Figure S1.

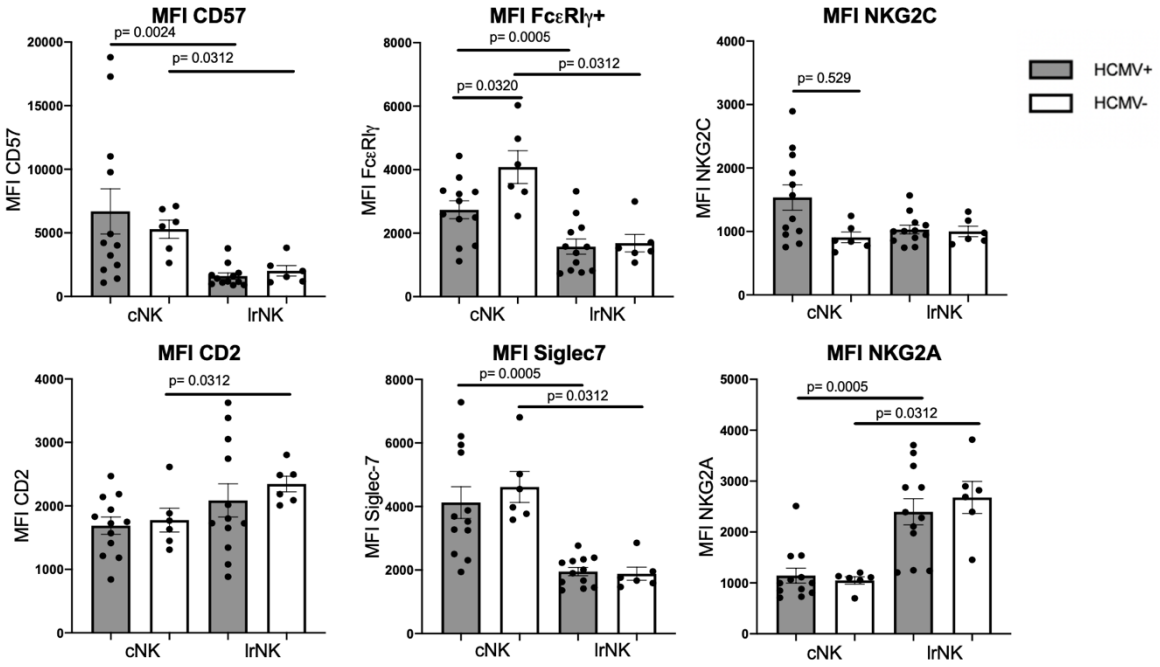

Figure S1. Expression phenotype of cNK or LrNK cells from HCMV seropositive or seronegative individuals. cNK and lrNK from HCMV seropositive (grey bars; n= 12) and seronegative (clear bars; n= 6) were analysed for their MFI expression of CD57, CD2, FcεRIγ, Siglec7, NKG2C, NKG2A. Significance was assessed using 2-tailed Wilcoxon's signed-rank sum test (paired data) or a 2-tailed Mann-Whitney U test (unpaired data).

Figure S2.

