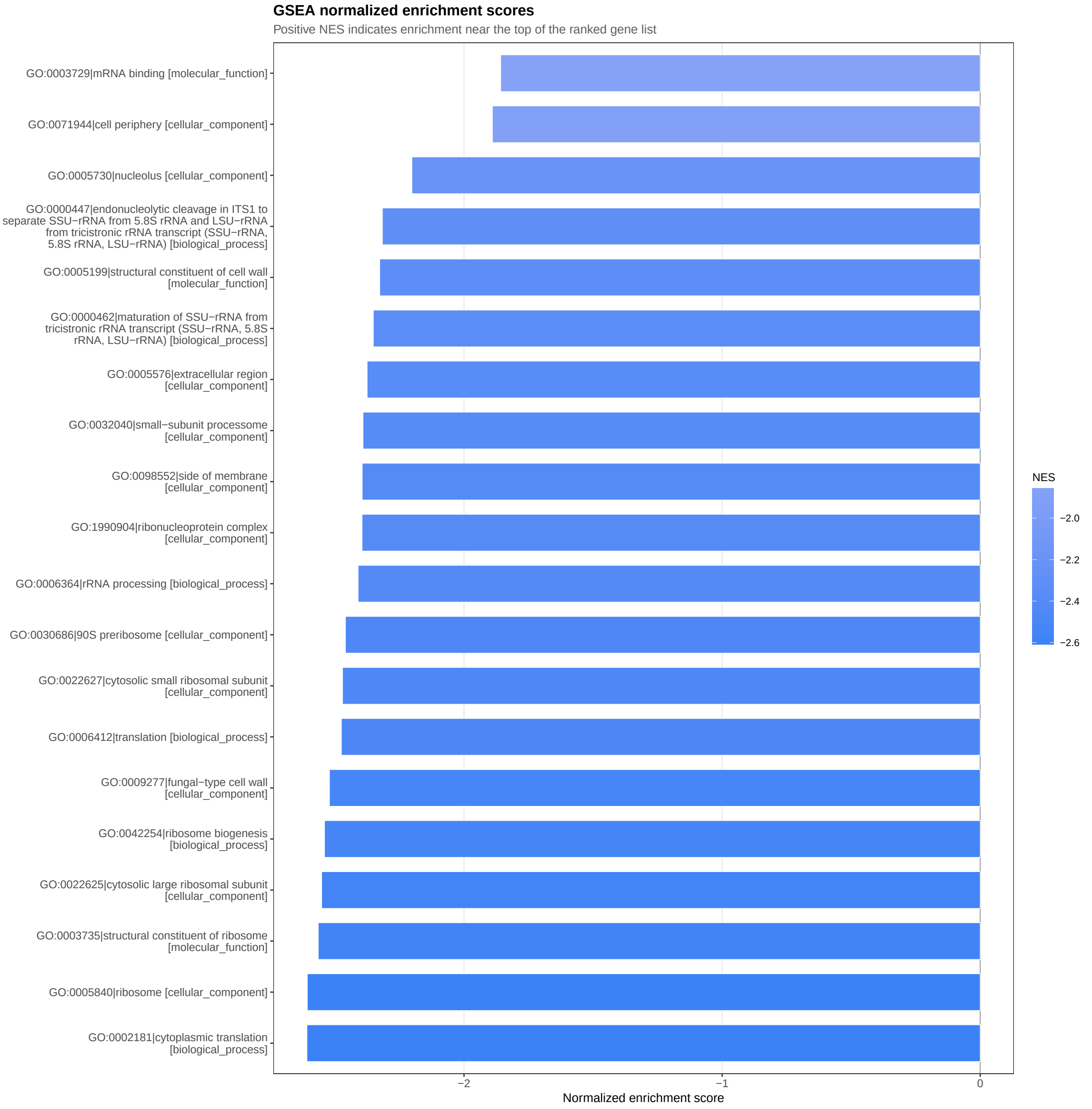
GSEA normalized enrichment scores
Positive NES indicates enrichment near the top of the ranked gene list
GO:0003729|mRNA binding [molecular_function]
GO:0071944|cell periphery [cellular_component]
GO:0005730|nucleolus [cellular_component]
GO:0000447|endonucleolytic cleavage in ITS1 to separate SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA) [biological_process]
GO:0005199|structural constituent of cell wall [molecular_function]
GO:0000462|maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA) [biological_process]
GO:0005576|extracellular region [cellular_component]
GO:0032040|small−subunit processome [cellular_component]
GO:0098552|side of membrane [cellular_component]
GO:1990904|ribonucleoprotein complex [cellular_component]
GO:0006364|rRNA processing [biological_process]
GO:0030686|90S preribosome [cellular_component]
GO:0022627|cytosolic small ribosomal subunit [cellular_component]
GO:0006412|translation [biological_process]
GO:0009277|fungal−type cell wall [cellular_component]
GO:0042254|ribosome biogenesis [biological_process]
GO:0022625|cytosolic large ribosomal subunit [cellular_component]
GO:0003735|structural constituent of ribosome [molecular_function]
GO:0005840|ribosome [cellular_component]
GO:0002181|cytoplasmic translation [biological_process]
−2
−1
0
Normalized enrichment score
NES
−2.0
−2.2
−2.4
−2.6