#### SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Adoptive transfer, detection and characterization of antigen-specific CD8<sup>+</sup> T cells. Peripheral blood leukocytes (PBLs) containing 500 WT or *Tcf7*<sup>-/-</sup> OT-I T cells  $(Thy 1.2^{+}CD45.2^{+})$  were adoptively transferred into B6.SJL recipient mice (Thy1.2<sup>+</sup>CD45.1<sup>+</sup>) alone, or in the presence of Thy1.1<sup>+</sup>CD45.2<sup>+</sup> WT OT-I reference T cells at 1:1 ratio. Twenty-four hours later, the recipient mice were infected with either attenuated LM-Ova or VacV-Ova as described previously (Badovinac and Harty, 2007). On various days post-infection, PBLs or splenocytes were isolated from the recipient mice, and donor-derived antigen-specific T cells were identified by surface staining of differential Thy1 and CD45 genetic markers. For additional phenotypic analysis, the cells were surface-stained for KLRG1 (clone 2F1), IL-7Rα (clone A7R34), CD62L (clone MEL-14, BD Biosciences), and IL-2R $\beta$  (clone TM- $\beta$ 1, BD Biosciences). CCR7 was stained indirectly with purified CCL19-Fc fusion protein followed by anti-human Fcy according to manufacturer's instructions (eBiosceince). For detection of IL-15 $\alpha$  chain, splenocytes were first blocked with rat serum, goat serum, and free streptavidin (1  $\mu$ g/ml), and stained with biotinylated IL-15R $\alpha$  (R&D Systems) or control goat IgG, followed by incubation with fluorochrome-conjugated streptavidin (McGill et al. 2010). For functional characterization of antigen-specific CD8<sup>+</sup> T cells, splenocytes were stimulated with 200 nM of Ova<sub>257-264</sub> peptide (SIINFEKL) for 5-6 hrs in the presence of GolgiStop and GlogiPlug (BD Biosciences). The stimulated cells were then surfaced stained, fixed and permeabilized using BD Cytofix/Cytoperm and BD Perm/Wash solutions (BD Biosciences), and intracellularly stained for IFN- $\gamma$  (clone XMG1.2), IL-2

(clone JES6-5H4), TNF-α (clone TN3-19), and Granzyme B (clone GB11, Invitrogen) following standard protocols (Haring et al., 2008). Bcl-2 was detected by intracellular staining with Bcl-2 PE set (clone 3F11, BD Biosciences). For intranuclear staining of transcription factors, surface-stained cells were fixed and permeabilized using Foxp3 staining buffer set (eBioscience), and stained with either PE-conjugated T-bet (clone 4B10, Santa Cruz Biotechnology) or Eomes antibody (clone Dan11mag, eBioscience). All fluorochrome-conjugated antibodies were from eBioscience unless indicated otherwise. The stained cells were analyzed on a FACSCalibur flow cytometer followed by data analysis using FlowJo software (Tree Star, Inc)(Jing et al., 2008).

# Detection of BrdU uptake and activated Caspase-3 and -7 in antigen-specific CD8<sup>+</sup> T cells

To determine the proliferation rate of antigen-specific T cells at early contraction phase, the mice were *i.p.* injected with 1 mg of 5-bromo-2-deoxyuridine (BrdU) on day 7 postinfection with *actA*<sup>-</sup>LM-OVA and given 0.8 mg/ml BrdU in drinking water for additional 18 hours. Splenocytes were isolated, surface-stained to identify donor-derived OT-I cells, followed by fixation and permeabilization procedures as recommended in the BrdU Flow Kit (BD Biosciences). For detection of activated caspase-3 and -7 in antigen-specific T cells, splenocytes were surface-stained as above and then incubated with the fluorescent inhibitor of caspases reagent at 37°C for 60 min as recommended in the Vybrant FAM Caspase-3 and -7 assay kit (Invitrogen).

# *In vitro* proliferation of memory CD8<sup>+</sup> T cells in response to IL-15

Splenocytes were isolated from B6.SJL recipients of WT or  $Tcf7^{-/-}$  OT-I T cells on day 90 after LM-Ova infection. The cells were labeled with 2.5  $\mu$ M CFSE as described (Jabbari and Harty, 2006), and 1×10<sup>6</sup> cells were cultured in 12-well plate in the presence or absence of 50 ng/ml (Peptrotech). IL-15 was refreshed at the end of 3-day culture. CFSE dilution on CD8<sup>+</sup>CD45.2<sup>+</sup> memory T cells was tracked daily during days 2-5 of culture. The total splenocytes were used to facilitate transpresentation of IL-15 to T cells (Dubois et al., 2002).

#### *In vivo* cytolytic assay

Splenocytes from C57BL/6 mice (CD45.2<sup>+</sup>) were labeled with 0.2  $\mu$ M or 2  $\mu$ M CFSE. The CFSE<sup>low</sup> cells were pulsed with 1  $\mu$ M OVA<sub>257-264</sub> peptide, mixed with unpulsed CFSE<sup>high</sup> cells at 1:1 ratio, and a total number of 8 × 10<sup>6</sup> mixed cells were injected into immune or naïve B6.SJL (CD45.1<sup>+</sup>) mice with the naïve mice as no-killing controls (Barber et al., 2003; Pham et al., 2009). Four hours later, spleens were harvested, and killing target cells were identified by CD45.2 positivity, within which the percentages of CFSE<sup>low</sup> and CFSE<sup>high</sup> cells were determined by flow cytometry. The specific killing was calculated using the following formula:

$$\left(1 - \frac{\frac{\text{Percent of CFSE}^{\text{low in immune mice}}}{\text{Percent of CFSE}^{\text{high in immune mice}}}\right) \times 100\%$$

# Detection of memory CD8<sup>+</sup> T cells in tissues

Isolation of lymphocytes from the livers and lungs was performed essentially as described (Masopust et al., 2001). Mice were first anesthetized, perfused with Hanks' balanced salt solution (HBSS), and then lungs and livers were removed. Lung tissue was minced and treated with Collagenase D (125 units/ml, Roche Applied Science) and DNase I (6 units/ml, Roche Applied Science). Liver tissue was mashed through a 70-µm strainer in HBSS and subjected to gradient centrifugation using Percoll. Cells at the gradient interface were harvested, washed, and surface-staining for CD8, CD45, and Thy1 markers to identify donor-derived memory CD8<sup>+</sup> T cells. Lymph nodes and bone marrow cells were harvested as previously described (Xue et al., 2007) and stained similarly.

#### **Retroviral transduction**

Bicistronic retroviral vector MigR1 and that expressing WT Eomes were obtained from Dr. Steven Reiner (Intlekofer et al., 2007). Retroviruses were packaged by transient transfection of 293T cells with the retroviral vector along with pCL<sup>eco</sup> as described (Xue et al., 2002). Retroviral transduction of antigen-specific CD8<sup>+</sup> T cells was performed following a previously described procedure (Joshi et al., 2007). In brief, WT or *Tcf7<sup>-/-</sup>* OT-I TCR transgenic mice were infected with  $2.5 \times 10^7$  CFU attenuated LM-Ova, and one day later the splenocytes were harvested and spin-infected with control or Eomes-expressing retrovirus in the presence of 8 µg/ml polybrene and 100 units/ml IL-2, followed by 30 min incubation at 37 degrees. The retrovirally infected cells were transferred into B6.SJL recipients ( $0.2 \times 10^6$  cells/mouse), and 24 hours later the

recipients were infected with  $5 \times 10^{6}$  CFU attenuated LM-Ova. Expansion and memory formation of antigen-specific CD8<sup>+</sup>T cells were monitored in PBLs on various days post-infection.

#### Microarray and bioinformatics analysis

On days 70-80 post-infection of B6.SJL recipient mice that had received 500 WT or  $Tcf7^{-/-}$  OT-I T cells, splenocytes were harvested and surface-stained to identify  $CD45.2^{+}CD8^{+}V\alpha-2^{+}$  cells. These donor-derived memory  $CD8^{+}$  T cells were sorted directly into Trizol LS reagent (Invitrogen). After chloroform extraction, the aqueous phase was mixed with 2 volumes of ethanol and loaded onto a purification column in RNeasy Mini Kit (Qiagen) for further purification. RNA quality was assessed using the Agilent Model 2100 Bioanalyzer. Total RNAs from 3 WT and 3 *Tcf7*<sup>-/-</sup> memory CD8<sup>+</sup> T cells (500 pg) were amplified using the NuGEN WT-Ovation Pico RNA Amplification System (NuGEN). The resulting cDNA probes were hybridized to the GeneChip Mouse GENE 1.0 ST arrays (Affymetrix), scanned with the Affymetrix Model 7G upgraded scanner, and the data were collected using the GeneChip Operating Software (GCOS). The data were imported into Partek Genomics Suite using RMA (Robust Multi-Chip Average) normalization. Differential expression and its statistical significance were calculated using linear contrasts with an ANOVA (analysis of variance) model. Functional annotation of these genes were performed using DAVID bioinformatics resources (http://david.abcc. ncifcrf.gov) (Huang da et al., 2009).

