**SUPPLEMENTAL MATERIAL AND METHODS**

***RNA-sequencing***

We performed whole transcriptome RNAseq analysis on the patients in cohort 2. Library preparation (polyA-selection) and multiplexed sequencing (Illumina HiSeq 3000, 1 X 50 nt, ~40 million reads per sample) were performed by the Genome Technology Access Center (GTAC) at Washington University.

RNA-seq reads were aligned to the Genome Reference Consortium Human Build 38 (GRCh38) using STAR2 with Ensembl genes for homo sapiens version 90 (17). Read counts were calculated using featureCounts with default parameters, and gene expression levels were calculated and normalized as reads per kilobase of transcript per million mapped read (FPKM) using Cufflinks with default parameters (18, 19). We excluded genes with consistently low expression levels (i.e., <1 FPKM or <200 reads) in ≥ 95% of samples, as previously described (20). ~17,000 expressed genes were remained for the following differential expression analysis and gene set enrichment analysis.

***Prevalence of Immune Cell Populations in Cervical Tumors Using a Tumor Microarray***

Staining for macrophages was done on a Ventana automated stainer (Ventana Medical Systems). Slides were deparaffinized and rehydrated, and then underwent antigen retrieval using Cell Conditioning 1 EDTA-based buffer (pH 8.0, Ventana) for 64 minutes at 95 °C. Primary antibodies were incubated for 20 minutes at 37 °C. Staining was performed with anti-CD68 (0.4 µg/mL, monoclonal mouse, Ventana) and anti-CD163 (0.3 µg/mL, monoclonal mouse, Cell Marque). A biotin-free multimer system using direct linkers between peroxidase and secondary antibodies was used for detection of the primary antibody.

Neutrophil staining was performed manually. Slides stained for neutrophil markers underwent antigen retrieval using a citrate buffer (pH 6.0) for 15 minutes at 100 °C in a pressure cooker. Slides were co-incubated overnight at 4° C with CD66b (1:600, BD Biosciences) and neutrophil elastase (1:200, Novus). Slides were then incubated with the secondary antibodies, 1:50 anti-mouse IgG Kappa biotin conjugated antibody (Santa Cruz Biotech) for neutrophil elastase, and 1:50 anti-mouse IgM alkaline phosphatase conjugated antibody (Sigma) for CD66b. Finally, slides were sequentially incubated with alkaline phosphatase substrate (Vector Labs) and HRP-streptavidin complex (Santa Cruz Biotech). Slides were then counterstained with hematoxylin.

***Macrophage Co-Culture and Conditioned Media Experiments***

Human monocytic THP-1 cells were maintained in Roswell Park Memorial Institute medium (RPMI 1640, Sigma) culture medium containing 10% heat inactivated fetal bovine serum and supplemented with 1% gentamycin. THP-1 monocytes were differentiated into macrophages by using 150 nM phorbol 12-myristate 13-acetate (PMA, Sigma) for 24 h. Macrophages were polarized to M1 macrophages by incubation with 20 ng/ml of IFN-γ (R&D system) and 10 pg/ml of LPS (Sigma). Macrophage were also polarized into M2 cells by incubation with 20 ng/ml of IL-4 (R&D Systems) and 20 ng/ml of IL-13 (R&D Systems).

For collection of conditioned media from differentiated macrophages, cells were washed twice with PBS to remove the cytokines used, and the medium was replaced with complete culture medium for additional 24 hrs. After 24 hrs, the supernatants were collected and centrifuged at 1950 g (5000 rpm) for 20 min. and then filtered through 0.22‐μm‐pore filters to remove cells and debris.