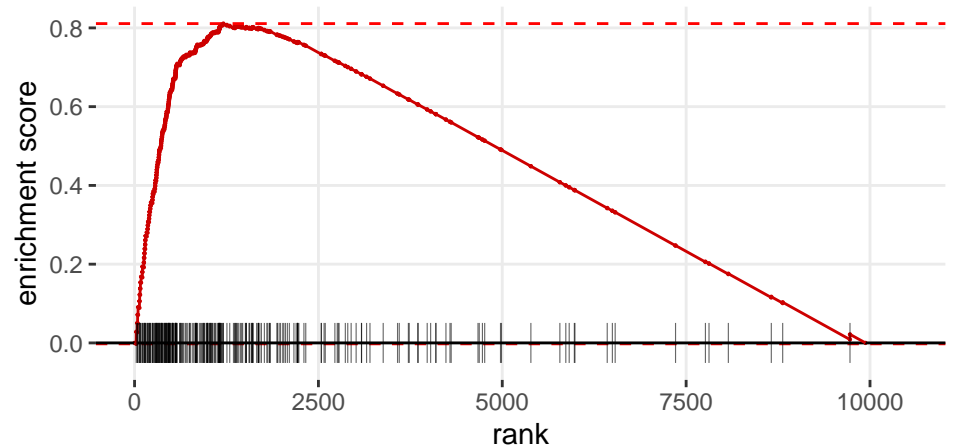


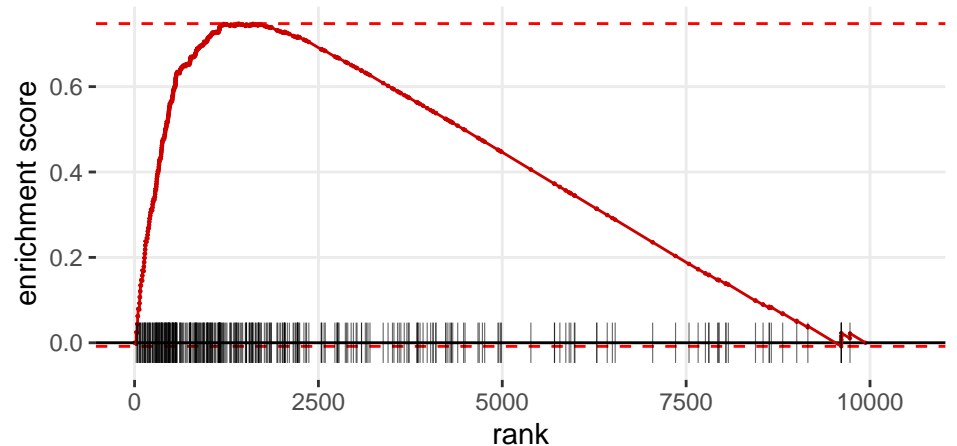
GSEA ImaxhmycVsNeg in GOBP Ribosome Biogenesis

NES = 2.29 p.adj = 7.32×10^{-18}



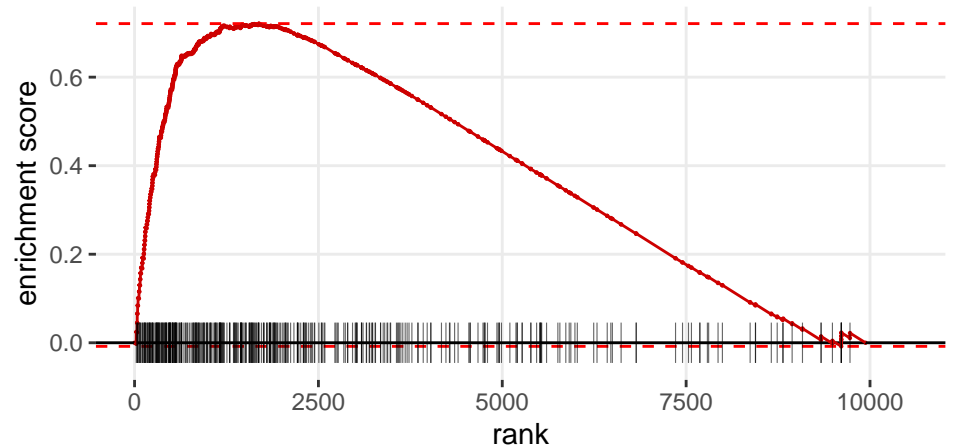
GSEA ImaxhmycVsNeg in GOBP Ribonucleoprotein Complex Biogenesis

NES = 2.23 p.adj = 1.69e-17



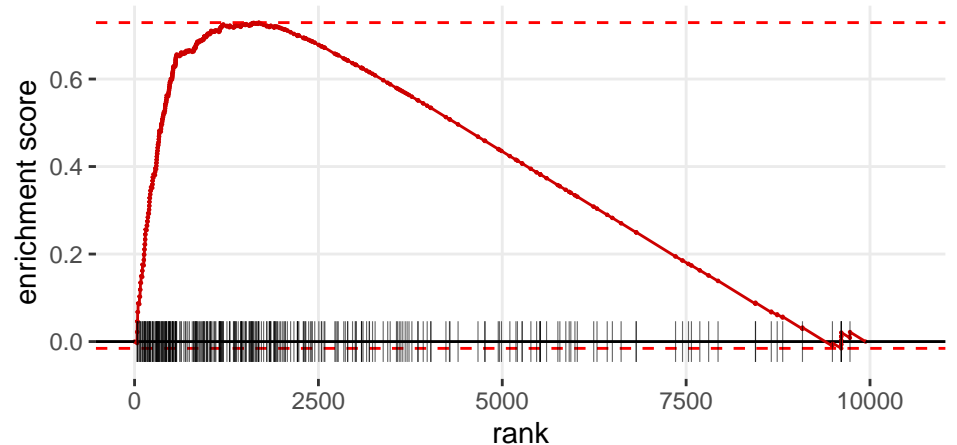
GSEA ImaxhmycVsNeg in GOBP ncRNA Metabolic Process

NES = 2.18 p.adj = 2.9e-16



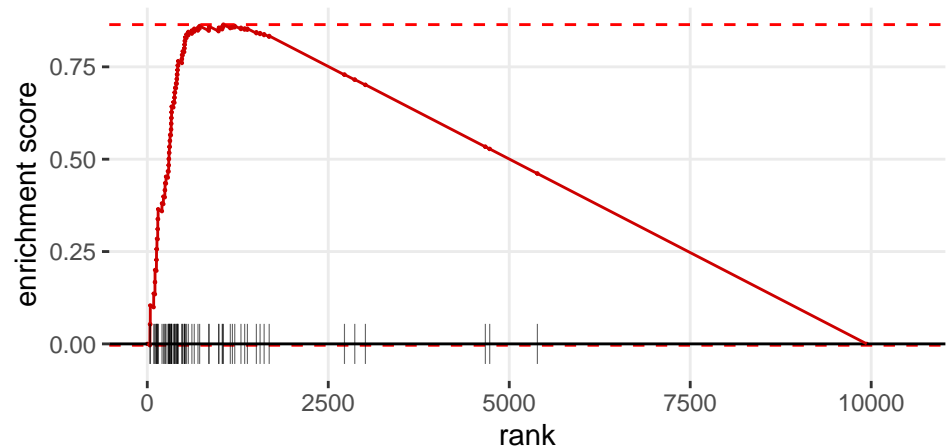
GSEA lmaxhmycVsNeg in GOBP ncRNA Processing

NES = 2.15 p.adj = 7.15e-14



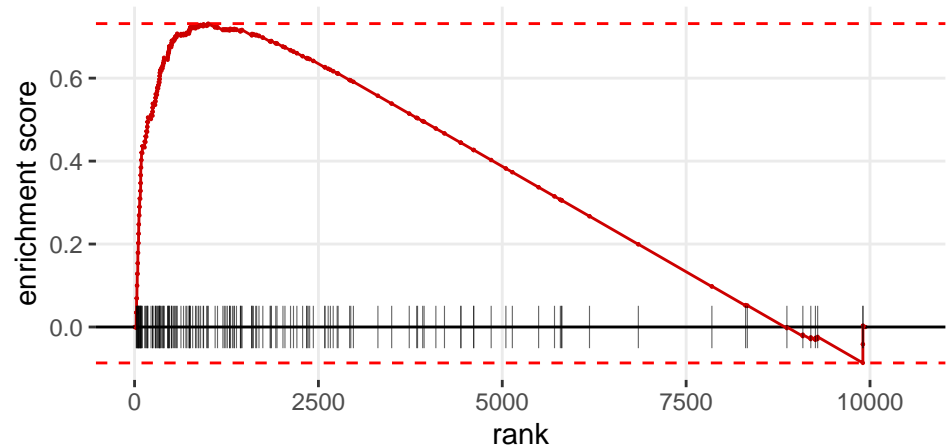
GSEA lmaxmycVsNeg in GOCC Preribosome

NES = 2.07 p.adj = 3.85e-06



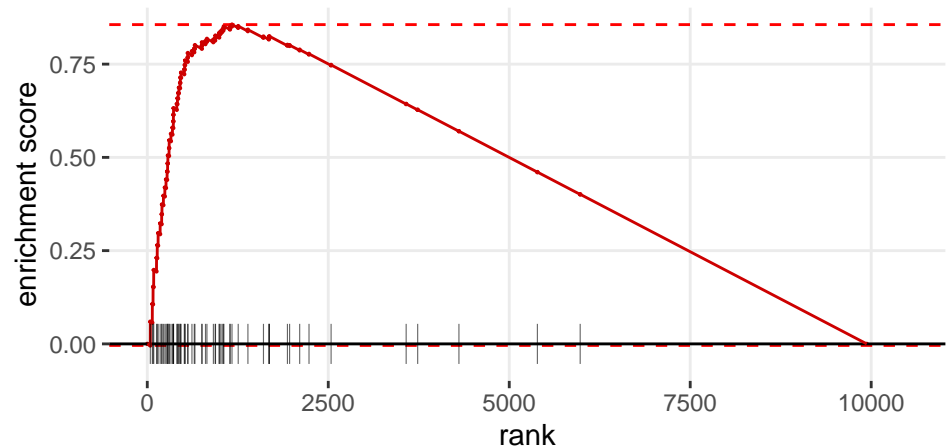
GSEA lmaxmycVsNeg in Hallmark Myc Targets V1

