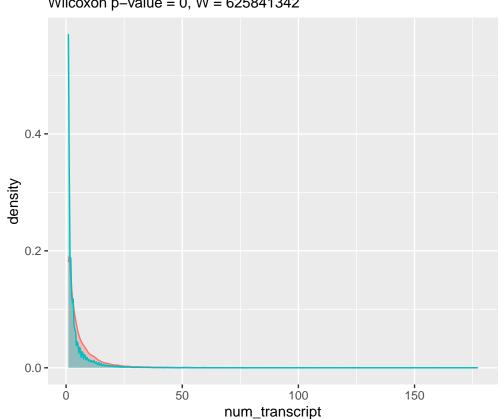
WHOLE-TRANSCRIPTOME VS ORTHOLOG DENSITY PLOTS

Figures below are density plots between whole-genome (red) and orthologs (light blue) for complexity metrics (TpG, EpT, and EpG) with densities on the y-axis and genetic element counts on the x-axis. Plots include every organism used in this study.

GCF_000001405.39_GRCh38.p13 TpG Wilcoxon p-value = 0, W = 625841342

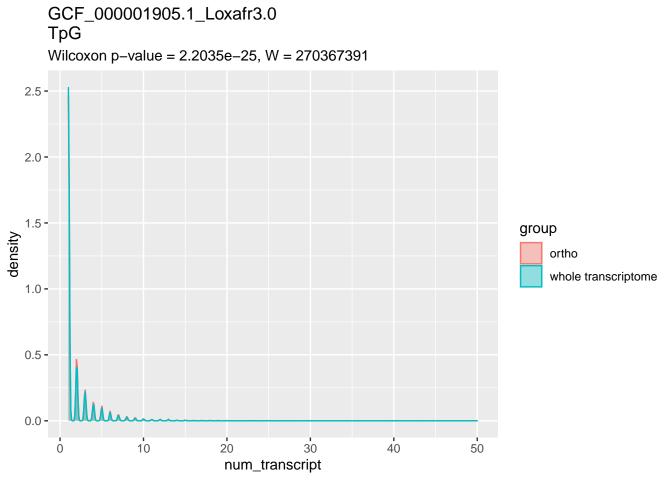


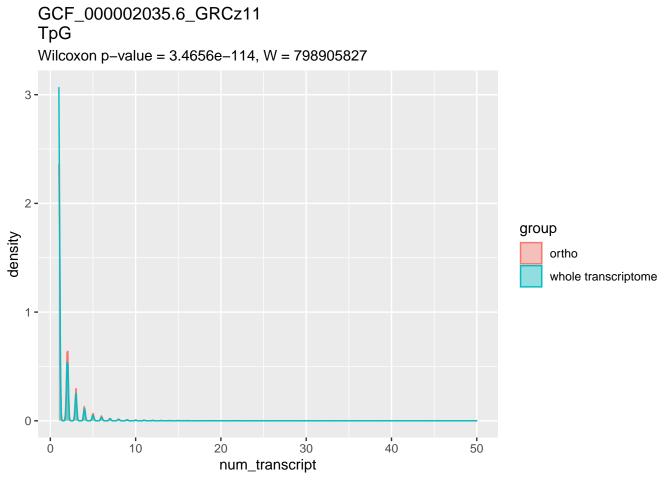
group

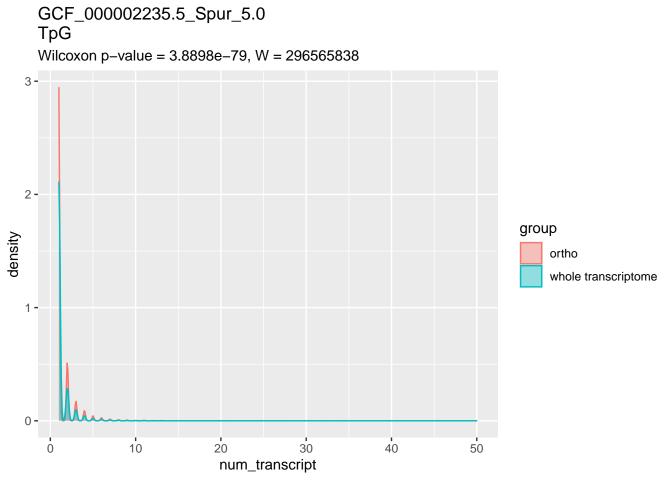
ortho

whole transcriptome

GCF_000001635.27_GRCm39 TpG Wilcoxon p-value = 0, W = 5160923201.00 -0.75 group density 0.50 ortho whole transcriptome 0.25 -0.00 -25 50 75 num_transcript

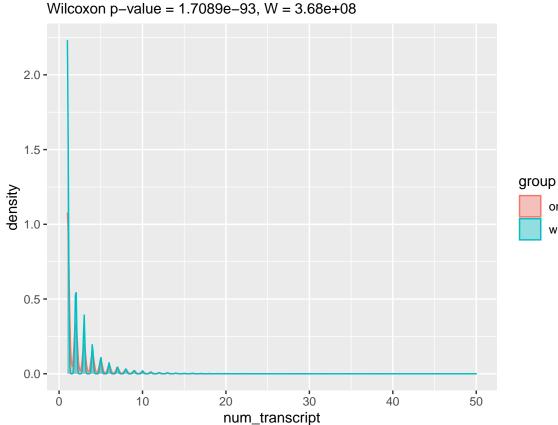






GCF_000002285.3_CanFam3.1 TpG Wilcoxon p-value = 7.4077e-107, W = 3.35e+081.2 -0.8 group density ortho whole transcriptome 0.4 -0.0 -10 20 30 40 50 num_transcript

GCF_000002295.2_MonDom5 TpG Wilcoxon p-value = 1.7089e-93, W = 3.68e+08

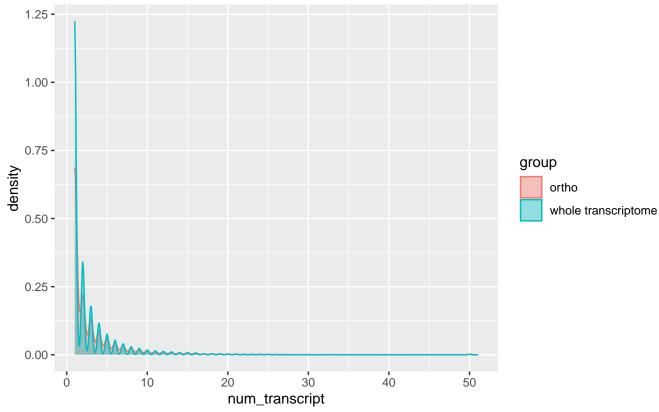


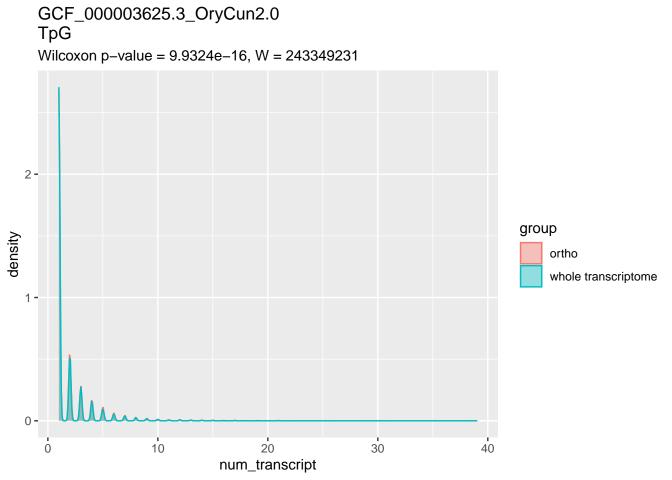
ortho

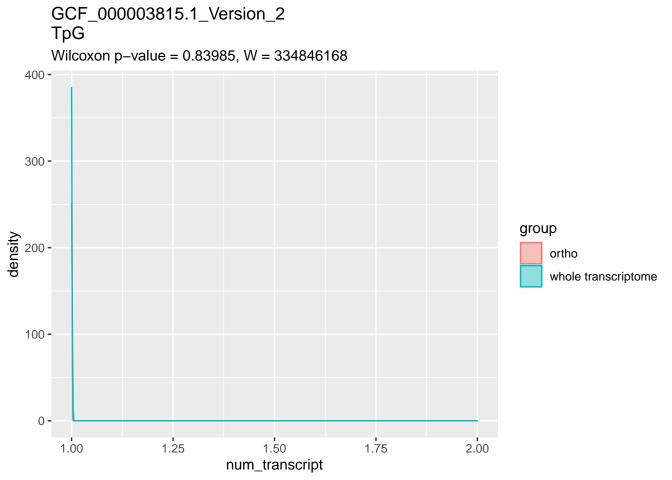
whole transcriptome

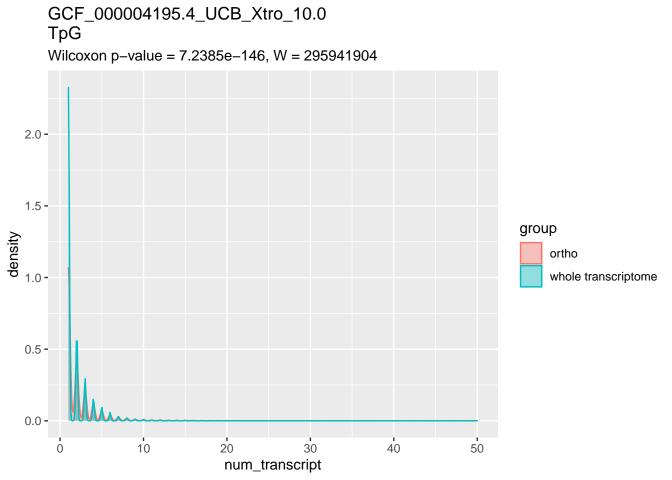
GCF_000003025.6_Sscrofa11.1 TpG

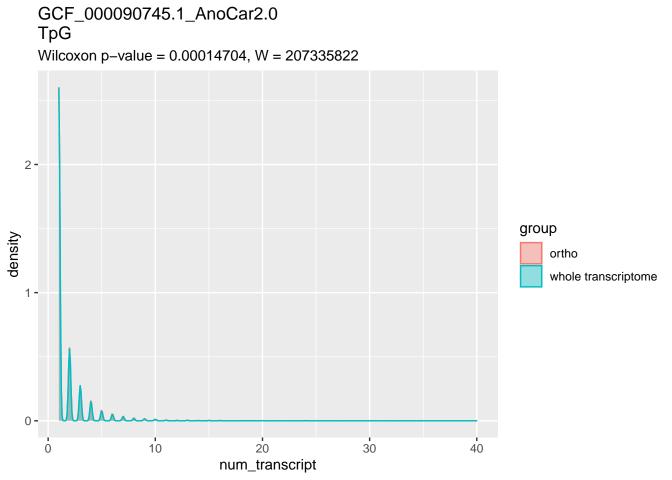
Wilcoxon p-value = 4.3091e-52, W = 290162832

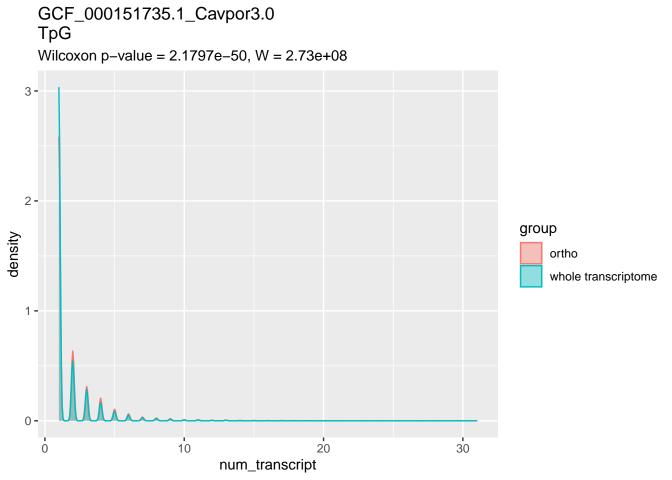








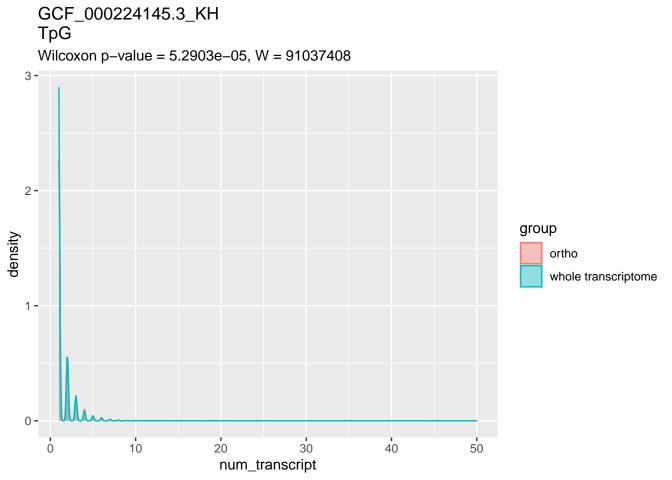


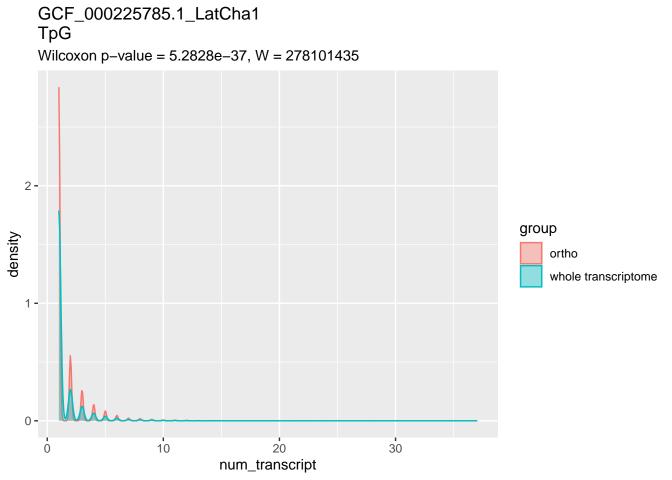


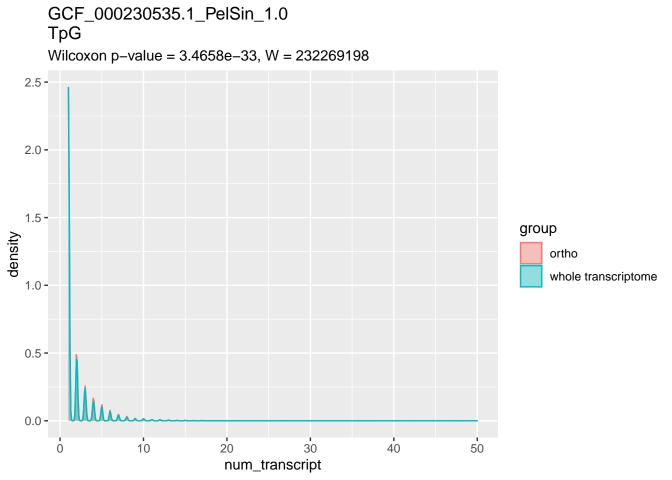
GCF_000165445.2_Mmur_3.0 TpG Wilcoxon p-value = 4.6076e-88, W = 3143525061.0 group density ortho whole transcriptome 0.5 -0.0 -10 20 30 40 50 num_transcript

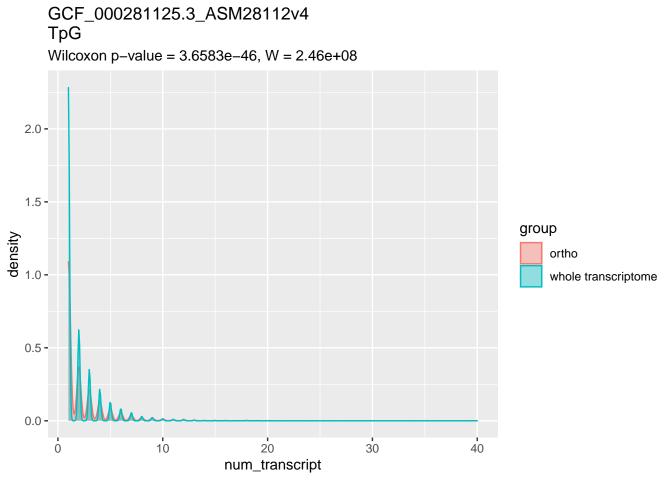
GCF_000181335.3_Felis_catus_9.0 TpG Wilcoxon p-value = 2.1429e-221, W = 3486793921.0 group density ortho whole transcriptome 0.5 -0.0 -10 20 30 40 50 num_transcript

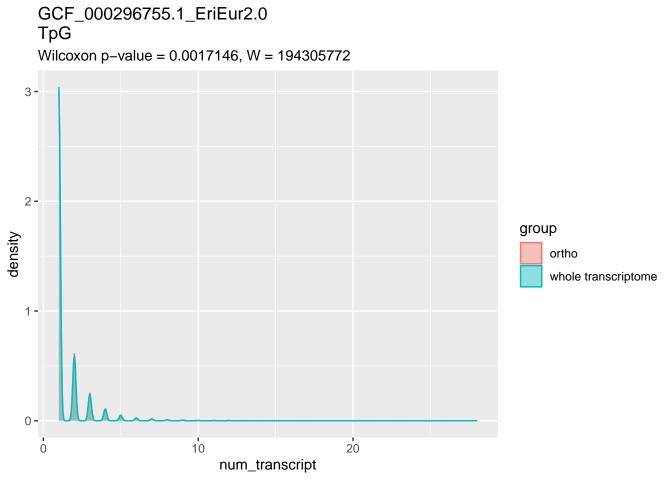
GCF_000186305.1_Python_molurus_bivittatus-5.0.2 TpG Wilcoxon p-value = 1.031e-16, W = 205306998 group density ortho whole transcriptome 10 20 30 num_transcript

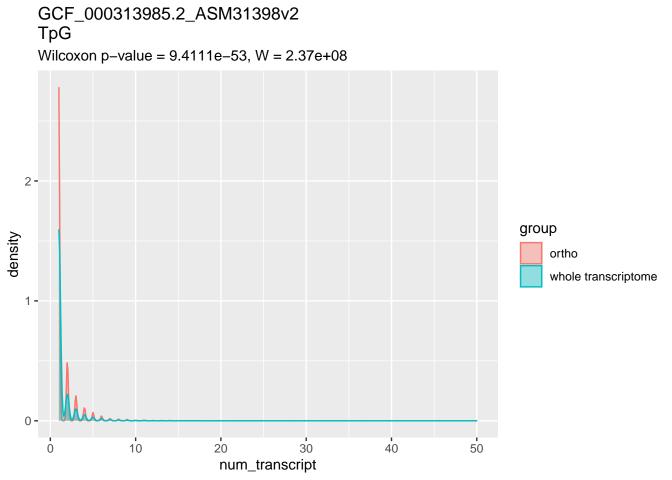




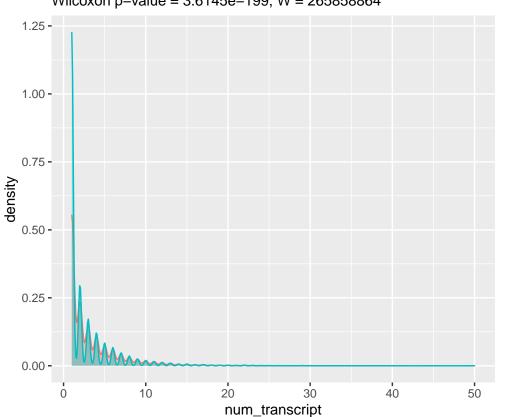








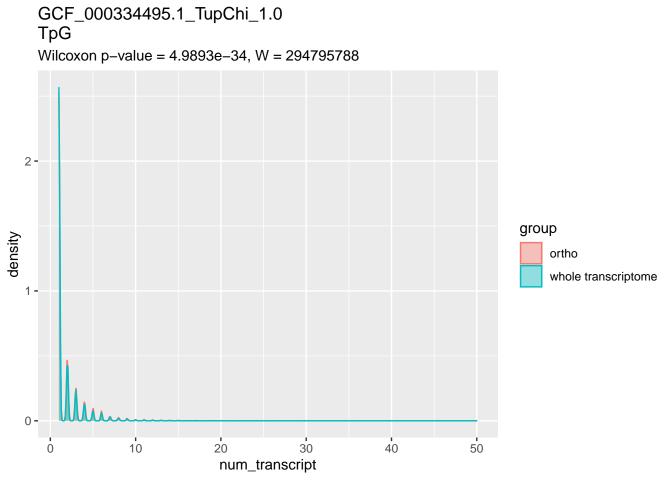
GCF_000331955.2_Oorc_1.1 TpG Wilcoxon p-value = 3.6145e-199, W = 265858864

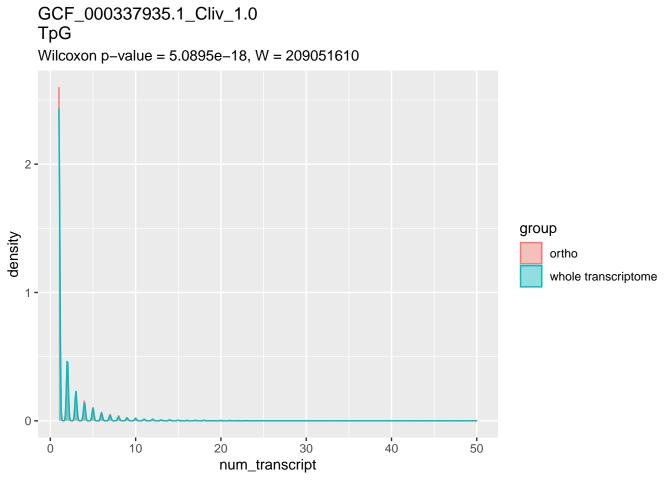


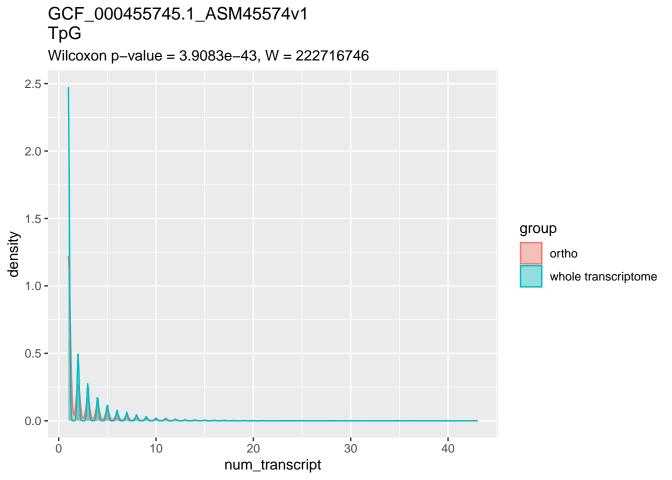
group

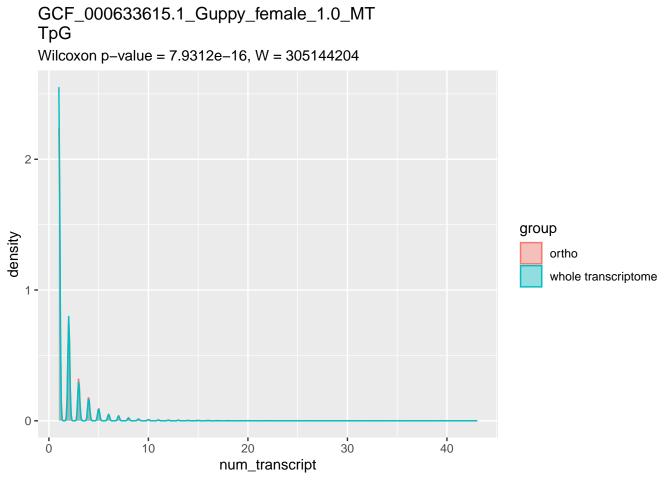
ortho

whole transcriptome









GCF_000696425.1_G_variegatus-3.0.2 TpG Wilcoxon p-value = 2.7091e-12, W = 2964314572.5 -2.0 -1.5 group density ortho whole transcriptome 1.0 -0.5 -

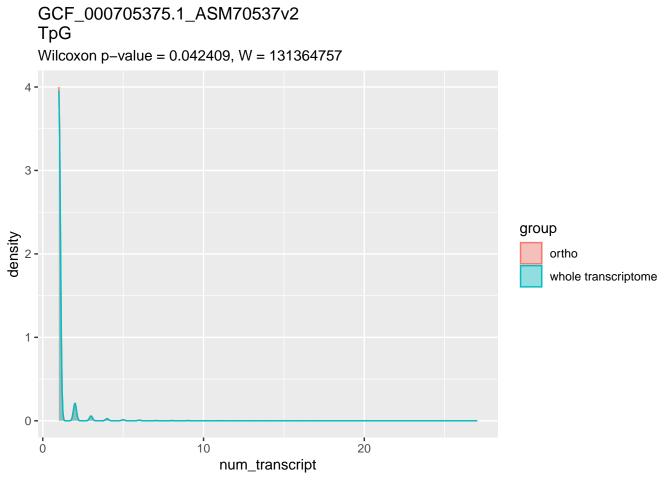
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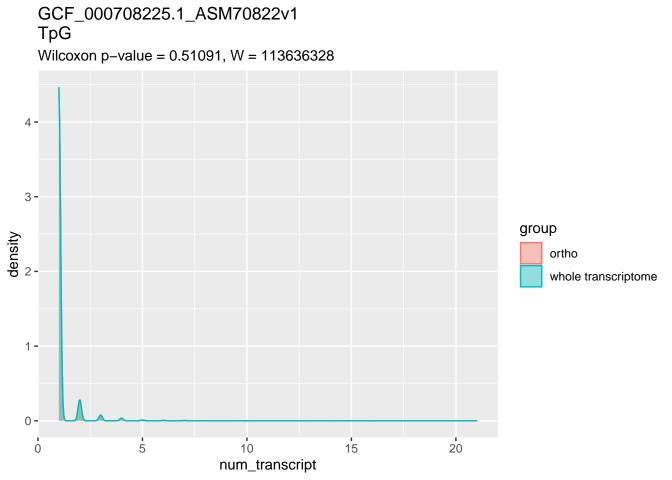
num_transcript

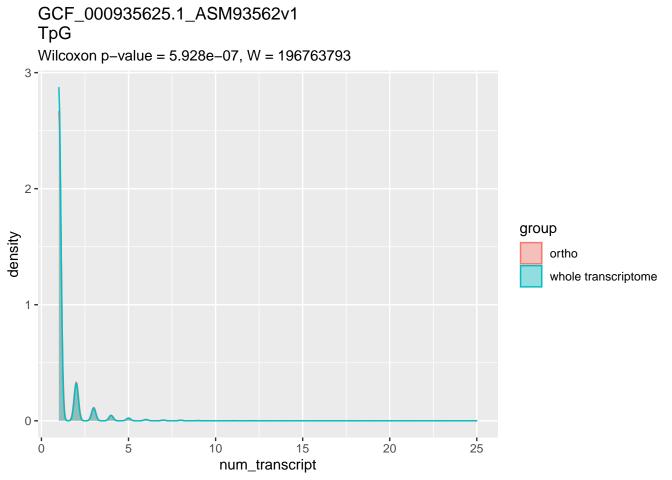
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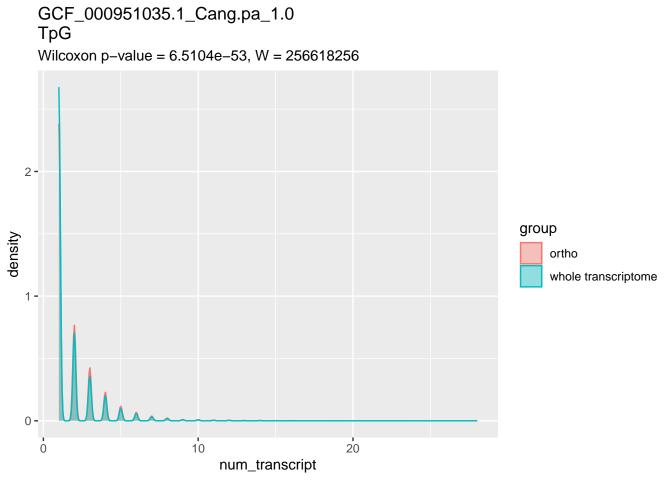
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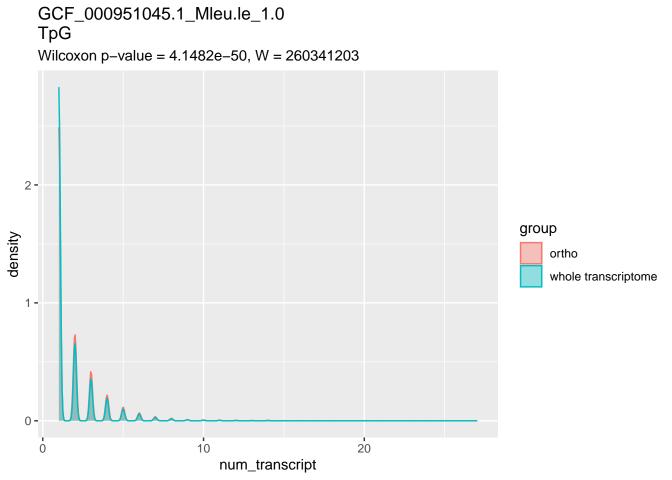
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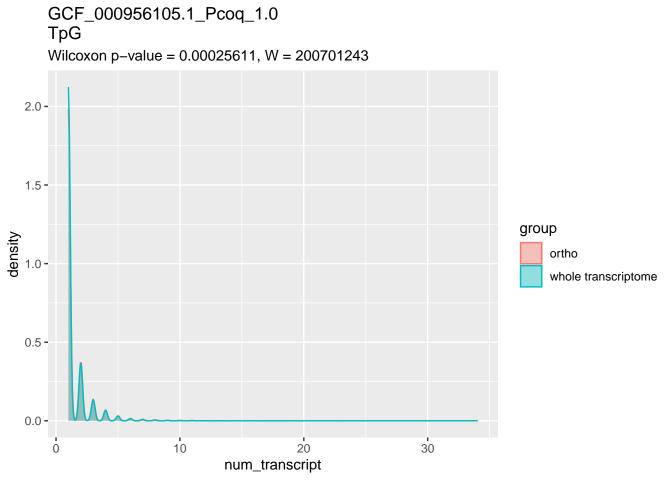


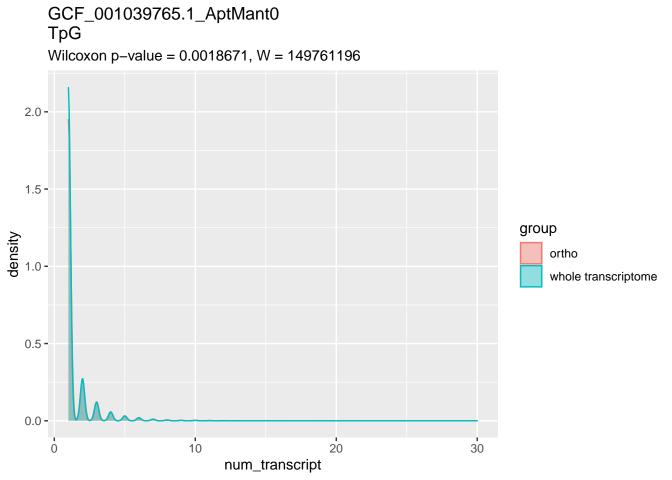


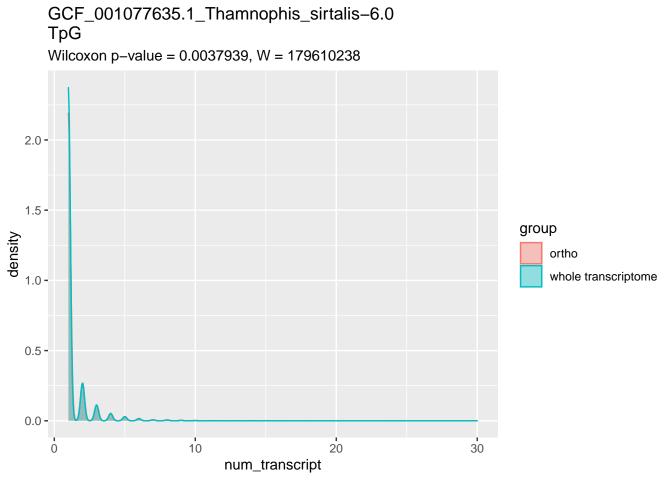


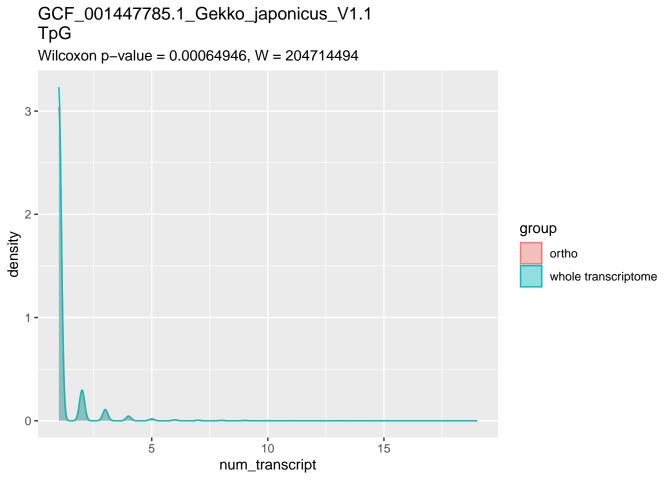


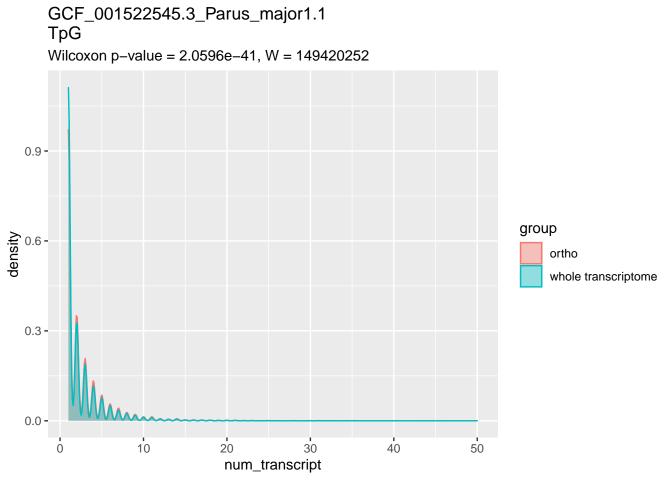


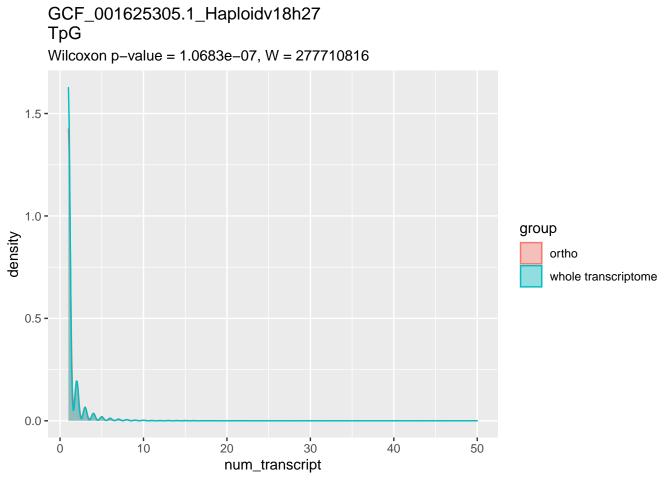


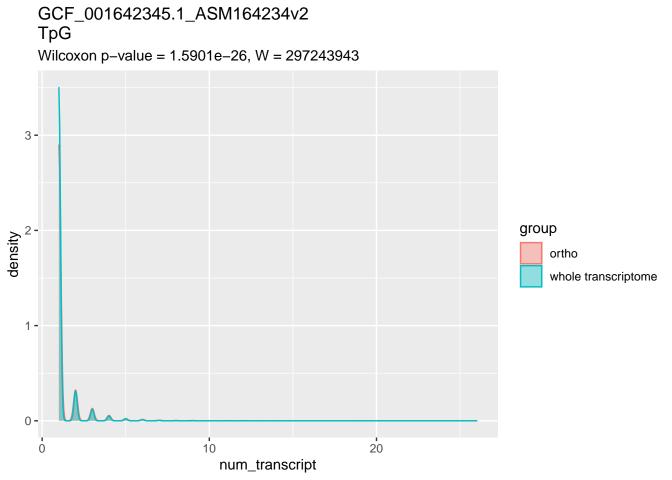


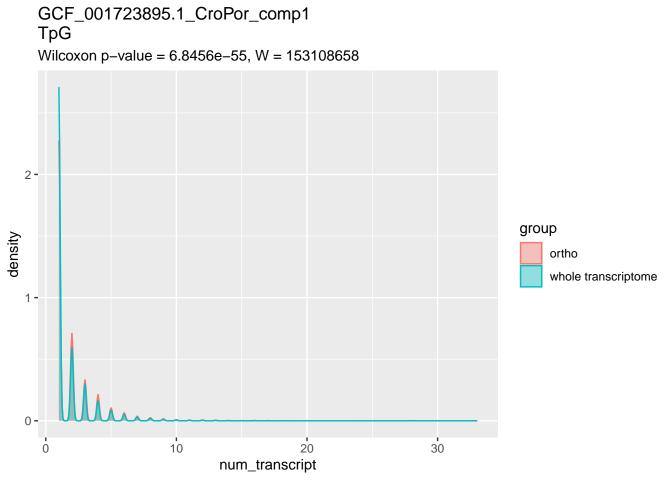


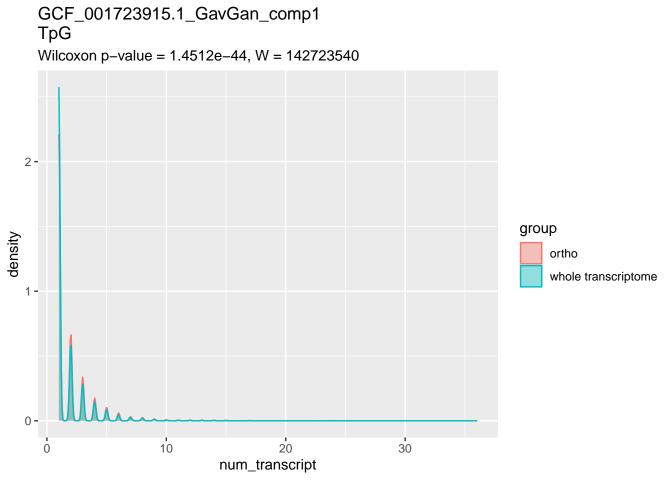


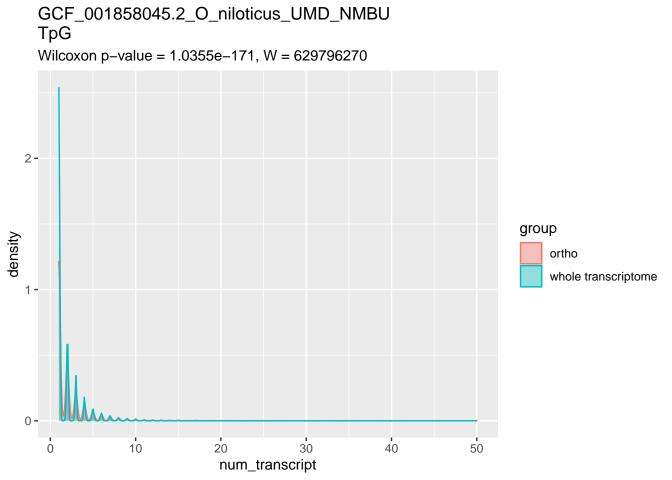


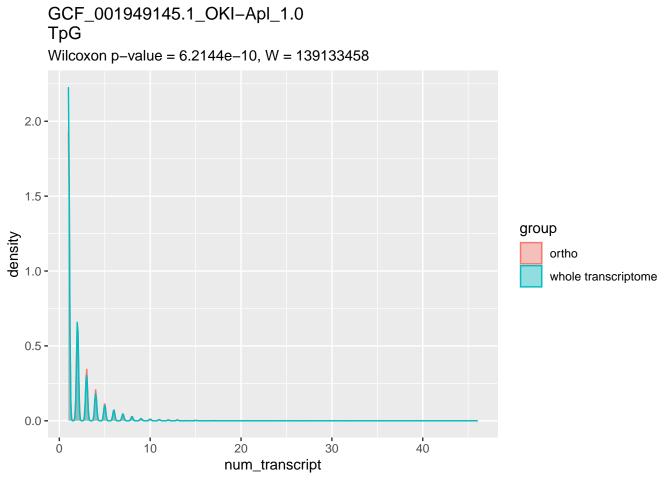


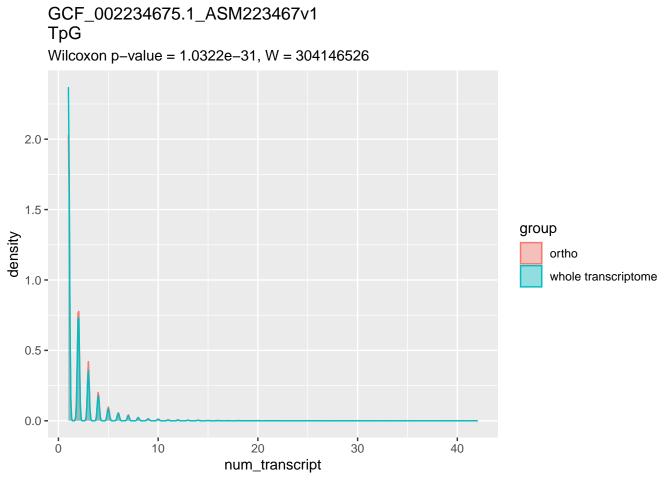






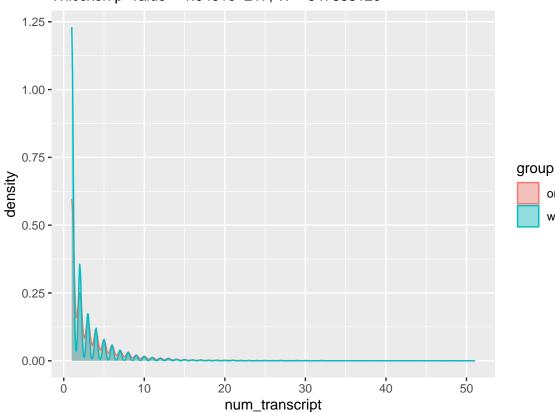






GCF_002263795.1_ARS-UCD1.2 TpG

Wilcoxon p-value = 1.0401e-217, W = 347888120

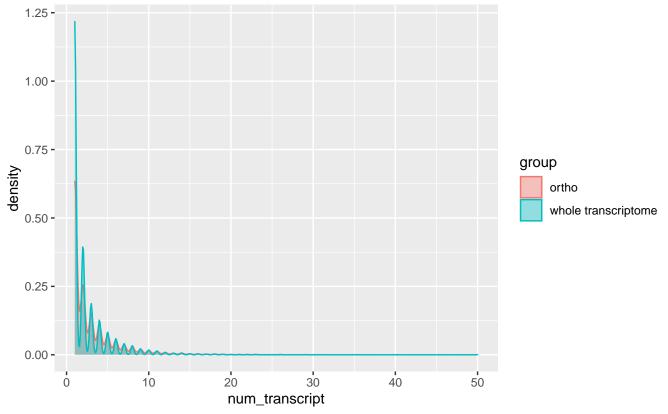


ortho

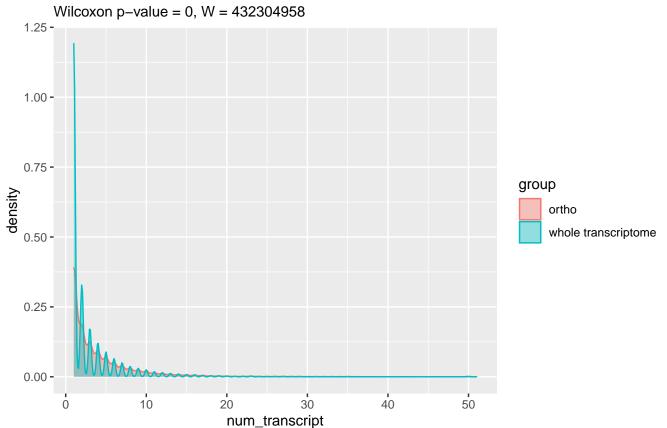
GCF_002288925.2_ASM228892v3 TpG Wilcoxon p-value = 1.3176e-85, W = 235054468 1.2 -0.9 group density - 9.0 ortho whole transcriptome 0.3 -0.0 -10 20 30 40 50 num_transcript

GCF_002863925.1_EquCab3.0 TpG

Wilcoxon p-value = 1.2409e-111, W = 343795446

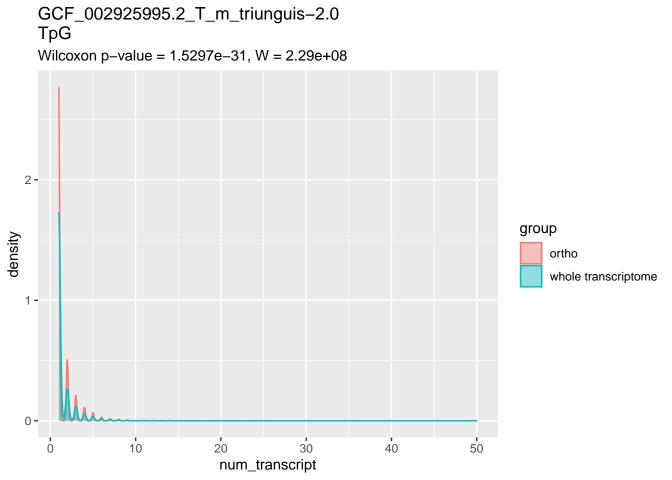


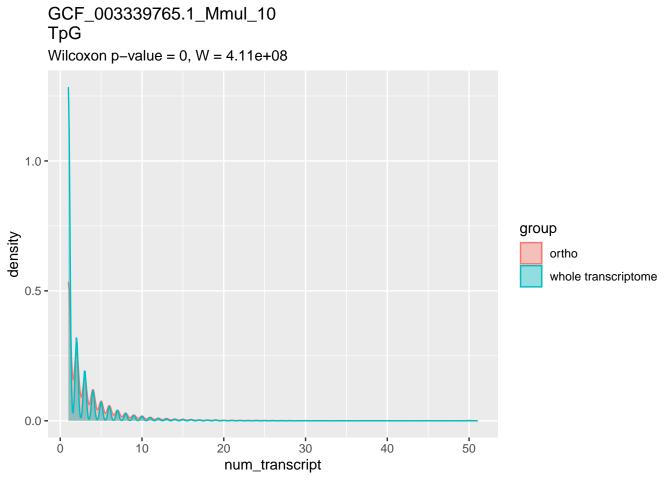
GCF_002880755.1_Clint_PTRv2 TpG



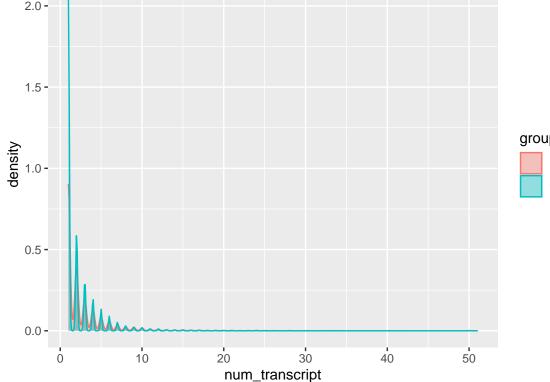
GCF_002880775.1_Susie_PABv2 TpG Wilcoxon p-value = 3.0402e-167, W = 318142192 2.0 -1.5 group density 1.0 ortho whole transcriptome 0.5 -10 20 30 40 50

num_transcript

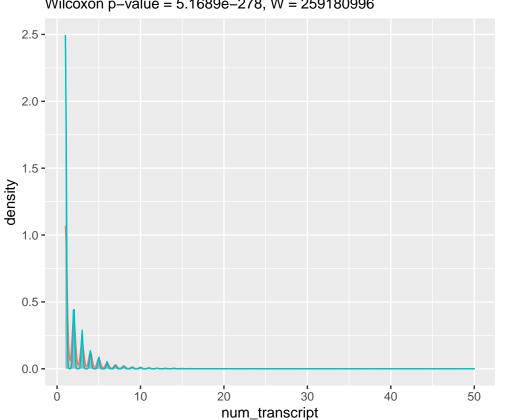




GCF_003957565.2_bTaeGut1.4.pri TpG Wilcoxon p-value = 5.9308e-119, W = 159196922 2.0 -1.5 group ortho whole transcriptome

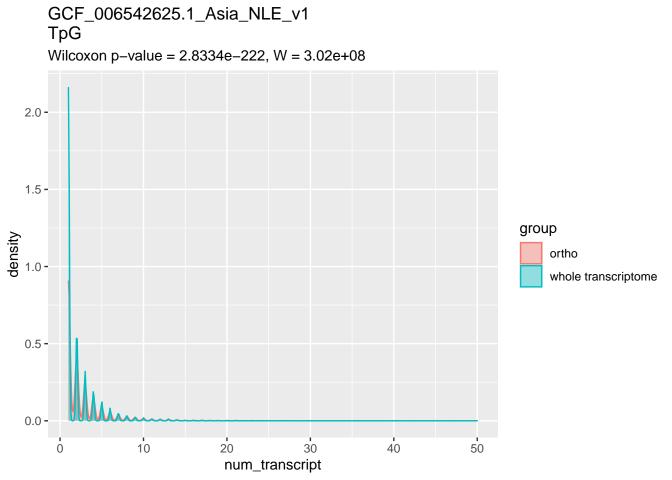


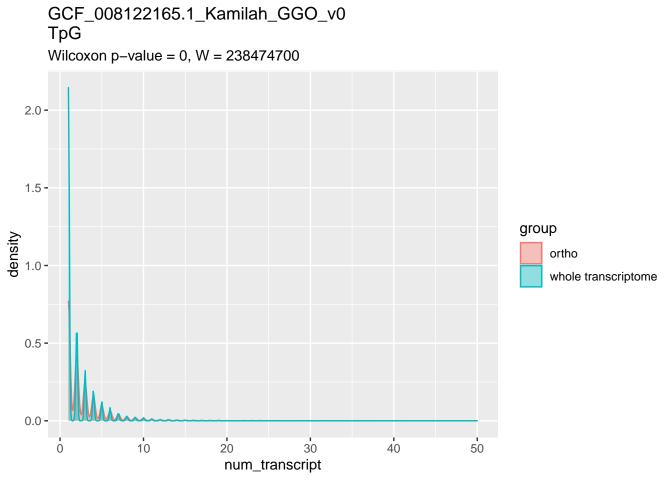
GCF_004115215.2_mOrnAna1.pri.v4 TpG Wilcoxon p-value = 5.1689e-278, W = 259180996



group

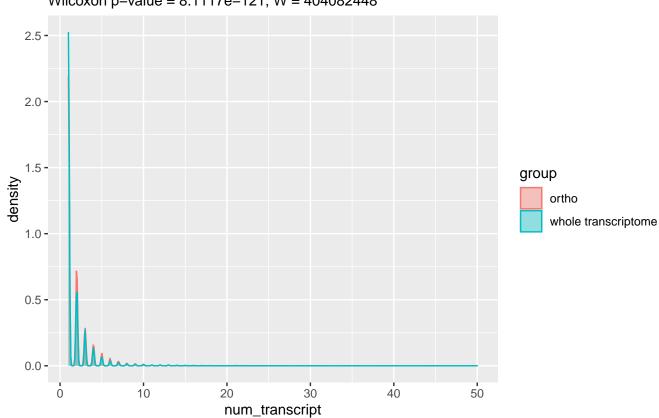
ortho





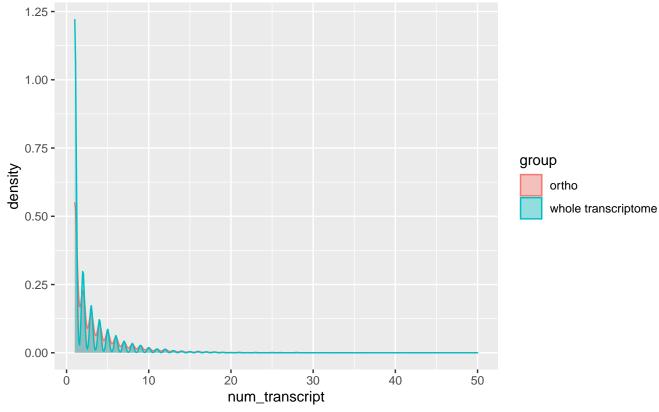
GCF_009663435.1_Callithrix_jacchus_cj1700_1.1 TpG Wilcoxon p-value = 0, W = 4.12e+081.0 group density ortho whole transcriptome 0.5 -0.0 -10 20 30 40 50 num_transcript

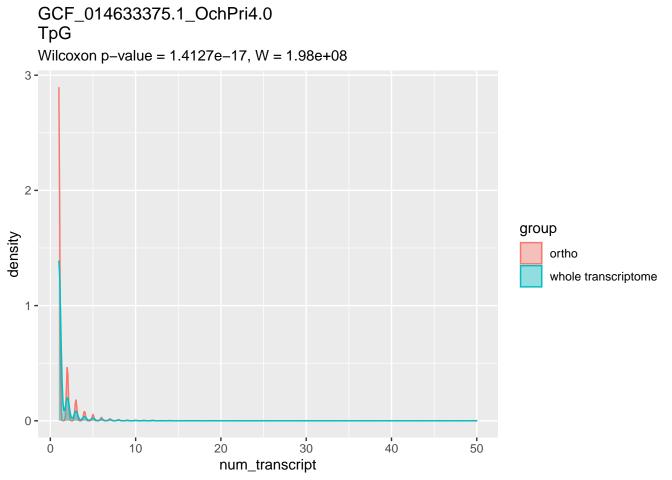
GCF_011125445.2_MU-UCD_Fhet_4.1 TpG Wilcoxon p-value = 8.1117e-121, W = 404082448



GCF_011762595.1_mTurTru1.mat.Y TpG

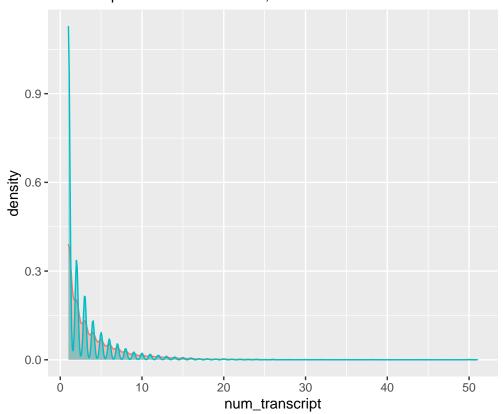
Wilcoxon p-value = 7.5471e-184, W = 233501265





GCF_015227675.2_mRatBN7.2 TpG

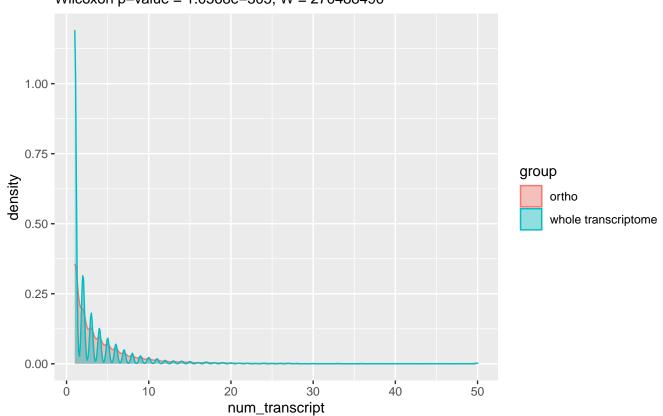
Wilcoxon p-value = 8.3603e-264, W = 403754368



group

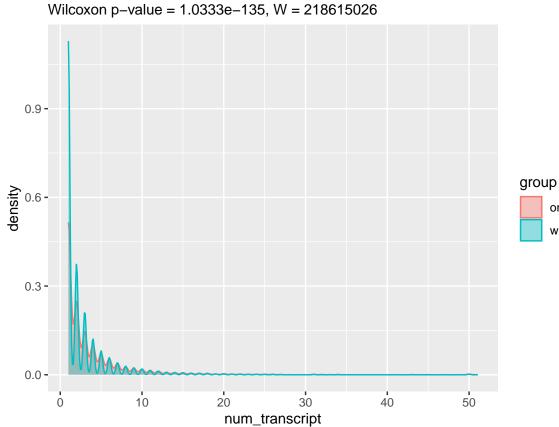
ortho

GCF_015237465.2_rCheMyd1.pri.v2 TpG Wilcoxon p-value = 1.0568e-305, W = 270488490

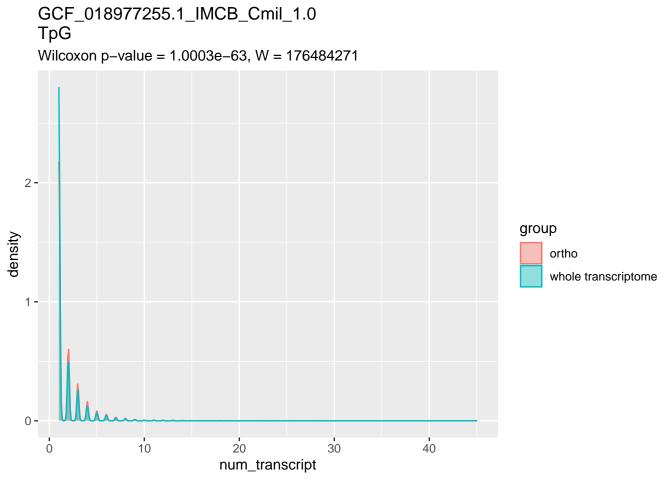


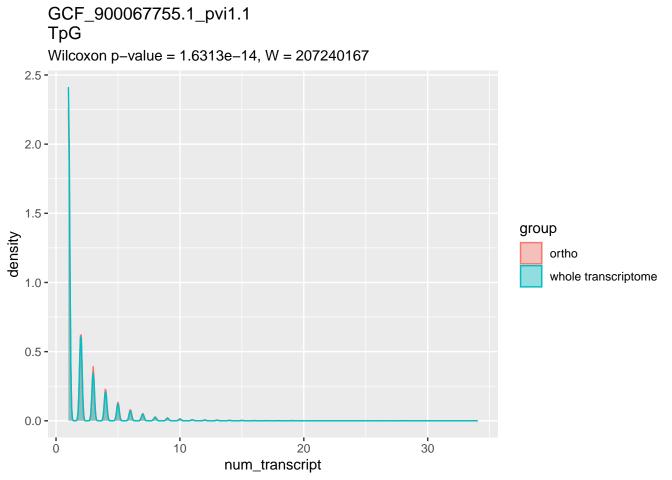
GCF_015476345.1_ZJU1.0 TpG Wilcoxon p-value = 8.9565e-157, W = 184234801 1.0 group density ortho whole transcriptome 0.5 -0.0 -10 20 30 40 50 num_transcript

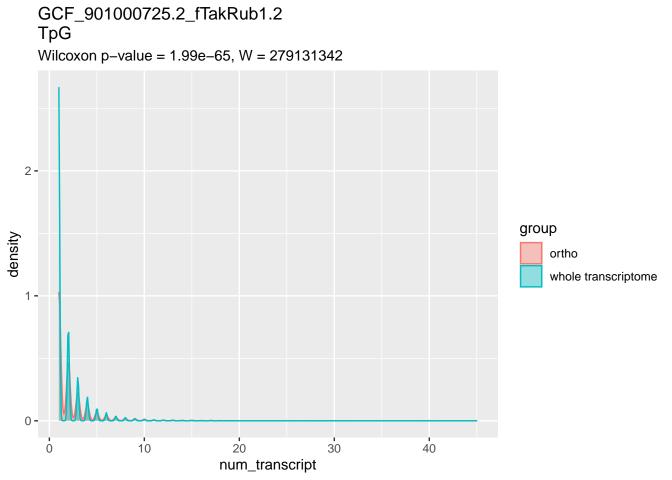
GCF_016699485.2_bGalGal1.mat.broiler.GRCg7b TpG

