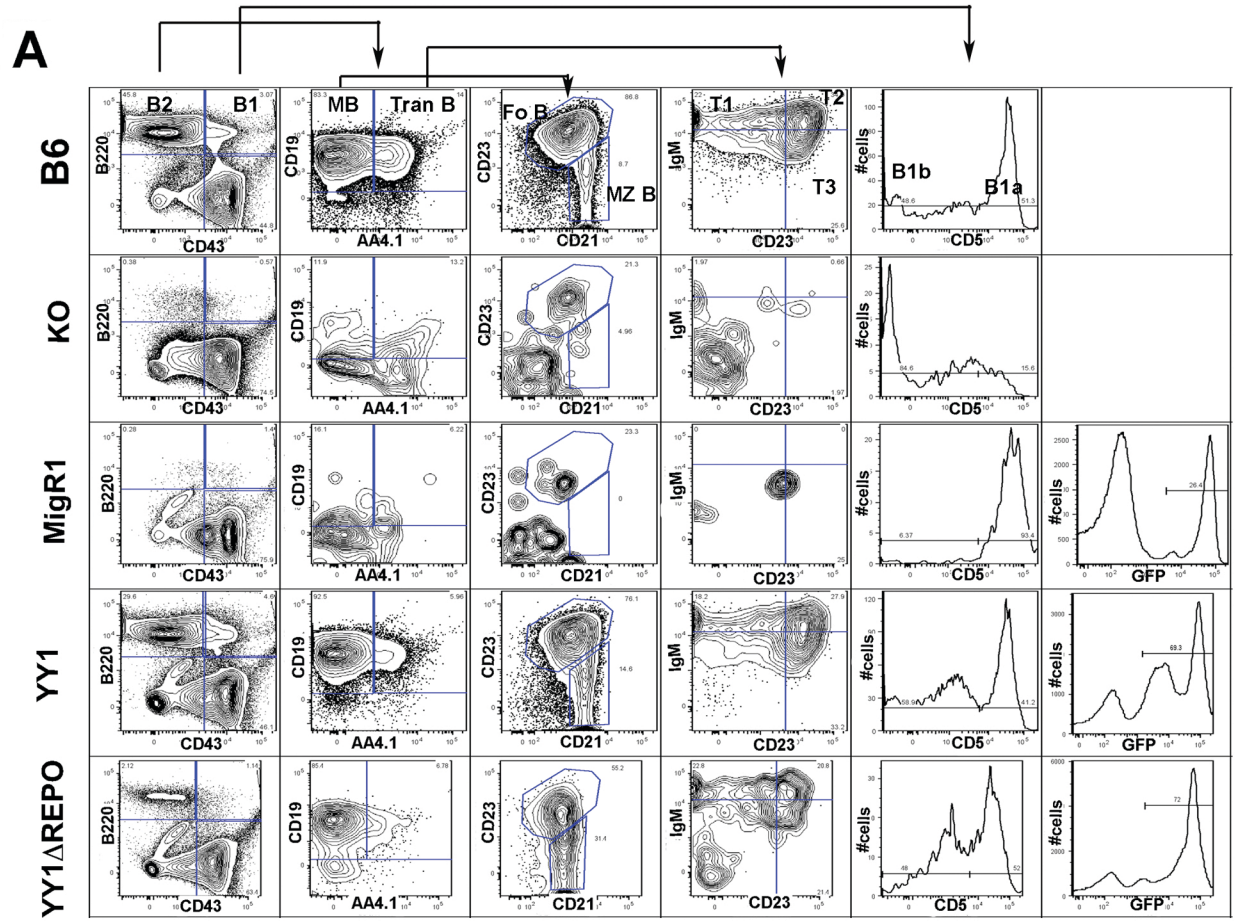
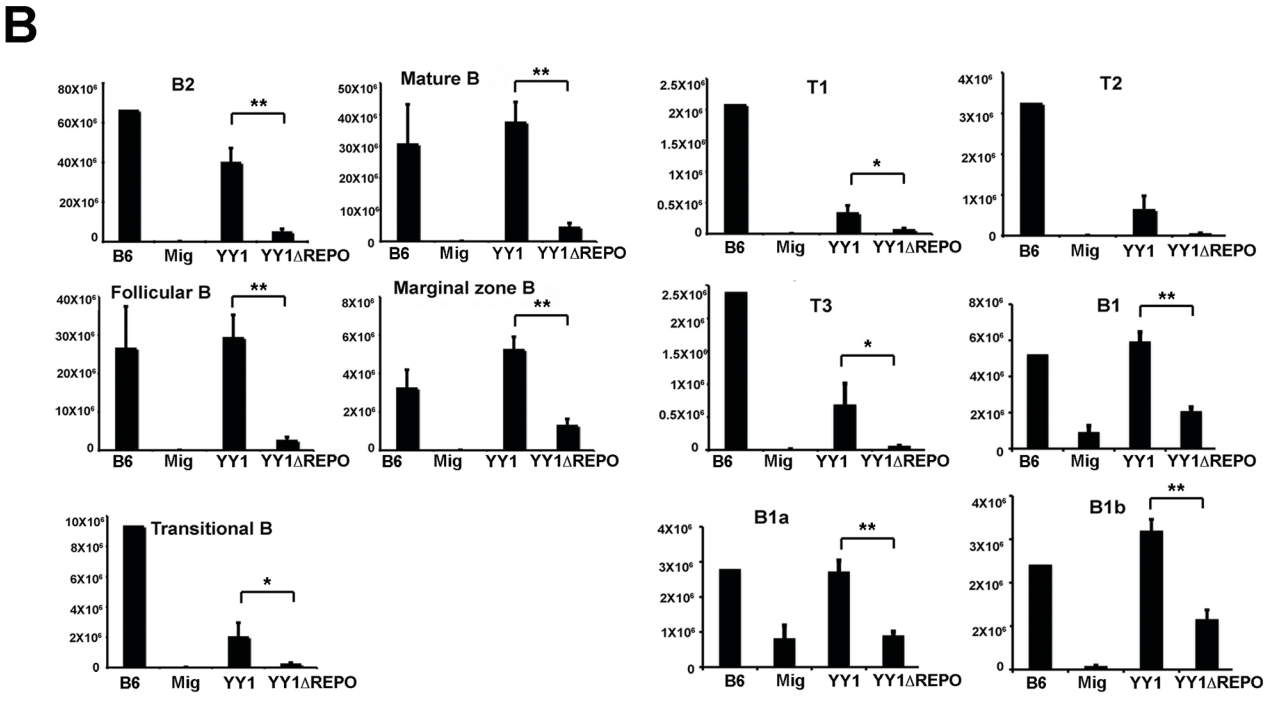