NES = 2.04 p.adj = 9.7e-07



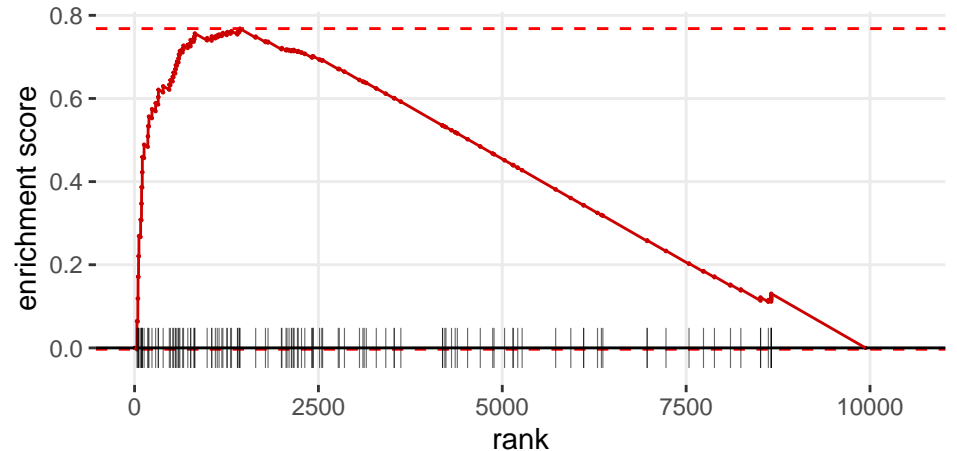
GSEA lmaxmycVsNeg in GOBP Ribosomal Large Subunit Biogenesis

NES = 2.02 p.adj = 4.42e-05



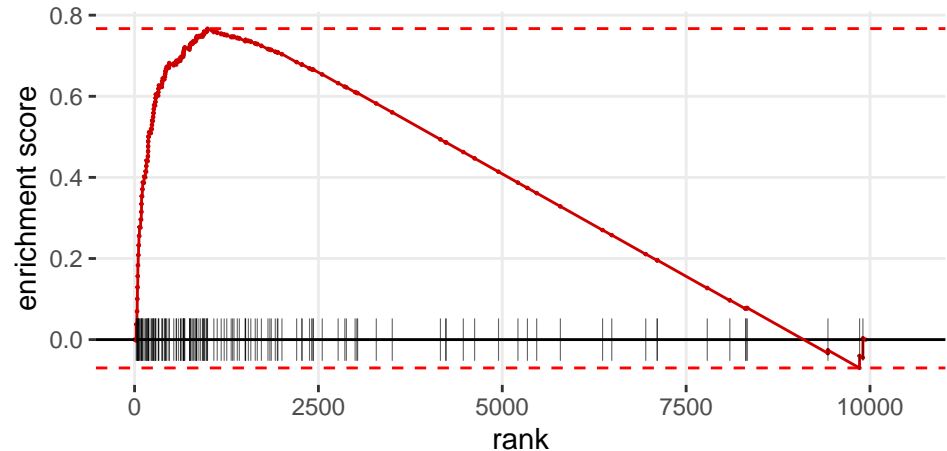
GSEA ImaxhmycVsNeg in GOMF Catalytic Activity Acting On DNA

NES = 2.02 p.adj = 1.58e-05



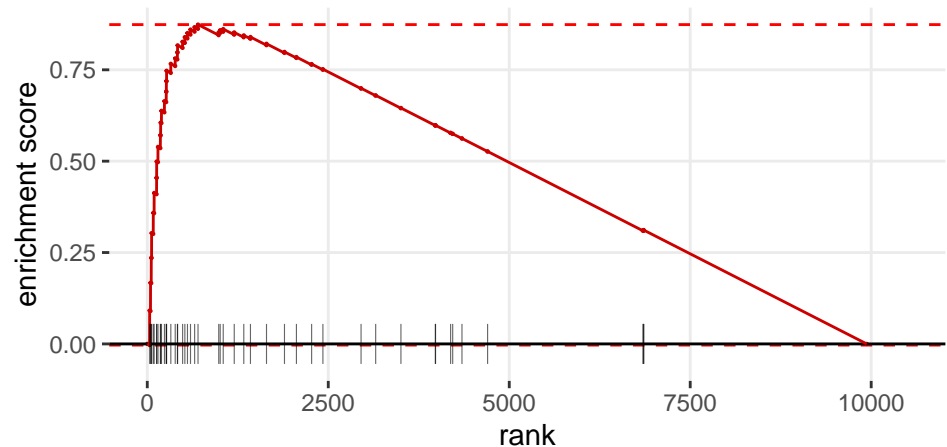
GSEA ImaxhmycVsNeg in Hallmark E2f Targets

NES = 2 p.adj = 2.61e-06



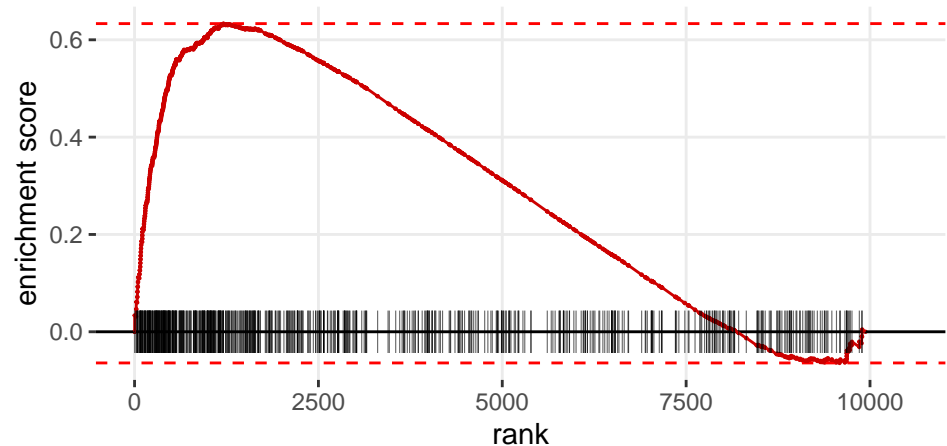
GSEA ImaxhmycVsNeg in GOBP Cell Cycle DNA Replication

NES = 1.94 p.adj = 0.000289



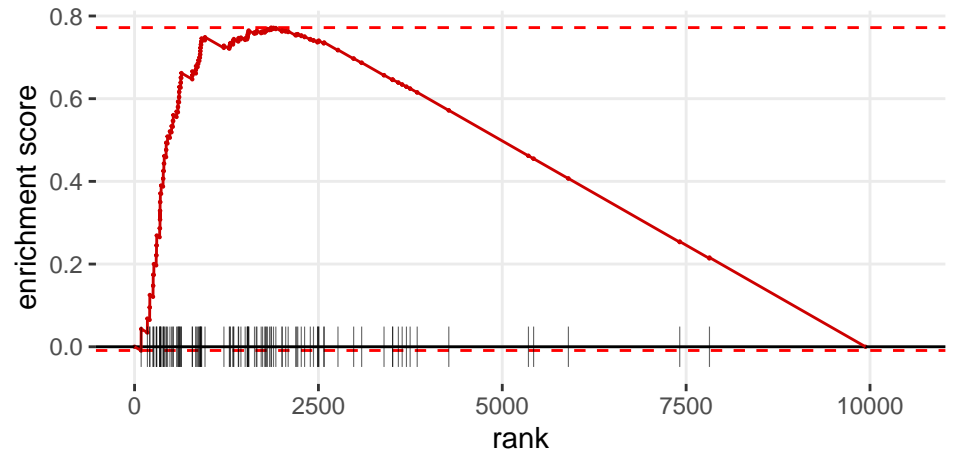
GSEA ImaxhmycVsNeg in GOCC Nucleolus

NES = 1.94 p.adj = 7.15e-14



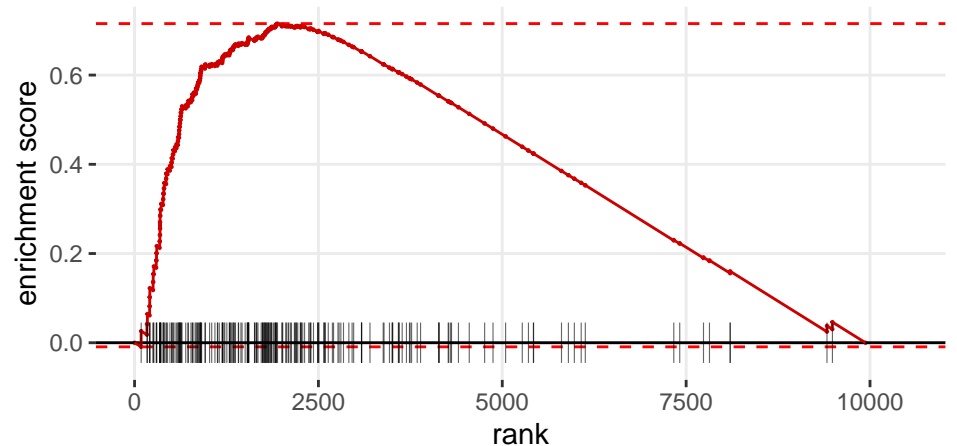
GSEA ImaxhmycVsNeg in GOCC Inner Mitochondrial Membrane Protein Complex

NES = 1.94 p.adj = 0.000245



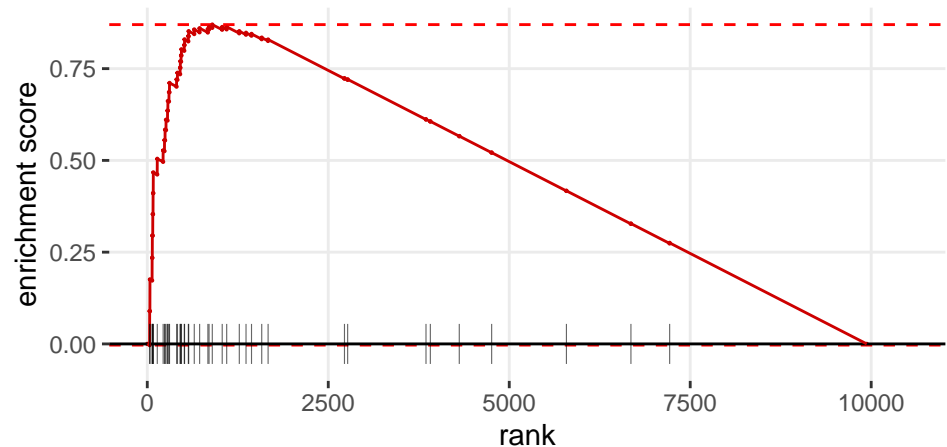
GSEA ImaxhmycVsNeg in GOCC Mitochondrial Protein Containing Complex