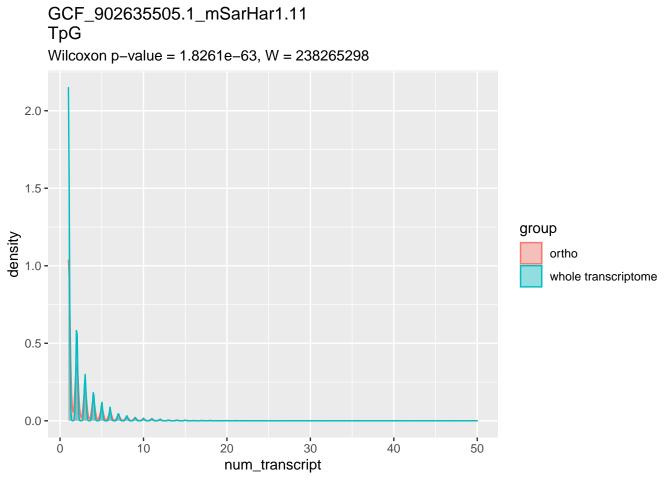


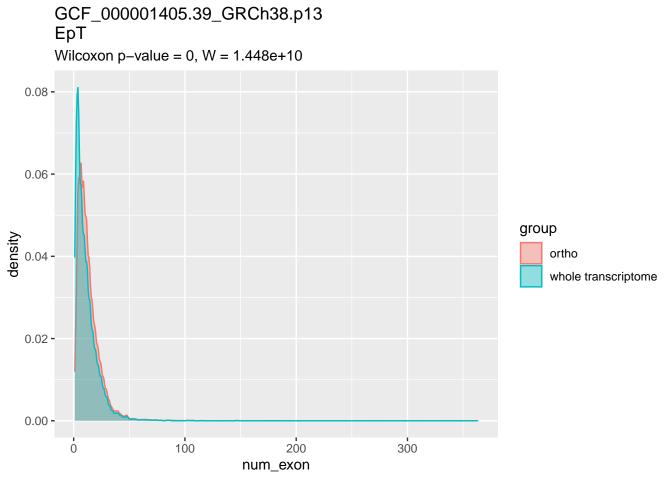
ortho

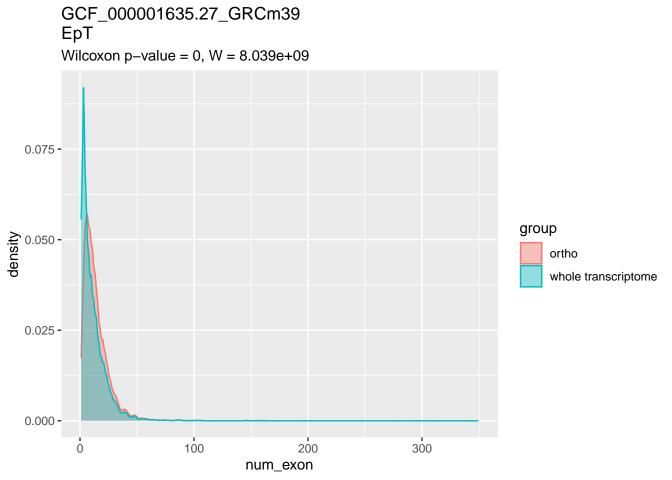


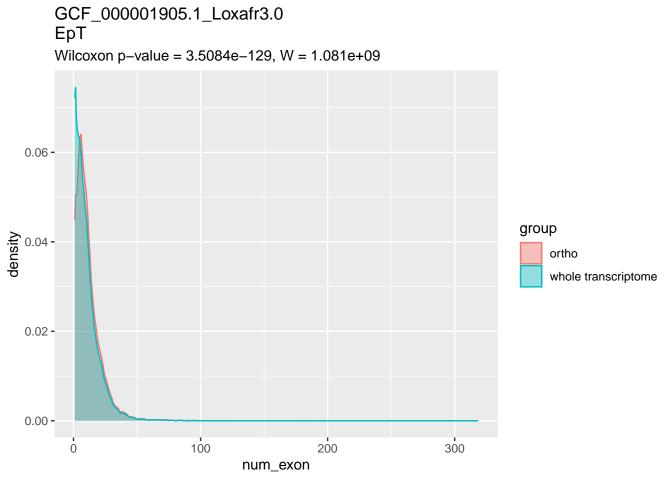


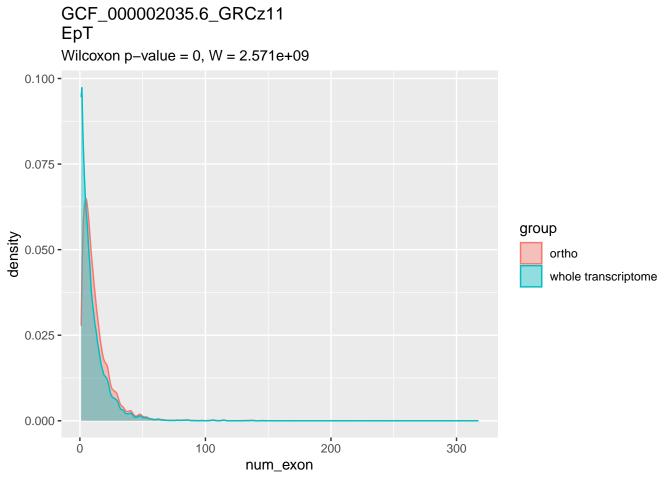


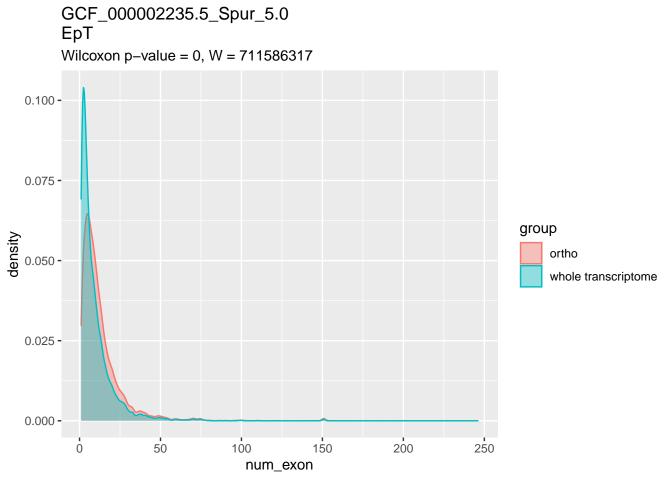


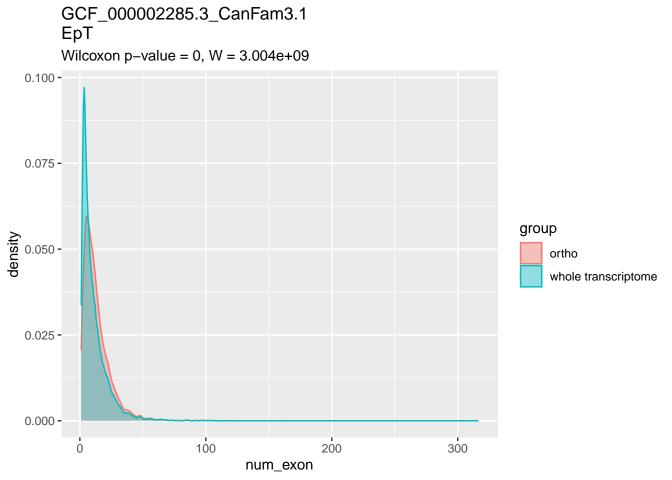




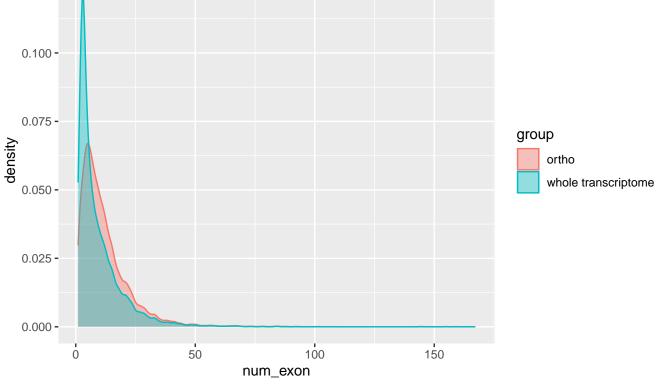




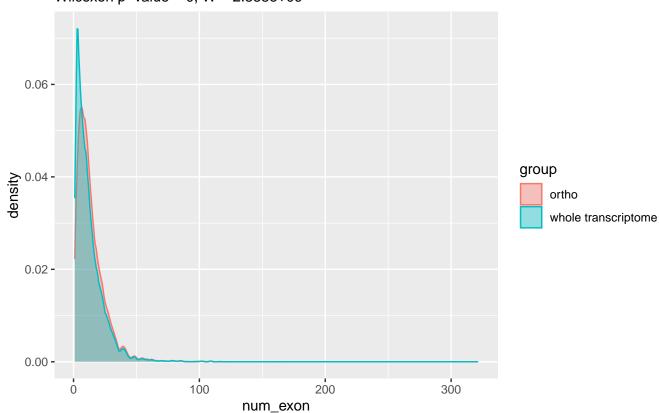


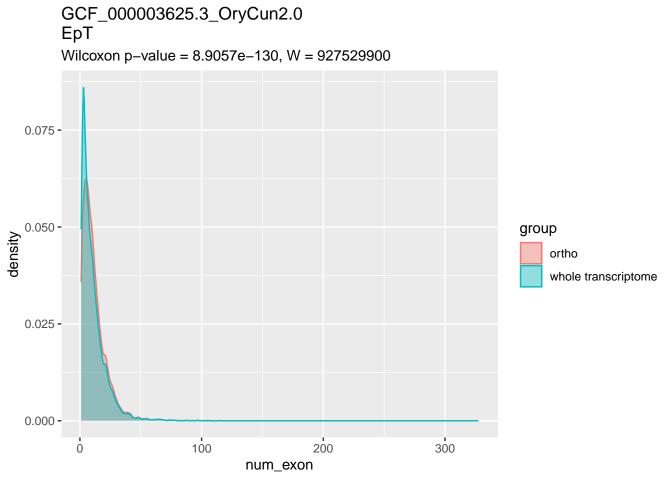


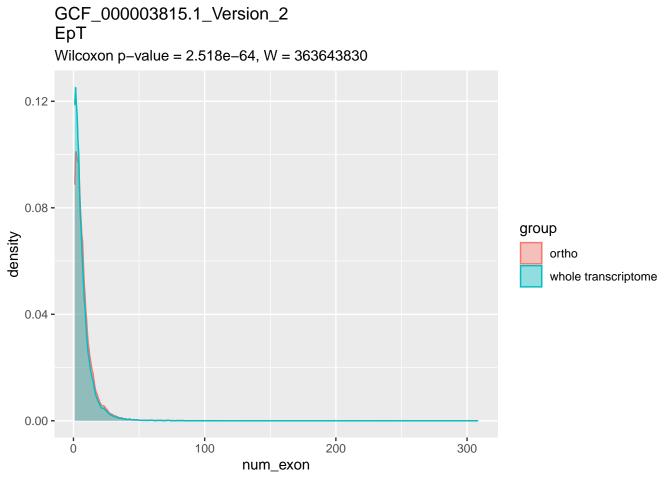
GCF_000002295.2_MonDom5 **EpT** Wilcoxon p-value = 0, W = 2.074e+090.125 group ortho whole transcriptome



GCF_000003025.6_Sscrofa11.1 EpT Wilcoxon p-value = 0, W = 2.888e+09

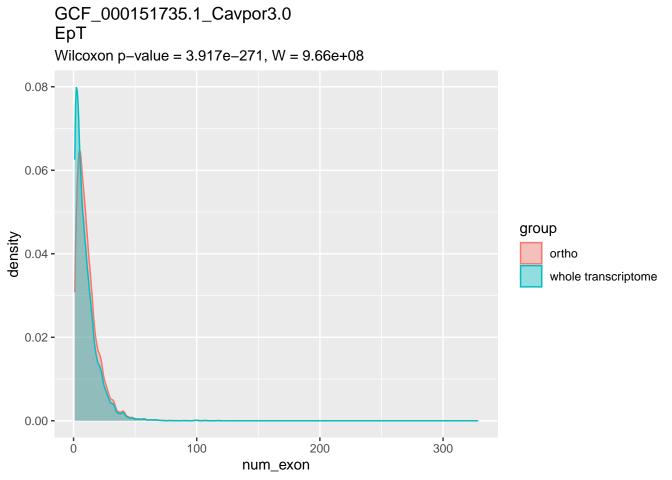


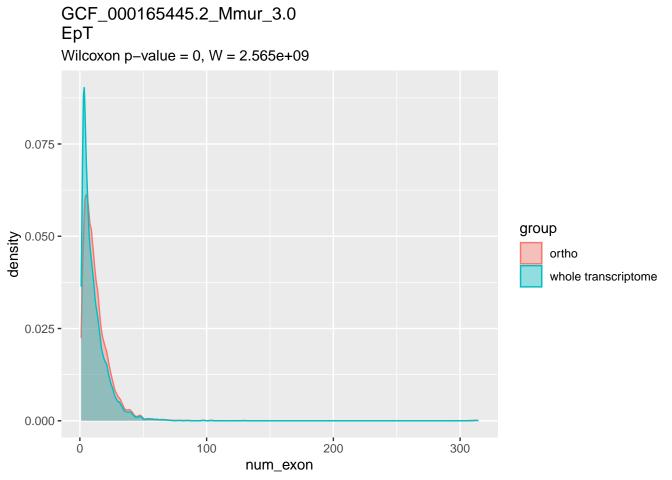


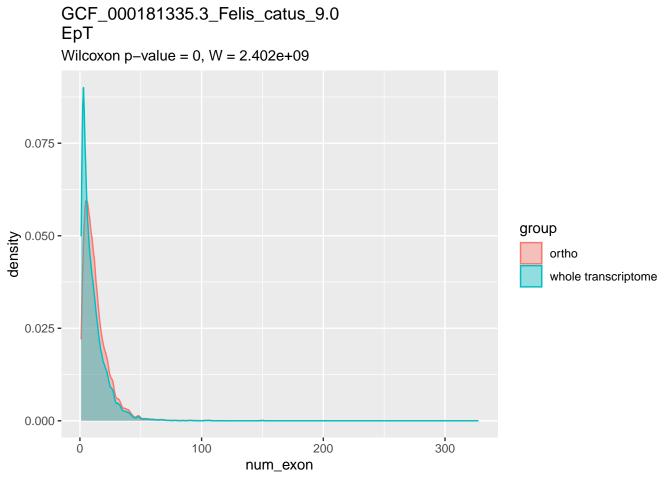


GCF_000004195.4_UCB_Xtro_10.0 **EpT** Wilcoxon p-value = 0, W = 1.269e+090.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

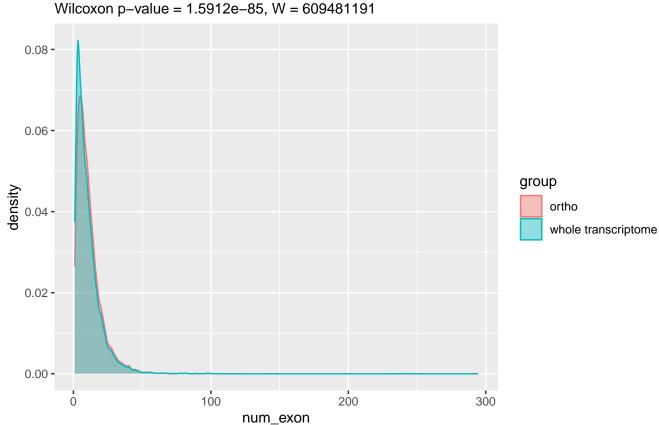
GCF_000090745.1_AnoCar2.0 **EpT** Wilcoxon p-value = 1.3657e-92, W = 7.24e+080.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -50 100 150 200 250 num_exon

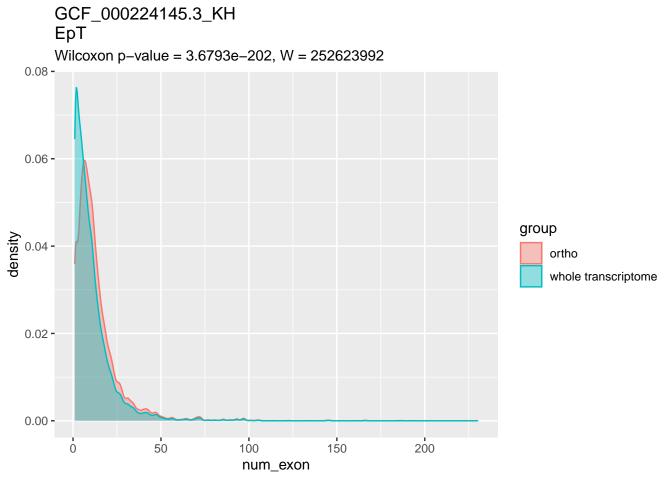




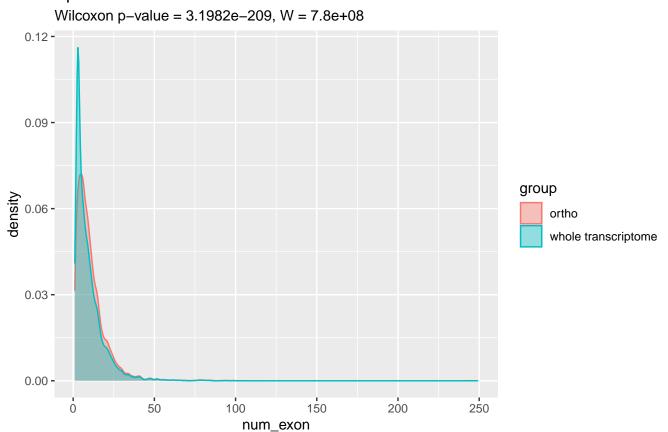


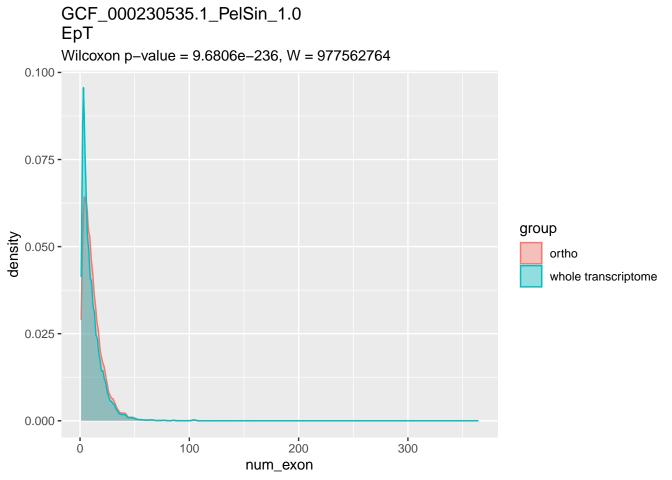
GCF_000186305.1_Python_molurus_bivittatus=5.0.2 EpT





GCF_000225785.1_LatCha1 EpT

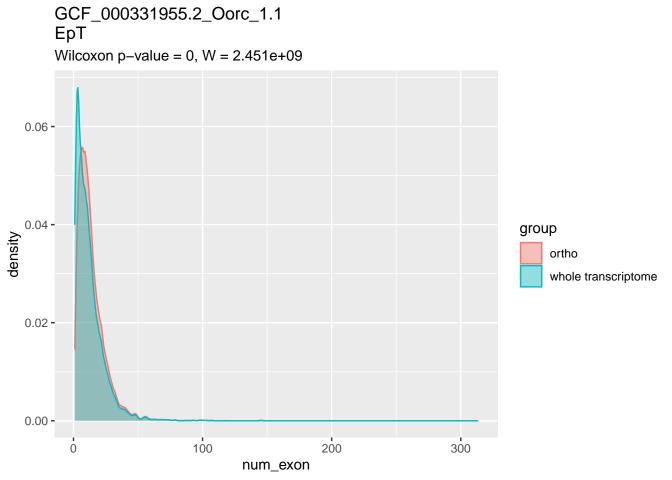


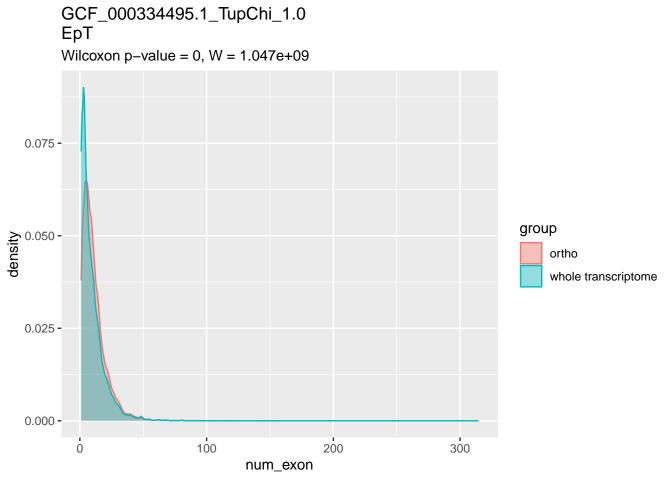


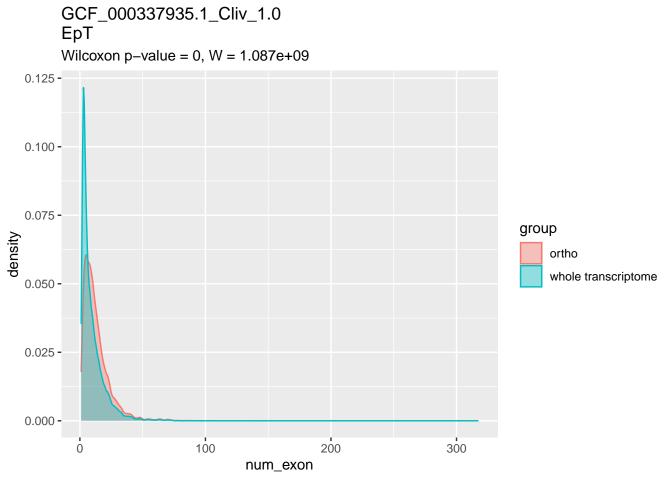
GCF_000281125.3_ASM28112v4 **EpT** Wilcoxon p-value = 5.8896e-261, W = 1.245e+090.075 density 0.050 group ortho whole transcriptome 0.025 -0.000 -100 200 300 num_exon

GCF_000296755.1_EriEur2.0 **EpT** Wilcoxon p-value = 5.0961e-11, W = 4564871170.06 -0.04 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

GCF_000313985.2_ASM31398v2 **EpT** Wilcoxon p-value = 5.2912e-285, W = 652147736 0.075 group density 0.050 ortho whole transcriptome 0.025 -0.000 -100 200 300 num_exon

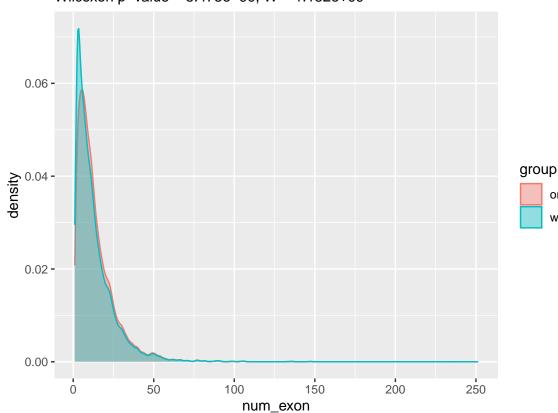






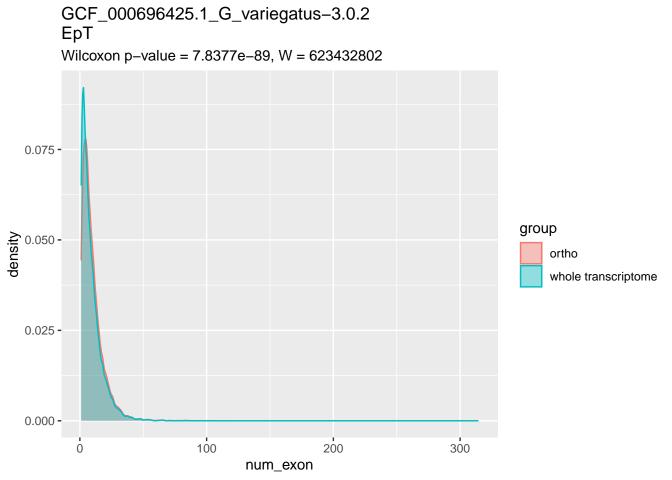
GCF_000455745.1_ASM45574v1 EpT Wilcoxon p-value = 4.4199e-187, W = 1.219e+09 0.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

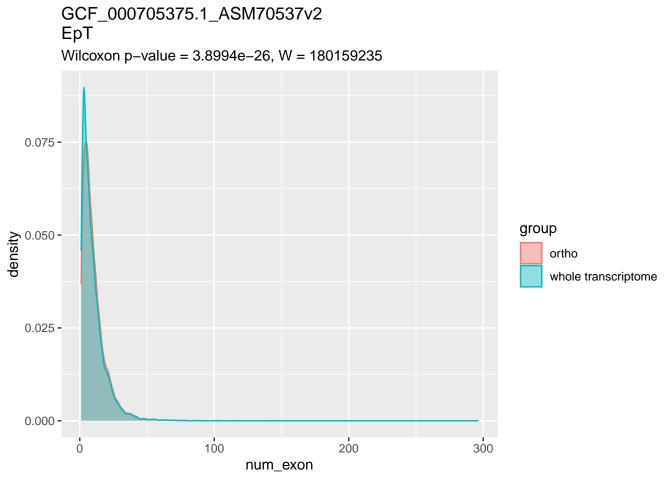
GCF_000633615.1_Guppy_female_1.0_MT EpT Wilcoxon p-value = 5.475e-90, W = 1.152e+09

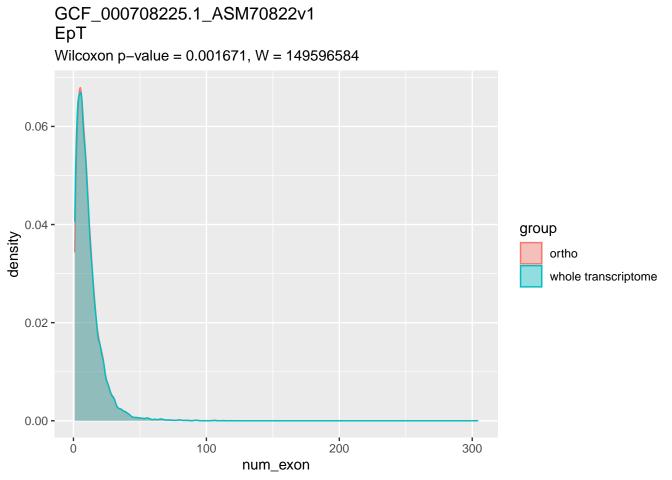


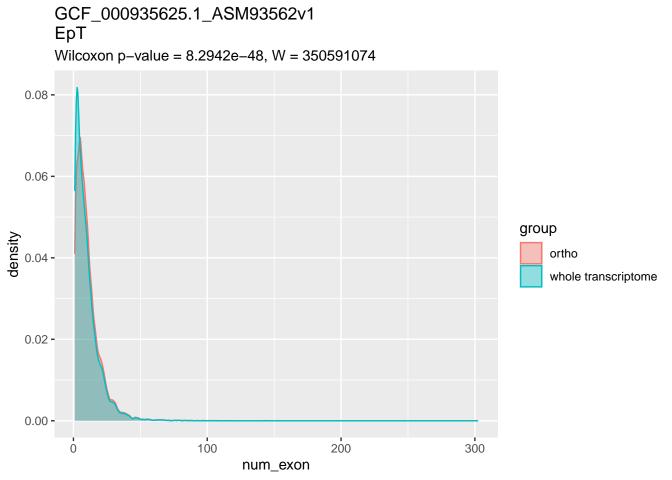
ortho

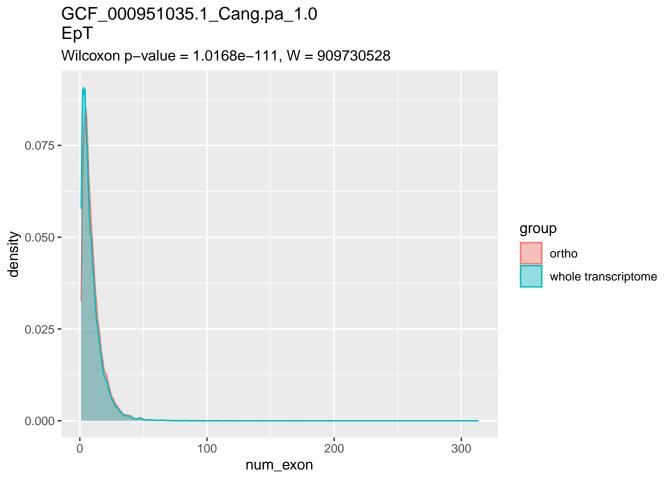
whole transcriptome

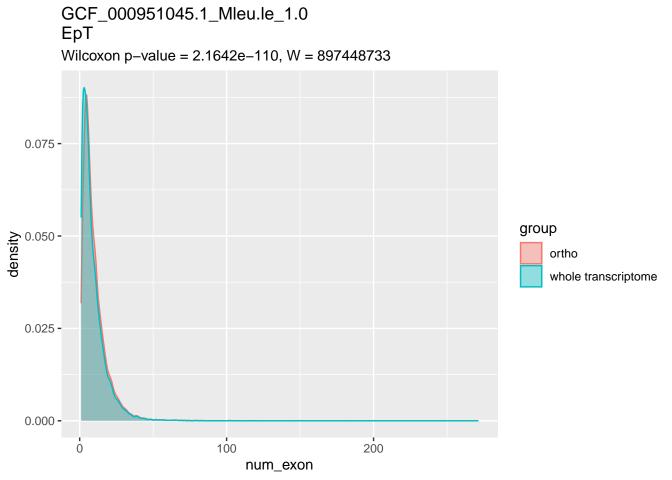


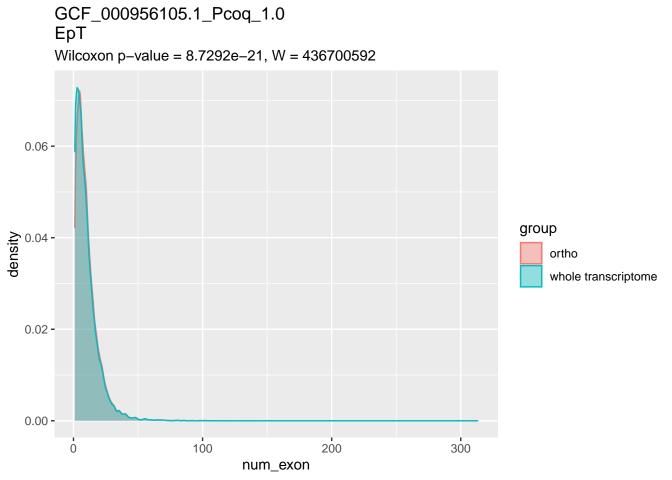


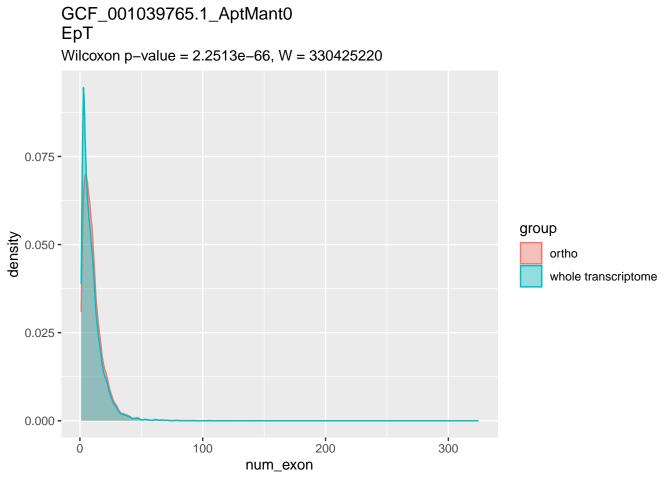


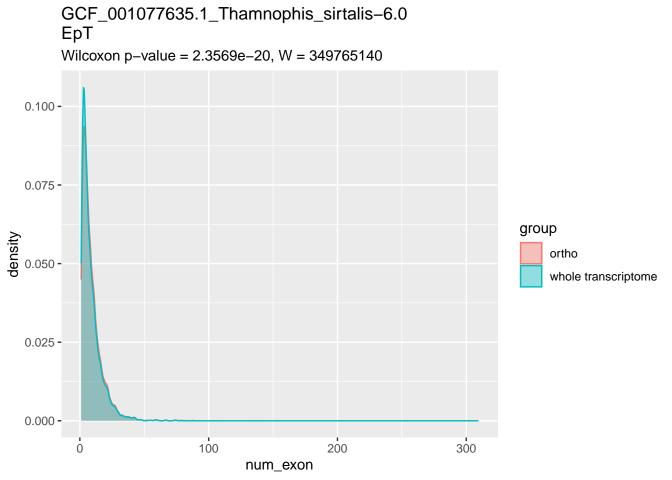


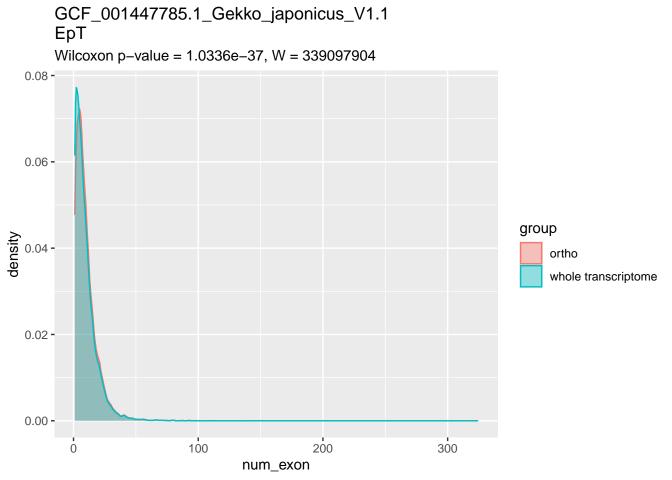


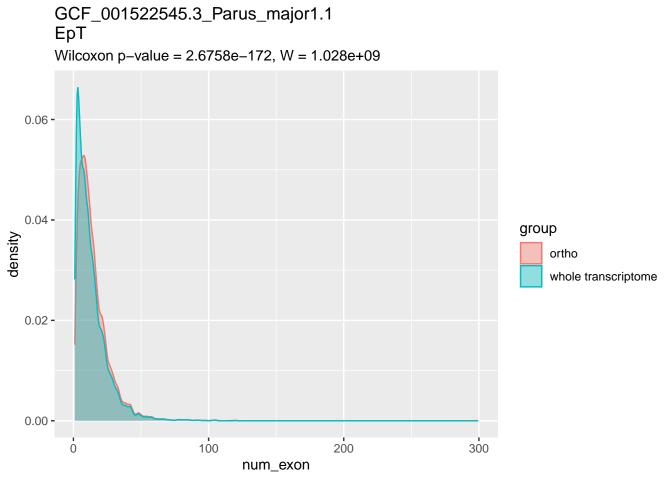




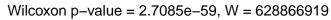


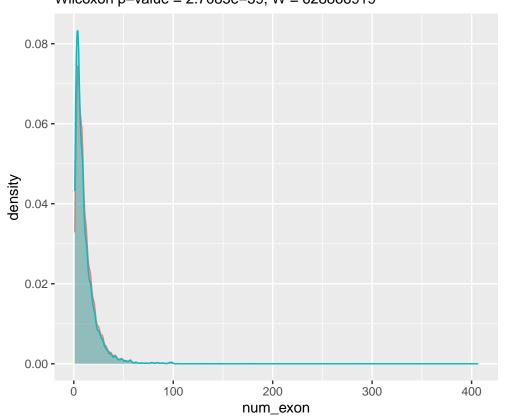






GCF_001625305.1_Haploidv18h27 EpT





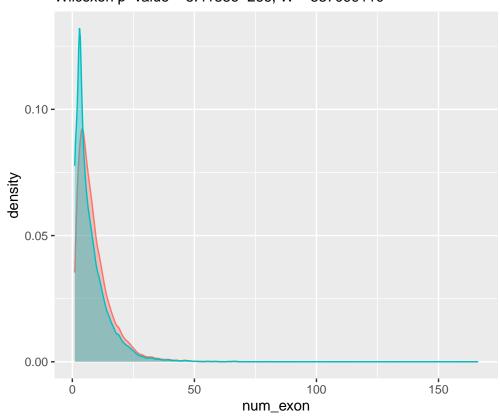
group

ortho

whole transcriptome

GCF_001642345.1_ASM164234v2 EpT





group

ortho

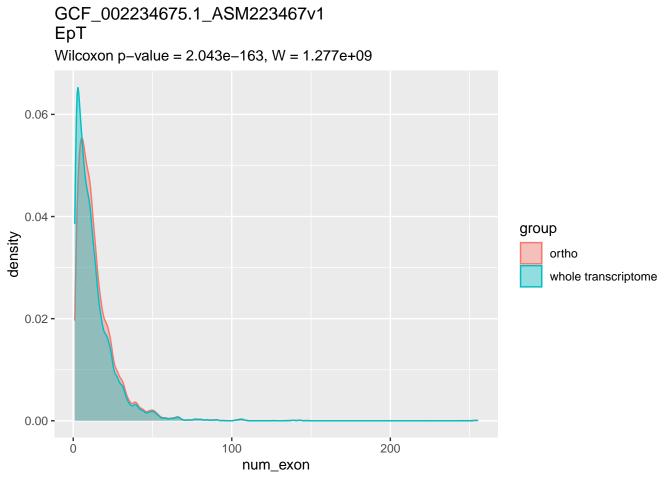
GCF_001723895.1_CroPor_comp1 **EpT** Wilcoxon p-value = 4.664e-176, W = 5644583720.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

GCF_001723915.1_GavGan_comp1 **EpT** Wilcoxon p-value = 4.7384e-167, W = 5083493050.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300

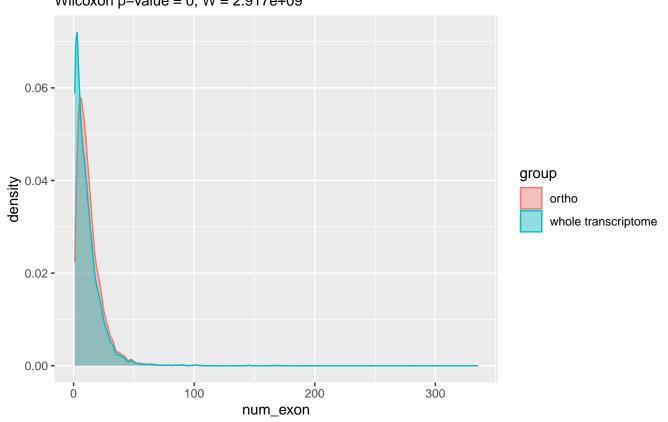
num_exon

GCF_001858045.2_O_niloticus_UMD_NMBU **EpT** Wilcoxon p-value = 0, W = 2.836e+090.100 -0.075 group density ortho whole transcriptome 0.025 -0.000 -50 100 150 200 250 num_exon

GCF_001949145.1_OKI-ApI_1.0 **EpT** Wilcoxon p-value = 3.919e-78, W = 6063706850.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -50 100 150 num_exon



GCF_002263795.1_ARS-UCD1.2 EpT Wilcoxon p-value = 0, W = 2.917e+09



GCF_002288925.2_ASM228892v3 **EpT** Wilcoxon p-value = 8.9185e-213, W = 1.739e+09 0.06 -0.04 group ortho whole transcriptome 0.02 -0.00 -

200

num_exon

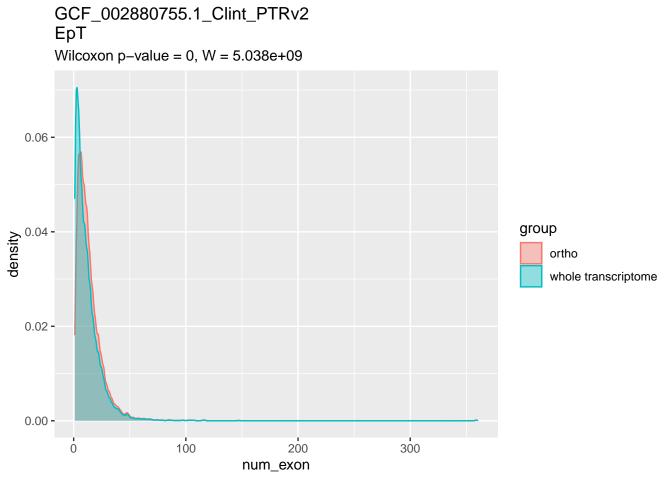
300

100

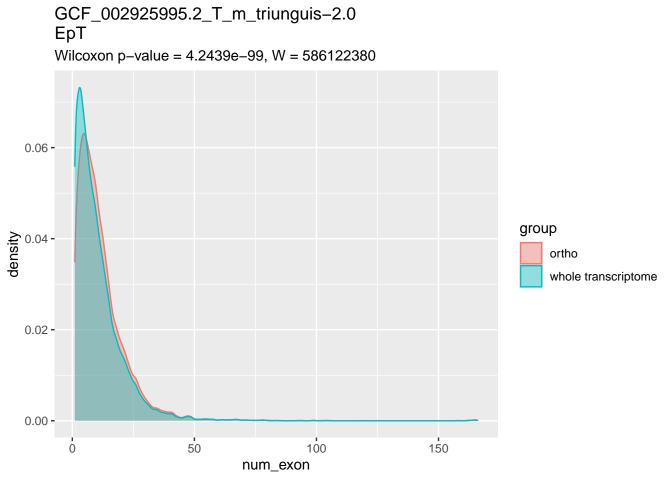
density

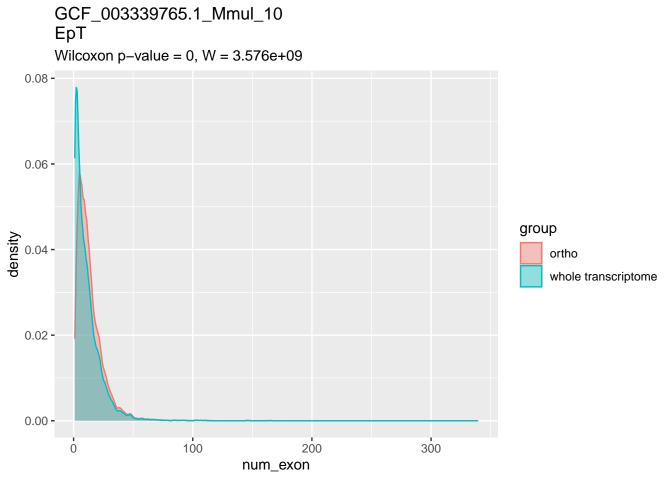
GCF_002863925.1_EquCab3.0 **EpT** Wilcoxon p-value = 0, W = 2.811e+090.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300

num_exon

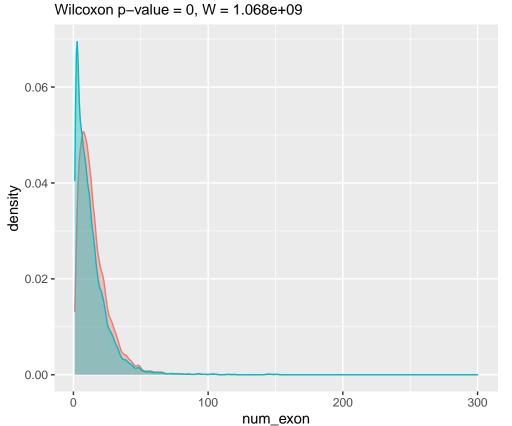


GCF_002880775.1_Susie_PABv2 **EpT** Wilcoxon p-value = 3.9447e-267, W = 1.653e+090.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon





GCF_003957565.2_bTaeGut1.4.pri EpT



group

ortho

GCF_004115215.2_mOrnAna1.pri.v4 **EpT** Wilcoxon p-value = 0, W = 1.16e+090.100 -0.075 group density ortho whole transcriptome 0.025 -0.000 -

150

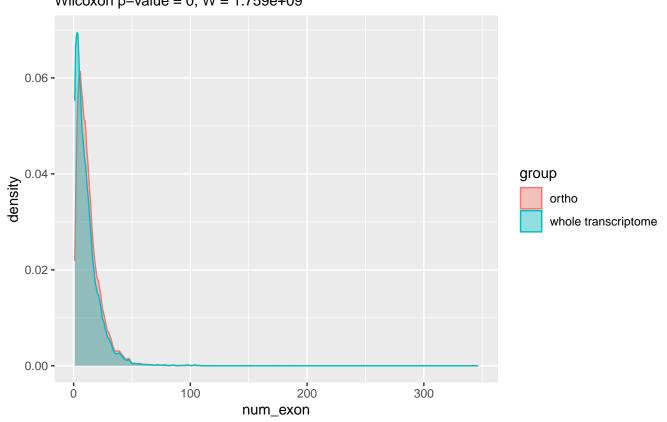
200

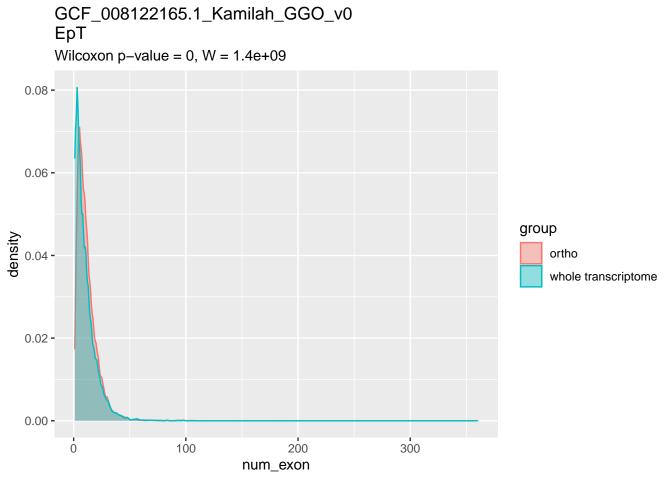
50

100

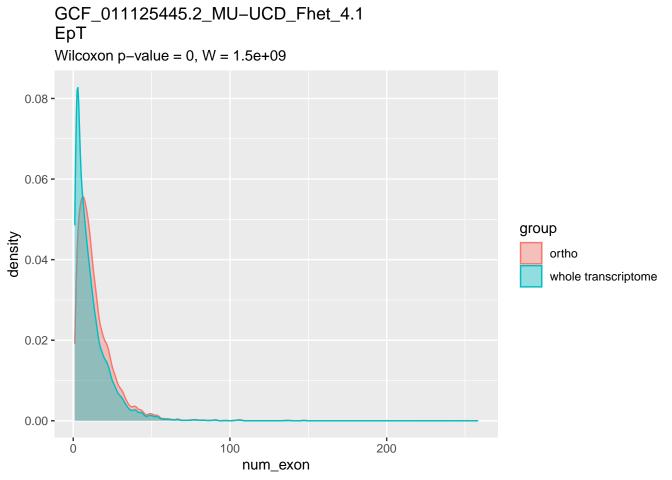
num_exon

GCF_006542625.1_Asia_NLE_v1 EpT Wilcoxon p-value = 0, W = 1.759e+09





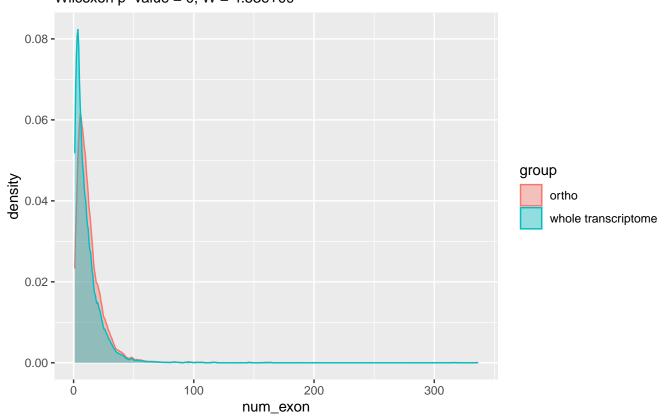
GCF_009663435.1_Callithrix_jacchus_cj1700_1.1 **EpT** Wilcoxon p-value = 0, W = 5.245e+090.06 -0.04 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon



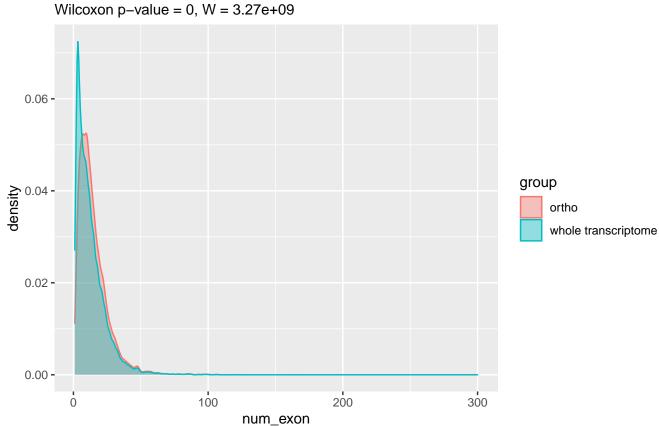
GCF_011762595.1_mTurTru1.mat.Y **EpT** Wilcoxon p-value = 0, W = 2.043e+090.06 -0.04 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

GCF_014633375.1_OchPri4.0 **EpT** Wilcoxon p-value = 2.8866e-81, W = 5072982920.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

GCF_015227675.2_mRatBN7.2 EpT Wilcoxon p-value = 0, W = 4.53e+09



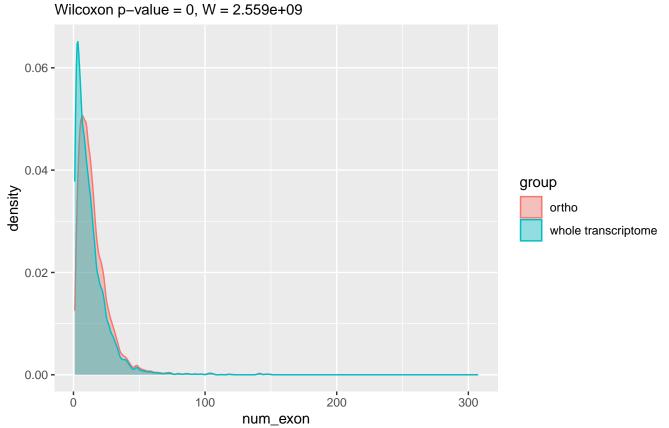
GCF_015237465.2_rCheMyd1.pri.v2 EpT

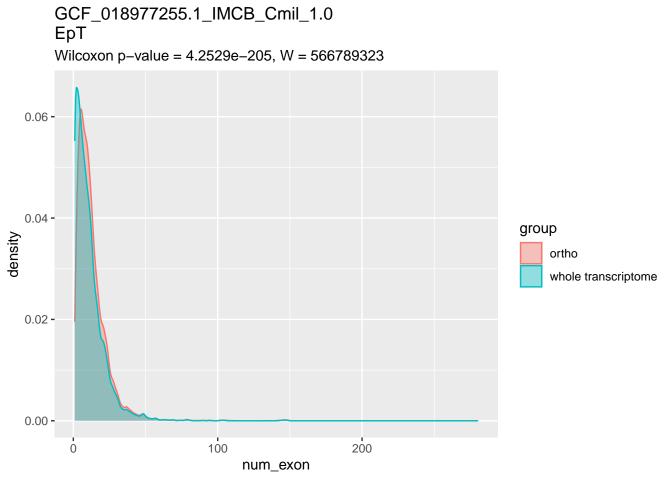


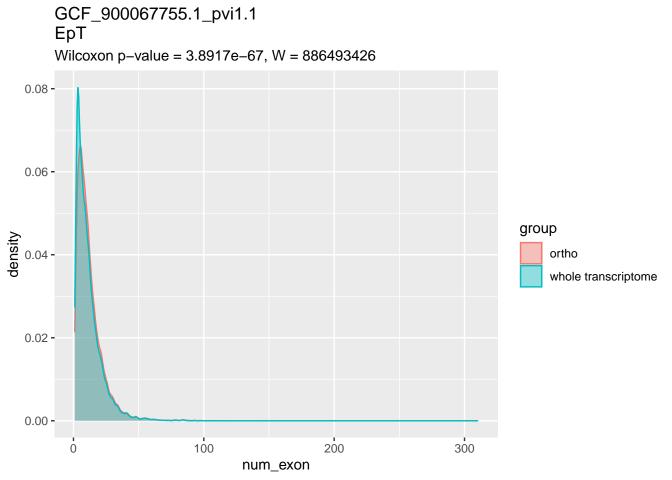
GCF_015476345.1_ZJU1.0 EpT Wilcoxon p-value = 0, W = 1.462e+090.08 -0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300

num_exon

GCF_016699485.2_bGalGal1.mat.broiler.GRCg7b EpT



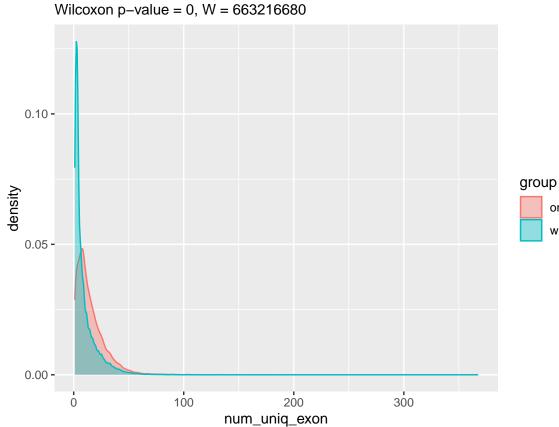




GCF_901000725.2_fTakRub1.2 **EpT** Wilcoxon p-value = 1.9828e-274, W = 1.331e+09 0.06 -0.04 group density ortho whole transcriptome 0.02 -0.00 -50 100 150 200 250 num_exon

GCF_902635505.1_mSarHar1.11 **EpT** Wilcoxon p-value = 3.1082e-209, W = 1.3e+090.06 density 0.04 group ortho whole transcriptome 0.02 -0.00 -100 200 300 num_exon

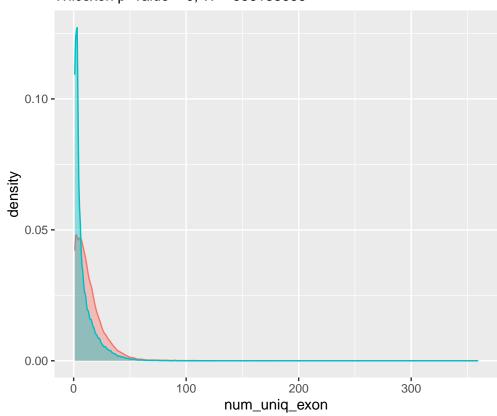
GCF_000001405.39_GRCh38.p13 EpG



ortho

GCF_000001635.27_GRCm39 EpG

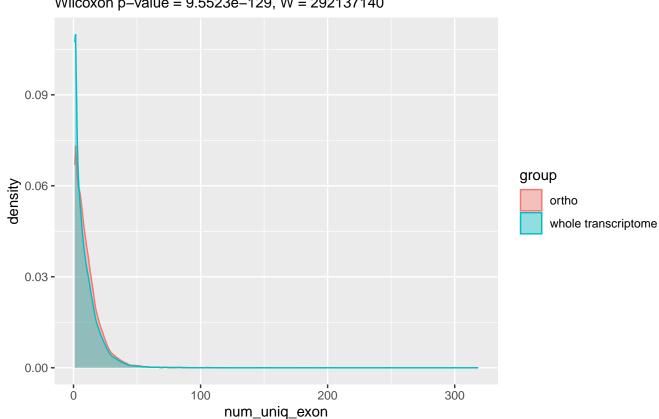
Wilcoxon p-value = 0, W = 556188686



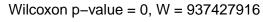
group

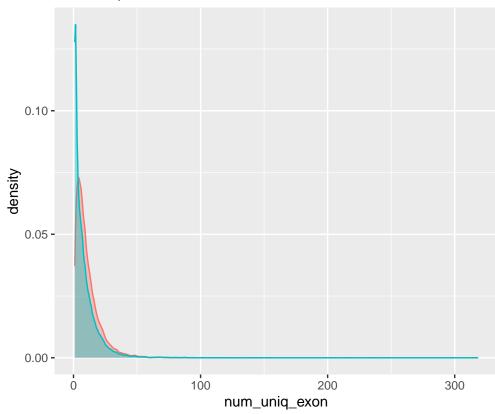
ortho

GCF_000001905.1_Loxafr3.0 EpG Wilcoxon p-value = 9.5523e-129, W = 292137140



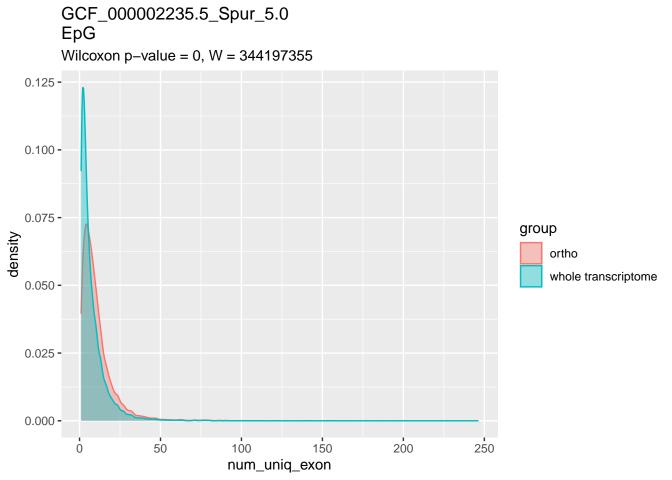
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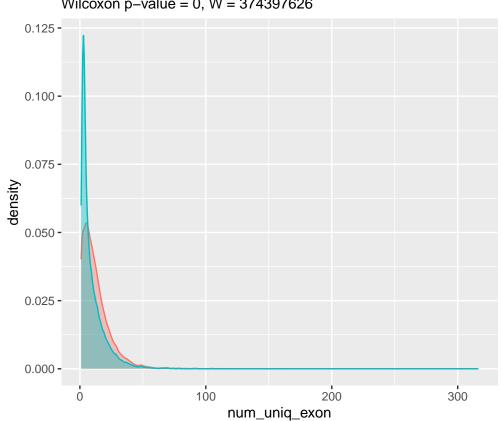


group

ortho

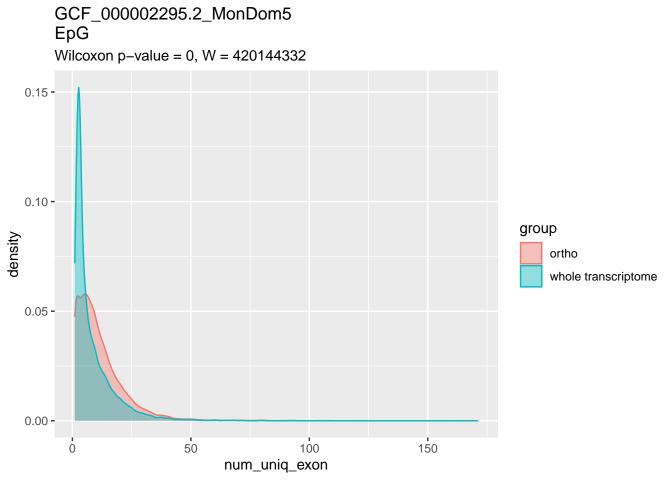


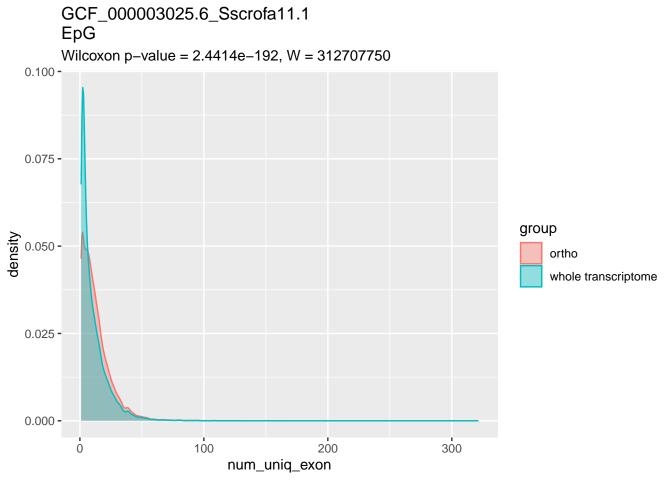
GCF_000002285.3_CanFam3.1 EpG Wilcoxon p-value = 0, W = 374397626

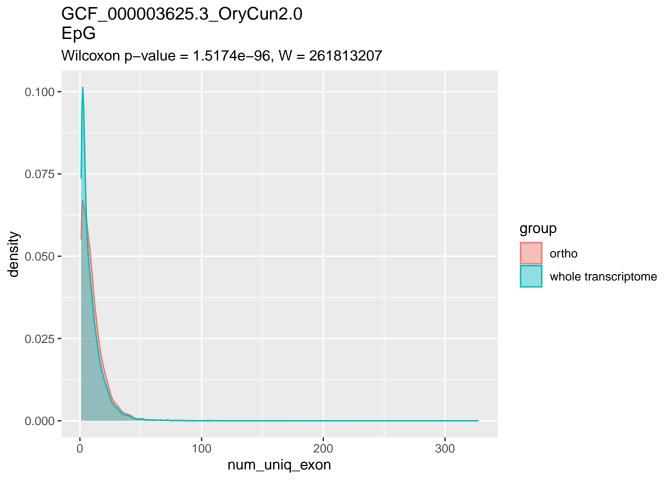


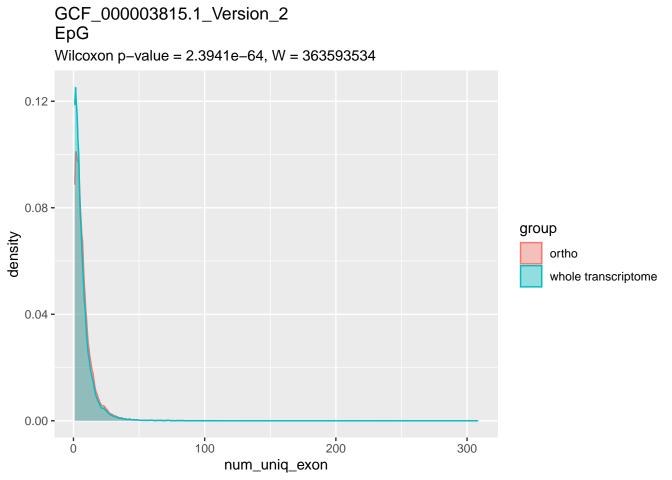
group

ortho





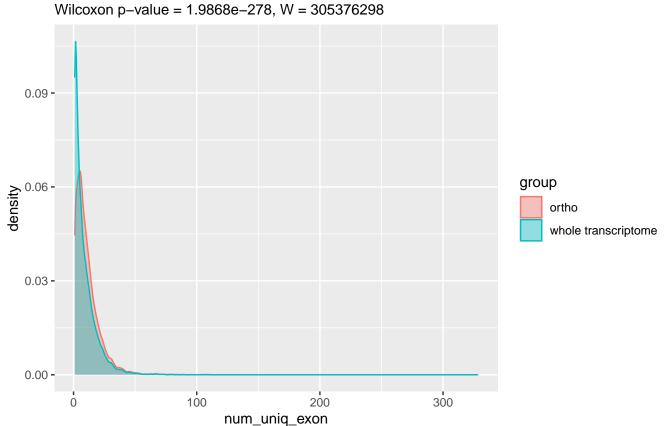


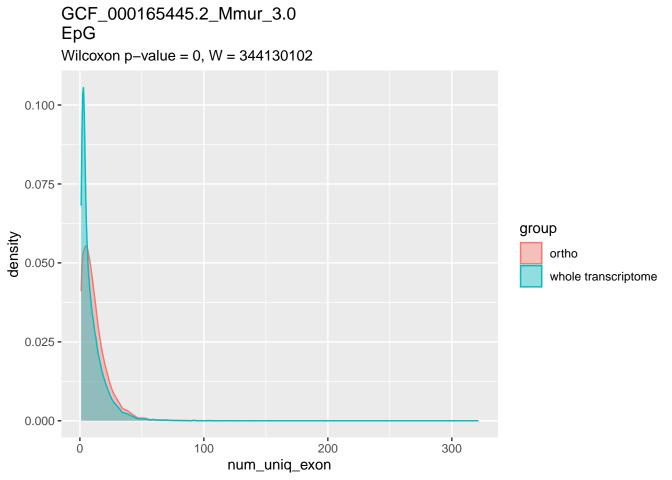


GCF_000004195.4_UCB_Xtro_10.0 EpG Wilcoxon p-value = 0, W = 327277446 0.100 -0.075 group density 0.050 ortho whole transcriptome 0.025 -0.000 -100 200 300 num_uniq_exon

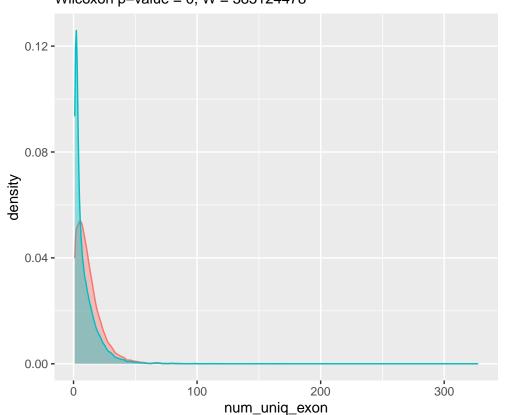
GCF_000090745.1_AnoCar2.0 EpG Wilcoxon p-value = 3.6558e-66, W = 223750716 0.100 -0.075 group density 0.050 ortho whole transcriptome 0.025 -0.000 -50 100 150 200 250 num_uniq_exon

GCF_000151735.1_Cavpor3.0 EpG





GCF_000181335.3_Felis_catus_9.0 EpG Wilcoxon p-value = 0, W = 385124478

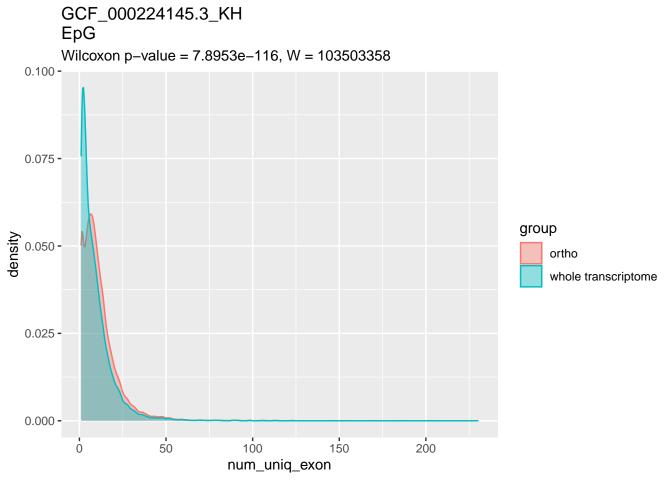


group

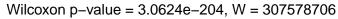
ortho

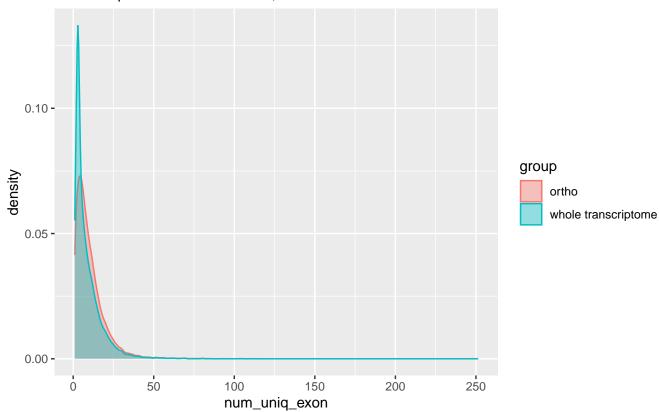
whole transcriptome

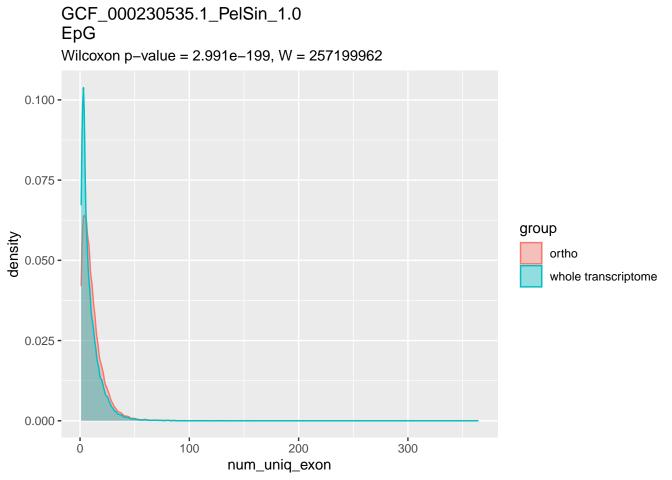
GCF_000186305.1_Python_molurus_bivittatus-5.0.2 EpG Wilcoxon p-value = 1.3206e-80, W = 2193451720.075 density 0.050 group ortho whole transcriptome 0.025 -0.000 -100 200 300 num_uniq_exon



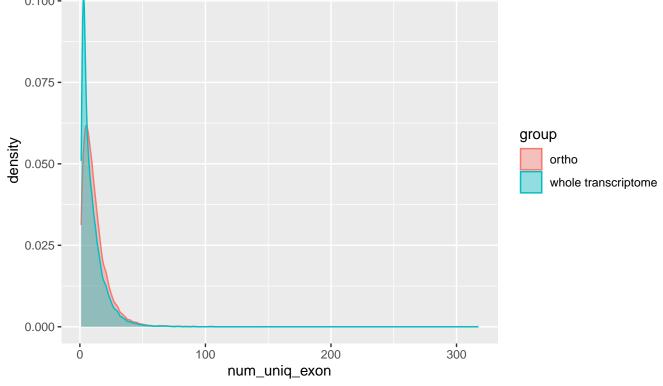
GCF_000225785.1_LatCha1 EpG







GCF_000281125.3_ASM28112v4 EpG Wilcoxon p-value = 5.4055e-218, W = 2.7e+080.100 group ortho whole transcriptome



GCF_000296755.1_EriEur2.0 EpG Wilcoxon p-value = 1.2782e-12, W = 199503692 0.06 group density ortho whole transcriptome 0.02 -0.00 -100 200 300 num_uniq_exon

GCF_000313985.2_ASM31398v2 EpG Wilcoxon p-value = 0, W = 269692960 0.125 -0.100 -0.075 group ortho whole transcriptome 0.050 -0.025 -0.000 -

