SUPPLEMENTAL MATERIAL

Heise et al., http://www.jem.org/cgi/content/full/jem.20132613/DC1

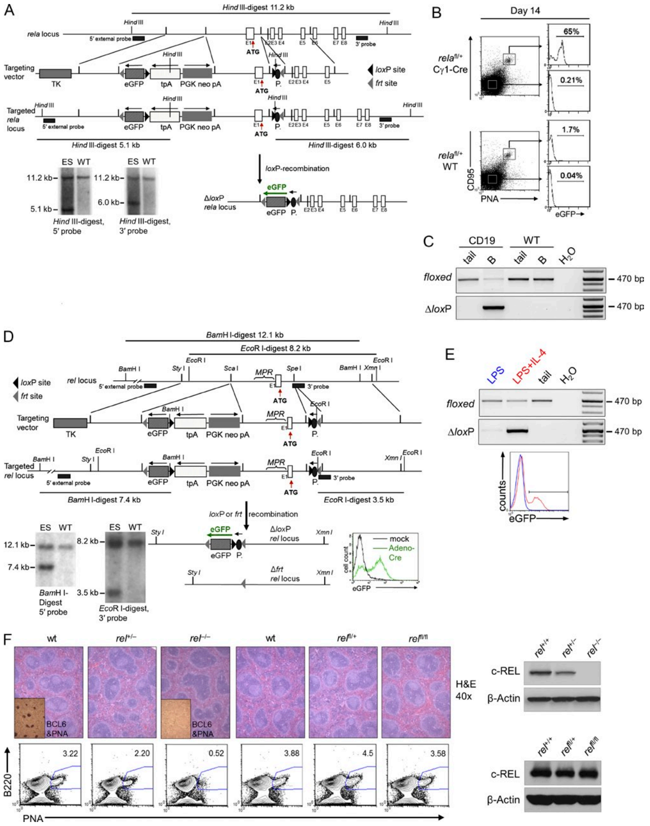

Figure S1. Generation and functional analysis of the conditional *rela* and *rel* alleles. (A) *Rela* (RELA) targeting strategy. Shown from top to bottom*:* the *rela* locus with the promoter region, exons, and translational start site in exon 1 (E1); the targeting vector comprising an eGFP, a triple SV40 polyA site (tpA), a PGK *neo*rpA cassette, a PGK promoter (P) downstream of exon 1, a TK gene, and *lox*P and *frt* sites; arrows denote the orientation; the targeted *rela* locus; and the locus after Cre-mediated recombination of *lox*P sites. Restriction sites, probes used for detection, and the expected fragments detected by Southern blot analysis are indicated. (Bottom left) Correctly targeted embryonic stem (ES) cell lines were identified by Southern blot analysis of HindIII-digested DNA that displayed the 5.1 kb band of the integrated transgene along with the 11.2 kb wild-type (WT) band. Co-integration of the 3′ *lox*P site was verified by the presence of the expected 6.0 kb transgenic band. (B) Flow cytometric analysis of splenic B cells (gated on B220$^+$) from *rela*$^{fl/+}$ Cγ1-Cre and *rela*$^{fl/+}$ control mice 14 d after SRBC immunization for the fraction of eGFP$^+$ GC (CD95^{hi}PNA^{hi}) and non-GC (CD95$^-$PNA$^-$) B cells. Numbers in histograms indicate percent eGFP$^+$ cells in the respective gates. (C) PCR to identify B cell–specific deletion of *rela*. DNA was isolated from the tail and purified B cells of *rela*$^{fl/+}$CD19-Cre and *rela*$^{fl/+}$ control mice. The forward primer is located in the eGFP gene, and the reverse primers are located in the junctions of the 5′ *lox*P site and the tpA gene, and the 3′ *lox*P site and the PGK promoter, respectively. (D) *Rel* (c-REL) targeting strategy. Shown from top to bottom: the *rel* locus with the minimal promoter region (MPR) and translational start site in exon 1 (E1); the targeting vector comprising an eGFP, a tpA site, a PGK *neo*rpA cassette, a PGK promoter (P) downstream of exon 1, a TK gene, and *lox*P and *frt* sites; arrows denote the orientation; the targeted *rel* locus; the locus after Cre-mediated recombination of *lox*P sites; and the locus after Flpe-mediated recombination of *frt* sites. Restriction sites, probes used for detection, and the expected fragments detected by Southern blot analysis are indicated. (Bottom left) Correctly targeted ES cell lines were identified by Southern blot analysis of BamHI-digested DNA that displayed the 7.4 kb band of the integrated transgene along with the 12.1 kb WT band. Co-integration of the 3′ *lox*P site was verified by analysis of EcoRI-digested DNA that displayed the 3.5 kb transgenic band along with the 8.2 kb WT band. (Bottom right) Flow cytometry of eGFP expression by Adeno-Cre–treated *rel*$^{fl/+}$ ES cells after *lox*P-mediated deletion of the *rel* locus. (E, top) PCR strategy to identify specific deletion of *rel* in B cells purified from *rel*$^{fl/+}$Cγ1-Cre mice upon induction of class-switch recombination with LPS+IL-4. DNA isolated from cultures treated with LPS alone and tail DNA of these mice served as negative control. The forward primer is located in the eGFP gene, and the reverse primers are located in the junctions of the 5′ *lox*P site and the tpA gene, and the 3′ *lox*P site and the PGK promoter, respectively. (E, bottom) Flow cytometric analysis of the same B cell cultures for eGFP expression. (F, left) IHC analysis of splenic sections for GCs by PNA and BCL6 co-staining (purple), and flow cytometric analysis of splenic B cells of *rel*$^{-/-}$, *rel*$^{+/-}$, *rel*$^{fl/fl}$, *rel*$^{fl/+}$, and wild-type littermates 14 d after SRBC immunization. *rel*$^{-/-}$ mice show impaired formation of GCs, in agreement with the literature (see main text), demonstrating that the newly generated conditional *rel* allele ablates the function of c-REL upon deletion. *rel*$^{fl/fl}$ mice show normal generation of GCs, demonstrating that the *lox*P-flanked conditional *rel* allele produces physiological amounts of c-REL despite the insertion of several gene cassettes into the *rel* locus. (Right) Western blot analysis of B cells isolated from *rel*$^{-/-}$, *rel*$^{+/-}$, *rel*$^{fl/fl}$, *rel*$^{fl/+}$, and wild-type littermates demonstrating that the newly generated conditional *rel* allele does not express c-REL protein upon deletion, and that the *lox*P-flanked allele in un-rearranged configuration produces normal amounts of c-REL protein.

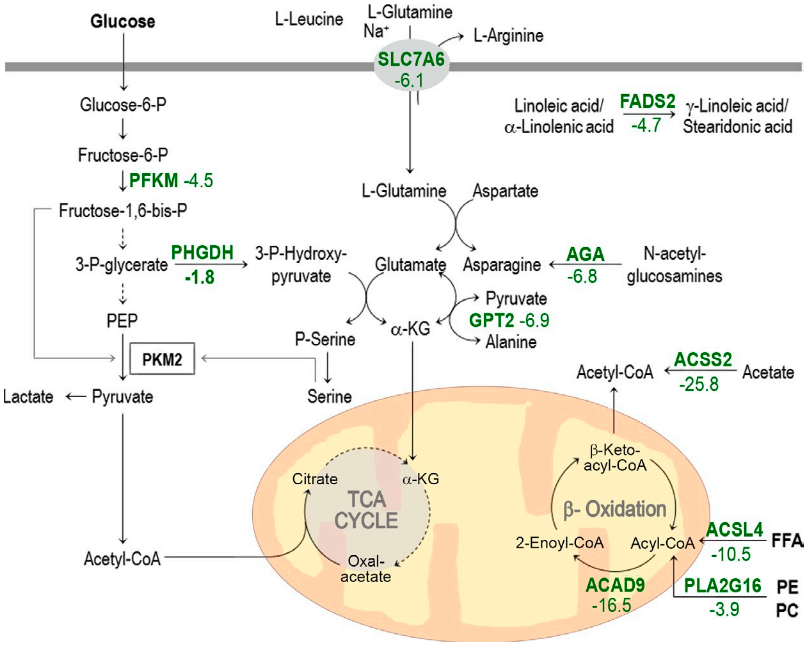

Figure S2. Chart depicting metabolic pathways that seem to be affected by the failed up-regulation of genes (indicated by green color) in c-REL–deficient GC B cells. The fold difference of the relative expression between the GC B cell fractions from *rel*$^{fl/fl}$Cγ1-Cre and Cγ1-Cre mice is indicated. α-KG, α-Ketoglutarate.

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Table S1. Genes differentially expressed in c-REL−deficient vs. wild-type GC B cells.