NES = 1.93 p.adj = 1.64e-06



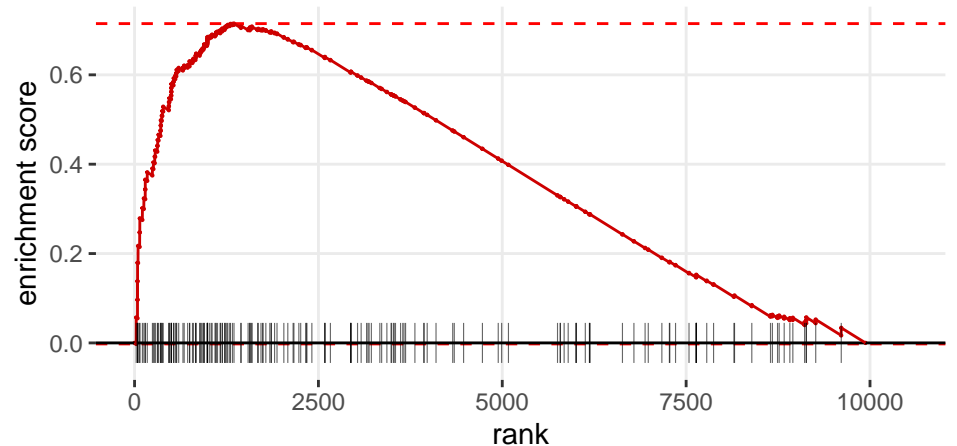
GSEA ImaxhmycVsNeg in Hallmark Myc Targets V2

NES = 1.93 p.adj = 0.000257



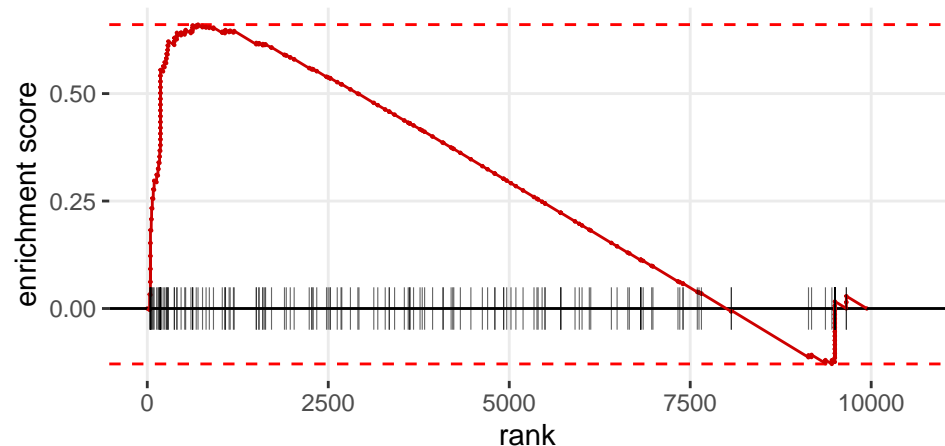
GSEA ImaxhmycVsNeg in GOBP RNA Localization

NES = 1.88 p.adj = 0.00018



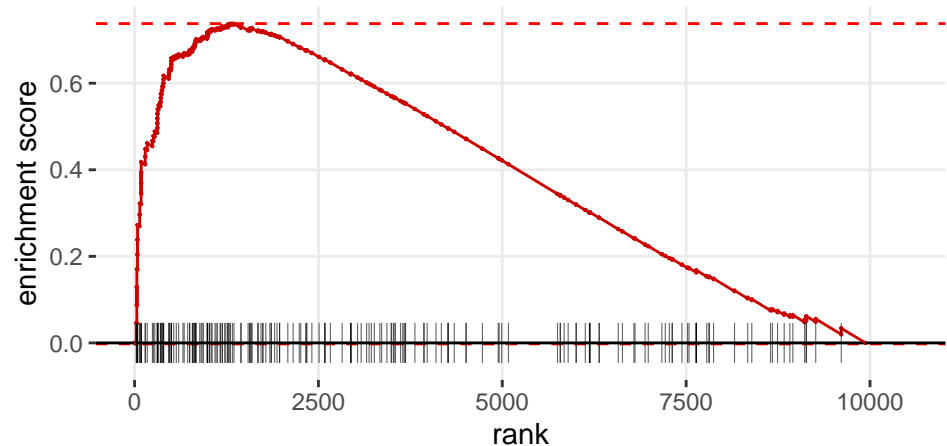
GSEA ImaxhmycVsNeg in GOBP Protein DNA Complex Subunit Organization

NES = 1.88 p.adj = 0.000815



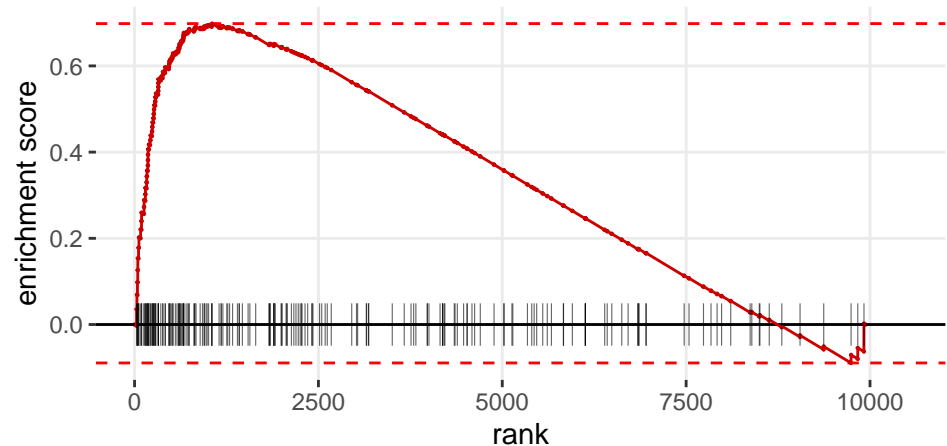
GSEA ImaxhmycVsNeg in GOBP Nucleobase Containing Compound Transport

NES = 1.88 p.adj = 0.000165



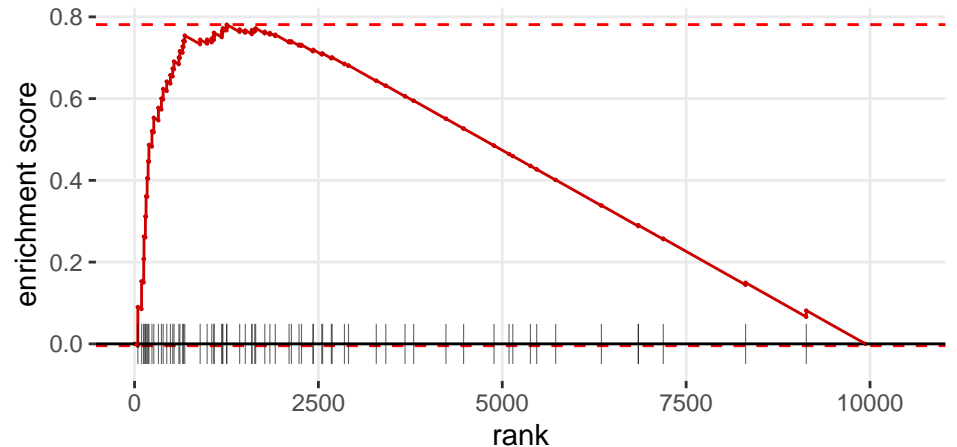
GSEA ImaxhmycVsNeg in GOBP DNA Replication

NES = 1.88 p.adj = 5.77e-05



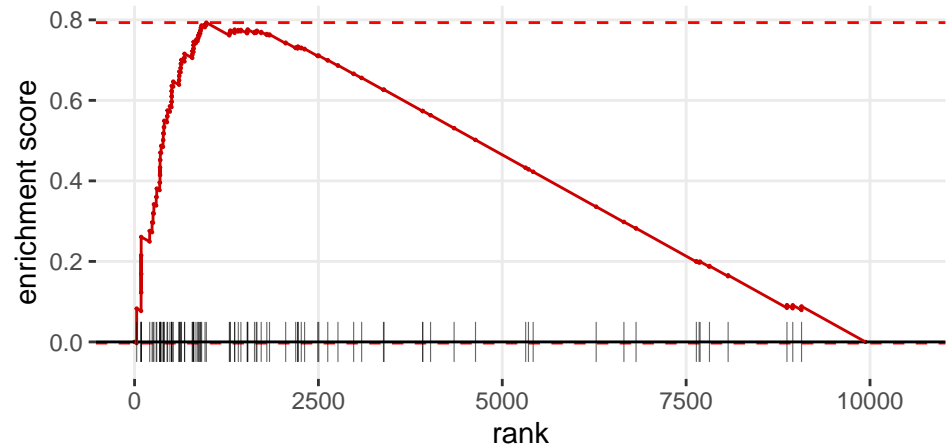
GSEA ImaxhmycVsNeg in WP DNA Repair Pathways Full Network

NES = 1.88 p.adj = 0.00544



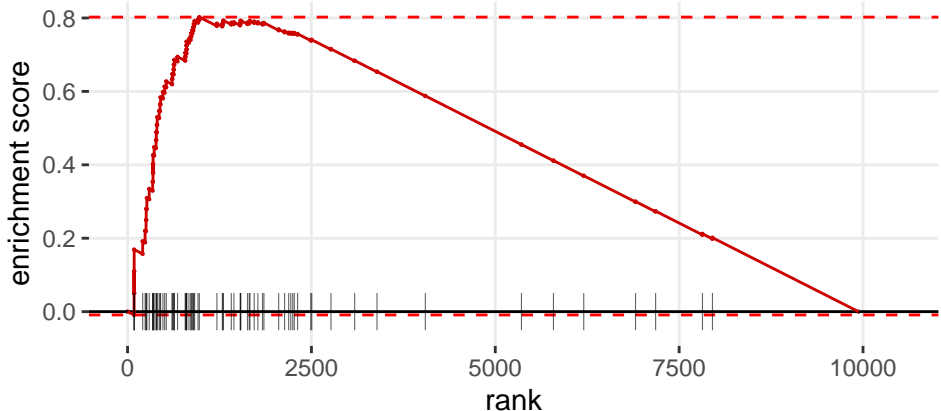
GSEA ImaxhmycVsNeg in Kegg Parkinsons Disease

NES = 1.87 p.adj = 0.00283



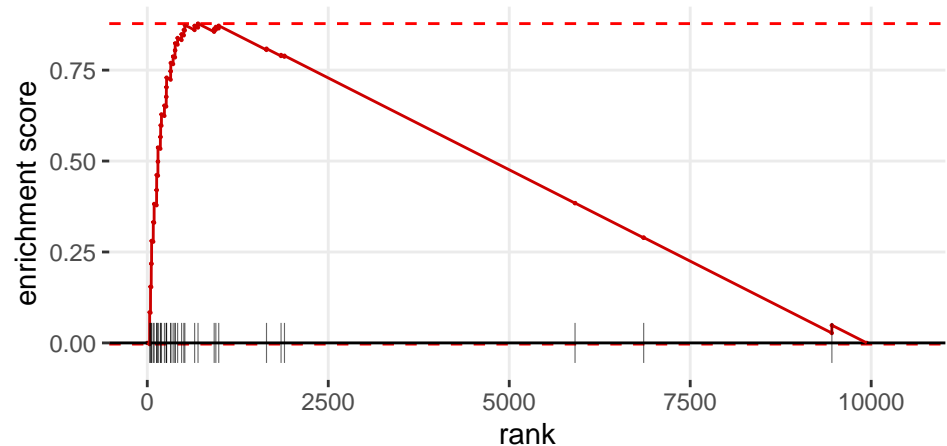
GSEA ImaxhmycVsNeg in WP Electron Transport Chain Oxphos System In Mitochondria

