A Genome-wide Regulatory Network Identifies Key Transcription Factors for Memory CD8⁺ T Cell Development

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Abstract

Memory $CD8^+$ T cell development is defined by the expression of a specific set of memory signature genes (MSGs). Despite recent progress, many components of the transcriptional control of memory $CD8^+$ T cell development are still unknown. To identify transcription factors (TFs) and their interactions in memory $CD8^+$ T cell development, we construct a genome-wide regulatory network and apply it to identify key TFs that regulate MSGs. Most of the known TFs in memory $CD8^+$ T cell development are rediscovered and about a dozen new TFs are also identified. *Sox4*, *Bhlhe40*, *Bach2* and *Runx2* are experimentally verified and *Bach2* is further shown to promote both development and recall proliferation of memory $CD8^+$ T cells through *Prdm1* and *Id3*. Gene perturbation study identifies the mode of interactions among the TFs with *Sox4* as a hub. The identified TFs and insights into their interactions should facilitate further dissection of molecular mechanisms underlying memory $CD8^+$ T cell development.

Immunological memory refers to faster and stronger responses to re-encountering of the same antigen. The basis for this enhanced response is the persistence of more abundant and intrinsically more reactive antigen-specific memory T and B lymphocytes that are generated following the initial antigen stimulation. Memory $CD8^+$ T cells are usually generated following antigen-stimulated T cell activation and expansion. In a typical $CD8^+$ T cell response, naïve $CD8^+$ T cells are activated to undergo clonal expansion when stimulated by appropriate antigen ¹. The resulting T cells acquire effector functions and migratory properties that allow them to clear antigens in both lymphoid and non-lymphoid organs. As antigen is cleared, most of the effector T cells die by apoptosis and only a small fraction survive and differentiate into memory $CD8^+$ T cells. Memory $CD8^+$ T cells are often divided into two subsets. Effector functions following antigen stimulation to confer faster memory response. Central memory T cells (T_{CM}) are $CD62L^{hi}CCR7^{hi}$ and proliferate extensively upon antigen restimulation to confer stronger memory response.

Memory CD8⁺ T cells are developmentally programmed as they express a specific set of memory signature genes (MSGs)^{2,3}, which confer them with characteristic memory phenotype and function. Like many developmental processes, memory CD8⁺ T cell development is ultimately controlled by transcription factors (TFs) that integrate external and internal signals to regulate the expression of the MSGs. In recent years, several studies have shed light on TFs that regulate the development of memory $CD8^+$ T cells. T-bet (encoded by Tbx21) and Eomesodermin (encoded by *Eomes*), both member of the T-box family, are essential for the differentiation of effector and memory CD8⁺ T cells ^{4, 5, 6}. *Tcf*7 is a TF downstream of the Wnt signaling. Consistent with the observation that activation of Wnt/β-catenin signaling promotes memory CD8⁺ T cell development by suppressing terminal differentiation of effector T cells ^{7, 8}, Tcf7-deficiency in CD8⁺ T cells impairs T_{CM} differentiation ⁹. Klf2 has been shown to be associated with memory CD8⁺ T cell development ¹⁰ probably by directly controlling the expression of cell surface receptors S1P1 and CD62L^{11, 12}. Id2 and Id3, the E-box-containing transcription suppressors, appear to regulate the development of memory CD8⁺ T cell subsets ¹³. Id2-knockout mice are deficient in memory CD8⁺ T cells, but effector T cells generated in these mice are CD127^{hi}CD62L^{hi}, a phenotype similar to T_{CM}¹⁴. Deficiency in Id3 inhibits, whereas

overexpression of *Id3* promotes memory CD8⁺ T cell development ¹⁵. The B-cell transcriptional repressor Blimp-1 (encoded by *Prdm1*) promotes the terminal differentiation of effector CD8⁺ T cells and is required for recall response of memory T cells ^{16, 17}. Despite these progresses, the current understanding of transcriptional regulation of memory CD8⁺ T cell development is still limited, as additional TFs as well as their coordination are likely required to respond to external and internal signals in order to establish the MSG program for memory CD8⁺ T cell development.

In this study, we assemble a genome-wide regulatory network associated with the development of CD8⁺ T cells using publicly available gene expression data and a reverse-engineering algorithm. This regulatory network is applied to identify key TFs that regulate memory CD8⁺ T cell development using the master regulator analysis (MRA) of the MSGs of CD8⁺ T cells. The inferred TFs include most of the known TFs as well as a dozen new TFs with limited functional information in CD8⁺ T cell differentiation. A regulatory module controlling the MSGs is constructed and the high accuracy of the regulations in the module is verified using ChIP-PCR. Gene perturbations identify multiple regulatory motifs among the key TFs, suggesting their complex regulations during the memory CD8⁺ T cell development. Four of the newly identified key TFs (*Sox4*, *Bhlhe40*, *Bach2*, and *Runx2*) are experimentally validated to regulate memory CD8⁺ T cell development and function. Bach2 is shown to promote memory CD8⁺ T cell development and recall proliferation through Id3 and Prdm1. Our study represents the most comprehensive analysis of TFs and their interactions in memory CD8⁺ T cell development to date. The identified TFs and the insights into their mode of interactions provide a foundation for further dissecting the molecular mechanisms underlying memory CD8⁺ T cell development.

Results

Identification of TFs associated with memory CD8⁺ T cells

We collected 386 gene expression profiles of naïve, effector and memory CD8⁺ T cells of the mouse from 35 independent GEO datasets (Supplementary Table S1). 1,445 genes coding putative TFs ¹⁸ were manually mapped to the latest mouse genome to eliminate redundant and erroneous annotations, resulting in a total of 1,038 putative TFs. Among these putative TFs, 464 were expressed during the naïve to effector to memory CD8⁺ T cell development (see Methods

for detail). Using a reverse-engineering algorithm CLR (context likelihood of relatedness)¹⁹, the 386 gene expression profiles and the 1,038 putative TFs, a genome-wide regulatory network was assembled. The network consisted of 107,157 interactions among 11,032 genes. 62,272 interactions (58%) were between the 276 of the 464 expressed putative TFs and 8,572 target genes, suggesting that interactions are enriched among the expressed genes (P<0.001, binomial test). Furthermore, 3,219 of these interactions involve 154 out of 196 (79%) identified MSGs ³ (Supplementary Fig. S1).

To identify key TFs that regulate MSGs, we applied the MRA to the CLR-inferred interactions (Fig. 1a, see Methods). The MRA algorithm computes the statistical significance of overlaps of all interactions of each TF (inferred by CLR) with MSGs or a control gene set by a binomial test. From the 1,038 putative TFs, MRA identified 60 MSG-specific TFs at P<0.05 (binomial test), all of which are expressed in CD8⁺ T cells (Supplementary Table S2). These 60 candidates were filtered by removing those whose knockout do not have any immune system phenotype as defined in MGI (Mouse Genome Informatics)²⁰. The positive candidates were then analyzed for enrichment of DNA-binding motifs among MSGs or differential expression among naïve, effector and memory CD8⁺ T cells (see Methods). This led to 21 key TFs that were ranked according to the numbers of MSG they regulate (Table 1). Text-mining of public references on these 21 TFs revealed that 8 of 12 known TFs, which have been reported to be involved in memory CD8⁺ T cell development and function ^{21, 22, 23, 24}, were identified by our analysis. These results show that our systematic approach is valid for identifying TFs that regulate memory CD8⁺ T cell development.

Validation of a regulatory module for memory signature genes

To further explore the relative importance of the 21 identified TFs in regulating MSGs, we constructed a regulatory module using the top 10-ranked TFs (Fig. 1b). The resulting module contained 56% (86 out of 154) of MSGs that were present in the entire network (Supplementary Fig. S1). To verify this regulatory module, chromatin immunoprecipitation (ChIP) was performed for the top 3 TFs, *Sox4*, *Tcf7* and *Eomes*, in CD8⁺ T cells followed by PCR amplification of promoter regions (within 1 kb upstream of the transcription-starting site) of randomly selected MSGs that were predicted to be regulated by *Sox4* or *Tcf7* or *Eomes*. As shown in Fig. 1c and 1d, promoter regions of 10 out of the 12 randomly selected *Sox4*-regulated

MSGs were amplified. Similarly, 12 out of 14 randomly selected *Tcf*7-regulated MSGs and 6 out of 9 randomly selected Eomes-regulated MSGs were amplified. On average, 80% of the tested promoter regions were immunoprecipitated with antibodies specific for each of the three TFs (Table 2), confirming the high accuracy of the constructed regulatory module. Furthermore, when the cumulative coverage of MSGs was plotted as a function of each of the 21 TFs, the top 2 TFs, *Sox4* and *Tcf7*, were shown to regulate 42% of MSGs (Supplementary Fig. S2).

Perturbation network of key TFs

Although the constructed regulatory module predicts interactions between TFs (Fig. 1b), the directions of regulation are not known. To find out these, the top 10 TFs and another two known memory-regulating TFs (*Id3* and *Tbx21*, #12 and #19 in the list, Table 1)^{6, 15, 25} were perturbed in CD8⁺ T cells *in vitro* by overexpression through retroviral transduction. The transcript level of each of the 12-selected TFs was measured by quantitative real-time PCR (Table 3). If changes in transcript level of \geq 2 fold were taken as directional regulations, the perturbation results identified 41 regulations among the 12x12 matrix (31%). Notably, the top 3 TFs (*Sox4*, *Tcf7* and *Eomes*) directed 19 of the 41 regulations. To verify these regulations, ChIP-PCR was performed using antibodies specific for Sox4, Tcf7 and Eomes. As shown in Fig. 2a, 18 of the 19 regulations were confirmed. ChIP-PCR also identified 4 more regulations that were not observed in the perturbation study. Thus, compared to ChIP-PCR, perturbation studies is able to identify the directional regulations with 82% sensitivity and 91% specificity.

We then constructed a perturbation network of the 12 TFs with directional regulations (Fig. 2b). The top 3 TFs (*Sox4*, *Tcf7* and *Eomes*) and *Bach2* had more downstream targets than the number of TFs that regulate them (Supplementary Fig. S3), suggesting that they are at the upstream of a regulatory structure. TFs in the perturbation network formed multiple motifs, such as feedback and feed-forward loops (Supplementary Fig. S4). For example, in a feedback motif of *Sox4-Tcf7-Eomes-Tbx21* (Fig. 2c), *Sox4* and *Tcf7* regulate each other and they also regulate expression of *Eomes* and/or *Tbx21*. The latter regulations were further confirmed at the protein level as indicated by suppression of Eomes and Tbx21 by overexpression of *Sox4* or *Tcf7* (Supplementary Fig. S5). These results suggest that complex regulations involving multiple regulatory motifs among these TFs are involved in memory CD8⁺ T cell development.

Validation of Sox4 and Bach2 in memory CD8⁺ T cells

Among the top 10 TFs (Table 1), 6 are known to play important roles in memory CD8⁺ T cell development and/or function. We then investigated whether the other 4 TFs (Sox4, Bhlhe40, *Bach2* and *Runx2*) are also involved in memory CD8⁺ T cell development/function by examining the effect of overexpression and knockdown of these TFs on the recall proliferation of memory CD8⁺ T cells *in vitro* and *in vivo*. CD8⁺ T cells expressing the 2C TCR were activated with cognate peptide SIYRYYGL (SIY) and then transduced with retroviruses expressing GFP plus Sox4, Bhlhe40, Bach2 or Runx2 or expressing GFP plus shRNA specific for one of the four TFs (Supplementary Table S3 and S4). The 2C T cells were then cultured in the presence of cytokine IL-7 to induce the development of memory $CD8^+$ T cells (Supplementary Fig. S6). To assay recall proliferation, the *in vitro* memory 2C T cells were restimulated with SIY and the number of transduced (GFP⁺) and non-transduced (GFP⁻) 2C T cells were quantified on day 4 and 6. Compared to the vector control, overexpression of Sox4 or Bach2 led to a significant increase in the proportions of GFP⁺ cells (Fig. 3a), suggesting a higher recall proliferation. When the *in vitro* generated memory 2C T cells were adoptively transferred into C57BL/6 (B6) mice followed by activation through infection with influenza virus that express SIY (WSN-SIY virus)²⁶, a significant increase in the proportion of GFP⁺ 2C T cells was also observed in the draining lymph nodes (DLN) (Fig. 3b), the blood, lung and spleen (Supplementary Fig. S7) 5 days post infection (dpi) if the transduced memory T cells expressed Sox4 or Bach2. Conversely, knockdown of Sox4 or Bach2 (Supplementary Fig. S8) resulted in a significant inhibition of the recall proliferation of memory 2C T cells both in vitro and in vivo (Fig. 3c,d). Although overexpression of *Bhlhe40* and *Runx2* inhibited the *in vivo* recall proliferation of the transduced memory 2C T cells (Fig. 3b), no significant change was observed in *in vitro* recall response (Fig. 3a) and in knockdown assay (Fig. 3c,d). As positive controls, we tested in parallel known TFs: overexpression of *Eomes* promoted the recall proliferation whereas overexpression of *Klf2* inhibited the recall proliferation (Supplementary Fig. S9), consistent with previous reports ^{9, 11}. These results show that *Sox4* and *Bach2* likely promote the recall proliferation of memory CD8⁺ T cells.

Enhanced memory T cell development by *Bach2* overexpression

To confirm the effect of overexpression of *Bach2* on recall proliferation of memory CD8⁺ T cells, we activated 2C T cells *in vitro* for two days, transduced the activated T cells with retroviruses expressing GFP alone or GFP plus Bach2. The cells were cultured in the presence of IL-2 for two more days and then adoptively transferred into antigen-free B6 mice to induce in vivo memory 2C T cells (Fig. 4a). Twenty-three days after transfer, the frequency, phenotype and function of persisting 2C T cells were analyzed. Both transduced (GFP⁺) and non-transduced (GFP⁻) 2C cells persisted in the recipient mice (Fig. 4b), GFP⁺ 2C cells exhibited a typical memory phenotype as indicated by expression of CD62L and IL-7 receptor (IL-7R), similar to the GFP⁻ 2C cells in the same recipient (Fig. 4c). The persisting memory 2C cells, both transduced and non-transduced, were rapidly induced to express IFNy and TNF α following antigen stimulation (Fig. 4d). Furthermore, some recipient mice were infected with WSN-SIY virus and the recall proliferation of persisting 2C cells in the spleen and DLN were analyzed 7 days later. As shown in Fig. 4e, if the 2C cells were originally transduced with GFP-expressing retrovirus, the proportion of GFP⁺ versus GFP⁻ 2C cells did not changed following WSN-SIY challenge. However, if the 2C cells were originally transduced with GFP and *Bach2*-expressing retrovirus, the proportion of GFP⁺ cells was significantly higher in both DLN and spleen, suggesting a stronger recall proliferation by *Bach2*-expressing memory 2C cells.

The observed stronger recall response by *Bach2*-expressing memory 2C cells could be due to the generation of more memory T cells and/or that the *Bach2*-expressing memory T cells are more responsive to restimulation. To investigate these possibilities, we activated 2C T cells *in vitro* for two days and transduced them with retroviruses expressing GFP alone (vector) or GFP plus *Bach2* (Fig. 5a). Twenty-four hours later, the T cells were adoptively transferred into B6 mice followed by WSN-SIY virus infection. 2C T cells, vector-transduced 2C T cells had the same expression profiles for CD62L, IL-7R, Klrg1 and CD27 in the same organs of the same mice (Fig. 5b, upper panel). In contrast, a significantly higher proportion of *Bach2*-transduced 2C T cells expressed CD62L and CD27, but a significantly lower fraction expressed Klrg1, in the DLN and spleen compared to non-transduced 2C cells in the same organs of the same recipients. When the persisting 2C T cells were analyzed 30 dpi, no significant differences in IFN γ and IL-2 expression were observed among non-transduced, vector-transduced and *Bach2*-transduced 2C T

cells in response to restimulation *in vitro* (Fig. 5c and Supplementary Fig. S10). Although no difference in CD62L and IL-7R expression was detected, CD27 was higher in *Bach2*-transduced than vector-transduced 2C T cells in the lung and DLN. (Fig. 5c and Supplementary Fig. S10). Importantly, significantly more *Bach2*-transduced 2C T cells persisted in the DLN, spleen and bone marrow (Fig. 5d,e). These result suggest that overexpression of *Bach2* likely promotes the generation of memory CD8⁺ T cells *in vivo*.

We further investigated the effect of *Bach2* overexpression in naïve 2C T cells on memory CD8⁺ T cell development *in vivo*. Bone marrow progenitor cells isolated from 2C TCR transgenic mice were transduced with retroviruses expressing GFP alone or GFP plus Bach2 and adoptively transferred into sublethally irradiated Rag2^{-/-} mice to generate naïve 2C T cells that express GFP or GFP plus Bach2 (Fig. 6a). The resulting transduced and non-transduced naïve 2C cells were then adoptively transferred into B6 mice followed by infection with WSN-SIY virus. The frequency, phenotype and function of 2C T cells were analyzed 7 dpi. Vector-transduced and non-transduced 2C T cells from the same recipient mice had the same expression profile of CD62L, IL-7R, Klrg1, IFNγ and TNFα (Fig. 6b). While *Bach2*-transduced 2C T cells expressed similar levels of IFNy and TNF α as non-transduced and vector-transduced 2C T cells, more cells expressed CD62L but fewer cells expressed Klrg1, resembling to CD62L^{hi}Klrg1^{low} memory precursors (Fig. 6b and Supplementary Fig. S11). By 30 dpi, no significant differences were observed among non-transduced, vector-transduced and Bach2-transduced 2C T cells in expression of CD62L, IL-7R, Klrg1, IFNy and TNFa (Fig. 6c). However, more Bach2transduced 2C T cells were found in the blood, lung, DLN and spleen 30 dpi (Fig. 6d.e). Together, these data suggest that overexpression of *Bach2* promotes the development of memory $CD8^+$ T cells.

Diminished memory T cell development due to Bach2 deficiency

We also examined the effect of Bach2 knockdown on memory T cell development. The approach was the same as outlined as in Figure 5a, except the retrovirus expressed shRNA specific for Bach2. Briefly, activated 2C T cells were transduced with shRNA-expressing retrovirus and adoptively transferred into B6 mice followed by infection with WSN-SIY influenza virus. The number and frequency of GFP⁺ and GFP⁻ 2C T cells in various organs were analyzed 7 and 30

dpi. No significant difference was observed among non-transduced, vector-transduced and shRNA-transduced 2C T cells in terms of CD62L, IL-7R, Klrg1, CD27 and IFNγ expression (Supplemental Fig. S12). However, the proportion of shRNA-transduced 2C T cells was reduced significantly in the blood, lung, DLN, spleen and bone marrow 30 but not 7 dpi (Fig. 5f). Consistently, the number of shRNA-transduced 2C T cells in the spleen was lower as compared to the numbers of non-transduced and vector-transduced 2C T cells 30 dpi (Supplemental Fig. S12c).

To investigate the effect of Bach2 knockout on memory T cell development, we constructed chimeric mice where T and B cells were deficient in Bach2 by adoptively transferring bone marrow cells from Bach2 knockout mice into sublethally irradiated Rag2^{-/-} mice. Three months after reconstitution, mice were infected with WSN-SIY influenza virus and analyzed for the presence of SIY-specific memory CD8⁺ T cells 30 days later. The percentage of SIY-specific CD8⁺ T cells was lower in the DLN and spleen of chimeric mice that were reconstituted with Bach2^{-/-} than Bach2^{+/+} bone marrow cells (Fig. 5g). Consistently, the number of SIY-specific CD8⁺ T cells in the spleen was lower in mice reconstituted with Bach2^{-/-} than Bach2^{+/+} bone marrow cells. Considering that *Bach2* expression was down-regulated in effector and then up-regulated in memory T cells during naïve to effector to memory cell transition (Table 1), together these results show that Bach2 promotes memory CD8⁺ T cell development.

Enhanced proliferation of T cells by *Bach2* overexpression

To further explore the mechanism underlying the observed effect of *Bach2* on memory T cell development and response, we examined whether *Bach2* affects T cell proliferation. 2C T cells were activated *in vitro* and transduced with either vector or *Bach2*-expressing retroviruses. The cells were cultured in the presence of either IL-2 or IL-7 and the proportion of transduced (GFP⁺) versus non-transduced (GFP⁻) cells in the same cultures was quantified over time. In the IL-7 culture, the proportion of transduced versus non-transduced 2C cells remained stable regardless whether the 2C T cells were transduced with vector or *Bach2* (Fig. 7a). Similarly, the proportion of vector-transduced versus non-transduced 2C cells remained stable in the IL-2 cultures. However, the proportion of *Bach2*-transduced 2C T cells increased significantly over time in the IL-2 cultures (Fig. 7a). When the cells were lableled with eFluor and followed over time, *Bach2*-

transduced 2C T cells diluted the flourescent dye more extensively than non-transduced 2C T cells (Fig. 7b). These data suggest that *Bach2* promotes proliferation of activated $CD8^+$ T cells.

We noticed a feed-forward regulatory motif of *Sox4-Bach2-Prdm1-Id3* in the perturbation network (Fig. 7c and Supplementary Fig. S4). We verified this regulatory motif by showing that overexpression of *Bach2* suppressed expression of *Prdm1* but stimulated expression of *Id3* at transcriptional (Table 3) and translational levels (Fig. 7d). ChIP-PCR analysis with anti-Bach2 antibody also confirmed that Bach2 binds directly to the promoter regions of *Prdm1* and *Id3* (Fig. 7e, f). Further supporting the regulatory motif, overexpression of *Prdm1* significantly reduced the *Bach2*-mediated proliferation of activated T cells (Supplementary Fig. S13). As *Prdm1* is known to inhibit T cell proliferation whereas *Id3* stimulates survival of effector T cells ^{15, 16}, we determined the effect of *Bach2* overexpression on molecules that regulate cell cycle and survival. Overexpression of *Bach2* stimulated CDK4, CDK6 and Bcl6 expression and Rb phosphorylation at amino acid residues 780 and 795 but inhibited expression of p27kip (Fig. 7g). These results suggest that *Bach2* regulates memory T cell development and recall proliferation by regulating cell cycle control possibly through *Prdm1* and *Id3*.

Discussion

At the molecular level, development of memory $CD8^+$ T cells is the establishment of MSG expression program, which ultimately is controlled by TFs. Although several TFs have been described to regulate memory $CD8^+$ T cell development, for a comprehensive understanding of transcriptional regulation of memory $CD8^+$ T cell development, it is necessary to identify most, if not all, key TFs that regulate MSGs and construct a genome-wide transcriptional network that supports memory $CD8^+$ T cell development. Using systems biology approaches and publically available gene expression data, here we have assembled a genome-wide regulatory network associated with $CD8^+$ T cells of the mouse. Applying MRA to this network, we have identified twenty-one key TFs, down-narrowed from 1038 putative TFs, which regulate the expression of 70% of MSGs. Our approach is valid based on the following considerations. First, our method identified eight of the twelve TFs known to be involved in memory $CD8^+$ T cell development, including *Tcf7*, *Eomes*, *Prdm1*, *Klf2*, *Id2*, *Stat4*, *Id3* and *Tbx21* (Table 1). Although *Bcl6*, *Stat3* and *Myc* are known to regulate memory $CD8^+$ T cell development, they were not within the top

21 TFs identified using our methodology because CLR-inferred targets do not overlap with MSGs possibly due to limited data on MSGs or the network. NF- κb plays important roles in both effector and memory T cell development $^{27, 28}$. We found that *NF-kb* was a key TF that regulates effector signature genes (ESG) when MRA was applied to the network and ESGs. Second, our method identified several TFs that are not known to function in the memory CD8⁺ T cell development, including Sox4, Bhlhe40, Bach2 and Runx2 in the top 10 TFs (Table 1). Follow-up experimentation showed that these newly identified TFs indeed play important roles in memory $CD8^+$ T cell development and function. Overexpression of Sox4 and Bach2 promoted a significantly higher recall proliferation of memory CD8⁺ T cells both *in vitro* and *in vivo*. Conversely knockdown of Sox4 and Bach2 inhibited the recall proliferation of the transduced memory T cells (Fig. 3). Overexpression of Bhlhe40 and Runx2 inhibited the in vivo recall proliferation, although no significant change was observed in *in vitro* recall response and in knockdown assay (Fig. 3). Further analysis showed that overexpression of Bach2 also promotes memory CD8⁺ T cell development (Fig. 4-6). Third, compared to the traditional method of differential gene expression analysis ^{2, 3}, which generates a long list of candidates using foldchange-based approaches, our network methods identify and rank order TFs according to their statistical importance. Reduction of hundreds of TFs to two-dozen key TFs makes direct experimental validation more manageable. The network approach and methodologies developed here can be applied to any phenotypic transition, such as effector T cells and exhausted T cells, to identify novel transcriptional modules and TFs.

