



Methylation UMAP plot

Close-up of UMAP for 20955530087_R05C01

Neighbors in UMAP for 209555530087_R05C01

A pie chart illustrating the distribution of GBM types. The chart is divided into four segments: a large red segment for GBM_RTK_II (47%), a large blue segment for GBM_MES (40%), and two smaller segments for GBM_RTK_I (7%, green) and HGNET_MN1 (7%, purple). The percentages are labeled directly on the chart segments.

GBM Type	Percentage
GBM_RTK_II	47 %
GBM_MES	40 %
GBM_RTK_I	7 %
HGNET_MN1	7 %

Figure 1: A Manhattan plot showing the association of 10,000 SNPs with the expression of 100 genes. The y-axis represents the association p-value on a log scale from -1.2 to 1.2. The x-axis shows chromosomes from chr1 to chrY. Blue dots represent SNPs associated with gene expression, while red dots represent SNPs not associated. A horizontal blue line at p=0.05 indicates the significance threshold. Several genes are labeled with their names and corresponding SNPs: NTRK1, MDM4, MYCN, FGF4, MLH1, OPA, SOX2, PDGFRA, KIT, CD274, CDKN2A, NTRK2, PTEN, MDM2, RB1, NUTM1, NTRK3, TP53, NF1, ESRB2, BRD4, NF2, and IL13RA2.