# Wnt responsiveness of naïve and memory CD8<sup>+</sup> T cells

Naïve OT-I CD8 T cells were purified by negative selection, and day 60-100 memory  $CD8^+$  T cells were isolated by cell sorting. The cells were treated with DMSO, BIOacetoxime or N-methylated BIO (each at 5  $\mu$ M) for 12 hours in 24-well plate. For responsiveness of CD8<sup>+</sup> T cells to a Wnt ligand, Wnt3a conditioned medium was used. L cells expressing Wnt3a or control L cells were cultured in complete DMEM containing 10% FBS. Exponentially growing cells were re-plated, and 6 days later the Wnt3a conditioned medium or control medium was collected and used for stimulation of CD8<sup>+</sup> T cells. The stimulated cells were then harvested, and gene expression was determined using quantitative PCR.

#### **Quantitative RT-PCR**

Total RNA was reverse-transcribed using QuantiTech Reverse Transcription Kit (Qiagen). The resulting cDNA was analyzed for expression of different genes by quantitative PCR using SYBR Advantage qPCR pre-mix (Clontech) on ABI 7300 Real Time PCR System (Applied Biosystems). Relative gene expression levels in each sample were normalized to that of a housekeeping gene, hypoxanthine phosphoribosyltransferase 1 (*Hprt1*). For each individual gene, its relative expression in DMSO-treated cells was arbitrarily set to 1, and its expression changes in BIO-acetoxime- or N-methylated BIOtreated cells were calculated as fold repression or induction.

Design of PCR primers was assisted by using the Primer3 program (Rozen and Skaletsky, 2000). The primers used in quantitative RT-PCR were as follows: *Eomes*: 5'-TCCTAACACTGGCTCCCACT and 5'-GTCACTTCCACGATGTGCAG; *Myc*: 5'-GTACCTCGTCCGATTCCACG and 5'-GCCTCTTCTCCACAGACACC; *Tbx21*: 5'-CAATGTGACCCAGATGATCG and 5'-GCGTTCTGGTAGGCAGTCAC; *Tcf7*: 5'-CAATCTGCTCATGCCCTACC and 5'-CTTGCTTCTGGCTGATGTCC; *Hprt1*: 5'-GCGTCGTGATTAGCGATGATG and 5'-CTCGAGCAAGTCTTTCAGTCC; *Axin2*: 5'-AAGAGAAGCGACCCAGTCAA and 5'-CTGCGATGCATCTCTCTCTG.

For assessing enrichment of genomic DNA segment in ChIP, the following primers were used.

Axin2 T2/3 cluster: 5'-AAATCCACAGCGCAGTTTTT and 5'-TTCAACCCAGGTCCTGTTTC;

Axin2 T7/8 cluster: 5'-TGTGTGGAGCTCAGATTTCG and 5'-

ATGTGAGCCTCCTCTCTGGA;

Rag2 promoter: 5'-CACTCTACCCTGCAGCCTTC and 5'-TCTGCCCTCTTGTAGCCAGT;

Tbx21 5'-regulatory region: 5'-GTGCCATGGTGCATGTTTAG and 5'-

GGGTGGTGGTTGGTTTGTCTGACT;

For the *Eomes* allele, -10 kb: 5'-CCCAGCGGGATGTTAATACT and 5'-

ACCCGGATCTCACTGTAGGA;

-3.5 kb (cluster a): 5'-AGAGAACAAAGGGCCAAACA and 5'-

ACTTTGCCTGGACTCTGGAA;

-2.6 kb (element b): 5'-CATGGAAGGTCCTGCTGTTT and 5'-

TCTGGTGTCTCAGGCACACT;

-1.8 kb (element c): 5'-CCTTGTGGAATCCTCACGTT and 5'-

CAGTCCAGAGATCCCAGCTC;

-0.8 kb (element d): 5'-CAGCTGCTAGGGAACCTTTG and 5'-

AATTCCCTCTGCTCGGTTTT; and

+3 kb: 5'-TCCTAACACTGGCTCCCACT and 5'-CACAGGCTTTTCCAGTCTCC.

# **Experimental Procedure-Associated References**

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Supplemental Figure 1 (related to Figure 1). TCF-1 deficiency limited expansion but did not affect survival of effector CD8<sup>+</sup> T cells.

(A) Schematic showing the experimental design for (B) - (D). Five hundreds of WT or  $Tcf7^{-/-}$  OT-I CD8<sup>+</sup> T cells (expressing CD45.2 and Thy1.2, as test cells) were mixed with CD45.2<sup>+</sup>Thy1.1<sup>+</sup> OT-I CD8<sup>+</sup> T cells (as reference cells, ref. cells) at approximately 1:1 ratio, and transferred into CD45.1<sup>+</sup> B6.SJL recipients, which were *i.v.* infected with 5 × 10<sup>6</sup> CFU of *actA*<sup>-</sup>LM-Ova. Donor-derived antigen-specific CD8<sup>+</sup> T cells were distinguished by differential Thy1.2 and Thy1.1 expression.

(B) Kinetics of  $CD8^+$  T cell response after LM infection. OT-I  $CD8^+$  T cells were tracked in the PBLs on different days post-infection, and their percentages in CD8 T cells are shown. Data are representative from 2 independent experiments with 5 recipient mice examined in each experiment.

(C) and (D) Proliferation of antigen-specific  $CD8^+$  T cells during expansion phase. LM-infected recipients were *i.p.* injected with 1 mg of BrdU on day 4 (C) or day 6 (D) after

infection, and 18 hrs later, BrdU uptake by OT-I T cells were measured. Data are representative from 2 independent experiments with similar results.

(E) Apoptosis of effector  $CD8^+$  T cells. In separate experiments where WT or  $Tcf7^{/-}$  OT-I T cells were transferred into B6.SJL recipients without Thy1.1<sup>+</sup> reference cells, on days 5 or 7 after infection, activation status of caspase-3/7 was determined in effector OT-I T cells. Percentages of cells with active caspase-3/7 are shown.

(F)  $Tcf7^{-/-}$  thymocytes showed increased caspase-3/7 activity. Thymocytes were isolated from WT or  $Tcf7^{-/-}$  mice, surface stained for CD4 and CD8, and then stained for active caspase-3/7. Percentages of caspase-3/7-positive subsets were shown for DP, CD4<sup>+</sup>, and CD8<sup>+</sup> thymocytes. Data are representative of analysis of 3 pairs of WT and  $Tcf7^{-/-}$  mice. This finding is consistent with previous observations that TCF-1-dependent signals are required for thymocyte survival (Ioannidis et al., Nat. Immunol. 2, 691-697, 2001).



Supplemental Figure 2 (related to Figure 2). Impaired Tcm differentiation of  $Tcf7^{/-}$ memory CD8<sup>+</sup> T cells generated in response to viral infection or from naïve precursors. (A) and (B) B6.SJL recipients of WT or  $Tcf7^{/-}$  OT-I CD8<sup>+</sup> T cells were infected with  $4 \times 10^{6}$  PFU of vaccinia virus expressing Ova (VacV-Ova). At days 45-75 post-infection, memory OT-I cells were characterized by cell surface or intracellular staining. (A) CD62L, IL-7R $\alpha$ , and KLRG1 expression on memory OT-I cells. Percentage of each subset was shown. (B) Production of IL-2, TNF- $\alpha$ , and granzyme B by memory OT-I cells. Splenocytes were stimulated with Ova-peptide for 6 hrs and intracellularly stained for the indicated effector molecules. Gating of the positive population was based on respective positive control. (C) Phenotypic analysis of splenic  $Tcf7^{-/-}$  OT-I T cells before adoptive transfer. Splenocytes were isolated from WT or  $Tcf7^{-/-}$  OT-I TCR transgenic mice and surfaced stained. Percentage of each subset was shown. Data are representative of at least 3 independent experiments with similar results.

(D) Functional analysis of splenic  $Tcf7^{-/-}$  CD8<sup>+</sup> T cells before adoptive transfer. CD44<sup>hi</sup> and CD44<sup>lo</sup> OT-I T cells were either cultured without stimulation or stimulated with plate-bound anti-CD3 (1 µg/ml) for 5 hrs. Brefeldin A was included for the last 4 hrs of incubation. The cells were then intracellularly stained for IFN- $\gamma$  and the percentages of IFN- $\gamma^+$  subsets are shown. Neither WT nor  $Tcf7^{-/-}$  CD44<sup>lo</sup> CD8<sup>+</sup> T cells constitutively expressed or were induced to express granzyme B or IL-2 (data not shown).

