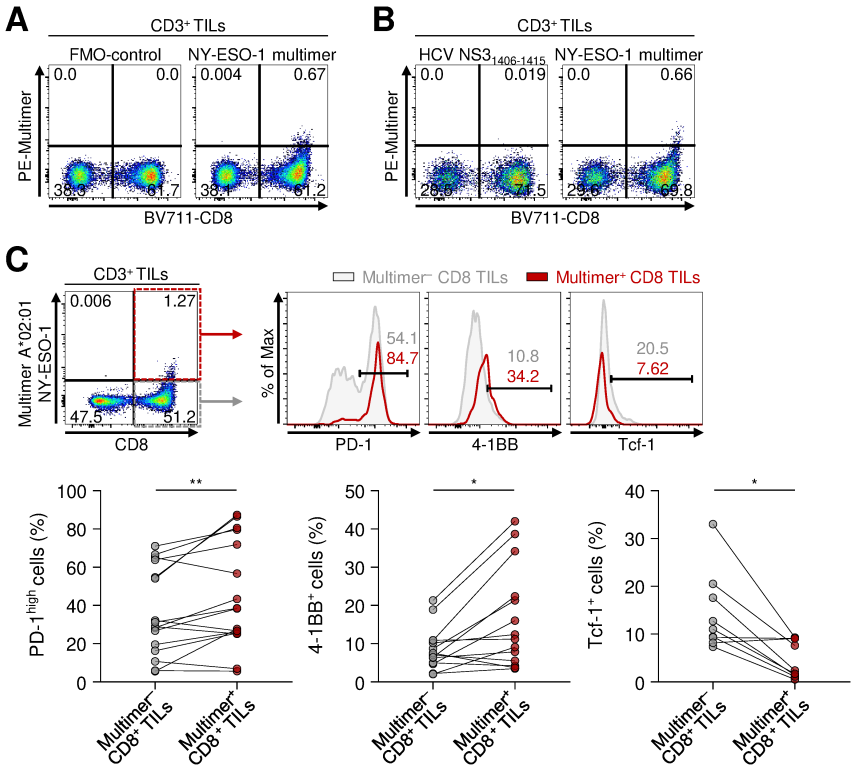
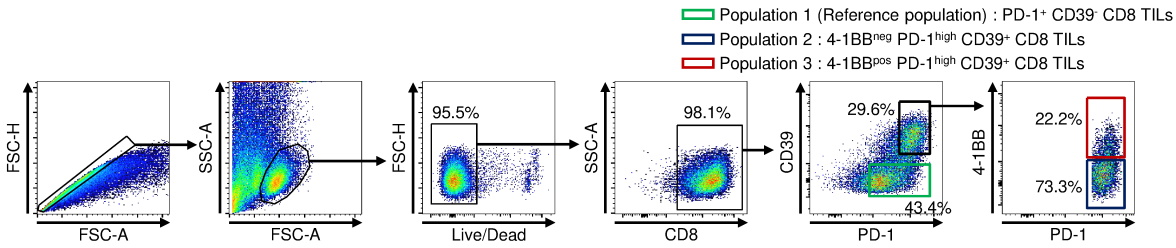
Supplementary Figure S1



