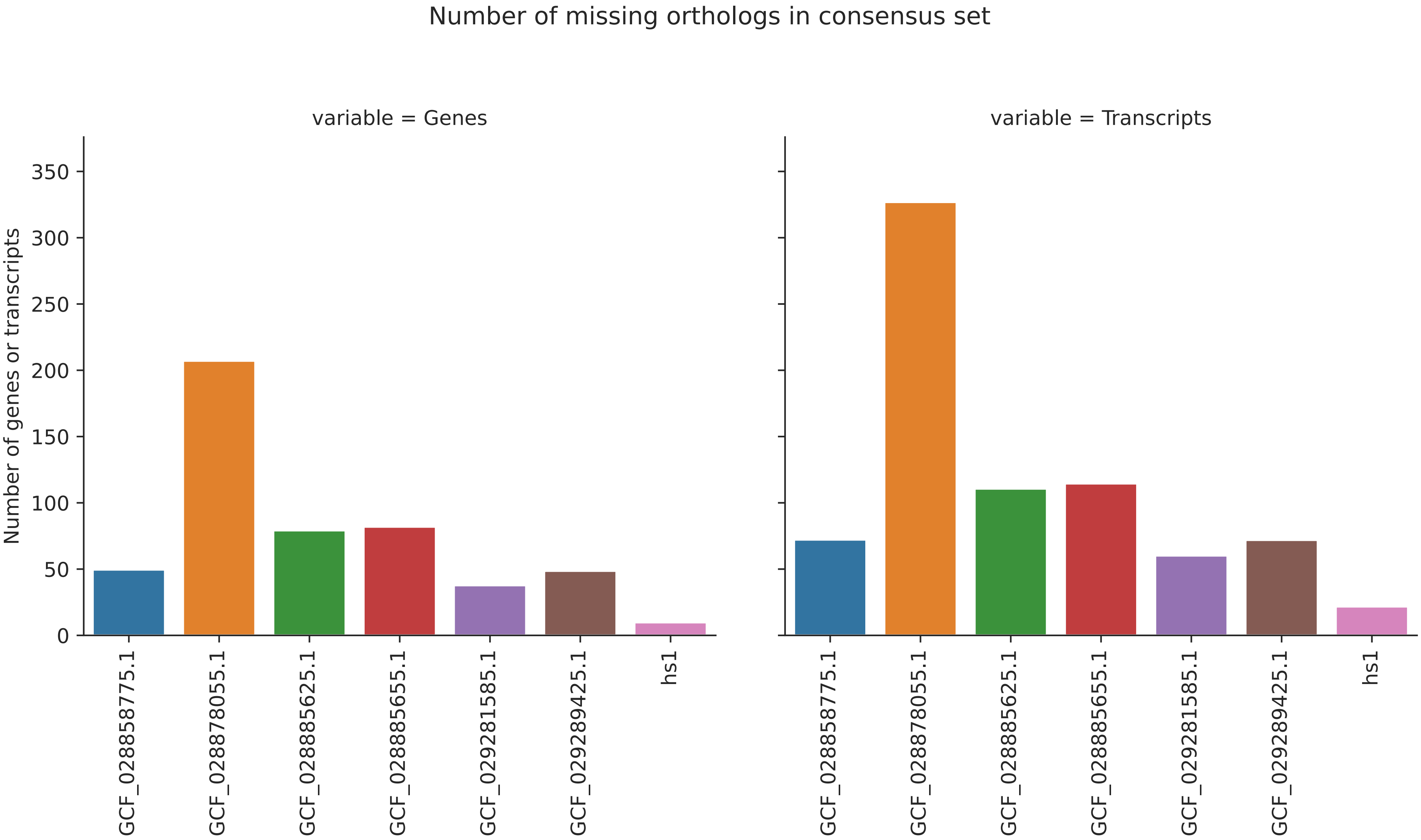
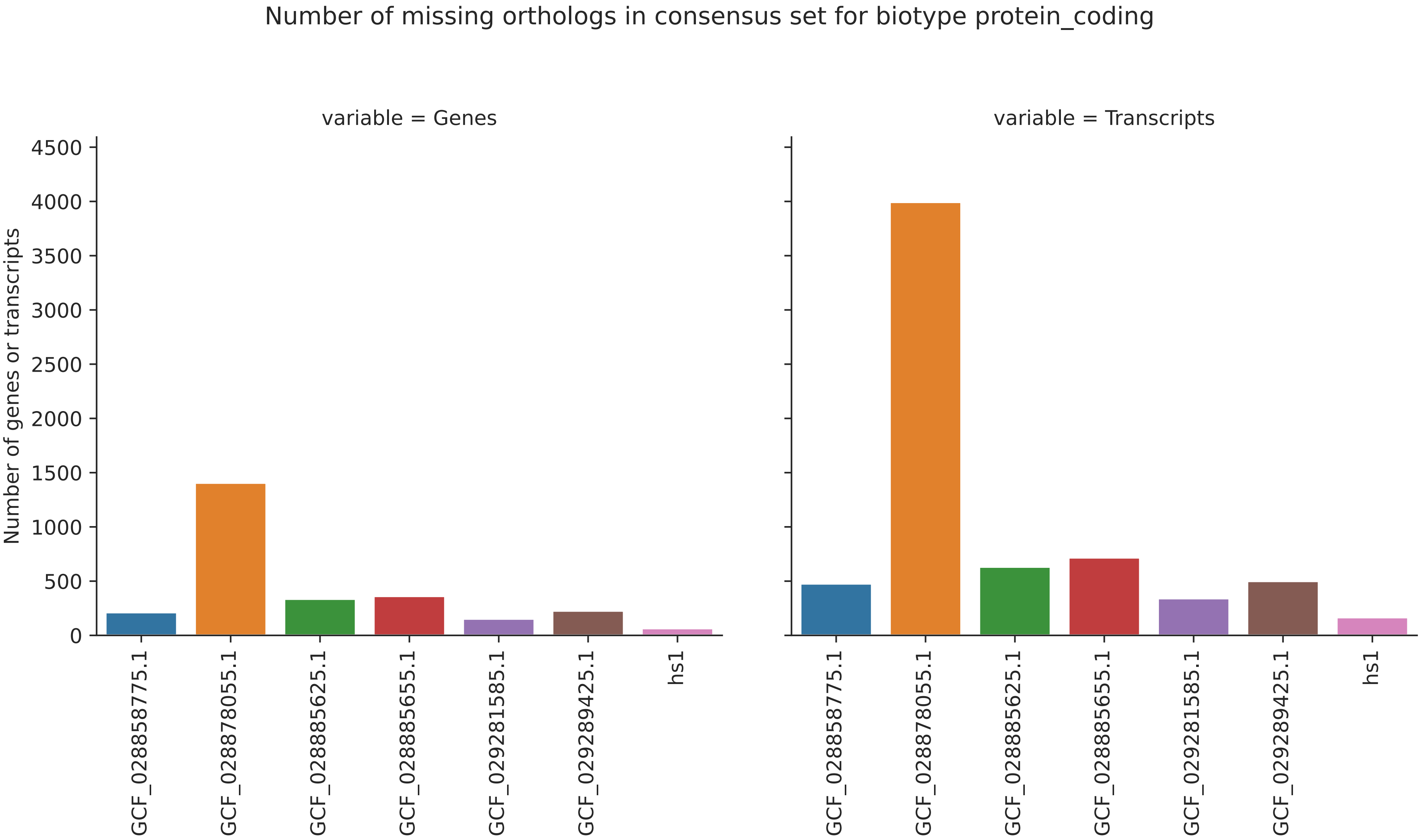
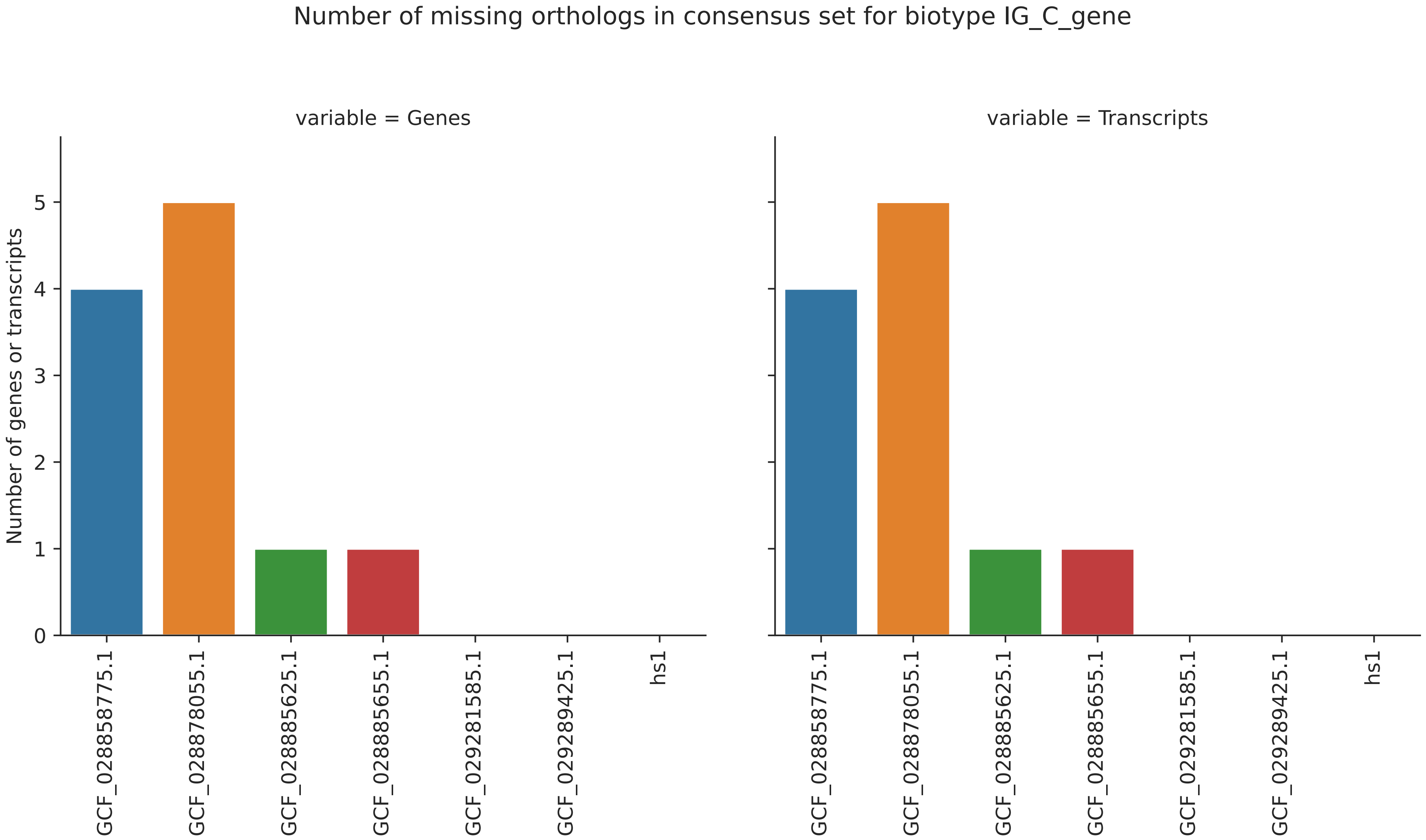
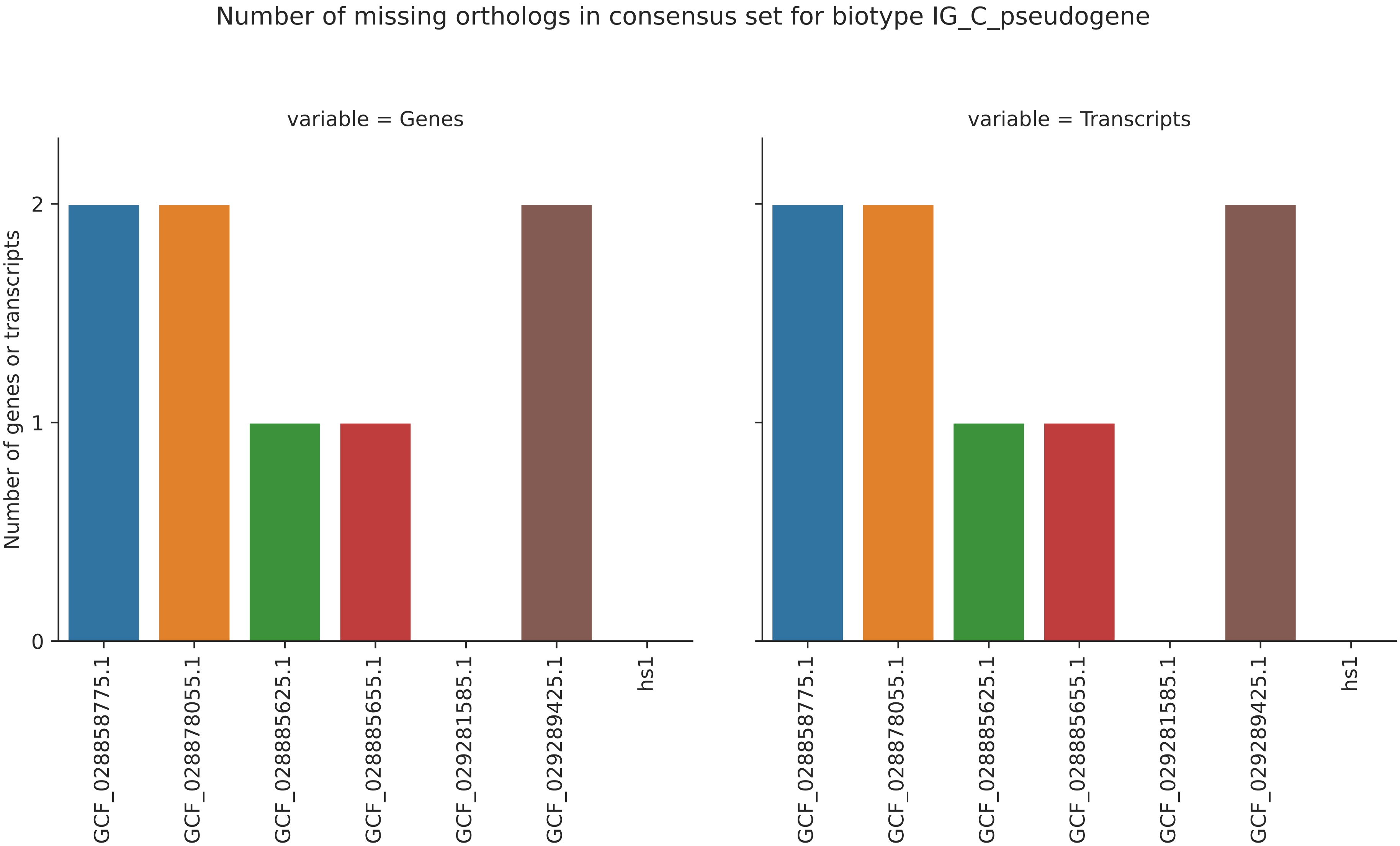

Number of missing orthologs in consensus set
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
50
100
150
200
250
300
350
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

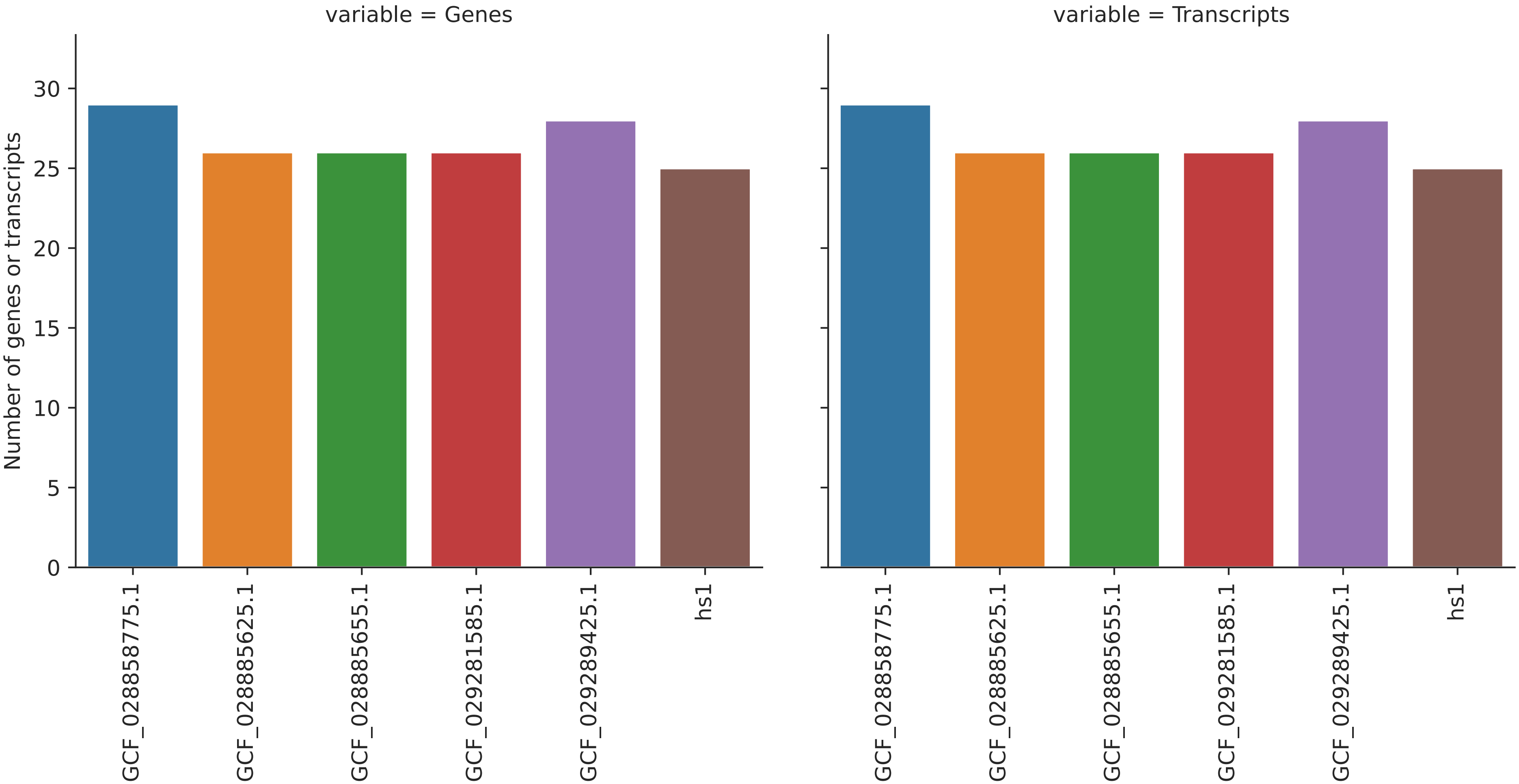

Number of missing orthologs in consensus set for biotype protein_coding
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
500
1000
1500
2000
2500
3000
3500
4000
4500
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1



