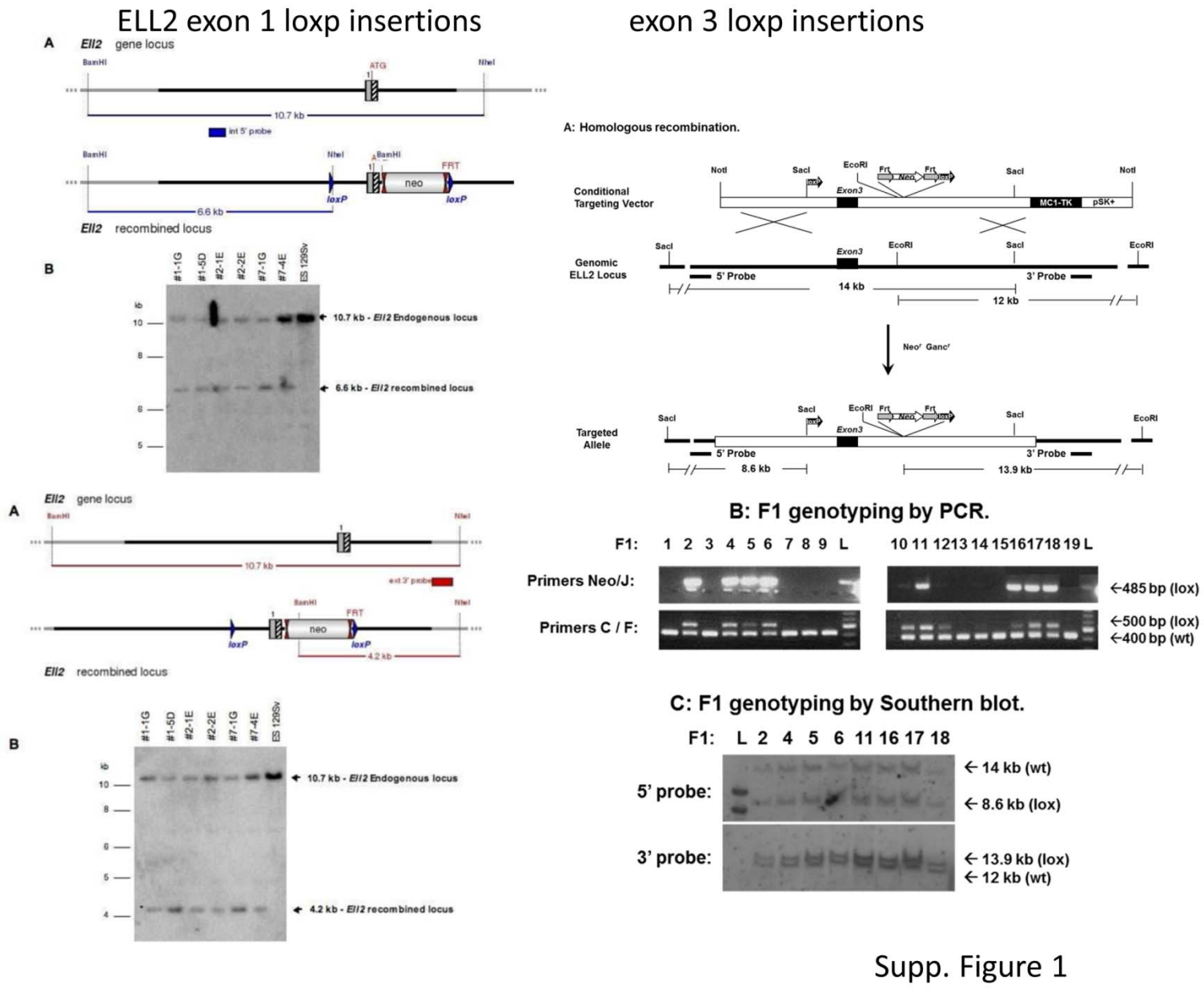


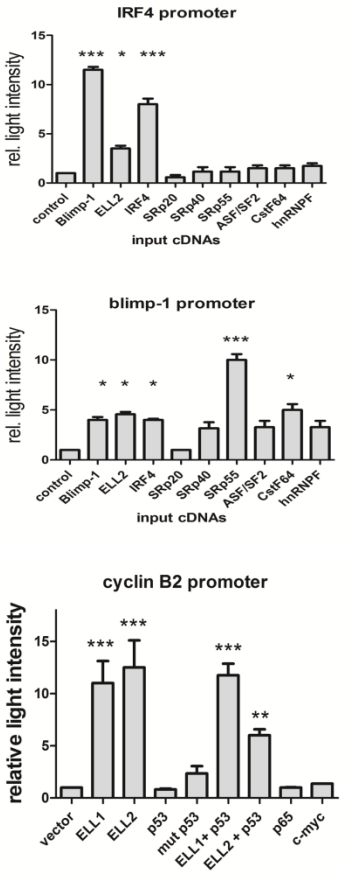
Supplemental Figure 1. Southern blots of gene insertion in Exon 1 and exon 3

