



**Supplementary Figure 1.** A) Dot plot of canonical markers extracted from Mei, Wang et al. 2023 (22). The figure shows the average expression of these genes in each cell type in the integrated object. The *dot.min* value was set to 0.05, meaning only genes with expression levels above 5% are represented by a dot. B) Table with the differential expression results from the analysis comparing glial cell clusters expressing *KLRC2* in newly diagnosed versus recurrent GBM patients. *pct.1* and *pct.2*: Proportion of cells expressing *KLRC2* in each cluster for newly diagnosed (*pct.1*) and recurrent patients (*pct.2*). *p\_val\_adj*: Adjusted p-value, accounting for multiple testing using the Benjamini-Hochberg procedure to control the false discovery rate. The remaining differentially expressed genes between the two conditions are listed in in Table S3A. C) Dot plot showing the percentage and average expression of activation and inhibition markers across the different conditions: control and GBM population (newly diagnosed and recurrent). The *dot.min* value was set to 0.01, meaning only genes with expression levels above 1% are represented by a dot.