# Supporting Information

## Wesemann et al. 10.1073/pnas.1210286109

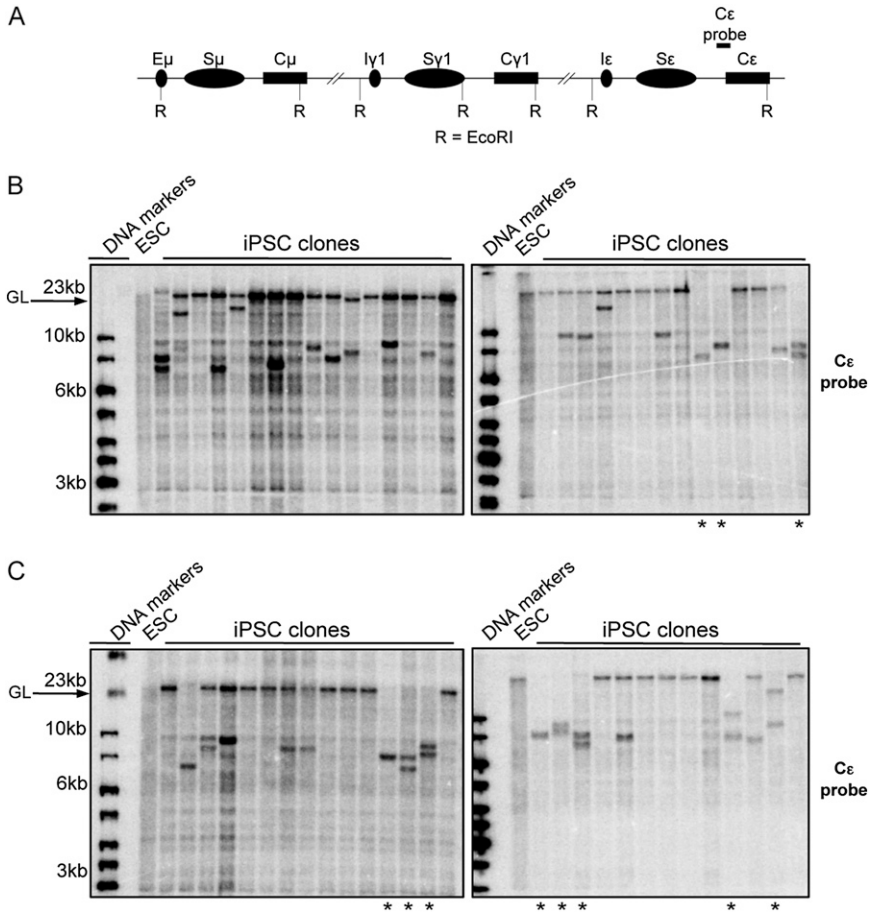


**Fig. S1.** *IgH* class-switched B cells can be reprogrammed to induced pluripotent stem cells (iPSCs). (*A*) A schematic of the IgH constant region. EcoRI (R) restriction sites and the location of the Cε probe are indicated. (*B* and *C*) Southern blot analysis of EcoRI-digested genomic DNA extracted from embryonic stem cells (ES cells) and iPSC clones reprogrammed from day 4 anti-CD40/IL-4–stimlulated B cells hybridized to a Cε probe. The germline (GL) band defined by EcoRI-digested ES cell DNA is indicated with an arrow and labeled. The first two lanes contain DNA size markers, and DNA sizes are indicated in kilobases on the left. Despite the relatively high amount of background signals arising with this probe, we mark lanes with asterisks (*) that clearly show two prominent bands that both differ from GL, indicating that these iPSC clones were likely derived from B cells that have undergone class-switch recombination (CSR) to IgE on both alleles.

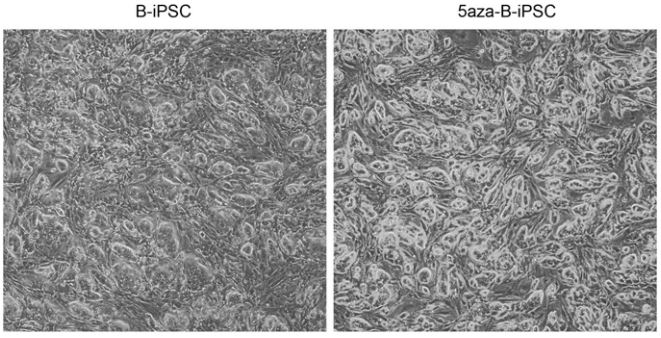


**Fig. S2.** (*Left*) iPSCs derived from activated B cells (B-iPSCs). (*Right*) iPSCs derived from activated B cells reprogrammed with the assistance of 5aza (5aza-B-iPSCs). These photographs are representative images indicating that there are no major morphological differences between B-iPSCs and 5aza-B-iPSCs.

