Supplementary Figures

Between innate and adaptive immune responses:
HLA-E restricted self-peptides acquired during an artificial hCMV infection determine the cell fate

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Supplementary Figures

Supplementary Fig. 1 Native PAGE of purified sNKG2/CD94 heterodimers

Lanes: 1, standard proteins sized in kDa at left; 2, sNKG2A/CD94; 3, sNKG2C/CD94. Purified sNKG2/CD94 heterodimers exhibit a molecular mass about ~ 66 kDa and no detectable monomers after purification. Proteins were detected with Coomassie blue G-250.
Supplementary Fig. 2 HLA-E surface expression on T2E cells

Histograms of HLA-E surface expression levels on T2E cells after incubation with the test peptides. HLA-E surface expression was detected after incubation with the anti-HLA-E 3D12-PE mab and differences in surface expression are indicated: filled grey: T2E cells without peptide, dashed graph: T2E cells with peptide.
Supplementary Fig. 3 NKG2/CD94 receptor binding to the p:HLA-E complexes

Receptor binding to T2E cells that were not pre-pulsed with peptide served as a negative control and are depicted by the filled grey graph and binding to T2E cells with peptide is indicated by the black graph.
Supplementary Fig. 4 Gating strategy for determination of CD8⁺ T cell proliferation and phenotype.

a) Proliferated CD8⁺ T cells were first gated on live cells (FSC-A versus SSC-A), followed by identification of CD3⁺CD8⁺ T cells (CD3 versus CD8). Proliferation of CD8⁺ T cells was analyzed by CFSE dilution. Subgating from live cells to identify CD8⁺ T cells (FSC-A versus CD8) leads to the determination of CD45RA and CD45RO phenotype of CD8⁺ T cells (CD45RO versus CD45RA). b) Gating from live cells to identify CD3⁺CD8⁺ T cells. CD3⁺CD8⁺ T cells were strictly gated on CD56⁻ cells and NKG2A/CD94 and NKG2C/CD94 phenotype of CD8⁺ T cells were determined (NKG2A/CD94 versus NKG2C/CD94).
Supplementary Fig. 5 Live/Dead discrimination of proliferated CD8\(^+\) T cells.

Gating on live cells (FSC-A versus SSC-A) was verified by 7-AAD staining (FSC-A versus 7-AAD) that represents the subgated population to determine the CD3\(^+\)CD8\(^+\) population.