

## Expanded View Figures

**Figure EV1. Gating strategies for the assessment of B- and T-cell populations in WT and *Shld2*<sup>-/-</sup> mice.**

- A Gating strategies used to quantitate Hardy fractions A-F of progenitor B-cells in bone marrows of WT and *Shld2*<sup>-/-</sup> mice.
- B Gating strategies used to quantitate immature, mature, T1, T2, MZ, and FO B-cell populations in the spleen of WT and *Shld2*<sup>-/-</sup> mice.
- C Gating strategies used to quantitate B1, B2, B1a, and B1b populations in the peritoneal cavity of WT and *Shld2*<sup>-/-</sup> mice.
- D Gating strategies used to quantitate various thymocyte populations in WT and *Shld2*<sup>-/-</sup> mice.
- E Insertion-deletion (indel) penetrance was measured by TIDE sequencing for the lentiCRISPRv2 constructs expressing the indicated sgRNAs targeting the *53bp1*, *Shld1*, *Shld2*, *Shld3*, and *Lig4* genes.
- F Baseline GFP frequency of bulk gene-edited A70.2 cells prior to imatinib stimulation (Fig 1F).

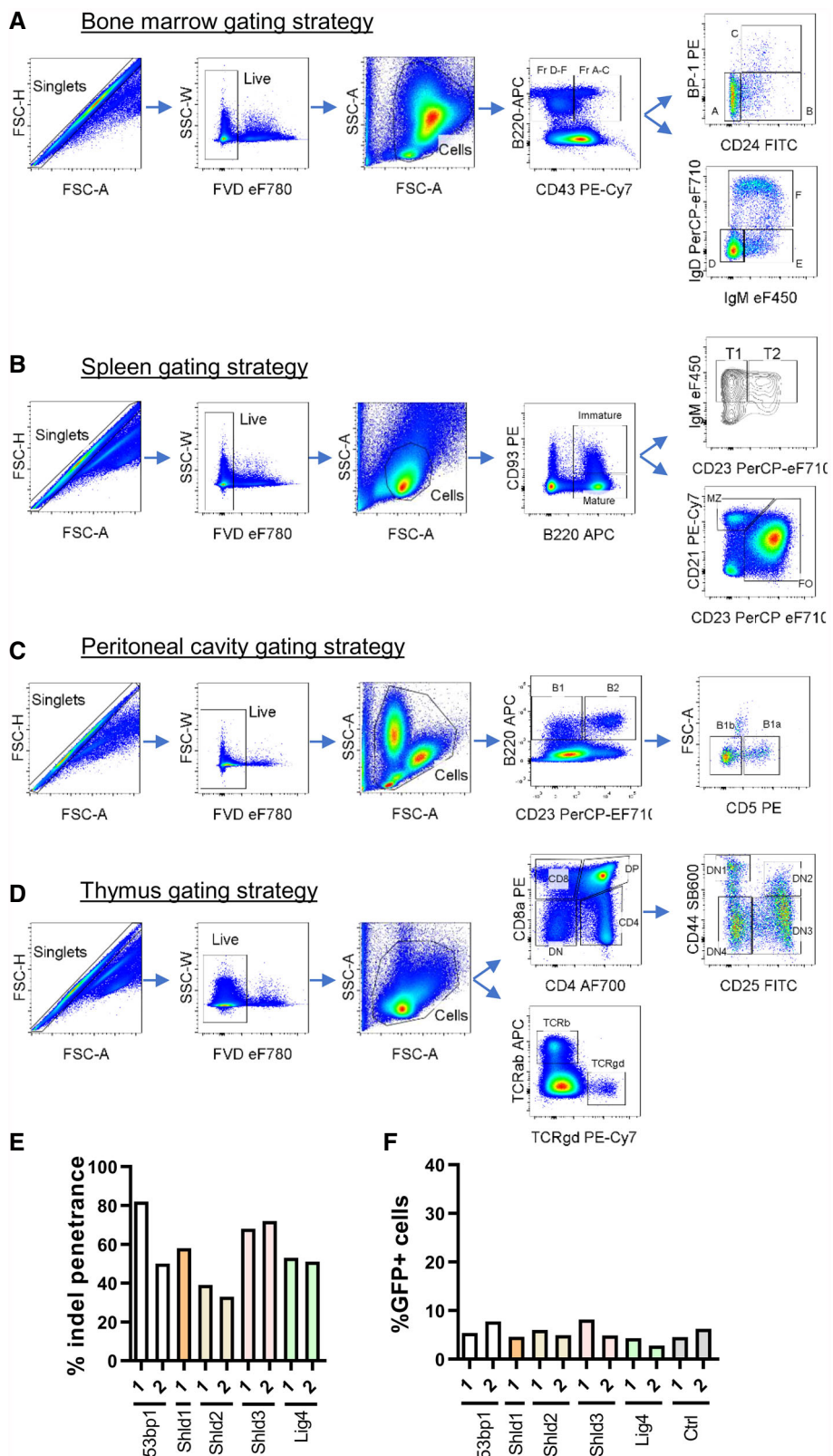
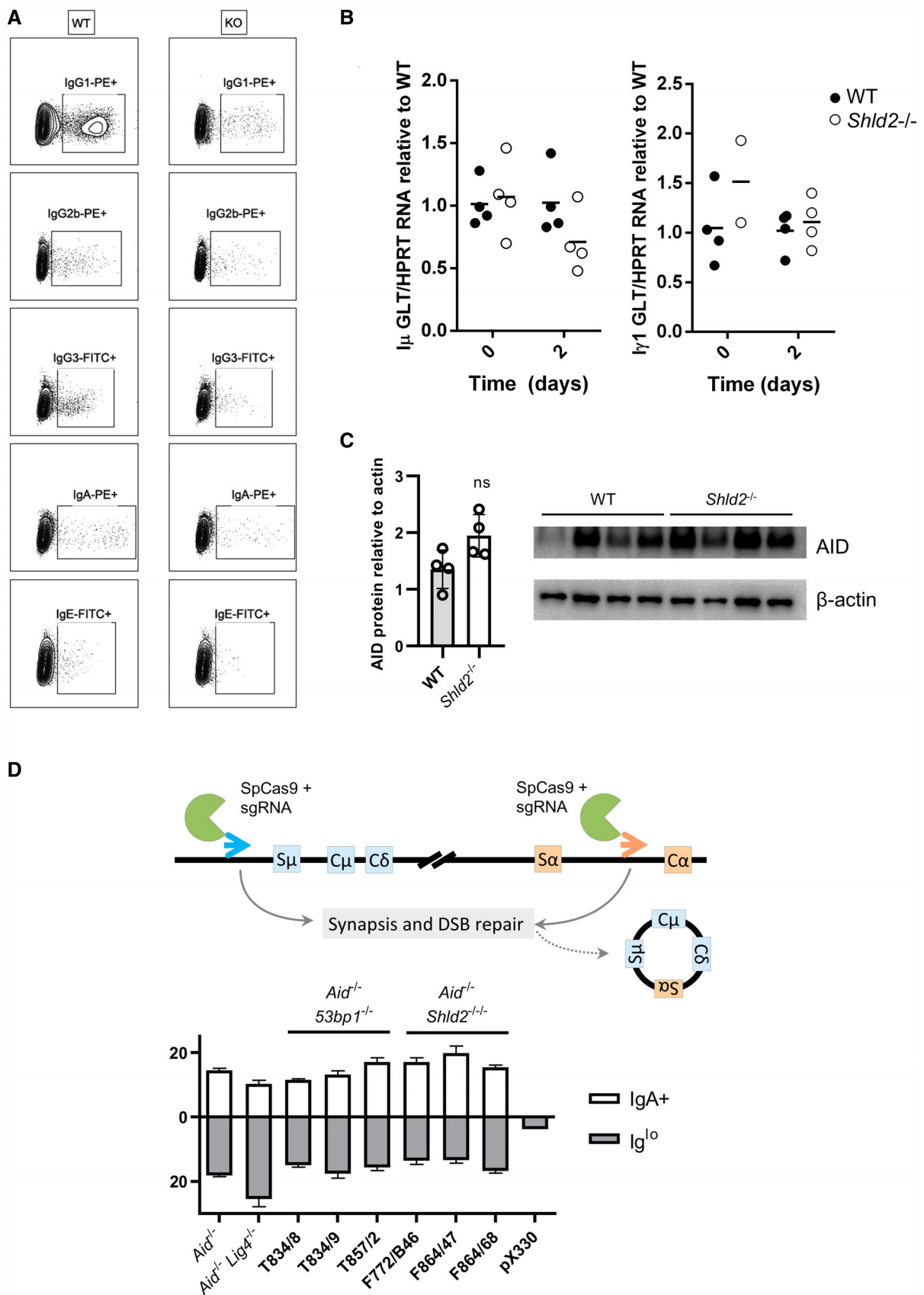
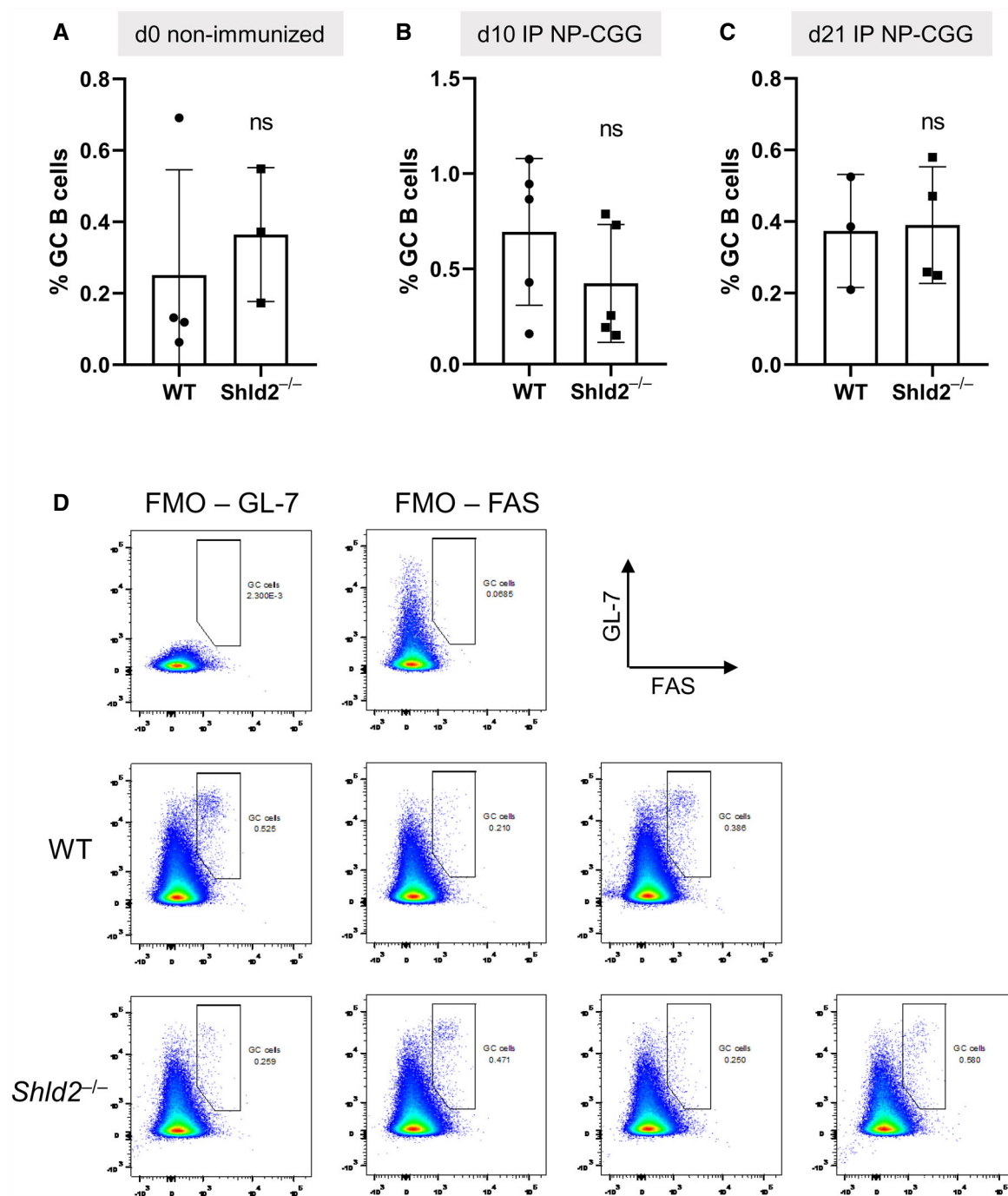