NES = 1.87 p.adj = 0.00424



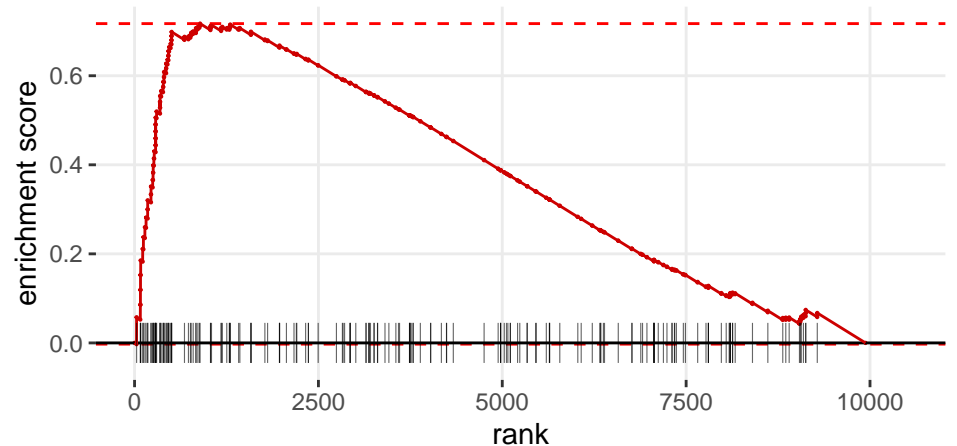
GSEA lmaxhmycVsNeg in WP DNA Replication

NES = 1.86 p.adj = 0.00329



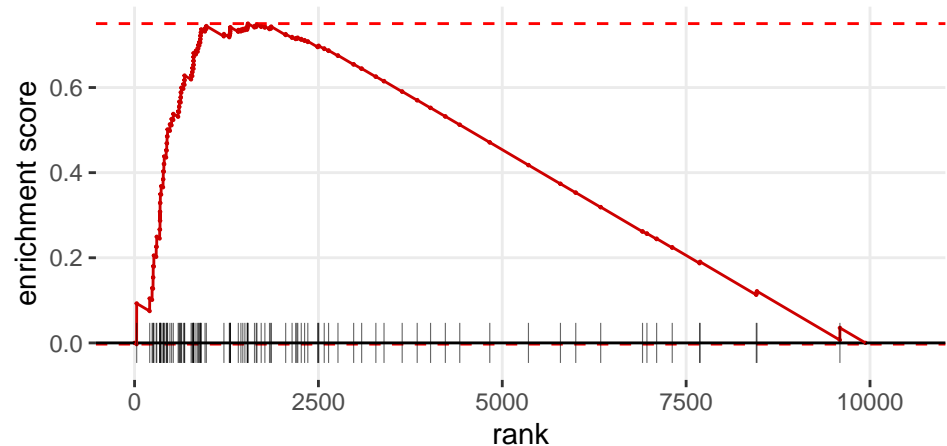
GSEA ImaxhmycVsNeg in GOBP Nucleoside Phosphate Biosynthetic Process

NES = 1.86 p.adj = 0.000329



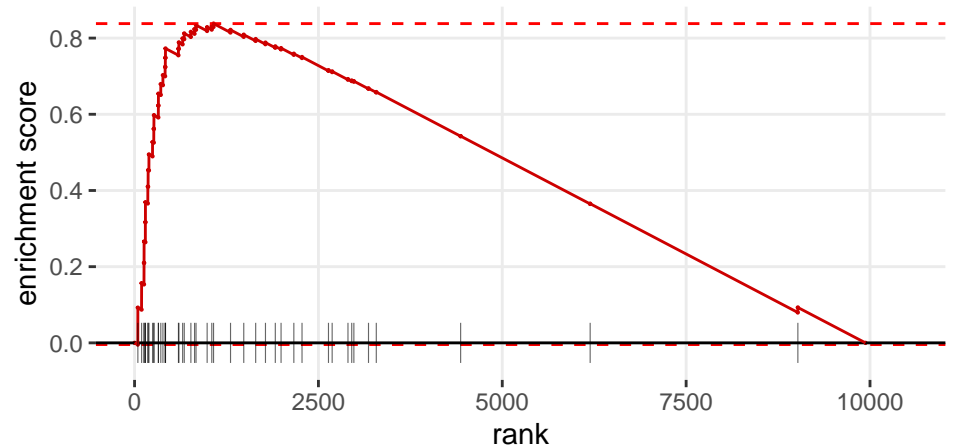
GSEA ImaxhmycVsNeg in GOBP Oxidative Phosphorylation

NES = 1.86 p.adj = 0.00283



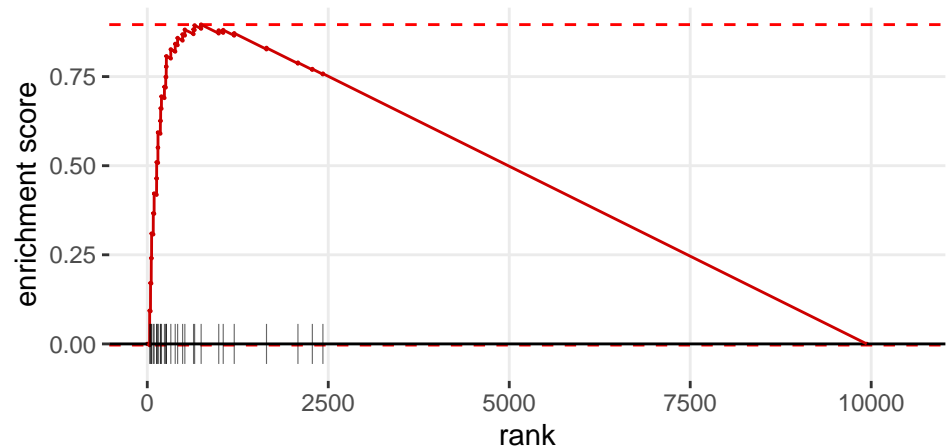
GSEA ImaxhmycVsNeg in GOCC Replication Fork

NES = 1.83 p.adj = 0.00526



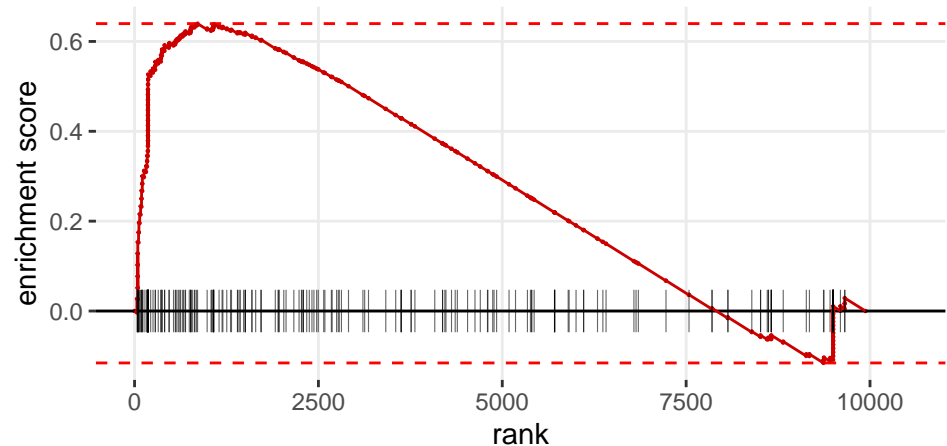
GSEA ImaxhmycVsNeg in Kegg DNA Replication

NES = 1.83 p.adj = 0.00496



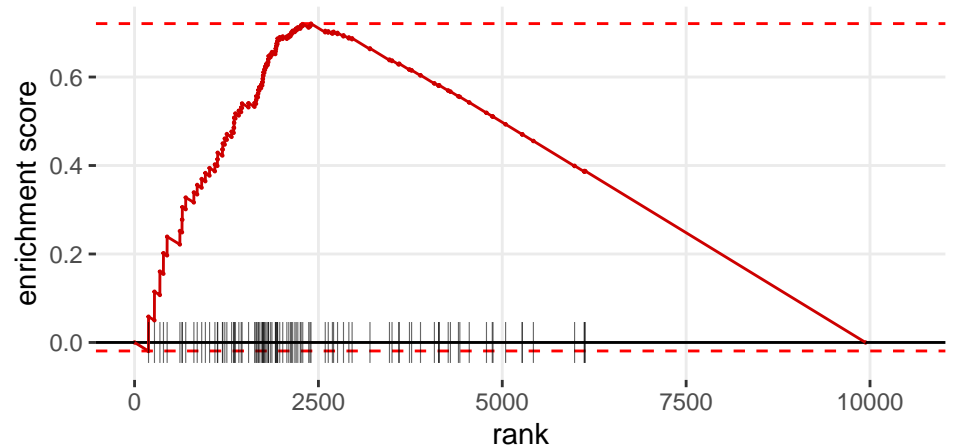
GSEA ImaxhmycVsNeg in GOBP DNA Conformation Change

NES = 1.82 p.adj = 0.000815



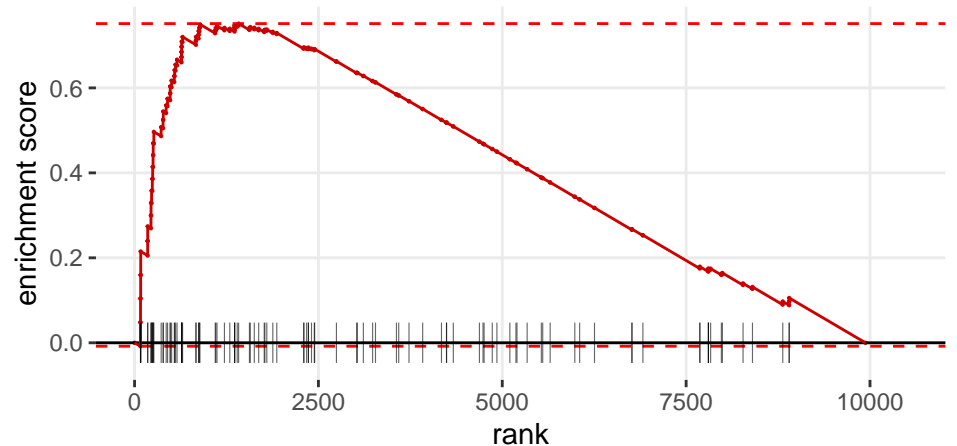
GSEA ImaxhmycVsNeg in GOBP Translational Elongation

