

# Sustained *Id2* regulation of E proteins is required for terminal differentiation of effector CD8<sup>+</sup> T cells

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CD8<sup>+</sup> T cells responding to infection differentiate into a heterogeneous population composed of progeny that are short-lived and participate in the immediate, acute response and those that provide long-lasting host protection. Although it is appreciated that distinct functional and phenotypic CD8<sup>+</sup> T cell subsets persist, it is unclear whether there is plasticity among subsets and what mechanisms maintain subset-specific differences. Here, we show that continued *Id2* regulation of E-protein activity is required to maintain the KLRG1<sup>hi</sup> CD8<sup>+</sup> T cell population after lymphocytic choriomeningitis virus infection. Induced deletion of *Id2* phenotypically and transcriptionally transformed the KLRG1<sup>hi</sup> "terminal" effector/effector-memory CD8<sup>+</sup> T cell population into a KLRG1<sup>lo</sup> memory-like population, promoting a gene-expression program that resembled that of central memory T cells. Our results question the idea that KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells are necessarily terminally programmed and suggest that sustained regulation is required to maintain distinct CD8<sup>+</sup> T cell states.

## INTRODUCTION

In response to acute infection, naive antigen-specific CD8<sup>+</sup> T cells become activated, proliferate, and differentiate into a heterogeneous population of effector cells with the functional capacity to eliminate the pathogen. Many effector CD8<sup>+</sup> T cells within this population are thought to be terminally fated to undergo apoptosis upon resolution of the infection. Others appear to be programmed for long-term survival and uniquely suited to protect the host upon reinfection (Chang et al., 2014). Considerable work in the field has focused on relating effector CD8<sup>+</sup> T cell phenotype to cell fate. Two cell-surface receptors, killer cell lectin-like receptor G1 (KLRG1) and interleukin 7 receptor  $\alpha$  (CD127), have been valuable in predicting the fates of CD8<sup>+</sup> T cell populations at the peak of the effector response. During the effector phase of infection, CD8<sup>+</sup> T cells expressing KLRG1 and low levels of CD127, called terminal effector (TE) cells, are often defined as terminally differentiated, have a shorter life span and exhibit minimal memory potential in adoptive transfer experiments. CD8<sup>+</sup> T cells with low KLRG1 and high CD127 surface expression in the effector phase have been defined as memory-precursor (MP) T cells and show a greater propensity to survive after infection and exhibit increased stem-like properties such as self-renewal (Kaech et al., 2003; Joshi et al., 2007; Sarkar et al., 2008).

At memory time points, the relationship of the canonical markers, KLRG1 and CD127, to cell fate becomes less clear. Memory CD8<sup>+</sup> T cells have been classified into subsets based on several criteria including location, effector function, capacity for self-renewal, and trafficking patterns. The best

characterized distinction is that of effector memory (T<sub>EM</sub>) and central memory (T<sub>CM</sub>) T cells, based on CD62L and CCR7 expression (Sallusto et al., 1999). T<sub>EM</sub> cells that lack CD62L and CCR7 expression circulate through nonlymphoid tissues and the blood and are poised to provide immediate effector function but have limited proliferation potential upon recall (Mueller et al., 2013). T<sub>CM</sub> cells express CD62L and CCR7 and thus home to lymphoid tissues and provide a long-term, self-renewing pool of T cells (Mueller et al., 2013). Overlaying the KLRG1 and CD127 phenotypic characterization of T cells adds a level of complexity to defining memory T cell subsets. Although CD127 expression supports long-term survival of memory T cells, the classification of T<sub>EM</sub> and T<sub>CM</sub> has not explicitly included the expression of CD127 or exclusion of KLRG1. Within the T<sub>EM</sub> population, KLRG1 expression can be detected on a portion of cells (Masopust et al., 2006; Hikono et al., 2007; Phan et al., 2016; Kakaradov et al., 2017). This observation is consistent with T<sub>EM</sub> exhibiting more effector-like properties and being more terminally differentiated (Kaech and Cui, 2012); however, variable KLRG1 expression suggests the T<sub>EM</sub> population itself is heterogeneous. Furthermore, a sizeable population of CD8<sup>+</sup> T cells defined as KLRG1<sup>hi</sup>CD127<sup>lo</sup> TE T cells at the effector stage survive after the infection has resolved and persist at memory time points, but the population continues to diminish relative to the KLRG1<sup>lo</sup> population, further supporting the idea that these cells are terminally fated (Olson et al., 2013).

Unique transcriptional programs have been described that drive the differentiation of CD8<sup>+</sup> T cells during infec-

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tion—with T-bet, Blimp-1, IRF4, Zeb2, and Id2 acting as critical regulators of the TE CD8<sup>+</sup> T cell population and Tcf1, Eomes, Bcl6, Foxo1, Id3, and E proteins regulating the MP CD8<sup>+</sup> T cell population (Kaech et al., 2003; Joshi et al., 2007; Zhou et al., 2010; Chang et al., 2014). Although it is clear that these transcriptional regulators are key for the generation of effector and memory CD8<sup>+</sup> T cell populations, little is known about their roles in maintaining subset-specific gene-expression programs. When considering the transition of CD8<sup>+</sup> effector T cells to memory populations, important questions arise: are effector CD8<sup>+</sup> T cell populations unconditionally committed to their specified fate after infection resolution, or does plasticity exist and is active transcriptional regulation necessary to continually enforce subset specificity?

E-protein transcription factors (TFs) and their repressors, Id (inhibitor of DNA binding) proteins, have emerged as key regulators of effector and memory CD8<sup>+</sup> T cell differentiation (Omlusik et al., 2013). E-protein activity increases upon T cell activation to induce a transcriptional network that promotes the formation of MP CD8<sup>+</sup> T cells; and loss of E2A and HEB, two E-protein family members, results in increased frequencies of KLRG1<sup>hi</sup> effector CD8<sup>+</sup> T cells after infection (D’Cruz et al., 2012). Id2 and Id3 are both thought to function by antagonizing E-protein activity, yet they differentially impact the formation of CD8<sup>+</sup> effector and memory T cell populations after acute infection (Cannarile et al., 2006; Ji et al., 2011; Yang et al., 2011; Knell et al., 2013; Masson et al., 2013). Loss of Id2 in naive CD8<sup>+</sup> T cells results in an effector CD8<sup>+</sup> T cell population that is highly susceptible to apoptosis with impaired survival after several bacterial or viral infections (Cannarile et al., 2006; Knell et al., 2016). Importantly, Id2-deficient CD8<sup>+</sup> T cells fail to form the KLRG1<sup>hi</sup> TE subset and instead adopt an MP phenotype (Cannarile et al., 2006; Knell et al., 2013; Masson et al., 2013). Conversely, CD8<sup>+</sup> T cells lacking Id3 have defects in formation and survival of long-lived memory (Ji et al., 2011; Yang et al., 2011). Here, we consider the transcriptional networks that actively maintain CD8<sup>+</sup> T cell commitment and the acquired phenotypic and functional subset-specific properties. In particular, we examine the role of Id2 and E-proteins in enforcing the TE CD8<sup>+</sup> T cell fate after resolution of infection. We find that memory T cell fates are more plastic than anticipated and that sustained regulation of E-protein activity is necessary to maintain the effector or TE CD8<sup>+</sup> T cell phenotype.

## RESULTS AND DISCUSSION

Id2 is expressed in CD8<sup>+</sup> T cells throughout the effector and into the memory phase after infection (Fig. S1 A; Cannarile et al., 2006). Id2 promotes survival and terminal differentiation of CD8<sup>+</sup> T cells at the peak of several acute infections (Cannarile et al., 2006; Knell et al., 2013; Fig. S1, B–H). Effector and TE CD8<sup>+</sup> T cells deficient for Id2 fail to accumulate after infection, and the lack of CD8<sup>+</sup> T cells makes it difficult to attribute a functional role for Id2 in homeostasis of T cell populations at later time points. To circumvent this, we crossed

mice with loxP-flanked *Id2* alleles (Id2<sup>fl/fl</sup>; Niola et al., 2012) to *Rosa26Cre-ERT2* mice (ERCre) to allow inducible deletion of *Id2* upon tamoxifen treatment. These mice were further mated with P14 transgenic mice that express an H-2D<sup>b</sup>-restricted T cell antigen-receptor specific for lymphocytic choriomeningitis virus (LCMV) glycoprotein<sub>33–41</sub>. Treatment of naive Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> P14 mice with tamoxifen induced a near complete deletion of *Id2* in CD8<sup>+</sup> T cells when compared with Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> P14 T cells that had been similarly treated (Fig. S1, B and C; mice called Id2WT or Id2KO after induced *Id2* deletion with tamoxifen). Upon mixed transfer of P14 T cells into congenically distinct hosts, CD8<sup>+</sup> T cells with induced deletion of *Id2* responding to LCMV infection had an accumulation and differentiation defect on day 8 of infection compared with Id2WT CD8<sup>+</sup> T cells consistent with our previously published results studying CD8<sup>+</sup> T cells with germline *Id2* deficiency after infection (Fig. S1, D and E; Cannarile et al., 2006; Knell et al., 2013). Further, when deletion was induced at the peak of infection (5–10 d), the *Id2*-deleted effector and TE CD8<sup>+</sup> T cells rapidly declined within days compared with the Id2WT cells (Fig. S1, F–H).