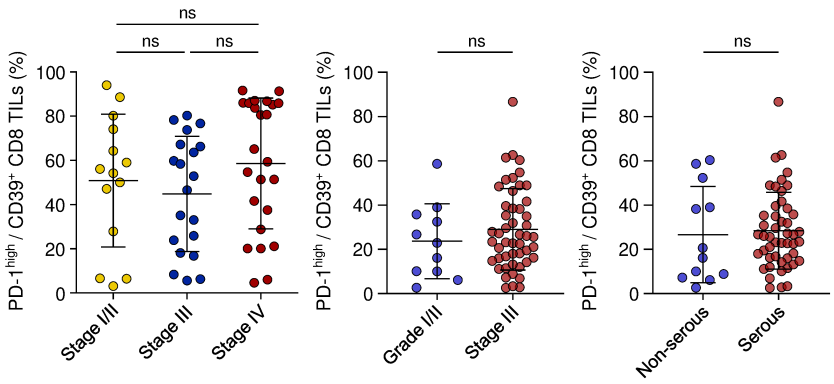
Supplementary Figure S1. The gating strategies of multimer-positive cells in flow cytometry. To clearly identify multimer-positive cells, we used FMO controls (**A**) and negative-epitope specific multimers (**B**) as control. **C**, Multimer$^+$ CD8 TILs (**red box**) and multimer$^-$ CD8 TILs (**grey box**) were compared in the expression of PD-1, 4-1BB, and Tcf-1. Upper plots are representative plots, and low graphs show cumulative data regarding the comparison of PD-1^{high} cells, 4-1BB$^+$ cells, and Tcf-1$^+$ cells between multimer$^+$ CD8 TILs and multimer$^-$ CD8 TILs. The statistical analyses were performed in pairs. *P < 0.05; **P < 0.01.

Supplementary Figure S2



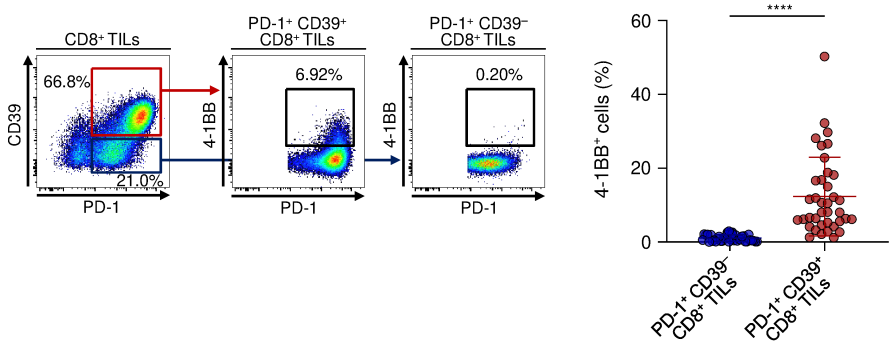
Supplementary Figure S2. The gating strategy of CD8 TIL sorting for RNA-seq. We first sorted PD-1^{+} CD39^{-} CD8 TILs as a reference population (green box), and in PD-1^{high} CD39^{+} CD8 TILs, we sorted 4-1BB-positive (red box) and -negative (blue box) cells separately.

Supplementary Figure S3



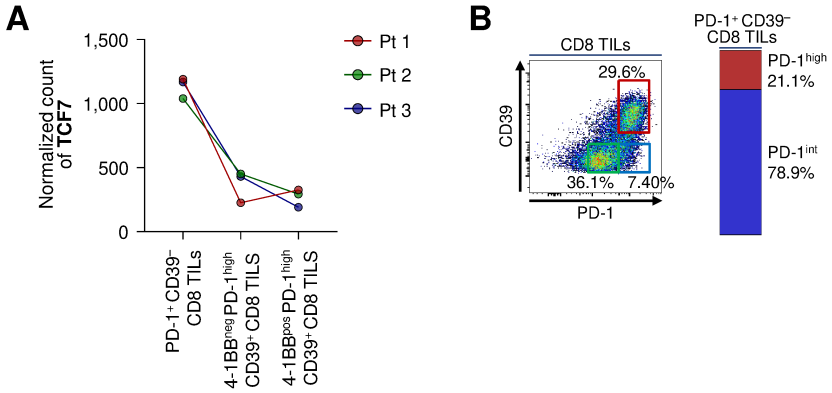
Supplementary Figure S3. Frequency of PD-1^{high} subpopulation among CD39^{+} CD8 TILs according to the cancer stage, tumor grade, and tumor histology. The mean and SD are shown. ns, not significant.

