



Supplementary Figure 2. Analysis of KLRC2 Expression in Tumor Core and Periphery A) Scatter plot displaying the log-transformed *KLRC2* expression levels for the average of peripheral samples (orange crosses) versus tumor core samples (gray crosses) in different patients. Each cross represents an individual patient measurement. B) Bar graph depicting the difference in log transformed *KLRC2* expression levels between matched tumor core and peripheral samples from individual patients (pair index). C) 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.