Having developed an efficient model in which to induce deletion of *Id2*, we sought to assess the role of Id2 in established memory CD8<sup>+</sup> T cells. Untreated Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> and Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were co-transferred at a 1:1 ratio into congenically distinct recipient mice 1 d before LCMV infection. After day 30 of infection, recipient mice were treated with tamoxifen to induce deletion of *Id2* (Fig. 1 A; and Fig. S1, I and J). After tamoxifen treatment (15–16 d), Id2WT and Id2KO CD8<sup>+</sup> T cells persisted in the blood, spleen, and lymph nodes (LNs) of the host at equivalent frequencies and numbers (Fig. 1, B and C; and Fig. S1 K). Strikingly, in this short duration of Id2 deficiency, the phenotype of the Id2KO CD8<sup>+</sup> T cell population significantly changed compared with that of the Id2WT cells. Most prominently in the blood and spleen, the shorter-lived, more effector-like KLRG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>hi</sup>CD127<sup>hi</sup> Id2KO CD8<sup>+</sup> T cell subsets almost completely disappeared, whereas the frequency of the more long-lived KLRG1<sup>lo</sup>CD127<sup>hi</sup> Id2KO CD8<sup>+</sup> T cells significantly increased (Fig. 1, B and D; Joshi et al., 2007; Sarkar et al., 2008). No differences in Ki67 were observed, indicating that the phenotypic changes occurred in the absence of proliferation (not depicted). Consistent with a conversion by the effector-like cells, the CD27<sup>lo</sup>CD43<sup>lo</sup> CD8<sup>+</sup> T cell population, a subset of long-lived effector T cells (Olson et al., 2013), was also lost upon *Id2* deletion, whereas a proportional increase in the CD27<sup>hi</sup>CD43<sup>lo/hi</sup> CD8<sup>+</sup> T cells was observed when compared with the Id2WT controls (Fig. 1, B and D). Furthermore, when analyzing the CD8<sup>+</sup> T cells from the blood and spleen based on CD62L, a marker classically used to define circulating memory CD8<sup>+</sup> T cells or T<sub>CM</sub> cells (Sallusto et al., 1999), we found that the frequency of the CD62L<sup>lo</sup>CD127<sup>lo</sup> long-lived effector Id2KO CD8<sup>+</sup> T cells declined compared with Id2WT CD8<sup>+</sup> T cells. (Fig. 1, E and F). The loss of cells with a KLRG1<sup>hi</sup> phenotype in the Id2KO

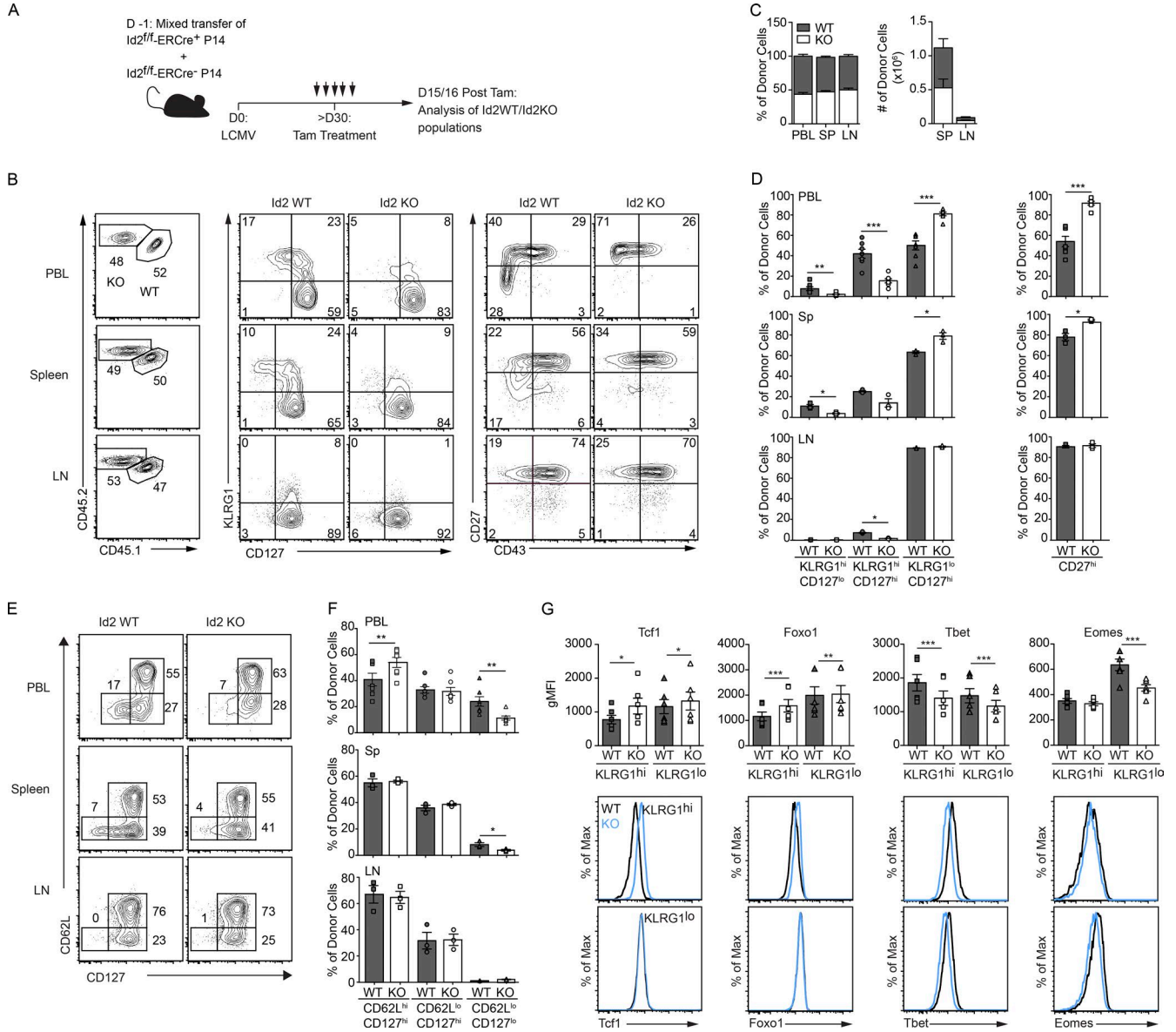
CD8<sup>+</sup> T cell population was accompanied by increased expression of memory-associated TFs, Tcf1 and Foxo1 (Zhou et al., 2010; Hess Michelini et al., 2013), and a decrease in the effector-associated protein, T-bet (Joshi et al., 2007; Fig. 1 G). There were not significant differences in CD122 or CD127 levels for the Id2-deficient cells that had converted to a KLRG1<sup>lo</sup> phenotype compared with WT cells, indicating a similar potential for cytokine responsiveness (not depicted). We did note that at >20 d after induced *Id2* deletion, the ratio of Id2KO to Id2WT donor cells began to fall, indicating that Id2 deficiency did eventually impair survival, in addition to profoundly affecting phenotype at earlier time points (Fig. S1 K). These results suggest that the effector differentiation state may be more actively controlled than previously appreciated and that continual Id2 transcriptional regulation is required to maintain the KLRG1<sup>hi</sup> effector/effector-memory CD8<sup>+</sup> T cell differentiation.