Supplementary Figure S4



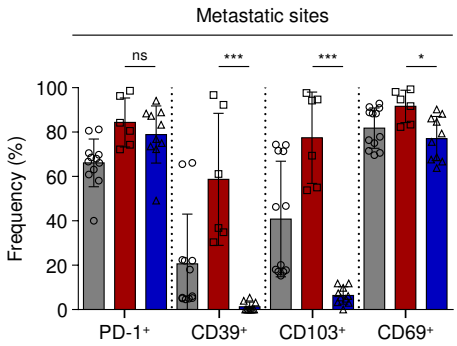
Supplementary Figure S4. The expression of 4-1BB in PD-1$^+$ CD39$^-$ CD8 TILs, compared to PD-1$^+$ CD39$^+$ CD8 TILs. Left flow cytometry plots are representative plots, and the right graph shows a cumulative data regarding the expression of 4-1BB in PD-1$^+$ CD39$^-$ CD8 TILs (blue dots) and PD-1$^+$ CD39$^-$ CD8 TILs (red dots). The mean and the SD are indicated in the graph. The statistical analysis was performed between PD-1$^+$ CD39$^-$ CD8 TILs and PD-1$^+$ CD39$^-$ CD8 TILs in pairs. ****P < 0.0001.

Supplementary Figure S5



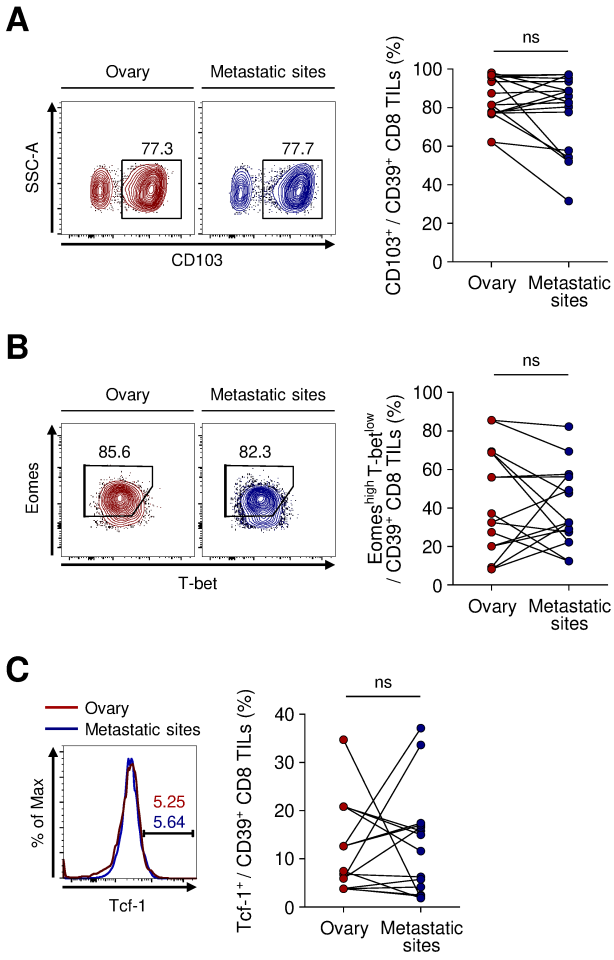
Supplementary Figure S5. Gene expression level of TCF7 and differential expression in PD-1 in PD-1^{+} CD39^{-} CD8 TILs. A, Gene expression level of TCF7 among PD-1^{+} CD39^{-} CD8 TILs, 4-1BB^{neg} PD-1^{high} CD39^{+} CD8 TILs, and 4-1BB^{pos} PD-1^{high} CD39^{+} CD8 TILs. Data is presented with normalized counts. **B**, Differential expression of PD-1 in PD-1^{+} CD39^{-} CD8 TILs. Left flow cytometry plot is a representative plot of 1 patient. The red box is for PD-1^{high} CD39^{+} population, the blue box is for PD-1^{high} CD39^{-} population, and the green box is for PD-1^{int} CD39^{-} population. The right bar graph shows cumulative mean of the frequency of PD-1^{high} population and PD-1^{int} population in PD-1^{+} CD39^{-} CD8 TILs (reference population in RNA-seq).

