Supp. Fig. 1

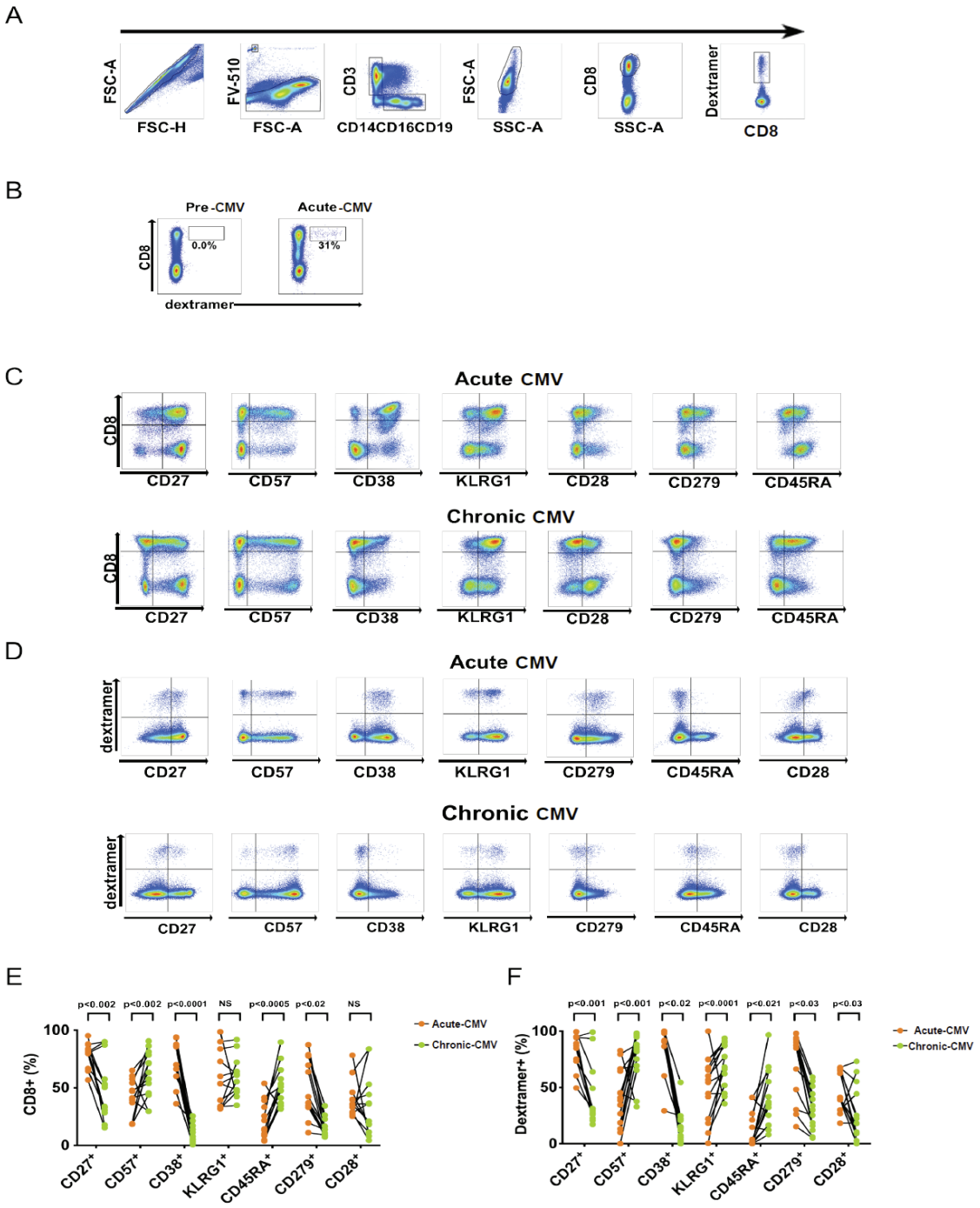

Figure S1. Gating Strategy and extended phenotypic analysis of total and CMV-specific CD8$^+$ T cells during acute and chronic CMV infection

