

Supporting Information

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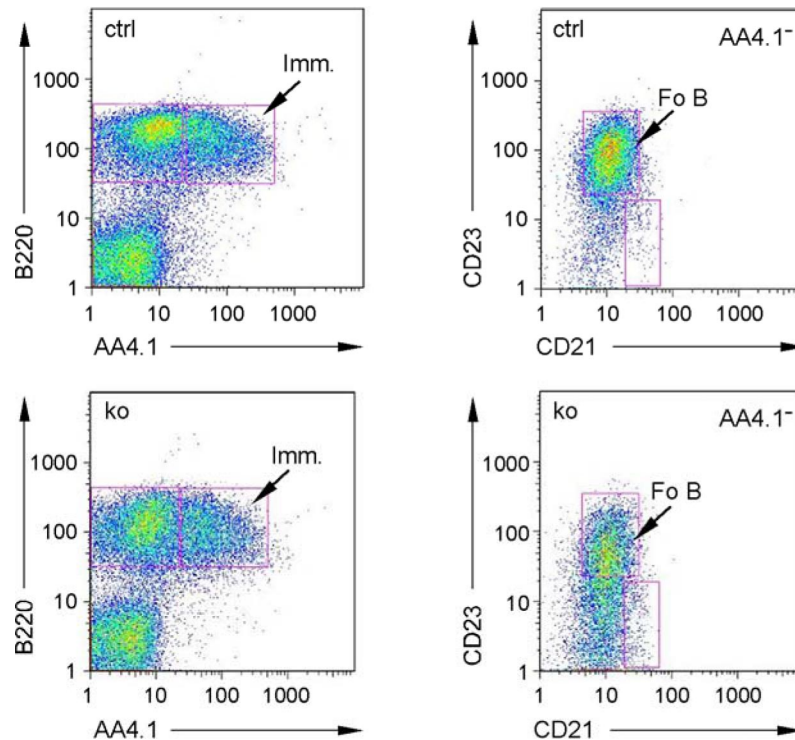


Fig. S1. Flow cytometry analyses of surface marker expression on splenic B cells from *Mef2c* conditional KO (ko) and control animals. Flow cytometry on spleens from *Mef2c* KO (ko, bottom row) and control (ctrl, top row) mice show a similar distribution of immature B cells (Imm., B220⁺, AA4.1⁺). Mature B cells (B220⁺, AA4.1⁻) were further separated by CD21 and CD23 expression (second column). For all experiments, Fo B cells (B220⁺, AA4.1⁻, CD21⁺, CD23⁺) expressing similar levels of CD21 and CD23 were used (denoted in panels on the right).

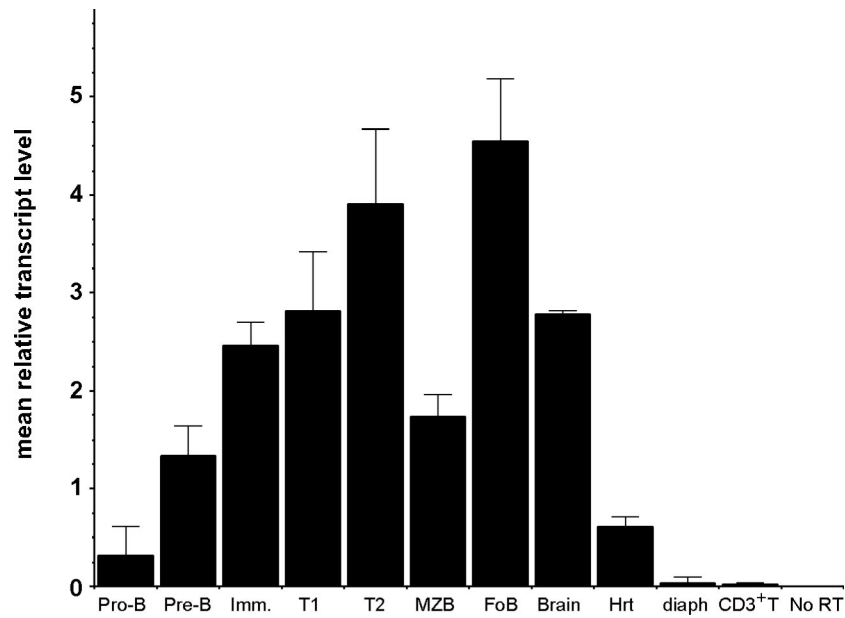


Fig. S2. *Mef2c* expression peaks in Fo B cells during B-cell development. *Mef2c* expression was relatively low in the B cells of the bone marrow, starting at the Pro-B-cell stage and slightly increasing at the Pre-B-cell and immature B-cell stages. In the spleen, *Mef2c* expression continued to increase as B cells matured from transitional 1 (T1) and transitional 2 (T2) stages. Fo B cell populations expressed the highest levels of *Mef2c*. *Mef2c* expression levels in MZ B cells (MZBs) were comparable to expression in the Pre-B-cell stage. Confirming earlier observations, *Mef2c* expression was nearly undetectable in T cells (CD3⁺T). Adult brain, heart (hrt), and diaphragm (diaph) were used as references for *Mef2c* expression. RT, reverse transcriptase.

