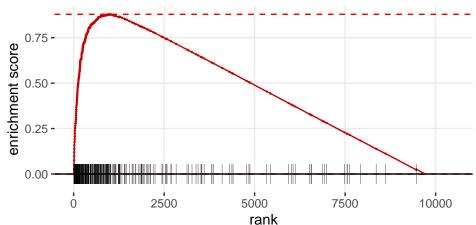
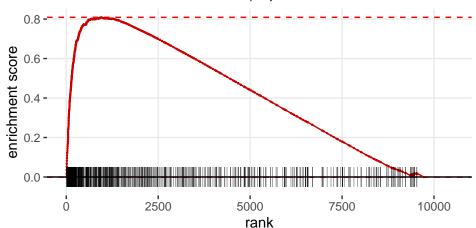
GSEA ImaxhmycVsImax in GOBP Ribosome Biogenesis

NES = 2.2 p.adj = 2.52e-22



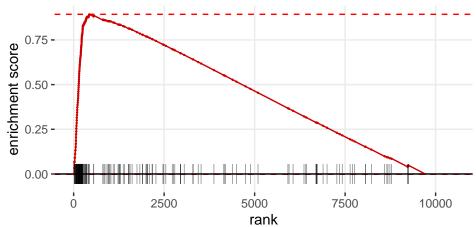
GSEA ImaxhmycVsImax in GOCC Ribonucleoprotein Complex

NES = 2.16 p.adj = 2.17e-28



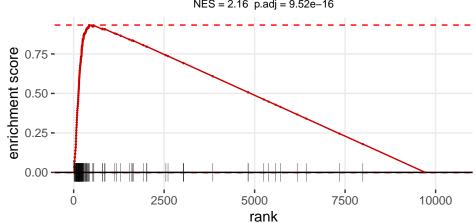
GSEA ImaxhmycVsImax in GOBP Viral Gene Expression

NES = 2.16 p.adj = 3.51e-16



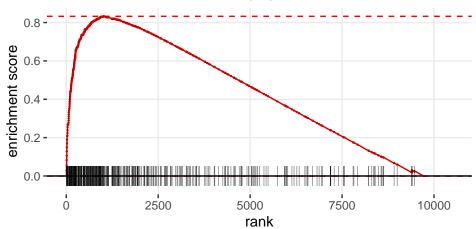
GSEA ImaxhmycVsImax in GOBP Establishment Of Protein Localization To Endoplasmic Reticulum

NES = 2.16 p.adj = 9.52e-16



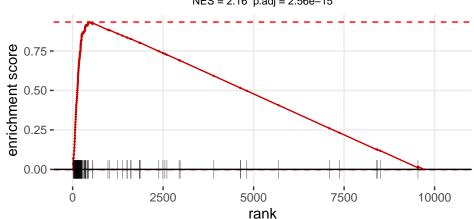
GSEA ImaxhmycVsImax in GOBP ncRNA Metabolic Process

NES = 2.16 p.adj = 5.82e-25



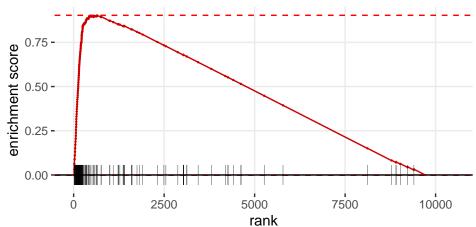
GSEA ImaxhmycVsImax in GOBP Nuclear Transcribed mRNA Catabolic Process Nonsense Mediated Decay

