



GSEA Down-regulated (BP)

This bubble plot displays the enrichment of biological processes (GOBP) in the GSEA Down-regulated set. The x-axis represents the Normalized Enrichment Score (NES), ranging from -2.50 to -1.75. The y-axis lists the pathway descriptions. The size of each bubble indicates the count of genes, and the color represents the  $-\log_{10}(\text{Adjusted p-value})$ . The most enriched pathways are GOBP\_PROTEIN\_PALMITOYLATION and GOBP\_PROTEIN\_DEUBIQUITINATION, with high NES and large counts.

Pathway Description	Normalized Enrichment Score (approx.)	Count (approx.)	$-\log_{10}(\text{Adjusted p-value})$ (approx.)
GOBP_PROTEIN_PALMITOYLATION	-2.60	30	15.0
GOBP_PROTEIN_DEUBIQUITINATION	-2.60	90	15.0
GOBP_PEPTIDYL_L_CYSTEINE_S_PALMITOYLATION	-2.62	30	12.5
GOBP_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	-2.50	60	10.0
GOBP_RNA_POLYMERASE_II_PREINITIATION_COMPLEX_ASSEMBLY	-2.50	30	10.0
GOBP_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	-2.38	60	7.5
GOBP_PROTEIN_POLYUBIQUITINATION	-2.00	90	7.5
GOBP_PROTEIN_K63_LINKED_UBIQUITINATION	-2.25	30	7.5
GOBP_NEUTRAL_AMINO_ACID_TRANSPORT	-2.25	60	7.5
GOBP_PEPTIDYL_CYSTEINE_MODIFICATION	-2.25	30	7.5
GOBP_CELLULAR_GLUCURONIDATION	-2.25	30	7.5
GOBP_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	-2.25	10	7.5
GOBP_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY	-2.15	30	7.5
GOBP_SUPPRESSION_OF_VIRAL_RELEASE_BY_HOST	-2.25	10	7.5
GOBP_PROTEIN_ACYLATION	-2.05	30	7.5
GOBP_PROTEIN_TARGETING	-1.80	90	7.5
GOBP_AMINO_ACID_TRANSPORT	-1.85	60	7.5
GOBP_RNA_METHYLATION	-2.10	30	7.5
GOBP_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	-2.10	10	7.5
GOBP_L_AMINO_ACID_TRANSPORT	-1.95	60	7.5