Number of missing orthologs in consensus set for biotype IG_C_gene

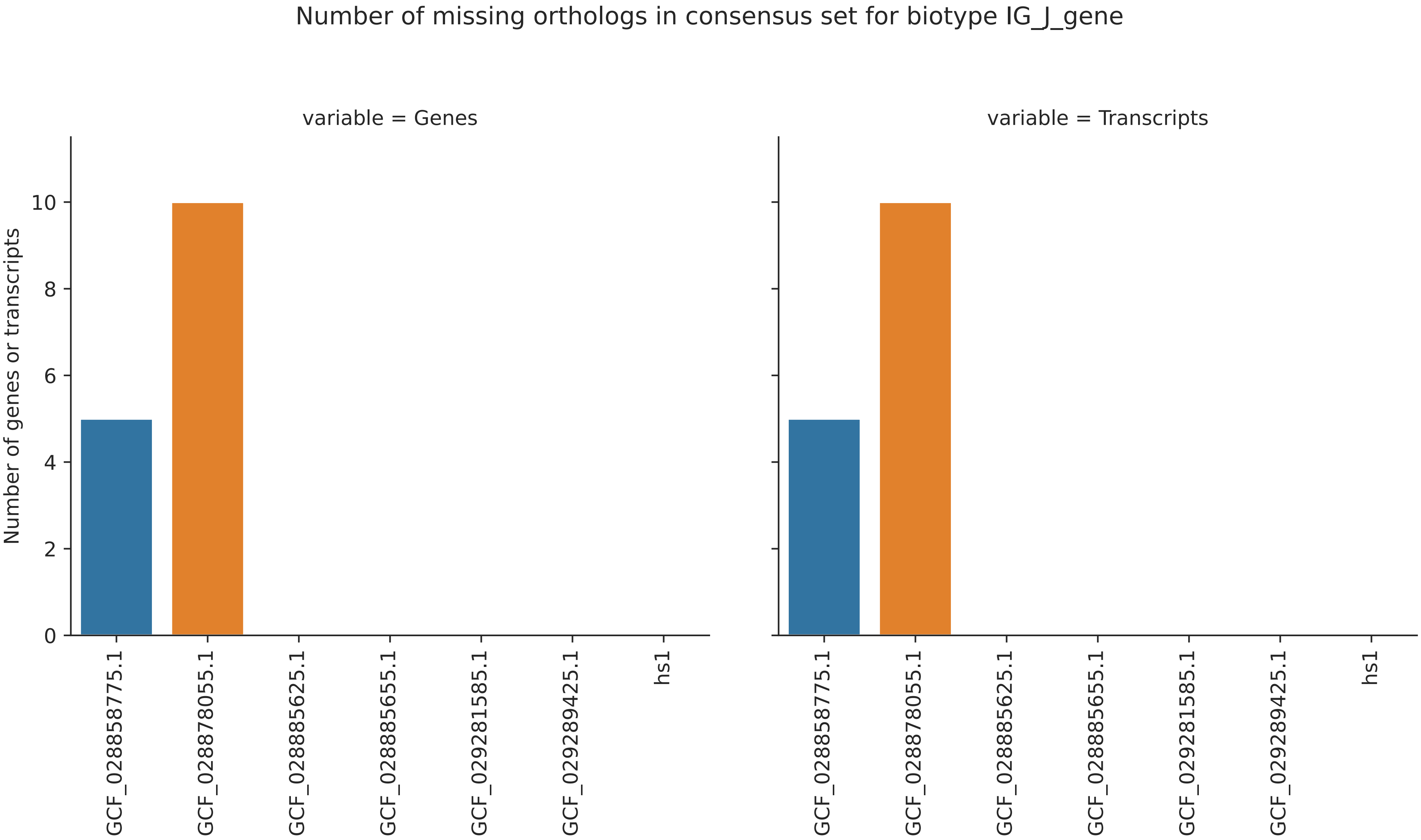

Number of missing orthologs in consensus set for biotype IG_C_pseudogene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
1
2
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

Number of missing orthologs in consensus set for biotype IG_D_gene

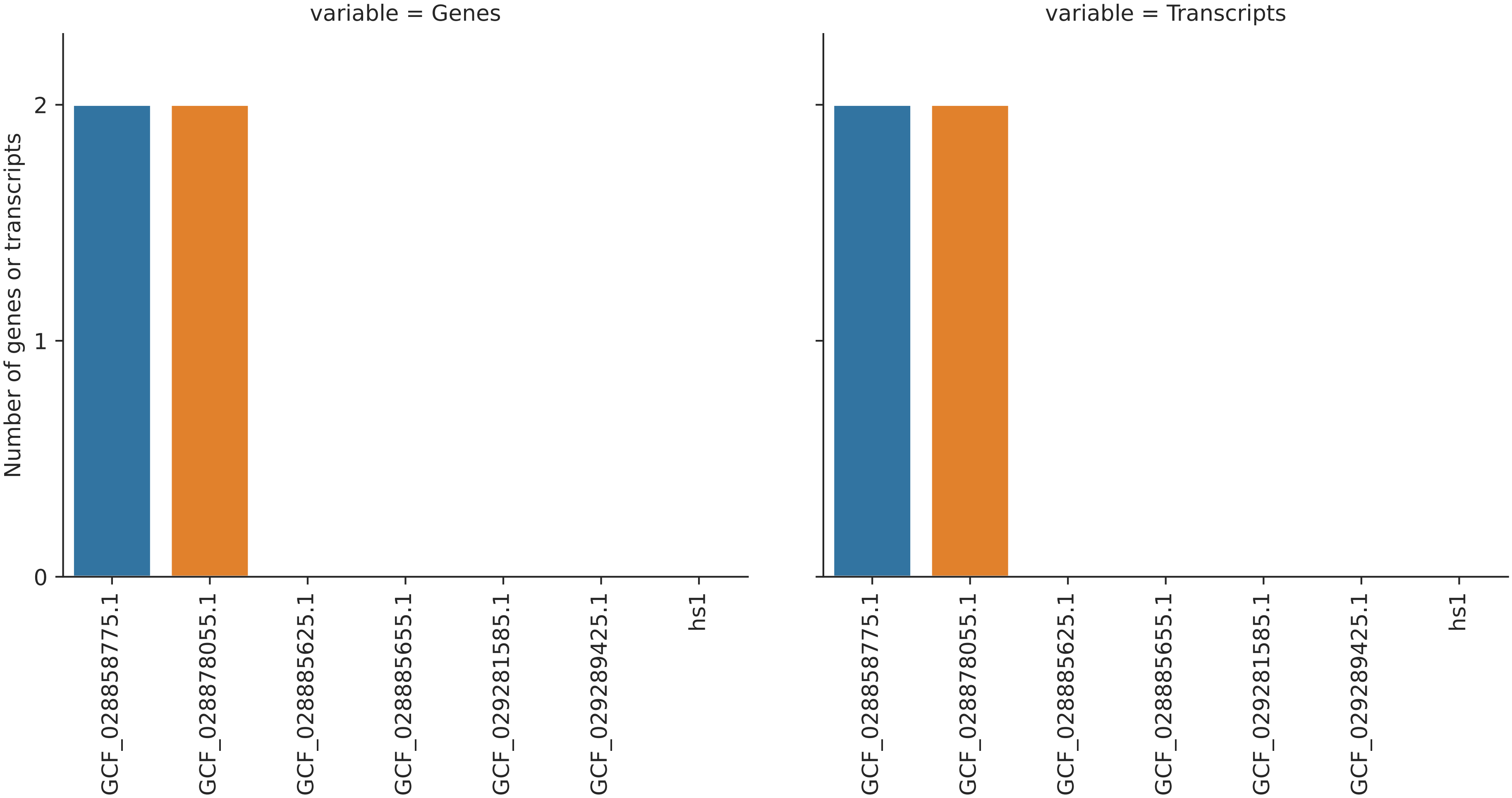


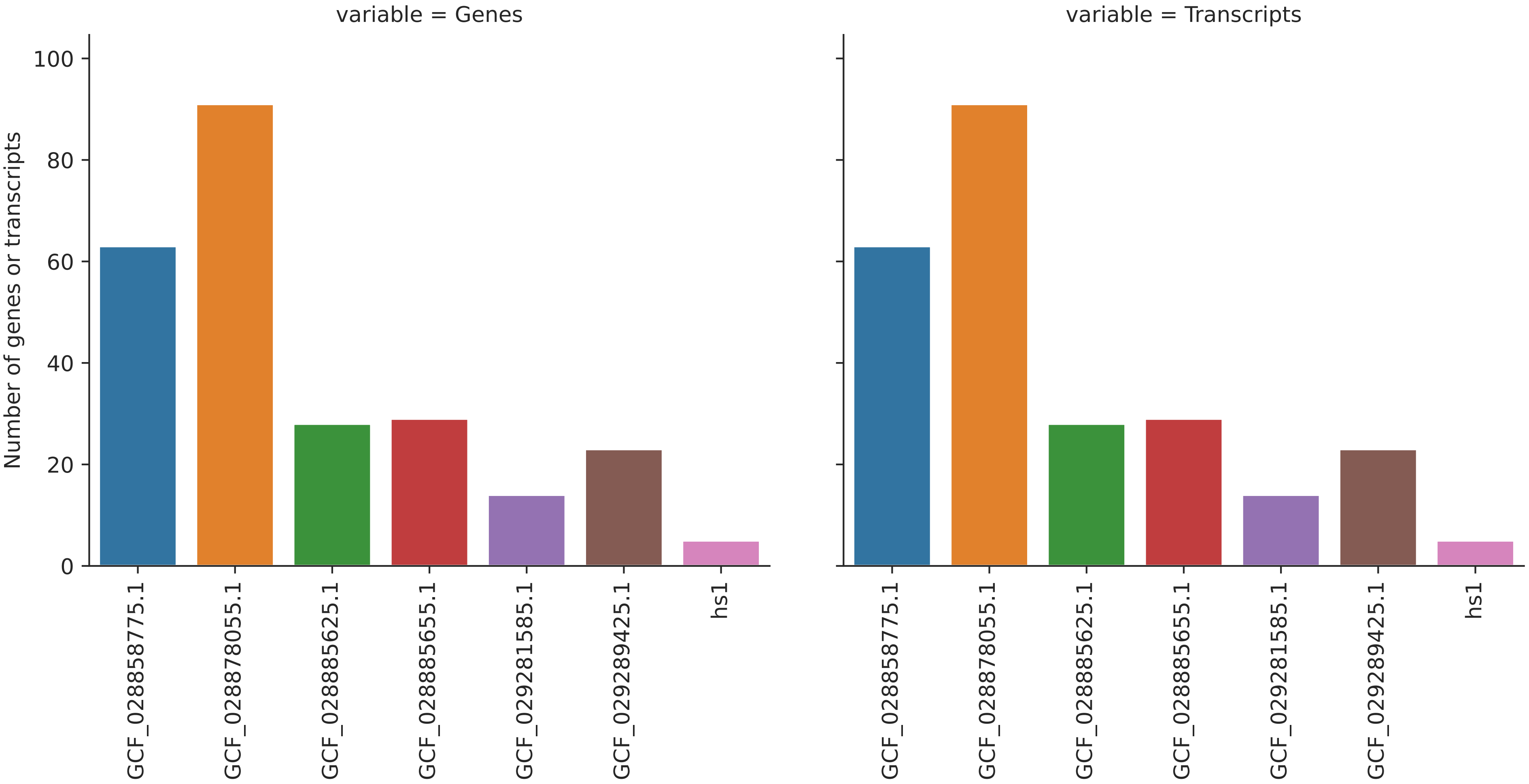
variable = Genes

variable = Transcripts


Number of missing orthologs in consensus set for biotype IG_J_gene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
2
4
6
8
10
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