NES = 2.16 p.adj = 2.56e-15

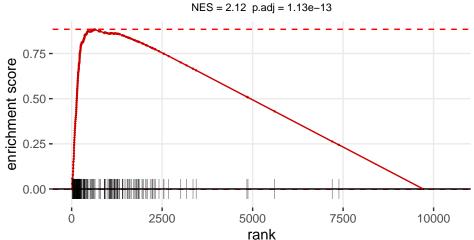


GSEA ImaxhmycVsImax in GOBP Translational Initiation

NES = 2.14 p.adj = 1.27e-13

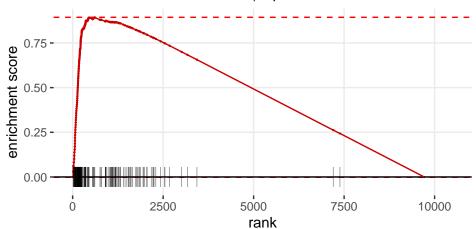


GSEA ImaxhmycVsImax in GOCC Ribosomal Subunit

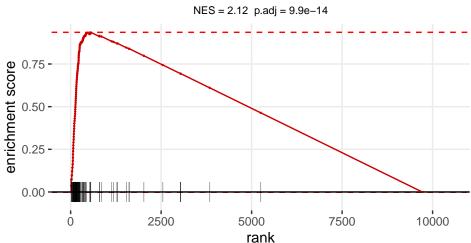


GSEA ImaxhmycVsImax in GOMF Structural Constituent Of Ribosome

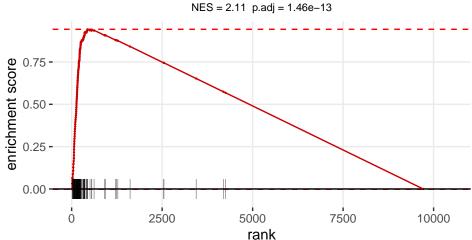
NES = 2.12 p.adj = 1.64e-12



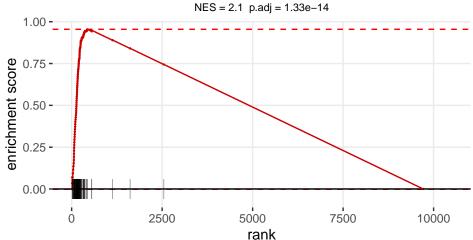
GSEA ImaxhmycVsImax in GOBP Cotranslational Protein Targeting To Membrane



GSEA ImaxhmycVsImax in GOCC Cytosolic Ribosome

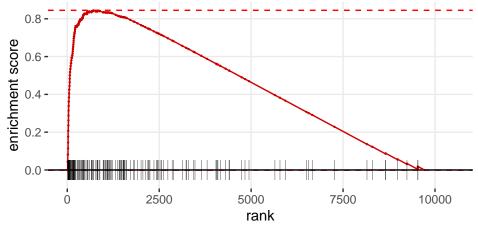


GSEA ImaxhmycVsImax in Kegg Ribosome



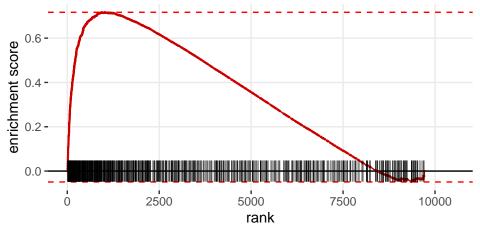
GSEA ImaxhmycVsImax in Hallmark Myc Targets V1

NES = 2.04 p.adj = 2.63e-09

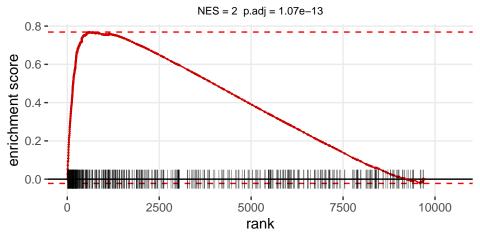


GSEA ImaxhmycVsImax in GOMF RNA Binding

NES = 2.02 p.adj = 9.25e-30

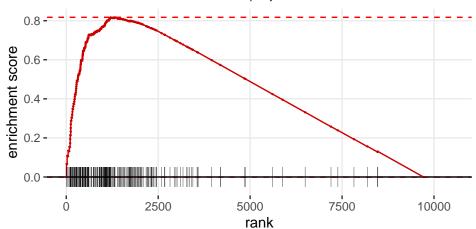


GSEA ImaxhmycVsImax in GOBP Establishment Of Protein Localization To Organelle



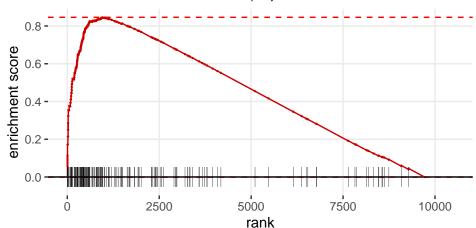
GSEA ImaxhmycVsImax in GOCC Mitochondrial Protein Containing Complex

