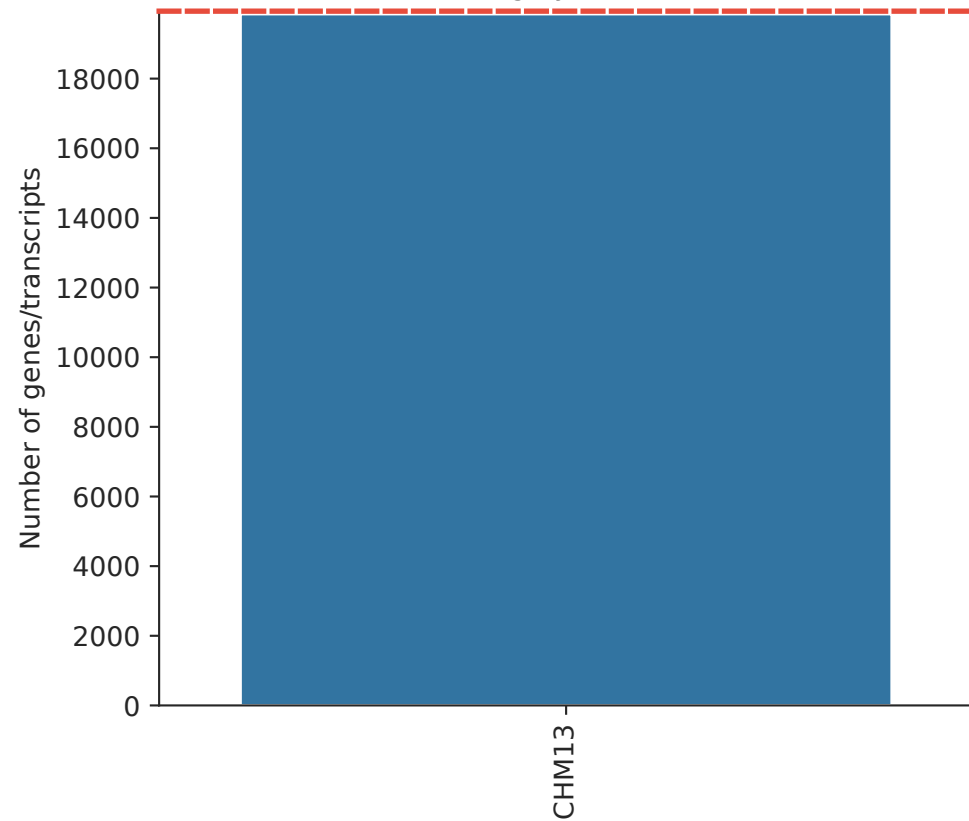


# Number of comparative genes/transcripts present

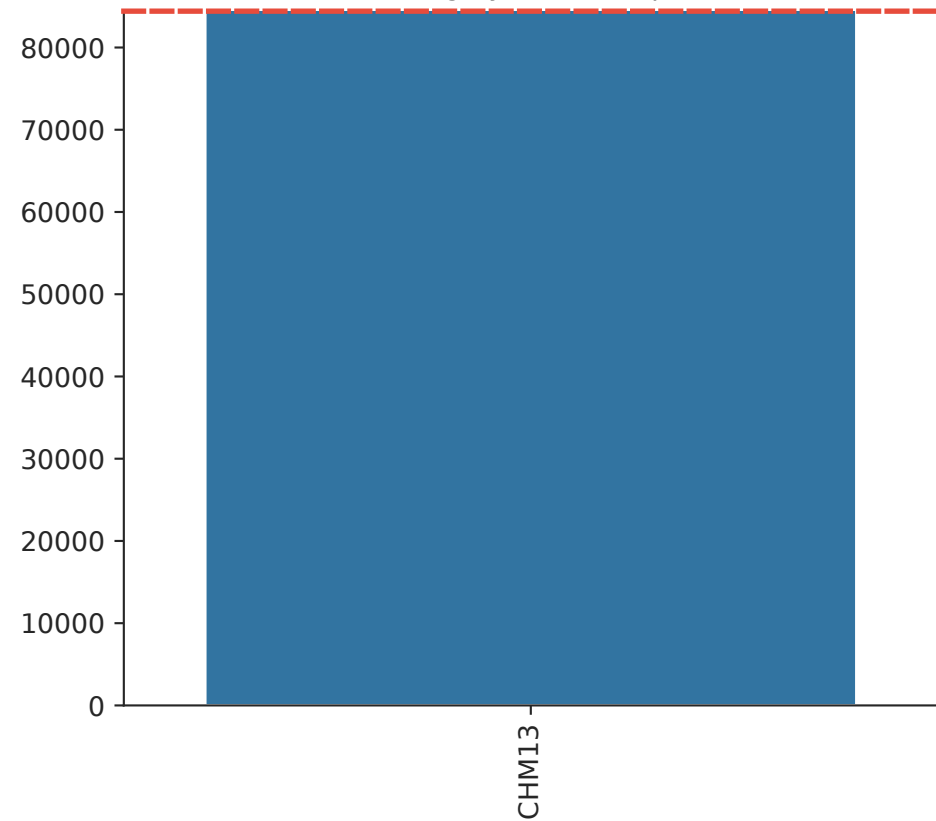


# Number of comparative genes/transcripts present for biotype protein\_coding

category = Gene

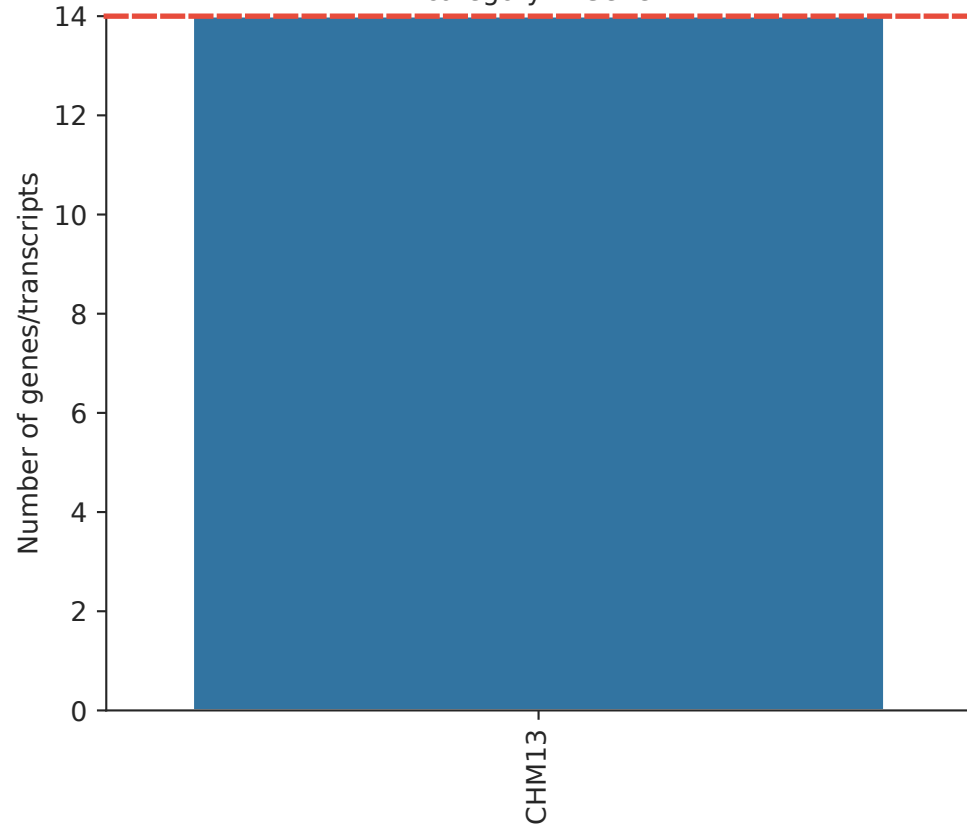


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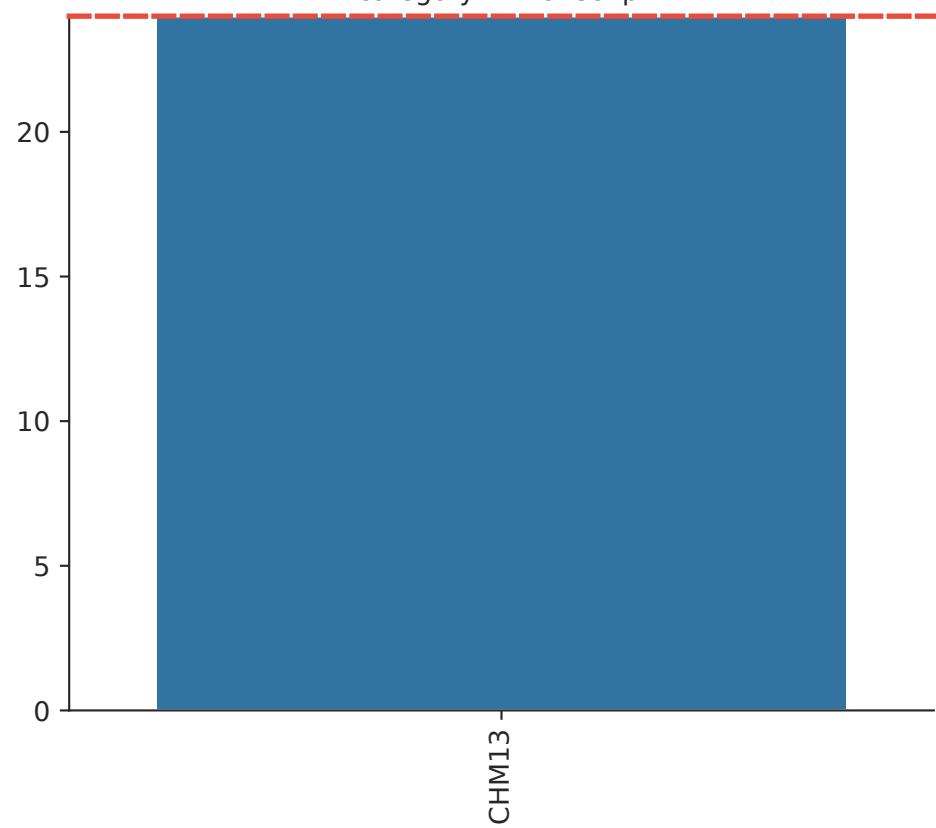


# Number of comparative genes/transcripts present for biotype IG\_C\_gene

category = Gene

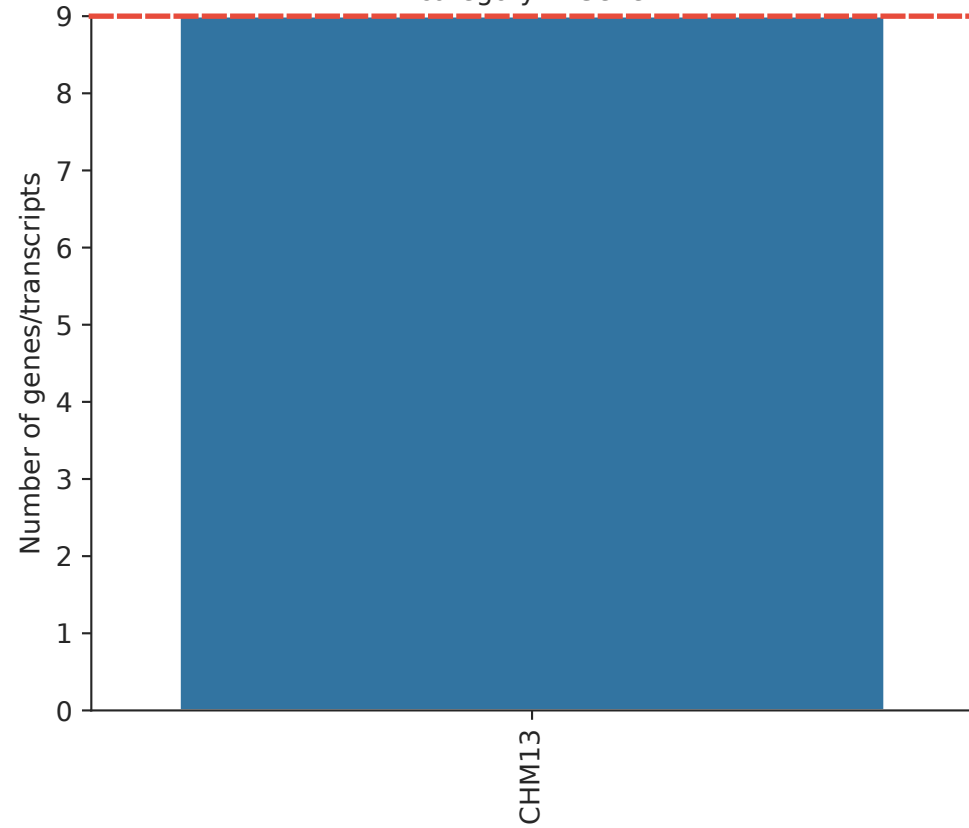


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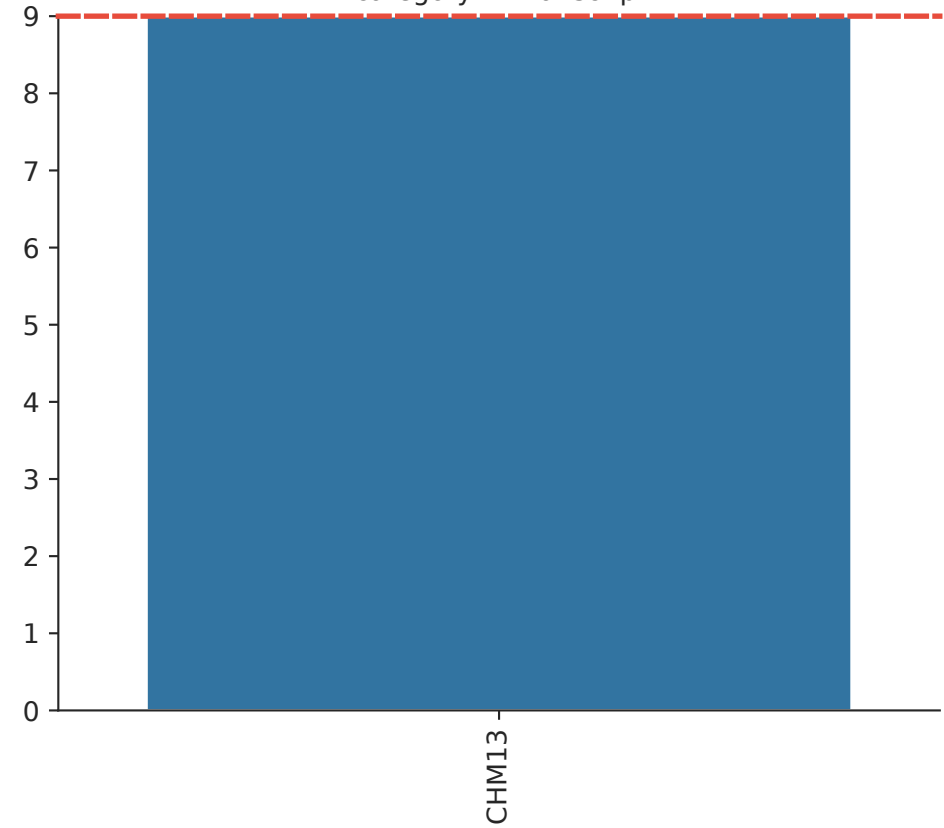


# Number of comparative genes/transcripts present for biotype IG\_C\_pseudogene

category = Gene

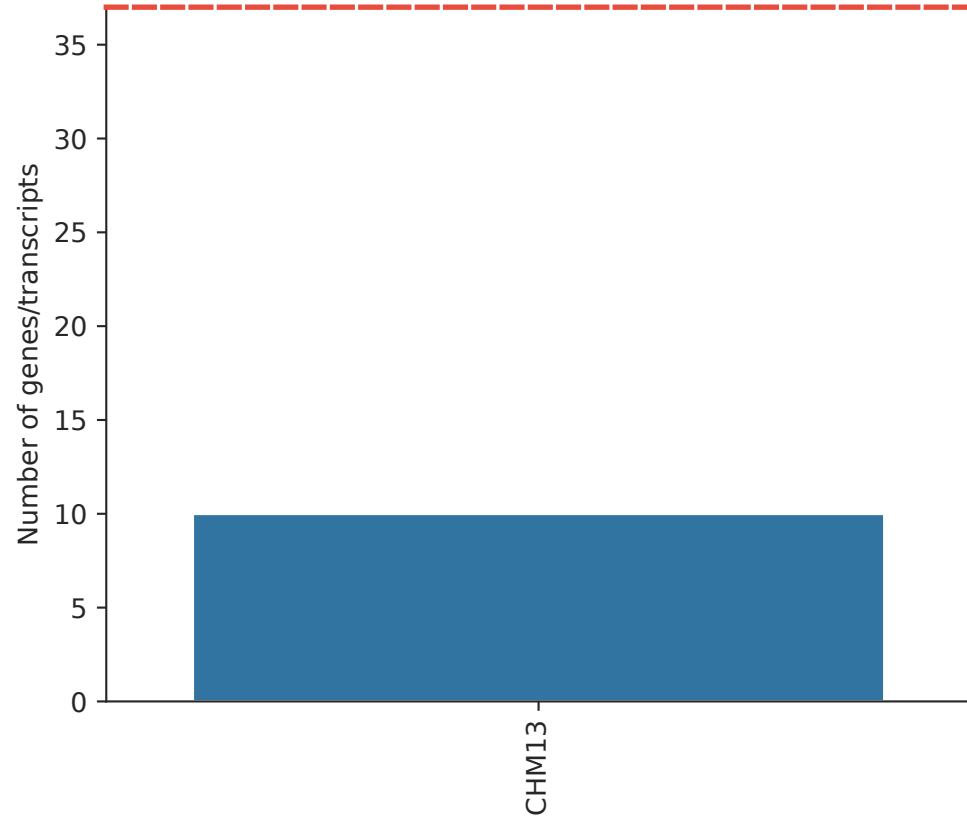


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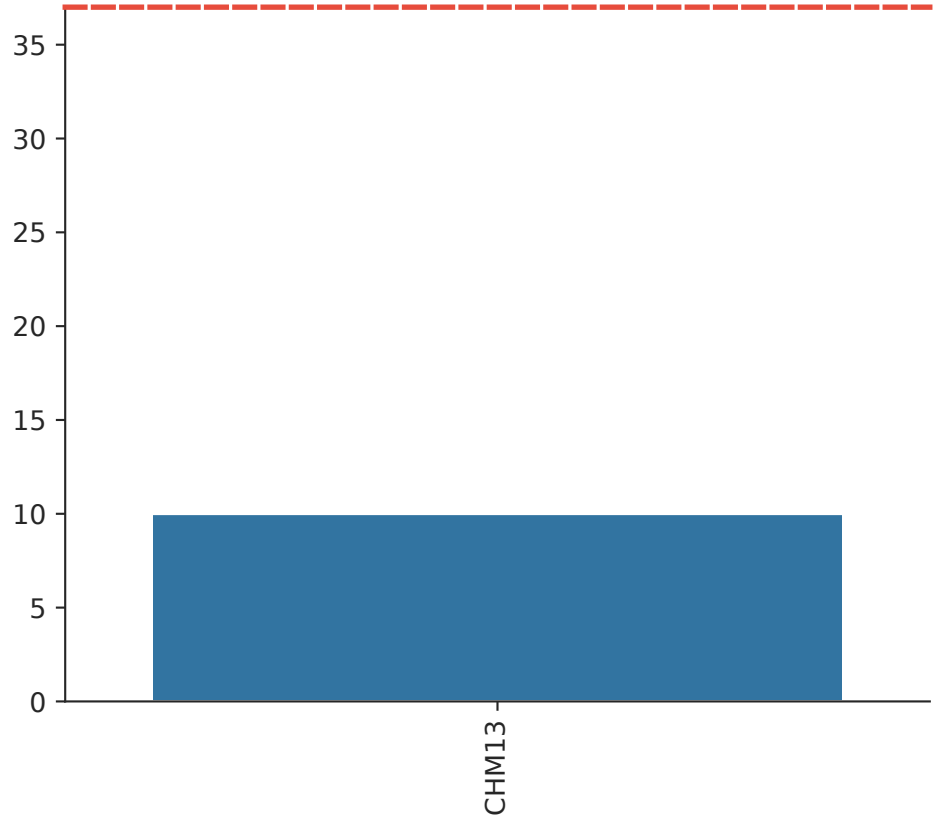


# Number of comparative genes/transcripts present for biotype IG\_D\_gene

category = Gene

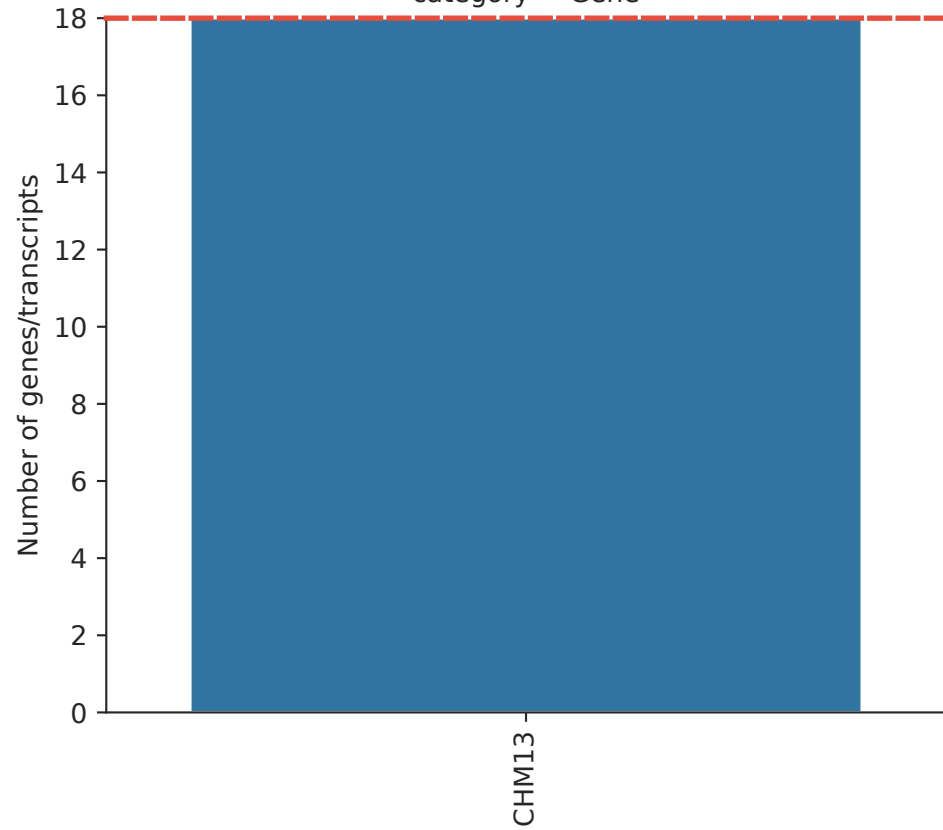


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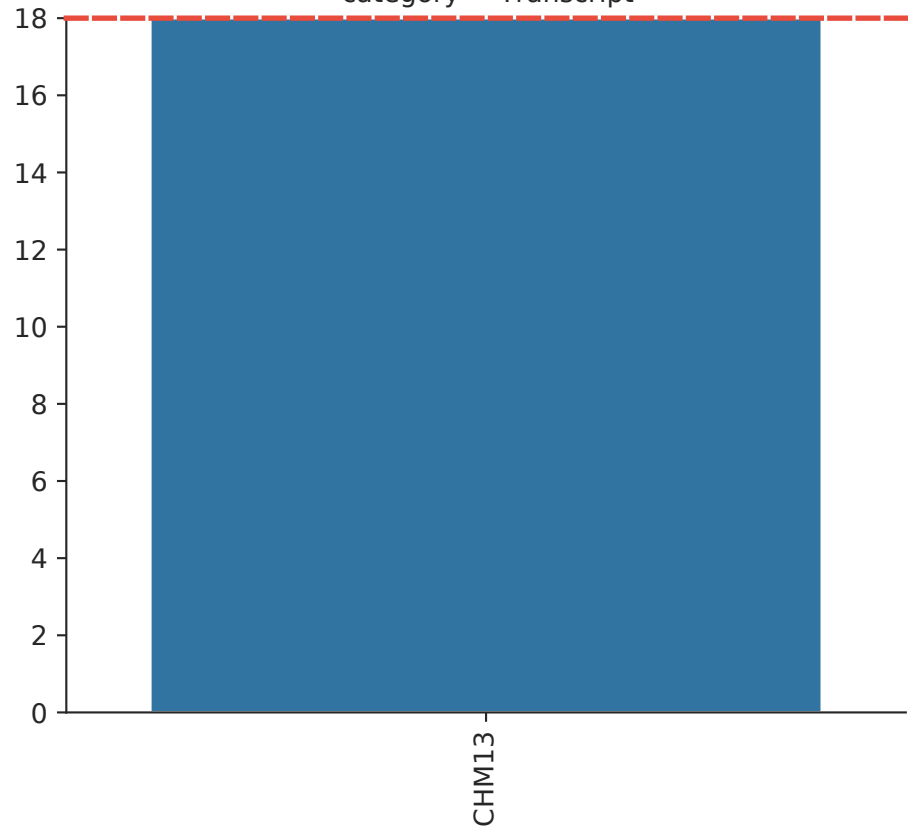