200

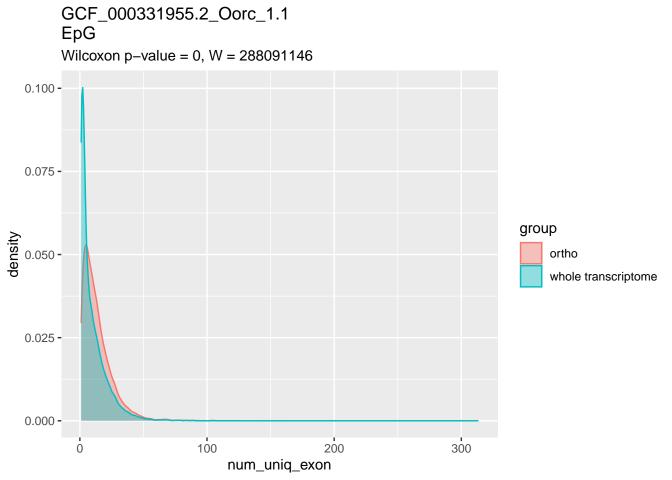
num_uniq_exon

300

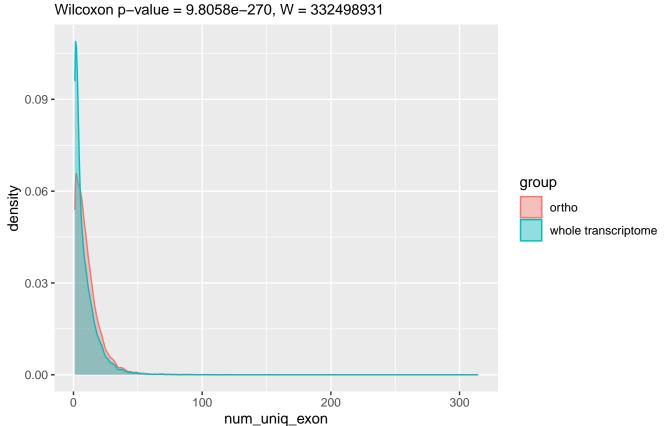
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density

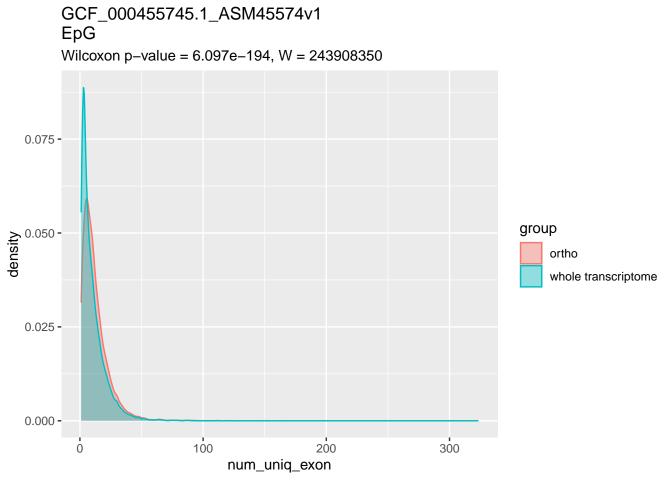
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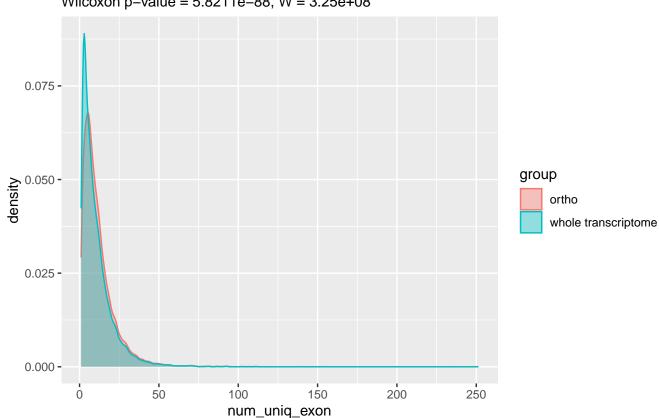
GCF_000334495.1_TupChi_1.0 EpG



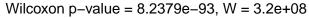
GCF_000337935.1_Cliv_1.0 EpG Wilcoxon p-value = 0, W = 257519666 0.10 group density ortho whole transcriptome 0.05 -0.00 -100 200 300 num_uniq_exon

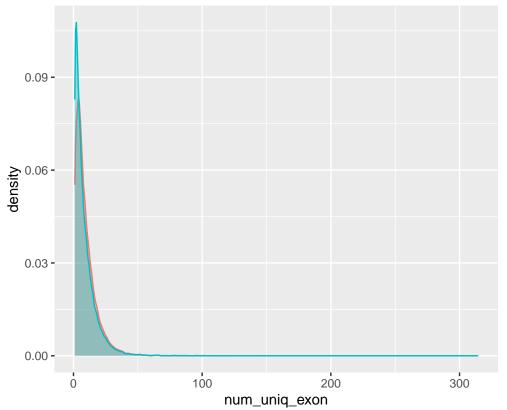


GCF_000633615.1_Guppy_female_1.0_MT EpG Wilcoxon p-value = 5.8211e-88, W = 3.25e+08



GCF_000696425.1_G_variegatus=3.0.2 EpG

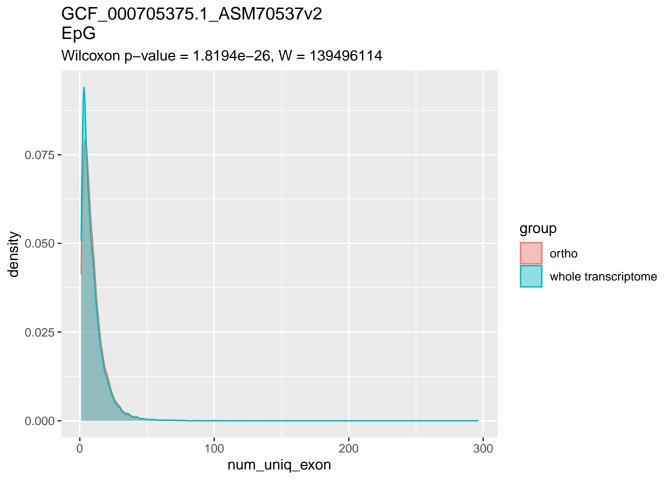


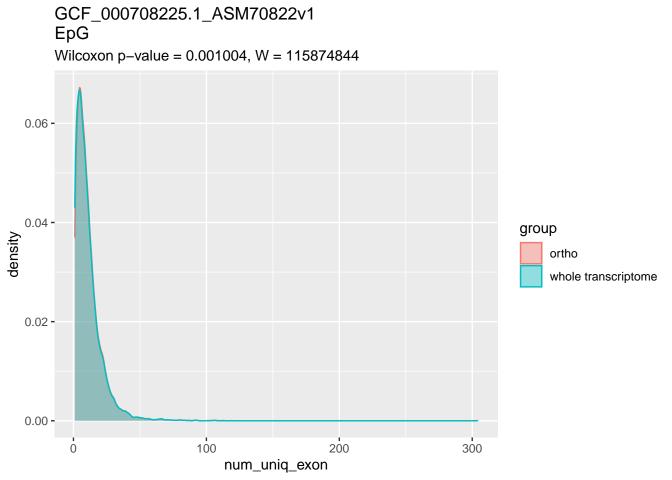


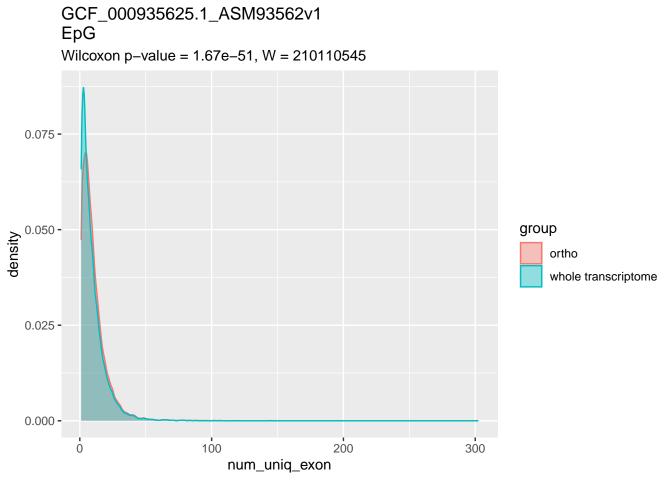
group

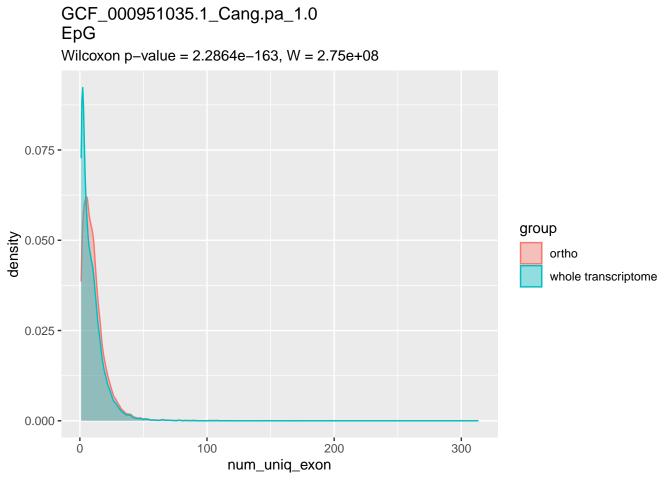
ortho

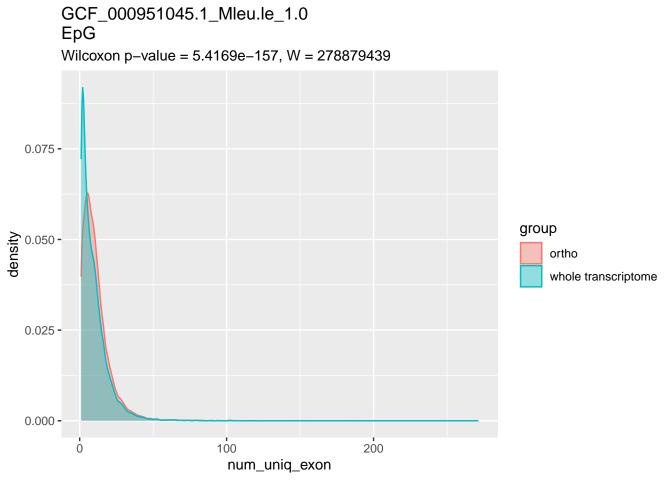
whole transcriptome

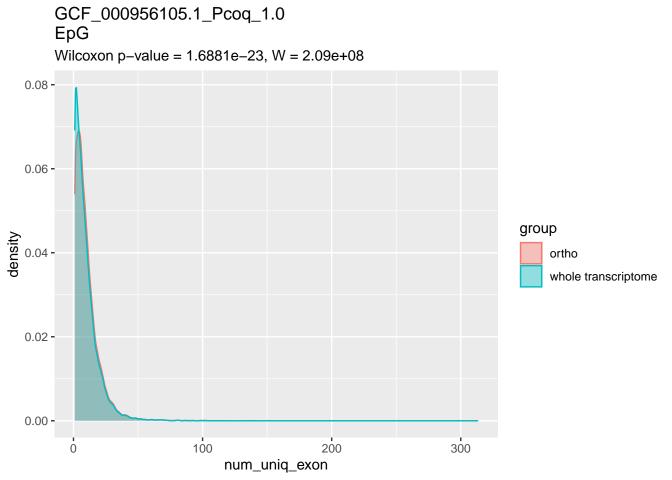


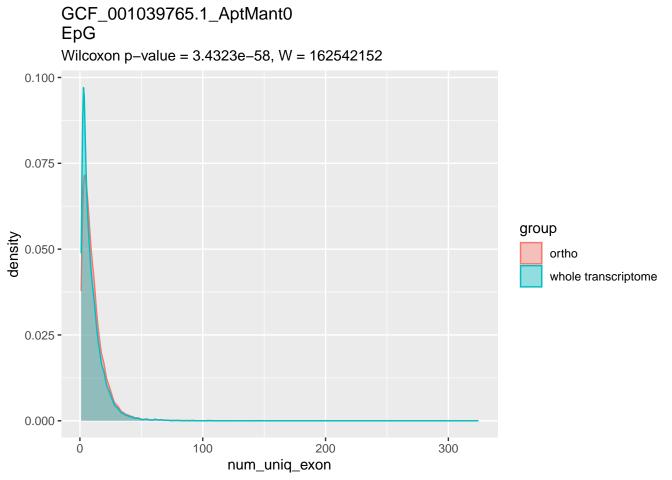








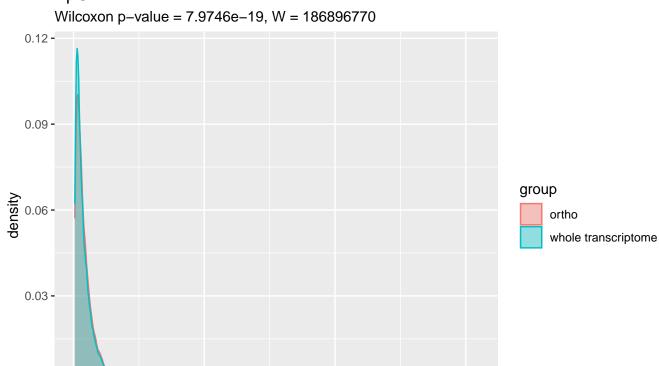




GCF_001077635.1_Thamnophis_sirtalis-6.0 EpG

100

0.00 -



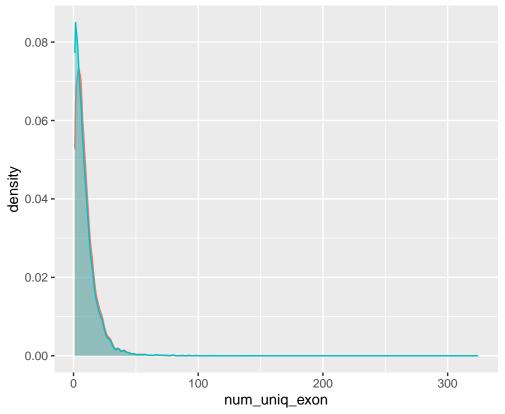
200

num_uniq_exon

300

GCF_001447785.1_Gekko_japonicus_V1.1 EpG

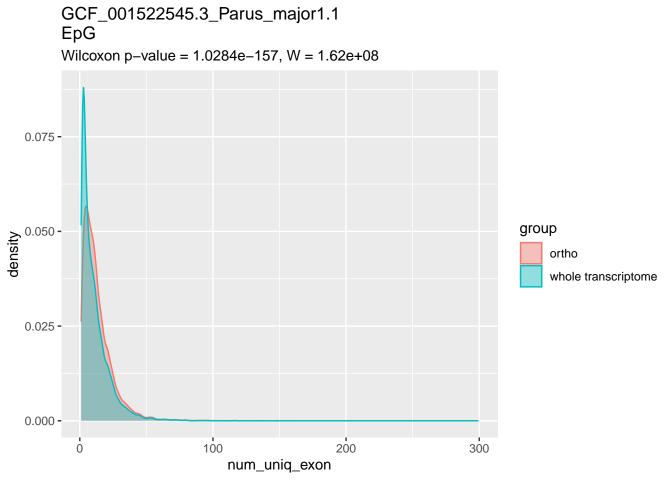
Wilcoxon p-value = 4.5196e-41, W = 2.18e+08

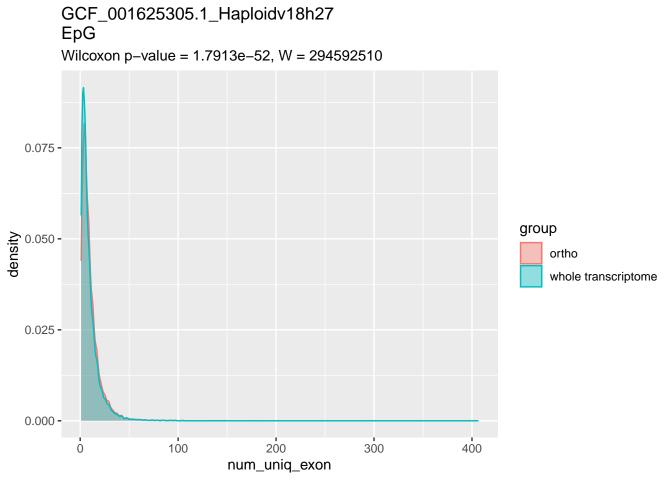


group

ortho

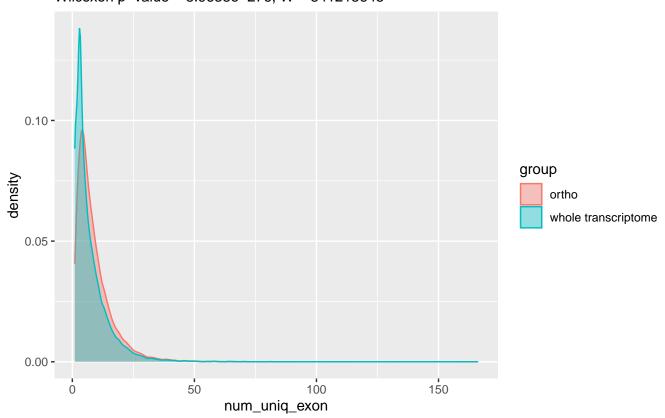
whole transcriptome





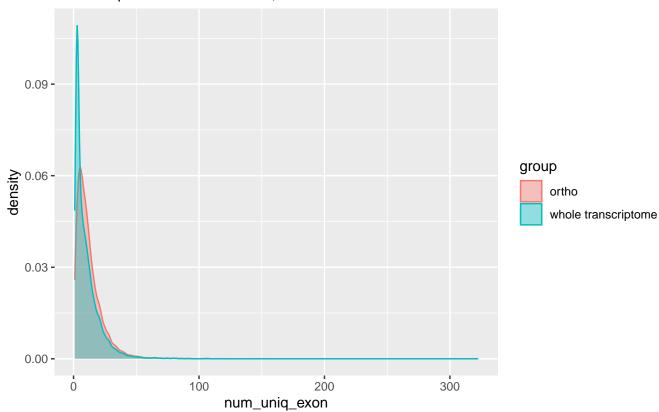
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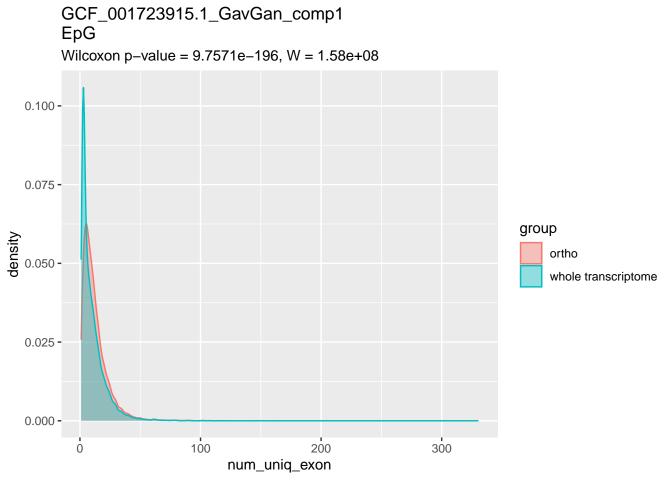
Wilcoxon p-value = 8.9638e-276, W = 341215648



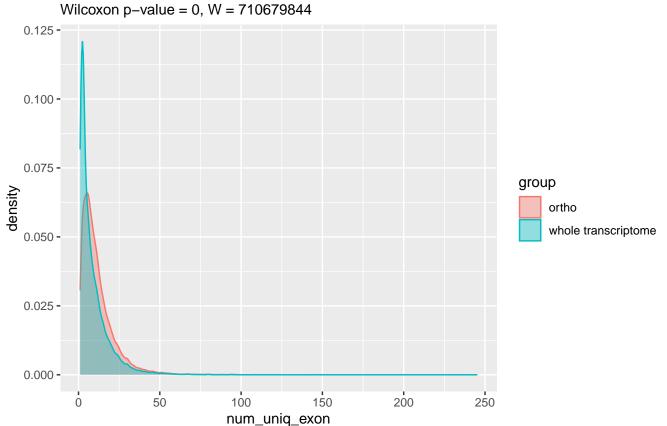
GCF_001723895.1_CroPor_comp1 EpG

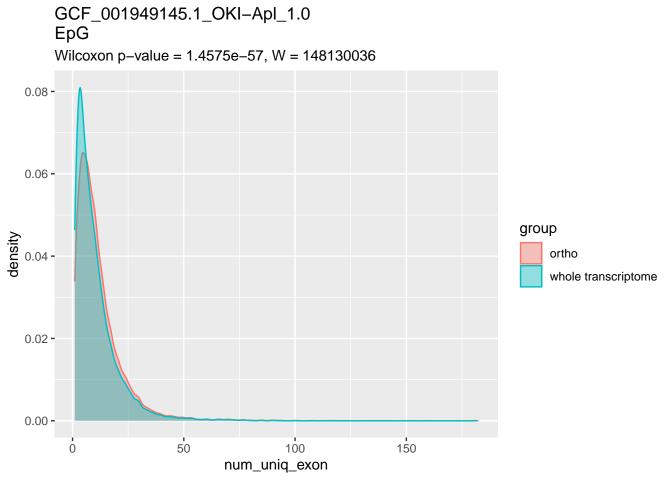
Wilcoxon p-value = 2.8947e-209, W = 168695824

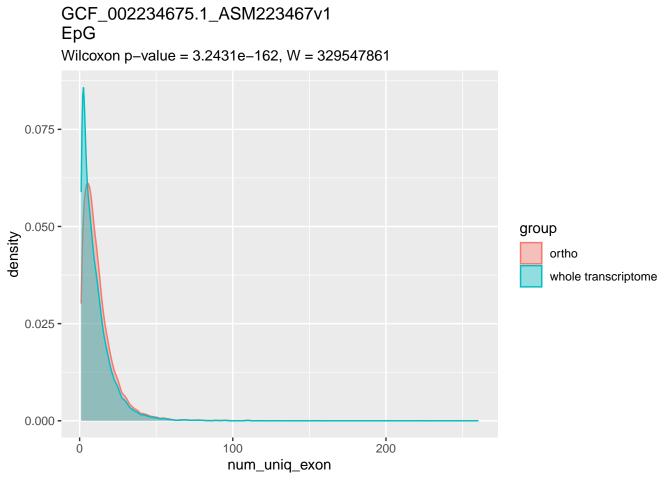




GCF_001858045.2_O_niloticus_UMD_NMBU EpG





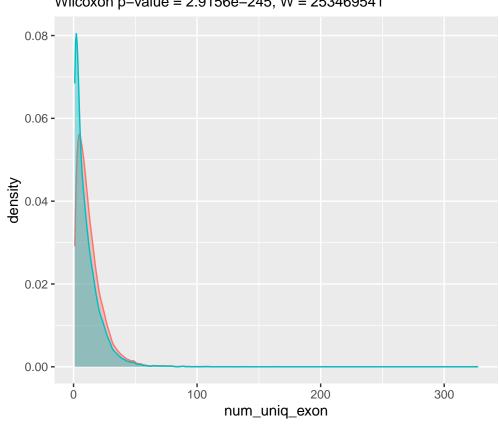


GCF_002263795.1_ARS-UCD1.2 EpG Wilcoxon p-value = 0, W = 3784741980.125 -0.100 -0.075 group ortho whole transcriptome 0.050 -0.025 -0.000 -100 0 200 300 num_uniq_exon

density

GCF_002288925.2_ASM228892v3 EpG

Wilcoxon p-value = 2.9156e-245, W = 253469541

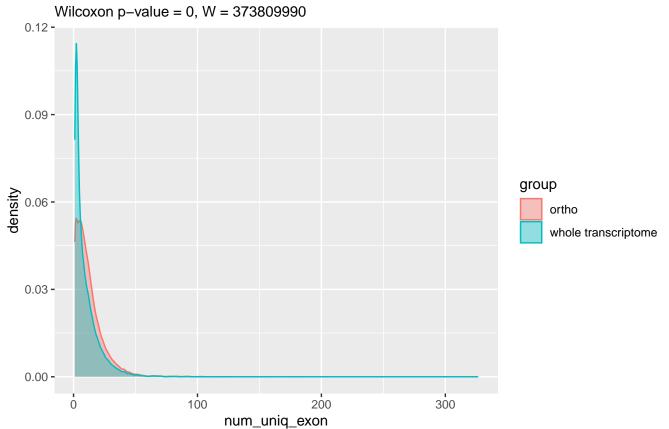


group

ortho

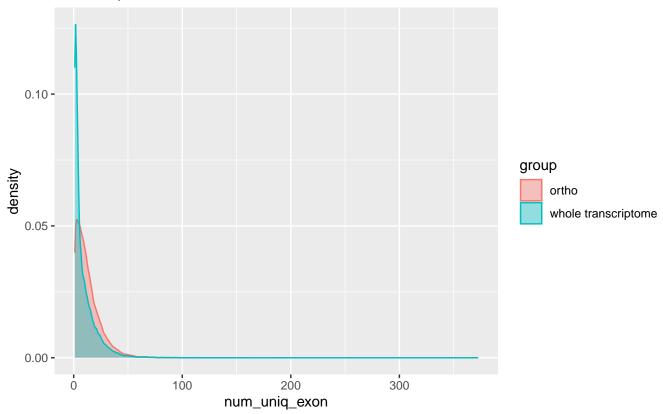
whole transcriptome

GCF_002863925.1_EquCab3.0 EpG



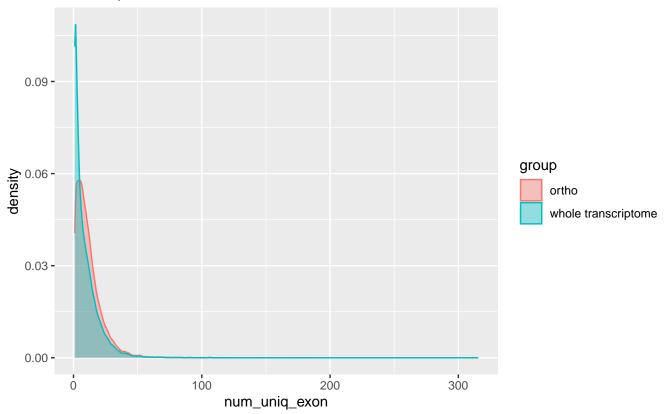
GCF_002880755.1_Clint_PTRv2 EpG

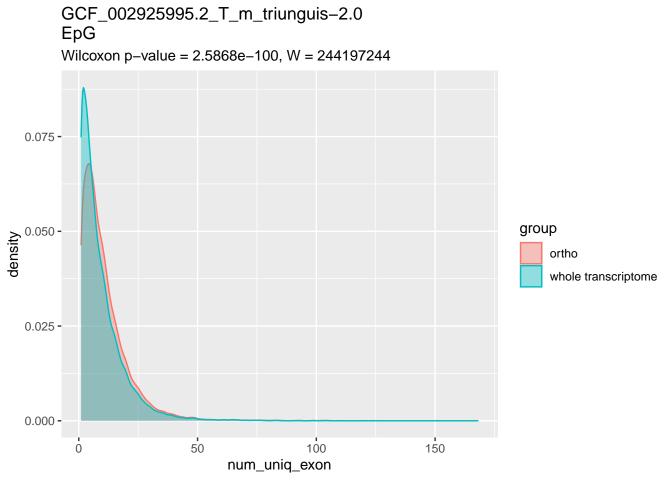
Wilcoxon p-value = 0, W = 463328730



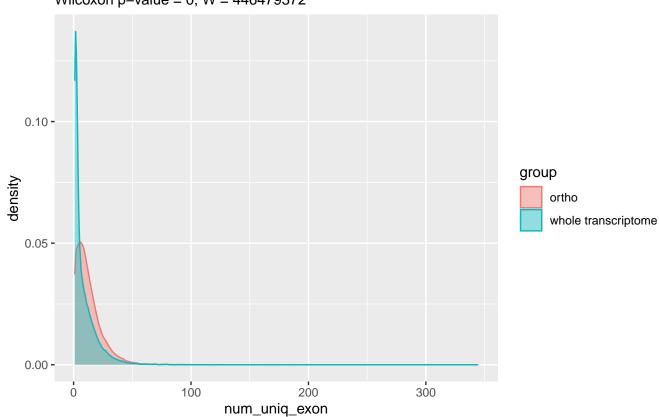
GCF_002880775.1_Susie_PABv2 EpG

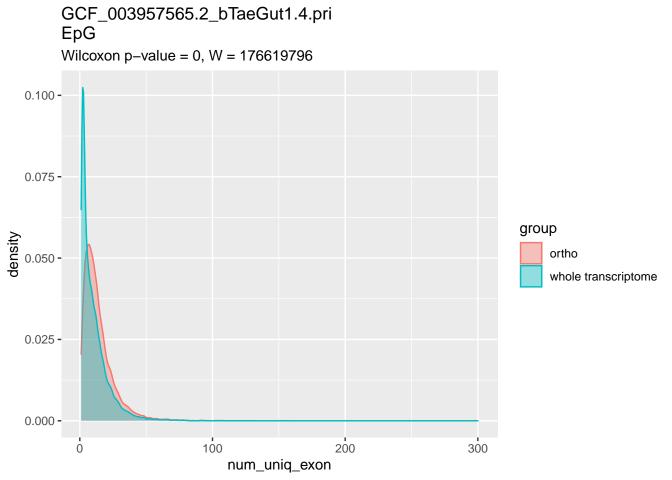
Wilcoxon p-value = 0, W = 343183737





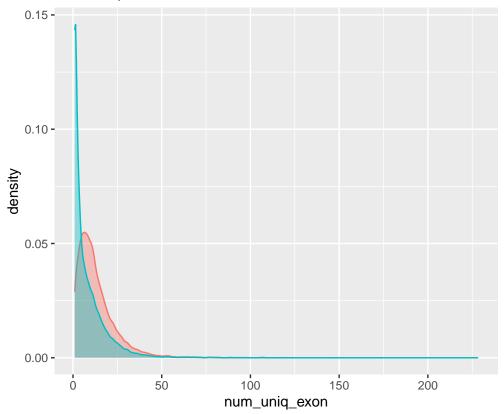
GCF_003339765.1_Mmul_10 EpG Wilcoxon p-value = 0, W = 446479372





GCF_004115215.2_mOrnAna1.pri.v4 EpG

Wilcoxon p-value = 0, W = 304506971



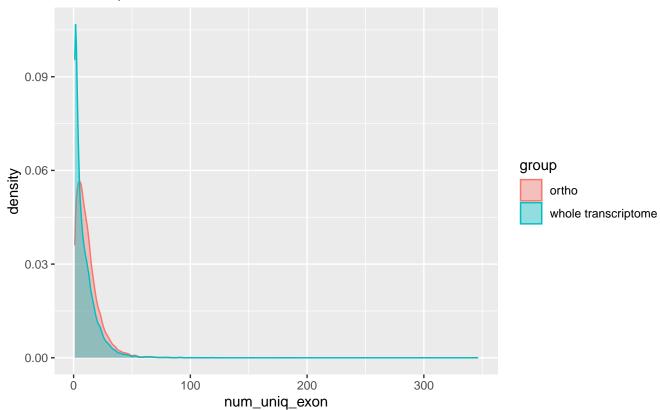
group

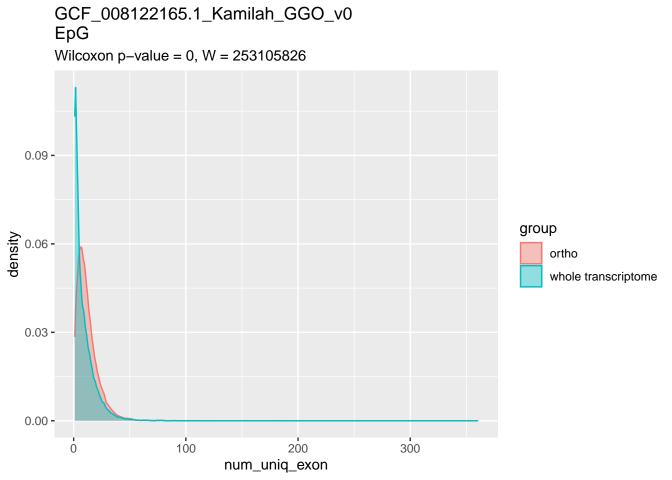
ortho

whole transcriptome

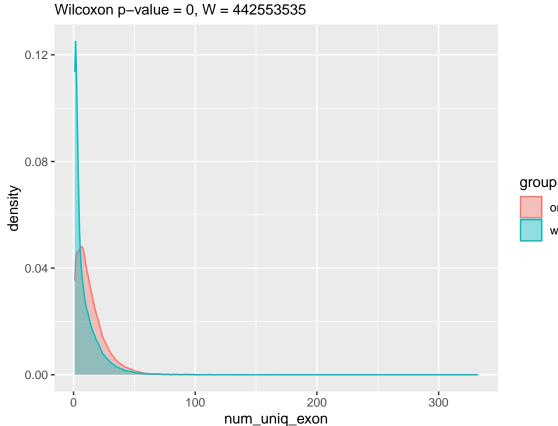
GCF_006542625.1_Asia_NLE_v1 EpG

Wilcoxon p-value = 0, W = 325375215



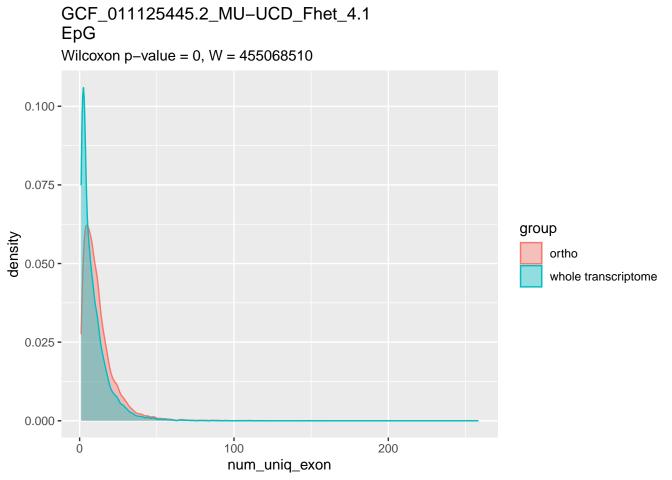


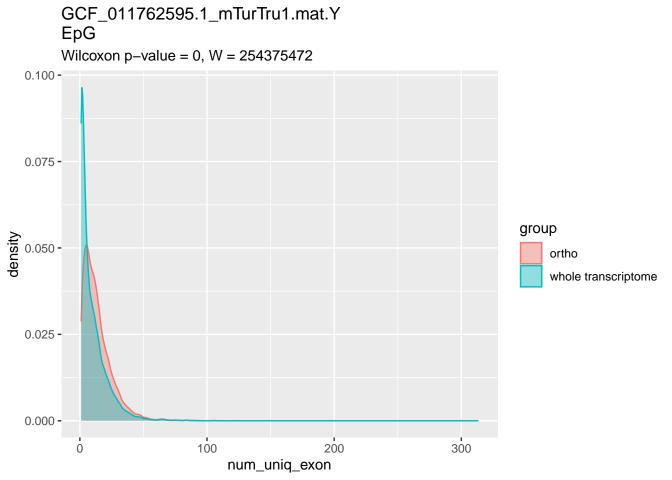
GCF_009663435.1_Callithrix_jacchus_cj1700_1.1 EpG

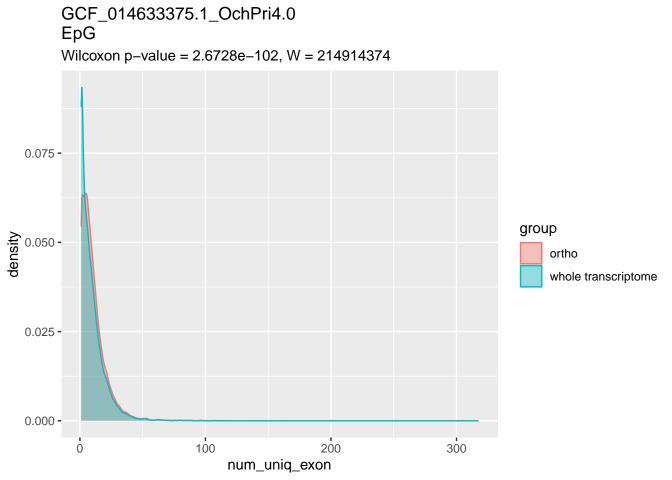


ortho

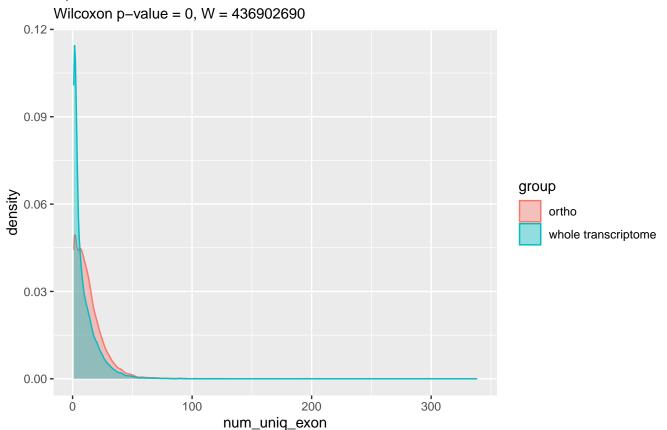
whole transcriptome



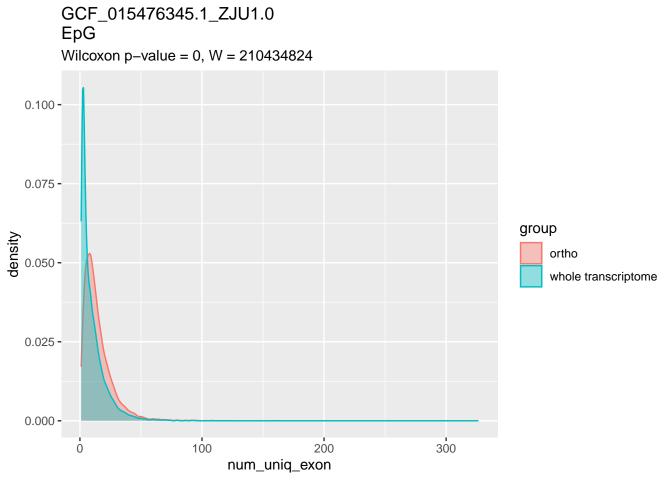




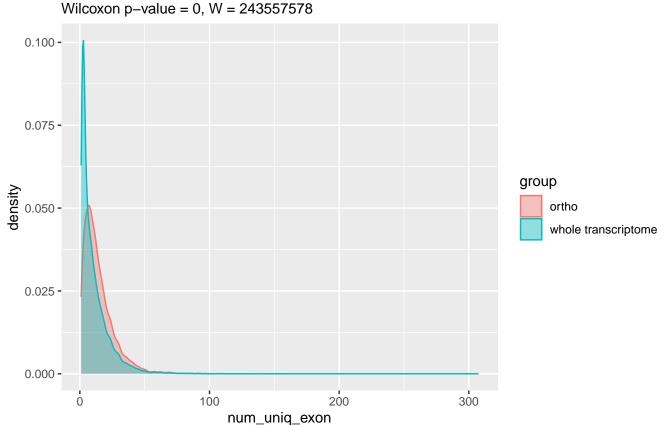
GCF_015227675.2_mRatBN7.2 EpG

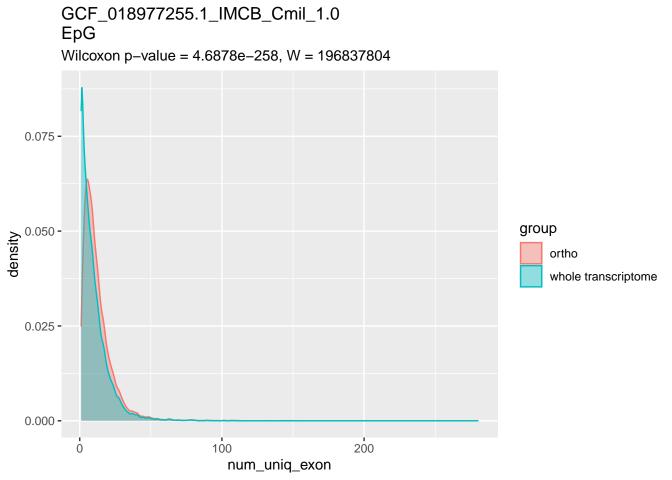


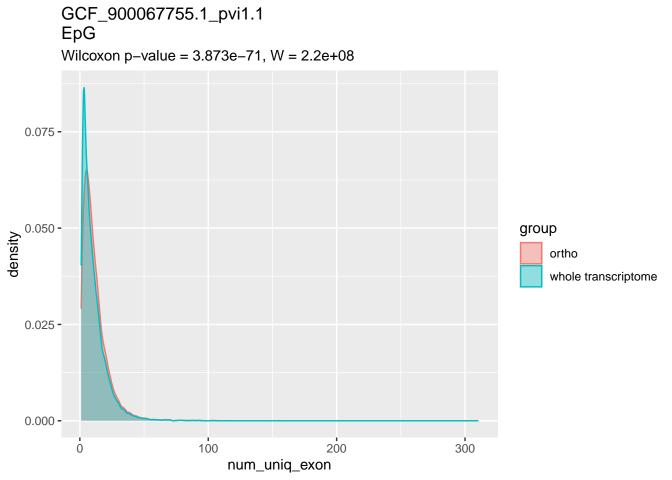
GCF_015237465.2_rCheMyd1.pri.v2 EpG Wilcoxon p-value = 0, W = 289281082 0.100 -0.075 group density 0.050 ortho whole transcriptome 0.025 -0.000 -100 200 300 num_uniq_exon



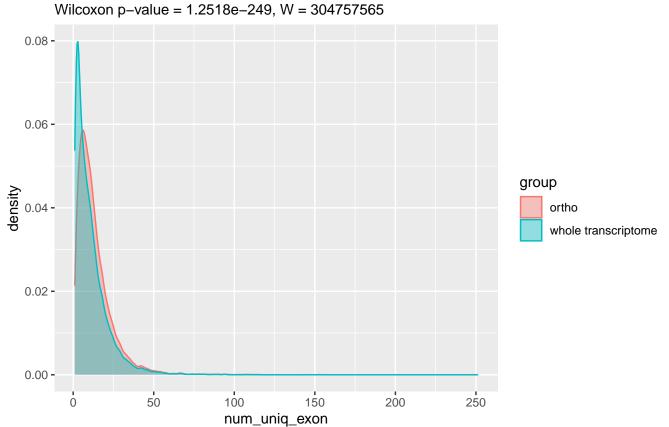
GCF_016699485.2_bGalGal1.mat.broiler.GRCg7b EpG

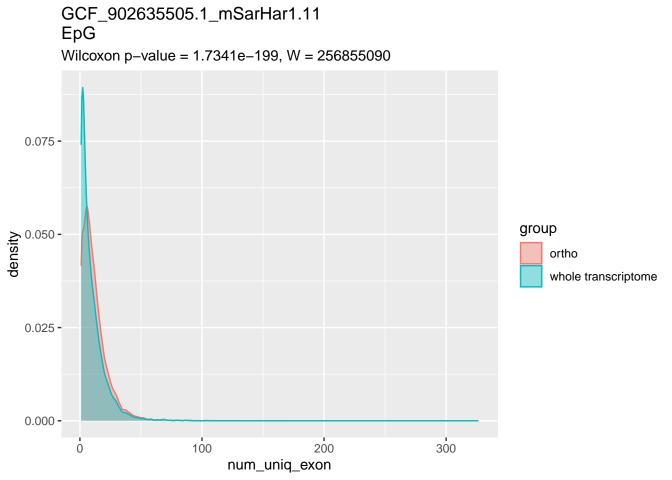




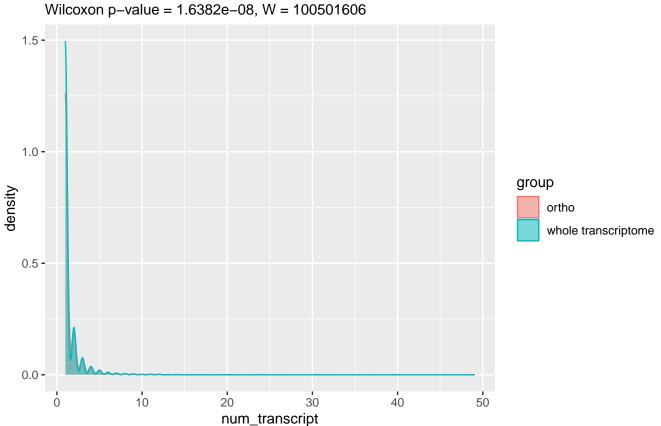


GCF_901000725.2_fTakRub1.2 EpG

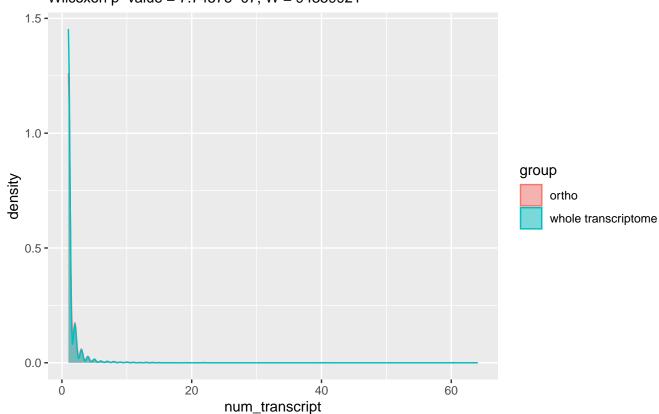


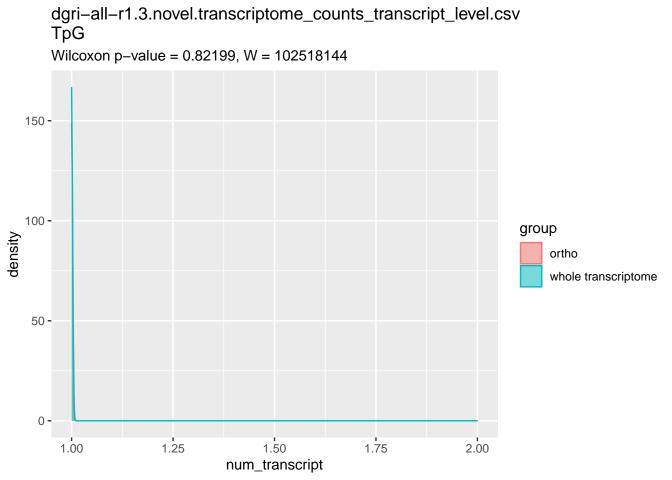


dana-all-r1.04.novel.transcriptome_counts_transcript_level.csv TpG

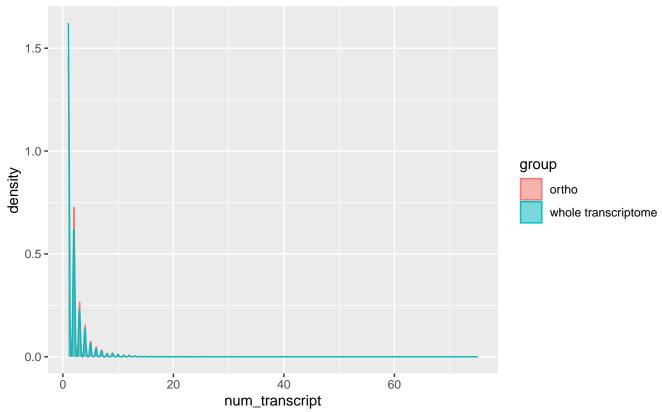


dere-all-r1.04.novel.transcriptome_counts_transcript_level.csv TpG Wilcoxon p-value = 7.7457e-07, W = 94359921





dmel-all-r6.07.novel.transcriptome_counts_transcript_level.csv TpG Wilcoxon p-value = 2.5723e-52, W = 1.29e+08

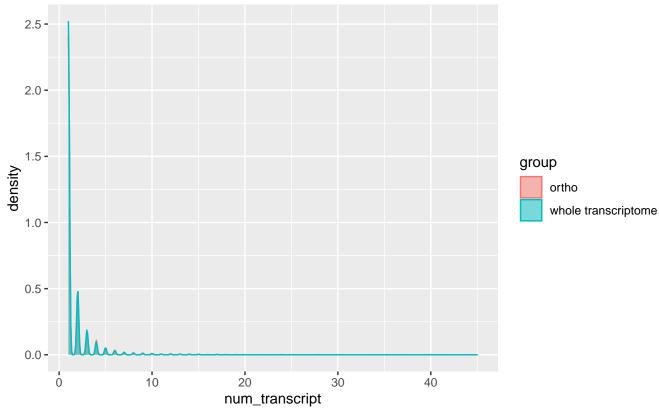


dmoj-all-r1.04.novel.transcriptome_counts_transcript_level.csv TpG Wilcoxon p-value = 0.00014577, W = 893056831.0 group density ortho whole transcriptome 0.5 -0.0 -20 40 60 num_transcript

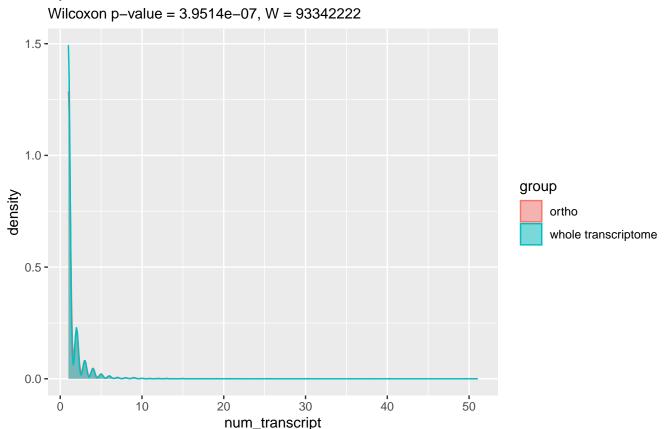
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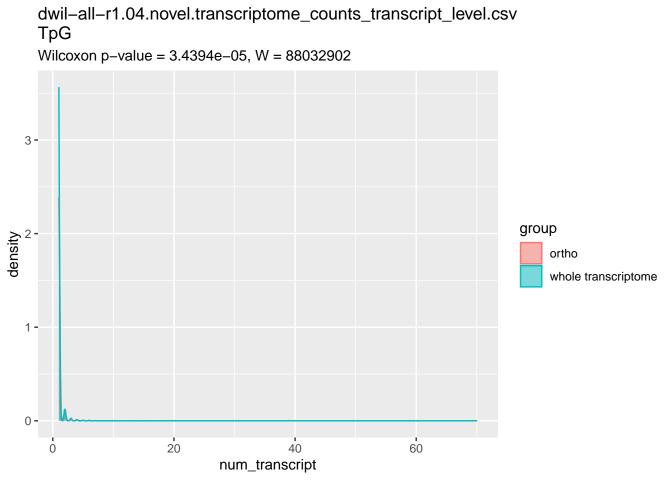
dsec-all-r1.3.novel.transcriptome_counts_transcript_level.csv TpG Wilcoxon p-value = 0.76122, W = 119305548 200 -150 group density ortho whole transcriptome 50 -0 -1.25 1.00 1.50 1.75 2.00 num_transcript

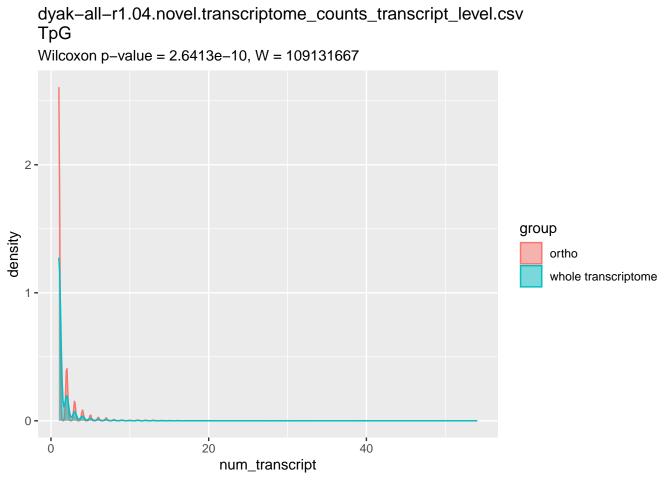
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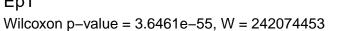
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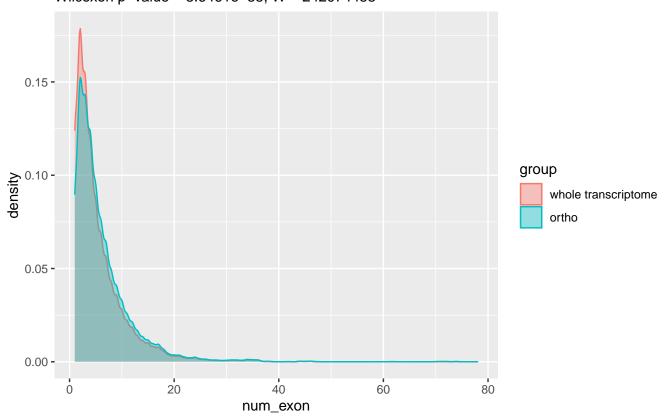




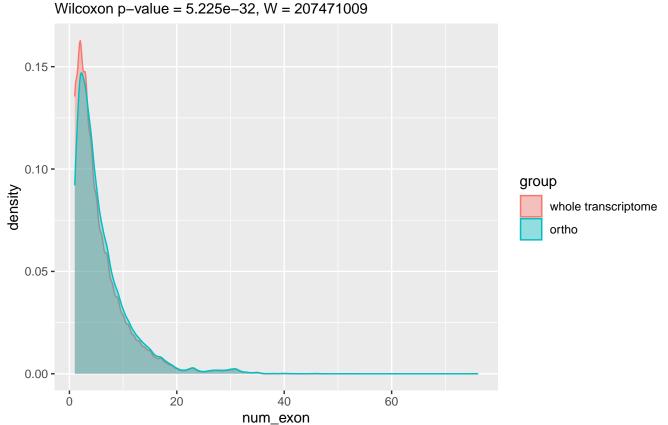


dana-all-r1.04.novel.transcriptome_counts_transcript_level.csv EpT

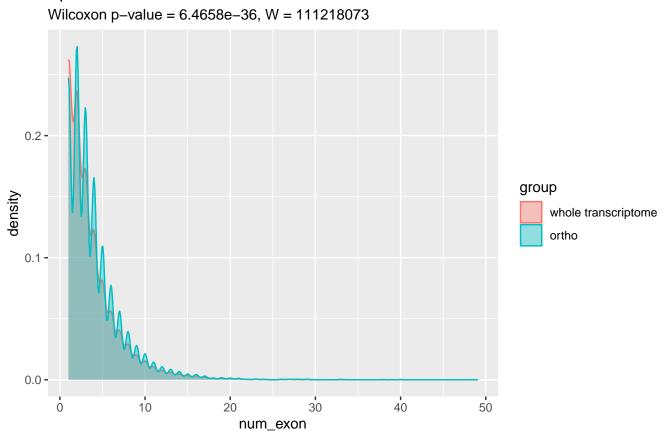




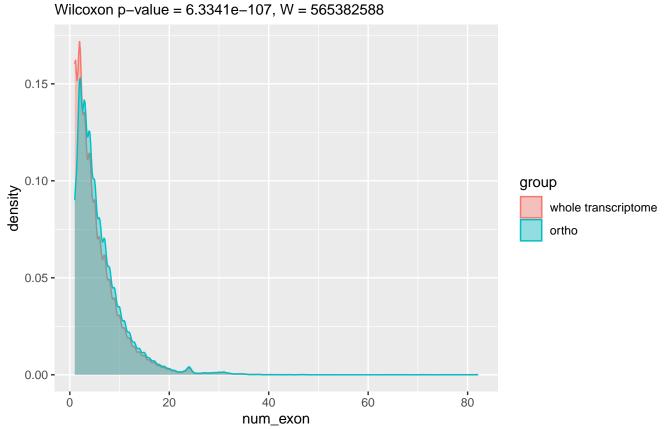
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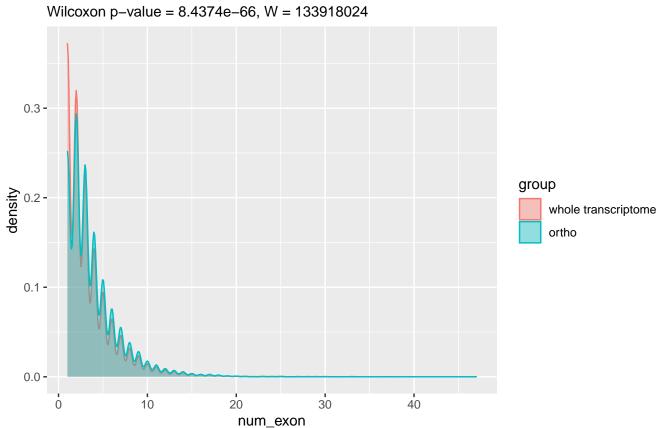
dmel-all-r6.07.novel.transcriptome_counts_transcript_level.csv EpT



dmoj-all-r1.04.novel.transcriptome_counts_transcript_level.csv EpT Wilcoxon p-value = 3.1819e-37, W = 2171794200.15 -0.10 group whole transcriptome ortho 0.05 -0.00 -20 40 60 num_exon

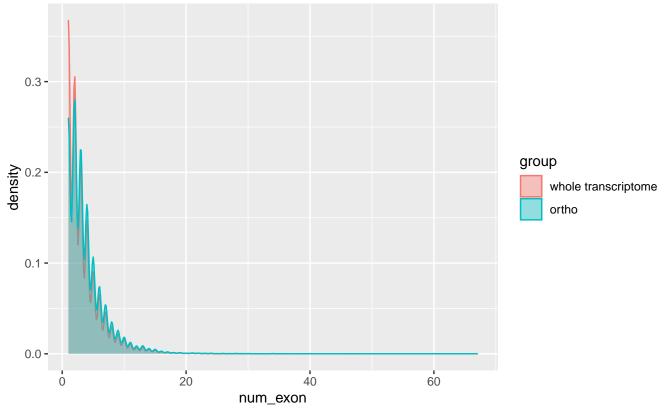
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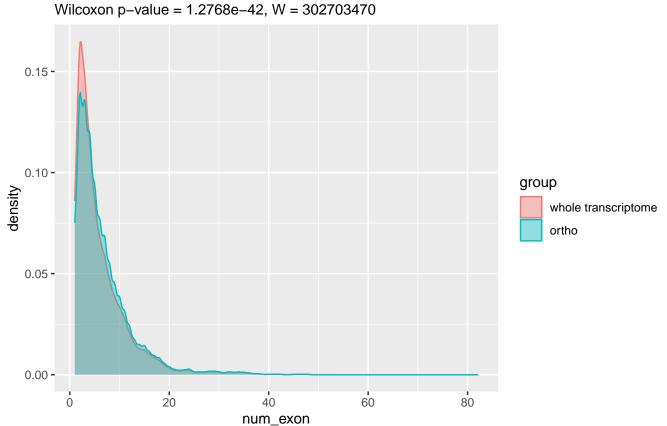


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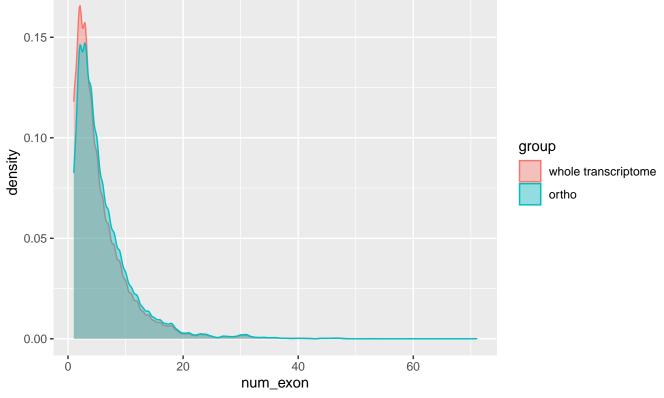
Wilcoxon p-value = 1.3151e-64, W = 132493764



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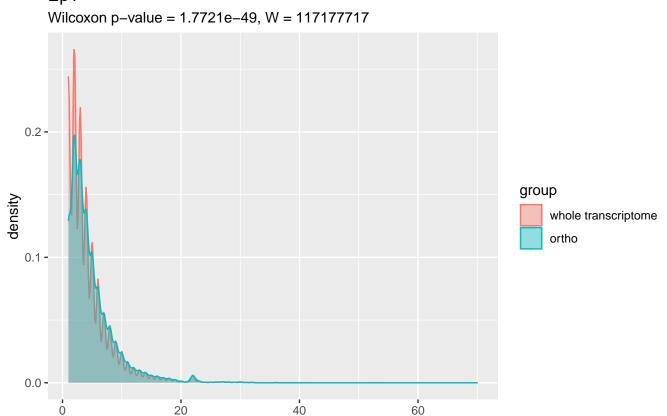


dvir-all-r1.03.novel.transcriptome_counts_transcript_level.csv **EpT** Wilcoxon p-value = 8.2806e-49, W = 230739586group whole transcriptome ortho

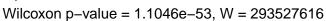


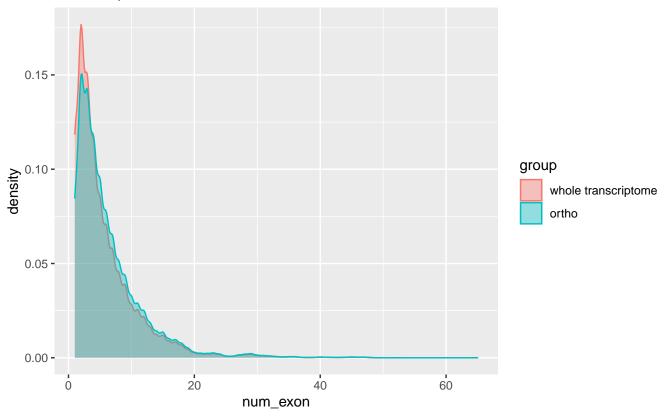
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num_exon



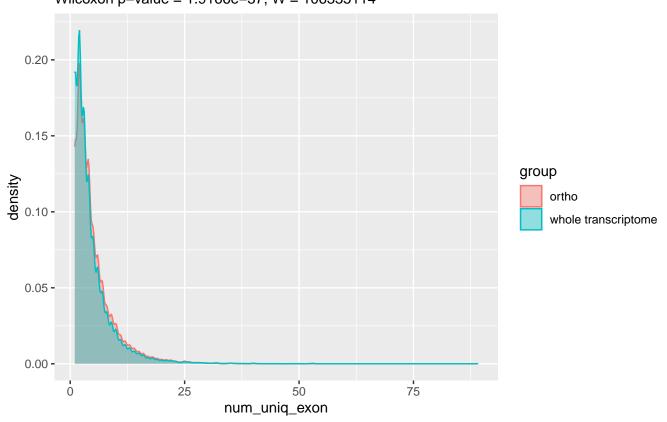
dyak-all-r1.04.novel.transcriptome_counts_transcript_level.csv EpT





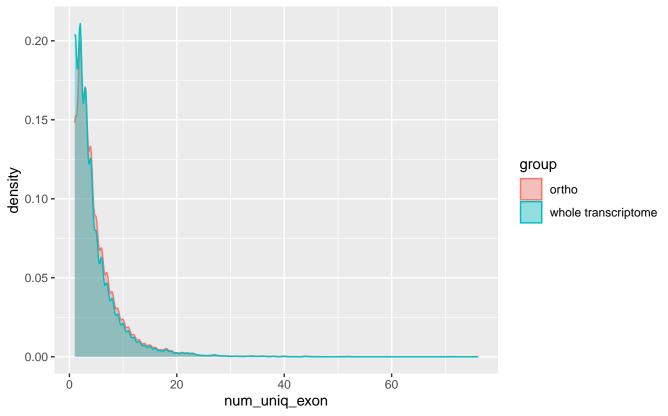
dana-all-r1.04.novel.transcriptome_counts_transcript_level.csv EpG

Wilcoxon p-value = 1.9166e-37, W = 106335114



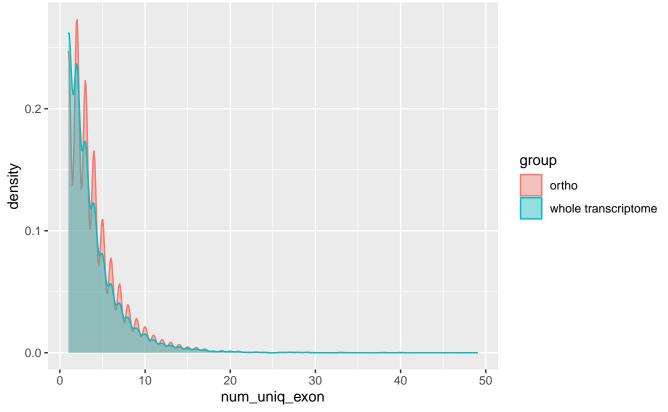
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Wilcoxon p-value = 5.5947e-29, W = 99357731

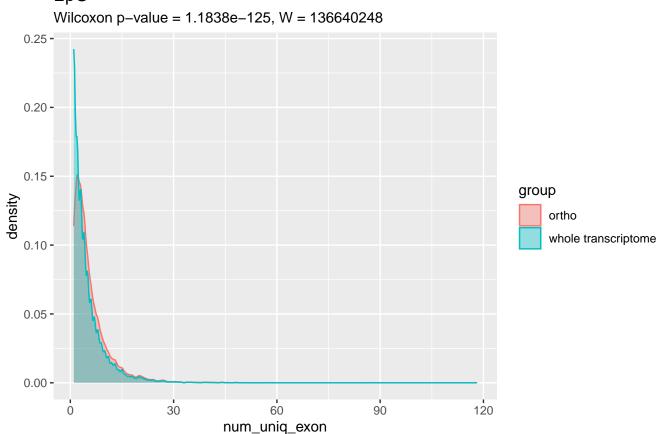


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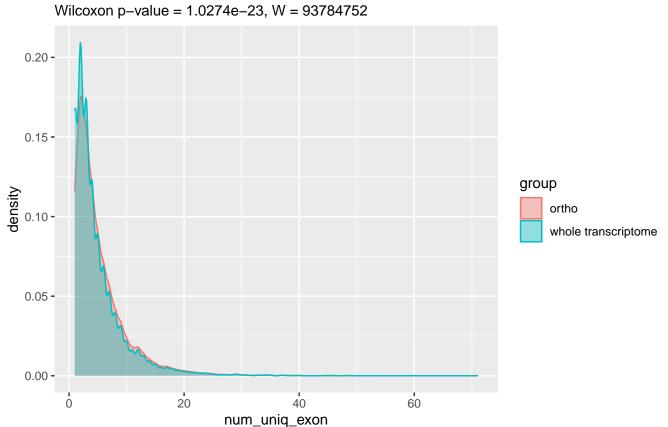
Wilcoxon p-value = 6.5294e-36, W = 111156382



