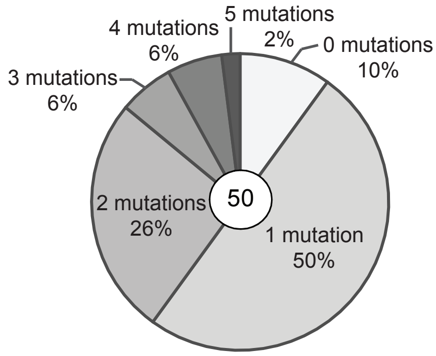
A

IgL(-)GFP2 2-3



Mutation Profile IgL(-)GFP2 2-3

From \ To	A	C	G	T
A		0	0	1
C	3		32	5
G	17	9		5
T	0	0	0	

1.5 mutations/seq
73 point mutations
58464 bp sequenced
1.25x10-3 mut/bp

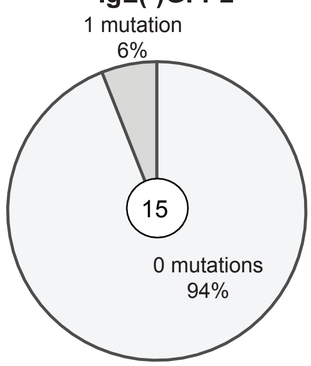
Published Profile IgL(+)GFP2 W

From \ To	A	C	G	T
A		0	2	0
C	21		73	33
G	25	67		2
T	1	0	0	

0.9 mutations/seq
224 point mutations
180,750 bp sequenced
1.24x10-3 mut/bp

B

IgL(-)GFP2



Mutation Profile IgL(-)GFP2

From \ To	A	C	G	T
A		0	0	0
C	0		0	0
G	0	0		0
T	1	0	0	

0.06 mutations/seq
1 point mutation
17661 bp sequenced
5.7x10-5 mut/bp

Published Profile IgL(-)GFP2

From \ To	A	C	G	T
A		0	3	1
C	1		0	2
G	7	0		0
T	0	1	0	

0.06 mutations/seq
15 point mutations
186,534 bp sequenced
8.04x10-5 mut/bp

Fig. S1. Sequence analysis of mutations supported by DIVAC 2-3. Genomic DNA was isolated from (A) IgL(-)GFP2 2-3 and (B) IgL(-)GFP2 cell lines on day 21 post-subcloning. A 1217 bp region of the GFP2 expression cassette was PCR amplified, cloned, and sequenced. The pie chart shows the proportion of sequences containing the indicated number of mutations; the middle circle denotes the number of sequences analyzed. Mutation spectra are depicted in the box diagrams (left, sequences from this analysis; right, published data from (34)). Further information concerning the mutations and mutation frequencies are detailed below the mutation spectra.

