Supplemental Figure 1, Related to Figure 1

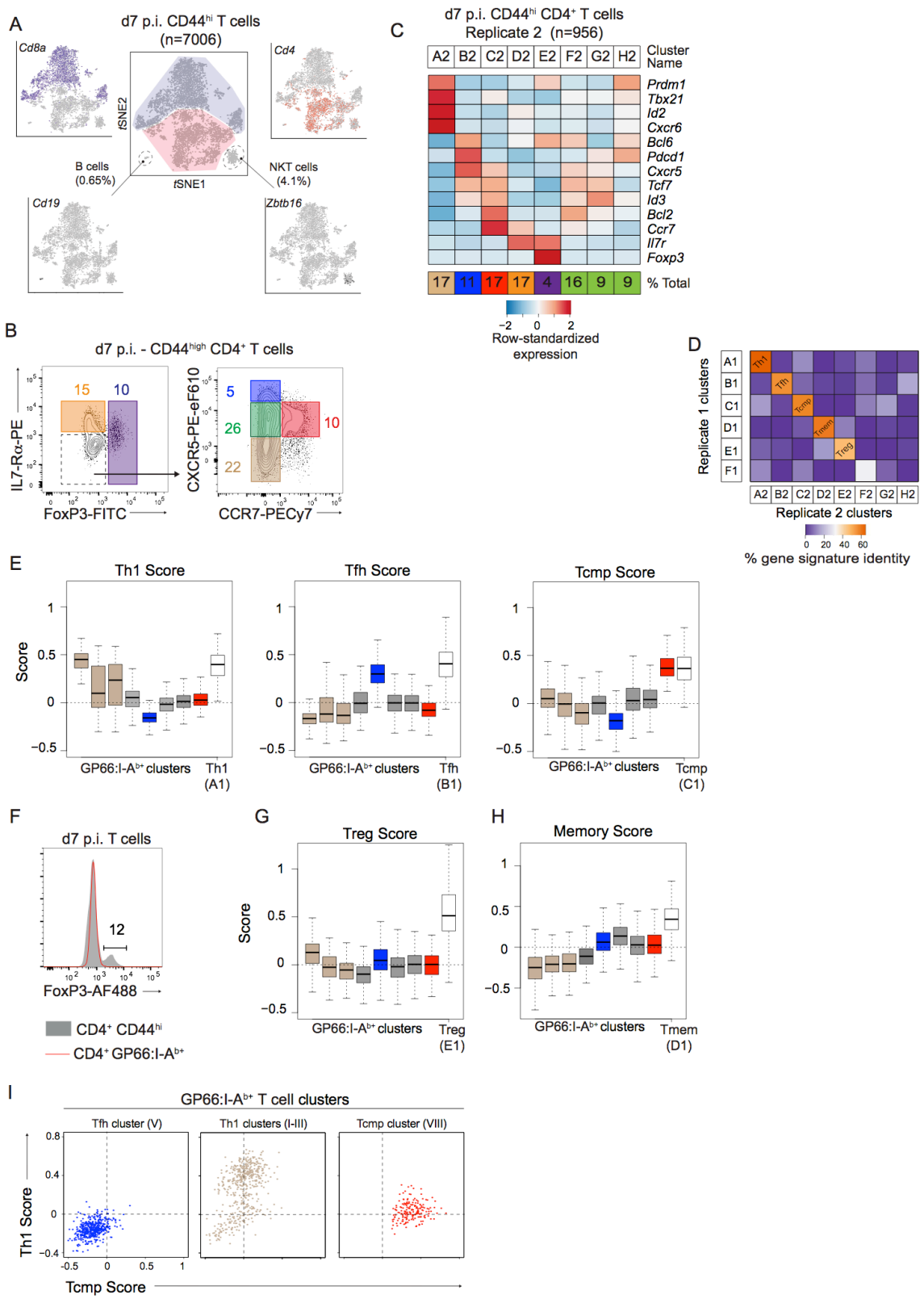

Figure S1: Identification and validation of CD4⁺ signatures by scRNAseq.

(**A**) CD44^{hi} spleen T cells from WT mice at d7 p.i. with LCMV Arm were analyzed by scRNAseq. Plot displays single CD44^{hi} T cells from experimental replicate 1, visualized with the t-SNE algorithm. Blue and red areas highlight the *Cd8a* and *Cd4* expressing cells respectively. Circles show B cells and iNK T cells, expressing *Cd19* and *Zbtb16* (encoding PLZF), respectively.

(**B**) Plots show the expression of CCR7 and CXCR5 on Foxp3^{-} IL-7Rα^{lo} spleen CD44^{hi} CD4^{+} T cells at d7 p.i. with LCMV Arm. Gates are colored according the code used for cell clusters defined in Fig. 1B, and numbers show the percentage of each subsets relative to the total population.
(**C**) Second replicate scRNAseq analysis of spleen WT CD44^{hi} T cells at d7 p.i. with LCMV Arm. Heatmap shows the relative expression of selected genes on the 8 unsupervised CD4^{+} clusters.
(**D**) Correlation matrix shows the percentages of identical genes between the gene signatures among the clusters of CD4^{+} T cells detected in Replicate 1 (Clusters A1 to F1, as shown in Fig. 1B, C) and in Replicate 2 (Clusters A2 to H2, Fig. S1C).
(**E, G, H**) Cells clusters from d7 p.i. GP66:I-A^{b+} WT spleen T cells (defined in Fig. 1F, G) are scored for the cell signatures. Boxplots show the centered distribution of cell scores for each cell signature. Clusters with high scores for Th1- (Clusters I-III), Tfh- (Cluster V) and Tcmp- (Cluster VIII) cell signatures are colored in brown, blue and red respectively. As a reference, the rightmost white box in each plot indicates the score of cells from the corresponding, cell signature-defining cluster in Replicate 1 (Cluster A1-E1, Fig. 1B, C).
(**F**) Plot shows Foxp3 expression on spleen CD4^{+} CD44^{hi} and CD4^{+} GP66:I-A^{b+} T cells from WT mice at d7 p.i. with LCMV Arm. The percentage of Foxp3^{+} among CD4^{+} CD44^{hi} T cells is shown.
(**I**) Dot plots show centered scores for Tcmp (x-axis) vs. Th1 (y-axis) signatures on cells from Cluster V (Tfh), Clusters I-III (Th1) and Cluster VIII (Tcmp) defined in Fig. 1F, G. Each dot represents a cell.

