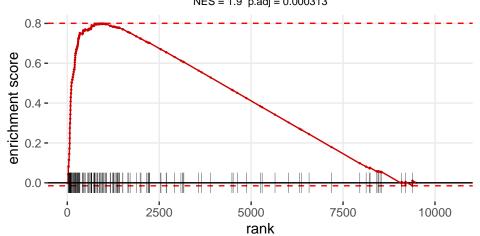
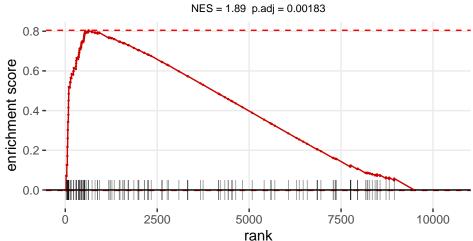
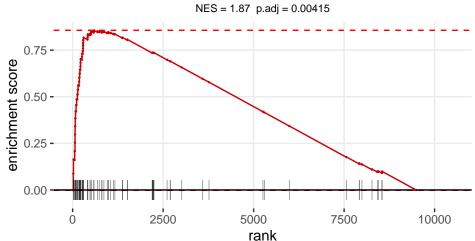
GSEA ImaxVsNeg in Hallmark E2f Targets NES = 1.9 p.adj = 0.000313



GSEA ImaxVsNeg in GOMF Catalytic Activity Acting On DNA

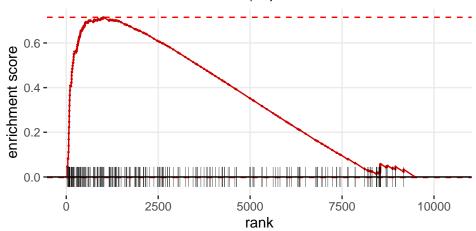


GSEA ImaxVsNeg in WP Retinoblastoma Gene In Cancer

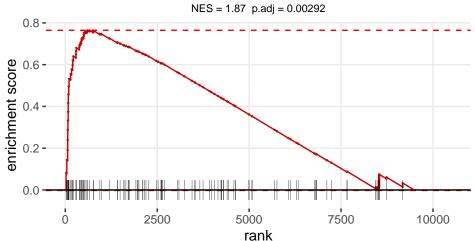


GSEA ImaxVsNeg in GOCC Chromosomal Region

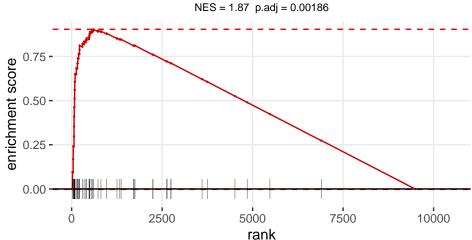
NES = 1.87 p.adj = 0.000277



GSEA ImaxVsNeg in GOCC Chromosome Telomeric Region

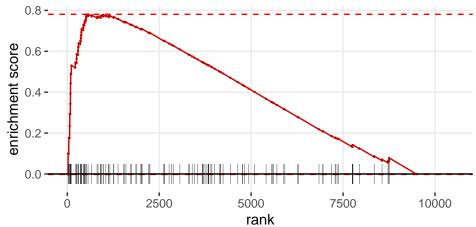


GSEA ImaxVsNeg in GOBP Cell Cycle DNA Replication



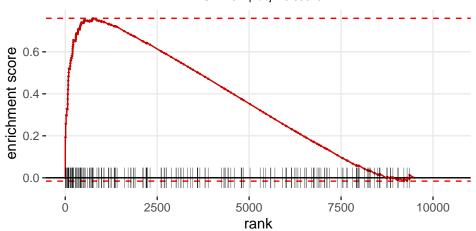
GSEA ImaxVsNeg in GOMF Helicase Activity

NES = 1.85 p.adj = 0.00632



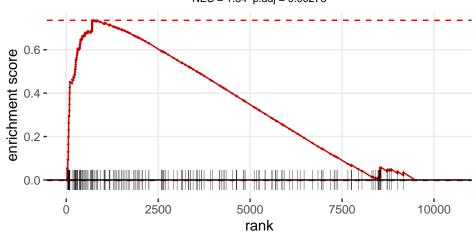
GSEA ImaxVsNeg in GOBP Cell Cycle G1 S Phase Transition

NES = 1.84 p.adj = 0.000492



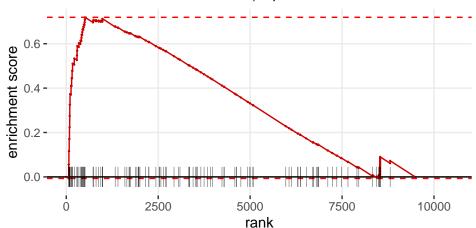
GSEA ImaxVsNeg in GOBP DNA Conformation Change

NES = 1.84 p.adj = 0.00273



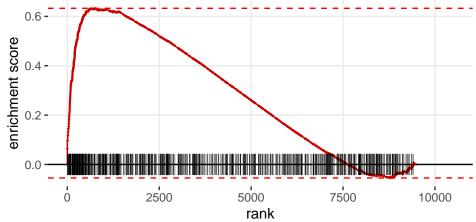
GSEA ImaxVsNeg in GOBP Telomere Organization

