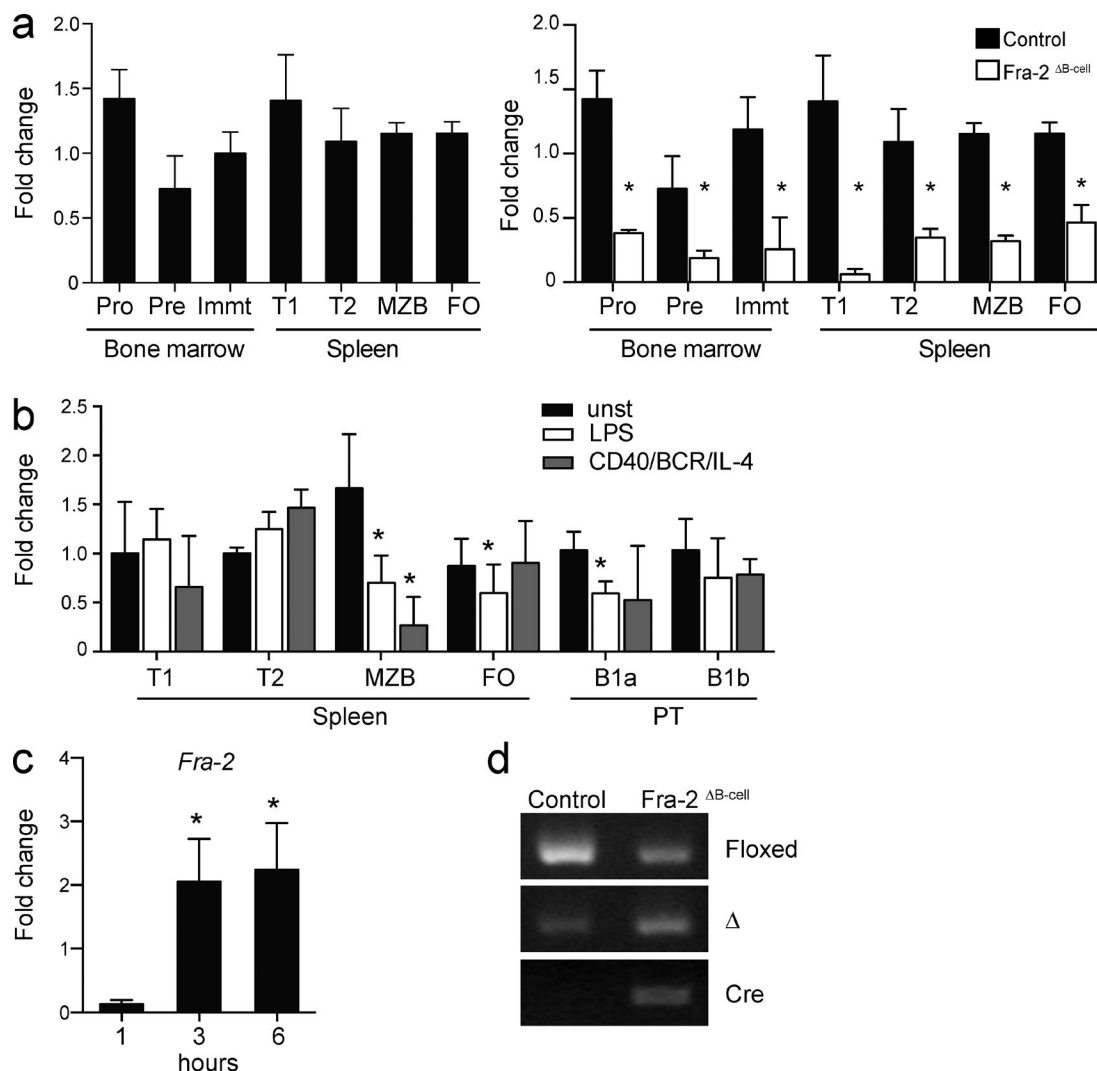


# SUPPLEMENTAL MATERIAL

Ubieta et al., <https://doi.org/10.1084/jem.20160514>



**Figure S1. Expression of *Fra-2* in B cell lineage.** (a) Real-time PCR analyses of *Fra-2* mRNA abundance in bone marrow B cell subsets (pro-, pre-, and immature [immt] B cells) and B cell subsets isolated from spleen (T1, T2, MZB, and FO B cells) of *Fra-2*<sup>ΔB-cell</sup> and littermate control mice. Relative expression to housekeeping genes ( $n = 5-6$ ). (b) Real-time PCR analyses of *Fra-2* mRNA levels in unstimulated or in 6 h LPS, LPS+IL4, or CD40/BCR/IL4 stimulated splenic T1, T2, MZB, and FO and peritoneal B1 littermate control B cells. (c) Real-time PCR analyses of *Fra-2* mRNA levels in pro-B cells after 3 and 6 h of IL-7 stimulation ( $n = 5$ ). Different B cell subsets were sorted by flow