NES = 1.82 p.adj = 0.00283



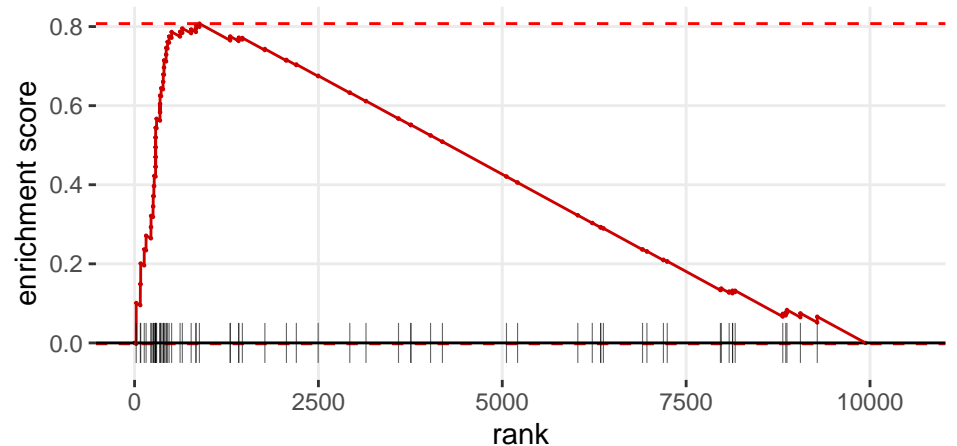
GSEA ImaxhmycVsNeg in GOMF Ligase Activity

NES = 1.82 p.adj = 0.00516



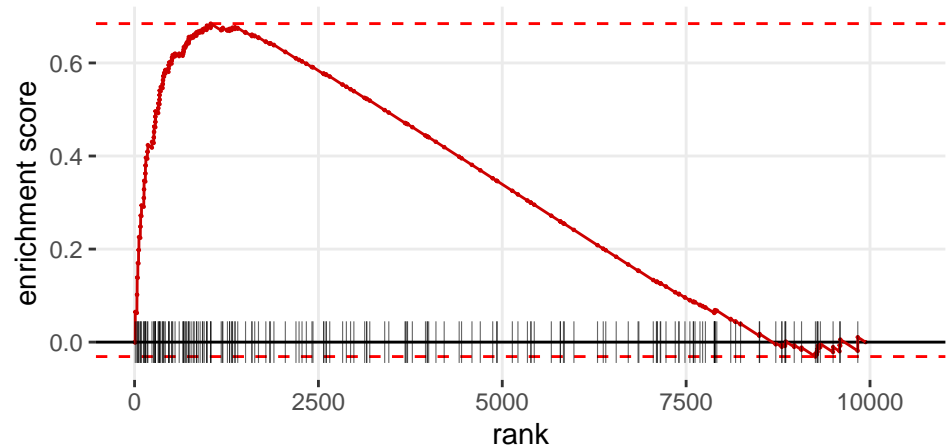
GSEA ImaxhmycVsNeg in GOBP Nucleoside Triphosphate Metabolic Process

NES = 1.82 p.adj = 0.00533



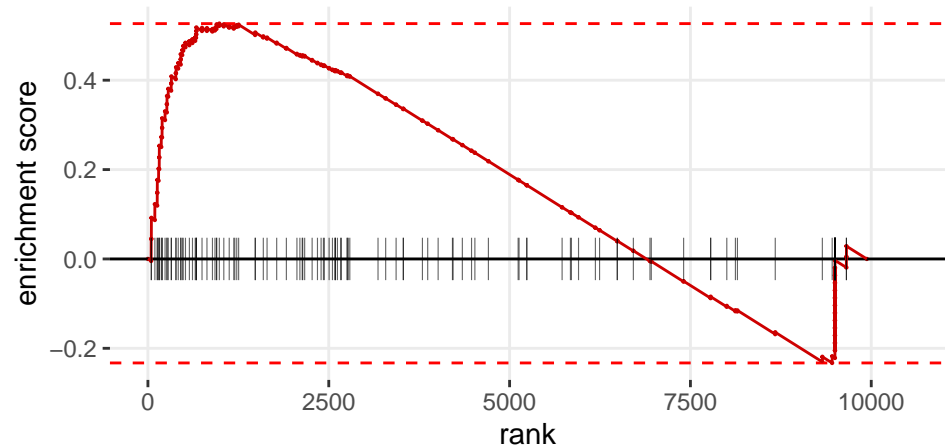
GSEA ImaxhmycVsNeg in GOBP Cell Cycle G1 S Phase Transition

NES = 1.81 p.adj = 0.00109



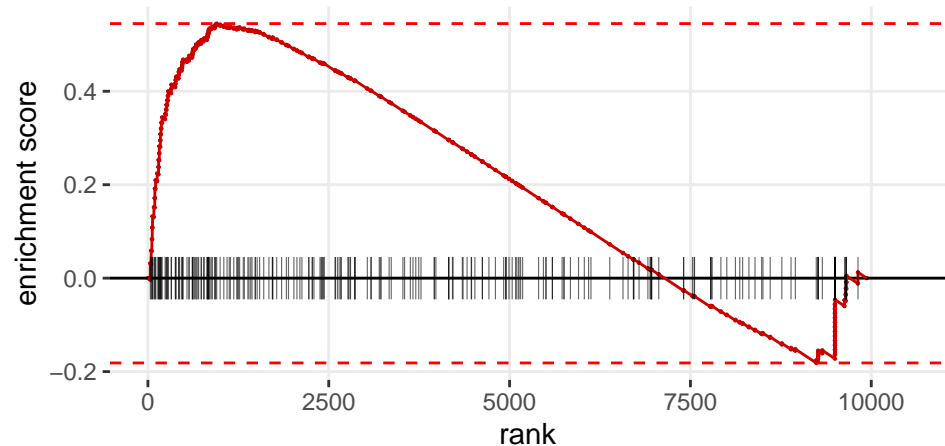
GSEA ImaxhmycVsNeg in GOBP Telomere Organization

NES = 1.79 p.adj = 0.00891



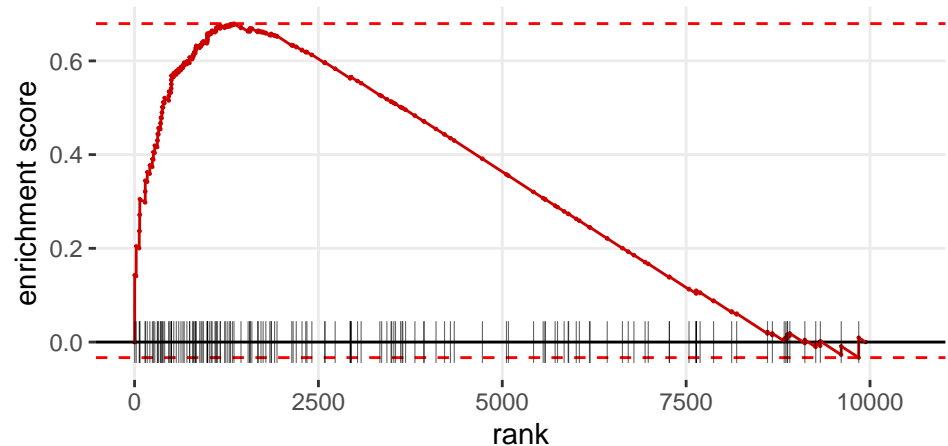
GSEA lmaxmycVsNeg in GOCC Chromosomal Region

NES = 1.78 p.adj = 0.000799



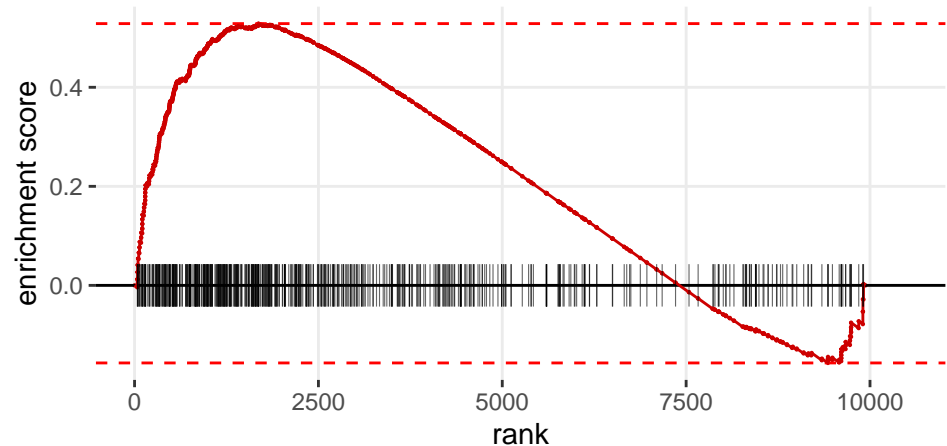
GSEA ImaxhmycVsNeg in GOBP Nuclear Export

NES = 1.77 p.adj = 0.00268



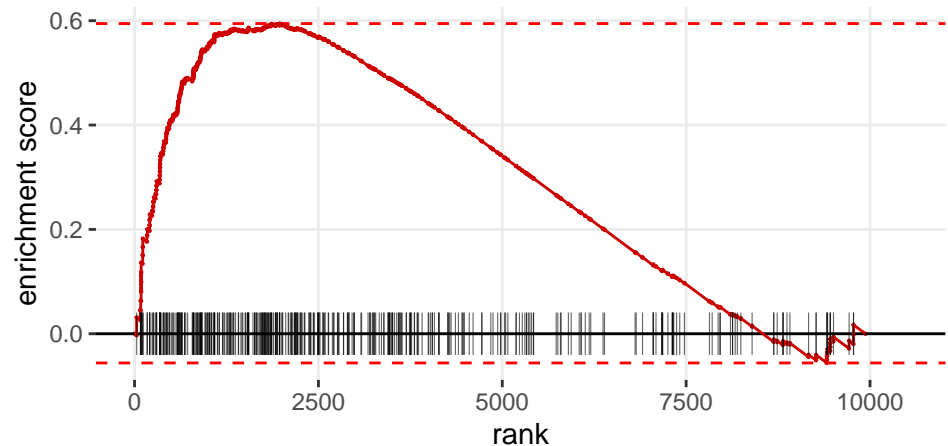
GSEA ImaxhmycVsNeg in GOCC Ribonucleoprotein Complex