(E) Kinetics or early CD8<sup>+</sup> T cell responses using naïve precursors. Naive CD62L<sup>+</sup>CD44<sup>lo</sup> CD8<sup>+</sup> T cells were isolated from the spleens of WT or  $Tcf7^{-}$  OT-I TCR transgenic mice by cell sorting. Five hundreds of the sorted naive precursors were adoptively transferred into B6.SJL recipients followed by infection with attenuated LM-Ova. Expansion and contraction of effector OT-I T cells were tracked in PBLs. Data are representative of 2 independent experiments with similar results (n = 5 for each time point).

(F) and (G) Characterization of memory OT-I cells derived from naïve precursors. During days 39-46 post-infection, memory OT-I cells were characterized by cell surface or intracellular staining. (F) CD62L, IL-7R $\alpha$ , and KLRG1 expression on memory OT-I cells. Percentage of each subset was shown. (G) Production of IL-2, TNF- $\alpha$ , and granzyme B by memory OT-I cells. Splenocytes were stimulated with Ova-peptide for 6 hrs and intracellularly stained for the indicated effector molecules. Gating of the positive population was based on respective isotype control.

Note that the reduced production of IL-2 by *Tcf7<sup>-/-</sup>* memory CD8<sup>+</sup> T cells may not have direct functional consequence on memory CD8<sup>+</sup> differentiation, as indicated by several recent studies showing that paracrine IL-2 signaling rather than intrinsic IL-2 production impacts primary and secondary CD8<sup>+</sup> T cell responses (Williams et al., Nature 441, 890-893, 2006; Kalia et al., Immunity 32, 91-103, 2010; Pipkin et al., Immunity 32, 79-90, 2010).



# Supplemental Figure 3 (related to Figure 3). Diminished expression of IL-2R $\beta$ , Bcl-2, and Eomes in *Tcf7*<sup>/-</sup> memory CD8<sup>+</sup> T cells generated in response to viral infection or from naïve precursors.

(A) and (B) B6.SJL recipients of WT or  $Tcf7^{-/-}$  OT-I CD8<sup>+</sup> T cells were infected with VacV-Ova as in Figure S2A, and memory OT-I cells were characterized by cell surface or intracellular staining during days 45-75 after infection.

(C) and (D) WT or  $Tcf7^{-/-}$  naïve CD62L<sup>+</sup>CD44<sup>lo</sup> OT-I T cells were sorted and transferred into B6.SJL recipients, followed by LM-Ova infection as in Figure S2E. Memory OT-I cells were analyzed during 39-46 days after infection.

(A) and (C) Expression of IL-2R $\beta$  and Bcl-2 in memory OT-I cells.

(B) and (D) Eomes and T-bet expression in memory OT-I cells. Percentage of each positive subset was shown. Also shown in the parenthesis is the  $\Delta$ MFI value between antibody- and isotype-stained whole cell populations without positivity gating as in Figure 3C. All data are representative of 2 independent experiments.



# Supplemental Figure 4 (related to Figure 5). Wnt responsiveness of CD8<sup>+</sup> T cells.

(A) BIO-acetoxime but not MeBIO induced  $\beta$ -catenin accumulation in naïve CD8<sup>+</sup> T cells. Naïve CD8 T cells were isolated from WT OT-I TCR transgenic mice and stimulated as indicated for 12 hrs.  $\beta$ -catenin and  $\beta$ -actin were detected by Western blotting.

(B) Induction of Eomes by BIO-acetoxime. Naïve CD8 T cells were isolated and stimulated for 12 hrs as in (A). The expression of selected genes was quantitatively determined, and all normalized to the samples treated with DMSO.

(C) Expression of Fzd receptor complex components in WT and  $Tcf7^{/-}$  memory CD8<sup>+</sup> T cells. The expression data of Fzd receptor complex components were extracted from microarray analysis of WT and  $Tcf7^{/-}$  memory CD8<sup>+</sup> T cells and shown in an intensity map. The color-coded relative expression scale is shown at the bottom. Also shown are expression changes between  $Tcf7^{/-}$  and WT memory CD8<sup>+</sup> T cells, with "+" denoting induction and "–" denoting repression. The p value of gene expression changes is shown for those reached statistical significance.

#### Cluster a

		-3527	
Mouse	ggaaacagggcagaagtagcagatctggccatcagagaa	caaag	ggccaaacagtgaacctgag
Rat	ggaaacagggctgaggtagtagatctggccatcagagaa	caaag	gggcgaacagtgaacctgag
Human	gaaagcacagcagaggtggcagatctggccatcagagaa	caaag	ggccaaagagtgaacctgag
Chimp	gaaagcacagcagaggtggcagatctggccatcagagaa	caaag	ggccaaagagtgaacctgag
Dog	${\tt caaaagcgcagtggaggtggcaggtctggccagcagagaa}$	caaag	ggccaaagagttaacctgag

2527

-2563

#### -3477

Mouse	atggtgaaataaaatgtaacatcaa	caaag	agagggccatagataaatagtaaaaggaccaact
Rat	acgctgaaataaaatgtaacatcaa	caaag	agagggccatagataaataggaaaaggaccaact
Human	ttggtgaaataaaatgtaacatcaa	caaag	aaagggccatagataaatagtaaaaggaccaact
Chimp	atggtgaaataaaatgtaacatcaa	caaag	aaagggccatagataaatagtaaaaggaccaact
Dog	atggtgaaataaaatgtaacatcaa	caaag	aaaaggccatagataaatagttaaaggaccaact

#### -3318

Mouse	${\tt ttttcctagggttaaaaggagagcatgcagcaagcctgttcagaatttagaatttagaggttaaaaggagagcatgcagcaagcctgttcagaatttagaatttagaggttagagggttagaggaggagg$	icaaag	tgtttgaata
Rat	${\tt ttttcctagggttaaaaggagagcatgcagcaagtctgttcagaatttagtcagaatttagtcagcaagtctgttcagaatttagtagtagtagtagtagtagtagtagtagtagt$	acaaag	tgtttgaata
Human	${\tt ttttcctagggttaaaaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaggagagaga$	acaaag	tgtttgaata
Chimp	${\tt ttttcctagggttaaaaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaagtctgctcagaatttaggagaaccggcagcaggagaaccggcaggagaaccggcagca$	acaaag	tgtttgaata
Dog	${\tt ttttcctagggttaaaaggagaaccggcagcaagtctgctcagaatttagattagaatttagattagagggtagaaggagaaccggcagcaagtctgctcagaatttagattggattagattggattggattggattggattggattggattggattggattggattggattggat$	icaaag	tgtttgaata

#### Element b

		-2303	
Mouse	tacaggaggtgctgcctgacatgtgccctcg	ctttg	ttttctcttcttacttctgg
Rat	taagtgagg-gctgcctggcccgtgc		ttctctttctct
Human	${\tt taaggagggtgctgcctgacatgttcacttaagccactg}$	ctttg	gctttcttttctattcctac
Chimp	${\tt taaggagggtgctgcctgacatgttcacttaagccactg}$	ctttg	gctttcttttctattcctac
Dog	ttaggagggtgctgcctgacatgttcactgaagccactg	cttta	gctttcttttctgttcctat

#### Element c

-1815 Mouse cactgtgccacgc-cagcgtttccccggtctctt-caaagtattttgaagggac-----Rat cactgtgccatgc-cagtgcttcccgggtctctt-caaagtattttgaagggacgccgagg Human cactttgccacgcgaagcgcttccctggctgcgtcaaaagcattttgaagggacgccgagg Chimp cactttgccacgcgaagcgcttccctggctgcgtcaaaagcattttgaagggacgccgagg Dog cactttgccacgcgagcgcttccctggccgcctcgaaagcagtctgaagggacaccgaag

Mouse	cttact-tctggctgtgtt
Rat	cctact-tctgactctgtt
Human	cccgct-tcttg <mark>ctttg</mark> tt
Chimp	cccgct-tcttg <mark>ctttg</mark> tt
Dog	cccgctttctctctgtgat

#### Element d

-837

Rat cagggaatettaactgeacagetgetagggaac <mark>etttg</mark> tgtettggtgteagteeceacea Human cagggaateetaactgtggggetgttagggaag <mark>etttg</mark> tttetteggtgteaggeetaactg	aag
Human cagggaateetaactgtggggetgttagggaag <mark>etttg</mark> tttettggtgtcaggeetaactg	aag
	aag
Chimp cagggaatcctaactgtggggctgttagggaag <mark>ctttg</mark> tttcttggtgtcaggcctaactg	aag
Dog cagggaatctcaaccgcactgctgctggggaac <mark>ctttg</mark> tctcttggtgccaggcccagctg	aag

Supplemental Figure 5 (related to Figure 6). Cross-species comparison of the conserved consensus TCF-1 binding motifs in the *Eomes* 5'-regulatory region. The conserved sequences are highlighted and their relative locations marked (based on UCSC genome browser).





