



Methylation UMAP plot

Close-up of UMAP for 210696120078_R05C01

Neighbors in UMAP for 210696120078_R05C01

A pie chart illustrating the distribution of GBM types. The chart is divided into five segments: a large purple segment (46.7%) for GBM_RTK_II, an orange segment (20%) for GBM_NOS, a blue segment (13.3%) for GBM_MES, a red segment (13.3%) for GBM_RTK_I, and a small green segment (6.67%) for GBM_LOW. A legend to the right of the chart lists the categories and their percentages.

GBM Type	Percentage
GBM_RTK_II	46.7%
GBM_NOS	20%
GBM_MES	13.3%
GBM_RTK_I	13.3%
GBM_LOW	6.67%

Figure 1: A Manhattan plot showing the results of a genome-wide association study (GWAS) for the number of metastatic sites. The x-axis represents chromosomes from 1 to 22, X, and Y. The y-axis represents the negative log₁₀(p-value), ranging from -1.2 to 1.2. A horizontal blue line at y=0 indicates the significance threshold. Numerous data points are plotted, with several points highlighted in red and labeled with gene names. The most significant association is on chromosome 7, near the EGFR gene, with a p-value exceeding 1.2. Other significant associations are found on chromosomes 1, 2, 3, 4, 9, 10, 12, 13, 15, 17, 18, 19, 21, and 22.