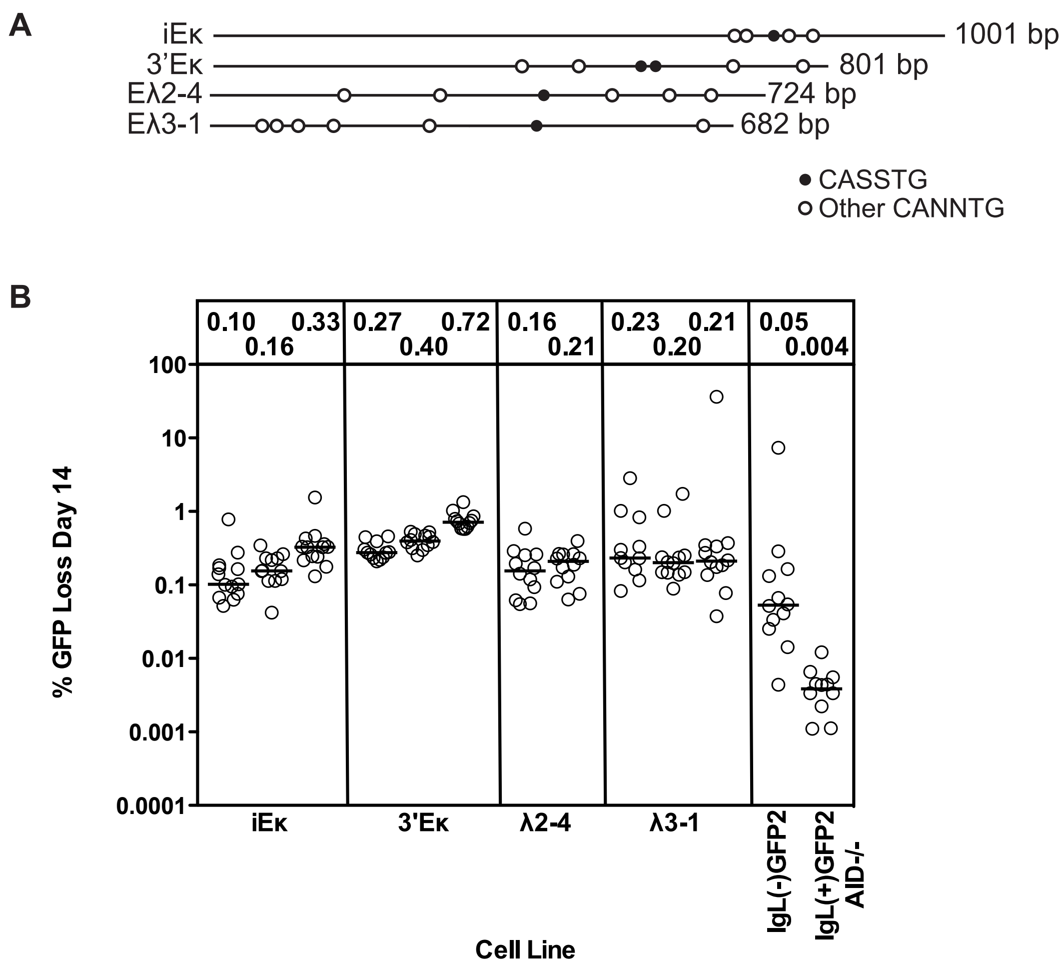


Fig. S2. Analysis of DIVAC function associated with murine Ig light chain enhancers. (A) Schematic diagram of the murine Ig light chain enhancers. The sizes of the fragments containing the intronic Igκ enhancer (iEκ), 3' Igκ enhancer (3'Eκ), Igλ 2-4 enhancer (Eλ2-4), and Igλ 3-1 enhancer (Eλ3-1), are indicated, as are the locations of E boxes conforming (closed symbols), or not conforming (open symbols) to the motif CASSTG. (B) Fluctuation analysis of GFP loss in subclones with data depicted as in Fig. 2D.

Fig. S3

A

AGCAGGCCGCATGGTACAGCTCCATCAGCA**CAGCTG**GGGCCACACAAAGAGCTGGGTTACTGTGGGCAGCAGGCT
GAAACCCGAAAACAAGAGCTGGGGGCTCAGAATAGCCCCGGGAGCAGGCAGGGCCTGGGGGAGAGGGCAAGCAC
CAGGCCCAGGGCCACACAGCCCTTCCAGGAAGGCACAGCGCTGTCAGGGTGCAGCACGCTCAGCCCCACCATG**CA**
GCTGTGCGGCCGGGGCATCCCCAAGCTAAATTTACTTCTCAGTCTCCAATCAGAAACTGAAGCTGAGGGGCCCACG
CCGGCCAAAAAAAGGAAACGAAACAGTCTCCAGAAAGCACTGACGTGTGAAGCAGAGCGAGCGCCGCGCAAACCG
GCCGCCATGTCACACACCTCAGGTTGGGGCTTTGCCAGACTGAGCTTTGCTGCTGCTCGGGGTGGGTGCCCACGGC
CTGGG**CACATG**GGATGGGGTACACACGTACACA**CACTTG**CACACCCACACCCCAACACTT**CAGGTG**ATGCTGGTGC
AGATGGGTGCCCCCCAGGCTGACCCCGCTTGCAAAGAGGAGAG**CATTTG**CATGGCTGTGGCAAAACAGCAACCGCC
TGTTGTG**CAGCTG**GGATGGTGTTATCTGGAAATGTACGCAGCCCAGGAGGGGTAAACAGCTCCAAACTGAGACCCT
GAGCTTGTCCACAGGTTGTAAACAGGCTGACATAAACACCTTTGTGCCGTGGAAAAATATTTATCACCTCAAATATAG
CAGGTTAATAAAATAAAACTCCCAACGGAGCTTCACACCTGCTTTGGAAGGGAAGCAGA**CACTTG**TTTTCTGCTTGAT
GTTGGCTGTAGGAAGCCATGTTTCCCGATGCAGGAGGGCCACAAAGCACTGACAACACAATGTGAGCTGAGCTTCG
CCCCTGTTTAAGCCCCCACCACAGGGCTTGTGGCCCTAGAGCAGACAGGGCGCAGGGGTGGCACCGGGCTGGGTG
ACATGGGCTGGTCCTGGGGTGTCTCACTGAGCTCTTTGGGGAGGGGTTGGAGCCCTGGGGCAATCACAGCACACAC
AGGAGGTGGGGGGATGCAGCCAG**CAGCTG**CCCTGCACTAAGAAAACCCCATCCGTGGGCTTT**CAGATG**GCCTTCC
CATCTCTCTGCAGCCTCTGCATGGGCTGAGCACAAGGTTTAAGTGTTTCTGCCATGTTTTTGGGCATGTTTGGAGGG
GCAGCGTGGGCCCGGGCATACGGGTACCGC**CACGTG**CTGCCAGCCCCA**CAGCTG**AGCCTGCACTCTCC**CAGATG**T
GCTGACCGCAGCCACGGGGGCAACAGTTTCTCTTGCTAAAAATTGTAGCCGGGAAGAAAA**CACGTG**GCAACTTCGG
CCAAACAG**CAGCTG**GAGGACAGGAATAGCCGTGGCCACGGCACGCTCTGCTTCCTCGGCACAAACATTCCAGTACG
TGGCACCACGAGCGCCGCTGCCCGGCACAGCAGCAAGCAGAGCCAGGAGCAGGAAATGCTGATTTGGGCCCCATT
TTGGCCATGGCTGAGAGAAGAGGCTTCCAGGGAGCTGGTCAGCTTGGTCCCCAAGCTGTGGCTTGGGGAAATGATG
GGGAGGGGATTGCCACTGCCCACCCTGCAGAGCAGGCTCTGGTCCCATCTCACTGCAGGGCACCAGGGCGTTTGC
ACTGCAGCAATTCACAGAAACATTGAAATGGCTCCT