Number of missing orthologs in consensus set for biotype IG_J_pseudogene



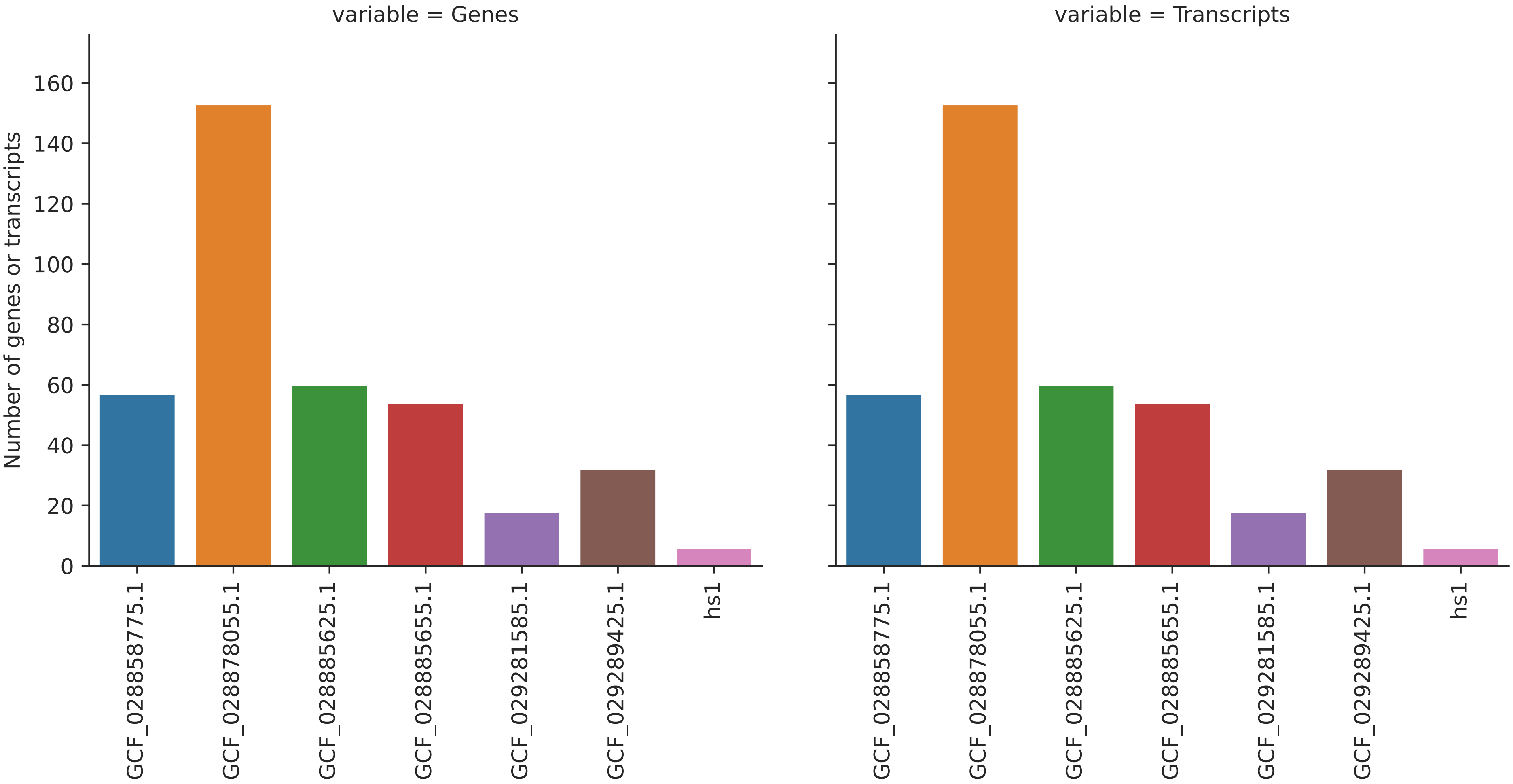


Number of missing orthologs in consensus set for biotype IG_V_gene

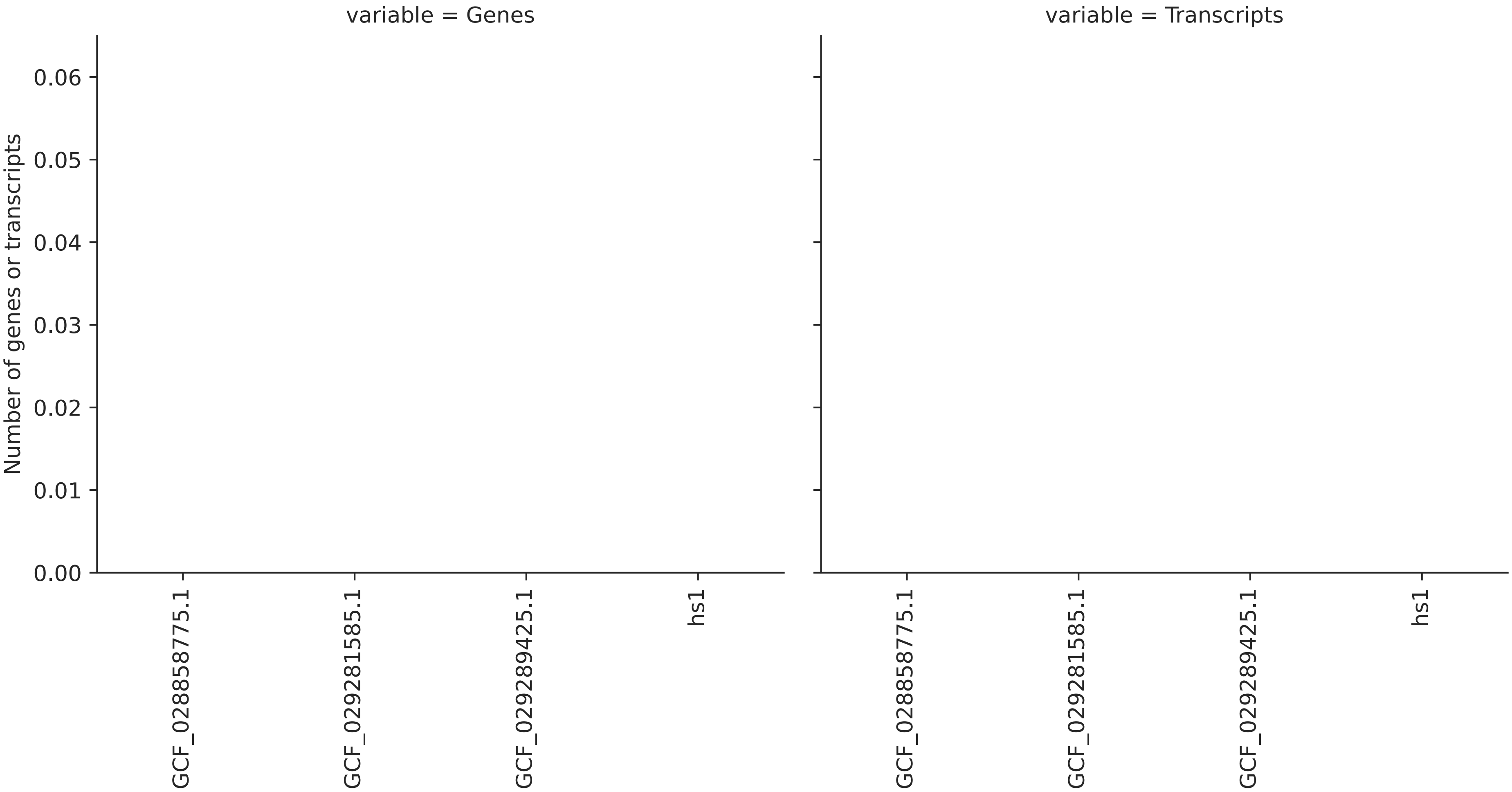
variable = Genes

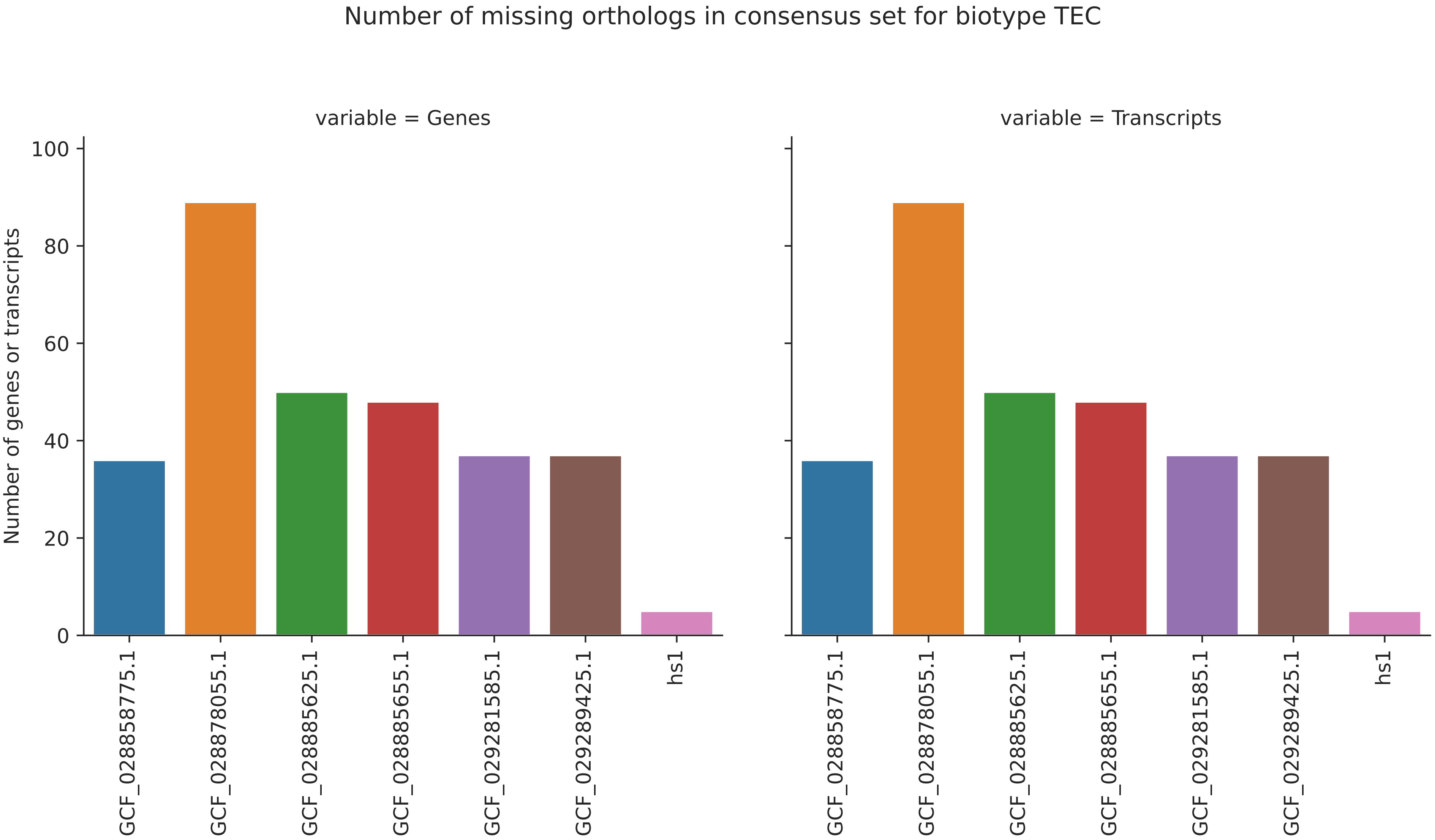
variable = Transcripts

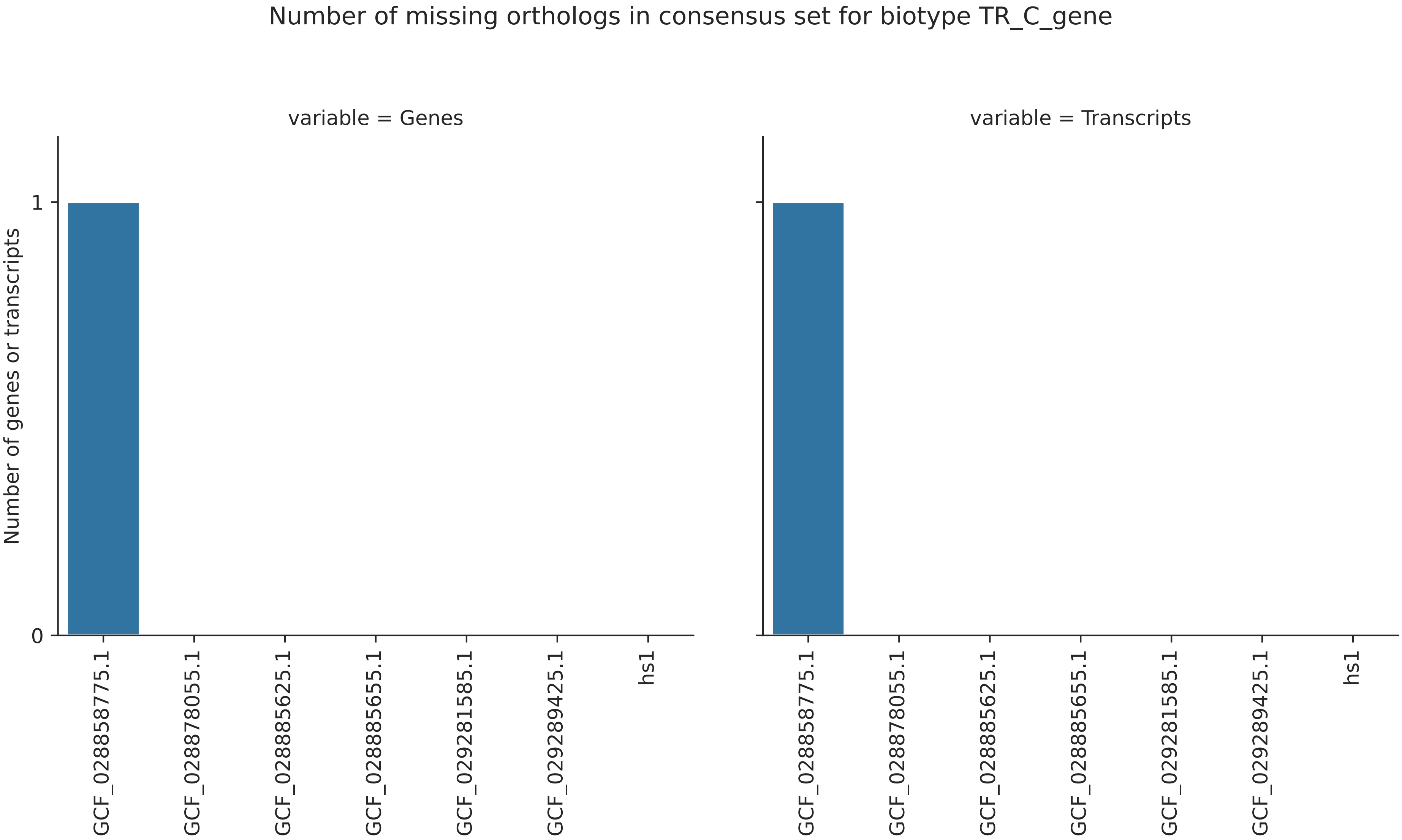
Number of missing orthologs in consensus set for biotype IG_V_pseudogene

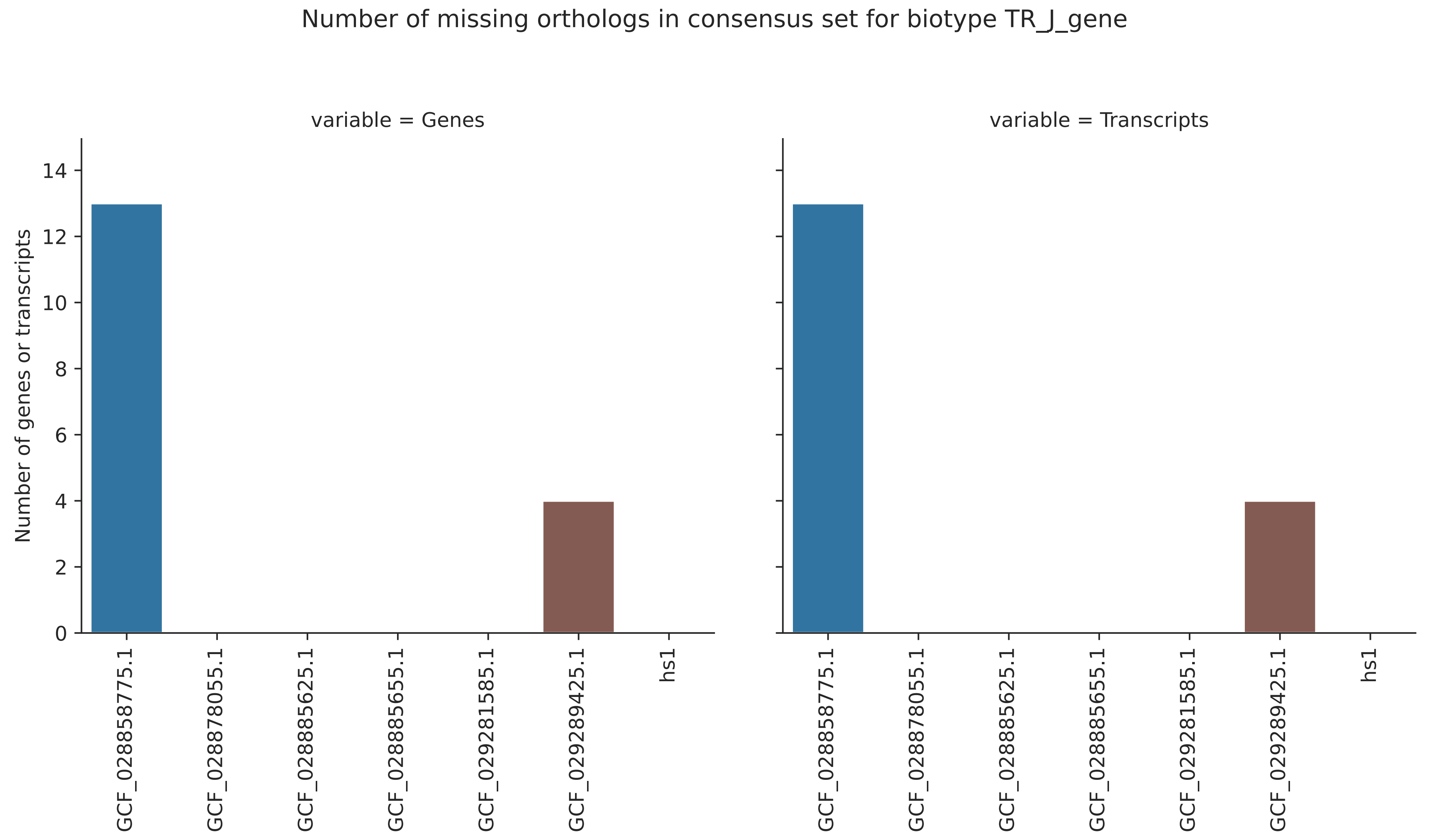


Number of missing orthologs in consensus set for biotype IG_pseudogene

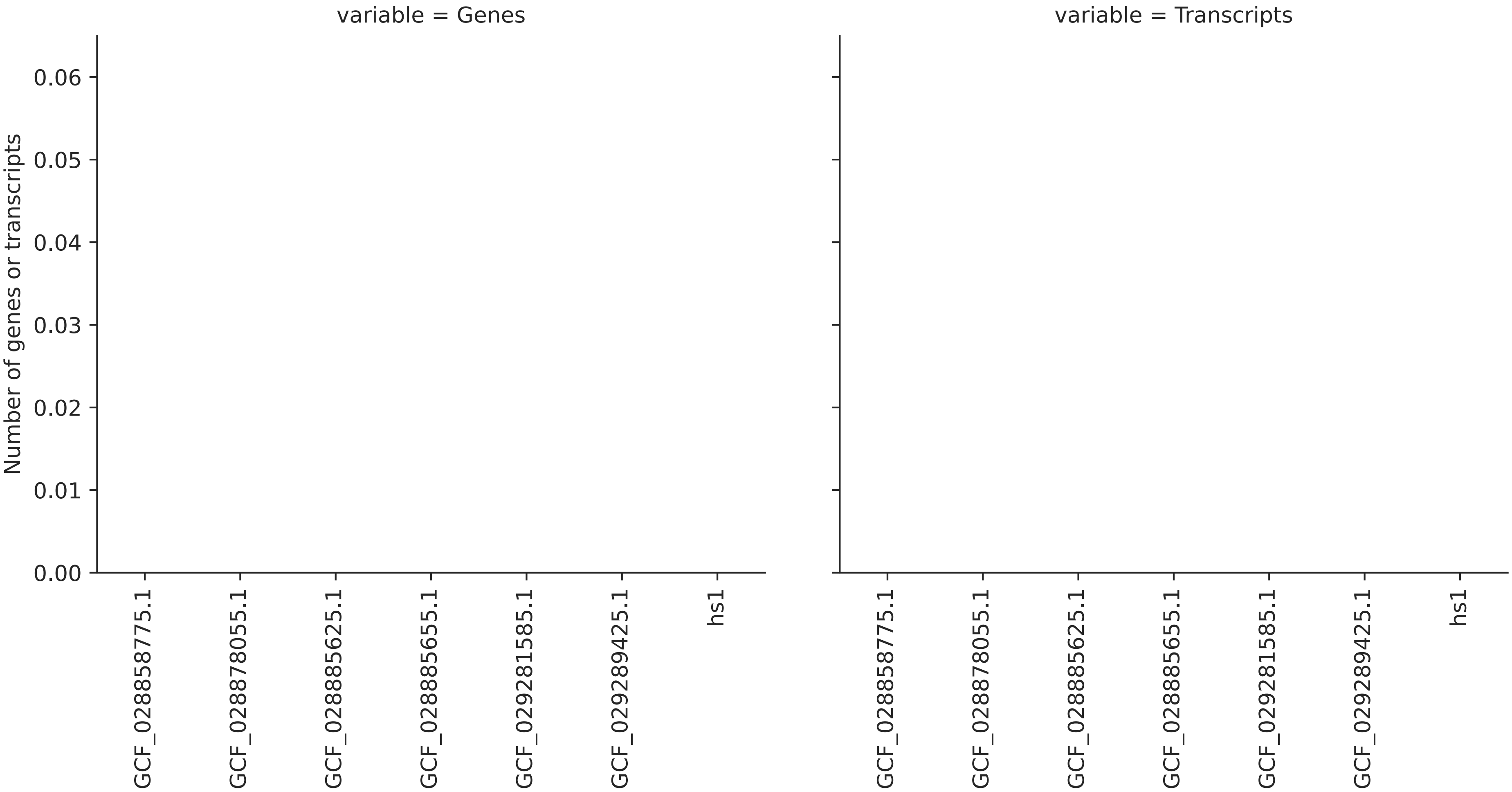


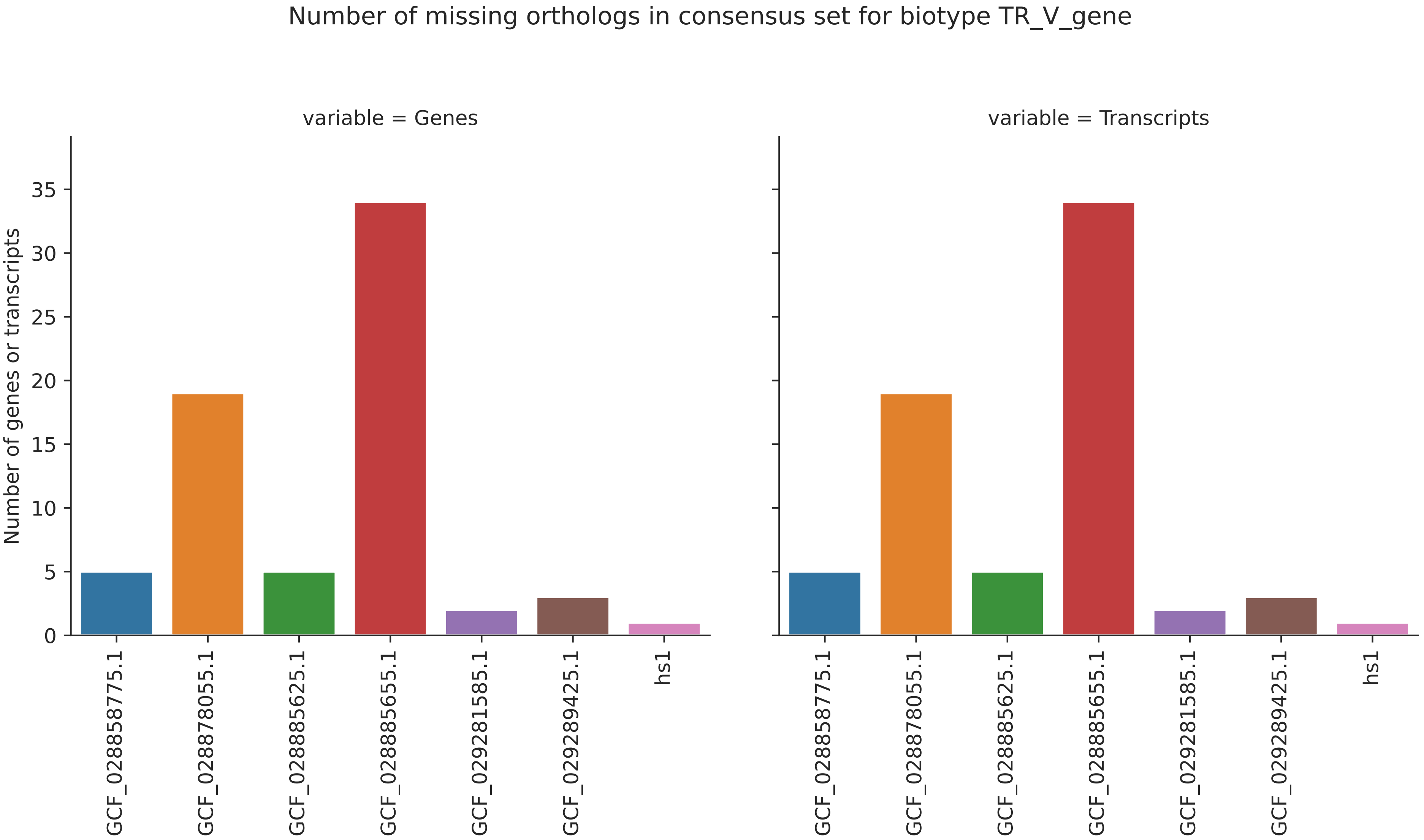

Number of missing orthologs in consensus set for biotype TEC
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
20
40
60
80
100
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1