Supplemental Figure 2, Related to Figures 2 and 3

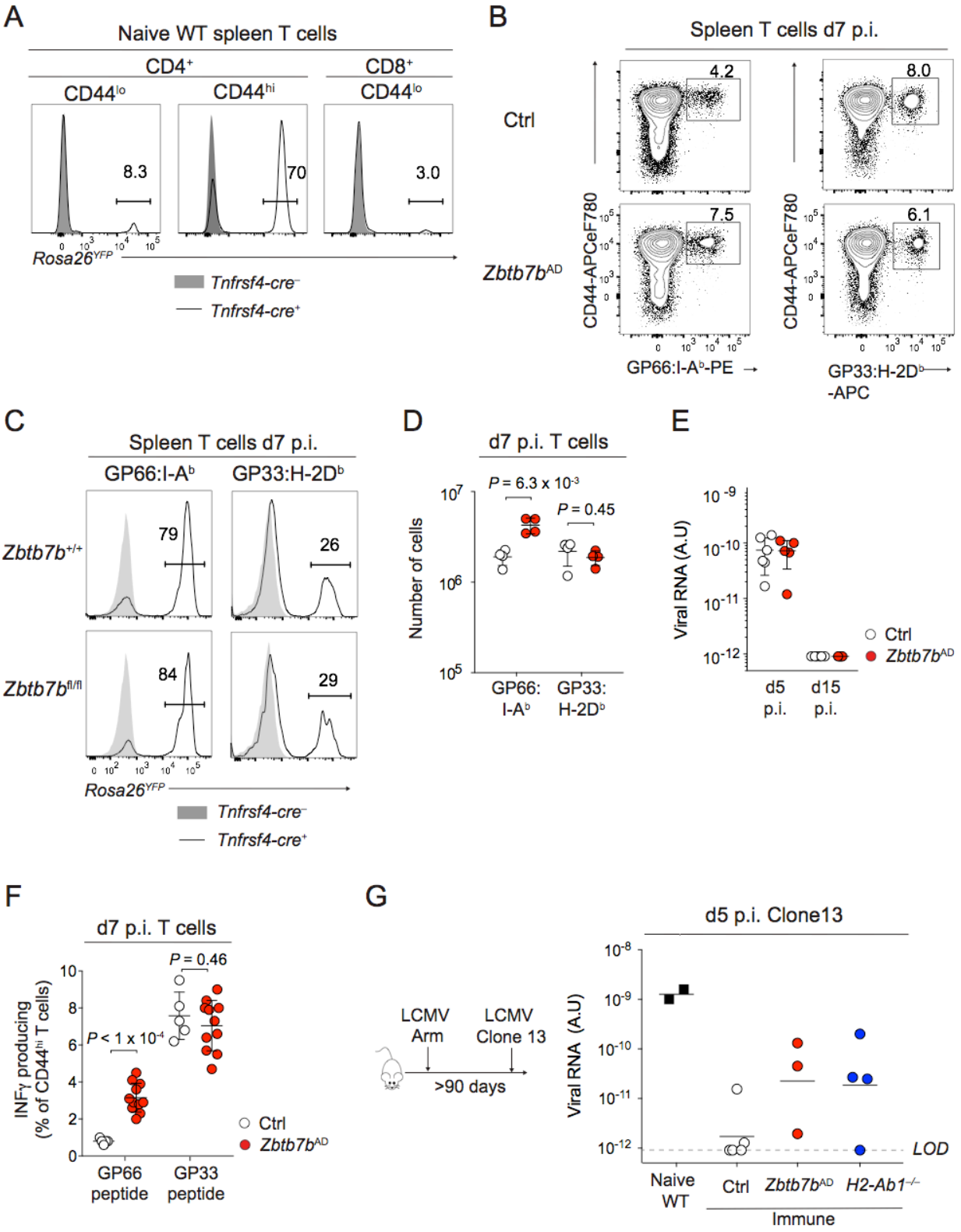

Figure S2: Post-activation disruption of *Zbtb7b* in LCMV-infected *Zbtb7b*^{AD} mice.

(**A**) Plots show Cre activity as reported by *Rosa26*^{YFP} expression on the indicated spleen T cell populations from *Tnfrsf4-cre*$^{+}$ (black line) or *Tnfrsf4-cre*$^{-}$ (grey histogram) uninfected animals. Data are representative of two independent experiments.
(**B**) Plots show GP66:I-A^{b} and GP33:H-2D^{b} staining at d7 p.i. with LCMV Arm on total spleen T cells from the indicated mice.

(**C**) Cre activity as reported by YFP expression was measured on spleen GP66:I-A^{b+} and GP33:H-2D^{b+} T cells from *Tnfrsf4-cre*$^{-}$ *Rosa26*^{YFP} (grey histogram) or *Tnfrsf4-cre*$^{+}$ *Rosa26*^{YFP} (black line) mice of the indicated genotype at d7 p.i.
(**D**) Graph shows the numbers of spleen GP66:I-A^{b+} and GP33:H-2D^{b+} T cells in *Zbtb7b*^{AD} (n=4) and control (n=5) mice analyzed as in (B). P-values from unpaired two-sided Welch's *t*-test are indicated. Data (B-D) are representative of two independent experiments.
(**E**) Serum virus titer at d5 and d15 p.i. of *Zbtb7b*^{AD} (n=5) and control (n=6) mice with LCMV Arm. Data are representative of two independent experiments.
(**F**) Percentage of IFNγ^{+} cells among *Zbtb7b*^{AD} (n=11) and control (n=5) CD44^{hi} spleen T cells after GP66 (MHC-II restricted) and GP33 (MHC-I restricted) peptide stimulation. P-values from unpaired two-sided Welch's *t*-test are indicated. Data are representative of two independent experiments.
(**G**) *Zbtb7b*^{AD}, *H2-Ab1*$^{-/-}$ (MHC-II-deficient) or control mice were infected with LCMV Arm and re-challenged with LCMV Clone 13 more than 90 days later. Graph shows serum virus titers in animals of the indicated genotype (red, blue and empty circles) 5 days after Clone 13 infection; black squares show titers in naive WT mice as controls. Dashed line shows the limit of detection (LOD) of the assay. Data are representative of two independent experiments.

