

Supplemental material

Guan et al., <https://doi.org/10.1084/jem.20171352>

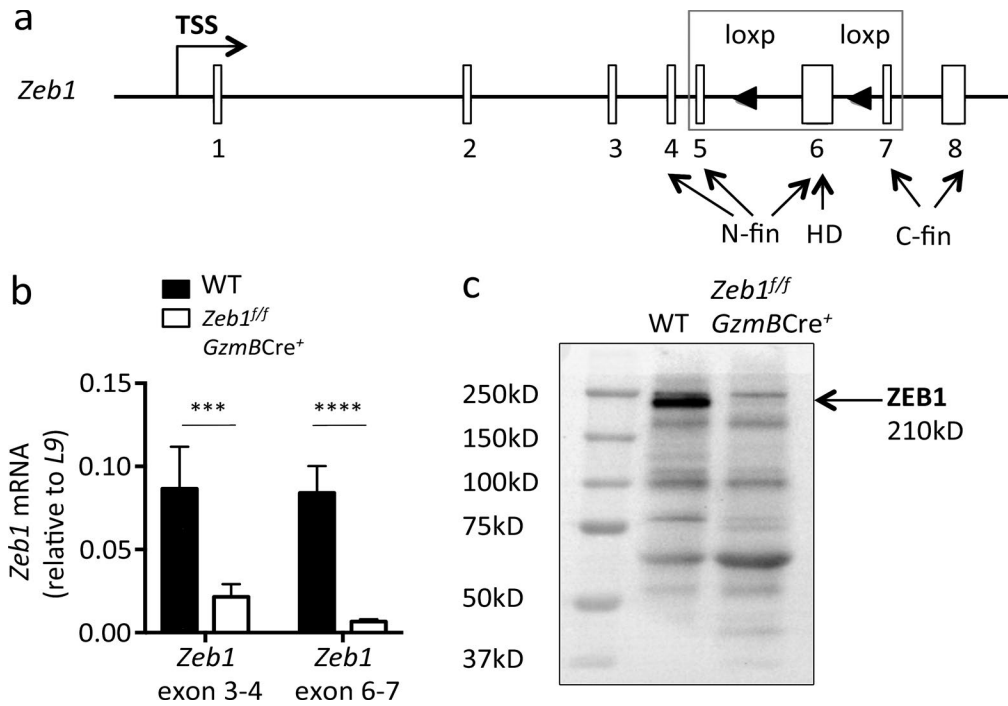


Figure S1. **Generation of *Zeb1* conditional KO mice and validation of deletion.** (a) A schematic representation of loxP inserts within *Zeb1* gene locus. (b) *Zeb1* transcript analysis comparing WT and *Zeb1<sup>ff/f</sup>* *CD4Cre<sup>+</sup>* naive CD8<sup>+</sup> T cells. Two sets of primers were used for the quantitative RT-PCR detection: one set flanking exon 3–4 (outside of loxP region) and the other flanking exon 6–7 (covering part of loxP region). (c) ZEB1 protein detection using Western Blotting comparing WT and *Zeb1<sup>ff/f</sup>* *CD4Cre<sup>+</sup>* naive CD8<sup>+</sup> T cells. Data shown are representative of two (b and c) independent experiments; *n* = 2–3 mice/group/experiment (b and c). Data are expressed as mean ± SEM. \*\*\*, *P* < 0.001; \*\*\*\*, *P* < 0.0001.