Figure EV1.

**Figure EV2. Sterile transcript or AID protein levels were unaffected in *Shld2*<sup>-/-</sup> B-cells.**

- A Representative flow plots of switched *ex vivo* B-cells in Fig 2B.
- B Purified splenic B-cells from WT and *Shld2*<sup>-/-</sup> mice were unstimulated or stimulated for 2 days with LPS + IL4, and germline (sterile) transcripts for I $\mu$  (left panel) and I $\gamma$ 1 (right panel) were quantitated by qPCR and compared to HPRT mRNA levels. Data are shown relative to WT, which is set at 1.
- C Lysates of purified splenic B-cells from WT and *Shld2*<sup>-/-</sup> mice that were stimulated for 3 days with LPS + IL4 and subjected to Western blot analyses for AID and the internal control  $\beta$ -actin.
- D Cas9-induced switching was carried out on *Aid*<sup>-/-</sup>, *Aid*<sup>-/-</sup> *Lig4*<sup>-/-</sup>, *Aid*<sup>-/-</sup> *53bp1*<sup>-/-</sup>, and *Aid*<sup>-/-</sup> *Shld2*<sup>-/-/-/-</sup> CH12 clones and switching to IgA was measured 3 days post-transfection. The percent of Ig<sup>lo</sup> cells is also reported. Transfection with the empty vector pX330 served as negative control. Values are mean frequency  $\pm$  SD of 3 biological replicates; \**P*  $\leq$  0.05, \*\**P*  $\leq$  0.01, \*\*\**P*  $\leq$  0.001, \*\*\*\**P*  $\leq$  0.0001, two-way ANOVA with *post hoc* Dunnett's test.





**Figure EV3. Germinal center B-cell frequency is not affected by SHLD2 deficiency.**

- A Germinal B-cell (GL-7<sup>+</sup> Fas<sup>+</sup>) frequency relative to all B-cells (B220<sup>+</sup>) in the spleen in unimmunized mice; mean  $\pm$  SD of 3 or 4 biological replicates, ns  $P \geq 0.05$ , unpaired two-tailed  $t$ -test.
- B As in A, but at day 10 post-NP-CGG immunization; mean  $\pm$  SD of 4 or 5 biological replicates, ns  $P \geq 0.05$ , unpaired two-tailed  $t$ -test.
- C As in A, but at day 21 post-NP-CGG immunization; mean  $\pm$  SD of 3 or 4 biological replicates, ns  $P \geq 0.05$ , unpaired two-tailed  $t$ -test.
- D Representative flow plots of fluorescence minus one (FMO) controls and day 21 data points.

**Figure EV4. CSR induces a permanent loss of Ig expression in CH12 cells.**

- A The indicated NHEJ-mutant CH12 clones were stimulated with CIT and analyzed by flow cytometry for IgM and IgA expression at days 3 and 7; mean  $\pm$  SD of 3 biological replicates.
- B WT, *53bp1*<sup>-/-</sup>, *Shd2*<sup>-/-</sup>, and *Shd3*<sup>-/-</sup> CH12 clones were stimulated with CIT for 3 days. The IgM<sup>+</sup>, IgA<sup>+</sup>, and Ig<sup>lo</sup> populations were sorted and reanalyzed for expression of IgM and IgA 12 days post-sort. Shown on bar graphs are sorted IgM<sup>+</sup>, IgA<sup>+</sup>, and Ig<sup>lo</sup> populations (each column, 1 technical replicate) from WT and mutant CH12 clones, and the percent of cells expressing IgM, IgA, or low for both isotypes (Ig<sup>lo</sup>) after 12 days of culture post-sort.