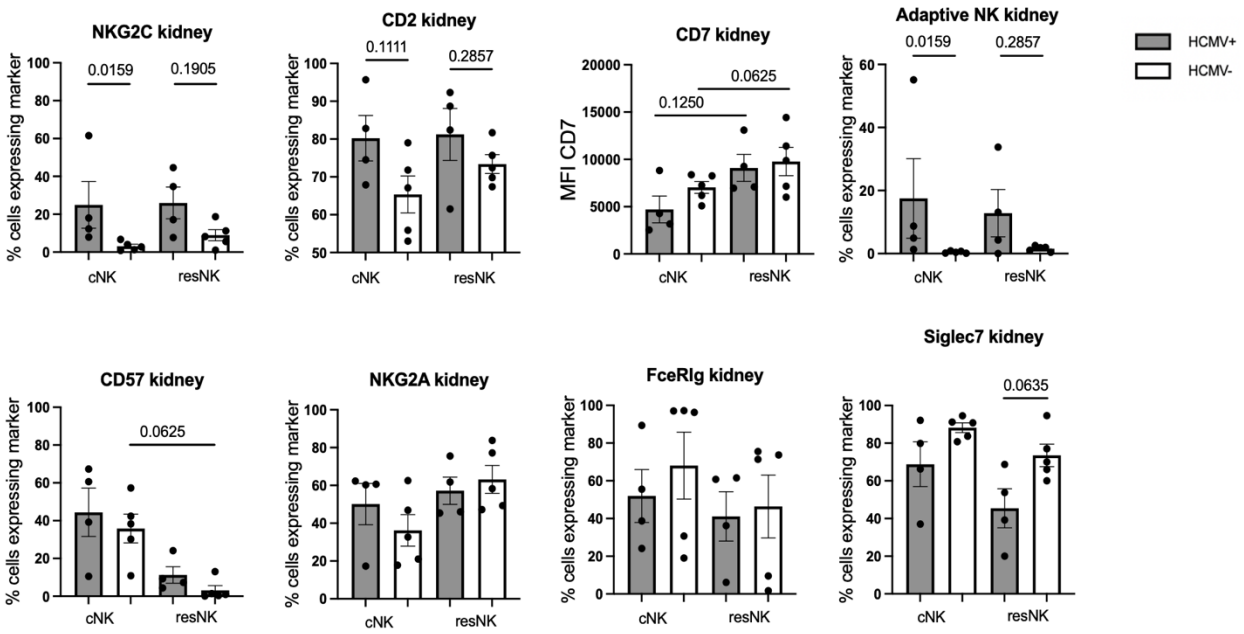

Figure S2. Expression phenotype observed in liver is recapitulated in the kidney. cNK and kidney-resident NK (krNK) from HCMV seropositive (grey bars; n= 4) and seronegative (clear bars; n= 5) were analysed for their MFI expression of CD57, CD2, FcεRIγ, Siglec7, NKG2C, NKG2A, and CD7. Significance was assessed using 2-tailed Wilcoxon's signed-rank sum test (paired data) or a 2-tailed Mann-Whitney U test (unpaired data).

Figure S3.