Top left: Southern blot analysis for 5' homologous recombination in ES cells. (A) schematic representation of the wild type ELL2 allele and the recombined allele with the relevant restriction sites for the Southern blot analysis is shown. The strategy for the 5' Southern blot analysis is indicated with a 10.7 kb endogenous ELL2 band plus 6.6 kb recombinant band. (B). the genomic DNA of the tested ES cell clones was compared with wild-type DNA (129SvPas). The digested DNAs were blotted on nylon membrane and hybridized with the 5' probe detecting the BamhH1-NheI fragment to screen for 5' homologous recombination event.

Bottom left: Southern blot analysis for 3' homologous recombination in ES cells. (A) schematic representation of the wild-type ELL2 allele and the recombined allele with the relevant restriction sites for the Southern blot analysis shown. The strategy for the Southern blot detection of the 3' targeting event is indicated with a 10.7 kb ELL2 endogenous band and a 4.2 kb recombinant band. (B) The genomic DNA of the tested ES cell clones was compared with wild-type DNA (129SvPas). The digested DNAs were blotted on nylon membrane and hybridized with the external 3' probe SA-E to screen for the 3' homologous recombination event.

Right panel: Southern blots of loxp gene insertion in Exon 3. (A) homologous recombination between the ELL2-cKO targeting vector and the ELL2 genomic locus. Correctly targeted ES cells have the cKO with 8.6 kb SacI band, in addition to a new 14 kb wild-type band, following hybridization with the 5' probe. These cKO clones also have a 13.9 kb EcoRI-targeted band as well as a 12 kb wild-type (129SvPas) band, following hybridization with the 3' probe as shown in the Southern blot of the F1 hybrids in (C). In (B) PCR showing 485 lox band with neo/J primer and 500 nt loxp containing band vs 400 nt wt band with C/F primers.

Supplemental Figure 2. Luciferase transcription assays with IRF4 Blimp-1 and cyclin B2 promoters



Supplemental Figure 2. Constructs with the (A) IRF4 (-2182 to 0) or (B) Blimp (-2973 to 0) promoters in the pGL4.11 luciferase vector were transfected into 293 T cells along with plasmids encoding the indicated cDNAs. In (C) the mouse cyclin B2 promoter cloned in pGL4.10 was obtained from Dr. Engeland as described in materials and methods. Two days after transfection the cell lysates were prepared and relative light units produced were determined in a luminometer. All transfections were performed at least three times. P values $\leq$0.05 is indicated by *; P$\leq$0.01 by **; and P$\leq$0.001 by *** .

Supplemental Table 1. Characterization of B cell subsets

population	**phenotypic definition**	
Bone marrow		
pro-B	B220+CD43+	
pre-B	B220+CD43-	
immature B	B220+IgM+	
recirc B	B220brightCD43-	
Spleen		
T1	B220+AA4.1+-	IgM+CD23
T2	B220+AA4.1+IgM+CD23hi	CD23hi
T3	B220+AA4.1+	IgMloCD23-
pPB	AA4hiB220intCD138-	
PC	AA4hiB220intCD138+	
FO	B220+CD21intCD23+	
FO Type I	B220+AA4.1-CD21intIgMloIgDhi	
FO Type II	B220+AA4.1-CD21intIgMhiIgDhi	
MZp	B220+AA4.1-CD21hiIgMhiCD23hi	
MZ	B220+CD21hiCD23lo	
MZ (alt)	B220+AA4.1-CD21hiIgMhiCD23lo	
CD4+ T	CD4+	
CD8+ T	CD8+	