Studies have suggested that memory $CD8^+$ T cell development is coordinately regulated by several TFs (reviewed in Refs. ^{22, 24}), including *Eomes* and *Tbx21*⁴. Our network and perturbation studies have now greatly expanded the understanding of the mode of interactions to the top 21 TFs. Our analysis reveals a dense overlapping regulation (DOR) among the key TFs (Fig. 2b). This mode of regulation is essential for sensing multiple external signals and integrate them into distinct cell fate outcomes ²⁹. As two classes of TFs have been proposed to control the developmental potentials of effector and memory fates in a quantitative manner ^{22, 24, 30}, the DOR might contribute to the quantitative regulations during effector to memory CD8⁺ T cell development. Our analysis also shows complex regulations with both feedback and feed-forward motifs among the key TFs (Table 3 and Fig. 2b). In the regulatory motif of *Sox4-Tcf7-Eomes*-

Tbx21, Tcf7, Eomes and Tbx21 are known to be critical for memory CD8⁺ T cell development. The association of *Sox4* with these three TFs and especially its "hub" position in this motif are intriguing. *Sox4* is not known to regulate memory CD8⁺ T cell development. However, it stabilizes β -catenin to modulate Wnt-Tcf7 signaling ^{31, 32}, which promotes memory CD8⁺ T cell development. *Sox4* also regulates 'stemness' of cancer cells ³³, a property shared by memory T cells. Furthermore, evidence suggests that *Sox4* might be a direct regulatory target of TGF β signaling ³⁴, which is essential for the differentiation of CD8⁺ T cells ³⁵. These previous observations, together with our finding of the "hub" position of *Sox4* in the regulatory motif of *Sox4-Tcf7-Eomes-Tbx21*, suggest that Sox4 is a critical TFs regulating memory CD8⁺ T cell development. While this hypothesis has yet to be validated, our finding that overexpression of Sox4 promotes recall proliferation of memory T cells suggests that Sox4 is involved in memory CD8⁺ T cell development.

In the regulatory motif of Sox4-Tcf7-Eomes-Tbx21, we found that Tcf7 binds to Eomes promoter (Fig. 2a) and retroviral expression of Tcf7 leads to a downregulation of Eomes transcript (Table 3) and protein (Supplementary Fig. S5). The latter results contradict with the previous report showing that the level of Eomes transcript and protein are decreased in memory CD8⁺ T cells from Tcf7-deficient mice⁹. Although we do not know the precise causes underlying the observed opposite effects, the following differences between the two studies may provide part of the explanation. First, our study was carried out in *in vitro*, using activated CD8⁺ T cells that are in transition to memory T cells, whereas the previous study used memory CD8⁺ T cells directly from mice. Second, in our study, we overexpressed Tcf7 for a short period (72 hrs) before assaying the effect on Eomes expression, whereas the previous study examined the accumulated effect of germline Tcf7 knockout on Eomes expression. The differences in the stage of T cells, in vitro vs. in vivo, overexpression vs. deficiency, and the length of Tcf7 overexpression or deficiency could all contribute to the observed differences in the two studies. Although the discrepancy raises concern of our approach, results from our perturbation study on the effect of Bach2 on Prdm1, Prdm1 on Tcf7, and Id2 on Id3 are all consistent with previous reports ^{17, 36, 37}, suggesting the validity of our in vitro assay in most cases.

Our detailed analysis of the feed-forward motif of Sox4-Bach2-Prdm1-Id3 (Fig. 7c) reveals new insight into memory CD8⁺ T cell development. This regulatory motif includes two known TFs (*Id3* and *Prdm1*) and two unknown TFs (*Sox4* and *Bach2*) in memory $CD8^+$ T cell development. Through both overexpression and knockdown/knockout in CD8⁺ T cells both *in vitro* and in mice, we provide extensive evidence showing that *Bach2* promotes memory CD8⁺ T cell development (Fig. 4-6). One mechanism appears to be by stimulating the induction of memory T cell precursors as Bach2-expression in effector T cells leads to a phenotype of CD62L^{hi}Klrg^{lo}CD27⁺ (Fig. 5b-c and Supplementary Fig. S10), which is considered as central memory T cell precursors with high proliferative potential ^{38, 39}. Recently, two studies report that Bach2 regulates CD4⁺ T cell development and function by suppressing effector gene expression ^{40, 41}. Our observation that Klrg1 is suppressed by Bach2 suggests that suppression of effector function may also be important for the development of memory CD8⁺ T cells. Another mechanism is by stimulating T cell proliferation. We showed that overexpression of Bach2 enhances IL-2 driven T cell proliferation in vitro and recall proliferation in vitro and in vivo. In addition, when in vitro memory 2C T cells were labeled with eFluro dye and adoptively transferred into Rag-/- mice, Bach2-transduced T cells diluted the flourescent dye more extensively than the non-transduced and vector-transduced T cells (Supplemental Fig. S14). The enhanced proliferation could lead to development and/or survival of memory T cells.

Our study further sheds light on the mechanisms by which Bach2 promotes T cell proliferation. In the regulatory motif, *Bach2* promotes *Id3* expression but suppresses *Prdm1* expression through direct binding to their promoter regions (Fig. 7c-f), the latter is consistent with *Bach2* suppression of *Prdm1* expression in B cells ³⁷. *Id3* is known to promote cell cycle and recall proliferation of memory CD8⁺ T cells by binding to and inhibiting E proteins ^{15, 42}. Thus, by promoting *Id3* expression, *Bach2* stimulates T cell proliferation. *Prdm1* is known to antagonize *Bcl6*, which promotes cell cycle by suppressing the expression of cell cycle inhibitor p27kip ⁴³. *Bcl6^{-/-}* mice exhibit a profound deficiency of memory T cells ^{44, 45}, whereas in the absence of p27kip, memory CD8⁺ T cells exhibit enhanced homeostatic and recall proliferation ⁴⁶. Consistently, we show that overexpression of Bach2 promotes Bcl6 expression but inhibits p27kip expression (Fig. 7g). Thus, Bach2 also stimulates T cell proliferation by suppressing

Prdm1 expression. Together, these findings suggest that *Bach2* promotes memory CD8⁺ T cell development and recall proliferation through Id3- and Prdm1-mediated cell cycle control.

Development of memory $CD8^+$ T cells requires integration of multiple external and internal signals to establish a new transcriptional program of MSGs that endows memory $CD8^+$ T cells with characteristic features in phenotype, tissue distribution, homeostasis and recall potentials. In this study, we have shown that integrated systems biology approaches can be effectively used to identify key TFs and their mode of interactions that underlies memory $CD8^+$ T cell differentiation and function. Further analysis of motifs in the regulatory network should help to elucidate in detail the molecular mechanisms underlying memory $CD8^+$ T cell development and function.

Methods

Regulatory network and master regulator analysis

386 public microarrays related to CD8⁺ T cells from 35 independent GEO datasets (till September 2009) were downloaded from the NCBI database of Gene Expression Omnibus (GEO) (Supplementary Table S1). All raw image files were reprocessed to normalize the data using R program with a gcRMA method. Gene expression data was used to construct the regulatory network with the putative TFs using a reverse engineering algorithm CLR ¹⁹. Among the 1,445 putative TFs identified according to the domain predictions of protein sequences ¹⁸, 1,038 were manually mapped to the latest mouse genome. To compare gene expression in different CD8⁺ T cells, samples were grouped into naïve, effector and memory based the cell types from which the microarray analysis were done (Supplementary Table S1). Gene was considered as expressed in CD8⁺ T cells if the average gene expression level in one of the three groups was more than 8 (gcRMA values).

To identify TFs associated with memory $CD8^+$ T cell development, we used Master Regulator Analysis (MRA) to compute the statistical significance of overlaps of all interactions of each TF (inferred by CLR) with MSGs or a control gene set by a binomial test. The MSGs were differentially expressed genes between memory $CD8^+$ T cells and naïve/effector $CD8^+$ T cells identified previously ³. 332 background genes were identified from the 386 gene expression profiles based on high levels of gene expression (gcRMA value >10) but minimal variation among 386 samples (variation from mean <0.5). This criterion minimizes the potential of the selected genes not being regulated by TFs in $CD8^+$ T cells. From the 1,038 putative TFs, MRA identified 60 MSG-specific TFs at *P*<0.05 (binomial test), all of which are expressed in $CD8^+$ T cells (Supplementary Table S2). These 60 candidates were filtered by removing those whose knockout does not have any immune system phenotype as defined in MGI ²⁰. The positive candidates were analyzed for enrichment of DNA-binding motifs in the promoter regions (-2000 to -1) of the MSGs using the program MatInspector ⁴⁷ or differential expression among naïve, effector and memory $CD8^+$ T cells. This led to 21 key TFs that exhibit immune system phenotype with either an enrichment of DNA-binding motifs among MSGs or differential expression.

Mice and virus

The 2C TCR transgenic mice on Rag2^{-/-} and C57BL/6 (B6 Thy1.1⁺) background (2C⁺Rag^{-/-}) were maintained in the animal facility at the Massachusetts Institute of Technology (MIT). These mice express the 2C TCR on CD8⁺ T cells specific for SIYRYYGL peptide (SIY) in association with MHC class I K^b molecule ⁴⁸. B6 and Rag2^{-/-} mice were from the Jackson Laboratory. Mice were used at 8-16 weeks of age. All animal studies and procedures were approved by the Massachusetts Institute of Technology's Committee for Animal Care. Recombinant WSN-SIY virus encoding the SIY epitope in the neuroaminidase stalk was constructed by plasmid-based reverse genetics and grown in Madin-Darby canine kidney cells ²⁶. For infection, mice were anesthetized and given 100 pfu (sublethal dose) intranasally.

Flow cytometry and cell sorting

Antibodies specific for CD8 α , Thy1.1, Klrg1, CD62L, CD127 (IL-7R), CD27, IFN γ , TNF α , IL-2, Eomes and T-bet (Tbx21) were purchased from BioLegend or eBiosciences and used at the recommended concentration. Single cell suspensions were prepared from spleens and mediastinal (draining) lymph nodes (DLN), peripheral blood, and lung. Splenocytes and lymphocytes were collected in 8 ml HBSS by crushing the spleen and lymph node with frosted glass slides and filtering the cell suspension through 80 µm nylon filters, respectively. Lungs were harvested and ground through a cell strainer, followed by incubation with 2 ml of digestion buffer (RPMI 1640 medium containing 3mg/ml of collagenase A (Roche), 5% FBS and 10mM HEPES) at 37°C for 1 hour. Red blood cells (RBCs) in the spleen, blood and lung were lysed with RBC lysis buffer (Gibco) and the cells were washed with complete RPMI. The cells were counted and 1-3 $\times 10^6$ cells were used for surface staining. Cells were washed twice with PBS plus 2% FBS before cytometry analsysis. For intracellular staining, splenocytes were stimulated with SIY peptide for 5 hours in the presence of GolgiPlug (BD Biosciences). Cells were washed twice with PBS and stained with indicated antibodies. The cells were then fixed and stained with labeled antibodies using an intracellular staining kit (Cytofix/Cytoperm kit; BD Biosciences) according to the manufacture's instructions. Stained cells were analyzed on either a FACSCalibur or AccuriTM C6 flow cytometer (BD Biosciences). 0.5-2 $\times 10^6$ events were collected and analyzed with FlowJo software. Cell sorting was carried out with a MoFlo cell sorter or FACSAria (BD Biosciences).

Retrovirus production and infection

Retroviral pMIGw-GW gateway vector was constructed by inserting a gateway cassette at EcoRI site of the pMIGw vector (Addgene #9044) using a gateway construction kit (Invitrogen). All ORFs encoding 12 TFs were amplified with primers (Supplementary Table S3) and cDNA from mouse splenocytes and cloned into pMIGw-GW using the gateway cloning technology. shRNAs for specific TFs (Supplementary Table S4) were chosen from the predicted TRC library and cloned into pMKO.1 GFP retroviral vector (Addgene #10676). Briefly, synthesized single-strand sense and antisense oligonucleotides were annealed into double-strand oligonucleotides for short hairpin RNA in the annealing buffer (10mM TrisCl (pH7.5), 50mM NaCl and 1mM EDTA). The double-strand oligonucleotides were directly treated with T4 polynucleotide kinase (NEB) and ligated into pMKO.1 GFP vector) between AgeI and EcoRI sites.

293FT cells were cultured to 60% confluency in 6-well plates. Cells were co-transfected with retroviral vector plasmid (4 μ g) and packing plasmids pCL-Eco (1 μ g) with 150 μ l DMEM and 15 μ l TransIT[®]-LT1 (Mirus) according to the manufacture's instructions. On the second day, the culture was replaced with fresh medium. On the third day, supernatant was collected and filtered through a 0.45 μ m low-protein binding membrane (Pall Life Science). Fresh viral supernatants were used for spin infection of CD8⁺ T cells in all experiments.

For infection, cells from spleens and lymph nodes were harvested from $2C^{+}RAG^{-/-}$ mice, pooled and cultured in 6-well plates in the presence of SIY peptide (1µg/ml) in the complete

RPMI medium (RPMI 1640 supplemented with 10% FBS, 5mM HEPES, 2 mM glutamine, 100U/ml penicillin, 100µg/ml streptomycin and 50µM β -mercaptoethanol (Invitrogen)). Two days later, activated 2C T cells were collected, washed and resuspended at 2 x 10⁶ cells per ml in the complete RPMI medium. 1ml fresh retrovirus supernatants and 0.25ml 2C cells with a final concentration of 5µg/ml polybrene (American Bioanalytical) were added to one well of a 24-well plate and spun for 90min at 2500rpm at 32°C to infect T cells. 24 hours later, cells were collected for direct adoptive transfer, or resuspended and cultured in 3ml fresh RPMI medium with 100U/ml IL-2 (eBioscience). After culture for 24 hours, 2C T cells were analyzed for GFP expression by flow cytometry and prepared for injection into mice to generate *in vivo* memory T cells or further culture to generate *in vitro* memory T cells.

Generation and recall proliferation of memory T cells

To generate *in vitro* memory T cells, activated (and transduced) 2C T cells were cultured in complete RPMI medium supplemented with 5ng/ml IL-7 (Peprotech) for 7 days with change of fresh IL-7-supplemented medium every two days. Cells were analyzed for memory phenotype by flow cytometry on day 7. To test the recall proliferation, *in vitro* memory 2C T cells ($1x10^5$) were cultured with B6 splenocytes ($5x10^5$) in a 12 well plate in complete RPMI medium supplemented with 1 µg/ml SIY peptide and 100 units/ml IL-2. The numbers and phenotype of 2C T cells were analyzed by flow cytometry 4 and 6 days later. Alternatively, *in vitro* memory 2C T cells ($2x10^5$) were transferred to B6 recipients and challenged with WSN-SIY virus. 2C cells were analyzed by flow cytometry 5 dpi.

To generate *in vivo* memory T cells, activated and transduced 2C T cells were adoptively transferred into B6 recipients. Twenty-third days later, the frequency, phenotype and function of persisting 2C T cells were analyzed by flow cytometry. To assay for recall response, mice were infected with 100pfu WSN-SIY virus and the number and phenotype of 2C T cells in different organs were analyzed by flow cytometry 7 dpi.

Bone marrow chimera mice

Bone marrow cells were collected from the tiba and femur of 2C⁺Rag^{-/-} mice. Stem and progenitor cells were enriched using a progenitor enrichment kit (Stemcell Technologies) according to the manufacture instructions. The enriched cells were cultured for 48 hours in

complete RPMI medium supplemented with IL-3 (30ng/ml), IL-6 (10ng/ml) and SCF (15ng/ml). The cells were resuspended at 2 x 10^6 cells per ml in complete RPMI. 600µl fresh retrovirus supernatants and 400µl cells plus a final concentration of 6 µg/ml polybrene were added to one well of a 24-well plate and spun for 90min at 2500rpm at 32°C. One the second day, cells were collected and washed and injected into Rag^{-/-} mice that had been irradiated for 500rads 4 hours earlier. Eight weeks later, mice were bleeded to determine the reconstitution of CD8⁺ T cells and GFP proportion by flow cytometry. Twelve weeks later, cells were collected from spleen and analyzed for 2C T cell percentage and phenotype. Splenocytes containing 5×10^4 2C T cells were adoptively transferred into B6 mice followed by WSN-SIY infection. The number, phenotype and function of 2C T cells in the recipient mice were analyzed 7 and 30 dpi. To generate Bach2^{-/-} chimeric mice, bone marrow cells from Bach2^{-/-} mice ⁴⁹ (kindly gift of Dr. Kazuhiko Igarash of Tohoko University, Japan) were directly injected into sublethally irradiated Rag2^{-/-} mice. Eight weeks later, reconstitution of CD8⁺ T cells were verified by flow cytometry of peripheral blood mononuclear cells. Twelve weeks later, mice were infected with 50 pfu WSN-SIY virus and 30 dpi SIY-specific CD8⁺ T cells in various tissues were identified by H-2K^b DimerX (BD Biosciences) loaded with SIY peptide plus anti-CD8 by flow cytometry.

Gene perturbations and quantitative PCR

To perturb the network, selected TFs were overexpressed in $CD8^+ 2C$ T cells by retrovirus transduction as described above. Transduced 2C T cells were cultured in the presence of IL-7 for 24 hours and GFP⁺ 2C T cells were purified by sorting (>95% viable by PI staining). Total RNA was extracted from the purified 2C T cells using RNeasy micro kit (Qiagen) according to the manufacture's instructions. First strand cDNA was synthesized from 1 µg total RNA using the TaqMan® Reverse Transcription Reagents (ABI). 2 µl of diluted cDNA (total 200 µl) were used as template for the quantitative PCR with LightCycler®480 SYBR Green and LightCycler®480 machine (Roche). For each TF transduced CD8⁺ T cells, the transcript levels of 12 TFs were measured by qPCR using gene specific primers (Supplementary Table S5). To measure the transcript level of TFs in naïve, effector and memory CD8⁺ T cells, naïve 2C T cells were adoptively transferred into B6 mice followed with WSN-SIY virus infection, effector and memory 2C T cells were sorted from spleen 7 dpi and 30 dpi, respectively. Total RNA was

isolated from naïve, effector and memory 2C T cells and used for quantification of the transcript level of each TF by PCR.

ChIP and ChIP-PCR

A Millipore ChIP kit was used for chromatin immunoprecipitation. DNA-protein complexes were cross-linked with formaldehyde at a final concentration of 1%, sheared by sonication to 800~1000bp, followed by precipitation with nonspecific goat anti-IgG (Sigma) or rabbit anti-IgG (Cell Signaling Technology) or chromatin ChIP-grade anti-Sox4 (C-20, Santa Cruz Biotechnology), anti-Tcf7 (H-118, Santa Cruz Biotechnology), and anti-Eomes (ab23345, Abcam). DNA-protein complex was eluted, and ChIP DNA was purified by PCR purification kit (Qiagen). The promoter regions of the indicated TFs or MSGs were amplified using specific primers (Supplementary Table S6). Primers used to amplify the promoter regions were all within this 1 kb upstream of the transcription-starting site. For ChIP of Bach2 with anti-Bach2 (E-16, Santa Cruz Biotechnology), cross-linked DNA-protein complexes were digested to 400~600bp by micrococcal nuclease (Cell Signaling Technology).

Protein extraction and western blotting

Proteins were extracted from transduced 2C T cells with the CelLyticTM Lysis Reagent (Sigma). Samples containing 20µg total protein (BCATM Protein Assay Kit, Pierce Biotechnology) were resolved on a 10% SDS-PAGE gel and electro-transferred onto a PVDF membrane (Millipore Corporation). The membrane was blocked in 5% (w/v) fat-free milk in PBST (PBS containing 0.1% Tween-20). The blot was hybridized overnight with primary antibodies: anti-GAPDH (HRP-conjugated, Cell Signaling Technology, 1:2000), anti-Sox4 (C-20, Santa Cruz Biotechnology, 1:500), anti-Bach2 (AP10133b, Abgent, 1:500), anti-Id3 (6-1, CalBioreagents, 1:2500), anti-Blimp-1 (6D3, eBioscience, 1:1000), anti-Bcl2 (BioLegend, 1:500), anti-Bcl6 (BioLegend, 1:2000), anti-pFoxO1 (Cell Signaling Technology, 1:1000), anti-CDK4 (Cell Signaling Technology, 1:1000), anti-Rb-p780 (Cell Signaling Technology, 1:1000), anti-Rb-p795 (Cell Signaling Technology, 1:1000) and anti-p27kip (Cell Signaling Technology, 1:1000) according to the recommended dilution in 5% fat free milk. The blot was washed twice in PBST and then incubated with HRP-conjugated secondary antibody (Cell Signaling Technology: anti-Rabbit, 1:2000; anti-mouse, 1:3000. Santa

Cruz Biotechnology: anti-Rat, 1:2000; anti-Goat 1:3000) in 5% fat-free milk. The membrane was washed twice in PBST and subjected to protein detection by ECL Plus Western Blotting Detection System (GE Healthcare) before being exposed to a Koda BioMax XAR film. The membrane was stripped and re-blotted with the rabbit anti-mouse HRP-conjugated anti-Gapdh antibody (Cell Signaling Technology) for protein loading control.

Statistical analysis

Statistical significance was determined with the two-tailed unpaired or paired Student's t-test. *P*-values for MRA and promoter enrichment results were calculated with a binomial test. The FDRs were computed with $q = p^*n/i$, (p = P value, n = total number of tests, i = sorted rank of P value).

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End notes

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Figure Legends

Figure 1 | Construction of regulatory network of memory $CD8^+$ T cells. (a) Schematic diagram of regulatory network analysis for identifying key TFs. N, E, and M, naïve, effector and memory $CD8^+$ T cells, respectively. (b) The regulatory module of the top 10 TFs (orchid circles) and their MSGs (blue). c, ChIP-PCR analysis of Sox4, Tcf7 and Emoes-regulated MSGs. ChIP was carried out with $CD8^+$ T cells expressing the 2C TCR using antibodies specific for Sox4, Tcf7 or Eomes or control IgG antibodies. Promoter regions of the indicted genes were amplified using the precipitated DNA. Shown are PCR products after electrophoresis.

Figure 2 | Construction of perturbation network of TFs in $CD8^+$ T cells. (a) ChIP-PCR analysis. ChIP was carried out with 2C T cells using antibodies specific for Sox4, Tcf7 or Eomes or control IgG antibodies. Promoter regions of the indicted genes were then amplified using the precipitated DNA. Shown are PCR products after electrophoresis. (b) Perturbation network based on Table 3. (c) An example of network motifs from the perturbation network.

Figure 3 | **Effect of overexpression and knockdown of TFs on memory CD8**⁺ **T-cell recall proliferation**. Naïve 2C T cells were activated *in vitro* with SIY peptide and then transduced with retroviruses expressing *Sox4*, *Bhlhe40*, *Bach2* or *Runx2* or expressing shRNA specific for one of the TFs. The cells were cultured in the presence of IL-7 to induce memory T cell development. The resulting memory 2C T cells were either activated *in vitro* with SIY peptide or transferred into mice and activated by WSN-SIY virus infection. The proportion of GFP⁺ (transduced) versus GFP⁻ (non-transduced) 2C T cells was quantified 4 and 6 days post stimulation *in vitro* and in draining lymph node (DLN) 5 days post infection (dpi). Shown are proportion of GFP⁺ 2C T cells that overexpressed *Sox4*, *Bhlhe40*, *Bach2* or *Runx2* among total 2C T cells is *in vitro* (**c**) and *in vivo* (**d**). Each line was one independent experiment with one sample per time point for the *in vitro* experiments and one or two mice per in vivo experiment. Data shown are mean \pm s.e.m. Pairwise two-tailed t-tests were used for statistical analyses. * *P*<0.05; ** *P*<0.01.