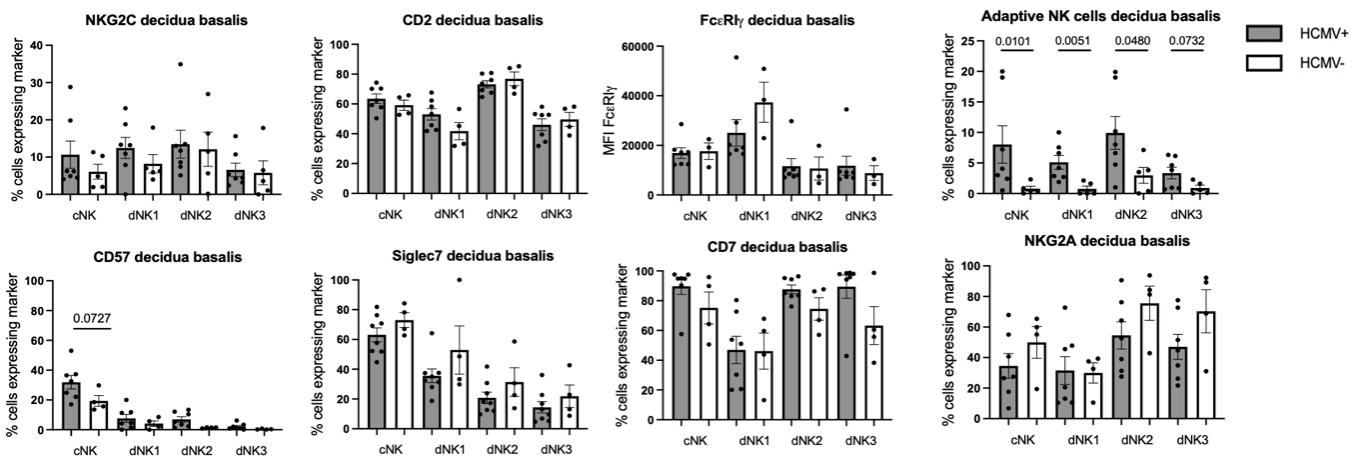

Figure S3. **Expression phenotype of decidual NK cells from HCMV seropositive or seronegative individuals.** Decidual NK cells from HCMV seropositive (grey bars; n= 7) and seronegative (clear bars; n= 5) were analysed for their MFI expression of CD57, CD2, FcεRIγ, Siglec7, NKG2C, NKG2A, and CD7. Significance was assessed using 2-tailed Wilcoxon's signed-rank sum test (paired data) or a 2-tailed Mann-Whitney U test (unpaired data).

Figure S4

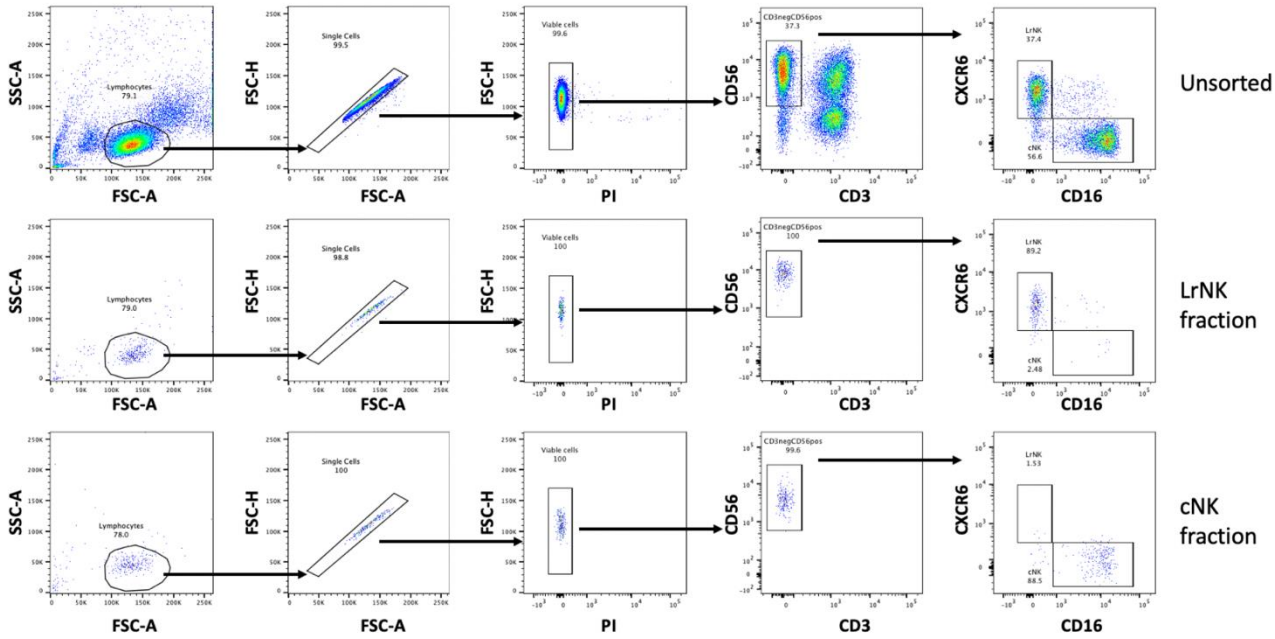

Figure S4. Gating strategy of sorted NK cell fractions from liver perfusates for use in functional assays. NK cells were separated from liver perfusates into cNK (CXCR6-CD16+) and LrNK (CXCR6+CD16) cell fractions by FACS. (Top) Unsorted lymphocyte fractions within perfusate. (Middle) Sorted LrNK cell fraction. (Bottom) Sorted cNK cell fraction.