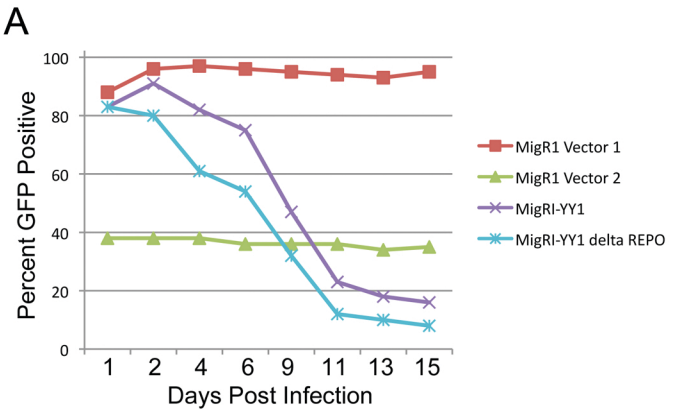
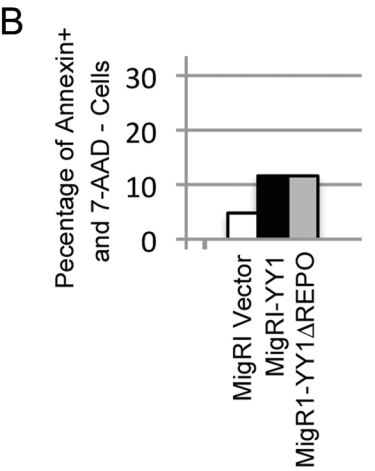
Pan et al Supplementary Fig. S1





