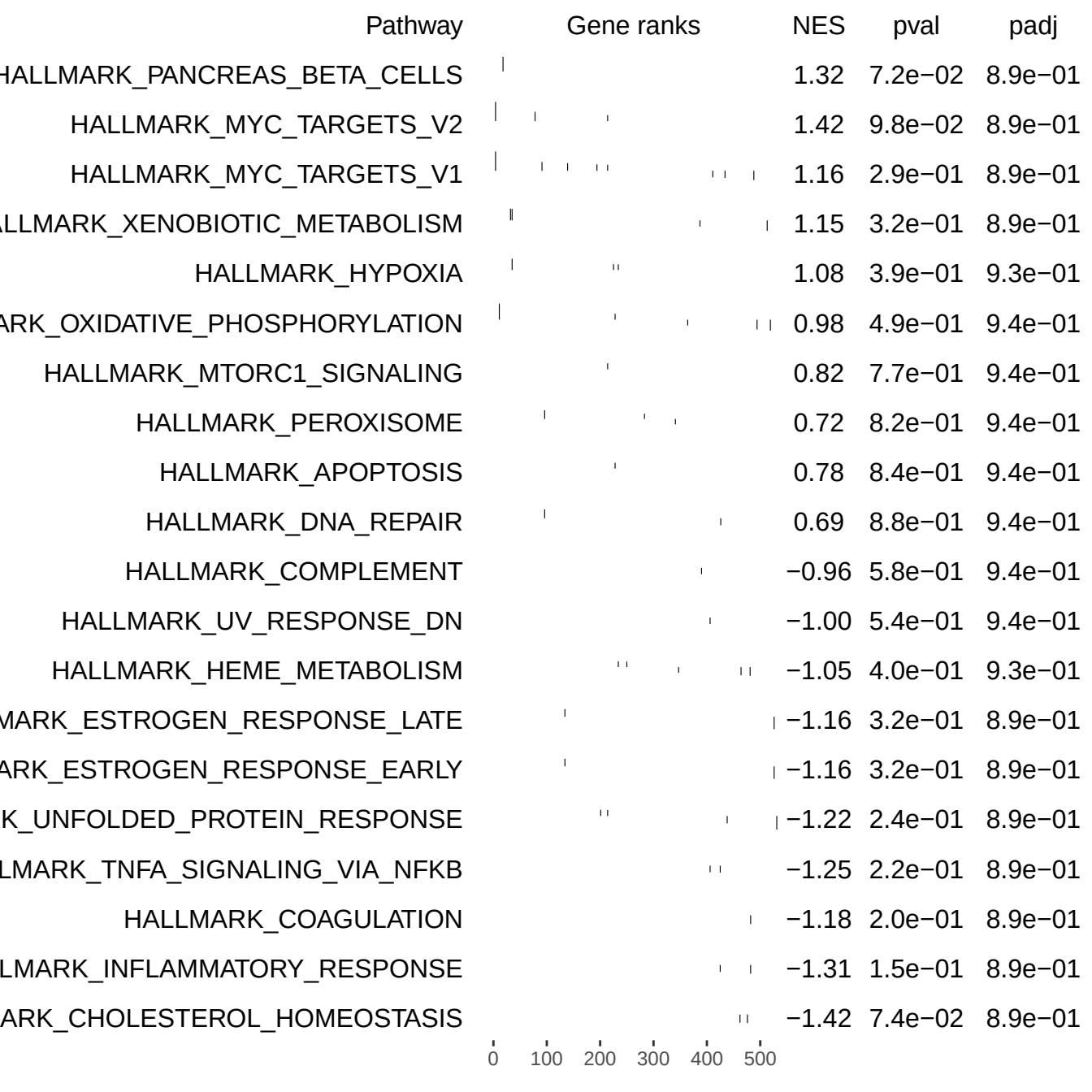
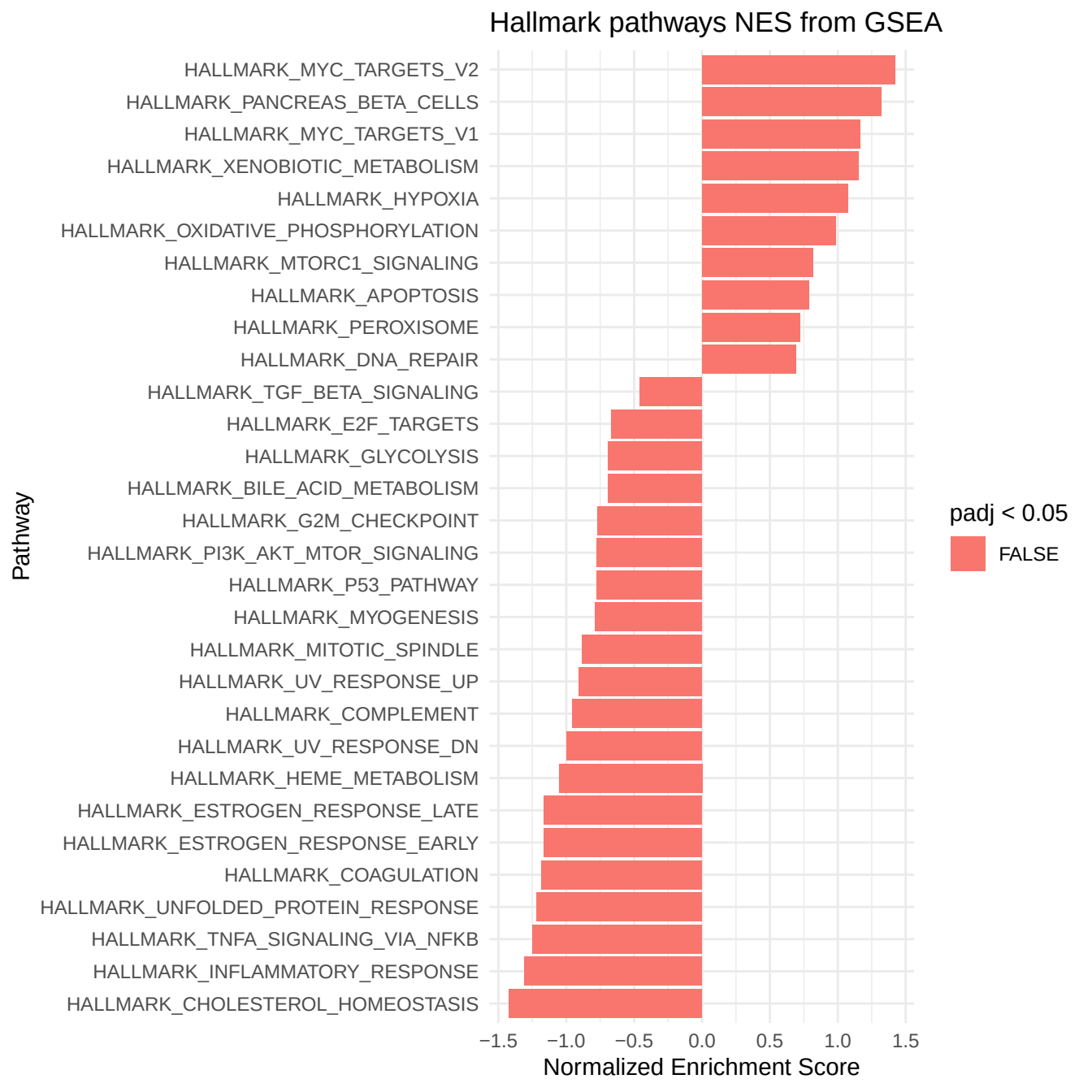

Pathway
Gene ranks
NES
pval
padj
HALLMARK_PANCREAS_BETA_CELLS 1.32 7.2e−02 8.9e−01
HALLMARK_MYC_TARGETS_V2 1.42 9.8e−02 8.9e−01
HALLMARK_MYC_TARGETS_V1 1.16 2.9e−01 8.9e−01
LLMARK_XENOBIOTIC_METABOLISM 1.15 3.2e−01 8.9e−01
HALLMARK_HYPOXIA 1.08 3.9e−01 9.3e−01
ARK_OXIDATIVE_PHOSPHORYLATION 0.98 4.9e−01 9.4e−01
HALLMARK_MTORC1_SIGNALING 0.82 7.7e−01 9.4e−01
HALLMARK_PEROXISOME 0.72 8.2e−01 9.4e−01
HALLMARK_APOPTOSIS 0.78 8.4e−01 9.4e−01
HALLMARK_DNA_REPAIR 0.69 8.8e−01 9.4e−01
HALLMARK_COMPLEMENT −0.96 5.8e−01 9.4e−01
HALLMARK_UV_RESPONSE_DN −1.00 5.4e−01 9.4e−01
HALLMARK_HEME_METABOLISM −1.05 4.0e−01 9.3e−01
MARK_ESTROGEN_RESPONSE_LATE −1.16 3.2e−01 8.9e−01
ARK_ESTROGEN_RESPONSE_EARLY −1.16 3.2e−01 8.9e−01
K_UNFOLDED_PROTEIN_RESPONSE −1.22 2.4e−01 8.9e−01
LMARK_TNFA_SIGNALING_VIA_NFKB −1.25 2.2e−01 8.9e−01
HALLMARK_COAGULATION −1.18 2.0e−01 8.9e−01
LMARK_INFLAMMATORY_RESPONSE −1.31 1.5e−01 8.9e−01