Figure S5

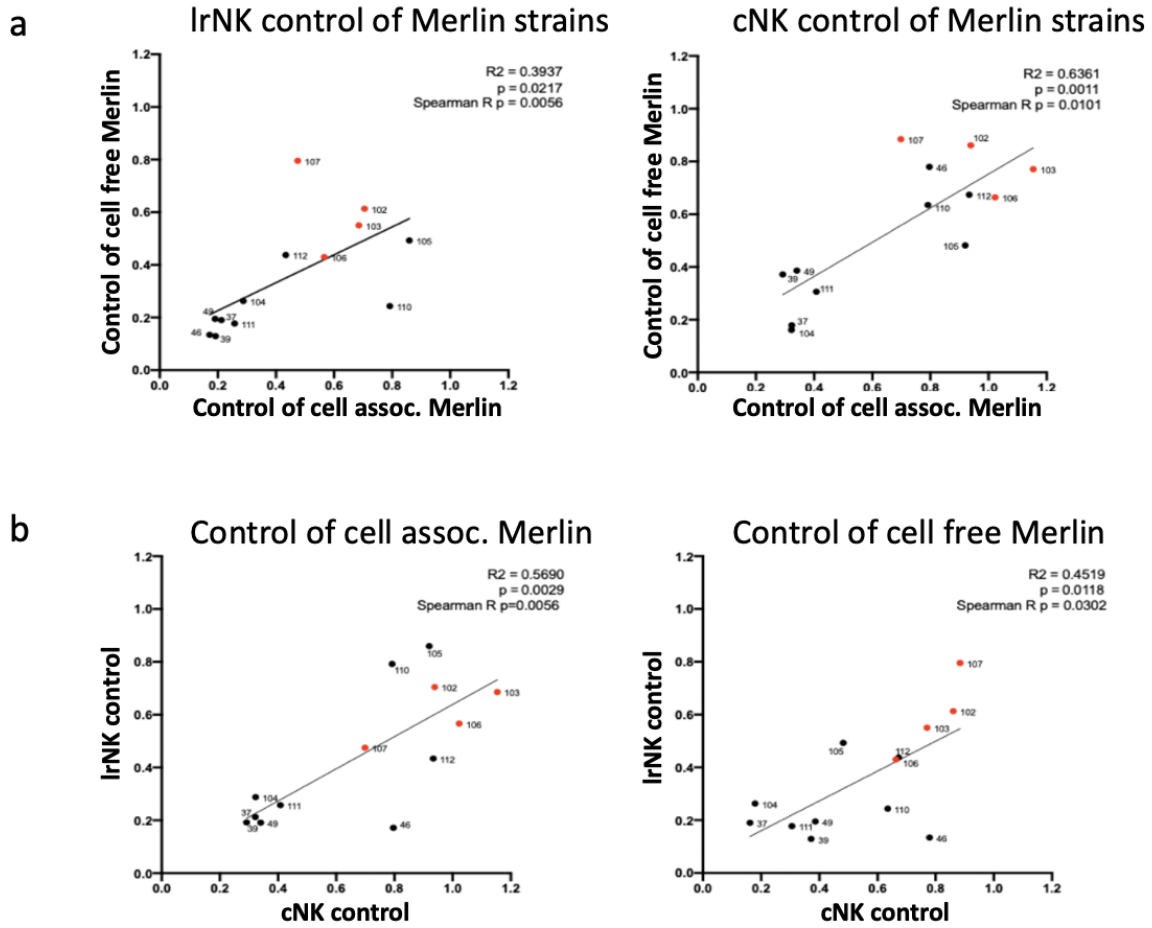

Figure S5. Correlation of NK cell mediated control between NK cell subsets and between HCMV strains. Data from virus spread assays plotted to assess correlation. HCMV seropositive donors (black; n= 9) and seronegative (red; n= 4) are plotted together. **(A)** Correlation between lrNK (left) and cNK (right) control of cell assoc. Merlin and cell free merlin. (B) Correlation between lrNK and cNK control of cell assoc. Merlin (left) and cell free merlin (right). Significance was assessed using linear regression analysis and Spearman's Rank correlation.

Figure S6.