NES = 1.76 p.adj = 2.61e-06



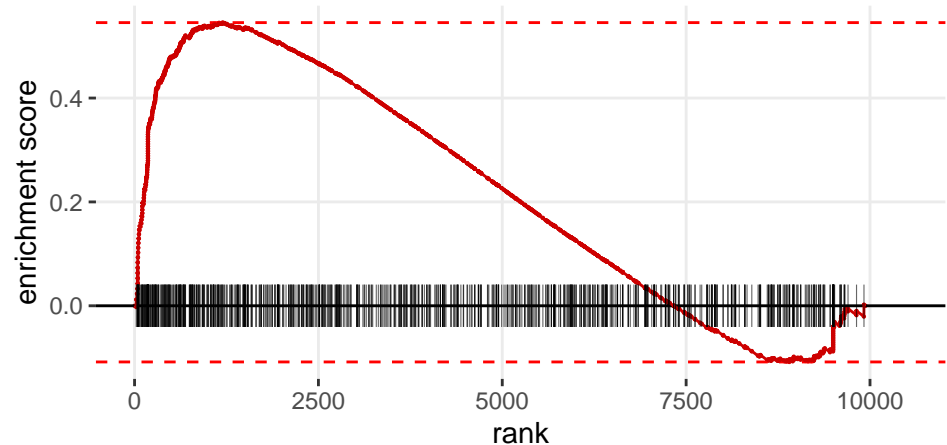
GSEA ImaxhmycVsNeg in GOCC Organelle Inner Membrane

NES = 1.75 p.adj = 5.63e-05



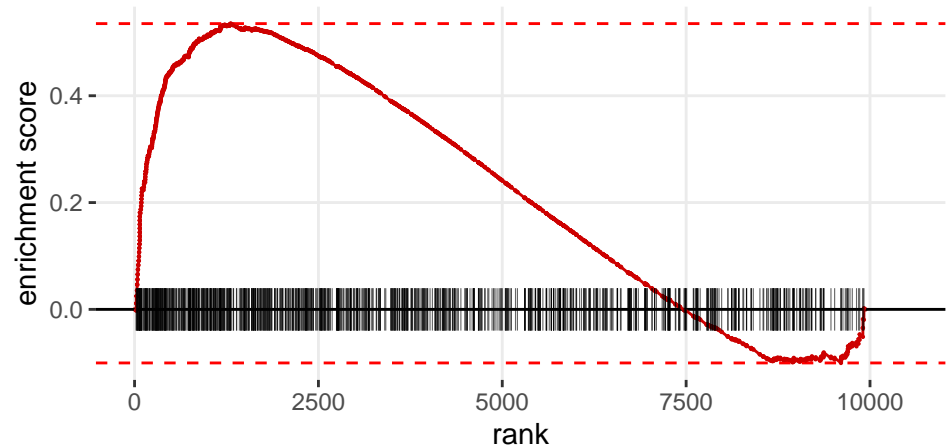
GSEA ImaxhmycVsNeg in GOBP Chromosome Organization

NES = 1.74 p.adj = 2.47e-08



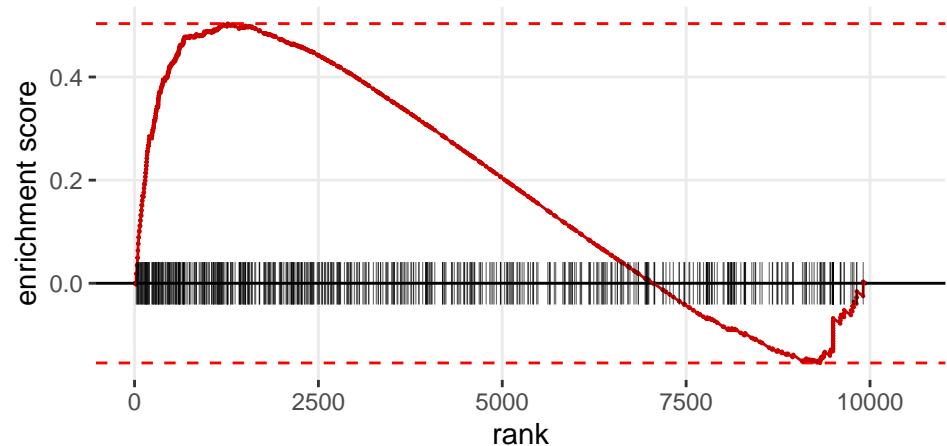
GSEA ImaxhmycVsNeg in GOCC Nuclear Protein Containing Complex

NES = 1.68 p.adj = 3.15e-08



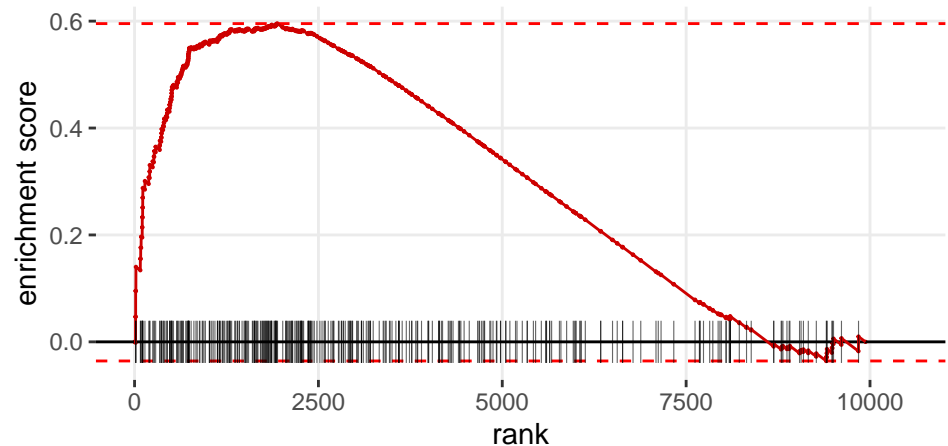
GSEA lmaxhmycVsNeg in GOBP DNA Metabolic Process

NES = 1.67 p.adj = 3.85e-06



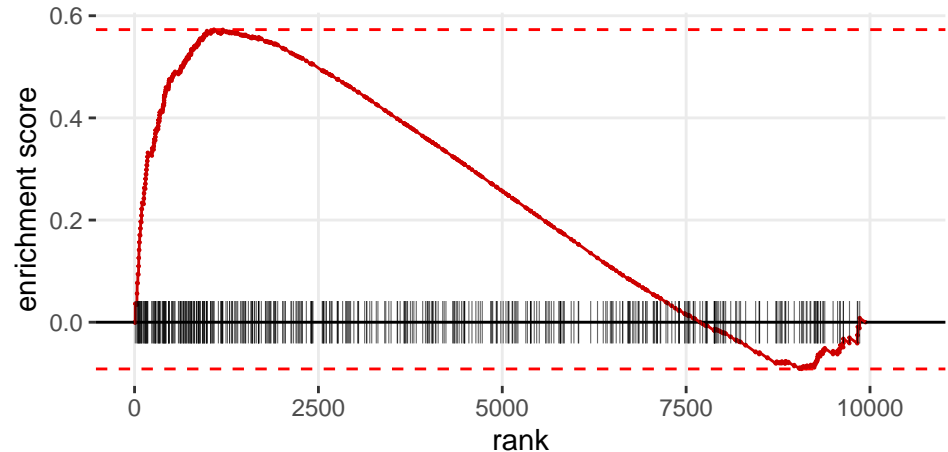
GSEA ImaxhmycVsNeg in GOCC Mitochondrial Matrix

NES = 1.66 p.adj = 0.000597



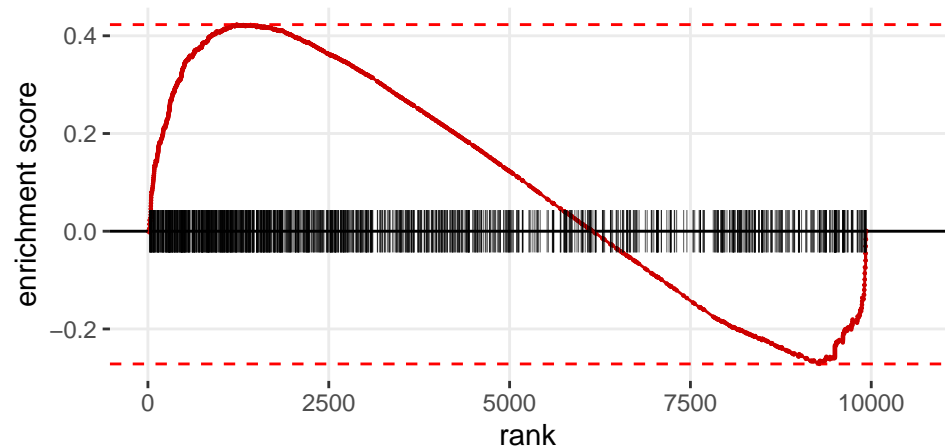
GSEA ImaxhmycVsNeg in GOBP Cell Cycle Phase Transition

