Supplemental Data Materials

Supplemental Tables 1-6

Supplemental Figures 1-11

Supplemental Tables

Supplemental Table 1: List of flow cytometry antibodies

| Antibody | Clone | Catalog number | Manufacturer | RRID |
|----------------|-------------|-------------------|--------------|-------------|
| CD3 | UCH-T1 | 555333 | BD | AB_395740 |
| CD3 | UCH-T1 | 555332 | BD | AB_395739 |
| CD3 | UCH-T1 | 563546 | BD | AB_2744387 |
| CD3 | UCH-T1 | 563109 | BD | AB_2732053 |
| CD3 | UCH-T1 | 555335 | BD | AB_398591 |
| CD4 | RPA-T4 | 560768 | BD | AB_1937323 |
| CD4 | RPA-T4 | 564724 | BD | AB_2738917 |
| CD8 | RPA-T8 | 560774 | BD | AB_1937325 |
| CD39 | TU66 | 563681 | BD | AB_2738370 |
| CD45RA | HI100 | 11-0458-42 | eBioscience | AB_11219672 |
| CD49a | SR84 | 559596 | BD | AB_397288 |
| CD69 | FN50 | 560737 | BD | AB_1727508 |
| CD86 | 2331 (FUN1) | 555658 | BD | AB_396013 |
| CD103 | BER-ACT8 | 550259 | BD | AB_393563 |
| CD152 (CTLA-4) | BNI3 | 563931 | BD | AB_2738491 |
| CD154 | TRAP1 | 555700 | BD | AB_396050 |
| PD-1 | EH12.1 | 565299 | BD | AB_2739167 |
| TIGIT | MBSA43 | 25-9500-42 | eBioscience | AB_2573548 |
| CD366 (TIM-3) | 7D3 | 565562 | BD | AB_2744369 |
| тох | TXRX10 | 50-6502-82 | eBioscience | AB_2574265 |
| IFN-γ | B27 | 557995 | BD | AB_396977 |
| TNF-α | MAb1 | 557647 | BD | AB_396764 |
| FOXP3 | PC5101 | 56-4776-41 | eBioscience | AB_1582210 |
| FOXP3 | PCH101 | 11-4776-42 | eBioscience | AB_1724125 |

| Antibody | Clone | Catalog number | Manufacturer | RRID |
|----------|------------|-------------------|--------------------|-------------|
| CD3 | UCH-T1 | 561027 | BD | AB_10561682 |
| CD4 | RPA-T4 | 555346 | BD | AB_395751 |
| CD8 | RPA-T8 | 560774 | BD | AB_1937325 |
| CD39 | TU66 | 563681 | BD | AB_2738370 |
| PD-1 | EH12.1 | 563789 | BD | AB_2738425 |
| CD127 | HIL-7R-M21 | 560551 | BD | AB_1645548 |
| CD25 | B1.49.9 | B09684 | Beckman Coulter | AB_2861133 |

Supplemental Table 2: List of antibodies for FACS cell sorting

Supplemental Table 3: List of NY-ESO-1 long peptides for CD4 T-cell stimulation

| Peptide | Sequence |
|-----------------------------|---------------------------|
| NY-ESO-1 ₁₋₂₀ | MQAEGRGTGGSTGDADGPGG |
| NY-ESO-1 ₁₁₋₃₀ | STGDADGPGGPGIPDGPGGN |
| NY-ESO-1 ₂₁₋₄₀ | PGIPDGPGGNAGGPGEAGAT |
| NY-ESO-1 ₃₁₋₅₀ | AGGPGEAGATGGRGPRGAGA |
| NY-ESO-1 ₄₁₋₆₀ | GGRGPRGAGAARASGPGGGA |
| NY-ESO-1 ₅₁₋₇₀ | ARASGPGGGAPRGPHGGAAS |
| NY-ESO-1 ₆₁₋₈₀ | PRGPHGGAASGLNGCCRCGA |
| NY-ESO-171-90 | GLNGCCRCGARGPESRLLEF |
| NY-ESO-1 ₈₁₋₁₀₀ | RGPESRLLEFYLAMPFATPM |
| NY-ESO-1 ₉₁₋₁₁₀ | YLAMPFATPMEAELARRSLA |
| NY-ESO-1 ₁₀₁₋₁₂₀ | EAELARRSLAQDAPPLPVPG |
| NY-ESO-1 ₁₁₁₋₁₃₀ | QDAPPLPVPGVLLKEFTVSG |
| NY-ESO-1 ₁₁₉₋₁₄₃ | PGVLLKEFTVSGNILTIRLTAADHR |
| NY-ESO-1 ₁₃₁₋₁₅₀ | NILTIRLTAADHRQLQLSIS |
| NY-ESO-1 ₁₃₉₋₁₆₀ | AADHRQLQLSISSCLQQLSLLM |
| NY-ESO-1 ₁₅₁₋₁₇₀ | SCLQQLSLLMWITQCFLPVF |
| NY-ESO-1 ₁₆₁₋₁₈₀ | WITQCFLPVFLAQPPSGQRR |