Figure 4 | *Bach2* promotes recall proliferation of memory $CD8^+$ T cells. (a) Scheme of experimental protocol. (b-d) Phenotype and function of persisting memory 2C cells. Twenty-two days post transfer, single cell suspension was prepared from spleen and analyzed for CD8, Thy1.1, GFP plus CD62L or IL-7R directly or stimulated in vitro with SIY peptide for 5 hours before staining for CD8, Thy1.1, GFP plus intracellular IFNy or TNFa. Comparison of GFP versus Thy1.1 (b) staining profiles of live cells between vector control and *Bach2* overexpression group. Comparison of CD62L and IL-7R (c) or IFN γ and TNF α expression (d) between GFP⁺ and GFP⁻ 2C T cells. Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells; dash gray trace, isotype control for intracellular staining; dash black trace, IL-7R staining of naïve 2C T cells. (e) Recall responses of persisting memory 2C T cells in vivo. Some recipient mice were infected with WSN-SIY 23-25 days post transfer and the proportions of GFP⁺ and GFP⁻ 2C T cells in the DLN and spleen was quantified by flow cytometry 7 dpi. Comparison of proportions of GFP⁺ 2C T cells in the DLN and spleen before (d23) and after antigen restimulation (7dpi). Representative data from three independent experiments with 2-3 mice per group per experiment are shown as mean \pm s.e.m. Two-tailed student's t-tests were used for statistical analyses. ** P<0.01; n.s., not significant.

Figure 5 | *Bach2* promotes memory CD8⁺ T cell development. (a) Scheme of experimental protocol for b-f. (b-e) Effect of Bach2 overexpression on memory T cell development. b,c, Persistence and phenotype of transferred 2C T cells over time. Seven and 30 dpi, 2C T cells in various organs were analyzed for CD62L, IL-7R, Klrg1, CD27 and IFNy as in Fig. 4. Shown are histograms of CD62L, IL-7R, Klrg1 and CD27 expression of Thy1.1⁺ CD8⁺ 2C T cells 7 (b) and 30 dpi (c). Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells. Representative data from 6 mice in 3 independent experiments are shown. (d) Proportion of GFP⁺ transduced 2C cells in different organs normalized to the average of the blood at 7 dpi. (e) Total Bach2-transduced 2C T cells (GFP⁺) in the spleen 7 and 30 dpi. (f) Effect of Bach2 knockdown on memory T cell development. Proportion of Bach2-knockdown 2C T cells (GFP⁺) in different organs normalized to the average of the blood at 7 dpi. (g) Effect of Bach2 knockout on memory T cell development. Chimera mice were constructed by injecting Bach2^{-/-} and Bach2^{+/+} bone marrow cells into sublethally irradieated Rag2^{-/-} recipient mice. Following reconstitution (3 months later), mice were infected with WSN-SIY virus and 30 dpi cells from DLN and spleen were stained for H-2K^b-SIY and anti-CD8. Shown are staining profiles of H-2K^b-SIY versus CD8. The numbers in the plots indicate percentage of SIY-specific memory CD8⁺ T cells. The numbers in the boxes indicate the number of SIY-specific memory CD8⁺ T cells (top) and total CD8⁺ T cells (bottom). Representative data from three independent experiments with 2-3 mice per group per experiment (d, e) and from two independent experiments with 3-4 mice per group per experiment (f) are shown as mean \pm s.e.m. Two-tailed student's t-tests were used for statistical analyses. * P < 0.05; ** P < 0.01.

Figure 6 | *Bach2* promotes memory CD8⁺ T cell development. (a) Scheme of experimental protocol. (b-e) Persistence and phenotype of transferred CD8⁺ T cells over time. Seven and 30 dpi, 2C T cells in various organs were analyzed as in Fig. 4. Shown are histograms of CD62L, IL-7R, Klrg1, IFN γ and TNF α expression of Thy1.1⁺ CD8⁺ 2C T cells 7 (b) and 30 dpi (c). Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells; dash gray trace, isotype control for intracellular staining. Representative data from 9-12 mice in 3 independent experiments are shown. (d) Proportion of GFP⁺ transduced 2C cells in different organs normalized to the average of the blood at 7 dpi. (e) Total Bach2-transduced 2C T cells

(GFP⁺) in the spleen 7 and 30 dpi. Data from three independent experiments with 3-4 mice per group per experiment are shown as mean \pm s.e.m. Two-tailed student's t-tests were used for statistical analyses. * *P*<0.05; ** *P*<0.01.

Figure 7 | *Bach2* promotes proliferation of CD8⁺ T cells. (a) 2C cells were activated *in vitro* and transduced with retroviruses expressing GFP alone (vector) or GFP plus Bach2 and cultured in the presence of either IL-2 or IL-7. The proportion of GFP⁺ 2C T cells was quantified. Shown (mean \pm s.e.m.) are changes in proportion of GFP⁺ cells over time from four independent experiments. Two-tailed student's t-tests were used for statistical analyses. ** P<0.01. (b) Bach2 transduced 2C T cells (day 4 in Fig. 7a) were labeled with eFluor®670 and cultured in the presence of IL-2 for four days. Shown are representative histograms of eFluor®670 from one of the two experiments. Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells. (c) Sox4-Bach2-Prdm1-Id3 regulatory motif identified in perturbation network. (d) Bach2 inhibits Prdm1 expression but promotes Id3 expression. Activated 2C T cells were transduced with retroviruses expressing GFP alone (vector) or GFP plus Bach2, Sox4 or Id3. The levels of the indicated TFs were assayed by Western blotting. Shown are representative Western blotting and the average expression level quantified from three independent experiments. (e-f) Bach2 binds to Prdm1 and Id3 promoter. Activated 2C T cells were cultured with IL-7 for 24 hours and harvested for ChIP using anti-Bach2. DNA was used to amplify different parts of the Prdm1 (e) and Id3 (f) promoter region indicated by i-v. The location of the predicted Bach2 binding motif was indicted as triangle. Data are from two independent experiments, error bar: SEM. (g) Bach2 affects Rb phosphorylation and p27kip expression. Activated 2C T cells were transduced with retroviruses expressing GFP alone (vector) or GFP plus Bach2 and cultured for 8 days (Fig. 7a). The levels of phosphorylated Rb and FoxO1, CDK4, CDK6, Bcl6, Bcl2 and p27kip in the transduced 2C T cells were assayed by Western blotting.

								qPCR	qPCR		
TF	#MSG	P-value	ISP*	DBM	FDR	ESG	MSG	E/N	M/N	Reference gene functions[#]	Ref.
Sox4	50	9.55E-10	YES	SORY	0.0001	YES	YES	-4.305	-5.845	Th2 differentiation	50
Tcf7	40	1.10E-06	YES	LEFF	0.0010	YES	NO	-3.71	-0.37	Promote memory	7, 9
Eomes	34	1.03E-06	YES	BRAC	0.0021	YES	YES	1.99	3.48	Effector and memory	4, 5
Bhlhe40	27	2.50E-05	YES	HESF	0.3353	YES	YES	2.72	4.215	CD8+ T cell activation	51
Prdml	26	2.90E-05	YES	PRDF	-	YES	NO	4.185	4.5	Effector/inhibit memory	16, 17
Klf2	24	0.000587	YES	KLFS	0.1135	NO	NO	-2.01	-0.63	Homeostasis/memory	10
Bach2	22	0.000229	YES	AP1R	0.0151	YES	NO	-3.77	-0.935	-	
Runx2	21	0.000365	YES	HAML	0.0031	YES	YES	0.19	2.775	Early T cell development	52
Id2	20	0.000319	YES	-	-	YES	YES	0.265	2.645	KO promotes memory	13, 14
Stat4	17	0.002650	YES	STAT	0.2503	NO	NO	-2.33	0.935	Effector and memory	53, 54
Runx3	15	0.002869	YES	HAML	0.0031	NO	NO	-2.37	-1.925	Cooperation with Tbx21	55
Id3	14	0.005424	YES	-	-	NO	NO	-3.695	-1.995	Promote memory	15
Nfatc2	12	0.007564	YES	NFAT	0.0127	NO	NO	-	-	TCR signaling	56
Gata3	11	0.012973	YES	GATA	0.0425	NO	NO	-	-	Th2 differentiation	57
Ikzfl	11	0.038617	YES	IKRS	0.0208	NO	NO	-	-	IL2/TCR signaling	58
Nfatc1	11	0.038617	YES	NFAT	0.0127	NO	NO	-	-	PD-1/TCR signaling	59
Jun	10	0.019089	YES	AP1F	0.0046	NO	NO	-	-	AP-1 complex	60
Nfe2l2	10	0.019089	YES	AP1R	0.0151	NO	NO	-	-	Protect memory	61
Tbx21	9	0.036556	YES	BRAC	0.0021	NO	NO	6.215	3.165	Effector and memory	4, 5
Jund	9	0.028085	YES	AP1F	0.0046	NO	NO	-	-	AP-1 complex	60
Maf	9	0.025971	YES	AP1R	0.0151	YES	NO	-	-	-	

Table 1. Ranking of the 21 key TFs identified by master regulator analysis.

#MSG: the total number of MSG regulated directly by the TF; * ISP: immune system phenotype; DBM, DNA binding motif; FDR, false discovery rate; ESG, effector signature genes; MSG, memory signature genes; qPCR E/N, log2 gene expression fold-changes between effector and naïve CD8⁺ T cells; qPCR M/N, log2 gene expression fold-changes between memory and naïve CD8⁺ T cells; [#]gene function reported in T cells. Grey marked TFs that have been reported as playing important roles in memory CD8⁺ T cell development or function.

Table 2. Summary of the ChIP-PCR results.

TF	Sox4	Tcf7	Eomes	Total
No. MSG target	41	36	26	103
No. tested target	12	14	9	35
No. positive	10 (83.3%)	12 (85.7%)	6 (66.7%)	28 (80%)

Gene	Sox4	Tcf7	Eomes	Bhlhe40	Prdm1	Klf2	Bach2	Id2	Runx2	Stat4	Id3	<i>Tbx21</i> *
Sox4	7.94	-1.38	1.77	-0.62	-3.17	-0.28	-0.93	-0.48	-0.05	-0.70	-0.83	1.21
Tcf7	-1.79	2.44	-0.03	-0.21	-2.01	-0.50	0.88	-0.39	0.04	-2.16	0.31	-0.64
Eomes	-2.28	-1.11	5.29	0.38	-0.08	-0.26	-0.64	-0.10	0.85	-0.55	0.54	-2.31
Bhlhe40	-2.03	0.41	1.09	3.88	0.02	1.99	0.32	0.31	0.14	-0.41	0.68	0.62
Prdm1	-0.14	-1.48	2.04	1.13	5.19	1.34	-1.62	-0.17	0.20	0.08	-0.39	1.30
Klf2	0.85	-0.78	-1.10	-0.55	-1.49	4.06	-1.52	-0.73	-0.07	-1.33	-1.51	-0.57
Bach2	1.37	0.75	0.35	0.00	0.22	1.40	4.41	-0.18	0.78	0.01	0.07	0.15
Id2	-2.24	1.10	0.46	0.38	0.24	0.66	0.09	4.98	0.93	-0.06	0.18	0.54
Runx2	-1.64	0.41	-0.51	-0.22	-0.02	0.91	-0.50	-0.82	3.71	-0.54	-0.03	-0.77
Stat4	-1.45	-0.26	-1.78	0.14	0.80	0.24	0.22	-0.01	0.85	2.32	0.41	-0.81
Id3	2.61	0.23	-1.32	0.47	-0.23	0.72	2.02	-1.03	0.25	0.73	7.44	-1.09
Tbx21	-1.68	-0.26	-0.22	0.12	-0.34	1.42	0.50	0.93	1.29	-2.29	1.17	6.54

Table 3. Perturbation analysis.

* The highlighted 12 TFs (first row) were overexpressed individually in 2C T cells and the level of their transcripts of each TFs was quantified by real-time PCR. Expression data was normalized to the empty vector control and then log2 transformed. Changes in transcript levels for \geq 2 fold are marked orange (up-regulated) or green (down-regulated). The overexpressed TFs are marked red.











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Supplementary information



Supplementary Figure S1. The regulatory network of $CD8^+$ T cells showing 3,219 interactions involving 154 MSGs and 276 expressed putative TFs. The gray nodes indicate TFs and the red nodes MSGs.



Supplementary Figure S2. (a) The cumulative percentage of MSGs that are regulated by the identified 21 TFs. The order that TFs were plotted is the same as they were ranked in Table 1. (b) The regulatory module of *Sox4* and *Tcf7* (orchid circles) and MSGs (blue circles).



Supplementary Figure S3: Identification of TFs in the upstream of the perturbation network. Shown is the plotting of the number of downstream and upstream interacting TFs for each TF in the perturbation network.



Supplementary Figure S4. Examples of network motifs from the perturbation network.



Supplementary Figure S5. Regulation of Eomes and Tbx21 by Sox4, Tcf7, Eomes and Tbx21. 2C T cells were transduced with retroviruses expressing GFP (vector) or GFP plus *Sox4*, *Tcf7*, *Eomes* or *Tbx21*. Expression of Eomes and Tbx21 was analyzed by intracellular staining and flow cytometry. Histograms compare Eomes and Tbx21 expression in non-transduced (GFP⁻, gray lines) and transduced (GFP⁺, black lines) T cells. The numbers indicate MFI.



Supplementary Figure S6. Phenotype of *in vitro* memory T cells. Activated 2C T cells were cultured *in vitro* with IL-7 for 7 days to induce *in vitro* memory T cells. (**a**) Naïve, effector and *in vitro* memory 2C T cells were stained for CD44, CD62L, IL-7R, CCR7 and CD122 followed by cytometry. (**b**) Quantitative PCR analysis of gene expression of key memory genes (*Eomes*, *Tbx21*, *Prdm1*, *Il7r*, *Sell* and *Klrg1*) in naïve, activated and *in vitro* memory 2C T cells.



Supplementary Figure S7. Effect of overexpression of *Sox4*, *Bhlhe40*, *Bach2* and *Runx2* on recall proliferation of memory $CD8^+$ T cells *in vivo*. Naïve 2C T cells were activated *in vitro* with SIY peptide and then transduced with retroviruses expressing *Sox4*, *Bhlhe40*, *Bach2* or *Runx2*. The cells were cultured in the presence of IL-7 to derive memory T cells. The resulting memory 2C T cells were transferred into B6 mice and activated with WSN-SIY virus. The proportion of GFP⁺ (transduced) versus GFP⁻ (non-transduced) 2C T cells was quantified in various organs 5 dpi. Shown is proportion of GFP⁺ 2C T cells that overexpressed *Sox4*, *Bhlhe40*, *Bach2* or *Runx2* among total 2C T cells *in vivo*. Data are from three independent experiments with 1-2 mice per group per experiment, shown as mean \pm s.e.m. Two-tailed student's t-tests were used for statistical analyses.



Supplementary Figure S8. Knowdown efficiency of shRNAs targeting *Sox4*, *Bhlhe40*, *Bach2* and *Runx2*. The indicated shRNA vectors were transduced individually in 2C T cells and the level of the target transcript was quantified by real-time PCR 48 hours later. Expression data was normalized to the empty vector control. Data from three independent experiments are shown as mean \pm s.e.m. Two-tailed student's t-tests were used for statistical analyses.



Supplementary Figure S9. Overexpression of *Eomes* and *Klf2* affects recall response of *in vitro* generated memory CD8⁺ T cells. 2C T cells were activated and transduced with retroviruses expressing GFP plus *Eomes* or *Klf2*. The cells were cultured in the presence of IL-7 to derive memory T cells. The resulting memory 2C cells were either activated *in vitro* with SIY peptide or transferred into mice and activated with WSN-SIY virus. The proportion of GFP⁺ (transduced) versus GFP⁻ (non-transduced) 2C T cells was quantified 4 and 6 days post stimulation *in vitro* and in DLN 5 dpi. Shown are Thy1.1 vs. GFP staining profiles of CD8⁺ 2C T cells (**a**) and proportion of GFP⁺ 2C T cells that overexpressed *Eomes* or *Klf2* among total 2C T cells *in vitro* (**b**) and *in vivo* (**c**). Each line was one independent experiment with one sample per time point for the *in vitro* experiments and one or two mice per *in vivo* experiment. * *P*<0.05; ** *P*<0.01. Pairwise two-tailed t-tests were used for statistical analyses.



Supplementary Figure S10. *Bach2* promotes memory CD8⁺ T cell development. Naïve 2C T cells were activated *in vitro* with SIY peptide and then transduced with retroviruses expressing *Bach2*. The cells were adoptively transferred into mice and activated with WSN-SIY virus. Phenotype of 2C T cells in various organs was analyzed for CD27.

Shown are histograms CD27 expression of Thy1.1⁺ CD8⁺ 2C T cells 7 (**a**) and 30 dpi (**b**). Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells. IL-2 and IFN γ expression 2C T cells 30 dpi were analyzed as **Fig.4**. Shown is IL-2 vs. IFN γ staining profile of Thy1.1⁺ CD8⁺ 2C T cells (**c**). Representative data from 6 mice in 3 independent experiments are shown.



Supplementary Figure S11. *Bach2* promotes memory CD8⁺ T cell development. Bone marrow progenitor cells isolated from 2C TCR transgenic mice were transduced with retroviruses expressing GFP alone (vector) or GFP plus *Bach2* and adoptively transferred into sublethally irradiated RAG2^{-/-} mice to generate naïve 2C T cells that express GFP or GFP plus *Bach2*. Three to 4 months later, 2C T cells generated in RAG2^{-/-} recipients were analyzed for Thy1.1, CD8 plus CD25, CD62L or IL-7R. (a) Comparison of CD25, CD62L and IL-7R expression between GFP⁺ and GFP⁻ 2C T cells (Thy1.1⁺ CD8⁺). The resulting transduced and nontransduced naïve 2C cells were adoptively transferred into B6 mice followed by infection with WSN-SIY influenza virus. The frequency, phenotype and function of 2C T cells were analyzed 7 dpi. (b) Quantification of CD62L⁺Klrg1⁻ memory 2C T cell precursors in the DLN and spleen. Data from three independent experiments with 3-4 mice per group per experiment are shown as mean ± s.e.m. Two-tailed student's t-tests were used for statistical analyses. **P*<0.05, ***P*<0.01.



Supplementary Figure S12. *Bach2* is required for memory CD8⁺ T cell development. Naïve 2C T cells were activated *in vitro* with SIY peptide and then transduced with retroviruses expressing the shRNA specific for *Bach2*. The cells were adoptively transferred into mice and activated with WSN-SIY virus. 2C T cells were analyzed 7 and 30 dpi as in **Fig. 4**. Shown are histograms of CD62L, IL-7R, CD27, Klrg1 and IFNγ expression of Thy1.1⁺ CD8⁺ 2C T cells in the spleen 7 (**a**) and 30 dpi (**b**). Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells. Representative data from 6-8 mice in two independent experiments are shown. (**c**) Total vector or shBach2 transduced 2C T cells (GFP⁺) in the spleen 7 and 30 dpi. Representative data from 6-8 mice in two independent experiments are shown as mean ± s.e.m. Two-tailed student's t-tests were used for statistical analyses. **P*<0.05;



Supplementary Figure S13. *Prdm1* inhibits *Bach2*-mediated proliferation of CD8⁺ T cells. 2C cells were activated *in vitro* and transduced with retroviruses expressing GFP alone (vector), GFP plus Bach2 or GFP plus Prdm1 and Bach2 (Prdm1-2A-Bach2) and cultured in the presence of IL-2. The proportion of GFP⁺ 2C T cells was quantified. Shown are changes in proportion of GFP⁺ cells over time from three independent experiments. Two-tailed student's t-tests were used for statistical analyses, error bar: s.e.m. ** *P*<0.01.



Supplementary Figure S14. Enhanced proliferation and survival of memory CD8⁺ T cells. Naïve 2C cells were activated *in vitro* and transduced with retroviruses expressing GFP alone (vector) or GFP plus Bach2 and cultured in the presence of IL-7 to derive memory T cells. *In vitro* memory 2C T cells were labeled with eFluor®670 and adoptively transferred into Rag2^{-/-} mice. 2C T cells in the spleen were analyzed 14 days later. Shown are representative histograms of eFluor®670 from one of the two experiments. Gray trace, nontransduced (GFP⁻) 2C T cells; black trace, transduced (GFP⁺) 2C T cells.



Supplementary Figure S15. The DNA gels of ChIP-PCR. (a) The DNA gels of ChIP-PCR for Fig. 1c. Representative data from 3 independent experiments. (b) The DNA gels of ChIP-PCR for Fig. 2a. Representative data from 3 independent experiments. 1, input chromatin; 2, IPed chromatin by TF Abs; 3, IPed chromatin by IgG.



Supplementary Figure S16. The Western blotting gels. (a) The protein gels of blotting Sox4, Bach2, Prdm1 and Id3 for Fig. 7d. Representative data from 3 independent experiments. (b) The protein gels of blotting pRb780, pRb795,pFoxO1, Bcl2,Bcl6, CDK4, CDK6 and p27kip for Fig. 7g. Marker is the PageRulerTM Prestained Protein Ladder (Thermo Scientific). Representative data are from 3 independent experiments.

