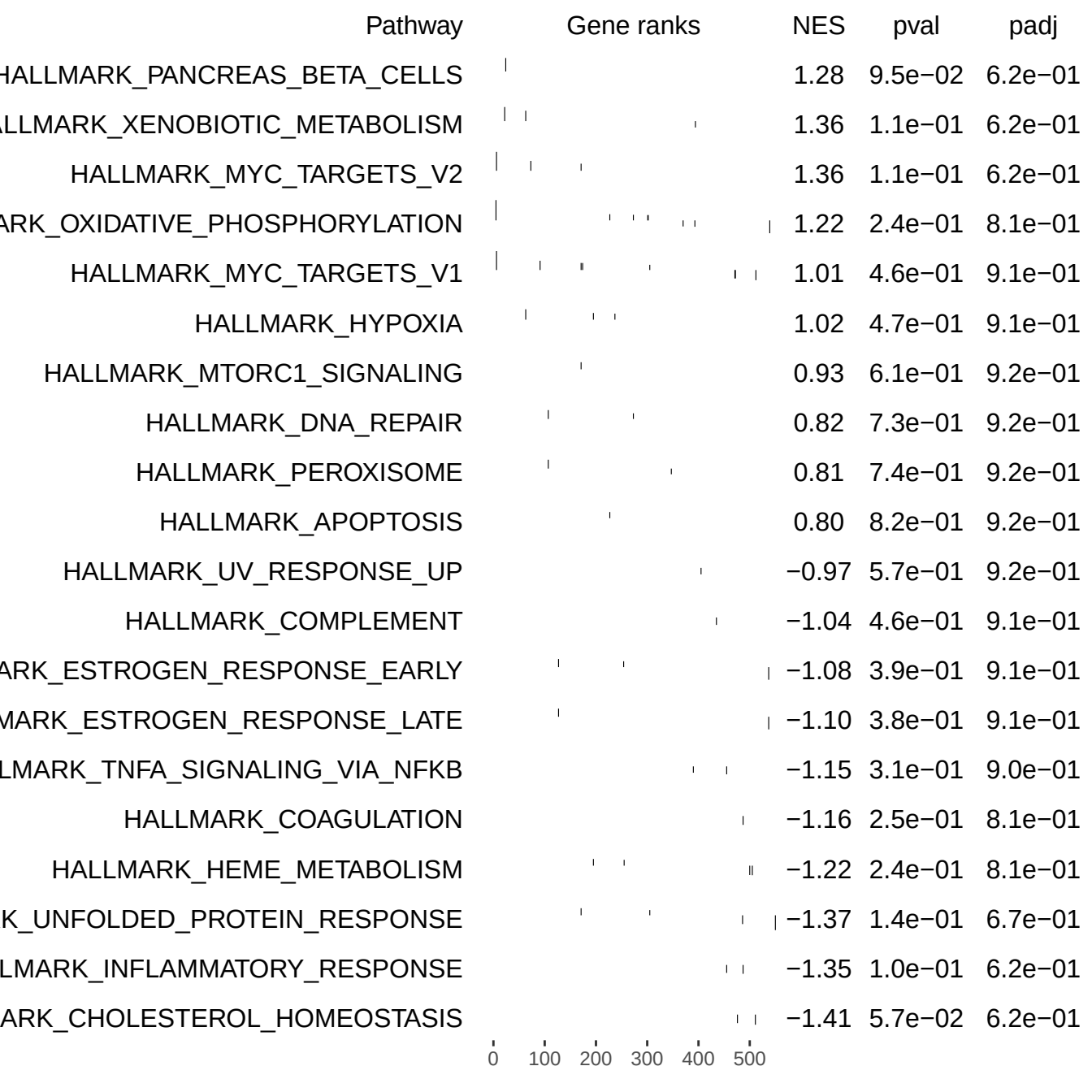
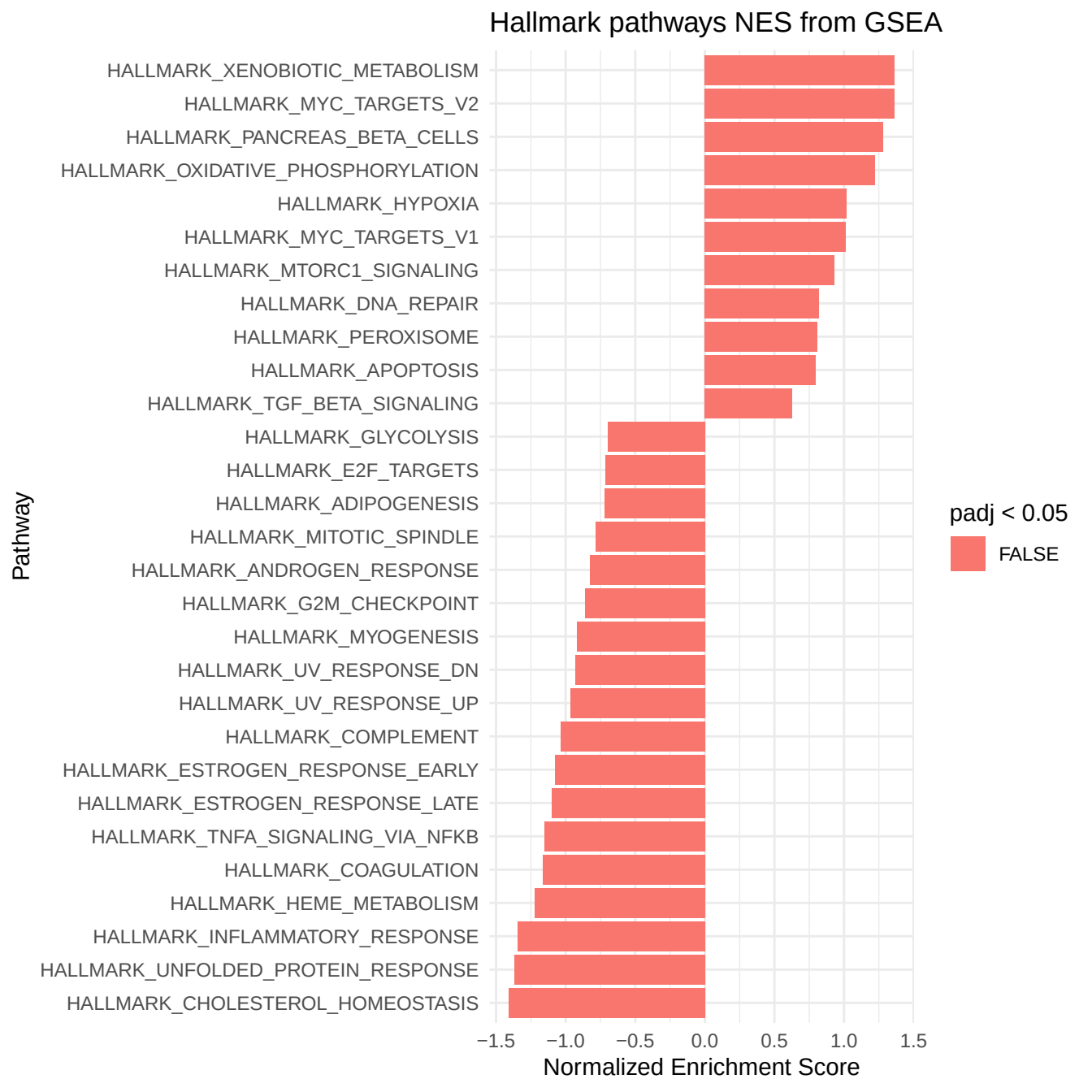

Pathway
Gene ranks
NES
pval
padj
HALLMARK_PANCREAS_BETA_CELLS 1.28 9.5e−02 6.2e−01
LLMARK_XENOBIOTIC_METABOLISM 1.36 1.1e−01 6.2e−01
HALLMARK_MYC_TARGETS_V2 1.36 1.1e−01 6.2e−01
ARK_OXIDATIVE_PHOSPHORYLATION 1.22 2.4e−01 8.1e−01
HALLMARK_MYC_TARGETS_V1 1.01 4.6e−01 9.1e−01
HALLMARK_HYPOXIA 1.02 4.7e−01 9.1e−01
HALLMARK_MTORC1_SIGNALING 0.93 6.1e−01 9.2e−01
HALLMARK_DNA_REPAIR 0.82 7.3e−01 9.2e−01
HALLMARK_PEROXISOME 0.81 7.4e−01 9.2e−01
HALLMARK_APOPTOSIS 0.80 8.2e−01 9.2e−01
HALLMARK_UV_RESPONSE_UP −0.97 5.7e−01 9.2e−01
HALLMARK_COMPLEMENT −1.04 4.6e−01 9.1e−01
ARK_ESTROGEN_RESPONSE_EARLY −1.08 3.9e−01 9.1e−01
MARK_ESTROGEN_RESPONSE_LATE −1.10 3.8e−01 9.1e−01
LMARK_TNFA_SIGNALING_VIA_NFKB −1.15 3.1e−01 9.0e−01
HALLMARK_COAGULATION −1.16 2.5e−01 8.1e−01
HALLMARK_HEME_METABOLISM −1.22 2.4e−01 8.1e−01
K_UNFOLDED_PROTEIN_RESPONSE −1.37 1.4e−01 6.7e−01
