SUPPLEMENTAL MATERIAL

Bednarski et al., http://www.jem.org/cgi/content/full/jem.20151048/DC1

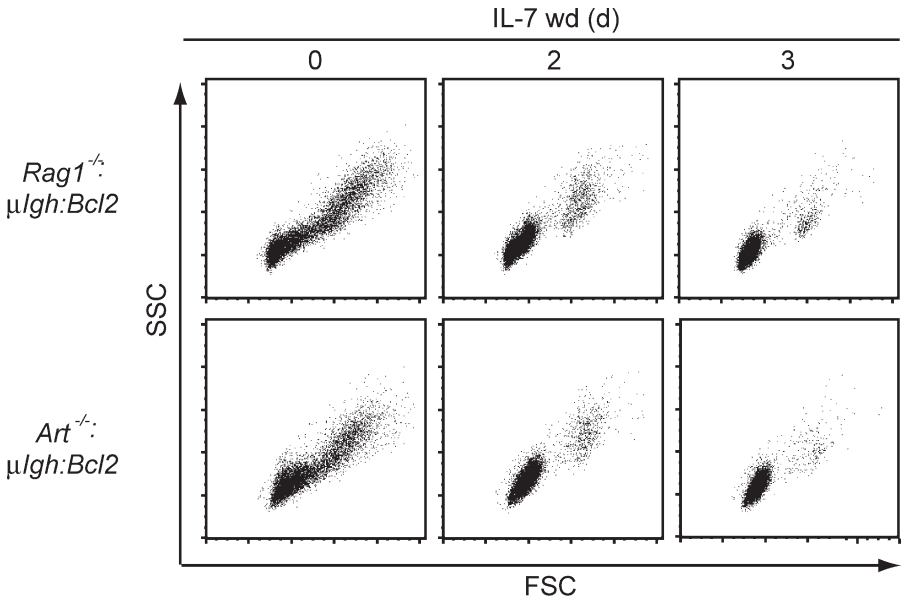

Figure S1. **Analysis of RAG DSB responses in pre–B cell cultures.** Bone marrow pre–B cells were cultured in the presence of IL-7 (0 d) and subsequently withdrawn from IL-7 (IL-7 wd) for the indicated days. Flow cytometric analysis of *Rag1*$^{-/-}$*:μIgH:Bcl2* and *Art*$^{-/-}$*:μIgH:Bcl2* pre–B cell cultures showing forward scatter (FSC, x axis) and side scatter (SSC, y axis).

Table S1, available as an Excel file, signals from RAG DSBs regulate the genetic program of small pre–B cells. Gene expression arrays were conducted on *Rag1*$^{-/-}$*:μIgH:Bcl2* and *Art*$^{-/-}$*:μIgH:Bcl2* pre–B cells in the presence of IL-7 (0 d) and 2 d after IL-7 withdrawal. Fold changes and p-values were calculated based on the mean of three cell lines for each genotype. Only those genes with a fold change of $\geq$1.5 and P $\leq$ 0.05 were considered for further analysis. Comparison of *Rag1*$^{-/-}$*:μIgH:Bcl2* pre–B cells in IL-7 (RAG_0d) and after IL-7 withdrawal (RAG_2d) identified genes changed upon transition from large (in IL-7) to small (2 d after IL-7 withdrawal) pre–B cells. *Rag1*$^{-/-}$*:μIgH:Bcl2* (RAG_2d) and *Art*$^{-/-}$*:μIgH:Bcl2* (ART_2d) were compared after IL-7 withdrawal to identify RAG DSB–dependent gene expression changes. Table includes all probes.

Table S2, available as an Excel file, NF-κB2 coordinates a cohort of gene expression changes in response to RAG DSBs. Gene expression arrays were conducted on *Art*$^{-/-}$*:μIgH:Bcl2* (ART) and *Art*$^{-/-}$*:Nfkb2*$^{-/-}$*:μIgH:Bcl2* (ART:NFkB2) small pre–B cells 2 d after IL-7 withdrawal. Data were analyzed as described in Fig. 3 A and Table S1. Table includes all probes.

Table S3, available as an Excel file, shows primer sequences used for RT-PCR and ChIP-qPCR.