Table 2. Primers used for RT-QPCR

gene	Oligo numbers	sequences
aicda	52002573/4	F: GGGCCAAGGGACGGCATGAG R: CCACGTGGCAGCCAGACTTGT
AFF1/af4	78065462/3	F: AGCGCCCAGGTCCTCCTCAG R: GCTGCTGGCACTTCTGGGGG
ATF6 4458	118235982/3	F: CTGGGCTCGGTAGTTTGTATC R: AGACCTGAATGGCTGCTTAC
ATF6 6076	118235984/5	F: GTGACCTGTAGCTCTGTCATAAG R: GTGGGTAAGGACTACGAGTTTG
Bcl6 Bcl6 Exon7/8	86298150/1 44582739/40	F: CATCGTGGTGAGCCGTGAGCA R: CAACTGGTCAGTGAAGATAC F: GCAACGAATGTGACTGCCGTTTCT R: CCGATTGAACTGCGCTCCACAAAT
BCMA / tnfrsf17	87205307/8	F: CATGCTTGCAAACCGTGTCA R: CACCGTGTACGTCCCTTTCA
BiP 663	118235978/9	F: CTGTTCCGCTCTACCATGAA R: GAGTAGATCCACCAACCAGAAC
BiP 347	118235980/1	F: CACCTTCGATGTGTCTCTTCTC R: ACCCGCTGATCAAAGTCTTC
Blimp-1 ex6/7/8	44582741/2	F: TTCAAGTGCCAGACCTGCAACAAG R: TCGAAGGTGGGTCTTGAGATTGCT
BRD4 ex5/6	48269793/4	F: TATGCCTGGCCTTTCTACAAGCCT R: ATCAGCACCAAATTCCTGGGCATC
Cdk8 ex12/13	50312483/4	F: GAACCAGGACAGCGGCCACG R: TCCCATGCTGCTCTGGGGCT
c/EBP-beta	78433471/2	F: TGCGCAACCTGGAGACGCAG R: AGGGTGCTGAGCTCTCGCGA
CstF2	16083678/9	F: GATCCTGAGATTGCGCTGAAA R: GGCTGAGGGTTGCCTGAAA
Cyclin B2 (CCNB2)	90368558/9	F: CCTCATGGCGCTGCTCCGACG R: CCGCCGGATAGTCACATGGCTCTT
Eaf1	78433465/6	F: CCGGGCAAGTGCAAGGCCAT R: TGCCAACCTGTAGTTCTCCTTCACA
Eaf2 exon 6/7/8	44582743/4	F: GCAACAGCAAATGTGGAATCTGCC R: AGTCCTCACTGTCGCTTTCTGACT
ELL1	87855970/1	F: GGAGTTACGGGTTGTCGTGT R: AGAGATGTGCCCTTGGCTTC
ELL2 ex3/4/5	23545157/8	F: CTGGCCAGGTTACAGTGAGA R: AGCGTCTTTGCTGGAACAC
ELL3	85776881/2 85776883/4	F: AGAGCCTCTCAGCTCCATCAGCC R: GCCCCAACTCGAGCATGCAG F: AGGGAGGAGAAGCATCGCTGT R: TCACCGGGGAAGATCCGAGC
Hif1-alpha	88741016/7	F: TGACGGCGACATGGTTTACA R: ACTGGGCCATTTCTGTGTGT
HPRT	16083680/1	F: CCTAAGATGAGCGCAAGTTGAA

		R: CCACAGGACTAGAACACCTGCTAA
HSP40	88741018/9	F: TCCCGTCTAAGAGTAAGGAAGACT R: GGTCATTGATCGTCACCTTCC
Ig kappa C region	53279371/2	F: ACAGACCCTGGCTTAAGGCCCT R: GCCTCTGTATGGCTTCCTTTGGTG
Igh mu CH4-M1 splice	42553248/9	F: TCCGGAGAGACCTATACCTGTGTT R: TTCTCAAAG CCTTCCTCCTCAGCA
Igh mu sec 3'UTR	42552350/1	F: TCTCCCTGATCATGTCTGACACAG R: ATACACAGAGCAACTGGACACCCA
IRE1 3'UT	118235972/3	F: AGGAAAGAGCAGTCCCAATTTA R: ATGTCTGGGTGTGGGTTTAC
IRF4 ex3/4/5	44582745/6	F: AAGATTGTTCCAGAGGGAGCCAAA R: ATGGGATTTCTGGGTGTGACTGGT
OcaB	78433473/4	F: TCCTTCCACGTGGGCTTTTATTCCT R: GACCCCAGAGACAGCCGGTGA
P50 of NF-kB	86298152/3	F: GGAGACCGGCAACTCACAGA R: GAAGCTGCCAGTGCTGTCAGG
P65 relA /NF-kB	52002569/70	F: TACTTTAGCGCGCCGTGGGC R: AGCCTGGGCTGGCTCTGAGG
Pax5	86298148/9 87205309	F: CGTCAGCTCCATCAACAGG R: CTCACCGATGACACCTGCG R: GTCGTACGCAGTGGCTG
PCNA	88741014/5	F: AGATGCCGTCGGGTGATTT R: ATGGTTACCGCCTCCTCTTC
Supt5h	52002571/2	F: GGGCTCAAAGCCCCGGGATG R: CCTGCTCATGCCACCTGGGC
XBP-1 "total" XBP Ex 2/3	86298154/5 44582749/50	F: GGCAGCAGGGTCGGAGGCGA R: CCGCTGCCGCTTGCGAGCCT F: GTGTCCATTCCCAAGCGTGTTCTT R: TAGAAAGAAAGCCCGGATGAGCGA
XBP-1 spliced	93215933 117556521	F: CCTTGTGGTTGAGAACCAGG R: CTGCACCTCGCGGACTCAG
XBP-1 unspliced	93215933 117556520	F: CCTTGTGGTTGAGAACCAGG R: AGGACGTGCACATAGTCTGAGTGC