# Number of comparative genes/transcripts present for biotype IG\_J\_gene

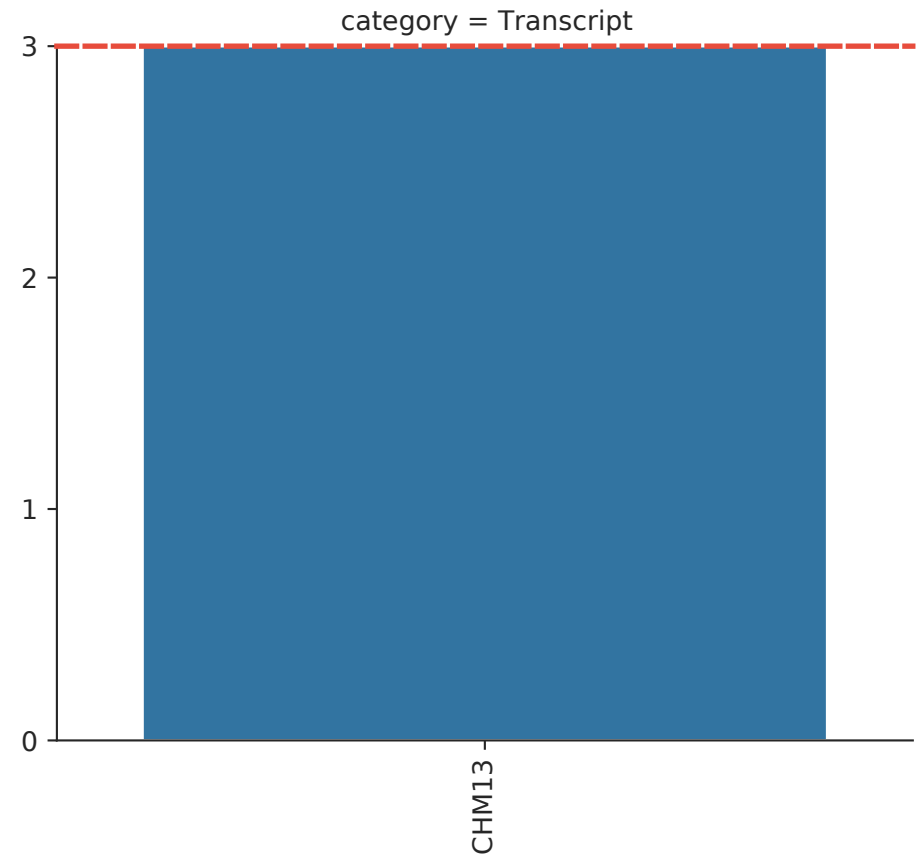
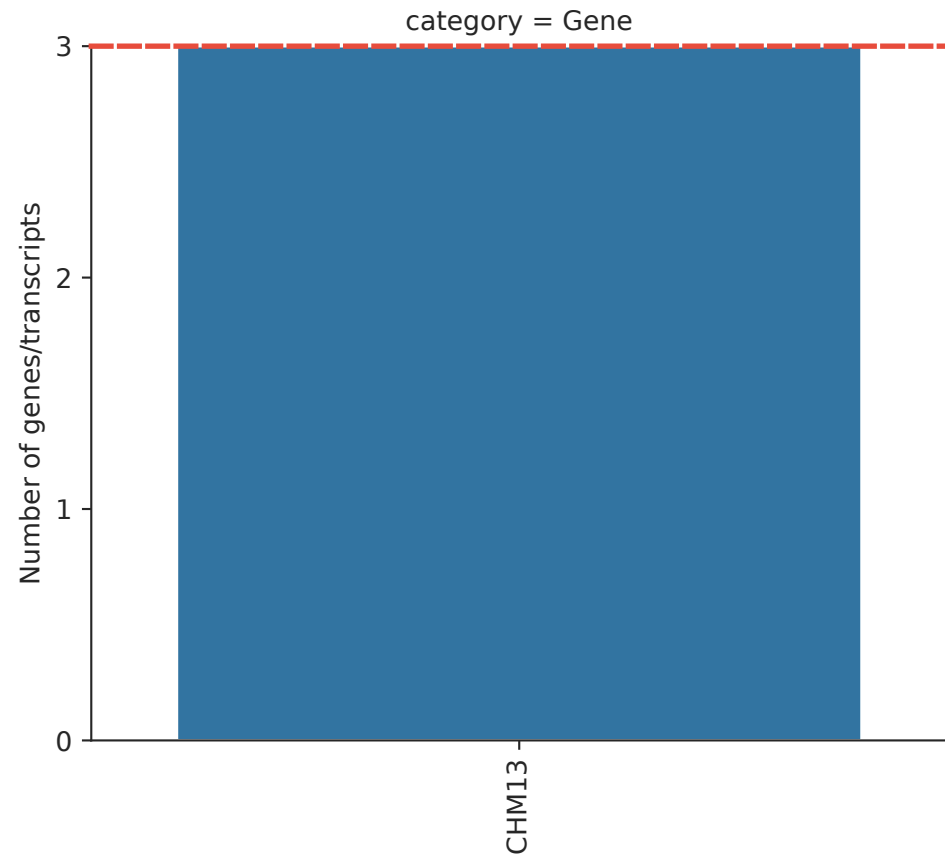
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category = Transcript

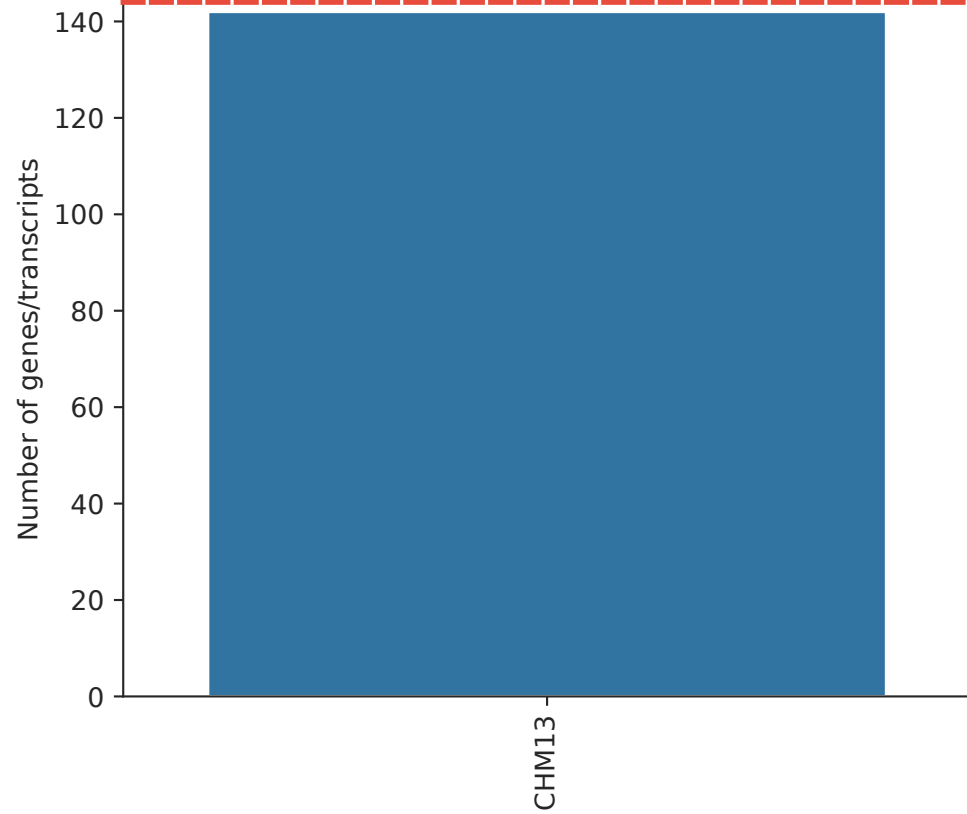


# Number of comparative genes/transcripts present for biotype IG\_J\_pseudogene

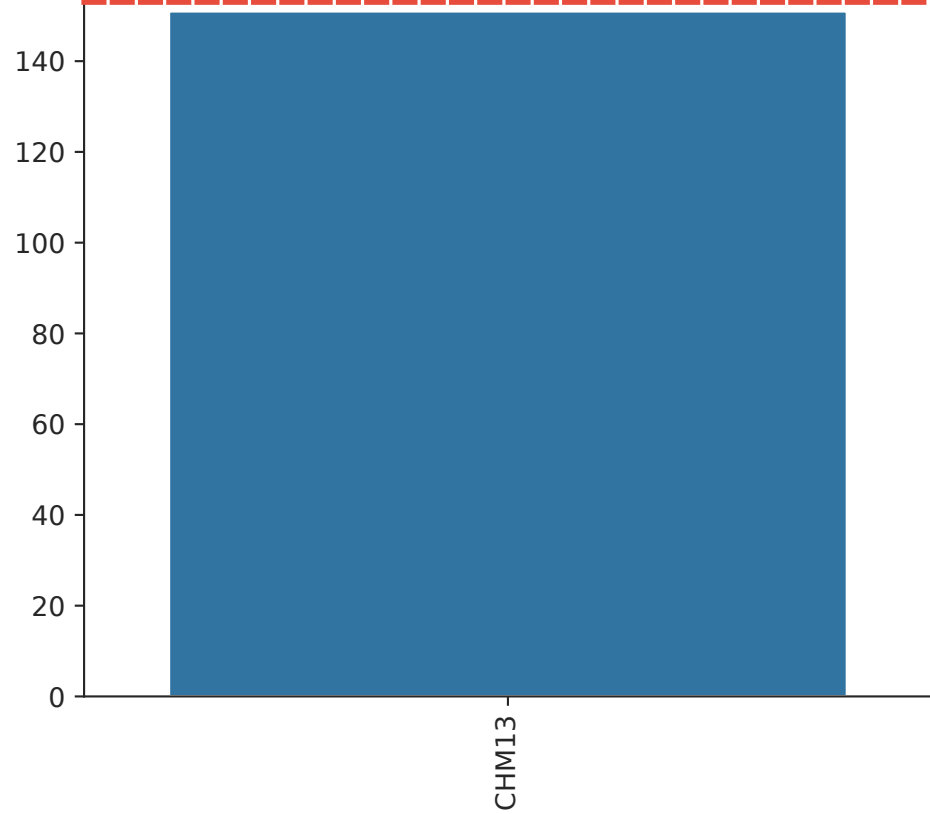


# Number of comparative genes/transcripts present for biotype IG\_V\_gene

category = Gene



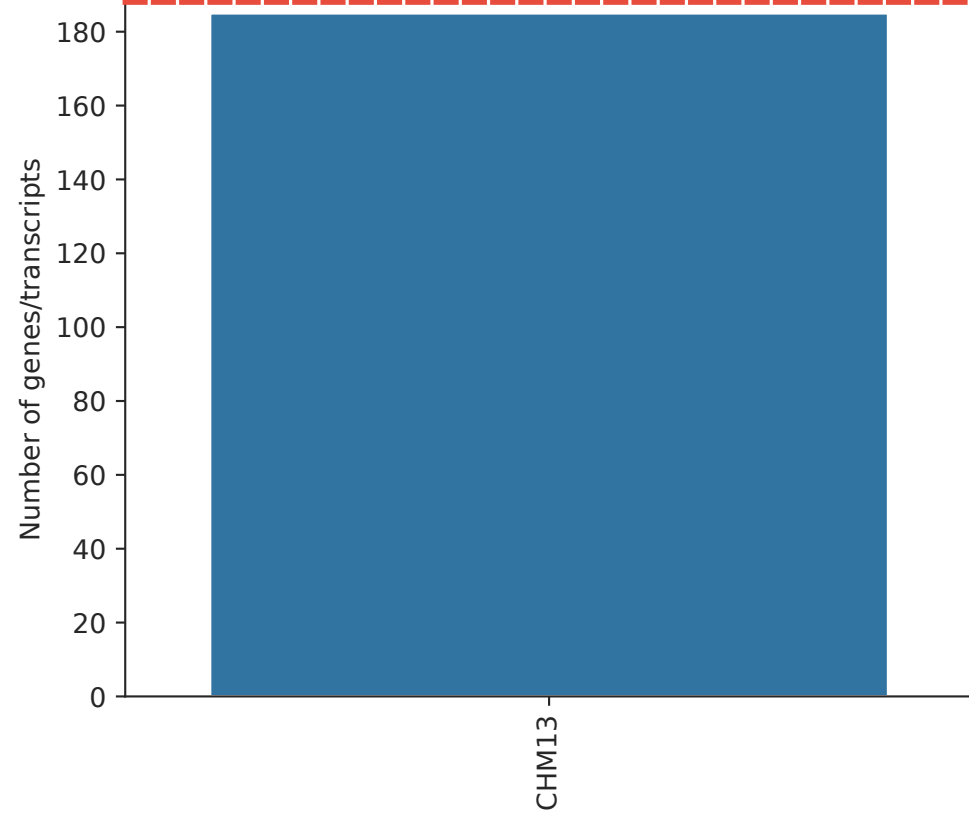
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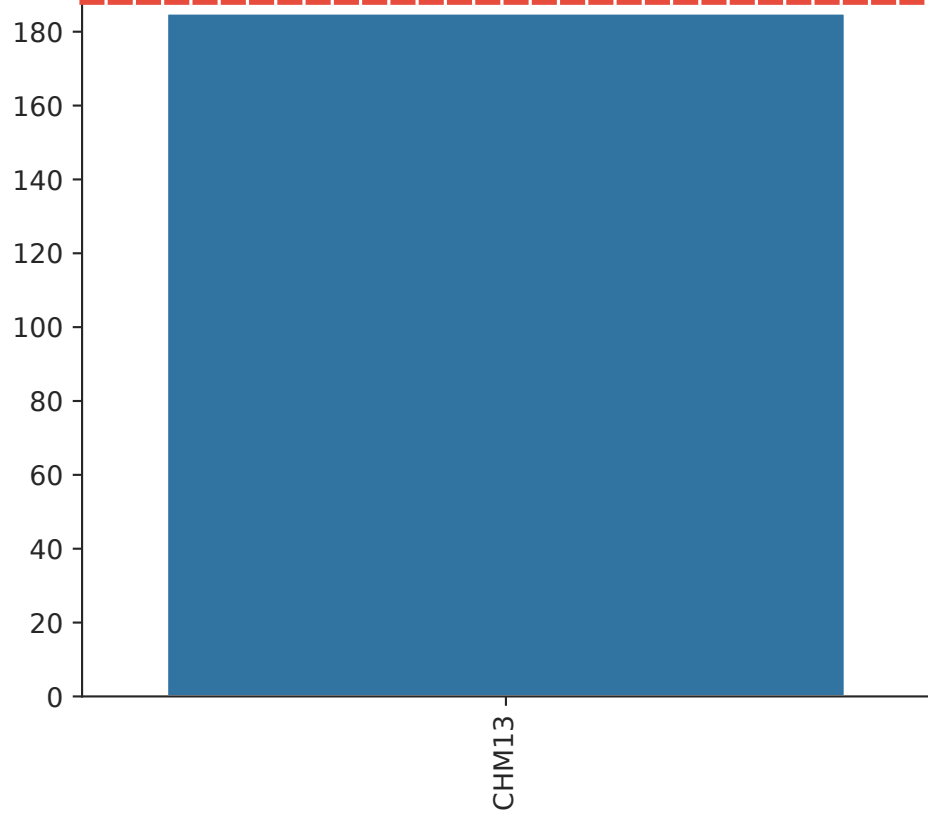


# Number of comparative genes/transcripts present for biotype IG\_V\_pseudogene

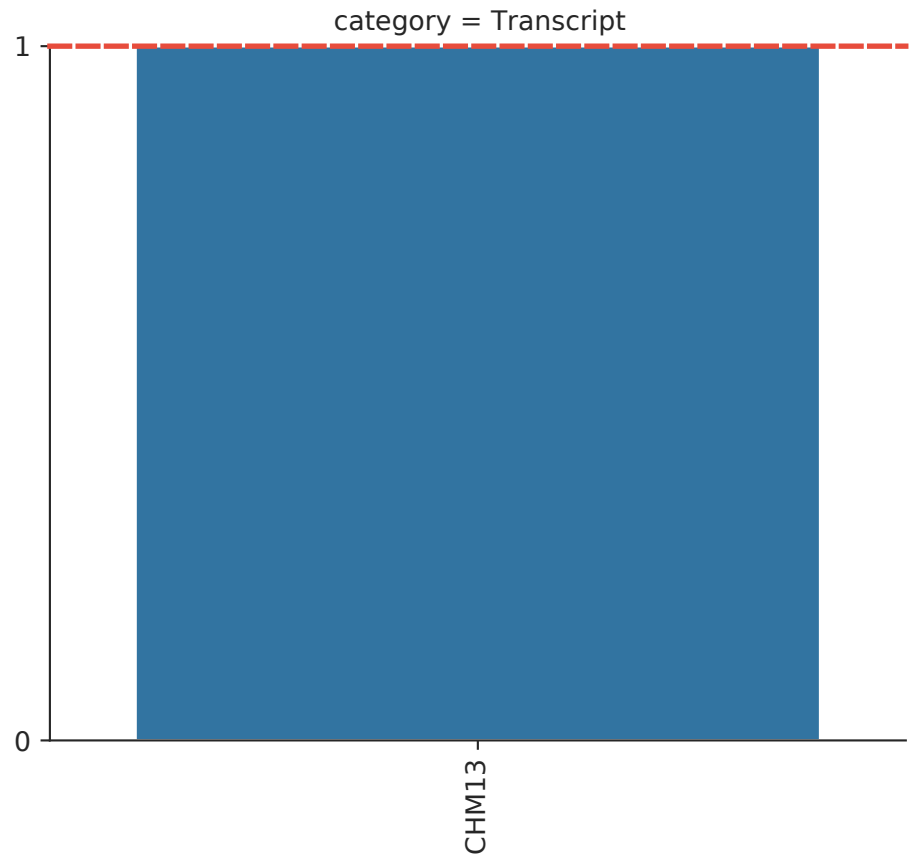
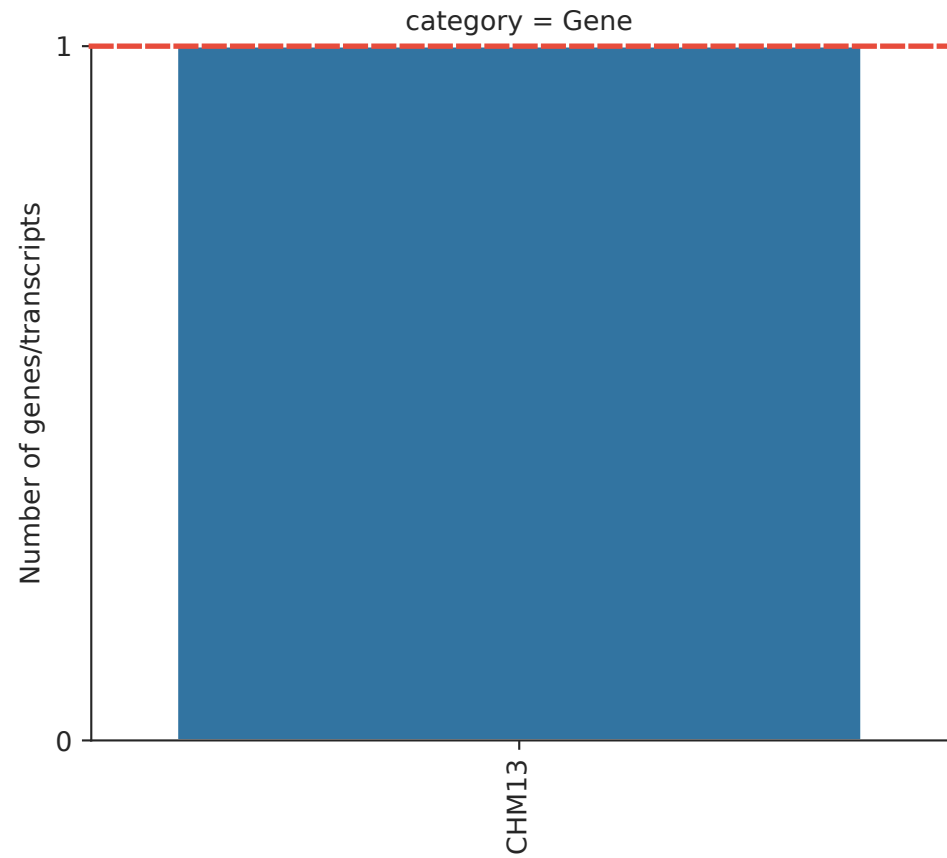
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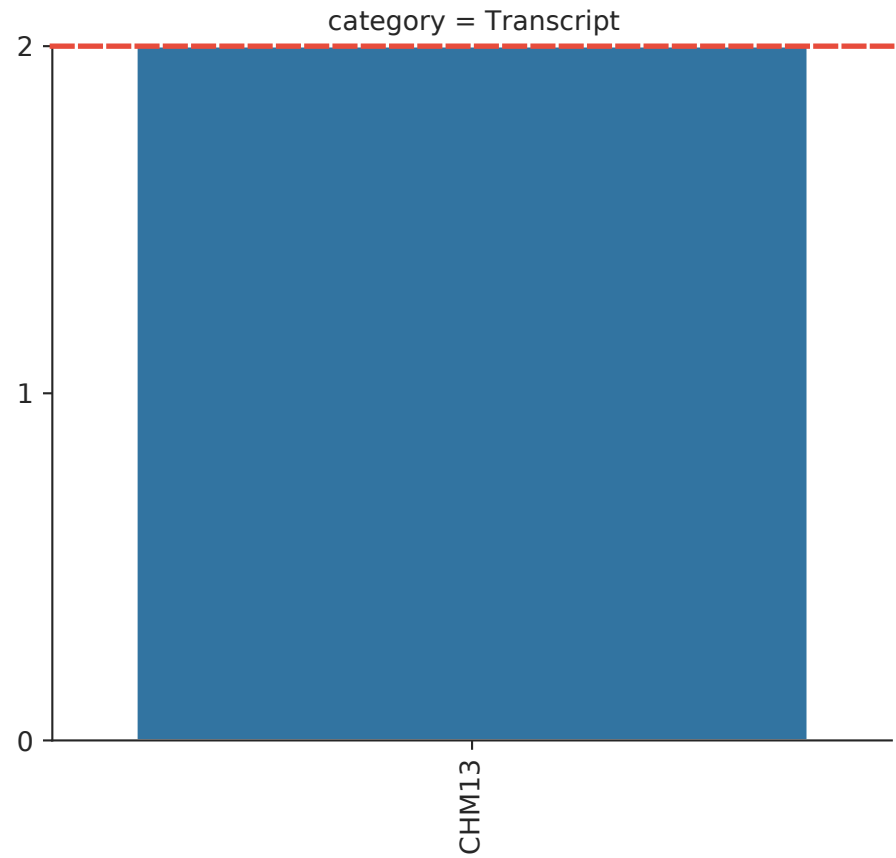
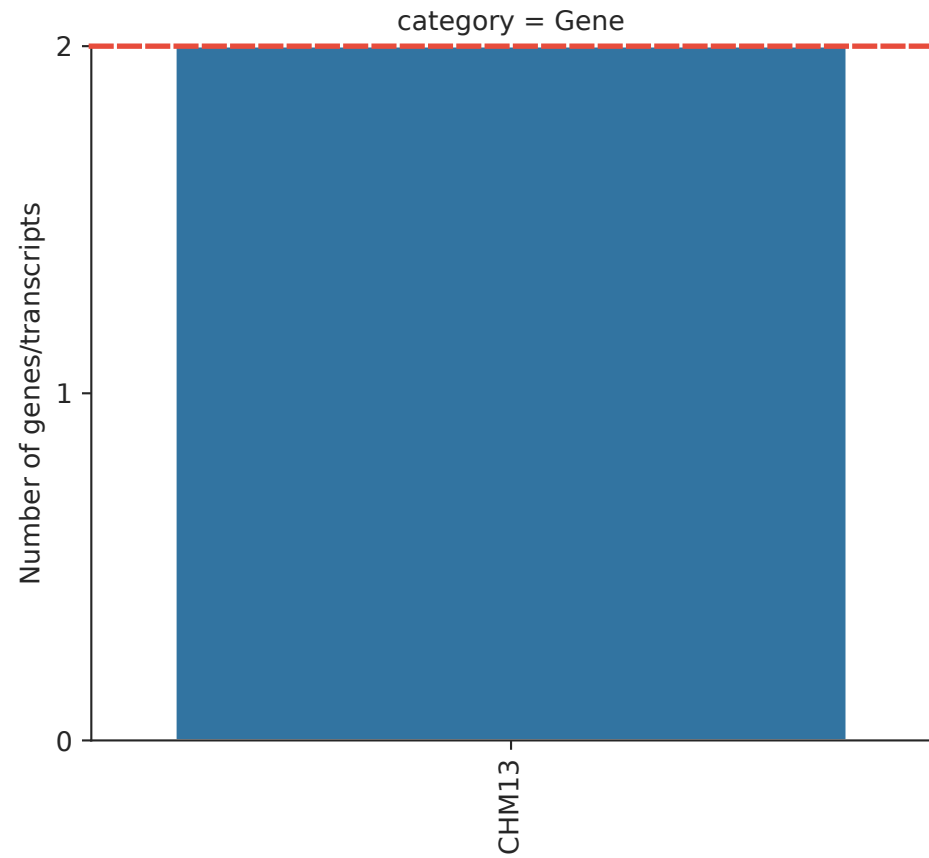
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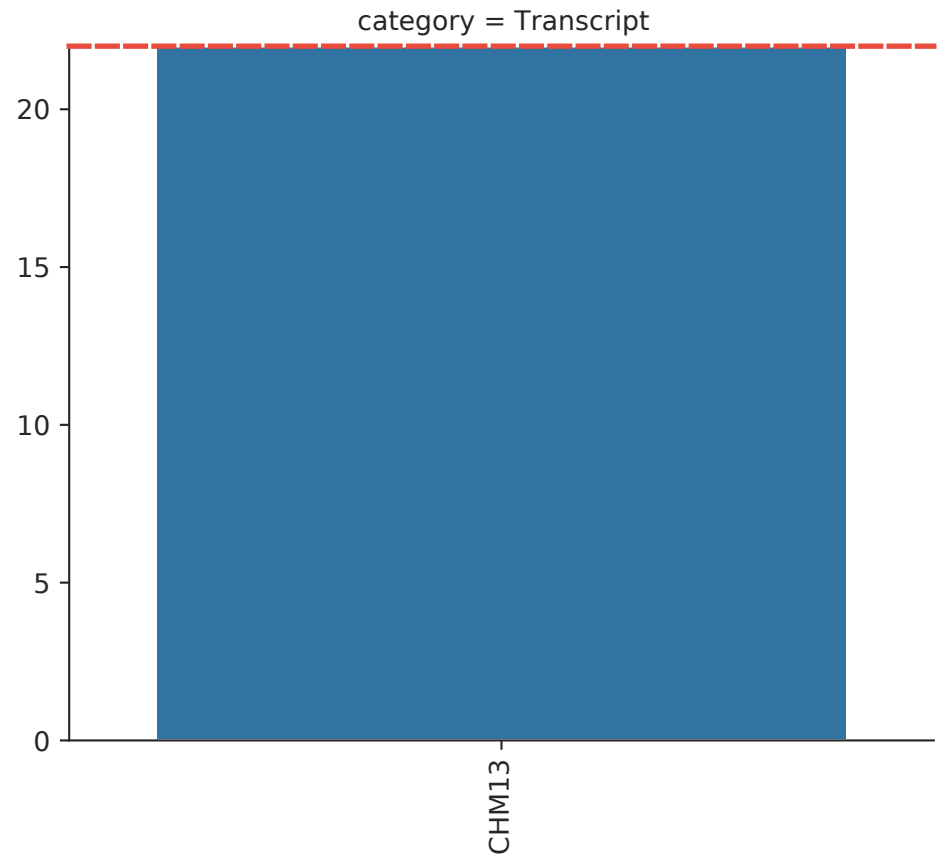
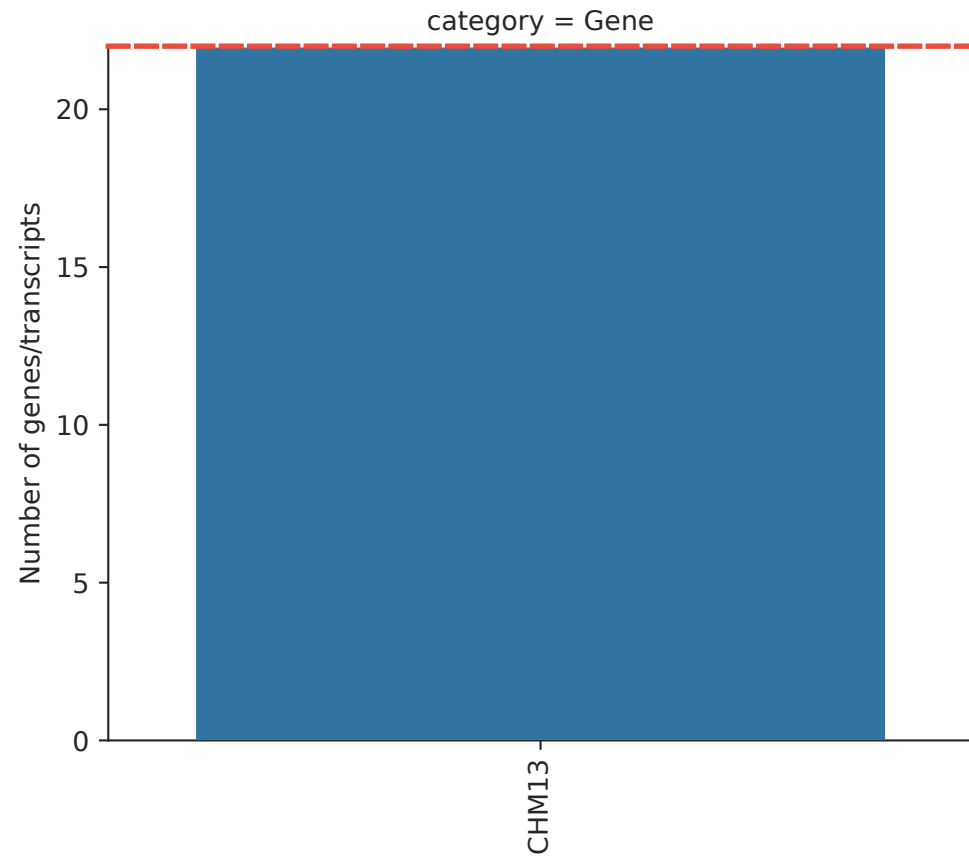
# Number of comparative genes/transcripts present for biotype IG\_pseudogene