The maintenance of Id2WT and Id2KO CD8<sup>+</sup> T cells in a 1:1 ratio after *Id2* deletion at early time points indicates that, in the absence of regulation of E-protein activity, effector-like Id2KO CD8<sup>+</sup> T cells that have been presumed to be terminally fated dedifferentiate to resemble the long-lived KLRG1<sup>lo</sup>CD127<sup>hi</sup>CD27<sup>hi</sup> T cell population. To understand if the loss of day 30 KLRG1<sup>hi</sup> effector/effector-memory Id2KO CD8<sup>+</sup> T cells was due to altered cell fates, cell death, or increased KLRG1<sup>lo</sup> cell proliferation, we sorted, transferred, and induced *Id2* deletion in CD8<sup>+</sup> T cell subsets and followed them over time (Fig. 2 A). Untreated Id2<sup>f/f</sup>-ERCre<sup>+</sup> and Id2<sup>f/f</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were co-transferred into congenically distinct recipient mice that were infected the next day with LCMV. After day 30 of infection, KLRG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>lo</sup>CD127<sup>hi</sup> P14 CD8<sup>+</sup> T cells subsets that were Id2<sup>f/f</sup>-ERCre<sup>+</sup> or Id2<sup>f/f</sup>-ERCre<sup>-</sup> were sorted from the spleen and LN of recipient mice. KLRG1<sup>hi</sup>CD127<sup>lo</sup> Id2<sup>f/f</sup>-ERCre<sup>+</sup> and Id2<sup>f/f</sup>-ERCre<sup>-</sup> (KLRG1<sup>hi</sup> transfer) or KLRG1<sup>lo</sup>CD127<sup>hi</sup> Id2<sup>f/f</sup>-ERCre<sup>+</sup> and Id2<sup>f/f</sup>-ERCre<sup>-</sup> (KLRG1<sup>lo</sup> transfer) were mixed at a 1:1 ratio and transferred to new congenically distinct recipient mice, which were subsequently treated with tamoxifen to induce *Id2* deletion (Fig. S2, A and B). The frequency and number of Id2WT and Id2KO CD8<sup>+</sup> T cells in the spleens of recipient mice receiving the KLRG1<sup>hi</sup> CD8<sup>+</sup> T cell transfer was not affected on day 6 or 32 after tamoxifen treatment (Fig. 2, B and C). However, by day 32, the proportion and number of Id2KO CD8<sup>+</sup> T cells from the KLRG1<sup>lo</sup> transfer were significantly reduced compared with the Id2WT CD8<sup>+</sup> T cells. The phenotype of the transferred KLRG1<sup>lo</sup> CD8<sup>+</sup> T cells remained KLRG1<sup>lo</sup> CD127<sup>hi</sup> and CD27<sup>hi</sup> after *Id2* deletion, whereas the KLRG1<sup>hi</sup> Id2KO CD8<sup>+</sup> T cells significantly down-regulated KLRG1 and up-regulated CD27, resembling a more long-lived T cell population (Fig. 2, B and D). The Id2WT cells in the KLRG1<sup>hi</sup> transfer partially up-regulated CD127, albeit not to the degree as the Id2KO CD8<sup>+</sup> T cells, likely to support the long-term survival of the transferred cells. Notably, there is an increase in CD62L expression among KLRG1<sup>hi</sup> trans-

ferred cells after *Id2* deletion (Fig. 2, E and F). The Id2KO KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells also significantly up-regulated Tcf1 expression and down-regulated T-bet expression consistent with reassignment from an effector-like phenotype to a memory-like phenotype (Fig. 2 G). The KLRG1<sup>lo</sup> transferred cells lost Eomes expression after *Id2* deletion (Figs. 1 G and 2 F), suggesting that *Id2* differentially affects the CD8<sup>+</sup> T cell populations consistent with multiple roles—promoting survival in the KLRG1<sup>lo</sup>CD127<sup>hi</sup> CD8<sup>+</sup> T cells and enforcing differentiation in the KLRG1<sup>hi</sup>CD127<sup>lo</sup> CD8<sup>+</sup> T cells. These results imply that differentiation to a KLRG1<sup>hi</sup> effector CD8<sup>+</sup> T cell subset is a reversible process and that sustained *Id2* regulation enforces the cell state of “terminal differentiation.”

The loss of *Id2* in long-lived KLRG1<sup>hi</sup> effector CD8<sup>+</sup> T cells leaves them phenotypically resembling CD8<sup>+</sup> T cells with more memory potential, so we sought to test their ability to recall after reinfection. After day 30 of LCMV infection, untreated KLRG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>lo</sup>CD127<sup>hi</sup> Id2<sup>f/f</sup>-ERCre<sup>+</sup> and Id2<sup>f/f</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were sorted and co-transferred as above (Fig. 2 A), and 6 d after tamoxifen treatment to induce *Id2* deletion, the host mice were rechallenged with LCMV. Following the kinetics of the CD8<sup>+</sup> T cell response in the blood, we found that the Id2KO CD8<sup>+</sup> T cells of the KLRG1<sup>hi</sup> transferred cells, which had largely lost KLRG1 expression, peaked 1 d sooner than the equivalent Id2WT CD8<sup>+</sup> T cells after infection (Fig. 3 A). As previously observed in primary responses (Cannarile et al., 2006; Knell et al., 2013; Fig. S1), the CD8<sup>+</sup> T cells deficient for *Id2* failed to accumulate in the late effector stage of the secondary response, and after day 7 of reinfection the proportion of Id2KO CD8<sup>+</sup> T cells of both the KLRG1<sup>hi</sup> and KLRG1<sup>lo</sup> transfer was largely diminished compared with the Id2WT CD8<sup>+</sup> T cells. We examined the phenotype of the responding Id2WT and Id2KO CD8<sup>+</sup> T cells in the spleen of recipients at day 9 after infection (Fig. 3, B–D). Although the Id2KO CD8<sup>+</sup> T cells of the KLRG1<sup>lo</sup> transfer were significantly impaired in their ability to differentiate into KLRG1<sup>hi</sup>CD127<sup>lo</sup> effector cells much like in a primary response (Cannarile et al., 2006; Knell et al., 2013; Masson et al., 2013; Fig. S1), ~60% of the Id2KO CD8<sup>+</sup> T cells of the KLRG1<sup>hi</sup> transfer, despite being largely KLRG1<sup>lo</sup> at the time of rechallenge (Fig. 2, B and D), were able to re-express KLRG1. Yet, the Id2KO CD8<sup>+</sup> T cells remained primarily CD27<sup>hi</sup> with increased expression of Tcf1 and Foxo1 and lower levels of T-bet compared with Id2WT CD8<sup>+</sup> T cells (Fig. 3, C and D; and Fig. S2 C). The Id2KO CD8<sup>+</sup> T cells likely persisted at a lower frequency at the late effector stage of rechallenge because of impaired survival demonstrated by reduced BCL2 (Fig. S2 C). Thus, KLRG1<sup>hi</sup> cells with induced *Id2* deletion responded more rapidly to reinfection than their WT counterparts, showing characteristics consistent with a memory phenotype.

To more thoroughly understand how *Id2* affects the gene-expression profile of established KLRG1<sup>hi</sup> effector/effector-memory CD8<sup>+</sup> T cell populations, we studied global transcriptional changes in CD8<sup>+</sup> T cells that resulted from

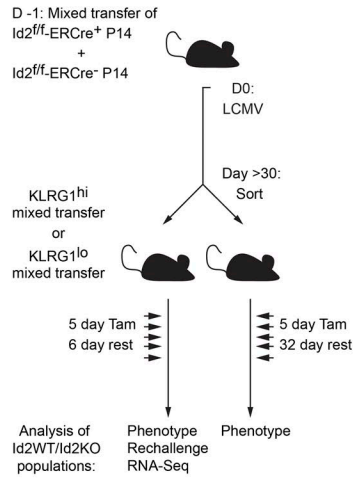


**Figure 1. Late deletion of *Id2* in antigen-specific CD8<sup>+</sup> T cells results in conversion from a KLRG1<sup>hi</sup> to KLRG1<sup>lo</sup> population.** (A) Schematic of experimental set-up. CD45.1 hosts were given a cotransfer of *Id2*<sup>flf</sup>-ERCre<sup>-</sup> (CD45.1.2) and *Id2*<sup>flf</sup>-ERCre<sup>+</sup> (CD45.2) P14 CD8<sup>+</sup> T cells then subsequently infected with LCMV. More than 30 d after infection, host mice were treated for 5 consecutive days with tamoxifen (Tam) to induce *Id2* deletion. *Id2*<sup>flf</sup>-ERCre<sup>-</sup> and *Id2*<sup>flf</sup>-ERCre<sup>+</sup> CD8<sup>+</sup> T cells are called Id2WT or Id2KO, respectively, after Tam treatment. (B) Flow cytometry of transferred P14 CD8<sup>+</sup> T cells from host peripheral blood lymphocytes (PBL) or spleen (Sp) and LN 15 or 16 d after the last Tam treatment, respectively. Frequency of Id2WT and Id2KO cells among P14 CD8<sup>+</sup> T cells (left), KLRG1 and CD127 expression (middle), and CD27 and CD43 expression (right) are shown. Numbers in plots represent the percentage of cells. (C) Quantification of donor cell frequency and number or (D) frequency of populations from B. (E) Flow cytometry of cells from B for CD62L and CD127 expression. (F) Quantification of donor populations from E. (G) Expression of indicated proteins on KLRG1<sup>hi</sup> or KLRG1<sup>lo</sup> Id2WT or Id2KO donor populations. Data shown are representative of three (B and D–F) independent or cumulative of two or three (C and G) independent experiments; *n* = 3–5 mice per group. Data are expressed as mean ± SEM. \*, *P* < 0.05; \*\*, *P* < 0.01; \*\*\*, *P* < 0.001 (two-tailed paired Student's *t* test).