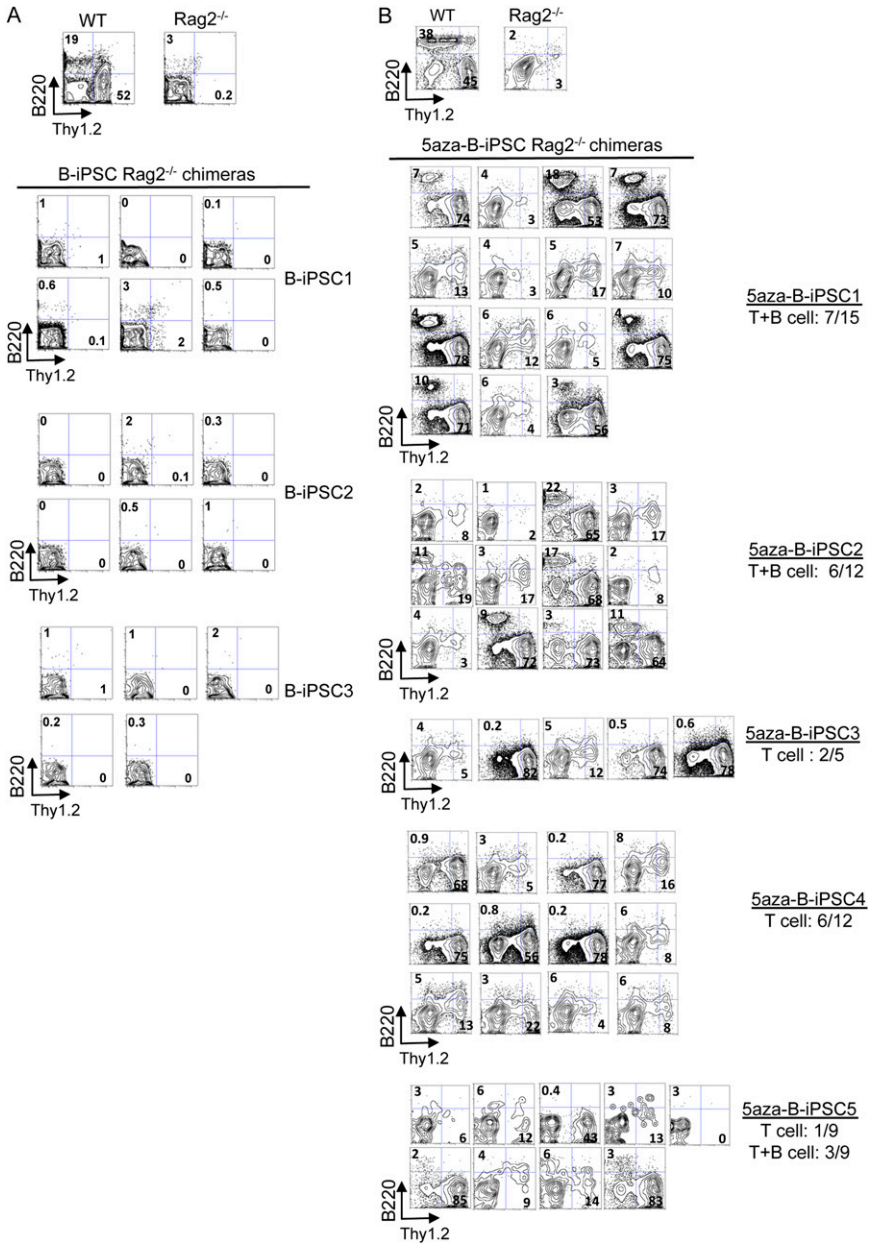


**Fig. S3.** *Meg3*$^{on}$ 5aza-B-iPSCs contribute to lymphocyte chimerism in *Rag2*$^{-/-}$ mice. (*A* and *B*) FACS plots of peripheral blood cells from *Rag2*-deficient blastocyst-complemented mice derived from B-iPSCs (*A*) or *Meg3*$^{on}$ 5aza-B-iPSCs (*B*) stained for surface expression of B220 and Thy1.2. Peripheral blood cells from WT and *Rag2*$^{-/-}$ were stained as positive and negative controls, respectively (*A* and *B*, *Top*). Each FACS plot represents an individual mouse derived from the iPSC clone indicated to the right. T-cell chimerism is defined by the presence of a distinct population of Thy1.2$^{+}$ cells in the lower right quadrant. T + B cell chimerism is defined by the presence of a distinct population of B220$^{+}$ cells in the upper left quadrants together with Thy1.2$^{+}$ cells in the lower right quadrants. There were no T or T + B-cell chimeras in the 17 mice