# Number of comparative genes/transcripts present for biotype Mt\_rRNA

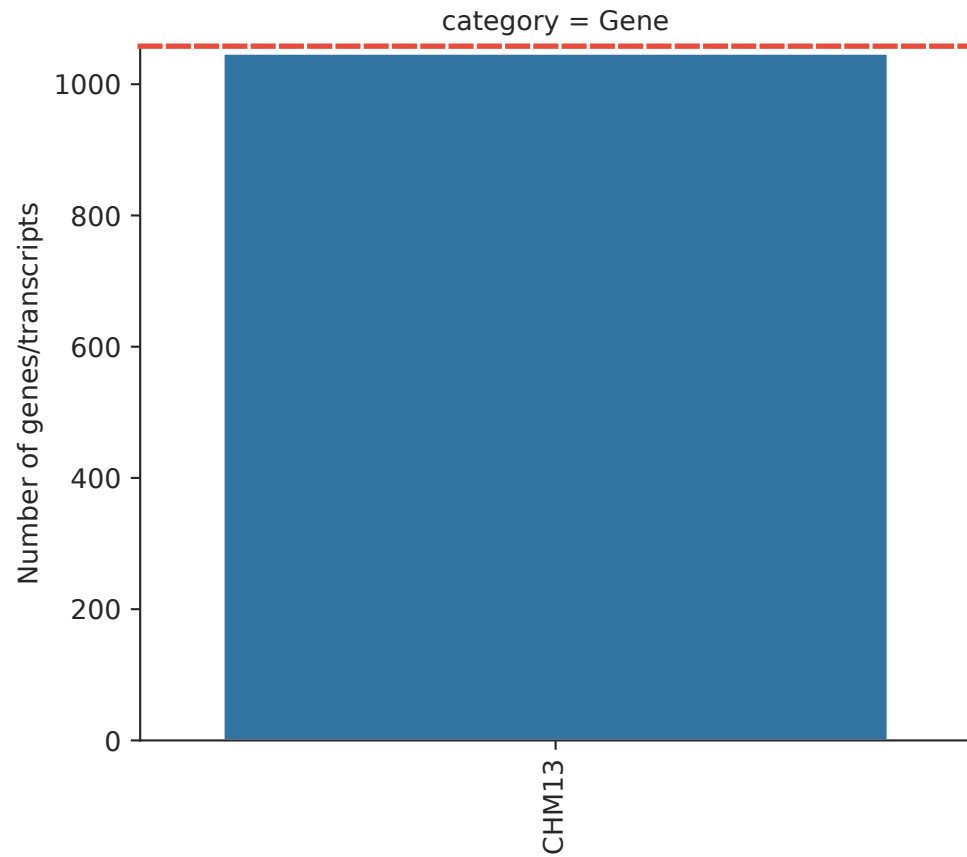


# Number of comparative genes/transcripts present for biotype Mt\_tRNA

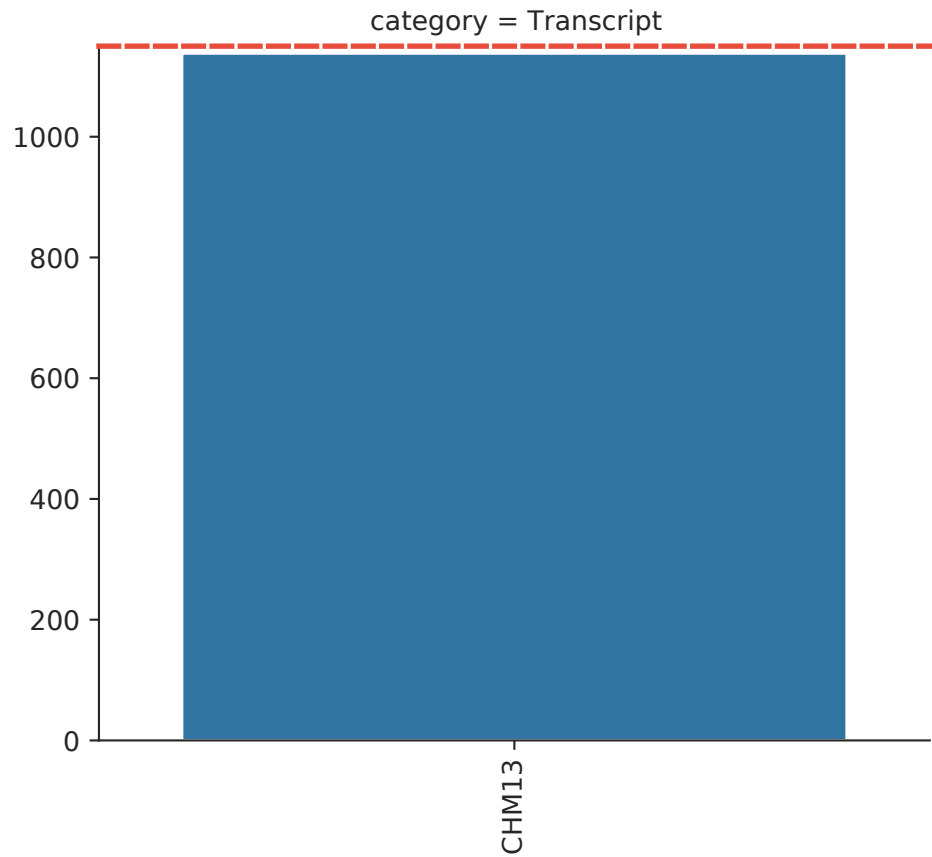


# Number of comparative genes/transcripts present for biotype TEC

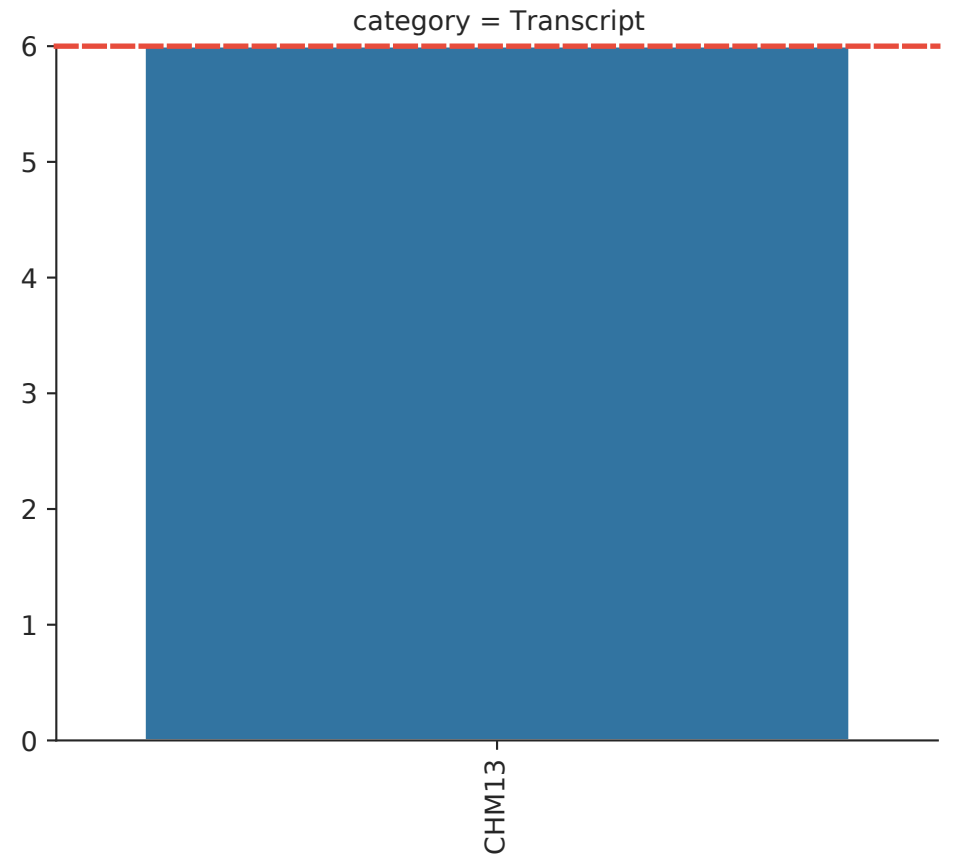
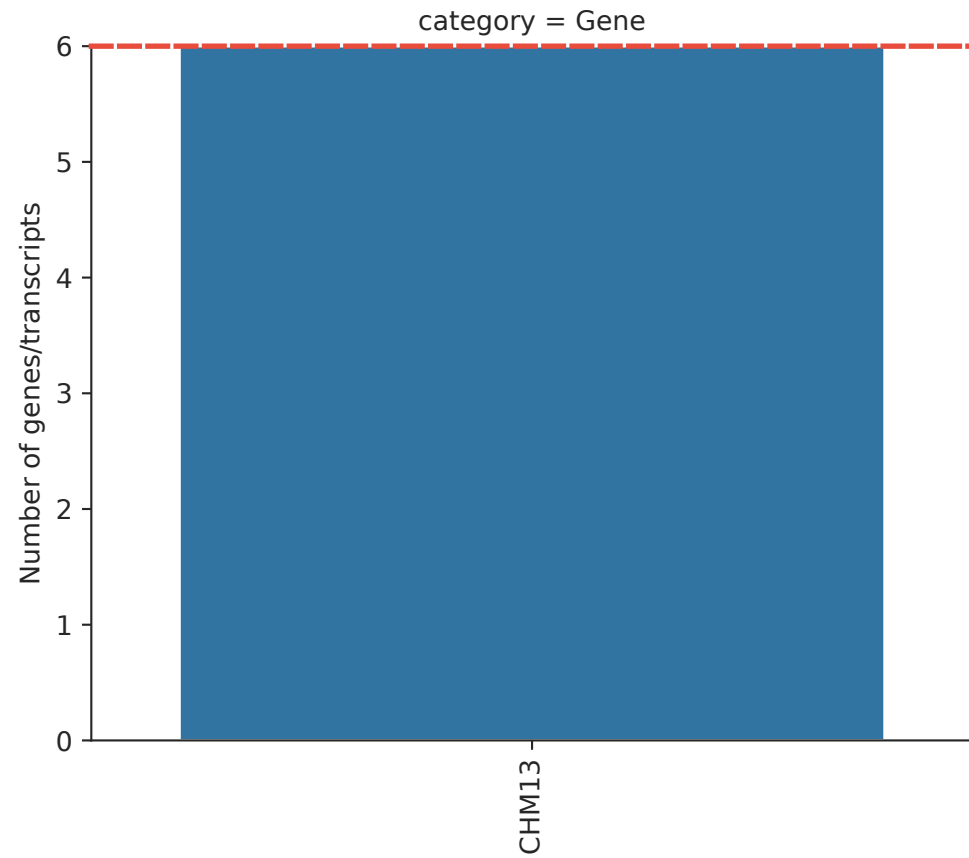
category = Gene



category = Transcript

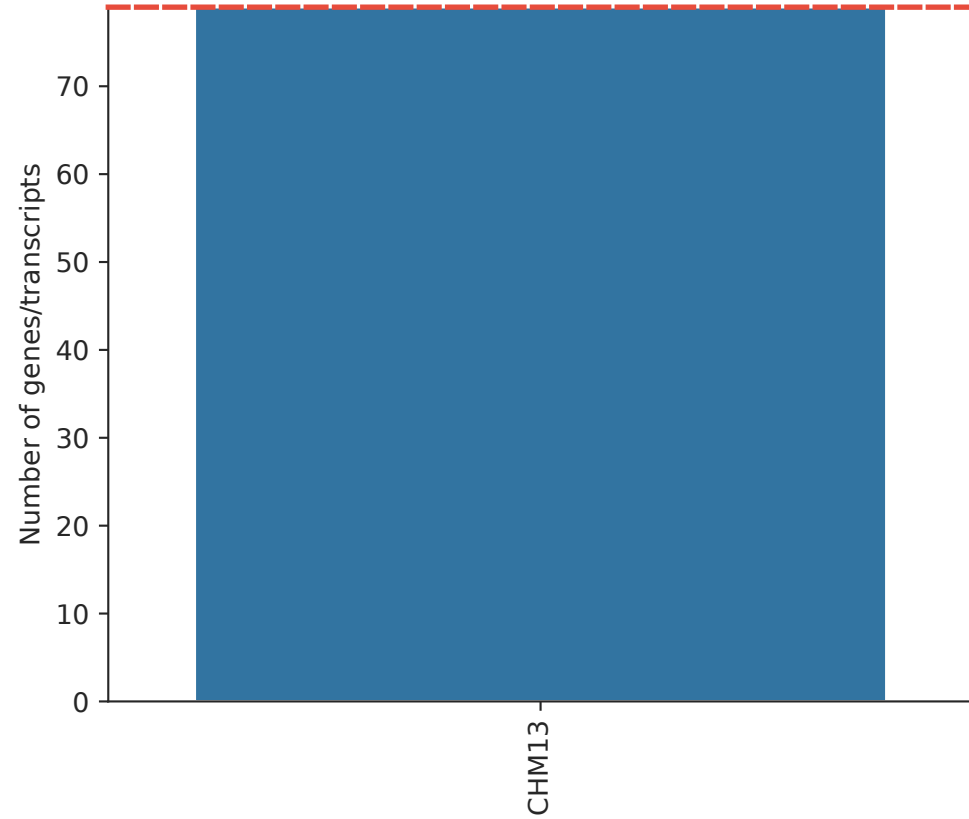


# Number of comparative genes/transcripts present for biotype TR\_C\_gene

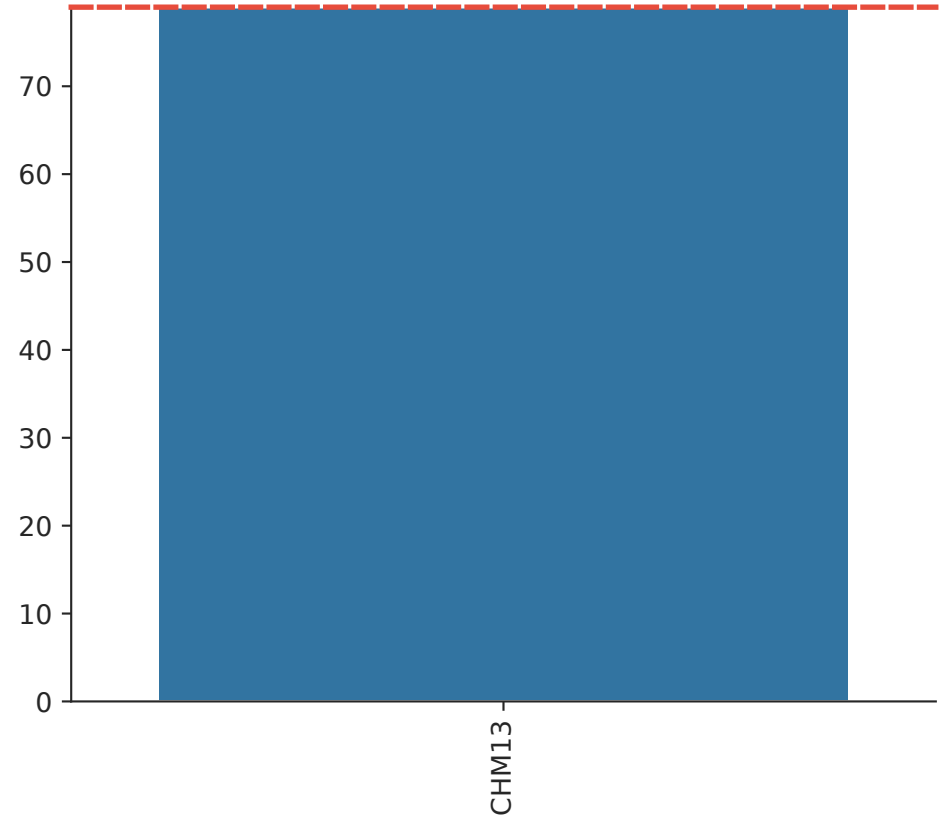


# Number of comparative genes/transcripts present for biotype TR\_J\_gene

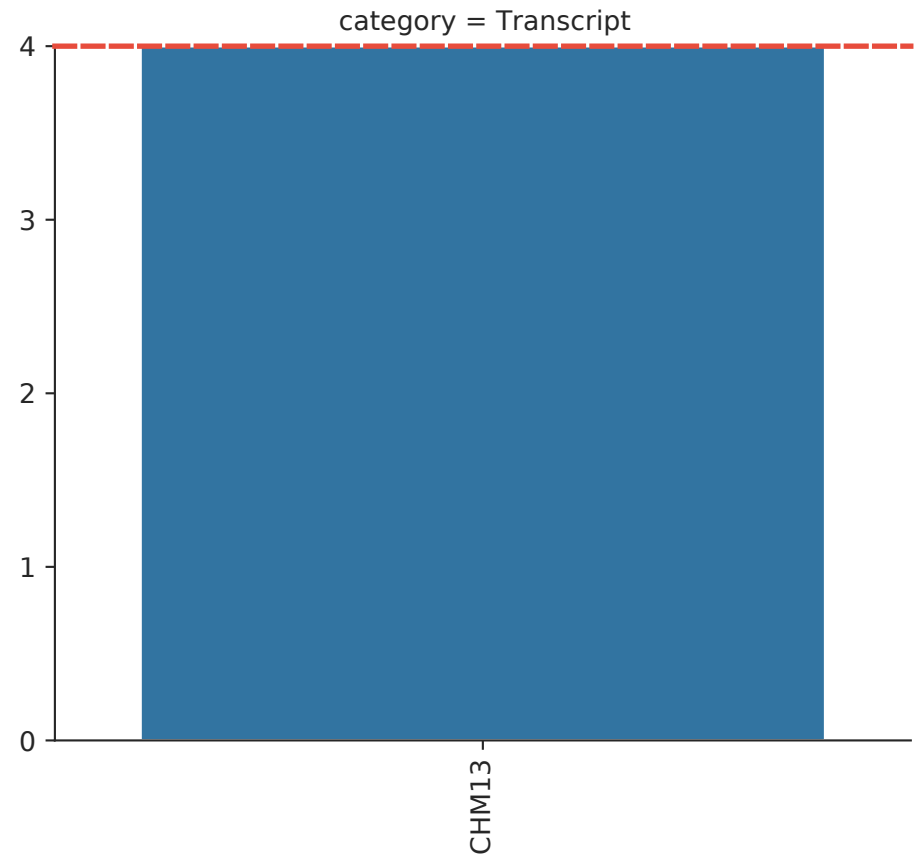
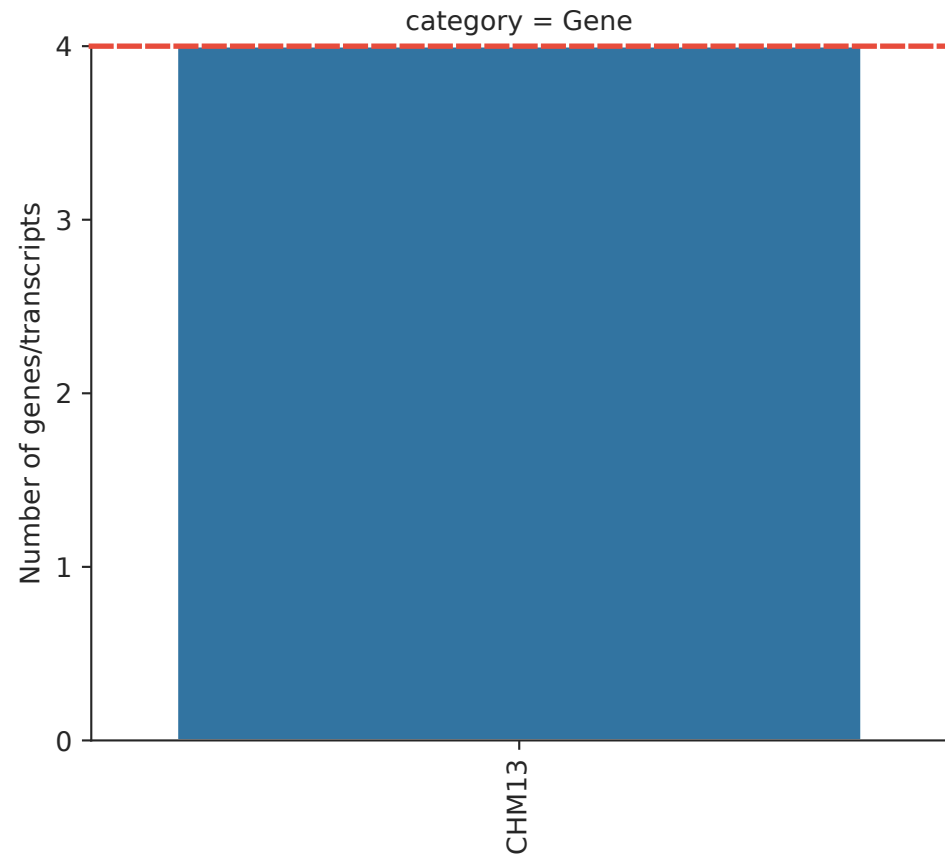
category = Gene



category = Transcript



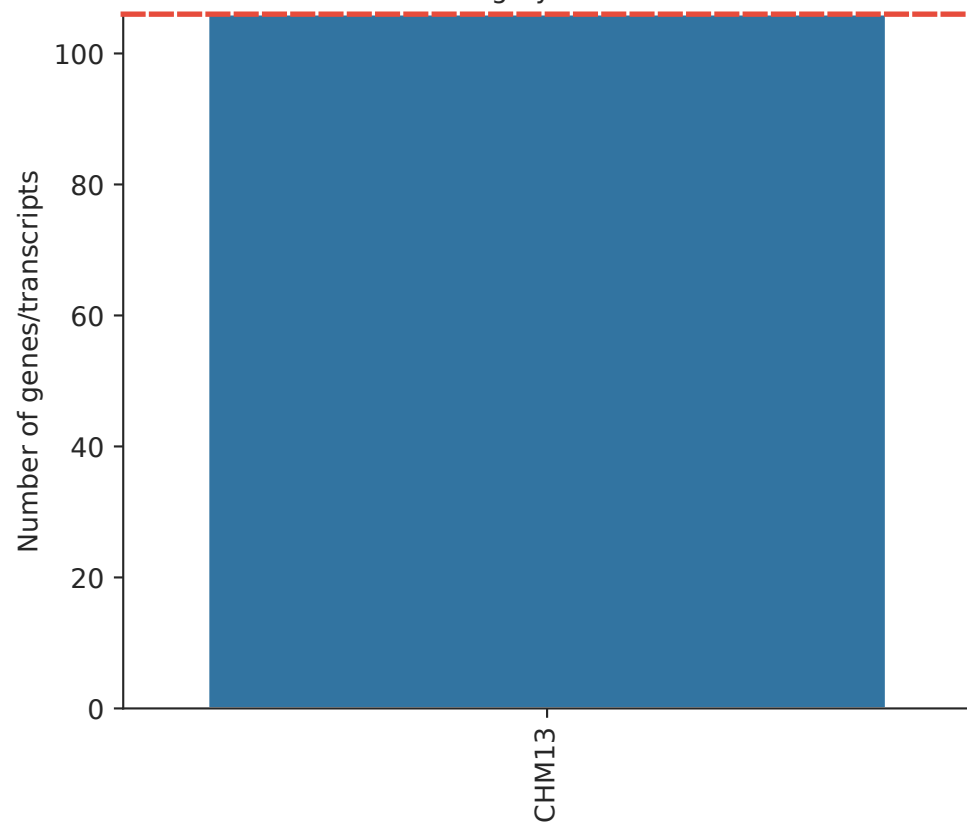
# Number of comparative genes/transcripts present for biotype TR\_J\_pseudogene