NES = 1.99 p.adj = 4.55e-09



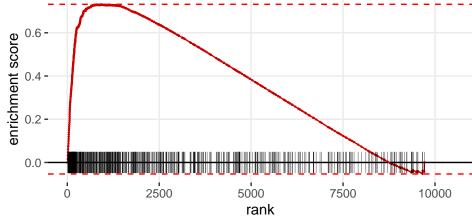
GSEA ImaxhmycVsImax in Hallmark Oxidative Phosphorylation

NES = 1.99 p.adj = 1.21e-07



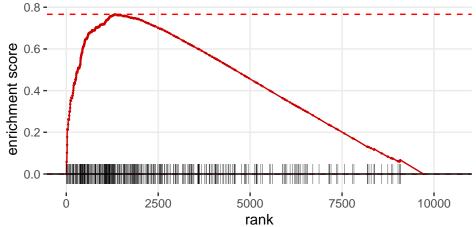
GSEA ImaxhmycVsImax in GOBP Amide Biosynthetic Process

NES = 1.95 p.adj = 1.35e-13



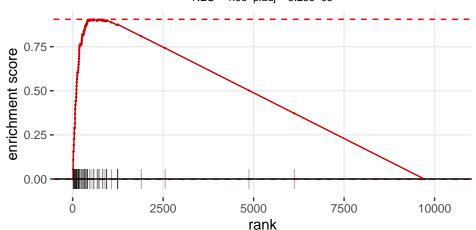
GSEA ImaxhmycVsImax in GOCC Mitochondrial Matrix

NES = 1.95 p.adj = 8.88e-10



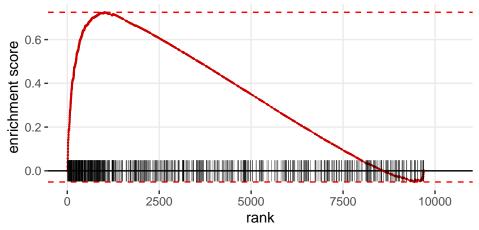
GSEA ImaxhmycVsImax in GOBP Ribosomal Large Subunit Biogenesis

NES = 1.95 p.adj = 5.23e-05



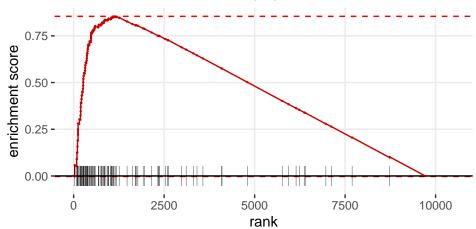
GSEA ImaxhmycVsImax in GOCC Nucleolus

NES = 1.94 p.adj = 2.56e-15

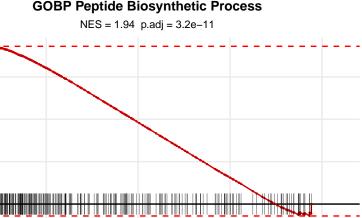


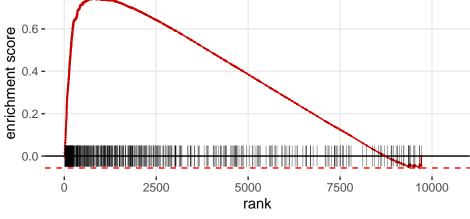
GSEA ImaxhmycVsImax in GOBP Oxidative Phosphorylation