Supplementary Table S	1. List of 386	gene express	ion profiles of CD8+ T cells used in the present study.
Index Platform	GSE ID	ArrayID	Array Name
1 GPL339	GSE2059	GSM35848	control 1
2 GPL339	GSE2059	GSM37078 GSM37070	control 2
4 GPL339	GSE2059 GSE2059	GSM37079 GSM37080	control 4
5 GPL339	GSE2059	GSM37081	control 5
6 GPL339	GSE2059	GSM37117	IL15 1
7 GPL339 8 GPL339	GSE2059 GSE2059	GSM37118 GSM37119	IL15 2 IL15 3
9 GPL339	GSE2059	GSM37120	IL15 4
10 GPL339	GSE2059	GSM37121	IL15 5
11 GPL339	GSE2059	GSM37122	IL21 1
12 GPL339 13 GPL339	GSE2059 GSE2059	GSM37123 GSM37124	IL21 2 IL21 3
14 GPL339	GSE2059	GSM37125	IL21 4
15 GPL339	GSE2059	GSM37126	IL21 5
16 GPL339	GSE2059	GSM37128	IL15+IL-21 1
17 GPL339 18 GPL339	GSE2059 GSE2059	GSM37165 GSM37164	IL15+IL-21 2 IL15+IL-21 3
19 GPL339	GSE2059	GSM37165	IL15+IL-21 4
20 GPL339	GSE2059	GSM37166	IL15+IL-21 5
21 GPL339	GSE4938	GSM111271 GSM111260	wt CD8 M
22 GPL339 23 GPL339	GSE4938 GSE4940	GSM111209 GSM111286	ko 501 0h
24 GPL339	GSE4940	GSM111287	ko 501_4h
25 GPL339	GSE4940	GSM111288	ko 501_8h
26 GPL339 27 GPL339	GSE4940 GSE4940	GSM111289 GSM111290	ko 501_24h wt 502_0h
28 GPL339	GSE4940 GSE4940	GSM111291	wt 502_0n
29 GPL339	GSE4940	GSM111292	wt 502_8h
30 GPL339	GSE4940	GSM111293	wt 502_24h
31 GPL339	GSE10093	GSM254977 GSM254082	Spleen CD8 T cells DMSO1 Spleen CD8 T cells DMSO2
32 GPL339 33 GPL339	GSE10093 GSE10093	GSM254985 GSM254976	Spleen CD8 T cells TCDD1
34 GPL339	GSE10093	GSM254978	Spleen CD8 T cells TCDD2
35 GPL339	GSE3565	GSM81921	DUSP1-/- control replicate 1
36 GPL339	GSE3565	GSM81922	DUSP1-/- control replicate 2
38 GPL339	GSE3565 GSE3565	GSM81923 GSM81924	DUSP1-/- LPS replicate 1
39 GPL339	GSE3565	GSM81925	DUSP1-/- LPS replicate 2
40 GPL339	GSE3565	GSM81926	DUSP1-/- LPS replicate 3
41 GPL339 42 GPL339	GSE3565 GSE3565	GSM81927 GSM81928	DUSP1+/+ control replicate 1 DUSP1+/+ control replicate 2
43 GPL339	GSE3565	GSM81929	DUSP1+/+ control replicate 3
44 GPL339	GSE3565	GSM81930	DUSP1+/+ LPS replicate 1
45 GPL339	GSE3565	GSM81931	DUSP1+/+ LPS replicate 2
46 GPL339 47 GPL330	GSE3565	GSM81932 GSM125705	DUSP1+/+ LPS replicate 3
47 GPL339 48 GPL339	GSE5811 GSE5811	GSM135705 GSM135706	B1_saline_overexpressor_422 B2_saline_overexpressor_422
49 GPL339	GSE5811	GSM135707	B3_saline_overexpressor_422
50 GPL339	GSE5811	GSM135708	B4_pseudomonas_overexpressor_422
51 GPL339	GSE5811	GSM135709	B5_pseudomonas_overexpressor_422
52 GPL339	GSE5811	GSM135711	R1 saline wildtype 422
54 GPL339	GSE5811	GSM135712	R2_saline_wildtype_422
55 GPL339	GSE5811	GSM135713	R4_saline_wildtype_422
56 GPL339 57 GPL339	GSE5811 GSE5811	GSM135714 GSM135715	R5_Pseudomonas_wildtype_422 R6_Pseudomonas_wildtype_422
58 GPL339	GSE5811 GSE5811	GSM135715 GSM135716	R7 Pseudomonas wildtype 422
59 GPL339	GSE5811	GSM135717	B2_saline_overexpressor_48
60 GPL339	GSE5811	GSM135718	B3_saline_overexpressor_48
61 GPL339 62 GPL339	GSE5811 GSE5811	GSM135719 GSM135720	B5_Pseudomonas_overexpressor_48 B6_Pseudomonas_overexpressor_48
63 GPL339	GSE5811	GSM135721	R2 saline wildtype 48
64 GPL339	GSE5811	GSM135722	R3_saline_wildtype_48
65 GPL339	GSE5811	GSM135723	R5_Pseudomonas_wildtype_48
66 GPL339 67 GPL339	GSE5811 GSE5811	GSM135724 GSM135725	R6_Pseudomonas_wildtype_48
68 GPL339	GSE5811	GSM135726	C2 CLP overexpressor 12
69 GPL339	GSE5811	GSM135727	C3_CLP_overexpressor_12
70 GPL339	GSE5811	GSM135728	C4_CLP_overexpressor_12
71 GPL339 72 GPL339	GSE5811 GSE5811	GSM135729 GSM135730	C5_CLP_overexpressor_12 C6_CLP_wildtype_12
73 GPL339	GSE5811	GSM135731	S1 sham overexpressor 12
74 GPL339	GSE5811	GSM135732	S2_sham_overexpressor_12
75 GPL339	GSE5811	GSM135733	S3_sham_overexpressor_12
76 GPL339 77 GPL339	GSE5811 GSE5811	GSM135734 GSM135735	S4_sham_overexpressor_12 S5_sham_overexpressor_12
78 GPL339	GSE5811	GSM135736	S6 Sham wildtype 12
79 GPL339	GSE5811	GSM135737	C1_CLP_wildtype_8
80 GPL339	GSE5811	GSM135738	C3_CLP_wildtype_8
81 GPL339 82 GPL339	GSE5811 GSE5811	GSM135739 GSM135740	C4_CLP_wildtype_8 C5star_CLP_wildtype_8
83 GPL339	GSE5811	GSM135741	C6star_CLP_wildtype_8
84 GPL339	GSE5811	GSM135742	S2_Sham_wildtype_8
85 GPL339	GSE5811	GSM135743	S3star_Sham_wildtype_8
86 GPL339 87 GPL339	GSE5811 GSE5811	GSM135744 GSM135745	54_Snam_wildtype_8 S6 Sham wildtype 8
88 GPL339	GSE7768	GSM188270	Ova, biological replicate 1
89 GPL339	GSE7768	GSM188271	Ova, biological replicate 2
90 GPL339	GSE7768	GSM188272	Ova, biological replicate 3
91 GPL339 92 GPI 339	GSE7768 GSE7768	GSM188273 GSM188274	OvaLPS, biological replicate 1 OvaLPS, biological replicate 2
93 GPL339	GSE7768	GSM188275	OvaLPS, biological replicate 3
94 GPL339	GSE7768	GSM188276	OvaMPL, biological replicate 1
95 GPL339	GSE7768	GSM188277	OvaMPL, biological replicate 2

Title	Classification
Control of naïve CD8+ T cells	N
Control of naïve CD8+ T cells	N
Control of naïve CD8+ T cells Control of naïve CD8+ T cells	N
IL15 of naïve CD8+ T cells	N
IL15 of naïve CD8+ T cells IL15 of naïve CD8+ T cells	N
IL15 of naïve CD8+ T cells	Ν
IL15 of naïve CD8+ T cells IL21 of naïve CD8+ T cells	N
IL21 of naïve CD8+ T cells	N
IL21 of naïve CD8+ T cells IL21 of naïve CD8+ T cells	N
IL21 of naïve CD8+ T cells	N
IL21 of naïve CD8+ T cells	N
IL15+IL21 of naïve CD8+ 1 cells IL15+IL21 of naïve CD8+ T cells	N
IL15+IL21 of naïve CD8+ T cells	N
IL15+IL21 of naïve CD8+ T cells CD8 M of Gfi1-WT	N
CD8 N of Gfi1-KO	N
0hr T Gfi1-KO activated by anti-CD3&CD28 4hr T Gfi1-KO activated by anti-CD3&CD28	N
8hr T Gfi1-KO activated by anti-CD3&CD28	E
24hr T Gfi1-KO activated by anti-CD3&CD28	Е
0hr T Gfi1-WT activated by anti-CD3&CD28 4hr T Gfi1-WT activated by anti-CD3&CD28	E
8hr T Gfi1-WT activated by anti-CD3&CD28	E
24hr T Gfi1-WT activated by anti-CD3&CD28	E
Spleen CD8 T cells with DMSO Spleen CD8 T cells with DMSO	N
Spleen CD8 T cells with TCDD	
Spleen CD8 T cells with TCDD	
DUSP1-/- control	
DUSP1-/- control	
DUSP1-/- LPS DUSP1-/- LPS	
DUSP1-/- LPS	
DUSP1+/+ control DUSP1+/+ control	
DUSP1+/+ control	
DUSP1+/+ LPS	
DUSP1+/+ LPS DUSP1+/+ LPS	
saline_overexpressor_422	
saline_overexpressor_422 saline_overexpressor_422	
pseudomonas_overexpressor_422	
pseudomonas_overexpressor_422	
saline_wildtype_422	
saline_wildtype_422	
Pseudomonas wildtype 422	
Pseudomonas_wildtype_422	
Pseudomonas_wildtype_422 saline_overexpressor_48	
saline_overexpressor_48	
Pseudomonas_overexpressor_48	
saline_wildtype_48	
saline_wildtype_48	
Pseudomonas_wildtype_48 Pseudomonas_wildtype_48	
CLP_overexpressor_12	
CLP_overexpressor_12 CLP overexpressor 12	
CLP_overexpressor_12	
CLP_overexpressor_12 CLP_wildtype_12	
sham_overexpressor_12	
sham_overexpressor_12	
sham_overexpressor_12 sham_overexpressor_12	
sham_overexpressor_12	
Sham_wildtype_12 CLP wildtype 8	
CLP_wildtype_8	
CLP_wildtype_8	
CLP_wildtype_8	
Sham_wildtype_8	
Snam_wildtype_8 Sham wildtype 8	
Sham_wildtype_8	
Ova Ova	
Ova	
OvaLPS OvaLPS	
OvaLPS	
OvaMP	
OvamP	

96 GPL339	GSE7768	GSM188278	OvaMPL, biological replicate 3
97 GPL339	GSE3997	GSM91280	B10 TCR double positive rep 1
98 GPL339	GSE3997	GSM91281	B10 TCR double positive rep 2
99 GPL339	GSE3997	GSM91282	B10 TCR double positive rep 3
100 GPL339	GSE3997	GSM91283	NOD TCR double positive rep 1
101 GPL339	GSE3997	GSM91284 GSM01285	NOD TCR double positive rep 2
103 GPL339	GSE3997	GSM91285	B10 Dbl double positive rep 1
104 GPL339	GSE3997	GSM91287	B10 Dbl double positive rep 2
105 GPL339	GSE3997	GSM91288	B10 Dbl double positive rep 3
106 GPL339	GSE3997	GSM91289	NOD Dbl double positive rep 1
107 GPL339	GSE3997	GSM91290	NOD Dbl double positive rep 2
108 GPL339	GSE3997	GSM91291	NOD Dbl double positive rep 3
109 GPL339	GSE2413	GSM45451	0h WT Sample 01
110 GPL339	GSE2413	GSM45452 GSM45452	0h WT Sample 13 0h WT Sample 16
112 GPI 339	GSE2413 GSE2413	GSM45455	0h WT Sample 36
113 GPL339	GSE2413	GSM45455	2h WT Cel.02
114 GPL339	GSE2413	GSM45456	2h WT Cel.17
115 GPL339	GSE2413	GSM45457	2h WT Cel.37
116 GPL339	GSE2413	GSM45458	6h WT Cel.03
117 GPL339	GSE2413	GSM45459	6h WT Cel.18
118 GPL339	GSE2413	GSM45460	6h WT cel.38
119 GPL339	GSE2413 GSE2413	GSM45461 GSM45462	24h WT Cel 19
121 GPL339	GSE2413 GSE2413	GSM45463	24h WT Cel 39
122 GPL339	GSE2413	GSM45464	0h Kin Cel.05
123 GPL339	GSE2413	GSM45465	0h Kin Cel.14
124 GPL339	GSE2413	GSM45466	0h Kin Cel.40
125 GPL339	GSE2413	GSM45467	0h Kin Cel.44
126 GPL339	GSE2413	GSM45468	2h Kin Cel.06
127 GPL339	GSE2413	GSM45469	2h Kin- Cel 41
128 GPL339	GSE2413 GSE2413	GSM45470 GSM45471	2n Kin- Cel 07
130 GPL339	GSE2413	GSM45472	6h Kin- Cel.42
131 GPL339	GSE2413	GSM45473	6h Kin- Cel.46
132 GPL339	GSE2413	GSM45474	24h kin- Cel.08
133 GPL339	GSE2413	GSM45475	24h Kin- Cel.43
134 GPL339	GSE2413	GSM45476	24h Kin Cel.47
135 GPL339	GSE9727	GSM245893	S49_untreated_time0,rep1
136 GPL339	GSE9/2/ CSE0727	GSM245894 CSM245805	S49_untreated_time0,rep2
138 GPI 339	GSE9727	GSM245896	S49_untreated_time0.rep3
139 GPL339	GSE9727	GSM245897	S49 treated 2h,rep1
140 GPL339	GSE9727	GSM245898	S49_treated_2h,rep2
141 GPL339	GSE9727	GSM245899	S49_treated_2h,rep3
142 GPL339	GSE9727	GSM245900	S49_treated_6h,rep1
143 GPL339	GSE9727	GSM245901	S49_treated_6h,rep2
144 GPL339	GSE9/2/	GSM245902	S49_treated_6h,rep3
145 GPL339 146 GPL 339	GSE9727 GSE9727	GSM245905 GSM245904	S49_treated_24h,rep1 S49_treated_24h ren2
147 GPL339	GSE9727	GSM245905	S49 treated 24h.rep3
148 GPL339	GSE9727	GSM248218	S49 untreated time0,rep1
149 GPL339	GSE9727	GSM248219	S49_untreated_time0,rep2
150 GPL339	GSE9727	GSM248220	S49_untreated_time0,rep3
151 GPL339	GSE9727	GSM248221	S49_untreated_time0,rep4
152 GPL339	GSE9/2/	GSM248222	S49_untreated_2h,rep1
153 GPL339	GSE9727 GSE9727	GSM248225 GSM248224	S49_untreated_2h.rep2 S49_untreated_2h.rep3
155 GPL339	GSE9727	GSM248225	S49_untreated_6h rep1
156 GPL339	GSE9727	GSM248226	S49 untreated 6h,rep2
157 GPL339	GSE9727	GSM248227	S49_untreated_6h,rep3
158 GPL339	GSE9727	GSM248228	S49_untreated_24h,rep1
159 GPL339	GSE9727	GSM248229	S49_untreated_24h,rep2
160 GPL339	GSE9/2/	GSM248230	S49_untreated_24h,rep3 WTL poive CD8 T colle
162 GPL 1261	GSE15324	GSM384858	WT2 naive CD8 T cells
163 GPL1261	GSE15324	GSM384859	WT1 activated CD8 T cells
164 GPL1261	GSE15324	GSM384866	WT2 activated CD8 T cells
165 GPL1261	GSE15324	GSM384867	Elf4 KO1 naive CD8 T cells
166 GPL1261	GSE15324	GSM384868	Elf4 KO2 naive CD8 T cells
167 GPL1261	GSE15324	GSM384869	Elf4 KO1 activated CD8 T cells
168 GPL1261	GSE15324 GSE6084	GSM384906 GSM140919	EII4 KO2 activated CD8 1 cells
170 GPL1261	GSE6084	GSM140920	T-cell Cycloheximide 30min rep2
171 GPL1261	GSE6084	GSM140921	T-cell_Cycloheximide_30min_rep3
172 GPL1261	GSE6084	GSM140922	T-cell_Cycloheximide_30min_rep4
173 GPL1261	GSE6084	GSM108343	T-cell_IL-2_Cycloheximide_4 hour_rep1
174 GPL1261	GSE6084	GSM108344	1-cell_IL-2_Cycloheximide_4 hour_rep2
175 GPL1261	GSE6084	GSM108345 GSM108346	T-cell II -2 Cycloneximide 4 hour rep3
177 GPL1261	GSE6084	GSM183635	T-cell Cycloheximide 4.5h rep1
178 GPL1261	GSE6084	GSM183636	T-cell_Cycloheximide 4.5h rep2
179 GPL1261	GSE6084	GSM183637	T-cell_Cycloheximide_4.5h_rep3
180 GPL1261	GSE6084	GSM183638	T-cell_Cycloheximide_4.5h_rep4
181 GPL1261	GSE11677	GSM296650	CD8 memory T cell_Expansion_rep1
182 GPL1261	CEE11(77	GSM296652	CD8 memory T cell_Expansion_rep2
192 CBL 12C1	GSEI1677	COM 100///2/	Lus memory L cell Expansion ren3
183 GPL1261 184 GPL1261	GSE11677 GSE11677	GSM296654 GSM296656	CD8 memory T cell Expansion rend
183 GPL1261 184 GPL1261 185 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677	GSM296654 GSM296656 GSM296651	CD8 memory T cell_Expansion_rep4 CD8 memory T cell PolyclonalAged rep1
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677	GSM296654 GSM296656 GSM296651 GSM296653	CD8 memory T cell_Expansion_rep4 CD8 memory T cell_PolyclonalAged_rep1 CD8 memory T cell_PolyclonalAged_rep2
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677	GSM296654 GSM296656 GSM296651 GSM296653 GSM296655	CD8 memory T cell_Expansion_rep4 CD8 memory T cell_PolyclonalAged_rep1 CD8 memory T cell_PolyclonalAged_rep2 CD8 memory T cell_PolyclonalAged_rep3
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261 188 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677	GSM296654 GSM296656 GSM296651 GSM296653 GSM296655 GSM296657	CD8 memory T cell_Expansion_rep4 CD8 memory T cell_PolyclonalAged_rep1 CD8 memory T cell_PolyclonalAged_rep2 CD8 memory T cell_PolyclonalAged_rep3 CD8 memory T cell_PolyclonalAged_rep4
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261 188 GPL1261 189 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE12388	GSM296654 GSM296656 GSM296651 GSM296653 GSM296655 GSM296657 GSM310897	CD8 memory T cell_spansion_rep4 CD8 memory T cell_spansion_rep4 CD8 memory T cell_PolyclonalAged_rep1 CD8 memory T cell_PolyclonalAged_rep3 CD8 memory T cell_PolyclonalAged_rep4 Splent Aire-wild-type A
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261 188 GPL1261 189 GPL1261 190 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE12388 GSE12388 GSE12388	GSM296654 GSM296656 GSM296651 GSM296653 GSM296655 GSM296657 GSM310897 GSM310900 GSM310900	CDB memory T cell_Expansion_rep4 CDB memory T cell_Expansion_rep4 CDB memory T cell_PolyclonalAged_rep1 CDB memory T cell_PolyclonalAged_rep3 CDB memory T cell_PolyclonalAged_rep3 CDB memory T cell_PolyclonalAged_rep3 Splen Aire-wild-type A Splen Aire-wild-type B Selama Aire Monchage A
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261 188 GPL1261 190 GPL1261 191 GPL1261 191 GPL1261 192 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE12388 GSE12388 GSE12388	GSM296654 GSM296656 GSM296651 GSM296655 GSM296655 GSM296657 GSM310897 GSM310897 GSM310898 GSM310801	CDS memory T cell Expansion rep4 CDS memory T cell Expansion rep4 CDS memory T cell PolyclonalAged rep2 CDS memory T cell PolyclonalAged rep3 CDS memory T cell PolyclonalAged rep4 Spleen Aire-wild-type A Spleen Aire-wild-type A Spleen Aire-midd-type B Spleen Aire-Mice-two R
183 GPL1261 184 GPL1261 185 GPL1261 186 GPL1261 187 GPL1261 188 GPL1261 189 GPL1261 190 GPL1261 191 GPL1261 192 GPL1261	GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE11677 GSE12388 GSE12388 GSE12388 GSE12388 GSE12388	GSM296654 GSM296656 GSM296651 GSM296653 GSM296655 GSM296655 GSM310897 GSM310897 GSM310900 GSM310898 GSM310901 GSM310903	CDS memory T cell_Expansion_rep4 CDS memory T cell_Expansion_rep4 CDS memory T cell_PolyclonalAged_rep2 CDS memory T cell_PolyclonalAged_rep3 CDS memory T cell_PolyclonalAged_rep4 Spleen Aire-wild-type A Spleen Aire-wild-type A Spleen Aire-knockout A Spleen Aire-knockout B Lymph node Aire-wild-type A

CD4+CD8+TCRhi CD4+CD8+TCRhi
CD4+CD8+TCRhi
CD4+CD8+TCRhi
CD4+CD8+TCRhi
CD4+CD8+TCRNI
CD4+CD8+TCRhi
CD4+CD8+TCRhi
CD4+CD8+CD69-TCRlow
CD4+CD8+CD69-TCRlow
CD4+CD8+CD69-TCRlow
CD4+CD8+CD60 TCRlow
CD4+CD8+CD09-TCKlow
CD4+CD8+CD69-TCRlow
CD4+CD8+CD69-TCRlow
S49 T-lymphoma cell line
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349 1-tymphonia cen me
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S49 T-lymphoma cell line S49 T-lymphoma cell line WT naive CD8 T cells
S49 T-lymphoma cell line S49 T-lymphoma cell Line S40 T-LOMB cell S40 T-LOMB
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194 GPL1261	GSE12388	GSM310899	Lymph node Aire-wild-type B
195 GPL1261	GSE12388	GSM310904	Lymph node Aire-knockout A
196 GPL1261	GSE12388	GSM310902	Lymph node Aire-knockout B
197 GPL1261	GSE11884	GSM300153	Naive_Furin_Wild-type_1
198 GPL1261	GSE11884	GSM300154	Naive_Furin_Wild-type_2
199 GPL1261	GSE11884	GSM300155	Naive_Furin_Knockout_1
200 GPL1261	GSE11884	GSM300156	Naive_Furin_Knockout_2
201 GPL1261	GSE11446	GSM288809	CD8 T cells_IL-2 complex treatment_0 h
202 GPL1261	GSE11446	GSM288810	CD8 T cells_IL-2 complex treatment_1 h
203 GPL1261	GSE11446	GSM288811	CD8 T cells_IL-2 complex treatment_3 h
204 GPL1261	GSE10239	GSM257826	CD8 P14 Naive cells-1
205 GPL1261	GSE10239	GSM257827	CD8 P14 Naive cells-2
206 GPL1261	GSE10239	GSM257828	CD8 P14 Naive cells-3
207 GPL1261	GSE10239	GSM257829	CD8 P14 Memory cells-1
208 GPL1261	GSE10239	GSM257830	CD8 P14 Memory cells-2
209 GPL1261	GSE10239	GSM257831	CD8 P14 Memory cells-3
210 GFL1201 211 GPL 1261	GSE10239	CSM257832	CD8 P14 day 4.5 post-infection KLRG-1 int sorted cells-1
211 GPL1201 212 GPL1261	GSE10239	GSM257834	CD8 P14 day 4.5 post-infection KLRG-1 Int sorted cells-2
213 GPL 1261	GSE10239	GSM257835	CD8 P14 day 4.5 post-infection KLRG-1 Hi sorted cells-1
213 GPL1261	GSE10239	GSM257836	CD8 P14 day 4.5 post-infection KLRG-1 Hi sorted cells-7
215 GPL1261	GSE10239	GSM257837	CD8 P14 day 4 5 post-infection KLRG-1 Hi sorted cells-3
216 GPL1261	GSE9997	GSM252716	Naive CD8+ T cells
217 GPL1261	GSE9997	GSM252717	Activated CD8+ T cells
218 GPL1261	GSE6085	GSM108334	T-cell IL-2 Ohour rep1
219 GPL1261	GSE6085	GSM108335	T-cell IL-2 Ohour rep2
220 GPL1261	GSE6085	GSM108336	T-cell IL-2 Ohour rep3
221 GPL1261	GSE6085	GSM108337	T-cell IL-2 Ohour rep4
222 GPL1261	GSE6085	GSM108338	T-cell_IL-2_0hour_rep5
223 GPL1261	GSE6085	GSM183455	T-cell_No IL-2_4 hour_rep1
224 GPL1261	GSE6085	GSM183456	T-cell_No IL-2_4 hour_rep2
225 GPL1261	GSE6085	GSM183457	T-cell_No IL-2_4 hour_rep3
226 GPL1261	GSE6085	GSM183458	T-cell_No IL-2_4 hour_rep4
227 GPL1261	GSE6085	GSM183459	T-cell_No IL-2_8 hour_rep1
228 GPL1261	GSE6085	GSM183460	T-cell_No IL-2_8 hour_rep2
229 GPL1261	GSE6085	GSM183461	T-cell_No IL-2_8 hour_rep3
230 GPL1261	GSE6085	GSM140923	T-cell_IL-2_0.5 hour_rep1
231 GPL1261	GSE6085	GSM140924	T-cell_IL-2_0.5 hour_rep2
232 GPL1261	GSE6085	GSM140925	1-cell_IL-2_0.5 hour_rep3
233 GPL1261	GSE6085	GSM140926	T-cell_IL-2_1 hour_rep1
234 GPL1261	GSE6085	GSM140927	T cell_IL-2_1 hour_rep2
235 GPL1261	GSE6085	GSM140928	T-cell_IL-2_1 hour_rep3
230 GPL1201	GSE6085	GSM140929	T cell II -2_2 hour rep1
238 GPI 1261	GSE6085	GSM140931	T-cell II -2 2 hour rep3
239 GPL1261	GSE6085	GSM108339	T-cell IL-2 4 hour repl
240 GPL1261	GSE6085	GSM108340	T-cell IL-2 4 hour rep2
241 GPL1261	GSE6085	GSM108341	T-cell_IL-2_4 hour_rep3
242 GPL1261	GSE6085	GSM108342	T-cell_IL-2_4 hour_rep4
243 GPL1261	GSE6085	GSM140932	T-cell_IL-2_6 hour_rep1
244 GPL1261	GSE6085	GSM140933	T-cell_IL-2_6 hour_rep2
245 GPL1261	GSE6085	GSM140934	T-cell_IL-2_6 hour_rep3
246 GPL1261	GSE6085	GSM140935	T-cell_IL-2_8 hour_rep1
247 GPL1261	GSE6085	GSM140936	T cell_IL-2_8 hour_rep2
248 GPL1201 249 GPL1261	GSE6085	GSM140937 GSM140938	T-cell II -2 10 hour repl
250 GPL1261	GSE6085	GSM140939	T-cell IL-2 10 hour rep2
251 GPL1261	GSE6085	GSM140940	T-cell IL-2 10 hour rep3
252 GPL1261	GSE6085	GSM140941	T-cell_IL-2_12 hour_rep1
253 GPL1261	GSE6085	GSM140942	T-cell_IL-2_12 hour_rep2
254 GPL1261	GSE6085	GSM140943	T-cell_IL-2_12 hour_rep3
255 GPL1261	GSE6085	GSM140944	T-cell_IL-2_16 hour_rep1
256 GPL1261	GSE6085	GSM140945	T-cell_IL-2_16 hour_rep2
257 GPL1261	GSE6085	GSM140946	T-cell_IL-2_16 hour_rep3
258 GPL1261	GSE6085	GSM140947	T-cell_IL-2_24 hour_rep1
259 GPL1261	GSE6085	GSM140948	T-cell_IL-2_24 hour_rep2
260 GPL1261	GSE6085	GSM140949	1-ceii_IL-2_24 hour_rep3
261 GPL1261	GSE8039	GSM198411	C1 peripheral lymph node
202 GPL1261	GSE8039	GSM198412	C2 peripheral lymph node
263 GPL1261	GSE8039	GSM198413	C3 peripheral lymph node
267 GEL1201	GSE8039	GSM198400	 T1 CD2-CD301 nerinheral lymph node
265 GPL1261	GSE8039	GSM198410	T2 CD2-CD30L peripheral lymph node
267 GPL1261	GSE8039	GSM198415	T3 CD2-CD30L peripheral lymph node
268 GPL1261	GSE8039	GSM198416	T4 CD2-CD30L peripheral lymph node
269 GPL1261	GSE8039	GSM198423	C1 mesenteric lymph node
270 GPL1261	GSE8039	GSM198424	C2 mesenteric lymph node
271 GPL1261	GSE8039	GSM198417	C3 mesenteric lymph node
272 GPL1261	GSE8039	GSM198418	C4 mesenteric lymph node
273 GPL1261	GSE8039	GSM198419	T3 mesenteric lymph node
2/4 GPL1261	GSE8039	GSM198420	14 mesenteric lymph node
275 GPL1261	GSE8039	GSM198421	T1 CD2-CD30L mesenteric lymph node
277 GPL1261	GSE8039	GSM198422 GSM198427	Cl spleen
278 GPL1261	GSE8039	GSM198428	C2 spleen
279 GPL1261	GSE8039	GSM198431	C3 spleen
280 GPL1261	GSE8039	GSM198432	C4 spleen
281 GPL1261	GSE8039	GSM198425	T1 CD2-CD30L spleen
282 GPL1261	GSE8039	GSM198426	T2 CD2-CD30L spleen
283 GPL1261	GSE8039	GSM198429	T3 CD2-CD30L spleen
284 GPL1261	GSE8039	GSM198430	T4 CD2-CD30L spleen
285 GPL1261	GSE8039	GSM198439	C1 Thymus
286 GPL1261	GSE8039	GSM198440	C2 Thymus
287 GPL1261	GSE8039	GSM198433	C3 Thymus
288 GPL1261	1.501.0020	GSM198434	C4 I nymus
	GSE8039	GSM108427	TI CD2 CD301 Thursus
200 GPL 1261	GSE8039 GSE8039	GSM198437 GSM198439	T1 CD2-CD30L Thymus T2 CD2-CD30L Thymus
290 GPL1261 291 GPL1261	GSE8039 GSE8039 GSE8039 GSE8039	GSM198437 GSM198438 GSM198435	T1 CD2-CD30L Thymus T2 CD2-CD30L Thymus T3 CD2-CD30L Thymus