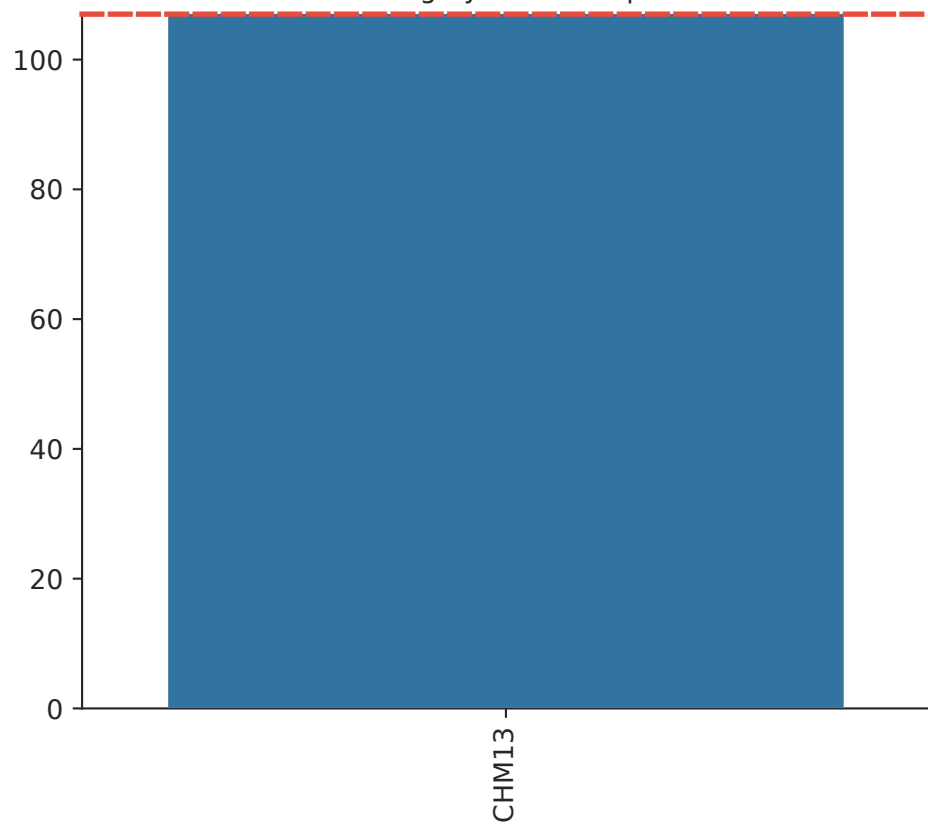


# Number of comparative genes/transcripts present for biotype TR\_V\_gene

category = Gene

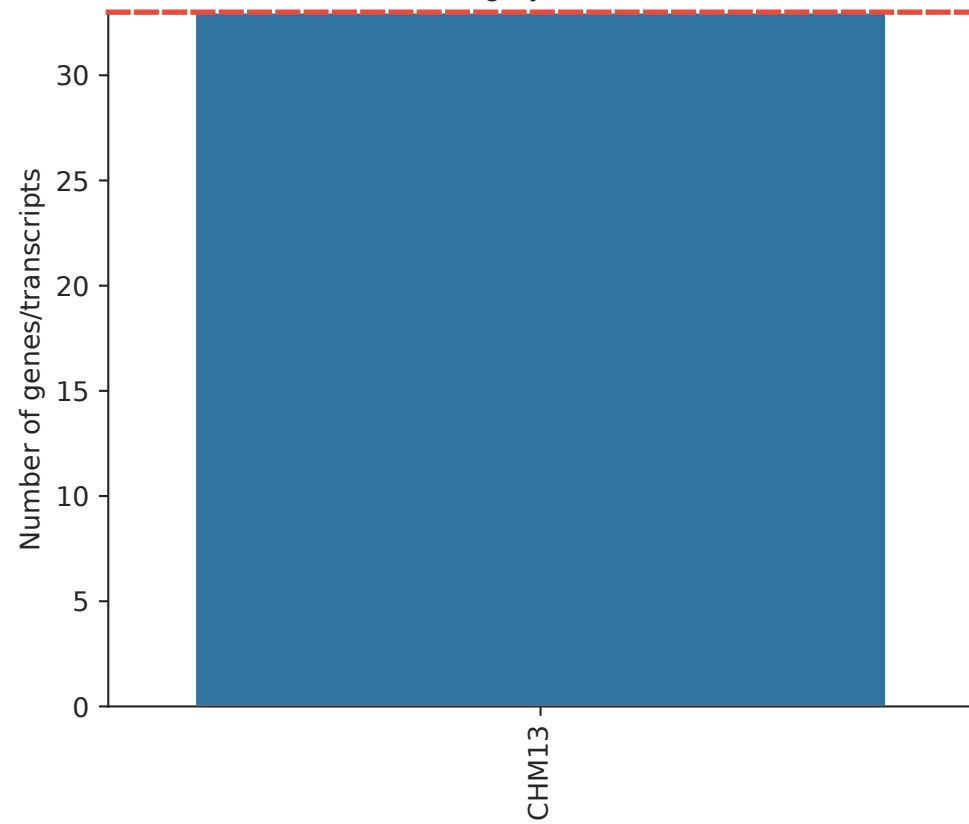


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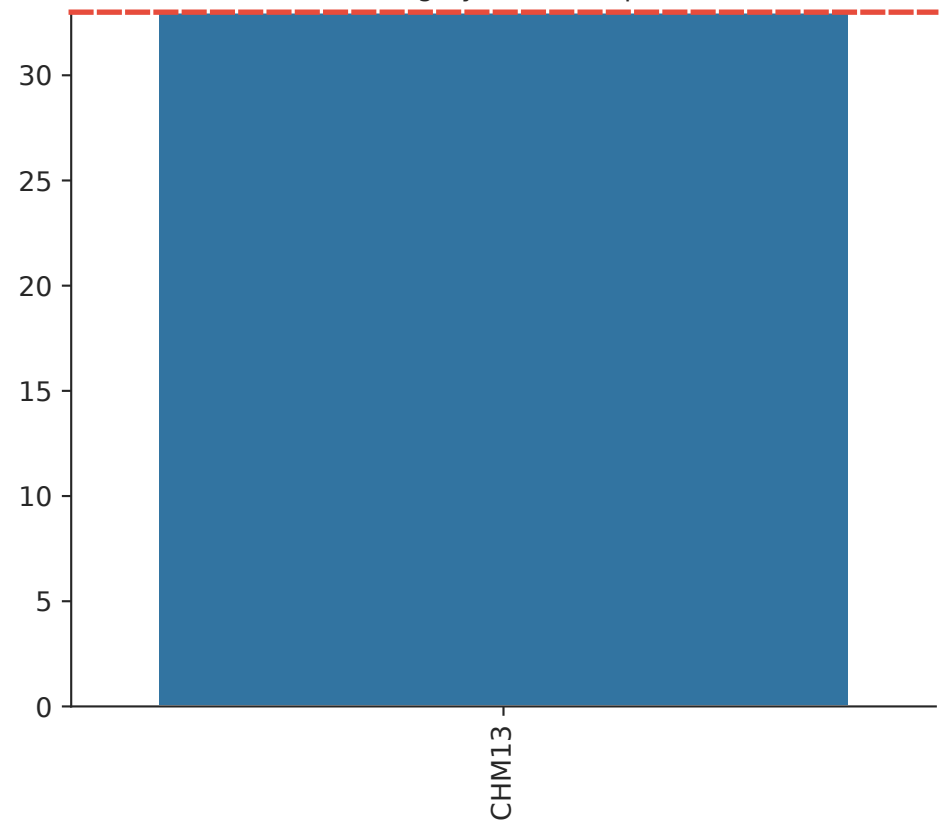


# Number of comparative genes/transcripts present for biotype TR\_V\_pseudogene

category = Gene

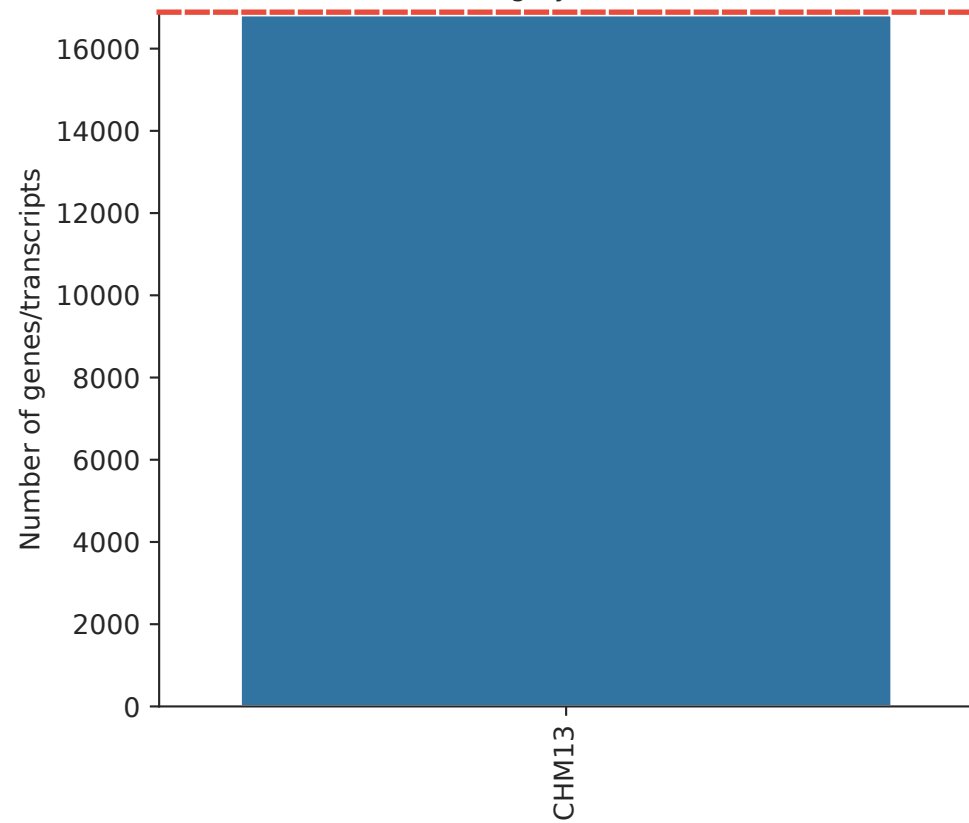


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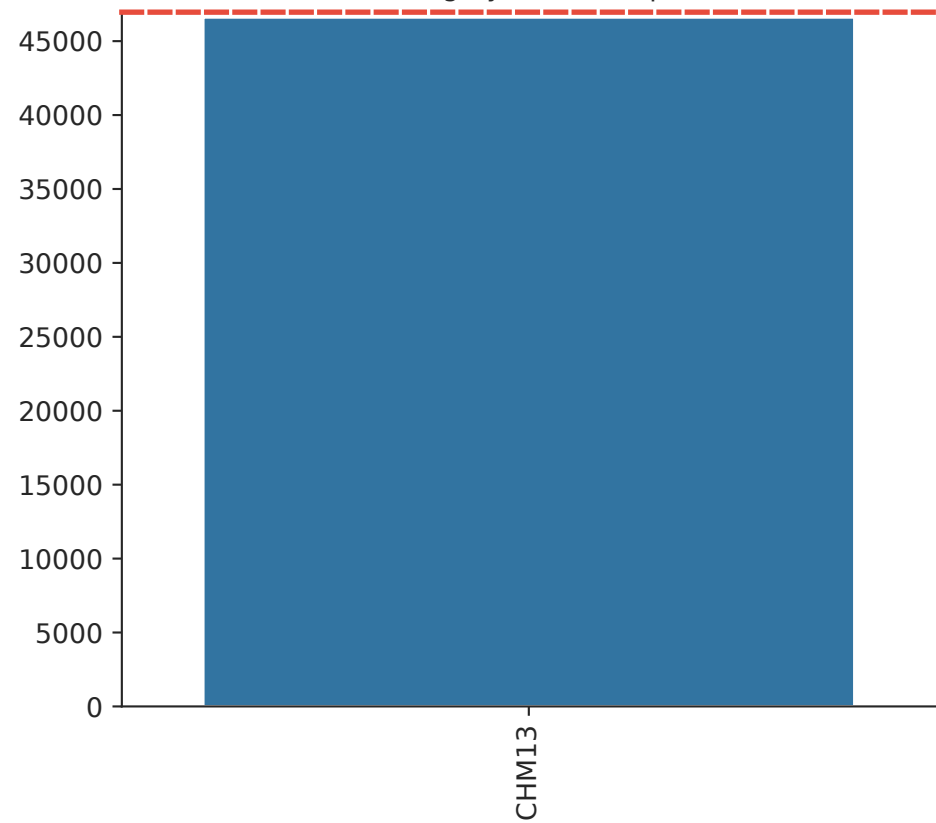


# Number of comparative genes/transcripts present for biotype lncRNA

category = Gene

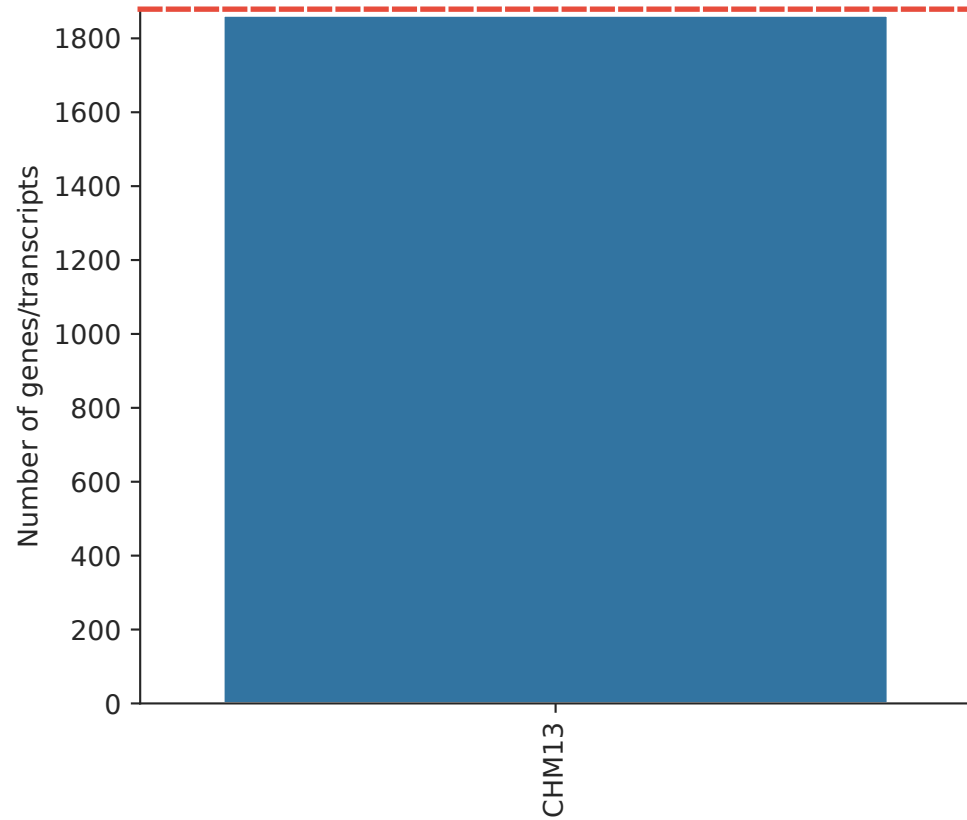


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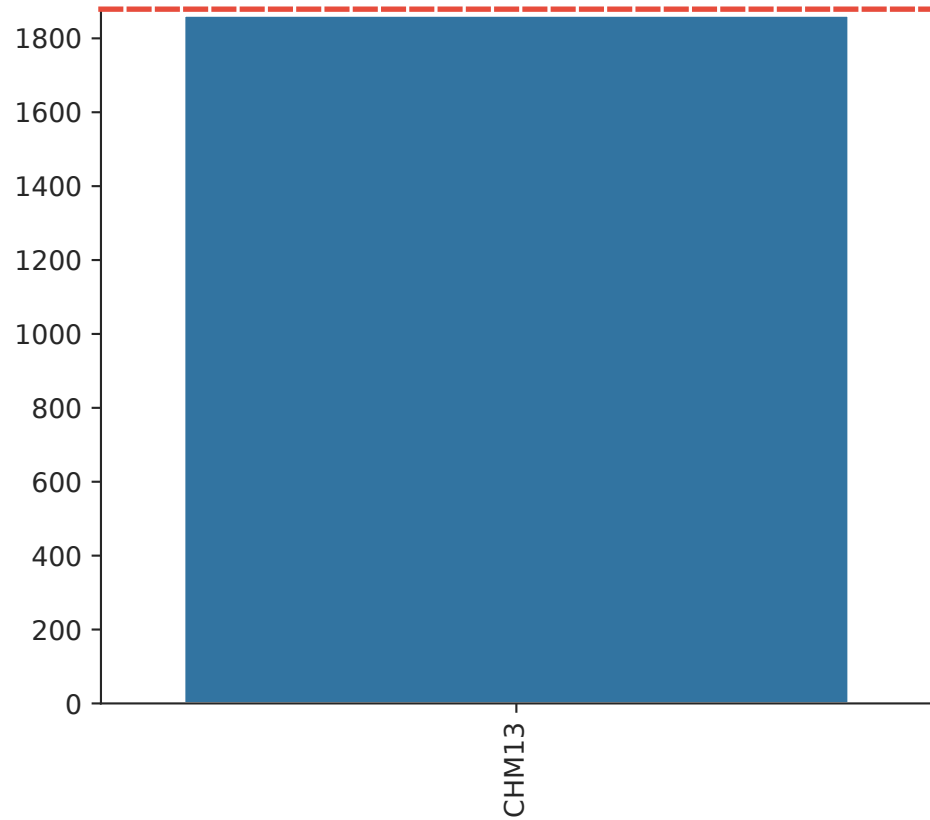


# Number of comparative genes/transcripts present for biotype miRNA

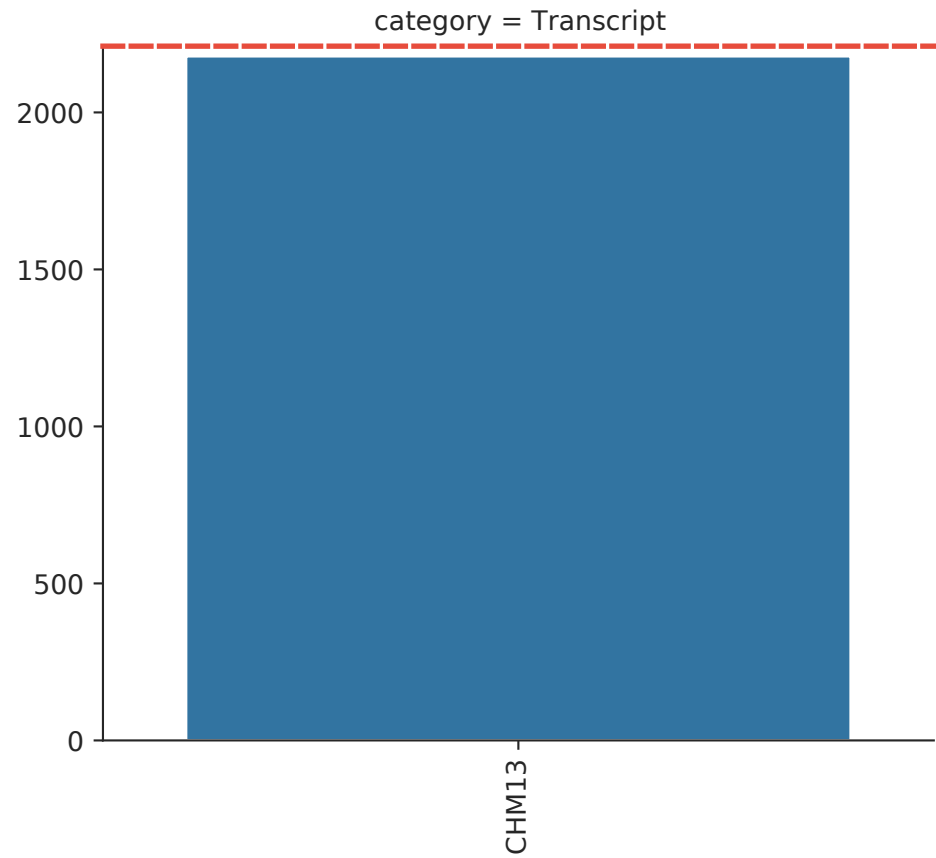
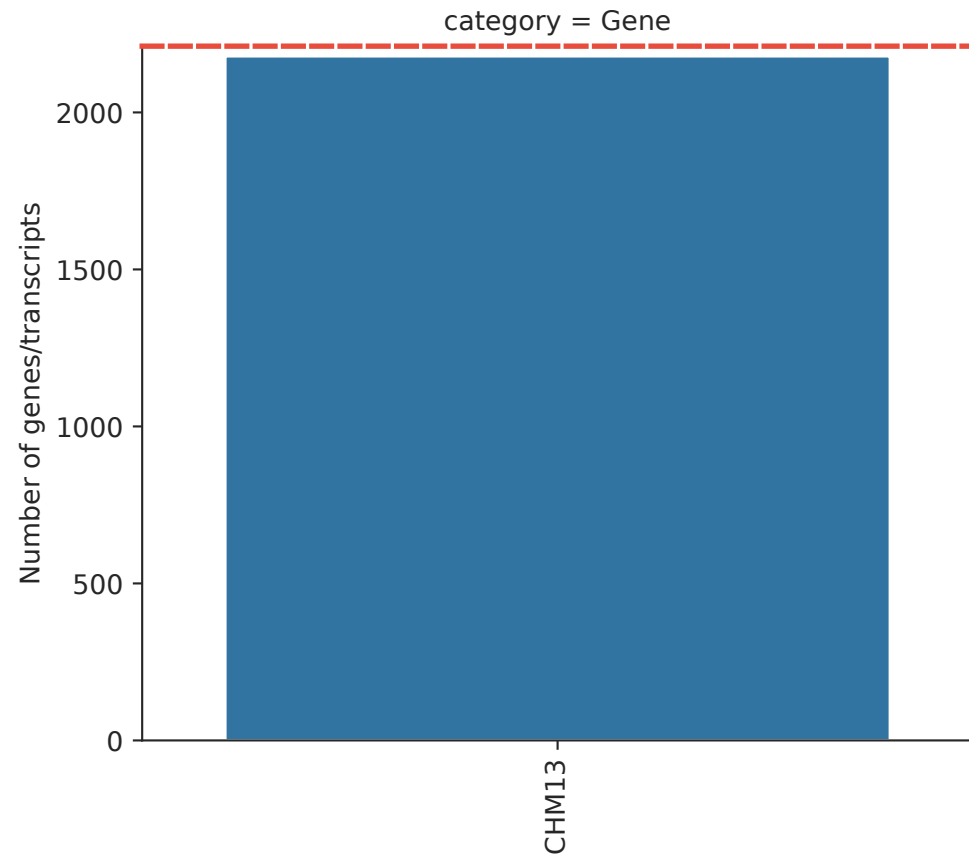
category = Gene



