CORRECTION

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Author Correction: Discovery of stimulation-responsive immune enhancers with CRISPR activation

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In this Letter, analysis of steady-state regulatory T (T_{reg}) cell percentages from *Il2ra* enhancer deletion (EDEL) and wild-type (WT) mice revealed no differences between them (Extended Data Fig. 9d). This analysis included two mice whose genotypes were incorrectly assigned. Even after correction of the genotypes, no significant differences in T_{reg} cell percentages were seen when data across experimental cohorts were averaged (as was done in Extended Data Fig. 9d). However, if we normalize the corrected data to account for variation among experimental cohorts, a subtle decrease in EDEL T_{reg} cell percentages is revealed and, using the corrected and normalized data, we have redrawn Extended Data Fig. 9d in Supplementary Fig. 1. The Supplementary Information to this Amendment contains the corrected and reanalysed Extended Data Fig. 9d. The sentence “This enhancer deletion (EDEL) strain also had no obvious T cell phenotypes at steady state (Extended Data Fig. 9)” should read: “This enhancer deletion (EDEL) strain had a small decrease in the percentage of T_{reg} cells (Extended Data Fig. 9)”. This error does not affect any of the main figures in the Letter or the data from mice with the human autoimmune-associated single nucleotide polymorphism (SNP) knocked in or with a 12-base-pair deletion at the site (12DEL). In addition, we stated in the Methods that we observed consistent immunophenotypes of EDEL mice across three founders, but in fact, we observed consistent phenotypes in mice from two founders. This does not change any of our conclusions and the original Letter has not been corrected.

Supplementary information is available for this Amendment at <https://doi.org/10.1038/s41586-018-0227-7>.