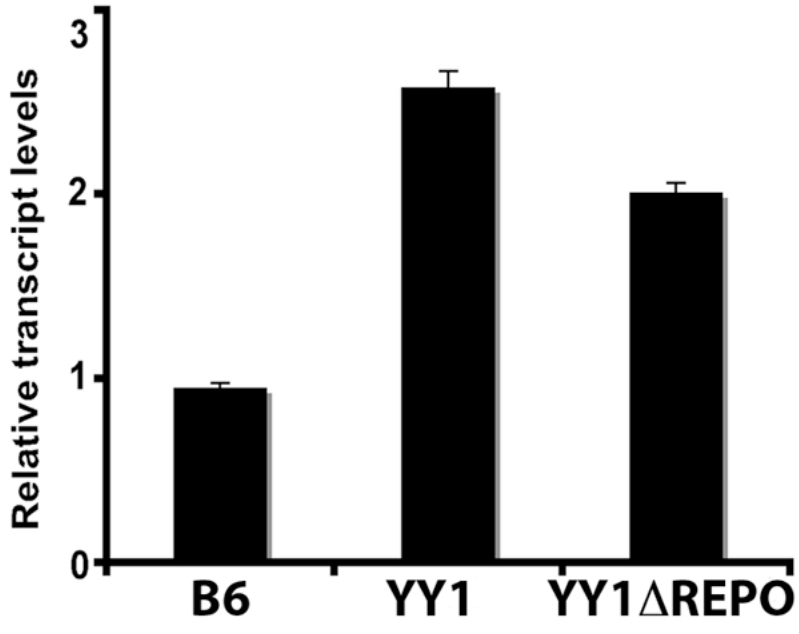
Pan et al Supplementary Fig. S2



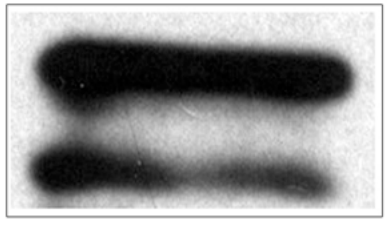


Pan et al Supplementary Fig. S3

A

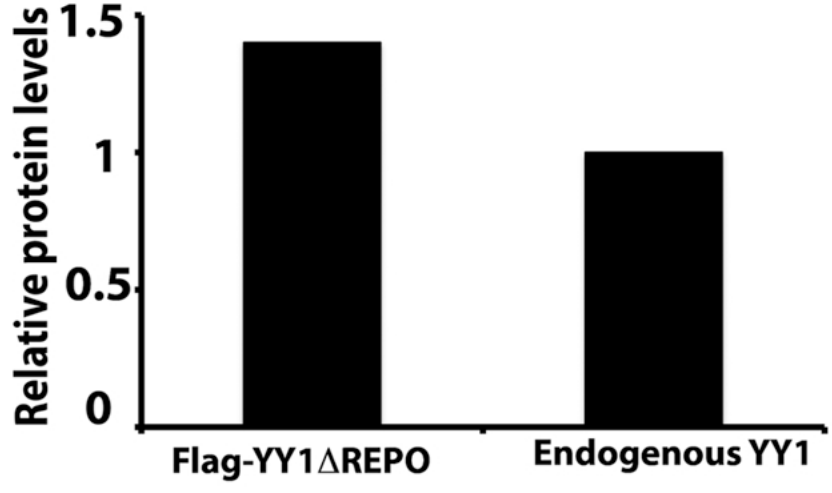


B

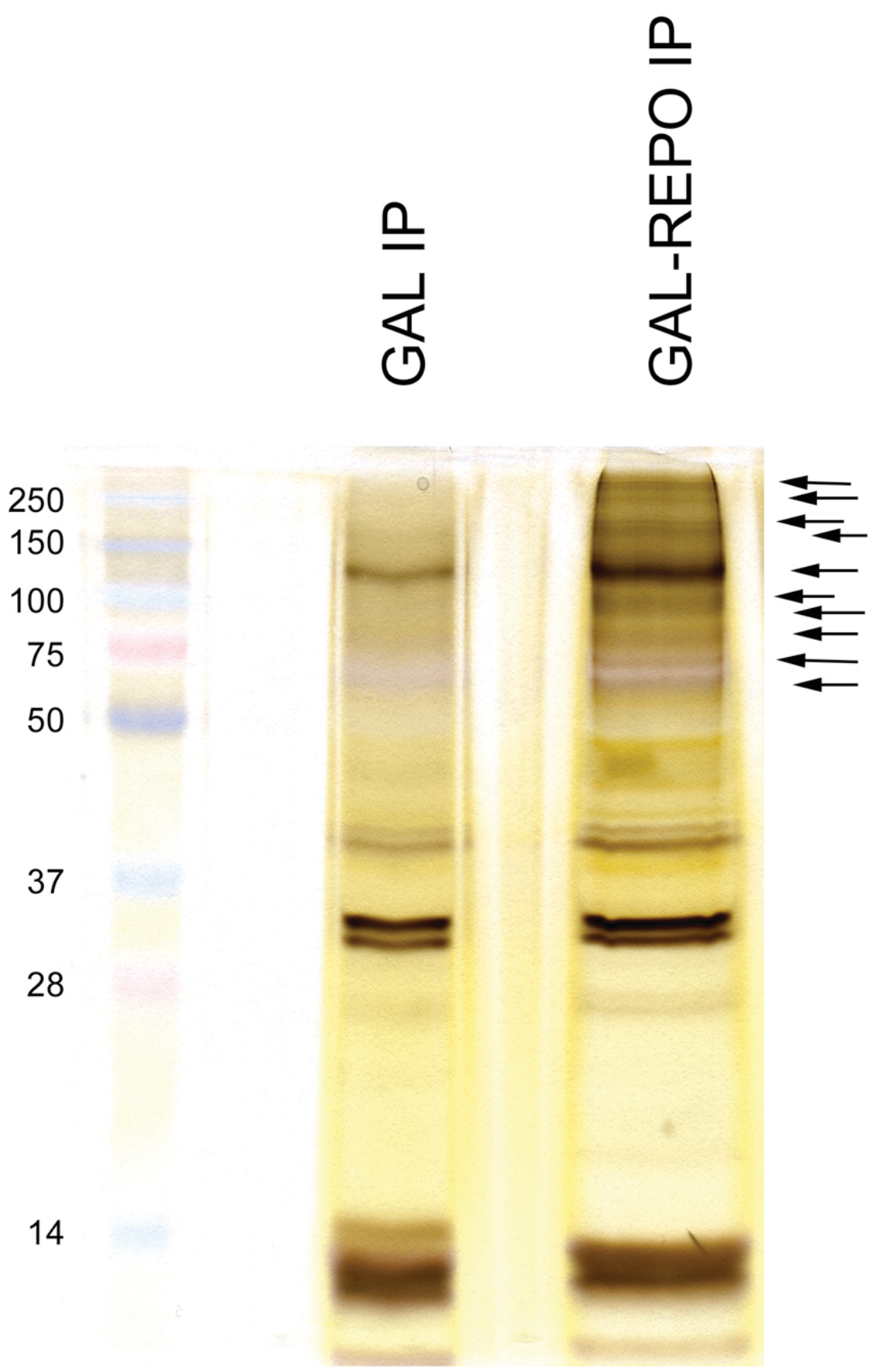


Flag-YY1ΔREPO

Endogenous YY1



Pan et al
Supplementary Fig. S4



Supplementary Figure Legends

Supplementary Figure S1. The YY1 REPO Domain is Needed for Splenic B Cell Development. MigR1, YY1 and YY1ΔREPO mice were made as described in Figure 1. Recipient mice were subject to analyses at 14 weeks post transplantation.
(A) FACS analyses of splenic B cells from mice reconstituted with *yy1$^{f/f}$ mb1CRE* bone marrow transduced with either MigR1, MigR1-FlagYY1, or MigR1-FlagYY1ΔREPO. Within the GFP$^+$ cell population, B2 cells were characterized as CD19$^+$CD43$^-$, B1 cells as CD19$^+$CD43$^+$, B1a cells as CD19$^+$CD43$^+$CD5$^+$, B1b as CD19$^+$CD43$^+$CD5$^-$, mature B cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^-$, transitional B cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^+$, follicular B cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^-$CD23^{hi} CD21/35$^+$, marginal zone B cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^-$CD23^{low} CD21/35$^-$, T1 cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^+$ IgM$^+$CD23$^-$, T2 cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^+$IgM$^+$CD23$^+$, and T3 cells as