Lymph node Aire-wild-type
Lymph node Aire-knockout
Lymph node Aire-knockout Naive Furin Wild-type 1
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Naive_Furin_Knockout_1
Naive_Furin_Knockout_1
CD8 T cells IL-2 complex treatment_0 ii CD8 T cells IL-2 complex treatment 1 h
CD8 T cells_IL-2 complex treatment_3 h
CD8 P14 Naive cells
CD8 P14 Naive cells
CD8 P14 Memory cells
CD8 P14 Memory cells
CD8 P14 Memory cells
CD8 P14 day4.5pi KLRG-1 Int sorted cells CD8 P14 day4 5pi KLRG-1 Int sorted cells
CD8 P14 day4.5pi KLRG-1 Int sorted cells
CD8 P14 day4.5pi KLRG-1 Hi sorted cells
CD8 P14 day4.5pi KLRG-1 Hi sorted cells
CD8 P14 day4.5pi KLRG-1 Hi sorted cells Naive CD8+ T cells
Activated_CD8+_T_cells
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cytotoxic T cell_IL-2_0hour
cytotoxic T cell_IL-2_0hour
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cytotoxic T cell_No IL-2_4 hour
cytotoxic T cell_No IL-2_4 hour
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cytotoxic T cell_IL-2_8 hour
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cytotoxic T cell_IL-2_10 hour
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cytotoxic T cell_IL-2_12 hour
cytotoxic T cell_IL-2_12 hour
cytotoxic T cell_IL-2_16 hour
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N N N M M E E E E E E E E E E

292 GPL1261	GSE8039	GSM198436	T4 CD2-CD30L Thymus	CD2-CD30L Thymus
293 GPL1261	GSE8678	GSM215223	Effector CD8 T cells, IL-7Rlo, rep1	Effector CD8 T cells, IL-7Rlo
294 GPL1261	GSE8678	GSM215224	Effector CD8 T cells, IL-7Rlo, rep2	Effector CD8 T cells, IL-7Rlo
295 GPL1261	GSE8678	GSM215225	Effector CD8 T cells, IL-7Rlo, rep3	Effector CD8 T cells, IL-7Rlo
296 GPL1261	GSE8678	GSM215226	Effector CD8 T cells, IL-7Rhi, rep1	Effector CD8 T cells, IL-7Rhi
297 GPL1261	GSE8678	GSM215227	Effector CD8 T cells, IL-7Rhi, rep2	Effector CD8 T cells, IL-7Rhi
298 GPL1261	GSE8678	GSM215228	Effector CD8 T cells, IL-7Rhi, rep3	Effector CD8 T cells, IL-7Rhi
299 GPL1261	GSE2924	GSM62977	CD8+Tet04	CD8+Tet-
300 GPL1261	GSE2924	GSM62978	CD8+Tet02	CD8+Tet-
301 GPL1261	GSE2924	GSM62979	CD8+Tet03	CD8+Tet-
302 GPL1261	GSE2924	GSM62980	CD8+Tet01	CD8+Tet-
303 GPL1261	GSE2924	GSM62981	CD8+Tet05	CD8+Tet-
304 GPL1261	GSE2924	GSM62982	CD8+HYTet+_01	CD8+HYTet+
305 GPL1261	GSE2924	GSM62983	CD8+HYTet+_02	CD8+HYTet+
306 GPL1261	GSE2924	GSM62984	CD8+HYTet+_03	CD8+HYTet+
307 GPL1261	GSE2924	GSM62985	CD8+HYTet+_04	CD8+HYTet+
308 GPL1261	GSE2924	GSM62986	CD8+H7aTet+_01	CD8+H7aTet+
309 GPL1261	GSE2924	GSM62987	CD8+H7aTet+_02	CD8+H7aTet+
310 GPL1261	GSE2924	GSM62988	CD8+H7aTet+_03	CD8+H7aTet+
311 GPL1261	GSE2924	GSM62876	CD8+H7aTet+_04	CD8+H7aTet+
312 GPL1261	GSE13493	GSM340091	DP thymocytes 1	CD4+CD8+ thymocytes
313 GPL1261	GSE13493	GSM340092	DP thymocytes 2	CD4+CD8+ thymocytes
314 GPL1261	GSE13493	GSM340093	CD4intCD8+ thymocytes 1	CD4intCD8+ thymocytes
315 GPL1261	GSE13493	GSM340094	CD4intCD8+ thymocytes 2	CD4intCD8+ thymocytes
316 GPL1261	GSE13493	GSM340095	CD8SP thymocytes 1	CD8SP thymocytes
317 GPL1261	GSE13493	GSM340096	CD8SP thymocytes 2	CD8SP thymocytes
318 GPL1261	GSE10813	GSM273000	Fresh CD8 rep1	Fresh CD8
319 GPL1261	GSE10813	GSM273001	Fresh CD8 rep2	Fresh CD8
320 GPL1261	GSE10813	GSM273005	Stimulated CD8 rep1	Stimulated CD8
321 GPL1261	GSE10813	GSM273006	Stimulated CD8 rep2	Stimulated CD8
322 GPL1261	GSE10813	GSM273002	Expanded CD8 Tcells with Suppression function rep2	Expanded CD8 Tcells with suppression function
323 GPL1261	GSE10813	GSM272995	Expanded CD8 Tcells with Suppression function rep1	Expanded CD8 Tcells with suppression function
324 GPL1261	GSE10813	GSM272996	Expanded CD8 Tcells with Suppression function rep3	Expanded CD8 Tcells with suppression function
325 GPL1261	GSE10813	GSM272997	Expanded CD8 Tcells with Suppression function rep4	Expanded CD8 Tcells with suppression function
326 GPL1261	GSE10813	GSM272998	Expanded CD8 Tcells with Suppression function rep5	Expanded CD8 Tcells with suppression function
327 GPL1261	GSE14699	GSM366905	OT-I T cell Naive repl	OT-I T cell Naive
328 GPL1261	GSE14699	GSM366912	OT-I T cell Naive rep2	OT-I T cell Naive
329 GPL1261	GSE14699	GSM366911	OT-LT cell Rag repl	OT-I T cell Rag
330 GPL1261	GSE14699	GSM366907	OT-I T cell RIP-OVAhi repl	OT-I T cell RIP-OVAhi
331 GPL1261	GSE14699	GSM366914	OT-L T cell RIP-OVAhi rep2	OT-L T cell RIP-OVAhi
332 GPL1261	GSE14699	GSM366909	OT-L T cell OCS/LPS ren]	OT-L T cell OCS/LPS
333 GPL1261	GSE14699	GSM366916	OT-L T_cell_OCS/LPS_rep2	OT L T cell OCS/LPS
334 GPI 1261	GSE4178	GSM05588	NK11 minus TGEbeta RILKO T calls T_KO	NK11-TGEbeta PILKO T celle T_KO
335 GPL 1261	GSE4178	GSM95589	NK11 minus rontrol T cells T WT	NK11- control T cells T WT
336 GPI 1261	GSE6810	GSM155205	Control renlicate 1	Control
337 GPL 1261	GSE6810	GSM155265	Control replicate 7	Control
338 GPI 1261	GSE6810	GSM155240	B abortue 2308 replicate 1	B shortus 2308
220 CBI 1261	CSE6810	CSM155251	B. abortus 2308 replicate 7	B. abortus 2308
339 GFL1201 340 GPL 1261	GSE6810	CSM155252	B. abortus 2.500 replicate 2	D. abortus 2508
340 GFL1201	GSE6810	CSM155252	B. abortus 3208 BA41 replicate 2	D. abortus DA41
341 GFL1201	GSE6810	CSM155254	B. abortus 2308 BA41 replicate 2	B. abortus 2208 A DH4 2
542 GFL1201	GSE6810	CSM155254	B. abortus 2308 ADH4.2 replicate 1	B. abortus 2208 ADH4.2
242 CBL 12(1	UNPOALU	GSM155255	B. adortus 2308 ADH4.2 replicate 2	B. abonus 2508 ADri4.2
343 GPL1261	CEE(010	COMPRESS	A menuensis i ovi replicate i	
343 GPL1261 344 GPL1261	GSE6810	GSM155256		B. memensis row
343 GPL1261 344 GPL1261 345 GPL1261	GSE6810 GSE6810	GSM155256 GSM155257	B. melitensis 16M replicate 2	B. melitensis 16M
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261	GSE6810 GSE6810 GSE15037	GSM155256 GSM155257 GSM375666	B. melitensis 16M replicate 1 B. melitensis 16M replicate 2 Wild-type CD8 T cell	B. melitensis 16M Wild-type CD8 T cell
 343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 	GSE6810 GSE6810 GSE15037 GSE15037	GSM155256 GSM155257 GSM375666 GSM375667	B melitensis How replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell	B. melitensis fow B. melitensis 16M Wild-type CD8 T cell Foxo IKO CD8 T cell
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 348 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964	E militensis How replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1	B. melitensis IoW B. melitensis IoW Wild-type CD8 T cell Foxo1KO CD8 T cell LN T cells-WT
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 348 GPL1261 349 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965	E-militarisi IGM replicate 2 Wild-type CD8 T cell FoxolKO CD8 T cell LNT-1 LNT-2	D. Internetists Town B. melitensis 16M Wild-type CD8 T cell Foxo1KO CD8 T cell LN T cells-WT LN T cells-WT
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 348 GPL1261 349 GPL1261 350 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965 GSM26966	B mellensis 10 repeate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1 LNT-2 LNT-2 LN-T-3	D. melitensis 16M Wild-type CD8 T cell Foxol KO CD8 T cell LN T cells-WT LN T cells-WT
343 GPL1261 344 GPL1261 345 GPL1261 347 GPL1261 347 GPL1261 348 GPL1261 349 GPL1261 350 GPL1261 351 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965 GSM26966 GSM26966 GSM26967	B militensis IoM replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4	D. mellensis 16M Wild-type CDS T cell Foxt IK C CDS T cell LN T cells-WT LN T cells-WT LN T cells-WT
343 GPL1261 344 GPL1261 345 GPL1261 347 GPL1261 348 GPL1261 348 GPL1261 350 GPL1261 350 GPL1261 351 GPL1261 352 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965 GSM26966 GSM26967 GSM26967	Emiliansis IoM replicate 2 Wild-type CD8 T cell FoxolKO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-4	D. melitensis 16M Wild-type CD8 T cell Foxo1KO CD8 T cell LN T cells-WT LN T cells-WT LN T cells-EA2 KO LN T cells-EA2 KO
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 349 GPL1261 349 GPL1261 350 GPL1261 351 GPL1261 352 GPL1261 353 GPL1261	GSE6810 GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965 GSM26966 GSM26967 GSM26968 GSM26968	B melinensis IoM replicate 2 Wild-type CD8 T cell FoxolKO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-4 LNT-5 LNT-6	D. melitensis 16M Wild-type CD8 T cell Foxol KO CD8 T cell LN T cells-WT LN T cells-WT LN T cells-EMT LN T cells-EM2 KO LN T cells-EM2 KO LN T cells-EM2 KO
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 348 GPL1261 350 GPL1261 351 GPL1261 352 GPL1261 353 GPL1261 354 GPL1261 354 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1506 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26966 GSM26966 GSM26966 GSM26968 GSM26969 GSM186666 GSM26969	B militensis HoM replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-5 CS7BL/04 female number 1, untreated control ear (#]_Wt-C-3)	D. melitensis 164 Wild-type CD8 T cell Foxol IX C OD8 T cell LN T cells-WT LN T cells-WT LN T cells-WT LN T cells-Exh2 KO LN T cells-Exh2 KO cutaneous T cell
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 349 GPL1261 349 GPL1261 350 GPL1261 351 GPL1261 353 GPL1261 353 GPL1261 353 GPL1261 355 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE7694 GSE7694	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26964 GSM26966 GSM26969 GSM26969 GSM186666 GSM186666 GSM186666	B militensis 16M replicate 2 Wild-type CD8 T cell FoxolKO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-5 C57BL/6/ female number 1, untreated control ear (#1_Wt-C-3) C57BL/6/ female number 2, untreated control ear (#2_Wt-C-4)	b. melitensis 1604 Wild-type CD8 T cell Foxol KO CD8 T cell LN T cells-WT LN T cells-WT LN T cells-WT LN T cells-EA2 KO LN T cells-EA2 KO LN T cells-EA2 KO cutaneous T cell cutaneous T cell
343 GPL1261 344 GPL1261 345 GPL1261 346 GPL1261 347 GPL1261 348 GPL1261 359 GPL1261 350 GPL1261 351 GPL1261 353 GPL1261 353 GPL1261 354 GPL1261 355 GPL1261 355 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE7694 GSE7694 GSE7694	GSM155256 GSM155257 GSM375666 GSM375667 GSM26964 GSM26965 GSM26966 GSM26967 GSM26968 GSM26969 GSM186666 GSM1866667 GSM1866667	B militensis HoM replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-5 LNT-5 C57BL/6J female number 1, untreated control ear (#1_Wt-C-3) C57BL/6J female number 2, untreated control ear (#2_Wt-C-4) C57BL/6J female number 3, untreated control ear (#3_Wt-C-7)	D. melitensis 1604 Wild-type CD8 T cell Foxol KO CD8 T cell LN T cells-WT LN T cells-WT LN T cells-Eh2 KO LN T cells-Eh2 KO LN T cells-Eh2 KO cutaneous T cell cutaneous T cell
343 GPL1261 344 GPL1261 345 GPL1261 347 GPL1261 347 GPL1261 348 GPL1261 349 GPL1261 350 GPL1261 351 GPL1261 353 GPL1261 353 GPL1261 354 GPL1261 355 GPL1261 355 GPL1261 357 GPL1261	GSE6810 GSE6810 GSE15037 GSE15037 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE1566 GSE7694 GSE7694 GSE7694	GSM155256 GSM155257 GSM375667 GSM26964 GSM26965 GSM26967 GSM26967 GSM26967 GSM26967 GSM26967 GSM186667 GSM186667 GSM186667 GSM186667	B militensis HoM replicate 2 Wild-type CD8 T cell Foxol KO CD8 T cell LNT-1 LNT-2 LNT-3 LNT-4 LNT-5 C57BL/6 female number 1, untreated control ear (#1_Wt-C-3) C57BL/6 female number 2, untreated control ear (#2_Wt-C-4) C57BL/6 female number 2, untreated control ear (#2_Wt-C-4) C57BL/6 female number 1, DNTB-treated allergic ear (#4_Wt-Tr-3) C57BL/6 female number 1, DNTB-treated allergic ear (#4_Wt-Tr-3)	D. inclusions for B. meltiensis for Wild-type CD8 T cell Foxol KO CD8 T cell LN T cells-WT LN T cells-WT LN T cells-WT LN T cells-Ezh2 KO LN T cells-Ezh2 KO cutaneous T cell cutaneous T cell cutaneous T cell cutaneous T cell
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* collected till Sept 2009 ** Classification: N, naïve; E,effector; M, memory;MP,memory precursor

TF Name	#MSG	#Rko	P-value		DNA Motif	FDR	FSG	MSG	۵۵۵. nD	CR F/N	aPCR M/N
Sov/	50		0 55F-10	VES	SORV	0.00012	VES	VES	٩r	-// 305	-5.8/15
7fn2611	JU 41	10	7 OFE 07	NO	3011	0.00012	NO	NO		-4.303	-3.645
ZIP3011	41	10	7.05E-07	NU	-	-	NU	NO	-	2 71	- 0.27
	40	10	1.10E-00	TES	LEFF	0.00104	TES	NU		-3./1	-0.37
норх	37	/	9.01E-07	NO	-	-	YES	YES	-	4.00	-
Eomes	34	4	1E-06	YES	BRAC	0.00209	YES	YES		1.99	3.48
Ets2	28	3	1.1/E-05	NO	EISF	0.16476	YES	NO	-		-
Bhlhe40	27	1	2.50E-05	YES	HESF	0.33531	YES	YES		2.72	4.215
Prdm1	26	2	2.9E-05	YES	PRDF	-	YES	NO		4.185	4.5
Klf2	24	9	0.00059	YES	KLFS	0.11349	NO	NO		-2.01	-0.63
Pou2af1	23	3	9.14E-05	YES	-	-	NO	NO	-		-
Bach2	22	5	0.00023	YES	AP1R	0.01508	YES	NO		-3.77	-0.935
Runx2	21	0	0.00036	YES	HAML	0.00308	YES	YES		0.19	2.775
Tcf4	21	9	0.00191	YES	EBOX	0.29778	NO	NO	-		-
ld2	20	2	0.00032	YES	-	-	YES	YES		0.265	2.645
Smad1	20	5	0.00052	NO	SMAD	0.76295	YES	NO	-		-
Stat4	17	6	0.00265	YES	STAT	0.25029	NO	NO		-2.33	0.935
Nr4a2	16	1	0.00187	NO	NBRE	-	NO	NO	-		-
Mef2c	16	4	0.00191	YES	MEF2	-	NO	NO	-		-
Zfp318	15	3	0.00234	-	-	-	YES	NO	-		-
Runx3	15	4	0.00287	YES	HAML	0.00308	NO	NO		-2.37	-1.925
Id3	14	0	0.00542	YES	-	-	NO	NO		-3.695	-1.995
Fosl2	12	1	0.00881	NO	ΔP1F	0 00459	NO	VES		0.000	-
Nfatc?	12	2	0.00001	VES	NEAT	0.00455	NO	NO	_		_
7fn422	12	2	0.00750	ILJ	NI AI	0.01205	NO	NO			
210422 1675	12	3	0.00781	-		- 0.0200	NO	NO	-		-
1K212 7fm5 2	12	4	0.00901	-	IKKS	0.0208	NO	NO	-		-
ZIµSZ Usalasa 1 al	12	5	0.01516	-	-	-	NO	NO	-		-
Juamia	12	6	0.01878	-	-	-	NO	NO	-		-
EtV3	12	/	0.02675	-	EISF	0.16476	NO	NO	-		-
Zfp238	11	0	0.01/0/	-	RP58	-	YES	NO	-		-
Gata3	11	1	0.01297	YES	GATA	0.04247	NO	NO	-		-
Bbx	11	2	0.01122	-	-	-	NO	NO	-		-
Enc1	11	3	0.01166	-	-	-	NO	NO	-		-
Cux1	11	4	0.01435	YES	CLOX	0.6281	NO	NO	-		-
Nsd1	11	4	0.01435	NO	-	-	NO	NO	-		-
lkzf1	11	7	0.03862	YES	IKRS	0.0208	NO	NO	-		-
Nfatc1	11	7	0.03862	YES	NFAT	0.01269	NO	NO	-		-
Phf3	11	7	0.03862	-	-	-	NO	NO	-		-
Jun	10	1	0.01909	YES	AP1F	0.00459	NO	NO	-		-
Nr4a1	10	1	0.01909	YES	NBRE	-	NO	NO	-		-
Nfe2l2	10	1	0.01909	YES	AP1R	0.01508	NO	NO	-		-
Egr1	10	4	0.0214	NO	EGRF	0.24216	NO	NO	-		-
Mxi1	9	0	0.03656	YES	EBOX	0.29778	NO	NO	-		-
Pbx3	9	0	0.03656	NO	-	-	YES	NO	-		-
Tbx21	9	0	0.03656	YES	BRAC	0.00209	NO	NO		6.215	3.165
Jund	9	1	0.02808	YES	AP1F	0.00459	NO	NO	-		-
Klf10	9	1	0.02808	NO	SP1F	0.9321	NO	NO	-		-
Tsc22d1	9	2	0.02469	NO	-	-	NO	NO	-		-
Ar	9	2	0.02469	YES	GREE	-	NO	NO	-		-
Maf	9	2	0.02103	VES		0 01508	VES	NO	-		-
Rfv1	9	3	0.02557	-	YRRE	0.01000	NO	NO	_		_
KIE2	0	5	0.02357		KIES	0.13030	NO	NO	_		-
Arntl	0	1	0.04237	NO		0.11345	NO	NO			
7fn700	ŏ о	1	0.04132	NU	11175	0.34390	NO	NO	-		-
21µ709	ð	1	0.04132	-		-	NO		-		-
	8	2	0.03666	NU	FKHD	0.00021	NO	NO	-		-
AFCC6	8	3	0.038//	1ES	-	-	NO	NO	-		-
smad3	8	3	0.038/7	YES	SIVIAD	0.76295	NU	NO	-		-
Atxn1	8	3	0.03877	NO	-	-	NO	NO	-		-
Ztp826	8	4	0.04742	YES	-	-	NO	NÖ	-		-
Sp1	8	4	0.04742	NO	SP1F	0.9321	NO	NO	-		-
Klf4	7	1	0.0608	NO	KLFS	0.11349	NO	YES	-		-

Supplementary Table S2. List of the 60 TFs identified by master regulator analysis.