derived from all three of the B-iPSCs tested (*A*). The T and T + B-cell chimeras from 5aza-B-iPSC–derived mice are indicated as a fraction of total chimeras on the right (*B*).

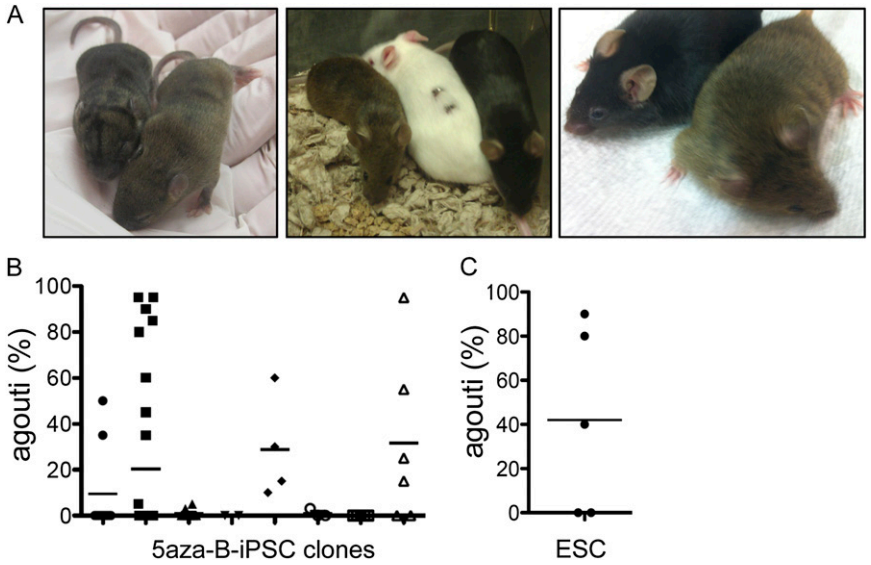


**Fig. S4.** *Meg3*$^{on}$ 5aza-B-iPSCs can form high-grade coat color chimeras. (*A*) Photographs of chimeric mice derived by injecting 5aza-B-iPSCs (agouti) into blastocysts derived from C57BL/6 mice (black). (*A*) (*Left*) Photograph of a 35% agouti chimera (*Left*) and an 85% agouti chimera (*Right*). (*Center*) Photograph of a 90% agouti chimera, a balb/c surrogate mother (white coat) and a 0% agouti chimera (black coat). (*Right*) Photograph of a 95% agouti chimera next to a 0% chimera. (*B* and *C*) Plots indicating percentage of agouti coat color. Each point on the graph indicates an individual chimeric mouse derived from separate *Meg3*$^{on}$ 5aza-B-iPSC (*B*) or TC1 ES cell (*C*) (also agouti) clones.