# Supplemental Figure 6 (related to Figure 7). Effect of forced expression Eomes on WT and $Tcf7^{-}$ memory CD8<sup>+</sup> T cells.

(A) Experimental design. WT and  $Tcf7^{-/-}$  OT-I mice were infected with high dose of LM-Ova, and 24 hours later the splenocytes were harvested, retrovirally transduced, and then transferred into naïve B6.SJL mice. The recipients were then infected with LM-Ova, the percentage of GFP<sup>+</sup> OT-I in PBL CD8<sup>+</sup> cells were determined on various days after infection. (B) Validation of increased Eomes expression in GFP<sup>+</sup> WT or  $Tcf7^{-/-}$  memory OT-I cells infected with MigR1-Eomes. On day 40 after LM infection, splenocytes were isolated from recipients of WT or  $Tcf7^{-/-}$  OT-I T cells that had been infected with MigR1-Eomes. GFP<sup>-</sup> and GFP<sup>+</sup> CD45.2<sup>+</sup>CD8<sup>+</sup> cells were separated by cell sorting, and the relative levels of Eomes transcripts were determined by quantitative RT-PCR.

(C) Phenotypic and functional analyses of retrovirally transduced WT or  $Tcf7^{-}$  memory T cells. On day 40 after infection, splenocytes were isolated from recipients of retrovirally infected WT or  $Tcf7^{-}$  OT-I T cells. The cells were surface or intracellularly stained after 5-hr Ova peptide stimulation. For surface staining, the percentages of subsets positive for IL-7R $\alpha$ , CD62L, or KLRG1 in GFP<sup>+</sup>CD45.2<sup>+</sup>CD8<sup>+</sup> T cells are shown. For intracellular staining, the percentages of subsets positive for TNF- $\alpha$ , Granzyme B (GzmB), or IL-2 in IFN- $\gamma^+$ GFP<sup>+</sup>CD45.2<sup>+</sup>CD8<sup>+</sup> T cells are shown. Note that  $Tcf7^{-/-}$  memory T cells reproducibly manifested phenotypes as shown in Figure 2, and forced expression of Eomes did not substantially improve/aggravate those phenotypic or functional alterations. Additionally, the numbers of GFP<sup>+</sup>  $Tcf7^{-/-}$  memory OT-I cells expressing Eomes in the spleen showed an approximately 1.6-fold increase compared with those of GFP<sup>+</sup>  $Tcf7^{-/-}$  memory OT-I cells infected with MigR1 (1.08 ± 0.32 × 10<sup>5</sup> vs. 0.69 ± 0.31 × 10<sup>5</sup>, n=3). The increase, however, did not reach a statistical significance, likely due to variations in retroviral infection efficiency and varied responses to LM infection when different recipients were cross-compared.