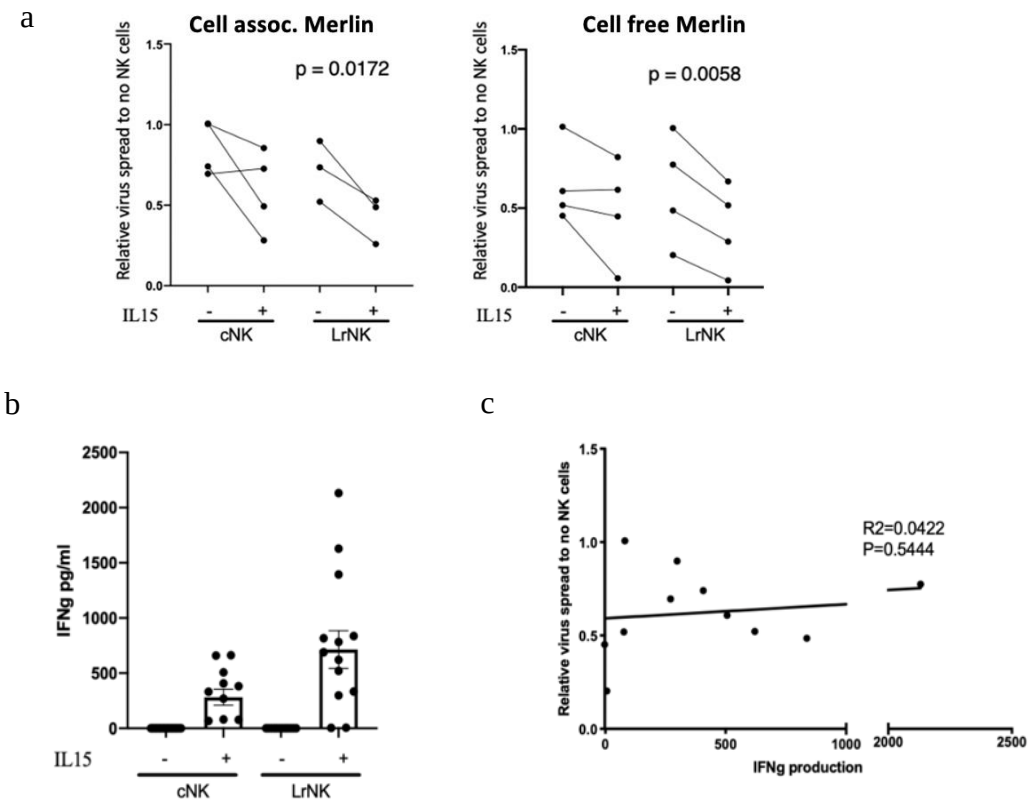

Fig S6. IL15 induced production of IFNγ is not associated with control. (A) cNK and lrNK were cultured with HCMV infected HFF alone (cNK n= 16; lrNK n=12) or in the presence of 10ng/ml human recombinant IL15 (cNK n= 12; lrNK n=14). (B) Culture supernatants were assessed for NK cell production of IFNγ by ELISA and (C) levels of IFNγ were plotted against in vitro control (n= 11). Significance was assessed using linear regression analysis (C) or with a mixed-effects model to determine the effect of IL-15 (A).