Supplemental Figure 3, Related to Figure 4

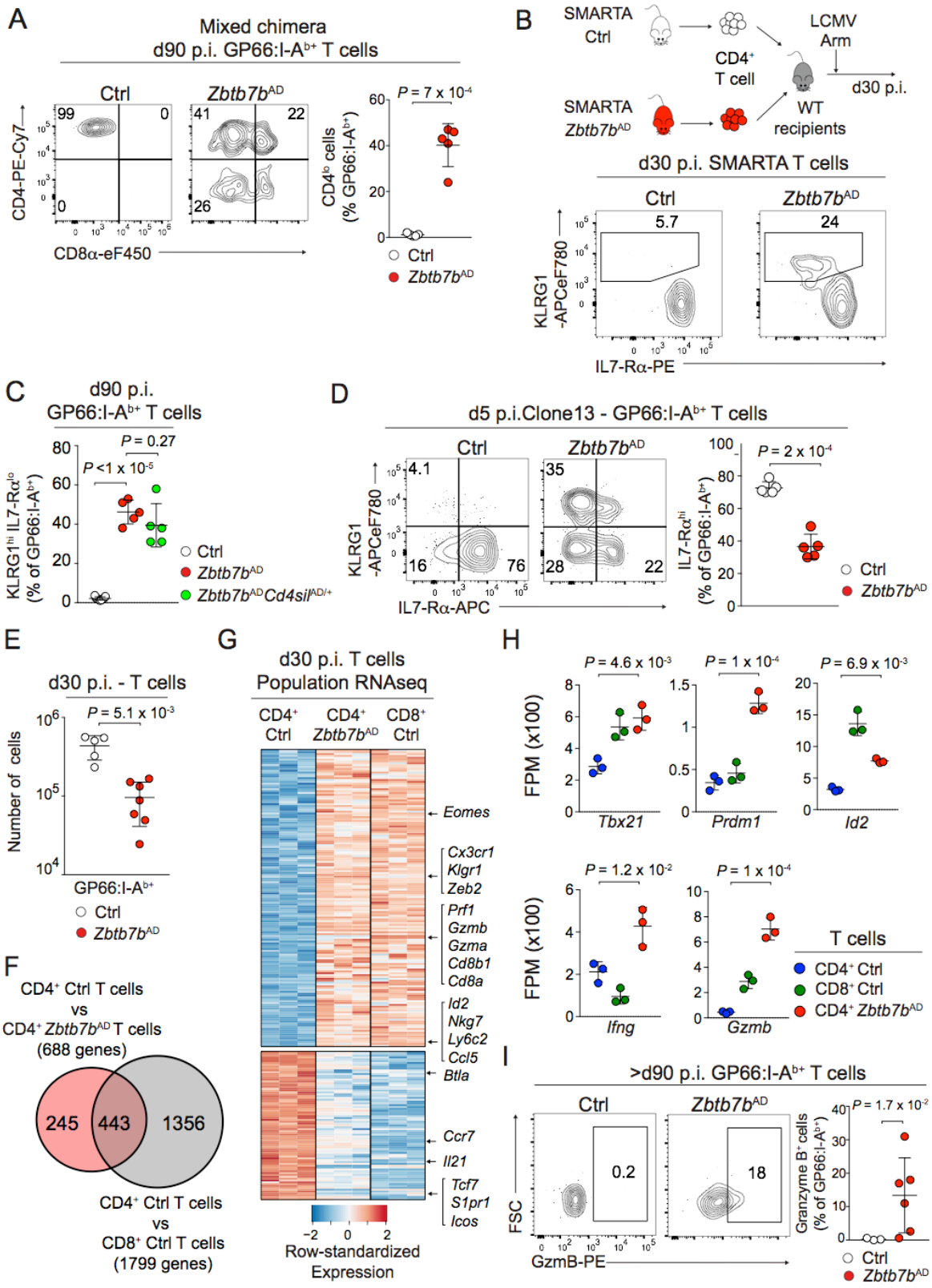

Figure S3: Phenotype and gene expression of Thpok-deficient memory CD4$^+$ T cells.

(**A**) *Zbtb7b*^{AD}:WT or Ctrl:WT mixed bone marrow chimeras were infected with LCMV Arm and analyzed at d90 p.i. Left panels show the expression of CD4 and CD8α on GP66:I-A^{b+} spleen T cells of the indicated genotype. Numbers indicate the percentage of cells in the box. Right panel shows the percentage of CD4^{lo} cells within the GP66:I-A^{b+} T cell population for each genotype (n=5 per group). P-values from unpaired two-sided Welch's *t*-test are indicated.

(**B**) Naive *Zbtb7b*^{AD} and control SMARTA TCR transgenic cells were adoptively transferred into CD45 congenic WT recipients one day before LCMV Arm infection. Flow cytometry plots show IL-7Rα and KLRG1 expression on adoptively transferred cells of the indicated genotype isolated from the spleen at d30 p.i. The percentages of cells in the indicated gates are shown.
(**C**) Percentage of KLRG1^{hi} IL-7Rα^{lo} cells within the GP66:I-A^{b+} T cell population in *Zbtb7b*^{AD} (n=5), *Zbtb7b*^{AD} *Cd4sil* ^{AD} (n=5) and control (n=9) mice analyzed at d90 p.i. with LCMV Arm. P-values from unpaired two-sided Welch's *t*-test are indicated. Data are from one experiment representative of two independent experiments.
(**D**) *Zbtb7b*^{AD} or control mice were infected with LCMV Arm and re-challenged more than 90 d p.i. with LCMV Clone 13. Left panels show the expression of KLRG1 and IL-7Rα on GP66:I-A^{b+} spleen T cells of the indicated genotype. Numbers indicate the percentage of cells in the box. Right panel shows the percentage of IL-7Rα^{hi} cells among GP66:I-A^{b+} T cells of each genotype (n=5 per group). P-value from unpaired two-sided Welch's *t*-test is indicated. Data are representative of two independent experiments.
(**E**) Numbers of spleen GP66:I-A^{b+} T cells in *Zbtb7b*^{AD} (n=7) and control (n=5) mice 30 d p.i. with LCMV Arm. P-value from unpaired two-sided Welch's *t*-test is indicated. Data are representative of two independent experiments.
(**F-H**) RNAseq analyses of gene expression at d30 p.i. with LCMV Arm was performed on sorted populations of GP66:I-A^{b+} spleen T cells from *Zbtb7b*^{AD} (CD4 *Zbtb7b*^{AD}) or control (CD4 Ctrl) mice, and of GP33:H-2D^{b+} spleen T cells from WT animals (CD8 Ctrl).
(F) Venn diagrams of the numbers of overlapping genes differentially expressed between CD4 *Zbtb7b*^{AD} vs CD4 Ctrl T cells and CD4 Ctrl vs CD8 Ctrl (adjusted p-value <0.01, log2 fold change > 1).
(**G**) Genes differently expressed between CD4 *Zbtb7b*^{AD} and CD4 Ctrl and also differently expressed between CD4 Ctrl and CD8 Ctrl as shown in (F).
(**H**) Graphs show RNAseq-determined expression (fragments per million, FPM) of selected genes in all three populations; P-values are from one-way ANOVA. Each symbol represents a biological replicate.
(**I**) Left panels show Granzyme B expression on GP66:I-A^{b+} spleen T cells of the indicated genotype. Right panel shows the percentage of Granzyme B expressing cells from *Zbtb7b*^{AD} (n=6) and control mice (n=3) more than 90 days p.i. LCMV Arm. P-value is from unpaired two-sided Welch's *t*-test. Data are representative of two independent experiments.

