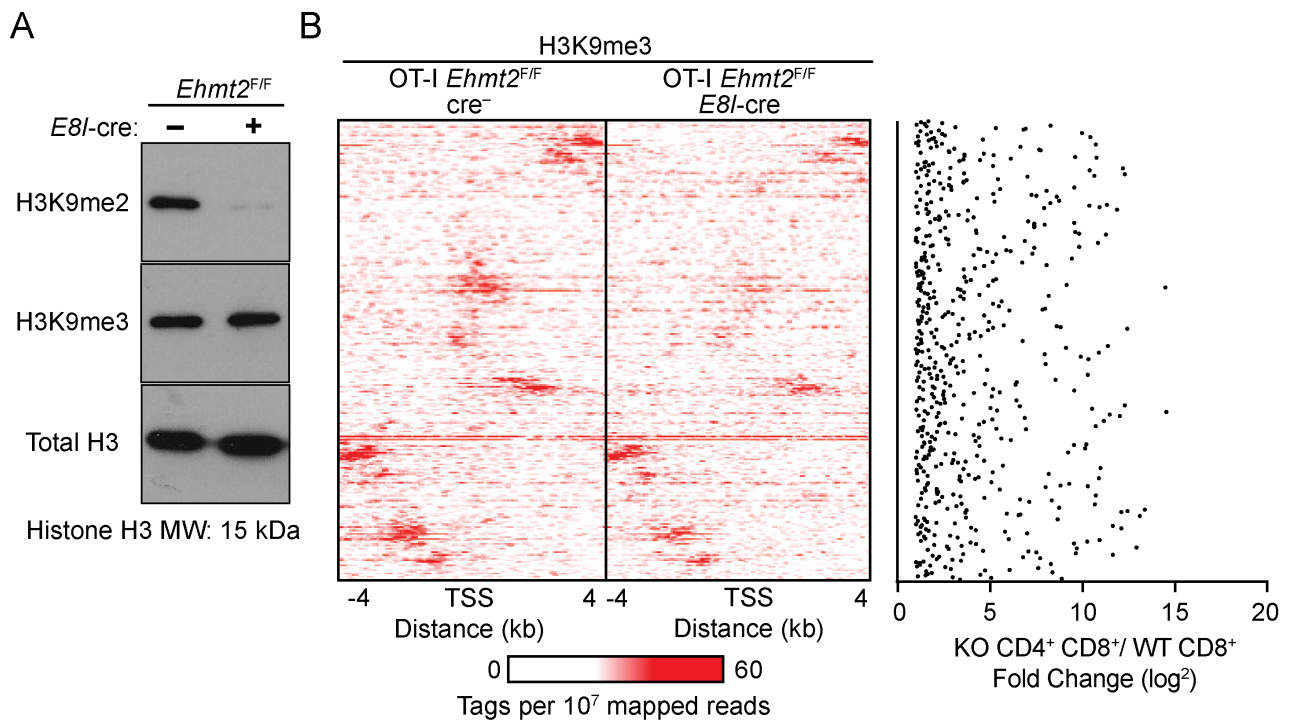


## Supplemental Data

Gene	Forward Primer	Reverse Primer
<i>Cd4</i>	5'-GGGCTGTGGCAGTGTCTACT-3'	5'-GACACAGCAGAGGATGCAGA-3'
<i>Rorc</i>	5'-TCTACGCTATGAGGAAGGAAGGC-3'	5'-GACTATGGAGGAGAAACAGGTCCC-3'
<i>Il21</i>	5'-GCTCCACAAGATGTAAAGGGGC-3'	5'-CCACGAGGTCAATGATGAATGTC-3'
<i>Cd40lg</i>	5'-GTGAGGAGATGAGAAGGCAA-3'	5'-CACTGTAGAACGGATGCTGC-3'
<i>Foxp3</i>	5'-AGAAGCTGGGAGCTATGCAG-3'	5'-TACTGGTGGCTACGATGCAG-3'
<i>Ctla4</i>	5'-GGATCCTTGTGCGAGTTAGC-3'	5'-TCACATTCTGGCTCTGTTGG-3'
<i>Aqp9</i>	5'-TGGGGATTTGAGGTCTTCAC-3'	5'-GTTTCGAGTGATGCATTTGGA-3'
<i>Zbtb7b</i>	5'-TGCTTCCGCATGTGGATC-3'	5'-GTGAGAAGCCCTTTGCCTGT-3'
<i>Ehmt2</i>	5'-TCATCCCTGTCCGGGTTTTTC-3'	5'-TCACCGTAGTCAAAGCCCA-3'
<i>Ehmt1</i>	5'-AAGCAAGAGACCAAGCAGGA-3'	5'-TGTGGAACCTTCATCAGCAG-3'
<i>Cd8a</i>	5'-CACAGGAGCCGAAAGCGT-3'	5'-GGGCTTGCCTTCCTGTCTG-3'
<i>Rora</i>	5'-CGCATTGATGGATTTATGGAG-3'	5'-TCGCATACTTCCCGTCAAAG-3'
<i>Kdm1a</i>	5'-TGGGATGGATGTCACACTTC-3'	5'-CTCGTCCACCTACTCGATCC-3'
<i>Kdm1b</i>	5'-GAGTATGCTTGTGGCAGCAG-3'	5'-GGGTATGGTCACCAGCAAAC-3'
<i>Kdm3a</i>	5'-TGTCGACTATTGAGCCACACA-3'	5'-TCCTTTGACAGCTCGTTTCC-3'
<i>Kdm3b</i>	5'-TGGAAGGCTCACTTGTTTGG-3'	5'-GGTATTCAACTGGCACCACAG-3'
<i>Kdm4c</i>	5'-ATGGATTGACTACGGCAAGG-3'	5'-CCATGTCATTCCGACAAGTG-3'