* ISP: immune system phenotype marked gray:known TFs that regulate memory CD8+ T cell development

Supplementary Table S3. Primers for gateway cloning of TFs

attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCT
attB2	GGGGACCACTTTGTACAAGAAAGCTGGGT
Sox4Fgw	AAAAAGCAGGCTACCATGGTACAACAGACCAACAACGCG
Sox4Rgw	AGAAAGCTGGGTTCAGTAGGTGAAGACCAGGTTAGAG
Tcf7Fgw	AAAAAGCAGGCTACCATGTACAAAGAGACTGTCTACTCTG
Tcf7Rgw	AGAAAGCTGGGTCTAGAGCACTGTCATCGGAAGG
Klf2Fgw	AAAAAGCAGGCTGCCATGGCGCTCAGCGAGCCTATCTTG
Klf2Rgw	AGAAAGCTGGGTCTACATGTGTCGCTTCATGTGC AAG
EomesFgw	AAAAAGCAGGCTAGCATGCAGTTGGGAGAGCAG
EomesRgw	AGAAAGCTGGGTCTAGGGACTTGTGTAAAAAGCATAATAAGC
Id2Fgw	AAAAAGCAGGCTagcATGAAAGCCTTCAGTCCGGTG
Id2Rgw	AGAAAGCTGGGTTTAGCCACAGAGTACTTTGCTATCAT
Prdm1Fgw	AAAAAGCAGGCTCAGATGAGAGAGGCTTATCTCAGATGTTG
Prdm1Rgw	AGAAAGCTGGGTTCTTAAGGATCCATCGGTTCAACTGT
Bach2Fgw	AAAAAGCAGGCTGGC ATGTCTGTGGATGAGAAGC
Bach2Rgw	AGAAAGCTGGGTGCTAGGCATAATCTTTCCTGGGC
Tbx21Fgw	AAAAAGCAGGCTCGGATGGGCATCGTGGAGC
Tbx21Rgw	AGAAAGCTGGGTCAGCGGCATTTTCTCAGTTGGG
Runx2Fgw	AAAAAGCAGGCTATGCTTCATTCGCCTCACAAACAAC
Runx2Rgw	AGAAAGCTGGGTTCAATATGGCCGCCAAACAGACTC
Id3Fgw	AAAAAGCAGGCTAACATGAAGGCGCTGAGCCCG
Id3Rgw	AGAAAGCTGGGTCCGGGTCAGTGGCAAAAGCTCC
Bhlhe40Fgw	AAAAAGCAGGCTATCATGGAACGGATCCCCAGC
Bhlhe40Rgw	AGAAAGCTGGGTCCCTCCAGAGTTTAGTCTTTGGTTTCTAAGTT
Stat4Fgw	AAAAAGCAGGCTAGCATGTCTCAGTGGAATCAAG
Stat4Rgw	AGAAAGCTGGGTCCGTCATTCAGCAGAATATGG

Supplementary Table S4. Sequences for shRNAs

shSox4F	CCGG <u>GCATCGTTCTCCCAGAGCAA</u> CTCGAG TTGCTCTGGAGAGAACGATGCTTTTTG
shSox4R	AATTCAAAAAGCATCGTTCTCTCCAGAGCAA CTCGAG TTGCTCTGGAGAGAACGATGC
shBhlhe40F	CCGG <u>GCGAGGTTACAGTGTTTATAT</u> CTCGAG ATATAAACACTGTAACCTCGCTTTTTG
shBhlhe40R	AATTCAAAAAGCGAGGTTACAGTGTTTATAT CTCGAG ATATAAACACTGTAACCTCGC
shBach2aF	CCGG <u>AAGAGCGAATTTGGTGCACAC</u> CTCGAG GTGTGCACCAAATTCGCTCTT TTTTG
shBach2aR	AATTCAAAAAAGAGCGAATTTGGTGCACAC CTCGAG GTGTGCACCAAATTCGCTCTT
shRunx2F	CCGG <u>GCACGCTATTAAATCCAAATT</u> CTCGAG AATTTGGATTTAATAGCGTGCTTTTTG
shRunx2R	AATTCAAAAAGCACGCTATTAAATCCAAATT CTCGAG AATTTGGATTTAATAGCGTGC

Gapdh 137	AGTATGACTCCACTCACGGC
Gapdh 402	GTTCACACCCATCACAAACA
Hprt 22	GTCGTGATTAGCGATGATGA
Hprt 245	ATGTAATCCAGCAGGTCAGC
Sox4FRT	GAGAACACTGAGGCTCTGCT
Sox4RRT	TGAACGGAATCTTGTCGCTG
Tcf7FRT	GTCTACTCTGCCTTCAATCTG
Tcf7RRT	GGGAAGTGCTGTCTATATCCG
Klf2FRT	CTATCTTGCCGTCCTTTGCC
Klf2RRT	CTCCGGGTAGTAGAAGGCAG
Eomes_1504	GTCAACACTTTGCCTCAAGC
Emoes_1862	AAGACAGGTGGGCTCATTCT
Tbx21_817	GAGGTGAATGATGGAGAGCC
Tbx21_1183	CATAACTGTGTTCCCGAGGT
Bhlh40_152	AAACTTACAAACTGCCGCAC
Bhlh40_502	ATTTCAGGTCCCGAGTGTTC
Id2_92	ACCCGATGAGTCTGCTCTAC
Id2_336	GATGCTGATGTCCGTGTTCA
Id3_107	AGCCTCTTAGCCTCTTGGAC
Id3_235	CGAGGATGTAGTCTATGACACG
Prdm1_1227	GAATGTTTCCTATGGTTCCG
Prdm1_1447	GGAGGTTACTGTAGACGGGAT
Bach2_1076	CTCAGCAACCCTTAGTCAGG
Bach2_1353	GCTCACCGCAGAGTATGAAT
Runx2_1409	CAGCCACCTTTACCTACACC
Runx2_1711	CGTCAACACCATCATTCTGG
Stat4_1063	TATCAGGTGAAAGTAAAGGCG
Stat4_1443	AACCAAGTTCTGGGAGTCG