(A) Shows gating strategy used in our flow cytometric analysis using FlowJo software. (B) Representative flow plots showing the CMV dextramer$^+$CD8$^+$ cells from a patient at Pre-CMV *(left panel)* and acute CMV infection *(right panel)* time points. (C) Representative flow plots showing CD8$^+$ T cells frequencies of phenotypic markers: CD27$^+$, CD57$^+$, CD38$^+$, KLRG1$^+$, CD28$^+$, CD279$^+$and CD45RA$^+$ in a patient during acute CMV infection *(upper panels)* and during Chronic CMV infection *(lower panels)*. (D) Representative flow plots shows frequencies of CMV dextramer$^+$CD8$^+$ cells of the same phenotypic markers: CD27$^+$, CD57$^+$, CD38$^+$, KLRG1$^+$, CD28$^+$, CD279$^+$and CD45RA$^+$ in a patient during acute CMV infection *(upper panels)* and during Chronic CMV infection *(lower panels)* time points. (E)(F) Cumulative data shows frequencies of total CD8$^+$ T cells (E) or CMV Dextramer$^+$ CD8$^+$ (F) of phenotypic markers: CD27$^+$, CD57$^+$, CD38$^+$, KLRG1$^+$, CD279$^+$ and CD28$^+$, in patients during acute CMV infection *(orange circles)* and during Chronic CMV infection *(green circles)*. Statistical analysis was performed using Wilcoxon matched pair signed rank test and p value of less than 0.05 considered statistically significant.

Supp. Fig. 2

A

Predicted T-bet binding Sites
KLRG1 Promoter

	start	end	score	strand
1	493	502	6.017168	+
2	676	685	1.808007	+
3	1017	1026	9.805924	+
4	240	249	2.104591	-
5	368	377	3.915415	-
6	505	514	5.799985	-
7	538	547	5.801434	-
8	697	706	7.413181	-
9	744	753	2.136272	-
10	944	953	6.354060	-
11	1217	1226	13.406233	-

B

Predicted T-bet binding Sites
B3GAT1 (CD57) Promoter

	start	end	score	strand
1	654	663	4.771764	+
2	441	450	4.859813	-

C

Figure S2. Predicted T-bet binding sites for KLRG1 and CD57 promoters.

(A) Predicted T-bet binding sites using *KLRG1* promoter using a consensus T-bet DNA binding matrix and a transcription factor binding site analysis tool (TFBS tools) and identified the T-bet binding site with the highest TFBS score (B) Lack of predicted T-bet binding sites for *B3GAT1* (CD57) promoter. (C)Targeted T-bet binding sites in the *KLRG1* promoter

Supp. Table I.

CMV dextramer CD8$^+$ T cell MHC Class I matches assessed during CMV infection

CD8$^+$ Class I Dextramers	Ethnicity	A*01 VTEHDTLLY[2] (pp50)[3]	A*02 NLVPMVATV (pp65)	B*07 TPRVTGGGAM (pp65)	B*08 ELRRKMMYM (IE1)
LTR Controllers					
28	W[1]		+		
34	W	+			+
37	W		+		
41	W		+	+	
51	W	+		+	
LTR Relapsers					
24	W	+			
29	W			+	
33	W		+		
46	W	+			+
53	W	+			+

[1]W=white

[2] HLA Class I dextramer and cognate peptide

[3] CMV antigen

Supp. Table II.

List of Primers used for ChIP Assay

Target	Forward	Reverse
KLRG1	AGCATCTACAGTGTCATGGGG	GATTCAAATTTGGGGGCTGCCT
CD57 (B3GAT1)	AGCAGACCCCGTGAAACCCC	AGTTAAAGCTCGGCCCCC
IFNγ	TACCAGGGCGAAGTGGGAGG	CACCTGTGCCATTCTGGTGGG
IL-4	CCAAGTGACTGACAATCTGGGTAACGAA	AATAGGTGTCGATTTGCAGTGACAATGTG
GAPGH	TCCTTCTGTTTCATCCAAGC	TACTAGCGGTTTTACGGGCG