

SUPPLEMENTAL MATERIAL

Schenten et al., <http://www.jem.org/cgi/content/full/jem.20080669/DC1>

A

genotype	clones	mutated clones	range (mut/clone)	mutations/bp	% mutations		
control mice:							
mouse #1	48	22	1-10	77/11000	0.70		
mouse #2	39	17	1-16	72/8488	0.85		
Pol$\zeta^{f/\Delta}$/CD21-cre mice:							
mouse #1	151	36	1-6	66/17942	0.37		
mouse #2	145	45	1-7	97/22330	0.43		
mutations in naive B cells [%]: 0.03							
B							
Pol$\zeta^{f/+}$							
n = 77	A	G	C	T	Sum	Tr./Tv.	
from	A	—	21	4	10	35	1.1
	G	12	—	5	3	20	
	C	4	6	—	5	15	
	T	8	8	14	—	30	
Pol$\zeta^{f/\Delta}$/CD21-cre							
n = 66	A	G	C	T	Sum	Tr./Tv.	
from	A	—	32	8	8	48	1.6
	G	8	—	8	0	16	
	C	1	3	—	6	10	
	T	5	6	17	—	28	
Pol$\zeta^{f/+}$/CD21-cre							
n = 72	A	G	C	T	Sum	Tr./Tv.	
from	A	—	18	11	4	33	1.3
	G	14	—	14	1	29	
	C	4	1	—	10	15	
	T	5	4	14	—	23	
Pol$\zeta^{f/\Delta}$/CD21-cre							
n = 97	A	G	C	T	Sum	Tr./Tv.	
from	A	—	21	11	5	37	1.3
	G	5	—	7	1	13	
	C	1	2	—	5	8	
	T	8	9	25	—	42	

Figure S1. SHM analysis of $\text{Pol}\zeta^{f/\Delta}/\text{CD21-cre}$ mice. (A) Frequency and range of mutations in a 500-bp-long region in the intron downstream of the rearranged $V_{\text{H}}D_{\text{H}}J_{\text{H}}4$ joints of splenic GC B cells of $\text{Pol}\zeta^{f/\Delta}/\text{CD21-cre}$ and control mice. After cell lysis, a 500-bp fragment was PCR amplified from 25,000 cell equivalents using a primer pair that anneals in the framework 3 region of most J558 V genes and in the intron downstream of $J_{\text{H}}4$ gene segment. (B) Patterns of mutations in the same intronic region. All values are shown in percentage and were rounded to the nearest whole number. n = the number of mutations; Tr./Tv, the transitions (Tr.) over transversions (Tv.) ratio. The mutation patterns are not corrected for the base composition of the $J_{\text{H}}4$ intron. Each pattern is derived from one mouse.

Table S1: Mutation frequencies in the S μ and S γ 3 regions near the S μ -S γ 3 junctions in class-switched B cells of Pol $\zeta^{f/\Delta}$ /CD21-cre mice.

Genotype	Clones	Percentage of mutated clones	Range (mutations/clone)	Percentage of mutations
Control mice				
S μ junctions	61	34.4	1 - 4	0.53
S γ 3 junctions	62	20.9	1 - 3	0.27
Pol $\zeta^{f/\Delta}$ /CD21-cre				
S μ junctions	36	20.0	1 - 2	0.21
S γ 3 junctions	38	18.4	1 - 2	0.22

The frequency of mutations was measured within a 100-bp region adjacent to either side of S μ -S γ 3 junctions.

Table S2. Types of genomic abnormalities in stimulated Pol $\zeta^{f/\Delta}$ /CD21-cre B cells measured by telomere-specific FISH

Genotype	Cytokine stimulation	Number of metaphases analyzed	Number of chromosomal aberrations	Number of chromatid breaks	Number of chromosome breaks	Number of other chromosome abnormalities
Pol $\zeta^{f/+}$	α -CD40 + IL-4	30	1	0	0	1
CD21-cre	α -CD40 + IL-4	30	2	0	2	0
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40 + IL-4	30	8	4	2	2
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40 + IL-4	30	9	6	3	0
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40 + IL-4	30	5	0	3	2
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40 + IL-4	30	4	0	2	0
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40 + IL-4	30	3	0	2	1
Pol $\zeta^{f/+}$ /CD21-cre	α -CD40	28	1	0	1	0
Pol $\zeta^{f/+}$ /CD21-cre	α -RP105	22	0	0	0	0
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	47	25	18	4
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	41	18	23	0
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	30	10	19	1
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	35	17	12	6
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	16	3	9	4
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40 + IL-4	30	19	7	8	4
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40	30	18	12	6	0
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40	20	10	1	9	0
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -CD40	23	1	0	1	0
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -RP105	30	31	10	13	8
Pol $\zeta^{f/\Delta}$ /CD21-cre	α -RP105	30	29	12	16	1

Each row represents the results from one individual mouse.