cytometry. Relative expression to housekeeping genes. (d) Genotyping PCR of MACS-sorted B220<sup>+</sup> cells from bone marrow of WT C57BL/6 mice. Bars represent mean values  $\pm$  SD. Data show one representative out of three independent experiments. Statistical analyses were performed using Student's  $t$  test; \*,  $P < 0.05$ . PT, peritoneal cavity; Unst, unstimulated.

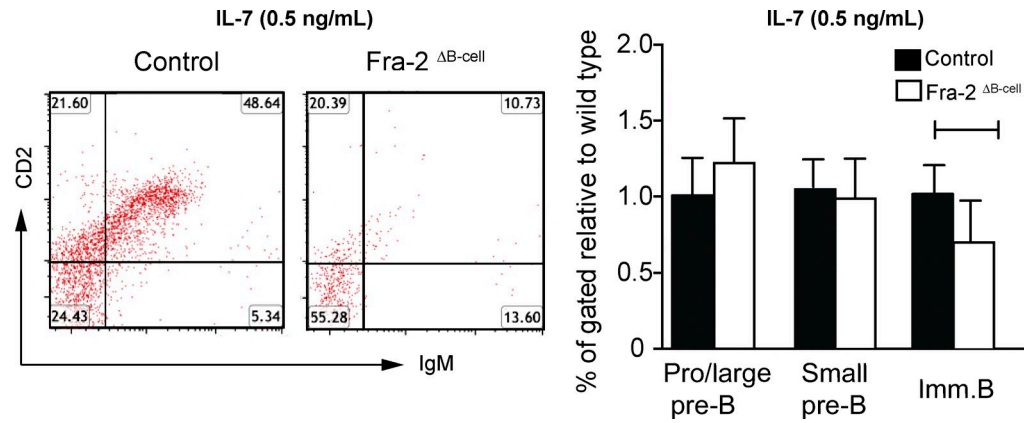


Figure S2. **In vitro IL-7 stimulations of B cells from Fra-2<sup>ΔB-cell</sup> and littermate control mice.** Flow cytometry analysis of pro/large pre-B cells, small pre-B cells, and immature B cells after 5 d of stimulation with IL-7 (0.05 and 5 ng/ml). Bars represent mean values ± SD (*n* = 5). Data show one representative out of three independent experiments. Statistical analyses were performed using Student's *t* test.