NES = 1.83 p.adj = 0.00446



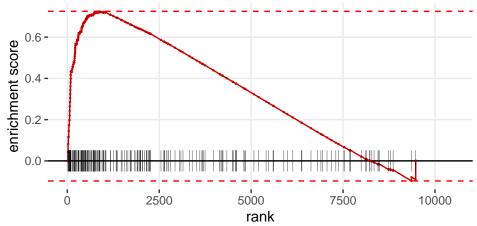
GSEA ImaxVsNeg in GOBP Cell Cycle Process

NES = 1.78 p.adj = 1.68e–09



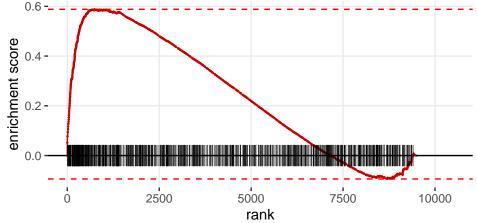
GSEA ImaxVsNeg in GOBP DNA Replication NES = 1.78 p.adj = 0.00527

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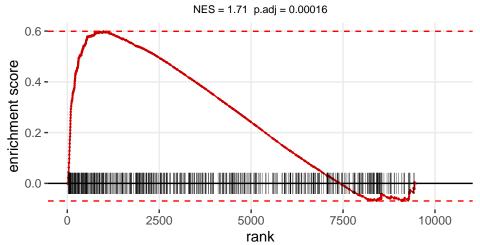


GSEA ImaxVsNeg in GOBP Cell Cycle NES = 1.75 p.adj = 7.14e-10

1120 = 1.70 p.auj = 7.14c=10

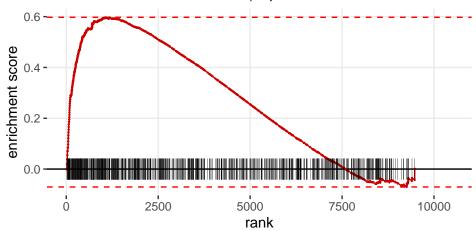


GSEA ImaxVsNeg in GOBP DNA Metabolic Process



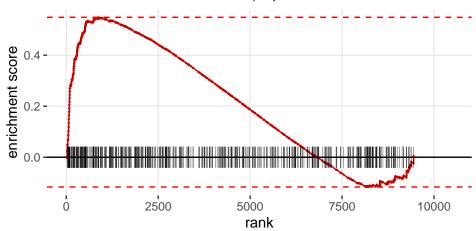
GSEA ImaxVsNeg in GOBP Chromosome Organization

NES = 1.71 p.adj = 1.39e-05

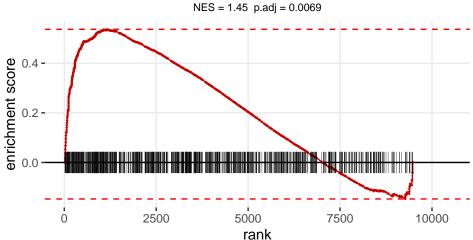


GSEA ImaxVsNeg in GOBP Cellular Response To DNA Damage Stimulus

NES = 1.57 p.adj = 0.00819

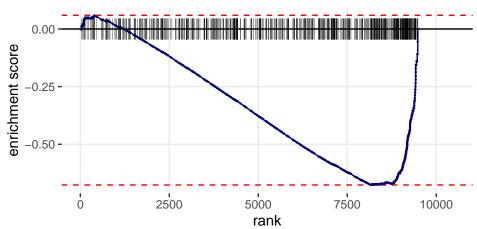


GSEA ImaxVsNeg in GOCC Nuclear Protein Containing Complex



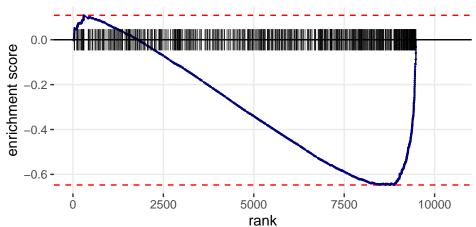
GSEA ImaxVsNeg in GOBP Peptide Metabolic Process

NES = -1.59 p.adj = 0.00605



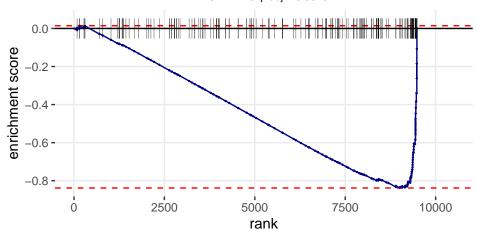
GSEA ImaxVsNeg in GOCC Endoplasmic Reticulum

NES = -1.61 p.adj = 5.49e-05

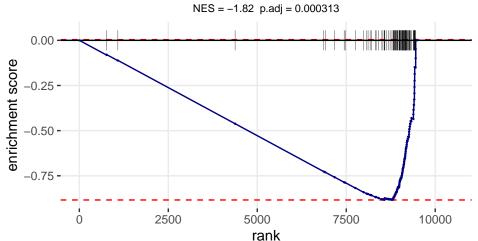


GSEA ImaxVsNeg in GOBP Response To Topologically Incorrect Protein

NES = -1.75 p.adj = 0.00461



GSEA ImaxVsNeg in GOBP Cotranslational Protein Targeting To Membrane



GSEA ImaxVsNeg in GOBP Establishment Of Protein Localization To Endoplasmic Reticulum