# Supplemental Table I. Select Genes Significantly Differentially Expressed

# between WT and TCF-1-deficient memory CD8 $^{+}$ T cells

#### (related to Figure 4)

ITeraseription factors           1-52         Acbp2         AE BINDING PROTEIN 2           1-53         Acbm         ATAXIA TELANGIECTASIA MUTATED HOMOLOG (HUMAN)           1-53         Churer         CHURCH CHURCHILL DOMAIN CONTAINING 1           1-53         Churer         CHURCH CHURCHILL DOMAIN CONTAINING 1           1-53         Gaot         WD REPEAT DOMAIN 39           2-55         Eomes         EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)           1-81         Gf2b         GENERAL TRANSCRIPTION FACTOR II I           1-79         Gf2i         GENERAL TRANSCRIPTION FACTOR II I           1-50         Hidorp2         HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 1           1-50         Miklz         MKL/MVOCARDIN-LIKE 2           1-67         Miklz         MKL/MVOCARDIN-LIKE 2           1-67         Miklz         MKL/MVOCARDIN-LIKE 2           1-77         Nabi         NGFL-ABINDING PROTEIN 1           2-46         Myc         WPELOCYTOMATOSIS ONCOGENE           1-77         Nabi         NGFL-AR RECEPTOR BINDING FACTOR 2 PSEUDOGENE           2-77         Nabi         NGLFLAR RECEPTOR BINDING FACTOR 2 PSEUDOGENE           2-72         Nrbf2         NUCLEAR RECEPTOR BINDING FACTOR 2 PSEUDOGENE           2-73	ED 1 • FACTOR FACTOR
Transcription factors         1-52       Acbp2       AE BINDING PROTEIN 2         1-58       Atm       ATAXIA TELANGIECTASIA MUTATED HOMOLOG (HUMAN)         1-53       Churct       CHURCHILL DOMAIN 20NTAINING 1         1-53       Churct       CHURCHILL DOMAIN 20NTAINING 1         1-53       Churct       CHURCHILL DOMAIN 20NTAINING 1         1-50       Hibep2       GENERAL TRANSCRIPTION FACTOR II B         1-79       Gf2i       GENERAL TRANSCRIPTION FACTOR II I         1-50       Hibep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 1         1-55       Khdribsi       KH IDOMAIN CONTAINING, RAA BINDING, SIGNAL TRANSDUCTION ASSOCIA'         1-50       Mikep2       MULTIPLE ENDOCRINE NEOPLASIA 1         1-55       Mikit       MUUTIPLE ENDOCRINE NEOPLASIA 1         1-50       Mikep2       MELAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 2         2-6       Myfz       METAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 2         2-6       Myfz       METAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 2         2-45       Nyfb       NUCLEAR FACTOR 1/B         1-77       Nabi       NOFI-A BINDING PROTEIN 1         2-72       Nyfb       NUCLEAR FACTOR 1/B         1-63       Tofio       TAF	ED 1 • FACTOR FACTOR
1:52       Aebp2       AE BINDING PROTEIN 2         1:58       Afm       ATAXIA TELANGIECTASIA MUTATED HOMOLOG (HUMAN)         1:53       Churcy       CHURCHILL DOMAIN CONTAINING 1         1:53       Cioat       WD REPEAT DOMAIN CONTAINING 1         1:53       Cioat       WD REPEAT DOMAIN 39         2:55       Eomes       EOMESODERMIN HOMOLOG (XENOPU'S LAEVIS)         1:81       Gfgbb       GENERAL TRANSCRIPTION FACTOR IIB         1:79       Gfgbb       GENERAL TRANSCRIPTION FACTOR III         1:50       Hidep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 1         1:50       Midrbsr       KH DOMAIN CONTAINING, RNA BINDING, SIGNAL TRANSDUCTION ASSOCIAT         1:50       Midl       MKL/MYOCARDIN-LIKE 2         1:67       Midl       MKL/MYOCARDIN-LIKE 2         1:67       Midl       MKL/MYOCARDIN-LIKE 2         1:77       Nabi       NUCLEAR FACTOR I/B         1:72       Nrbf2       NUCLEAR FACTOR I/B         1:72       Nrbf2       NUCLEAR FACTOR I/B         1:75       Jfib       NUCLEAR RECEPTOR BINDING FACTOR 2 PSEUDOGENE         1:43       PURINE RUCH ELEMENT BINDING PROTEIN (TBP)-ASSOCIATE         1:45       Purb       PURINERASE II, TATA BOX BINDING ROTEIN (TBP)-ASSOCIAT	ED 1 ) FACTOR FACTOR
1.58       Affan       ATAXIA TELANOLECTASIA MUTATED HOMOLOG (HUMAN)         1.53       Churet       CHURCHILL DOMAIN 30         1.53       Churet       CHURCHILL DOMAIN 30         2-55       Eomes       EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)         1.81       G(fz)       GENERAL TRANSCRIPTION FACTOR IIB         1-79       G(fz)       GENERAL TRANSCRIPTION FACTOR IIB         1-79       G(fz)       GENERAL TRANSCRIPTION FACTOR IIB         1-50       Hikep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEINS :         1-50       Mklz       MELL/IPLE ENDOCINEN ENOPLASIA 1         1-50       Mklz       MEL/(MYOCARDIN-LIKE 2         1-67       Mfz       METAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 2         2-6       Myz       MELOCYTOMATOSIS ONCOGENE         1-77       Nabi       NOFI-A BINDING PROTEIN 1         2-45       Nfb       NUCLEAR FACTOR 1/B         1-72       Nrbf2       NUCLEAR RACTOR 1/B         1-72       Nrbf2       NUCLEAR RACTOR 1/B         1-74       Pac2q       PROLIFERATION-SACTOR 1/B         1-75       Tgf1       TAF10 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI         1-75       Tgf10       TAF10 RNA POLYMERASE II, TATA BOX BIND	ED 1 ) FACTOR FACTOR
-1.53       Churct       CHURCHILL DOMAIN CONTAINING 1         1.53       Churct       WD REPEAT DOMAIN 39         2.55       Eomese       EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)         -1.81       Gf2b       GENERAL TRANSCRIPTION FACTOR IIB         -1.79       Gf2i       GENERAL TRANSCRIPTION FACTOR III         -1.50       Hivep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCE BINDING PROTEIN :         -1.65       Khdrbis       KH DOMAIN CONTAINING, NA BINDING, SIGNAL TRANSDUCTION ASSOCIAT         -1.65       Khdrbis       MULTIPLE ENDOCRINE NEOPLASIA 1         -1.65       Mkl2       MKL/MYOCARDIN-LIKE 2         -1.67       Mf2       MKL/MYOCARDIN-LIKE 2         -1.67       Mf2       MULLEAR RESPONSE ELLEMENT BINDING FRANSCRIPTION FACTOR 2         -2.45       Mf0       NUCLEAR RACTOR I/B         -1.77       Nobi NOFI-A BINDING PROTEIN 1       -         -2.45       J/Ib       NUCLEAR RECEPTOR BINDING FACTOR 2 PSEUDOGENE         -1.79       Nobi NOFI-A BINDING PROTEIN 1       -         -1.72       Nbd2       NUCLEAR RECEPTOR BINDING FACTOR 2 PSEUDOGENE         -1.73       TAFIN BRUTHOR HACTOR A MITOCHONDRIN B       -         -1.65       Purb FURINE RICH ELEMENT BINDING PROTEIN B         -1.66       Tafio	ED 1 ) FACTOR FACTOR
1.33       Ciaol       WD REPEAT DOMAIN 30         22.55       Eomes       EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)         22.55       Eomes       EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)         22.56       Eomes       EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)         22.50       Hivep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 3         1.50       Hivep2       HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 3         1.53       Ment       MULTIPLE ENDOCRINE NEOPLASIA 1         1.50       Mikl2       MKL/MYOCARDIN-LIKE 2         2.60       Mye       MYELOCTOMATOSIS ONCOGENE         2.77       Nabr       NGFI-A BINDING PROTEIN 1         2.43       Nfib       NUCLEAR FACTOR 1/B         1.72       Nrbf2       NUCLEAR FACTOR 1/B         1.72       Nrbf2       NUCLEAR FACTOR 1/B         1.72       Nrbf2       NUCLEAR FACTOR 1/B         1.73       TIM       PURINE RICH ELEMENT BINDING PROTEIN B         1.63       Purb       PURINE RICH ELEMENT BINDING PROTEIN B         1.64       Tafri T AF11 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI         1.67       Tafri T AF11 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI         1.67       Tafri       TAF11	ED 1 ) FACTOR FACTOR
255         Eomes         EOMESODERMIN HOMOLOG (XENOPUS LAEVIS)           1-181         Gf2b         GENERAL TRANSCRIPTION FACTOR IIB           1-79         Gf2i         GENERAL TRANSCRIPTION FACTOR III           1-150         Hivep2         HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN :           1-65         Khdrbst         KH DOMAIN CONTAINING, RAN BINDING, SIGNAL TRANSDUCTION ASSOCIAT           1-53         Ment         MULTIPLE ENDOCRINE NEOPLASIA 1           1-55         Mkl2         MKL/MYOCARDIN-LIKE 2           1-67         Mf2         METAL RESPONDSE ELEMENT BINDING TRANSCRIPTION FACTOR 2           2-46         Myc         MYELOCYTOMATOSIS ONCOGENE           2-47         Ndb         NUCLEAR FACTOR I/B           1-77         Nabi         NUCLEAR FACTOR I/B           2-14         Pagg4         PROLIFERATION-ASSOCIATED 2G4           1-63         Pdlimi         PDZ AND LIM DOMAIN I (ELFIN)           1-85         Purb         PURINE RICH ELEMENT BINDING FACTOR 2 PSEUDOGENE           1-75         Tsg101         TAFIO RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATED           1-68         Taf10         TAFIO RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATED           1-75         Tsg101         TANGCRIPTION FACTOR A, MITOCHONDRIAL	ED 1 ) FACTOR FACTOR
1.81         G(f2b)         GENERAL TRANSCRIPTION FACTOR IIB           1-7.9         G(f2i)         GENERAL TRANSCRIPTION FACTOR II           1-7.9         G(f2i)         GENERAL TRANSCRIPTION FACTOR II           1-7.9         Hivep:         HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN :           1-5.0         Ment         MULTIPLE ENDOCRINE NEOPLASIA 1           1-5.3         Ment         MULTIPLE ENDOCRINE NEOPLASIA 1           1-5.0         Mf2         MKL/MYOCARDIN-LIKE 2           1-1.7         Mb1         NGFI-A BINDING PROTEIN 1           2-2.6         Myc         MYELOCYTOMATOSIS ONCOGENE           1-1.77         Nabi         NGFI-A BINDING PROTEIN 1           2-2.45         Nfib         NUCLEAR FACTOR 1/B           1-1.72         Nvhf2         NUCLEAR FACTOR 1/B           1-1.73         Nabi         NGFI-A BINDING PROTEIN 1           2-1.63         Pulimi         PDZ AND LIM DOMAIN 1 (ELFIN)           1-1.65         Tufto         TAFin RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI           1-1.65         Tufto         TAFin RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI           1-1.75         Tgam         TRANSCRIPTION FACTOR A. MITOCHONDRIAL           1-1.75         Tgam	ED 1 ) FACTOR FACTOR
1.79Gf[2]GENERAL TRANSCRIPTION FACTOR II 11.79Gf[2]GENERAL TRANSCRIPTION FACTOR II 11.70Hivep2HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER BINDING PROTEIN 21.65KhdrbsiKH DOMAIN CONTAINING, RNA BINDING, SIGNAL TRANSDUCTION ASSOCIA"1.53MeniMULTIPLE ENDOCRINE NEOPLASIA 11.50Mkl2MKI/LYOYOARDOSIS ONCOGENE1.67Mfg2METAL RESPONSE ELEMENT BINDING TRANSCRIPTION FACTOR 22.60MgcMYELOCYTOMATOSIS ONCOGENE1.77NabiNGFI-A BINDING PROTEIN 12.43NfbNUCLEAR FACTOR I/B1.74Nrbf2NUCLEAR FACTOR I/B1.75Nrbf2NUCLEAR FACTOR I/B2.14Pagg4PROLIFERATION-ASSOCIATED 2G41.63PdlimuPDZ AND LIM DOMAIN 1 (ELFIN)1.85PurbPURINE RICH ELEMENT BINDING PROTEIN B1.66TaftoTAF10 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI1.75TafuinTAF10 RNA POLYMERASE II, TATA BOX BINDING PROTEIN (TBP)-ASSOCIATEI1.75TagtoiTUMOR SUSCEPTIBILITY GENE 1011.75TagtoiTUMOR SUSCEPTIBILITY GENE 1011.66Ubp2UDP-GLUCOSE PYROPHOSPHORYLASE 21.67Yg1Y1 TRANSCRIPTION FACTOR1.68Egr1EARLY GROWTH RESPONSE 11.69Foxfilead BOX D21.60Foxfilead BOX D22.79Foxd21.60Homez1.61Homez1.62Egr12.79Foxd22.79<	ED 1 ) FACTOR FACTOR
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-1.64Zeb1ZINC FINGER HOMEOBOX 1A1.62Egr1EARLY GROWTH RESPONSE 11.60Foxc1FORKHEAD BOX C12.79Foxd2FORKHEAD BOX D21.56Foxf1aFORKHEAD BOX T1A1.61HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.64HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.65Hoxb2HOMEO BOX B21.64Hsm2INSULINOMA-ASSOCIATED 22.39JundJUN PROTO-ONCOGENE RELATED GENE D11.53Ldb2LIM DOMAIN BINDING 21.64Msv2HOMEO BOX, SH-LIKE 21.55Nkv2HOMEO BOX, SH-LIKE 21.56Nkv2NESCIENT HELIX LOOP HELIX 21.56Nkv2-3NECIENT HELIX LOOP HELIX 21.56Nkv2-3NEURONAL PAS DOMAIN PROTEIN 31.66Rhox4pREERODUCTIVE HOMEOBOX 4B1.61Npas3NEURONAL PAS DOMAIN PROTEIN 31.65Rhox4pRIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 54300432L21 GENE1.59Rhox9RIKEN CDNA 54300432L21 GENE1.59Rhox9RIKEN CDNA 54300432L21 GENE1.59Rhox4pRIKEN CDNA 54300432L21 GENE1.59Rhox9RIKEN CDNA 54300432L21 GENE1.59Rhox9RIKEN CDNA 54300432L21 GENE1.54Smad6MAD HOMOLOG 6 (DROSOPHILA)1.54Smad6MAD HOMOLOG 6 (DROSOPHILA)	