| Antibody | Clone | Catalog number | Manufacturer | RRID |
|----------|-------|-------------------|---------------------|------------|
| HLA-DP | B7/21 | H260 | Leinco Technologies | AB_2737518 |
| HLA-DQ | SPVL3 | IM0416 | Beckman Coulter | AB_2861134 |
| HLA-DR | G46-6 | 555809 | BD | AB_396143 |

Supplemental Table 4: List of anti-HLA class II functional antibodies

Supplemental Table 5: List of NY-ESO-1 short peptides for CD8 T-cell stimulation

| Peptide | Sequence |
|------------------------------|-------------|
| NY-ESO-1 ₉₂₋₁₀₀ | LAMPFATPM |
| NY-ESO-1 _{157-165A} | SLLMWITQA |
| NY-ESO-1 ₉₄₋₁₀₂ | MPFATPMEA |
| NY-ESO-1 ₉₄₋₁₀₄ | MPFATPMEAEL |
| NY-ESO-1 ₉₆₋₁₀₄ | FATPMEAEL |

Supplemental Table 6: List of HLA class I/peptide multimers

| Peptide | HLA | Multimer type | Catalog number | Manufacturer |
|----------------------------|---------|---------------|-------------------|--------------|
| NY-ESO-1157-165A | A*0201 | Dextramer | WB-3247-PE | Immudex |
| NY-ESO-1 ₉₄₋₁₀₂ | B*3501 | Dextramer | WK2701-PE | Immudex |
| NY-ESO-1 ₉₄₋₁₀₄ | B*3501 | Dextramer | WK5341-PE | Immudex |
| NY-ESO-1 ₉₂₋₁₀₀ | Cw*0304 | Dextramer | WS3694-PE | Immudex |
| NY-ESO-1 ₉₆₋₁₀₄ | Cw*0304 | Dextramer | WS5342-PE | Immudex |

Figures Supplemental Figure 1



Supplemental Figure 1. Immune checkpoints expression in CD4 Tconv TILs. Isolated CD4⁺ TILs were stained ex vivo with fluorochrome-labeled mAbs specific for CD3, CD4, CD45RA, PD-1, TIGIT, CTLA-4, TIM-3 and FOXP3 and analyzed by flow cytometry. (**A**) Gating strategy for CD4 Tconv TILs assessment. Left dot plot shows CD3 versus CD4 expression in CD4⁺ TILs, center histogram plot shows CD45RA expression in gated CD3⁺CD4⁺ T cells and right dot plot shows FOXP3 expression in gated memory (CD45RA⁻) CD4⁺ T cells where CD4 Tconv are gated as FOXP3⁻ cells. (**B**) Dot plots show PD-1 versus TIGIT, CTLA-4 and TIM-3 expression in gated memory CD4 Tconv TILs. Proportions of PD-1⁺, TIGIT⁺, CTLA-4⁺ and TIM-3⁺ cells in CD4 Tconv are summarized for ovarian (OC, *n=10*, purple), head and neck (HNC, *n=16*, green) and cervical (CC, *n=7*, yellow) cancer patients (middle). Correlation between the proportions of PD-1⁺ and those of TIGIT⁺ (*n=19*), CTLA-4⁺ (*n=31*) or TIM-3⁺ (*n=19*) CD4 Tconv TILs from the three tumor types (bottom). Data are presented as mean ± SD. Mann-Whitney test (middle) and Pearson correlation (bottom) were used to compare variables (**B**).