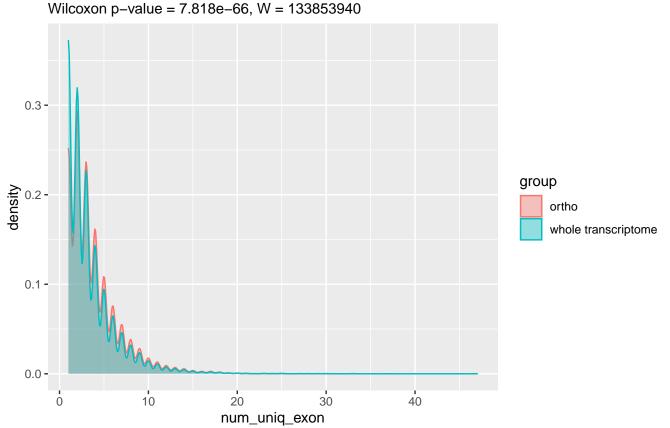
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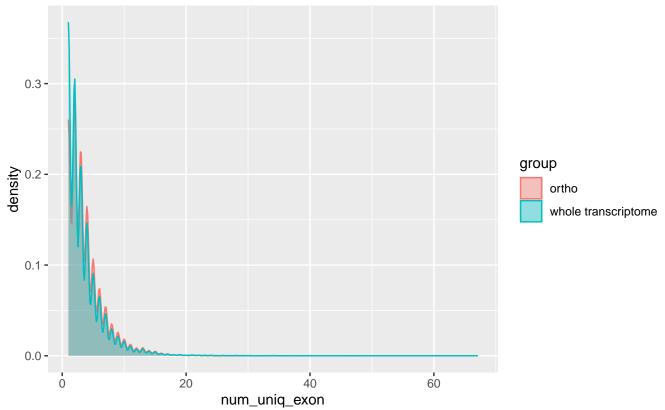


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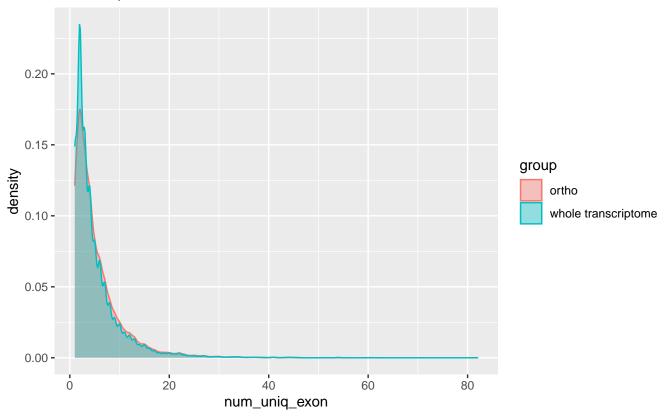
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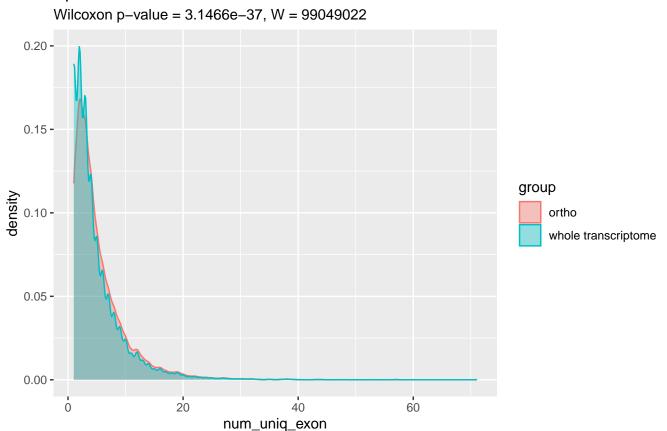


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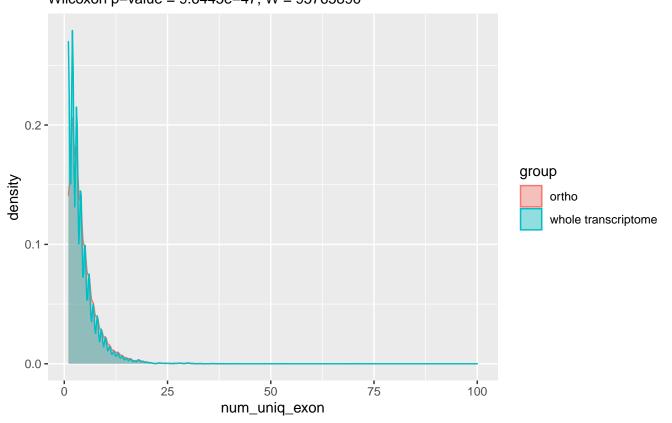


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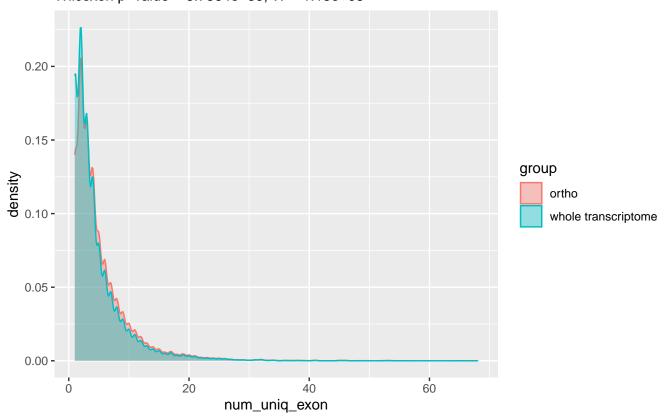
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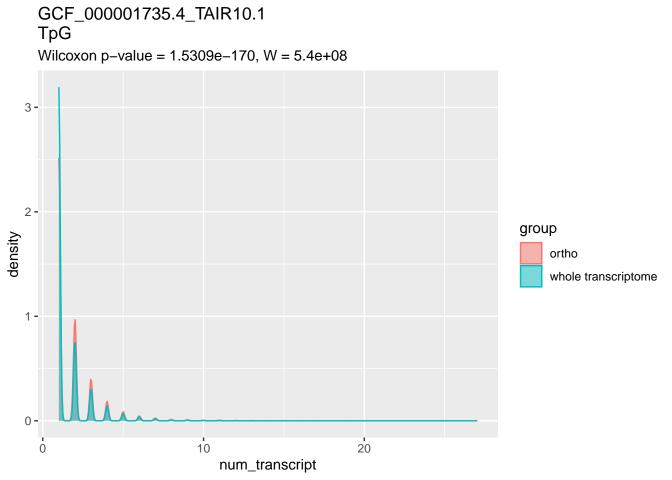
EpG Wilcoxon p-value = 9.6445e-47, W = 95765890

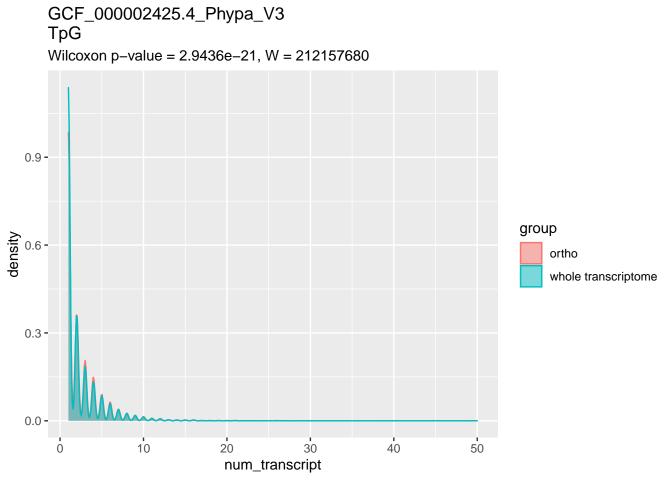


dyak-all-r1.04.novel.transcriptome_counts_transcript_level.csv EpG

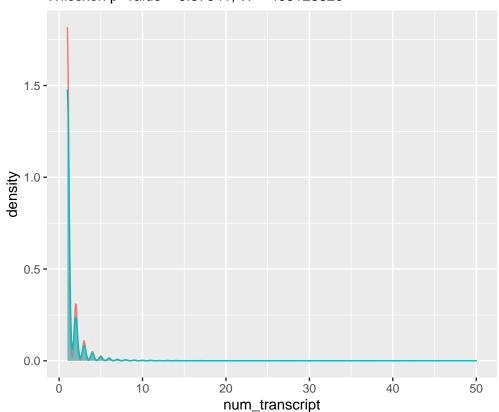
. Wilcoxon p-value = 8.7364e-39, W = 1.15e+08







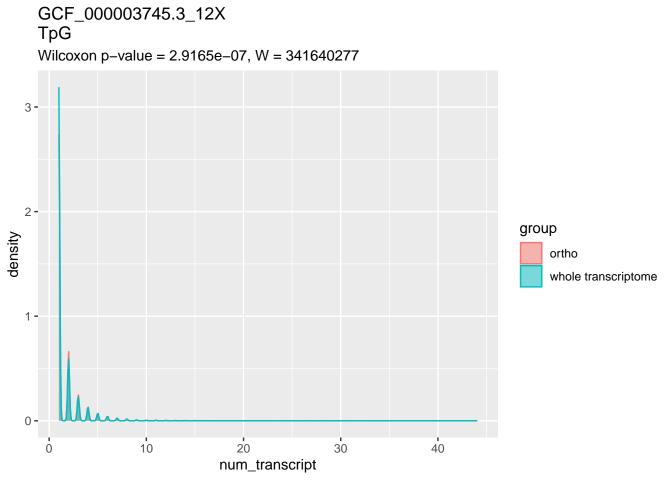
GCF_000003195.3_Sorghum_bicolor_NCBIv3 TpG Wilcoxon p-value = 0.37941, W = 405128820

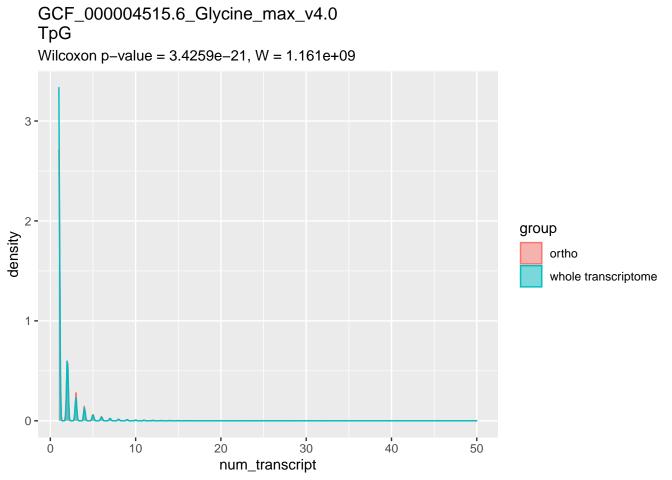


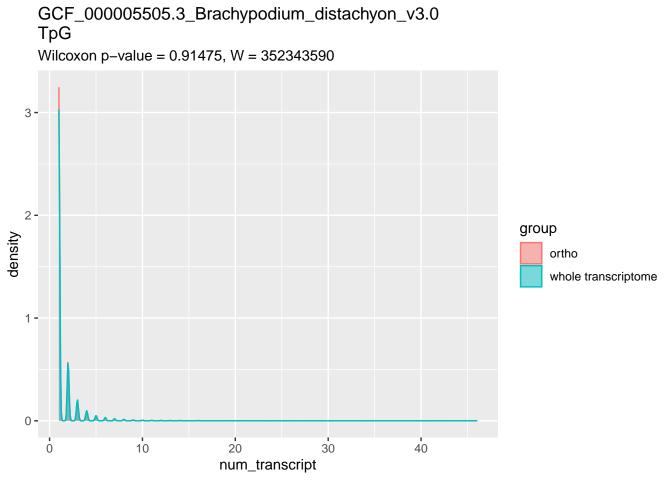
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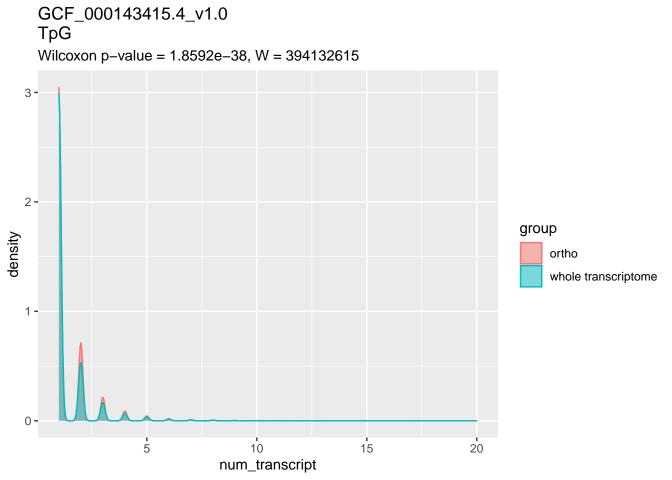
ortho

whole transcriptome

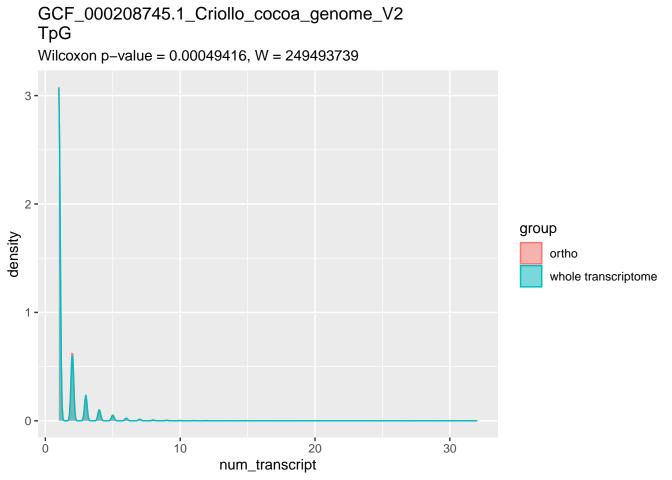






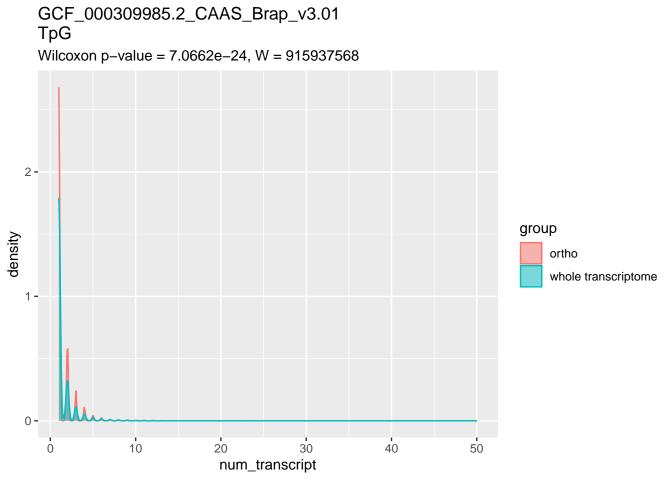


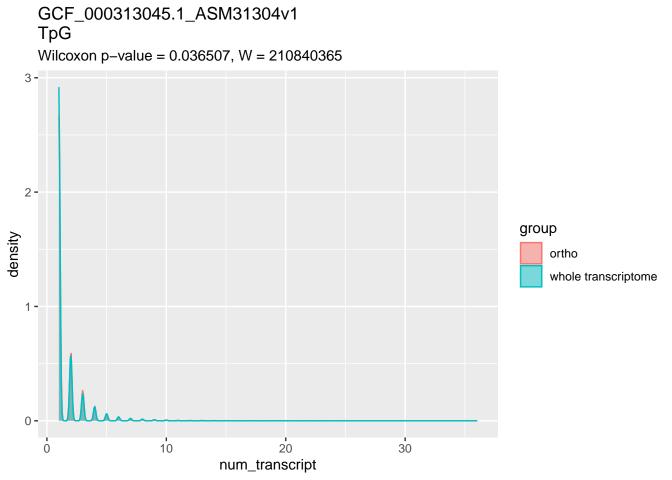
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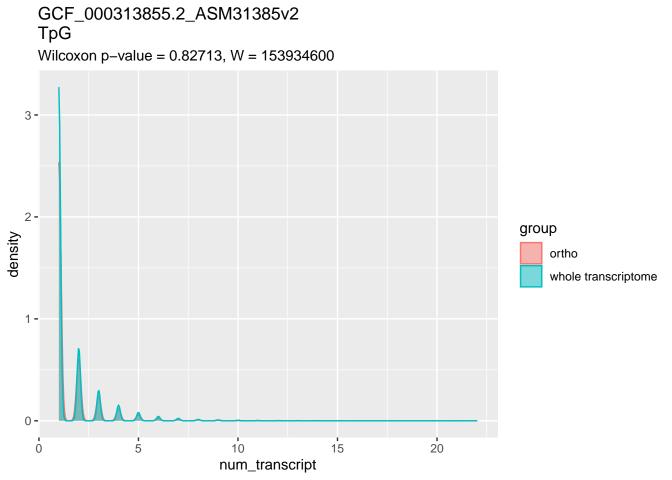


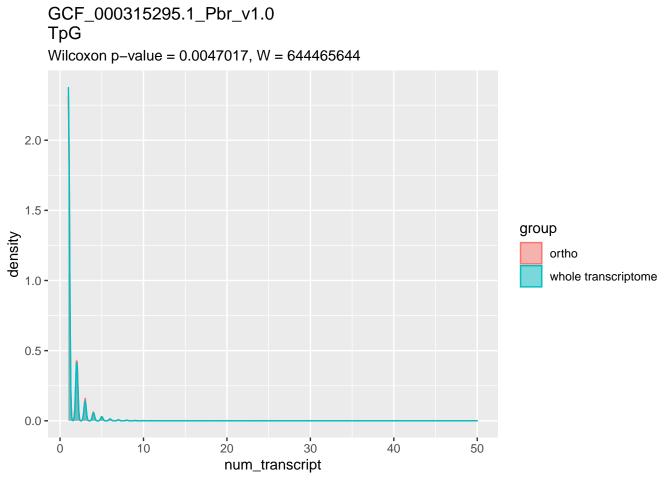
GCF_000226075.1_SolTub_3.0 TpG Wilcoxon p-value = 0.51236, W = 4.22e+082.5 -2.0 -1.5 group density ortho whole transcriptome 1.0 -0.5 -10 20 30 40 50

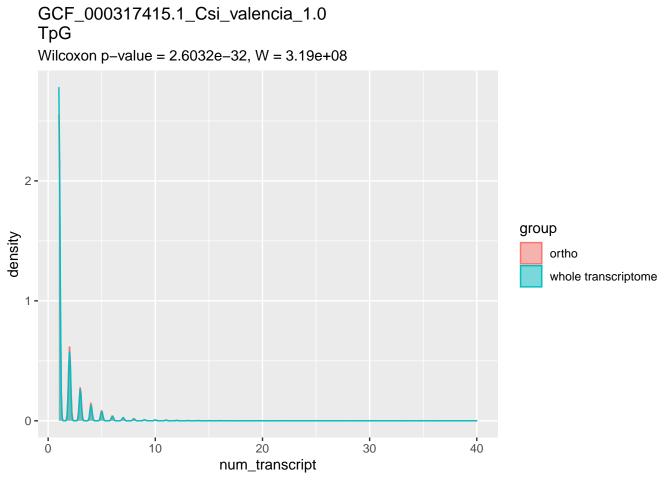
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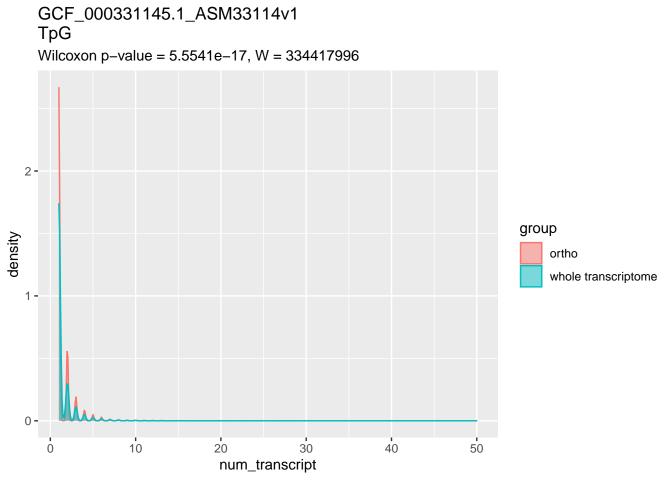


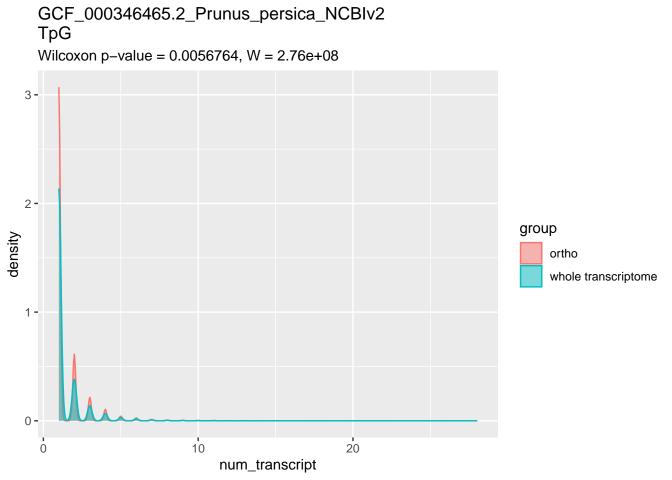


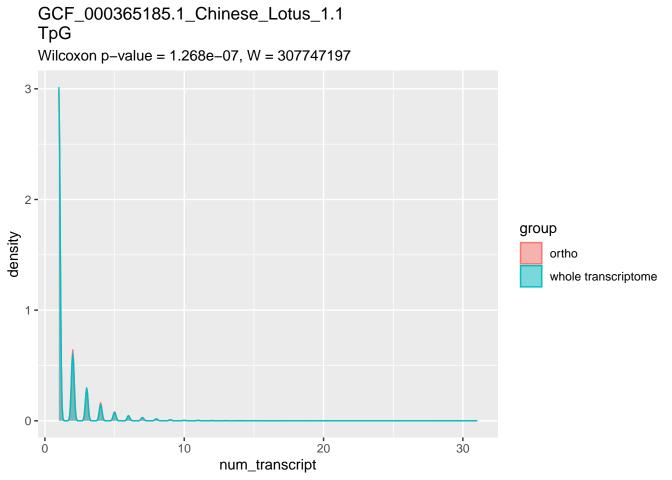




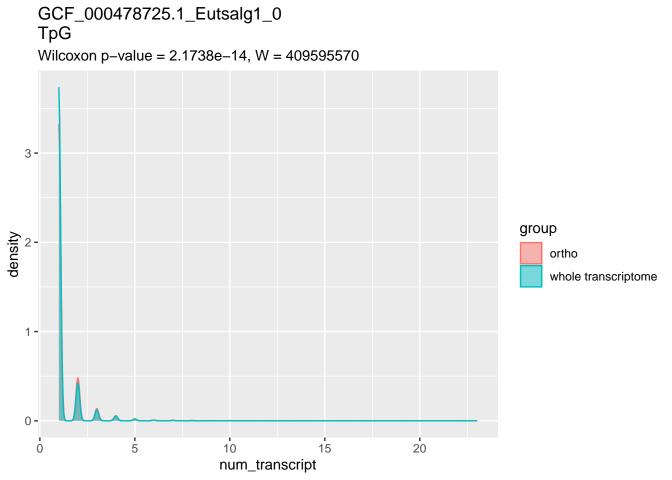


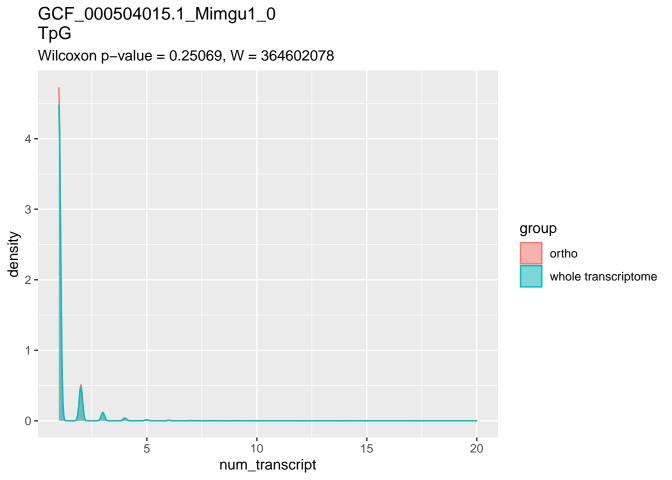




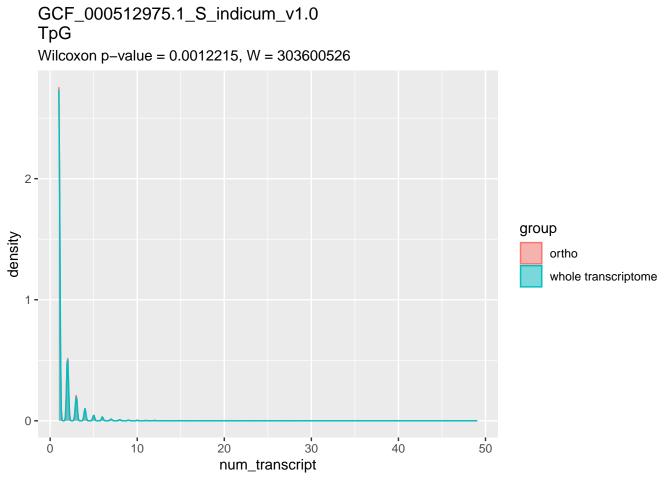


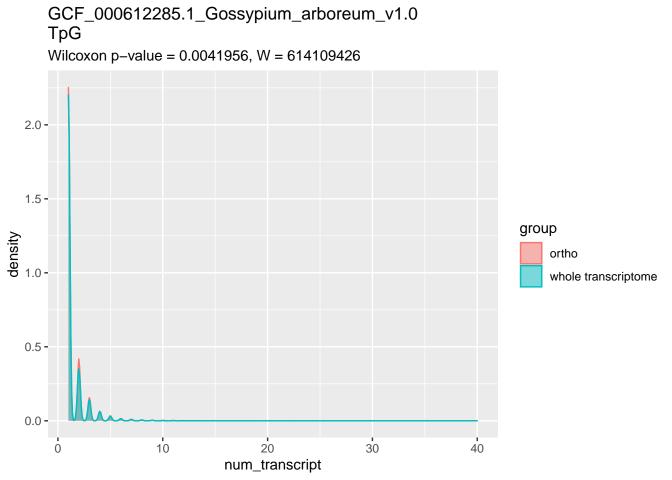
GCF_000471905.2_AMTR1.0 TpG Wilcoxon p-value = 1.076e-07, W = 1496997062.5 -2.0 -1.5 group density ortho whole transcriptome 1.0 -0.5 -10 20 30 40 50 num_transcript

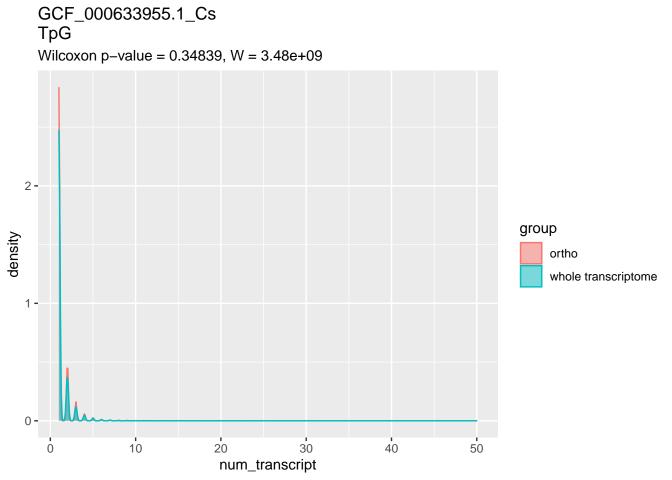


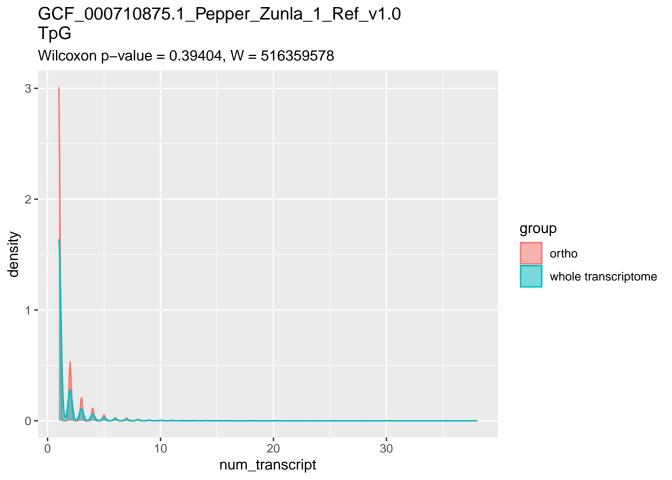


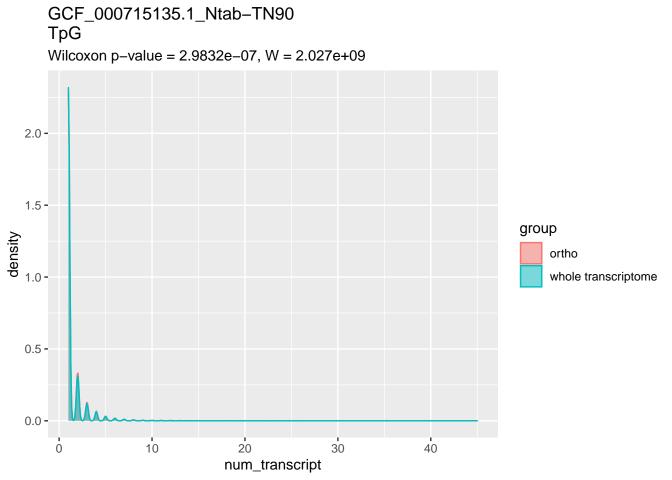
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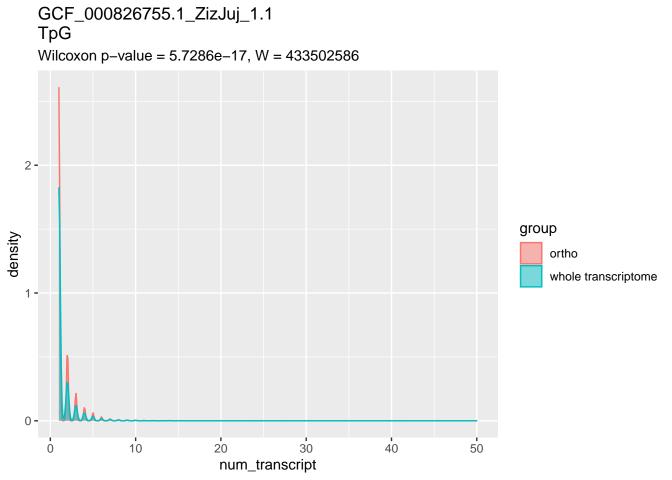


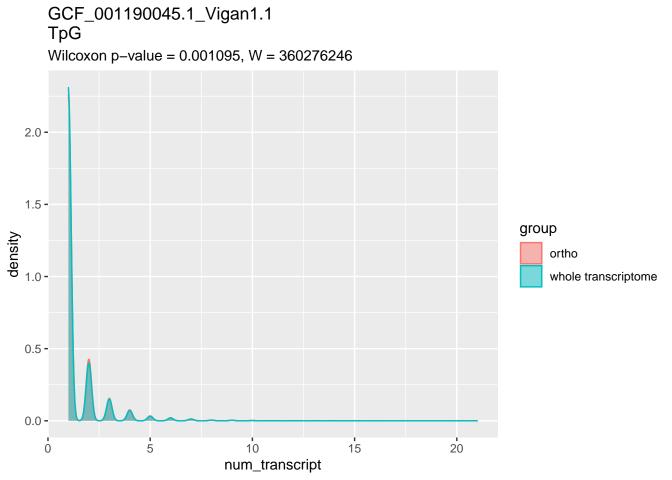


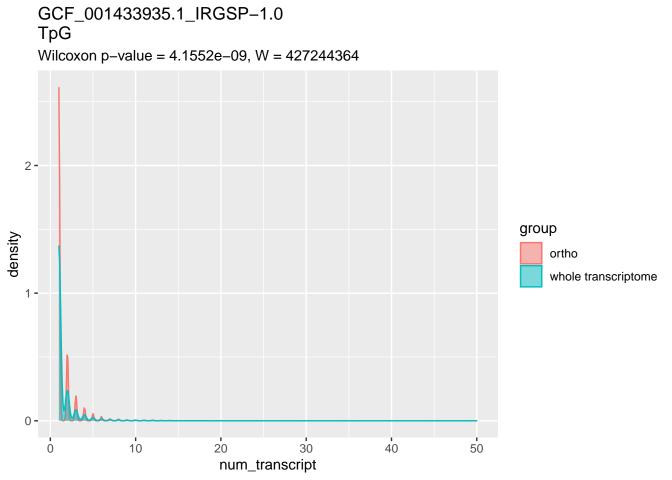


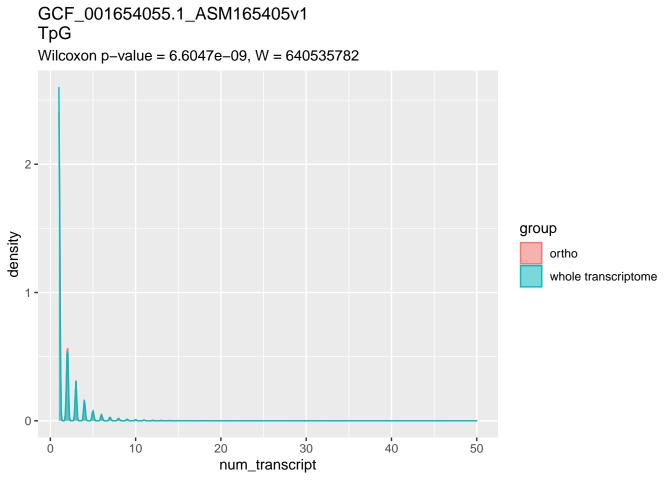




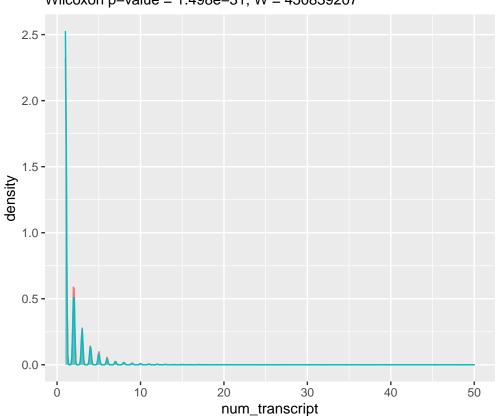








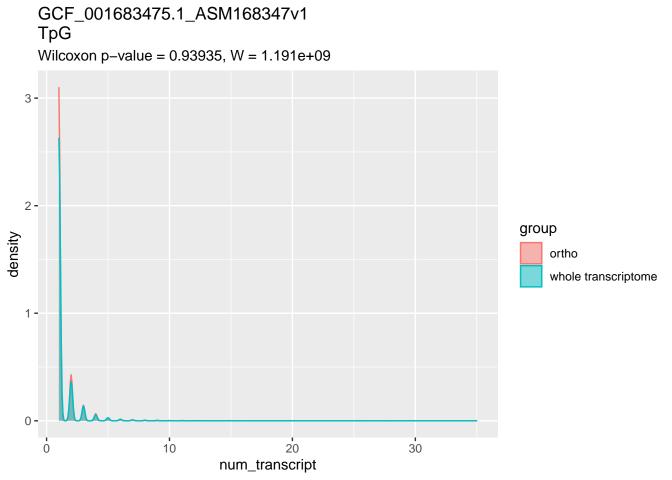
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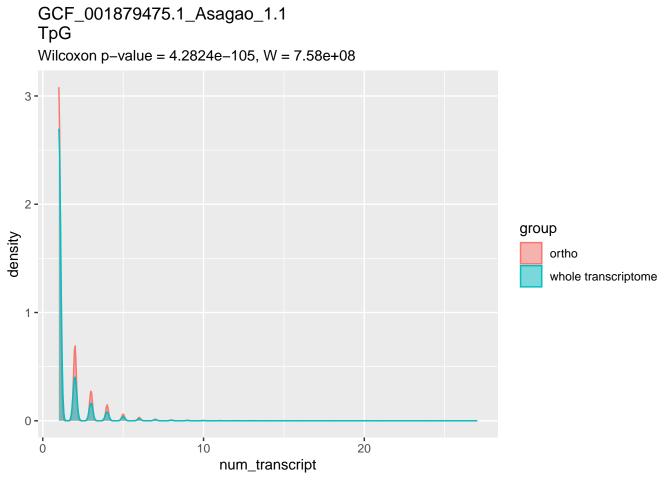


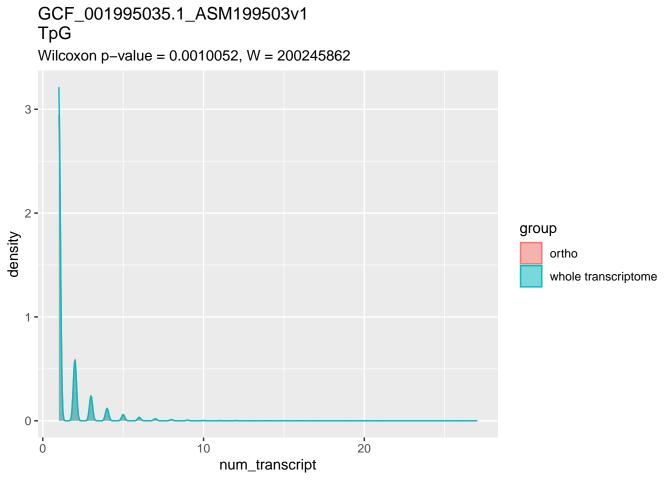
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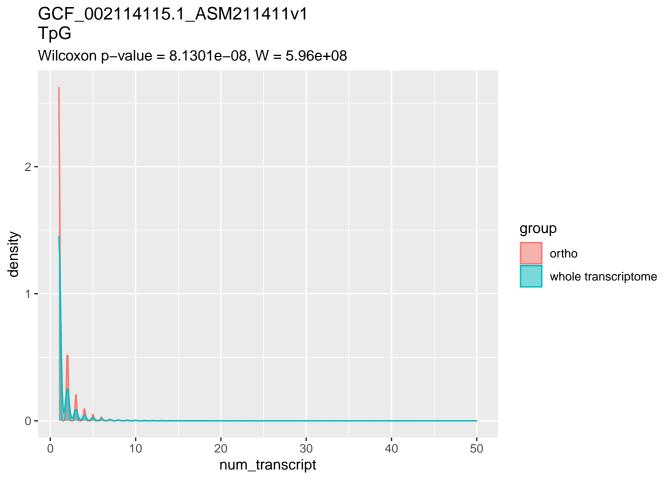
ortho

whole transcriptome

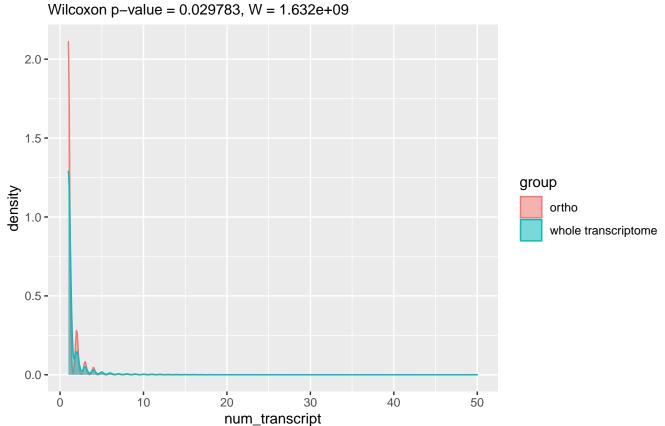


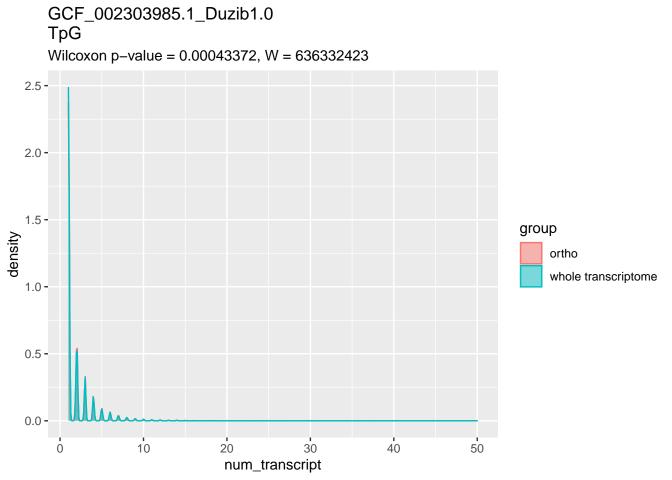


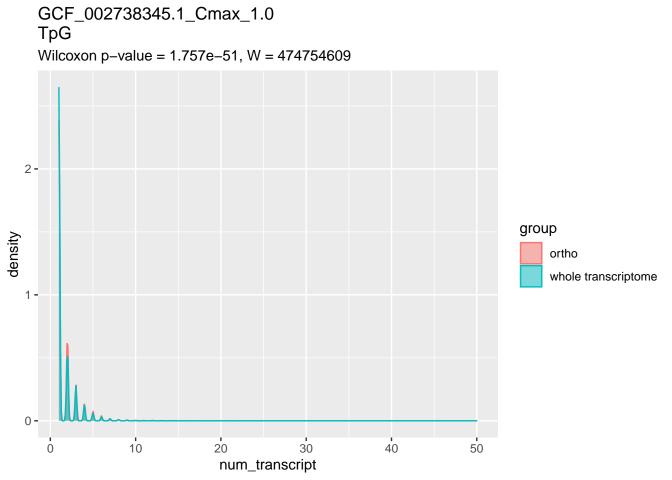


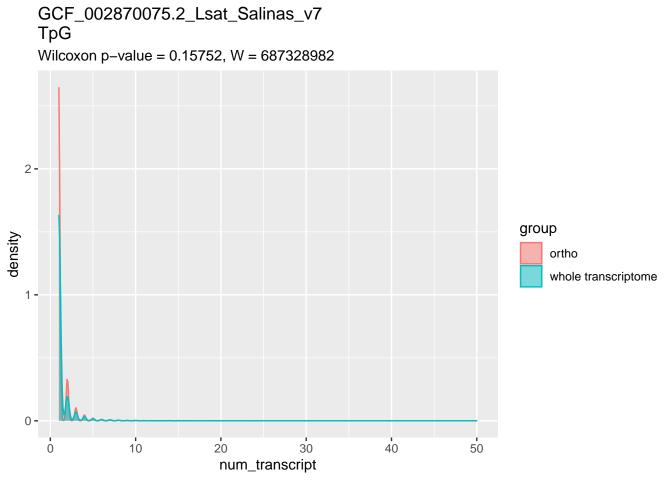


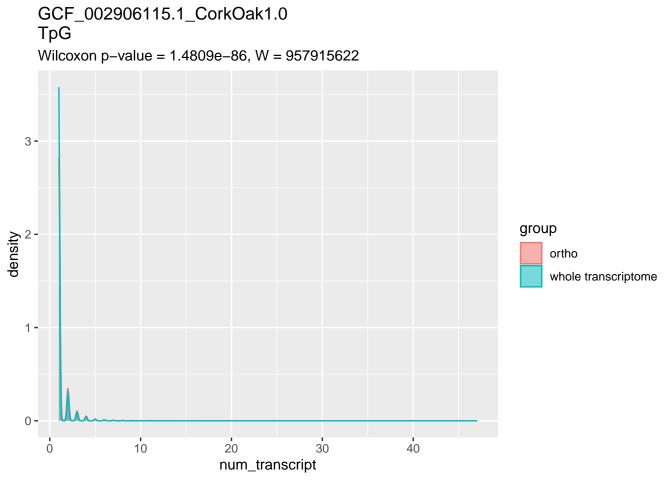
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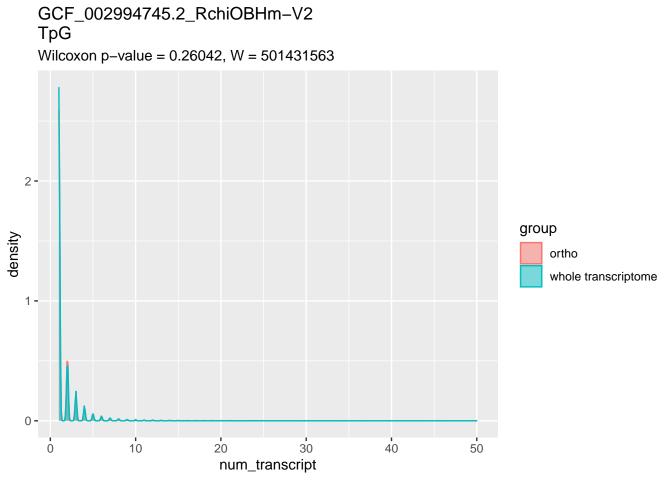


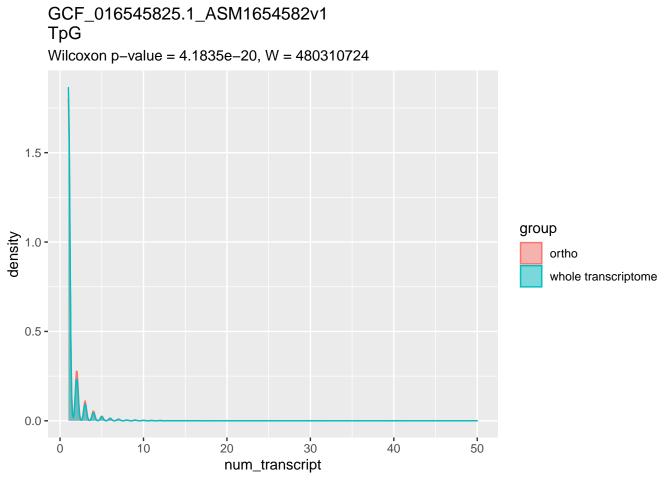




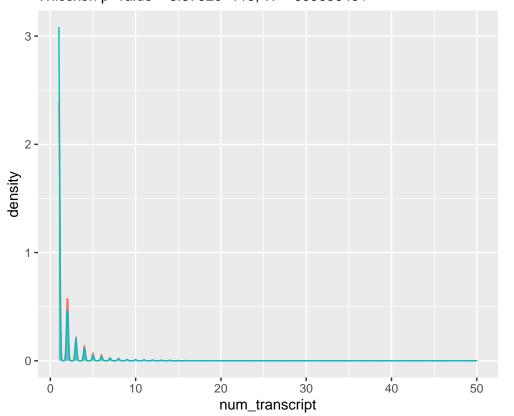








GCF_902167145.1_Zm-B73-REFERENCE-NAM-5.0 TpG Wilcoxon p-value = 3.3792e-113, W = 695636431

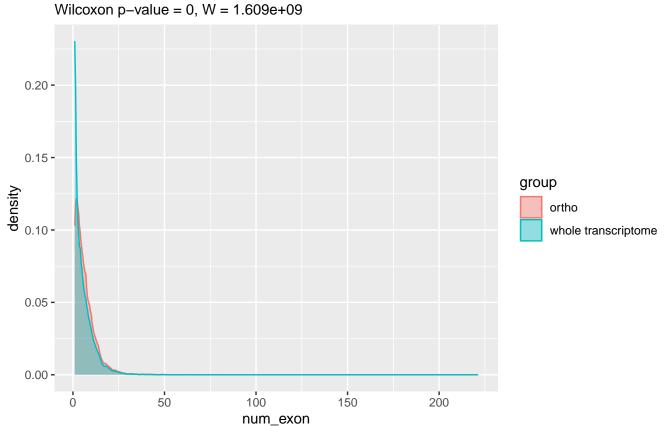


group

ortho

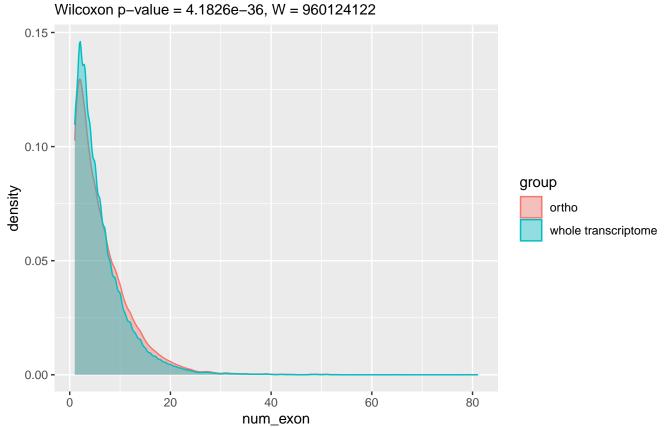
whole transcriptome

GCF_000001735.4_TAIR10.1 EpT



GCF_000002425.4_Phypa_V3 **EpT** Wilcoxon p-value = 6.6779e-167, W = 1.35e+09 0.100 -0.075 group density 0.050 ortho whole transcriptome 0.025 -0.000 -20 40 60 80 num_exon

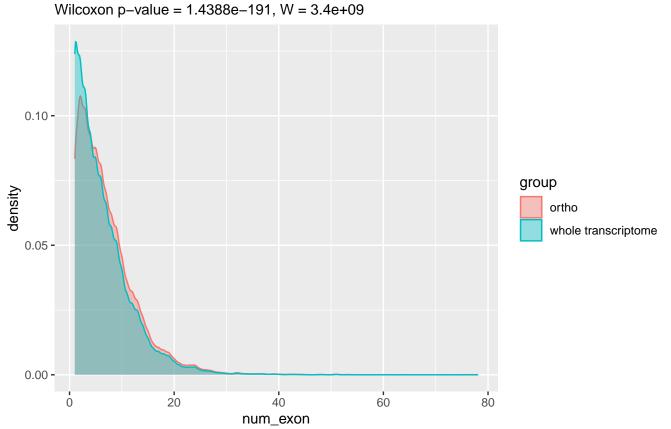
GCF_000003195.3_Sorghum_bicolor_NCBIv3 EpT



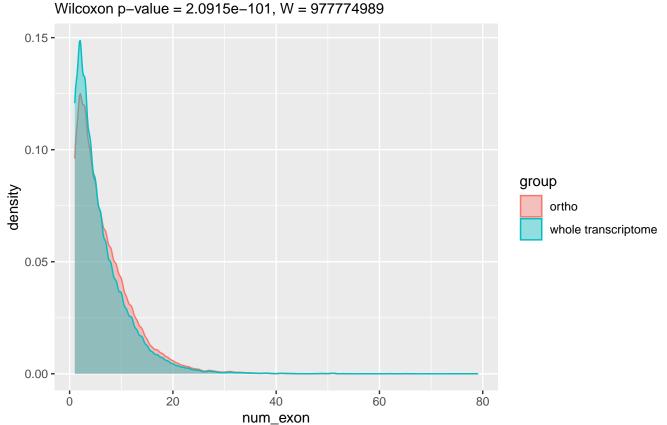
GCF_000003745.3_12X **EpT** Wilcoxon p-value = 6.0129e-61, W = 1.013e+090.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80

num_exon

GCF_000004515.6_Glycine_max_v4.0 EpT



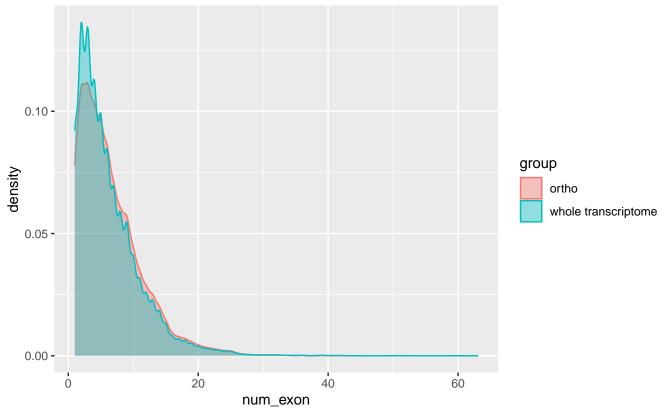
GCF_000005505.3_Brachypodium_distachyon_v3.0 EpT



GCF_000143415.4_v1.0 **EpT** Wilcoxon p-value = 0, W = 8755414270.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80 num_exon

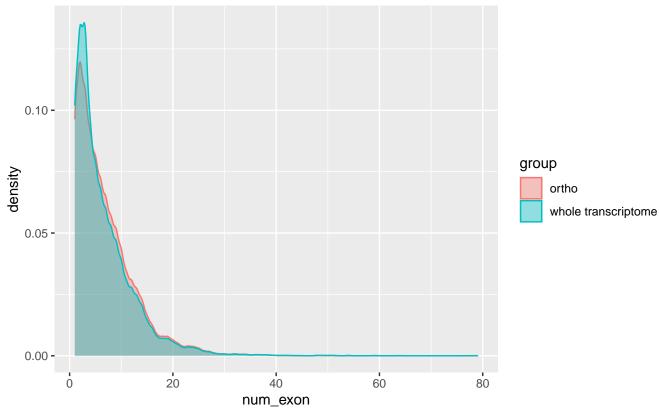
GCF_000150535.2_Papaya1.0 EpT

Wilcoxon p-value = 2.1857e-32, W = 410716315



GCF_000208745.1_Criollo_cocoa_genome_V2 EpT

Wilcoxon p-value = 1.7635e-29, W = 574331424



GCF_000226075.1_SolTub_3.0 **EpT** Wilcoxon p-value = 3.1217e-47, W = 865174096 0.15 -0.10 group ortho whole transcriptome 0.05 -0.00 -20 40 60 80

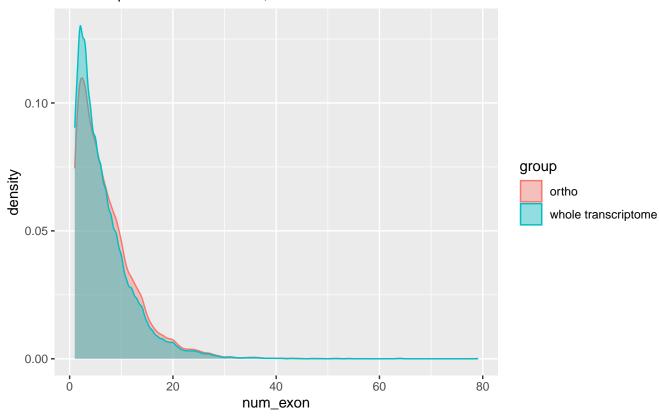
num_exon

density

GCF_000309985.2_CAAS_Brap_v3.01 **EpT** Wilcoxon p-value = 4.2308e-227, W = 2.225e+09 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80 num_exon

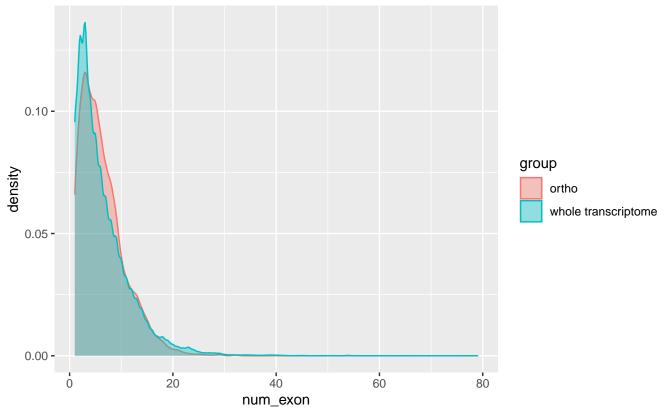
GCF_000313045.1_ASM31304v1 EpT





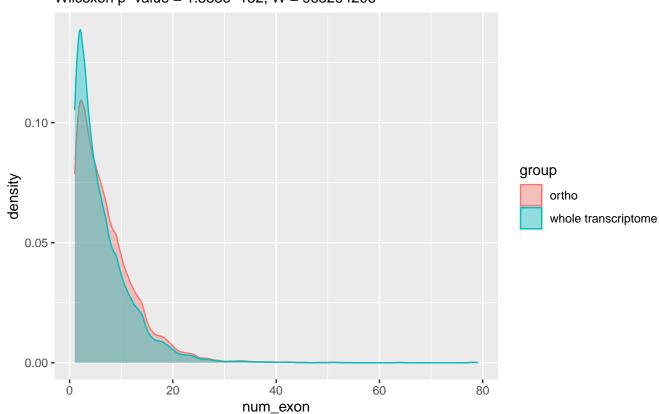
GCF_000313855.2_ASM31385v2 EpT

Wilcoxon p-value = 3.5778e-22, W = 414855524

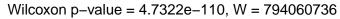


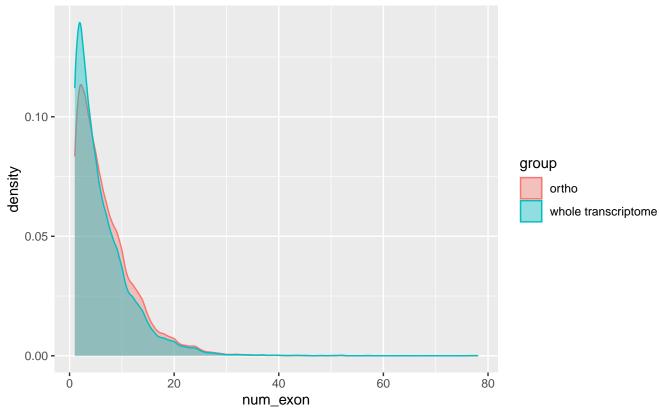
GCF_000315295.1_Pbr_v1.0 **EpT** Wilcoxon p-value = 2.1632e-34, W = 1.308e+090.10 group density ortho whole transcriptome 0.05 -0.00 -30 60 90 num_exon

GCF_000317415.1_Csi_valencia_1.0 EpT Wilcoxon p-value = 1.588e-152, W = 965294206

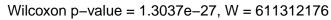


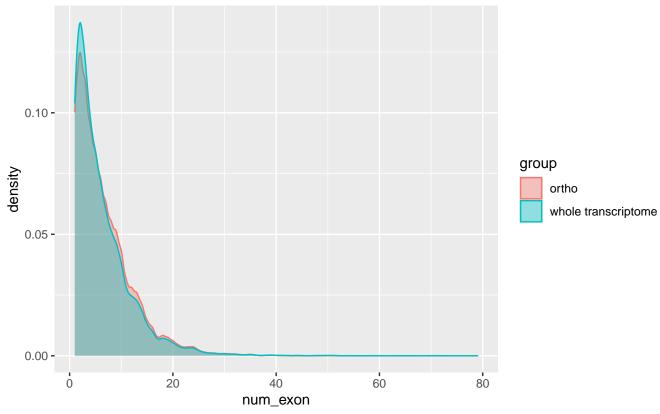
GCF_000331145.1_ASM33114v1 EpT



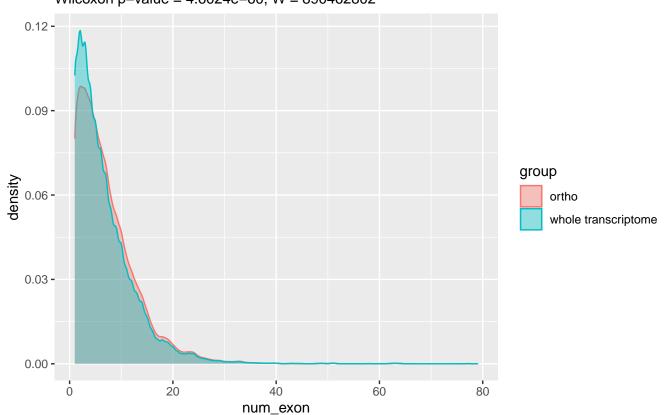


GCF_000346465.2_Prunus_persica_NCBIv2 EpT

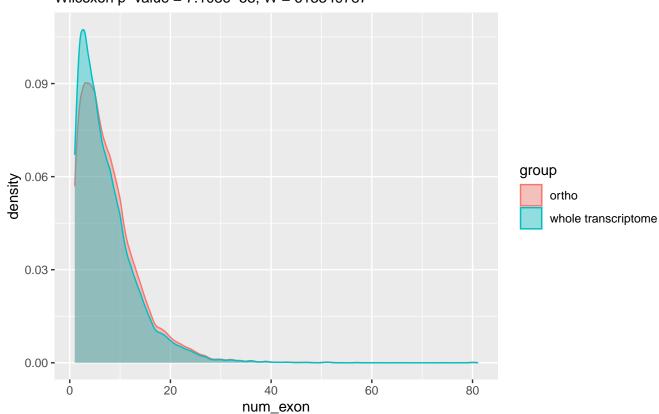




GCF_000365185.1_Chinese_Lotus_1.1 EpT Wilcoxon p-value = 4.6024e-60, W = 890462802



GCF_000471905.2_AMTR1.0 EpT Wilcoxon p-value = 7.108e-53, W = 613349787



GCF_000478725.1_Eutsalg1_0 **EpT** Wilcoxon p-value = 3.1891e-122, W = 702622725 0.20 -0.15 group density ortho whole transcriptome 0.05 -

60

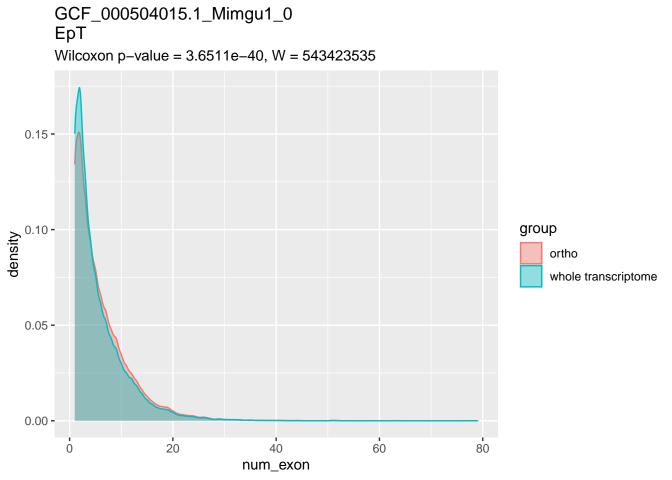
80

0.00 -

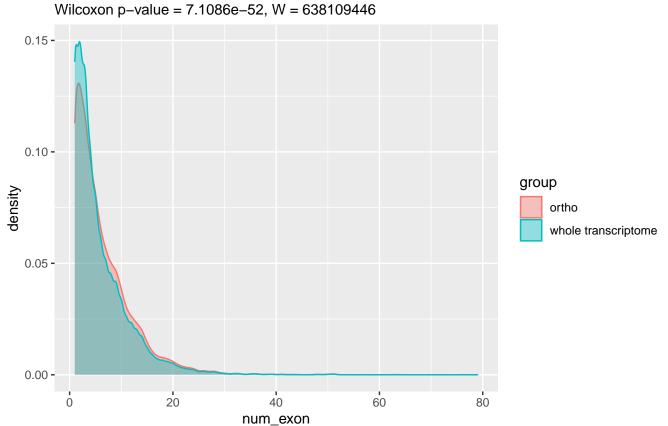
20

40

num_exon



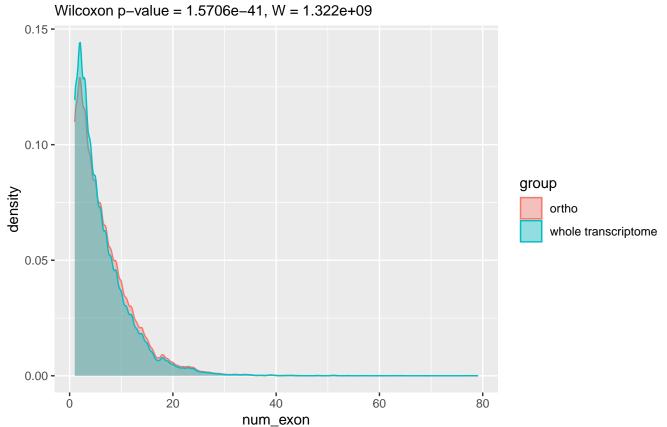
GCF_000511025.2_RefBeet-1.2.2 EpT

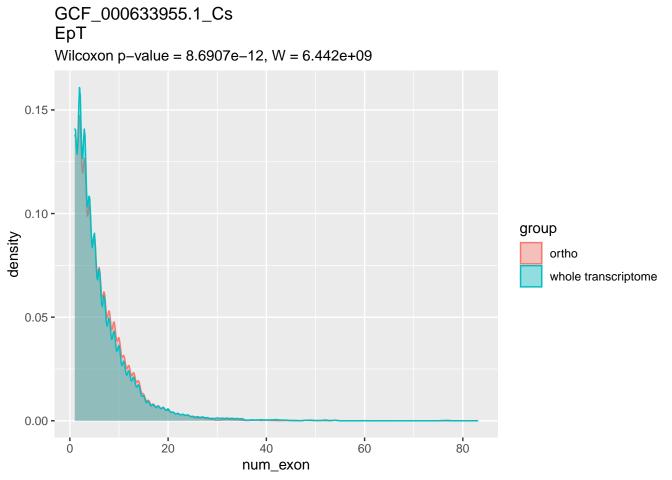


GCF_000512975.1_S_indicum_v1.0 **EpT** Wilcoxon p-value = 4.3093e-24, W = 726387150 0.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80