Genes downregulated in c-REL-deficient GC B cells

Z-score	Probe set	Gene Symbol	Category	Fold change
29.519	1432604_at	Rbl1	Cell Cycle/Proliferation	23.5
28.997	1425604_at	Crkl	Signaling	18.4
21.892	1425307_at	Dnahc1	Cytoskeleton/Structure	9.0
18.823	1430460_at	Fam188a	Unknown	21.4
17.842	1425124_at	Rnf183	Unknown	8.3
14.727	1432027_a_at	Tbc1d14	Unknown	5.1
12.871	1446136_at	Sik3	Unknown	11.6
11.85	1435276_a_at	Dgcr2	Migration/Adhesion	16.8
11.638	1418389_at	2810453I06Rik	Unknown	9.5
11.586	1420044_at	Osbpl9	Transporter Protein	3.0
10.188	1441062_at	Ddx11	RNA Metabolism	7.3
9.386	1442566_at	C78878	Unknown	13.5
9.044	1452801_at	Pigk	Miscellaneous	10.8
9.008	1453490_at	Sass6	Cell Cycle/Proliferation	4.0
8.897	1452650_at	Trim62	Unknown	192.2
8.64	1439710_at	Tgs1	RNA Metabolism	8.7
8.445	1449170_at	Piwil2	Miscellaneous	18.1
8.432	1438317_a_at	Endog	DNA Metabolism	3.5
7.848	1440054_at	Pik3ca	Signaling	19.1
7.793	1439387_x_at	Ctu2	RNA Metabolsim	2.4
7.778	1457964_at	1810044D09Rik	Unknown	12.0
7.684	1453743_x_at	Phf14	Transcription Factor	5.8
7.671	1457216_at	-	Unknown	90.1
7.492	1416507_at	Cnpy2	Miscellaneous	25.9
7.366	1416262_at	Tmem19	Unknown	5.0
7.325	1449629_s_at	-	Unknown	42.1
7.305	1442433_at	-	Unknown	16.8
7.301	1457031_at	Fsd2	Unknown	13.7
7.202	1448190_at	Mrpl33	Miscellaneous	2.9
7.189	1439932_at	Ubxn2b	Cell Cycle/Proliferation	5.1
7.177	1429939_at	Ppp6r3	Signaling	32.5
7.139	1435215_at	-	Unknown	4.9
7.102	1434588_x_at	Tbca	Cytoskeleton/Structure	17.9
6.999	1441163_at	Med12l	Transcription	15.7
6.917	1447409_at	-	Unknown	18.2
6.851	1422616_s_at	Wdr54	Unknown	12.9
6.843	1454243_at	Ick	Signaling	36.9
6.832	1451363_a_at	Dennd2d	Unknown	3.1
6.805	1444394_at	Acad9	Metabolism	16.5
6.671	1420594_at	Bard1	DNA Metabolism	5.0
6.645	1421087_at	Per3	Miscellaneous	31.6
6.573	1436058_at	Rsad2	Immune Response	30.3
6.476	1416319_at	Adk	Metabolism	3.5
6.464	1439738_at	Mettl13	Miscellaneous	9.5
6.459	1453168_at	1700029J07Rik	Unknown	118.8
6.411	1440183_x_at	2810002N01Rik	Miscellaneous	36.8
6.343	1435403_at	1700007L15Rik	Unknown	21.2
6.262	1436833_x_at	Ttll1	Cytoskeleton/Structure	35.9
6.241	1446405_at	Myst3	DNA metabolism	9.1
6.182	1439876_at	Vti1a	Cellular Trafficking	62.6
6.12	1438294_at	Atxn1	Transcription	105.4
6.045	1434173_s_at	D19Bwg1357e	Unknown/Miscellaneous	2.9
5.928	1422479_at	Acss2	Metabolism	25.8
5.897	1453359_at	Exosc1	RNA Metabolism	3.4
5.893	1436737_a_at	Sorbs1	Signaling	43.0
5.837	1417985_at	Nrarp	Signaling	8.4

5.766	1419773_at	Aplf	DNA metabolism	64.2
5.727	1433658_x_at	Pcbp4	RNA Metabolism	3.4
5.727	1456844_at	Camk2d	Signaling	4.2
5.689	1433266_at	2810416A17Rik	Unknown	101.0
5.591	1439422_a_at	Fam132a	Metabolism	26.9
5.553	1430904_at	Arfgap3	Cellular Trafficking	40.2
5.527	1435554_at	Tmcc3	Unknown	27.9
5.508	1436024_at	Fam113a	Unknown	5.8
5.469	1452757_s_at	Hba-a1 Hba-a2	Miscellaneous	23.0
5.452	1447904_s_at	Fnta	Miscellaneous	1.9
5.449	1424580_at	Slc35a3	Membrane Transport	13.3
5.412	1423672_at	Ttc30b	Cellular Trafficking	23.8
5.4	1431618_a_at	Pibf1	Immune Response	10.5
5.27	1431252_a_at	Zfp655	Unknown	21.9
5.26	1442594_at	Ttk	Cell Cycle/Proliferation	2.8
5.256	1423432_at	Phip	Signaling	2.8
5.168	1444312_at	Slc22a15	Membrane Transport	3.1
5.104	1459020_at	Amigo1	Miscellaneous	20.7
5.081	1434576_at	Tsga14	Unknown	6.9
4.979	1455007_s_at	Gpt2	Metabolism	6.9
4.951	1437980_at	9130230N09Rik	Unknown	7.9
4.934	1445984_at	-	Unknown	4.4
4.912	1429173_at	Dnase1l1	DNA metabolism	18.1
4.896	1423266_at	2810405K02Rik	Unknown	18.9
4.893	1453622_s_at	Mllt3	Transcription	4.3
4.875	1445329_at	Dtnb	Miscellaneous	6.9
4.854	1456805_a_at	Ppp4r1l-ps	Unknown	24.2
4.853	1426147_s_at	Cldn10	Cytoskeleton/Structure	24.2
4.828	1460098_at	-	Unknown	17.2
4.648	1427005_at	Plk2	Cell Cycle/Proliferation	14.2
4.641	1434919_at	Agps	Metabolism	2.5
4.639	1454018_at	Tlk2	Chromatin	8.8
4.612	1428568_at	B230217C12Rik	Unknown	9.5
4.606	1446177_at	-	Unknown	34.6
4.603	1460632_at	Rdh10	Metabolism	6.1
4.559	1432548_at	Parp14	Metabolism	7.1
4.524	1419269_at	Dut	DNA metabolism	3.6
4.522	1443057_at	-	Unknown	5.7
4.508	1444571_at	-	Unknown	27.9
4.363	1426383_at	Cry2	Miscellaneous	6.5
4.358	1427073_at	Lace1	Unknown	3.7
4.335	1453386_at	Tusc1	Unknown	28.4
4.326	1441685_at	Prosc	Unknown	11.6
4.324	1441373_at	-	Unknown	4.4
4.31	1419031_at	Fads2	Metabolism	4.7
4.294	1418967_a_at	St7	Unknown/Miscellaneous	172.1
4.267	1440781_at	B830007D08Rik	Unknown	8.8
4.258	1416780_at	Pfkm	Metabolism	4.5
4.253	1434168_at	Peo1	DNA Metabolism	3.3
4.202	1455787_x_at	Minpp1	Metabolism	2.0
4.187	1445597_s_at	Pla2g16	Metabolism	3.9
4.182	1434926_at	Arhgef11	Signaling	5.9
4.162	1438169_a_at	Frmd4b	Signaling	11.1
4.111	1460164_at	Spin1	Cell Cycle/Proliferation	5.1
4.086	1438970_x_at	1700034F02Rik	Unknown	13.2
4.074	1428269_a_at	Glt8d1	Miscellaneous	3.0
4.061	1440254_at	Snord104	RNA metabolism	3.6
3.994	1448520_at	Dclre1b	DNA metabolism	13.8
3.993	1451611_at	Pla2g16	Metabolism	3.6
3.987	1415943_at	Sdc1	Miscellaneous	5.8
3.958	1421692_at	Cacna1e	Membrane Transport	10.2
3.956	1421895_at	Eif2s3x Gm2223	Translation	5.1

3.938	1439913_at	Pabpc1l	Unknown	10.2
3.91	1437828_s_at	Wdr46	Unknown	12.0
3.898	1458896_at	Gmeb1	Transcription	13.4
3.894	1426965_at	Rap2a	Signaling	5.9
3.888	1418301_at	Irf6	Transcription Factor	17.4
3.878	1457873_at	-	Unknown	13.0
3.847	1437279_x_at	Sdc1	Miscellaneous	15.1
3.846	1418942_at	Ift74	Cellular Trafficking	7.3
3.84	1452504_s_at	Ctbs	Miscellaneous	10.9
3.817	1446926_at	Pycard	Immune Response	5.7
3.811	1430127_a_at	Ccnd2	Cell Cycle/Proliferation	6.8
3.806	1441880_x_at	Tmem149 U2af1l4	RNA Metabolism	6.1
3.758	1424760_a_at	Smyd2	Miscellaneous	6.7
3.758	1422709_a_at	Wdr46	Unknown	5.9
3.756	1416002_x_at	Cotl1	Cytoskeleton/Structure	4.6
3.74	1437800_at	Edaradd	Signaling	13.0
3.732	1418826_at	Ms4a6b	Signaling	3.3
3.727	1438452_at	Nebl	Cytoskeleton/Structure	6.7
3.702	1445655_at	-	Unknown	29.7
3.698	1433670_at	Emp2	Cytoskeleton/Membrane Function	13.0
3.685	1443763_at	-	Unknown	7.3
3.681	1437621_x_at	Phgdh	Metabolism	1.8
3.657	1437374_at	Zfp865	Miscellaneous	3.6
3.656	1448626_at	Cdk5rap1	Miscellaneous	5.3
3.645	1452977_at	Zhx3	Transcription Factor	16.0
3.632	1436376_s_at	Srbd1	Unknown	3.3
3.583	1439648_at	Anln	Cytoskeleton/Structure	6.5
3.58	1429205_at	Mllt3	Transcription	5.4
3.573	1421167_at	Atp11a	Membrane Transport	5.5
3.573	1419801_x_at	-	Unknown	4.6
3.565	1429337_at	Tmem87b	Unknown	17.8
3.555	1432073_at	Aarsd1 Ptges3l	Miscellaneous	9.9
3.497	1438796_at	Nr4a3	Transcription Factor	16.7
3.418	1428471_at	Sorbs1	Signaling	6.4
3.388	1449374_at	Pipox	Metabolism	4.8
3.324	1417512_at	Evi5	Cell Cycle/Proliferation	6.0
3.303	1420784_at	Scn11a	Membrane Transport	14.2
3.262	1428142_at	Etv5	Transcription Factor	4.7
3.241	1446757_at	-	Unknown	8.0
3.238	1445625_at	-	Unknown	8.9
3.21	1435342_at	Kcnk6	Membrane Transport	2.3
3.202	1416163_at	Cops4	Signaling	2.3
3.188	1418911_s_at	Acsl4	Metabolism	10.5
3.166	1435503_at	C330006K01Rik	DNA metabolism	6.4
3.146	1427269_at	Srsf11	Miscellaneous	4.8
3.126	1455433_at	Zfp942	Unknown	2.8
3.125	1446345_at	-	Unknown	12.9
3.071	1437163_x_at	Gtf2h4	RNA Metabolism	4.3
2.969	1430131_at	Cr1l	(Innate) Immune Response	3.6
2.954	1431127_at	Zbtb43	Unknown	9.6
2.947	1440308_at	Cmpk1	DNA metabolism	17.9
2.938	1450914_at	Ppp1r14b	Signaling	2.7
2.867	1434951_at	Armc8	Unknown	9.5
2.858	1429712_at	Etohi1	Unknown	4.5
2.812	1424331_at	Rab40c	Protein Degradation	4.5
2.793	1440388_at	-	Unknown	8.5
2.763	1435252_at	B3galt6	Miscellaneous	4.9
2.756	1456000_at	Ddx18	RNA Metabolism	6.2
2.737	1438957_x_at	Cds2	Signaling	4.5
2.72	1436635_at	Ube2z	Protein Degradation	4.7
2.7	1421600_a_at	Trim26	Unknown	5.1
2.685	1432352_at	Ccny	Cell Cycle/Proliferation	10.6