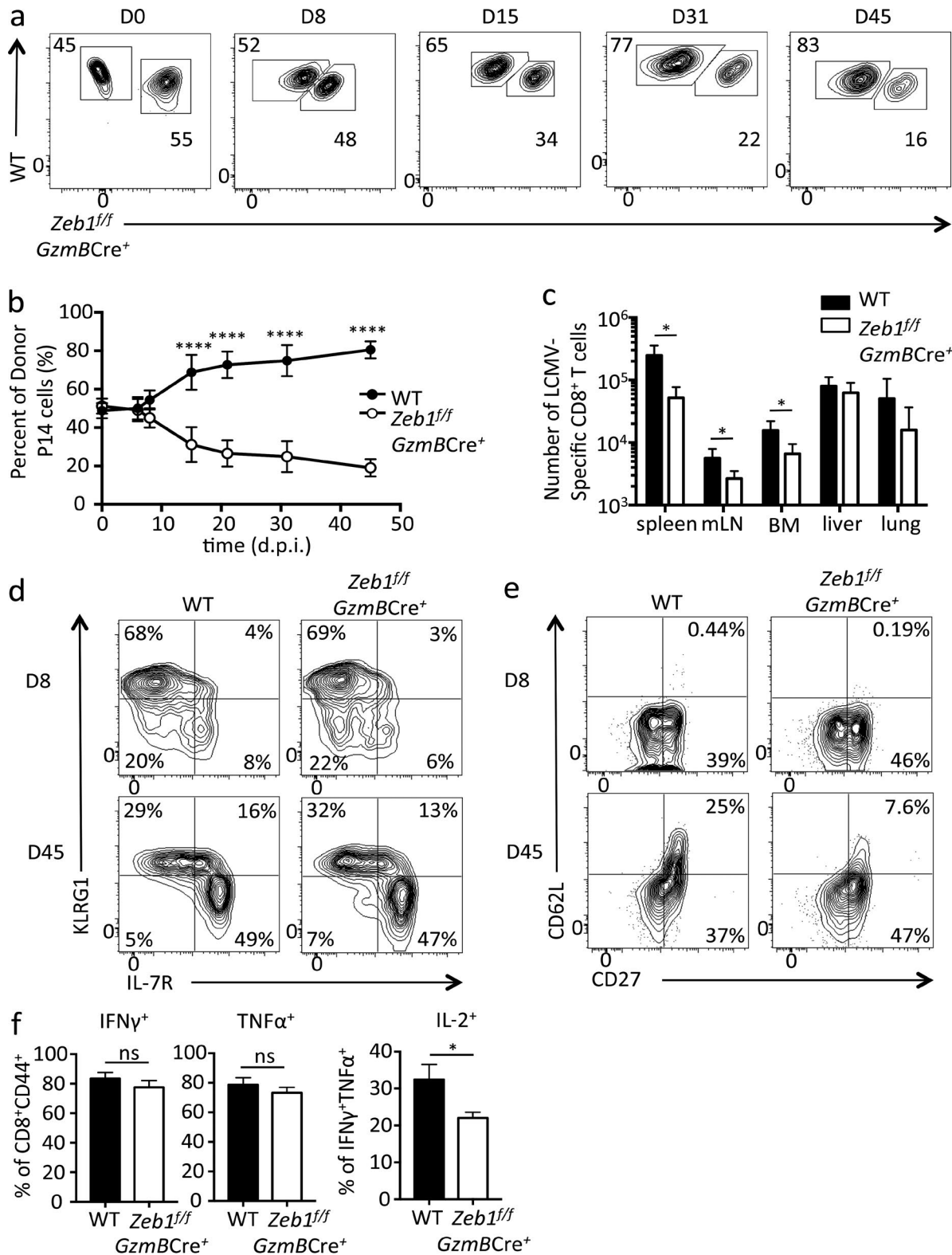


Figure S2. **ZEB1 plays an intrinsic role in promoting memory CD8<sup>+</sup> T cell survival.** (a–c) Time course analysis of the frequency (a and b) of WT and *Zeb1<sup>ff</sup>* *GzmBCre<sup>+</sup>* P14<sup>+</sup> CD8<sup>+</sup> T cells (Thy1.2/1.2) cotransferred equally into congenically mismatched (Thy1.1/1.1) naive B6 mice after LCMV-Arm infection. (c) Combined number ( $\pm$ SEM) of WT and *Zeb1<sup>ff</sup>* *GzmBCre<sup>+</sup>* P14<sup>+</sup> CD8<sup>+</sup> T cells in various tissues 30 dpi including spleen, mLN, bone marrow (BM), liver, and lung. (d and e) Flow plots show expression of KLRG1 and IL-7R (d) and CD62L and CD27 (e) of donor WT and *Zeb1<sup>ff</sup>* *GzmBCre<sup>+</sup>* P14<sup>+</sup> CD8<sup>+</sup> T cells at 8 and 45 dpi. (f) WT and *Zeb1<sup>ff</sup>* *GzmBCre<sup>+</sup>* P14<sup>+</sup> CD8<sup>+</sup> T cells from 30 dpi were analyzed for IFN $\gamma$  and TNF $\alpha$  (left two bar graphs) or IL-2 (right bar graph) expression using intracellular cytokine staining after a 5-h GP<sub>33–41</sub> peptide stimulation. Note, IL-2 producing cells were gated on IFN $\gamma$ <sup>+</sup> TNF $\alpha$ <sup>+</sup> P14<sup>+</sup> CD8<sup>+</sup> T cells. Data shown are representative of two (a, d, and e) or cumulative of two (b, c, and f) independent experiments;  $n = 3–5$  mice/group/experiment (a, d, and e);  $n = 6–10$  (b, c, and f). Data are expressed as mean  $\pm$  SEM. \*,  $P < 0.05$ ; \*\*\*\*,  $P < 0.0001$ .