NES = 1.94 p.adj = 4.71e-05

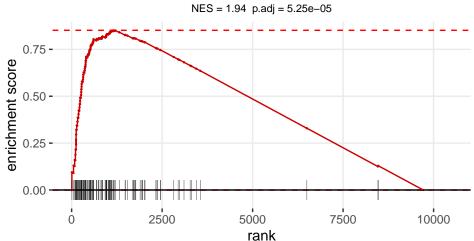


GSEA ImaxhmycVsImax in GOBP Peptide Biosynthetic Process

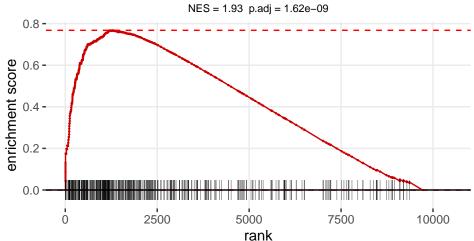




GSEA ImaxhmycVsImax in GOCC Inner Mitochondrial Membrane Protein Complex

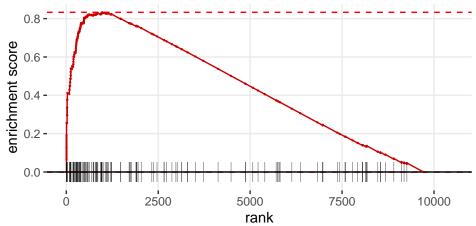


GSEA ImaxhmycVsImax in GOCC Organelle Inner Membrane



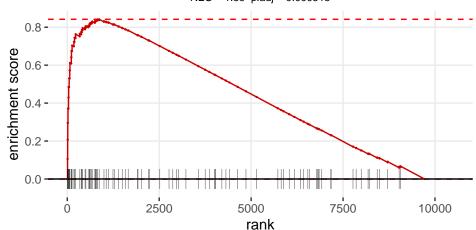
GSEA ImaxhmycVsImax in Kegg Huntingtons Disease

NES = 1.9 p.adj = 0.000523



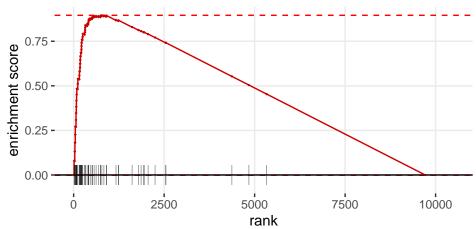
GSEA ImaxhmycVsImax in Hallmark Unfolded Protein Response

NES = 1.89 p.adj = 0.000515

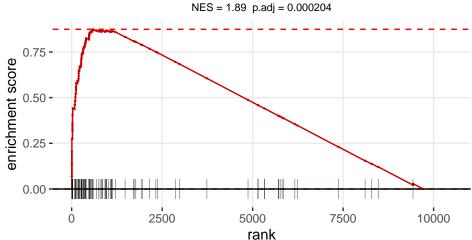


GSEA ImaxhmycVsImax in GOBP Ribosome Assembly

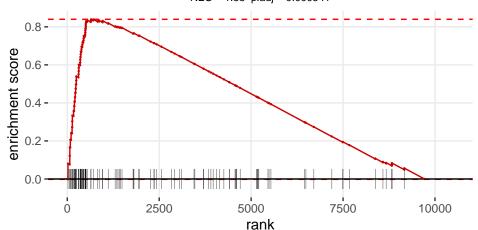
NES = 1.89 p.adj = 0.000137



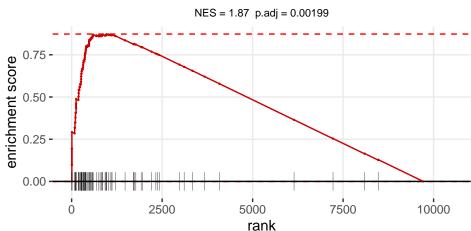
GSEA ImaxhmycVsImax in Kegg Parkinsons Disease



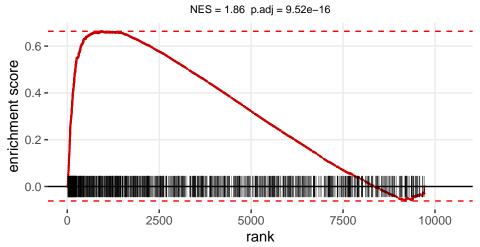
GSEA ImaxhmycVsImax in GOMF Ligase Activity NES = 1.88 p.adj = 0.000541



