Background To identify novel molecular mechanisms used by triple negative breast cancer (TNBC) to facilitate metastasis, we manipulated oncogenic epithelial-to-mesenchymal transition (EMT) by restoring the microRNA-200c (miR-200c), termed ‘the guardian of the epithelial phenotype’. We identified several tumor cell catabolizing enzymes, including tryptophan 2,3-dioxygenase (TDO2) and heme oxygenase-1 (HO-1). The Richer lab has published that TDO2 promotes anchorage independent cell survival during TNBC metastasis via its catabolite kynurenine, which also induces CD8+ T cell death. Similarly, published studies have demonstrated that HO-1 supports BC anchorage independent survival. However, effects of the HO-1 catabolite bilirubin on the tumor microenvironment had not been studied. We postulated that TNBC utilize targetable catabolizing enzymes, like HO-1, to simultaneously support tumor cell survival and dampen the anti-tumor immune response.

Methods To test our hypothesis in an immune competent mouse model, Met-1 mammary carcinoma cells from a late stage MMTV-PyMT tumor were engineered to inducibly express miR-200c. Tumor cell infiltrates were analyzed by immunohistochemistry (IHC), flow cytometry and multispectral fluorescence. RAW264.7 mouse macrophages were cultured with conditioned medium from carcinoma cells ± miR-200c or the HO-1 competitive inhibitor tin mesoporphyrin (SnMP). RAW264.7 macrophages were also treated with 0–20 μM bilirubin and macrophage polarization and efferocytic capacity, the ability to engulf dead tumor cells, were assessed using qRT-PCR and IncuCyte assays.

Results MiR-200c restoration to Met-1 orthotopic tumors decreased growth by 45% and increased infiltration of CD11c+ dendritic cells and activation, determined by CD44 expression, of CD4+ and CD8+ T cells. While the number of F4/80+ macrophages was unchanged by miR-200c, the percent of M1 anti-tumor macrophages (F4/80+iNOS+/total cells) increased by >6-fold in miR-200c-tumors. RAW264.7 macrophages cultured with conditioned medium from miR-200c-restored mammary carcinoma cells had a 25–95% decrease in M2 pro-tumor genes (Arg1, Il4 and Il13) and a 15–5% increase in M1 genes (Nos2, Tnfa and Cxcl10). A similar expression in vulvar melanoma including miR-200b-3p, miR-494-3p, and miR-200a-5p, and 44 demonstrated a significant increase in expression including hsa-miR-17-5p, hsa-miR-19b-3p, hsa-miR-20a-5p, and hsa-miR-20b-5p. 45 DE miRs were identified between vulvar melanoma and PCM, among which 3 demonstrated a significant decrease in expression in vulvar melanoma relative to NAT, including hsa-miR-145-5p, hsa-miR-99a-5p, and hsa-miR-1972, and 15 exhibiting a significant increase in expression including hsa-miR-17-5p, hsa-miR-19b-3p, hsa-miR-20a-5p, and hsa-miR-20b-5p. 45 DE miRs were identified between vulvar melanoma and PCM, among which 3 demonstrated a significant decrease in expression in vulvar melanoma including miR-200b-3p, miR-494-3p, and miR-200a-3p, and 44 demonstrated a significant increase in expression including miR-17-5p, miR-146a-5p, and miR-19b-3p (fold change > 2, p < 0.01). Among these DE miRs, both miR-17-5p and miR-146a-5p have recently been experimentally validated as direct or indirect regulators of PD-L1 expression in melanoma. Pathway analysis for DE miRs in vaginal and vulvar melanoma revealed significant enrichment of 35 and 30 pathways, respectively, each including TGF-β signaling, for which 57 genes in the pathway are validated target genes of differentially expressed (DE) miRs.

Conclusions Use of miR-200c to reverse EMT revealed that HO-1 promotes simultaneous TNBC cell survival and immune suppression. These studies are the first to show that tumor cell-HO-1 activity and subsequent bilirubin production may alter macrophage function in the tumor microenvironment. This finding could be clinically relevant since HO-1 inhibitors like SnMP are already FDA approved for treatment of other diseases.