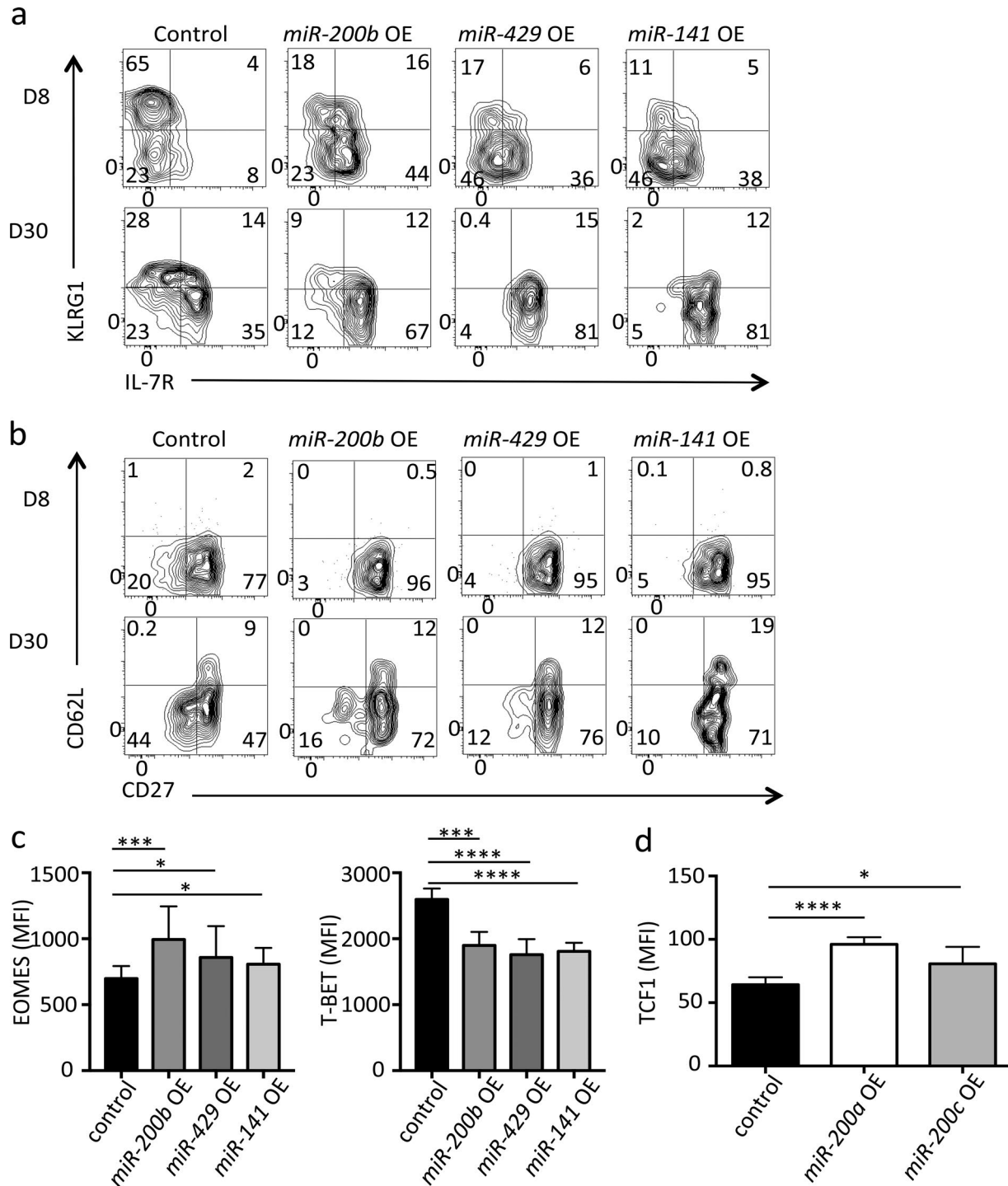


Figure S3. **Overexpression of *miR-200* family promotes memory CD8<sup>+</sup> T cell differentiation.** (a and b) Flow plots show expression of KLRG1 and IL-7R (a) CD62L and CD27 (b) in control, *miR-200b*, *miR-429*, and *miR-141* overexpressing P14<sup>+</sup> CD8<sup>+</sup> T cells 8 and 30 dpi. (c and d) Bar graphs show amounts of Eomes, T-bet (c), and TCF1 (d) in control, *miR-200a*, and *miR-200c* overexpressing P14<sup>+</sup> CD8<sup>+</sup> T cells 30 dpi. Data shown are representative of two (a and b) or cumulative of three (c and d) independent experiments; *n* = 3–5 mice per group per experiment (a and b), *n* = 8–10 (c). Data are expressed as mean ± SEM. \*, *P* < 0.05; \*\*\*, *P* < 0.001; \*\*\*\*, *P* < 0.0001.