CD19$^+$CD43$^-$B220$^+$AA4.1$^+$IgM$^-$CD23$^-$. (B) Compared with YY1 reconstituted mice, YY1ΔREPO reconstituted mice have a significant decrease in mature splenic B cell subpopulations. Total cell numbers are shown of each splenic B cell subpopulation in MigR1, YY1, YY1ΔREPO reconstituted chimeric mice and B6 control mice. Mean and standard error of the mean of 4 experiments with 10 mice per cohort are shown. Single and double asterisks indicate significant differences between YY1 and YY1ΔREPO reconstituted mice at $p < 0.05$ or $p < 0.01$, respectively.

Supplementary Figure S2. YY1 and YY1ΔREPO Show Similar Effects on Growth and Apoptosis. (**A**) 38B9 pro-B cells were transduced with MigR1, MigR1-FlagYY1, or MigRIYY1ΔREPO and percent GFP-positive cells were plotted through time. (B) The

same retroviruses were transduced into 3-1 pro-B cells and percent of cells that were Annexin positive and 7-AAD negative were plotted after four days.

Supplementary Figure S3. Exogenous YY1 and YY1ΔREPO were Well Expressed in Chimeric Mice. Bone marrow from 5-FU-treated *mb1-CRE yy1$^{f/f}$* donor mice were retrovirally transduced with MigR1, MigR1-FlagYY1 or MigR1-FlagYY1ΔREPO. Lethally irradiated C57BL6 mice were reconstituted with the transduced bone marrow cells. Recipient mice were subject to analysis at 14 weeks post transplantation. (A) Exogenous YY1 and YY1ΔREPO are well expressed at the transcript level in GFP$^+$ bone marrow pre-B