GSEA ImaxhmycVsImax in WP Electron Transport Chain Oxphos System In Mitochondria

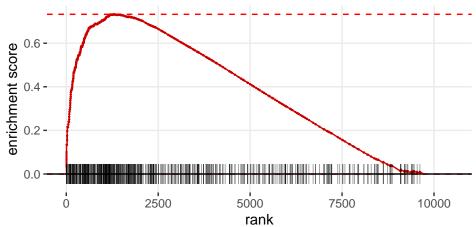


GSEA ImaxhmycVsImax in GOBP Organonitrogen Compound Biosynthetic Process

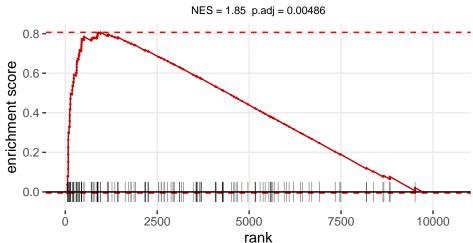


GSEA ImaxhmycVsImax in GOCC Mitochondrial Envelope

NES = 1.85 p.adj = 1.4e-08

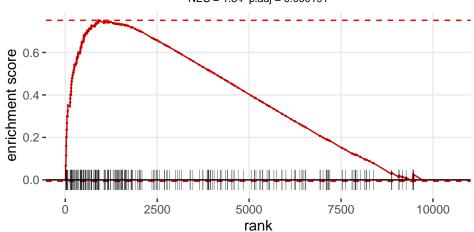


GSEA ImaxhmycVsImax in GOBP Ribose Phosphate Biosynthetic Process

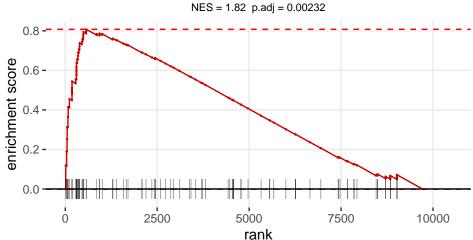


GSEA ImaxhmycVsImax in GOBP Cellular Amino Acid Metabolic Process

NES = 1.84 p.adj = 0.000191

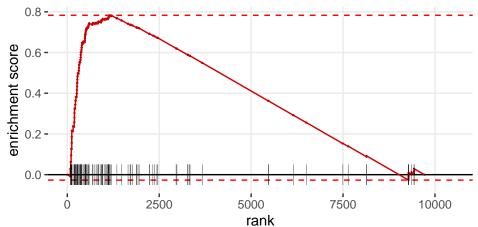


GSEA ImaxhmycVsImax in GOMF Unfolded Protein Binding



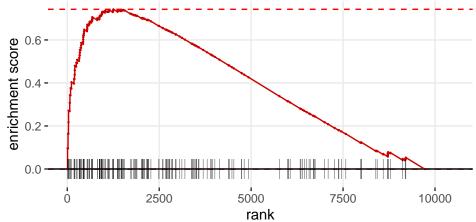
GSEA ImaxhmycVsImax in Kegg Oxidative Phosphorylation

NES = 1.82 p.adj = 0.00823

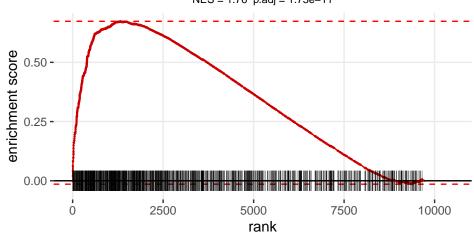


GSEA ImaxhmycVsImax in GOBP RNA Localization

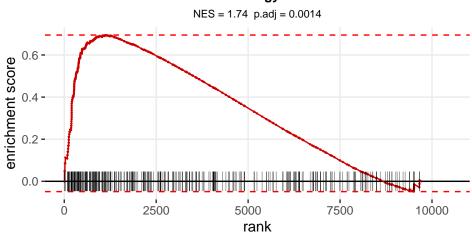
NES = 1.81 p.adj = 0.00277



GSEA ImaxhmycVsImax in GOCC Mitochondrion NES = 1.76 p.adj = 1.73e-11

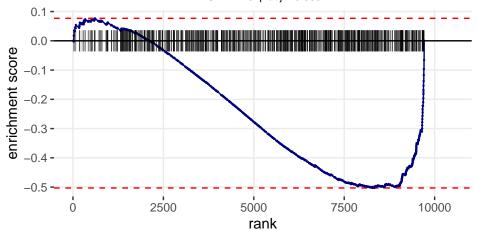


GSEA ImaxhmycVsImax in GOBP Generation Of Precursor Metabolites And Energy



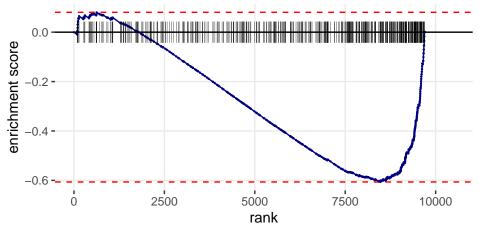
GSEA ImaxhmycVsImax in GOCC GOLGI Apparatus