category = Transcript

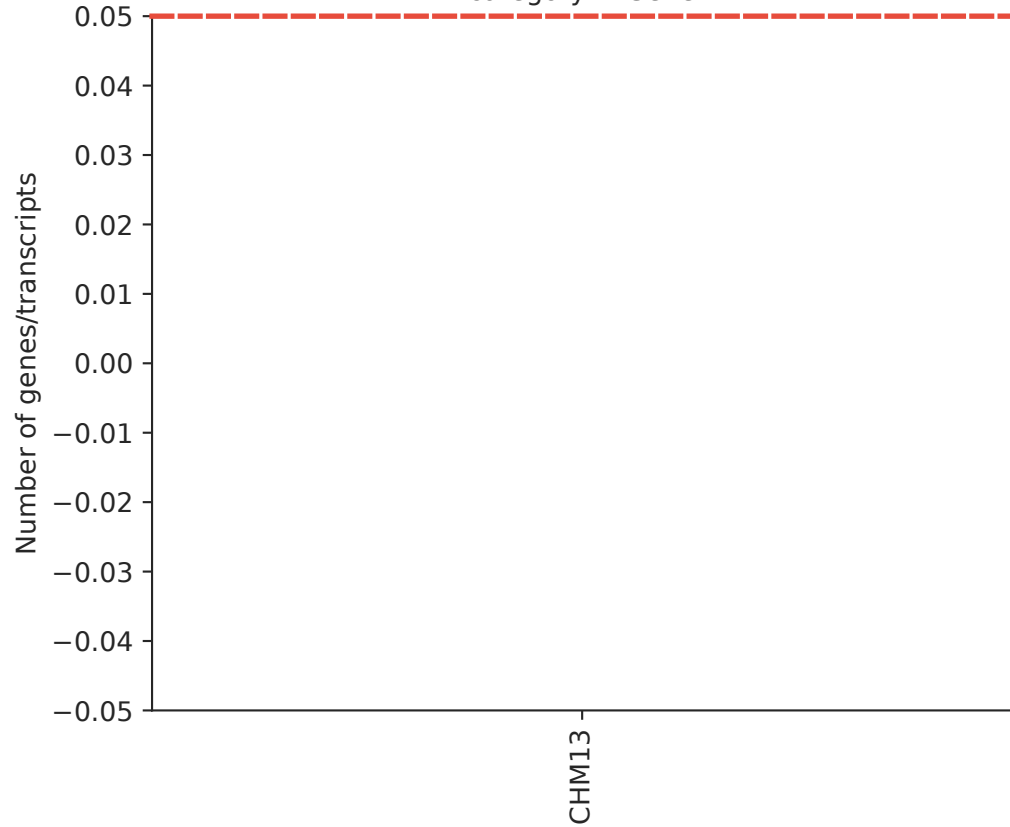


# Number of comparative genes/transcripts present for biotype misc\_RNA

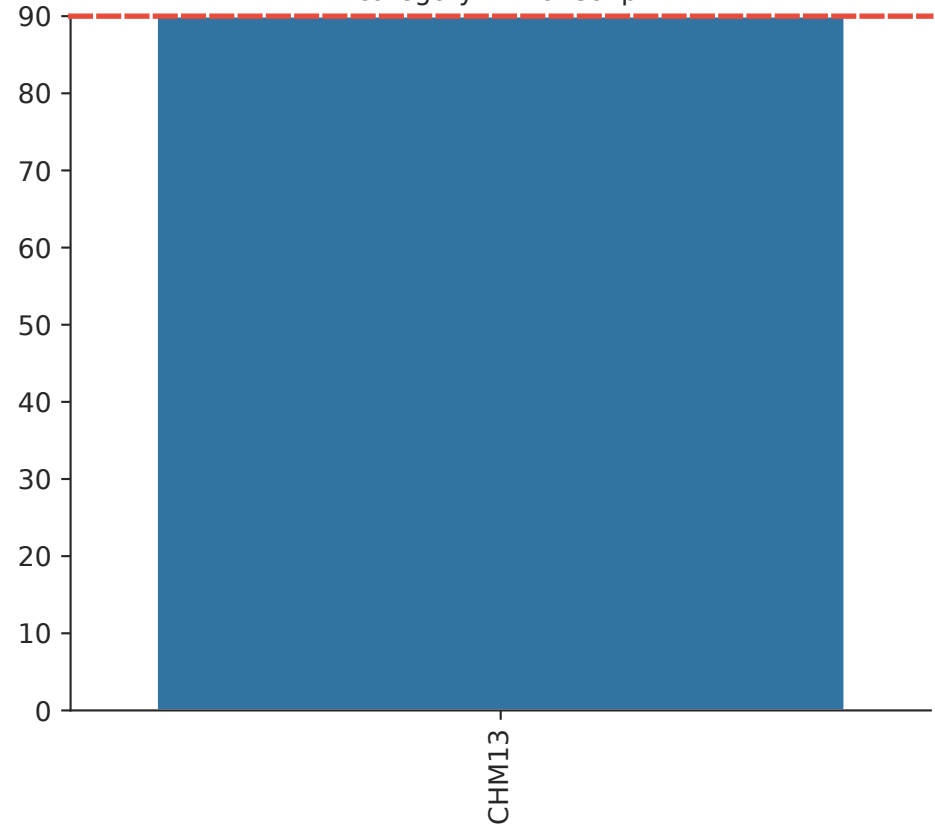


# Number of comparative genes/transcripts present for biotype non\_stop\_decay

category = Gene

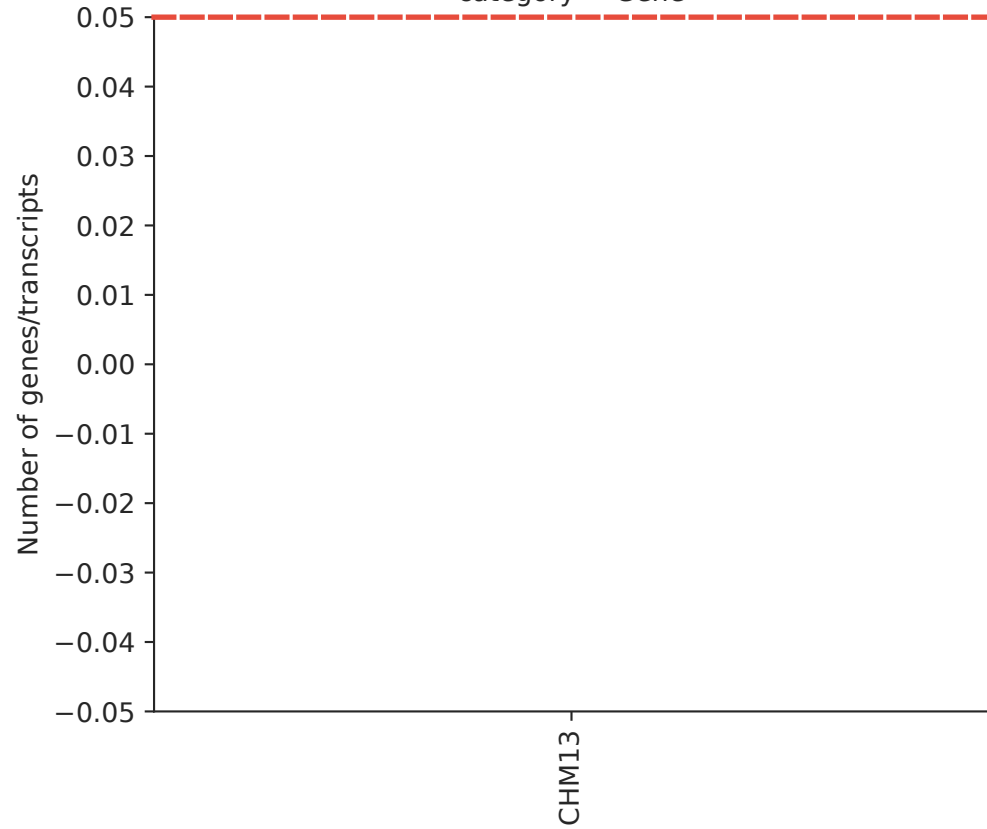


category = Transcript

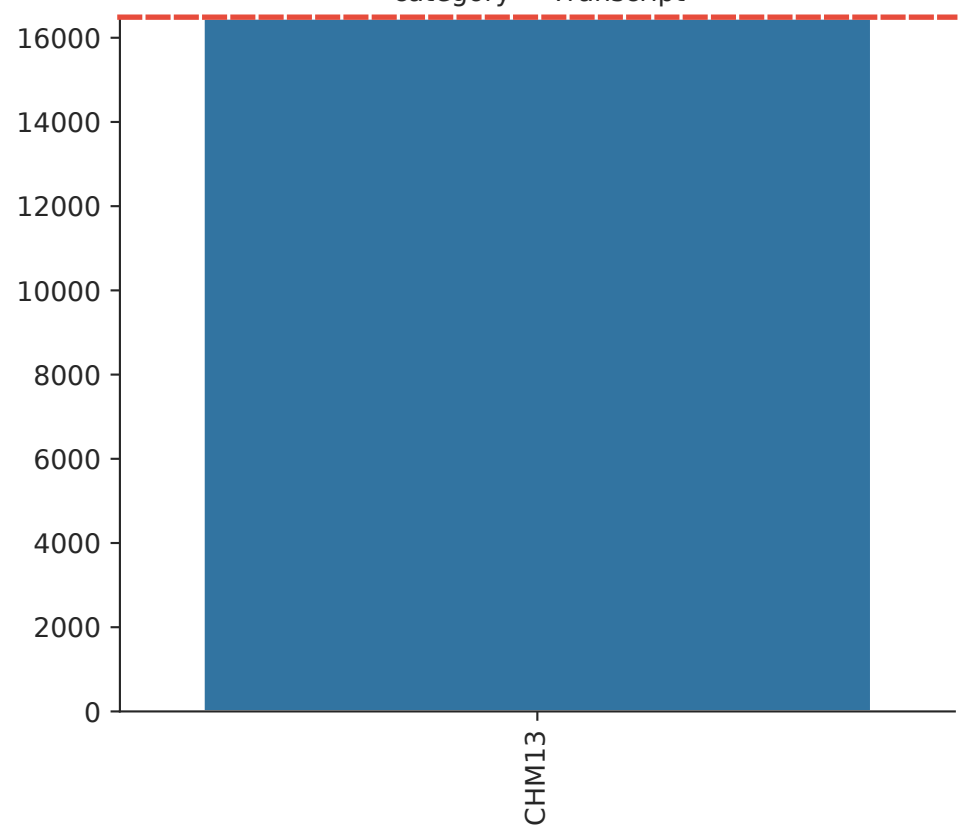


# Number of comparative genes/transcripts present for biotype nonsense\_mediated\_decay

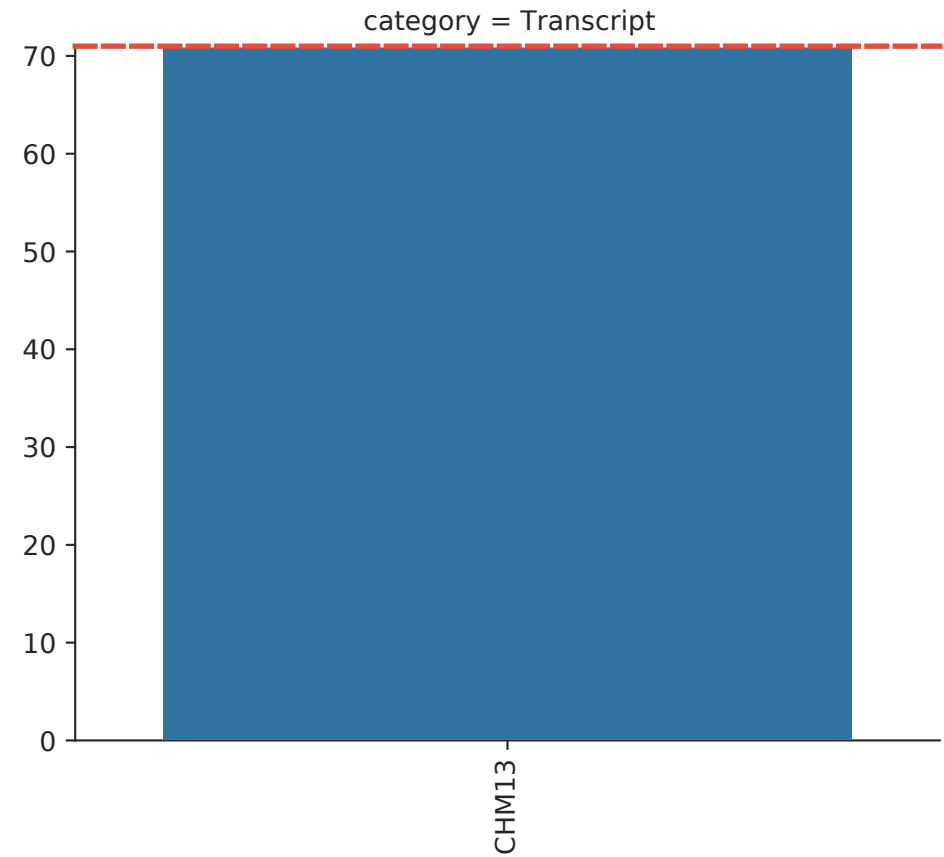
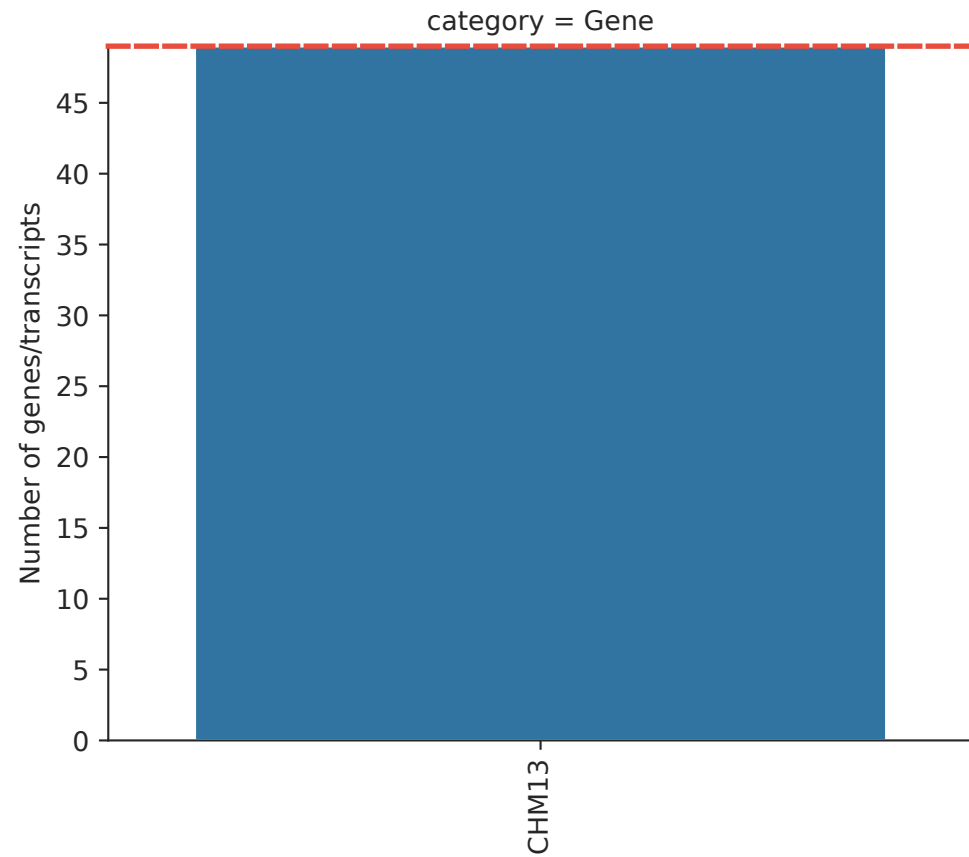
category = Gene



category = Transcript



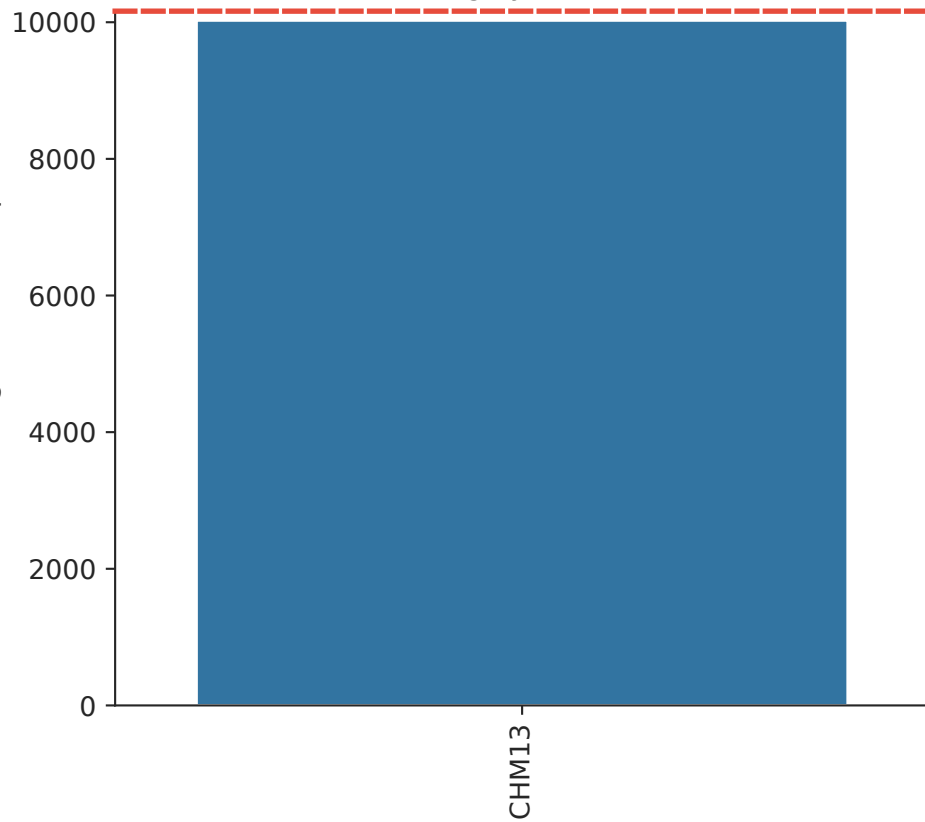
# Number of comparative genes/transcripts present for biotype polymorphic\_pseudogene



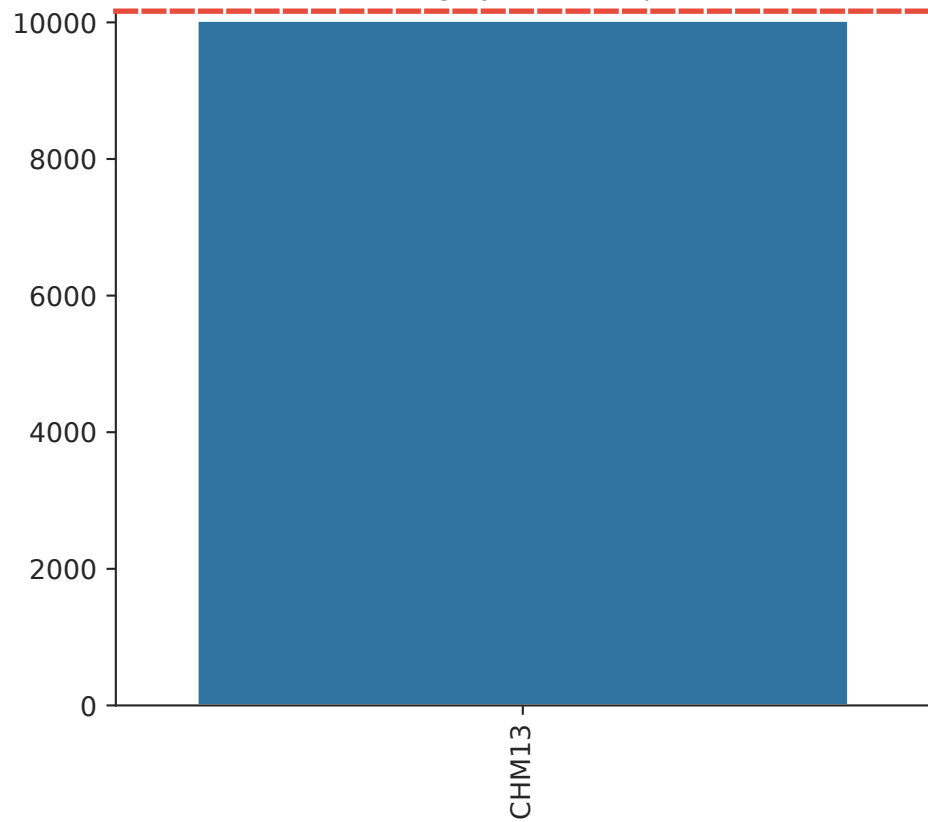


# Number of comparative genes/transcripts present for biotype processed\_pseudogene

category = Gene

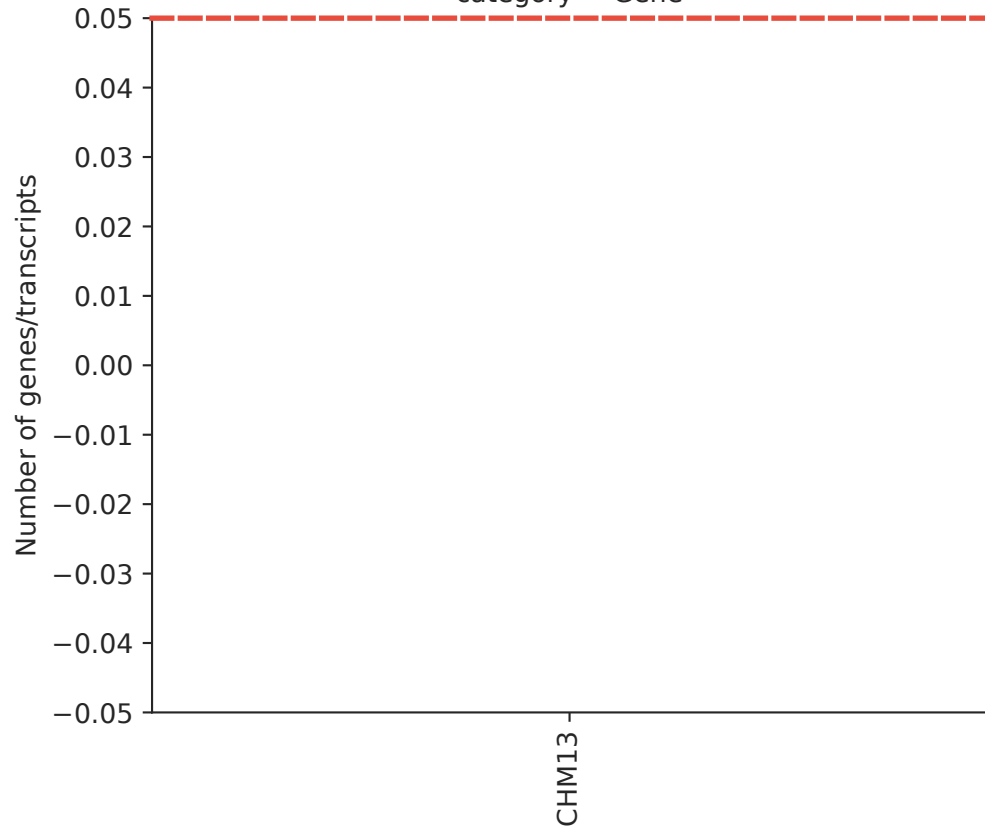


category = Transcript

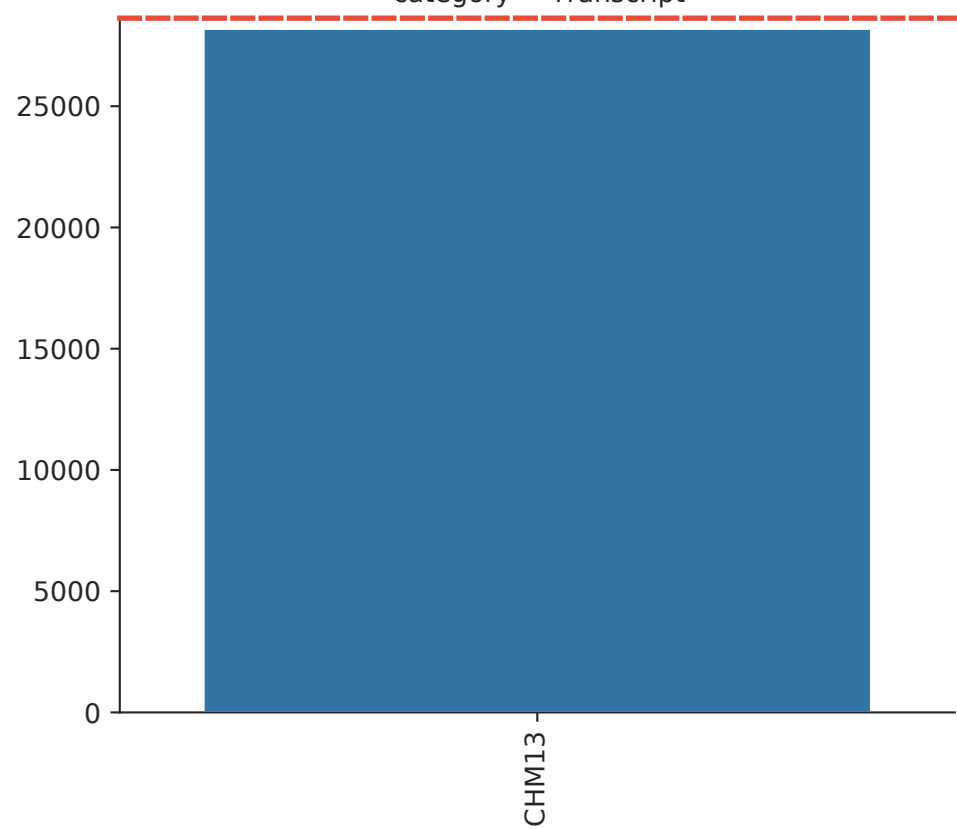


# Number of comparative genes/transcripts present for biotype processed\_transcript

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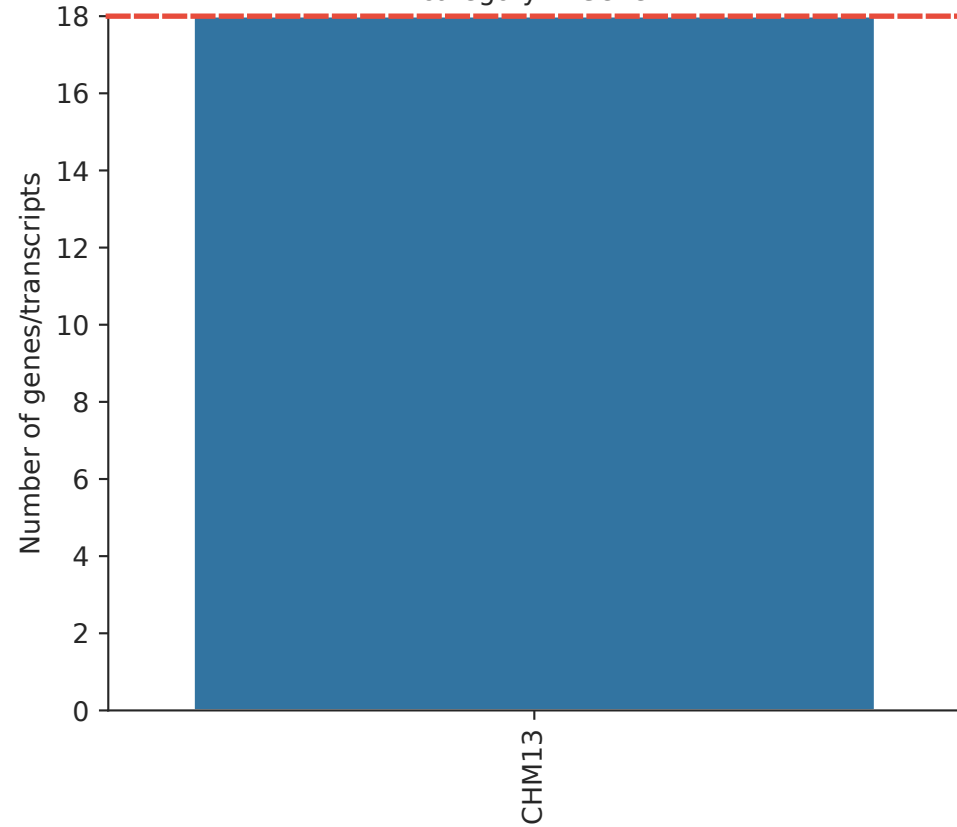


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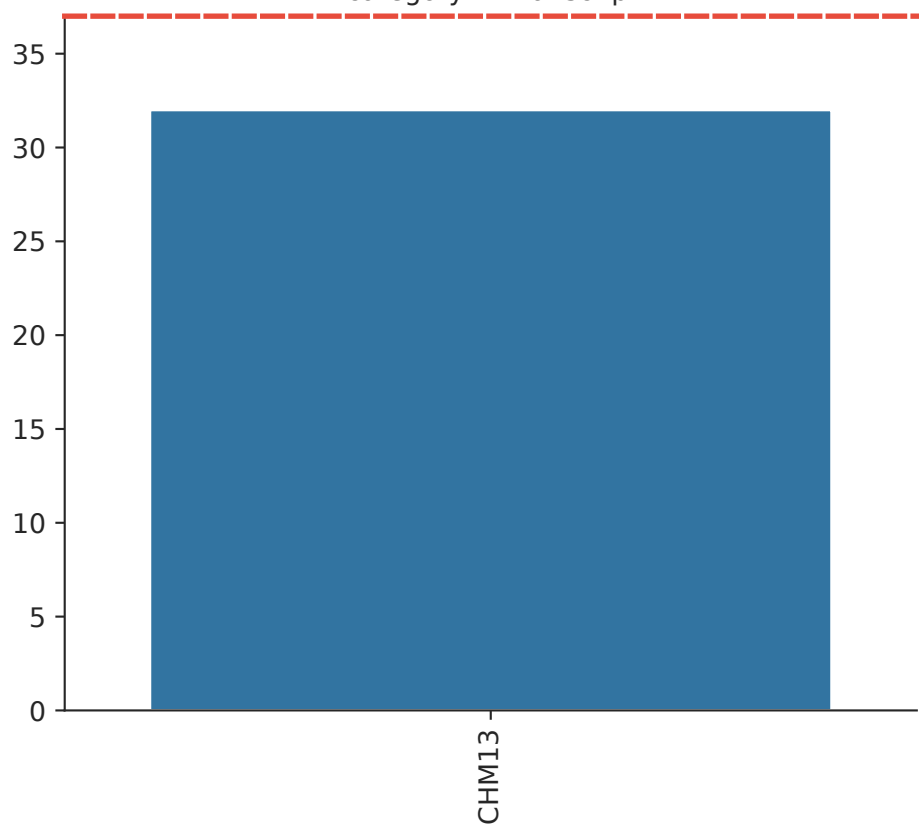


