Cancer cells impair monocyte-mediated T cell stimulation to evade immunity

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Supplementary Table Legends:

Supplementary Table 1: **Top 20 markers from scRNA-seq populations**. Gene lists depicting the top differentially expressed genes of each identified population in the scRNA-seq from the immune TME of YUMM1.7^{OVA} tumors.

Supplementary Table 2: **scRNA-seq gene signatures**. Publicly available T cell signatures used to probe the scRNA-seq data of OT-1 T cells isolated from YUMM1.7^{OVA} tumors, publicly available inflammatory gene signatures and the Monocyte 1 and Inflammatory Monocyte gene signatures generated with the scRNA-seq dataset from our study.

Supplementary Table 3: **Differentially expressed genes in N^{TT} and R^{TT} cancer cells.** Differentially expressed genes (log2FC > 2, p-value < 0.05) from YUMM1.7^{OVA} N^{TT} and R^{TT} cancer cells sorted from tumors and analyzed by RNA-sequencing.

Supplementary Table 4: **Differentially expressed genes in the TME and TME signatures.** Gene lists depicting the differentially expressed genes in the immune TME of *Ptgs1/2* KO and IRF3/7 R^{TT} compared to CTRL R^{TT} YUMM1.7^{OVA} tumors (log2FC > 1, p-value < 0.05) analyzed by scRNA-seq. Gene signatures derived (TME-COX and TME-IRF3/7) and their human orthologs are included.

Supplementary Table 5: Meta-analysis studies. Main characteristics of studies included in the meta-analysis, including cancer type, numbers of patients, COX inhibitors used and immunotherapy specification.

Supplementary Table 6: Search query for meta-analysis. Contains the exact search query that was used for the meta-analysis in this study.

Supplementary Table 7: RT-qCPR primer and sgRNA list. Contains a list with all primer pairs used for RT-qPCR experiments and sgRNAs used for CRISPR/Cas9 knockouts.

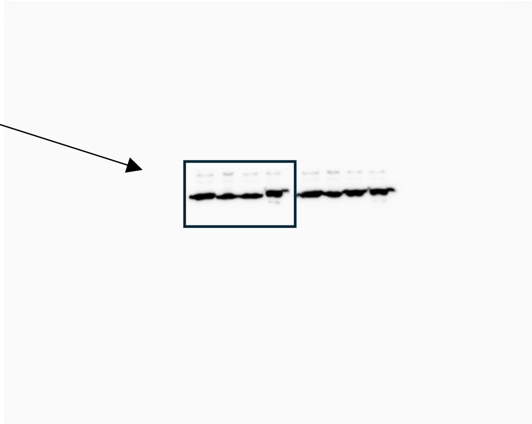
Supplementary Table 8: Antibody list. Contains a list with all antibodies used in this study for flow cytometry, immunofluorescence, western-blotting and *in vivo* and *in vitro* depletion experiments.

UNCROPPED WESTERN BLOT IMAGES

1. A375 Melanoma BLOT: **Extended Data Fig. 5s**

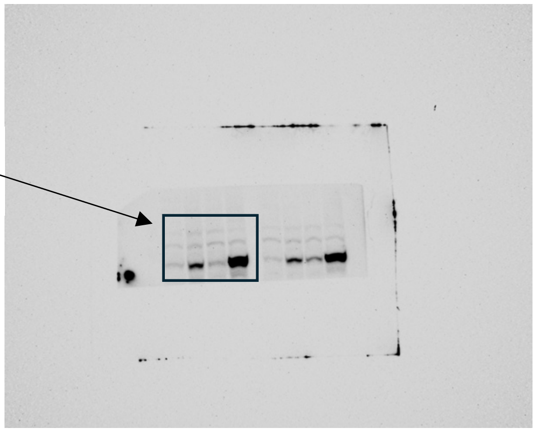
    - HISTONE3 (18kDa)