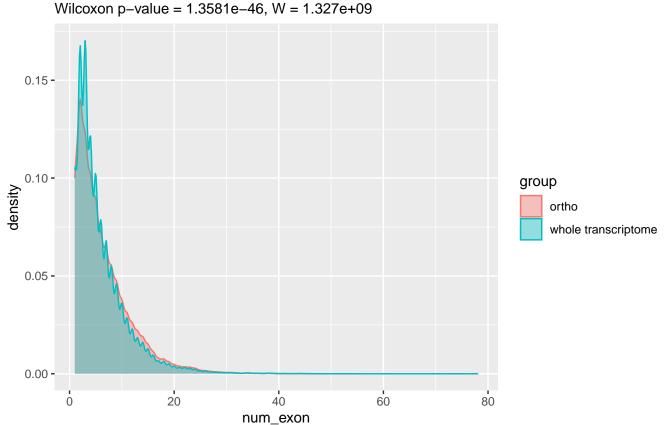
num_exon

GCF_000612285.1_Gossypium_arboreum_v1.0 EpT





GCF_000710875.1_Pepper_Zunla_1_Ref_v1.0 EpT

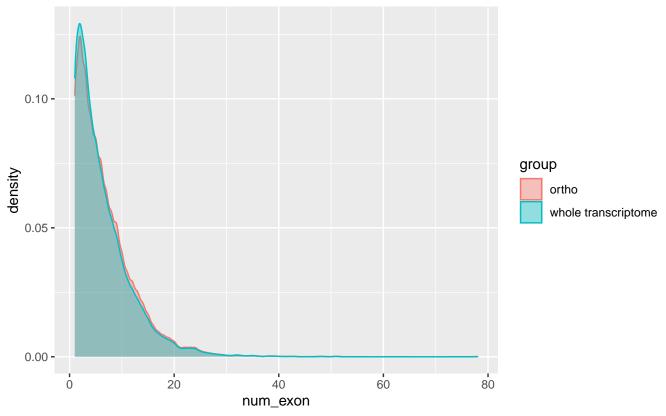


GCF_000715135.1_Ntab-TN90 **EpT** Wilcoxon p-value = 1.0145e-133, W = 4.475e+090.20 -0.15 group density 0.10 ortho whole transcriptome 0.05 -0.00 -20 40 60 80 num_exon

GCF_000826755.1_ZizJuj_1.1 **EpT** Wilcoxon p-value = 5.1426e-106, W = 1.065e+09 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80 num_exon

GCF_001190045.1_Vigan1.1 EpT

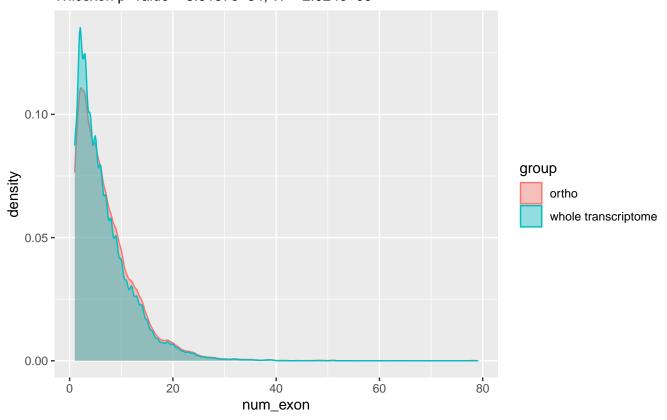
Wilcoxon p-value = 1.1405e-23, W = 785391376

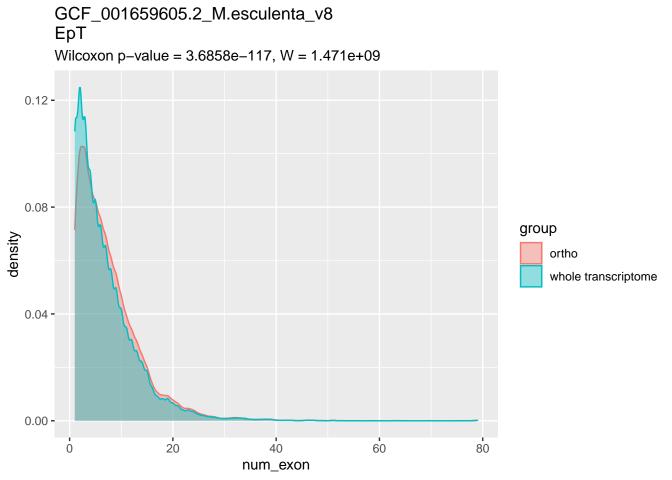


GCF_001433935.1_IRGSP-1.0 **EpT** Wilcoxon p-value = 7.8074e-122, W = 1.17e+09 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80 num_exon

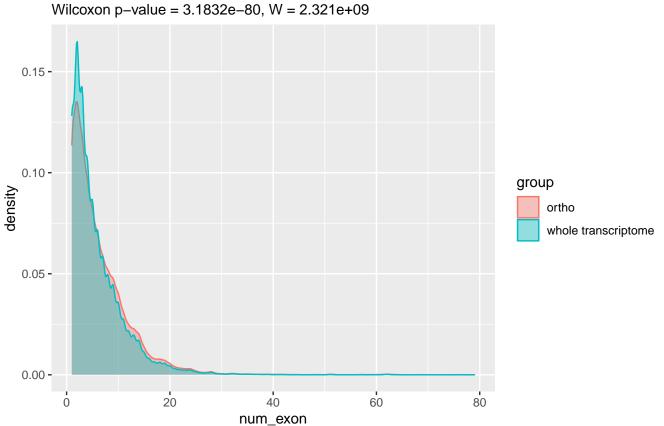
GCF_001654055.1_ASM165405v1 EpT

Wilcoxon p-value = 3.0157e-54, W = 2.024e+09



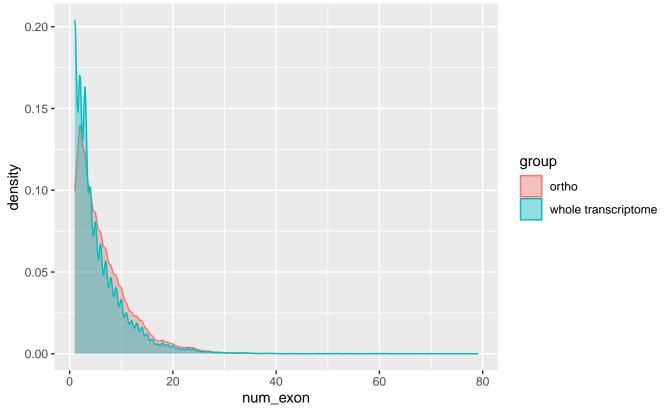


GCF_001683475.1_ASM168347v1 EpT



GCF_001879475.1_Asagao_1.1 EpT

Wilcoxon p-value = 0, W = 1.762e+09



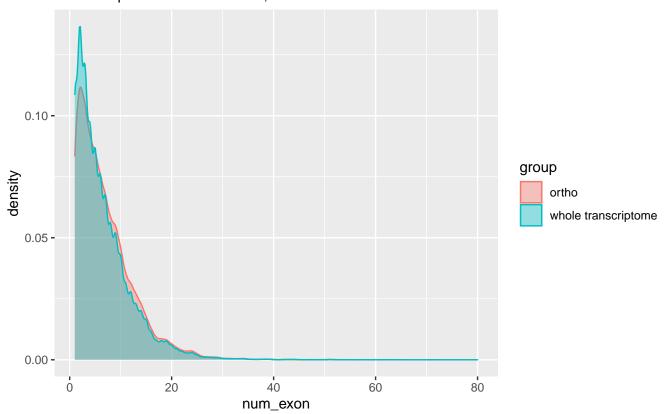
GCF_001995035.1_ASM199503v1 **EpT** Wilcoxon p-value = 9.9827e-28, W = 492738858 0.12 -0.08 group ortho whole transcriptome 0.04 -0.00 -20 40 60 80

num_exon

density

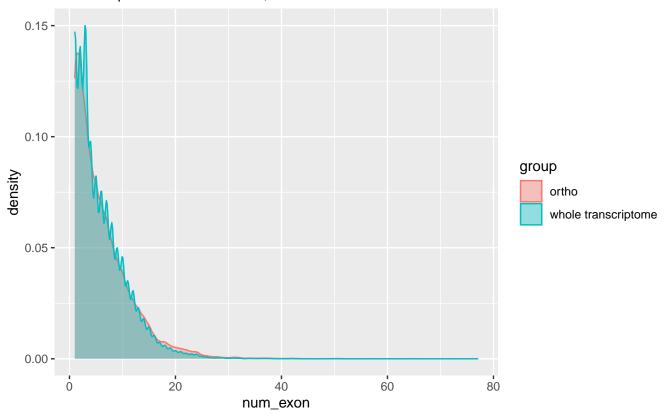
GCF_002114115.1_ASM211411v1 EpT

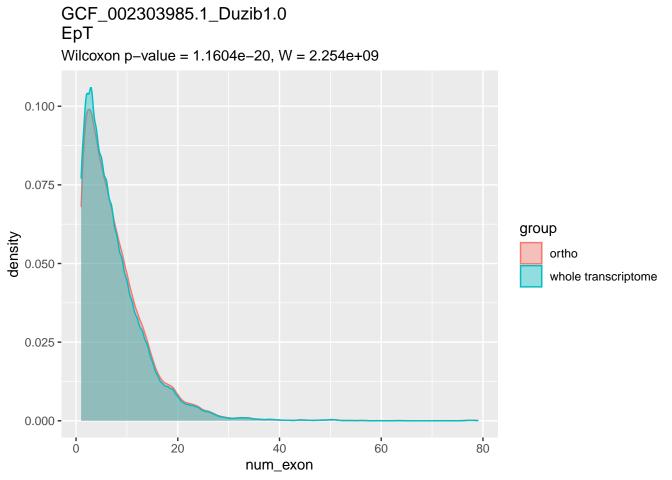
Wilcoxon p-value = 2.3214e-71, W = 1.485e+09



GCF_002127325.2_HanXRQr2.0-SUNRISE EpT

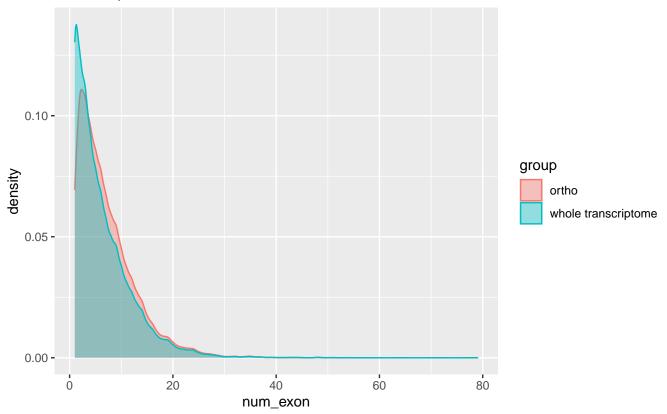
Wilcoxon p-value = 2.5433e-06, W = 3.865e+09





GCF_002738345.1_Cmax_1.0 EpT

Wilcoxon p-value = 2.832e-229, W = 1.285e+09

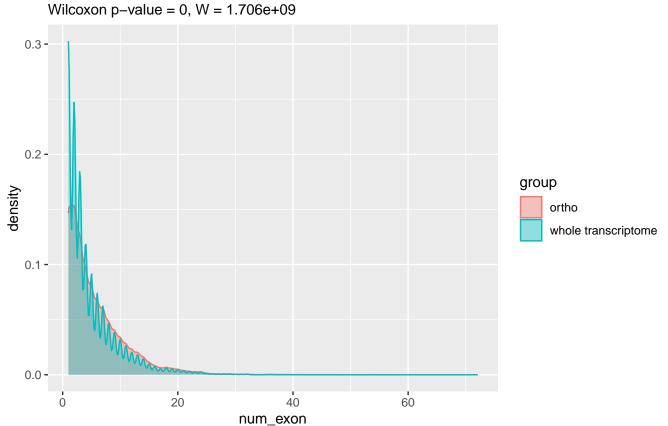


GCF_002870075.2_Lsat_Salinas_v7 **EpT** Wilcoxon p-value = 2.5238e-83, W = 1.429e+090.15 -0.10 group ortho whole transcriptome 0.05 -0.00 -20 40 60 80

num_exon

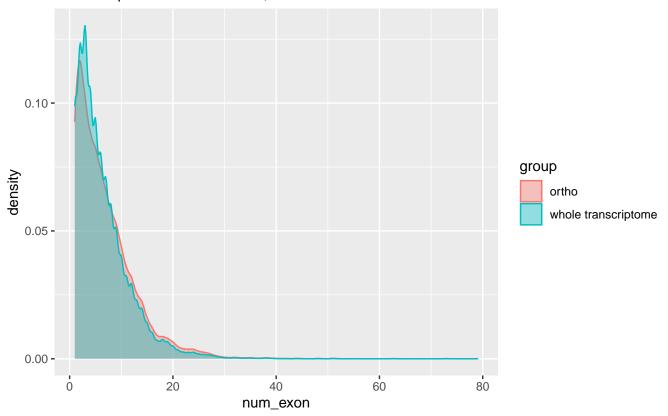
density

GCF_002906115.1_CorkOak1.0 EpT

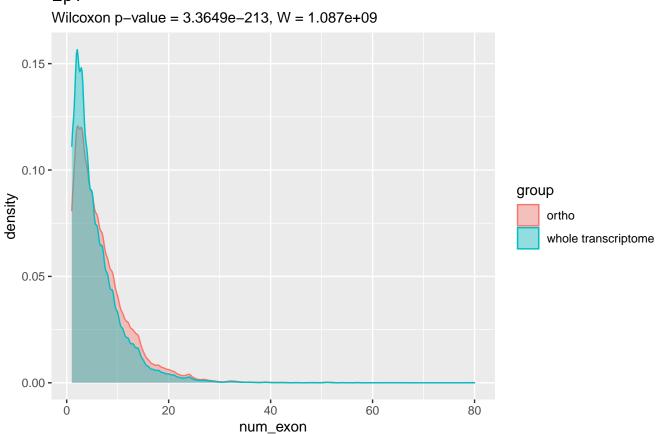


GCF_002994745.2_RchiOBHm-V2 EpT

Wilcoxon p-value = 2.2738e-34, W = 1.466e+09

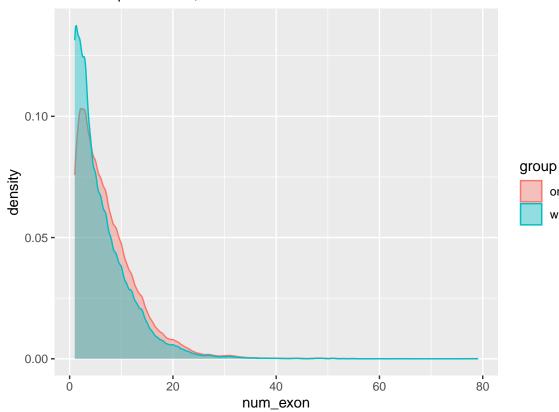


GCF_016545825.1_ASM1654582v1 EpT



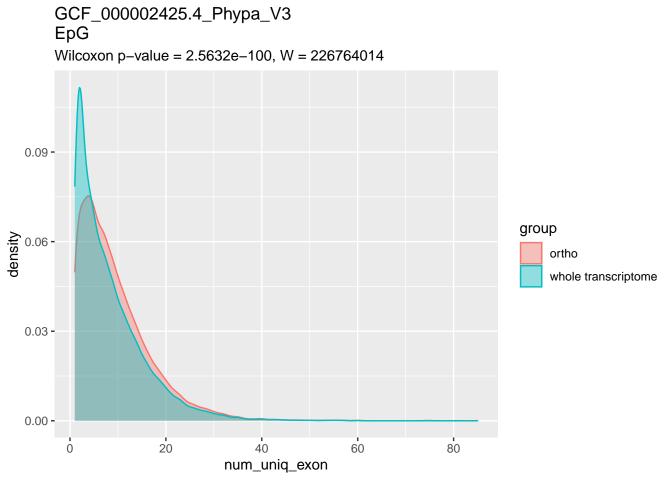
GCF_902167145.1_Zm-B73-REFERENCE-NAM-5.0 EpT

Wilcoxon p-value = 0, W = 2.391e+09



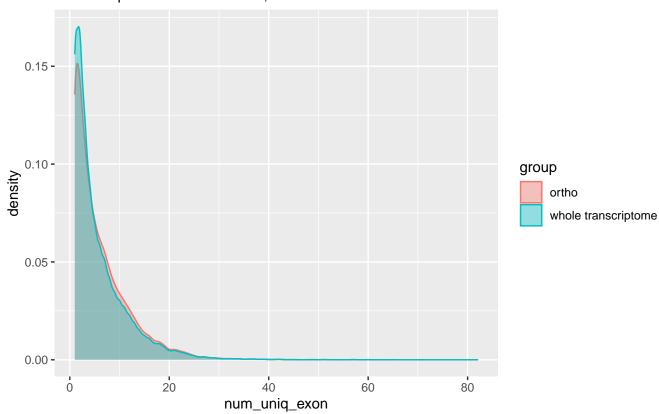
ortho

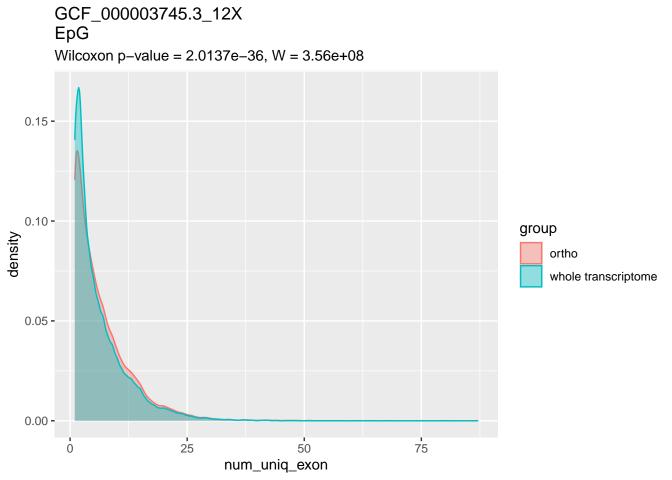
GCF_000001735.4_TAIR10.1 EpG Wilcoxon p-value = 0, W = 5944231450.3 -0.2 group density ortho whole transcriptome 0.1 -0.0 -20 40 60 80 num_uniq_exon



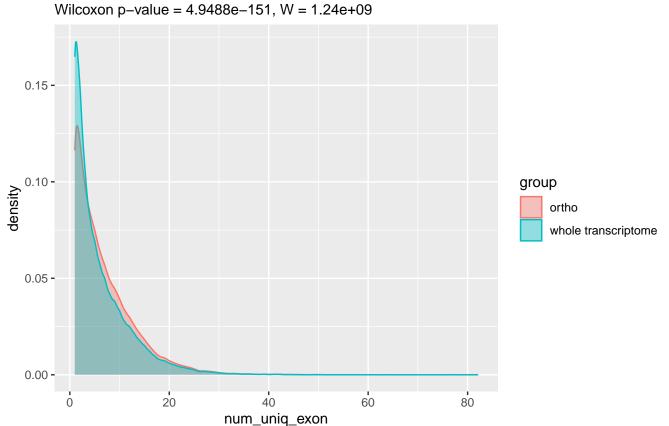
GCF_000003195.3_Sorghum_bicolor_NCBIv3 EpG

Wilcoxon p-value = 1.8857e-21, W = 4.25e+08



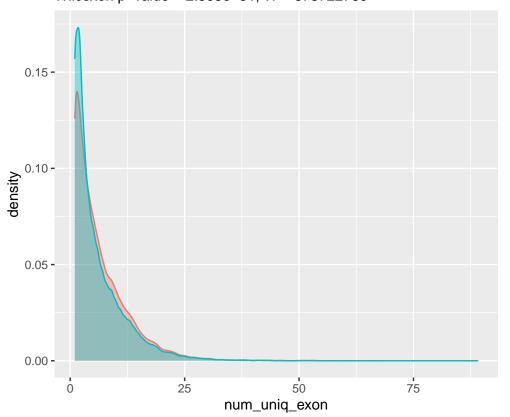


GCF_000004515.6_Glycine_max_v4.0 EpG



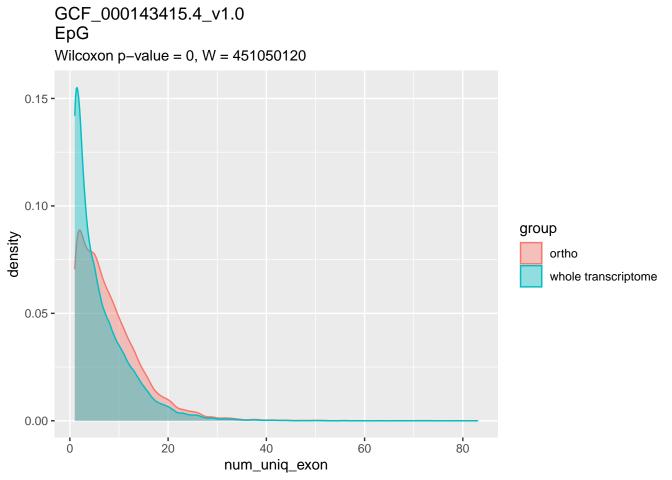
 $\begin{array}{l} {\sf GCF_000005505.3_Brachypodium_distachyon_v3.0} \\ {\sf EpG} \end{array}$





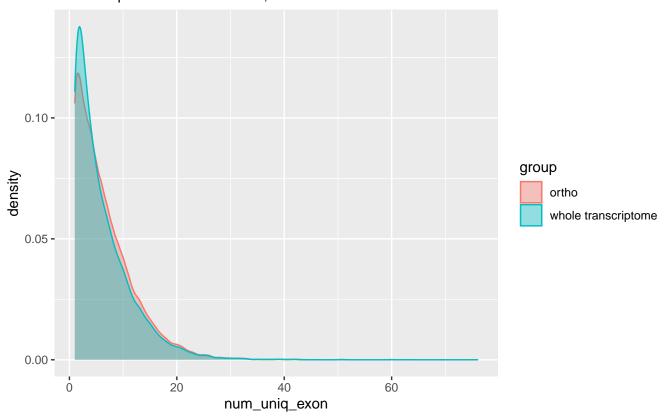
group

ortho

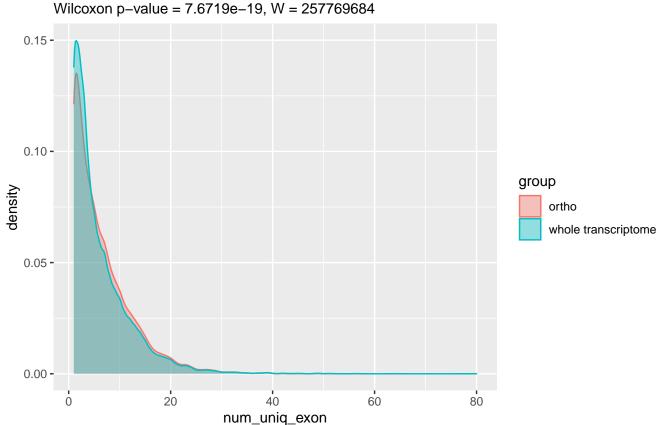


GCF_000150535.2_Papaya1.0 EpG

Wilcoxon p-value = 5.6899e-24, W = 177202184

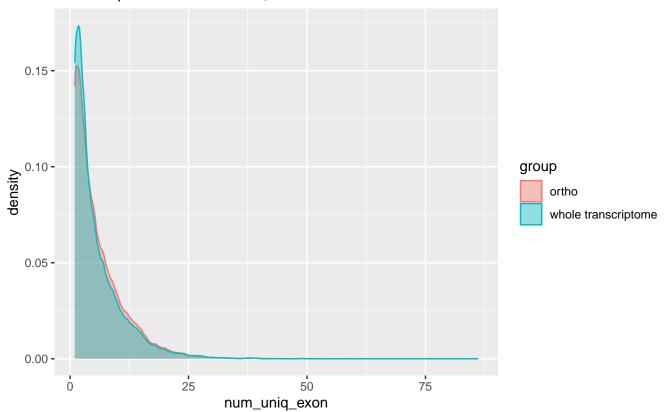


GCF_000208745.1_Criollo_cocoa_genome_V2 EpG

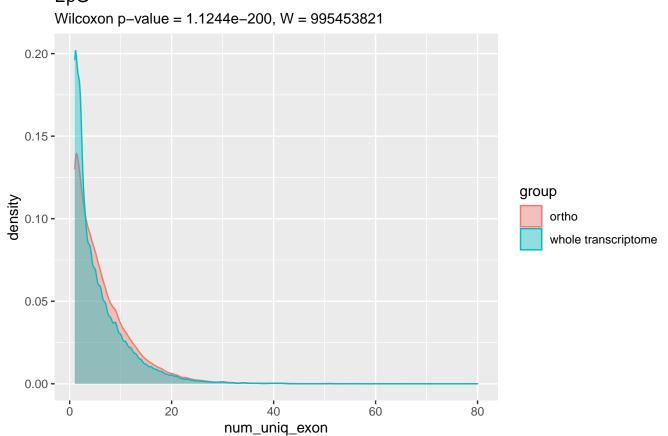


GCF_000226075.1_SolTub_3.0 EpG

Wilcoxon p-value = 4.4589e-30, W = 4.44e+08

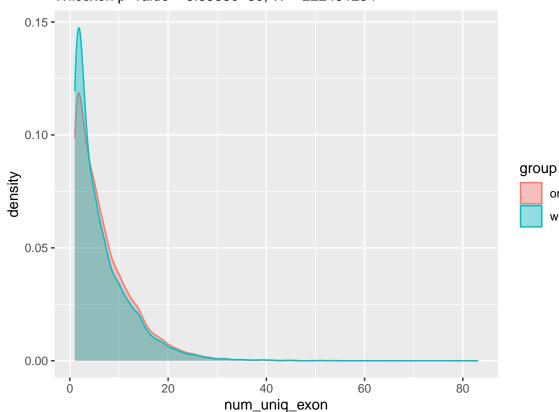


GCF_000309985.2_CAAS_Brap_v3.01 EpG Wilcoxon p-value = 1.1244e-200, W = 995453821



GCF_000313045.1_ASM31304v1 EpG

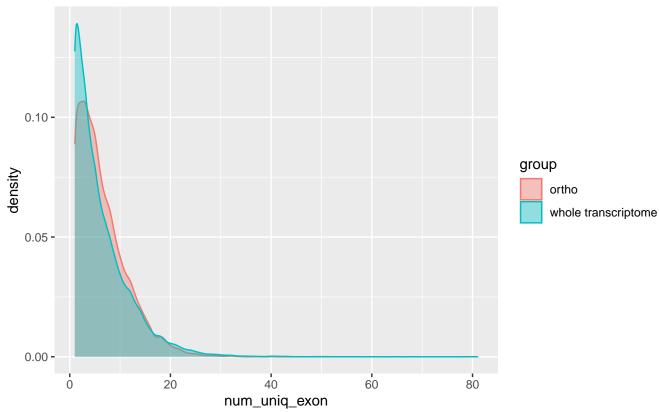
Wilcoxon p-value = 3.6588e-30, W = 222431294

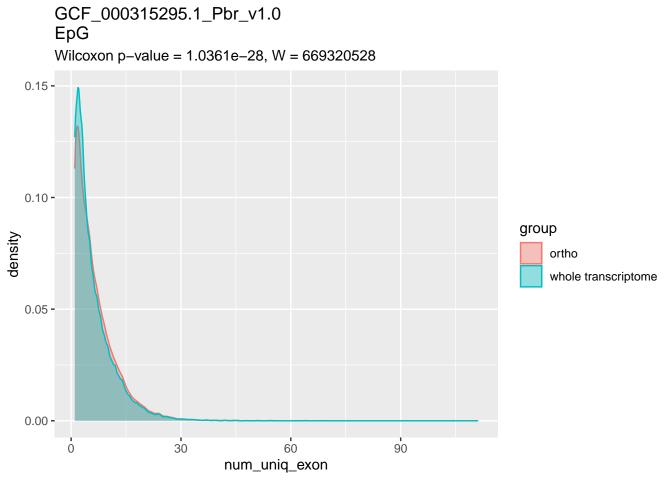


ortho

GCF_000313855.2_ASM31385v2 EpG

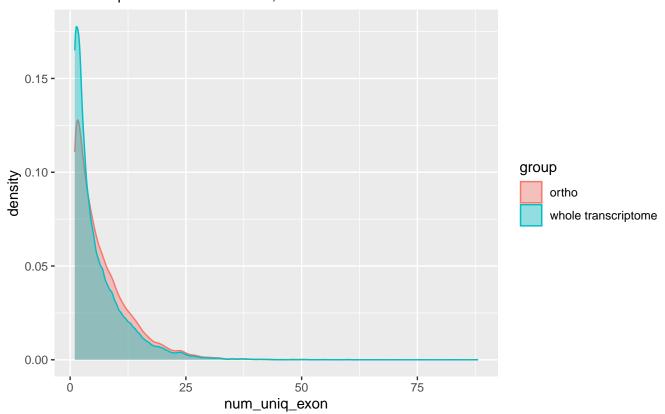
Wilcoxon p-value = 6.5722e-27, W = 164915926



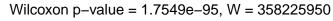


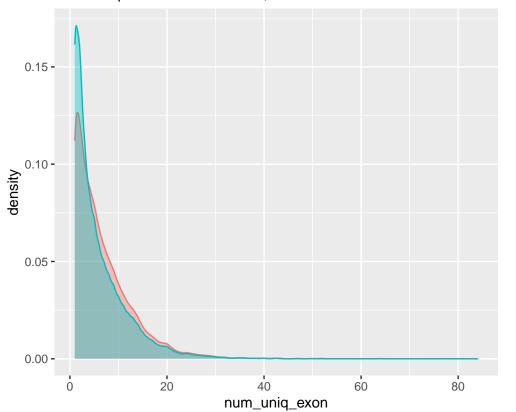
GCF_000317415.1_Csi_valencia_1.0 EpG

Wilcoxon p-value = 2.7237e-106, W = 338381280



GCF_000331145.1_ASM33114v1 EpG

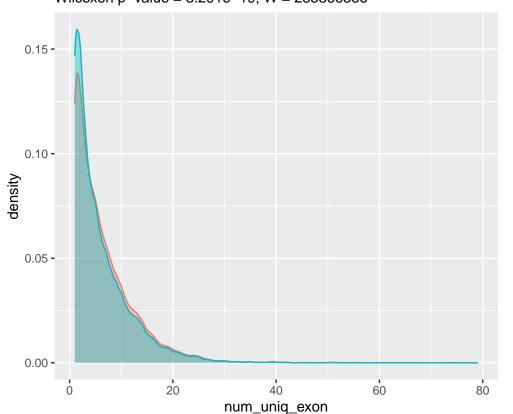




group

ortho

GCF_000346465.2_Prunus_persica_NCBIv2 EpG Wilcoxon p-value = 8.291e-19, W = 285866586

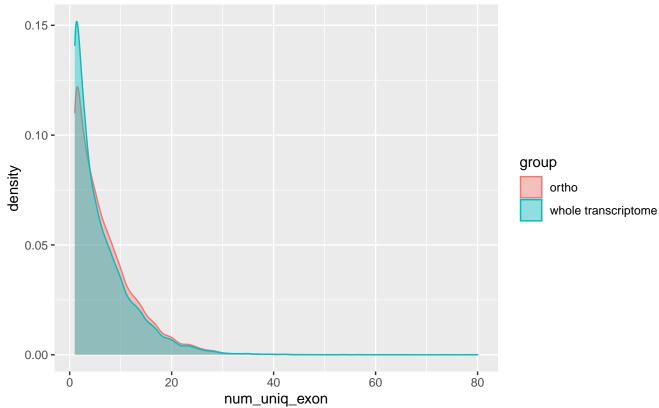


group

ortho

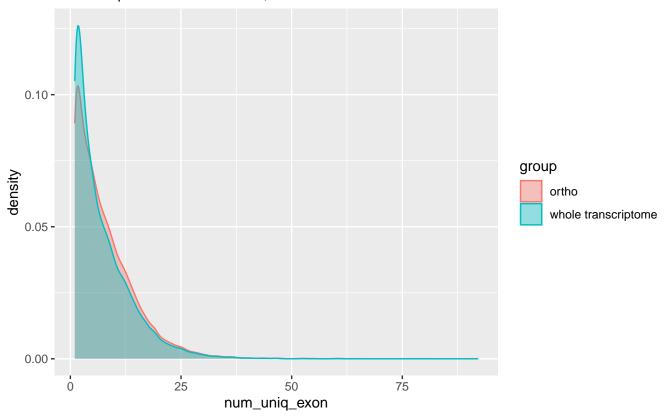
GCF_000365185.1_Chinese_Lotus_1.1 EpG

Wilcoxon p-value = 2.3943e-41, W = 322052429

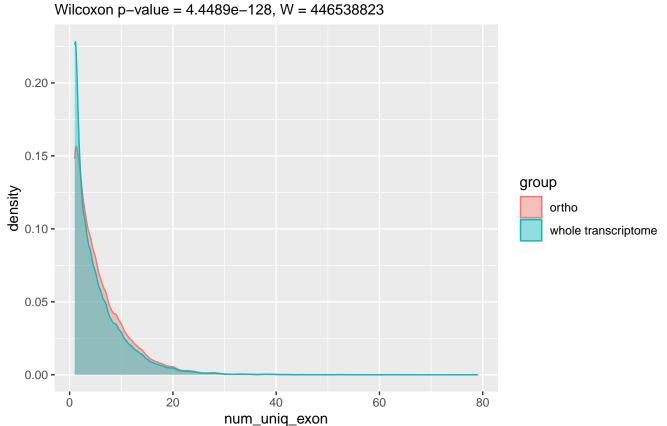


GCF_000471905.2_AMTR1.0 EpG

Wilcoxon p-value = 1.6531e-29, W = 155726614



GCF_000478725.1_Eutsalg1_0 EpG

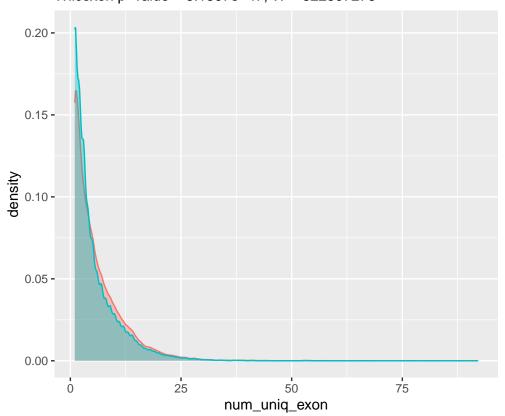


GCF_000504015.1_Mimgu1_0 EpG Wilcoxon p-value = 6.217e-34, W = 3852237930.20 -0.15 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 80

num_uniq_exon

GCF_000511025.2_RefBeet-1.2.2 EpG



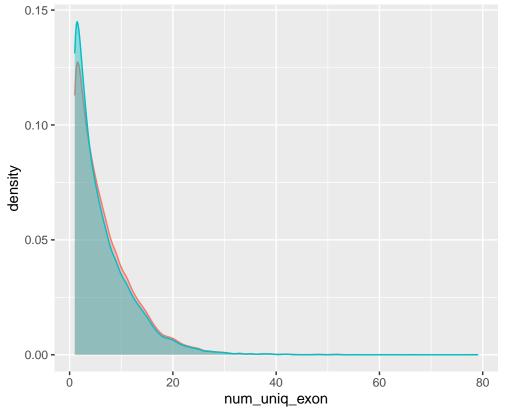


group

ortho

GCF_000512975.1_S_indicum_v1.0 EpG

Wilcoxon p-value = 6.8147e-22, W = 314671742

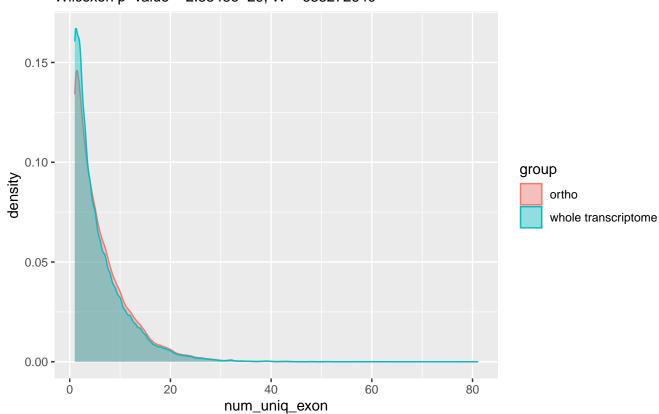


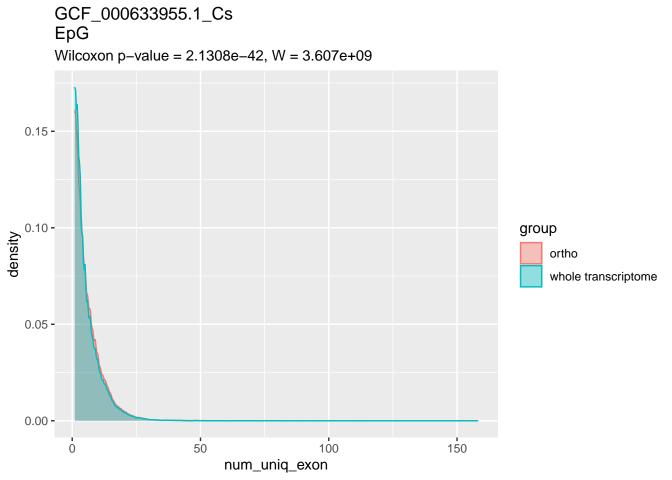
group

ortho

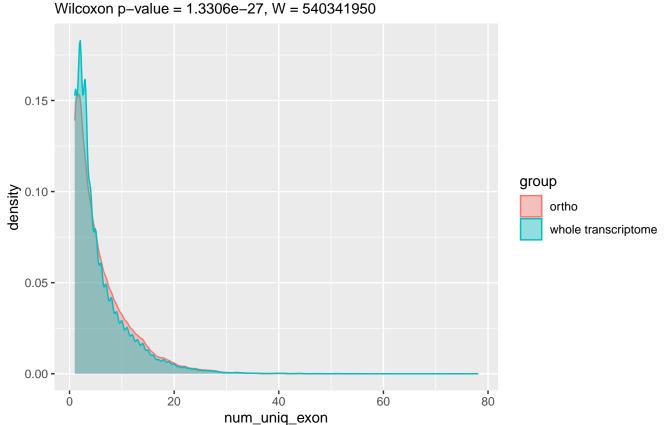
GCF_000612285.1_Gossypium_arboreum_v1.0 EpG

. Wilcoxon p-value = 2.8348e-29, W = 638272640



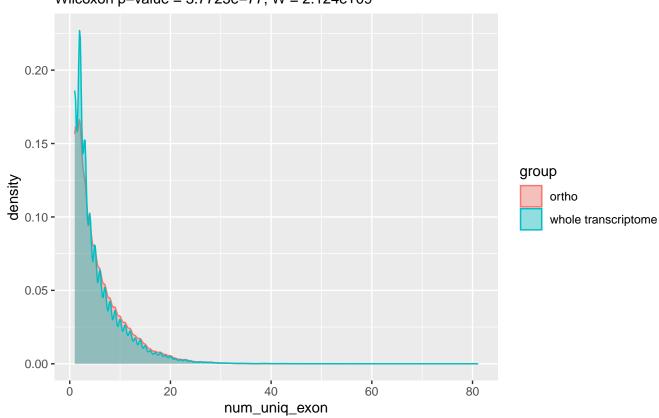


GCF_000710875.1_Pepper_Zunla_1_Ref_v1.0 EpG



GCF_000715135.1_Ntab-TN90 EpG

Wilcoxon p-value = 3.7725e-77, W = 2.124e+09

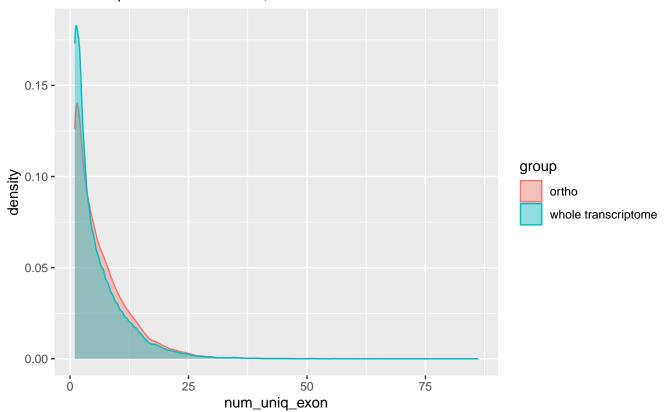


GCF_000826755.1_ZizJuj_1.1 EpG Wilcoxon p-value = 2.6058e-76, W = 4578697660.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -25 50 75 num_uniq_exon

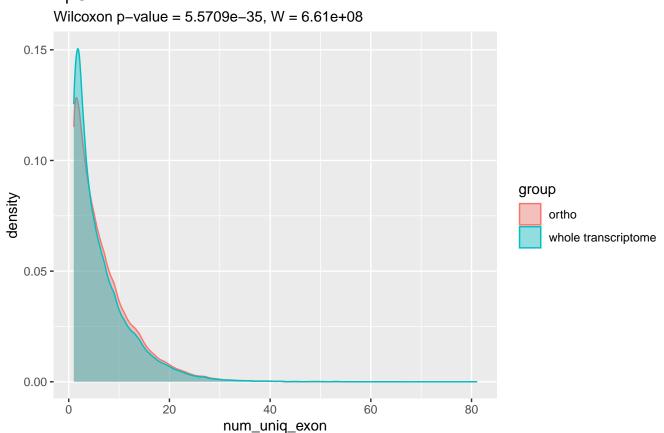
GCF_001190045.1_Vigan1.1 EpG Wilcoxon p-value = 3.9446e-20, W = 372216514 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -25 50 75 num_uniq_exon

GCF_001433935.1_IRGSP-1.0 EpG

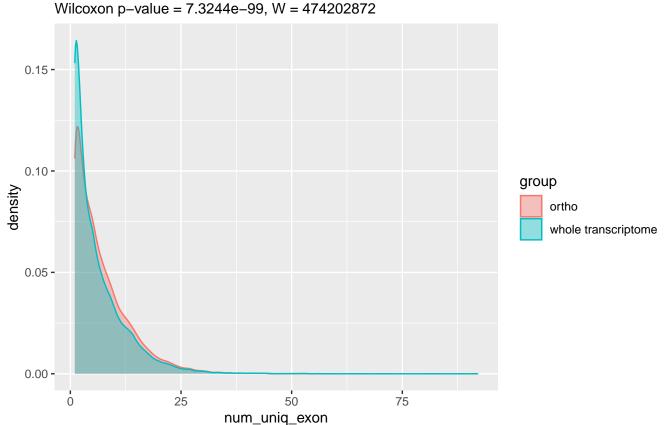
Wilcoxon p-value = 4.2661e-97, W = 460130084



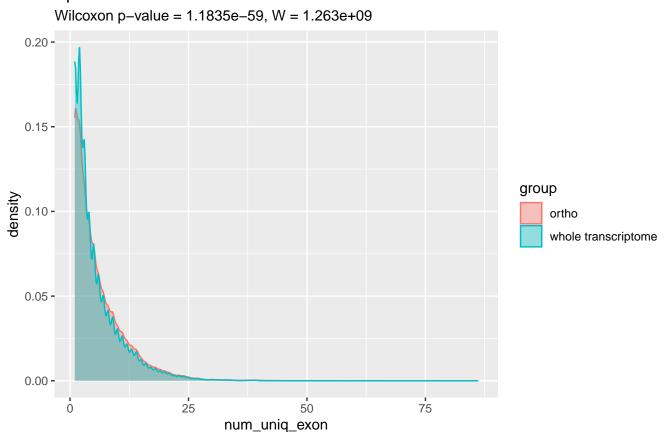
GCF_001654055.1_ASM165405v1 EpG



GCF_001659605.2_M.esculenta_v8 EpG

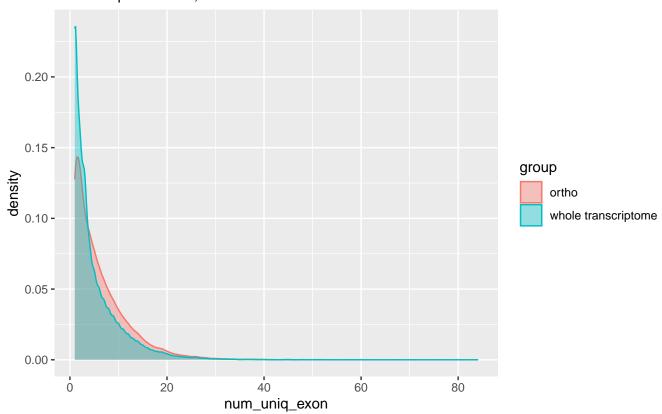


GCF_001683475.1_ASM168347v1 EpG



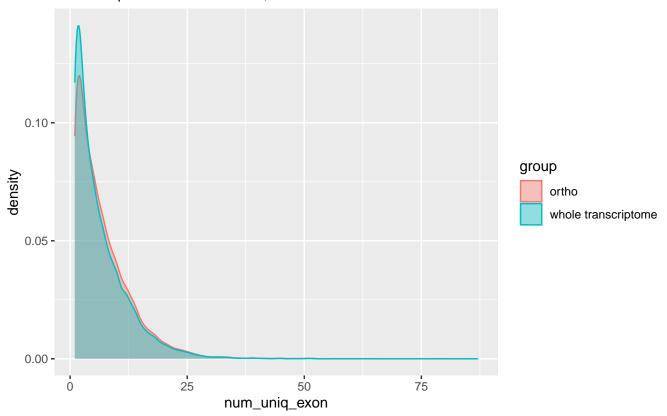
GCF_001879475.1_Asagao_1.1 EpG

Wilcoxon p-value = 0, W = 834789628

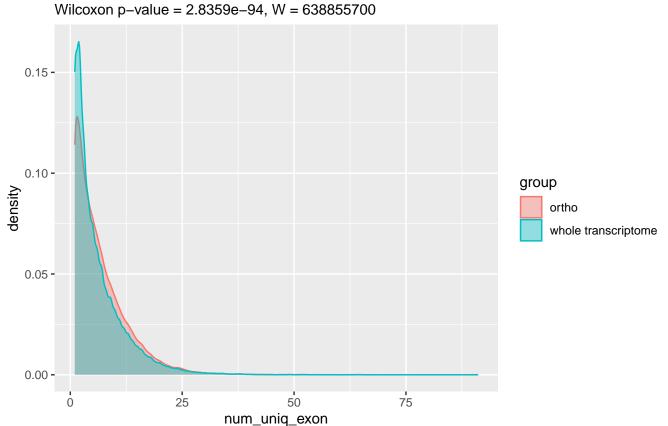


GCF_001995035.1_ASM199503v1 EpG

Wilcoxon p-value = 1.9306e-24, W = 208942580

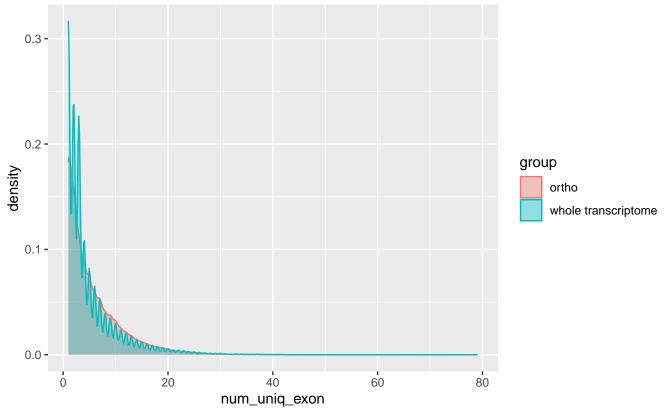


GCF_002114115.1_ASM211411v1 EpG

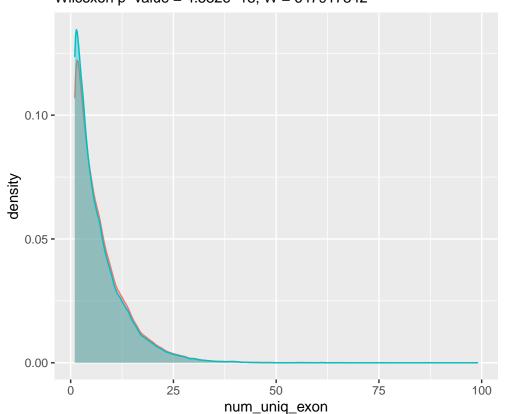


GCF_002127325.2_HanXRQr2.0-SUNRISE EpG

Wilcoxon p-value = 1.3717e-172, W = 1.8e+09



GCF_002303985.1_Duzib1.0 EpG Wilcoxon p-value = 4.532e-13, W = 647917342

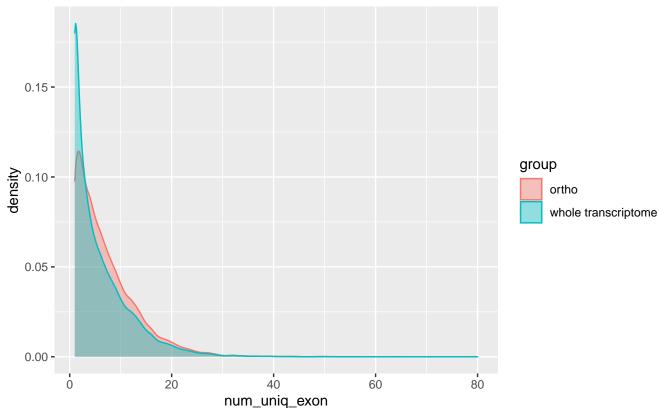


group

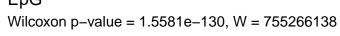
ortho

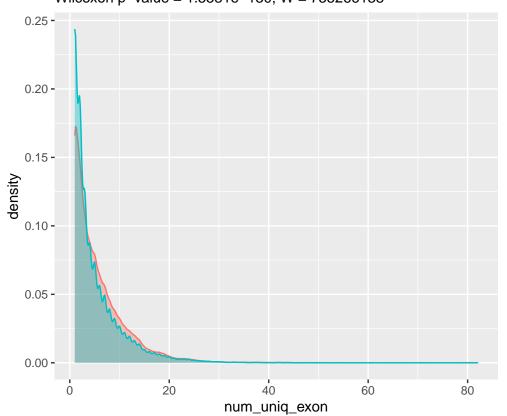
whole transcriptome

GCF_002738345.1_Cmax_1.0 EpG Wilcoxon p-value = 3.4986e-245, W = 519635797



GCF_002870075.2_Lsat_Salinas_v7 EpG





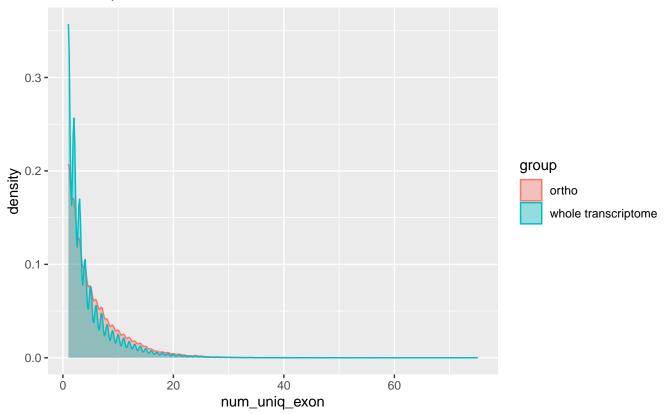
group

ortho

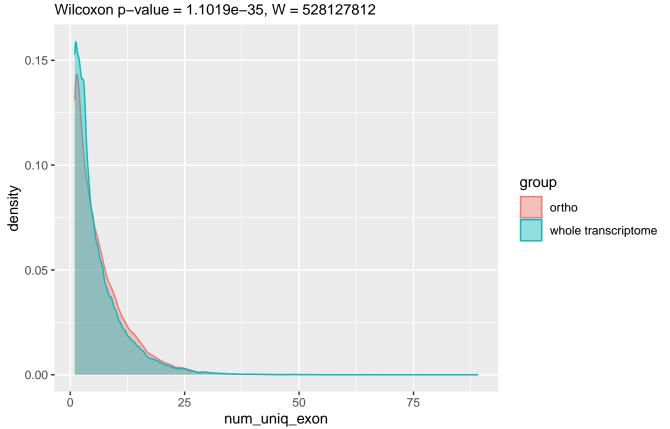
whole transcriptome

GCF_002906115.1_CorkOak1.0 EpG

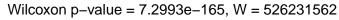
Wilcoxon p-value = 8.1907e-308, W = 1.049e+09

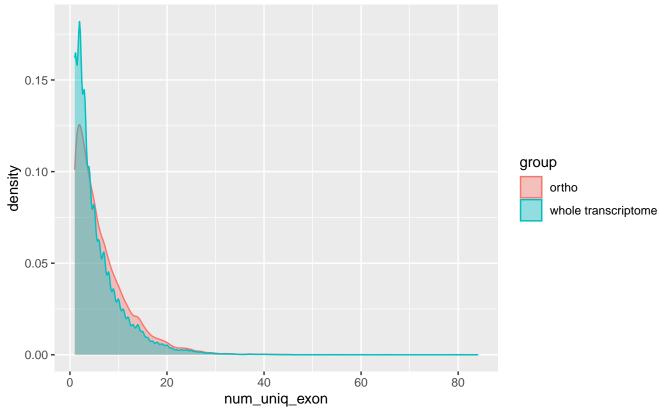


GCF_002994745.2_RchiOBHm-V2 EpG



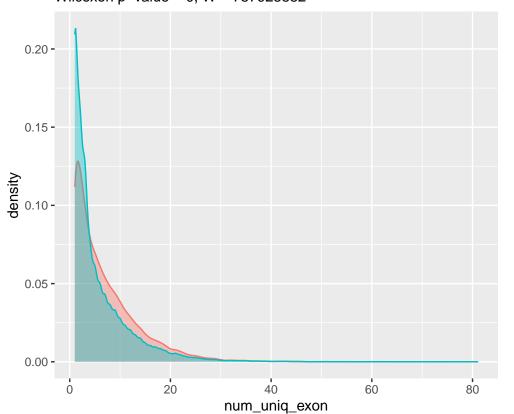
GCF_016545825.1_ASM1654582v1 EpG





GCF_902167145.1_Zm-B73-REFERENCE-NAM-5.0 EpG

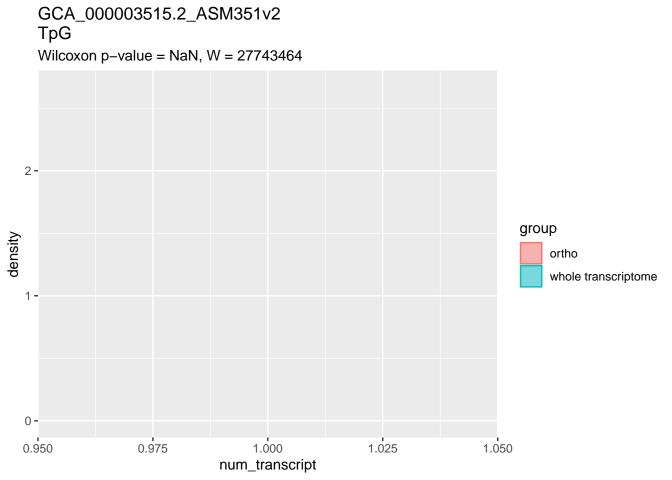
Wilcoxon p-value = 0, W = 757925882

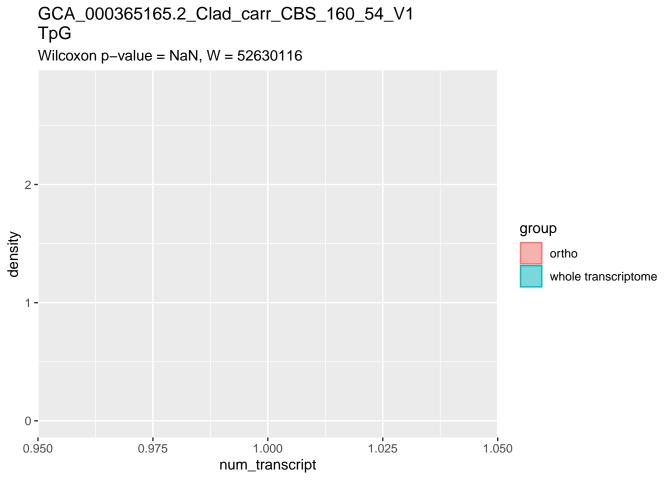


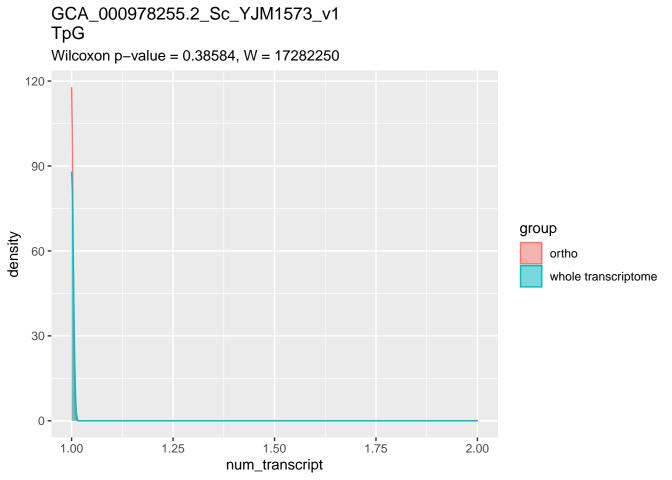
group

ortho

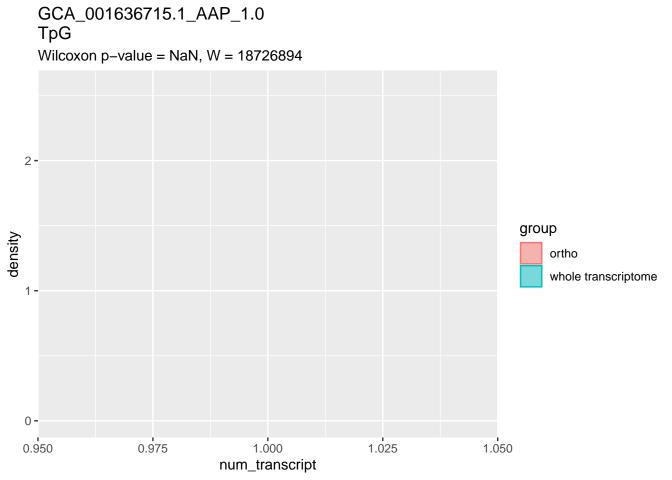
whole transcriptome

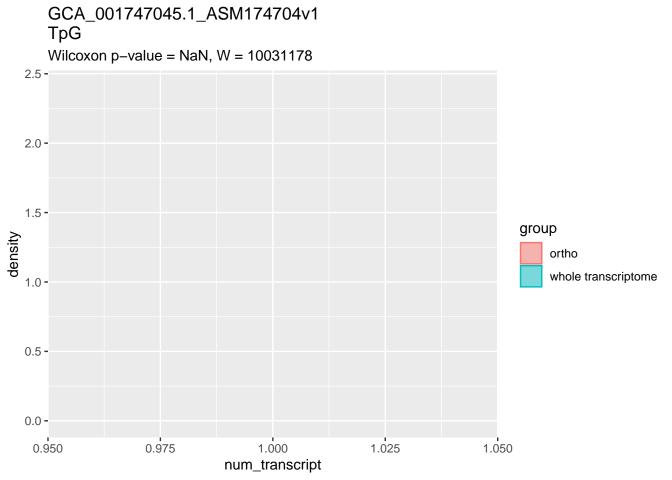


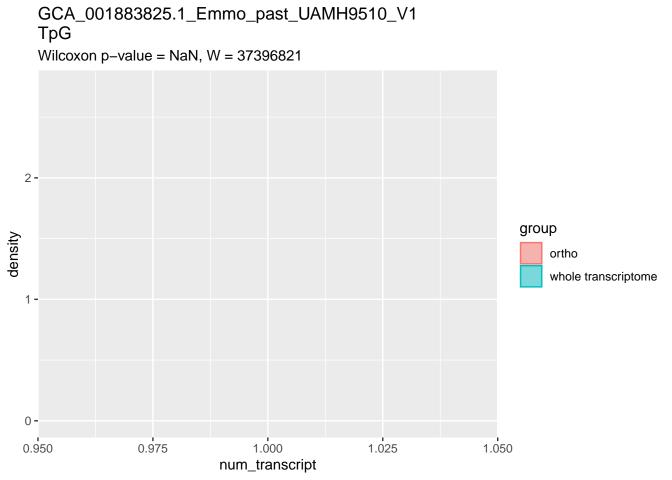


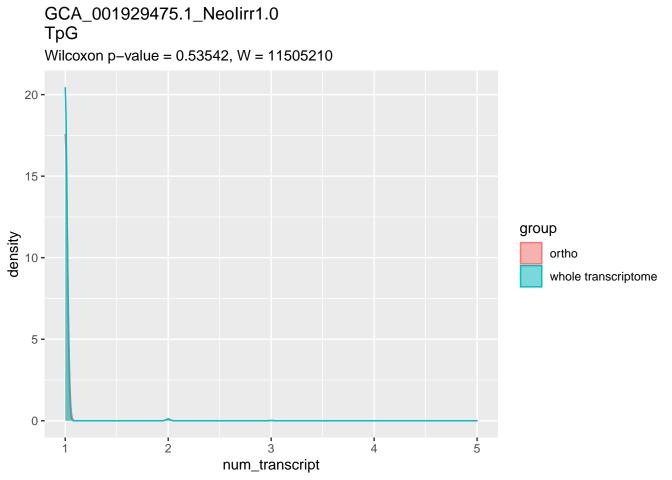


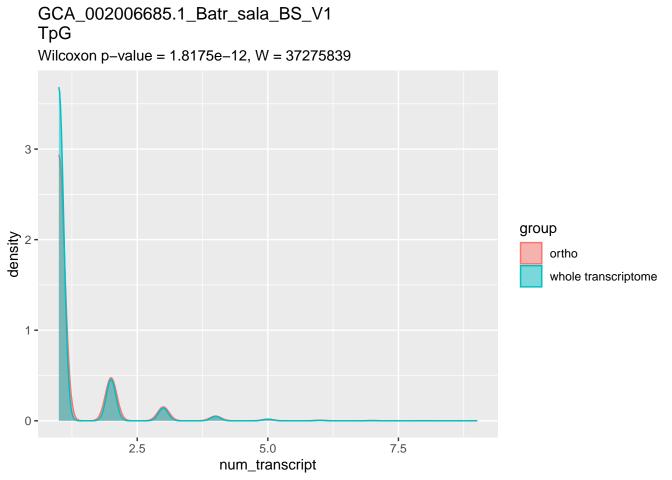
GCA_001574975.1_Ganpr1 TpG Wilcoxon p-value = 0.78061, W = 58698720150 **-**100 group density ortho whole transcriptome 50 -0 -1.25 1.50 1.75 1.00 2.00 num_transcript