# Number of comparative genes/transcripts present for biotype pseudogene

category = Gene

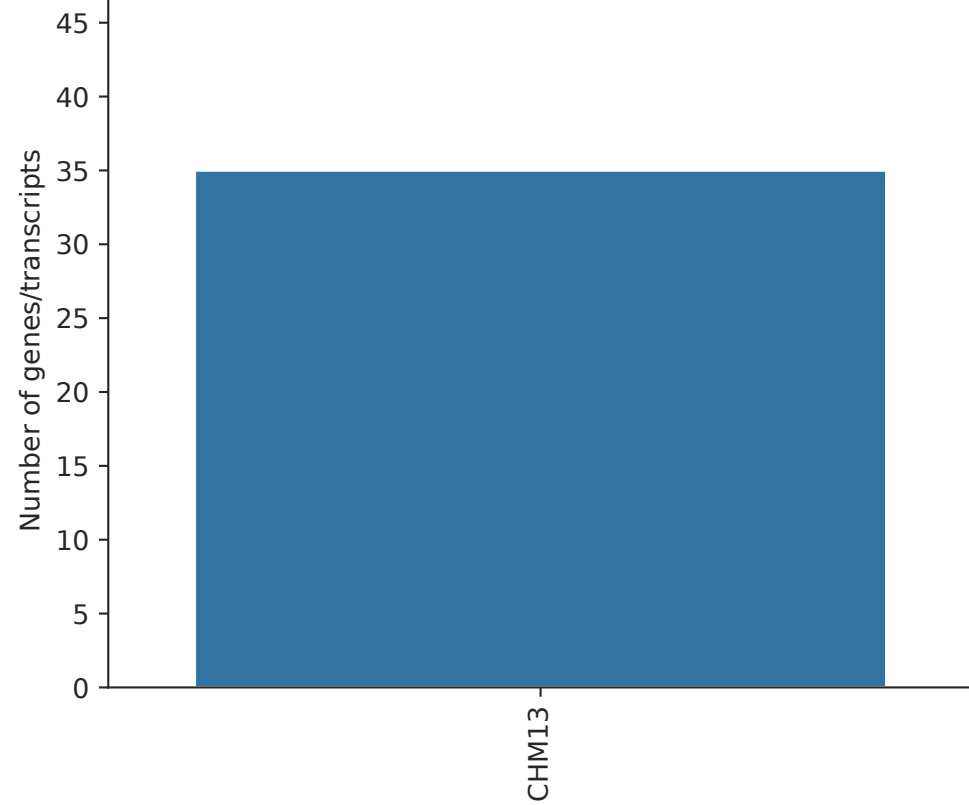


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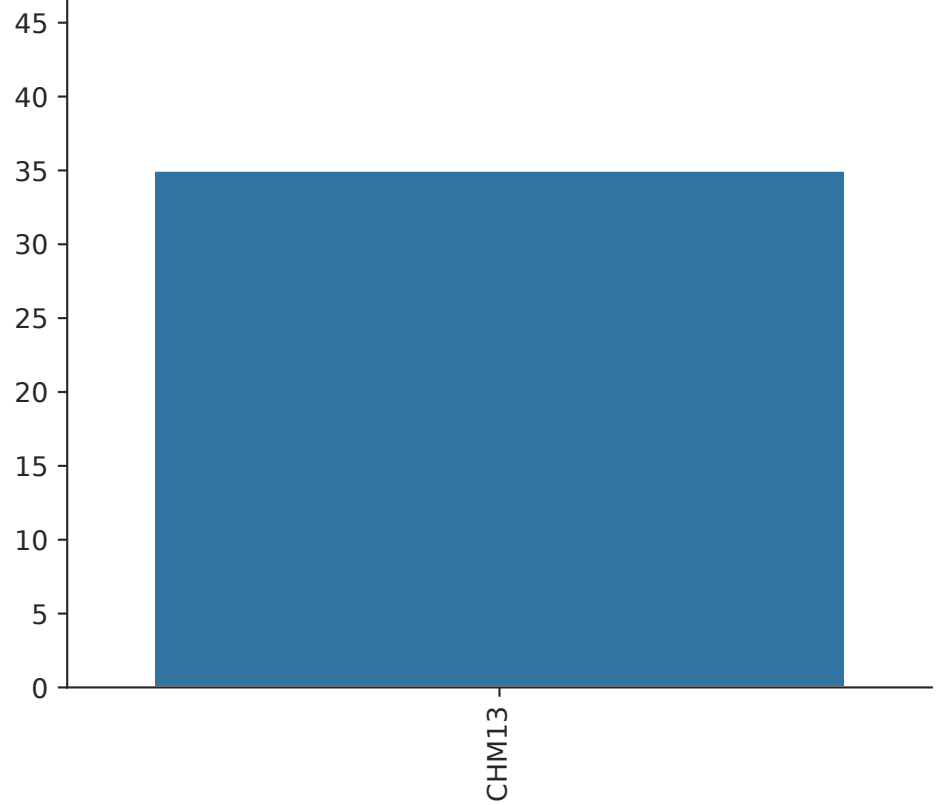


# Number of comparative genes/transcripts present for biotype rRNA

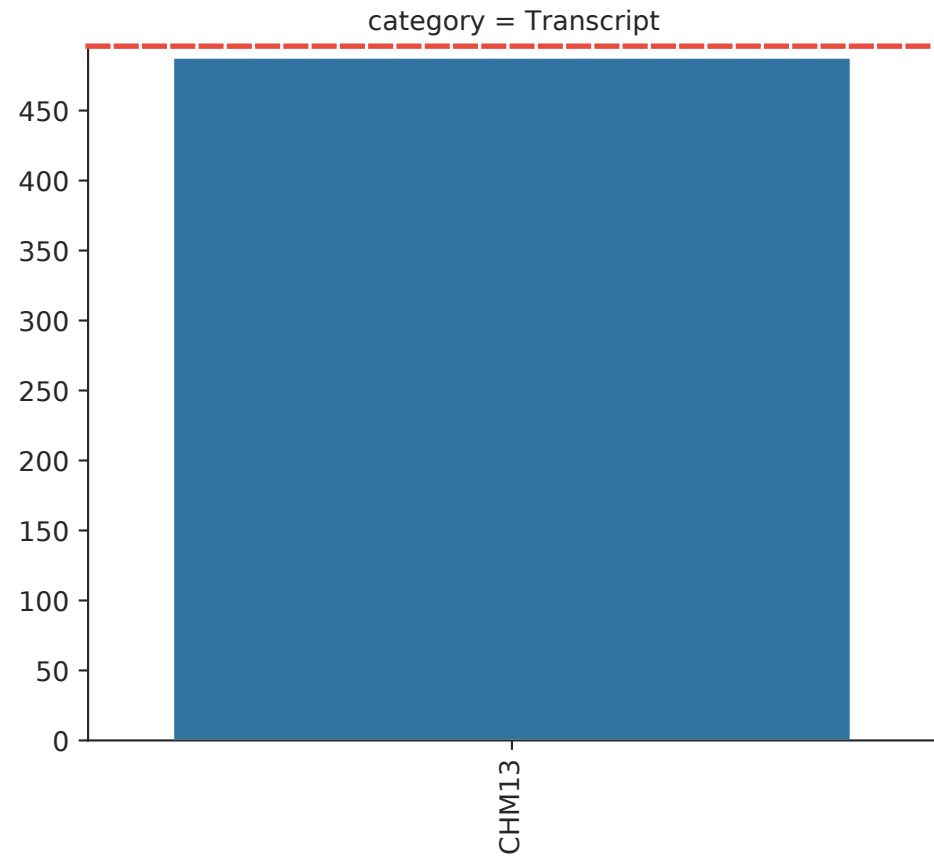
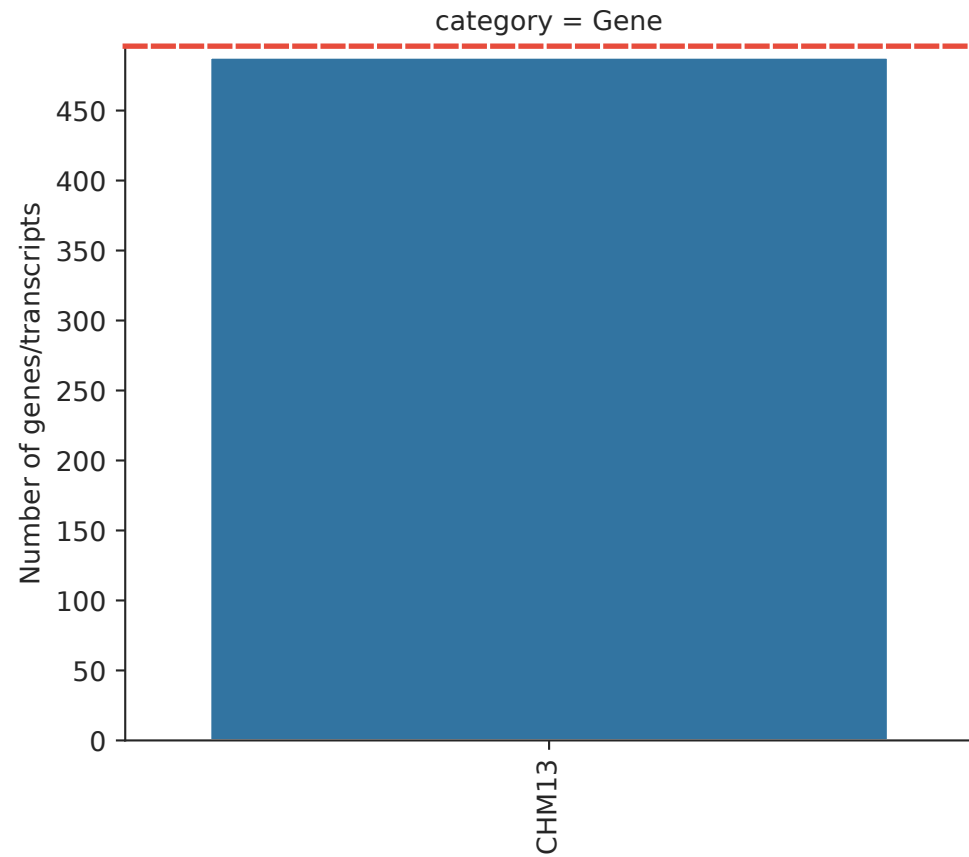
category = Gene



category = Transcript

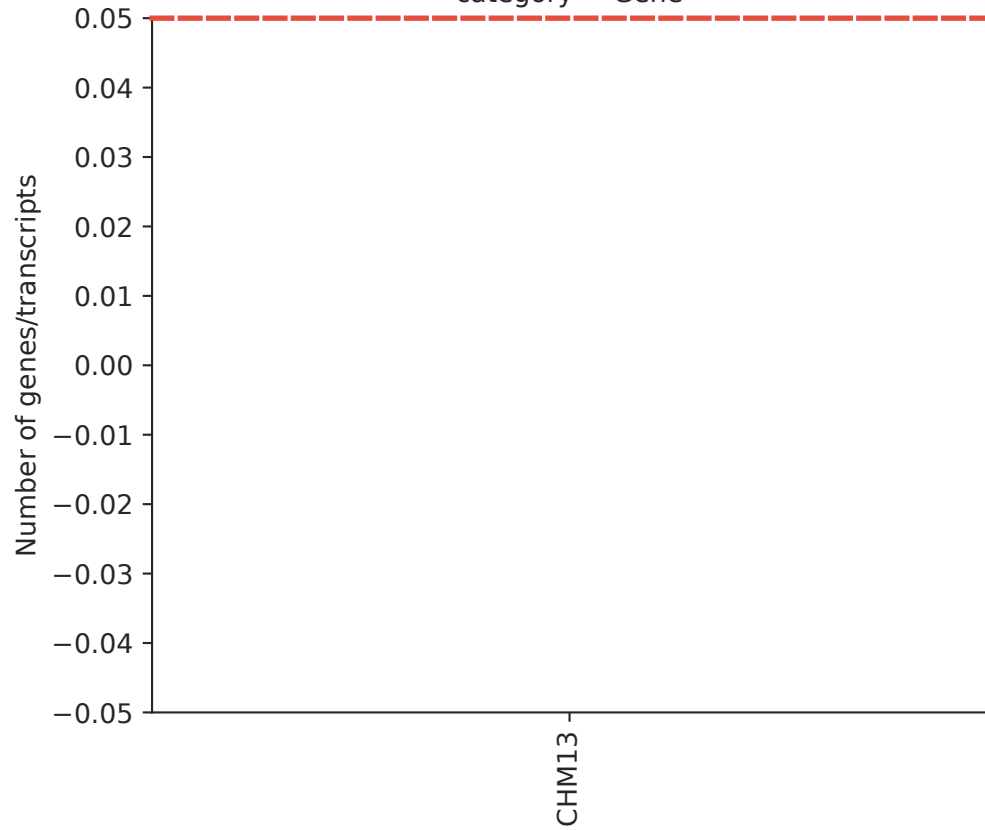


# Number of comparative genes/transcripts present for biotype rRNA\_pseudogene

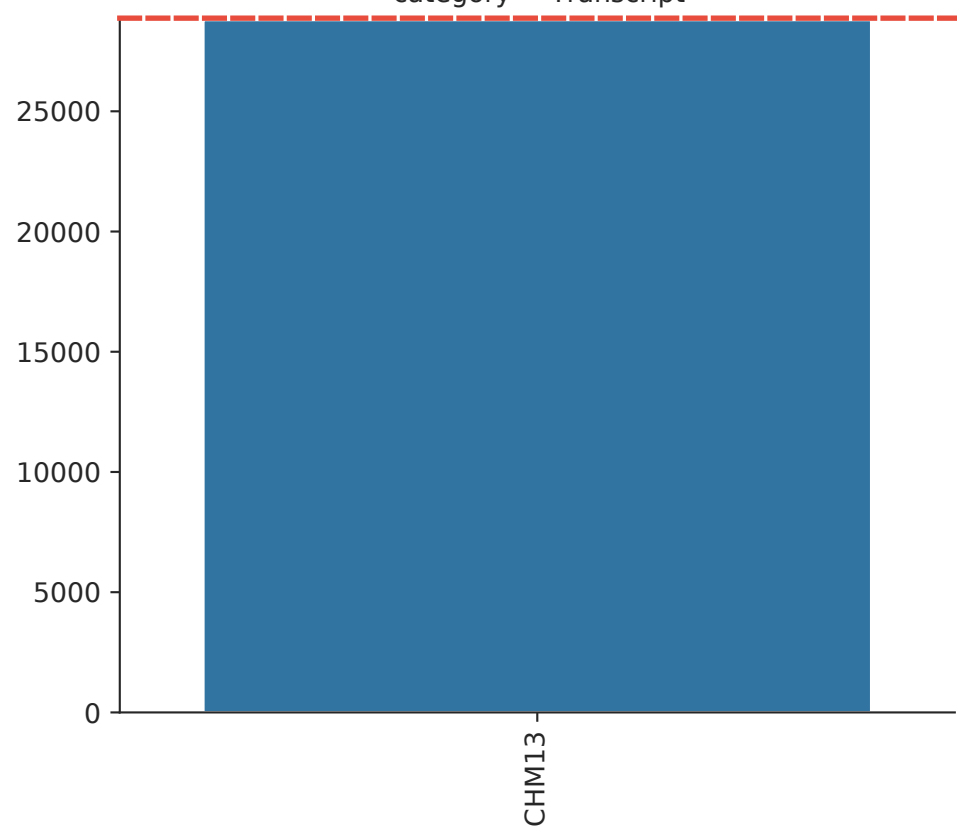


# Number of comparative genes/transcripts present for biotype retained\_intron

category = Gene

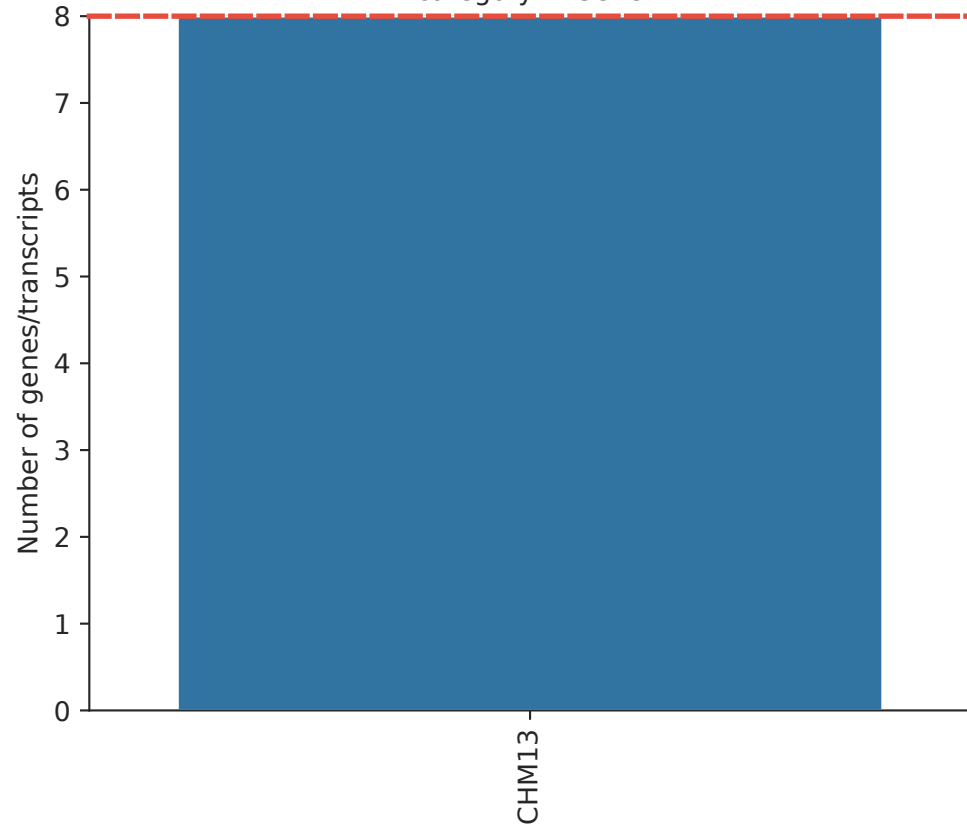


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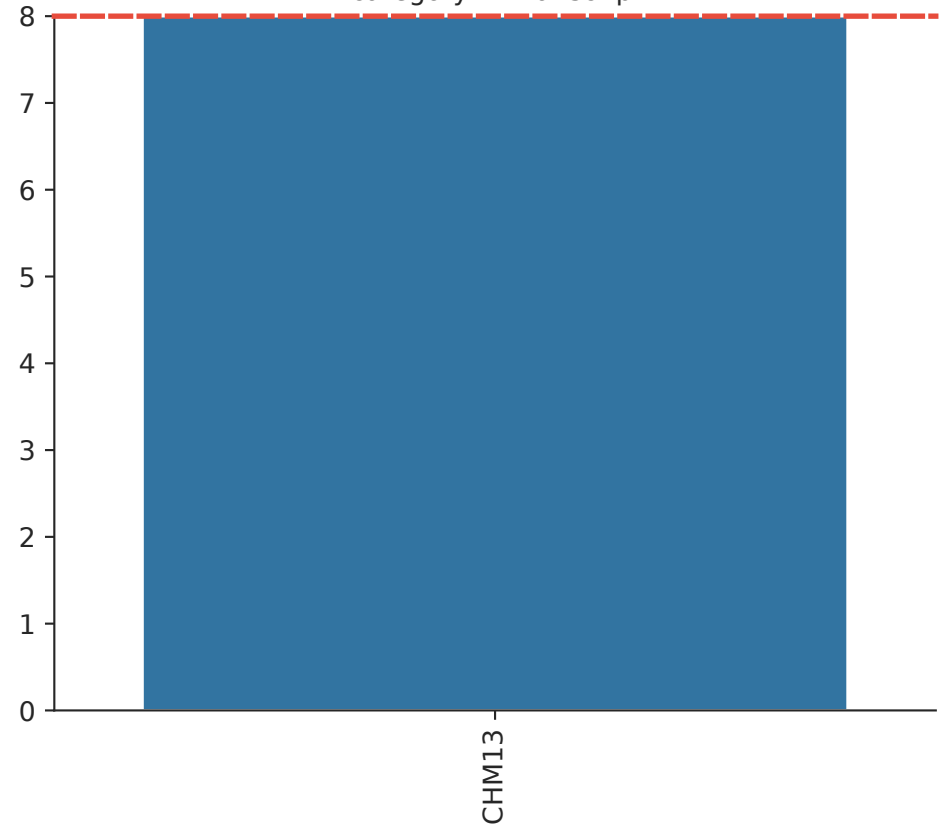


# Number of comparative genes/transcripts present for biotype ribozyme

category = Gene

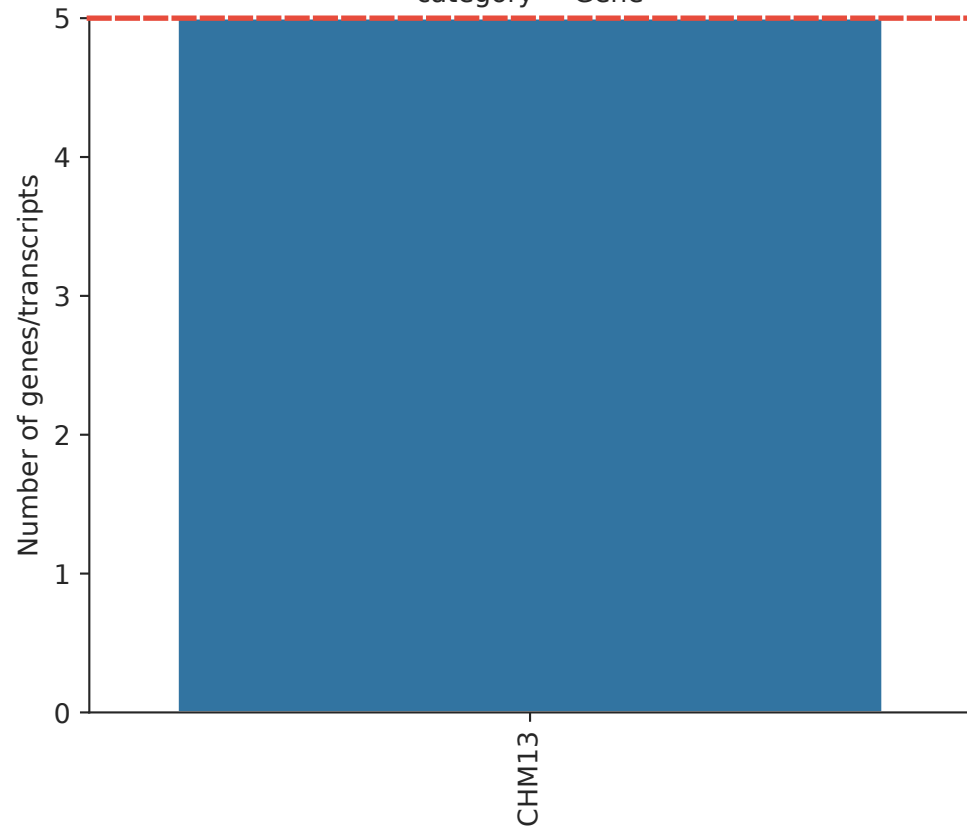


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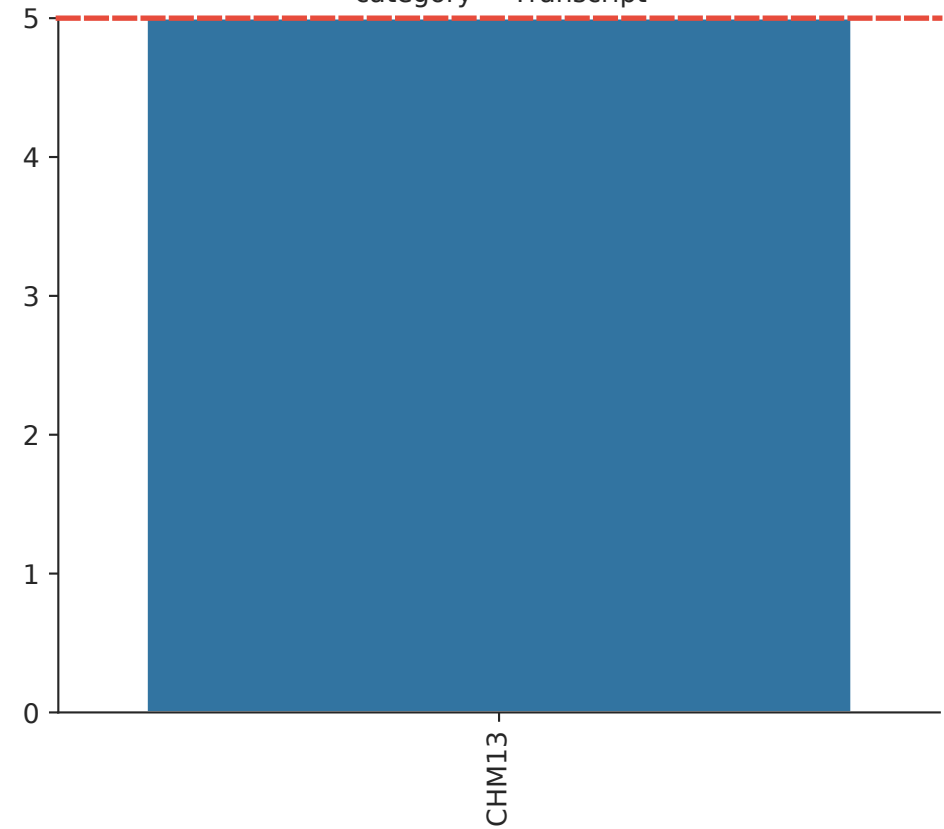