Number of missing orthologs in consensus set for biotype TR_C_gene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
1
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

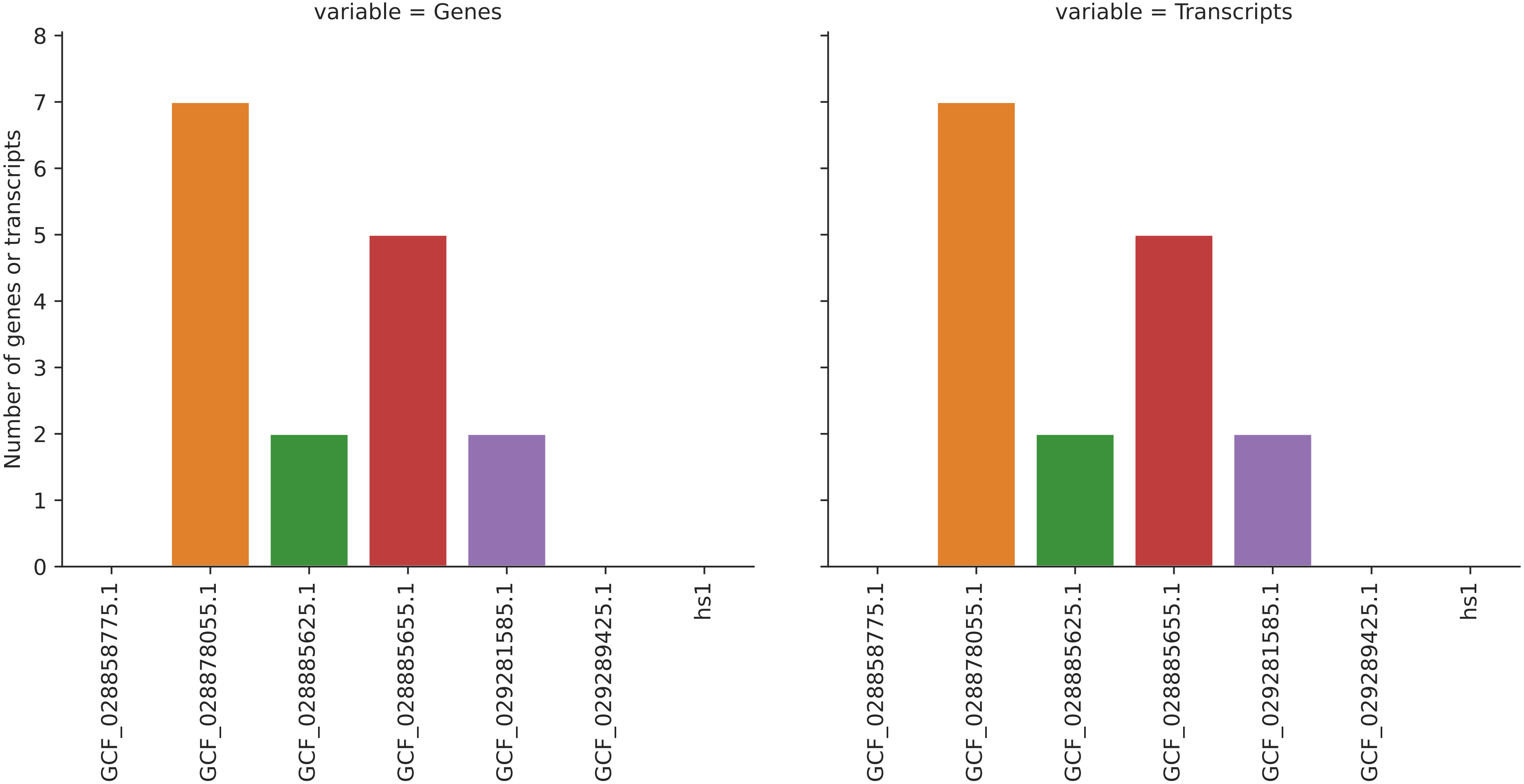

Number of missing orthologs in consensus set for biotype TR_J_gene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
2
4
6
8
10
12
14
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

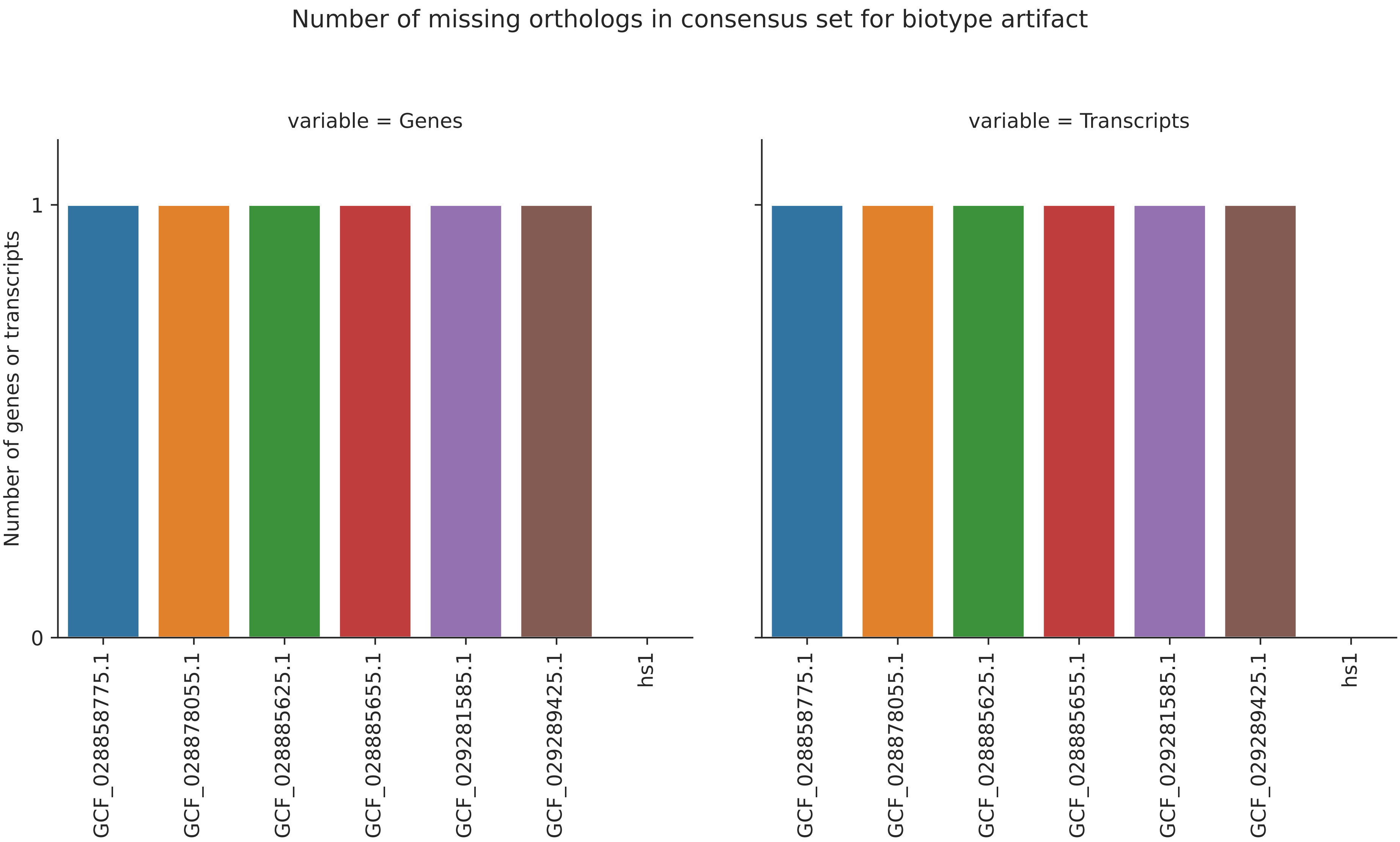
Number of missing orthologs in consensus set for biotype TR_J_pseudogene

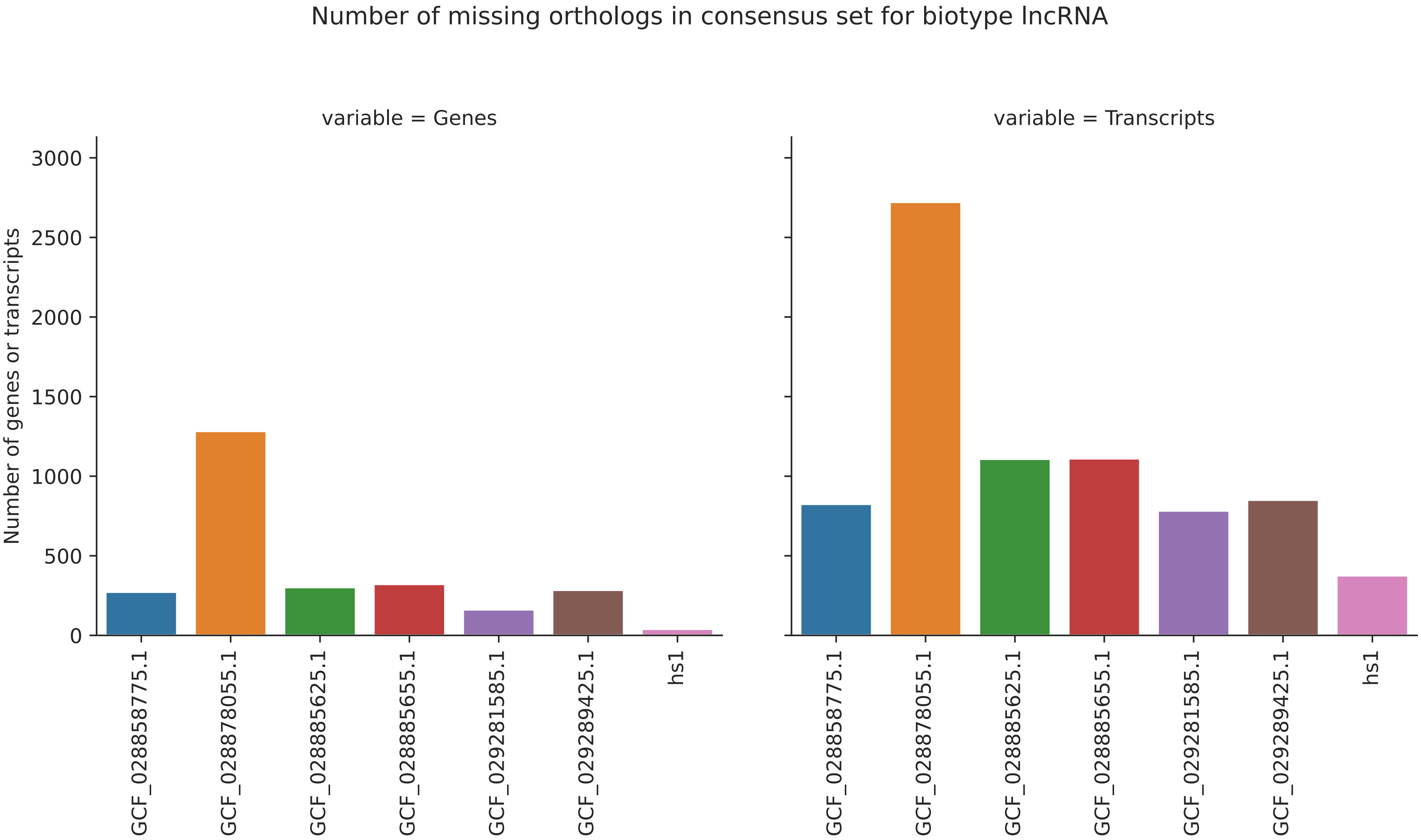


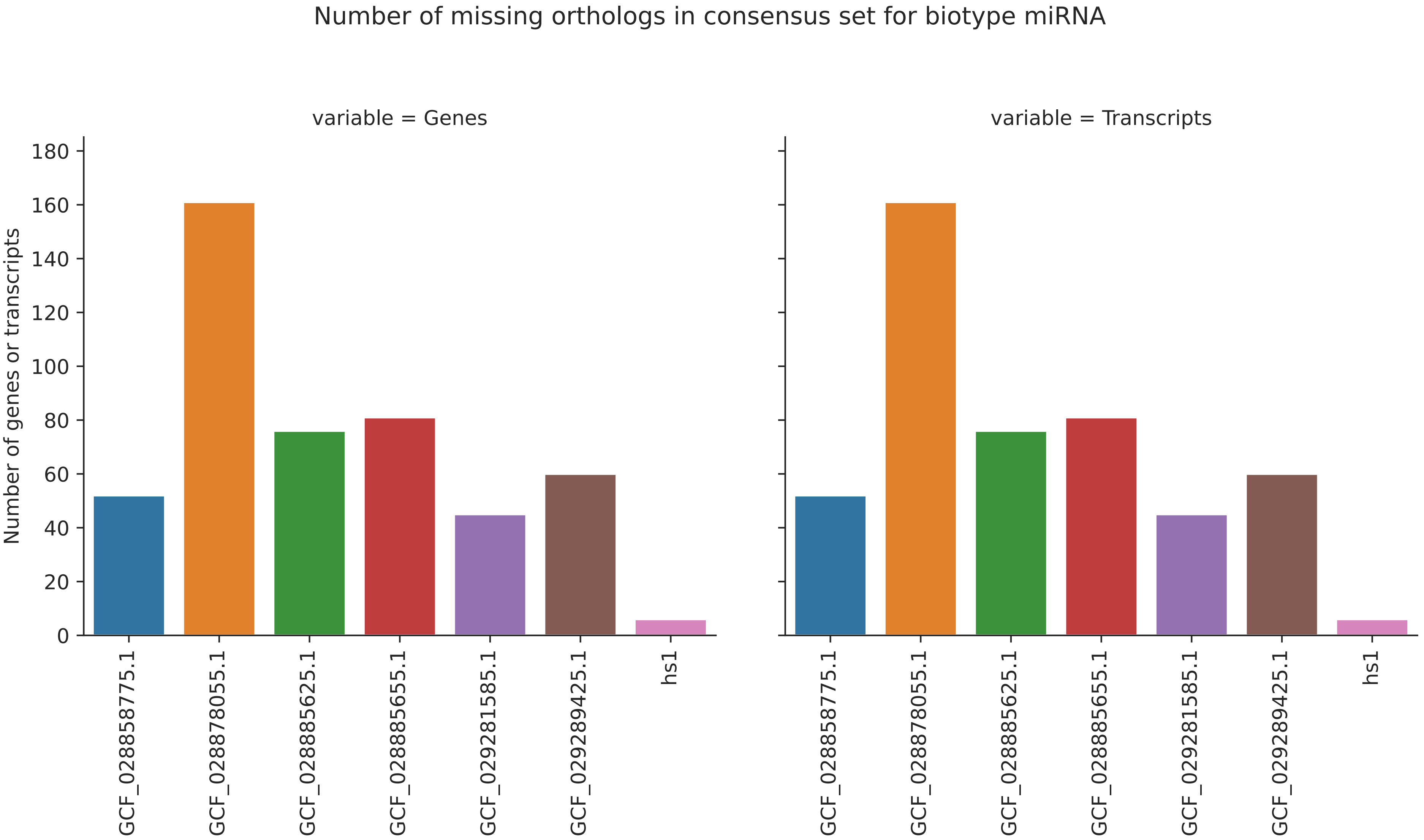

Number of missing orthologs in consensus set for biotype TR_V_gene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
5
10
15
20
25
30
35
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

Number of missing orthologs in consensus set for biotype TR_V_pseudogene




Number of missing orthologs in consensus set for biotype artifact
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
1
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