Supplemental Figure 4, Related to Figure 4

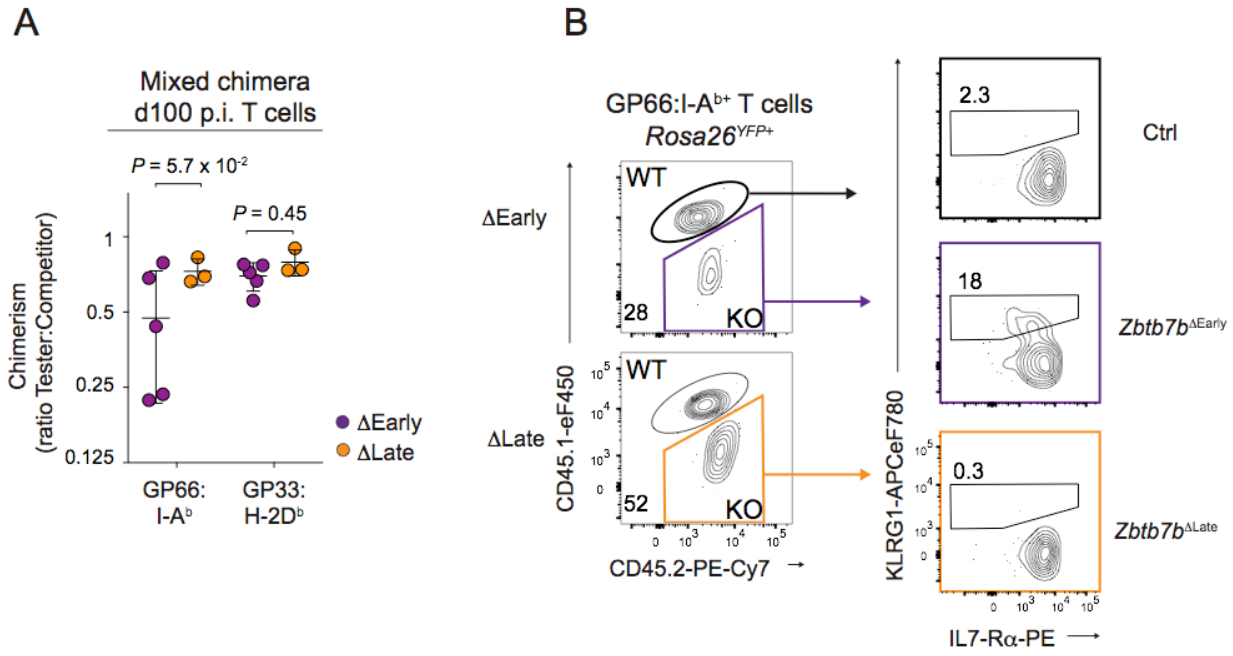

Figure S4: Early requirement for Thpok in the differentiation of memory CD4⁺ T cells.

Mixed bone marrow chimeras (*Cd4-creER*$^{T2+}$ *Zbtb7b*$^{fl/fl}$ tester: *Cd4-creER*$^{T2+}$ *Zbtb7b*$^{+/+}$ competitor) were infected with LCMV Arm after (ΔEarly) or 3 weeks before (ΔLate) tamoxifen treatment.
(**A**) Graph shows tester-competitor chimerism among spleen GP66:I-A^{b+} *Rosa26*$^{YFP+}$ and GP33:H-2D^{b+} T cells at d100 p.i. (ΔEarly, n=5; ΔLate, n=3). P-values from two-way ANOVA are indicated.
(**B**) Right panels show the expression of IL-7Rα and KLRG1 on the GP66:I-A^{b+} cell populations defined in the left panels. The percentages of cells in the indicated gates are shown. Data are representative of 2 independent mixed bone marrow experiments and 3 non-chimeric experiments.