# Number of comparative genes/transcripts present for biotype sRNA

category = Gene

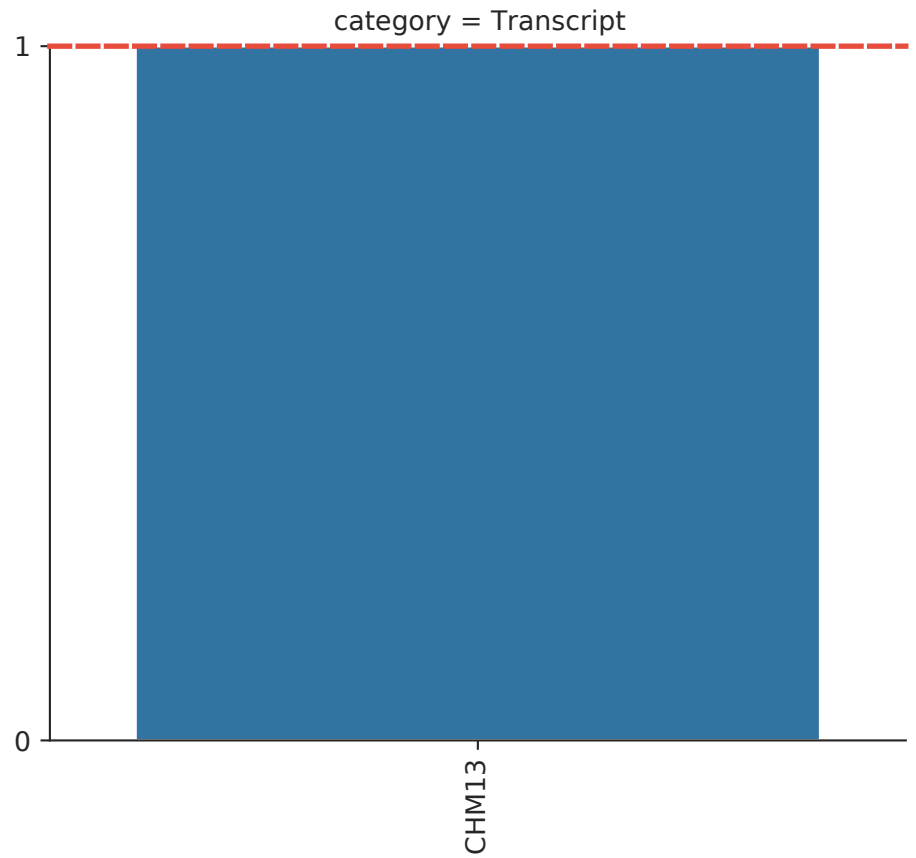
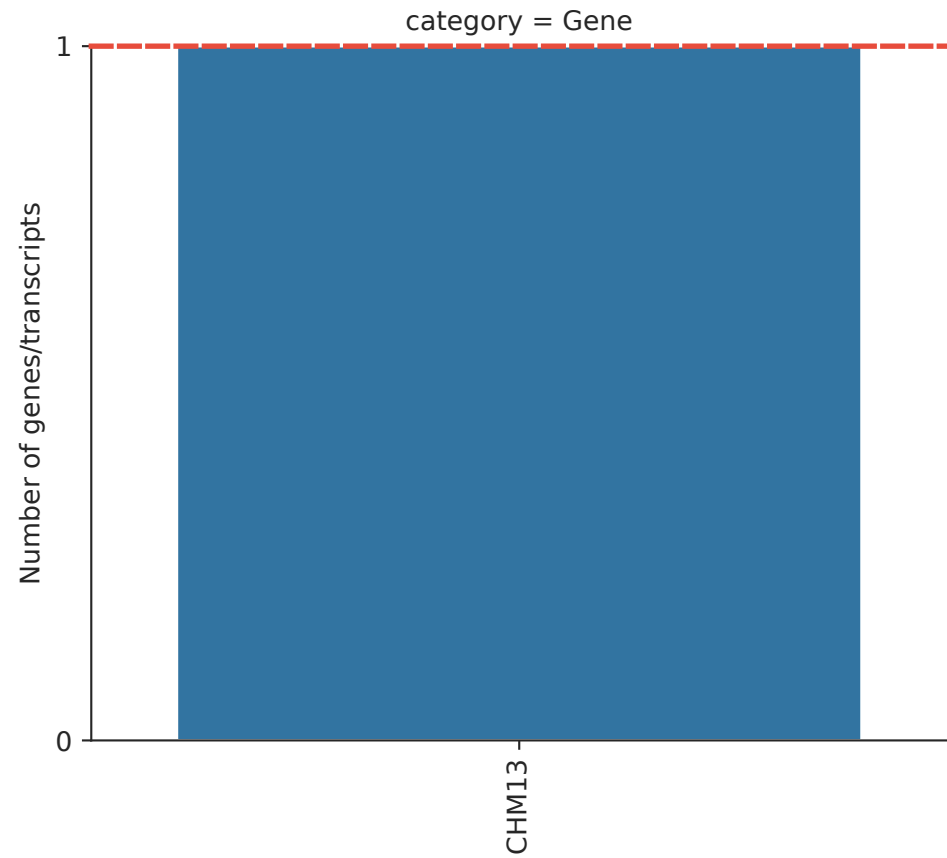


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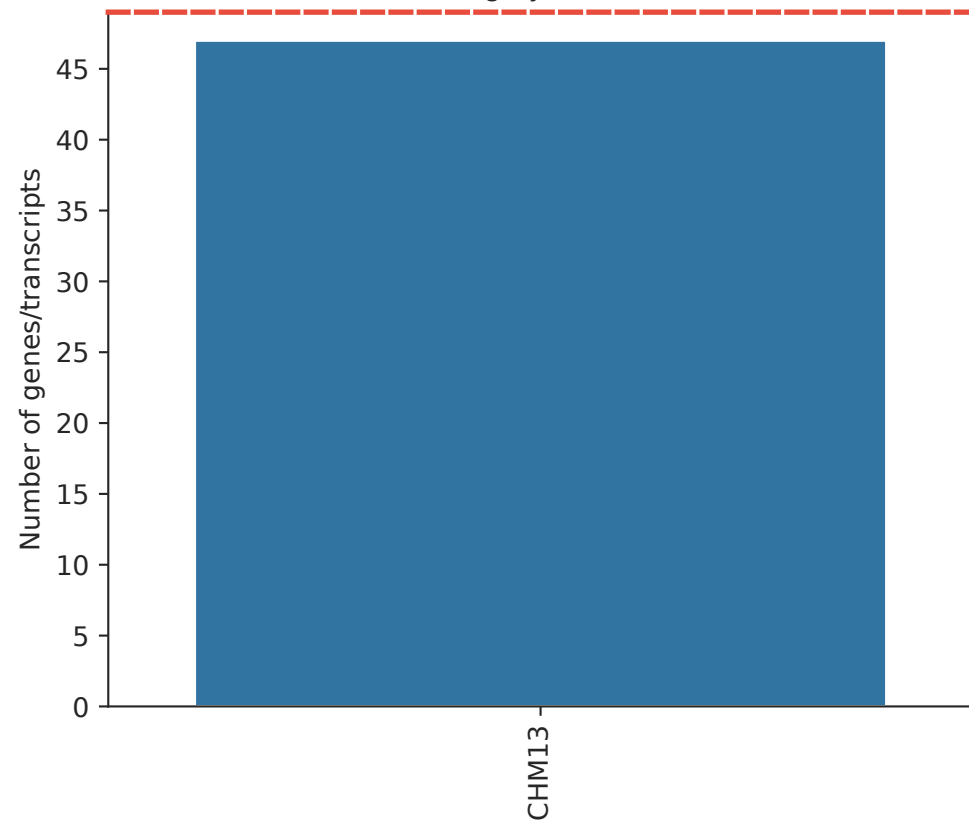


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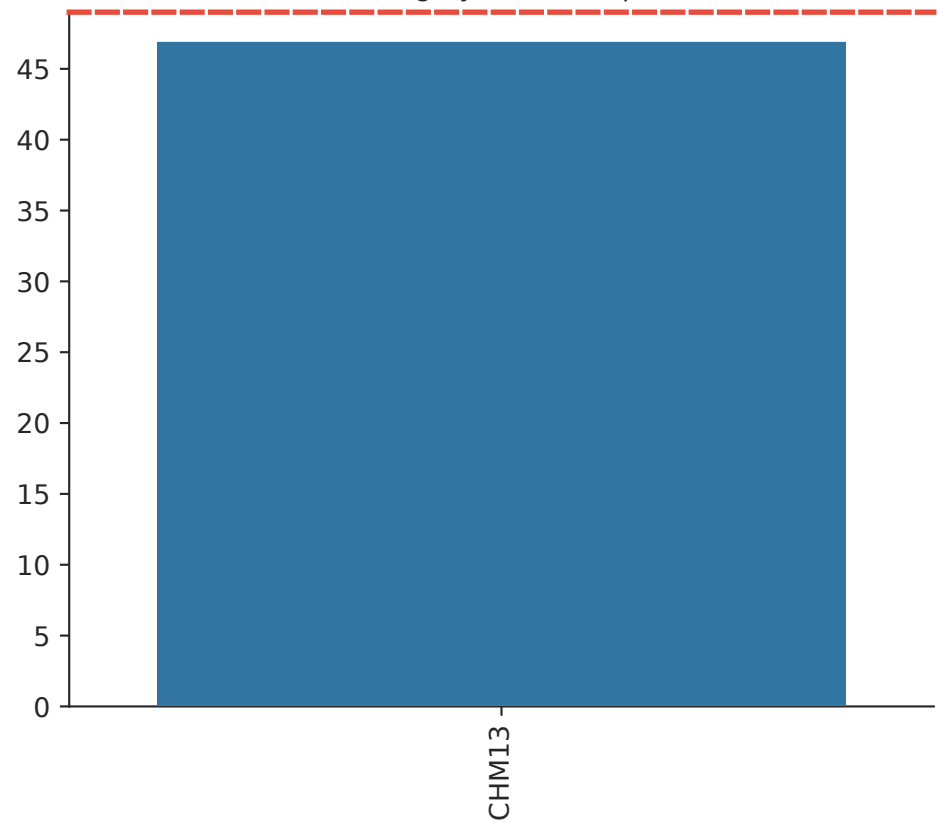


# Number of comparative genes/transcripts present for biotype scaRNA

category = Gene

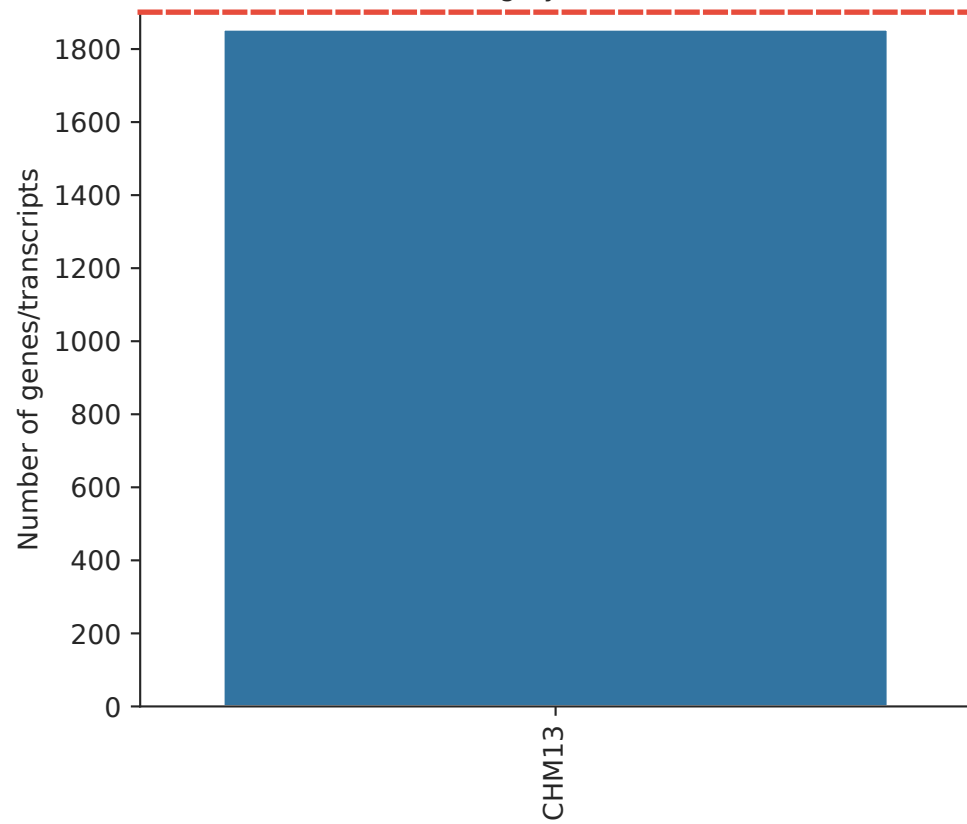


category = Transcript

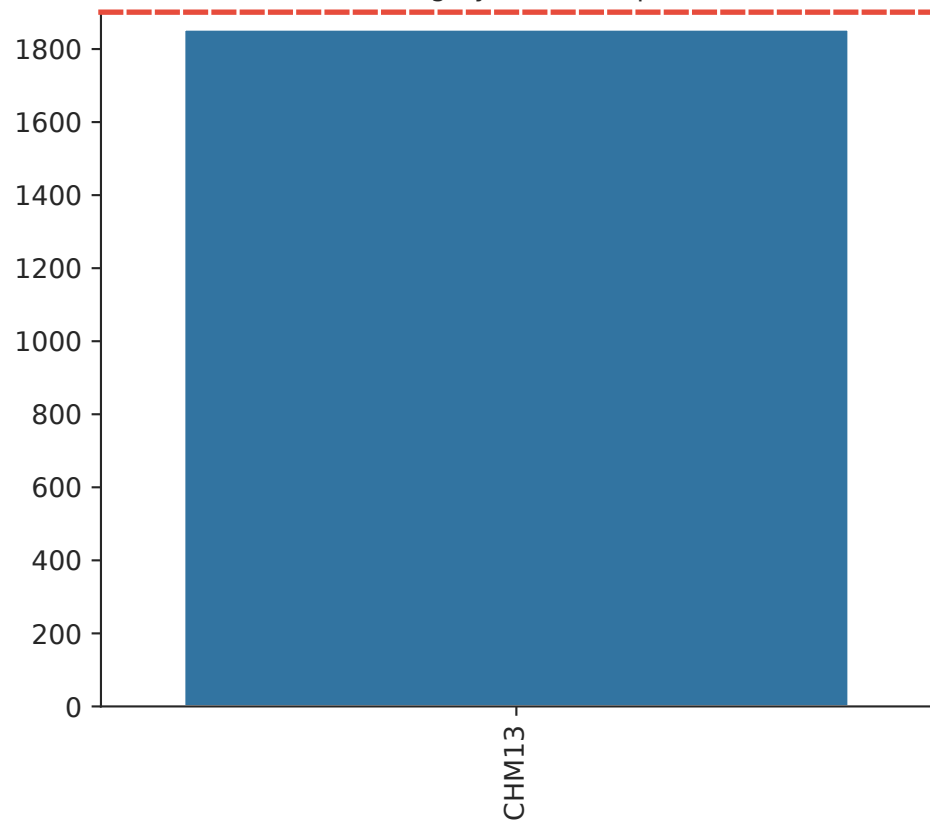


# Number of comparative genes/transcripts present for biotype snRNA

category = Gene

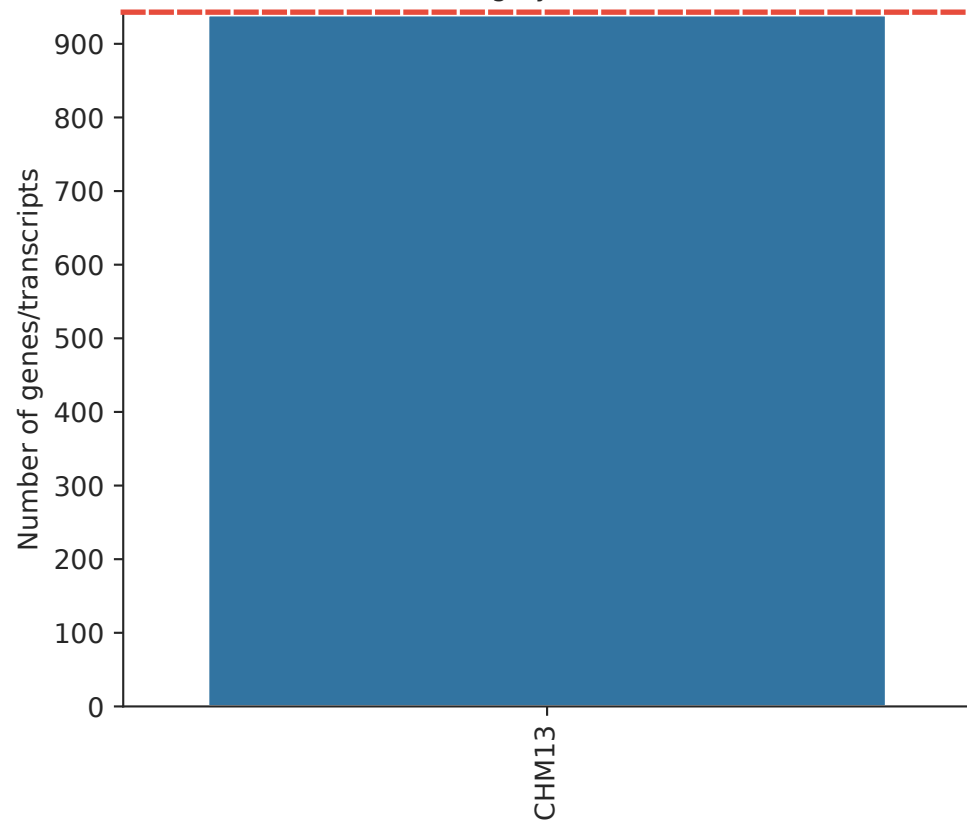


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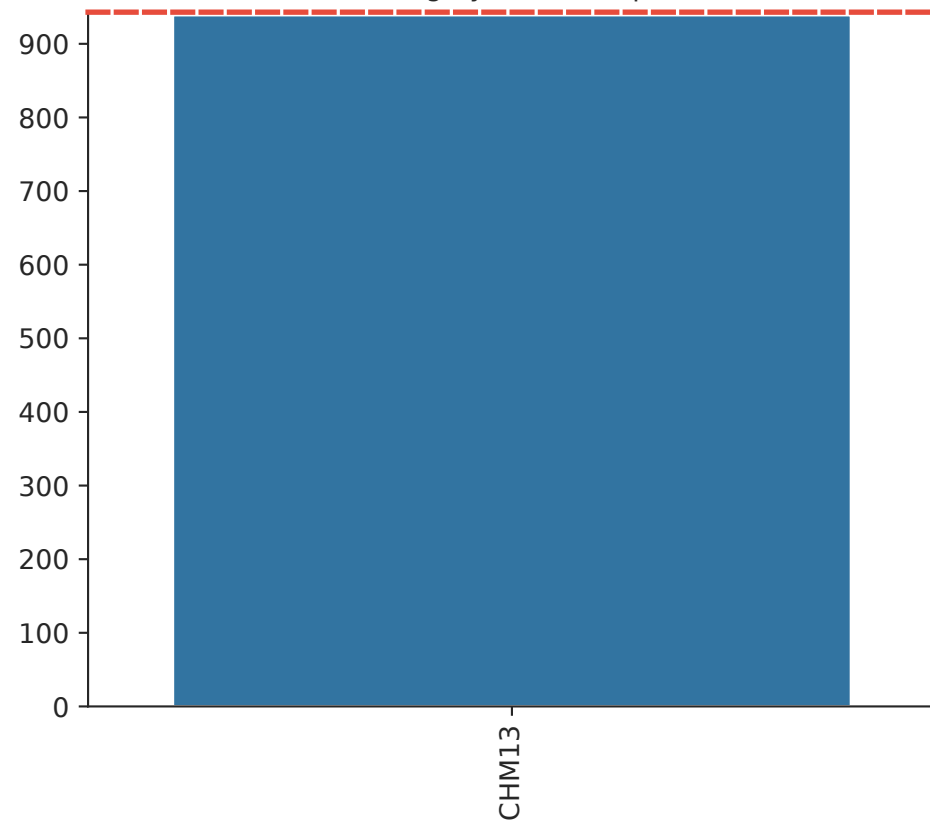


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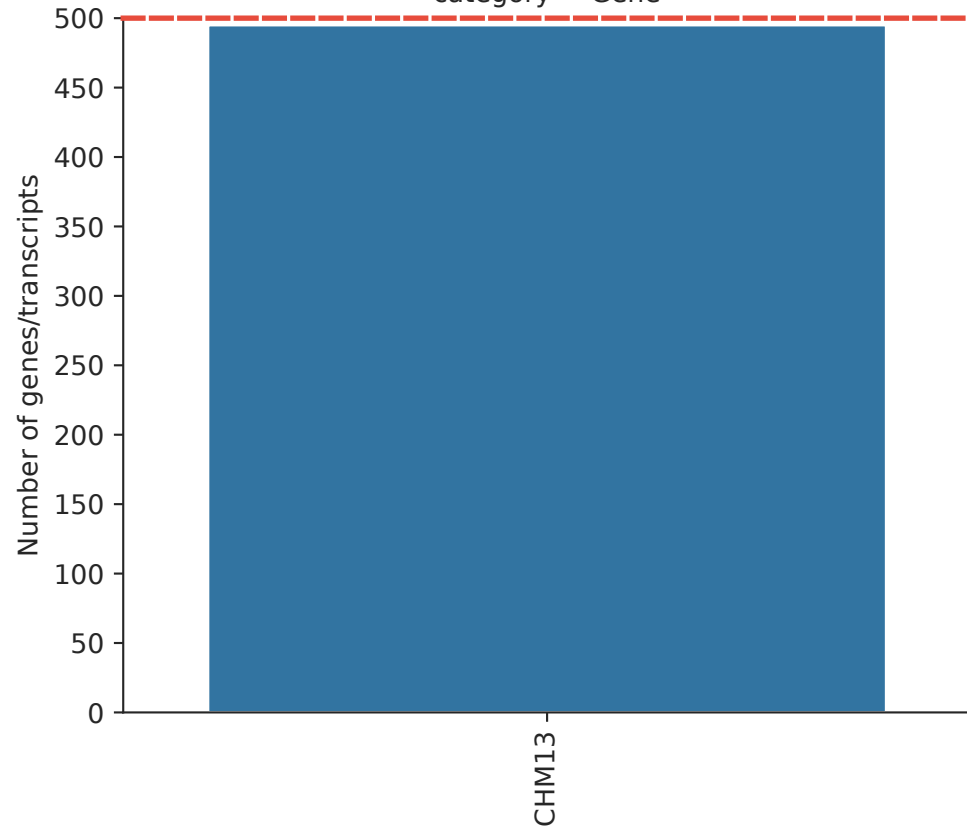


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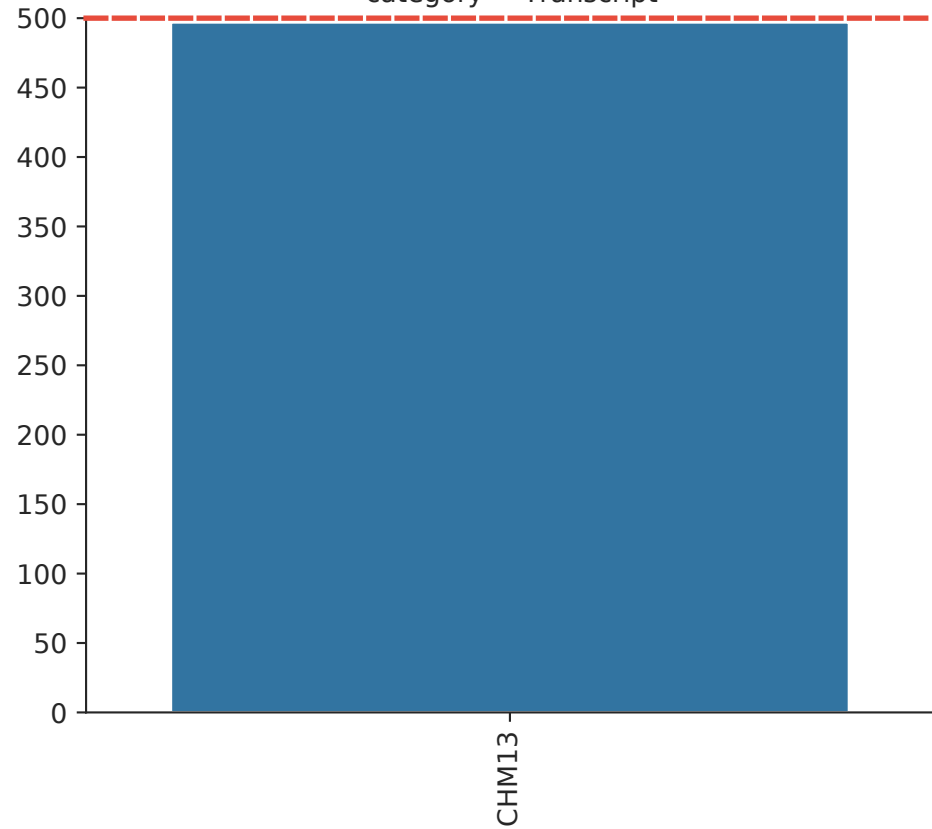


# Number of comparative genes/transcripts present for biotype transcribed\_processed\_pseudogene

category = Gene

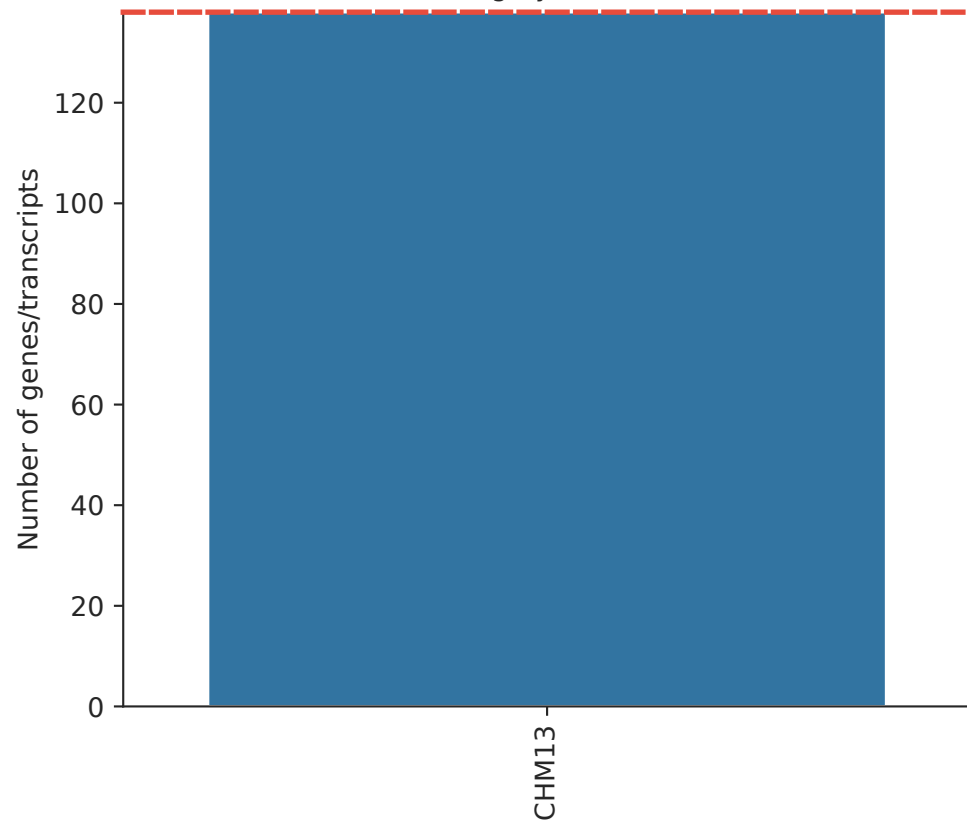


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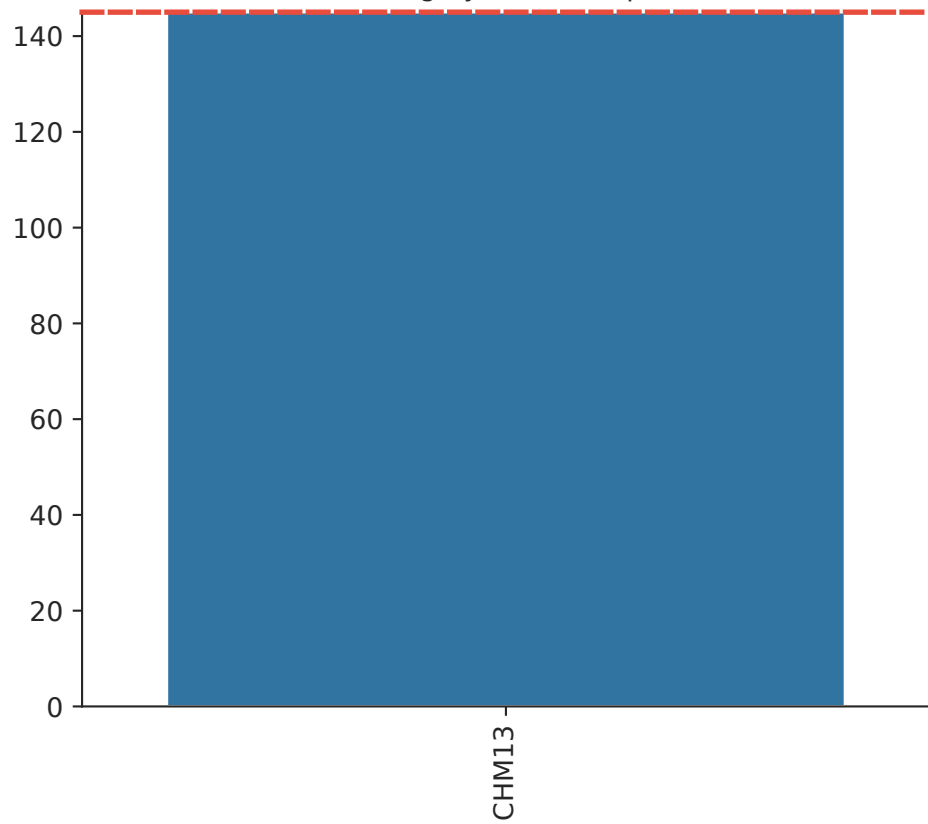