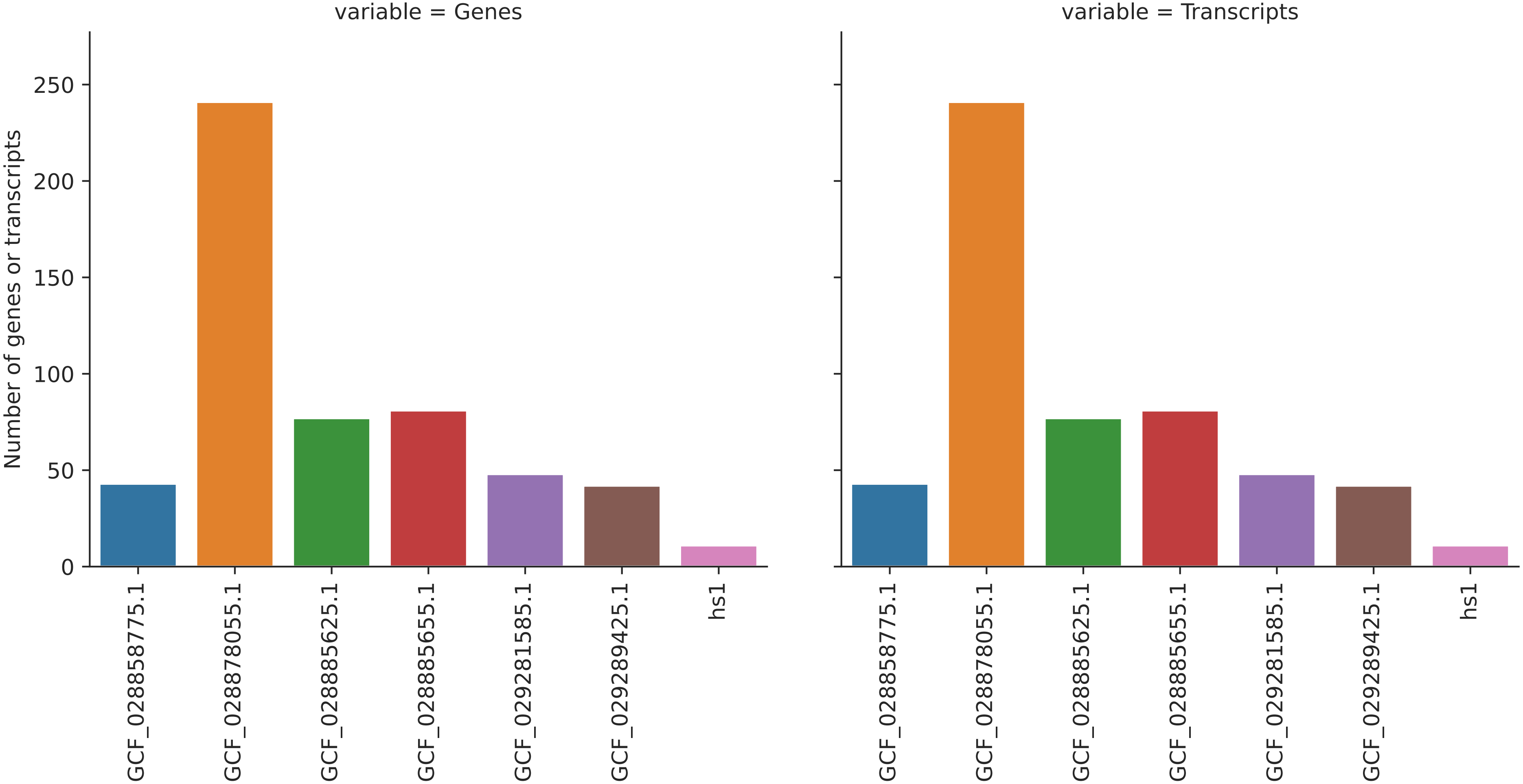

Number of missing orthologs in consensus set for biotype lncRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
500
1000
1500
2000
2500
3000
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1



Number of missing orthologs in consensus set for biotype miRNA

variable = Genes

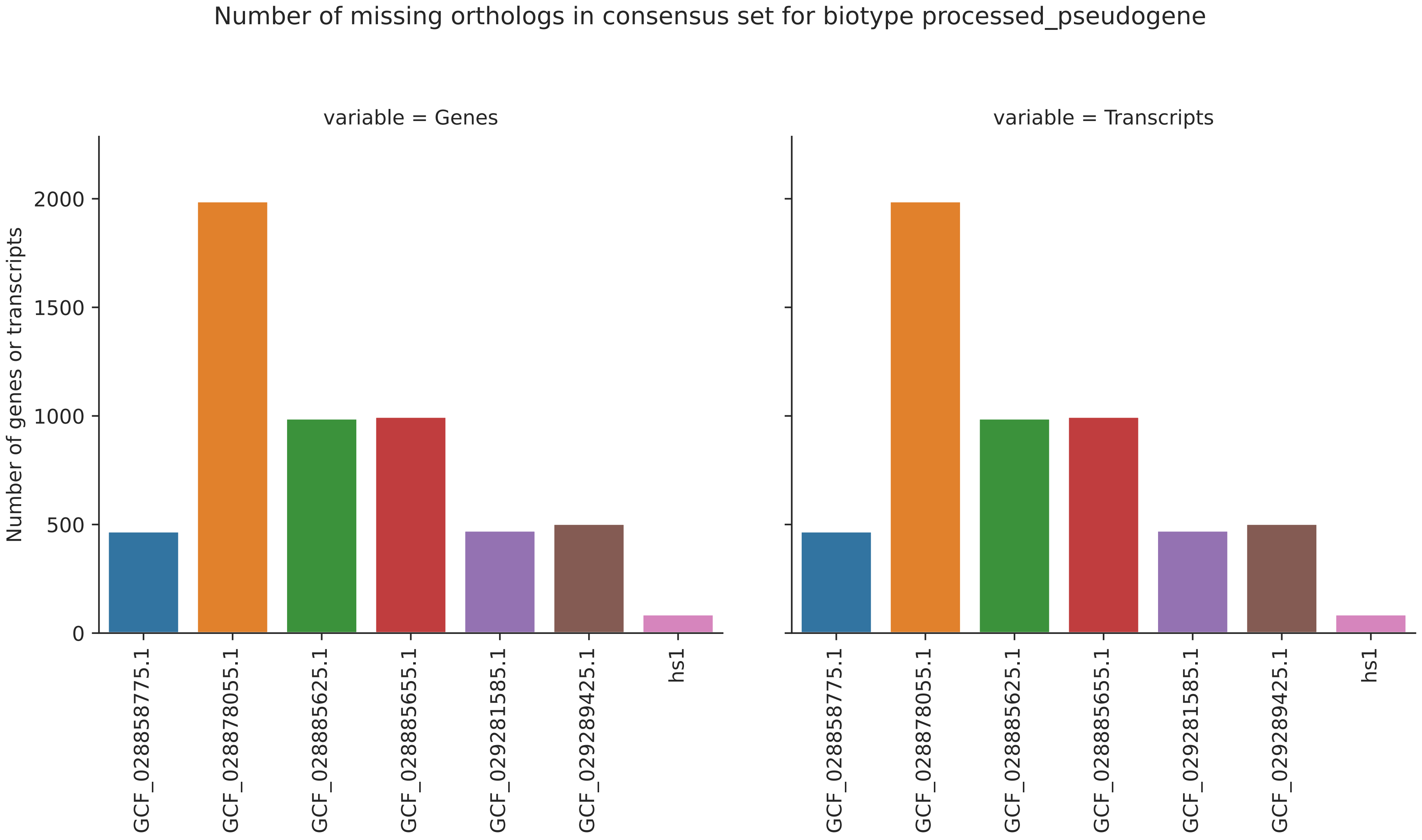
variable = Transcripts

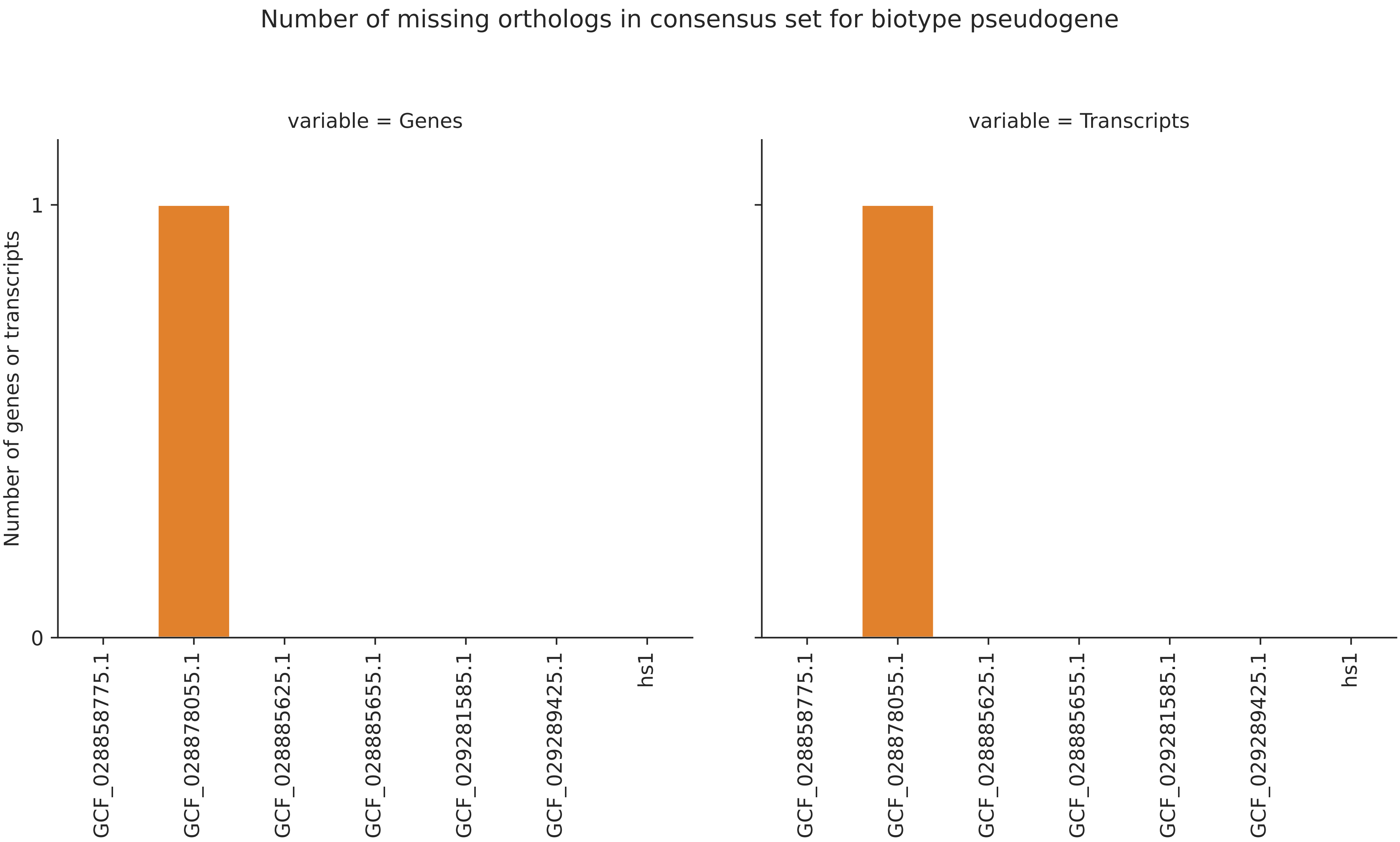


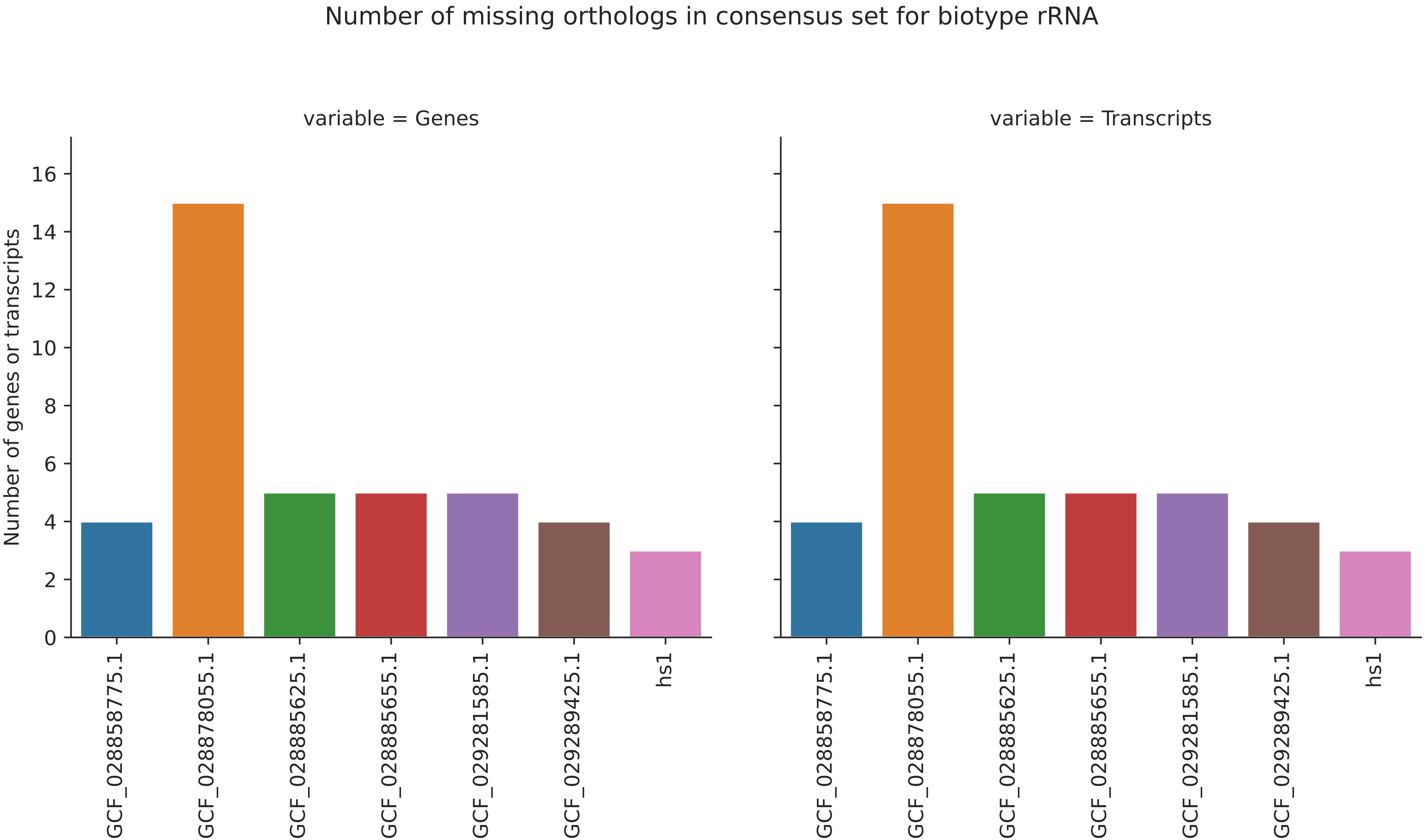
Number of missing orthologs in consensus set for biotype misc_RNA

variable = Genes

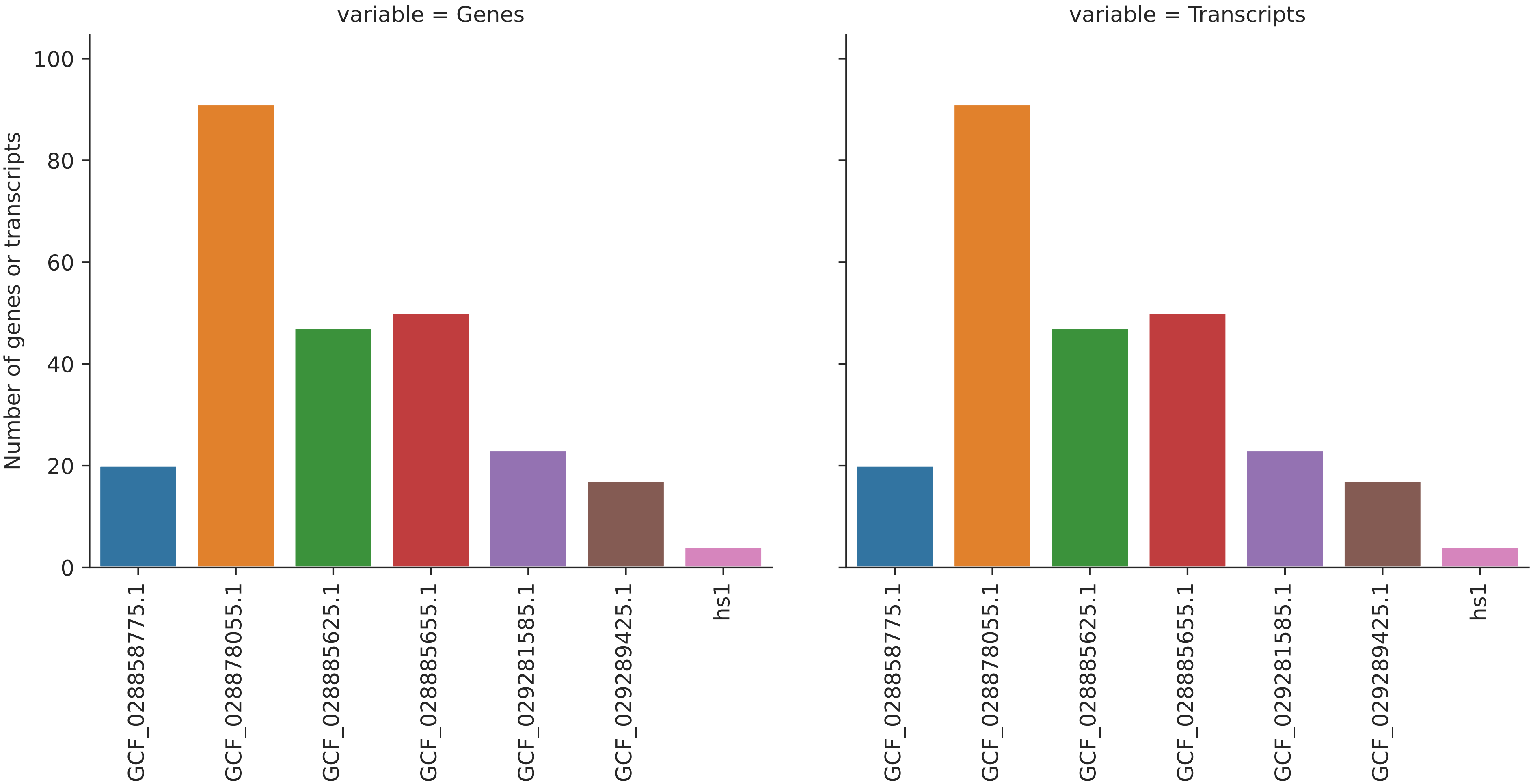
variable = Transcripts


Number of missing orthologs in consensus set for biotype processed_pseudogene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
500
1000
1500
2000
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