Supplemental Figure 2. Co-expression of immune checkpoints and CD39 defines distinct CD4 Tconv TIL subsets. Isolated CD4⁺ TILs were stained ex vivo with mAbs specific for CD3, CD4, CD45RA, PD-1, TIGIT, CTLA-4, TIM-3, CD39 and FOXP3 and analyzed by flow cytometry. (A) Contour plots (right), showing CTLA-4 and TIM-3 expression, are gated on PD-1⁻TIGIT⁻, PD-1⁺TIGIT⁻, PD-1⁻TIGIT⁺ and PD-1⁺TIGIT⁺ CD4 Tconv populations as shown in the left contour plot. Proportions of each of the 16 possible combinations of immune checkpoint (IC) expression are summarized (*n*=33). Tconv TIL subpopulations with a median proportion > 5% are represented in blue. QP, quadruple positive cells expressing the 4 ICs, i.e. PD-1⁺TIGIT⁺CTLA-4⁺TIM-3⁺ Tconv TILs. (B) Mean fluorescence intensity (MFI) of PD-1 and TIGIT in CD4 Tconv TIL subpopulations defined in A (with a median proportion > 5%) expressing PD-1 or TIGIT, respectively (numbers of samples are as in A). (C) Histogram plots showing CD39 expression in CD4 Tconv TIL subpopulation are summarized (*n*=16). (D) Proportions of CD39⁺ cells in CD4 Tconv are summarized for ovarian (OC, *n*=13, purple), head and neck (HNC, *n*=4, green) and cervical (CC, *n*=4, yellow) cancer patients. Data are presented as mean ± SD. Wilcoxon test or two-tailed paired test were used to compare variables (B). **, *P* < 0.001; ****, *P* < 0.0001.



Supplemental Figure 3. PD-1^{hi} **CD4 Tconv TILs are effector memory T cells.** CD4⁺ TILs were stained ex vivo with mAbs specific for CD3, CD4, CD45RA, CCR7 and PD-1 and the percentages of naïve (N, CD45RA⁺CCR7⁺), central memory (CM, CD45RA⁻CCR7⁺), effector memory (EM, CD45RA⁻CCR7⁻), and effector (E, CD45RA⁺CCR7⁻) cells among PD-1⁻, PD1^{int} and PD1^{hi} subsets are represented (*n*=11). Data are presented as mean ± SD. Wilcoxon test was used to compare variables. **, *P* < 0.01; ***, *P* < 0.001; ****, *P* < 0.0001.



Supplemental Figure 4. PD-1^{hi}CD39⁺ CD4 Tconv TILs have reduced cytokine production capacities. CD4⁺ TILs were stained ex vivo with mAbs specific for CD3, CD4, CD8, CD127, CD25, PD-1 and CD39, and CD4 Tconv (CD3⁺CD8⁻CD4⁺CD25⁻CD127⁺) were sorted into PD-1⁻CD39⁻(grey), PD-1^{lo}CD39⁻(green), PD-1^{hi}CD39⁻(blue) and PD-1^{hi}CD39⁺ (red) subsets that were stimulated or not in vitro with PMA/ionomycin overnight. TNF- α , IFN- γ and IL-2 were quantified by ELISA in the supernatant (*n=4*). Data are presented as mean ± SD.



Supplemental Figure 5. TOX expression in CD4 Tconv TIL subsets. Isolated CD4⁺ TILs were stained ex vivo with mAbs specific for CD3, CD4, CD45RA, PD-1, CD39, TOX and FOXP3 and analyzed by flow cytometry. Examples of histogram plots showing TOX expression in CD4 Tconv TIL populations defined according to PD-1 and CD39 expression; PD-1⁻CD39⁻, PD-1^{lo}CD39⁻, PD-1^{hi}CD39⁻ and PD-1^{hi}CD39⁺.



Supplemental Figure 6. Pseudotime analysis of scRNA-seq data. Pseudotime maturation trajectory of CD4 Tconv based on scRNA-Seq data presented in dendrograms color-coded according to *ENTPD1*, *CTLA4*, *HAVCR2* and *LAG3* gene expression levels (*n=4*).



Supplemental Figure 7. *ENTPD1*⁺ CD4 Tconv TILs exhibit features of T-cell activation, late differentiation and tumor residency. Differential gene expression analysis between *ENTPD1*⁺ and *ENTPD1*⁻ CD4 Tconv was performed using scRNA-Seq data (Figure 3B). (A-F) Violin plots of expression of 14 genes shown to be significantly differentially expressed in *ENTPD1*⁺ versus *ENTPD1*⁻ CD4 Tconv TILs (n=4). (G) t-SNE plot color-coded by levels of expression (grey to red) of *NT5E* (CD73) gene.