1.62 $Egr1$ EARLY GROWTH RESPONSE 1 $1.60$ $Foxct$ FORKHEAD BOX C1 $2.79$ $Foxd2$ FORKHEAD BOX D2 $1.56$ $Foxfa$ FORKHEAD BOX FIA $1.61$ $Homez$ HOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE $1.64$ $Homez$ HOMEO BOX B2 $1.54$ $Insm2$ INSULINOMA-ASSOCIATED 2 $2.39$ $Jund$ JUN PROTO-ONCOGENE RELATED GENE D1 $1.53$ $Ldb2$ LIM DOMAIN BINDING 2 $1.64$ $Msx2$ HOMEO BOX, SRATELAKE 2 $1.55$ $Nhx2$ HOMEO BOX, SRATELAKE 2 $1.56$ $Nkx2$ HOMEO BOX, SRATELAKE 2 $1.56$ $Nkx2$ -3NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA) $1.61$ $Npas3$ NEURONAL PAS DOMAIN PROTEIN 3 $1.66$ $Rhox4p$ RIERO DUCTIVE HOMEOBOX 4B $1.61$ $Rhox4p$ RIKEN CDNA 4540432L21 GENE $1.59$ $Rhox9$ RIKEN CDNA 4600026001 GENE $1.79$ $Rybp$ RING1 AND YY1 BINDING PROTEIN $1.98$ $Six6$ SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA) $1.54$ $Smad6$ MAD HOMOLOC 6 (DROSOPHILA)	
1.60FOX:1FORKHEAD BOX C12.79Foxd2FORKHEAD BOX D21.56FoxfiaFORKHEAD BOX F1A1.61HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.60Hoxb2HOMEO BOX B21.54Insm2INSULINOMA-ASSOCIATED 22.39JundJUN PROTO-ONCOGENE RELATED GENE D11.53Ldb2LIM DOMAIN BINDING 21.64Msx2HOMEO BOX, MSH-LIKE 21.50Nhlh2NESCIENT HELIX LOOP HELIX 21.56Nkx2-3NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)1.61Npas3NEURONAL PAS DOMAIN PROTEIN 31.66Rhox4bREPRODUCTIVE HOMEOBOX 4B1.61Rhox4eRIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 1600026001 GENE1.79RybpRING1 AND YY1 BINDING PROTEIN1.98Six6SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)1.54Smad6MAD HOMOLOG 6 (DROSOPHILA)	
2.79Foxd2FORKHEAD BOX D21.56FoxfraFORKHEAD BOX F1A1.61HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.60Hoxb2HOMEO BOX B21.54Insm2INSULINOMA-ASSOCIATED 22.39JundJUN PROTO-ONCOGENE RELATED GENE D11.53Ldb2LIM DOMAIN BINDING 21.64Msx2HOMEO BOX, MSH-LIKE 21.55Nhlh2NESCIENT HELIX LOOP HELIX 21.56Nkx2-3NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)1.61Npas3NEURONAL PAS DOMAIN PROTEIN 31.66Rhox4bREPRODUCTIVE HOMEOBOX 4B1.61Rhox4eRIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 1600026001 GENE1.79RybpRING1 AND YY1 BINDING PROTEIN1.98Six6SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)1.54Smad6MAD HOMOLOG 6 (DROSOPHILA)	
1.56FoxfraFORKHEAD BOX F1A1.61HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.60Hoxb2HOMEO BOX B21.54Insm2INSULINOMA-ASSOCIATED 22.39JundJUN PROTO-ONCOGENE RELATED GENE D11.53Ldb2LIM DOMAIN BINDING 21.64Msx2HOMEO BOX, BY1.55Nhln2NESCIENT HELIX LOOP HELIX 21.56Nkx2-3NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)1.61Npas3NEURONAL PAS DOMAIN PROTEIN 31.66Rhox4bREPRODUCTIVE HOMEOBOX 4B1.61Rhox4cRIKEN CDNA 4630432L21 GENE1.59Rhox9RIKEN CDNA 1600026001 GENE1.79RybpRING1 AND YY1 BINDING PROTEIN1.98Six6SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)1.54MadbMAD HOMOLOG 6 (DROSOPHILA)	
1.61HomezHOMEODOMAIN LEUCINE ZIPPER-ENCODING GENE1.60Hoxb2HOMEO BOX B21.54Insm2INSULINOMA-ASSOCIATED 22.39JundJUN PROTO-ONCOGENE RELATED GENE D11.53Ldb2LIM DOMAIN BINDING 21.64Msx2HOMEO BOX, MSH-LIKE 21.50Nhh2NESCIENT HELIX LOOP HELIX 21.56Nkx2-3NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)1.61Npas3NEURONAL PAS DOMAIN PROTEIN 31.66Rhox4bREPRODUCTIVE HOMEOBOX 4B1.61Rhox4eRIKEN CDNA 5430432L21 GENE1.59Rhox9RIKEN CDNA 1600026001 GENE1.79RybpRING1 AND Y1 BINDING PROTEIN1.98Six6SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)1.54Mad6MAD HOMOLOG 6 (DROSOPHILA)	
1.60       Hoxb2       HOMEO BOX B2         1.54       Insm2       INSULINOMA-ASSOCIATED 2         2.39       Jund       JUN PROTO-ONCOGENE RELATED GENE D1         1.53       Ldb2       LIM DOMAIN BINDING 2         1.61       Lhx9       LIM HOMEOBOX PROTEIN 9         1.64       Msx2       HOMEO BOX, MSH-LIKE 2         1.50       Nhlh2       NESCIENT HELIX LOOP HELIX 2         1.56       Nkx2-3       NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)         1.61       Npas3       NEURONAL PAS DOMAIN PROTEIN 3         1.66       Rhox4b       REPRODUCTIVE HOMEOBOX 4B         1.61       Rhox4e       RIKEN CDNA 5430432L21 GENE         1.59       Rhox9       RIKEN CDNA 1600026001 GENE         1.79       Rybp       RING1 AND Y1 BINDING PROTEIN         1.98       Six6       SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)         1.98       Six6       SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)	
154       Insm2       INSULINOMA-ASSOCIATED 2         2:39       Jund       JUN PROTO-ONCOGENE RELATED GENE D1         1:53       Ldb2       LIM DOMAIN BINDING 2         1:64       Msx2       HOMEOBOX PROTEIN 9         1:55       Nhla2       NESCIENT HELIX LOOP HELIX 2         1:56       Nkx2-3       NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)         1:66       Rhox4p       REPRODUCTIVE HOMEOBOX 4B         1:61       Rhox4p       RIKEN CDNA 1600026001 GENE         1:59       Rhox9       RIKEN CDNA 1600026001 GENE         1:79       Rybp       RING1 AND YY1 BINDING PROTEIN         1:98       Six6       SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)         1:54       Smad6       MAD HOMOLOC 6 (DROSOPHILA)	
2.39       Jund       JUN PROTO-ONCOGENE RELATED GENE D1         1.53       Ldb2       LIM DOMAIN BINDING 2         1.61       Lhx9       LIM HOMEOBOX PROTEIN 9         1.64       Msx2       HOMEO BOX, MSH-LIKE 2         1.50       Nhln2       NESCIENT HELIX LOOP HELIX 2         1.56       Nkx2-3       NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)         1.61       Npas3       NEURONAL PAS DOMAIN PROTEIN 3         1.66       Rhox4b       REPRODUCTIVE HOMEOBOX 4B         1.61       Rhox4e       RIKEN CDNA 4540432121 GENE         1.59       Rhox9       RIKEN CDNA 1600026001 GENE         1.79       Rybp       RING1 AND YY1 BINDING PROTEIN         1.98       Six6       SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)         1.54       Smad6       MAD HOMOLOG 6 (DROSOPHILA)	
1.53     Ldb2     LIM DOMAIN BINDING 2       1.61     Lhx9     LIM HOMEOBOX PROTEIN 9       1.64     Msx2     HOMEO BOX, MSH-LIKE 2       1.50     Nhh2     NESCIENT HELIX LOOP HELIX 2       1.56     Nkx2-3     NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)       1.61     Npas3     NEURONAL PAS DOMAIN PROTEIN 3       1.66     Rhox4b     REPRODUCTIVE HOMEOBOX 4B       1.59     Rhox9     RIKEN CDNA 1600026001 GENE       1.79     Rybp     RING1 AND Y1 BINDING PROTEIN       1.98     Six6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
1.53         Lab2         Link DOMINIC DIA Dia 2           1.54         Link DOMINIC DIA DIA 2         1           1.64         Msx2         HOMEO BOX, MSH-LIKE 2           1.50         Nhh2         NESCIENT HELIX LOOP HELIX 2           1.56         Nkx2-3         NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)           1.61         Npas3         NEURONAL PAS DOMAIN PROTEIN 3           1.66         Rhox4p         REPRODUCTIVE HOMEOBOX 4B           1.61         Rhox4e         RIKEN CDNA 5430432L21 GENE           1.59         Rhox9         RIKEN CDNA 1600026001 GENE           1.79         Rybp         RING1 AND Y1 BINDING PROTEIN           1.98         Six6         SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)           1.54         Smad6         MAD HOMOLOG 6 (DROSOPHILA)	
1.64     Msv2     HOMEO BOX, MSH-LIKE 2       1.50     Nhh2     NESCIENT HELIX LOOP HELIX 2       1.56     Nkx2-3     NK2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)       1.61     Npas3     NEURONAL PAS DOMAIN PROTEIN 3       1.66     Rhox4p     REPRODUCTIVE HOMEOBOX 4B       1.59     Rhox9     RIKEN CDNA 1600026001 GENE       1.79     Rybp     RING1 AND YY1 BINDING PROTEIN       1.98     Six6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
1.50         Nhh2         INSTED FIGURATION           1.50         Nhh2         NESCIENT HELIX LOOP HELIX 2           1.56         Nkx2-3         NE2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)           1.61         Npas3         NEURONAL PAS DOMAIN PROTEIN 3           1.66         Rhox4b         REPRODUCTIVE HOMEOBOX 4B           1.61         Rhox4e         RIKEN CDNA 5430432L21 GENE           1.59         Rhox9         RIKEN CDNA 1600026001 GENE           1.79         Rybp         RING1 AND YY1 BINDING PROTEIN           1.98         Six6         SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)           1.54         Smad6         MAD HOMOLOG 6 (DROSOPHILA)	
1.56     Nku2     Nku2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)       1.56     Nku2     NKu2 TRANSCRIPTION FACTOR RELATED, LOCUS 3 (DROSOPHILA)       1.61     Npas3     NEURONAL PAS DOMAIN PROTEIN 3       1.66     Rhox4b     REPRODUCTIVE HOMEOBOX 4B       1.61     Rhox4e     RIKEN CDNA 5430432L21 GENE       1.59     Rhox9     RIKEN CDNA 1600026001 GENE       1.79     Rybp     RING1 AND YY1 BINDING PROTEIN       1.98     Six6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
1.50     NA225     NA225     NA225     NA225       1.51     Npas3     NEURONAL PAS DOMAIN PROTEIN 3       1.66     Rhox4b     REPRODUCTIVE HOMEOBOX 4B       1.61     Rhox4e     RIKEN CDNA 5430432L21 GENE       1.59     Rhox9     RIKEN CDNA 1600026001 GENE       1.79     Rybp     RING1 AND Y1 BINDING PROTEIN       1.98     Six6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
Information         Information <thinformation< th=""> <thinformation< th=""></thinformation<></thinformation<>	
1.66 <i>R10x40</i> REPRODUCTIVE HOMEOBOX 4B           1.61 <i>Rhox4e</i> RIKEN CDNA 5430432L21 GENE           1.59 <i>Rhox9</i> RIKEN CDNA 1600026001 GENE           1.79 <i>Rybp</i> RING1 AND YY1 BINDING PROTEIN           1.98         Six6         SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)           1.54 <i>Smad6</i> MAD HOMOLOG 6 (DROSOPHILA)	
1.61 <i>Rhox4p</i> RIKEN CDNA 5430432L3 GENE           1.59 <i>Rhox9</i> RIKEN CDNA 1600026001 GENE           1.79 <i>Rybp</i> RING1 AND YY1 BINDING PROTEIN           1.98         Six6         SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)           1.54         Smad6         MAD HOMOLOG 6 (DROSOPHILA)	
1.59         κποχ9         ΚΙΚΕΝ CDNA 1600020001 GENE           1.79         Rybp         RING1 AND YY1 BINDING PROTEIN           1.98         Six6         SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)           1.54         Smad6         MAD HOMOLOG 6 (DROSOPHILA)	
kybp     RING1 AND YY1 BINDING PROTEIN       1.98     Six6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
1.98     Stx6     SINE OCULIS-RELATED HOMEOBOX 6 HOMOLOG (DROSOPHILA)       1.54     Smad6     MAD HOMOLOG 6 (DROSOPHILA)	
1.54 Smad6 MAD HOMOLOG 6 (DROSOPHILA)	
1.52 Sox7 SRY-BOX CONTAINING GENE 7	
1.62 Sp3 TRANS-ACTING TRANSCRIPTION FACTOR 3	
1.55 Spib SPI-B TRANSCRIPTION FACTOR (SPI-1/PU.1 RELATED)	
1.51 Tbpl2 TBP-RELATED FACTOR 3	
1.54 Yapı YES-ASSOCIATED PROTEIN 1	
1.70 Zeb2 ZINC FINGER HOMEOBOX 1B	
1.53 Zfp213 ZIN CINGER PROTEIN 213	
1.55 Zfp354a ZINC FINGER PROTEIN 354A	
1.59 Zhu ZINC FINGER PROTEIN 1. Y LINKED	
1.54 Zscan2 ZINC FINGER AND SCAN DOMAIN CONTAINING 2	
Effector molecules	
5.34 Gzma GRANZYME A	
4.58 Gzmb GRANZYME B	
Cytokines, chemokines, and secreted factors	
3 64 Cleft CARDIOTROPHINLIKE CVTOKINE FACTOR 1	
104 CASI CARDITATI INVERSE FICALIVE FACTOR I	
1.05 Lev Linki investori a Billion a transmission exercises $1.05$ MacDadit a Ce MicDatrion investori exercises	
-1.95 MU MACKOFIAGE MIGKATION INHIBITORY FACTOR	
11-51 Spreuz SPKOU I I -KELAI EL, EVHI DOMAIN CONTAINING 2 10-51 THAON DECODORE EACTOR (TACANDA SUPERDAVILY AND SPEC	
-1.59 <i>Injsg8</i> IUMOK NECKOSIS FACTOR (LIGAND) SUPERFAMILY, MEMBER 8	
-1.01 Acti CHEMOKINE (CMOTHF) LIGAND 1	
1.57 Gdf9 GROWTH DIFFERENTIATION FACTOR 9	
1.53 Ifna11 INTERFERON ALPHA FAMILY, GENE 11	