NES = 1.63 p.adj = 0.000799



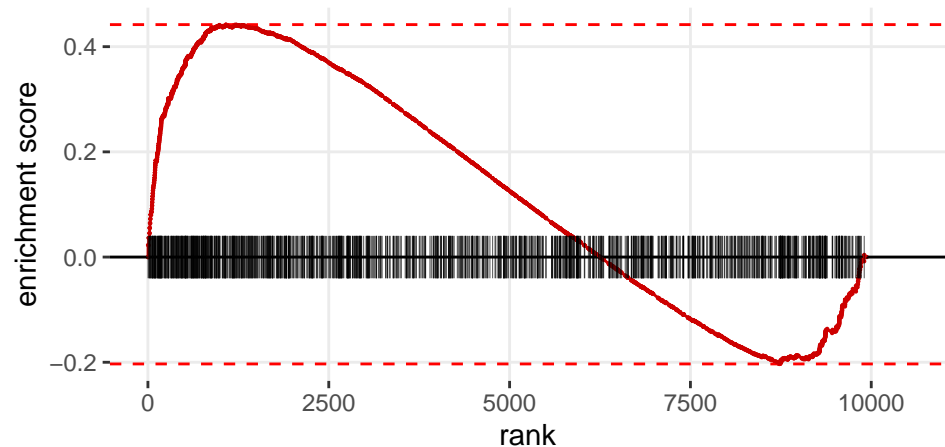
GSEA lmaxhmycVsNeg in GOMF RNA Binding

NES = 1.49 p.adj = 5.15e-06



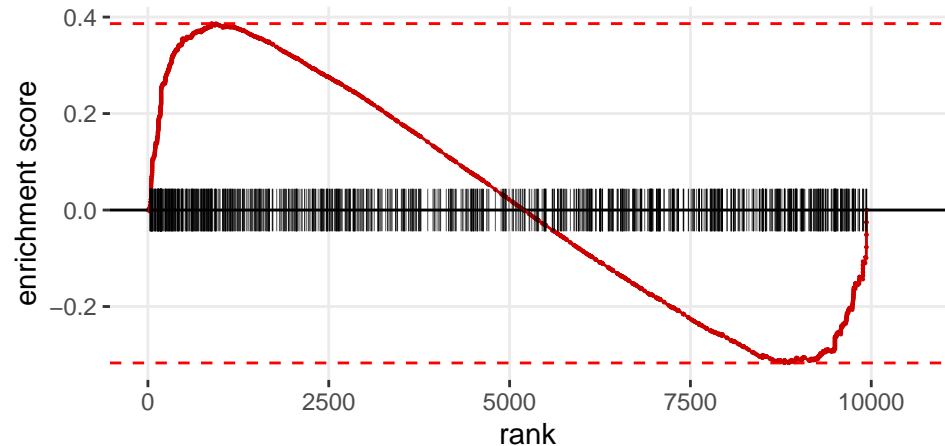
GSEA lmaxhmycVsNeg in GOBP Cell Cycle

NES = 1.47 p.adj = 1.9e-05



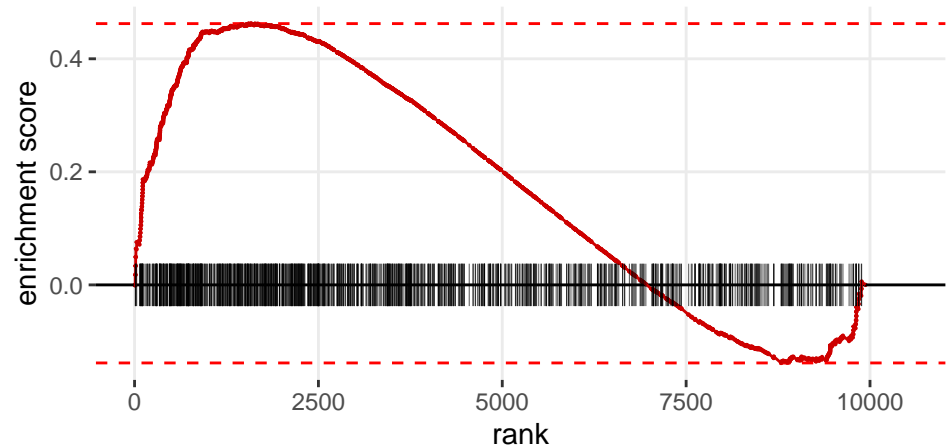
GSEA lmaxmycVsNeg in GOCC Chromosome

NES = 1.37 p.adj = 0.00413



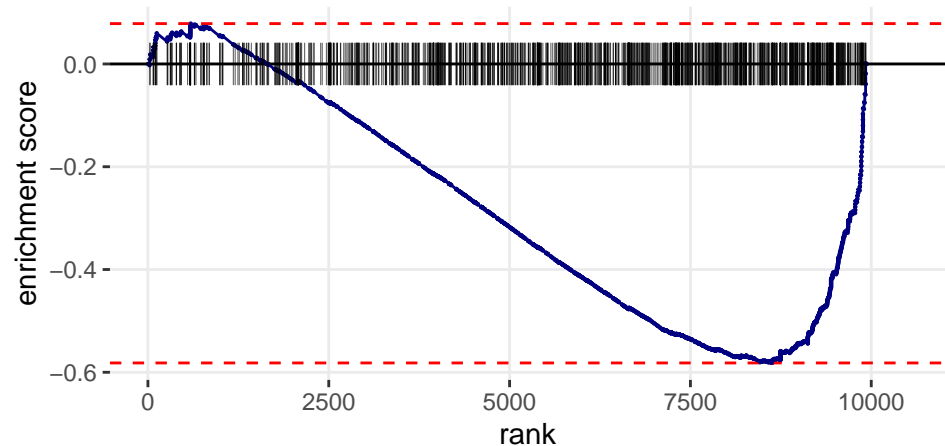
GSEA ImaxhmycVsNeg in GOCC Mitochondrion

NES = 1.34 p.adj = 0.00177



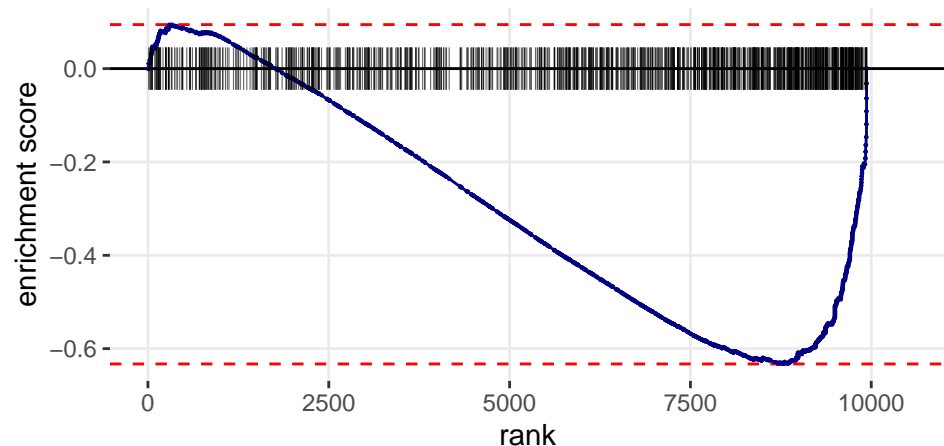
GSEA lmaxmycVsNeg in GOCC Organelle Subcompartment

NES = -1.45 p.adj = 0.00496



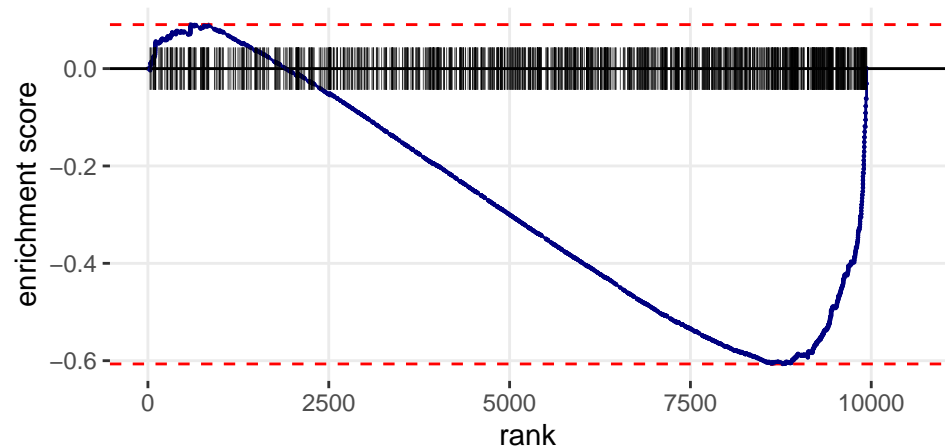
GSEA lmaxmycVsNeg in GOBP Regulation Of Cell Differentiation

NES = -1.49 p.adj = 0.00329



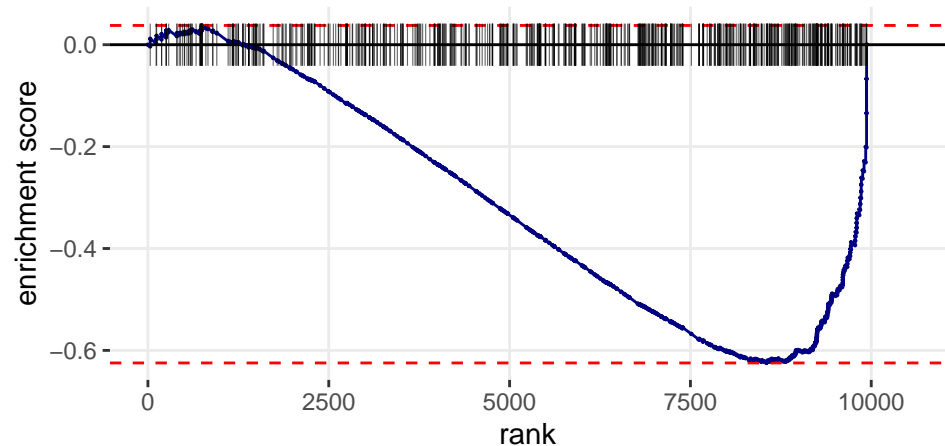
GSEA ImaxmycVsNeg in GOCC Endoplasmic Reticulum

NES = -1.51 p.adj = 0.000185



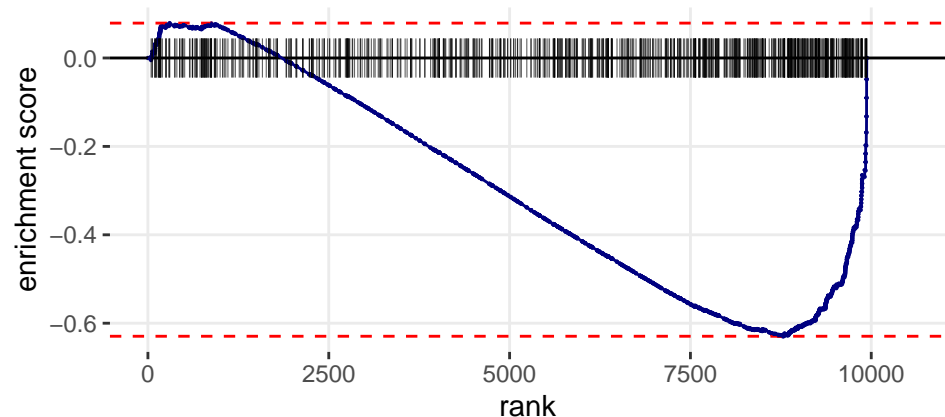
GSEA lmaxmycVsNeg in GOCC Secretory Vesicle

NES = -1.51 p.adj = 0.00762



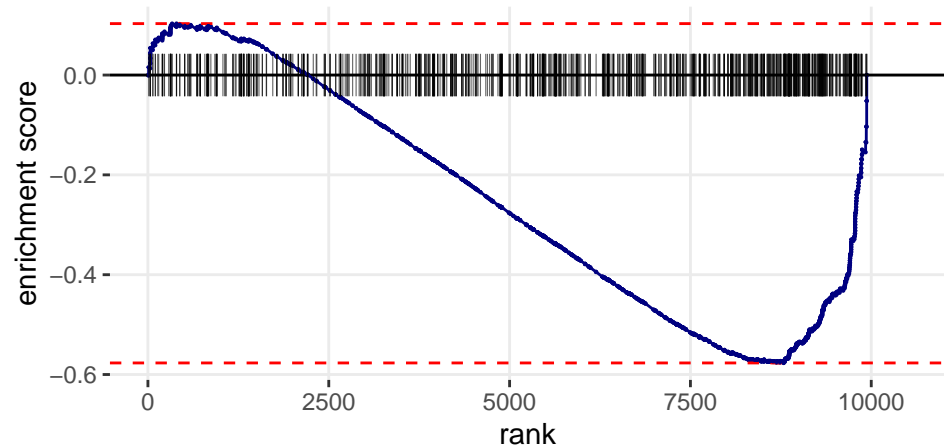
GSEA ImaxhmycVsNeg in GOBP Positive Regulation Of Multicellular Organismal Process