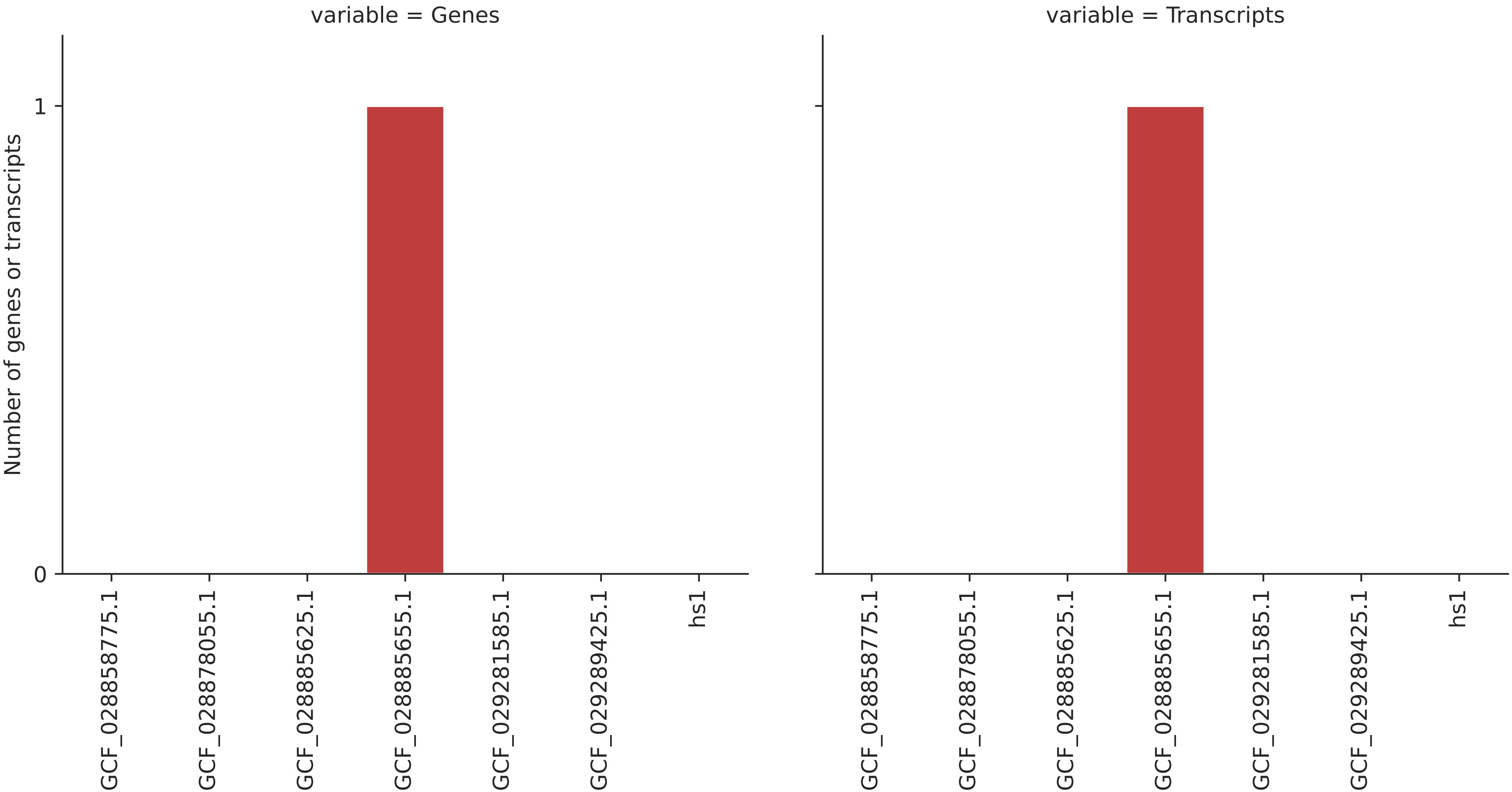
Number of missing orthologs in consensus set for biotype pseudogene
variable = Genes
variable = Transcripts
Number of genes or transcripts
1
0
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

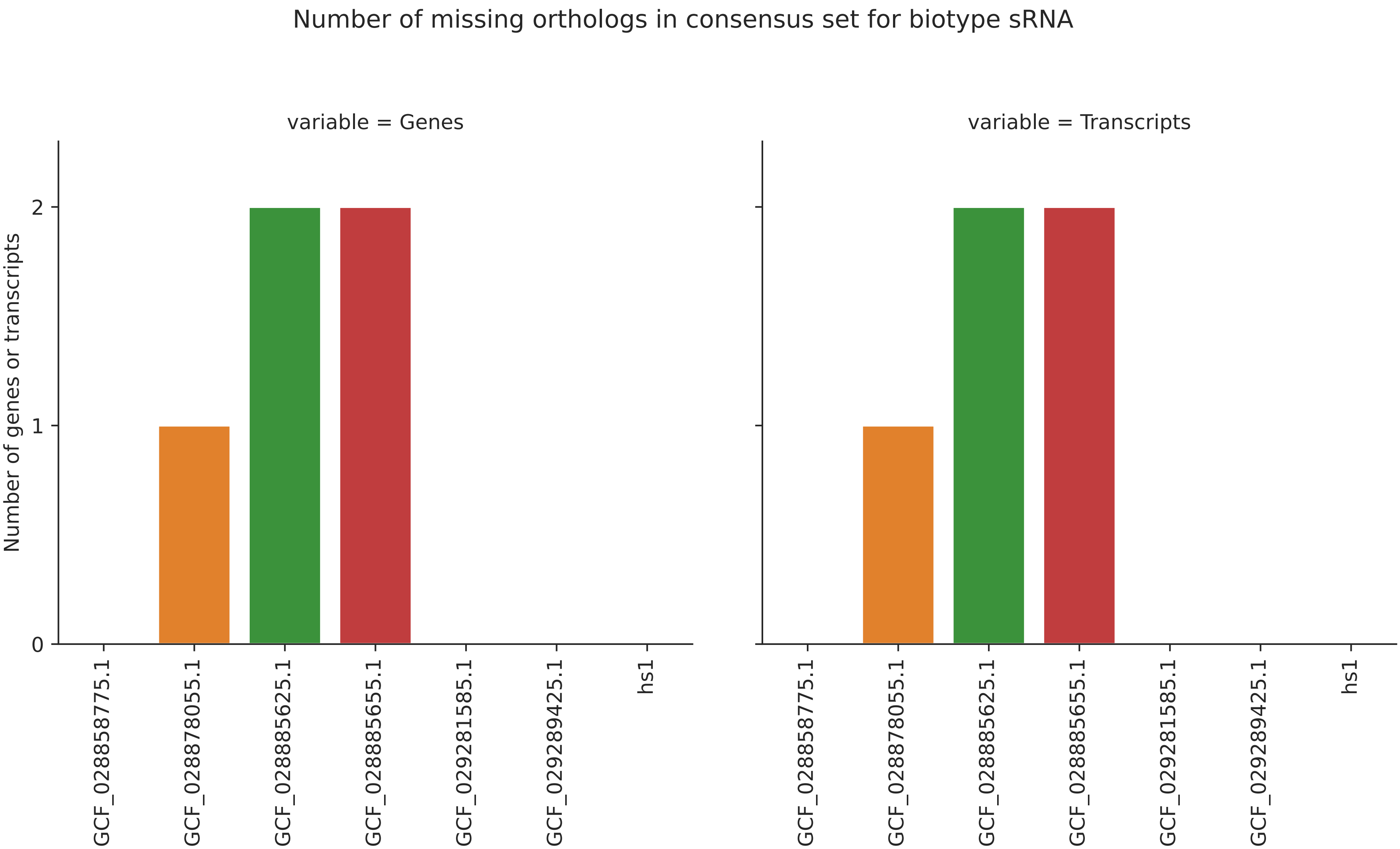

Number of missing orthologs in consensus set for biotype rRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
2
4
6
8
10
12
14
16
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

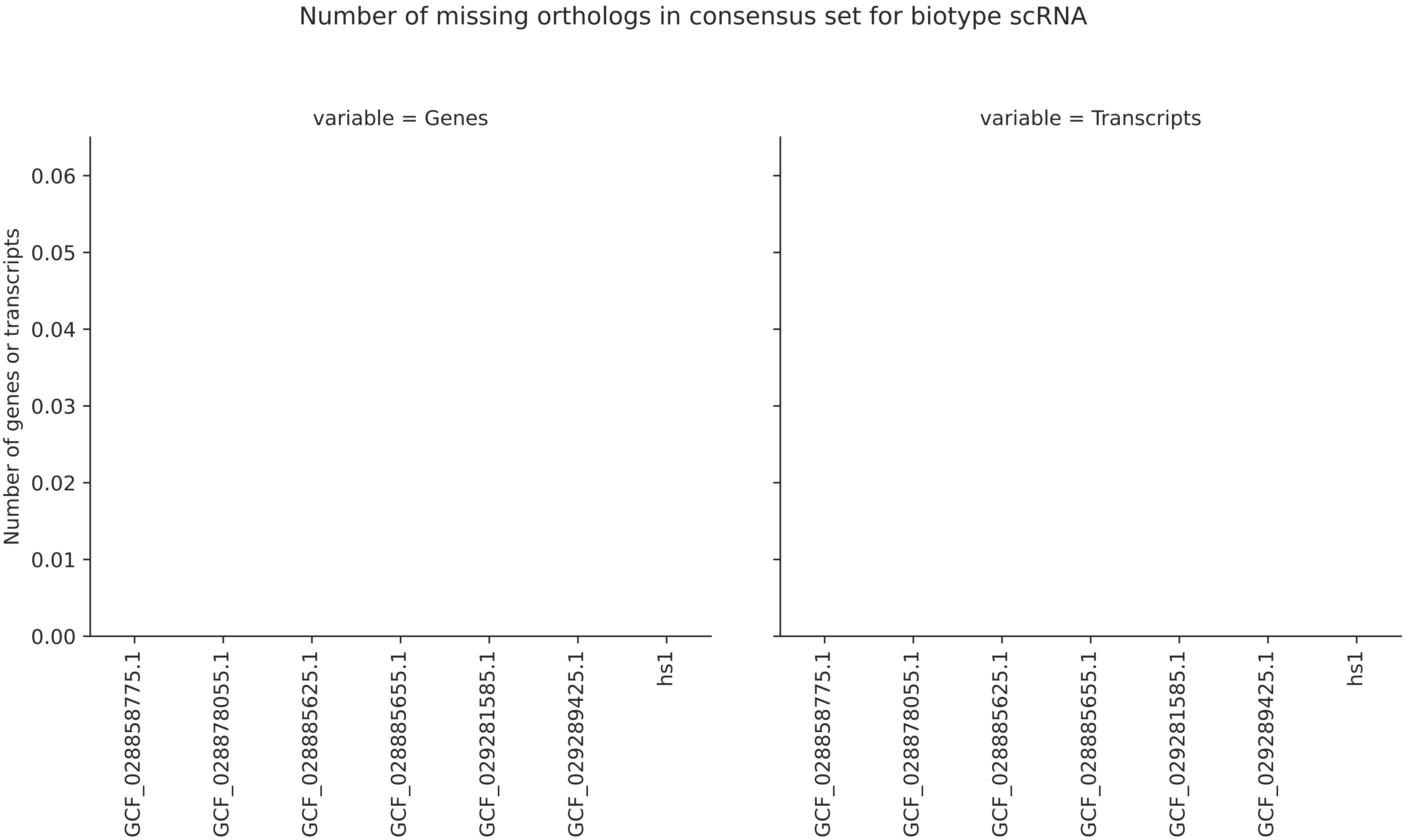
Number of missing orthologs in consensus set for biotype rRNA_pseudogene



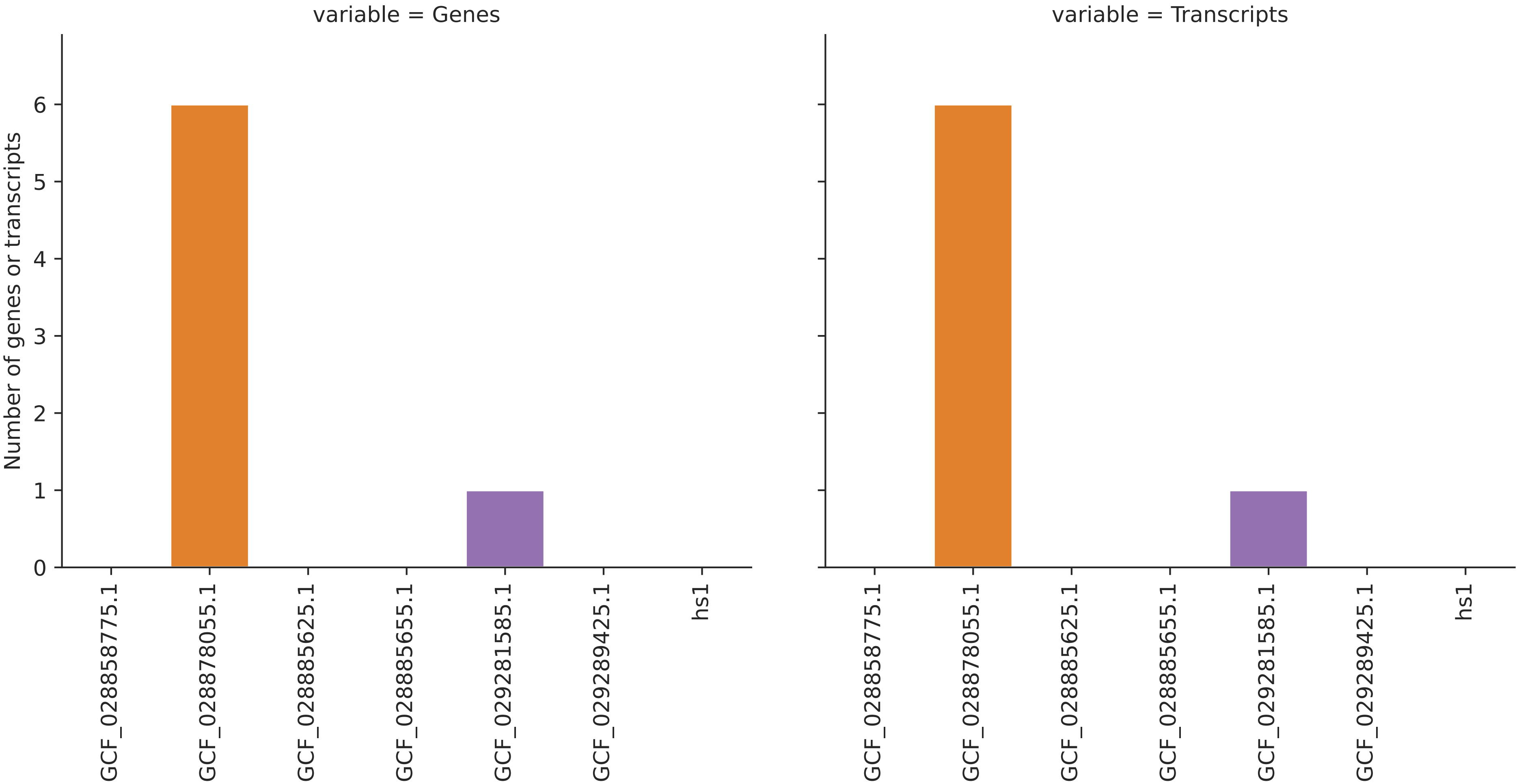
Number of missing orthologs in consensus set for biotype ribozyme

