



Methylation UMAP plot

Figure 1: A Manhattan plot showing the results of a genome-wide association study (GWAS) for the number of differentially expressed genes (DEGs) in breast cancer. The x-axis represents chromosomes (chr1 to chr22, chrX, chrY) and the y-axis represents the negative log10(p-value). The plot shows a significant association on chromosome 9, with a peak at the NTRK2 gene. Other genes shown include NTRK1, MDK4, MYCN, MLH1, PDGFRA, KIT, ODC1, EGF, MET, PTEN, RB1, NTRK3, NUTM1, TSC3, ERBB2, NF1, BRD4, NFKB1, and IL13RA2.