NES = -1.52 p.adj = 0.00369



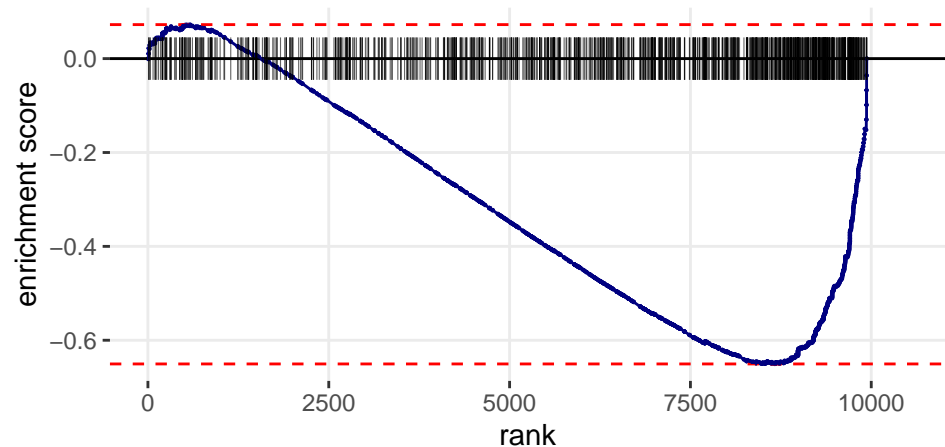
GSEA lmaxmycVsNeg in GOCC Plasma Membrane Region

NES = -1.54 p.adj = 0.00151



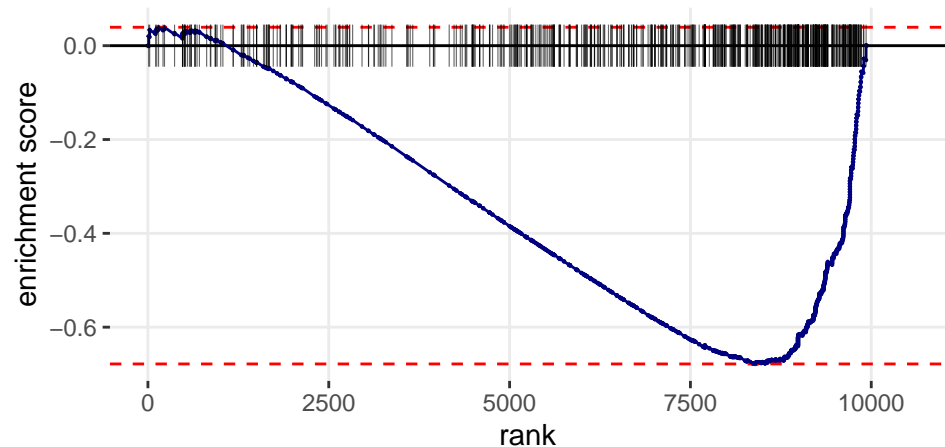
GSEA lmaxmycVsNeg in GOBP Locomotion

NES = -1.62 p.adj = $2.57e-06$



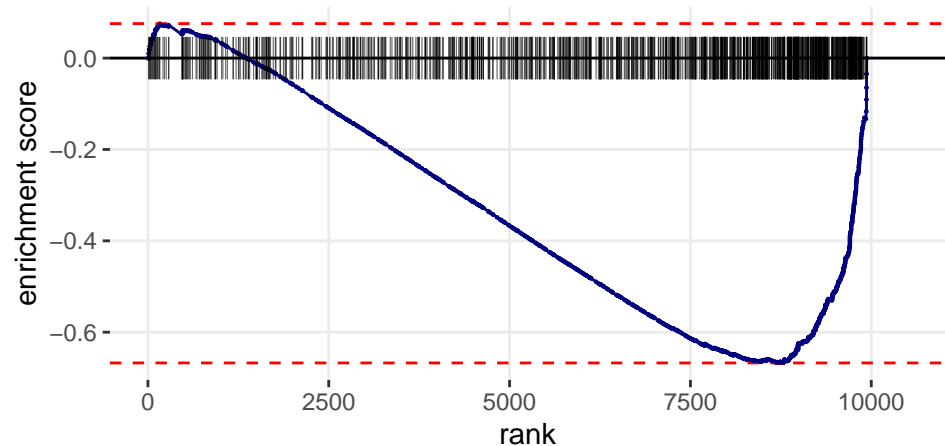
GSEA lmaxmycVsNeg in GOBP Cell Morphogenesis

NES = -1.63 p.adj = 0.000165



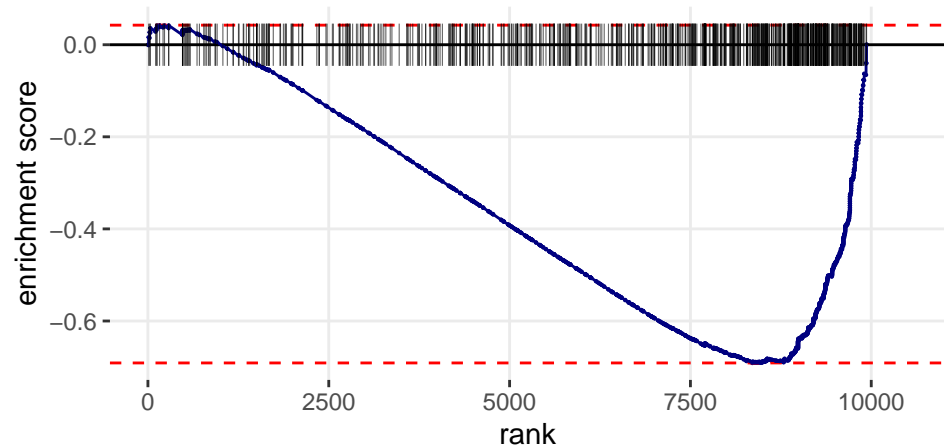
GSEA lmaxmycVsNeg in GOBP Neurogenesis

NES = -1.63 p.adj = $1.63\text{e-}06$



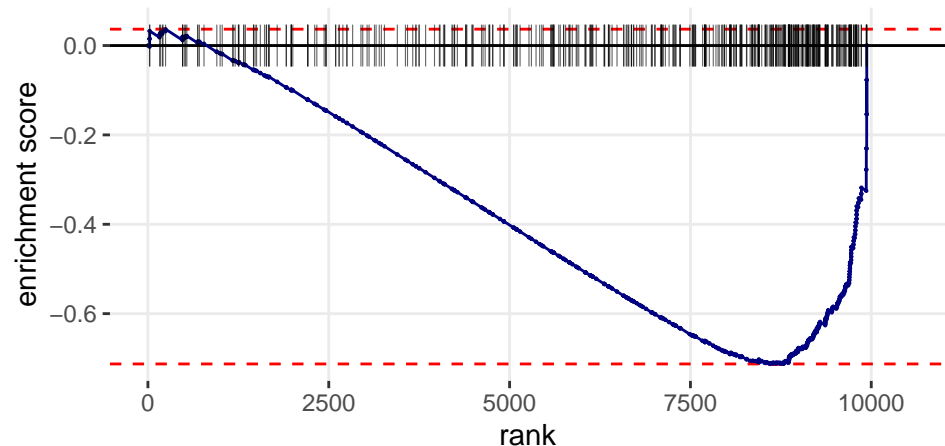
GSEA lmaxmycVsNeg in GOBP Neuron Development

NES = -1.66 p.adj = $1.66e-05$



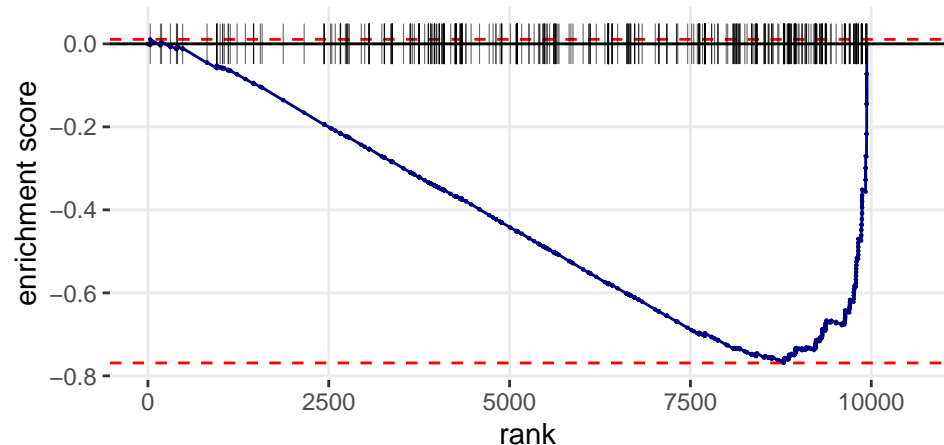
GSEA ImaxhmycVsNeg in GOBP Cell Junction Organization

NES = -1.67 p.adj = 0.000631



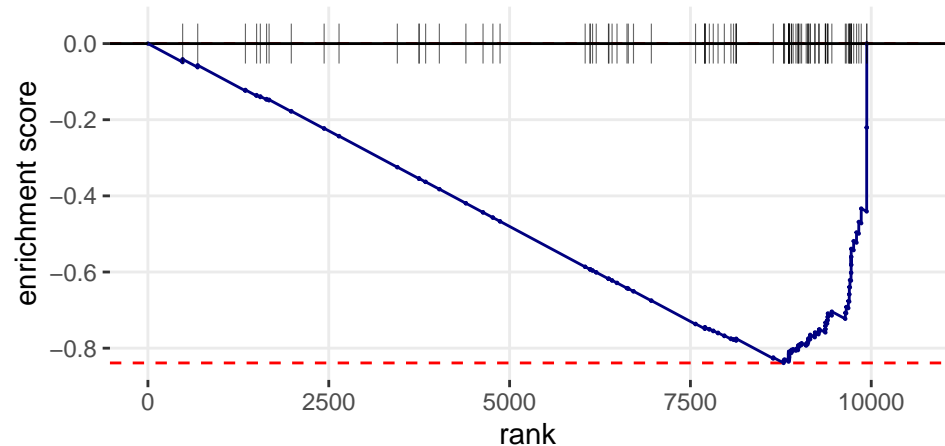
GSEA lmaxhmycVsNeg in GOMF Molecular Transducer Activity

NES = -1.76 p.adj = 0.000299



GSEA lmaxmycVsNeg in GOBP Synapse Assembly

NES = -1.76 p.adj = 0.00786



GSEA lmaxmycVsNeg in GOBP Regulation Of Cell Junction Assembly

NES = -1.8 p.adj = 0.000443