Supplemental Figure 5, Related to Figure 5

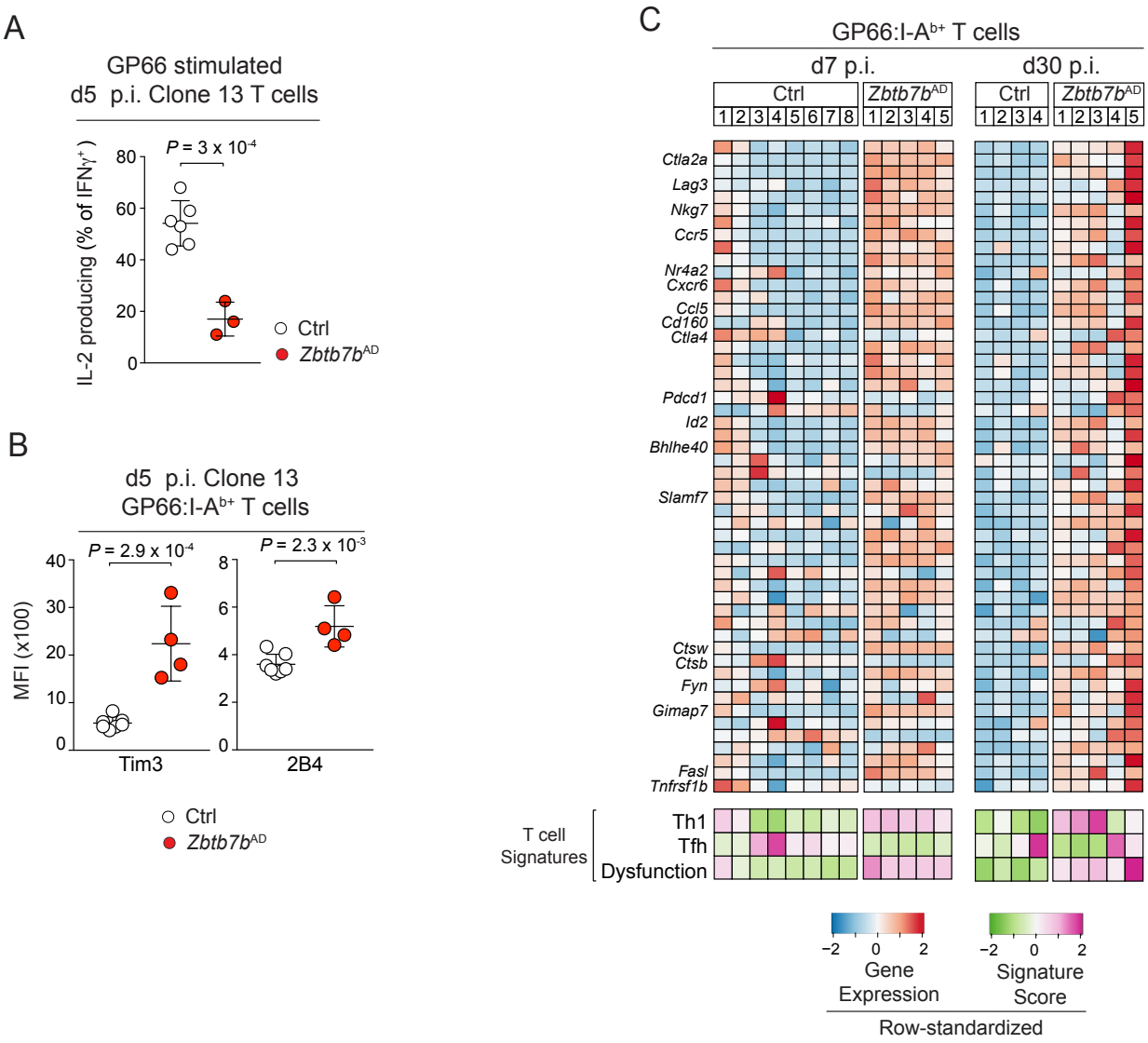

Figure S5: Thpok represses a dysfunctional program in CD4⁺ T cells.

(**A, B**) *Zbtb7b*^{AD} or control mice were infected with LCMV Arm and re-challenged more than 90 p.i. with LCMV Clone 13. (**A**) Graph shows the percentage of IL-2 producing among IFNγ-producing *Zbtb7b*^{AD} (n=3) or *Ctrl* (n=6) spleen T cells after GP66 peptide stimulation at d5 post-rechallenge.
(**B**) Graph shows Tim3 and 2B4 surface expression (mean fluorescence intensities, MFI) on spleen GP66:I-A^{b+} T cells of the indicated genotype 5 days after re-challenge. (A, B) P-values from unpaired two-sided Welch's *t*-test are indicated. Data are representative of two independent experiments.
(**C**) The "Dysfunction signature" was defined on Cluster d30 *Zbtb7b*^{AD}5 (Fig. 5C) compared to all other d30 clusters. Heatmap shows signature scores and relative expression of dysfunction signature genes across clusters of d7 and d30 cells (as defined respectively in Fig. 2A, B and Fig. 5B, C).