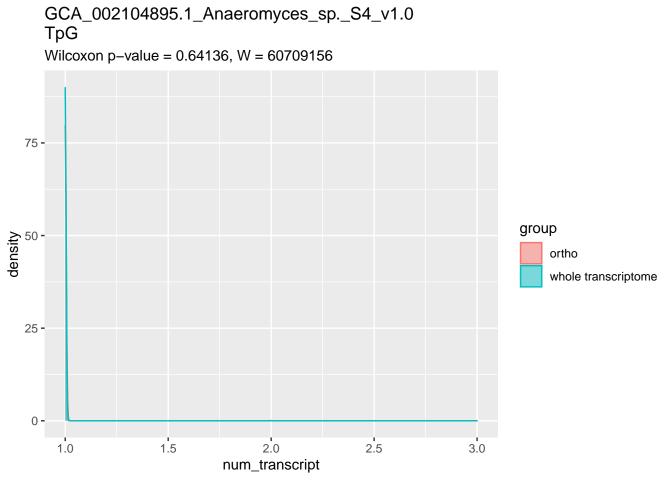


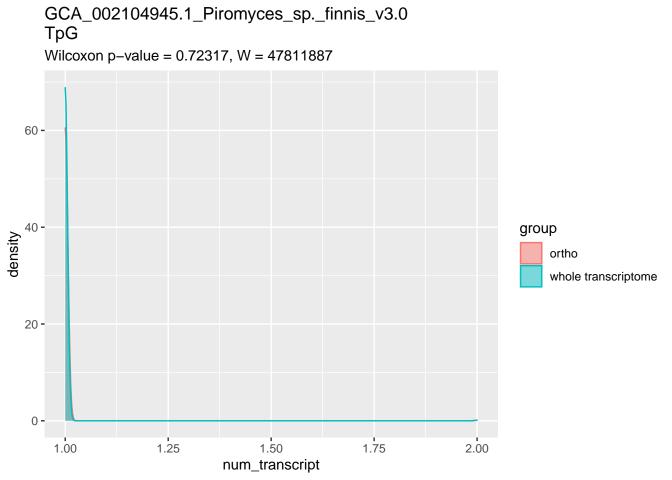


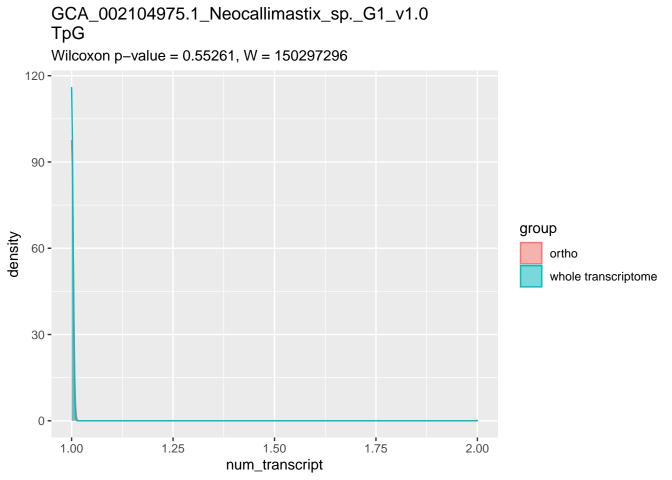


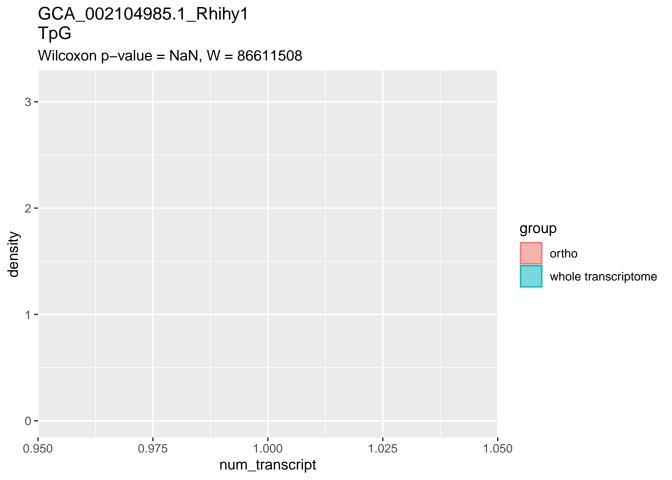


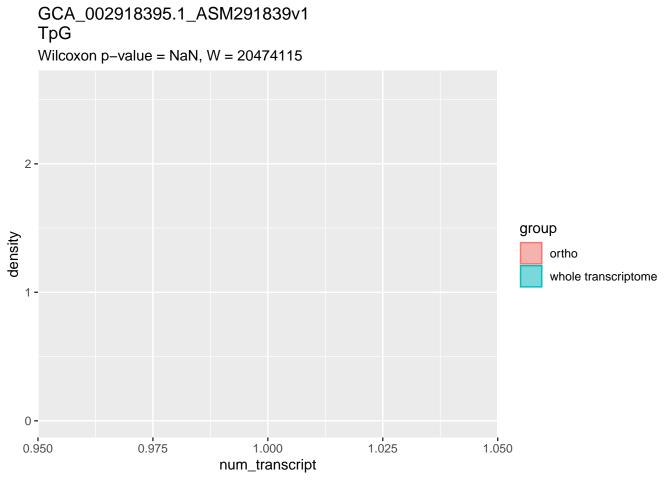


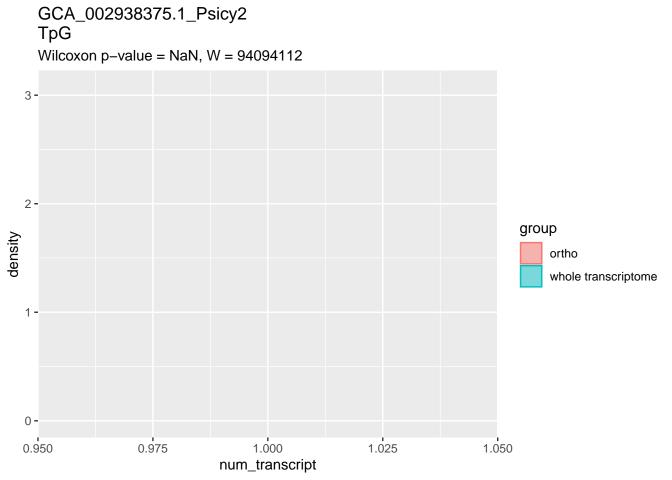


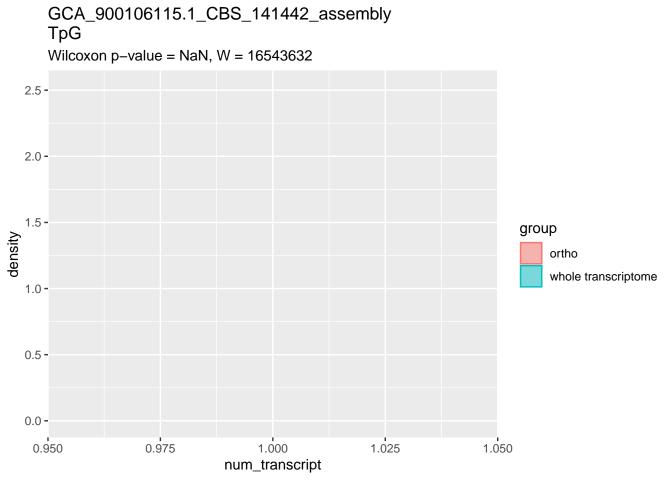








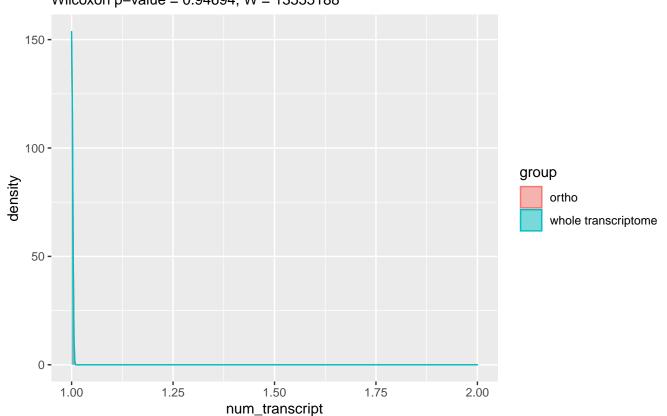


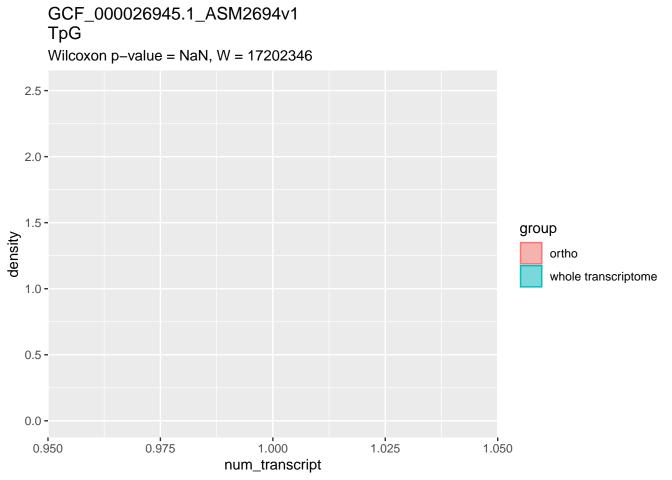


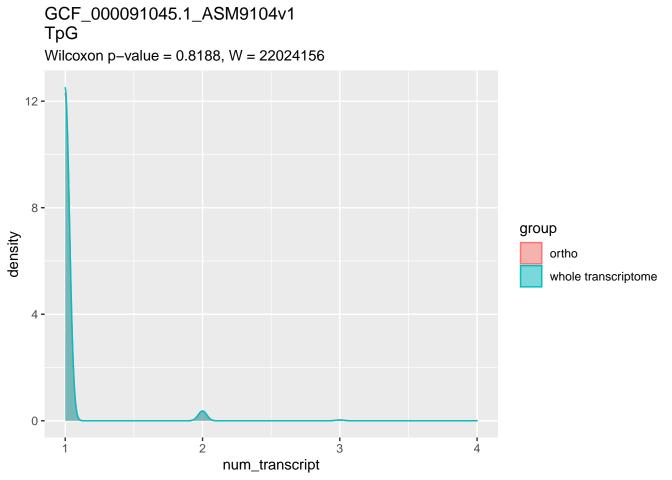
GCF_000001985.1_JCVI-PMFA1-2.0 TpG Wilcoxon p-value = 0.64175, W = 49373246 7.5 group density density ortho whole transcriptome 2.5 -0.0 -

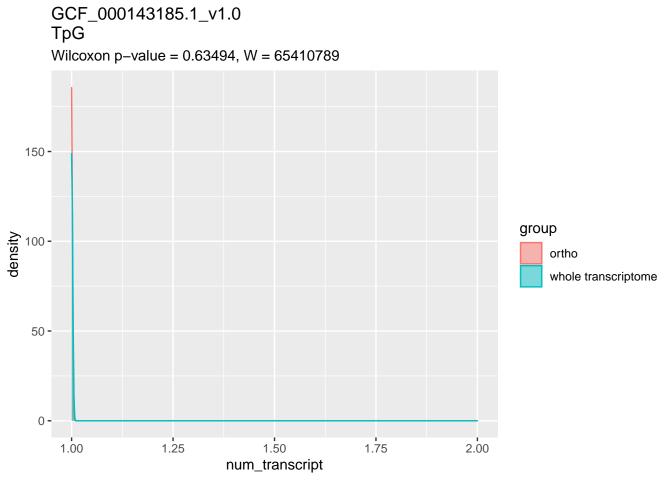
num_transcript

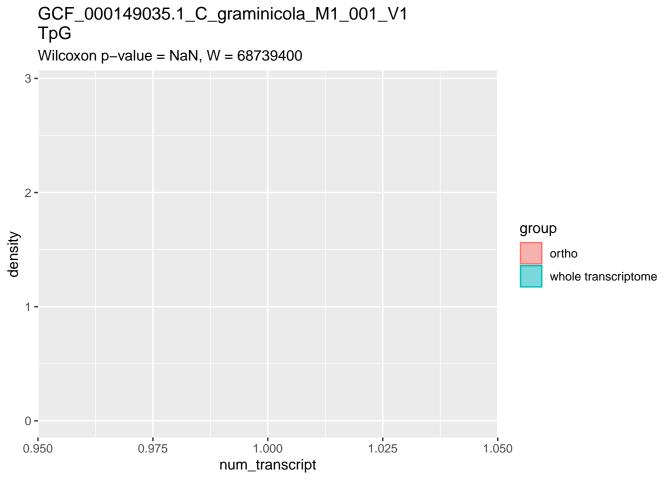
GCF_000002545.3_ASM254v2 TpG Wilcoxon p-value = 0.94694, W = 13555188



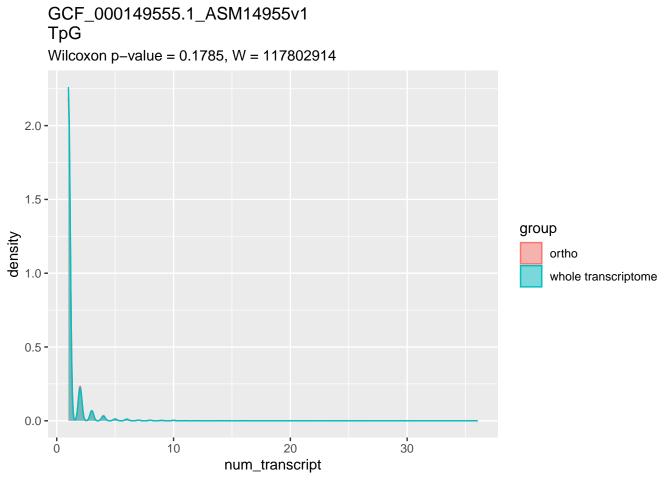


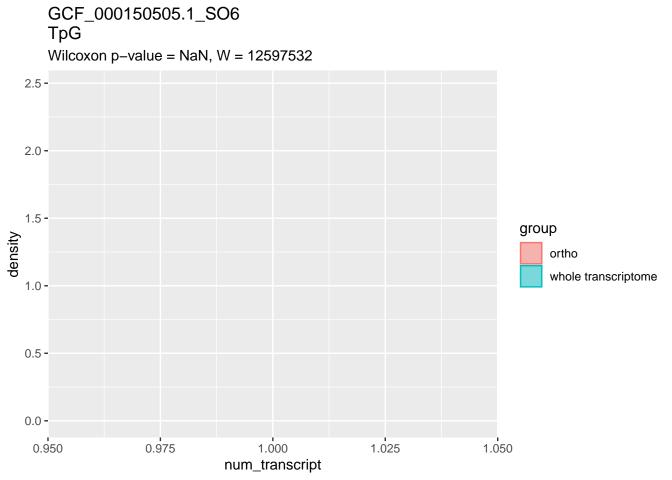


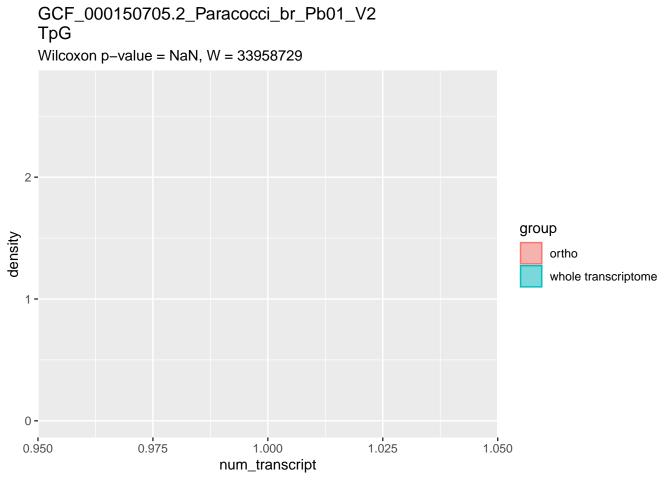


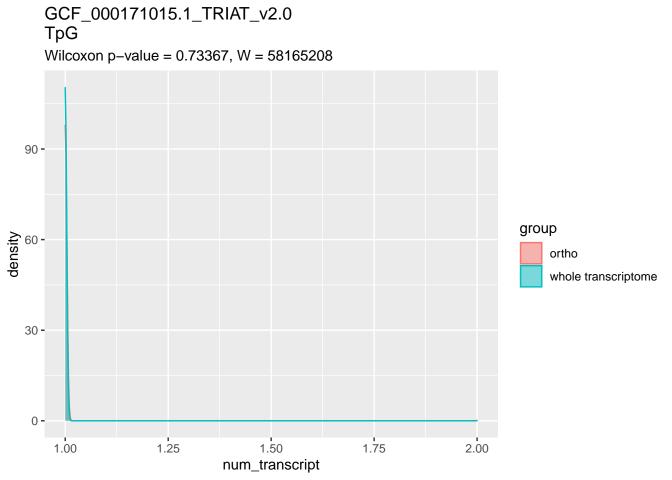


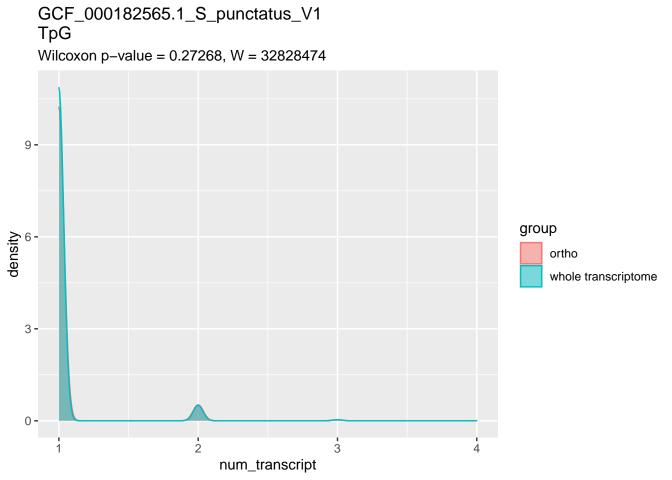
GCF_000149335.2_ASM14933v2 TpG Wilcoxon p-value = 0.078434, W = 38400634 20 -15group density o ortho whole transcriptome 5 -0 -1.5 2.0 2.5 1.0 3.0 num_transcript

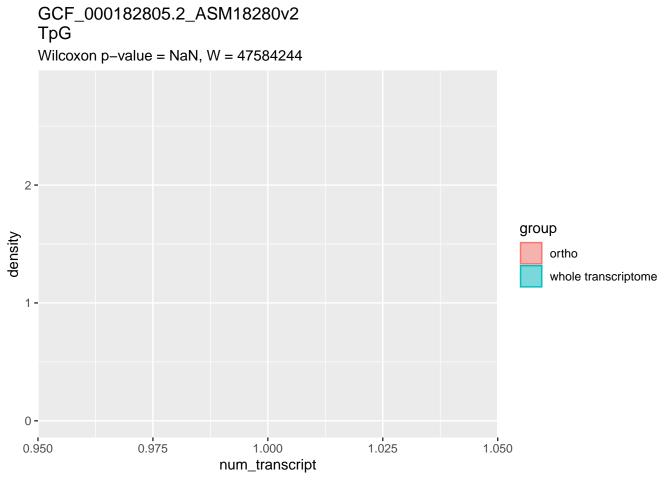


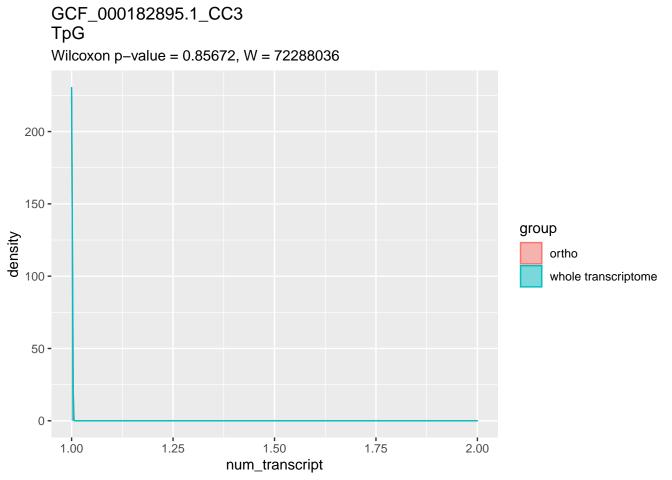


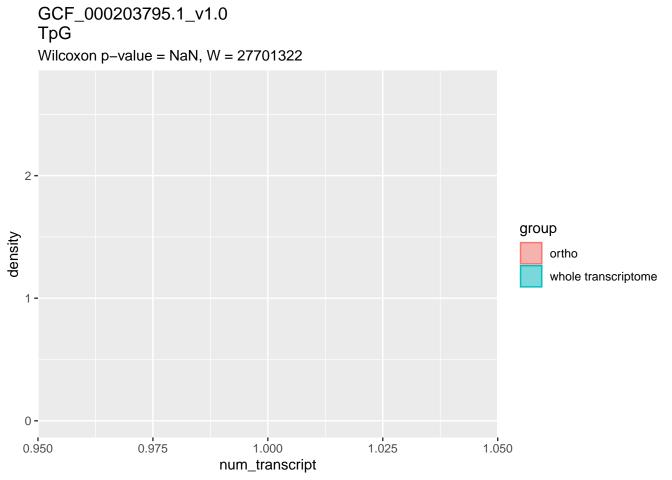


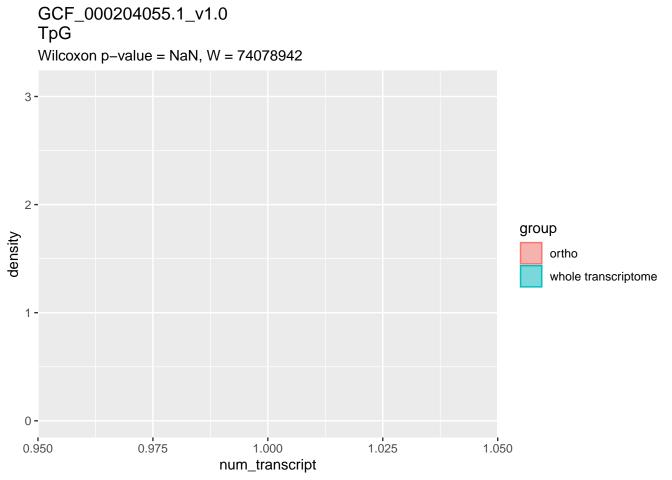


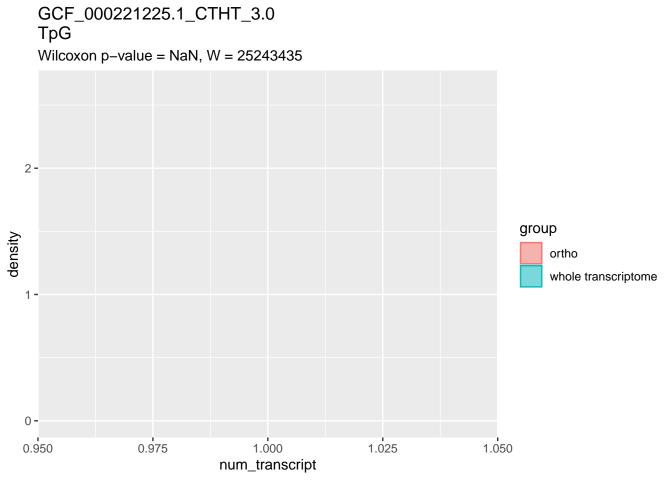


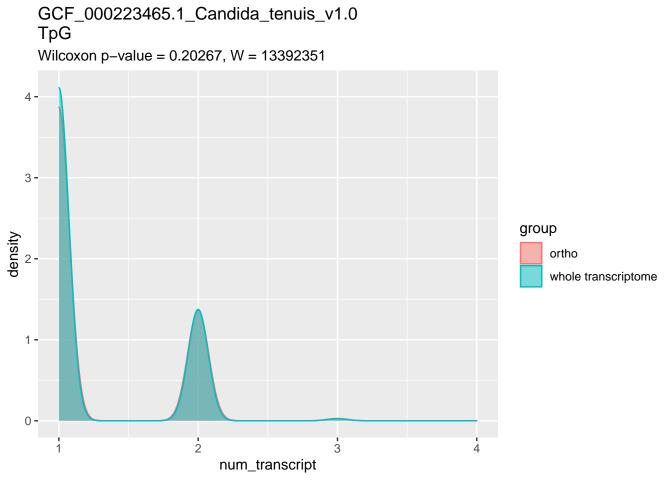


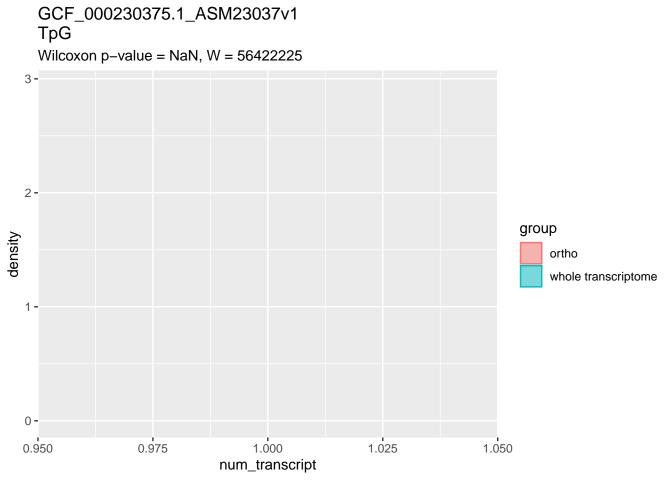


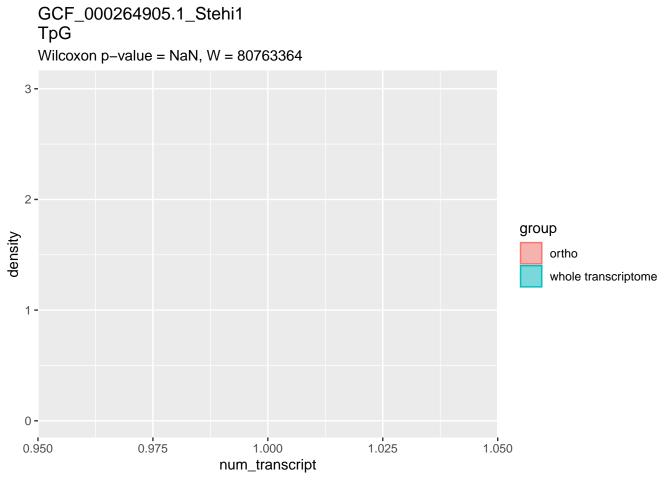


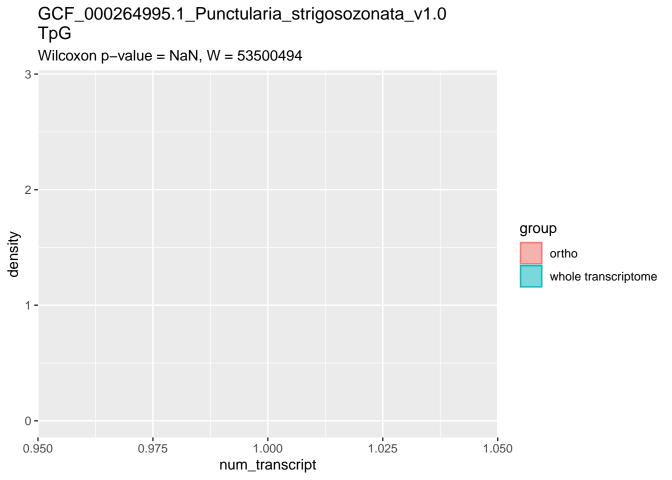


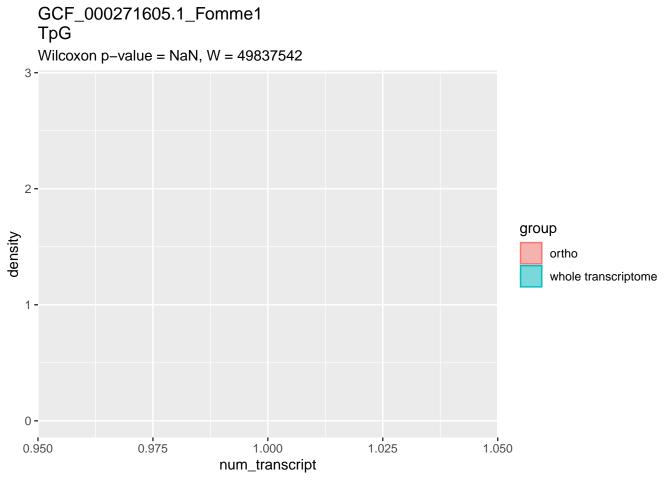


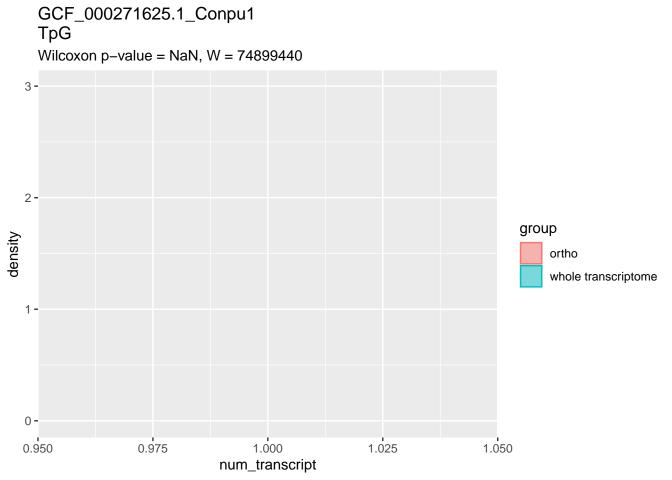


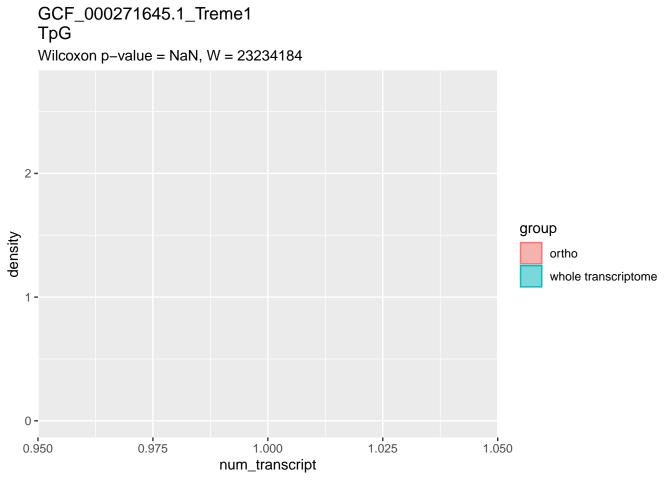


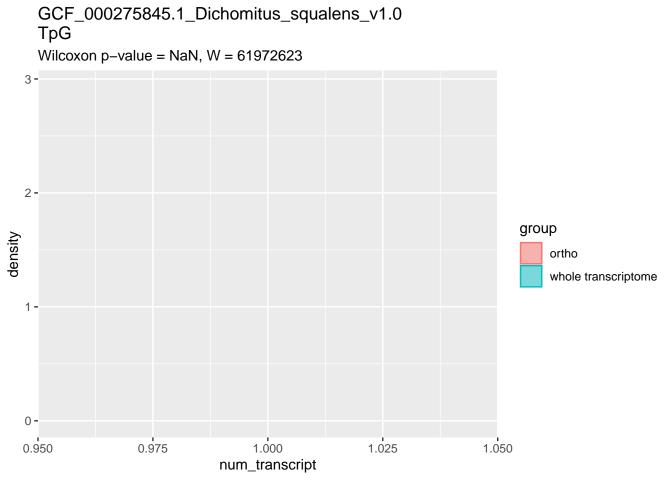


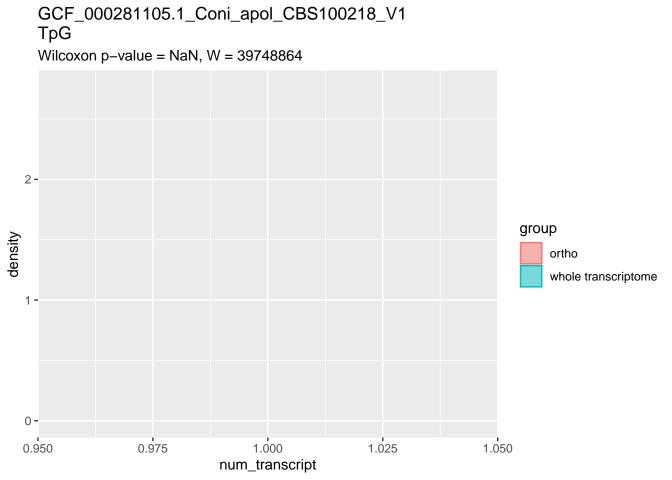


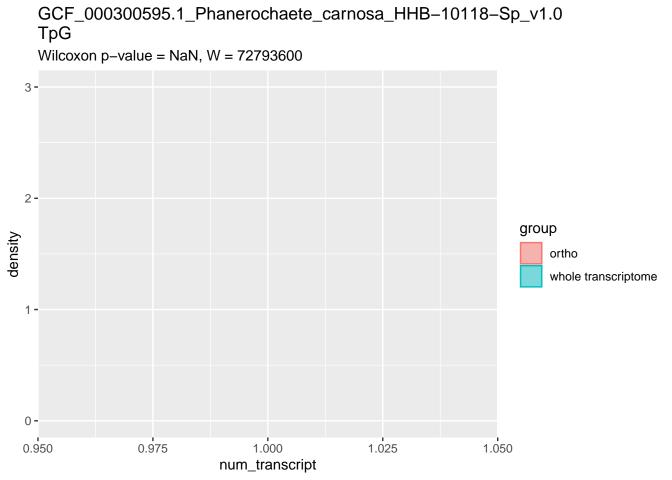


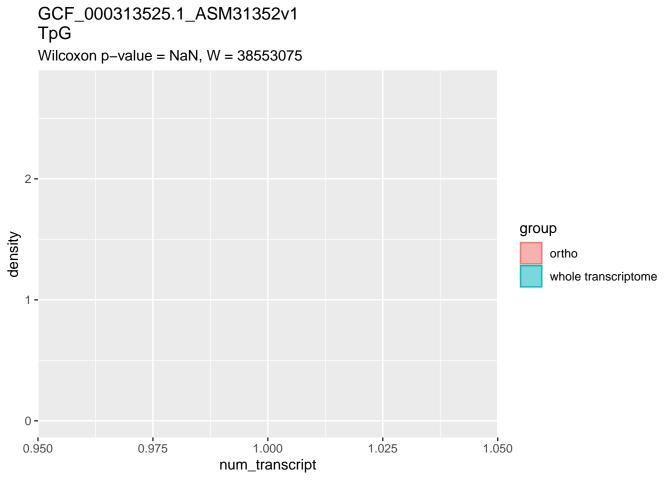




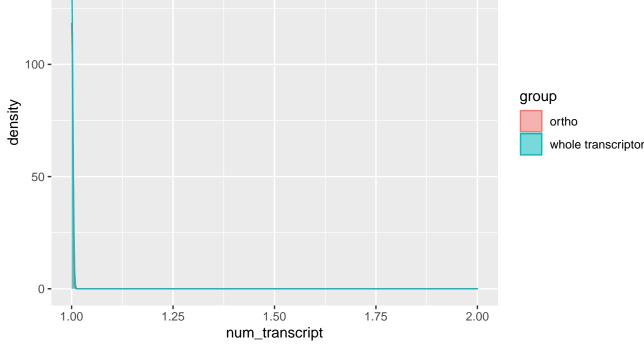


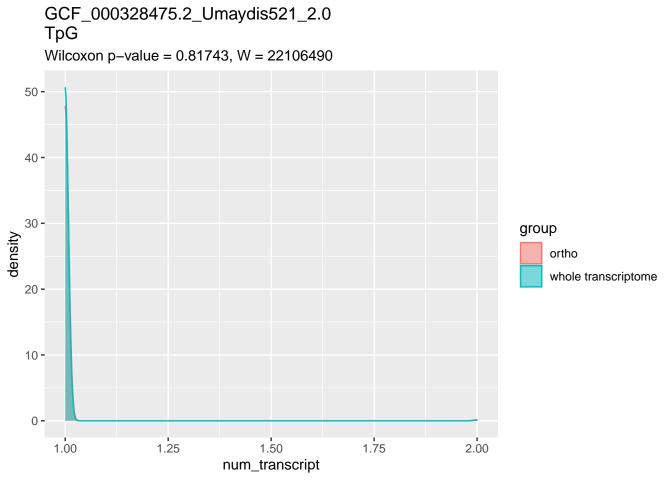


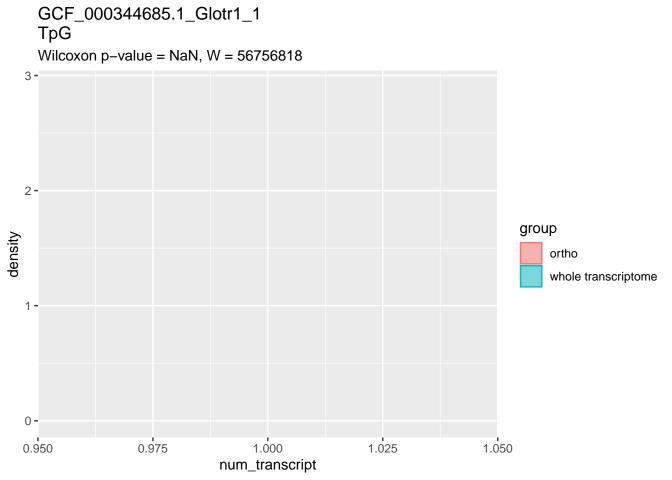


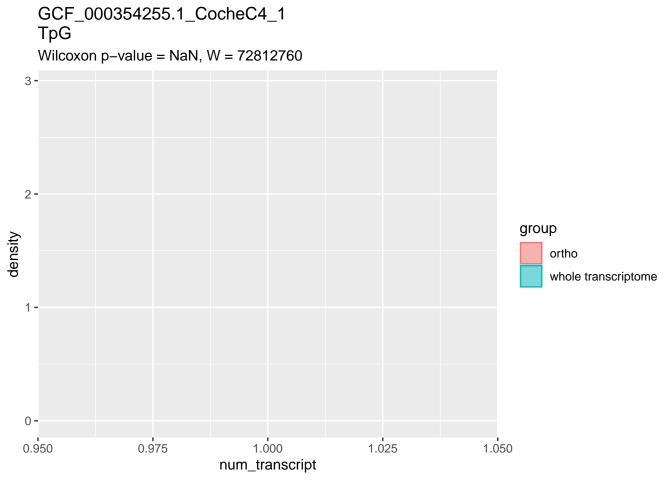


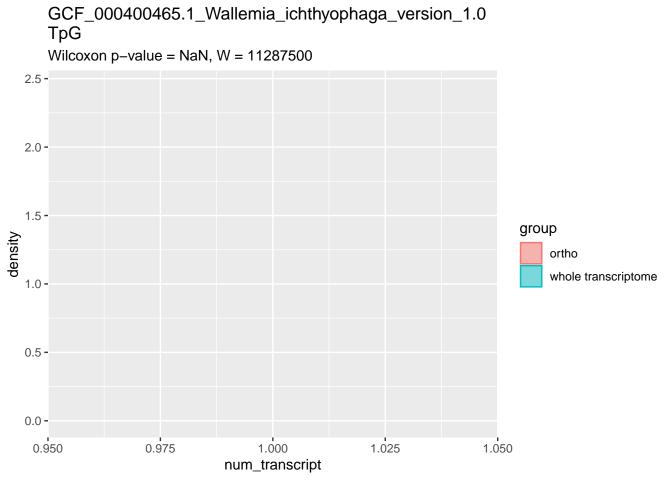
GCF_000320585.1_Heterobasidion_irregulare_v2.0 TpG Wilcoxon p-value = 0.55163, W = 5.8e+07150 **-**100 group ortho whole transcriptome 50 -

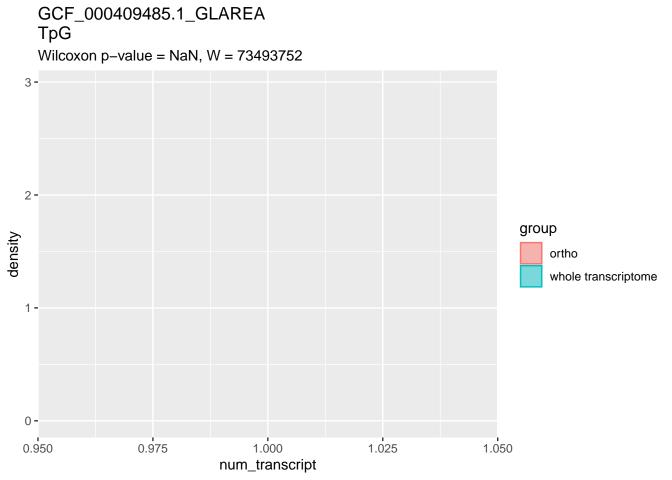


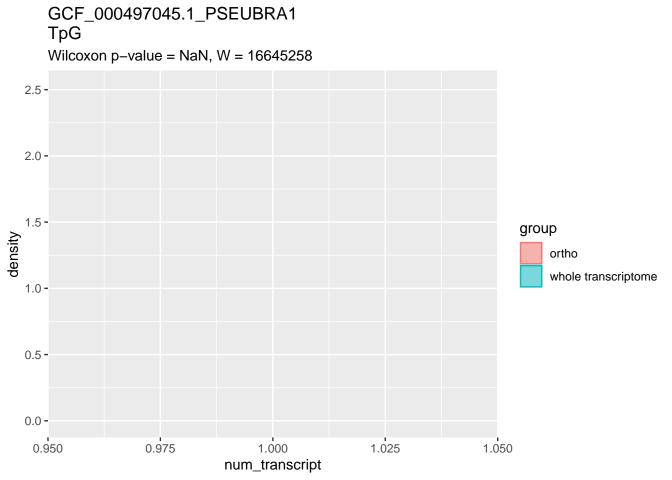


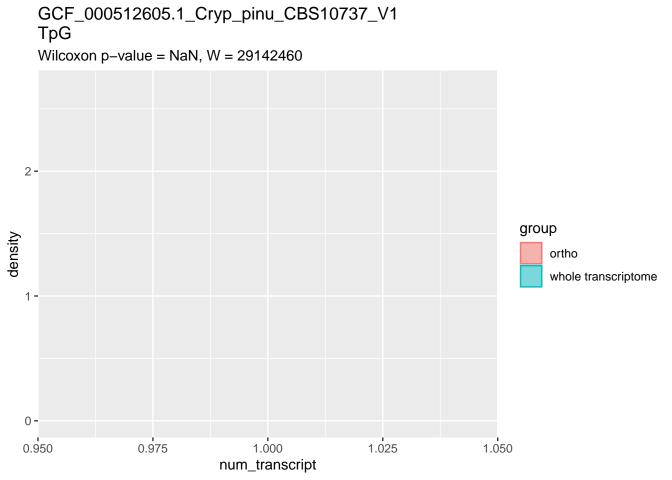


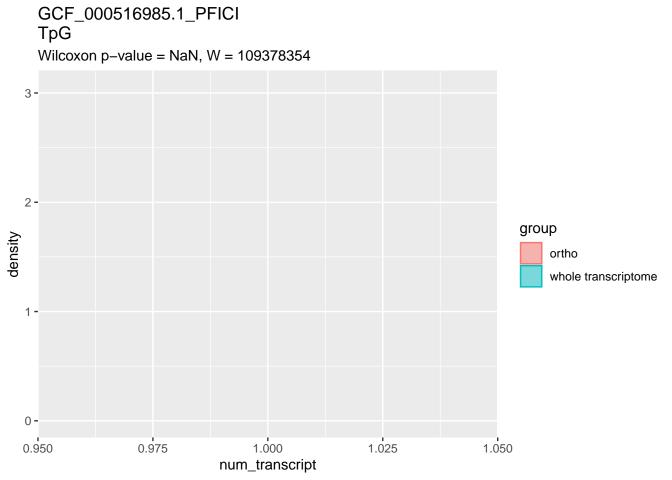


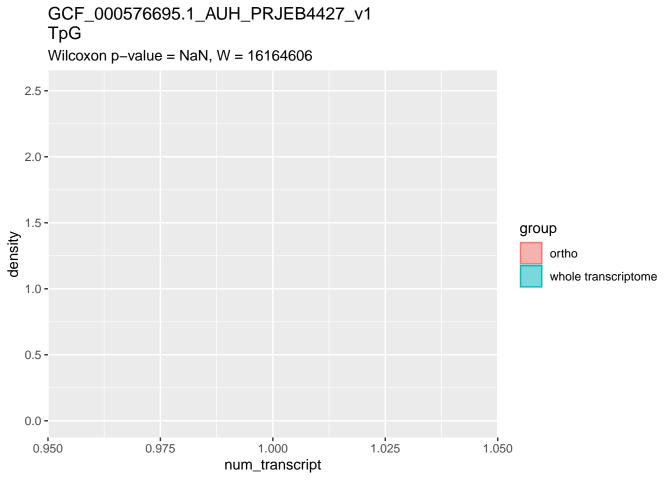


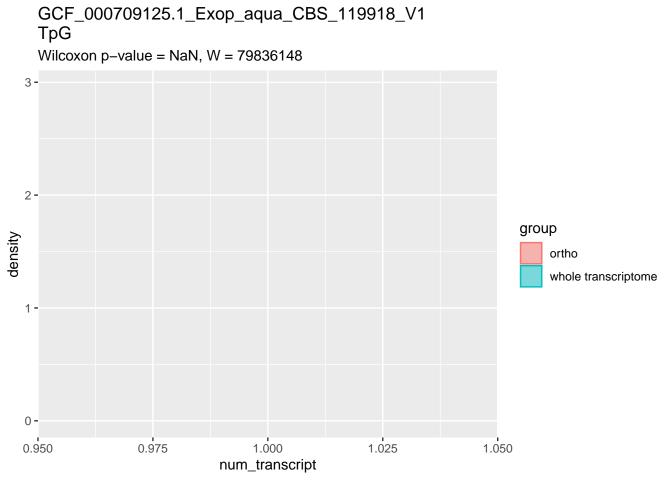


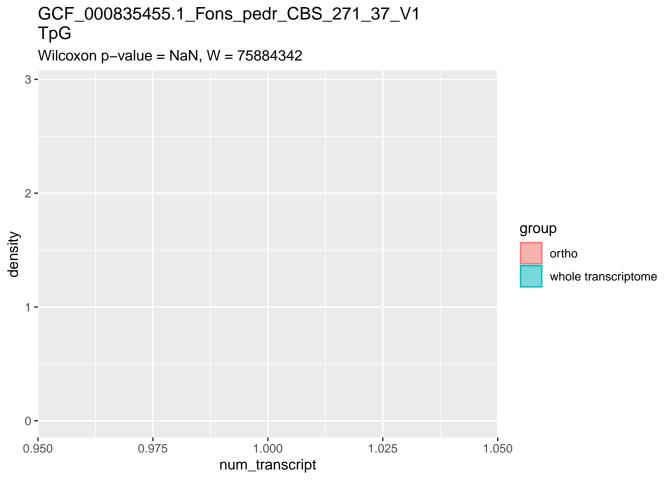


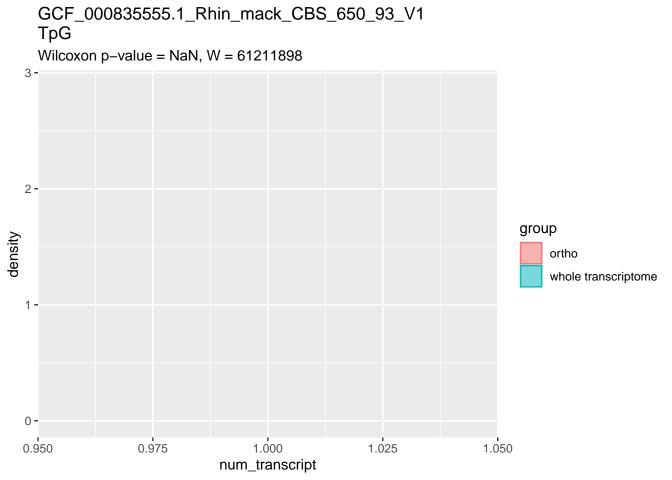


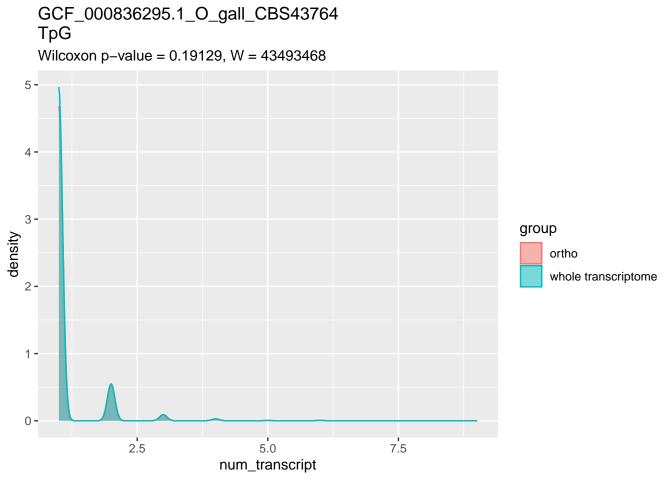


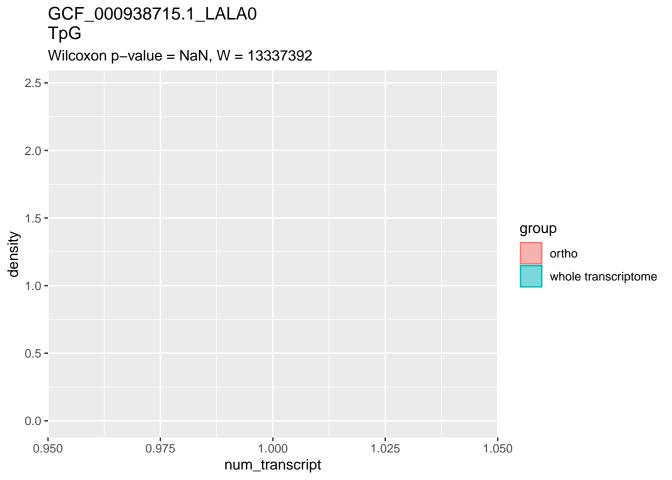


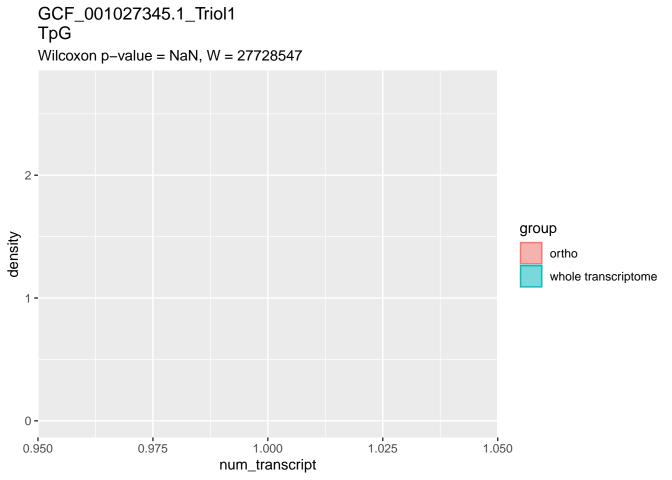


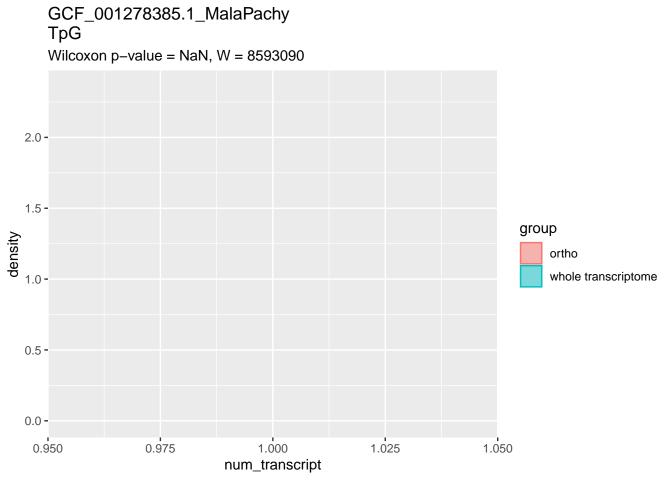


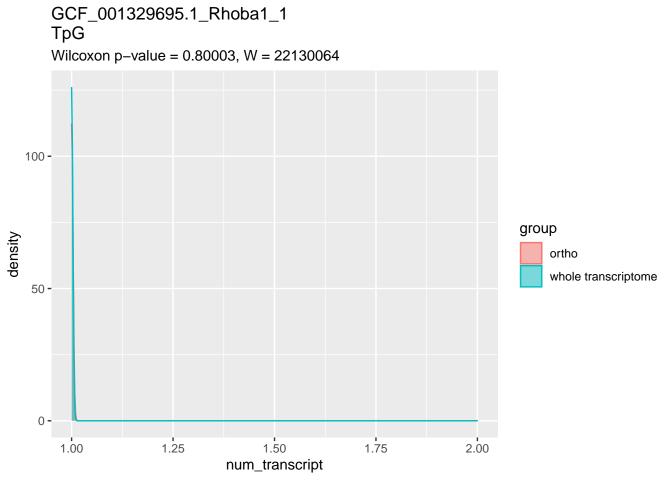


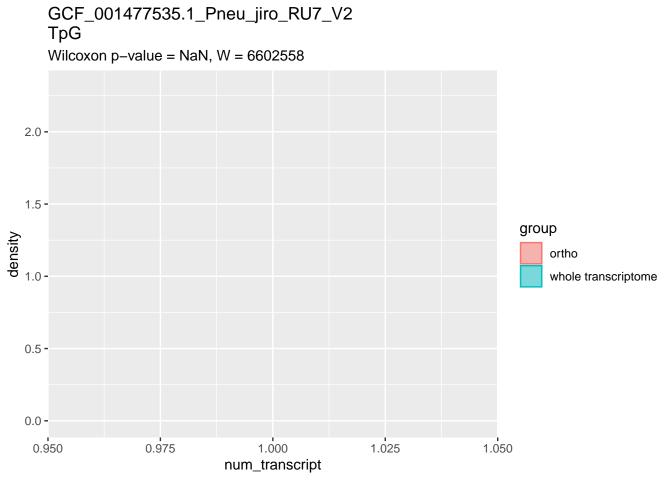


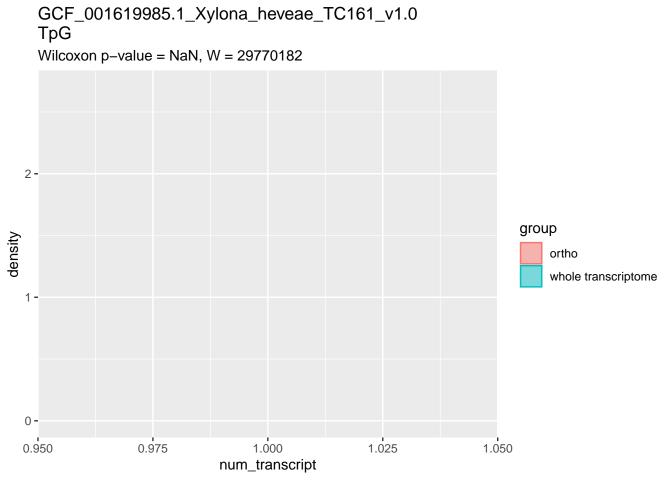


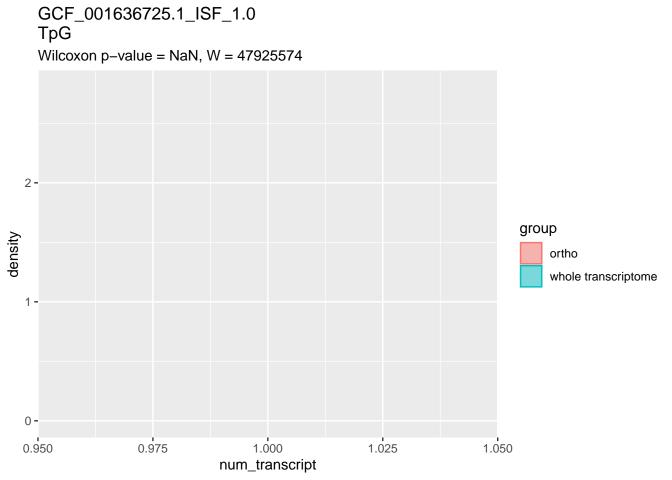


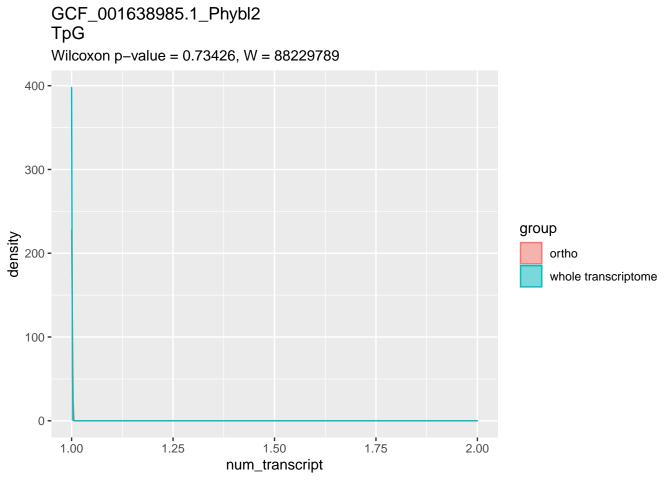


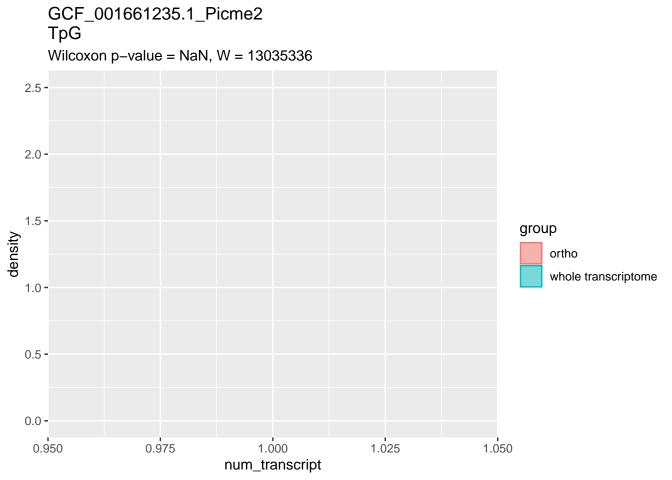


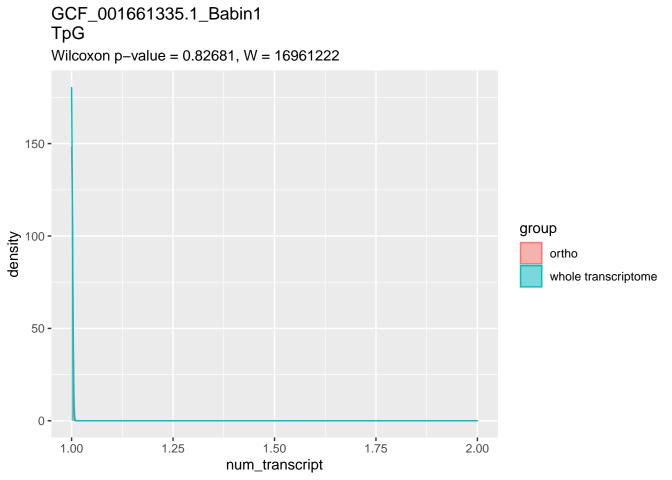


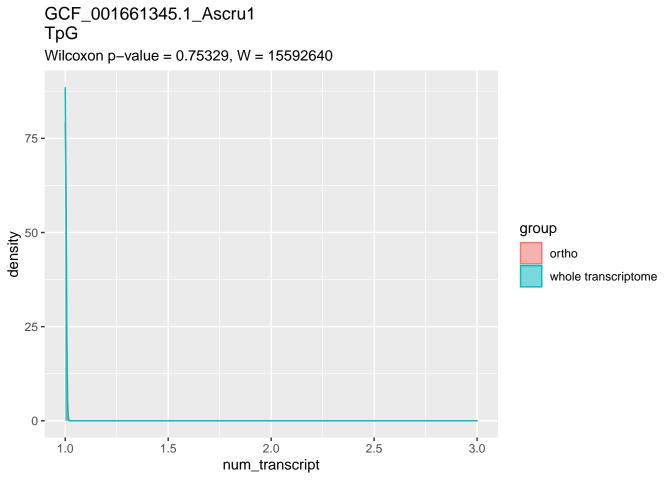


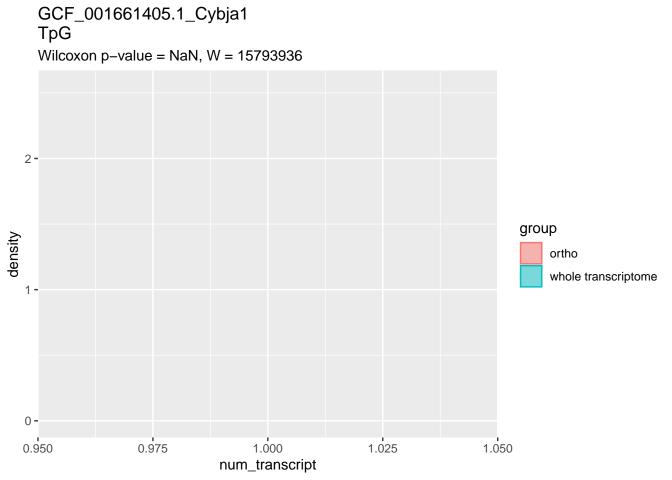


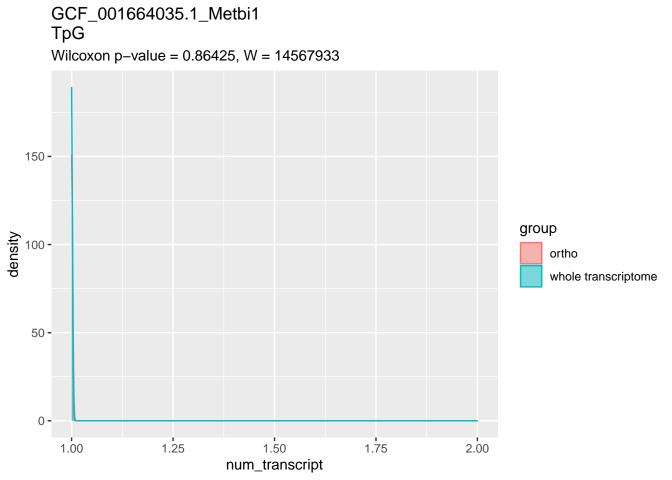


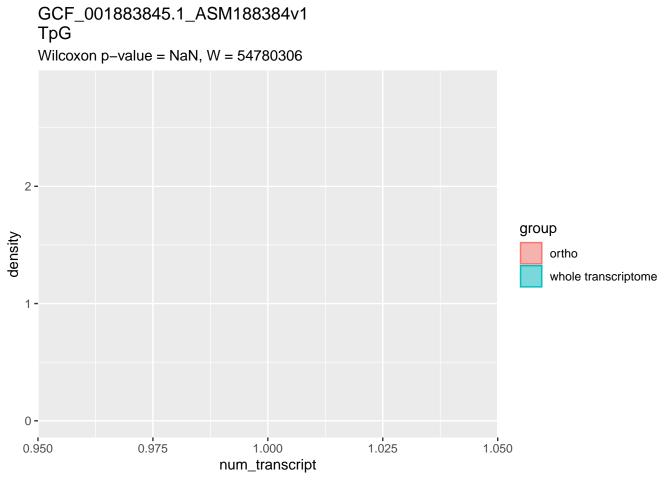




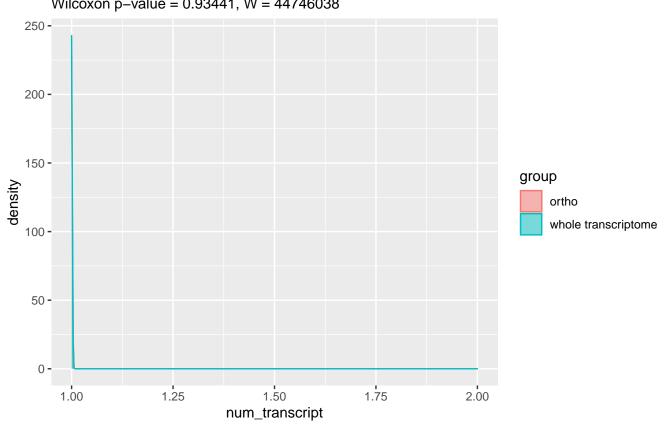


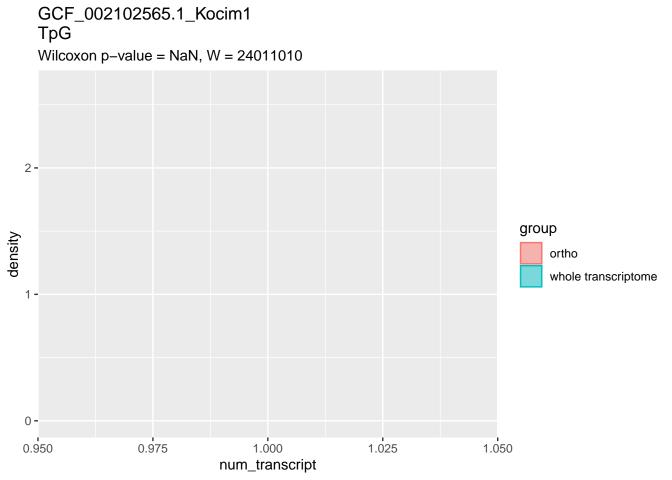


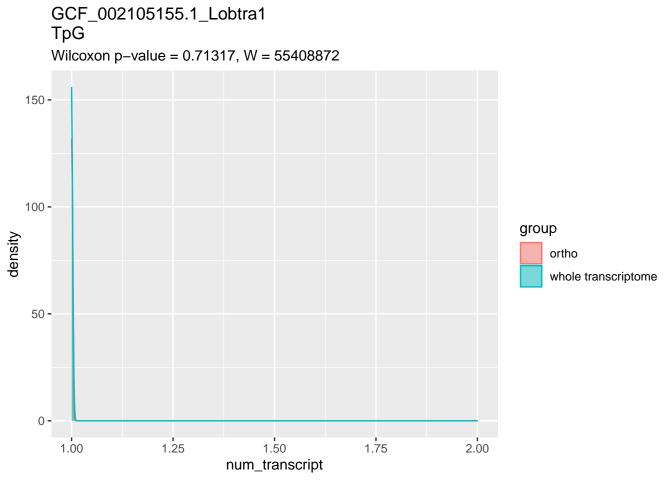


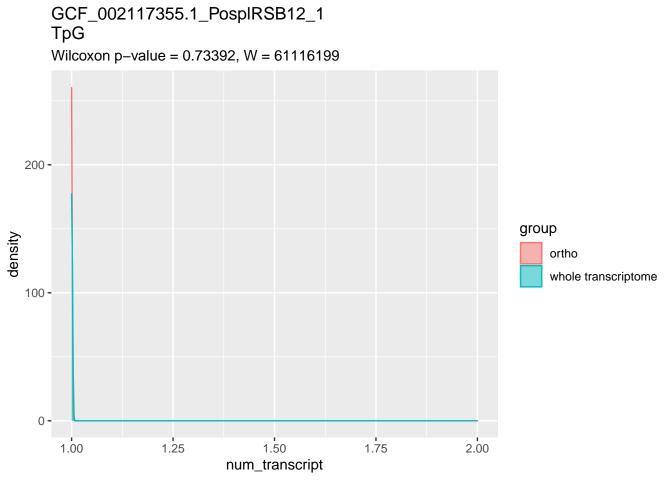


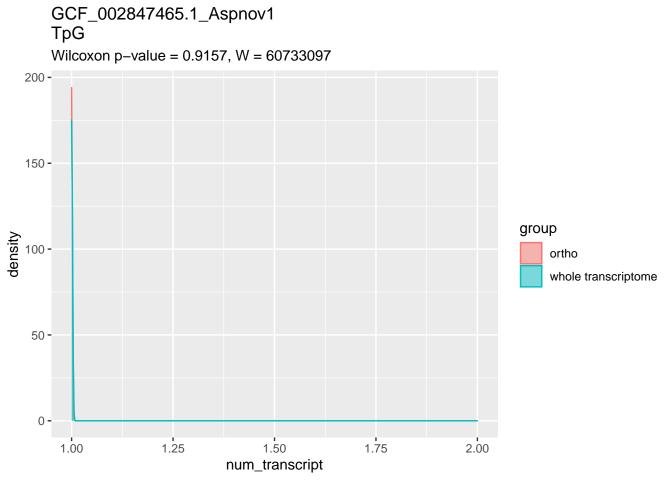
GCF_001890105.1_Aspzo1 TpG Wilcoxon p-value = 0.93441, W = 44746038