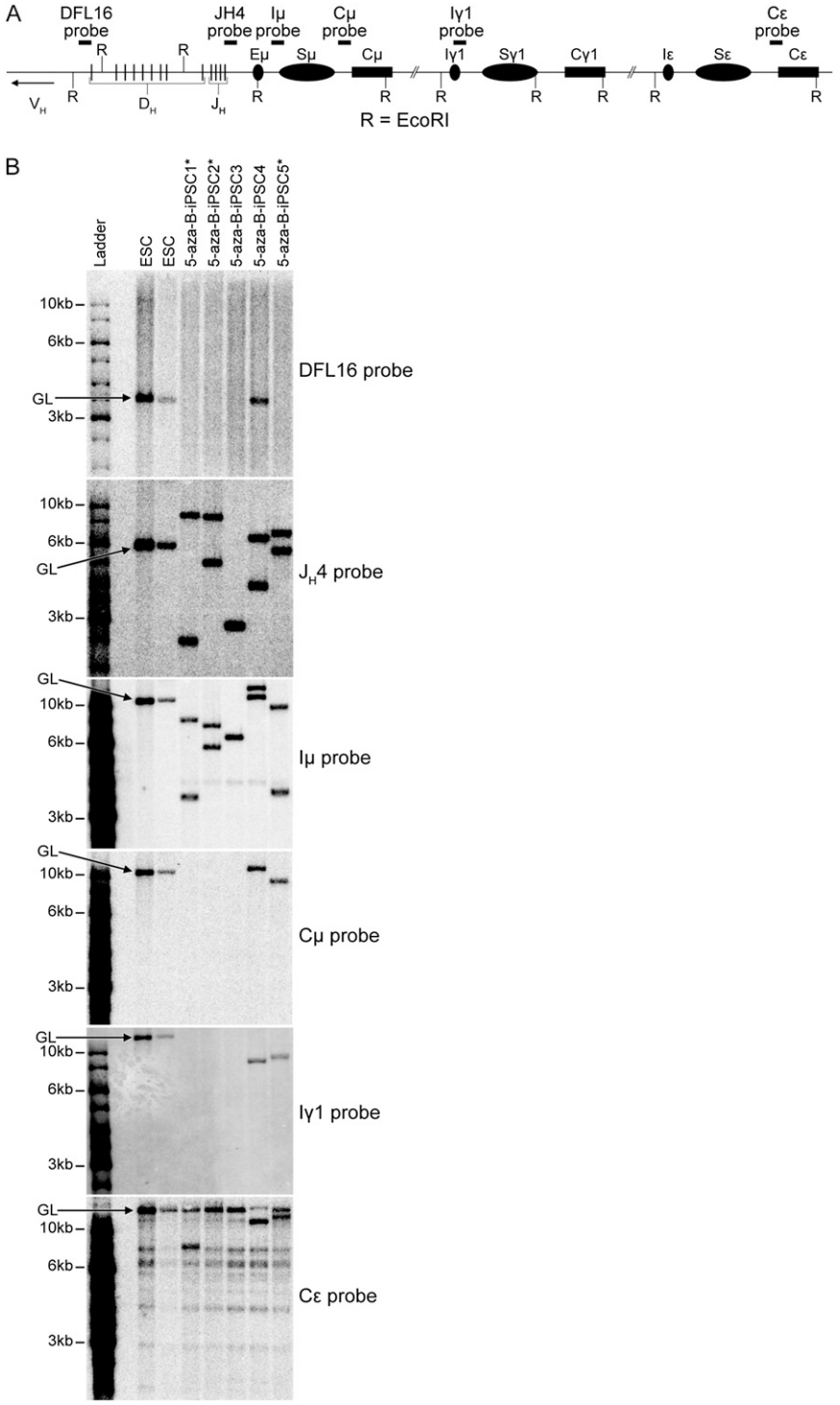


**Fig. S5.** Southern blot analysis of 5aza-B-iPSC. (*A*) A schematic of the IgH constant region. EcoRI (R) restriction sites and the location of the Southern blot probes are indicated. (*B*) Southern blot analysis of EcoRI-digested genomic DNA extracted from ES cells and the 5aza-B-iPSCs used for RDBC. The germline band defined by EcoRI-digested ES cell DNA is indicated with an arrow and labeled as GL. The lane contains a DNA size marker, and DNA sizes are indicated in kilobases on the left. 5aza-B-iPSCs that support T- + B-cell chimerism are marked with an asterisk (*). The absence of a DFL16 signal indicates an allele that has undergone V-to-DJ recombination. The presence of a $J_H$4 signal that differs from germline configuration indicates an allele that has undergone D-to-J or V-to-DJ recombination. The presence of an Iμ signal that differs from germline indicates an allele that has undergone either internal switch deletions (ISD) or CSR. The absence of a Cμ or Iμ signal indicates an allele that has undergone CSR. The presence of a Cε signal that differs from germline configuration indicates an allele that has undergone CSR or ISD involving Sε.