<i>Kdm7a</i>	5'-CAGCTCTACACGGCTCTTCC-3'	5'-ACAGGTTTGGAGCCATCATC-3'
<i>Phf8</i>	5'-GTGTGACATGTGCCAGGACT-3'	5'-TCCTCCTCAACACCAACACA-3'
<i>Setdb1</i>	5'-CACAAAGGCACCCTTATTGC-3'	5'-CGGGAGGGTGGTAATCATAG-3'
<i>Suv39h1</i>	5'-AGGGGAGGAAGAAGTGGAAC-3'	5'-CAGGTCCTGCAGTTGATTCC-3'
<i>Prdm2</i>	5'-CTCCACCTCTGCAAACATGA-3'	5'-ACTGCATCCTGGCTTACCAC-3'
<i>18S rRNA</i>	5'-CGGCTACCACATCCAAGGAA-3'	5'-GCTGGAATTACCGCGGCT-3'

**Supplemental Table 1. Sequences of primers used for quantitative PCR.**



**Supplemental Figure 1. De-repression of the helper lineage-associated genes in *Ehmt2<sup>-/-</sup>* cells is independent of H3K9 trimethylation.**

(A) Western blots showing amounts of H3K9me2, H3K9me3 or total H3 in CD8 T cells from *Ehmt2<sup>F/F</sup> Cd8-E8I-cre* mice and control *Ehmt2<sup>F/F</sup> cre<sup>-</sup>* mice. Data are representative of two experiments. (B) A heat map displaying the distribution of H3K9me3 ChIP-seq tags at the 637 genes that were identified from the RNA-sequencing data with at least a 2-fold higher expression in the CD4<sup>+</sup> CD8<sup>+</sup> *Ehmt2<sup>F/F</sup> Cd4-cre* mice compared to CD8<sup>+</sup> cells from control *Ehmt2<sup>F/F</sup> cre<sup>-</sup>* in Fig. 2C. Fold-changes of expression of those genes are plotted on the right panel.