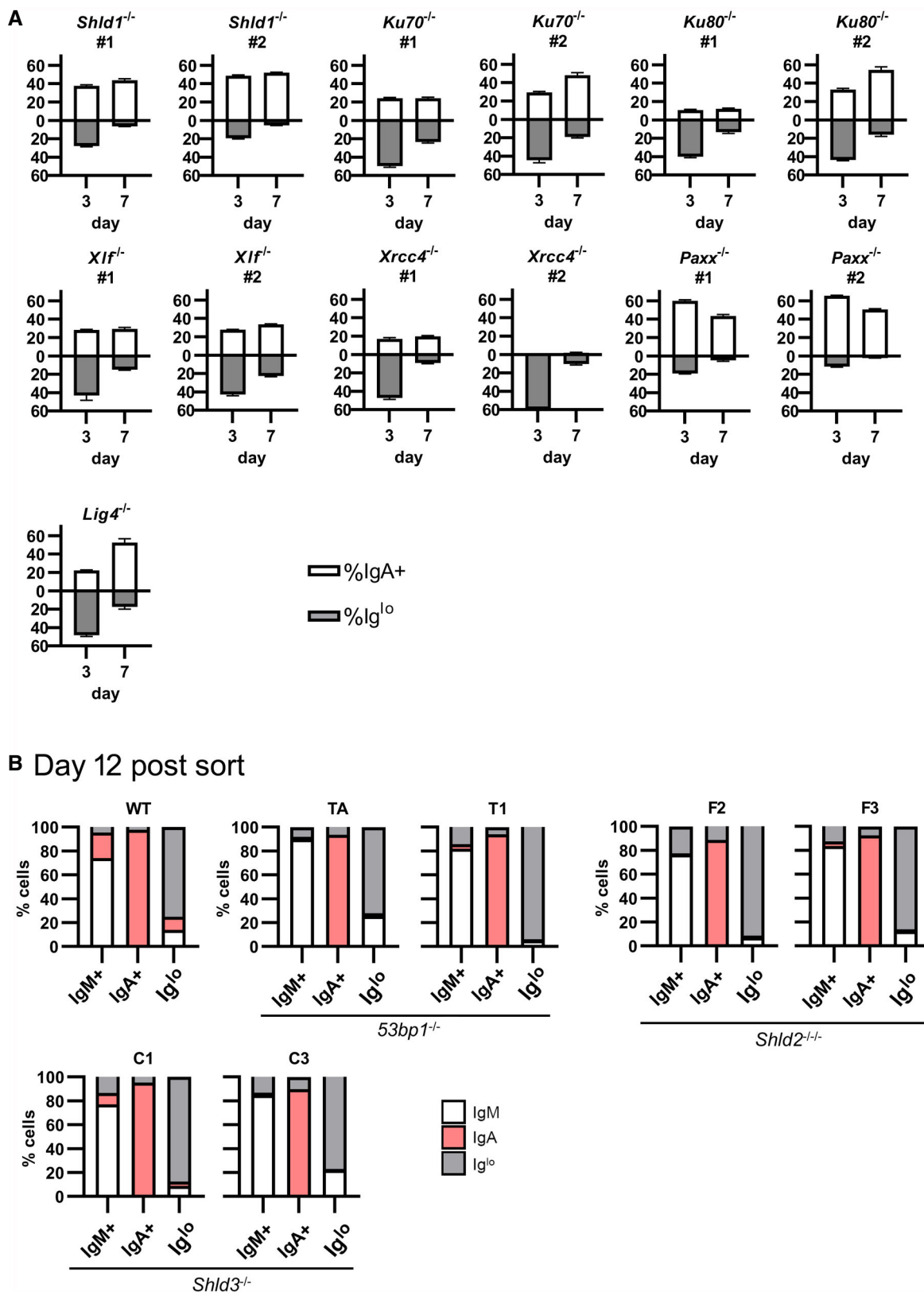
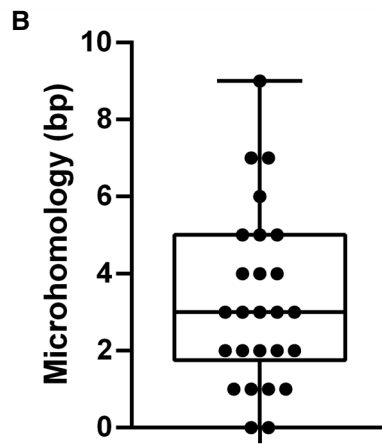
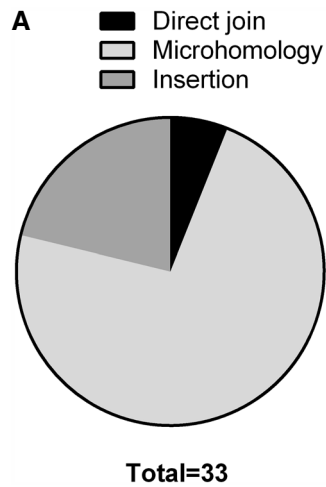


Figure EV4.



**Figure EV5. Repair junctions in  $Ig^{lo}$  cells have characteristics of alternative end joining.**

- A Categorization of *Ighm-Igha* junctions from sequences in Fig 6D, separated into junctions incorporating DNA insertion, microhomology, or neither in the form of direct joins.
- B Microhomology distribution of *Ighm-Igha* junctions from sequences in Fig 6D, except for those with insertions (26 independent sequences from one experiment). Median and lower/upper quartiles defined by box, and whiskers represent minimum and maximum values.