2.639	1433467_at	Slc7a6	Metabolism	6.1
2.606	1424772_at	H2afj	Chromatin	7.6
2.576	1418647_at	Gnl1	Miscellaneous	7.9
2.576	1450385_at	Kpna3	Membrane Transport	12.5
2.572	1439249_at	Wac	Miscellaneous	8.1
2.54	1451146_at	Zfp386	Unknown	5.1
2.526	1451570_a_at	Fam92a	Unknown	3.5
2.507	1434665_at	Aga	Metabolism	6.8
2.499	1436196_at	C030046G05	Unknown	2.6
2.493	1446680_at	-	Unknown	9.2
2.46	1426695_at	9030624J02Rik	Unknown	3.9
2.357	1424630_a_at	Brca1	DNA Metabolism	4.9
2.345	1451313_a_at	1110067D22Rik	Miscellaneous	5.5
2.307	1456038_at	Fbxl4	Protein Degradation	5.7
2.162	1423403_at	Mapkbp1	Signaling	9.3
2.136	1454402_at	Zfp942	Unknown	7.5

Genes upregulated in c-REL-deficient GC B cells

Z-score	Probe set	Gene Symbol	Category	Fold change
-70.296	1422562_at	Rrad	Signaling	8.5
-25.151	1443489_at	-	Unknown	4.6
-17.106	1446134_at	C78115	Unknown	33.0
-16.527	1435527_at	Nfic	Transcription	12.7
-15.190	1449184_at	Pglyrp1	(Innate) Immune Response	2.8
-14.473	1448162_at	Vcam1	Migration/Adhesion	300.0
-10.099	1417061_at	Slc40a1	Membrane Transport	18.7
-8.920	1448048_at	Nmrk1	Metabolism	7.0
-8.556	1440604_at	8030494B02Rik	Unknown	5.9
-8.366	1460466_at	1700047I17Rik2	Unknown	4.7
-8.159	1442132_at	-	Unknown	16.9
-7.652	1417063_at	C1qb	(Innate) Immune Response	22.8
-7.509	1442685_at	-	Unknown	43.2
-7.092	1424598_at	Ddx6	RNA Metabolism	3.4
-6.767	1457503_at	-	Unknown	4.7
-6.726	1419873_s_at	Csf1r	(Innate) Immune Response	22.0
-6.682	1425740_at	Suv420h1	Unknown	6.4
-6.492	1420954_a_at	Add1	Cytoskeleton/Structure	11.8
-6.416	1418728_at	Star	Metabolism	8.8
-6.206	1434366_x_at	C1qb	(Innate) Immune Response	33.0
-6.161	1419872_at	Csf1r	(Innate) Immune Response	25.3
-6.003	1433804_at	Jak1	Signaling	3.3
-5.726	1449401_at	C1qc	(Innate) Immune Response	64.5
-5.703	1447137_at	-	Unknown	94.7
-5.683	1450430_at	Mrc1	Miscellaneous	19.2
-5.645	1449134_s_at	Spic	Transcription Factor	13.2
-5.615	1446838_at	Atad1	Miscellaneous	5.0
-5.604	1450068_at	Baz1b	Chromatin	3.0
-5.541	1443684_at	Gm10034	Unknown	12.1
-5.535	1438425_at	Gtf3c1	Transcription	15.5
-5.349	1437726_x_at	C1qb	Innate Immune Response	34.6
-5.270	1457053_at	-	Unknown	6.0
-5.270	1456378_s_at	Fbxl20	Protein Degradation	5.6
-5.241	1453122_at	Fam135a	Unknown	14.6
-5.184	1424986_s_at	Fbxw7	Protein Degradation	4.4
-5.092	1431355_s_at	Trpm7	Membrane Transport	5.0
-5.057	1440331_at	Kdsr	Metabolism	17.1
-4.991	1437021_at	Arl13b	Cellular Trafficking	7.0
-4.987	1457678_at	2310035C23Rik	Unknown	3.6
-4.849	1435471_at	Zfp708	Unknown	9.3
-4.844	1449838_at	Crisp3	Unknown	7.0
-4.673	1443125_at	Trip12	Protein Degradation	8.4
-4.596	1453512_at	5830407P18Rik	Unknown	26.5

-4.595	1429583_at	2900053A13Rik	Unknown	7.3
-4.567	1436491_at	Gm11346	Unknown	9.3
-4.406	1441493_at	Erc1	Signaling	5.2
-4.343	1440577_at	-	Unknown	11.9
-4.323	1426998_at	Zfand3	Unknown	4.3
-4.301	1429871_at	Hmmr	Miscellaneous	4.3
-4.259	1458151_at	4833444G19Rik	Unknown	5.0
-4.250	1425398_at	Hist1h2bf	Chromatin	8.1
-4.235	1428423_at	Pcgf3	Unknown	4.1
-4.012	1459924_at	Atp6v0a1	Membrane Transport	22.2
-3.995	1424585_at	Ranbp10	Miscellaneous	3.5
-3.967	1438714_at	-	Unknown	3.9
-3.951	1445103_at	-	Unknown	8.3
-3.947	1441142_at	2700081L22Rik	Unknown	29.6
-3.903	1432798_at	Slc12a6	Membrane Transport	16.2
-3.842	1456276_at	-	Unknown	28.1
-3.814	1439041_at	Slc39a10	Membrane Transport	6.7
-3.762	1458064_at	-	Unknown	8.4
-3.761	1441178_at	Dtwd2	Unknown	12.5
-3.743	1424498_at	Atl3	Cytoskeleton/Structure	6.9
-3.737	1446735_at	-	Unknown	3.2
-3.722	1444159_at	-	Unknown	4.3
-3.715	1458017_at	Phf20	Chromatin	4.6
-3.661	1424944_at	Pcp2	Miscellaneous	5.0
-3.640	1441848_at	-	Unknown	29.2
-3.634	1458051_at	A230048O21Rik	Unknown	4.4
-3.633	1456494_a_at	Trim30a; Trim30d	Signaling	6.5
-3.617	1426516_a_at	Lpin1	Metabolism	6.0
-3.588	1428878_a_at	Pitpnc1	Membrane Transport	4.2
-3.553	1444519_at	Lgr5	Signaling	6.5
-3.550	1441565_at	-	Unknown	9.5
-3.447	1419604_at	Zbp1	(Innate) Immune Response	6.2
-3.423	1439930_at	-	Unknown	5.5
-3.378	1430404_at	LOC75771	Unknown	3.4
-3.372	1443517_at	Fam178a	Unknown	5.6
-3.370	1457628_at	Ccdc53	Cytoskeleton/Structure	4.5
-3.332	1459384_at	-	Unknown	13.7
-3.328	1436780_at	Ogt	Chromatin	4.1
-3.249	1416702_at	Serpini1	Miscellaneous	5.5
-3.239	1418327_at	1110058L19Rik	Unknown	3.0
-3.204	1457685_at	Zfp81	Miscellaneous	6.3
-3.191	1444962_at	Gm7609	Unknown	4.5
-3.191	1419798_at	2610019E17Rik	Unknown	5.8
-3.184	1441324_at	-	Unknown	5.2
-3.123	1442804_at	Fgr	Migration/Adhesion	3.7
-3.101	1443082_at	-	Unknown	5.2
-3.039	1439938_at	Stk38	Signaling	8.2
-3.035	AFFX-18SRNAMur/X00686_5_at			
-2.935	1459955_at	-	Unknown	9.5
-2.922	1441200_at	Klf3	Miscellaneous	12.8
-2.896	1431316_at	Itch	Protein Degradation	10.6
-2.882	1452940_x_at	Pitpnc1	Membrane Transport	6.5
-2.848	1456172_at	-	Unknown	8.8
-2.847	1424990_at	Orai1	Membrane Transport	3.8
-2.829	1438033_at	Tef	Transcription Factor	10.1

Table S2. Genes not induced in c-REL−deficient vs. wild-type B cells by ≥2-fold.