Figure S7

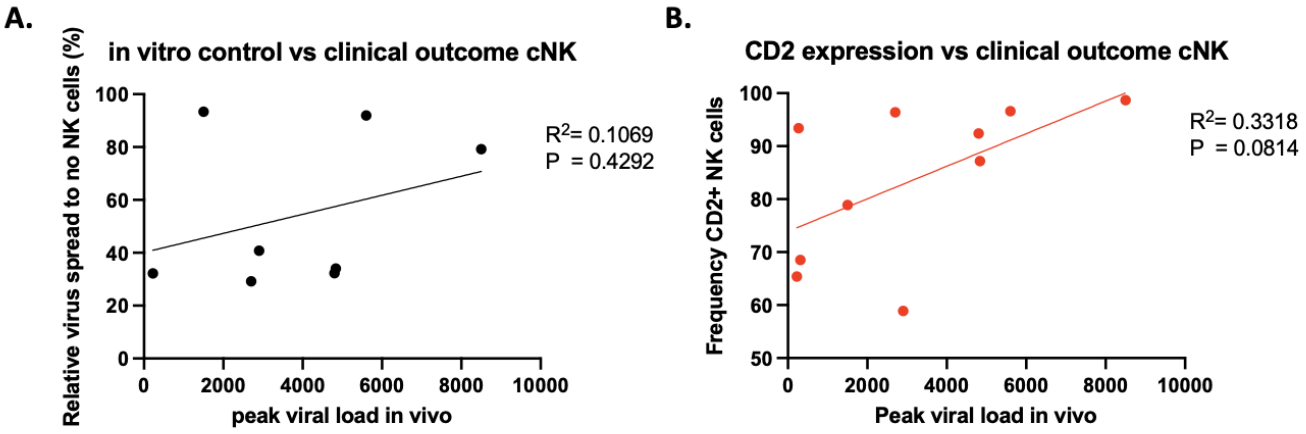

Figure S7. No correlation was observed between cNK cells and post-transplant outcome. Peak viral load (genome copies/ml blood) within one year post-transplant in all transplant recipients who received a liver from a HCMV-seropositive donor is plotted against (A) *in vitro* control of HCMV spread by cNK cells (black; n= 8) or (B) frequency of CD2+ cNK cells (red: n=10) isolated from the donor liver prior to transplant. Significance was assessed using linear regression analysis.

Figure S8

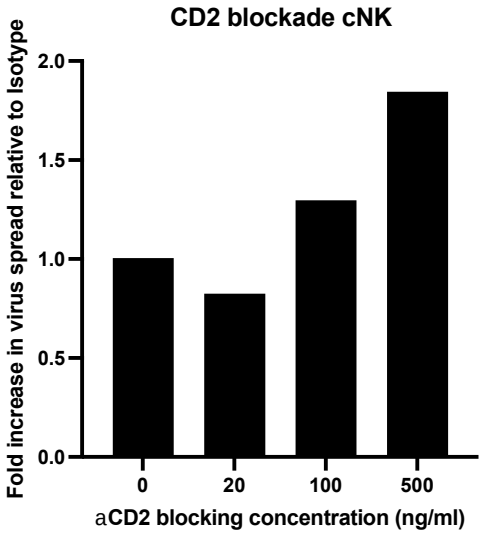

Figure S8. CD2 blockade inhibits control of HCMV infection by cNK cells. FACS sorted CD2+ cNK cells were blocked with aCD2 antibody or isotype control and then analysed for in vitro control of cell assoc. Merlin in a virus dissemination assay.

Figure S9.