cells. GFP$^+$B220$^+$CD43$^-$ IgM$^-$AA4.1$^+$ bone marrow pre-B cells from C57BL/6 control, YY1 and YY1ΔREPO reconstituted mice were sorted and RNA was prepared. Endogenous YY1 transcript and exogenous Flag-YY1 or Flag-YY1ΔREPO transcripts were detected by RT-PCR. HPRT was used as an internal control for normalization and the quantitation was determined by the ΔΔCT method. Mean and standard error of the mean are shown. (B) Exogenous Flag-YY1ΔREPO is well expressed compared with endogenous YY1. GFP$^+$ lymphocytes (T cells and B cells) were sorted from the blood of MigR1-FlagYY1ΔREPO reconstituted mice 14 weeks post reconstitution and crude cell lysates were made. Western blot was performed for detection of both endogenous YY1 and exogenous Flag tagged YY1ΔREPO. The upper band indicates Flag-tagged exogenous YY1ΔREPO and the lower band indicates endogenous YY1. The intensities of bands are quantified and are normalized to the endogenous YY1 level.

Supplementary Figure S4. Identification of Proteins that Bind to the YY1 REPO Domain. 293 cells were transfected with plasmids expressing either the GAL4 DNA binding domain (GAL) or the GAL4 DNA binding domain fused to the YY1 REPO domain. Two days later lysates were immunoprecipitated with GAL4 antibodies and proteins were separated by SDS-PAGE. Arrows show bands specific for GAL-REPO compared to GAL alone. Bands were excised from the gel and analyzed by MALDI-TOF mass spec (Table I).