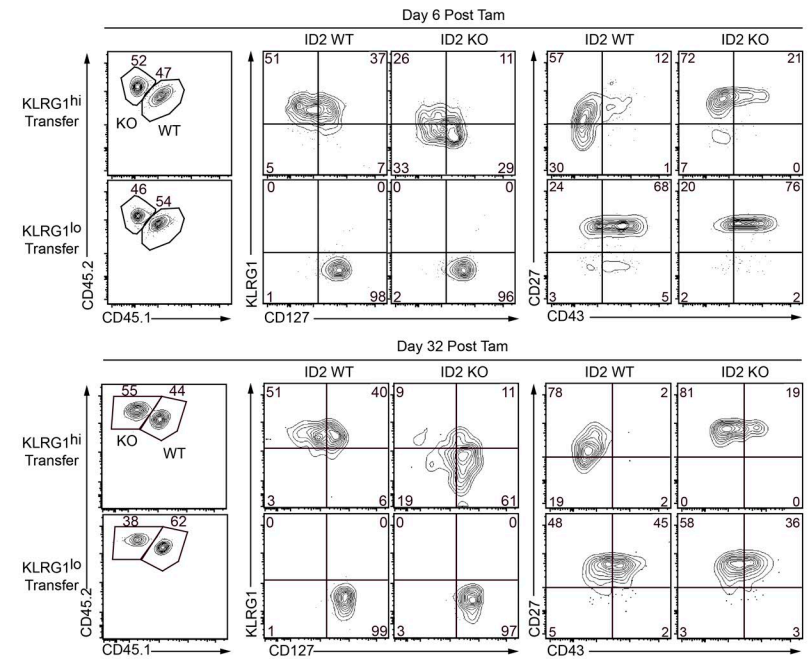
induced deletion of *Id2*. On day 26 of LCMV infection, KLRG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>lo</sup>CD127<sup>hi</sup> *Id2*<sup>flf</sup>-ERCre<sup>+</sup> and *Id2*<sup>flf</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were sorted and co-transferred as in Fig. 2 A, and 6 d after tamoxifen treatment Id2WT and Id2KO T cell populations were sorted for

RNA sequencing (RNA-Seq) analysis. Differential expression of genes associated with KLRG1<sup>hi</sup>CD127<sup>lo</sup> or KLRG1<sup>lo</sup>CD127<sup>hi</sup> CD8<sup>+</sup> T cell populations from 30 or more days of infection was confirmed by comparison of Id2WT CD8<sup>+</sup> T cells from the KLRG1<sup>hi</sup> or KLRG1<sup>lo</sup> transfers (Fig. 4 A,

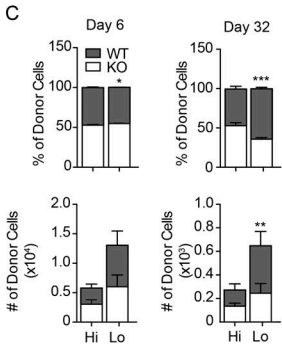
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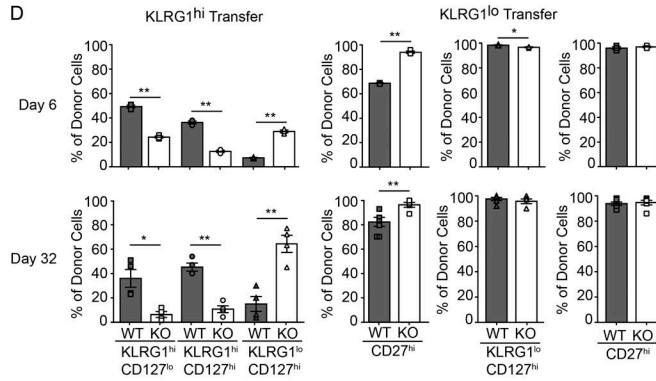
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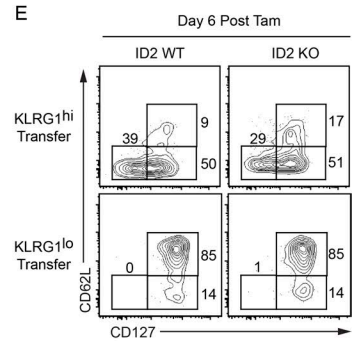
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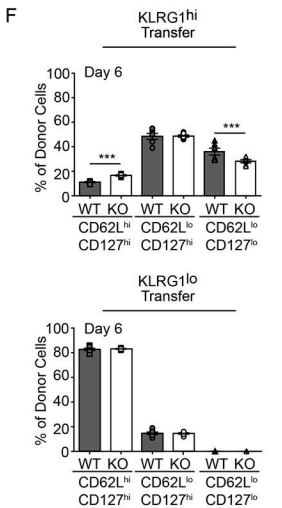
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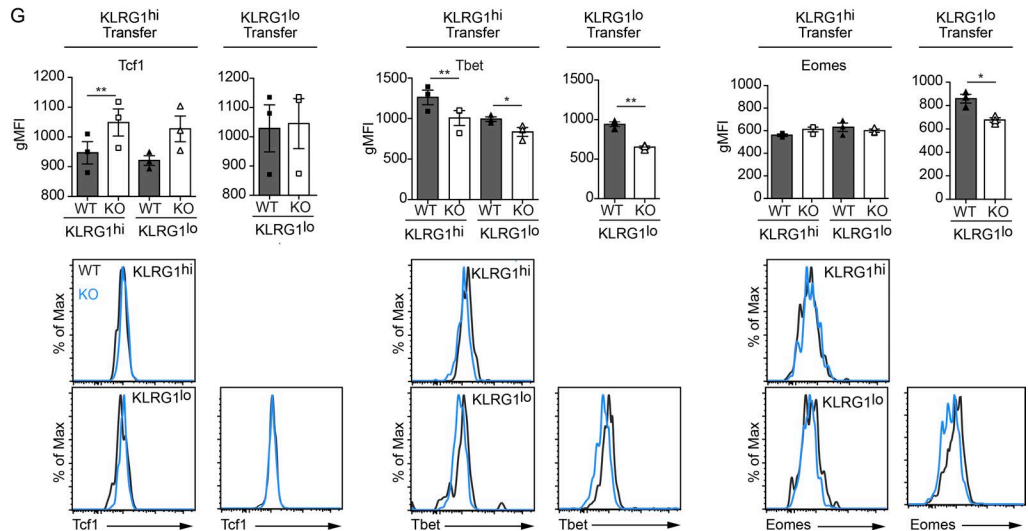
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G



left). We compared gene expression between the Id2WT and Id2KO CD8<sup>+</sup> T cells from the KLRG1<sup>hi</sup> transfer and found that Id2KO KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells, in addition to down-regulating KLRG1 and T-bet protein expression, down-regulated mRNA of effector-associated genes (*Prdm1*, *Tbx21*, *Zeb2*, and *Gzmb*) and up-regulated mRNA of memory-associated genes (*Id3*, *Ccr7*, and *Tcf7*) upon *Id2* deletion (Fig. 4 A, right). Principal component analysis confirmed that the induced deletion of *Id2* resulted in the Id2KO KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells rapidly adopting a transcriptional profile that was distinct from WT KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells and more closely resembling MP or memory (T<sub>EM</sub>, T<sub>CM</sub>) cells (Fig. 4 B).