6 hours CD40 + IgM stimulation

gene	gene name	fold change	padj
Cytoskeleton&structure			
Myo1g	myosin IG	2.6	1.96E-155
Shank1	SH3 and multiple ankyrin repeat domains 1	2.2	1.15E-77
Coro2a	coronin, actin binding protein, 2A	2.0	1.37E-66
Psrc1	proline/serine-rich coiled-coil 1	2.9	8.05E-32
Agrn	agrin	2.0	2.72E-31
Kank3	KN motif and ankyrin repeat domains 3	2.1	9.97E-11
Zfp365	zinc finger protein 365	3.9	2.37E-10
Bmp1	bone morphogenetic protein 1	3.0	5.57E-05
Spon1	spondin 1, extracellular matrix protein	2.1	3.29E-03
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	5.0	0.002266505
Apoptosis			
Bcl2l1	BCL2-like 1	9.2	3.86E-244
Bcl2a1d	B cell leukemia/lymphoma 2 related protein A1d	3.3	1.80E-44
Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1b	2.0	1.59E-27
Proliferation			
Ccnd2	cyclin D2	2.6	3.77E-145
Cdk5r1	cyclin-dependent kinase 5, regulatory subunit 1	4.1	2.05E-52
Immune response			
Fam129c	family with sequence similarity 129, member C	6.0	0
Il2ra	interleukin 2 receptor, alpha	5.5	0
Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	2.0	3.99E-91
Lrrc32	leucine rich repeat containing 32	3.7	1.53E-51
Mfhas1	malignant fibrous histiocytoma amplified sequence 1	2.1	5.18E-35
Ikbke	inhibitor of kappaB kinase epsilon	2.5	1.58E-33
Havcr1	hepatitis A virus cellular receptor 1	2.2	1.22E-28
Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	3.2	1.38E-15
Ebi3	Epstein-Barr virus induced 3	2.5	6.76E-11
Dusp14	dual specificity phosphatase 14	2.3	1.66E-06
Timd2	T cell immunoglobulin and mucin domain containing 2	2.0	0.003190434
Signalling			
Axl	AXL receptor tyrosine kinase	6.0	1.73E-283
Gng4	guanine nucleotide binding protein (G protein), gamma 4	4.3	9.50E-212
Fam129a	family with sequence similarity 129, member A	3.3	1.27E-56
Grm6	glutamate receptor, metabotropic 6	6.1	3.79E-47
Phlda3	pleckstrin homology-like domain, family A, member 3	3.1	2.14E-23
Gpr56	G protein-coupled receptor 56	2.4	4.60E-11
Melk	maternal embryonic leucine zipper kinase	2.4	3.00E-08
Other			
Tmem132a	transmembrane protein 132A	3.6	8.73E-34
Reep2	receptor accessory protein 2	2.1	0.005524572
Unknown			
AI848285		3.7	3.62E-35
Tmcc3	transmembrane and coiled-coil domain family 3	2.3	1.06E-28
9030617O03Rik		2.3	7.57E-15
6530418L21Rik		2.1	9.44E-13
Rbm47	RNA binding motif protein 47	2.0	1.42E-11
BC048355		2.0	5.92E-06
Metabolism			
Slc15a3	solute carrier family 15, member 3	3.3	3.84E-171
Dhrs3	dehydrogenase/reductase (SDR family) member 3	4.1	4.98E-18
Mgll	monoglyceride lipase	10.6	7.30E-12
Nucb2	nucleobindin 2	2.0	1.26E-07
Fads2	fatty acid desaturase 2	2.2	0.000198501
Cell trafficking			
Sytl3	synaptotagmin-like 3	9.7	8.88E-32
Kifc3	kinesin family member C3	2.4	4.34E-10
Transport			
Plscr1	phospholipid scramblase 1	3.4	9.79E-67
Transcription			
Rel	reticuloendotheliosis oncogene	12.2	0
Phf15	PHD finger protein 15	2.9	1.50E-156
Grhl1	grainyhead-like 1	2.5	1.00E-33
Snai1	snail homolog 1	2.4	6.68E-06
Prdm16	PR domain containing 16	2.2	0.005844837
Nr1d1	nuclear receptor subfamily 1, group D, member 1	2.0	0.002266505

ordered within groups by p value (less than or equal to 0.01 p adj)

blue color: indicates genes that were identified in both 6 and 24 hour time-points

24 hours CD40 + IgM stimulation

gene	gene name	fold change	padj
Apoptosis			
Bcl2l1 (BclxL)	BCL2-like 1	4.9	4.04E-240
Bcl2a1d (BFL1)	BCL2-related protein A1	2.5	1.30E-89
Pim1	pim-1 oncogene	2.8	2.88E-70
Cytoskeleton&structure			
Mid1	midline 1	2.4	6.34E-70
Myo1g	myosin IG	2.1	6.53E-69

Hmmr	hyaluronan-mediated motility receptor (RHAMM)	3.3	2.55E-44
Inf2	Inverted Formin, FH2 And WH2 Domain Containing	2.0	4.42E-34
Tjp2	tight junction protein 2	2.1	4.82E-30
Lad1	ladinin 1	3.9	6.54E-19
Mtap2	Microtubule-Associated Protein 2	2.3	9.24E-18
Bmp1	Bone Morphogenetic Protein 1	4.9	1.37E-15
Col9a3	collagen, type IX, alpha 3	4.3	8.03E-10
Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	2.3	1.82E-09
Jph1	Junctophilin 1	12.6	3.39E-07
Celsr2	cadherin, EGF LAG seven-pass G-type receptor 2	2.0	1.37E-05
Dnalc1	dynein, axonemal, light chain 1	2.1	3.92E-05
Palm	paralemmin	2.8	3.94E-05
Grasp	GRP1 (General Receptor For Phosphoinositides 1)-Associated Scaffold Protein	2.8	9.88E-05
Jup	junction plakoglobin	2.2	2.53E-04
Gjc1	gap junction protein, gamma 1, 45kDa	3.6	9.99E-03
DNA regulation			
Hells	helicase, lymphoid-specific	2.0	6.45E-52
Hmgb2	high mobility group box 2	2.2	3.92E-45
Chaf1a	Chromatin Assembly Factor 1, Subunit A	2.0	9.40E-42
Chaf1b	chromatin assembly factor 1, subunit B (p60)	2.0	1.34E-33
Smyd2	SET and MYND domain containing 2	2.5	2.48E-19
Recql4	RecQ protein-like 4	2.0	1.62E-18
Hist1h3c	histone cluster 1, H3c	2.4	1.48E-05
Hist1h2bj	histone cluster 1, H2bj	2.0	7.21E-04
DNA repair			
Brip1	BRCA1 interacting protein C-terminal helicase 1	2.8	4.11E-44
Rad51ap1	RAD51 associated protein 1	2.3	3.54E-34
Brca1	breast cancer 1, early onset	2.0	2.29E-33
Neil3	nei endonuclease VIII-like 3 (E. coli)	2.2	3.78E-11
Immune response			
Il2ra	interleukin 2 receptor, alpha	3.6	1.20E-152
Fam129c	family with sequence similarity 129, member C	3.3	1.34E-145
Ccl22	chemokine (C-C motif) ligand 22	7.0	9.16E-124
Havcr1	hepatitis A virus cellular receptor 1	2.3	4.60E-63
Tnfsf14	tumor necrosis factor (ligand) superfamily, member 14 (LIGHT, LTg)	3.8	2.76E-55
Spp1	secreted phosphoprotein 1	3.0	1.97E-54
Ccl3	chemokine (C-C motif) ligand 3	2.3	2.58E-54
Ifih1	1 interferon induced with helicase C domain 1 (MDA5)	2.8	5.56E-51
Selplg	selectin P ligand	2.0	2.65E-42
Cst7	cystatin F (leukocystatin)	2.5	5.76E-26
Tnfsf9	tumor necrosis factor (ligand) superfamily, member 9	5.4	2.10E-23
Lrrc32	leucine rich repeat containing 32	38.6	4.18E-21
Dusp14	dual specificity phosphatase 14	11.8	1.91E-19
Timd2		2.7	6.93E-18
Ccl1	chemokine (C-C motif) ligand 1	2.7	1.20E-08
Mnda	myeloid cell nuclear differentiation antigen	2.2	3.46E-07
Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	2.7	2.96E-05
Cd70	CD70 molecule	3.3	5.04E-05
Il12rb1	interleukin 12 receptor, beta 1	2.1	2.89E-04
Metabolism			
Lipg	lipase, endothelial	3.4	2.71E-82
Fads2	fatty acid desaturase 2	8.2	4.59E-69
Dhfr	dihydrofolate reductase	2.2	1.61E-50
Dhrs3	dehydrogenase/reductase (SDR family) member 3	3.3	1.37E-43
Ppap2a	phosphatidic acid phosphatase type 2A	3.1	6.83E-40
Slc15a3	Solute Carrier Family 15, Member 3	2.0	4.78E-35
Fads1	fatty acid desaturase 1	2.3	6.68E-35
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1 (GLUT1)	2.0	2.93E-33
Tpi1	triosephosphate isomerase 1	2.0	9.09E-33
Pask	PAS domain containing serine/threonine kinase	2.1	4.53E-31
Chst7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	3.7	1.93E-26
Gcat	glycine C-acetyltransferase	2.5	3.18E-25
Asns	asparagine synthetase (glutamine-hydrolyzing)	2.2	7.87E-19
Akap1	A kinase (PRKA) anchor protein 1	2.1	2.62E-17
Nampt	nicotinamide phosphoribosyltransferase	2.1	1.06E-15
Slc25a13	solute carrier family 25 (aspartate/glutamate carrier), member 13	2.1	1.33E-15
Ak4	adenylate kinase 4	4.1	9.58E-13
Maoa	monoamine oxidase A	2.4	1.42E-11
Fam54a	Mitochondrial Fission Regulator 2	2.1	1.27E-10
Pcx	pyruvate carboxylase	2.2	3.22E-10
Mgll	monoglyceride lipase	5.1	4.27E-10
Kcnk10	potassium channel, subfamily K, member 10	2.4	5.50E-10
Car2	Carbonic Anhydrase II	2.2	9.73E-10
Fam72a	family with sequence similarity 72, member A	2.6	5.02E-09
Xylb	xylulokinase homolog (H. influenzae)	2.6	3.49E-08
Tyms-ps	thymidylate synthase, pseudogene	4.3	4.64E-08
Ppp1r3b	protein phosphatase 1, regulatory subunit 3B	5.5	2.37E-07
Car13	carbonic anhydrase XIII	2.0	8.72E-07
Slc16a3	Solute Carrier Family 16, Member 3 (Monocarboxylic Acid Transporter 4)	4.7	8.87E-07
Hilpda	hypoxia inducible lipid droplet-associated	3.6	2.31E-06
Slc39a8	solute carrier family 39 (zinc transporter), member 8	2.1	3.62E-06
Car12	Carbonic Anhydrase XII	2.7	5.99E-06
Qpct	glutaminyl-peptide cyclotransferase	6.7	6.46E-06