Supplementary Table SI

Proteins identified by Mass Spec analyses that co-IP with GAL-REPO

Protein	Mass	Identified Peptides
Topoisomerase 2A (36 queries matched)	174,276	R.EIVNNIR.R
		K.IPNFDVR.E
		R.GYDSDPVK.A
		K.FTVETASR.E
		R.AYDIAGSTK.D
		K.IIIENKPK.K
		K.EQELDTLK.R
		K.FLYDDNQR.V
		R.RAYDIAGSTK.D
		K.NYEDEDSLK.T
		K.TLAVSGLGVVGR.D
		R.EVTFVPGLYK.I
		K.TQMAEVLPSPR.G
		K.SVVSDLEADDVK.G
MSH6 (18 queries matched)	152,689	K.QVISLQTK.N
		R.YSDSLVQK.G
		R.NLPEEYELK.S
		K.LANLINAEER.R
		R.LANLPEEVIQK.G
		R.AIMYEETTYSK.K
		K.GMTSESDSIGLTPGEK.S
		K.GTQTYSVLEGDPSENYSK.Y
MBB1A (12 queries matched)	148,762	K.SPLSALAR.K
		R.LITGLGVGR.E
		K.YDLHQVK.K
		R.SPSLLQSGAK.K
		K.EIPSATQSPISK.K
SMC4 (15 queries matched)	147,091	K.FTASIQR.L
		K.TEYDAVAEK.A
		K.VLDAIIQEK.K
		R.LGDLGAIDEK.Y
		K.LTQEETNFK.S
		K.LLEENVSAFK.T
		K.SNNIINETTTR.N
SMC1A (14 queries matched)	143,144	R.ISSIYAR.E
		K.YQIAVTK.V
		K.LVIDVIR.Y
		R.VIVGGSSEYK.I
		R.TALFEEISR.S
		R.AATLAQELEK.F
		K.YSQSDLEQTK.T
		K.LNEQQSVLQR.I

PARP1 (19 queries matched)	112,881	K.ELLIFNK.Q K.AEPVEVVAPR.G -.AESSDKLYR.V K.TLGDFAAEYAK.S K.QQVPSGESAILDR.V R.VVSEDFLQDVSASTK.S
LAMA (25 queries matched)	74,095	R.LQLELSK.V K.LEAALGEAK.K R.DLEDSLAR.E R.LSPSPTSQR.S K.LLEGEEER.L R.ITESEEVVSR.E K.AAYEAELGDAR.K R.SGAQASSTPLSPTR.I
HSP7C_CRIGR (37 queries matched)	70761	R.IPKIQK.L R.GTLDPVEK.A K.DAGTIAGLNVLR.I K.VEIIANDQGNR.T K.NSLESYAFNMK.A R.TTPSYVAFTDTER.L K.TVTNAVVTVPAYFNDSQR.Q
DDX5 (29 queries matched)	69,105	R.GLDVEDVK.F K.TIVFVETK.R K.LLQLVEDR.G R.TAQEVETYR.R K.QVSDLISVLR.E K.APILIATDVASR.G R.TTYLVLDEADR.M
LAM2 (22 queries matched)	67,647	R.LQIEIGK.L R.QQEYDFK.M K.LLEGEEER.L R.EGELTVAQGR.V R.GLESDVAELR.A R.AGGPATPLSPTR.L K.ALYESELADAR.R R.QVLEGEEIAYK.F
LAM1 (47 queries matched)	66,237	K.LQIELGK.C R.EELMESR.M K.IGDTSVSYK.Y K.LLEGEEER.L R.EYEAALNSK.D K.QLADETLLK.V K.DAALATALGDK.K K.ESDLNGAQIK.L

		R.AGGPTTPLSPTR.L R.IQELEDLLAK.E K.DAALATALGDKK.S K.ALYETELADAR.R R.IESLSSQLSNLQK.E R.LSSEMNTSTVNSAR.E
RL1D1 (46 queries matched)	54,939	K.FFTTPSK.S K.TEQFYR.K R.LLPSLIGR.H K.ALPASETPK. K.VPVSVNLLSK.N K.TPANEKVEIQK.H K.DDVAPESGDTTVK.K K.ATNESEDEIPQLVPIGK.K K.TASVLSKDDVAPESGDTTVK.K

Supplementary Table SII. Primers for Ig rearrangement assays.