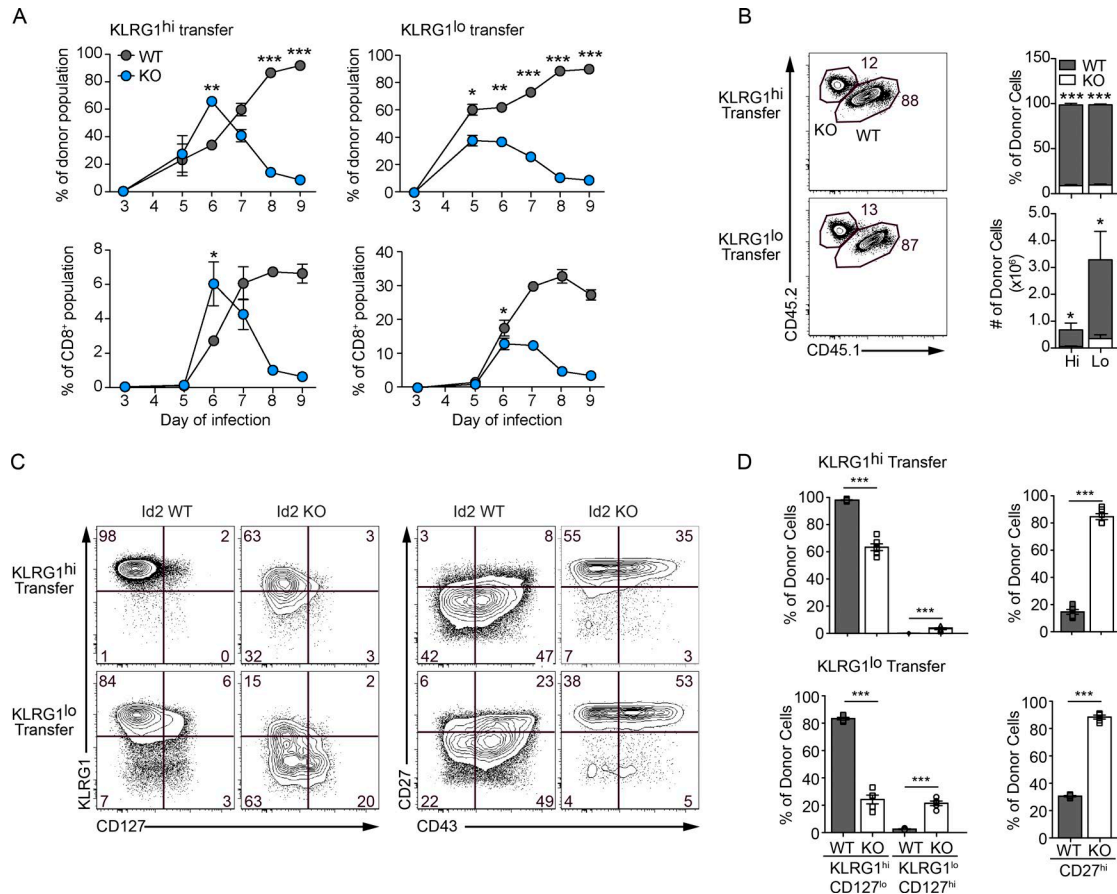
To more carefully characterize the effect of induced *Id2* deletion on genes that are effector or memory associated, we compared expression of genes differentially expressed between Id2WT and Id2KO CD8<sup>+</sup> T cells from the KLRG1<sup>hi</sup> transfer to TE and MP gene signatures and T<sub>EM</sub> and T<sub>CM</sub> gene signatures previously established in our laboratory (Milner et al., 2017; Yu et al., 2017). It should be noted that T<sub>EM</sub> and T<sub>CM</sub> populations were isolated by sorting on the CD62L<sup>lo</sup> or CD62L<sup>hi</sup> P14 CD8<sup>+</sup> T cell populations and did not exclude KLRG1 to be consistent with other studies (Chang et al., 2014); therefore, it is likely that long-lived TE may be a component of our T<sub>EM</sub> signature. Id2KO CD8<sup>+</sup> T cells lost expression of 79% of the TE signature genes and up-regulated expression of 69% of the MP-associated genes compared with the Id2WT CD8<sup>+</sup> T cells (Fig. 4 C, top; P < 0.001). Similarly, Id2KO CD8<sup>+</sup> T cells lost expression of 83% or up-regulated expression of 88% of T<sub>EM</sub> or T<sub>CM</sub> signature genes, respectively (Fig. 4 C, bottom; P < 0.001). These analyses indicate a substantial skewing away from an effector-like and toward a T<sub>CM</sub> CD8<sup>+</sup> T cell transcriptional program by the so-called “terminally differentiated” KLRG1<sup>hi</sup>CD127<sup>lo</sup> Id2KO CD8<sup>+</sup> T cells, rapidly following induction of *Id2* deletion.

The dedifferentiation of long-lived KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells to memory-like KLRG1<sup>lo</sup>CD127<sup>hi</sup> CD8<sup>+</sup> T cells in the absence of continual *Id2* regulation suggests that restrained E-protein activity is necessary to maintain a KLRG1<sup>hi</sup> effector CD8<sup>+</sup> T cell phenotype. To confirm that E-protein activity, the presumed target of *Id2*, determines and maintains

the fate of CD8<sup>+</sup> T cells after infection, we analyzed genes differentially expressed between Id2WT or Id2KO KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells that are identified E2A targets (Leong et al., 2016) and are defined in the TE and MP or T<sub>EM</sub> and T<sub>CM</sub> gene signatures (Fig. 4 D). We found a substantial number of E2A-bound genes that were differentially up-regulated (*Id3*, *Ccr7*, *Tcf7*, and *Cd27*) and down-regulated (*Prdm1*, *Ccl3*, and *Gzma*) upon induced deletion of *Id2*. This suggests that *Id2* mediation of E-protein activity plays a key role in enforcing effector CD8<sup>+</sup> T cell terminal differentiation. It then follows that diminished levels of E2A would “rescue” the effector CD8<sup>+</sup> T cell dedifferentiation observed in *Id2*-deficient cells. Therefore, we transduced Id2<sup>ff</sup>-ERCre<sup>+</sup> and Id2<sup>ff</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells with a retroviral shRNA vector targeting the gene encoding E2A (sh*Tcf3*) or control shRNA (sh*Cd19*; Fig. 4 E and Fig. S3 A) as previously described (Shaw et al., 2016). Id2<sup>ff</sup>-ERCre<sup>+</sup> and Id2<sup>ff</sup>-ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells transduced with sh*Tcf3* or sh*Cd19* were mixed in a 1:1 ratio and co-transferred to congenically distinct recipients that had been infected 1 d earlier with LCMV. On day 15 of infection, recipient mice were treated with tamoxifen to induce deletion of *Id2*, and the phenotype of the transferred CD8<sup>+</sup> T cells in recipient spleens was analyzed. As expected, the Id2KO CD8<sup>+</sup> T cells expressing control sh*Cd19* were unable to maintain a differentiated population of CD8<sup>+</sup> T cells defined as KLRG1<sup>hi</sup>CD127<sup>lo</sup> and CD27<sup>lo</sup>CD43<sup>lo</sup>. However, the Id2KO CD8<sup>+</sup> T cells with diminished expression of *Tcf3* were almost completely rescued with the frequency of KLRG1<sup>hi</sup>CD127<sup>lo</sup> and CD27<sup>lo</sup>CD43<sup>lo</sup> populations nearly equivalent to Id2WT CD8<sup>+</sup> T cell population (Fig. 4, F and G). Therefore, the loss of the effector-like CD8<sup>+</sup> T cell population we observed upon *Id2* deletion can be attributed largely to increased E-protein activity.

