



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 dexramer⁺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 dexramer⁺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 Dexramer⁺ 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.

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

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GCCTTGTGTGCTTGCATGTGTTGATTTTGATTGGAGAGTAAGTCTAATGCCATTCTGTCATGGC
TGGAAAGCAGAAATATATTTGTTTTTATAATATAAAACAAATTAATATAAAGCACTCCCTGTTTCTCTTC
TTTTATCCTTATGCAGCTATCTTGATGATCTTATCCACTCTTAAGAGTTTCAATACTCTTTCTGTTTC
CTTACTTTAACTTTTGTTTTTTTAGACGGAGTTTCACTCTTGTGCCAGGCTAGATAGAGTACAAT
GGTGCAGTCTGGGCTCGCTGCAACCTCCGCCTCCCGGTTTCAAGCCATTCTCCTGCCTCAGCCT
CCTGAGCAGCTGAGATTACAGCCCCCACCACCACACCAGCTAATTTTTTTGATTTTTAGTAGAG
ACGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAATTCCTGACCTGAGGTGATCCACCCTGCTT
GGCCTCCCAAAGTCTGGGATTACAGCCGTGAGCCACCACACCTGGCCTACTCTAACTTTTTTATTA
ACTTTTCACCTACTAAAAACAAATTAAGATGTTAGAATGATTTGTTTACTTTGCTCTTTTTTA
GTTATCTTTGCATGAAGTATAATAATAAAAAAATAAGACAACAAAGAGAAAAATATAATGGAATTC
TGATACTGTGAAGGGTAAAGACCATCACACAATTTGGACAAGGTTTTGGGGAGATGTGGTCATGTC
ATATTCACAAAATATATCTGGGTAATAGTCTATTTCTCCCGTGATTCCAGGCATATGCACCCAACAGT
CCATTTCTGTTATTGCTTATCACTGCCAAAAGTTCCAAGAAATGATGAAGTCAGTCTCATTGGCAT
ACATCTACTTTTTTCAGAAGGAAACAAAGCAGAGAAAAAATCCGAGAGAAATTCATAGCTAGTAACC
ACTCTCACTTTTATTTTATTTCCATAACTGAAATTGCTGGACTTGAGAGCAATTTTCCCTTGCTCAA
CAGAATTAGGTGAGATCGGGAATCAATTTAATATATTTAGTGAGCATCTACAGTGTTCATGGGGCA
AAAAAATAGCAACTTACAATATTAATTTCTATAGGCAGCCCCCAAATTTGAATCATTTCCTGAAAAATT
ACTTCTGCTTTTGTGAAGTTTCTGCTAGCAGTTTAGAGATTGGGCTGTTTCTCCTCACTGATACATAT
CTTCACACTTCTATAATTTAACTCTCTCAACTGCAITGTGAAAGATCTTAGCTGAAGATG
    
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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	A*02	B*07	B*08
		VTEHDTLLY ² (pp50) ³	NLVPMVATV (pp65)	TPRVTGGGAM (pp65)	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	+			+

¹W=white

²HLA Class I dextramer and cognate peptide

³CMV antigen

Supp. Table II.

List of Primers used for ChIP Assay

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