Supplemental Figure 6, Related to Figure 6

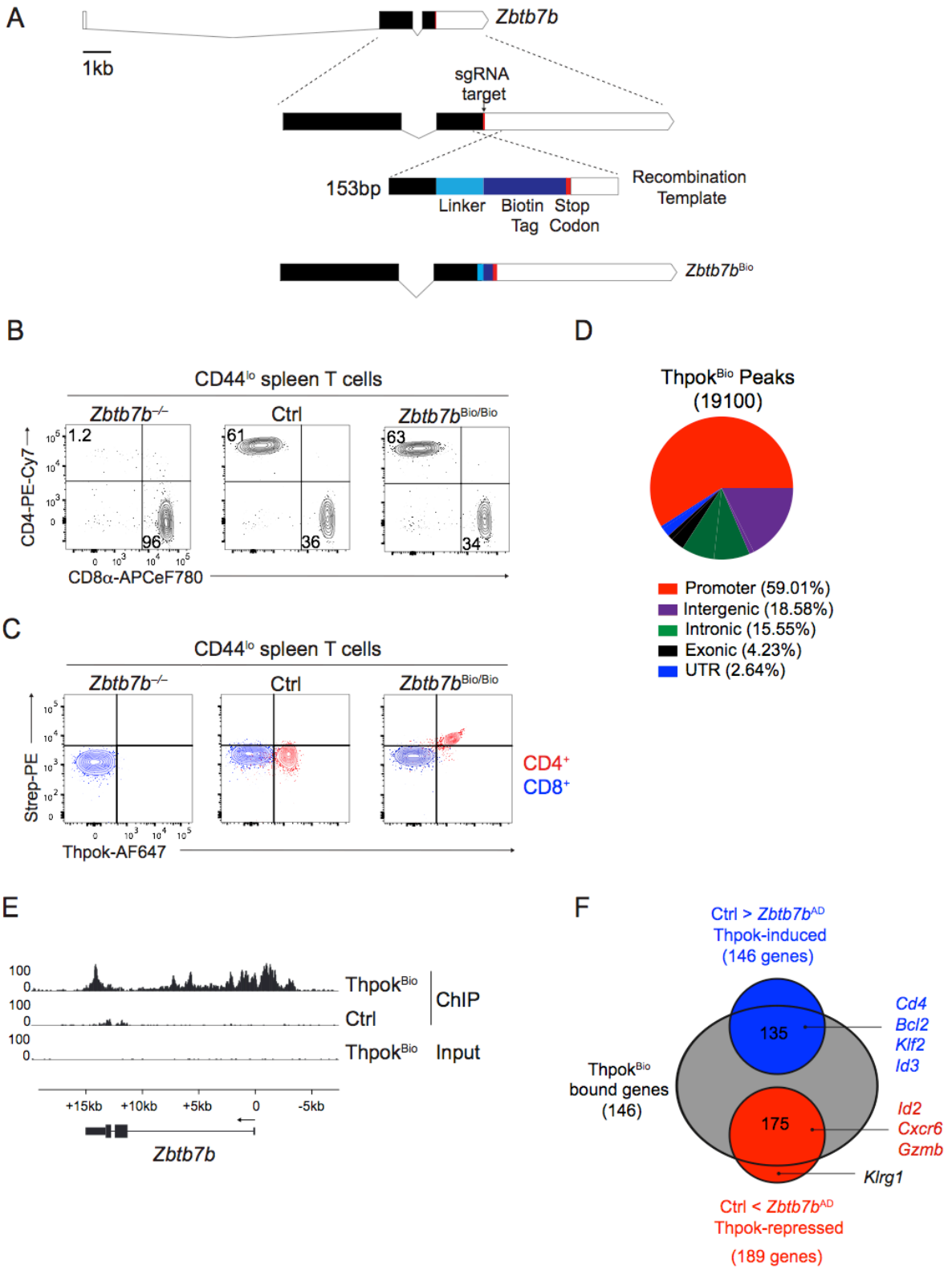

Figure S6: Generation and characterization of *Zbtb7b*^{Bio} mice.

(**A**) Schematic representation of the generation of the *Zbtb7b*^{Bio} allele.
(**B, C**) *Zbtb7b*^{Bio} animals were crossed with *Rosa26*^{BirA} mice and *Zbtb7b*$^{Bio/Bio}$ *Rosa26*^{BirA} (*Zbtb7b*$^{Bio/Bio}$), *Zbtb7b*$^{-/-}$ and *Zbtb7b*$^{+/+}$ *Rosa26*^{BirA} (Ctrl) animals were analyzed. (**B**) Expression of CD4 and CD8α in the spleen T cell population from the indicated animals. The percentages of cells in the indicated gates are

shown. (**C**) Intra-cellular Thpok and biotinylated Thpok were assessed on spleen T cells by anti-Thpok antibody (x axis) and streptavidin (y-axis). Data are representative of two independent experiments.
(**D-F**) Thpok DNA binding was assessed by ChIP-seq in activated $CD4^+$ T cells from $Thpok^{Bio/+}$ *Rosa26*$^{BirA+}$ ($Thpok^{Bio}$) or *Rosa26*$^{BirA+}$ (Ctrl) animals. (**D**) Pie chart shows the genome-wide distribution of Thpok binding. (**E**) IGV browser tracks show binding by $Thpok^{Bio}$ molecules on the *Zbtb7b* locus ($Thpok^{Bio}$ ChIP), compared to background signals from streptavidin pull-down on Ctrl cells (Ctrl ChIP), and input DNA signal from $Thpok^{Bio}$ cells. (**F**) Gene occupancy by Thpok molecules was compared to Thpok-dependent genes defined on d7 p.i. GP66:I-A^{b+} T cells by scRNAseq.

Supplemental Figure 7, Related to Figure 7

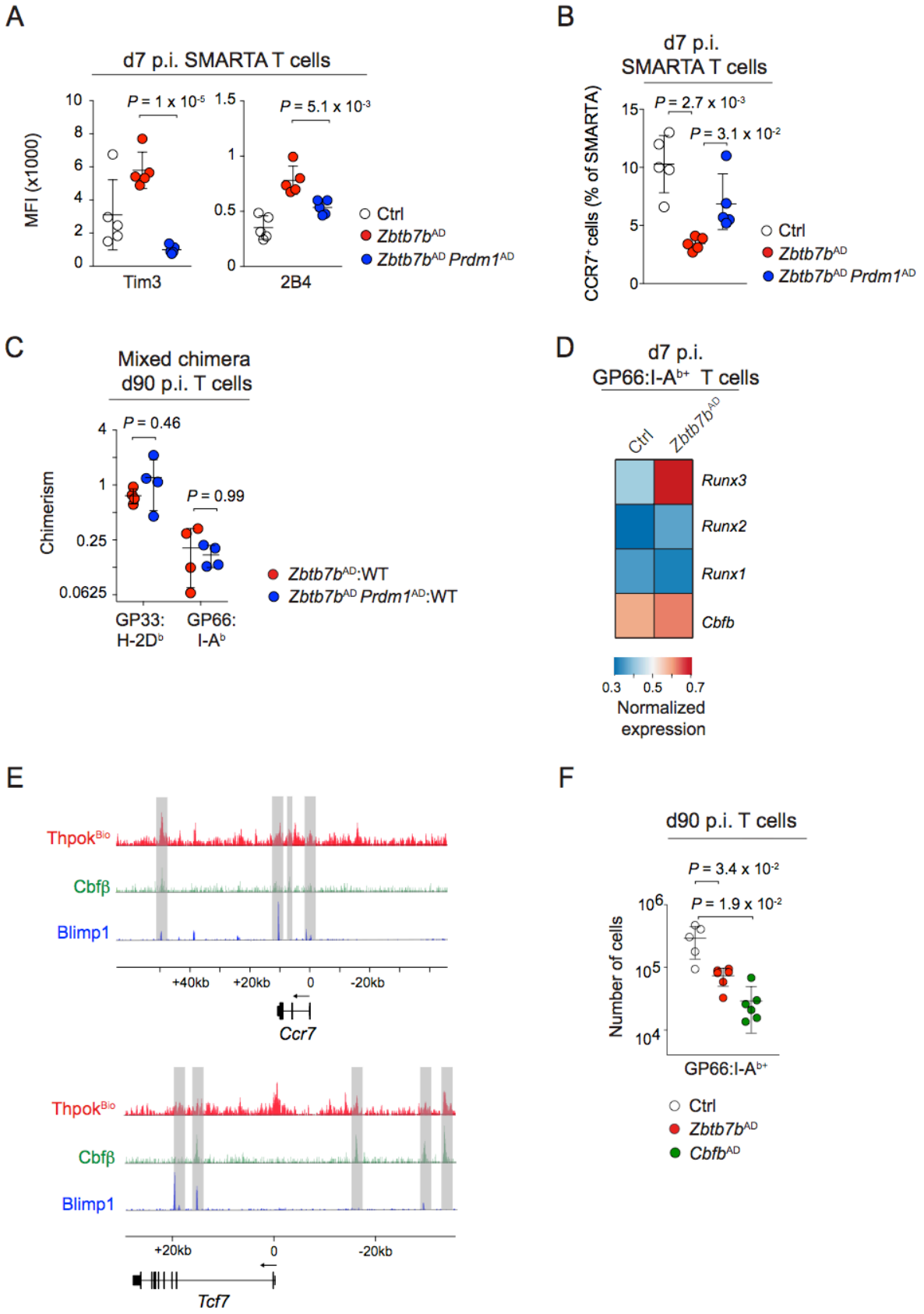

Figure S7: Thpok repression of Blimp1 and Runx3 and memory CD4⁺ T cell differentiation.