Supplementary Figure S6



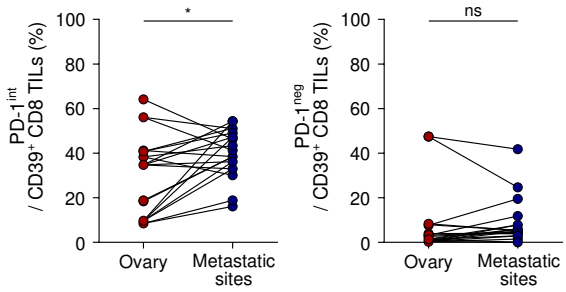
Supplementary Figure S6. Comparison of the expression of PD-1, CD39, CD103, and CD69 between tumor-specific multimer$^+$ CD8 TILs and tumor-unrelated multimer$^+$ (virus-specific) CD8 TILs from metastatic sites. The mean and SD are shown. *P < 0.05; ***P < 0.001; ns, not significant.

Supplementary Figure S7



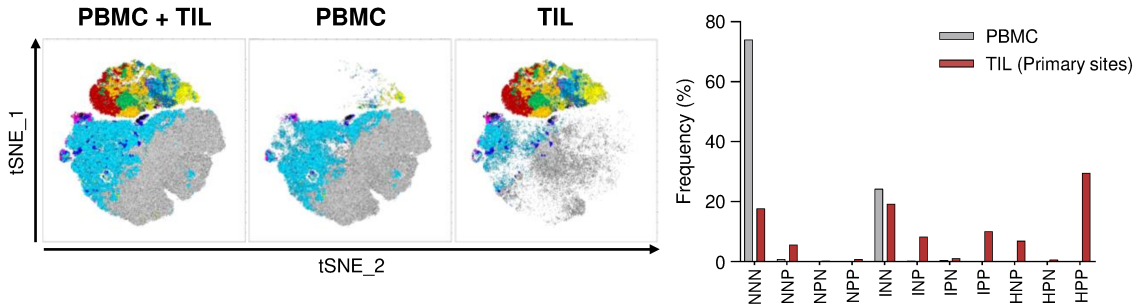
Supplementary Figure S7. CD39⁺ CD8 TILs from metastatic sites show similar phenotypes regarding tumor reactivity and exhaustion compared to CD39⁺ CD8 TILs from primary sites. A–C, Direct comparison of the percentages of CD103⁺ **(A)**, Eomes^{high} T-bet^{low} **(B)**, and Tcf-1⁺ **(C)** cells among CD39⁺ CD8 TILs, compared between the ovary and metastatic sites. Representative flow cytometry plots are shown to the left, and cumulative data are shown to the right. ns, not significant.

Supplementary Figure S8



Supplementary Figure S8. Pairwise comparison of the PD-1^{int} subpopulation and PD-1^{neg} subpopulation among CD39^{+} CD8 TILs between ovary (primary site) and metastatic sites. **P* < 0.05; ns, not significant.

Supplementary Figure S9



Supplementary Figure S9. t-SNE analysis of PBMCs and TILs. Left flow cytometry plots are t-SNE plots of merged PBMC and TILs, separated PBMCs, and separated TILs in the order from the left. Right bar graphs show the frequency of each population defined by the differential expression of PD-1, CD39 and CD103. Gray bars for PBMCs and red bars for TILs (from primary sites). NNN; PD-1^{neg} CD39^{-} CD103^{-}, NNP; PD-1^{neg} CD39^{-} CD103^{+}, NPN; PD-1^{neg} CD39^{+} CD103^{-}, NPP; PD-1^{neg} CD39^{+} CD103^{+}, INN; PD-1^{int} CD39^{-} CD103^{-}, INP; PD-1^{int} CD39^{-} CD103^{+}, IPN; PD-1^{int} CD39^{+} CD103^{-}, IPP; PD-1^{int} CD39^{+} CD103^{+}, HNP; PD-1^{high} CD39^{-} CD103^{+}, HPN; PD-1^{high} CD39^{+} CD103^{-}, HPP; PD-1^{high} CD39^{+} CD103^{+}.