Loss of *Id2* and enhanced E-protein activity disproportionately impact the KLRG1<sup>hi</sup> effector-like CD8<sup>+</sup> T cell population at memory time points with a rapid and dramatic shift in phenotype and overall gene expression of KLRG1<sup>hi</sup> CD8<sup>+</sup> T cells to a memory-like state, whereas the KLRG1<sup>lo</sup> CD8<sup>+</sup> T cells showed moderately lower Eomes expression and impaired survival at later time points (by day 32). Al-

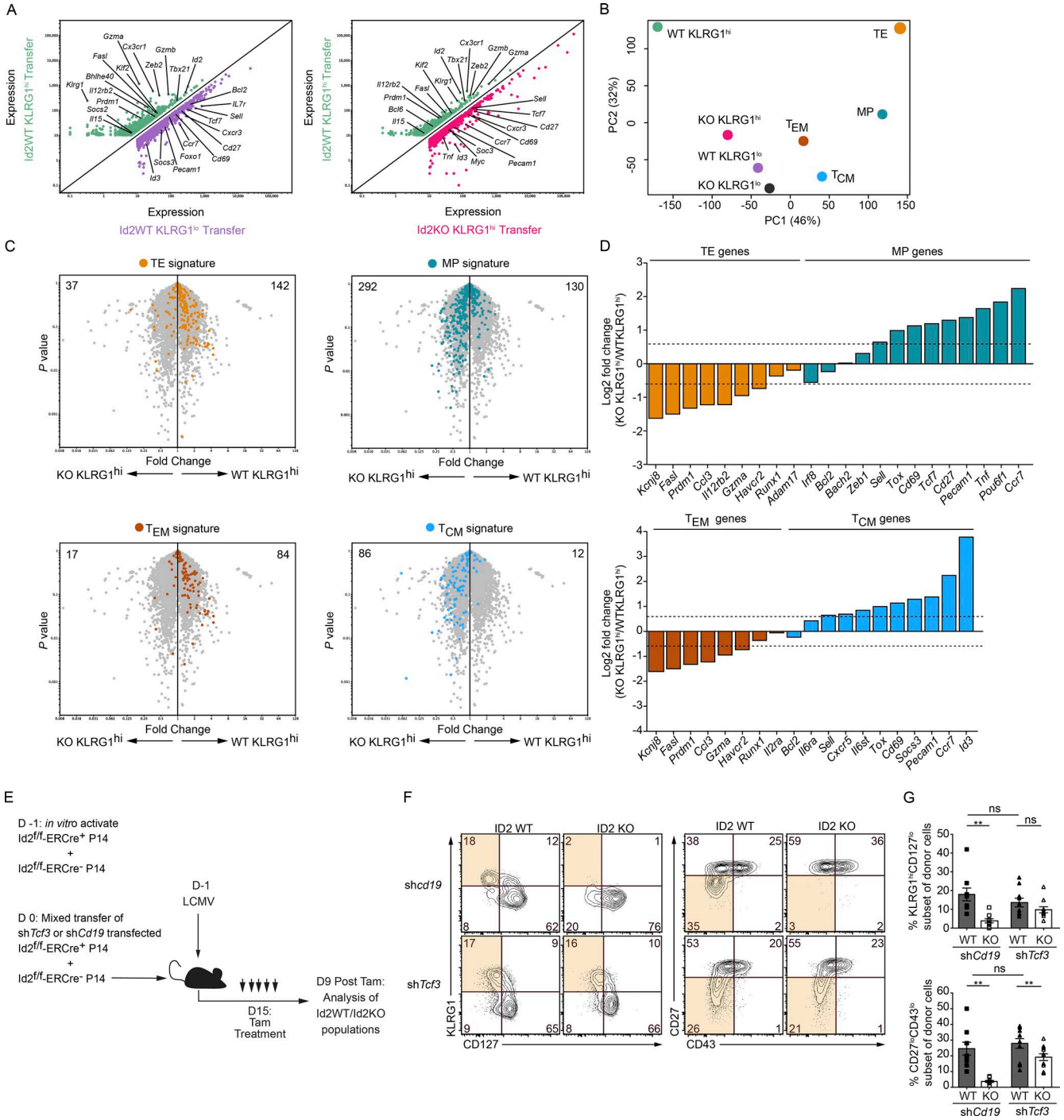
**Figure 2. Id2 is necessary to maintain the terminal differentiation of antigen-specific CD8<sup>+</sup> T cells.** (A) Schematic of experimental set-up. CD45.1 hosts were given a cotransfer of Id2<sup>ff</sup>-ERCre<sup>-</sup> (CD45.1.2) and Id2<sup>ff</sup>-ERCre<sup>+</sup> (CD45.2) P14 CD8<sup>+</sup> T cells and then subsequently infected with LCMV. At >30 d after infection, KLRG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>lo</sup>CD127<sup>hi</sup>, Id2<sup>ff</sup>-ERCre<sup>-</sup>, and Id2<sup>ff</sup>-ERCre<sup>+</sup> P14 CD8<sup>+</sup> T cells were sorted purified. Id2<sup>ff</sup>-ERCre<sup>-</sup> and Id2<sup>ff</sup>-ERCre<sup>+</sup> KLRG1<sup>hi</sup>CD127<sup>lo</sup> (KLRG1<sup>hi</sup> transfer) or Id2<sup>ff</sup>-ERCre<sup>-</sup> and Id2<sup>ff</sup>-ERCre<sup>+</sup> KLRG1<sup>lo</sup>CD127<sup>hi</sup> (KLRG1<sup>lo</sup> transfer) populations were co-transferred into naive CD45.1 hosts that were treated with tamoxifen (Tam). Id2<sup>ff</sup>-ERCre<sup>-</sup> and Id2<sup>ff</sup>-ERCre<sup>+</sup> CD8<sup>+</sup> T cells are called Id2WT or Id2KO, respectively, after Tam treatment. (B) Flow cytometry of transferred P14 CD8<sup>+</sup> T cells from host spleen 6 d (top) or 32 d (bottom) after last Tam treatment. Frequency of Id2WT and Id2KO cells among P14 CD8<sup>+</sup> T cells (left), KLRG1 and CD127 expression (middle), and CD27 and CD43 expression (right) for the KLRG1<sup>hi</sup> and KLRG1<sup>lo</sup> transfer are shown. Numbers in plots represent the frequency of cells in that quadrant. (C) Quantification of donor cell frequency and number from KLRG1<sup>hi</sup> (Hi) or KLRG1<sup>lo</sup> (Lo) transfers from B. (D) Quantification of donor populations from KLRG1<sup>hi</sup> (left) and KLRG1<sup>lo</sup> (right) transfer. (E) Flow cytometry of transferred P14 CD8<sup>+</sup> T cells from host spleen 6 d after last Tam treatment. CD62L and CD127 expression for the KLRG1<sup>hi</sup> and KLRG1<sup>lo</sup> transfers is shown. (F) Quantification of donor populations from E. (G) Expression of indicated transcription factors on KLRG1<sup>hi</sup> or KLRG1<sup>lo</sup> Id2WT or Id2KO donor populations from hosts receiving KLRG1<sup>hi</sup> transferred (left) and KLRG1<sup>lo</sup> transferred (right) cells 6 d after last Tam treatment. Data shown are representative (B, E, and G) or cumulative (C, D, and F) of two independent experiments; n = 3–4 mice per group. Data are expressed as mean ± SEM. \*, P < 0.05; \*\*, P < 0.01; \*\*\*, P < 0.001 (two-tailed paired Student's *t* test).



**Figure 3. Deletion of *Id2* in *KLRG1<sup>hi</sup>* memory *CD8<sup>+</sup>* T cells results in the faster initiation of a recall response.** *Id2<sup>fl/fl</sup>-ERCre<sup>-</sup>* and *Id2<sup>fl/fl</sup>-ERCre<sup>+</sup>* *KLRG1<sup>hi</sup>* or *KLRG1<sup>lo</sup>* P14 *CD8<sup>+</sup>* T cells were co-transferred into naive *CD45.1* hosts, and *Id2* deletion was induced as described in Fig. 2 A. Host mice were infected with LCMV 7 d after the last tamoxifen treatment. *Id2<sup>fl/fl</sup>-ERCre<sup>-</sup>* and *Id2<sup>fl/fl</sup>-ERCre<sup>+</sup>* *CD8<sup>+</sup>* T cells are called *Id2WT* or *Id2KO*, respectively, following tamoxifen treatment. **(A)** The frequency of total *Id2WT* and *Id2KO* P14 donor cells (top) or *Id2WT* and *Id2KO* P14 cells of total *CD8<sup>+</sup>* T cells (bottom) in PBL on indicated days after infection is shown. **(B)** Flow cytometry (left) and quantification (right) of the frequency of *Id2WT* and *Id2KO* P14 *CD8<sup>+</sup>* T cells from host spleen 9 d after infection for *KLRG1<sup>hi</sup>* and *KLRG1<sup>lo</sup>* transfers. **(C)** Flow cytometry of *KLRG1* and *CD127* expression (left) and *CD27* and *CD43* expression (right) for *KLRG1<sup>hi</sup>* and *KLRG1<sup>lo</sup>* transfers are shown. **(D)** Quantification of donor populations from C after *KLRG1<sup>hi</sup>* (top) and *KLRG1<sup>lo</sup>* (bottom) transfer. Numbers in plots represent the percentage of cells. Data shown are cumulative (total donor frequency; A, top) or representative (total *CD8<sup>+</sup>* population frequency; A, bottom), representative (B), or cumulative (C) of two independent experiments;  $n = 2-4$  mice per group. Data are expressed as mean  $\pm$  SEM. \*,  $P \leq 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$  (one-tailed paired [A and B] or two-tailed paired [D] Student's *t* test).