(**A, B**) Naive *Zbtb7b*^{AD} , *Zbtb7b*^{AD} *Prdm1*^{AD} or control SMARTA cells were adoptively transferred into WT recipients a day before LCMV Arm infection. Graphs show (**A**) Graphs show Tim3 and 2B4 surface

expression and (**B**) percentage of CCR7 positive cells on the adoptively transferred SMARTA cells of the indicated genotype at d7 p.i. (per group n=5). P-values from unpaired two-sided Welch's *t*-test are indicated. Data are representative of one adoptive transfer experiment and 2 independent experiments on *Zbtb7b*^{AD} or *Zbtb7b*^{AD} *Prdm1*^{AD} and control animals.

(**C**) *Zbtb7b*^{AD}:WT and *Zbtb7b*^{AD} *Prdm1*^{AD}: WT mixed bone marrow chimeras were analyzed at d90 p.i with LCMV Arm. Graph shows Tester:Competitor ratios among spleen GP33:H-2D^{b+} and GP66:I-A^{b+} T cells in *Zbtb7b*^{AD}:WT (red) and *Zbtb7b*^{AD} *Prdm1*^{AD}:WT (empty circles) chimeras (n=4 per group). Data are representative of one mixed bone marrow experiment and 3 non-chimeric experiments *Zbtb7b*^{AD}, *Zbtb7b*^{AD} *Prdm1*^{AD} and control animals.

(**D**) Heatmap shows the expression of Runx-related genes on GP66:I-A^{b+} T cells measured by scRNAseq at d7 p.i. with LCMV Arm.

(**E**) IGV browser tracks show ChIP-seq binding of Thpok, Cbfβ and Blimp1 on the *Ccr7* and *Tcf7* loci. Grey shading highlights detected Thpok peaks overlapping with detected CBFβ or Blimp1 peaks

(**F**) *Zbtb7b*^{AD}, *Cbfb*^{AD} or control mice were infected with LCMV Arm. Graph shows the number of spleen GP66:I-A^{b+} cells in *Zbtb7b*^{AD} (n=6), *Cbfb*^{AD} (n=6) and control (n=5) animals at d90 p.i. P-values from unpaired two-sided Welch's *t*-test are indicated. Data are representative of 2 independent experiments.

Supplemental Table 1, Related to Figures 1, 2 and 5

Cell designation	Capture Session Number	Figure Panel	Timepoint	Cell Type	Genotype	Number of cell capture	Number of cells after filtering	Median Number UMI per cell	Median Number genes per cell
d7 Replicate 1	**1**	Fig. 1B-D Fig. S1A, D, E	d7 p.i.	$CD44^+$ T cells	WT	7911	7006	3982	1446
d7 Replicate 2	**2**	Fig. 1D Fig. S1C-E	d7 p.i.	$CD44^+$ T cells	WT	2416	2185	5039	1808
d7 GP66:I-A^{b+} Ctrl	**2**	Fig. 2A, B Fig. S5C	d7 p.i.	GP66:I-A^{b+} *Rosa26*$^{YFP+}$ T cells	*Tfnrsf4-cre*$^+$ *Zbtb7b*$^{+/+}$	2459	2154	5277	1758
d7 GP66:I-A^{b+} *Zbtb7b*^{AD}	**2**	Fig. 2A, B Fig. S5C	d7 p.i.	GP66:I-A^{b+} *Rosa26*$^{YFP+}$ T cells	*Tfnrsf4-cre*$^+$ *Zbtb7b*$^{fl/fl}$	1414	1330	5889	1984
d30 GP66:I-A^{b+} Ctrl	**2**	Fig. 5B, C Fig. S5C	d30 p.i.	GP66:I-A^{b+} *Rosa26*$^{YFP+}$ T cells	*Tfnrsf4-cre*$^+$ *Zbtb7b*$^{+/+}$	1355	723	2017	832
d30 GP66:I-A^{b+} *Zbtb7b*^{AD}	**2**	Fig. 5B, C Fig. S5C	d30 p.i.	GP66:I-A^{b+} *Rosa26*$^{YFP+}$ T cells	*Tfnrsf4-cre*$^+$ *Zbtb7b*$^{fl/fl}$	827	703	2385	1030
d7 GP66:I-A^{b+} WT	**3**	Fig. 1E-G Fig S1E-I	d7 p.i.	GP66:I-A^{b+} T cells	WT	2717	2213	5620	1936