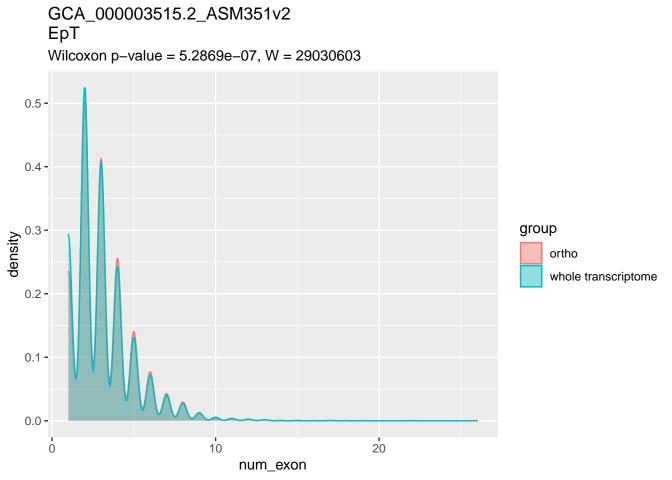


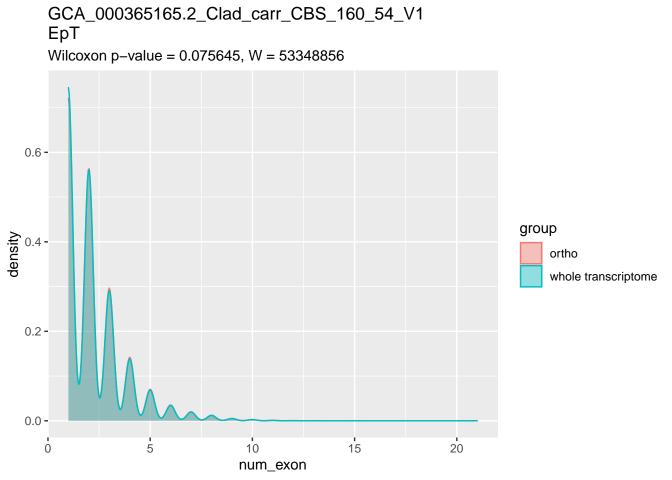


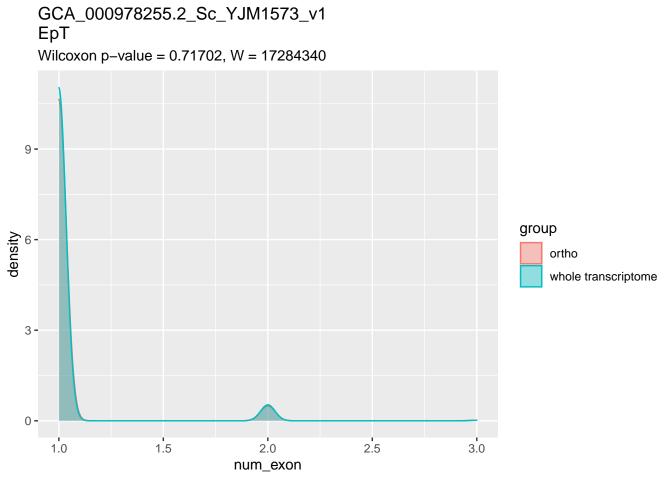






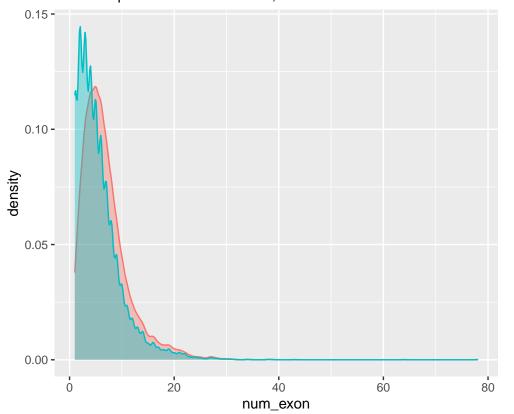






GCA_001574975.1_Ganpr1 EpT

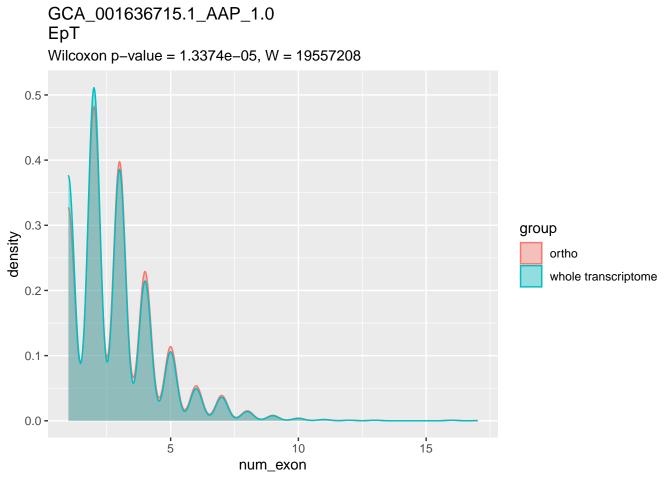
Wilcoxon p-value = 1.0995e-158, W = 71233330



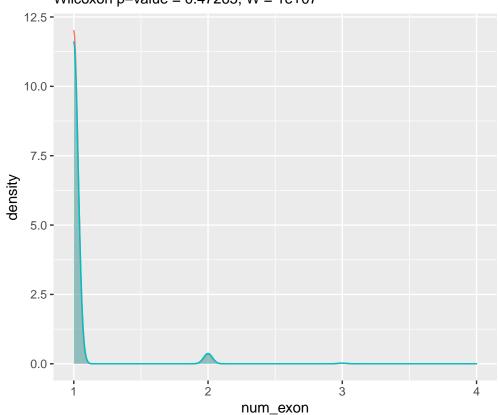
group

ortho

whole transcriptome



GCA_001747045.1_ASM174704v1 EpT Wilcoxon p-value = 0.47265, W = 1e+07

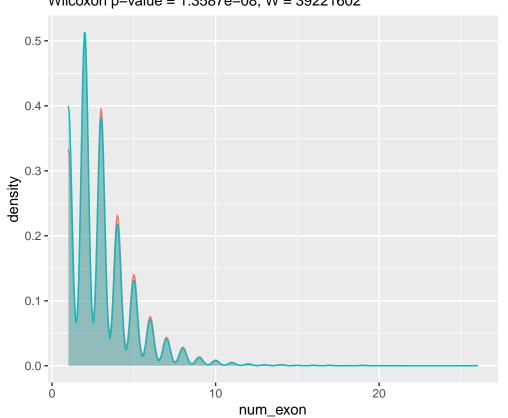


group

ortho

whole transcriptome

GCA_001883825.1_Emmo_past_UAMH9510_V1 EpT Wilcoxon p-value = 1.3587e-08, W = 39221602



group

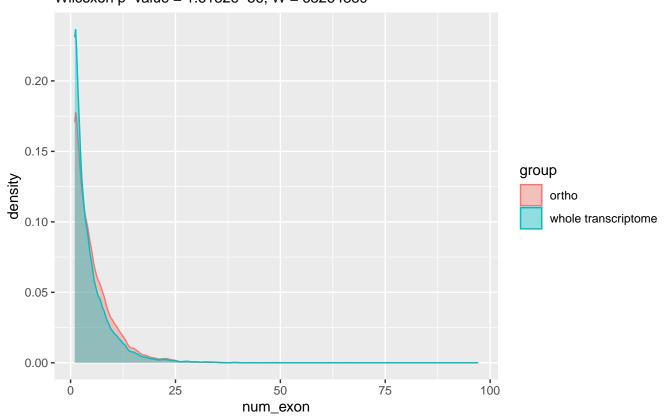
ortho

whole transcriptome

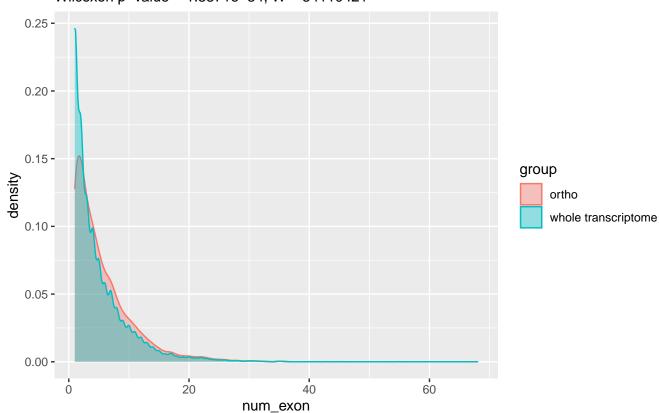
GCA_001929475.1_Neolirr1.0 EpT Wilcoxon p-value = 8.0961e-28, W = 13213286 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -10 20 30 num_exon

GCA_002006685.1_Batr_sala_BS_V1 **EpT** Wilcoxon p-value = 5.3926e-101, W = 66485014 0.20 -0.15 group density ortho whole transcriptome 0.05 -0.00 -10 20 30 40 num_exon

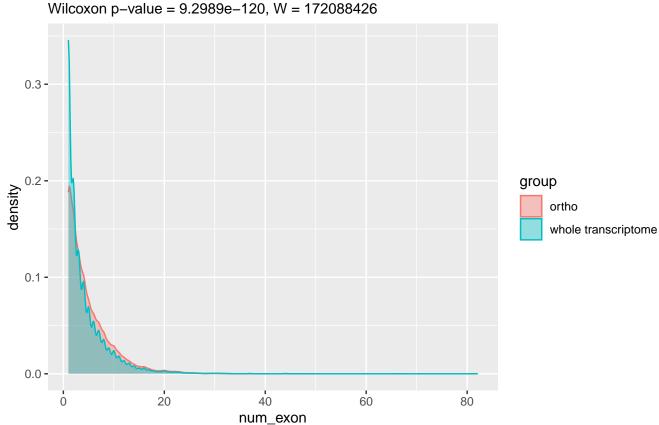
GCA_002104895.1_Anaeromyces_sp._S4_v1.0 EpT Wilcoxon p-value = 1.6182e-56, W = 68264889



GCA_002104945.1_Piromyces_sp._finnis_v3.0 EpT Wilcoxon p-value = 1.3371e-54, W = 54110421

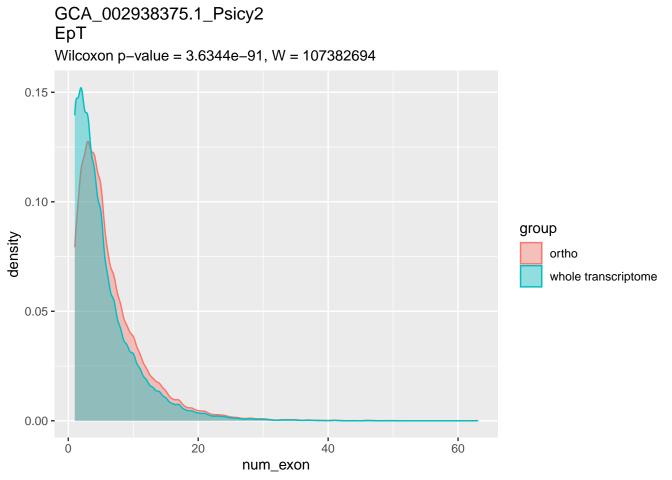


GCA_002104975.1_Neocallimastix_sp._G1_v1.0 EpT



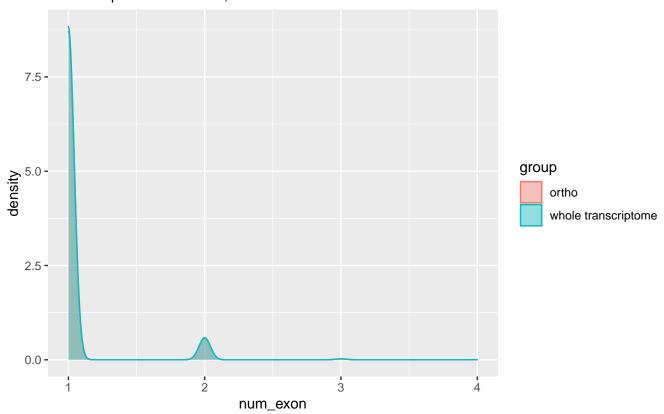
GCA_002104985.1_Rhihy1 EpT Wilcoxon p-value = 2.8699e-188, W = 104853940 0.3 -0.2 group density ortho whole transcriptome 0.1 -0.0 -10 20 50 30 40 num_exon

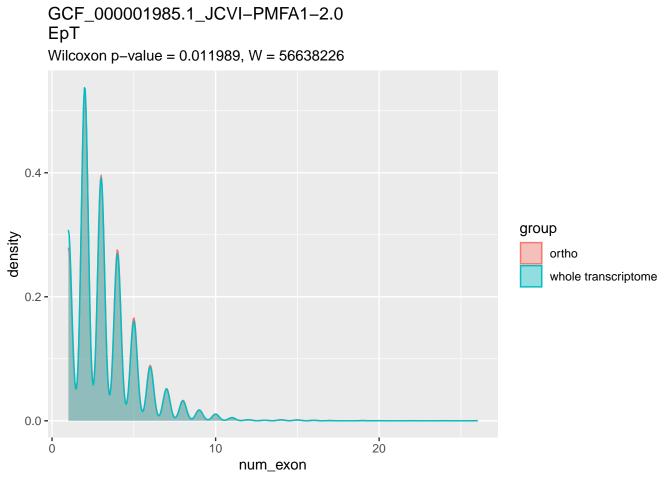
GCA_002918395.1_ASM291839v1 **EpT** Wilcoxon p-value = 0.00069673, W = 21165694 0.4 group density ortho whole transcriptome 0.2 -0.0 -12 16 num_exon



GCA_900106115.1_CBS_141442_assembly EpT

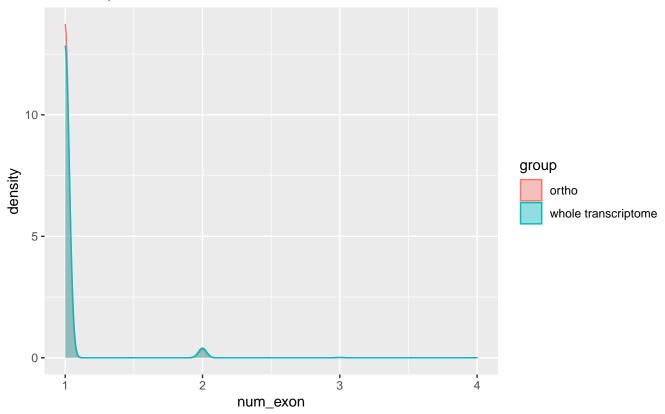
Wilcoxon p-value = 0.9859, W = 16542289



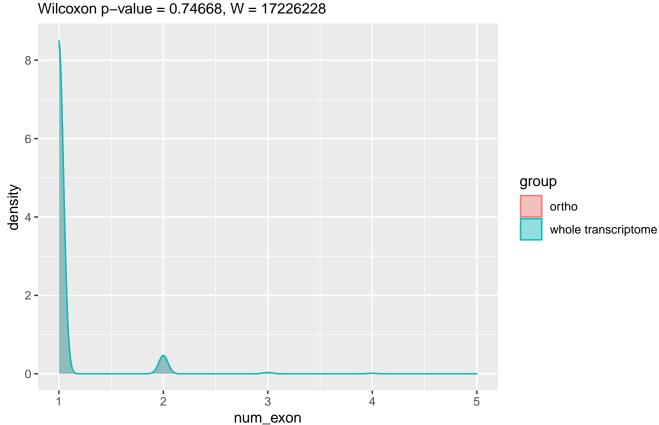


GCF_000002545.3_ASM254v2 EpT

Wilcoxon p-value = 0.062028, W = 13477208

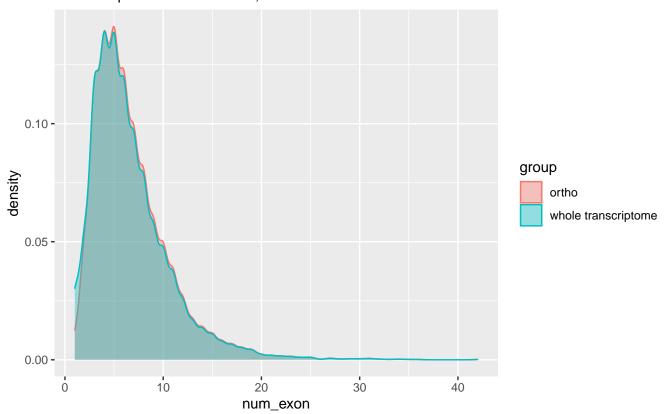


GCF_000026945.1_ASM2694v1 EpT



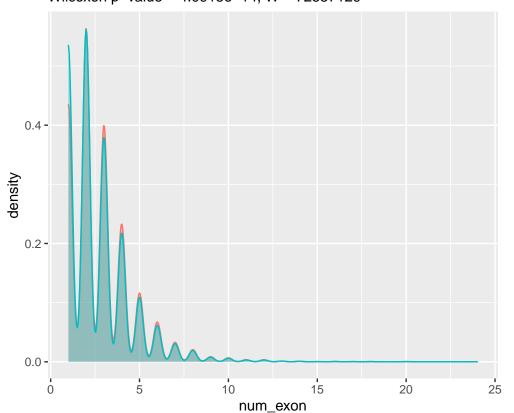
GCF_000091045.1_ASM9104v1 EpT

Wilcoxon p-value = 0.0023912, W = 24252288



GCF_000143185.1_v1.0 EpT Wilcoxon p-value = 1.6727e-40, W = 72109412 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -20 40 60 num_exon

GCF_000149035.1_C_graminicola_M1_001_V1 EpT Wilcoxon p-value = 4.0915e-14, W = 72557129

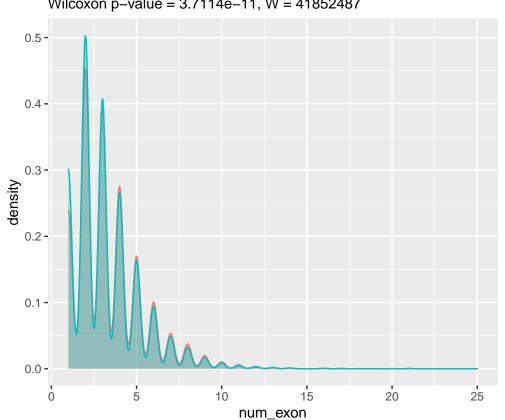


group

ortho

whole transcriptome

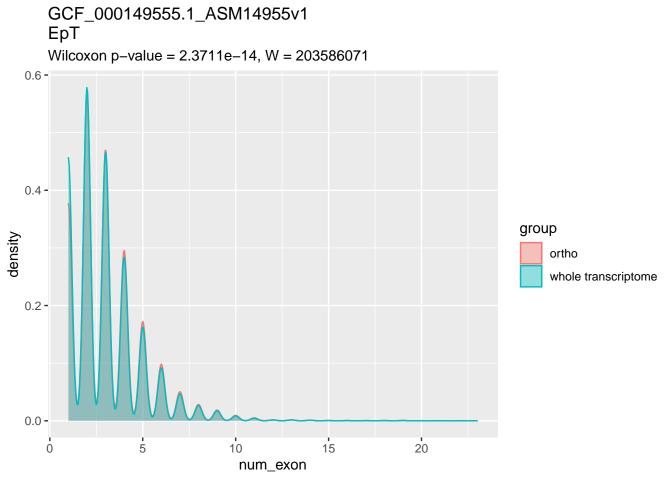
GCF_000149335.2_ASM14933v2 EpT Wilcoxon p-value = 3.7114e-11, W = 41852487

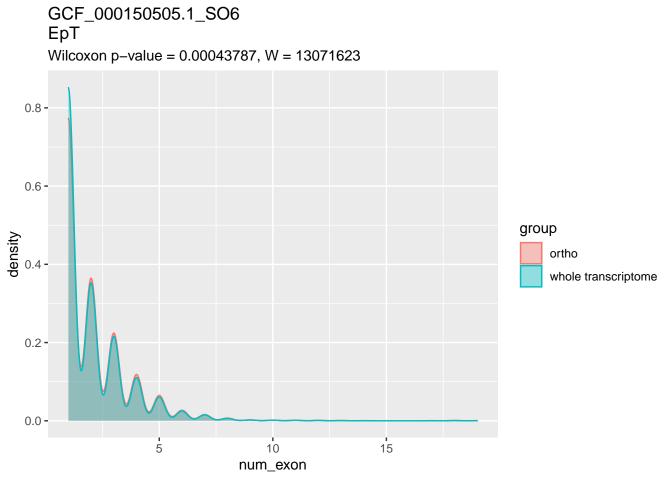


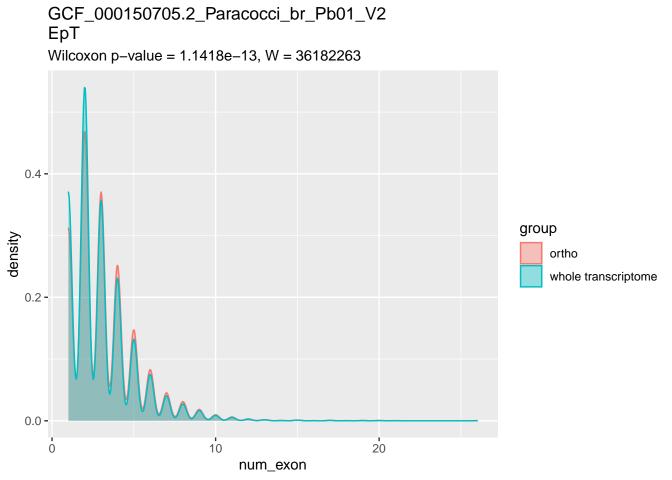
group

ortho

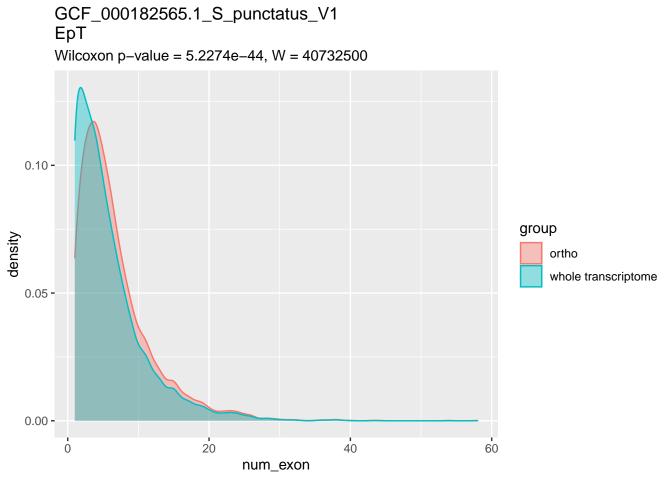
whole transcriptome

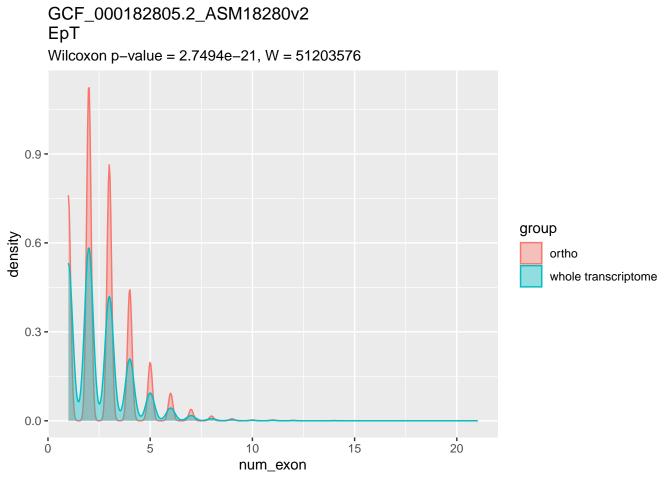






GCF_000171015.1_TRIAT_v2.0 **EpT** Wilcoxon p-value = 1.91e-12, W = 613882820.4 group density ortho whole transcriptome 0.2 -0.0 -10 20 5 15 num_exon

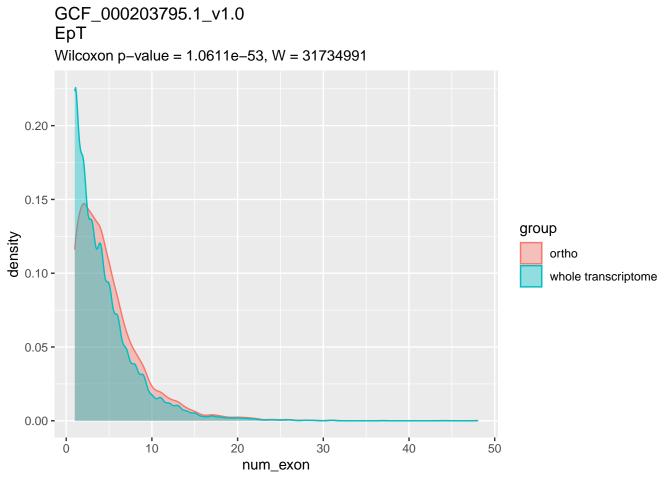




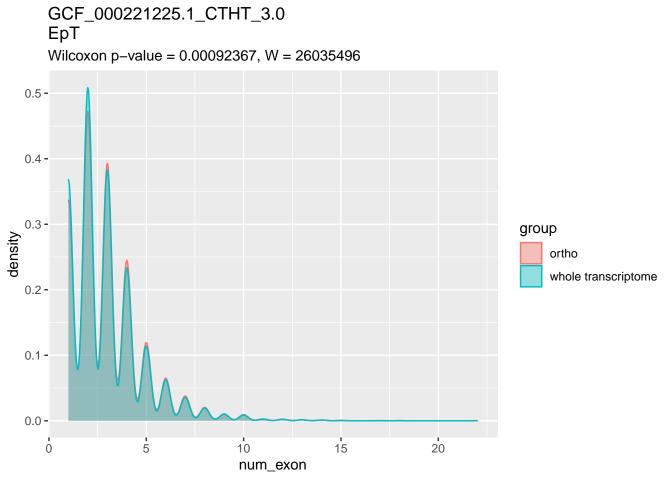
GCF_000182895.1_CC3 EpT Wilcoxon p-value = 1.229e-63, W = 81356712 0.15 -0.10 group density ortho whole transcriptome 0.05 -0.00 -20

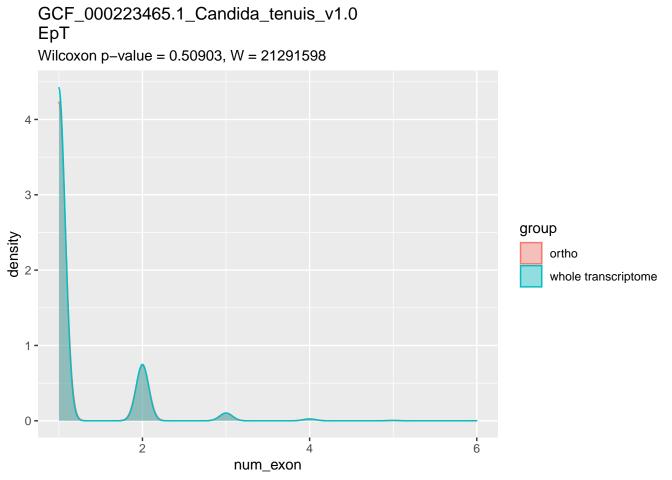
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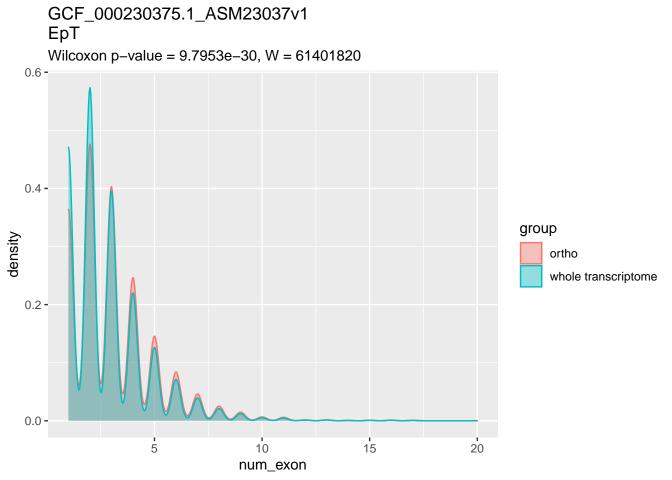
num_exon



GCF_000204055.1_v1.0 **EpT** Wilcoxon p-value = 1.0391e-122, W = 87177470 0.15 density 0.10 group ortho whole transcriptome 0.05 -0.00 -20 30 10 40 num_exon

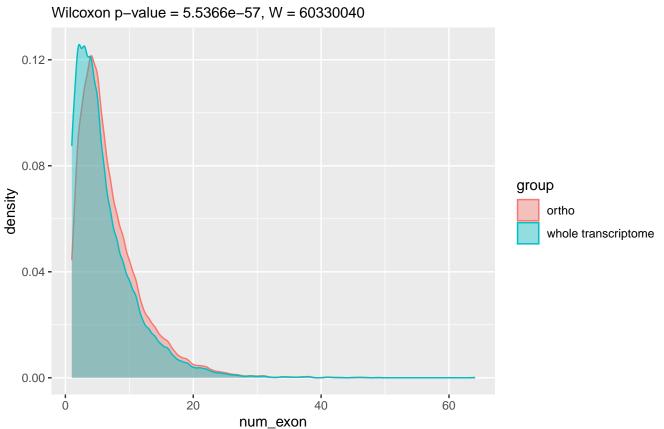






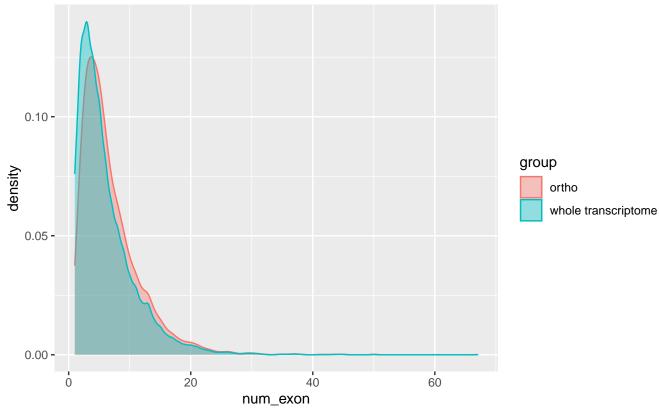
GCF_000264905.1_Stehi1 **EpT** Wilcoxon p-value = 6.8178e-69, W = 91028688 0.125 -0.100 -0.075 group density ortho whole transcriptome 0.050 -0.025 -0.000 -20 40 60 80 num_exon

GCF_000264995.1_Punctularia_strigosozonata_v1.0 EpT



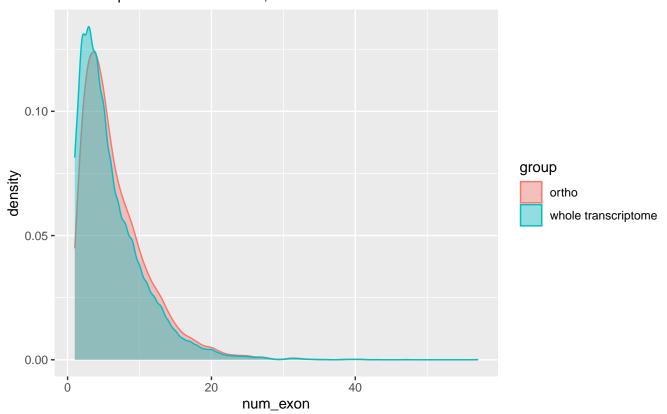
GCF_000271605.1_Fomme1 EpT

Wilcoxon p-value = 2.1102e-59, W = 56456622

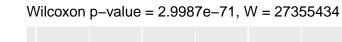


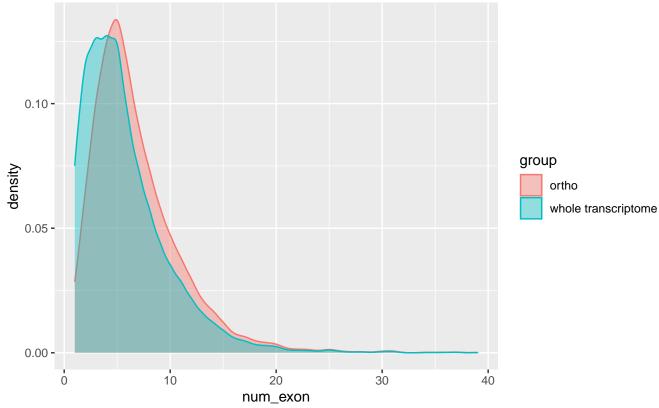
GCF_000271625.1_Conpu1 EpT

Wilcoxon p-value = 4.3283e-48, W = 82951852



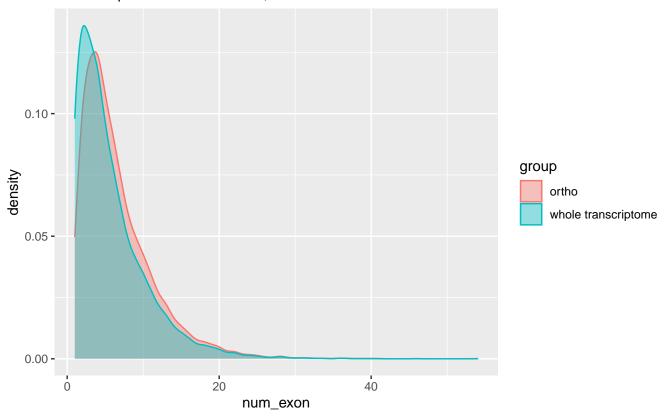
GCF_000271645.1_Treme1 EpT





GCF_000275845.1_Dichomitus_squalens_v1.0 EpT

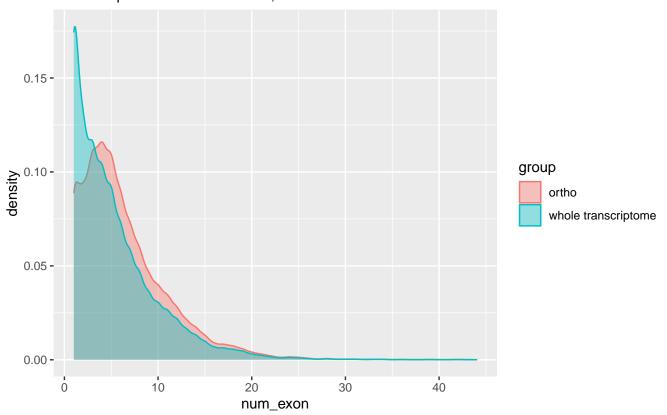
Wilcoxon p-value = 1.5407e-67, W = 70290322



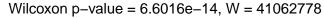
GCF_000281105.1_Coni_apol_CBS100218_V1 **EpT** Wilcoxon p-value = 4.9957e-07, W = 41436016 0.4 group density ortho whole transcriptome 0.2 -0.0 -5 10 . 15 num_exon

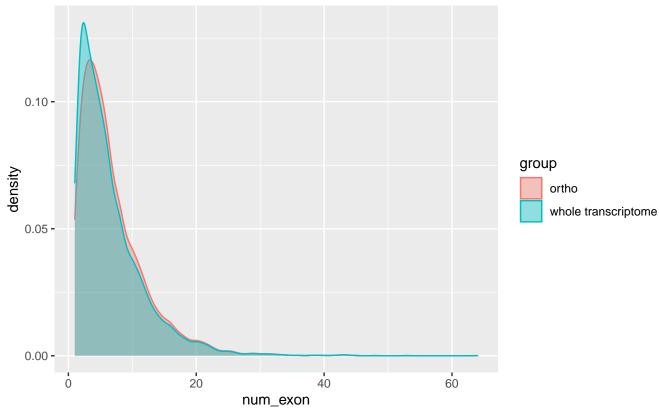
GCF_000300595.1_Phanerochaete_carnosa_HHB-10118-Sp_v1.0 EpT

Wilcoxon p-value = 1.8906e-111, W = 84941675

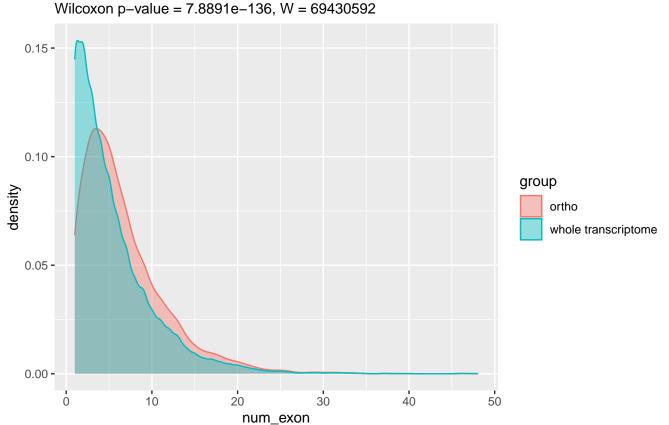


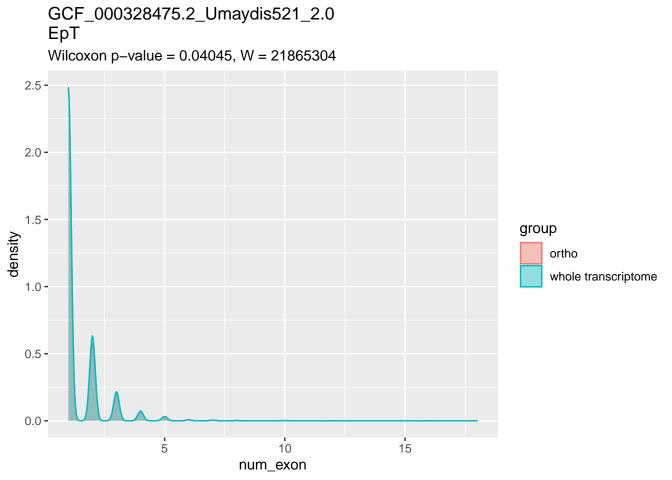
GCF_000313525.1_ASM31352v1 EpT

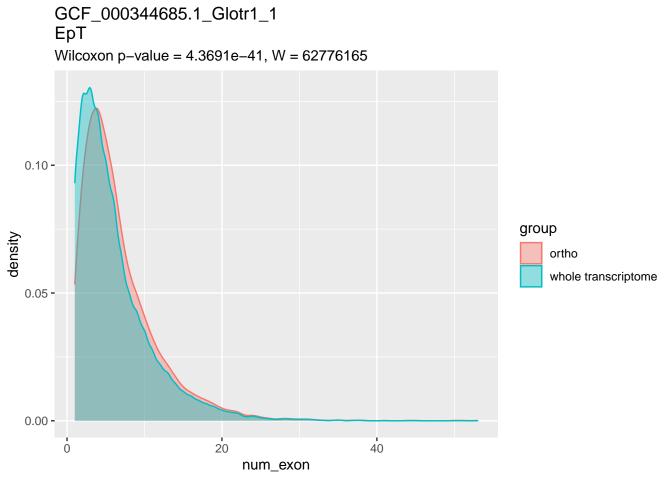


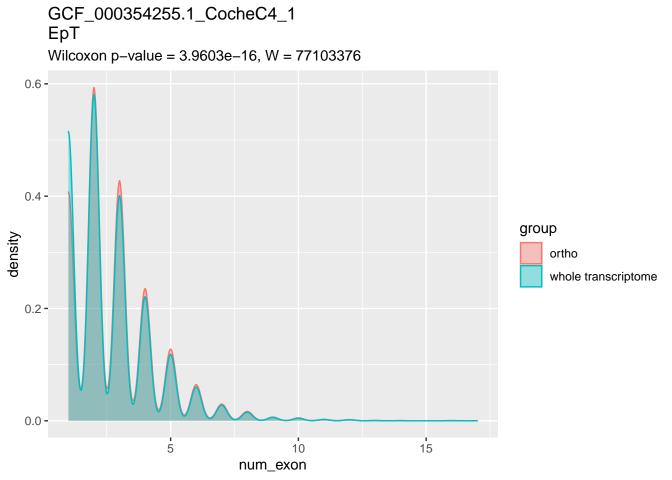


GCF_000320585.1_Heterobasidion_irregulare_v2.0 EpT

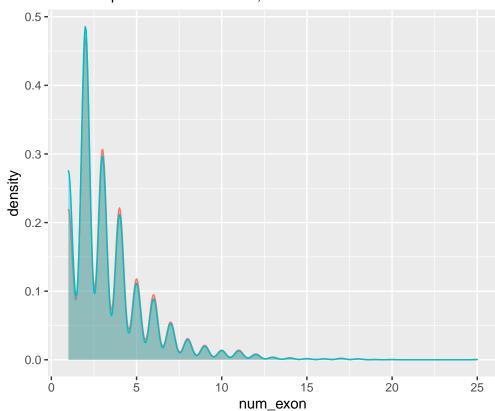








GCF_000400465.1_Wallemia_ichthyophaga_version_1.0 EpT Wilcoxon p-value = 4.0854e-05, W = 11825388



group

ortho

whole transcriptome

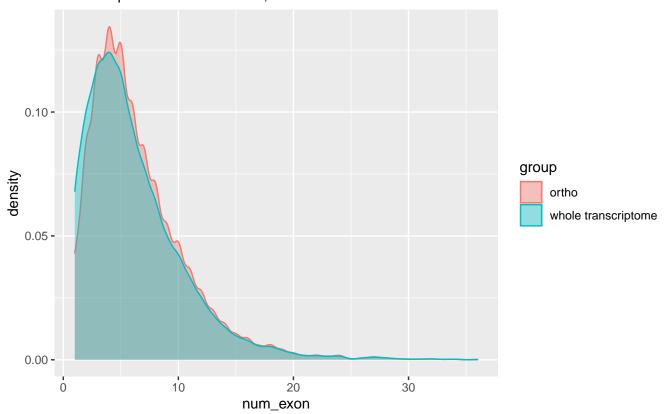
GCF_000409485.1_GLAREA EpT Wilcoxon p-value = 3.2847e-20, W = 78415741 0.5 -0.4 density 0.3 group ortho whole transcriptome 0.2 -0.1 -0.0 -10 20 30 num_exon

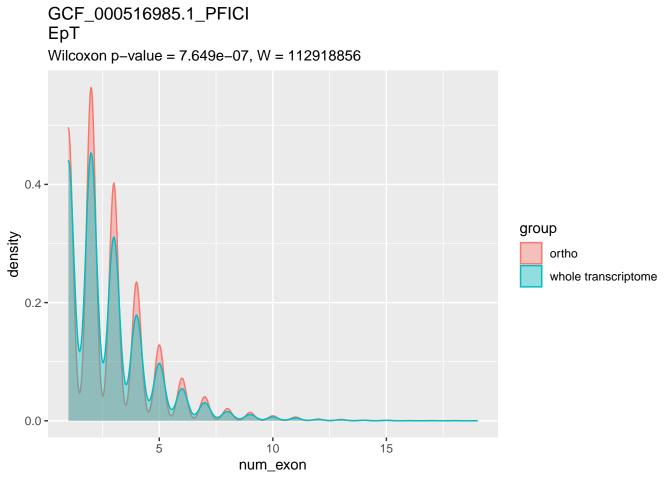
GCF_000497045.1_PSEUBRA1 EpT Wilcoxon p-value = 0.1247, W = 16409746 2.0 -1.5 group density ortho whole transcriptome 0.5 -0.0 -5.0 2.5 7.5 10.0 12.5

num_exon

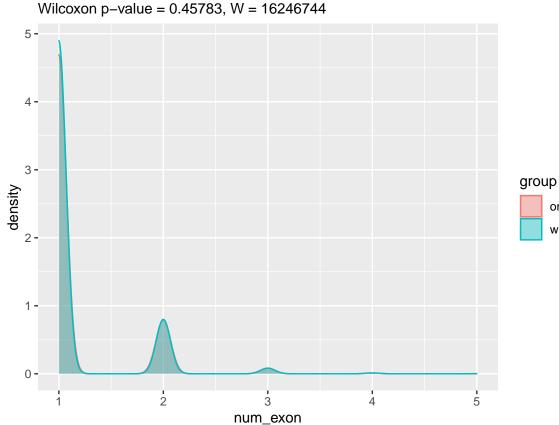
GCF_000512605.1_Cryp_pinu_CBS10737_V1 EpT

Wilcoxon p-value = 1.8916e-10, W = 30870323



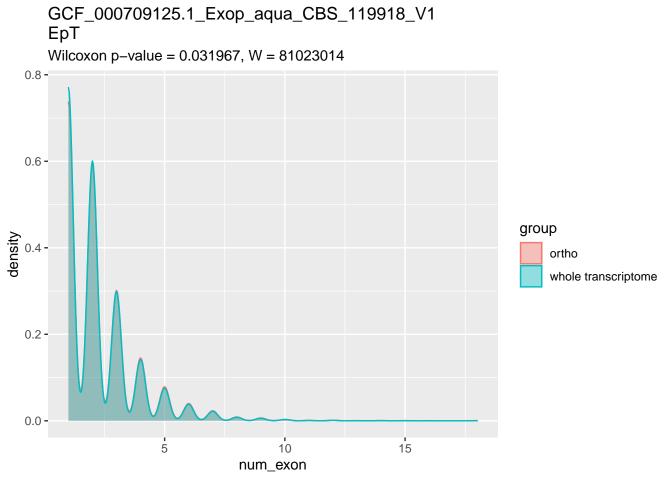


GCF_000576695.1_AUH_PRJEB4427_v1 EpT



ortho

whole transcriptome



GCF_000835455.1_Fons_pedr_CBS_271_37_V1 **EpT** Wilcoxon p-value = 0.1242, W = 76710654 0.6 density 0.4 group ortho whole transcriptome 0.2 -0.0 -10 15 num_exon

GCF_000835555.1_Rhin_mack_CBS_650_93_V1 **EpT** Wilcoxon p-value = 0.031178, W = 621976570.6 density 0.4 group ortho whole transcriptome 0.2 -0.0 -12 num_exon

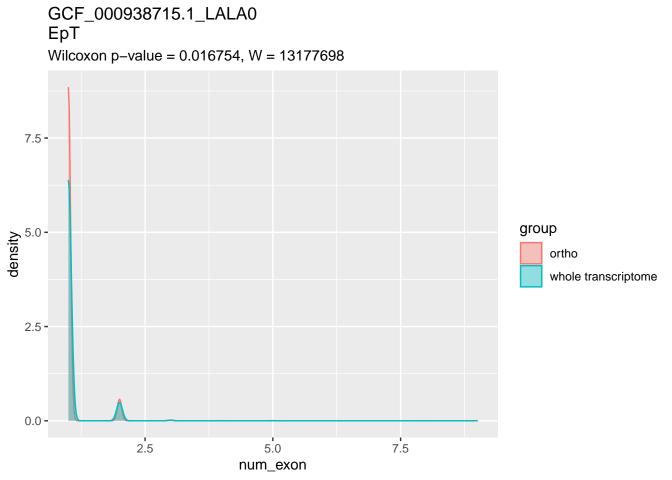
GCF_000836295.1_O_gall_CBS43764 EpT Wilcoxon p-value = 1.2554e-09, W = 608753480.6 -0.4 group density ortho whole transcriptome 0.2 -0.0 -5 10

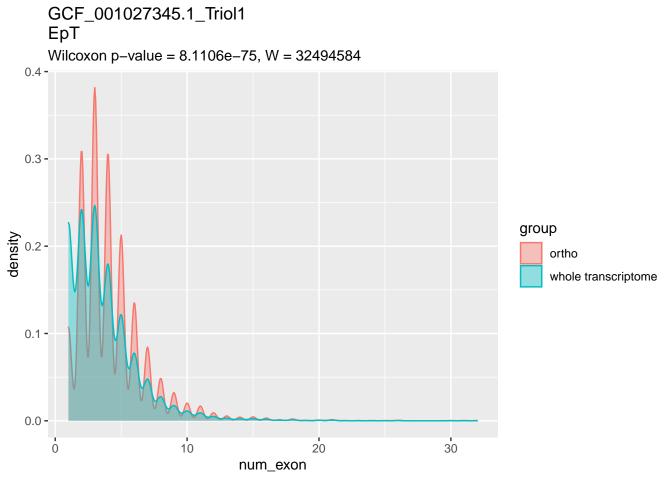
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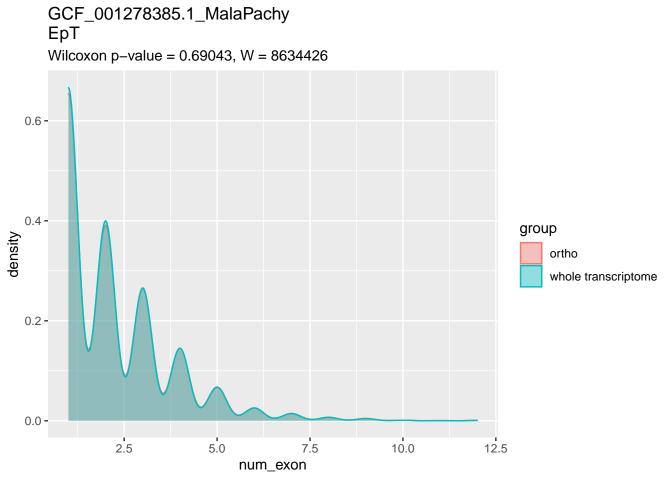
num_exon

20

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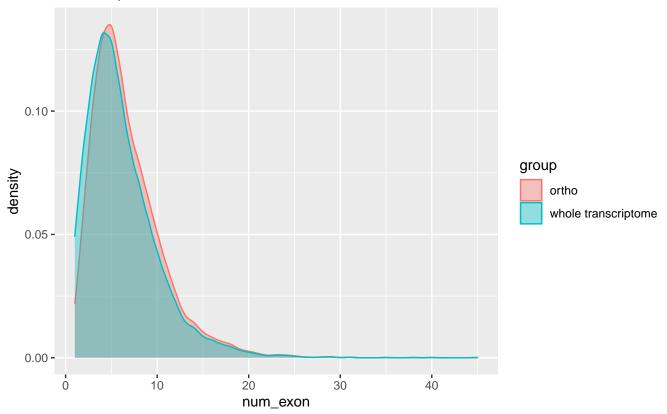




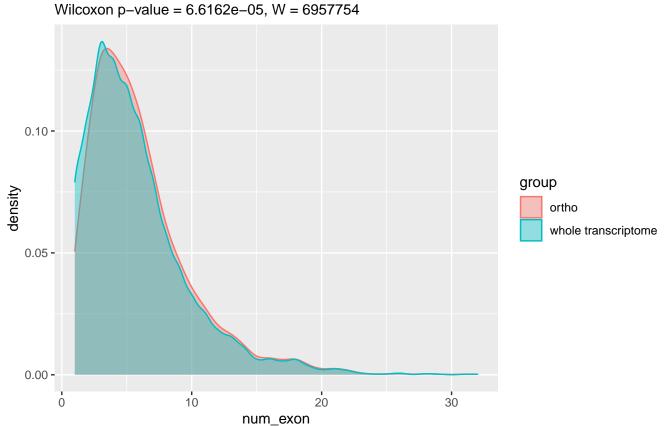


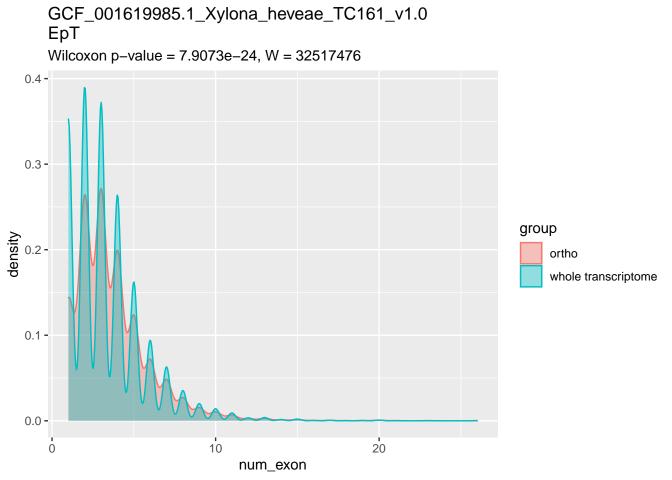
GCF_001329695.1_Rhoba1_1 EpT

Wilcoxon p-value = 2.2047e-22, W = 24300781

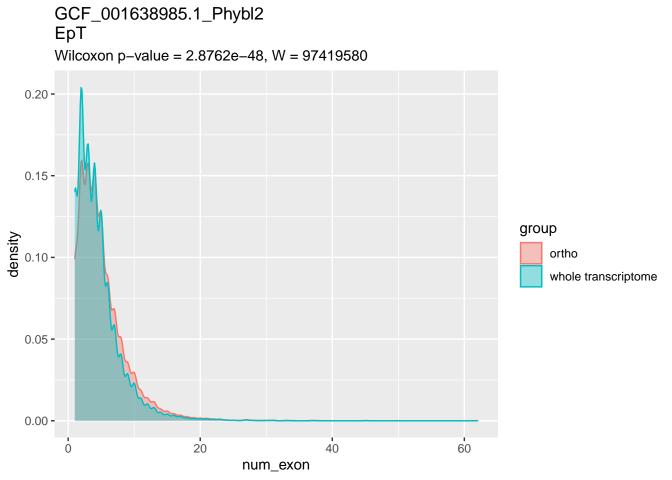


GCF_001477535.1_Pneu_jiro_RU7_V2 EpT



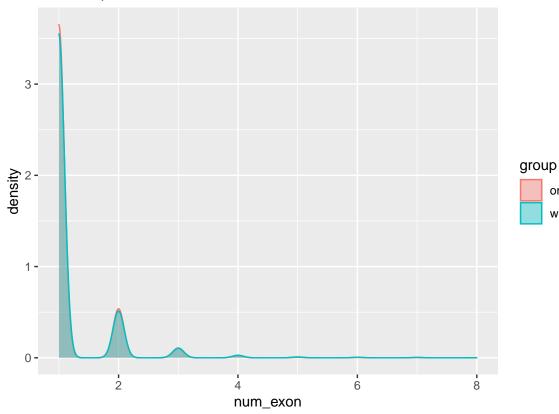


GCF_001636725.1_ISF_1.0 EpT Wilcoxon p-value = 0.023964, W = 487919980.4 group density ortho whole transcriptome 0.2 -0.0 -10 5 15 20 num_exon

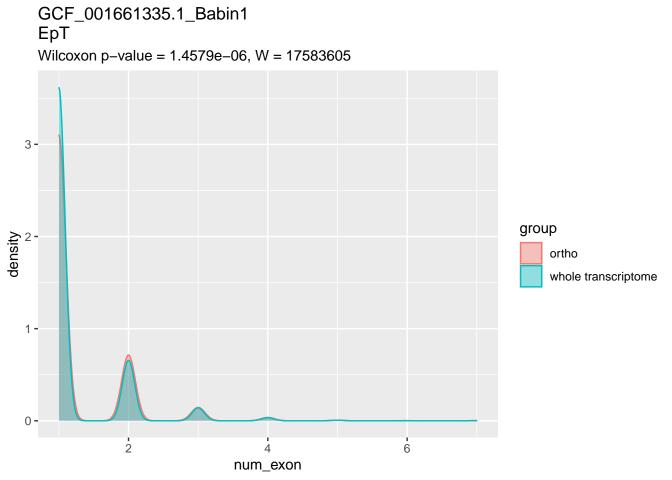


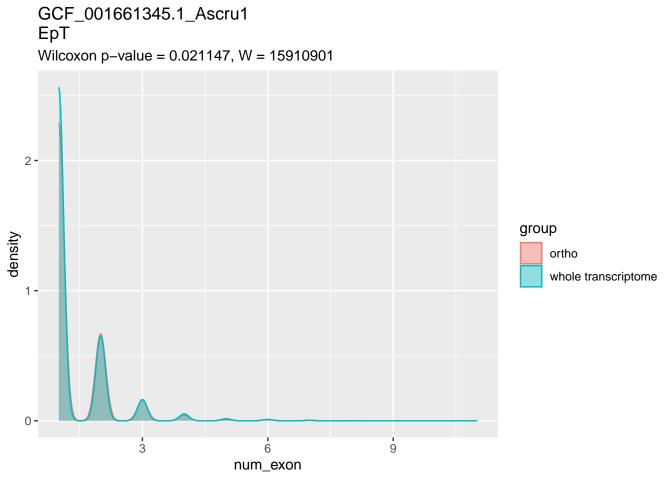
GCF_001661235.1_Picme2 EpT

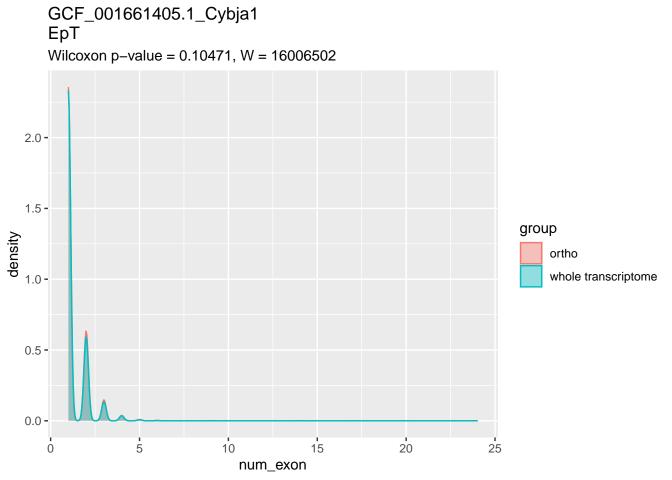
Wilcoxon p-value = 0.74992, W = 13005198

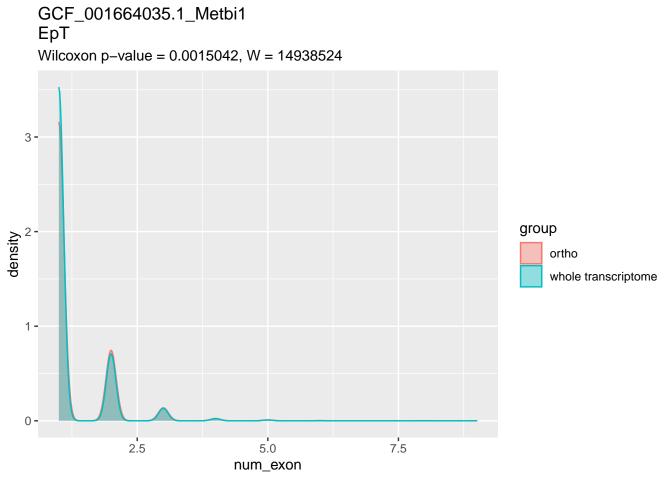


ortho



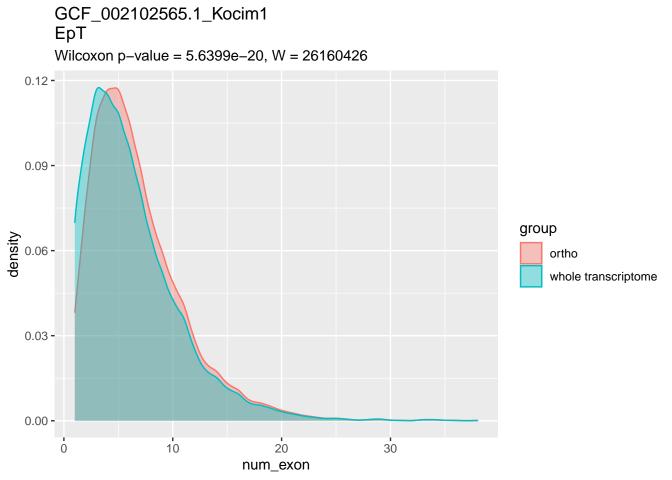






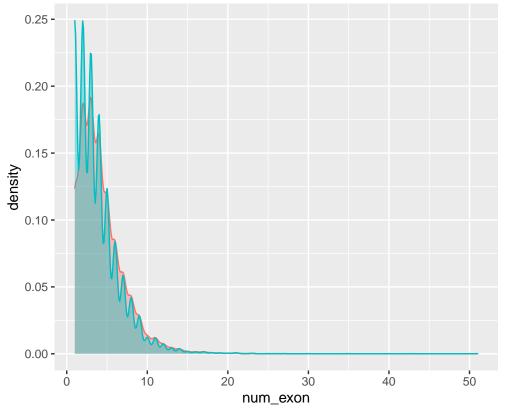
GCF_001883845.1_ASM188384v1 EpT Wilcoxon p-value = 0.00014592, W = 564066560.5 -0.4 density 0.3 group ortho whole transcriptome 0.2 -0.1 -0.0 -5 10 20 15 25 num_exon

GCF_001890105.1_Aspzo1 EpT Wilcoxon p-value = 2.2334e-10, W = 47097161 0.4 -0.3 density 0.2 group ortho whole transcriptome 0.1 -0.0 -10 20 num_exon



GCF_002105155.1_Lobtra1 EpT

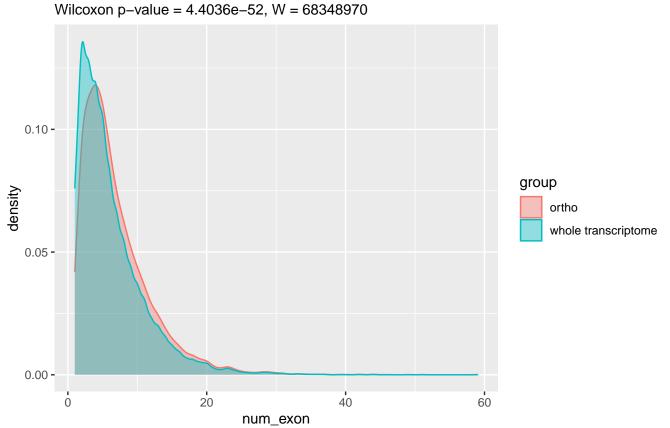




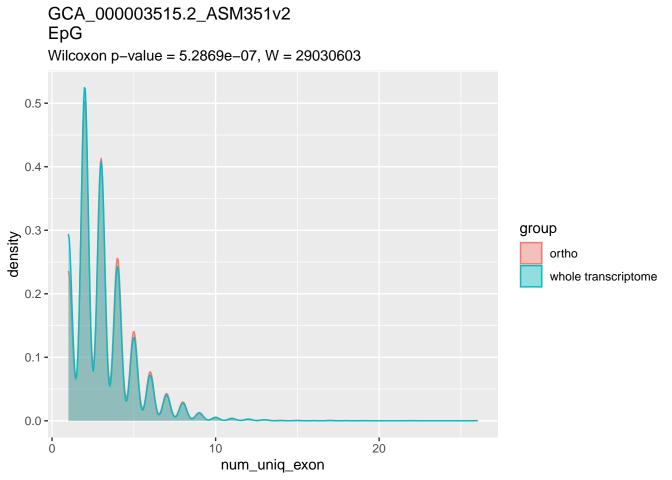
group

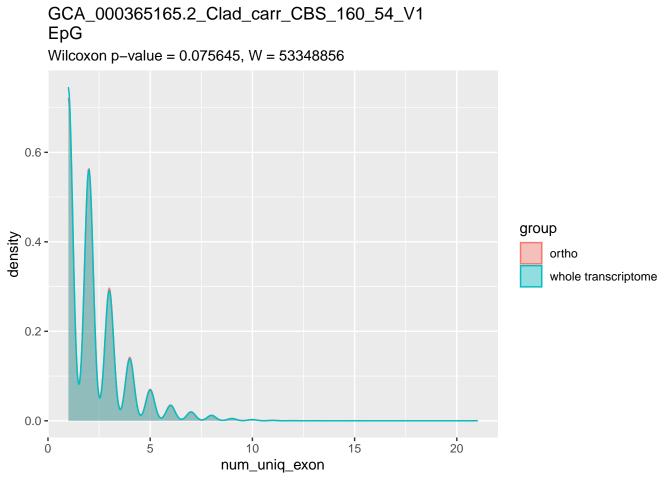
ortho

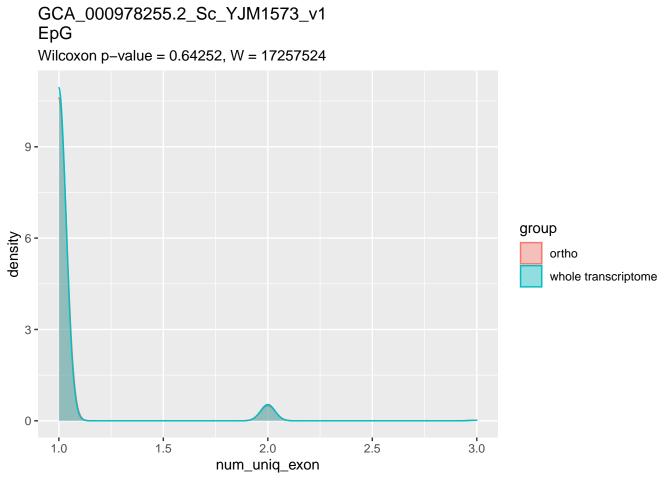
GCF_002117355.1_PosplRSB12_1 EpT



GCF_002847465.1_Aspnov1 EpT Wilcoxon p-value = 7.9483e-15, W = 643656580.4 -0.3 density 0.2 group ortho whole transcriptome 0.1 -0.0 -10 20 num_exon