Supplemental Figure 8. Trm markers expression in CD4 Tconv TIL subsets. Isolated CD4⁺ TILs were stained ex vivo with mAbs specific for CD3, CD4, CD45RA, PD-1, CD39, CD49a, CD69, CD103 and FOXP3 and analyzed by flow cytometry. (**A-C**) Examples of histogram plots showing CD103 (**A**), CD49a (**B**) and CD69 (**C**) expression in CD4 Tconv TIL populations defined according to PD-1 and CD39 expression; PD-1⁻CD39⁻, PD-1^{lo}CD39⁻, PD-1^{hi}CD39⁻ and PD-1^{hi}CD39⁺ (*n=8*). Data are presented as mean ± SD.



Supplemental Figure 9. Fine specificity and MHC restriction of PD-1^{hi}CD39⁺ Tconv TILs-derived NY-ESO-1-specific clones. (A-D) PD-1^{hi}CD39⁺ CD4 Tconv TILs-derived clones responding to NY-ESO-1 peptide pool (Figure 4C) were stimulated or not with each single peptide for 4 hours in the presence of HLA-matched iDCs from HDs and IFN- γ , TNF- α and CD154 expression were analyzed by intracellular staining and flow cytometry. (A) Examples of dot plots showing IFN- γ versus TNF- α production of the indicated NY-ESO-1–specific clones in the absence or presence of the indicated NY-ESO-1 peptides (B) Proportions of cytokine⁺ (IFN- γ and or TNF- α) cells after stimulation or not of the five NY-ESO-1–specific clones with single NY-ESO-1 peptides (C) Examples of histogram plots showing CD154 expression in the indicated NY-ESO-1–specific clones in the absence or presence of the indicated NY-ESO-1 peptides. (D) Proportions of CD154⁺ cells after stimulation or not of the five NY-ESO-1 peptides. (D) Proportions of CD154⁺ cells after stimulation or not of the five NY-ESO-1 peptides. (E) Proportions of cytokine⁺ (IFN- γ and/or TNF- α) cells after stimulation with HLA-matched iDCs from HDs with corresponding NY-ESO-1 single peptides for C9B5, C5D8 and C10F4 clones, in the presence or absence of blocking anti-HLA-DR, anti-HLA-DP and anti-HLA-DQ mAbs. (B,D,E) One experiment representative of two independent experiments.



Supplemental Figure 10. Ag specificity of Tconv TIL subets. Ex vivo isolated CD4 TILs (*n*=3) were stimulated or not for 6 hours with the NY-ESO-1 peptide pool in presence of autologous circulating CD14⁺ cells and IFN- γ and CD154 expression were analyzed by intracellular staining and flow cytometry. (**A**) Dot plots show IFN- γ versus CD154 expression for the PD-1⁻CD39⁻, PD-1^{hi}CD39⁻ and PD-1^{hi}CD39⁺ Tconv subsets (CD3⁺CD4⁺FOXP3⁻) in presence or absence of the NY-ESO-1 peptide pool. (**B**, **C**) Proportions of IFN- γ ⁺ and CD154⁺ cells in the three subsets are summarized. Data are presented as mean ± SD.



Supplemental Figure 11. Graphical representation of circulating CD8 T-cell stimulation experiment with NY-ESO-1 peptides in the presence of autologous CD4⁺ TILs and iDCs. CD14⁺ cells were sorted from PBMCs of ovarian cancer patients exhibiting antibody and CD8 T-cell responses to the NY-ESO-1 Ag and were differentiated into iDCs by culture for 5 days in the presence of GM-CSF and rhIL-4. At day 5, CD4⁺ TILs were isolated from the same patients, pre-incubated or not with anti-PD-1 mAbs for 30 minutes at 4°C and washed twice. In parallel, autologous circulating CD8 T cells were sorted from PBMCs and co-cultured with iDCs, anti-PD-1 pre-treated or non-pre-treated CD4⁺ TILs in the presence of NY-ESO-1 peptides, as detailed in Materials and Methods, and rhIL-2. At day 10, cells were stained with MHC-I/NY-ESO-1 multimers and analyzed by flow cytometry.