a

Rank	Motif	P-value	log P-value	% of Targets	% of Backgrounds	STD (Bg STD)	Best Match/Details	Motif File
1	AAAAAAAAAAAA	1e-136	-3.143e+02	84.41%	21.13%	13.9bp (126.5bp)	PB0182.1_Srf_2/Jaspar(0.837) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
2	GAGAAACCTCTGT	1e-41	-9563e+01	35.29%	8.66%	42.8bp (110.7bp)	PH0163.1_Six3/Jaspar(0.610) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
3	CCATTCCATCC	1e-35	-8.174e+01	4.71%	0.02%	33.6bp (27.3bp)	PB0098.1_Zfp410_1/Jaspar(0.635) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
4	TGTATCCTCGG	1e-35	-8.139e+01	42.35%	14.32%	54.5bp (108.4bp)	TEAD2(TEA)/Py2T-Tea2-ChIP-Seq(GSE55709)/Homer(0.580) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
5	CCCTGCT	1e-32	-7.418e+01	45.88%	17.72%	58.7bp (107.9bp)	SD0002.1_at_AC_acceptor/Jaspar(0.677) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
6	GCCTCAGGCTCA	1e-29	-6.812e+01	27.94%	7.35%	48.0bp (111.9bp)	MA0146.2_Zfx/Jaspar(0.632) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
7	CGAGTCTTAGGA	1e-27	-6290e+01	26.76%	7.24%	59.3 bp (110.3bp)	PB0181.1_Spdef_2/Jaspar(0.573) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
8	CTGGGATTAG	1e-23	-5291e+01	18.24%	3.93%	62.7bp (113.6bp)	Pitx1(Homeobox)/Chicken-Pitx1-ChIP-Seq(GSE38910)/Homer(0.706) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
9	CACTCCACTCCA	1e-20	-4.767e+01	2.65%	0.01%	27.3bp (38.9bp)	MA0130.1_ZNF354C/Jaspar(0.645) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
10	GTGGAGTCTCAT	1e-20	-4.767e+01	2.65%	0.01%	9.4bp (24.0bp)	MA0130.1_ZNF354C/Jaspar(0.696) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
11	TGGAAGCTCAG	1e-20	-4.704e+01	30.29%	11.32%	55.1bp (106.0bp)	PH0037.1_Hdx/Jaspar(0.623) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
12	GCAGGCCT	1e-20	-4.617e+01	28.82%	10.51%	45.8bp (109.5bp)	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer(0.817) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
13	AAATCCGCCT	1e-16	-3.739e+01	21.76%	7.43%	47.2bp (103.3bp)	PH0122.1_Obox2/Jaspar(0.643) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
14	GAGCTAATA	1e-14	-3.352e+01	7.65%	1.00%	60.7bp (105.4bp)	MA0072.1_RORA_2/Jaspar(0.652) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
15	TTATCTTAGCT	1e-13	-3.079e+01	2.06%	0.01%	31.5bp (28.1bp)	MA0029.1_Mecom/Jaspar(0.686) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
16	GCTGAACATGTA	1e-12	-2.879e+01	2.35%	0.03%	57.5bp (33.1bp)	PH0085.1_Irx4/Jaspar(0.679) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
17*	GGTGGTTTTGAT	1e-11	-2.759e+01	1.47%	0.00%	2.4bp (31.0bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer(0.699) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
18*	ATTAAGG	1e-11	-2.618e+01	14.41%	4.69%	61.9bp (103.8bp)	MA0151.1_ARID3A/Jaspar(0.806) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
19*	GGCTCATGCC	1e-10	-2.448e+01	2.65%	0.08%	47.0bp (58.4bp)	PB0147.1_Max_2/Jaspar(0.597) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
20*	TAACAAATGG	1e-10	-2.402e+01	7.35%	1.41%	58.5bp (90.2 bp)	PB0119.1_Foxa2_2/Jaspar(0.831) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>

Motif 17 RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer

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Score: 0.70  
Offset: -2  
Orientation: reverse strand  
Alignment: --GGTGGTTTTGAT  
NNTGGTTTT---

PB0035.1\_Irf5\_1/Jaspar

Match rank: 2  
Score: 0.67  
Offset: -1  
Orientation: reverse strand  
Alignment: GGTGGTTTTGAT----  
-NTGGTTTCGGTNNN

PB0034.1\_Irf4\_1/Jaspar

Match rank: 3  
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Orientation: reverse strand  
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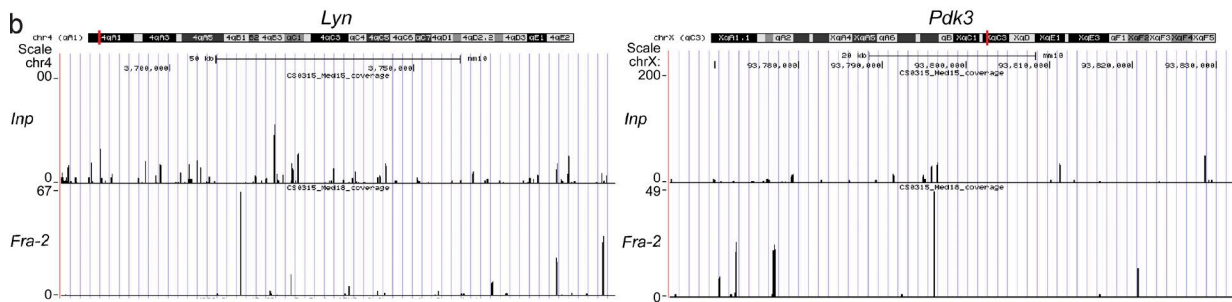


Figure S3. **Fra-2** recognition sequence in B220<sup>+</sup> bone marrow B cells. (a) Consensus Fra-2 recognition sequence in B220<sup>+</sup> bone marrow B cells of WT mice identified by ChIP-seq analyses. (b) ChIP-seq analysis of the binding of Fra-2 at *Lyn* and *pdk3* promoters ( $n = 3$ ) performed in B220<sup>+</sup> B cells from control mice.