though we noted a 1.9-fold increase in mRNA expression of *Id2* in the *KLRG1<sup>hi</sup>CD127<sup>lo</sup>* compared with the *KLRG1<sup>lo</sup>CD127<sup>hi</sup>* *CD8<sup>+</sup>* T cells (Fig. 4 A, left) and higher *Id2* reporter expression has been observed in *T<sub>EM</sub>* cells versus *T<sub>CM</sub>* cells after influenza infection (Masson et al., 2013), we did not detect differential *Id2* reporter levels between *KLRG1<sup>hi</sup>CD127<sup>lo</sup>* and *KLRG1<sup>lo</sup>CD127<sup>hi</sup>* *CD8<sup>+</sup>* T cells or *Id2* protein levels between *T<sub>EM</sub>* and *T<sub>CM</sub>* in our experiments (Fig. S3 B). This suggests that the increased dependency on *Id2* observed in the *KLRG1<sup>hi</sup>* compared with *KLRG1<sup>lo</sup>* *CD8<sup>+</sup>* T cells was not due to substantially differing expression levels. Using the assay for transposase-accessible chromatin-sequencing (ATAC-Seq) data for naive, TE, and MP or *T<sub>CM</sub>* and *T<sub>EM</sub>* *CD8<sup>+</sup>* T cells assessed 0, 7, 30, or 180 d after LCMV infection, we analyzed chromatin accessibility of MP or *T<sub>CM</sub>* E-protein

target genes that were differentially regulated upon *Id2* deletion (Fig. 4 D). E-protein binding sites in *Tcf7*, *Cd27*, *Cxcr5*, *Ccr7*, and *Id3*, identified by using E2A chromatin immunoprecipitation-sequencing (ChIP-Seq; Leong et al., 2016), were accessible in the naive, TE, MP, *T<sub>CM</sub>*, and *T<sub>EM</sub>* populations analyzed (Fig. S3 C and not depicted). This suggests that other factors contribute to *CD8<sup>+</sup>* T cell subset-specific E-protein regulation. For example, *Zeb2*, a transcription factor highly expressed in TE and *T<sub>EM</sub>* *CD8<sup>+</sup>* T cells and found to be important for terminal differentiation (Dominguez et al., 2015; Omilusik et al., 2015; Kakaradov et al., 2017), can bind DNA at tandem, separated E-protein binding sites (Sekido et al., 1994; Remacle et al., 1999). We identified such a site within the *Tcf7* gene (Fig. S3 C), suggesting *Zeb2* may function in *KLRG1<sup>hi</sup>* effector-like *CD8<sup>+</sup>* T cell populations



**Figure 4. Id2 regulation of E2A binding regulates expression of key effector CD8<sup>+</sup> T cell genes.** (A–D) Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> (CD45.1.2) and Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> (CD45.2) KLRG1<sup>hi</sup> or KLRG1<sup>lo</sup> P14 CD8<sup>+</sup> T cells were co-transferred into naive CD45.1 hosts, and Id2 deletion was induced as described in Fig. 2 A. Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> and Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> CD8<sup>+</sup> T cells are called Id2WT or Id2KO, respectively, after tamoxifen (Tam) treatment. On day 6 after the last Tam treatment, Id2WT and Id2KO cells were sorted for RNA-Seq. (A) Gene expression by cells from the Id2WT KLRG1<sup>hi</sup> transfer versus Id2WT KLRG1<sup>lo</sup> transfer (left) or from the Id2WT KLRG1<sup>hi</sup> transfer versus Id2KO KLRG1<sup>hi</sup> transfer (right) for genes differentially expressed by 1.5-fold or more, a coefficient of variation of  $\leq 0.50$ , and an expression value of  $\geq 10$ ; colors indicate genes up-regulated 1.5-fold or more in the cells from the Id2WT KLRG1<sup>hi</sup> transfer relative to their expression in cells from the Id2WT KLRG1<sup>lo</sup> transfer (green) or vice versa (purple), or genes up-regulated in cells from the Id2WT KLRG1<sup>hi</sup> transfer relative to cells from the Id2KO KLRG1<sup>hi</sup> transfer (green) or vice versa (magenta). Labels in plots indicate genes of published relevance to CD8<sup>+</sup> T cell differentiation and memory formation. (B) Principal component analysis of gene expression in Id2WT and Id2KO P14 CD8<sup>+</sup> T cells from the KLRG1<sup>hi</sup> and KLRG1<sup>lo</sup> transfers, in TE and MP P14 CD8<sup>+</sup> T cell populations at day 7 of LCMV infection, and in T<sub>CM</sub> and T<sub>EM</sub> P14 CD8<sup>+</sup> T cell populations at day 180 of LCMV infection. (C) Expression of TE- or



to repress E-protein activity and thus the memory-gene expression program. Perhaps enhanced E-protein activity upon the loss of Id2 expression may outcompete Zeb2 for E-box sites, resulting in greater expression of *Tcf7*, which then could promote the T<sub>CM</sub>, long-lived memory phenotype.

Ultimately these results show that the concept of terminal differentiation may be flawed in the context of CD8<sup>+</sup> memory T cell differentiation. KLRG1 may not be a definitive marker of terminal differentiation, and bona fide, terminally differentiated CD8<sup>+</sup> T cells may die shortly after resolution of the infection, leaving a less-differentiated KLRG1<sup>hi</sup> population that persists at memory time points. Instead, we support the notion that CD8<sup>+</sup> T cell differentiation is flexible and sustained inhibition of E-protein activity by Id2 allows the survival of an effector-like population that can reacquire at least a portion of the T<sub>CM</sub>, or long-lived memory gene-expression program, favoring the idea of plasticity of cell states over fixed cell fates among the heterogeneous, post-infection CD8<sup>+</sup> T cell population.

## MATERIALS AND METHODS

### Mice

All mouse strains were bred and housed in specific pathogen-free conditions in accordance with the Institutional Animal Care and Use Guidelines of the University of California San Diego. Id2-YFP mice (Yang et al., 2011), Id2<sup>fl/fl</sup> mice (Niola et al., 2012), *Rosa26Cre-ERT2* (ERCre) mice (Hess Michelini et al., 2013), P14 mice (with transgenic expression of H-2D<sup>b</sup>-restricted TCR specific for LCMV glycoprotein gp33), and CD45.1 and CD45.1.2 congenic mice were bred to obtain a fully C57BL/6J background. Both male and female mice were used throughout the study, with sex- and age-matched T cell donors and recipients.

### Cell transfer, LCMV infection, and tamoxifen treatment

Congenically distinct Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> and Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> P14 CD8<sup>+</sup> T cells were mixed at a 1:1 ratio and adoptively transferred at  $5 \times 10^4$  cells per CD45.1 recipient mouse. Mice were then infected with  $2 \times 10^5$  PFU LCMV-Armstrong by intraperitoneal injection. At day 5 or >30 d after infection, *Rosa26Cre-ERT2*-mediated deletion of floxed alleles was induced by intraperitoneal injection for 5 consecutive days of 1 mg tamoxifen (Cayman Chemical Company) emulsified in 100 ml sunflower seed oil (Sigma-Aldrich). Alternatively, >30 d (or at 26 d for RNA-Seq analysis) after infection, KL-

RG1<sup>hi</sup>CD127<sup>lo</sup> and KLRG1<sup>lo</sup>CD127<sup>hi</sup> populations from total P14 CD8<sup>+</sup> T cells were sorted from recipient spleen and LN, mixed in a 1:1 ratio of KLRG1<sup>hi</sup>CD127<sup>lo</sup> Id2<sup>fl/fl</sup>-ERCre<sup>+</sup>/Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> or KLRG1<sup>lo</sup>CD127<sup>hi</sup> Id2<sup>fl/fl</sup>-ERCre<sup>+</sup>/Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> and then transferred at  $1.5 \times 10^5$  total cells per CD45.1 recipient mouse. The next day, tamoxifen was administered as above for five consecutive days to induce *Id2* deletion. At 6 or 32 d after the last tamoxifen treatment, Id2WT and Id2KO populations were assessed by flow cytometry or sorted for RNA-Seq (as described in the RNA-Seq section), or recipients were rechallenged intraperitoneally with  $2 \times 10^5$  PFU LCMV-Armstrong.