Gatm	Glycine Amidinotransferase (L-Arginine:Glycine Amidinotransferase)	5.4	1.06E-05
B4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	5.6	5.84E-05
B4galt4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	2.2	1.76E-04
Nme4	NME/NM23 nucleoside diphosphate kinase 4	2.1	3.25E-04
Sord	sorbitol dehydrogenase	2.0	1.09E-03
Nkain1	Na+/K+ transporting ATPase interacting 1	4.0	1.14E-03
Gls2	glutaminase 2 (liver, mitochondrial)	2.9	1.70E-03
Pon3	Paraoxonase 3	2.0	1.80E-03
Fads3	fatty acid desaturase 3	3.2	2.02E-03
Cth	cystathionase (cystathionine gamma-lyase)	3.0	2.75E-03
Dgat2	Diacylglycerol O-Acyltransferase 2	2.0	4.90E-03
Other			
Xist	X inactive specific transcript (non-protein coding)	3.4	1.42E-226
Atxn1	ataxin 1	2.1	4.39E-55
Fignl1	fidgetin-like 1	2.1	5.51E-49
Nefh	neurofilament, heavy polypeptide	2.4	1.69E-30
Troap	trophinin associated protein	3.6	1.14E-22
Mreg	melanoregulin	2.2	1.58E-18
Adm	adrenomedullin	2.9	1.28E-15
Alpl	alkaline phosphatase, liver/bone/kidney	2.4	2.00E-11
Mlf1	myeloid leukemia factor 1	5.6	2.33E-10
Fam20c	family with sequence similarity 20, member C	3.2	7.62E-08
Maged1	melanoma antigen family D, 1	2.1	3.18E-07
F9	coagulation factor IX	2.0	1.45E-06
Mlkl	mixed lineage kinase domain-like	2.0	1.25E-05
Bmp6	bone morphogenetic protein 6	2.9	3.35E-04
Gtf2ird1	GTF2I repeat domain containing 1	2.6	3.36E-04
Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	2.1	1.22E-03
Unc13b	unc-13 homolog B (C. elegans)	2.4	2.05E-03
Necab3	N-terminal EF-hand calcium binding protein 3	3.3	3.31E-03
Rarres1	Retinoic Acid Receptor Responder (Tazarotene Induced) 1	5.9	3.62E-03
Gbp1	guanylate binding protein 1, interferon-inducible	3.4	6.31E-03
Penk	proenkephalin	6.4	7.18E-03
Rbm24	RNA binding motif protein 24	19.7	7.48E-03
Tspan33	tetraspanin 33	2.5	7.57E-03
Proliferation			
Mki67 (KI-67)	antigen identified by monoclonal antibody Ki-67	3.1	1.32E-133
Top2a	topoisomerase (DNA) II alpha 170kDa	2.6	6.67E-113
Ccna2	cyclin A2	3.6	2.58E-104
Rrm2	ribonucleotide reductase M2	2.9	7.11E-103
Cdk1	cyclin-dependent kinase 1	3.6	1.47E-92
Kif11	kinesin family member 11	2.7	3.80E-77
Espl1	extra spindle pole bodies homolog 1 (S. cerevisiae)	3.4	1.73E-76
Lig1	ligase I, DNA, ATP-dependent	2.1	2.48E-72
Cdk5r1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	8.1	6.82E-66
Ncapg2	non-SMC condensin II complex, subunit G2	2.3	1.33E-64
Tyms	thymidylate synthetase	2.7	1.74E-63
Tpx2	TPX2, microtubule-associated, homolog (Xenopus laevis)	3.0	1.60E-61
Bub1	BUB1 mitotic checkpoint serine/threonine kinase	3.1	1.31E-59
Birc5	baculoviral IAP repeat containing 5	3.1	2.08E-57
Mcm10	minichromosome maintenance complex component 10	2.7	2.45E-57
Ncapg	Non-SMC Condensin I Complex, Subunit G	2.8	1.43E-56
Cdc45	cell division cycle 45	2.4	4.19E-55
Kntc1	kinetochore associated 1	2.3	2.82E-54
Rad51	RAD51 homolog (S. cerevisiae)	2.3	1.61E-53
Clspn	claspin	2.6	1.35E-52
Mybl2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	3.8	2.69E-47
Kif4	kinesin family member 4A	2.9	5.72E-47
Cdc6	cell division cycle 6	2.3	1.41E-46
Spag5	sperm associated antigen 5	2.7	1.74E-45
Gins2	GINS complex subunit 2 (Psf2 homolog)	2.2	1.73E-42
Aurkb	aurora kinase B	2.4	4.15E-41
Nek2	NIMA-related kinase 2	3.1	1.40E-40
E2f8	E2F transcription factor 8	2.8	3.04E-40
Nuf2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	2.8	7.15E-40
Cenpf	centromere protein F, 350/400kDa	3.0	1.68E-39
Ncaph	non-SMC condensin I complex, subunit H	2.2	2.74E-39
Kif20a	kinesin family member 20A	2.4	5.51E-39
Fancd2	Fanconi anemia, complementation group D2	2.3	6.45E-39
Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	2.1	1.43E-38
Cep55	centrosomal protein 55kDa	2.4	6.41E-38
Rad54l	RAD54-like (S. cerevisiae)	2.2	7.98E-38
Exo1	exonuclease 1	2.2	1.26E-37
Spc24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	2.5	1.32E-37
Aspm	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	2.7	1.68E-37
Racgap1	Rac GTPase activating protein 1	2.4	4.96E-37
Cks1b	CDC28 protein kinase regulatory subunit 1B	2.0	9.80E-36
Cdca8	cell division cycle associated 8	2.3	1.26E-35
Cenpe	centromere protein E, 312kDa	2.3	1.62E-34
Stmn1	stathmin 1	2.3	2.26E-34
Kif2c	kinesin family member 2C	3.1	5.30E-33
Dna2	DNA replication helicase 2 homolog (yeast)	2.9	3.11E-32
Kif18b	kinesin family member 18B	2.9	8.75E-32