Table S1: scRNAseq captures and metrics

Supplemental Table 2, Related to Figure 1

Signature:	Th1	Th1 (continued)	Tfh	Tcmp	Tmem	Treg	Dysfuntion
	4930453N24Rik	*Il18rap*	*2310001H17Rik*	*1810058I24Rik*	*Btg1*	*Bmyc*	*2010111I01Rik*
	Abracl	*Il2rb*	*Aldoa*	*Ablim1*	*Ccnd2*	*Btg1*	*Arl6ip1*
	Acot7	*Itga4*	*Angptl2*	*Acot7*	*Eif4a2*	*Capg*	*AW112010*
	Actb	*Itgb2*	*Asap1*	*Acp5*	*Gm10073*	*Ccnd2*	*Bhlhe40*
	Actg1	*Itgb7*	*Batf*	*Actn1*	*Il7r*	*Cd2*	*Ccl3*
	Actr3	*Klrc1*	*BC021614*	*Adgre5*	*Malat1*	*Cd74*	*Ccl4*
	Adgre5	*Krtcap2*	*Bcl2a1b*	*Adk*	*Rabac1*	*Ctla4*	*Ccl5*
	Agpat4	*Lfng*	*Borcs8*	*Ahnak*	*Rpl12*	*Foxp3*	*Ccr5*
	Ahnak	*Lgals1*	*Cd160*	*Anp32a*	*Rpl13*	*Gbp7*	*Cd160*
	Anxa1	*Lgals3*	*Cd200*	*Anxa2*	*Rpl13-ps3*	*Gimap7*	*Cd27*
	Anxa2	*Lsp1*	*Cd3g*	*Arl5c*	*Rpl18a*	*Gpx4*	*Cd3g*
	Anxa5	*Ly6c2*	*Cd82*	*Atp1b3*	*Rpl36*	*H2-T22*	*Cd7*
	Anxa6	*Mrpl33*	*Cox14*	*Atp2b1*	*Rpl36a*	*Ifngr1*	*Cst7*
	Ap2s1	*Ms4a4b*	*Ctsb*	*Bcl2*	*Rpl37a*	*Ikzf2*	*Ctla2a*
	Aprt	*Ms4a6b*	*Cxcr5*	*Bin2*	*Rpl38*	*Il7r*	*Ctla4*
	Arhgdib	*Mtpn*	*Ddit4*	*Ccdc28b*	*Rpl9*	*Izumo1r*	*Ctsb*
	Arl6ip5	*Myl12a*	*Dennd2d*	*Ccr7*	*Rpl9-ps6*	*Ltb*	*Ctsw*
	Arpc5	*Myl6*	*Eea1*	*Cd9*	*Rplp1*	*Mbnl1*	*Cxcr6*
	Atp1a1	*Myo1f*	*Fam162a*	*Cdc25b*	*Rplp2*	*Peli1*	*Cyba*
	Atp5c1	*Myo1g*	*Fyn*	*Cdc42se1*	*Rps14*	*Rgs1*	*Dnaja1*
	Atp5h	*Ndufb7*	*Gapdh*	*Cdkn2d*	*Rps15*	*Samsn1*	*Efhd2*
	Atp5l	*Nkg7*	*Gdi2*	*Crip1*	*Rps15a*	*Sdf4*	*Fasl*
	AW112010	*Nptn*	*Gimap5*	*Crip2*	*Rps16*	*Sell*	*Fyn*
	Bhlhe40	*Ostf1*	*Gna13*	*Dock2*	*Rps19*	*Serinc3*	*Gadd45b*
	Calm1	*Pglyrp1*	*Gng2*	*Emb*	*Rps21*	*Shisa5*	*Gimap7*
	Capzb	*Plac8*	*Hif1a*	*Ezr*	*Rps23*	*Tnfrsf18*	*Gpr65*
	Ccl5	*Plek*	*Hmgb1*	*Fam177a*	*Rps24*	*Tnfrsf4*	*Gzmk*
	Ccr2	*Podnl1*	*Icos*	*Fam65b*	*Rps27*		*H2-K1*
	Cd2	*Ppib*	*Ifi27l2a*	*Glud1*	*Rps27rt*		*Hspa1a*
	Cd47	*Ppp1ca*	*Isg15*	*Hint1*	*Rps28*		*Hspa8*
	Cd48	*Ppp3ca*	*Izumo1r*	*Id3*	*Rps29*		*Hsph1*
	Cd52	*Prelid1*	*Limd2*	*Il6ra*	*Rps5*		*Id2*
	Cdc42	*Psmb3*	*Lpp*	*Iqgap1*	*Rps9*		*Lag3*
	Cdc42ep3	*Pycard*	*Lrmp*	*Itgb1*			*Lilr4b*
	Cfl1	*Rap1b*	*Maf*	*Itpkb*			*Nkg7*
	Clic1	*Rasgrp2*	*Marcksl1*	*Jund*			*Nr4a2*
	Clta	*Rbm3*	*Matk*	*Klf2*			*Pdcd1*
	Coro1a	*Reep5*	*Mif*	*Klf3*			*Plac8*
	Cox17	*Rnf138*	*Mmd*	*Klf6*			*Psmb10*
	Cox5a	*Rnf166*	*Nsg2*	*mt-Co1*			*Psmb8*
	Cox5b	*Rora*	*Nt5e*	*Pbxip1*			*Rgs1*
	Crip1	*Rpa2*	*P2rx7*	*Pdlim1*			*Rnaset2b*
	Crot	*Runx3*	*Pdcd1*	*Prr13*			*Samsn1*
	Ctla2a	*S100a10*	*Pfkl*	*Psma6*			*Serpina3g*
	Ctsc	*S100a11*	*Pfkp*	*Raf1*			*Sh2d2a*
	Ctsd	*S100a13*	*Pgam1*	*Rasa3*			*Shisa5*
	Ctsw	*S100a4*	*Pkm*	*Rasgrp2*			*Slamf7*
	Cxcr6	*S100a6*	*Ppp1r14b*	*Rora*			*Sub1*
	Cyba	*S1pr4*	*Prkca*	*Rpa1*			*Tapbpl*
	Cyth4	*Sec61b*	*Ptp4a2*	*S100a10*			*Tnfrsf1b*
	Dnajc15	*Sec61g*	*Ptpn11*	*S100a11*			*Traf4*
	Dok2	*Selplg*	*Ptprcap*	*S100a4*			*Ubb*
	Ech1	*Sept11*	*Ptrh1*	*S100a6*			
	Emp3	*Serpinb6b*	*Rab37*	*Sfr1*			
	Eno1	*Serpinb9*	*Rgs10*	*Slamf6*			
	Epsti1	*Sh3bgrl3*	*Rnaset2a*	*Spn*			
	Esyt1	*Slamf1*	*Rnaset2b*	*Srpk1*			
	Fam107b	*Sms*	*Rpsa*	*Stk24*			
	Gabarapl2	*Spn*	*Scd2*	*Stk38*			
	Gapdh	*St3gal6*	*Sept7*	*Tagap*			
	Gbp7	*Stmn1*	*Sh2d1a*	*Tagln2*			
	Ggh	*Sub1*	*Smco4*	*Tcf7*			
	Gimap7	*Tagln2*	*Sostdc1*	*Tcp11l2*			
	Glipr2	*Taldo1*	*Tbc1d4*	*Tspan13*			
	Glrx	*Tbx21*	*Tnfaip8*	*Tuba1a*			
	Gm4950	*Tceb2*	*Tnfsf8*	*Vim*			
	Gmfg	*Thy1*	*Tox*	*Vsir*			
	Gna15	*Tmed2*	*Tox2*	*Xrn2*			
	Gramd3	*Tmsb4x*	*Tpi1*				
	Gzmb	*Tpm4*	*Trim8*				
	H2afy	*Tpst2*	*Zap70*				
	H2afz	*Tspo*	*Zfp36l1*				
	Hmgb2	*Txn1*					
	Hsp90b1	*Txndc5*					
	Id2	*Ube2g2*					
	Idh3a	*Vim*					
	Ifngr1	*Zyx*					
	Il18r1						

Table S2: T cell gene signatures