LMARK_INFLAMMATORY_RESPONSE −1.35 1.0e−01 6.2e−01
ARK_CHOLESTEROL_HOMEOSTASIS −1.41 5.7e−02 6.2e−01
0
100
200
300
400
500


Hallmark pathways NES from GSEA
HALLMARK_XENOBIOTIC_METABOLISM
HALLMARK_MYC_TARGETS_V2
HALLMARK_PANCREAS_BETA_CELLS
HALLMARK_OXIDATIVE_PHOSPHORYLATION
HALLMARK_HYPOXIA
HALLMARK_MYC_TARGETS_V1
HALLMARK_MTORC1_SIGNALING
HALLMARK_DNA_REPAIR
HALLMARK_PEROXISOME
HALLMARK_APOPTOSIS
HALLMARK_TGF_BETA_SIGNALING
HALLMARK_GLYCOLYSIS
HALLMARK_E2F_TARGETS
HALLMARK_ADIPOGENESIS
HALLMARK_MITOTIC_SPINDLE
HALLMARK_ANDROGEN_RESPONSE
HALLMARK_G2M_CHECKPOINT
HALLMARK_MYOGENESIS
HALLMARK_UV_RESPONSE_DN
HALLMARK_UV_RESPONSE_UP
HALLMARK_COMPLEMENT
HALLMARK_ESTROGEN_RESPONSE_EARLY
HALLMARK_ESTROGEN_RESPONSE_LATE
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_COAGULATION
HALLMARK_HEME_METABOLISM
HALLMARK_INFLAMMATORY_RESPONSE
HALLMARK_UNFOLDED_PROTEIN_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