### RT-PCR and qPCR

To confirm *Id2* deletion or *Tcf3* knockdown, total RNA was extracted by using Trizol (Life Technologies) from sorted Id2WT and Id2KO P14 CD8<sup>+</sup> T cells. cDNA was synthesized by using Superscript II kit (Life Technologies) following the manufacturer's instructions. For qPCR, cDNA was quantitatively amplified by using Stratagene Brilliant II Syber Green master mix (Agilent Technologies). The abundance of transcripts was normalized to that of the housekeeping gene *Hprt*. The following primers were used: *Id2* forward, 5'-TCCCTTCTGAGCTTATGTCCG-3' and *Id2* reverse, 5'-GTCCATTCAACGTGTTCTCC-3'; *Tcf3* forward, 5'-CATCCATGTCCTGCGAAGCCA-3' and *Tcf3* reverse, 5'-TTCTTGTCTCTTTCGGCGT-3'; *Hprt* forward, 5'-GGCCAGACTTTGTTGGATTT-3', and *Hprt* reverse: 5'-CAACTTGCGCTCATCTTAGG-3'.

### Flow cytometry and cell sorting

Single-cell suspensions were prepared from spleen, LN, or blood. The following antibodies were used for surface staining (all from eBioscience): CD8 (53-6.7), CD27 (LG-7F9), CD43 (1B11), CD45.1 (A20-1.7), CD45.2 (104), CD62L (MEL-14), CD122 (TM-b1), CD127 (A7R34), CXCR3 (CXCR3-173), and KLRG1 (2F1). Cells were incubated for 30 min at 4°C in PBS supplemented with 2% bovine growth serum and 0.1% sodium azide. Intracellular staining was performed by using the Foxp3 Transcription Factor Staining Buffer kit (eBioscience) and the following antibodies (all from eBioscience unless otherwise specified): BCL2 (3F11; BD PharMingen), Eomes (Dan11mag), Foxo1 (C29H4; Cell Signaling), Gzmb (GB12; Invitrogen), Id2 (ILCID2; Thermo Fisher Scientific), Tbet (eBio4B10), and Tcf1 (C63D9; Cell

MP-associated genes (top) or T<sub>EM</sub>- or T<sub>CM</sub>-associated genes (bottom) assessed in cells from the Id2KO KLRG1<sup>hi</sup> transfer versus cells from the Id2WT KLRG1<sup>hi</sup> transfer and plotted against p-value. Numbers in the corners indicate the total of those genes up-regulated in cells from the Id2KO KLRG1<sup>hi</sup> transfer (top left) or from the Id2WT KLRG1<sup>hi</sup> transfer (top right). P < 0.001 ( $\chi^2$  test). (D) Relative expression of TE and MP genes (top) and T<sub>EM</sub> and T<sub>CM</sub> genes (bottom) from C that are putative E2A-target genes identified by ChIP-Seq (bar colors match dot colors in C). (E) Schematic of experimental set-up. CD45.1 host mice infected 1 d before received a cotransfer of Id2<sup>fl/fl</sup>-ERCre<sup>-</sup> and Id2<sup>fl/fl</sup>-ERCre<sup>+</sup> P14 CD8<sup>+</sup> T cells transduced with control shRNA targeting *Cd19* or with sh*Tcf3*. At 15 d of infection, host mice were treated with tamoxifen (Tam) to induce *Id2* deletion. (F) Flow cytometry of transferred cells 9 d after the last Tam treatment for KLRG1 and CD127 expression (left) and CD27 and CD43 expression (right). Numbers in the plots represent the percentage of cells. (G) Quantification of donor populations from highlighted populations in F. Data are representative of two (A–D) or three (F) and cumulative of three (G) independent experiments; n = 3–5 mice per group. Data are expressed as mean  $\pm$  SEM. \*\*, P < 0.01 (two-tailed paired Student's *t* test).

Signaling). Stained cells were analyzed by using LSRFortessa or LSRFortessa X-20 (BD) and FlowJo software (TreeStar). All sorting was performed on BD FACSAria or BD FACSAria Fusion instruments.

#### shRNA-mediated knockdown by retroviral transduction

DNA fragments encoding shRNA targeting mouse *Tcf3* or *Cd19* were subcloned into a custom retroviral vector containing ametrine as a reporter. Naive congenically distinct  $Id2^{f/f}$ -ERCre<sup>+</sup> and  $Id2^{f/f}$ -ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were stimulated for 18 h in 6-well plates precoated with anti-CD3 and anti-CD28. After stimulation, cells were transduced by adding retroviral supernatants supplemented with 100 U/ml human IL-2 and 8 μg/ml polybrene, followed by centrifugation for 90 min at 2000 *g* at 37°C. After transduction, cells were incubated for 3 h at 37°C.  $Id2^{f/f}$ -ERCre<sup>+</sup>/ $Id2^{f/f}$ -ERCre<sup>-</sup> P14 CD8<sup>+</sup> T cells were mixed 1:1 and 10<sup>6</sup> cells were transferred into day -1 LCMV-infected hosts, and remaining cells were cultured *in vitro* with 50 U/ml human IL-2 for 4 d to assess for knockdown efficiency by qPCR. On day 15 of infection, tamoxifen was administered as described in the tamoxifen treatment section for 5 consecutive days to induce *Id2* deletion. At 9 d after the last tamoxifen treatment,  $Id2^{WT}$  and  $Id2^{KO}$  populations were assessed by flow cytometry.

#### RNA-Seq, ChIP-Seq, and ATAC-Seq

6 d after the last tamoxifen treatment, 10<sup>3</sup>  $Id2^{WT}$  and  $Id2^{KO}$  P14 cells from recipients receiving mixed transfers of KLRG1<sup>hi</sup>CD127<sup>lo</sup> or KLRG1<sup>lo</sup>CD127<sup>hi</sup> transfer were sorted into Buffer TCL (Qiagen) with 1% 2-mercaptoethanol. RNA was isolated, and libraries were prepared following Immgen protocols (<https://www.immgen.org/Protocols/11Cells.pdf>). Libraries were analyzed on an Illumina HiSeq2500 sequencer. Samples were generated from two biological replicates, and ~10 million paired-reads were generated per sample. Reads were mapped by using Tophat, and aligned reads in transcripts were counted with HTseq. Analysis was performed by using the GenePattern Multiplot Studio module. TE and MP (Yu et al., 2017) and T<sub>EM</sub> and T<sub>CM</sub> gene signatures (Milner et al., 2017) represent genes that have a 1.5-fold increased expression in that CD8<sup>+</sup> T cell population. Principal component analysis used RNA-Seq data for TE and MP or T<sub>EM</sub> and T<sub>CM</sub> P14 CD8<sup>+</sup> T cells from day 7 or 180 after LCMV infection. E2A Bio-Chip analysis was deposited by Leong et al. (2016) (GEO accession code GSE84974), and ATAC-Seq data from Immgen (<http://rstats.immgen.org/Chromatin/chromatin.html>) was analyzed in the University of California, Santa Cruz, genome browser.

#### Statistics

The one- or two-tailed paired Student's *t* test was used for comparisons between groups as stated in the figure legends. The  $\chi^2$  test was used to determine significant enrichment of gene sets in the RNA-Seq data. Statistical analysis was performed by using GraphPad Prism software.

#### Online supplemental material

Fig. S1 shows analysis of CD8<sup>+</sup> T cells responding to LCMV infection when *Id2* deletion is induced in naive cells or at the peak of infection, as well as knockout efficiency when *Id2* deletion is induced >30 d after infection. Fig. S2 shows the mix of  $Id2^{WT}$  and  $Id2^{KO}$  CD8<sup>+</sup> T cells for KLRG1<sup>hi</sup> and KLRG1<sup>lo</sup> transfers and additional phenotyping after LCMV rechallenge. This relates to Figs. 2 and 3. Fig. S3 shows *Tcf3* knockdown efficiency in  $Id2^{WT}$  and  $Id2^{KO}$  P14 CD8<sup>+</sup> T cells transduced with retroviral shRNA constructs. Also, ATAC-Seq and E2A ChIP-Seq analysis of the *Tcf7* loci for CD8<sup>+</sup> T cell populations after LCMV infection is shown. This relates to Fig. 4.

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The authors declare no competing financial interests.

Author contributions: K.D. Omilusik designed and performed experiments, analyzed the data, and wrote the paper. M.S. Nadjisombati, L.A. Shaw, B. Yu, and J.J. Milner performed experiments and assisted with data analysis. A.W. Goldrath supervised the project, designed the experiments, analyzed the data, and wrote the paper.

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