Pimer sequence disance to TSS (bp) Hprt_806 CCCAGATAATCACTCCGCA -194 Gaph_738 CCTATCAGTTCGGAGCCCA -262 Gaph_902 GCCCTGCTTATCCAGTCCTA -98 Sox4_915 GAAGCGTTAGTTACAGCGGC -85 Sox4_915 GAACGGTACTGACTAATCC -308 Tef7_876 ACTGACAGGGAACAGCGACA -143 Tbx21_579 GACCAGGACACAGCGAGCAAAC -481 Tbx21_579 GACCAGGACACAGCGAGCAAAC -481 Tbx21_579 GGATTCATTCTCCTGGTAACTG -223 Prdm1_509 GGATTTCATTCTCCTGGTAACTG -491 Ktr2_760 AACAACCAGGCAACACGG -264 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_364 TTCATCAAAGGGAAAGCCG -636 Bhihe0_951 GCTACAACCAGTCAGCAGCAGC -262 Bhihe0_951 GCTGCGCGAGAGCAGCAACA 26 Gamb_951 GCACAGCCTAAGGAGCAGC -166 Ga_1020 GAGACCACCACAGCGAAGCC -187 Gamb_959 GACACACACCAGGACATACC -293 GCACATGCCCACTTAGG	Supplementary	Table S6. Primers for ChIP-PCR.	
Hprt.803 GCCTTGAACTCAGAAATCCG -397 Hprt.806 CCCAAGTATACCACTCCGCA -262 Gapdn.902 GCCCAGGTAATCACACTCCGCA -282 Gapdn.902 GCCCAGGTAATCACCAGCGCA -285 Sox4_113 GTTTTCTCCCCCCCCTCTG 136 TGT7.802 GCCCAGGTACTAATCC -308 Ter7.803 GCCCAGGTAGCACATATCC -308 Ter7.804 ACCTGACGACAACAGCGGA -124 Eomes.804 ACCACGGTTGATCATCCCAGGGG -396 Eomes.804 ACCACGGTTGCATCGTCGTGGTG -431 Thx21_77 AACCAGGATTTCCATCGTGGG -396 Firm1.509 GCACAGCTTTCCTTCCTCCAACCTG -431 KII2_566 CAAAGATTTCACAGAGCGACAACCG -434 KII2_566 CAAAGATTCCATGGGAGCACACAGC -226 Bihledo_914 GCTGTGGGAACTAGCGGAGAGAGC -240 Bach2a_39 GCTGTGGGAACTAGCGGAGGAGT -370 Id2_530 GTCTGCTGTAGGGAGAGAGC -166 Bihledo_944 AGCCAATGCCTAAAGCAGCAGCAACA 26 Gamb_070 CAAGAGACCACCAATGAGCAGCAATCA 26 <	Pimer	sequence	disance to TSS (bp)
Hprt_806 CCCACAGATAATCACTCCGCA -194 Gapch, 738 CCTATCAGTTCGGAGCCCA -262 Gapdh, 738 CCTATCAGTTCGAGCCCA -262 Sox4_915 GAAGCGTTAGTCAGAGCGCA -268 Sox4_915 GATCGCAGGGAACAGCGGCA -124 Eomes,850 ACCAGGATCAGTCGACTAATCC -308 Eomes,857 GACCAGCTTGGACAGCAGCAAAC -481 Thx21_579 GACAAGAGACAGCGAGCAAAC -481 Thx21_579 GACAAGAGACAGCGAGCAAAC -481 Prim1_192 GGATGTCCTTCCTCTCCTCCCCCAGA -413 Thx21_579 GACAAGAGACAGCGACACACG -434 Kif2_566 CAAAGATTTCAATCAGAGGAGCAGCA -431 Kif2_560 CAACAACCAGGCAGCAACAGCG -236 Barba2_379 GCTGTGGTGGAAGTCAGTGGAGG -221 Barba2_91 GCTGTGCTGGGAGAGAGCCG -152 Barba2_93 GCTGTGCTGGGAGAAGAGCC -166 Id3_934 CAGAACCACTAAGCAGCAAACAC 26 Rum2_983 GGCAGTCCCAAGGAGAGCC -117 Rum2<193	Hprt_603	GCCTTGAACTCAGAAATCCG	-397
Gapdh, 738 CCTATCAGTTCGGAGCCCA -262 Sox4_915 GAAGCGTTAGTCAGCCTA -98 Sox4_915 GAAGCGTTAGTACAGCGGC -85 Sox4_1136 TGTTTCTCCCCCCTCG 136 Td7_876 ACTGGACAGCGAACAGCGAC -124 Eomes, 504 ACCAGGATTCGATTCCCAGTGG -396 Eomes, 504 ACCAGGATTCGATTCCCAGTGG -396 Eomes, 504 ACCAGGATTCGATTCCCAGTGG -431 Thx21_77 AATCTGGGAAAGCTCGACACCTG -491 Kitz_566 CAAAGATTCATTTCTCCCGGAACCTG -491 Kitz_566 CAAAGATTCAGTGGAAG -222 Prim1_120 GGATTCGATTCACAGGCACAACCAGC -434 Kitz_566 CAAAGACTCAGTGGAAGCGG -256 Bihle40_916 GCTACAACCAATCAGCGGAAGCC -434 Kitz_566 CAAAGCCAGCTAAGGAAGCCG -256 Bihle40_951 GCTACCAACCAATCAGCGACG -266 Bihle40_951 GCTACCACCATAGGAAGCCC -166 1d2_948 AGCCACTCAAGGAAGACC -166 1d3_91026 GGACACCTAAAGCAGCACAAACA 26 <td< td=""><td>Hprt_806</td><td>CCCAGATAATCACTCCGCA</td><td>-194</td></td<>	Hprt_806	CCCAGATAATCACTCCGCA	-194
Gapdh.902 GCCCTGCTTATCCAGTCCTA -98 Sox4_915 GAAGCGTTAGTTACACGGC -85 Sox4_1138 TGTTTCCCCTCCCTCTG 136 TdT_927 ACTTGACAGGGAACAGCGAC -124 Eomes.857 GACCGCTTGGAACTGACTCATCC -308 TdT_927 ACTTGACAGGGAACAGCGAGCAAAC -481 Tbx21_519 GACAGCTTGCTTCTCTCTCCAG -818 Prim1_125 GGATTCATTTCACAGGCACACCG -233 Prim1_1509 GGATTTCATTTCCCTGGTAACTG -491 Kit2_568 CAAAGATTCATTCACAGGCACACGC -240 Bach2a_394 TTCATCAAGGGAAAGCCG -636 Bhhe40_744 AGTGTCGTGGCGAAGAGCG -161 Id2_630 GTCTGCTGTGCGGAGAGAGGT -370 Id2_648 ACGCACACCTAAGCAGCAAACAG 26 Rmv2_88 GGCAGTCCACTTATGTGG -117 Run2_1087 AAACGCCAGGCCAATGCC -293 Garmb_707 CAAGAGCAGCAGCAATGACC 240 II7_813 TGAAGCACACAGCGAATGACC 240 II7_813 TGAAGCACACAGCAATGACC 240 II7_813	Gapdh_738	CCTATCAGTTCGGAGCCCA	-262
Sox4_915 GAAGCGTTAGTTACAGCGGC -85 Td7_s92 GCCCAGGTGACTGACTAATCC -308 Td7_s76 ACTTGACAGGAACAGCGAC -124 Eomes_604 ACCAGGATIGATTCTCAGTGG -396 Eomes_614 ACCAGGATIGATTCTCAGTGG -396 Eomes_614 ACCAGGAGAGCAGCAGCACAC -481 Tbx21_57 GACAGGAGAGCAGCAGCACACTG -223 Prim1_509 GGATTCATTTCTCCTGCTCAGAA -818 Prim1_509 GGATTGCATTTCTCCTGCTGCAACTG -491 Kil2_760 AACAACCAGGCACAACAGC -240 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -221 Bach2a_79 GCTGTGGGAAACCAGTGGACG -256 Bhihe40_44 AGTCATCAGGGAAAGCCG -266 Bhihe40_951 GTCACACCAATCAGCGGAACAC 26 Balhe40_951 GCTGTGGGGAAGAGCC -166 1d2_303 GGCAGTCCCACTTAAGGAGAGC -26 Runx2_883 GCAGTCCCACTAAGCAGCACAACA 26 Runx2_883 GGCAGTCACAGGCCAAAGCC -40 ITr_1024 CTAGAGGACTAAGGCCCAAATGCCC -111 <t< td=""><td>Gapdh_902</td><td>GCCCTGCTTATCCAGTCCTA</td><td>-98</td></t<>	Gapdh_902	GCCCTGCTTATCCAGTCCTA	-98
Sox4_136 TGTTTCCCCTCCCTGTG 136 Torf_982 GCCCAGGGTGACTGACTATCC -308 Torf_876 ACTTGACAGGGAACAGCGAC -124 Eomes_857 ACCAGGATTGATTCTCAGTGG -139 Eomes_857 GACCGCTTGGGAACTGATCG -223 Primi_129 GCATGGTTCTCTCTCTCCAGA -818 Primi_1509 GGATTCATTTCCACGAGCGACAACGC -240 Bach2a_79 GCTGTGGAAACAGCGCACAACGC -240 Bach2a_94 TTCATCAAGGGAAGCGG -636 Bihhe40_744 AGTGTTGCGGAGCAACGGC -256 Bihhe40_744 AGTGTTCGTGGAGAGGAGGC -166 Id3_84 CGCCATGCTGTGGGGAGG -152 Id3_84 CGCCAAGCCAATCAGCGGGA 26 Runx2,883 GGCAGTCCCAATGCGCAAACA 26 Runx2,883 GGACACCTAAGCAGCAAACA 26 Scmb_889 GAACCCCAAGCCAATGCC -116 ITr_1024 CCAGTGGCAAGACCT -348 GCTTGCTGCACACTGGTACACCA 24 -117 Runx2,883 GGCAGTCCACATGGCCAATGCC -190 Sell_800 T	Sox4_915	GAAGCGTTAGTTACAGCGGC	-85
Teff_892 GCCCAGGTGACTGACTAATCC -308 Teff_876 ACTTGACAGGGAACAGCGAC -124 Eomes_64 ACCAGGATTGATTCTCAGTGG -396 Eomes_657 GACCAGGAGACAGGGACAAC -481 Tbx21_579 AATCTGGGAAAGAGTCAACCTG -223 Prdm1_509 GGATTCCTTCCTCTGCAGA -491 KllZ_568 CAAAGCAGGCACAACAGC -434 KllZ_760 AACAACCAGGCACAACAGC -240 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -221 Bach2a_964 TTCATCAAAGGGAAAGCGG -256 Bhihe40_44 AGTGTTCGTGGAGACGGG -256 Bhihe40_951 GCTACCACCTATAGGAGAGCC -166 Id2_848 AGCCAATCAGCCTATAGGACGC -268 Bhihe40_451 GGAGACCCAAAGCACAAACA 26 Rum2_83 GGACACCTAAAGCAAACA 26 Rum2_83 GGACACCCACAGCCAAATGACC -166 Id3_1026 GGACACCACAGCCAAATGACCC -161 Rum2_83 GGACACCACAGCCAAATGACCC -161 Rum2_83 GGACACCTAAAGCACACATGACTC -111 Sell_980	Sox4_1136	TGTTTCTCCCTCCTCCTG	136
Tcf.2786 ACTGACAGGAACAGCGAC -124 Eomes_04 ACCAGGATIGATTCTAGTGG -396 Eomes_057 GACCGCTTGGAAACTTGTG -143 Tbx21_777 AATCTGGGAAAGAGTCACACCTG -223 Prdm1_509 GGATGTCCTTCCTTCTCCAGAA 481 Prdm1_509 GGATTTCATTTCCCTGGTAACTG 491 Klt2_760 AACAAACCAGGCAACACGC -240 Bach2a_78 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_78 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_78 GCTGTGCGTGGCAGAACCGC -636 Bihle40_744 AGTGTCTGCTGGAGGAAGCGC -161 Id2_848 AGCCAATGCCTGTAGGGGG -49 Id2_848 AGCCAATGCCTGTAGGAGGC -166 Id3_1026 GAACACCACATCAAGCAGCAAACA 26 Grmb_707 CAAAGAGTGAGCCCACTTTGTG -111 Runx2_818 GGACCACCACCACTAAGCAC 240 Grmb_707 CAAGAGACTCAAGGAGTAGTC -111 Sell_960 TGCTTCTCCATGCTGCACAC -40 It7_e131 TGAAGGCCACTAAGGGAGGAGC -171 Prd1	Tcf7_692	GCCCAGGTGACTGACTAATCC	-308
Eomes_804 ACCAGGATTGATTCTCAGTGG -396 Eomes_857 GACCAGCTTGGAAACTTGTG -143 Tbx21_519 GACAAGAGAGAGCAGCAAAC 481 Tbx21_519 GACAGCTTGGAAACTTGTG -223 Prdm1_1509 GGATTTCATTTCTCCTGCAACTG 491 KI2_566 CAAAGATTCACAGGCACAACAGC -434 KI2_566 CAAAGAGATTCAGTGGAAAGCGG -240 Bach2a_97 GCTGTGGGAAACTCAGTGGAAAG -221 Bach2a_94 TTCATCAAAGGGAAAGCCG -266 Bhihed_744 AGTGTTCGTGGAAGAGCAGC -266 Bhihed_951 GCTACAACCAATCAGCGCGAACCG -266 Bhihed_951 GCTACAACCAATCAGCGCAACACC 26 Runz_883 GGCAGTCCCACTTAAGGAGAGCC -166 102_910 AAACGCCAGGCAAATGACCC 293 Gzmb_70 CAAGCAGCACACACGGAATGACTC -111 Sell_810 TGCTCACACACGTGTGTACACCAC 24 Car_652 CTGCTGCTAACAGACCAC 24 Car_652 CTGCTGCGACAATGACCAC 24 Car_7652 CTGCTGCTACACTGTGTCTAAC 24 Car_	Tcf7_876	ACTTGACAGGGAACAGCGAC	-124
Eomes.857 GACCGCTTGGAAACTTGTG -143 Tbx21_579 GACAAGAGAACAGCGAGCAAAC -481 Tbx21_579 GACAAGAGACAGCGAGCAAAC -223 Prdm1_1509 GGATTCCTTCCTCCCGCAAACTG -223 Prdm1_509 GGATTTCACAGAGCGTTCC -434 Klf2_566 CAAAGATTTCACAGAGCGTTCC -434 Klf2_760 AACCAAGCAACCAGGCACAACCAG -240 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_364 TTCATCAAAGGGAAAGCCG -636 Bhihe40_744 AGTGTCGTGGCGGAGAGGGT -370 Id2_848 AGCCACACCATCAGCGGGGG -152 Id3_384 CAGACCACCTAAGCAGCAAACA 26 Runx2_883 GGCAGTCCACTTTAGTTGGG -117 Runx2_883 GGCAGTCCACTTAGCTTGGG -293 Gzmb_889 GAACCCACAGCGAATGACCC -40 II7_813 TGAGTCACACGGAAGAGCAC -40 II7_8190 TGGTTGCTGCGTGTAACCAC 24 Car_acc2 CTGTGGCGGACAATGCCCACT -348 Car_acc2 TGGTGCTGCGGACAGGAGAGGACG -171 II7_81	Eomes_604	ACCAGGATTGATTCTCAGTGG	-396
Tbx21_579 GACAAGAGACAGCGAGCAAAC 481 Tbx21_777 AATCTGGGAAAGAGTCAACCTG -223 Prdm1_182 GGATITCATTCTTCTCCAGA -818 Prdm1_509 GGATTTCATTTCTCCTGCTAACTG -491 Klf2_566 CAAAGATTTCACAGGCGACCAACAGC -240 Bach2a_34 TTCATCAAGGGAAAGCCG -236 Bhihe40_744 AGTGTTCGTGGGAAGTGACCG -256 Bhihe40_951 GTCTGCTGTGCGGAGAGAGCT -370 Id2_630 GTCTGCTGTGCGGAGAAGCC -166 Id3_1026 GAGACACCTAAGGAAGCC -166 Id3_1026 GAGACCACTAAGCAAGCAAACA 26 Rumx2_1087 AAACCCACCACAGCCATAGGAAGCC -166 Id3_1026 GAGACCCACACACTAAGCAACACA 26 Rumx2_1087 AAACCCACCACAGCCTTCTTG 87 Gzmb_707 CAAGAGATGAGCCCAAATGC -293 Gzmb_707 CAAGAGATGAGCCCAATGC -111 ITr_112 IGATCCACCACACGCAATGACTC -111 ITr_112 IGATCCACCACTGCTGCTCA -187 ITr_112 IGATGCGGAGAGAGTGATAATGCACT -240	Eomes_857	GACCGCTTGGAAACTTGTG	-143
Tbx21_777 AATCTGGGAAAGAGTCAACCTG -223 Prdm1_182 GGATTTCATTTCTCCTCCTCAGA -818 Prdm1_500 GGATTTCATTTCTCCTGCTAACTG 491 KIZ_566 CAAAGATTTCACAGAGCGTTCC -434 KIZ_566 CAACAACCAGGCCAACAGC -240 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_79 GCTGTGGGAAACTCAGTGGAAG -921 Bach2a_79 GCTGTGGGAAGGGCACCG -256 Bhlhe40_951 GCTACAACCAATCAGCGGG -256 Bhlhe40_951 GCTACAACCAATCAGCGAAGCG -166 Id2_848 AGCCAATGCCTTAAGGAAGCC -166 Id3_1026 GAGACCCTAAAGCAGCAAACG 26 Runx2_883 GGCAGTCCAATTACTTTGTGG -117 Runx2_1087 AAACGCCCACAGCGATGACTC -111 Sell_960 TGCTTTTCATTTCTCATGC -40 It7_813 TGAAGAGCCAATAGCCAC 24 Ca7_652 CTGTGGGACATAGCCACT -348 Ca7_652 TGTAGAGACTCACGGGAGGAGGAC -111 Prf1_1036 CTTCCTCTACCTGCACAGCT -362 Caf_663 </td <td>Tbx21_519</td> <td>GACAAGAGACAGCGAGCAAAC</td> <td>-481</td>	Tbx21_519	GACAAGAGACAGCGAGCAAAC	-481
Prdm1_182 GGATTCCTTCCTCCCGCAACGA -818 Prdm1_509 GGATTCCTTTCCCTGCTAACTG -491 Ktl2_566 CAAAGATTCCATTTCTCCTGCTAACTG -434 Ktl2_566 CAAAGATTCCATGGCAACGC -240 Bach2a_364 TTCATCAAAGGGAAAGCCG -636 Bhihe40_744 AGTGTTCGTGGGAGAGGCG -266 Bhihe40_744 AGTGTTCGTGGGAGAGGGGG -499 1d2_630 GTCTGCTGTGCGGAGAAGCCG -166 1d3_1026 GAGACCCAAAGGAAGCC -166 1d3_1026 GAGACACCTAAGGCAAGCACAACA 26 Runx2_1087 AAACGCAGGCAAGCACAAAGCA 26 Runx2_1087 AAACGCACGCAAAGCACCAAATGACC -293 Gzmb_707 CAAGAGATGACCTC -111 Sell_980 TGCTTACTTTCTTCATTGG -190 Sell_980 TGCTTACTTTCAATGGGAGC -244 Ccrf_652 CTGCTGGGAAATAGCCAC -44 Crf_822 TGCTGGGACAATAGCCAC -44 Crf_823 CTGCTGCTCAAAGGAGAGGC -111 Frl138 CAGGACGAGAGAGTAGAGATATGATATG -112 Prl1303 </td <td>Tbx21_777</td> <td>AATCTGGGAAAGAGTCAACCTG</td> <td>-223</td>	Tbx21_777	AATCTGGGAAAGAGTCAACCTG	-223
Prdm1_509 GGATTTCATTTCTCCTGCTAACTG 491 Kll2_566 CAAAGATTTCACAGAGCGTTCC -434 Kll2_760 AACAAACCAGGCACAACAGC -240 Bach2a_79 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_364 TTCATCAAAGGGAAAGCCG -266 Bhihed_951 GCTACAACCAATCAGCGGG -256 Bhihed_951 GCTACAACCAATCAGCGGG -49 Id2_630 GTCTGCTGTGCGGAGAGAGC -162 Id3_84 CAGACCAGCCTAAGGAGCACA 26 Runx2_883 GGCAGTCCCACTTACTTGGG -117 Runx2_1087 AAACGACCAGCCAAATGACCC -266 Gramb_707 CAAGAGATGAGCCCAAATGACTC -111 Sell_980 GAACCCACAGCGAATGACTC -111 Sell_980 GACCCACAGCGAATGACTC -111 Sell_980 GACTCTACAGCAATGACCAC 24 Cor7_552 CTGCTGGCGACATAGCCACT -348 Car7_629 TGTAGAGACTCAGGGAGGAGC -171 Prf_188 CAGGCCAGAGAGTAGTAGTAGATGT -112 Prf_813 TGAGAGACTCAGGGAGGAGGC -292 Car7_629 <td>Prdm1_182</td> <td>GGATGTCCTTCCTTCCAGA</td> <td>-818</td>	Prdm1_182	GGATGTCCTTCCTTCCAGA	-818
Kif2_566 CAAAGATTTCACAGAGCGTTCC 434 Kif2_760 AACAAACCAGGCACAACAGC -240 Bach2a_70 GCTGTGGAAACTCAGTGGAAG 921 Bach2a_74 AGTGTTCGTGGAAAGCCG -266 Bhihe40_951 GCTACACCAACCAGCGGG -49 Id2_630 GCTGTGCTGTGGGAGAGGGT -370 Id2_848 AGCCAATCCTAAGGAAGCC -166 Id3_934 CAGACCACCTAAAGCAACACACA 26 Runx2_883 GGCAGTCCCACTTTAGTTTGAG -117 Runx1_087 CAAGGCAATGAGCCCAAACA 26 Sell_910 CGCTGCCACATGCGTGTTCTTG 87 Gzmb_889 GAACCCACCGCAAGGCAATGACTC -111 Sell_910 TGGTCCACTACTGTGTCTTGG -187 I77_1813 TGAAGACTACACACCTTGCTCAA -187 I77_1813 TGAAGACTACAGGAAGAGCC -44 Car7_829 TGTAGAGACTCAGGGAGAGGAC -111 Prf1_988 CAGGCAGTAGAGAGAGTC -192 Cd5_808 AGGCAGTAGAGGAGAGTG -122 Car7_829 TGTAGAGACTCAGGGAGAGAGTG -372 Grmk_708	Prdm1_509	GGATTTCATTTCTCCTGCTAACTG	-491
Kif2_760 AACAAACCAGGCACAACAGC -941 Bach2a_364 TTCATCAAAGGGAAACCCG -921 Bach2a_364 TTCATCAAAGGGAAAGCCG -836 Bhihe40_744 AGTGTTCGTGGGAAGTGACCG -256 Bhihe40_951 GCTACAACCAATCACCGGGG -49 Jd2_848 AGCCAATGCCTGTAGGGAGC -162 Jd3_1026 GAGACACCTAAAGCAGCAACAA 26 Runx2_883 GGCAGTCCCACTTTACTTTGAG -117 Runx2_1087 AAAGGCCAAGCCAAATGACC 26 Runx2_1087 AAAGGCCAAGCCAATGAGCCT -111 Sell_980 GAACCCACAGCGAATGACTC -111 Sell_980 GAACCCACAGCCAATGGCCACAC 24 Carb_707 CAAGGAGTGACCCACACTGCAATGC -40 Sell_980 GACCTACACCACTTGCTCAA -187 IJ7_613 TGAAGTCACACCACTTGCAA -187 IJ7_813 TGAAGACTCAAGGGAAGGACC -124 Carf_652 CTGCTGCTCAACACCAC 24 Carf_652 CTGCTGCTCTACCACCTGAAGTGC -122 Ccf_983 CAGGCAGTAGAGGACGAGGACC -112 Prf1_1036 </td <td>Klf2_566</td> <td>CAAAGATTTCACAGAGCGTTCC</td> <td>-434</td>	Klf2_566	CAAAGATTTCACAGAGCGTTCC	-434
Bach2a_79 GCTGTGGAAACTCAGTGGAAG -921 Bach2a_364 TTCATCAAAGGGAAAGCCG -636 Bhlhe40_951 GCTACAACCAATCAGCGGG -49 Id2_630 GTCTGCTGGCGAGAGAGT -370 Id2_848 AGCCAATCCTAAGGAGAGC -166 Id3_1026 GAGACACCTAAAGCAACCAAACA 26 Runx2_883 GGCAGTCCCACTTAGTGAGCACAAAGCA 26 Gzmb 289 GAACCCACGAGAGCCTTCTTG 87 Gzmb_707 CAAGAGAGCCCAAAGCG -111 Sell_810 TGGTCCACTACTGTGTTCTTGG 190 Sell_80 TGCTTCTTCTTTCATTTCCCAGC -40 IT7_1024 CTCTGTGGCACATAGCCCAA -187 II7_1024 CTCTGTGGCACATAGCCACA 24 Ccrd_522 CTGCTGGGACAATAGCCACT -348 Crd_552 CTGCTGGGACAATAGCCACT -348 Crd_552 CTGCTGGGACAGTAGAGGC -171 Prf1_88 CAGGGCAGGAAGTAGTAATGATAGTG -112 Prf1_88 CAGGGCAGGAAGTAGGCAGAGTC -192 Cd5_963 CCAGGGTTAGAGAGGCAGAGTC -192 Cd5_963	Klf2_760	AACAAACCAGGCACAACAGC	-240
Bach2a_364 TTCATCAAAGGGAAAGCCG -636 Bhlhe40_744 AGTGTTCGTGGAAGTGACCG -256 Bhlhe40_51 GCTACAACCAATCAGCGGGG -49 Id2_630 GTCTGCTGTGCGGAGAGAGT -370 Id2_844 AGCCAATGCCTAAGGAAGCC -166 Id3_1026 GAGACACCTAAAGCAGCAAACA 26 Rumx2_1087 AAACGCACCCACGTTAGGTTGTGG 87 Gzmb_707 CAAGAGATGAGCCCCAAATGC -293 Gzmb_889 GAACCCACAGCGAATGACTC -111 Sell_810 TGGTCACTACTGTGTTTTCTGG -190 Sell_960 TGCTTTTTTTCTTTCACTGCAGC -40 ITr_813 TGAAGTCACCACCTGCTAAA -187 IT_91024 CTCTGTGGCAAATGCCACC 24 Cor7_829 TGTAGAGCACTAAGGGAAGGAGC -111 Prf1_9186 CAGGGCAGGAAGTAGTAGTAATGATATG -112 Prf1_9188 CAGGGCAGGTAGCAAGGGAAGCC -192 Cd5_808 AGGGCAGTTAGAGGCAGAGGTC -192 Cd5_808 AGGGCAGTTAGAGACAGCGCTGC -362 GTmk_708 GTGGTCTGAGTAGAACAGCGCTC -355 <t< td=""><td>Bach2a_79</td><td>GCTGTGGAAACTCAGTGGAAG</td><td>-921</td></t<>	Bach2a_79	GCTGTGGAAACTCAGTGGAAG	-921
Bhihe40_744 AGTGTTCGTGGAAGTGACCG -256 Bhihe40_951 GCTACAACCAATCACCGGG -49 Id2_630 GTCTGCTGTGCGGAGAGAGT -370 Id2_631 CACACCACCTGTAGGGAGGACA 26 Id3_1026 GAGACACCTAAGCAAGCACAACA 26 Runx2_883 GGCAGTCCCACTTAGCTTGAGG -117 Runx2_1087 AAACGCCAAGCCAAATGC -293 Gzmb_707 CAAGAGATGAGCCCAAATGC -293 Gzmb_889 GAACCCACAGCGAATGACTC -111 Sell_810 TGGTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTCTCCACC -40 II7_1024 CTCTGTGGCACATAGCCACT -348 Corf_629 TGTAGAGACTACAGGAGAGGC -171 Pf1_88 CAGGCAGAAGTAGTAATGGTAAT -348 Corf_630 CCACAGGTTAGAGGCAGAAGTG -182 Cdf_803 CCACGGCAGAGAGAGTG -192 Cdf_803 CCACGGCAGAGAGAGTG -192 Cdf_803 CCACGGCAGAGAGAGC -292 Gzmk_708 GTGACCCACAGGAGAAGTG -373 Gzmk_973 ACCG	Bach2a_364	TTCATCAAAGGGAAAGCCG	-636
Bhlhedu_961 GCTACAACCAATCAGCGGG -49 Id2_630 GTCTGCTGTGCGGAGAGAGT -370 Id2_848 AGCCAATGCCTTAGGGTG -152 Id3_834 CAGACCAGCCTAAGGAAGCC -166 Id3_1026 GAGACACCTAAAGCAGCAAACA 26 Runx2_883 GGCAGTCCCACTTTACTTTAGT 87 Gzmb_707 CAAGAGATGAGCCCAAATGAC -293 Gzmb_889 GAACCACACGAGAGCTTC -111 Sell_810 TGCTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTTCCCAGC -40 IT7_1024 CTCTGTGCCTGCTAACCAC 24 Cc7_652 CTGCTGGGACAATAGCCACT -348 Ccr_829 TGTAGAGCACGAAGTGGTAGTAATGATATG -112 Prf1_88 CAGGCAGCAGGAGAGTAGTAATGATATG -112 Prf1_80 CTCCCTCCTCTACCTGAAGCC -292 Gzmk_708 GTGACCAACAGGAGAGAGC -192 Cd5_908 CGGGACAATAGCACAGC -292 Gzmk_973 ACGGACGACAGTGGCAGC -362 Ill*1_638 GTGTTCAGTTCGTGCCTC -573 Illøra_427 <t< td=""><td>Bhlhe40_744</td><td>AGTGTTCGTGGAAGTGACCG</td><td>-256</td></t<>	Bhlhe40_744	AGTGTTCGTGGAAGTGACCG	-256
Id2_630 GTCTGCTGTGCGGAGAGAGT -370 Id2_848 AGCCAATGCCTGTAGGGAG -152 Id3_834 CAGGACCAGCCTAAAGGAAGCC -166 Id3_1026 GAGACACCTAAAGCAGCAAACA 26 Runx2_883 GGCAGTCCCACATTTAGTTTGAG -117 Runx2_1087 AAACGCCAGAGCACTTAGC -293 Gzmb_707 CAAGAGATGACCCAAATGC -293 Sell_960 TGGTTCTTTTTTTTTTTCTCAGG -101 Sell_980 GAACCCACAGCGAATAGCTC -40 II7r_813 TGAAGTCTACCACCTTGCTCAAA -187 II7r_1024 CTCTGTGCCTGCTAAACCAC 24 Car7_652 CTGCTGGGACAATAGCACT -348 Ccr7_829 TGTAGAGACTCAGGGAGGAGGC -117 Prf1_888 CAGGCAGTAGCAGAGGAGAGTC -192 Cd5_963 CCAGGGTAGCAGAGGAGAGTG 37 Gzmk_973 ACGGACAAACTGCTGGCTTC -27 Ilf81_886 GCTTCCAGTTAGGAGAGAGC -282 Gmk_973 TTCCAATCTGGGCAGGAGC -362 Ilf81_84 640 CAACGGACAACGCTGC -362 Ilf81_	Bhlhe40_951	GCTACAACCAATCAGCGGG	-49
Id2_848 AGCCAATGCCTGTAGGAGCG -152 Id3_834 CAGACCAAGCCTAAGGAAGCC -166 Id3_1026 GAGACACCTAAAGCAAGCAACAA 26 Rumx2_1087 AAACGCCAGGCCTTTACTTTGAG -117 Rumx2_1087 AAACGCCACAGAGCCTTACTG 293 Gzmb_889 GAACCCACAGGCCAAATGC -293 Gzmb_89 GAACCCACAGGCGAATGACTC -111 Sell_810 TGGTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTTCTCCAGC -40 Il7r_813 TGAAGTCACCACCACC 24 Cc7_652 CTGCTGGCACAATAGCCAC 24 Cc7_652 CTGCTGCGCACAAGTAGTAGTATGG -112 Prf1_88 CAGGCACGAGAGTAGTAGTAGTATG -112 Prf1_88 CAGGCACGAAGAGTGGAGAGTG 37 Cd5_963 CCAGGGTAGCAAGACGCTGC -292 Gzmk_708 GTGACCACACAACTGCTGCAGAGAGC -135 Il6ra_611 GGTGCTTACGGGAAGCACAGGCTGC -362 Il18r1_865 GCTTCAGTTCTGGGAAGCACA -389 S100a4_737 TTCTAATTCGGGAAGCACAGGCTGC -263 S	ld2_630	GTCTGCTGTGCGGAGAGAGT	-370
Id3_834 CAGACCAGCCTAAGGAAGCC -166 Id3_1026 GAGACACCTAAAGCAGCAAACA 26 Runx2_818 GGCAGCCCCACTITACTITGAG -117 Runx2_818 GGCAGCCCACATTACCTITGG 87 Gzmb_889 GAACCCACAGCGAATGACCC -293 Gzmb_889 GAACCCACAGCGAATGACCC -111 Sell_960 TGCTTTCTTTCATTTCCCAGC -40 II7_813 TGAAGTCTACCACCTIGCTCAA -187 II7_1024 CTCTGTGCCACAACAGCACC 24 Cor7_652 CTGCTGGGCACAATAGCCACC 24 Cor7_829 TGTAGAGACTCAGGGAAGAGACACT -348 Cor7_829 TGTAGAGACCCACAGGAGAGAGACC -171 Prf1_808 CAGGGCAGGAAGAGAGAGAGAGC -172 Prf1_808 CAGGGCAGGAGAGAGAGAGGC -292 Cd5_983 CCAGGATAGACAGGCAGAGAGTC -192 Cd5_983 CCGGACAAACTGCTTGCTC -277 II181_638 GTGGTTCAGTAGACAGGCTGC -362 II187_1638 GTGGTTAGGGAAGACAGGCTGC -363 S100a4_906 TGATTAGTAGTAATGTCATAGCACCC -273	ld2_848	AGCCAATGCCTGTAGGGTG	-152
Id3_1026 GAGACACCTAAAGCAGCAGAACA 26 Runx2_883 GGCAGTCCCACTTTACTTTGAG -117 Runx2_1087 AAACGCCAGAGCCTTCTTG 87 Gzmb_07 CAAGAGATGAGCCCAAATGC -293 Gzmb_189 GAACCCACAGCGAATGACTC -111 Sell_960 TGCTTTCTTTCATTTCTCAGC 40 II7r_813 TGAAGTCTACCACCTTGCTCAA -187 II7r_1024 CTCTGTGCCTGCTAAACCAC 24 Cor7_652 CTGCTGGGACAATAGCCACT -348 Cor7_652 CTGCTGGGACAGGAGGAGGAGC -171 Prf1_888 CAGGGCAGGAAGTAGCAAGTG 36 Ccl5_963 CCAGGGTAGCAGGAGGCGAGC -192 Ccl5_963 CCAGGGTAGCAGAGGCAGGC -292 Gzmk_708 GTGACCCACAGGTTGAGAGC -292 Gzmk_973 ACGGCAGTAGCAGAGGCGC -292 Gzmk_973 ACGGCAGCAACTGCTGC -362 Ilf8r1_635 GCTTTCAGTTGCTGCCC -573 Il6ra_611 GGTGCTTACGGGAACCAACCC -389 S100a4_906 TGATGTAGAAGAGCACCACCCC -94 S100a6_936	ld3_834	CAGACCAGCCTAAGGAAGCC	-166
