



Supplementary Figure 12. Expression of tissue-resident memory T cell, co-stimulatory and co-inhibitory markers within the intratumoral CD8, CD4, Treg, Tother and NK cell cluster in OPSCC.

Single-cell transcriptome RNA sequencing analysis was performed on magnetic-bead sorted CD3⁺ T cells and CD56⁺ NK cells from 13 OPSCC samples. Dot plots depict the expression levels of **A**) tissue-resident memory T cell, **B**) co-stimulatory and **C**) co-inhibitory genes (Y-axis) for all identified CD8, CD4, Treg, Tother and NK clusters (X-axis, from left to right). The size of the dots represent the percentage of cells expressing the genes, and the color scale indicates the mean expression of the genes.