Cdca7l	cell division cycle associated 7-like	2.3	1.73E-31
Pbk	PDZ binding kinase	3.3	3.38E-30
Casc5	cancer susceptibility candidate 5	2.3	7.25E-30
Plk1	polo-like kinase 1	3.1	1.36E-28
Stil	SCL/TAL1 interrupting locus	2.2	4.51E-28
Cit	citron (rho-interacting, serine/threonine kinase 21)	2.3	1.29E-27
Prc1	protein regulator of cytokinesis 1	2.4	1.69E-27
Fanca	Fanconi anemia, complementation group A	2.0	5.37E-27
Trip13	thyroid hormone receptor interactor 13	2.0	2.31E-26
Kif14	kinesin family member 14	3.0	5.04E-26
Kif23	kinesin family member 23	2.2	1.83E-25
Foxm1	Forkhead Box M1	2.0	2.46E-25
Cdca5	cell division cycle associated 5	2.2	5.73E-25
Sgol1	shugoshin-like 1 (S. pombe)	2.5	5.98E-25
Cenph	centromere protein H	2.2	1.33E-24
Cenpi	centromere protein I	2.4	2.68E-24
Kif22	kinesin family member 22	2.1	5.23E-24
Bard1	BRCA1 associated RING domain 1	2.1	6.83E-24
Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	2.6	1.82E-22
Nusap1	nucleolar and spindle associated protein 1	3.2	7.34E-22
Cdca2	cell division cycle associated 2	2.1	1.69E-21
Ccnb1	cyclin B1	2.9	2.08E-21
E2f7	E2F transcription factor 7	3.1	5.08E-21
Ccnb2	cyclin B2	2.8	7.99E-21
Ccne2	cyclin E2	2.6	2.81E-20
Syce2	synaptonemal complex central element protein 2	2.1	3.76E-20
E2f1	E2F transcription factor 1	2.2	8.99E-20
Cenpn	centromere protein N	2.1	1.28E-19
Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	2.9	3.27E-19
Cenpm	centromere protein M	2.4	6.42E-18
Mis18bp1	MIS18 binding protein 1	2.2	8.42E-18
Kif15	kinesin family member 15	2.7	4.35E-17
Spc25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	2.2	5.18E-17
Kifc1	kinesin family member C1	2.5	3.81E-15
Ckap2	cytoskeleton associated protein 2	2.1	4.16E-15
Ska1	spindle and kinetochore associated complex subunit 1	2.8	1.47E-14
Oip5	Opa interacting protein 5	2.2	3.96E-13
Cenpw	centromere protein W	2.1	3.45E-11
Mastl	Microtubule Associated Serine/Threonine Kinase-Like	2.0	1.48E-10
Myh10	myosin, heavy chain 10, non-muscle	2.2	1.55E-09
Rad54b	RAD54 homolog B (S. cerevisiae)	2.1	9.69E-09
Cenpp	centromere protein P	2.3	1.27E-08
Pard3b	par-3 partitioning defective 3 homolog B (C. elegans)	2.2	2.44E-08
Anln	anillin, actin binding protein	2.7	9.82E-08
Fgd2	FYVE, RhoGEF and PH domain containing 2	2.0	2.03E-07
Kifc3	kinesin family member C3	4.4	8.26E-07
Mnd1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	2.6	5.04E-06
Fam64a	family with sequence similarity 64, member A	2.9	2.70E-05
Fam83d	Family With Sequence Similarity 83, Member D	2.6	7.24E-05
Cdc25c	cell division cycle 25C	2.6	1.38E-03
Psrc1	proline/serine-rich coiled-coil 1	2.4	4.12E-03
Protein degradation			
Siah2	siah E3 ubiquitin protein ligase 2	2.6	6.74E-53
Dtl	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	2.1	5.39E-51
Uhrf1	Ubiquitin-Like With PHD And Ring Finger Domains 1	2.1	9.78E-49
Cdca3	cell division cycle associated 3	3.1	7.01E-47
Ube2c	ubiquitin-conjugating enzyme E2C	3.7	5.56E-37
Ccnf	cyclin F	2.1	3.94E-28
Protein stabilization			
Hspa1a	heat shock 70kDa protein 1A	2.9	1.39E-03
Hspa1b	heat shock 70kDa protein 1B	2.3	1.81E-03
RNA metabolism			
Rpp25	ribonuclease P/MRP 25kDa subunit	3.9	1.05E-03
Signalling			
Axl	*AXL* receptor tyrosine kinase	4.4	1.89E-256
Spry2	sprouty homolog 2 (Drosophila)	3.2	1.53E-65
Cst6	cystatin E/M	3.5	1.37E-61
Melk	maternal embryonic leucine zipper kinase	3.3	1.57E-52
Fam129a	family with sequence similarity 129, member A	2.8	9.49E-48
St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	2.1	1.35E-47
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	2.1	2.63E-46
Shcbp1	SHC SH2-domain binding protein 1	2.6	5.78E-34
Rgs9bp	regulator of G protein signaling 9 binding protein	6.0	2.39E-33
Baiap2	BAI1-associated protein 2	2.0	4.07E-27
Sh3rf1	SH3 domain containing ring finger 1	2.2	4.99E-27
Gpr176	G protein-coupled receptor 176	3.4	7.29E-26
Ppp1r15a	protein phosphatase 1, regulatory subunit 15A	2.1	7.48E-22
Ttk	TTK protein kinase	2.2	3.70E-18
Pdgfa	platelet-derived growth factor alpha polypeptide	2.0	3.78E-18
Stk39	serine threonine kinase 39	4.8	3.15E-16
Lrr1	leucine rich repeat protein 1	2.8	2.61E-15
Chac1	ChaC, cation transport regulator homolog 1 (E. coli)	3.9	1.48E-10
Bag2	BCL2-associated athanogene 2	2.8	2.02E-10

Lrp5	low density lipoprotein receptor-related protein 5	2.6	4.15E-08
Gpr56	G protein-coupled receptor 56	4.6	6.64E-08
Apold1	apolipoprotein L domain containing 1	6.2	1.15E-07
Rhobtb1	Rho-Related BTB Domain-Containing Protein 1	2.0	2.45E-07
Ptpn3	protein tyrosine phosphatase, non-receptor type 3	2.3	1.79E-06
Tiam1	T-cell lymphoma invasion and metastasis 1	2.3	5.45E-06
Gng4	guanine nucleotide binding protein (G protein), gamma 4	3.9	6.78E-06
Rap1gap2	RAP1 GTPase activating protein 2	2.3	1.36E-05
Dmxl2	Dmx-like 2	2.3	4.55E-05
Ier3	immediate early response 3	4.3	1.65E-04
Epha2	EPH receptor A2	2.3	4.20E-04
Arl5b	ADP-ribosylation factor-like 5B	2.0	7.99E-04
Plekhg4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	3.7	8.01E-04
Prkar2b	protein kinase, cAMP-dependent, regulatory, type II, beta	2.1	9.27E-04
Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	3.6	1.55E-03
Kif7	kinesin family member 7	2.7	1.89E-03
Ryk	receptor-like tyrosine kinase	2.1	2.30E-03
Dact3	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	2.8	4.08E-03
Phlda3	pleckstrin homology-like domain, family A, member 3	3.0	9.96E-03
Transcription			
Rel	-	12.3	2.94E-184
Tfdp1	transcription factor Dp-1	2.0	3.03E-47
Tcf19	transcription factor 19	2.2	1.11E-32
Grhl1	grainyhead-like 1 (Drosophila)	2.9	4.18E-32
Snai1	snail homolog 1 (Drosophila)	2.6	2.42E-11
Maff	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.5	2.44E-08
Trim29	Tripartite Motif Containing 29	5.8	9.31E-07
Etv4	ets variant 4	3.1	1.32E-06
Nr4a3	nuclear receptor subfamily 4, group A, member 3	2.2	1.49E-05
Nr4a2	nuclear receptor subfamily 4, group A, member 2	2.4	1.51E-05
Zik1	zinc finger protein interacting with K protein 1	2.1	2.82E-05
Egr4	early growth response 4	6.9	4.38E-05
Ctdspl	CTD (Carboxy-Terminal Domain, RNA Polymerase II, Polypeptide A) Small Phosphatase-Like	3.5	8.96E-05
Msi1	musashi RNA-binding protein 1	3.5	5.72E-04
Mxd3	MAX dimerization protein 3	2.0	5.77E-04
Atf3	activating transcription factor 3	2.2	8.66E-04
Transport			
Plscr1	phospholipid scramblase 1	3.2	2.44E-58
Unknown			
2810417H13Rik		3.0	5.93E-108
AI848285		2.8	2.02E-81
5730590G19Rik		2.2	4.52E-39
Gm11974	predicted gene 11974	2.1	2.01E-34
Iqgap3	IQ motif containing GTPase activating protein 3	3.3	4.44E-34
Ckap2l	Cytoskeleton-Associated Protein 2-Like	2.5	1.01E-29
BC030867		3.0	1.26E-28
BC048355		3.1	1.54E-27
Ankle1	ankyrin repeat and LEM domain containing 1	3.4	1.36E-21
2610002D18Rik		3.3	7.61E-21
2010317E24Rik		3.2	6.28E-20
Gdap10	ganglioside-induced differentiation-associated-protein 10	2.0	9.18E-19
Nkg7	natural killer cell group 7 sequence	6.9	3.93E-18
Fam46c	family with sequence similarity 46, member C	5.0	1.62E-17
F630043A04Rik		2.2	5.37E-17
Nt5dc2	5'-nucleotidase domain containing 2	2.9	8.52E-16
C330027C09Rik		2.0	1.57E-14
Ankrd37	ankyrin repeat domain 37	3.9	1.45E-12
Diap3	diaphanous homolog 3 (Drosophila)	2.1	2.75E-11
4930547N16Rik		2.3	3.54E-11
1190002F15Rik		2.6	6.37E-07
Syna	syncytin a	2.8	8.49E-07
9830001H06Rik		2.6	2.57E-06
Tnfaip8l1	tumor necrosis factor, alpha-induced protein 8-like 1	2.4	5.59E-06
Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	2.2	7.46E-06
D630045J12Rik		2.5	1.33E-05
Armcx4	armadillo repeat containing, X-linked 4	2.0	2.12E-05
Armcx6	armadillo repeat containing, X-linked 6	2.0	2.31E-05
Depdc1b	DEP domain containing 1B	3.6	3.87E-05
Stac2	SH3 and cysteine rich domain 2	2.2	5.15E-05
4931417G12Rik		5.4	1.28E-04
Hpdl	4-hydroxyphenylpyruvate dioxygenase-like	2.0	1.77E-04
Tex15	testis expressed 15	2.6	2.44E-04
Xkr5	XK, Kell blood group complex subunit-related family, member 5	2.4	3.23E-04
Kctd17	potassium channel tetramerisation domain containing 17	2.4	5.13E-04
A330009N23Rik		2.2	7.04E-04
AI607873		3.5	1.15E-03
Tmem98	transmembrane protein 98	3.3	1.82E-03
AI854703		4.2	2.11E-03
Ildr1	immunoglobulin-like domain containing receptor 1	2.0	3.00E-03
Tm4sf19	transmembrane 4 L six family member 19	2.4	3.26E-03
Ccdc102a	coiled-coil domain containing 102A	3.4	9.26E-03

ordered within groups by p value (less than or equal to 0.01 p adj)

blue color: indicates genes that were identified in both 6 and 24 hour time-points

Table S3. A c-REL−dependent metabolic program precedes a proliferation program in activated B cells.