ARK_CHOLESTEROL_HOMEOSTASIS −1.42 7.4e−02 8.9e−01
0
100
200
300
400
500


Hallmark pathways NES from GSEA
HALLMARK_MYC_TARGETS_V2
HALLMARK_PANCREAS_BETA_CELLS
HALLMARK_MYC_TARGETS_V1
HALLMARK_XENOBIOTIC_METABOLISM
HALLMARK_HYPOXIA
HALLMARK_OXIDATIVE_PHOSPHORYLATION
HALLMARK_MTORC1_SIGNALING
HALLMARK_APOPTOSIS
HALLMARK_PEROXISOME
HALLMARK_DNA_REPAIR
HALLMARK_TGF_BETA_SIGNALING
HALLMARK_E2F_TARGETS
HALLMARK_GLYCOLYSIS
HALLMARK_BILE_ACID_METABOLISM
HALLMARK_G2M_CHECKPOINT
HALLMARK_PI3K_AKT_MTOR_SIGNALING
HALLMARK_P53_PATHWAY
HALLMARK_MYOGENESIS
HALLMARK_MITOTIC_SPINDLE
HALLMARK_UV_RESPONSE_UP
HALLMARK_COMPLEMENT
HALLMARK_UV_RESPONSE_DN
HALLMARK_HEME_METABOLISM
HALLMARK_ESTROGEN_RESPONSE_LATE
HALLMARK_ESTROGEN_RESPONSE_EARLY
HALLMARK_COAGULATION
HALLMARK_UNFOLDED_PROTEIN_RESPONSE
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_INFLAMMATORY_RESPONSE
HALLMARK_CHOLESTEROL_HOMEOSTASIS
Pathway
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Normalized Enrichment Score
padj < 0.05
FALSE