



Figure S1. Extended Data for Mass Cytometry Analysis & Aggregate UMAPs for Endometrial Tumor Samples. (A) Resultant UMAP clusters derived from total CD45+ cells from endometrial patient tumors (N=3) as analyzed by mass cytometry (left). Immune subpopulations were defined by manual gating and immune subtypes projected onto the UMAP. Expression pattern of CD103 across CD45+ cells overlaid onto the UMAP (right). (B) Frequency of immune cell subpopulations amongst CD45+ cells across nine patient tumor samples (N=6 NSCLC, solid dots; N=3 Endometrial, open dots) (left). Frequency of cells expressing CD103 within the indicated immune subsets (right). (C) UMAPs of CD8+ T cells for each individual patient sample depicting variation in cellular distribution amongst immune subpopulations for NSCLC (top two rows) or Endometrial (bottom row) tumors. Aggregate UMAPs were generated separately for each tumor indication. (D) Expression of proliferation and dysfunction markers in Endometrial tumors (N=3) overlaid onto the aggregate UMAP of CD8+ T cells. (E) Correlation of the percentage of PD-L1-expressing cells out of total CD45+ cells to the

frequency of CD8+ T cells (top), CD103+ cells within CD8+ T cells (middle), or proliferating (Ki-67+) CD103+ CD8+ T cells (bottom) as analyzed by mass cytometry on freshly procured tumors. Data from NSCLC tumors is indicated by solid dots and endometrial tumors depicted by open dots. The Spearman correlation coefficient is displayed on each plot alongside the resultant p-value. * $p < 0.05$, ** $p < 0.01$, n.s.= not significant.