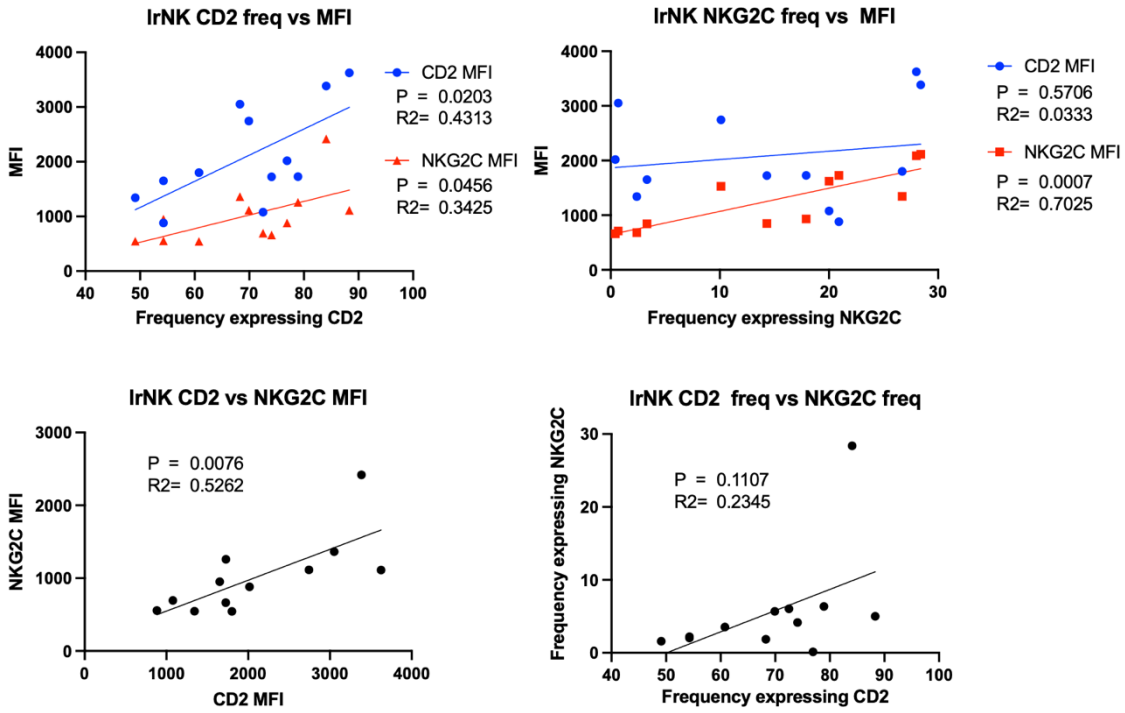

Figure S9. Association of NKG2C and CD2 expression by lrNK cells. Phenotypic analysis of NKG2C and CD2 expression on lrNK cells measured through frequency of positive cells or MFI. Significance was assessed using linear regression analysis.

Figure S10.

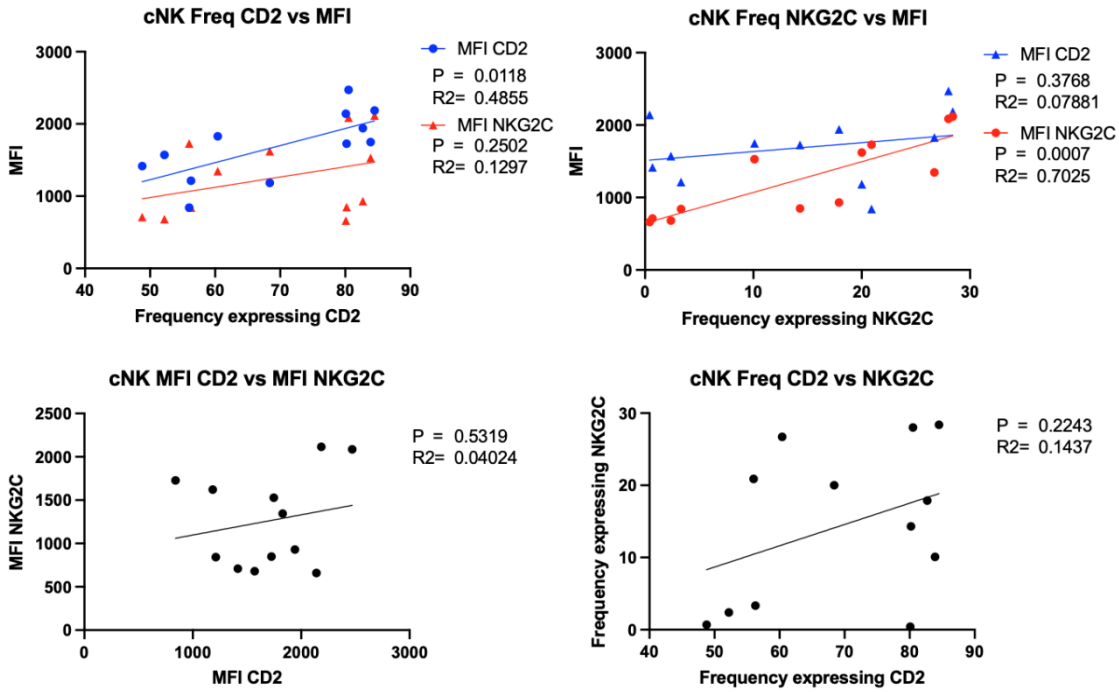

Figure S10. Association of NKG2C and CD2 expression by cNK cells. Phenotypic analysis of NKG2C and CD2 expression on cNK cells measured through frequency of positive cells or MFI. Significance was assessed using linear regression analysis.

