Abstract 1420 Figure 1  Comparison of most significant gene differences between black and white patients ovarian TME. A FFPE tissue array was made consisting of ovarian tumor tissue for 3 white patients and 2 black patients with HGSOC and 1 patient with polycystic ovarian disease. Immunofluorescence staining was performed for CD3 (T cells), CD68 (macrophages) and panCK (tumor). Regions of interest (ROI) were selected in the CD3, CD68 and PanCK stained regions of each patient tissue for sequencing on a NanoString Digital Spatial Profiling DSP platform. Differential analysis between genes was performed by the linear mix model (LNM) using FDR (false discovery rate) < 0.05 as cutoff. (A) volcano plot is for the most significant genes between black and white patients in the CD3 ROIs, (B) in the CD68 ROIs, (C) in the PanCK ROIs. (D) shows the most significant genes in the PanCK region between the white and control patients (273 genes were differentially expressed). There were 175 differentially expressed genes in black versus control patients in the PanCK ROIs (not shown).

REFERENCES

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