Rumx2_883 GGCAGTCCCACTTTACTTTGAG -117 Rumx2_1087 AAACGCCAGAGCCTTCTTG 87 Gzmb_289 GAACCCACAGCCCAATGACC -293 Gzmb_289 GAACCCACAGCGCAATGACTC -111 Sell_810 TGGTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTTCTCCAGC -40 Il7r_813 TGAAGTCACCACCTGCTAAACCAC 24 Ccr7_652 CTGCTGGGACAATAGCCAC 24 Ccr7_652 CTGCTGGGACAATAGCCAC 24 Ccr7_652 CTGCTGCGGACAGTAGTAGTATGATATG -112 Prf1_888 CAGGGCAGGAGAGTAGTAGTATGATATG -112 Prf1_888 CAGGGCAGGAGGAGGAGGTAGT -36 Ccl5_808 AGGGCAGTTAGAGGCAGAGAGTC -192 Ccl5_983 CCAGGGATGACAGAGCAGGCTGC -27 Ill8r1_638 GTGGTTCAGTTGCGTC -27 Ill8r1_865 GCTTTCAGTTCGTGCAGGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACC -135 Il6ra_417 ACACACAACTTGAGAGACACC -38 S100a4_936 GACTCCTGGGACACAGGCAGG -219	ld3 1026	GAGACACCTAAAGCAGCAAACA	26
Rumx2_1087 AAACGCCAGAGCCTTCTTG 87 Gzmb_707 CAAGAGATGAGCCCAAATGC -293 Gzmb_889 GAACCCACAGCGATGACTC -111 Sell_810 TGGTCCACTACTGTGTTTTGG -190 Sell_960 TGCTTTCTTTCATTTCTCCAGC -40 II7r_813 TGAAGTCTACCACCTTGCTCAA -187 II7r_1024 CTCTGTGCGACAATACCAC 24 Cc7_652 CTGCTGGGACATAGCACC -348 Cc7_652 CTGCTCCTCCTTACCTGAAGTATGG -112 Prf1_1036 CTTCCTCCTCTACCTGAAGTATG -112 Prf1_1036 CTTCCTCCTTACCTGAAGGCAGGTC -192 Cd5_808 AGGGCAGTTAGAGGCAGAGTG 37 Gzmk_708 GTGACCAACAGCTGCTGC -223 Gzmk_973 ACGGACAACAGCTTGAGTAGACGCTGC -362 Il18r1_865 GCTTTCAGTTCGGGAACCAAA -389 S100a4_906 TGATGTAGTAGACAGGCTGC -363 S100a4_906 TGATGTAGTAAAATGCAAAA -389 S100a4_906 TGATGTAGTAAAATGCAACAG -219 S100a6_936 GAACTCCACACACTGAGT -64 Stat4		GGCAGTCCCACTTTACTTTGAG	-117
Gzmb_707 CAAGAGATGAGCCCAAATGC -293 Gzmb_889 GAACCCACAGCGAATGACTC -111 Sell_960 TGCTTTCTTTCATTTCTCCAGC -40 II7r_813 TGAAGTCTACCACCTTGCTCAA -187 II7r_1024 CTCTGTGCCTGCTAAACCAC 24 Cor7_652 CTGCTGGGACAATAGCCACT -348 Cor7_652 CTGCTGGGACAATAGCCACC 24 Crf_652 CTGCTGGGACATAGCCAGGAGGAGC -171 Prf1_88 CAGGGCAGGAAGTAGTAATGATATG -112 Prf1_1036 CTTCCTCCTCCTTACCTGAAGTC 36 Ccd5_963 CCAGGGTAGCAAGGAGAGTG 37 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Ilf8r1_865 GCTTTCAGTTCAGGAAGCC -135 Ilf8r4_87 ACACTGGTTTCGTGGCACC -362 Ill8r1_865 GCTTTACGGGAACAACTGCTGC -363 S100a4_737 TTCCTAAACTTGTGGCAGC -263 S100a6_936 GAACTGGGAACACACCACACTGAT -64 S100a6_936 GAACTGGGACCAGGCAG -105 Infga645 CTGTGCGGCACCAGGCAG -388 S100a6_936 <td></td> <td>AAACGCCAGAGCCTTCTTG</td> <td>87</td>		AAACGCCAGAGCCTTCTTG	87
Gzmb_889 GAACCCACAGCGAATGACTC -111 Sell_810 TGGTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTTCCCAGC -40 Il7r_813 TGAAGTCTACCACCTTGCTCAA -187 II7r_1024 CTCTGTGCCTGCTAAACCAC 24 Cor7_652 CTGCTGGGACAATAGCCACT -348 Cdr7_829 TGTAGAGACTCAGGGAGGAGC -171 Prfl_888 CAGGGCAGGTAGCAGGGAGGAGC -192 Cd5_808 AGGGCAGTTAGAGGCAGAGTG 36 Cd5_963 CCAGGGTAGCAGAGGAGAGTG -292 Gzmk_708 GTGACCCACAGGTTGAGAGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Ilf8r1_865 GCTTTCAGTTCGGGAACAAA -389 S100a4_737 TTCCTAAGTTCTGGGCAGC -362 Ilf8r1_865 GCTTTCAGGGAATCAAA -389 S100a4_906 TGATGTAGTAGACAGCC -135 If6ra_427 ACACCGGGACCACATGAGA -389 S100a4_906 TGATGTAGTAAACTGCACC -94 S100a4_906 TGATGTAGTAACACACACATGAT -64 Stat4_812	Gzmb 707	CAAGAGATGAGCCCAAATGC	-293
Sell_810 TGGTCCACTACTGTGTTCTTGG -190 Sell_960 TGCTTTCTTTCATTTCCTCAGC -40 Il7r_813 TGAAGTCTACCACCTTGCTCAA -187 Il7r_1024 CTCTGTGCGGACAATAGCCAC 24 Cor7_652 CTGCTGGGACAATAGCCAC 24 Cor7_829 TGTAGAGACTCAGGGAGGAGC -171 Prff_888 CAGGGCAGGAAGTAGTAATGATATG -112 Prf1_1036 CTTCCTCCTCTACCTGAAGGC 36 Cd5_808 AGGGCAGTTAGAGGCAGAGGC -192 Cd5_963 CCAGGGTAGCAGAGGAGAGTG 37 Gzmk_973 ACGGACAACTGCTTGCTC -27 Ilf8r1_865 GCTTTCAGTTCGGGAAGACC -135 Ilf8r_427 ACACTGGTTCGGTGCTC -573 Il6ra_427 ACACTGGTTCGTGCTCAGAG -289 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_936 GGACTGGGAACCACACGGAG -219 S100a6_936 GACATTGAGGACCAGGGGAC -388 Stat4_612 AGACATTGAGGCCTGATCAAAGGC -219 S100a6	Gzmb 889	GAACCCACAGCGAATGACTC	-111
Sell_960 TGCTTTCTTTCATTTCTCCAGC -40 II7r_813 TGAAGTCTACCACCTTGCTCAA -187 II7r_1024 CTCTGTGCCTGCTAAACCAC 24 Cor7_652 CTGCTGGGACAATAGCCACT -348 Cor7_829 TGTAGAGACTCAGGGAGGAGC -171 Prff_888 CAGGGCAGGAAGTAGTAATGATATG -112 Prf1_1036 CTTCCTCCTCCTTACCTGAAGTC 36 Ccl5_963 CCAGGGTAGCAGGGCAGGTC -192 Ccl5_963 CCAGGGTAGCAGGGCAGAGTC -27 II8r_1638 GTGCTTCAGTAGAGAGGAAGC -222 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 II8r_1638 GTGCTTCAGTCTGGGAAGACC -135 Il6ra_411 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGACTGGGAACCACACAGACTGAT -64 S100a6_781 ACCACCACACACTGATGAAACGGCTG -94 S100a6_936 GAACTATGAGAACAGGCTG -199 S100a6_936 GAACTATGAGAACAGGCTGC -388 Stat4_895 AGACATTGAGGACCAGACGCAC -343	Sell 810	TGGTCCACTACTGTGTTCTTGG	-190
II7_813 TGAAGTCTACCACCTTGCTAA -187 II7_1024 CTCTGTGCCTGCTAAACCAC 24 Cc7_852 CTGCTGGGACATAGCCACT -348 Cc7_829 TGTAGAGACTCAGGGAGGACC -171 Prf1_888 CAGGGCAGGAAGTAGTAATGATATG -112 Prf1_1036 CTTCCTCCTCCTTACCTGAAGTC 36 Ccl5_963 CCAGGGTAGCAGAGGAGAGTG -192 Ccl5_963 CCAGGGTAGCAGAGGAGGAGTG -292 Gzmk_708 GTGACCCACAGGTTGAGAGC -292 Gzmk_708 GTGACCCACAGGTTGCCTC -362 II18r1_638 GTGGTTGAGTAGACAGGCTGC -362 II18r1_865 GCTTTCAGTTCTGGGAAGACC -135 II6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_731 ACCACCACACACTGAT -64 Stat4_895 AGACATTGAGGACCAGGCAG -219 S100a6_936 GACTCTTGGCTCTGTGCAC -388 Stat4_895 AGACATTGAGACAGGCAGG -105 Ing_823 GACCCCCTGGTCTGTGAC -443 Acxr3_857	Sell 960	TGCTTTCTTTCATTTCTCCAGC	-40
II7_1024 CTCTGTGCCTGCTAAACCAC 24 Cc77_652 CTGCTGGGACAATAGCCACT -348 Cc77_829 TGTAGAGACTCAGGGAGGAGGC -171 Prff_888 CAGGGCAGGAAGTAGTAATGGTATG -112 Prf1_1036 CTTCCTCCTCCTCCTCACCAGAGTC 36 Cc5_808 AGGGCAGTTAGAGGCAGAGTG 37 Gzmk_708 GTGACCACAGAGTGAGAGGAGGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Il8r1_638 GTGGTTGAGTAGACAGGCTGC -362 Il8r1_635 GCTTTCAGTTCGGGAAGACC -135 Il6ra_427 ACACTGGTTTCGTGCCTC -573 Il6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTAGC -263 S100a4_906 TGATGAAAACTGCTGAGGC -263 S100a6_936 GGACTGGGAACCACACATGAT -64 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Img_e45 CTGTGGCTGTGTCTGAGC -43 Cxcr3_557 ATGCAGGACTGTTACAAGGCAC -44 Cxcr3_557 </td <td></td> <td>TGAAGTCTACCACCTTGCTCAA</td> <td>-187</td>		TGAAGTCTACCACCTTGCTCAA	-187
Cc7_652 CTGCTGGGACAATAGCCACT -348 Cc7_622 TGTAGAGACTCAGGGAGGAGC -171 Prf1_888 CAGGGCAGGAAGTAGTAAGTATGATATG -112 Prf1_1036 CTTCCTCCTCTTACCTGAAGTC 36 Ccl5_808 AGGCAGTAGGAGGAGGAGTG -192 Ccl5_963 CCAGGGTAGCAGAGGC -292 Gzmk_708 GTGACCCACAGGTTGAGAGAGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Il18r1_658 GTGGTTGAGTAGACAGGCTGC -362 Il18r1_865 GCTTTCAGTTCTGGGGAACCAGGCTGC -363 Il6ra_417 ACACTGGTTTCGTGCTC -573 Il6ra_417 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCAC -94 S100a6_781 ACCACCACACACTGAT -64 Stat4_612 AGACATTGAGGACCAGGCAG -105 Img_823 GACTCCTTGGGCTCTGTGGAC -388 Stat4_95 AGCAAGAAGAGTCAAGAGGAGGAG -105 Img_845 CTGGCAGCTGATTCAACC -443 Cxcr		CTCTGTGCCTGCTAAACCAC	24
Cc7_829 TGTAGAGACTCAGGGAGGAGC -171 Prf1_888 CAGGGCAGGAAGTAGTAATGATATG -112 Prf1_1036 CTTCCTCCTCTTACCTGAAGTC 36 Ccl5_963 CCAGGGTAGCAGAGGAAGTG -192 Ccl5_963 CCAGGGTAGCAGAGGAAGTG 37 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Ill8r1_638 GTGGTTGAGTAGACAGGCTGC -362 Ill8r1_865 GCTTTCAGTTCGTGGCAGAGACC -135 Il6ra_611 GGTGCTTACGGGAATCAAA -389 S1100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_781 ACCACCACAACTTGAAGAACAG -219 S100a6_936 GGACTGGGAACCACACACGAT -64 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATGAGAGGAGAGAACC -105 Ifmg_823 GACTCCTTGGGCTCTGTGAC -117 Cxcr3_557 ATGCCAGGGCAGAGAGAGCC -443 Cxcr3_857 ACTGCAGGACAGAGTGAGAGAGGG -105	Ccr7 652	CTGCTGGGACAATAGCCACT	-348
Prff_888 CAGGGCAGGAAGTAGTAATGATATG -112 Prff_1036 CTTCCTCCTCCTTACCTGAAGTC 36 Ccd5_808 AGGGCAGTTAGAGGCAGAGTG 37 Gzmk_708 GTGACCCACAGGTGAGAGGAGGC -292 Gzmk_708 GTGGTGAGCAGAGAGCC -362 Ill8r1_638 GTGGTTGAGTAGCAGAGCC -362 Ill8r1_638 GTGGTTGAGTAGCAGAGCC -135 Il6ra_427 ACACTGGTTTCGGGAAGACC -135 Il6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGAGAACCACACTGAA -389 S100a4_936 GGACTGGGAACCACACTGAT -64 S100a6_936 GGACTGGGACCAACTGAGCAC -388 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Img_645 CTGTGCTGTGCTCTGTGAC -177 Cxcr3_857 ACTTGGGACTAAGAGTGGAAGAGG -503 Abca3_497 TTGGTGACAAGAGTGAGATGG -503 Abca3_672 AACAGTAGGCGTTACTATAGTGAGG -328	 Ccr7_829	TGTAGAGACTCAGGGAGGAGC	-171
Prif_1036 CTTCCTCCTCCTTACCTGAAGTC 36 Cd5_808 AGGGCAGTTAGAGGCAGAGTC -192 Cd5_963 CCAGGGTAGCAGAGGCAGAGTG 37 Gzmk_708 GTGACCCACAGGTTAGAGAGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Ill8r1_638 GTGGTCAGTAGACAGGCTGC -362 Ill8r1_638 GTGGTTCAGTAGACAGGCTGC -362 Ill8r1_865 GCTTTCAGTTGTGGCAAGACC -135 Ilf6ra_427 ACACTGGTTTCGTTGCCTC -573 Ill8r1_865 GCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_936 GGACTGGGAACCACACTGAT -64 Stat4_812 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Img_645 CTGTGCTGTGCTCTGTGGCAC -388 Stat4_895 AGACATTGAGGACTGAAGACCT -143 Abca3_497 TTGGGACTGATTCAACC -443 Cxcr3_857 ACTTGGGACTGATACTAAGCGA -120 Blk	Prf1 888	CAGGGCAGGAAGTAGTAATGATATG	-112
Cd-AGGGCAGTTAGAGGCAGAGTC-192Cd5_963CCAGGGTAGCAGAGGGAAGTG37Gzmk_708GTGACCCACAGGTTGAGAGC-292Gzmk_973ACGGACAAACTGCTTGCTTC-27Il18r1-638GTGGTTGAGTAGACAGGCTGC-362Il18r1-865GCTTTCAGTTCTGGGAAGACC-135Il6ra_427ACACTGGTTTCGTGGCAGAGACC-135Il6ra_611GGTGCTTACGGGAATCAAA-389S100a4_737TTCCTAAACTTCTGGCTGAGC-263S100a4_737TTCCTAAACTTCTGGCTGAGC-263S100a6_781ACCACCACAACTGAAGAACAG-219S100a6_936GGACTGGGAACCACACTGAT-64Stat4_612AGAGAAGAATCCAGGTGGCAC-388Stat4_895AGACATTGAGGACCAGGCAG-105Ifmg_645CTGTGCTGTGCTCTGTGGAT-355Ifmg_823GACTCCTTGGGCTCTCTGAC-177Cxcr3_557ATGCCAGGTCTGATCAAAGGCGT-143Abca3_497TTGGTGACAAGAGTGAGAGAGG-503Abca3_497TTGGTGACAAGAGTGAGAGTGG-328Dusp14_595GCCAACCTGGTCTACATAGTGAG-405Dusp14_880CACCTGGACTTACTGCCAGA-120Blk_801AGTCCAGTCACATCTGTTCTGC-199Blk_102CCCTTGGTTGGTTGCTACAGGAGTGG-221Cct5_779TTCGATTTCCACCTCCTCGGGC-334Ms4a1_913ACCTTGCTTTGCCACCTCCTGGGC-70KIrc1_843TTGTTACCACAGCACTGG-157KIrc1_1049AGTTCTTTGCCACCTCCAGGTC-157KIrc1_1049AGTTCTTTGCCACCTCCAGGTC-159Cd38_1017GAAGAGAGCACAGGGCTGAC-159 <td>Prf1 1036</td> <td>CTTCCTCCTCCTTACCTGAAGTC</td> <td>36</td>	Prf1 1036	CTTCCTCCTCCTTACCTGAAGTC	36
Ccl5_963 CCAGGGTAGCAGAGGAAGTG 37 Gzmk_708 GTGACCCACAGGTTGAGAGAGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Il18r1_638 GTGGTTGAGTAGACAGGCTGC -362 Il18r1_865 GCTTTCAGTTCTGGGAAGACC -135 Il6ra_427 ACACTGGTTTCGTTGCCTC -573 Il6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAGAAATGTCATAGCACCC -94 S100a6_781 ACCACCACAACTTGAAGAACAG -219 S100a6_936 GGACTGGGAACCACACATGAT -64 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Ifng_645 CTGTGCTGTGCTCTTGGACT -177 Cxcr3_857 ACTGGACAGGCGTAGTTACAAGC -443 Cxcr3_857 ACTGGACAAGAGGTGAGAGAGG -503 Abca3_672 AACAGTAGCGGTATACTAGCAGAG -120 Blk_801 AGTCCATGGACATCTGTTCTGGCA -334 Ms4a1_913 ACCTTGCTTCCAGGGATTCCGAC -334 <	Ccl5 808	AGGGCAGTTAGAGGCAGAGTC	-192
Gzmk_708 GTGACCCACAGGTTGAGAGC -292 Gzmk_973 ACGGACAAACTGCTTGCTTC -27 Ill8r1_638 GTGGTTGAGTAGACAGGCTGC -362 Ill8r1_865 GCTTTCAGTTCTGGGAAGACC -135 Ilfa_427 ACACTGGTTTCGTGCCTC -573 Ilfar_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_781 ACCACCACACACTGAT -64 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Ifng_645 CTGTGCTGTGCTCTGTGGAT -355 Ifng_823 GACTCCTTGGGCTCTCTGAC -443 Accar3_87 ACTGGGACAAGAGCGT -143 Abca3_497 TTGGTGACAAGAGTGAGAGAGG -503 Abca3_672 AACAGTAGCACACTGTTACTGCGCAG -328 Dusp14_595 GCCAACCTGGTCTACATAGTGAGA -120 Blk_801 AGTCCAGGCATTACTGCGAGA -120 Blk_801 AGTCCAGTCACATCTGTTCTGGC -199 B	Ccl5 963	CCAGGGTAGCAGAGGAAGTG	37
Gzmk 973 ACGGACAAACTGCTTGCTTC -27 II18r1_638 GTGGTTGAGTAGACAGGCTGC -362 II18r1_865 GCTTTCAGTTCTGGGAAGACC -135 II6ra_427 ACACTGGTTTCGTTGCCTC -573 II6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a4_906 TGATGTAGGAACACCACACTGAT -64 S100a6_936 GGACTGGGAACCACACACGAGT -64 S1at4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Ifng_645 CTGTGCTGTGCTCTGTGGAT -355 Ifng_823 GACTCCTTGGGCTCTCTGAC -177 Cxcr3_857 ACTGGGACAAGAGTGAGAGTGG -503 Abca3_497 TTGGTGACAAGAGTGAGAGTGG -503 Abca3_497 TTGGTGACTACTGTGCTACATAGTGAGA -120 Blk_801 AGTCCAGGTCACATCTGTTCTGC -199 Blk_1002 CCCTTGGTTGCTTACCATAGTGAGA -120 Blk_801 AGTCCAGTCACATCTGTTCCGAGA -120	 Gzmk 708	GTGACCCACAGGTTGAGAGC	-292
II18r1_638 GTGGTTGAGTAGACAGGCTGC -362 II18r1_865 GCTTTCAGTTCTGGGAAGACC -135 II6ra_427 ACACTGGTTTCGTTGCCTC -573 II6ra_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAATAGTCATAGCACCC -94 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_781 ACCACCACAACTTGAGGAACAGC -219 S100a6_936 GGACTGGGAACCACACATGAT -64 Stat4_612 AGAGAAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Ifng_645 CTGTGCTGTGCTCTGTGGAT -355 Ifng_823 GACTCCTTGGGCTCTGTGAC -143 Abca3_497 TTGGTGACAAGAGTGAGATGG -503 Abca3_497 TTGGTGACAAGAGTGAGATTGGCAGA -120 Blk_801 AGTCCAGGTCACATTGTTGCGCAGA -120 Blk_801 AGTCCAGTCACATTGTTCGCAGA -120 Blk_801 AGTCCAGTCACTCTGTTGCGAG -334 Ms4a1_913 ACCTTGCTTTCCAGGAGATTCCGAC -334 <td>Gzmk 973</td> <td>ACGGACAAACTGCTTGCTTC</td> <td>-27</td>	Gzmk 973	ACGGACAAACTGCTTGCTTC	-27
II18r1/865GCTTTCAGTTCTGGGAAGACC-135II6ra_427ACACTGGTTTCGTTGCCTC-573II6ra_611GGTGCTTACGGGAATCAAA-389\$100a4_737TTCCTAAACTTCTGGCTGAGC-263\$100a4_906TGATGTAGTAAATGTCATAGCACCC-94\$100a6_781ACCACCACAACTTGAAGAACAG-219\$100a6_936GGACTGGGAACCACACTGAT-64\$tat4_612AGAGAAGAATCCAGGTGGCAC-388\$tat4_895AGACATTGAGGACCAGGCAG-105Ifng_645CTGTGCTGTGCTCTGTGGAT-355Ifng_823GACTCCTTGGGCTCTGTGAC-1177Cxcr3_557ATGCCAGGTCTGATTCAACC-443Cxcr3_857ACTTGGGACTAGTTACAAAGCCT-143Abca3_497TTGGTGACAAGAGTGAGATGG-503Abca3_672AACAGTAGGCGTTACTACAAGGCGT-1120Blk_801AGTCCATGGTCTGACTACATAGTGAG-405Dusp14_880CACCTGGACTTACTGGCAGA-120Blk_1002CCCTTGGTTGGTTTGTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTTGCCTTACCAGG-87Ccr5_779TTCGATTTCCAACGACAGCAGTGG-221Ccr5_1070GATGTCTACCACCTCCTCTGGC70KIrc1_843TTGTGTTACCACAGCACTCG-157KIrc1_1049AGTTCTTGCAGGAAGTAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGACC17	ll18r1 638	GTGGTTGAGTAGACAGGCTGC	-362
IIGra_427ACACTGGTTTCGTTGCCTC-573IIGra_611GGTGCTTACGGGAATCAAA-389\$100a4_737TTCCTAAACTTCTGGCTGAGC-263\$100a4_906TGATGTAGTAAATGTCATAGCACCC-94\$100a6_781ACCACCACACTTGAAGAACAG-219\$100a6_936GGACTGGGAACCACGTGAACCACTGAT-64\$tat4_612AGAGAAGAATCCAGGTGGCAC-388\$tat4_895AGACATTGAGGACCAGGTGGGAC-355Ifmg_645CTGTGCTGTGCTCTGTGGAT-355Ifmg_823GACTCCTTGGGCTCTGTGAC-1177Cxcr3_557ATGCCAGGTCTGATTCAACC-443Cxcr3_857ACTTGGGACAAGAGTGAGATGG-503Abca3_497TTGGTGACAAGAGTGAGATGG-328Dusp14_595GCCAACCTGGTCTACTAGTGAGG-405Dusp14_880CACCTGGACTACTGTTCTGC-199Blk_801AGTCCAGTCACATCTGTTCTGGC-334Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGACATGTGTG-221Ccr5_779TTCTGATTTCCACCTCCTGGGC70Klrc1_843TGTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTCCAGGTC-157Klrc1_1049AGTTCTTGCAGAGAAGTAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGACC17	ll18r1_865	GCTTTCAGTTCTGGGAAGACC	-135
Ilfara_611 GGTGCTTACGGGAATCAAA -389 S100a4_737 TTCCTAAACTTCTGGCTGAGC -263 S100a4_906 TGATGTAGTAAATGTCATAGCACCC -94 S100a6_936 GGACTGGGAACCACACTGAT -64 Stat4_612 AGAGAAGAATCCAGGTGGCAC -388 Stat4_895 AGACATTGAGGACCAGGCAG -105 Ifng_645 CTGTGCTGTGCTCTGTGGAT -355 Ifng_823 GACTCCTTGGGGCTCTGTGAC -177 Cxcr3_557 ATGCCAGGTCTGATTCAAAGCC -443 Cxcr3_857 ACTTGGGACCAGGAGGAG -503 Abca3_497 TTGGTGACAAGAGTGAGAATGG -503 Abca3_672 AACAGTAGCGGTTAGTTACAAAGCCT -143 Abca3_672 AACAGTAGCACACATGTTACTAGTGAG -405 Dusp14_595 GCCAACCTGGACTACTGTGTCTGC -199 Blk_801 AGTCCAGGACTACATGTGTTCTGC -199 Blk_1002 CCCTTGGTTGCTTACCAGG -334 Ms4a1_666 TACCTTCCAGGAGATCCGGAC -334 Ms4a1_913 ACCTTGCTTCCTCTCTGGC 70 Kirc1_843 TTGTTACCACAGCACTCG -221 <tr< td=""><td>ll6ra 427</td><td>ACACTGGTTTCGTTGCCTC</td><td>-573</td></tr<>	ll6ra 427	ACACTGGTTTCGTTGCCTC	-573
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S100a6_936GGACTGGGAACCACACACTGAT-64Stat4_612AGAGAAGAATCCAGGTGGCAC-388Stat4_895AGACATTGAGGACCAGGCAG-105Ifng_645CTGTGCTGTGCTCTGTGGAT-355Ifng_823GACTCCTTGGGCTCTCTGAC-177Cxcr3_557ATGCCAGGTCTGATTCAACC-443Cxcr3_857ACTTGGGACTGTTACAAAGCCT-143Abca3_497TTGGTGACAAGAGTGAGATGG-503Abca3_672AACAGTAGGCGTTACATAGTGGG-328Dusp14_595GCCAACCTGGTCTACATAGTGAGA-120Blk_801AGTCCAGTCACATCTGTTCTGC-199Blk_1002CCCTTGGTTGGTTTGTAGG2Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTCCACGCAGTGTGGTGG-221Cr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTGTTACCACAGCACTCG-157Klrc1_049AGTTCTTGCGAGAGTAGGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGACC17		ACCACCACAACTTGAAGAACAG	-219
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Ifing_645CTGTGCTGTGCTCTGTGGAT-355Ifing_645CTGTGCTGTGCTCTGTGGAT-355Ifing_823GACTCCTTGGGCTCTGTGAC-177Cxcr3_557ATGCCAGGTCTGATTCAACC-443Cxcr3_857ACTTGGGACAGGTGTGACAAGGCCT-143Abca3_497TTGGTGACAAGAGTGGAGATGG-503Abca3_672AACAGTAGGCGTTAGTTTGGG-328Dusp14_595GCCAACCTGGTCTACATAGTGAG-405Dusp14_880CACCTGGACTTACTCGCAGA-120Blk_801AGTCCAGTCACATCGTTCTGC-199Blk_1002CCCTTGGTTGGTTGTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Cr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTGCCACCTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Stat4 895	AGACATTGAGGACCAGGCAG	-105
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Cxcr3.857ACTTGGGACTGTTACAAAGCCT-143Abca3_497TTGGTGACAAGAGTGAGAGAGG-503Abca3_672AACAGTAGGCGTTAGTTTGGG-328Dusp14_595GCCAACCTGGTCTACATAGTGAG-405Dusp14_880CACCTGGACTTACTCGCAGA-120Blk_801AGTCCAGTCACATCTGTTCTGC-199Blk_1002CCCTTGGTTGGTTTGTTAGG2Ms4a1_666TACCTTCCCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Cxcr3 557	ATGCCAGGTCTGATTCAACC	-443
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Dusp14_595GCCAACCTGGTCTACATAGTGAG-405Dusp14_880CACCTGGACTTACTCGCAGA-120Blk_801AGTCCAGTCACATCTGTTCTGC-199Blk_1002CCCTTGGTTGGTTTGTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Abca3 672	AACAGTAGGCGTTAGTTTGGG	-328
Dusp14_880CACCTGGACTTACTCGCAGA-120Bik_801AGTCCAGTCACATCTGTTCTGC-199Bik_1002CCCTTGGTTGGTTTGTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Kirc1_843TTGTTGTTACCACAGCACTCG-157Kirc1_1049AGTTCTTTGCCACCTCCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Dusp14 595	GCCAACCTGGTCTACATAGTGAG	-405
Bik_801AGTCCAGTCACATCTGTTCTGC-199Bik_801AGTCCAGTCACATCTGTTCTGC-199Bik_1002CCCTTGGTTGGTTGGTTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Kirc1_843TTGTTGTTACCACAGCACTCG-157Kirc1_1049AGTTCTTTGCCACCTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACACAGGGCTGAC17	Dusp14 880	CACCTGGACTTACTCGCAGA	-120
Bik_1002CCCTTGGTTGGTTGTTAGG2Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Kirc1_843TTGTTGTTACCACAGCACTCG-157Kirc1_1049AGTTCTTTGCCACCTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGGACACAGGGCTGAC17	Blk 801	AGTCCAGTCACATCTGTTCTGC	-199
Ms4a1_666TACCTTCTCAGGGATTCCGAC-334Ms4a1_913ACCTTGCTTGCCTTACCAG-87Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Blk 1002	CCCTTGGTTGGTTGTTGTTAGG	2
Ms4a1_913 ACCTTGCTTTGCCTTACCAG -87 Ccr5_779 TTCTGATTTCCAACGAAGTGTG -221 Ccr5_1070 GATGTCTCACCTCCTCTGGC 70 Klrc1_843 TTGTTGTTACCACGACACTCG -157 Klrc1_1049 AGTTCTTTGCCACCTTCAGTTC 49 Cd38_841 TCTGGAGTCTGGAAGTAAGCAGT -159 Cd38_1017 GAAGAGAGCACAGGGCTGAC 17	Ms4a1 666	TACCTTCTCAGGGATTCCGAC	-334
Ccr5_779TTCTGATTTCCAACGAAGTGTG-221Ccr5_1070GATGTCTCACCTCCTCTGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Ms4a1 913	ACCTTGCTTTGCCTTACCAG	-87
Car5_1070GATGTCTCACCTCACCTCGGC70Klrc1_843TTGTTGTTACCACAGCACTCG-157Klrc1_1049AGTTCTTTGCCACCTTCAGTTC49Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Ccr5 779	TTCTGATTTCCAACGAAGTGTG	-221
Klrc1_843 TTGTTGTACCACAGCACTCG -157 Klrc1_1049 AGTTCTTTGCCACCTTCAGTTC 49 Cd38_841 TCTGGAGTCTGGAAGTAAGCAGT -159 Cd38_1017 GAAGAGAGCACAGGGCTGAC 17	Ccr5 1070	GATGTCTCACCTCCTCTCGC	70
Klic1_1049 AGTTCTTTGCCACCTTCAGTTC 49 Cd38_841 TCTGGAGTCTGGAAGTAAGCAGT -159 Cd38_1017 GAAGAGAGCACAGGGCTGAC 17	Kirc1 843	TIGTIGTIACCACAGCACTCG	-157
Cd38_841TCTGGAGTCTGGAAGTAAGCAGT-159Cd38_1017GAAGAGAGCACAGGGCTGAC17	Kirc1 1049	AGTICTTIGCCACCTTCAGTTC	49
Cd38_1017 GAAGAGAGCACAGGGCTGAC 17	Cd38_841	TCTGGAGTCTGGAAGTAAGCAGT	-159
	Cd38 1017	GAAGAGAGCACAGGGCTGAC	17