NES = -1.43 p.adj = 0.00612



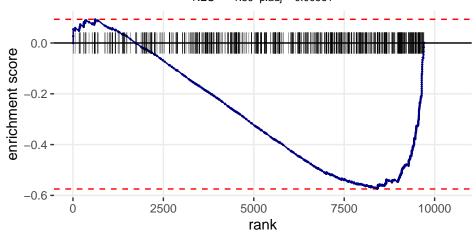
GSEA ImaxhmycVsImax in GOBP Tube Morphogenesis

NES = -1.58 p.adj = 0.00823



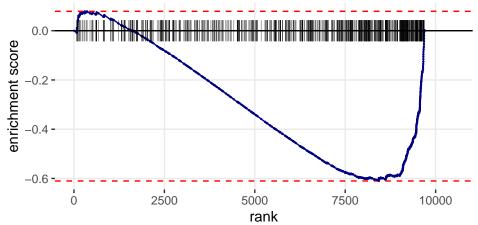
GSEA ImaxhmycVsImax in GOCC Intrinsic Component Of Plasma Membrane

NES = -1.59 p.adj = 0.00561



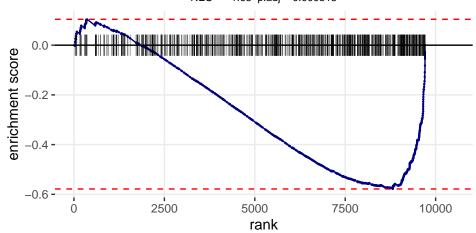
GSEA ImaxhmycVsImax in GOBP Biological Adhesion

NES = -1.61 p.adj = 0.00116



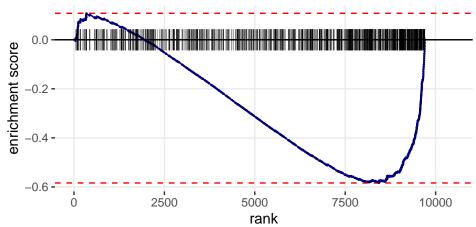
GSEA ImaxhmycVsImax in GOCC Plasma Membrane Region

NES = -1.63 p.adj = 0.000515



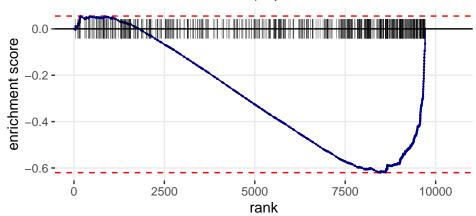
GSEA ImaxhmycVsImax in GOBP Locomotion

NES = -1.7 p.adj = 2.58e-07



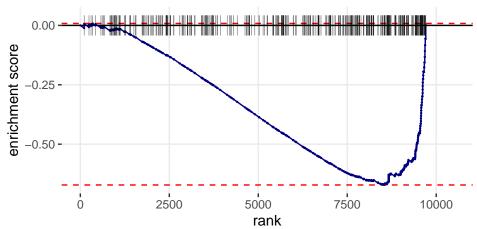
GSEA ImaxhmycVsImax in GOBP Regulation Of Anatomical Structure Morphogenesis

NES = -1.7 p.adj = 0.000118



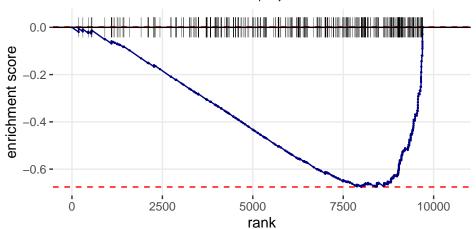
GSEA ImaxhmycVsImax in GOBP Developmental Growth

NES = -1.75 p.adj = 0.00159



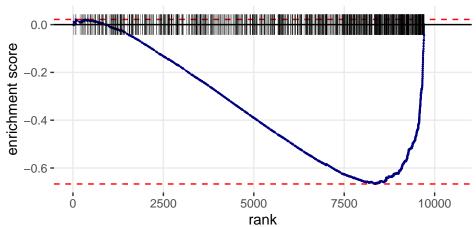
GSEA ImaxhmycVsImax in GOMF Molecular Transducer Activity