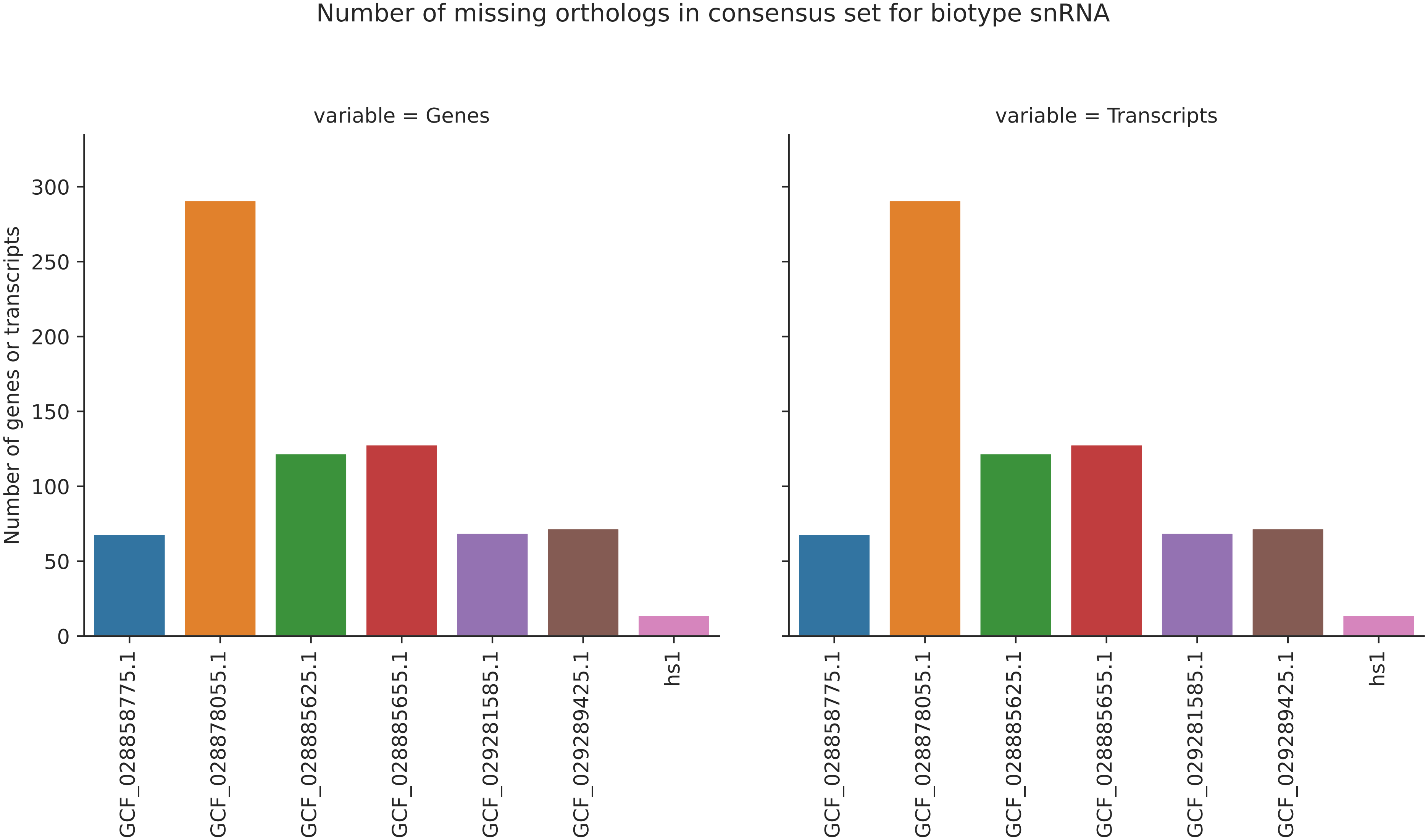


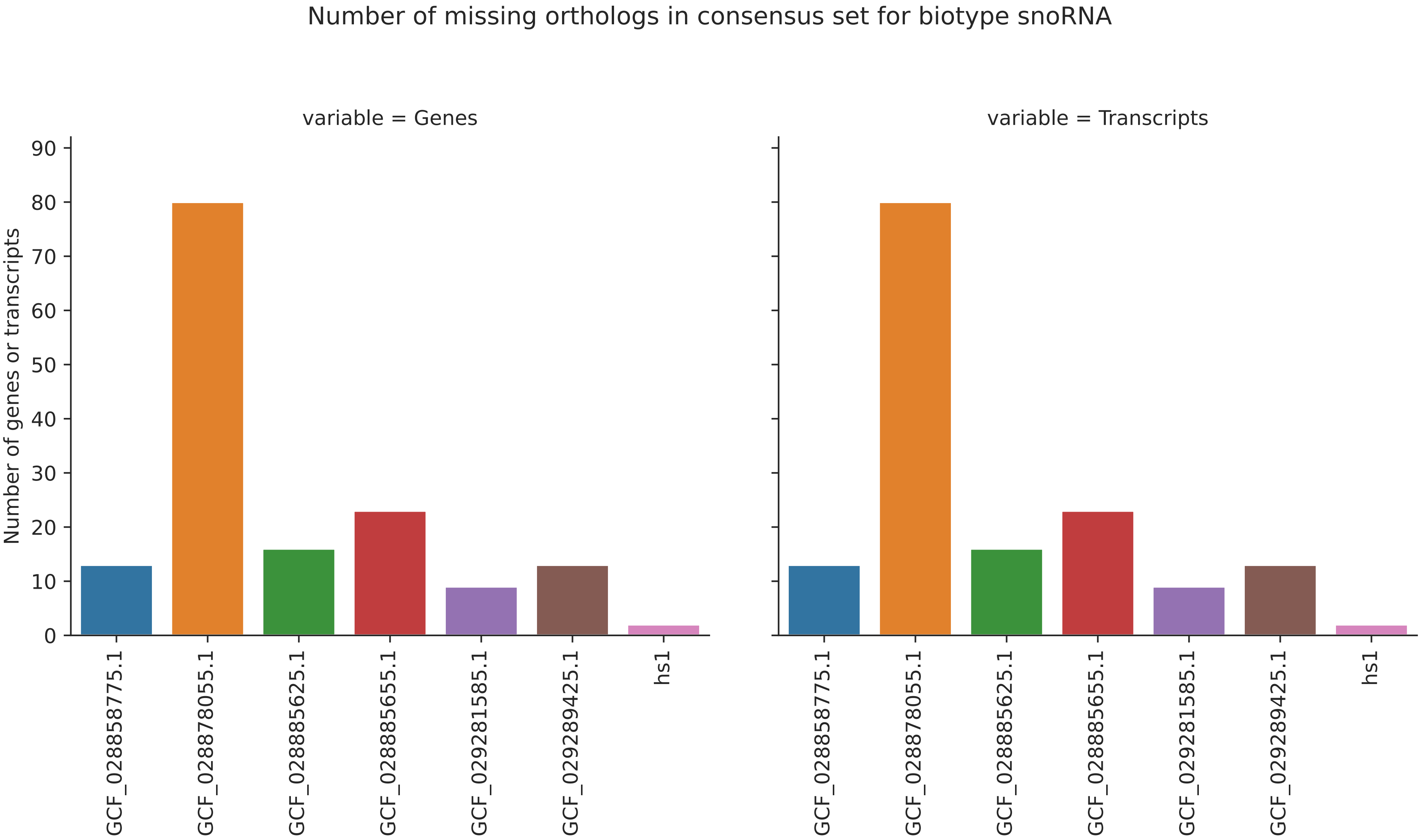

Number of missing orthologs in consensus set for biotype sRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
1
2
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

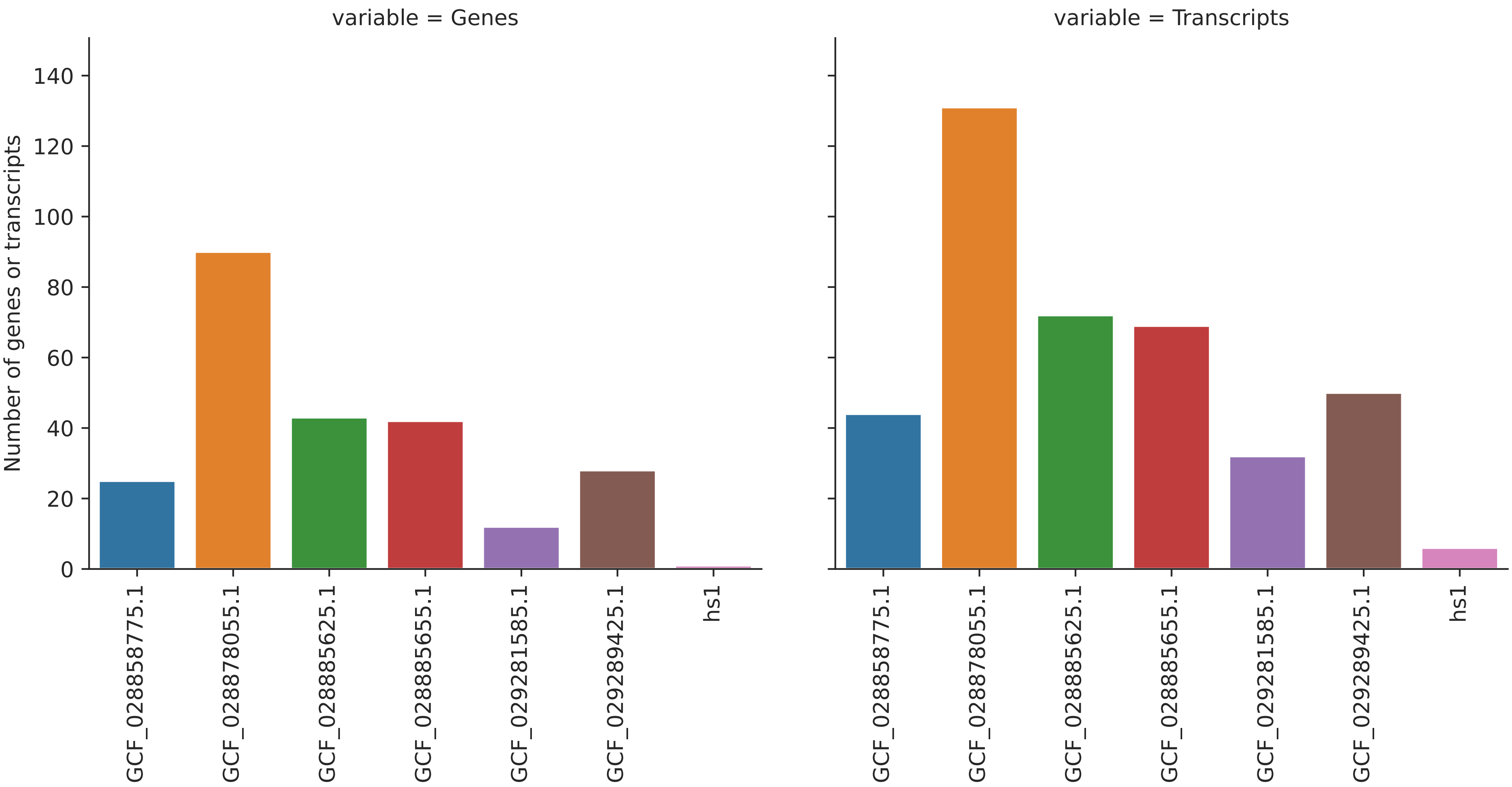

Number of missing orthologs in consensus set for biotype scRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0.00
0.01
0.02
0.03
0.04
0.05
0.06
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

Number of missing orthologs in consensus set for biotype scaRNA

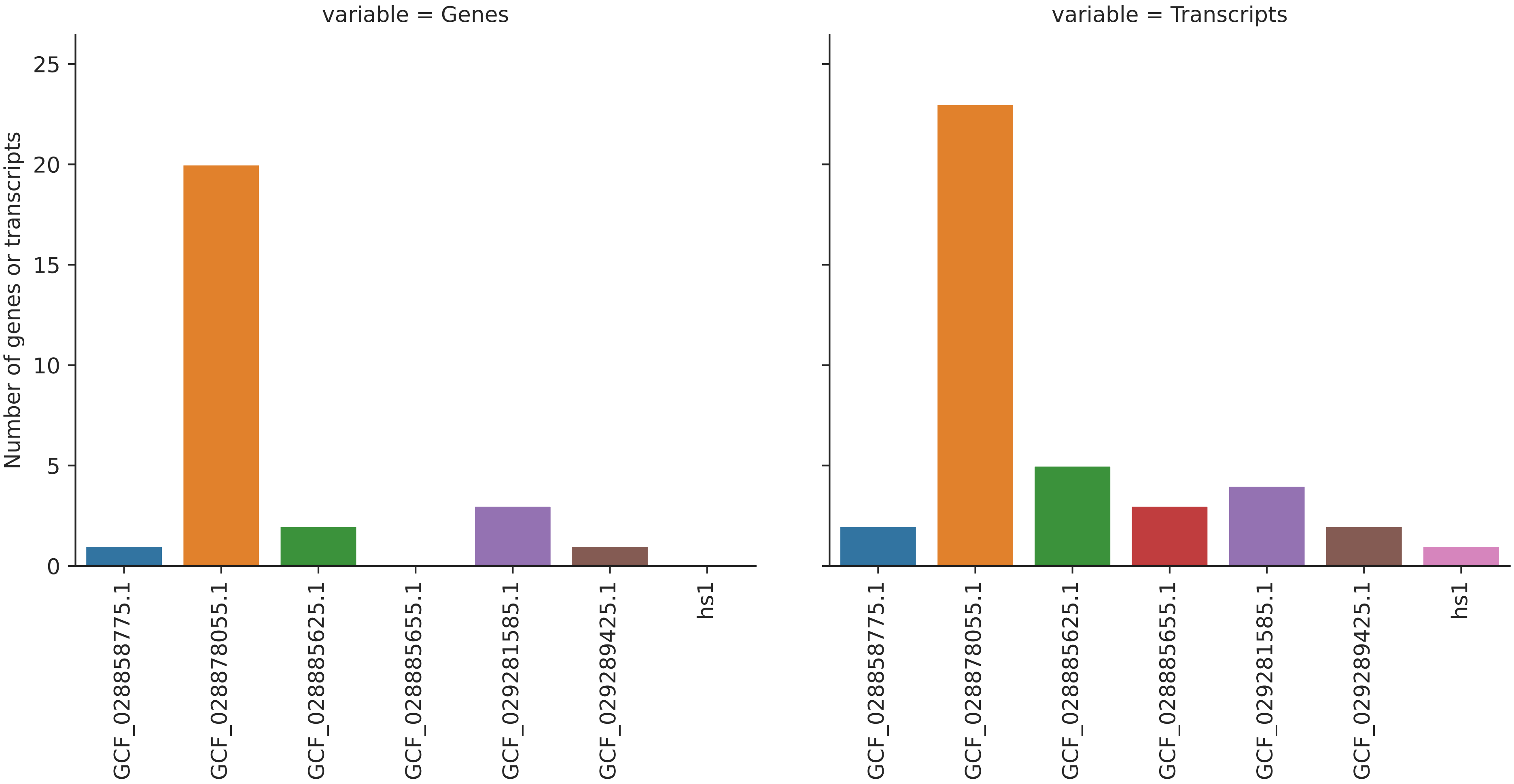



Number of missing orthologs in consensus set for biotype snRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
50
100
150
200
250
300
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1

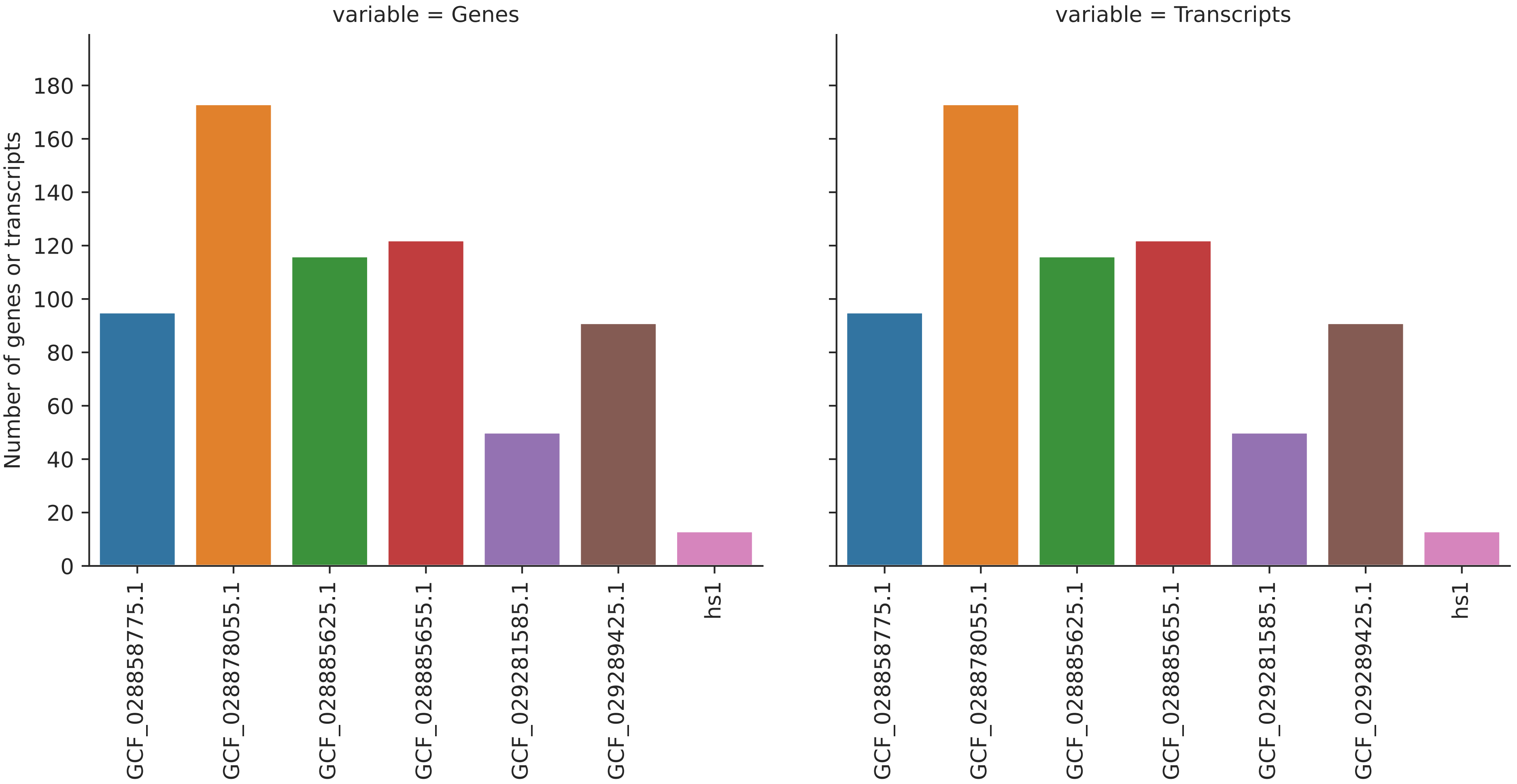

Number of missing orthologs in consensus set for biotype snoRNA
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
10
20
30
40
50
60
70
80
90
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1



