



Supplemental Figure 11. T cell expansion among the different T cell clusters.

Integrated single-cell transcriptome and TCR repertoire RNA sequencing analysis was performed on magnetic-bead sorted CD3+ T cells and CD56+ NK cells from 13 OPSCC samples. A-C) Box plots displaying the percentage of expanded cells within the identified CD8 (A), CD4 (B) and Treg (C) clusters in HPV- (red, n=3), HPV16+IR- (blue, n=4) and HPV16+IR+ (green, n=6) OPSCC patients. Data are represented as percentage of total expanded CD8, CD4 and Treg cells.