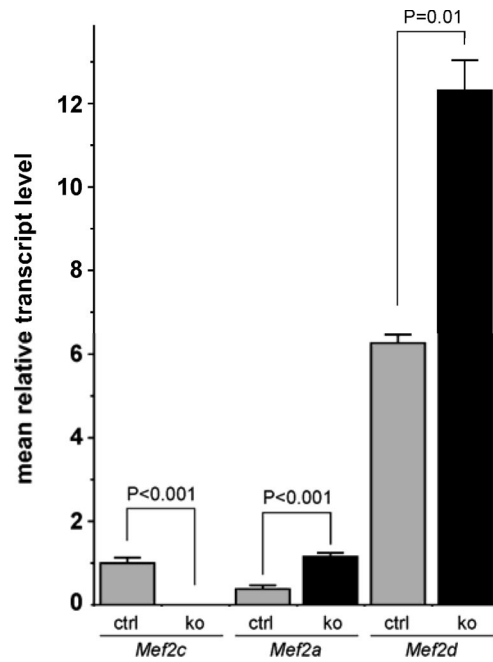


Fig. S3. Expression of *Mef2c*, *Mef2a*, and *Mef2d* in Fo B cells from *Mef2c* B cell KO (ko) and littermate control (ctrl) mice. *Mef2c* expression was not detectable in B-cell KO mice. Expression of *Mef2a* and *Mef2d* increased in primary Fo B cells in the absence of *Mef2c*. Relative expression (*Mef2c* in control Fo B cells equals 1) is indicated on the y axis. The data presented represent the mean plus SEM for three independent expression analyses from primary Fo B cells isolated from three KO and three control mice. *P* values were calculated by the unpaired two-tailed Student's *t* test.

Table S1. MEF2C is required for the activation of many cell cycle genes

Gene name	Fold change	P
Araf	-3.61	0.001136
Atf2	-4.17	0.026319
Ccna1	-3.71	0.01426
Ccna2	-10.41	0.05887
Ccnb1	-5.66	0.029677
Ccnb2	-3.94	0.011774
Ccnd1	-3.21	0.009506
Ccnd2	-2.87	0.06755
Ccnd3	-6.08	0.013067
Ccne1	-1.88	0.017151
Cdc42	-3.86	0.054512
Cdk2	-3.85	0.025312
Cdk4	-1.74	0.014033
Cdk6	-2.75	0.011096
Cdkn1a	-9.59	0.050013
Cdkn1b	-7.79	0.017502
Cdkn1c	-4.62	0.013574
Cdkn2a	-3.70	0.034863
Cdkn2b	-2.52	0.049855
Cdkn2c	-2.70	0.013206
Cdkn2d	-2.26	0.144003
Chuk	-1.12	0.776621
Col1a1	-2.37	0.234316
Creb1	-6.29	0.196178
Crebbp	-7.54	0.050784
DLK1	-4.84	0.587851
E2f1	-4.76	0.717268
Egfr	-2.68	0.605971
Egr1	-3.14	0.661391
Elk1	-3.51	0.06049
Ets1	-1.62	0.401633
Ets2	-2.17	0.485416
Fos	-2.01	0.59343
Grb2	-1.61	0.900978
Hras1	-1.37	0.180299
Hspa5	-2.56	0.682536
Hspb1	-3.22	0.289003
Jun	-3.26	0.043844
Kcnn1	-3.97	0.191843
Kras	-6.74	0.364158
Ksr1	-2.39	0.01257
Map2k1	-3.13	0.925675
Hsp90ab1	-1.05	0.04039
Gapdh	-1.08	0.240559
Actb	1.72	0.050558
Gusb	-3.15	0.046355
Hprt1	-1.52	0.026495
Map2k1ip1	-1.17	0.692906
Map2k2	-1.34	0.995945
Map2k3	1.01	0.939548
Map2k4	-1.11	0.017166
Map2k5	2.84	0.042799
Map2k6	-1.87	0.493096
Map2k7	-4.54	0.116385
Map3k1	-2.70	0.324276
Map3k2	-3.72	0.555791
Map3k3	-2.14	0.351709
Map3k4	-6.09	0.286642
Map4k1	-2.07	0.629011
Mapk1	1.36	0.882588

Table S1. Continued

Gene name	Fold change	P
Mapk10	-1.51	0.8337
Mapk11	-1.41	0.560768
Mapk12	1.57	0.473684
Mapk13	3.56	0.045239
Mapk14	-1.06	0.56543
Mapk3	-3.31	0.463476
Mapk6	-3.39	0.045957
Mapk7	-2.73	0.584072
Mapk8	-2.37	0.945837
Mapk8ip1	-1.17	0.980257
Mapk8ip2	1.06	0.008416
Mapk8ip3	-1.32	0.870214
Mapk9	1.23	0.062914
Mapkapk2	-1.91	0.888216
Mapkapk5	1.29	0.607717
Max	-1.30	0.496133
Mef2c	-3.32	0.031053
Mknk1	-3.03	0.767517
Mos	-2.14	0.302586
Myc	-3.06	0.864793
Nfatc4	-1.49	0.412855
Nras	-1.35	0.831375
Pak1	-1.67	0.638628
Rac1	1.23	0.847943
Raf1	-1.15	0.807132
Rb1	-1.28	0.045106
Sfn	-1.57	0.895166
Smad4	-1.25	0.937582
Trp53	-1.08	0.046798

Select genes involved in the MAPK pathway were analyzed by Taqman real-time PCR for expression in sorted splenic Fo B cells isolated from *Mef2c* B-cell KO mice compared with littermate controls. Data are expressed as fold change compared with controls. Blue numbers indicate fold decrease in gene expression; pink numbers indicate fold increase in gene expression. *P* values were determined using a two-tailed *t* test; *n* = 6 independent replicates.