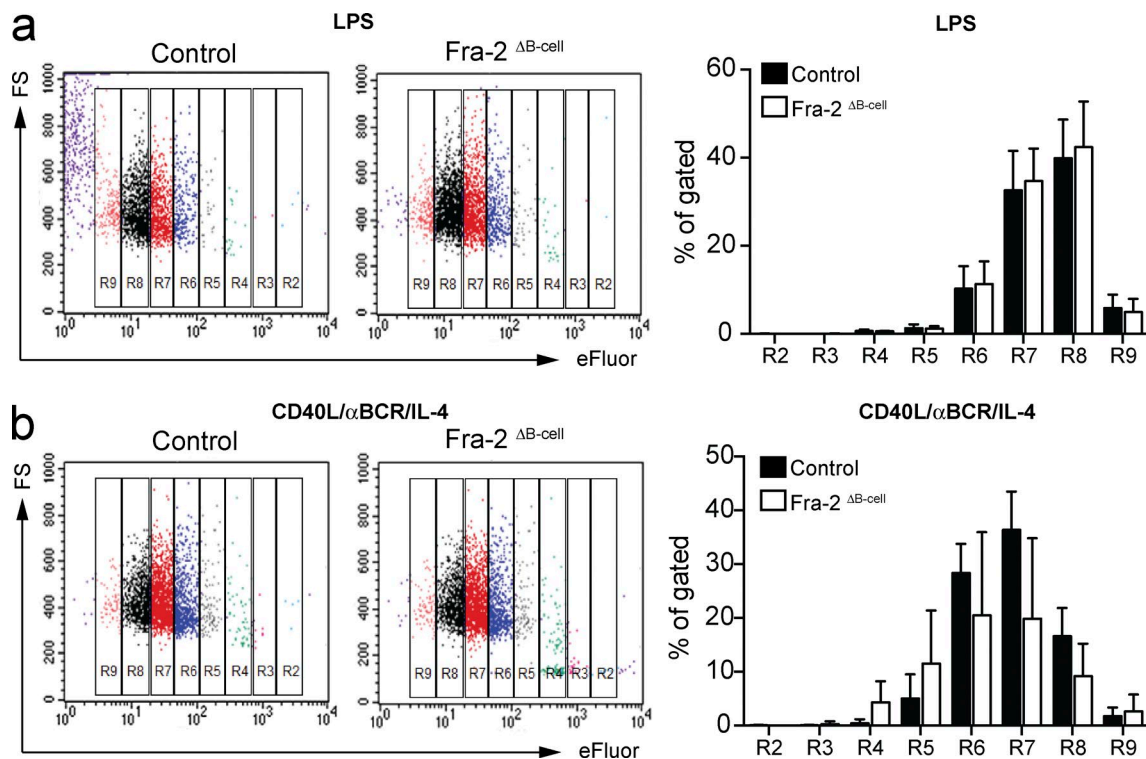


Figure S4. **In vitro LPS or CD40/BCR/IL-4 stimulations of Fra-2 $\Delta$ B cell and littermate control B cells.** (a and b) Flow cytometry analysis of the proliferation rate in Fra-2 $\Delta$ B cell and littermate control pro-B cells after 3 d of LPS or CD40/BCR/IL-4 stimulation. Bars represent mean values  $\pm$  SD ( $n = 3$ ). Data show one representative out of three independent experiments.

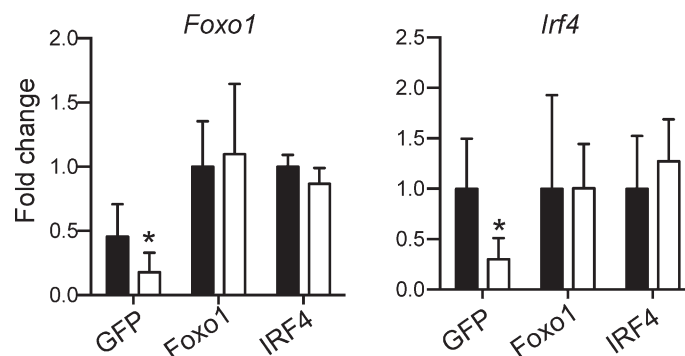


Figure S5. **Rescue expression of B cell genes.** Real-time PCR analysis of *Foxo1* and *Irf4* genes of pro-B cell culture after infection with IRES-GFP, IRES-Foxo1-GFP, and IRES-Irf4-GFP expressing retrovirus and after stimulation with IL-7 for 5 d ( $n = 5$ ). Bars represent mean values  $\pm$  SD ( $n = 5$ ). Data show one representative out of three independent experiments. Statistical analyses were performed using Student's *t* test; \*,  $P < 0.05$ .