# Number of comparative genes/transcripts present for biotype transcribed\_unitary\_pseudogene

category = Gene

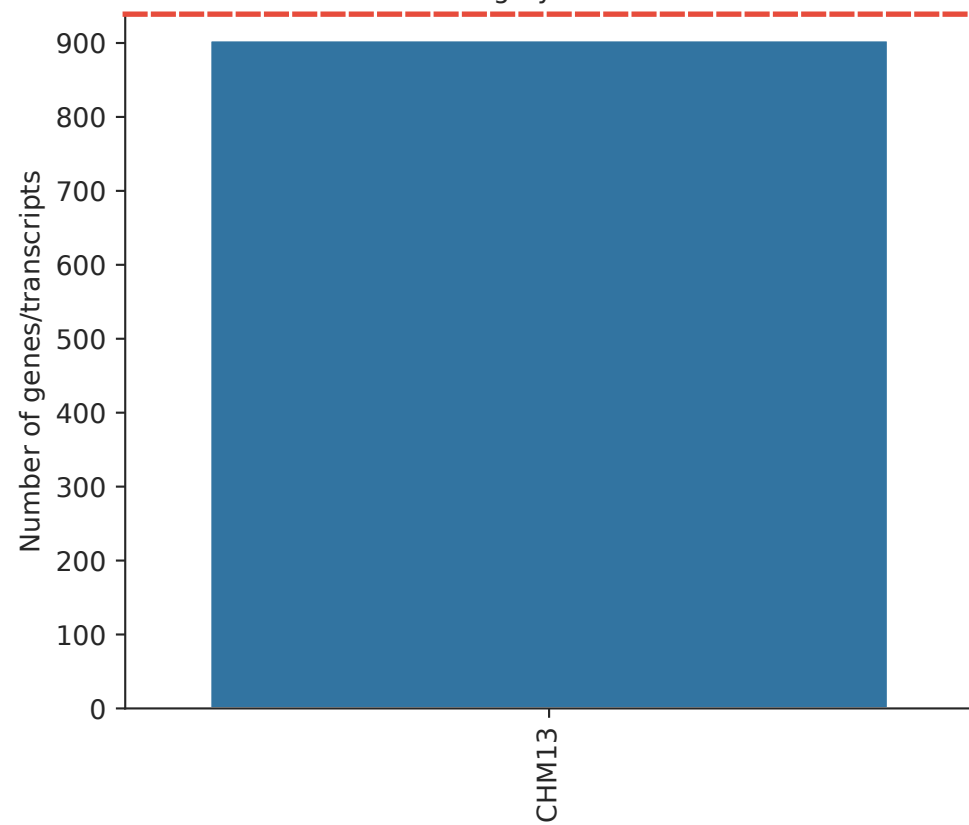


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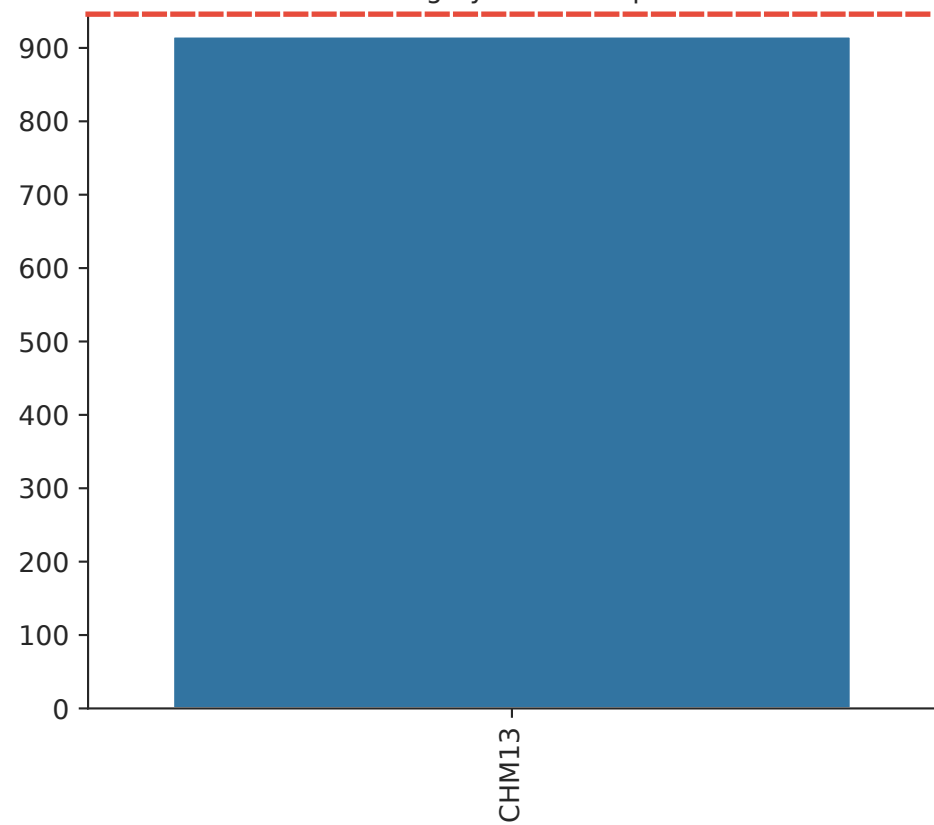


# Number of comparative genes/transcripts present for biotype transcribed\_unprocessed\_pseudogene

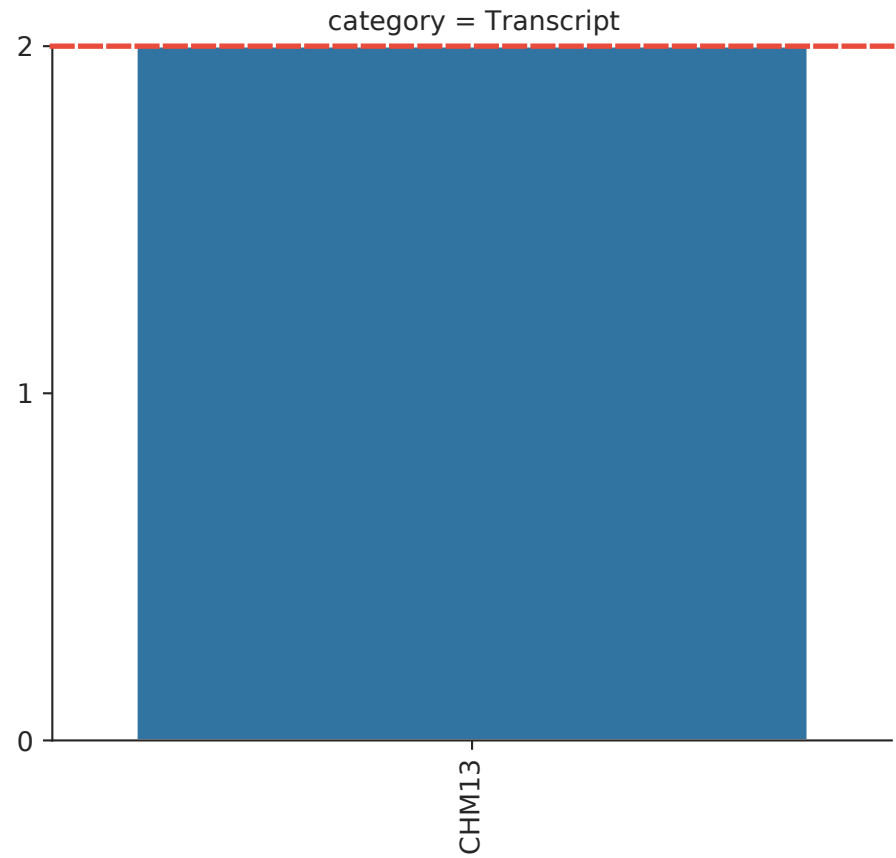
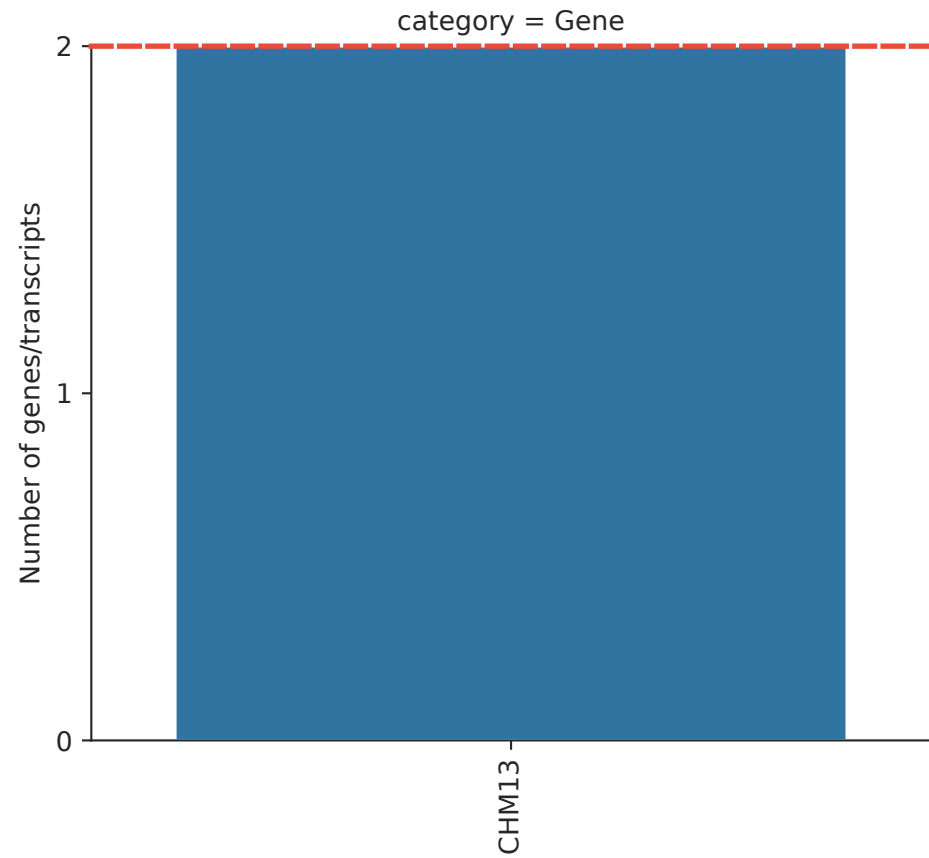
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category = Transcript

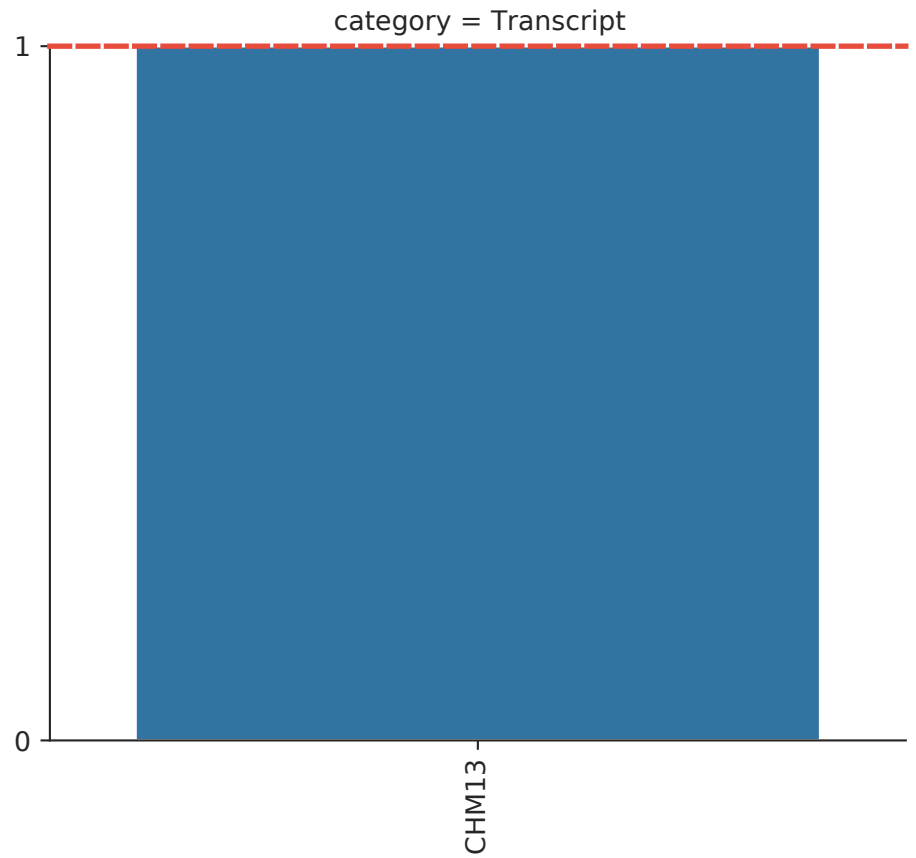
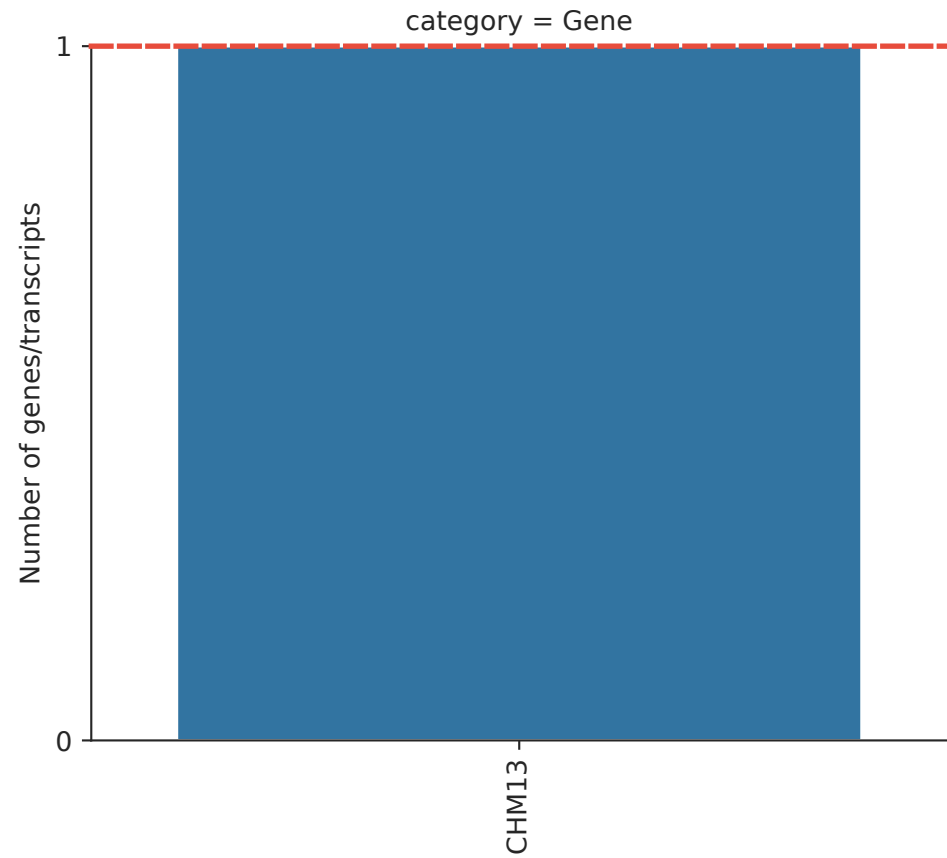


# Number of comparative genes/transcripts present for biotype translated\_processed\_pseudogene

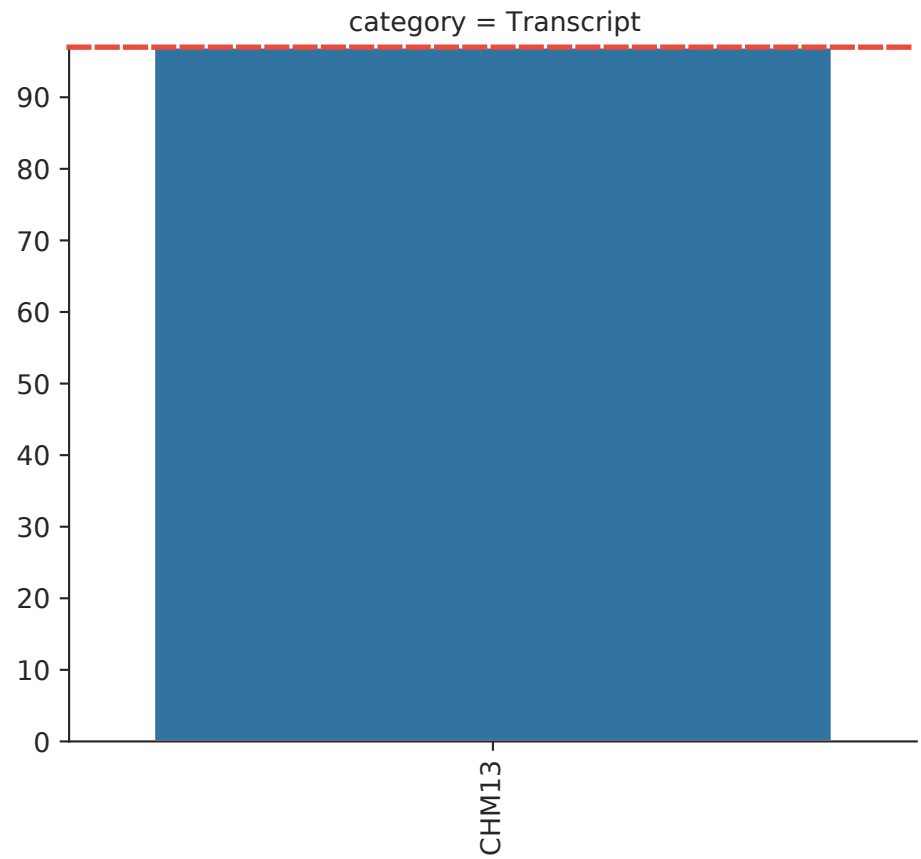
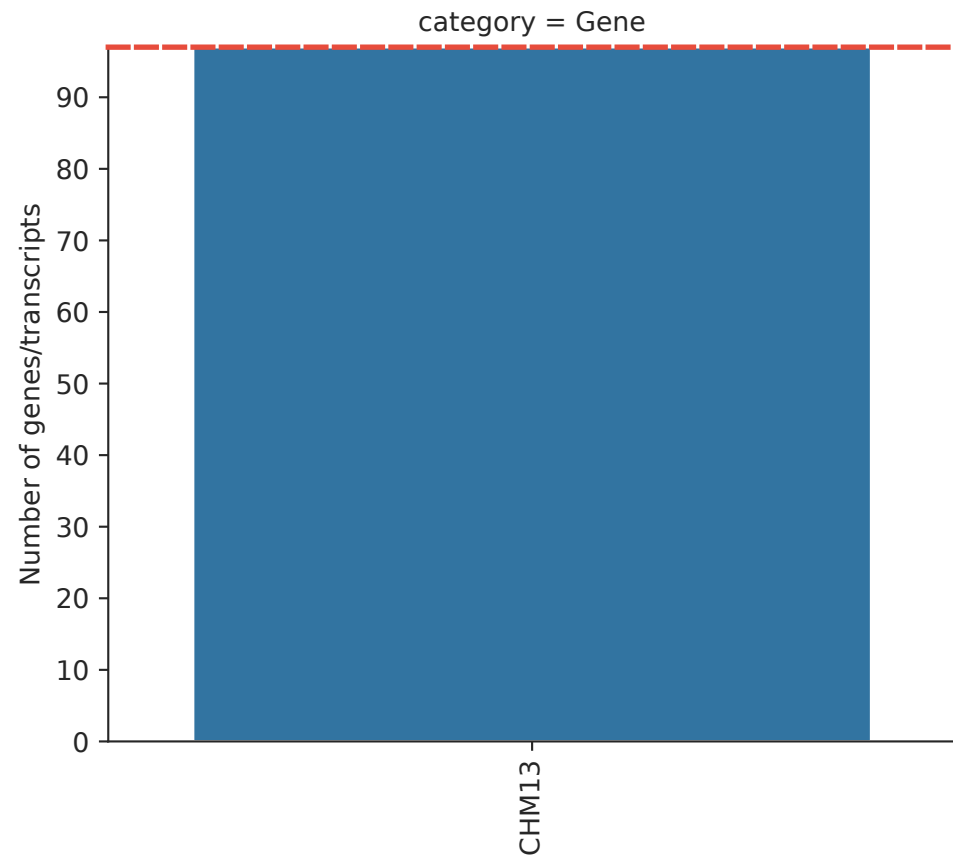




# Number of comparative genes/transcripts present for biotype translated\_unprocessed\_pseudogene

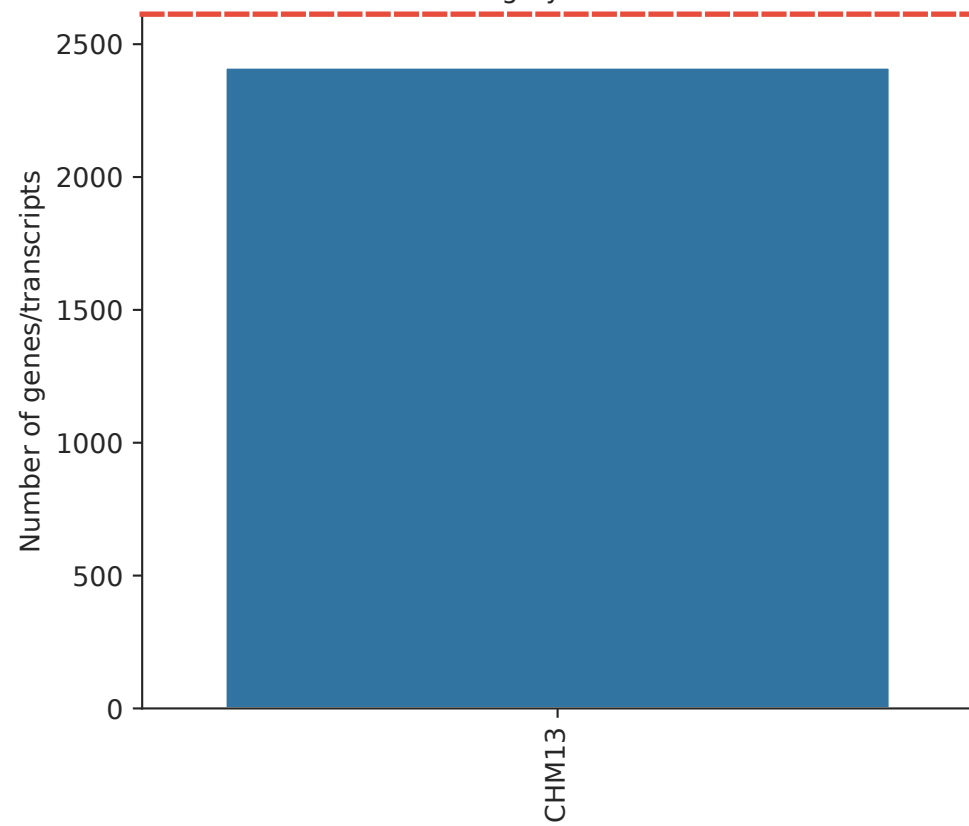


# Number of comparative genes/transcripts present for biotype unitary\_pseudogene

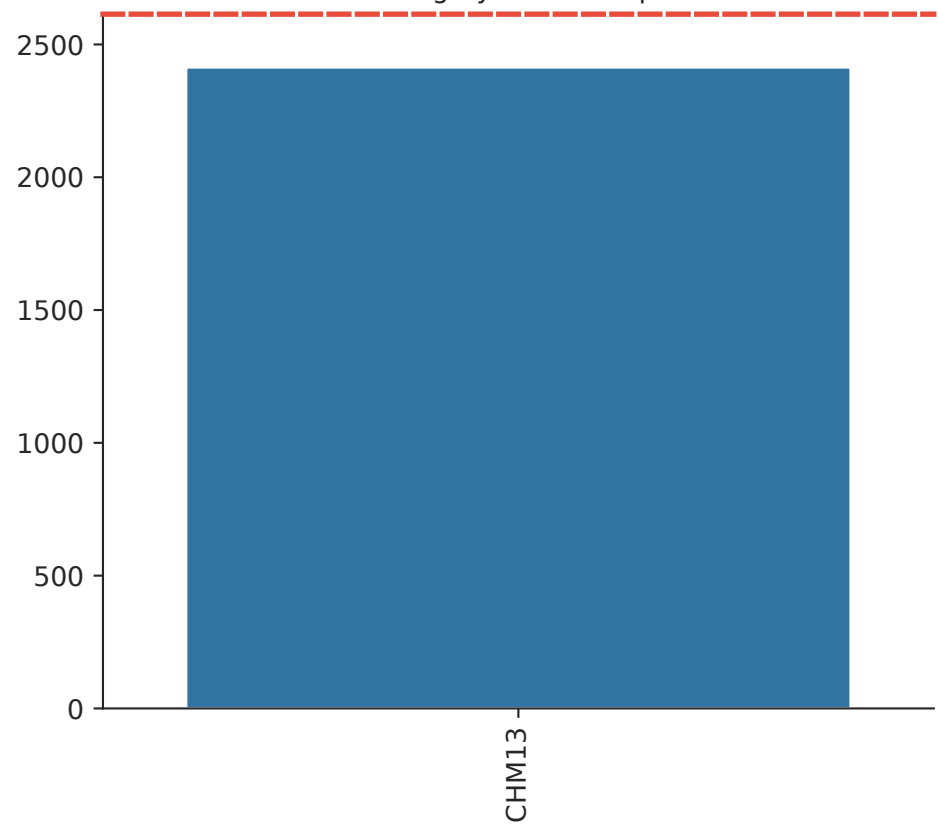


# Number of comparative genes/transcripts present for biotype unprocessed\_pseudogene

category = Gene



category = Transcript



# Number of comparative genes/transcripts present for biotype vault\_RNA