Table S1.

Freq %	Merlin BAC	HCMV+	HCMV-	
cNK	NKG2A	0.9299	0.1045	
cNK	Siglec7	0.5288	0.0516	neg assoc
cNK	FcεRIγ	0.6151	0.7568	
cNK	NKG2C	0.0841	0.5888	neg assoc
cNK	CD2	0.4792	0.4244	
cNK	CD57	0.2087	0.7988	
LrNK	NKG2A	0.3788	0.0628	neg assoc
LrNK	Siglec7	0.2105	0.5584	
LrNK	FcεRIγ	0.4355	0.4055	
LrNK	NKG2C	0.388	0.1807	
LrNK	CD2	0.0462	0.1442	pos assoc
LrNK	CD57	0.1308	0.8307	

Freq %	Merlin isolate	HCMV+	HCMV-	
cNK	NKG2A	0.0482	0.2519	neg assoc
cNK	Siglec7	0.1186	0.1486	
cNK	FcεRIγ	0.1228	0.1521	
cNK	NKG2C	0.0084	0.6914	neg assoc
cNK	CD2	0.8424	0.7749	
cNK	CD57	0.66	0.8936	
LrNK	NKG2A	0.1565	0.7905	
LrNK	Siglec7	0.0317	0.2933	neg assoc
LrNK	FcεRIγ	0.7798	0.9228	
LrNK	NKG2C	0.2951	0.9367	
LrNK	CD2	0.129	0.9367	
LrNK	CD57	0.3588	0.2257	

MFI	Merlin BAC	HCMV+	HCMV-	
cNK	CD57	0.9659	0.6027	
cNK	NKG2A	0.302	0.4717	
cNK	NKG2C	0.1045	0.7769	
cNK	Siglec7	0.7157	0.0396	neg assoc
cNK	CD7	0.7871	0.2824	
cNK	FcεRIγ	0.942	0.8407	
cNK	CD2	0.4737	0.4891	
LrNK	CD57	0.9289	0.4742	
LrNK	NKG2A	0.1128	0.735	
LrNK	NKG2C	0.7562	0.6051	
LrNK	Siglec7	0.5269	0.7847	
LrNK	CD7	0.3087	0.2271	
LrNK	FcεRIγ	0.6289	0.259	
LrNK	CD2	0.5203	0.7512	

MFI	Merlin isolate	HCMV+	HCMV-	
cNK	CD57	0.5649	0.896	
cNK	NKG2A	0.9959	0.7014	
cNK	NKG2C	0.5158	0.5215	
cNK	Siglec7	0.9251	0.2878	
cNK	CD7	0.2652	0.0505	neg assoc
cNK	FcεRIγ	0.6187	0.3602	
cNK	CD2	0.5207	0.7926	
LrNK	CD57	0.6912	0.9636	
LrNK	NKG2A	0.3005	0.813	
LrNK	NKG2C	0.8668	0.4154	
LrNK	Siglec7	0.0529	0.8924	neg assoc
LrNK	CD7	0.4884	0.0936	neg assoc
LrNK	FcεRIγ	0.3174	0.6344	
LrNK	CD2	0.2736	0.4594	

Linear regression P value	<0.05	< 0.1

Table S1. Association of NK cell phenotypic markers with in vitro control of HCMV.

Expression frequency and MFI expression of NK cell markers CD57, CD2, FcεRIγ, Siglec7, NKG2C, NKG2A and CD7 were assessed for association with in vitro control of HCMV. Positive or negative association is indicated on relevant rows. Significance was assessed using linear regression analysis (p=<0.05 green, <0.1 yellow).