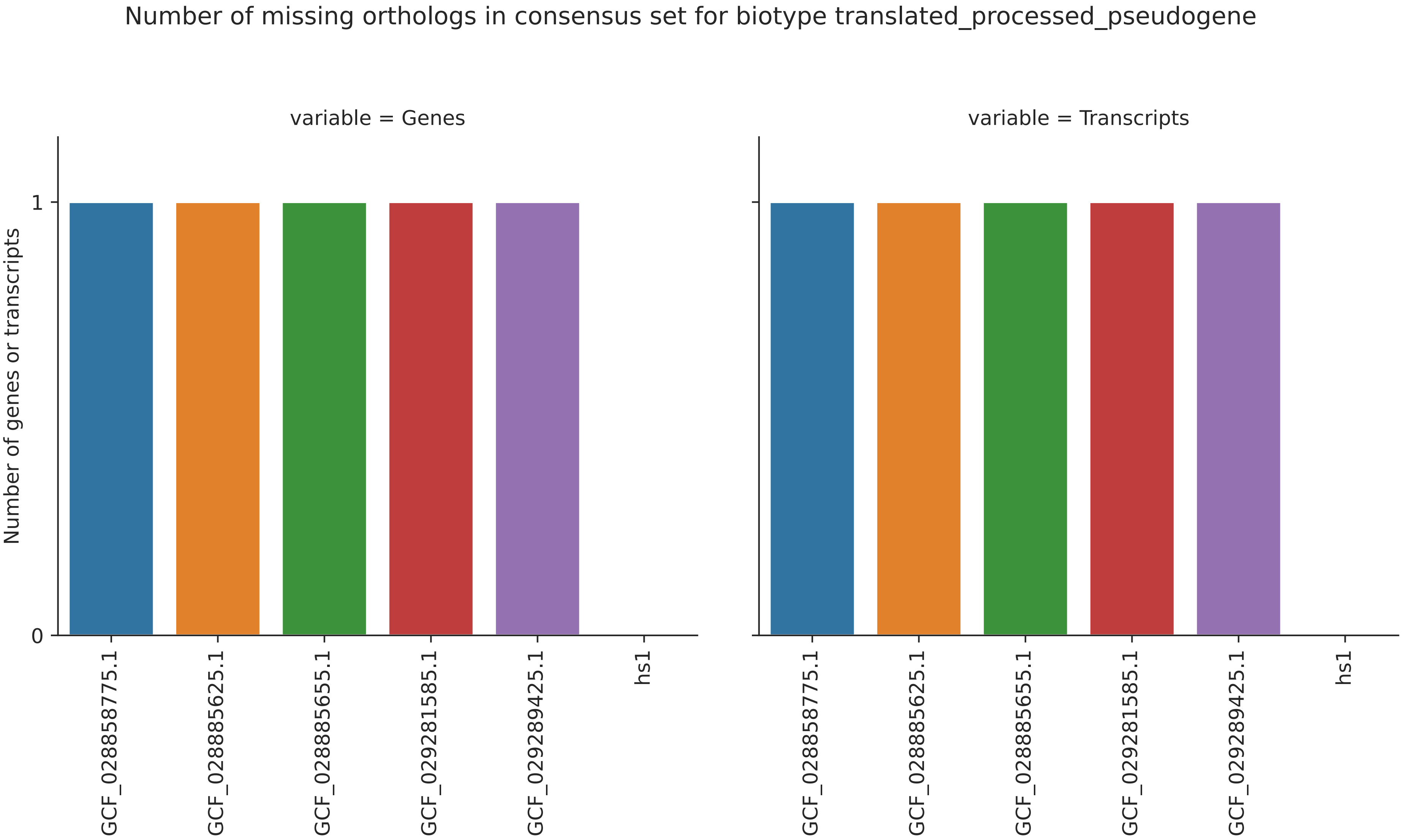
Number of missing orthologs in consensus set for biotype transcribed_processed_pseudogene

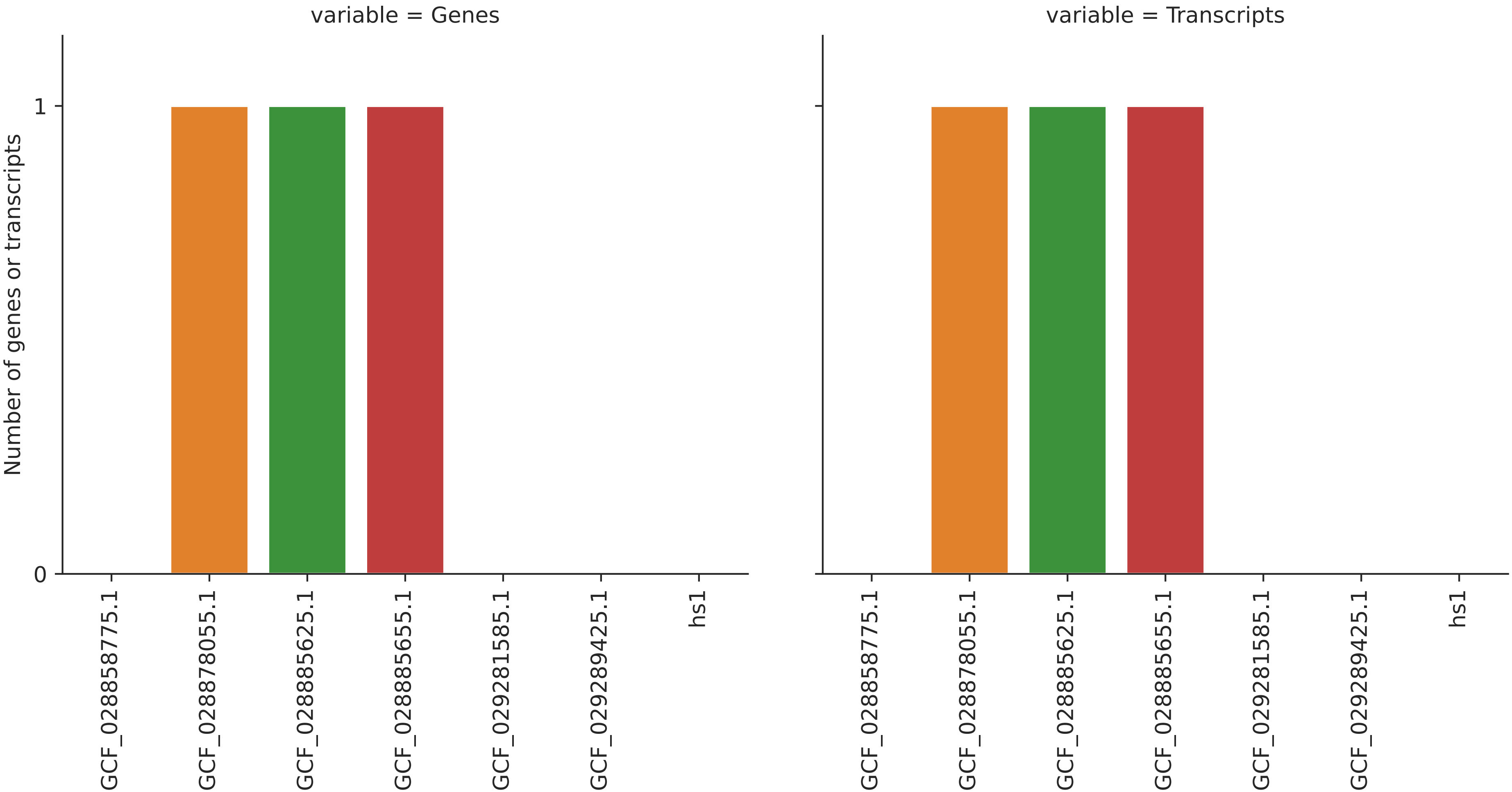


Number of missing orthologs in consensus set for biotype transcribed_unitary_pseudogene

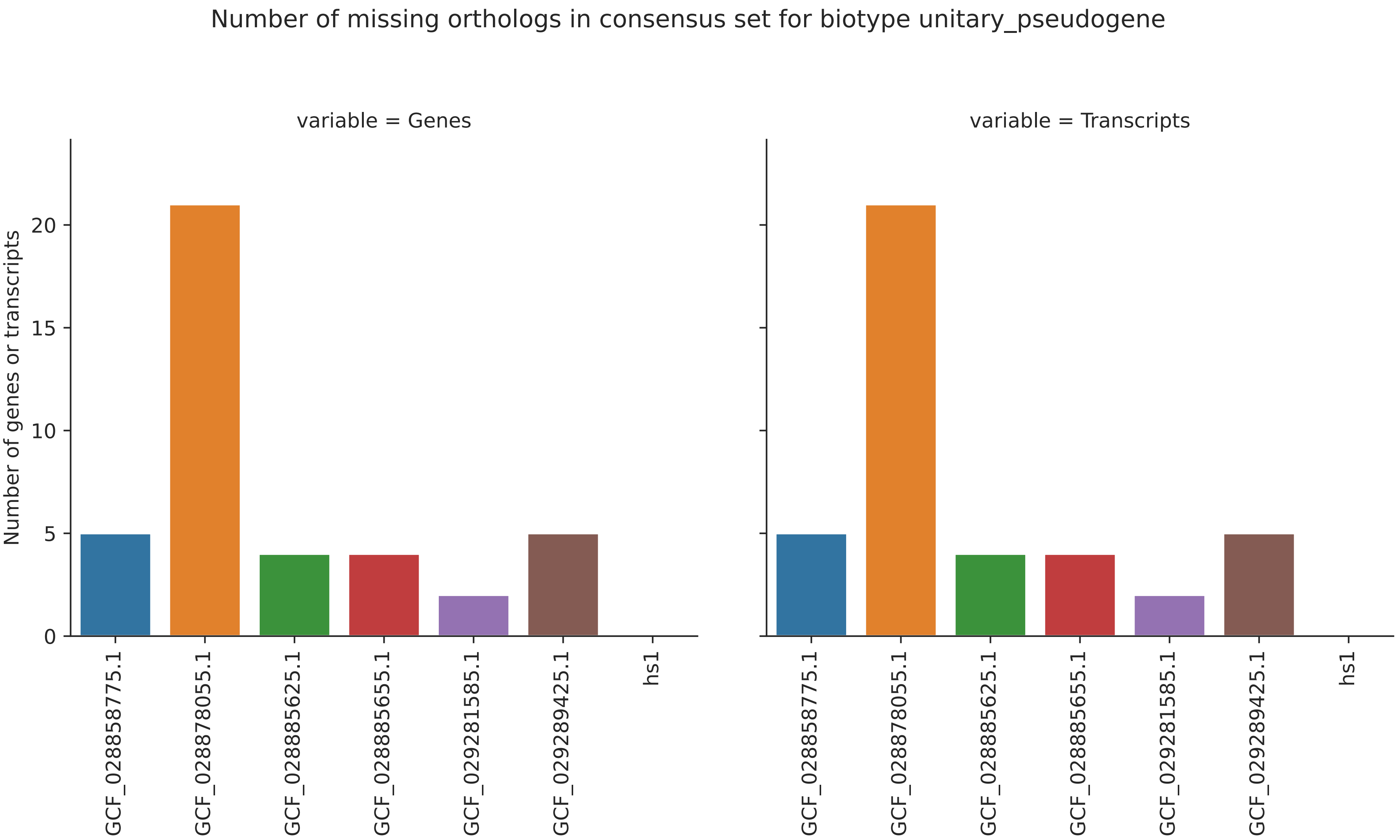


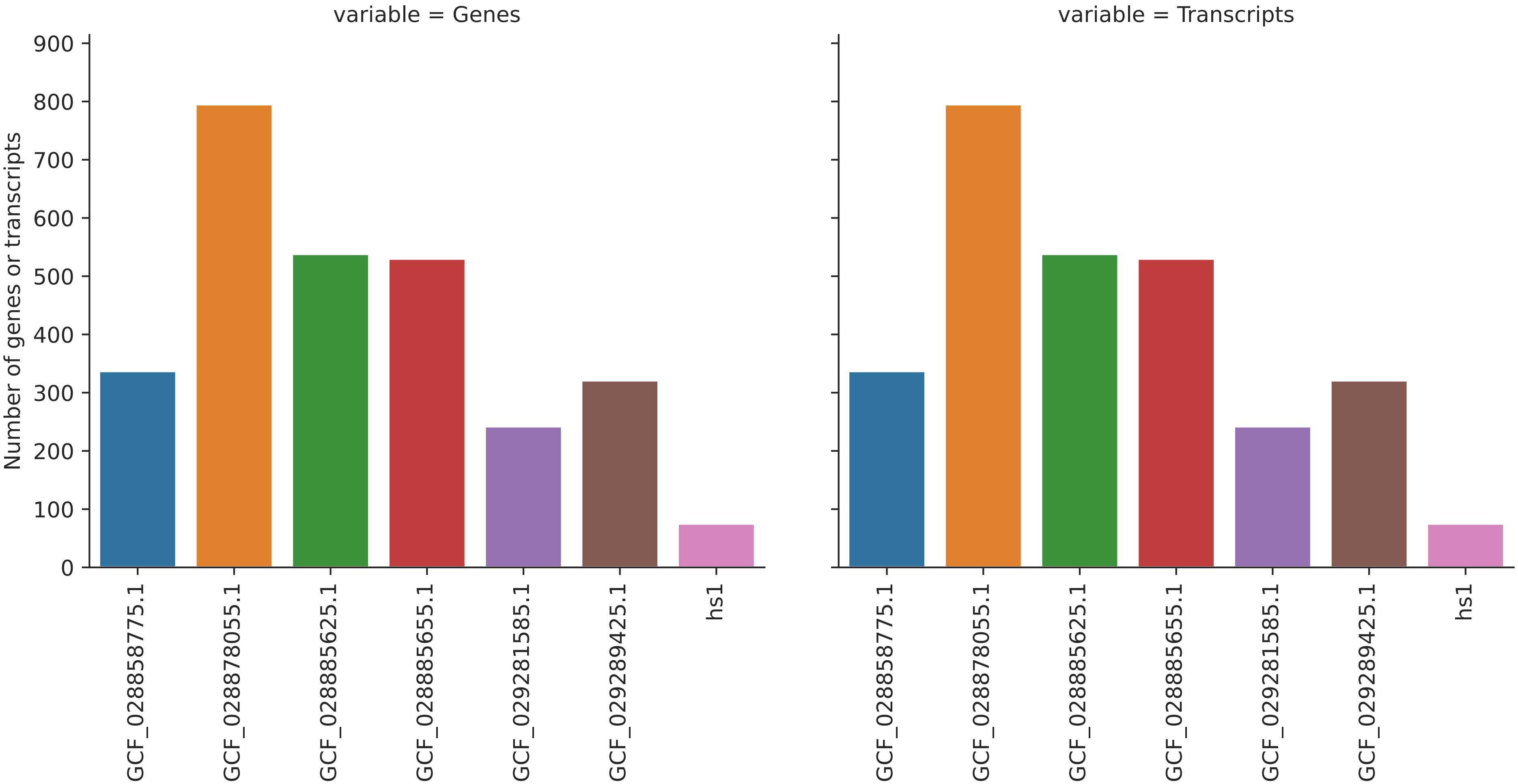
Number of missing orthologs in consensus set for biotype transcribed_unprocessed_pseudogene


Number of missing orthologs in consensus set for biotype translated_processed_pseudogene
variable = Genes
variable = Transcripts
Number of genes or transcripts
1
0
GCF_028858775.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1



Number of missing orthologs in consensus set for biotype translated_unprocessed_pseudogene

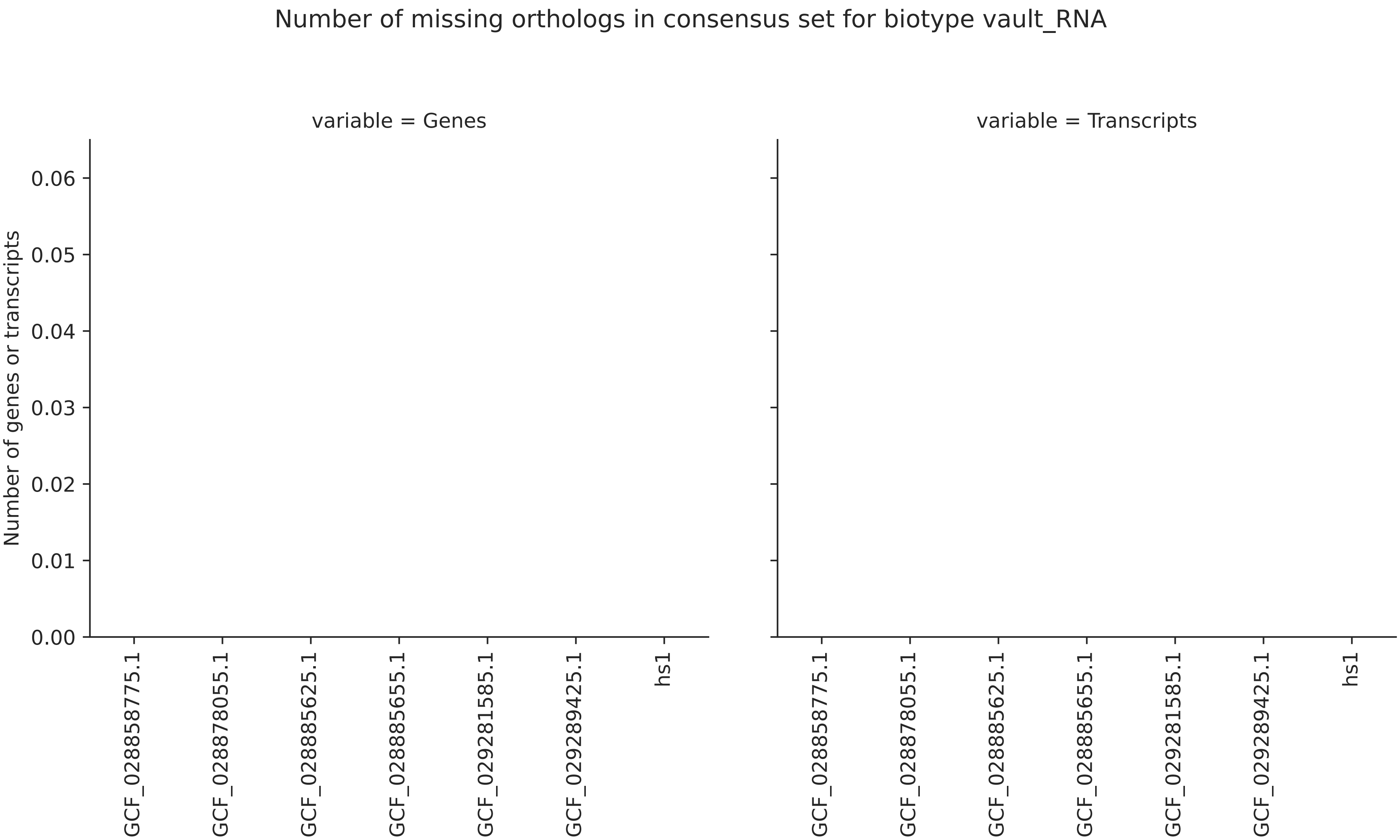

Number of missing orthologs in consensus set for biotype unitary_pseudogene
variable = Genes
variable = Transcripts
Number of genes or transcripts
0
5
10
15
20
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1



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
Number of genes or transcripts
0.06
0.05
0.04
0.03
0.02
0.01
0.00
GCF_028858775.1
GCF_028878055.1
GCF_028885625.1
GCF_028885655.1
GCF_029281585.1
GCF_029289425.1
hs1