BP: GO biological process	CATEGORY	GENESET NAME	NES	NOM p-value	FDR q-value
6 HRS CD40+IgM	CELLULAR METABOLISM	GLUTAMATE_SIGNALING_PATHWAY	1.647767	0	0.1978507
		CARBOXYLIC_ACID_TRANSPORT	1.5978355	0.002205072	0.22779933
		ORGANIC_ACID_TRANSPORT	1.5591958	0.003351955	0.17676894
		AMINO_ACID_TRANSPORT	1.5285233	0.00462963	0.21097836
	RNA METABOLISM	RNA_SPLICING	1.5812175	0	0.20395255
		RNA_PROCESSING	1.569541	0	0.18833303
	OTHER	RIBOSOME_BIOGENESIS_AND_ASSEMBLY	1.5433053	0.004872107	0.1939141
24 HRS CD40+IgM	CELL CYCLE ENTRY and PROGRESSION and DNA METABOLISM	MITOTIC_CELL_CYCLE	2.2562175	0	0
		M_PHASE_OF_MITOTIC_CELL_CYCLE	2.2156723	0	0
		CELL_CYCLE_PROCESS	2.2120438	0	0
		MITOSIS	2.1836686	0	0
		CELL_CYCLE_PHASE	2.1727412	0	0
		M_PHASE	2.1434066	0	0
		CELL_CYCLE_GO_0007049	2.1251442	0	0
		CHROMOSOME_SEGREGATION	2.0214539	0	0
		REGULATION_OF_MITOSIS	1.942693	0	2.24E-04
		DNA_DEPENDENT_DNA_REPLICATION	1.9354295	0	4.16E-04
		DNA_REPLICATION	1.9259895	0	5.68E-04
		INTERPHASE_OF_MITOTIC_CELL_CYCLE	1.9095057	0	8.60E-04
		SISTER_CHROMATID_SEGREGATION	1.8863707	0	0.001110423
		MITOTIC_SISTER_CHROMATID_SEGREGATION	1.8790002	0	0.001314917
		CELL_CYCLE_CHECKPOINT_GO_0000075	1.8742197	0	0.001356966
		REGULATION_OF_CELL_CYCLE	1.8621807	0	0.001654028
		INTERPHASE	1.85156	0	0.002106091
		CELL_DIVISION	1.8444518	0	0.002326212
		DNA_METABOLIC_PROCESS	1.8121154	0	0.004350767
		MICROTUBULE_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	1.7850782	0	0.00738802
		MITOTIC_CELL_CYCLE_CHECKPOINT	1.745789	0.005415163	0.013186095
		ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION	1.7273105	0.003703704	0.01766416
		REGULATION_OF_MITOTIC_CELL_CYCLE	1.7160944	0.001912046	0.01961962
		DNA_REPAIR	1.7033104	0.001547988	0.02305555
		ORGANELLE_LOCALIZATION	1.6685276	0.014571949	0.031142432
		G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	1.6450824	0.003717472	0.040345866
		RESPONSE_TO_DNA_DAMAGE_STIMULUS	1.6312721	0	0.046828076
		REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	1.6239511	0.005535055	0.049538534
		DNA_RECOMBINATION	1.5927386	0.005424955	0.063328385
		DNA_INTEGRITY_CHECKPOINT	1.5717627	0.012411348	0.07375563
		DNA_PACKAGING	1.5389353	0.005145798	0.09855357
		CHROMOSOME_ORGANIZATION_AND_BIOGENESIS	1.5399941	0.003246753	0.100344524
		CELL_PROLIFERATION_GO_0008283	1.523904	0	0.112375684
		DOUBLE_STRAND_BREAK_REPAIR	1.5045915	0.035650622	0.123235166
		REGULATION_OF_DNA_METABOLIC_PROCESS	1.4797735	0.015679443	0.13732934
		MICROTUBULE_BASED_PROCESS	1.4801308	0.010084034	0.13956076
		REGULATION_OF_DNA_REPLICATION	1.4817907	0.048387095	0.14019424
		NUCLEOBASENUCLEOSIDE_AND_NUCLEOTIDE_METABOLIC_PROCESS	1.4351289	0.021543985	0.18732354
		ORGANELLE_ORGANIZATION_AND_BIOGENESIS	1.4290395	0	0.19066665
	CELLULAR METABOLISM	CARBOXYLIC_ACID_TRANSPORT	1.6121563	0.003424658	0.054313682
		TRNA_METABOLIC_PROCESS	1.5933466	0.009487666	0.06477512
		ORGANIC_ACID_TRANSPORT	1.5833919	0.003552398	0.06900686
		ELECTRON_TRANSPORT_GO_0006118	1.5214355	0.013400335	0.11254809
		LIPID_BIOSYNTHETIC_PROCESS	1.5081948	0.003252032	0.12241391
		STEROID_BIOSYNTHETIC_PROCESS	1.4741639	0.028933093	0.14141886
		HORMONE_METABOLIC_PROCESS	1.4864851	0.031894933	0.14327794
		MITOCHONDRIAL_TRANSPORT	1.4295087	0.041825093	0.19332403
		ALCOHOL_METABOLIC_PROCESS	1.403899	0.017152658	0.21728891
		STEROID_METABOLIC_PROCESS	1.4005066	0.03305785	0.21976508
		CARBOXYLIC_ACID_METABOLIC_PROCESS	1.388847	0.011217949	0.23711126
		CELLULAR_BIOSYNTHETIC_PROCESS	1.3856027	0.004273505	0.2394752
		ORGANIC_ACID_METABOLIC_PROCESS	1.3765271	0.01898734	0.24176563
		CELLULAR_LIPID_METABOLIC_PROCESS	1.3737426	0.001529052	0.24321777
	RNA METABOLISM	RRNA_METABOLIC_PROCESS	1.7201879	0.009578544	0.019018956
		RNA_PROCESSING	1.69008	0	0.02604897
		RRNA_PROCESSING	1.6769708	0	0.028756496
		RNA_SPLICING	1.5803995	0.001694915	0.06952343
		MRNA_PROCESSING_GO_0006397	1.4589359	0.023728814	0.15953502
	OTHER	RESPONSE_TO_ENDOGENOUS_STIMULUS	1.519018	0	0.112858325
		PATTERN_SPECIFICATION_PROCESS	1.4820087	0.025089607	0.1428012
		REGULATION_OF_BLOOD_PRESSURE	1.483316	0.042513862	0.14440466
		PROTEIN_FOLDING	1.4254373	0.031914894	0.1924746
		RIBOSOME_BIOGENESIS_AND_ASSEMBLY	1.6836034	0.009328358	0.02707364

CP: KEGG: KEGG gene sets	CATEGORY	GENESET NAME	NES	NOM p-value	FDR q-value
6 HRS CD40+IgM	CELLULAR METABOLISM	KEGG_PYRIMIDINE_METABOLISM	1.514874	0.001044932	0.091122
		KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	1.5207639	0.004581902	0.10584206
		KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	1.5249261	0.003348214	0.13237898
		KEGG_PENTOSE_PHOSPHATE_PATHWAY	1.4355496	0.019630484	0.21421596
		KEGG_LINOLEIC_ACID_METABOLISM	1.4221715	0.022836538	0.22587317
	RNA METABOLISM	KEGG_SPLICEOSOME	1.5285051	0	0.19070262
	OTHER	KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	1.586597	0.00234192	0.13196608

		KEGG_P53_SIGNALING_PATHWAY	1.4687734	0.003181336	0.15700944
24 HRS CD40+IgM	CELLULAR METABOLISM	KEGG_ONE_CARBON_POOL_BY_FOLATE	1.837495	0	0.006142664
		KEGG_ARGININE_AND_PROLINE_METABOLISM	1.7927383	0	0.006493236
		KEGG_PYRIMIDINE_METABOLISM	1.7951747	0	0.007861392
		KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	1.7267377	0	0.009907804
		KEGG_OXIDATIVE_PHOSPHORYLATION	1.7130511	0	0.010289431
		KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	1.7414619	0.001831502	0.010306698
		KEGG_PENTOSE_PHOSPHATE_PATHWAY	1.6541762	0.005725191	0.017636057
		KEGG_RETINOL_METABOLISM	1.6565747	0.00177305	0.018445348
		KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	1.5795099	0.010733453	0.031617846
		KEGG_PHENYLALANINE_METABOLISM	1.5569662	0.009505703	0.03917478
		KEGG_GLYCEROLIPID_METABOLISM	1.5388736	0.01048951	0.04598379
		KEGG_GALACTOSE_METABOLISM	1.5277787	0.033158813	0.04707884
		KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	1.5217346	0.02559415	0.04811833
		KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	1.5278103	0.009225092	0.04912575
		KEGG_PURINE_METABOLISM	1.5087196	0.006319115	0.052561156
		KEGG_GLYCOLYSIS_GLUCONEOGENESIS	1.4797087	0.014010508	0.06643744
		KEGG_DRUG_METABOLISM_CYTOCHROME_P450	1.4458034	0.035185184	0.077699766
		KEGG_CITRATE_CYCLE_TCA_CYCLE	1.446333	0.035916824	0.07969638
		KEGG_PYRUVATE_METABOLISM	1.4476432	0.027874565	0.08090103
		KEGG_TYROSINE_METABOLISM	1.4495525	0.021937843	0.08252497
		KEGG_PPAR_SIGNALING_PATHWAY	1.3579651	0.042517006	0.14217804
	CELL CYCLE ENTRY and	KEGG_DNA_REPLICATION	2.115131	0	0
	PROGRESSION	KEGG_CELL_CYCLE	2.0138788	0	0
	and DNA METABOLISM	KEGG_HOMOLOGOUS_RECOMBINATION	1.7834507	0	0.006396068
		KEGG_MISMATCH_REPAIR	1.7401252	0.001683502	0.009271333
		KEGG_NUCLEOTIDE_EXCISION_REPAIR	1.6489205	0.003378379	0.017707538
		KEGG_BASE_EXCISION_REPAIR	1.617916	0.005300353	0.025743468
	RNA METABOLISM	KEGG_SPLICEOSOME	1.6973053	0	0.011115047
	OTHER	KEGG_PARKINSONS_DISEASE	1.5905601	0.004761905	0.03230945
		KEGG_HUNTINGTONS_DISEASE	1.5820765	0	0.032353114
		KEGG_OOCYTE_MEIOSIS	1.5840557	0	0.03334049
		KEGG_PROTEASOME	1.4845436	0.025773196	0.06570404
		KEGG_DRUG_METABOLISM_CYTOCHROME_P450	1.4458034	0.035185184	0.077699766
		KEGG_ALZHEIMERS_DISEASE	1.4576428	0.003095975	0.07904794
		KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	1.426582	0.021630615	0.089418225
		KEGG_P53_SIGNALING_PATHWAY	1.4183191	0.024263432	0.093365915

Table S4. Genes not induced in RELA-deficient vs. wild-type B cells by ≥2-fold.

