





Expression levels of *CD19*, *MS4A1* (*CD20*) and *BLK* are depicted in color code. Violin plot (right) displaying expression of *BLK* within B cells from HPV16<sup>+</sup>IR<sup>+</sup> (blue; left) and HPV16<sup>+</sup>IR<sup>-</sup> (orange; right) OPSCC. **D)** Kaplan-Meier survival curves based on high/low *BLK* or *CXCL12* expression (classification based on median *BLK* or *CXCL12* expression) upregulated in HPV16<sup>+</sup>IR<sup>+</sup> compared to HPV16<sup>+</sup>IR<sup>-</sup> OPSCC patients for all OPSCC patients analyzed by Nanostring Pancancer IO360 (n=21; left), for the HPV16<sup>+</sup> patients within this cohort (n=13; middle), and for a large independent TCGA cohort of HPV16<sup>+</sup> OPSCC (n=69; right). **E)** Kaplan-Meier survival curves based on high/low expression of the top 3 DEGs (*CCL20*, *BMP2* and *CXCL3*) upregulated in HPV16<sup>+</sup>IR<sup>-</sup> compared to HPV16<sup>+</sup>IR<sup>+</sup> OPSCC patients for all OPSCC patients analyzed by Nanostring Pancancer IO360 (n=21, left), for the HPV16<sup>+</sup> patients within this cohort (n=13; middle), and for a large independent TCGA cohort of HPV16<sup>+</sup> OPSCC (n=69; right). **F)** Linear regression analysis of top upregulated DEGs *BLK* and *CXCL12* in HPV16<sup>+</sup>IR<sup>+</sup> compared to HPV16<sup>+</sup>IR<sup>-</sup> OPSCC versus cell type profiles of CD8 (*CD8A*), CD4, Tbet<sup>+</sup> T cells (*TBX21*) and DC (*ITGAX*, *CD11c*). Upper 2 panels display all OPSCC patients analyzed by Nanostring Pancancer IO360 (n=21). Each patient is represented by a colored dot: HPV<sup>-</sup> (red), HPV16<sup>+</sup>IR<sup>-</sup> (blue) and HPV16<sup>+</sup>IR<sup>+</sup> (green). The lower 2 panels show the regression analysis of the 69 HPV16<sup>+</sup> OPSCC patients of the independent TCGA cohort. **G)** Linear regression analysis of *LTB* versus indicated genes involved in tumor cell migration (metastases) and cell activation.