1.55	Pdqfc	PLATELET-DERIVED GROWTH FACTOR, C POLYPEPTIDE
1.53	Scgb3a1	SECRETOGLOBIN, FAMILY 3A, MEMBER 1
1.67	Shh	SONIC HEDGEHOG
1.54	Tafa	TRANSFORMING GROWTH FACTOR ALPHA
1.72	Wnt2b	WINGLESS RELATED MMTV INTEGRATION SITE 2B
Cytokine an	d chemokine recep	tors
-1.51	Ccr7	CHEMOKINE (C-C MOTIF) RECEPTOR 7
-1.78	Ccr9	CHEMOKINE (C-C MOTIF) RECEPTOR 9
-1.69	Cxcr3	CHEMOKINE (C-X-C MOTIF) RECEPTOR 3
-1.54	Ifnar2	INTERFERON (ALPHA AND BETA) RECEPTOR 2
-1.69	Ilıora	INTERLEUKIN 10 RECEPTOR, ALPHA
2.31	Cx3cr1	CHEMOKINE (C-X3-C) RECEPTOR 1
2.52	Il12rb2	INTERLEUKIN 12 RECEPTOR, BETA 2
Costimulate	ory and inhibitor re	ceptors, and adhesion molecules
-1.53	Cd28	CD28 ANTIGEN
-1.65	Cd5	CD5 ANTIGEN
-2.81	Sell	L-SELECTIN/CD62L
-2.82	Tlr1	TOLL-LIKE RECEPTOR 1
1.76	Itga1	INTEGRIN ALPHA 1
1.72	Itgad	INTEGRIN, ALPHA D
1.65	Itgam	INTEGRIN ALPHA M
1.5	Itgb6	INTEGRIN BETA 6
2.88	Klrg1	KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY G, MEMBER 1
	1.1	
Cell cycle re		
-1.60	Cede5	COLLED-COLL DOMAIN CONTAINING 5
-1.70	Cdk6	CYCLIN-DEPENDENT KINASE 6
-1.60	Cks1b	CDC28 PROTEIN KINASE 1B
-1.53	Ctef	CCCTC-BINDING FACTOR
-1.56	Dmtf1	CYCLIN D BINDING MYB-LIKE TRANSCRIPTION FACTOR 1
-1.86	Eef1e1	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 EPSILON 1
-1.52	Gmnn	GEMININ
-2.29	Gnl3	GUANINE NUCLEOTIDE BINDING PROTEIN-LIKE 3 (NUCLEOLAR)
-1.69	Gspt1	G1 TO S PHASE TRANSITION 1
-1.60	Htatip2	HIV-1 TAT INTERACTIVE PROTEIN 2, HOMOLOG (HUMAN)
-2.53	Lzts1	LEUCINE ZIPPER, PUTATIVE TUMOR SUPPRESSOR 1
-1.60	Mcm6	MINICHROMOSOME MAINTENANCE DEFICIENT 6 (MIS5 HOMOLOG, S. POMBE)
-1.77	Mnat1	MENAGE A TROIS 1
-1.67	Mns1	MEIOSIS-SPECIFIC NUCLEAR STRUCTURAL PROTEIN 1
-1.72	Npm1	NUCLEOPHOSMIN 1
-1.74	Prdmo	VPR DOMAIN CONTAINING 9
-1 52	Radzo	RADEO HOMOLOG (S. CEREVISIAE)
-1.60	Rassf9	RASS ASSOCIATION (RAIGDS/AF-6) DOMAIN FAMILY 2
-1.00	Soen 2	RESTRIN 0
-1.05	Sesil	SECTATING SMC4 STRINGTIDAT MAINTENANCE OF CHDOMOSOMES 4-TIKE 4 (VEAST)
-1.05	Smc4	SINCE STRUCTORAL MAINTENANCE OF CHROMOSOMES 4-LIKE I (TEAST)
-1.55	Terrfo	SI INDEN TEL OMEDIC DEDEAT DINDING EACTOD &
-2.02	Cablest	CDV-AND ADI ENZYME SUBSTDATE 1
1.52	Dahoin	$CDK_{2}$ AND ADD EVALUATE SO BATATE I DISABLED HOMALOG $_{0}$ (DROODHILLA) INTED ACTING DROTEIN
1.55	Dub2ip	DISABLED HOMOLOG 2 (DRUSOFAILA) IN IERACI ING FROI EIN
1.08	Gaaa450	GROWITH ARREST AND DIA-DAMAGE-INDUCIBLE 45 BEIA
1.74	Gasi	GROWIH ARREST SPECIFIC 1
1.64	Gas2	GROWTH ARREST SPECIFIC 2
1.77	Yes1	YAMAGUCHI SARCOMA VIRAL (V-YES) ONCOGENE HOMOLOG 1
Apontosis r	egulation	
-1.90	Bcan20	B-CELL RECEPTOR-ASSOCIATED PROTEIN 29
-1 51	Beap_ 9 Bean 21	B-CELL RECEPTOR-ASSOCIATED PROTEIN 21
-1.69	Birce	BACULOVIRAL JAP REPEAT-CONTAINING 3
-2.16	Casni	CASPASE 1
-1.64	Cleft	CARDIOTROPHIN-LIKE CYTOKINE FACTOR 1
-1.04	Cloud	CARDITACITINI-LIKE CITOKINE FACTORI
-1.64	Ciec2u Cues	C-11FE LECTIN DOMAIN FAMILI 2, MEMBER D
-2.43	Cycs	CYTOCHROME C, SOMATIC
-1.53	Fisi	FISSION 1 (MITOCHONDRIAL OUTER MEMBRANE) HOMOLOG (YEASI)
-1.66	11go3op	INTEGRIN BETA 3 BINDING PROTEIN (BETA3-ENDONEXIN)
-1.69	Mlh1	MUTL HOMOLOG 1 (E. COLI)
-1.63	Msh6	MUTS HOMOLOG 6 (E. COLI)
-1.85	Prdx2	PEROXIREDOXIN 2
-1.69	Rnf130	RING FINGER PROTEIN 130
1.58	Acur1c	ACTIVIN A RECEPTOR, TYPE IC
1.51	Alox12	ARACHIDONATE 12-LIPOXYGENASE
1.68	Bag2	BCL2-ASSOCIATED ATHANOGENE 2
1.73	Egln3	EGL NINE HOMOLOG 3 (C. ELEGANS)
1.64	Fadd	FAS (TNFRSF6)-ASSOCIATED VIA DEATH DOMAIN
1.58	Ntf3	NEUROTROPHIN 3
<b>61</b> , <b>1</b> ,		
Signaling m	olecules	
-1.53	Cacel6	CELL DIVISION CYCLE 2-LIKE 6 (CDK8-LIKE)
-1.69	Cdc42se2	CDU42 SMALL EFFECTOR 2
-1.73	Csnk2a1	CASEIN KINASE II, ALPHA 1 POLYPEPTIDE
-1.79	Ddx1	DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 1
-1.55	Etnk1	ETHANOLAMINE KINASE 1
-1.51	Gnb2l1	GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), BETA POLYPEPTIDE 2 LIKE 1

