



Methylation UMAP plot

Close-up of UMAP for 20955540073_R03C01

Neighbors in UMAP for 20955540073_R03C01

A pie chart illustrating the distribution of GBM types. The chart is divided into three segments: a large blue segment representing GBM_RTK_I at 67%, a green segment representing GBM_RTK_II at 27%, and a small red segment representing GBM_NOS at 7%. A legend to the right of the chart identifies each segment with its corresponding color and percentage.

GBM Type	Percentage
GBM_RTK_I	67 %
GBM_RTK_II	27 %
GBM_NOS	7 %

A Manhattan plot displaying the association of various genes with cancer risk. The x-axis represents chromosomes 1 through 22, plus X and Y. The y-axis represents the negative logarithm of the p-value (-log₁₀(p-value)), ranging from -1.2 to 1.2. Genes are plotted as points, with their names labeled above or below them. Points are colored blue for positive values and red for negative values. Horizontal dashed lines indicate significance thresholds at approximately ±1.3.

Gene	Chromosome	-log ₁₀ (p-value)
NTRK1	chr1	0.1
MDM4	chr1	1.1
MYCN	chr2	0.2
PDCD1	chr3	0.0
VHL	chr3	-0.1
MLH1	chr3	-0.2
SOX2	chr4	0.2
PDGFRA	chr4	0.1
OPA1	chr4	-0.1
EGFR	chr7	1.1
MET	chr7	0.1
CDKN2A	chr9	-1.1
CDKN2B	chr9	-0.1
PTEN	chr10	-0.8
NTRK2	chr9	0.1
CDK4	chr12	0.5
MDM2	chr12	-0.1
RB1	chr13	-0.1
NUTM1	chr15	-0.1
NTRK3	chr16	0.0
TP53	chr17	0.0
ERBB2	chr17	-0.1
BRD4	chr19	0.1
NF2	chr22	-0.1
IL13TAD	chrX	-0.5