6 hours CD40 + IgM stimulation

gene	**gene name**	**fold change**	**padj**
Cytoskeleton&structure			
Marcksl1	MARCKS-like 1	2.0	1.07E-87
Hspg2	perlecan (heparan sulfate proteoglycan 2)	2.9	1.74E-80
Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	2.6	1.92E-47
Psrc1	proline/serine-rich coiled-coil 1	2.6	3.59E-41
Sdc3	syndecan 3	2.2	1.43E-22
Mid1 (TRIM18)	midline 1	2.1	2.88E-19
Zfp365	zinc finger protein 365	3.2	1.86E-11
Stag3	stromal antigen 3	2.1	2.45E-10
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	5.2	0.008894984
Apoptosis			
Xaf1	XIAP associated factor 1	2.3	3.09E-49
Tnfrsf10b	tumor necrosis factor receptor superfamily, member 10b	2.5	1.48E-24
Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	2.2	3.62E-11
Immune response (antimicrobial)			
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	2.1	1.65E-80
Zbp1	Z-DNA binding protein 1	2.5	1.05E-79
Oas3	2'-5' oligoadenylate synthetase 3	2.5	1.17E-57
Slfn5	schlafen 5	2.7	1.68E-57
Mx1	myxovirus (influenza virus) resistance 1	2.5	4.06E-49
Rtp4	receptor transporter protein 4 (28kD interferon responsive protein)	2.7	1.23E-47
Trim30d	tripartite motif-containing 30D	2.0	1.13E-43
Irf7	interferon regulatory factor 7	2.5	4.39E-35
Trim30a	tripartite motif-containing 30A	2.0	5.42E-34
Isg20	interferon-stimulated protein	2.5	8.93E-30
Oasl2	2'-5' oligoadenylate synthetase-like 2	2.3	8.43E-26
Isg15	ISG15 ubiquitin-like modifier	2.3	1.78E-23
Mx2	myxovirus (influenza virus) resistance 2	2.5	1.19E-21
Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	2.1	6.39E-19
Gbp6	guanylate binding protein 6	2.1	9.07E-19
Ifitm3	interferon induced transmembrane protein 3	2.0	9.37E-15
Rsad2	radical S-adenosyl methionine domain containing 2	2.2	2.35E-13
Usp18	ubiquitin specific peptidase 18	2.3	9.50E-13
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	2.8	5.95E-12
Ifit1	interferon-induced protein with tetratricopeptide repeats 1	2.5	7.31E-08
Gbp10	guanylate-binding protein 10	2.6	1.01E-06
Ifit2	interferon-induced protein with tetratricopeptide repeats 2	2.2	1.07E-06
Ifi44	interferon-induced protein 44	2.4	5.51E-05
Immune response			
Csf1	colony stimulating factor 1 (macrophage)	2.2	4.06E-47
Tnfrsf9 (CD137)	tumor necrosis factor receptor superfamily, member 9	2.0	4.68E-19
Igj	immunoglobulin joining chain	2.2	3.50E-12
Tnfsf4 (CD134L)	tumor necrosis factor (ligand) superfamily, member 4	2.2	4.24E-06
Il15	interleukin 15	2.2	0.009964831
Signalling			
Axl	AXL receptor tyrosine kinase	2.0	2.23E-111
Phlda3	pleckstrin homology-like domain, family A, member 3	2.6	8.88E-27
Other			
Epha2	Eph receptor A2	2.1	8.10E-08
Smoc1	SPARC related modular calcium binding 1	3.0	3.51E-06
Unknown			
9030617O03Rik		2.7	3.17E-34
Pydc4	pyrin domain containing 4	2.4	2.33E-30
6530418L21Rik (Fam212b)	family with sequence similarity 212, member B	2.6	4.94E-30
Pydc3	pyrin domain containing 3	2.2	6.11E-30
Gm12250		2.0	2.81E-16
G530011O06Rik		2.0	1.84E-14
I830012O16Rik		2.6	5.05E-09
Gm5431	predicted gene 5431	2.4	6.12E-05
C130083M11Rik		2.0	0.000270942
Lmo7	LIM domain only 7	2.1	0.000659593
Metabolism			
Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	2.1	4.20E-14
Pla1a	phospholipase A1 member A	2.2	0.002062752
Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	2.7	0.002559054
Cell trafficking			
Cxcl10	chemokine (C-X-C motif) ligand 10	2.5	3.80E-08
Cxcr7	chemokine (C-X-C motif) receptor 7	2.7	3.83E-08
Ccrl2	chemokine (C-C motif) receptor-like 2	2.0	0.000369833
S1pr2	sphingosine-1-phosphate receptor 2	2.1	0.001110386
Madcam1	mucosal vascular addressin cell adhesion molecule 1	27.9	0.001360544
Transcription			
Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	5.3	1.29E-195

ordered within groups by p value (less than or equal to 0.01 p adj)

blue color: indicates genes that were identified as not upregulated in both RELA and c-REL-deficient cultures

Table S5. Antibodies used for flow cytometry (FC), immunohistochemistry (IHC), ELISA (EL) and Western blot (WB) analysis.

Molecule/ Antigen	Application	Species	Fluorochrome/ Conjugate	Source	Clone	Manufacturer
β-Actin	WB	mouse	−	mouse	AC-15	Sigma
B220	IHC	mouse	Biotin	rat	RA3-6B2	BD Pharmingen
B220	FC	mouse	PE-CF594	rat	RA3-6B2	BD Horizon
B220	FC	mouse	PerCP	rat	RA3-6B2	BD Pharmingen
BCL2	WB	human	−	rabbit	SC-783	Santa Cruz
BCL6	IHC	mouse	−	rabbit	N-3	Santa Cruz
BLIMP1	WB	mouse	−	rat	6D3	Santa Cruz
CD16/CD32	FC	mouse	−	rat	2.4G2	BD Pharmingen
CD38	FC	mouse	Alexa Fluor 700	rat	90	eBioscience
CD138	FC	mouse	PE	rat	281-2	BD Pharmingen
CD86	FC	mouse	APC	rat	GL1	eBioscience
CD95	FC	mouse	PE	hamster	Jo2	BD Pharmingen
c-Myc	WB	mouse	−	rabbit	Y69	Abcam
c-Rel	WB, IHC	mouse	−	rabbit	C	Santa Cruz
CXCR4	FC	mouse	PerCP-eFluor 710	rat	2B11	eBioscience
Cyclin D3	IHC	mouse	−	rabbit	DCS22	Cell Signaling
GFP	IHC	mouse	Alexa Fluor 555	rabbit	−	Invitrogen
IgG1	FC	mouse	APC	rat	X56	BD Pharmingen
IgG1	IHC, EL	mouse	AP	goat	−	Southern Biotech
IgM	IHC, EL	mouse	AP	goat	−	Southern Biotech
IRF4	WB	mouse	−	goat	M-17	Santa Cruz
NF-κB p65	WB	mouse	−	rabbit	C-20	Santa Cruz
NP(8)	FC	mouse	PE	−	−	Biosearch Technologies
PNA	FC	mouse	Biotin	−	−	Vector Laboratories
Streptavidin	FC	mouse	APC	−	−	BD Pharmingen
Streptavidin	FC	mouse	eFluor 450	−	−	eBioscience
Secondary antibodies:						
Anti-Goat IgG	WB		HRP	donkey		Santa Cruz
Anti-Mouse IgG	WB		HRP	goat		Thermo Scientific
Anti-Rabbit IgG	WB		HRP	donkey		GE Healthcare
Anti-Rat IgG	WB		HRP	goat		GE Healthcare

Table S6. Primer sequences used for quantitative RT-PCR analysis. All primer pairs were validated by analysis of standard curves (efficiency of 90-110%) and dissociation curves to yield one single peak.

Gene symbol	***Forward primer***	***Reverse primer***	***Source***
Fads2	GGTGGTTGTAGGGCAGGTATT	ACCGACATTTCCAACACCAT	NCBI Mouse PrimerDepot
Hprt1	AGCTACTGTAATGATCAGTCAACG	AGAGGTCCTTTTCACCAGCA	RTPrimerDB (www.rtprimerdb.org)
Phgdh	AGGTGGTGGAGAAGCAGAACTTG	CAGCAGTGACCTTAGTAGCAGAC	In-house design
Pla2g16	GTCTGCTTTGACTGACAAGGC	GTGTACTCCTCGTCATGTTTGTT	In-house design
Slc7a6	AAGATGGTAGGTGGGTGTGG	GAGGAGGTAGCTGGCGAGG	NCBI Mouse PrimerDepot