-1.50	Map3k7	MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 7
-1.69	Mpp6	MEMBRANE PROTEIN, PALMITOYLATED 6 (MAGUK P55 SUBFAMILY MEMBER 6)
-1.60	Nme1	EXPRESSED IN NON-METASTATIC CELLS 1, PROTEIN
-1.80	Nme2	EXPRESSED IN NON-METASTATIC CELLS 2, PROTEIN
-1.77	Nme7	NON-METASTATIC CELLS 7, PROTEIN EXPRESSED IN
-1.52	Nt5c	5',3'-NUCLEOTIDASE, CYTOSOLIC
-1.64	Pank1	PANTOTHENATE KINASE 1
-1.52	Pdk1	PYRUVATE DEHYDROGENASE KINASE, ISOENZYME 1
-1.62	Pfkp	PHOSPHOFRUCTOKINASE, PLATELET
-1.68	Pgk1	PHOSPHOGLYCERATE KINASE 1
-1.79	Phpt1	PHOSPHOHISTIDINE PHOSPHATASE 1
-1.74	Pik3ca	PHOSPHATIDYLINOSITOL 3-KINASE, CATALYTIC, ALPHA POLYPEPTIDE
-1.53	Pip4k2a	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, TYPE II, ALPHA
-1.62	Ppp2r2a	PROTEIN PHOSPHATASE 2 (FORMERLY 2A), REGULATORY SUBUNIT B (PR 52), ALPHA ISOFORM
-1.58	Prps1	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1
-1.70	Prps2	RIKEN CDNA 2610101M19 GENE
-1.53	Pstk	PHOSPHOSERYL-TRNA KINASE
-1.52	Ptpn3	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3
-1.86	Ripk2	RECEPTOR (TNFRSF)-INTERACTING SERINE-THREONINE KINASE 2
-1.61	Rngtt	RNA GUANYLYLTRANSFERASE AND 5'-PHOSPHATASE
-1.56	Rock2	RHO-ASSOCIATED COILED-COIL FORMING KINASE 2
-1.52	Rps6ka3	RIBOSOMAL PROTEIN S6 KINASE POLYPEPTIDE 3
-1.55	Scyl2	SCY1-LIKE 2 (S. CEREVISIAE)
-1.51	Smg7	SMG-7 HOMOLOG, NONSENSE MEDIATED MRNA DECAY FACTOR (C. ELEGANS)
-1.51	Srpk1	SERINE/ARGININE-RICH PROTEIN SPECIFIC KINASE 1
-1.55	Ssh2	SLINGSHOT HOMOLOG 2 (DROSOPHILA)
-1.69	Stk38	RIKEN CDNA 5830476G13 GENE
-1.65	Stk38l	SERINE/THREONINE KINASE 38 LIKE
-1.72	Styx	PHOSPHOSERINE/THREONINE/TYROSINE INTERACTION PROTEIN
-1.81	Traf3ip2	TRAF3 INTERACTING PROTEIN 2
1.62	Cish	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN
1.51	Mst1r	MACROPHAGE STIMULATING 1 RECEPTOR (C-MET-RELATED TYROSINE KINASE)
1.56	Met	MET PROTO-ONCOGENE
1.51	Mapk6	MITOGEN ACTIVATED PROTEIN KINASE 4
1.54	Flrt2	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE KINASE 5
1.67	Pip5kl1	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE-LIKE 1
1.56	Prkch	PROTEIN KINASE C, ETA
1.62	Pdk4	PYRUVATE DEHYDROGENASE KINASE, ISOENZYME 4
1.68	Mapk13	SAPK/ERK/KINASE 4
1.69	Snrk	SNF RELATED KINASE

 1.69
 Snrk
 SNF RELATED KINASE

 Data represtnt the average of 3 indipendent samples of WT and  $Tef7^{/r}$  memory OT-1 T cells analyzed on Mouse GENE 1.0 ST arrays.

 Negative fold changes indicate downregulated genes in  $Tef7^{/r}$  memory OT-1 cells and are shown in bold.

 Positive fold changes indicate upregualted genes in  $Tef7^{/r}$  memory OT-1 cells. All fold changes are statistically significant, p < 0.05.</td>

 Each subset was listed on alphabetical order based on the gene symbols.

 Genes highlighted in yellow are those among the top 20 upregulated or downregulated genes.