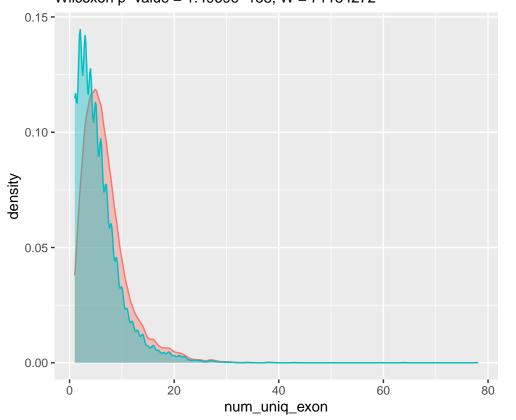






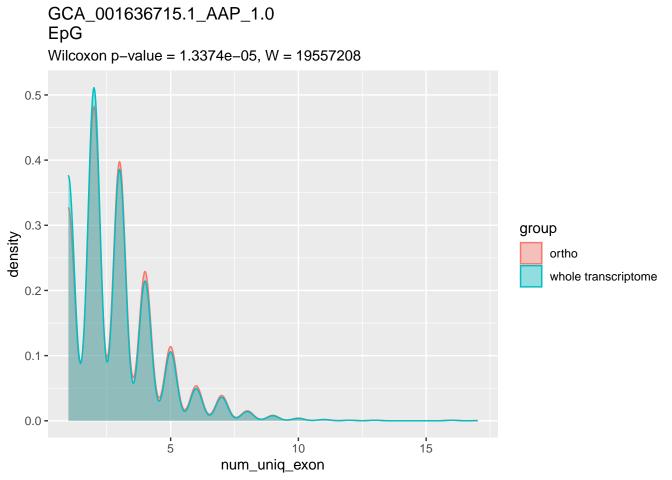
GCA_001574975.1_Ganpr1 EpG

Wilcoxon p-value = 1.4969e-158, W = 71184272

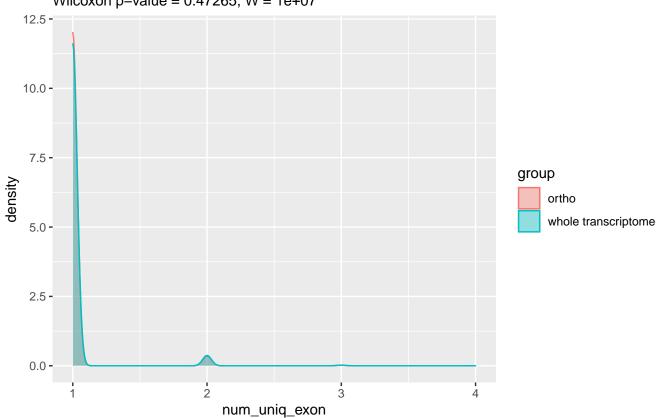


group

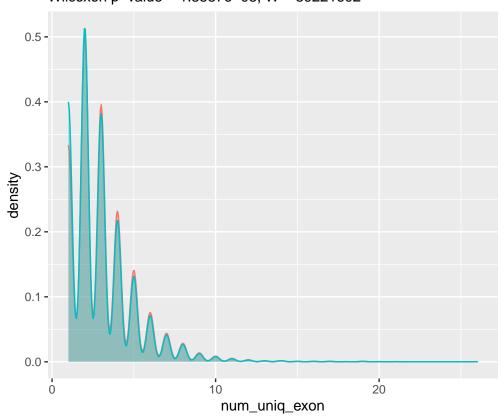
ortho



GCA_001747045.1_ASM174704v1 EpG Wilcoxon p-value = 0.47265, W = 1e+07



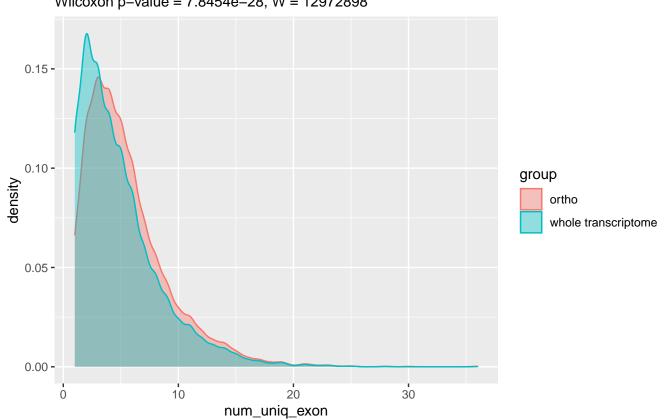
GCA_001883825.1_Emmo_past_UAMH9510_V1 EpG Wilcoxon p-value = 1.3587e-08, W = 39221602



group

ortho

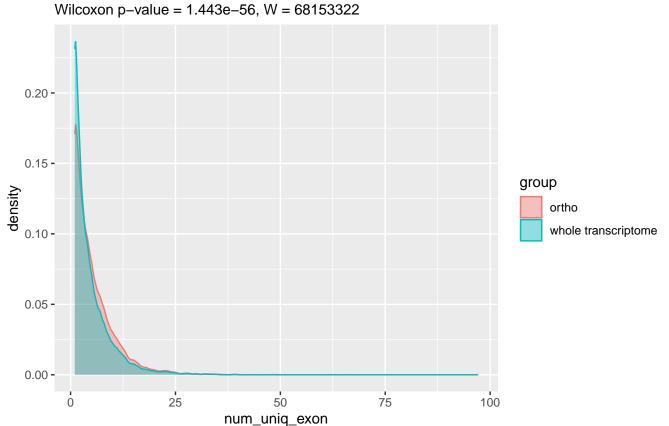
GCA_001929475.1_Neolirr1.0 EpG Wilcoxon p-value = 7.8454e-28, W = 12972898



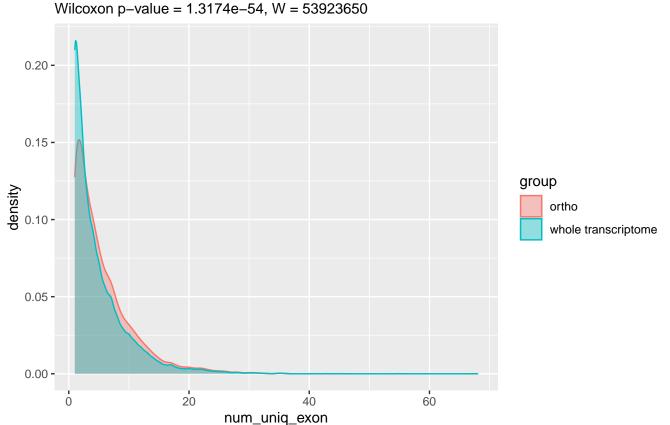
GCA_002006685.1_Batr_sala_BS_V1 EpG Wilcoxon p-value = 1.5824e-102, W = 42634718 0.20 -0.15 group density ortho whole transcriptome 0.05 -0.00 -10 20 30 40

num_uniq_exon

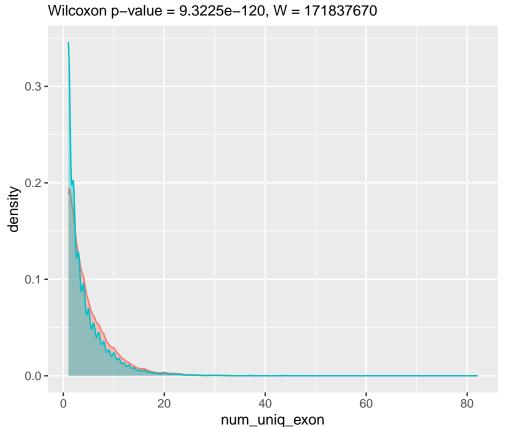
GCA_002104895.1_Anaeromyces_sp._S4_v1.0 EpG



GCA_002104945.1_Piromyces_sp._finnis_v3.0 EpG



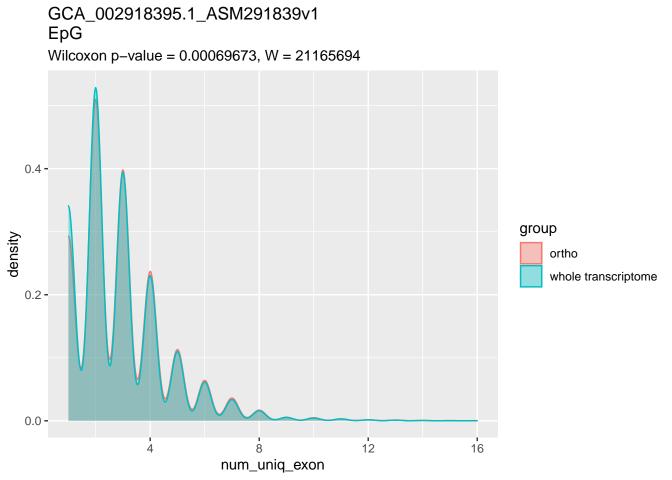
GCA_002104975.1_Neocallimastix_sp._G1_v1.0 EpG Wilcoxon p-value = 9.3225e-120, W = 171837670

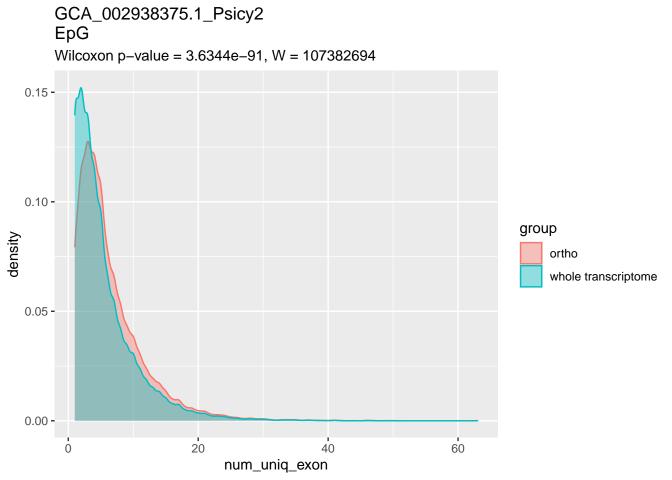


group

ortho

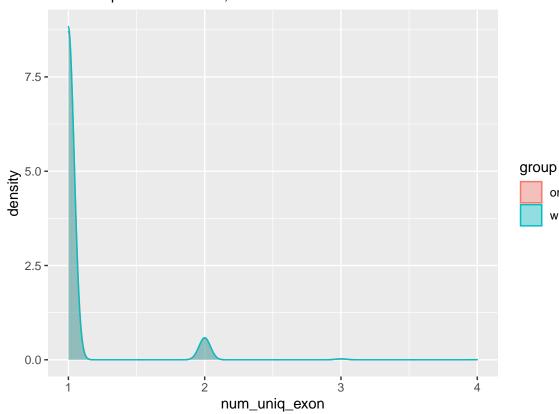
GCA_002104985.1_Rhihy1 EpG Wilcoxon p-value = 2.8699e-188, W = 104853940 0.3 -0.2 group density ortho whole transcriptome 0.1 -0.0 -10 20 30 50 40 num_uniq_exon



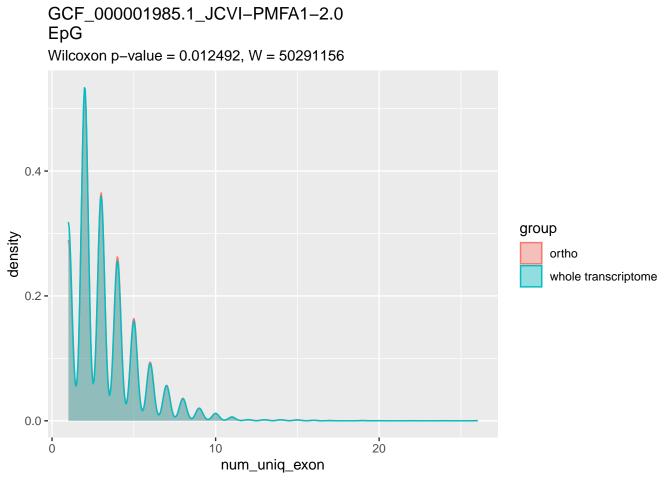


GCA_900106115.1_CBS_141442_assembly EpG

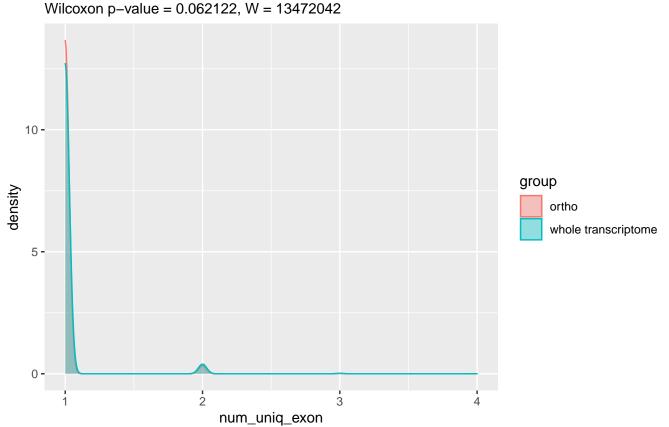
Wilcoxon p-value = 0.9859, W = 16542289

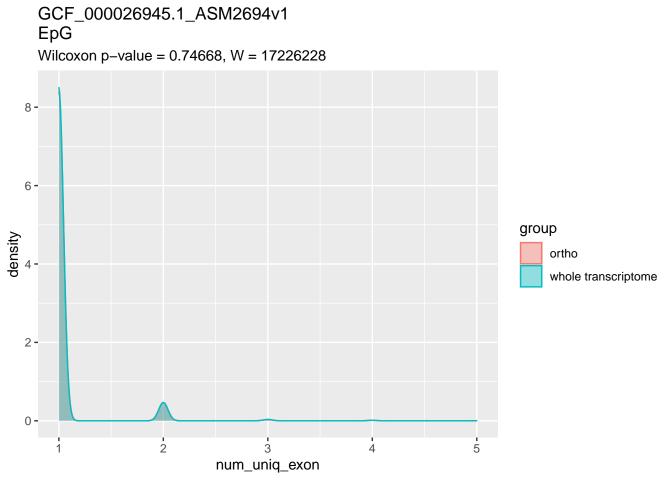


ortho



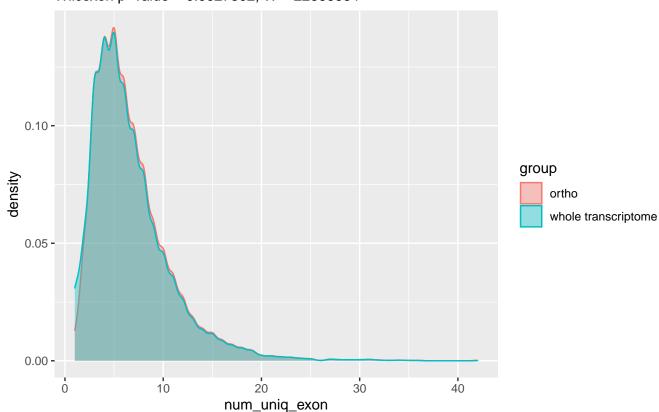
GCF_000002545.3_ASM254v2 EpG



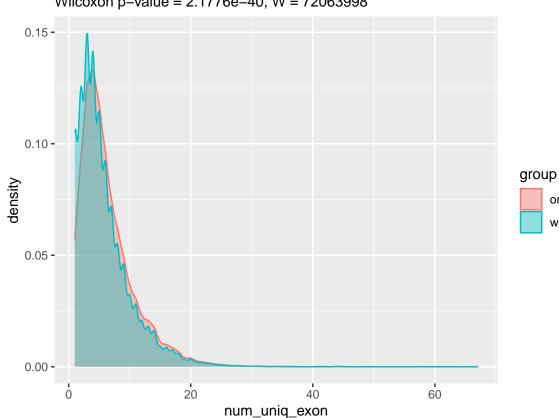


GCF_000091045.1_ASM9104v1 EpG

Wilcoxon p-value = 0.0027302, W = 22666664



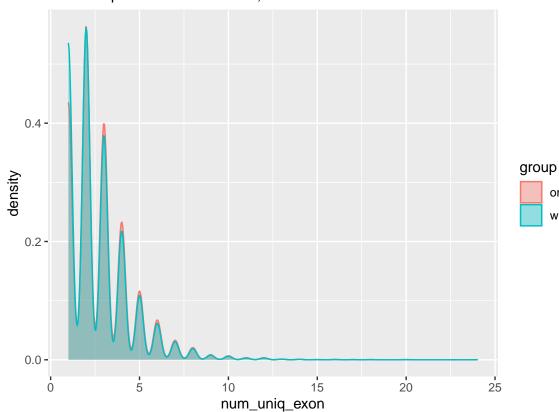
GCF_000143185.1_v1.0 EpG Wilcoxon p-value = 2.1776e-40, W = 72063998



ortho

whole transcriptome

GCF_000149035.1_C_graminicola_M1_001_V1 EpG Wilcoxon p-value = 4.0915e-14, W = 72557129



ortho

whole transcriptome

GCF_000149335.2_ASM14933v2 EpG Wilcoxon p-value = 6.25e-11, W = 404298320.5 -0.4 -0.3 group density ortho whole transcriptome 0.2 -0.1 -0.0 -5 10 20 15 25

num_uniq_exon

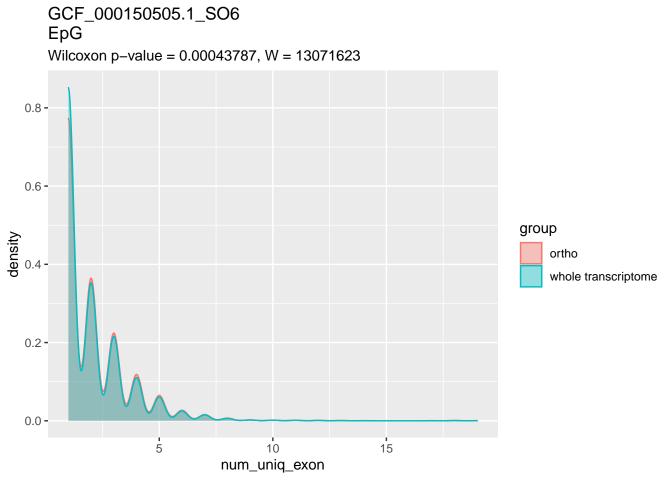
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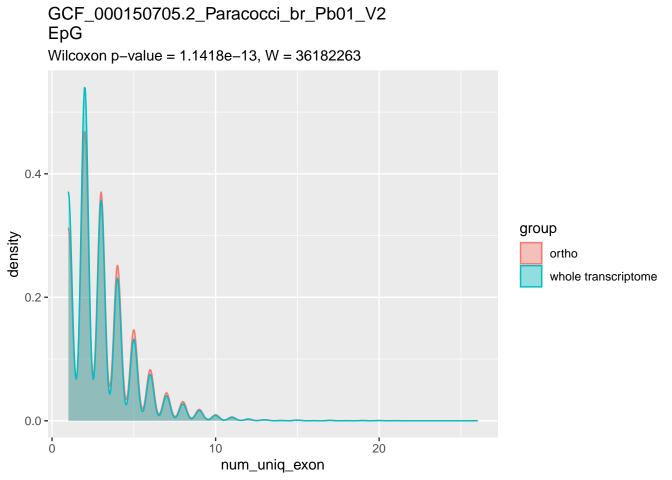
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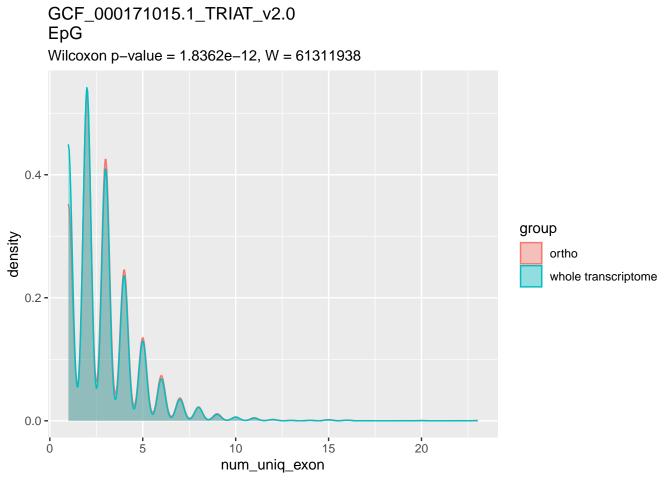
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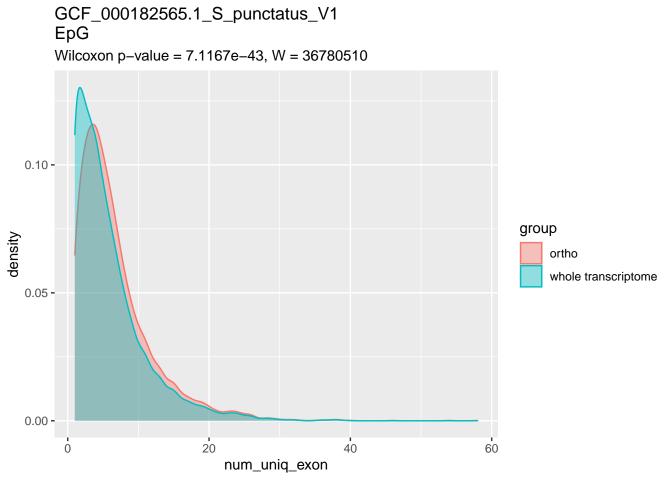
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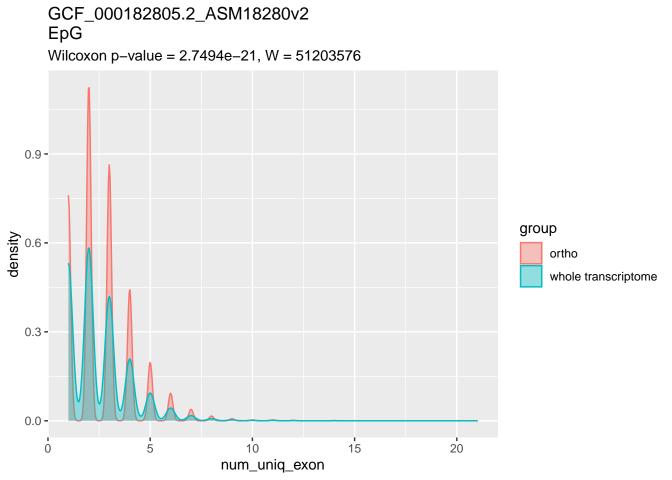
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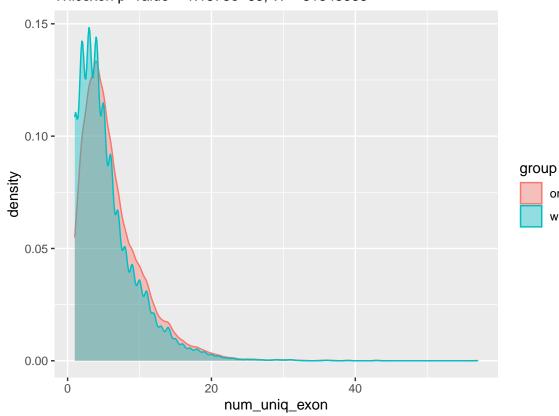






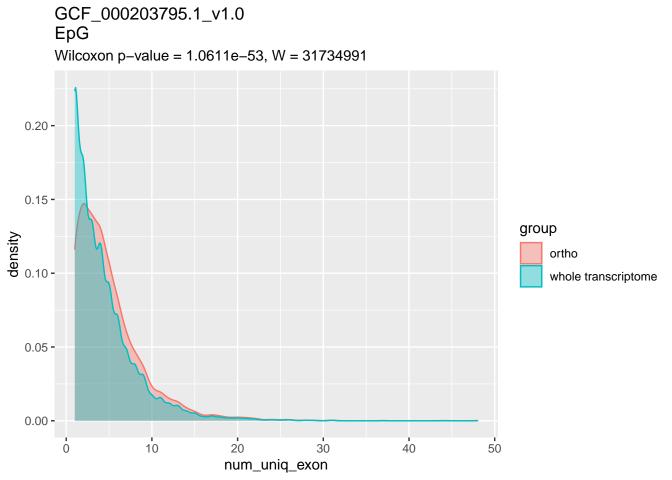
GCF_000182895.1_CC3 EpG

Wilcoxon p-value = 1.1573e-63, W = 81345388

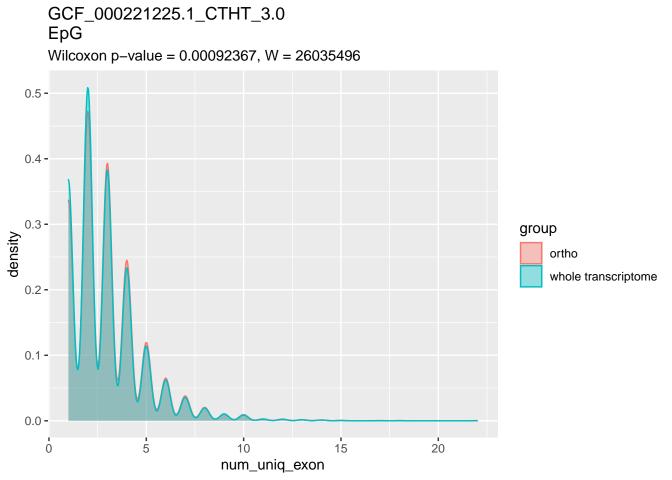


ortho

whole transcriptome



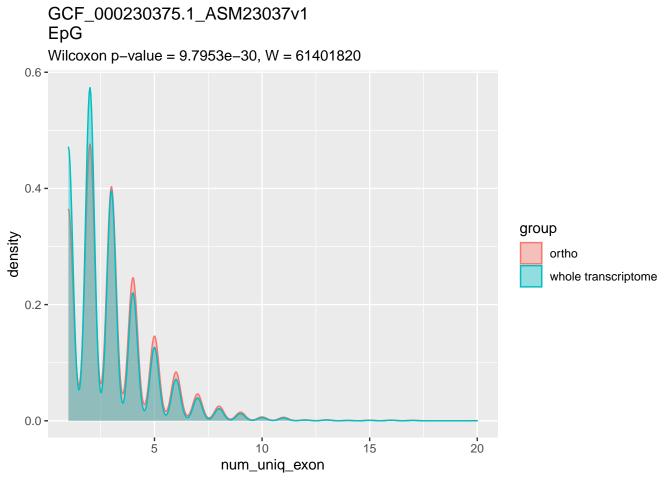
GCF_000204055.1_v1.0 EpG Wilcoxon p-value = 1.0391e-122, W = 87177470 0.15 density 0.10 group ortho whole transcriptome 0.05 -0.00 -20 30 10 40 num_uniq_exon



GCF_000223465.1_Candida_tenuis_v1.0 EpG Wilcoxon p-value = 0.11882, W = 13448629 2.0 -1.5 group density ortho whole transcriptome 0.5 -0.0 -

num_uniq_exon

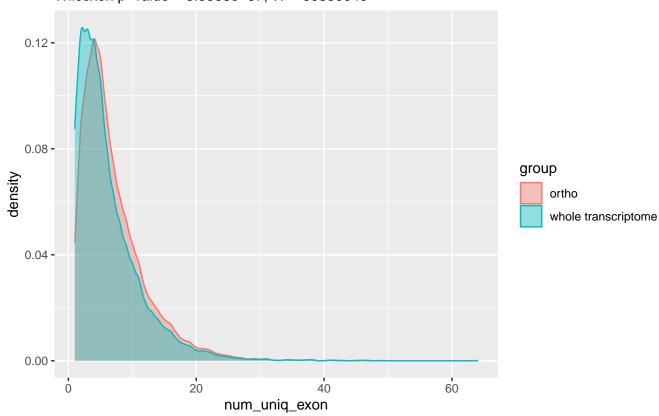
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GCF_000264905.1_Stehi1 EpG Wilcoxon p-value = 6.8178e-69, W = 91028688 0.125 -0.100 -0.075 group density ortho whole transcriptome 0.050 -0.025 -0.000 -20 40 60 80 num_uniq_exon

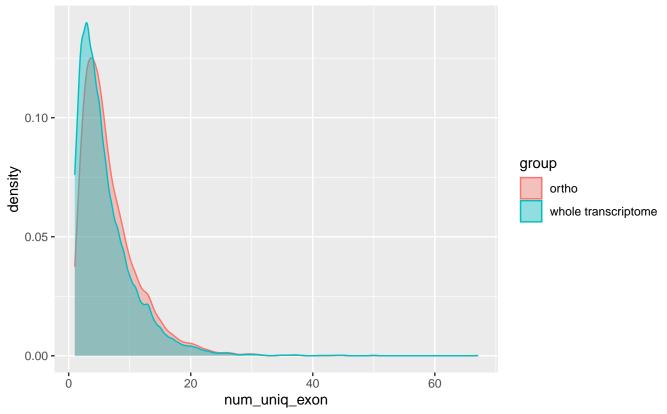
GCF_000264995.1_Punctularia_strigosozonata_v1.0 EpG

Wilcoxon p-value = 5.5366e-57, W = 60330040



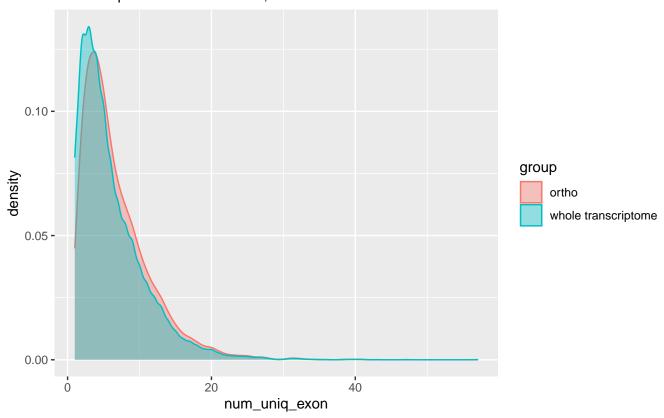
GCF_000271605.1_Fomme1 EpG

Wilcoxon p-value = 2.1102e-59, W = 56456622



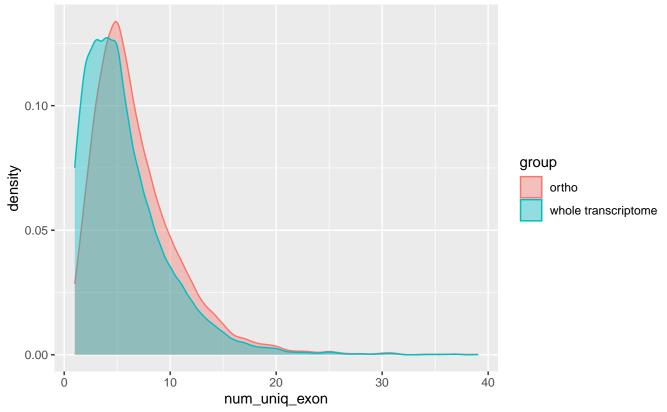
GCF_000271625.1_Conpu1 EpG

Wilcoxon p-value = 4.3283e-48, W = 82951852



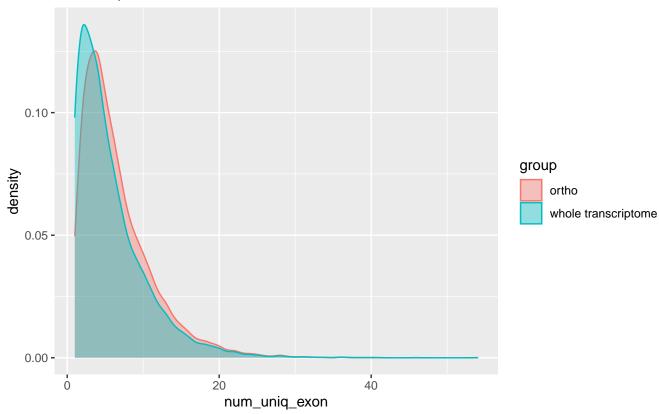
GCF_000271645.1_Treme1 EpG

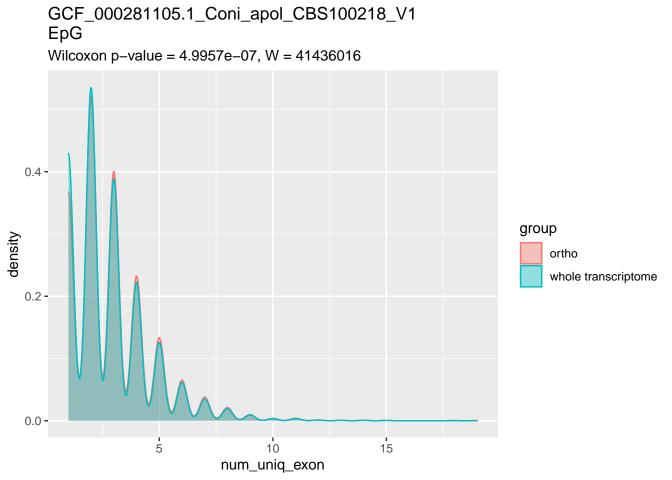
Wilcoxon p-value = 2.9987e-71, W = 27355434



GCF_000275845.1_Dichomitus_squalens_v1.0 EpG

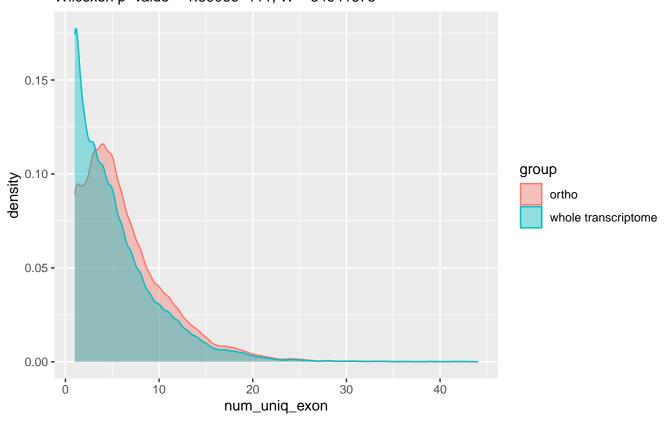
Wilcoxon p-value = 1.5407e-67, W = 70290322





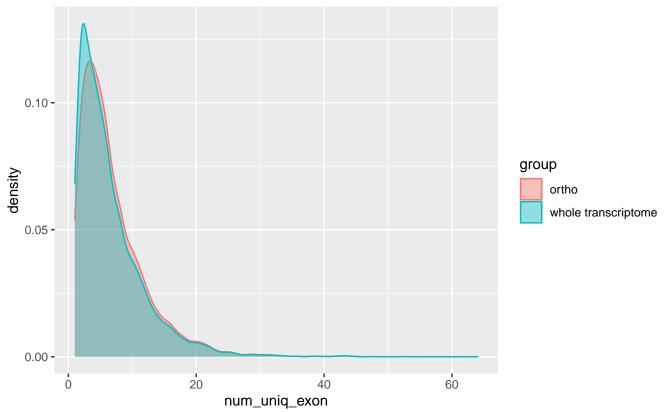
GCF_000300595.1_Phanerochaete_carnosa_HHB-10118-Sp_v1.0 EpG

. Wilcoxon p-value = 1.8906e-111, W = 84941675

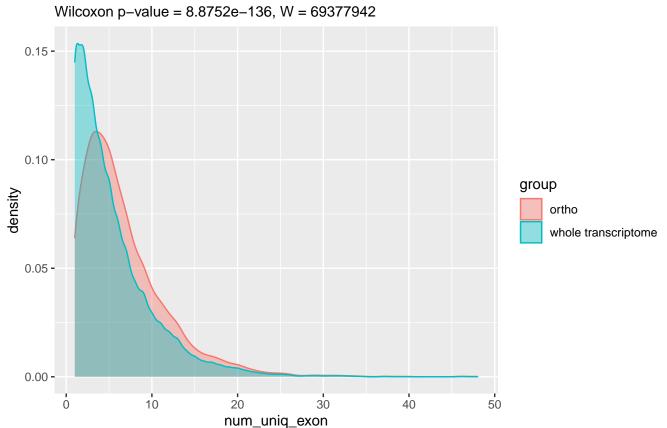


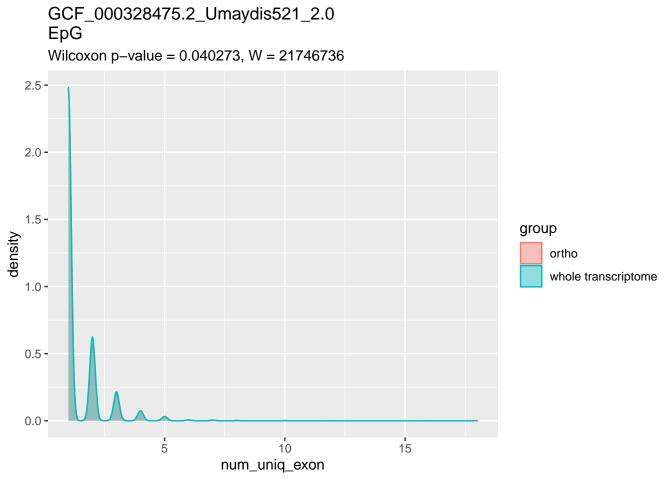
GCF_000313525.1_ASM31352v1 EpG

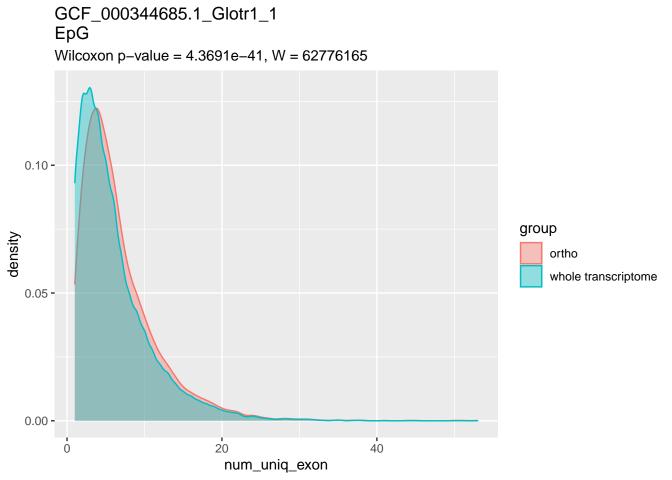
Wilcoxon p-value = 6.6016e-14, W = 41062778

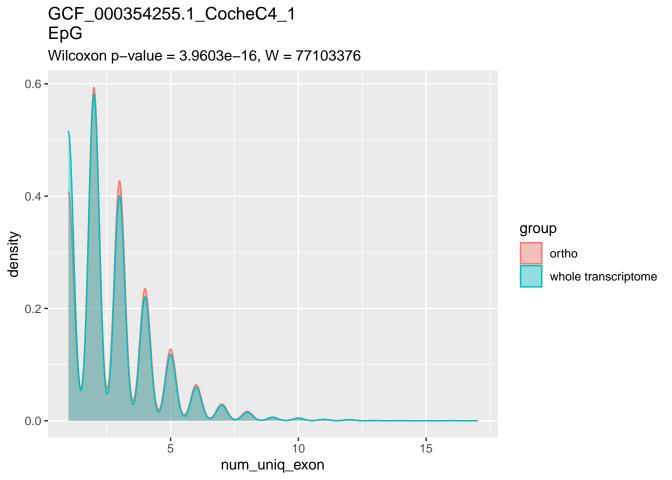


GCF_000320585.1_Heterobasidion_irregulare_v2.0 EpG

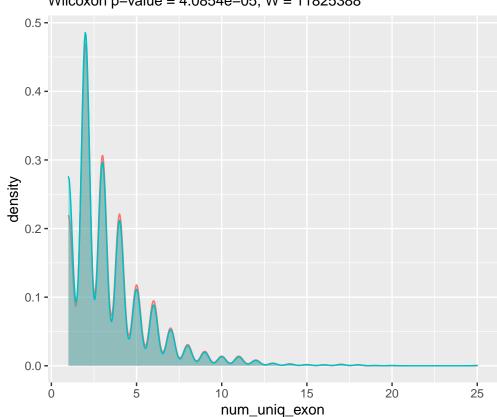








GCF_000400465.1_Wallemia_ichthyophaga_version_1.0 EpG Wilcoxon p-value = 4.0854e-05, W = 11825388



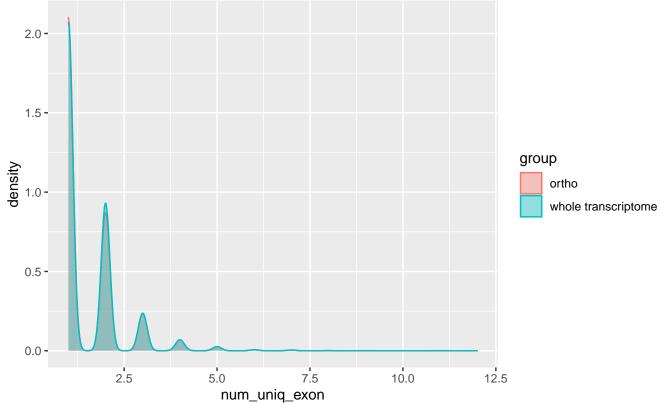
group

ortho

whole transcriptome

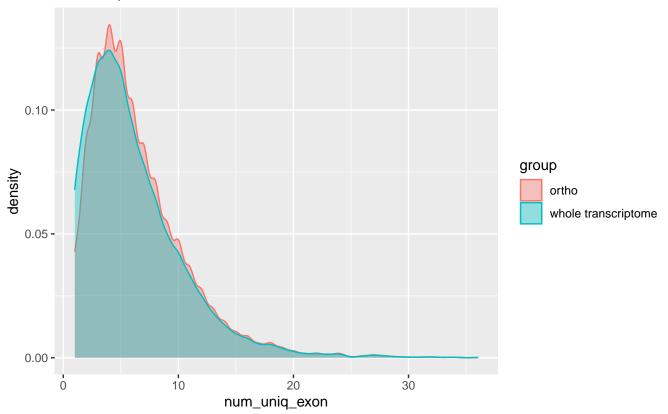
GCF_000409485.1_GLAREA EpG Wilcoxon p-value = 3.2847e-20, W = 78415741 0.5 -0.4 density 0.3 group ortho whole transcriptome 0.2 -0.1 -0.0 -10 20 30 num_uniq_exon

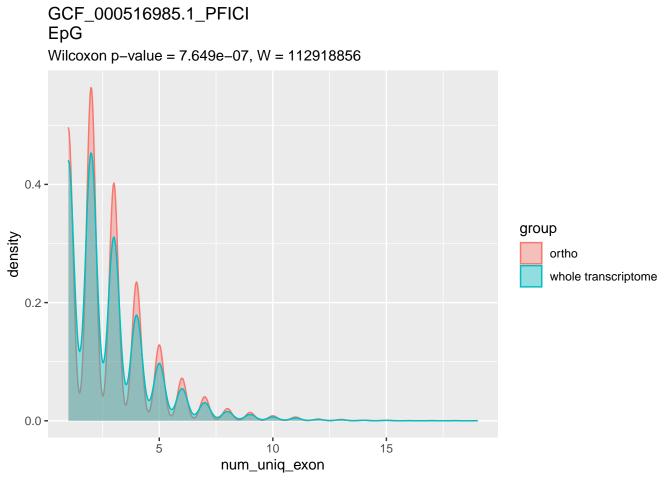
GCF_000497045.1_PSEUBRA1 EpG Wilcoxon p-value = 0.1247, W = 16409746



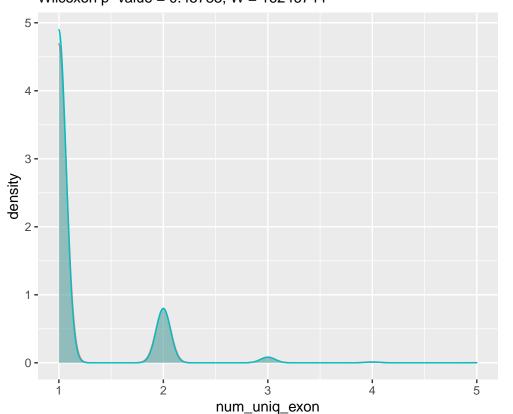
GCF_000512605.1_Cryp_pinu_CBS10737_V1 EpG

Wilcoxon p-value = 1.8916e-10, W = 30870323





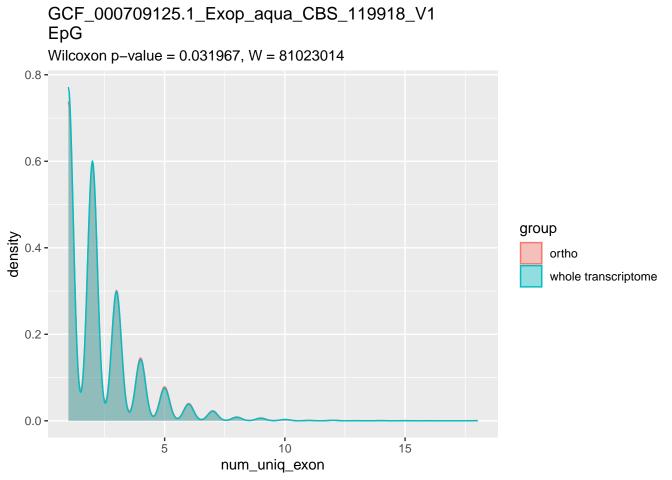
GCF_000576695.1_AUH_PRJEB4427_v1 EpG Wilcoxon p-value = 0.45783, W = 16246744

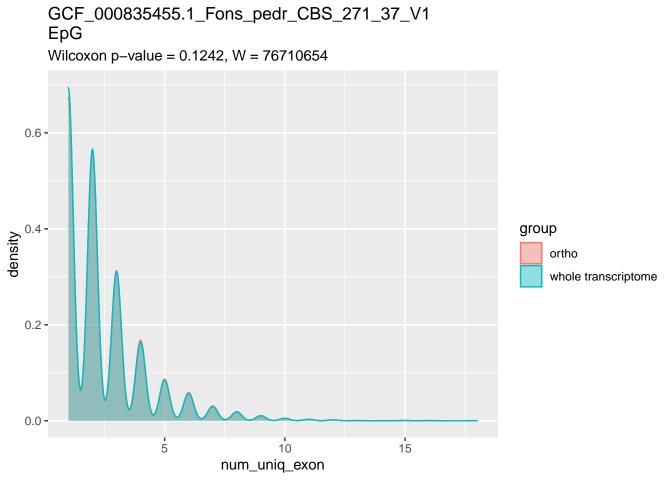


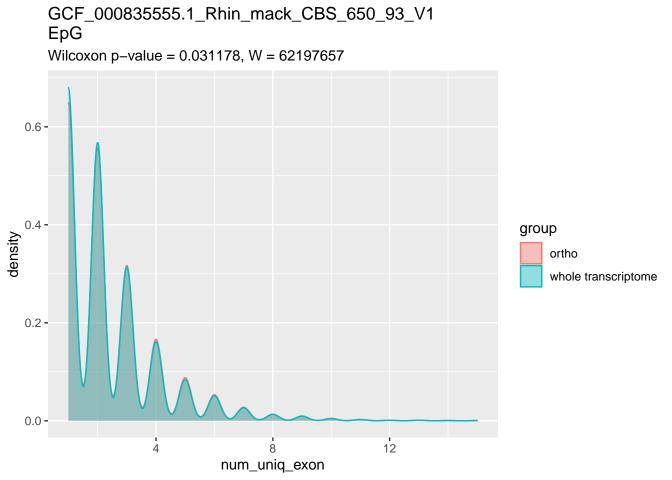
group

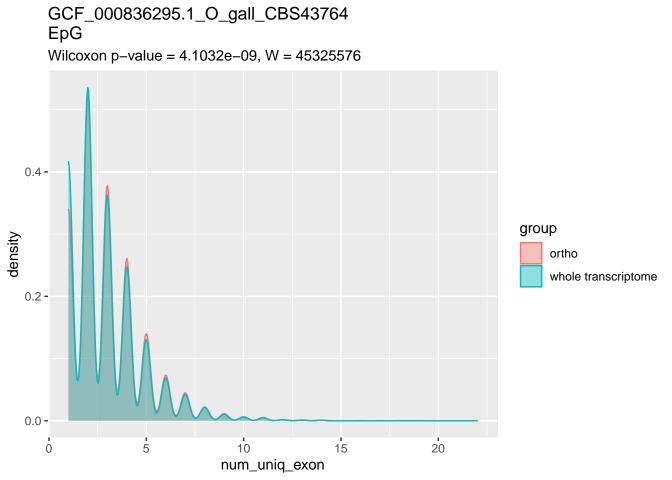
ortho

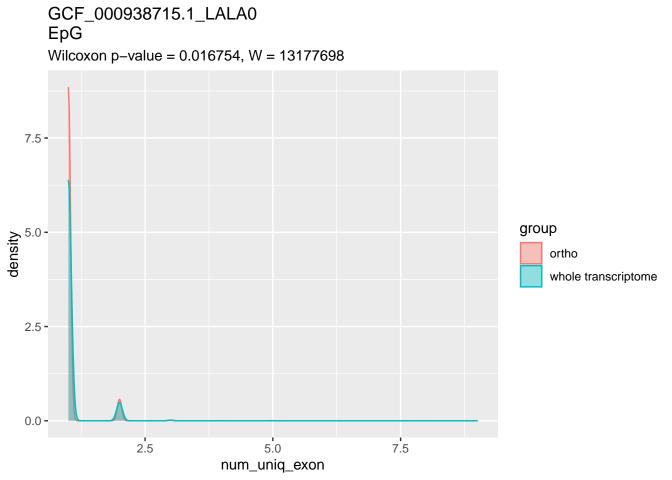
whole transcriptome

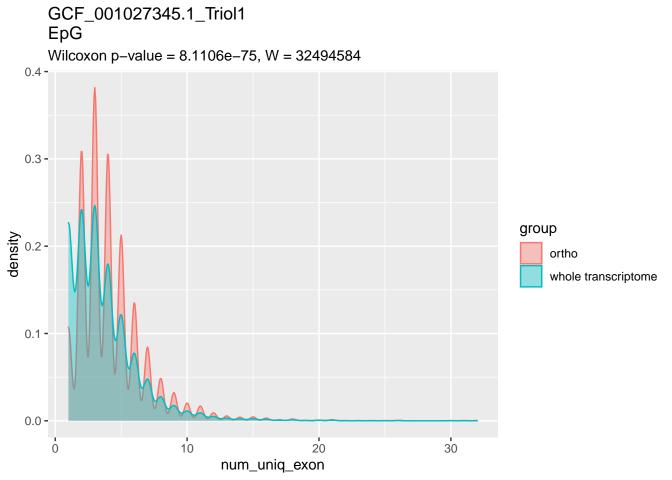


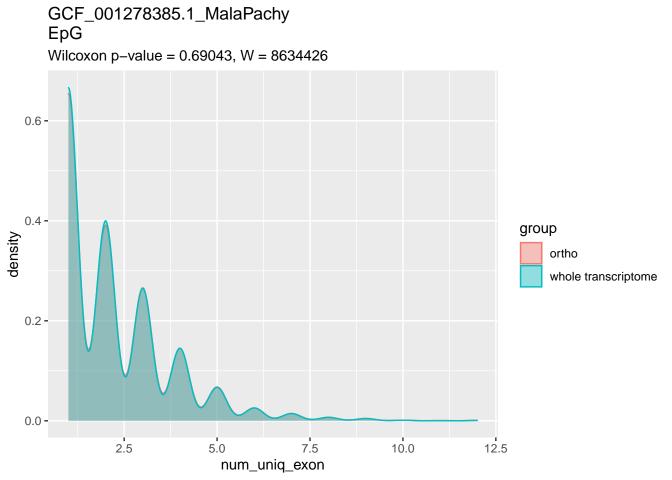




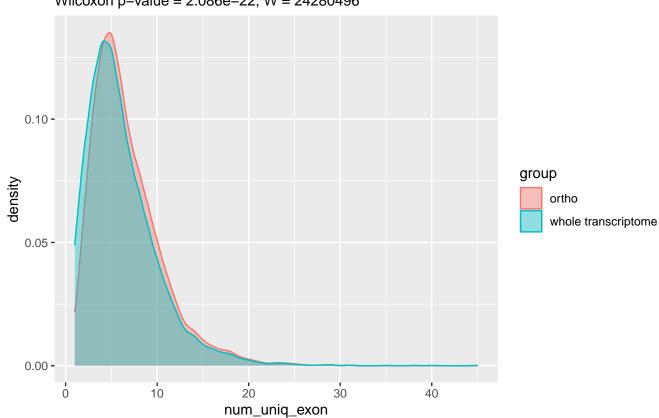






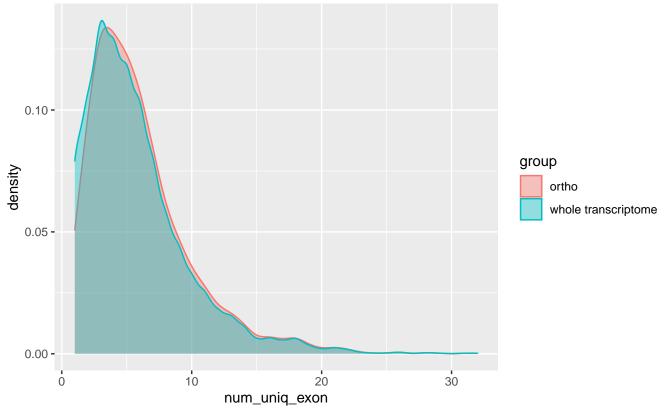


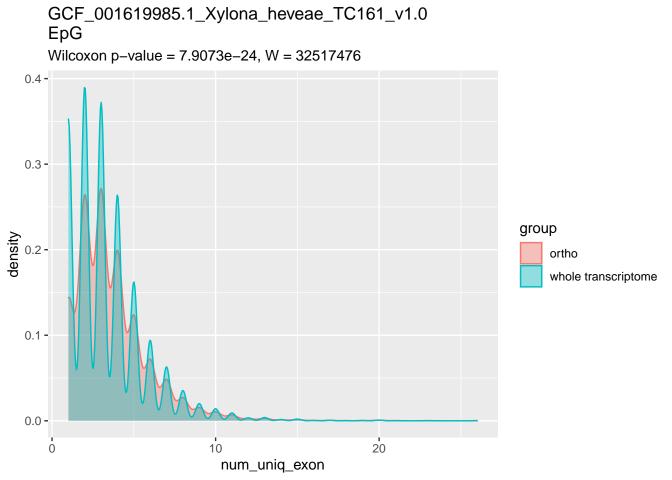
GCF_001329695.1_Rhoba1_1 EpG Wilcoxon p-value = 2.086e-22, W = 24280496

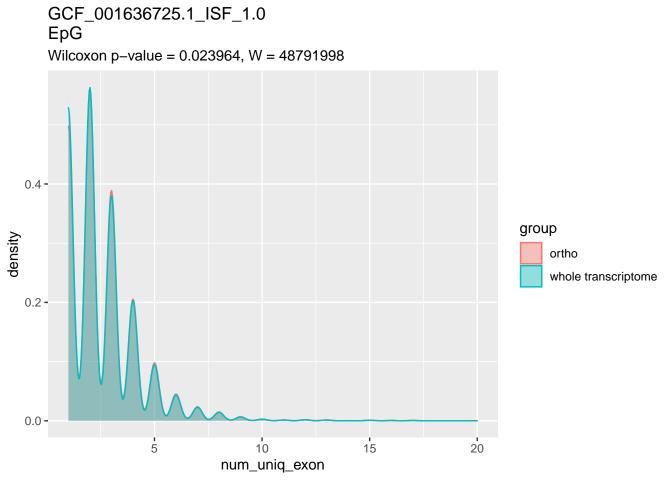


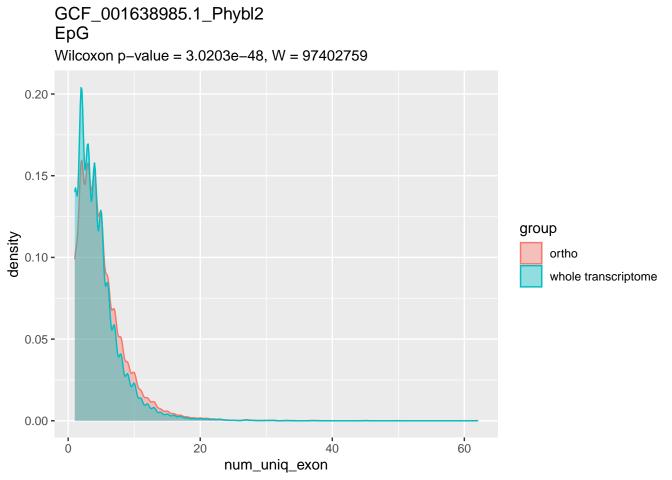
GCF_001477535.1_Pneu_jiro_RU7_V2 EpG

Wilcoxon p-value = 6.6162e-05, W = 6957754

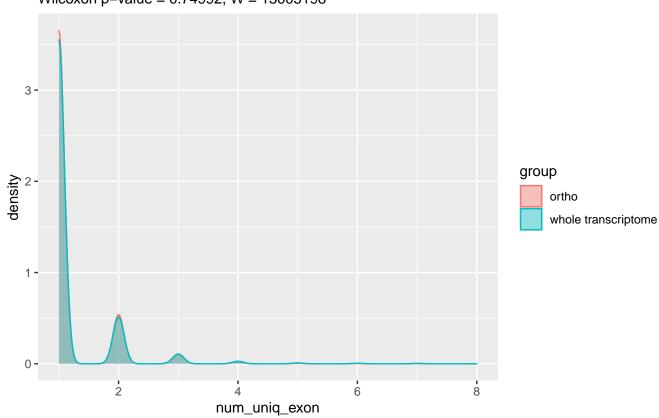


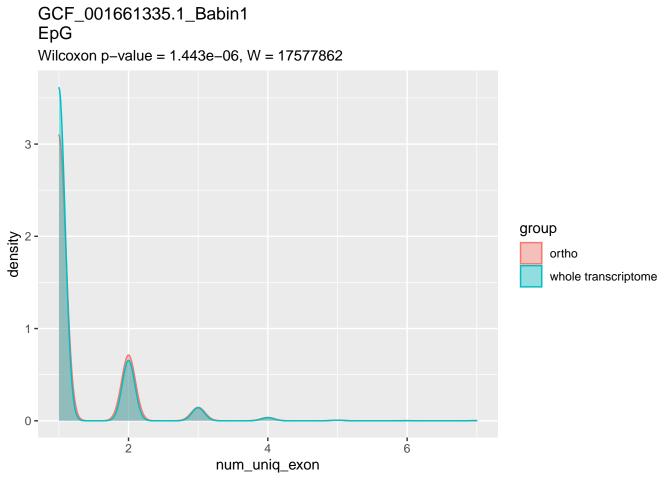


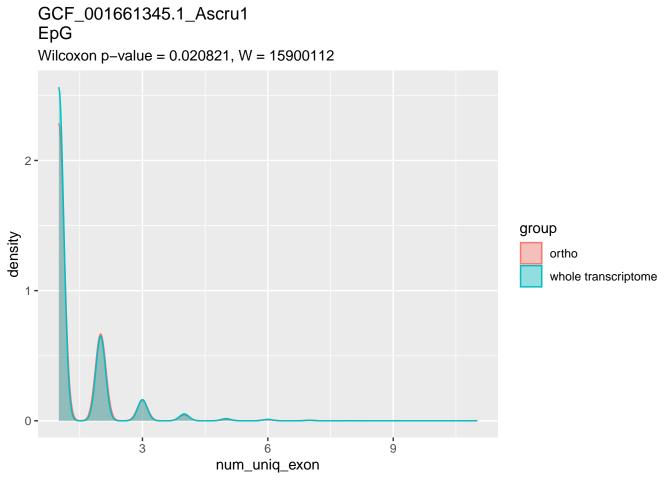


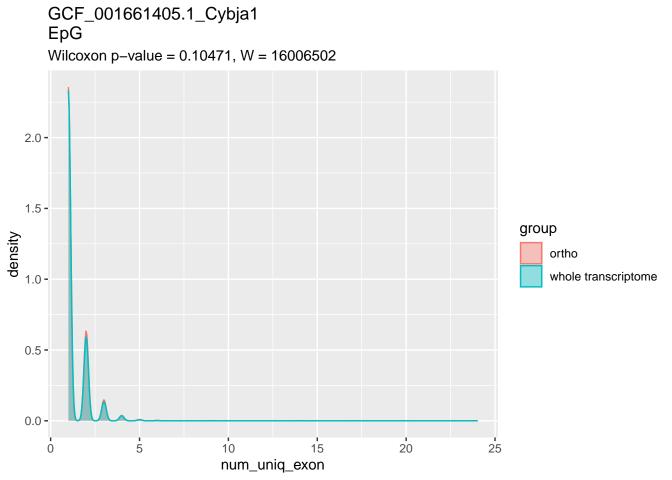


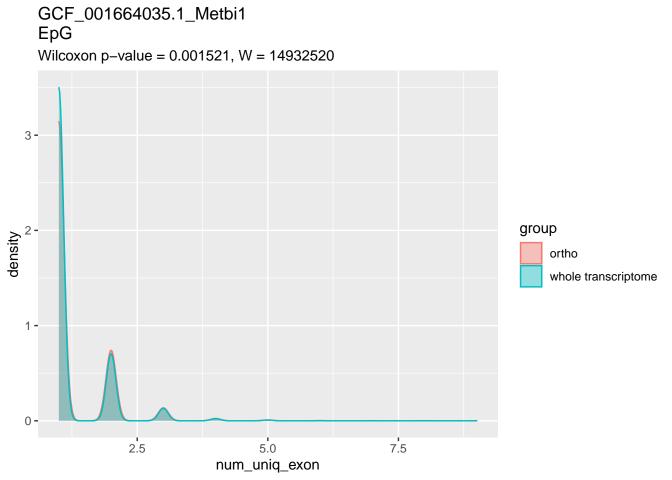
GCF_001661235.1_Picme2 EpG Wilcoxon p-value = 0.74992, W = 13005198

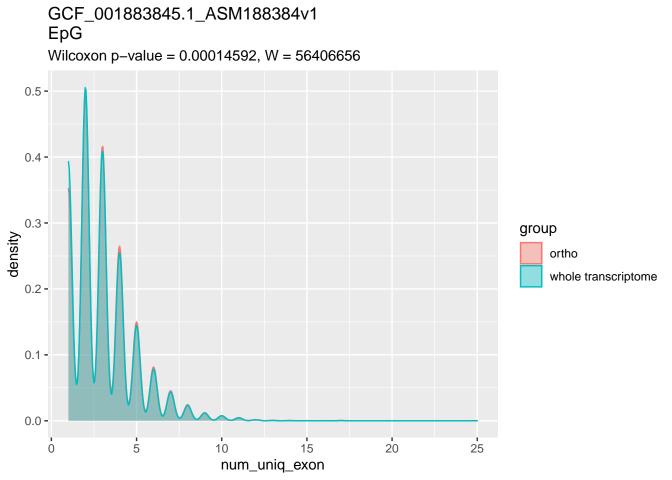


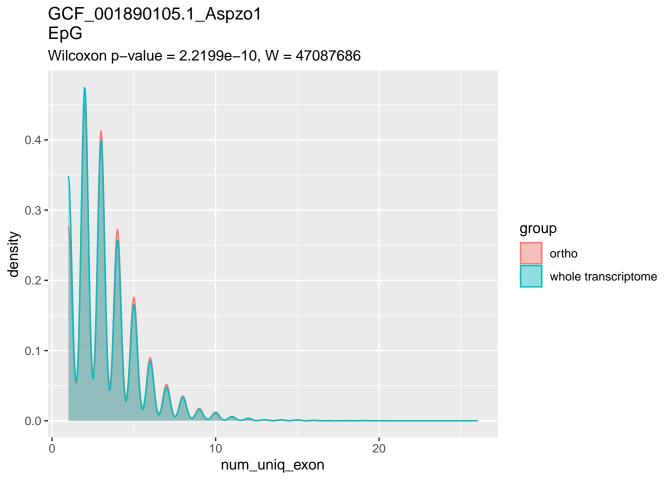












GCF_002102565.1_Kocim1 EpG Wilcoxon p-value = 5.6399e-20, W = 261604260.12 -0.09 group density ortho whole transcriptome 0.03 -

30

20

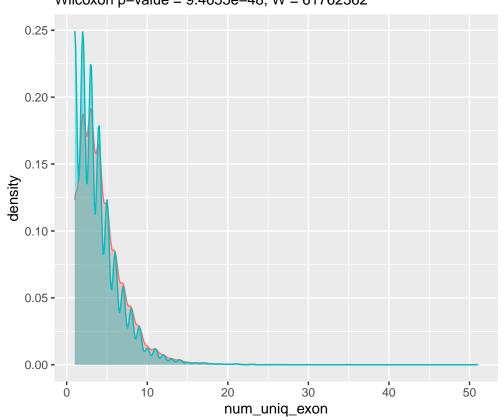
num_uniq_exon

10

0.00 -

GCF_002105155.1_Lobtra1 EpG





group

ortho

whole transcriptome

GCF_002117355.1_PospIRSB12_1 EpG

Wilcoxon p-value = 3.8467e-52, W = 68335786