Primer name	Sequence
D_H	TTC AAA GCA CAA TGC CTG GCT
V_HJ558	CGA GCT CTC CAR CAC AGC CTW CAT GCA RCT CAR C
V_H7183	CGG TAC CAA GAA SAM CCT GTW CCT GCA AAT GAS C
V_HQ52	CGG TAC CAG ACT GAR CAT CAS CAA GGA CAA YTCC
J_H3	GTC TAG ATT CTC ACA AGA GTC CGA TAG ACC CTG G
Vκ19-15	TTA CTC GGC ATC CTA CCG GTA CAG
Vκ21-5	AGG ACA GAC TTC ACC CTC ACC ATT AA
Vκ2-139	CCT CTT AGA TAG TGA TGG AAA GAC A
Vκ9-122	GGC AAG TCA GGA CAT TGG TAG TAG
Vκ4-52	GCA CTG GTA CCA GCA GAA GTC AGA A
Vκ21-4	CTC ATC TAT GCT GCA TCC AAT CTA GAA TC
Vκ12-44	CGA GCA AGT GAG AAT ATT TAC AGT AAT TTA GC
Vκ38-93	CTC ATA CAT TAC ACA TCT ACA TTA CAG CC
Vκ20-137	ACC AGC ACT GAT ATT GAT GAT
Jκ1	GAC AAC GGA AGA AAG AGA CTT TGG A
Jκ2	GGT TAG ACT TAG TGA ACA AGA GTT GAG AA
Jκ5	TGC CAC GTC AAC TGA TAA TGA GCC CTC TC

Supplementary Table SIII. Primers for Igκ locus ChIP assays.

Name	Forward Primer	Reverse Primer
01	CAGAGCCCTCAGCTGCAACT	CCAGGGAAATCTCCTTAGCCC
02	CCTGATCCACTGCCACTGAA	CCTGTTGCTCTGGTTTCCAAG
1	GCCAGGCAACTCAAGACATTG	GGTCAGCCAAGCCTCTCACTT
2	TCTGCCCTACACACCCTGAAA	CAACGGTCACAGCTAGCAACA
3	TGCCAGGCTAGTCAGAGCATT	AACACTCCTGCCTTCCAGAGG
4	AGATGTGAGGTCCAGATGACTCCA	TCAGTACCTCTCCCTCTCACAAAGA
5	TCACCATGACTTGCCAGGC	TGTGGGAGGGAGATAACTATGCTG
6	GCAGTCCAGCCTCTCACTTTG	TCAGCAGAAACCAGGTGGAAC
7	TCTGGTGTCCCATCAAGGTTC	TGGTACACTCCTGCCTTCCAG
8	TGTGACGTCCAGATGACTCCA	CAGAGCCCTCAGCTGCAACT
10	CCATCCTCCCTGTCTGCATC	TGTCCCATATCCACTGCCACT
11	CCAGCAGAAACCAGGGAAATC	TTAGGAGGAACAGCTGAGGCA
13	GCAGCAGAAACCAGGGAAATC	GGCAGCCCAGCCTCTTAGTT
15	TCACCATGAGGAACATCTGGAG	CTCAGGAGTCCCATCAAGGTTC
16	TCCAGGTTGCTGATGGTGAG	TGCAAGTCAGGGCATTAGCA
19	GCTTCCCTGGGTGGTTTATGT	GCACCTGTGGGAGAAAGTGTC
20	CTTCTGCTTCCCTGCATGGT	AGCTCCTGGTCTATGCTGCAA
24	TGGCTTGAATCACTGTGGGA	CAGCTCCTGGTCTATGATGCG
25	TGTGAAGCGATCAGGGACC	CTCCATCCTCCCTGACTGTGA
29	TGGTGACTGGCCTGAGAAGAT	GAGGAGGATGGGAGCGAAA

24-140	TGCACCAAGCAGGGGATTTGCA	TCCCCAGAGTCACCCACATTCT
9-128	ATGCTCTGGACAGGCAAACT	TCAAGGCAGCACACATTCTC
12-89	TGAGTCCTGCAGCTGTGCCTA	AGCAACAGGAGCTGAGTGGGT
33-84	CTGCACCCTCTCTACTGGAGCA	TCCCATTGGCTCTGAACT6GGGT
dv-36	ACCAGGAAGGTGACGAGTGTGT	ATAAGGAGCCGGGGAACTTGCT