NES = -1.78 p.adj = 0.00345



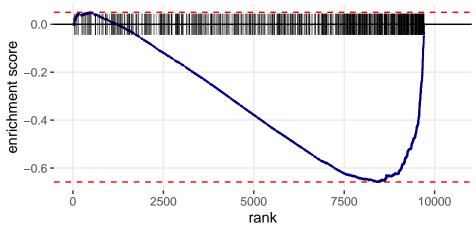
GSEA ImaxhmycVsImax in GOBP Cell Projection Organization

NES = -1.78 p.adj = 2.58e-09



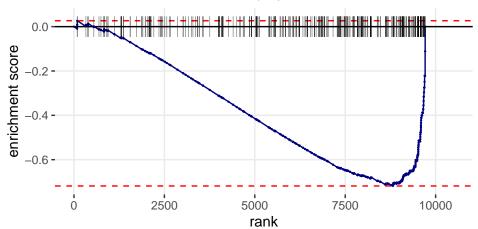
GSEA ImaxhmycVsImax in GOBP Neurogenesis

NES = -1.8 p.adj = 9.99e-11



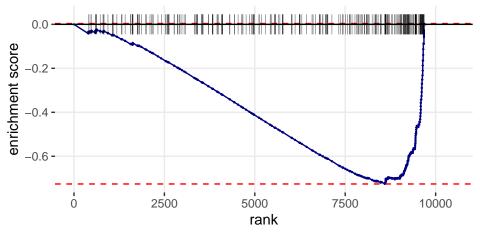
GSEA ImaxhmycVsImax in GOBP Small Gtpase Mediated Signal Transduction

NES = -1.8 p.adj = 0.00218



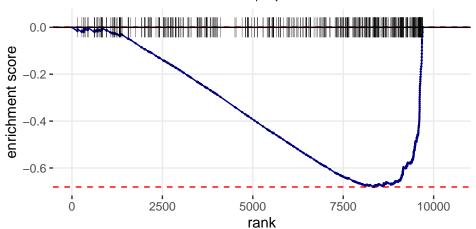
GSEA ImaxhmycVsImax in GOCC Cell Cell Junction

NES = -1.83 p.adj = 0.00326



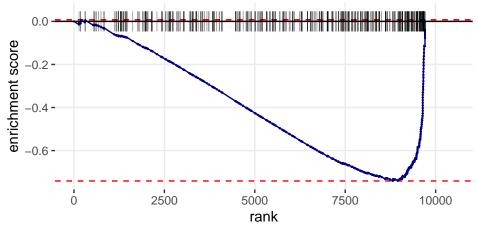
GSEA ImaxhmycVsImax in GOBP Actin Filament Based Process

NES = -1.83 p.adj = 2.35e-05



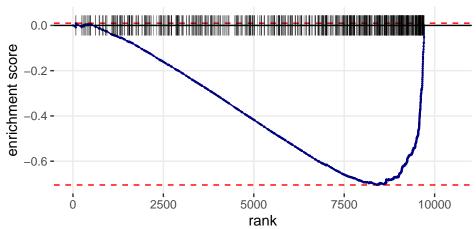
GSEA ImaxhmycVsImax in GOCC Axon

NES = -1.85 p.adj = 4.06e-05



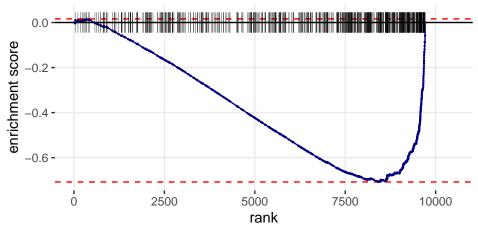
GSEA ImaxhmycVsImax in GOBP Neuron Development

NES = -1.88 p.adj = 2.38e-09



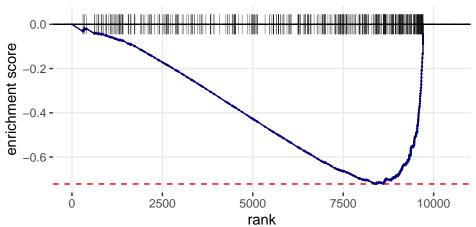
GSEA ImaxhmycVsImax in GOBP Cell Morphogenesis

NES = -1.89 p.adj = 3.9e-09



GSEA ImaxhmycVsImax in GOBP Cell Junction Organization

NES = -1.93 p.adj = 1.27e-06



GSEA ImaxhmycVsImax in GOBP Cellular Component Morphogenesis

NES = -1.97 p.adj = 1.4e-09