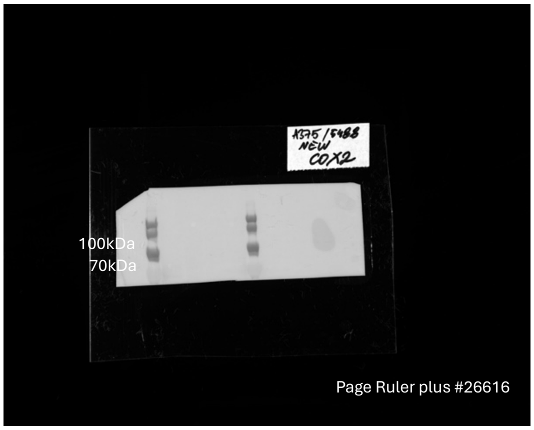
Cropped area



    - COX2 (74 kDa)

Cropped area



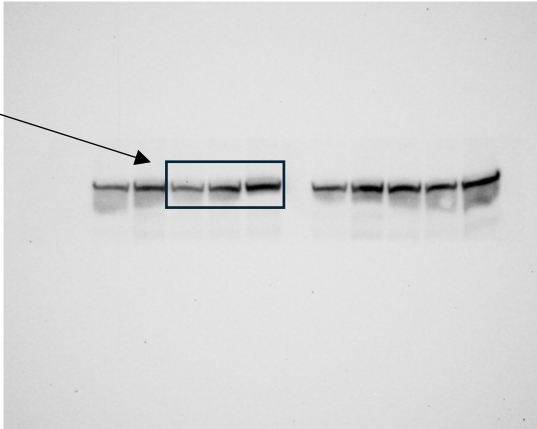


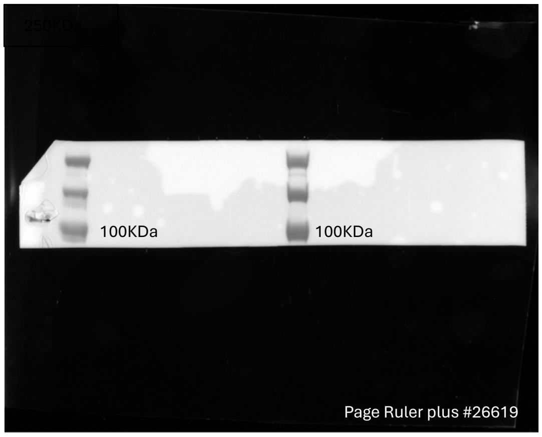
Histone control run on the same gel. Gel was cut for antibody incubation and development.

2. YUMM1.7 Melanoma BLOT: **Extended Data Fig. 5m**

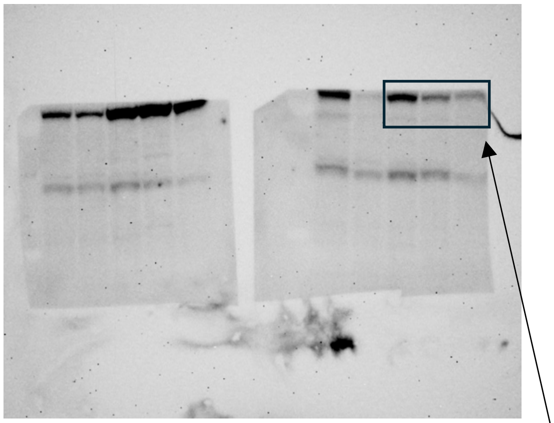
   - Vinculin (~116kDa)
     *on left side for COX2 samples on right side for COX1 samples

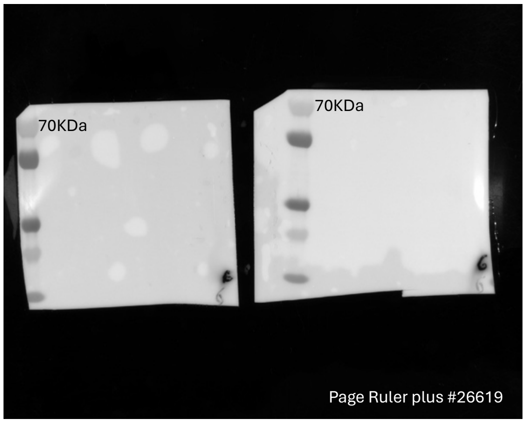
Cropped area





   - COX 1 (left) COX2 (right) ~74KDa





Cropped area

Vinculin control run on the same gel. Gel was cut for antibody incubation and development.