



### Methylation UMAP plot

Close-up of UMAP for 209340850183\_R01C01

Neighbors in UMAP for 209340850183\_R01C01

A pie chart illustrating the distribution of two categories: OS\_CONV and OS\_HG. The OS\_CONV category, represented by a blue slice, accounts for 66.7% of the total. The OS\_HG category, represented by a red slice, accounts for 33.3% of the total. A legend on the right side of the chart identifies the colors and their corresponding percentages.

Category	Percentage
OS_CONV	66.7%
OS_HG	33.3%

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. Red dots indicate SNPs associated with down-regulation, and blue dots indicate SNPs associated with up-regulation. Genes are labeled with their names and the chromosome and position of the associated SNPs. For example, NTRK1 is on chr1, MYCN is on chr2, PDCD1 is on chr3, and so on.