B

AACATCCCACCAGCACACGGGGCTCAGCACGCCTGGCGACGTGGCATCAGCAGAGCAGGCCGCATGGTACAGCTC
CATCAGCA**CAGCTG**GGGCCACACAAAGAGCTGGGTTACTGTGGGCAGCAGGCTGAAACCCGAAAACAAGAGCTGG
GGGCTCAGAATAGCCCCGGGAGCAGGCAGGGCCTGGGGGAGAGGGCAAGCACCAGGCCCAGGGCCACACAGCCC
TTCCAGGAAGGCACAGCGCTGTCAGGGTGCAGCACGCTCAGCCCCACCATG**CAGCTG**TGCGGCCGGGGCATCCCC
AAGCTAAATTTACTTCTCAGTCTCCAATCAGAAACTGAAGCTGAGGGGCCCACGCCGGCCAAAAAAAGGAAACGAAA
CAGTCTCCAGAAAGCACTGACGTGTGAAGCAGAGCGAGCGCCGCGCAAACCGGCCGCCATGTCACACACCTCAGGT
TGGGGCTTTGCCAGACTGAGCTTTGCTGCTGCTCGGGGTGGGTGCCCACGGCCTGGG**CACATG**GGATGGGGTACA
CACGTACACA**CACTTG**CACACCCACACCCCAACACTT**CAGGTG**ATGCTGGTG**CAGATG**GGTGCCCCCCAGGCTGAC
CCCCCCACGCATGGGCCTGGCCCCACACTGCTCCATCCGTGTCTCTGACTAGCGGCGGAGCCC**CAGCTG**TAGGAA
GCTCAGAGCCATCACACAGCAATTAAAGAGGAATTAAATTAAATCAATAAATGTTTTAGGCGGGCT**CAGCTG**CCAGCA
C**CACCTG**ACCGAAACAGCCCGCTTGCAAAGAGGAGAG**CATTTG**CATGGCTGTGGCAAAACAGCAACCGCCTGTTGT
G**CAGCTG**GGATGGTGTTATCTGGAAATGTACGCAGCCCAGGAGGGGTAAACAGCTCCAAACTGAGACCCTGAGCTT
GTCCACAGGTTGTAAACAGGCTGACATAAACACCTTTGTGCCGTGGAAAAATATTTATCACCTCAAATATAGCAGGTT
AATAAAATAAAACTCCCAACGGAGCTTCA**CACCTG**CTTTGGAAGGGAAGCAGA**CACTTG**TTTTCTGCTTGATGTTGGC
TGTAGGAAGCCATGTTTCCCGATGCAGGAGGGCCACAAAGCACTGACAACACAATGTGAGCTGAGCTTCGCCCCTG
TTTAAGCCCCCACCACAGGGCTTGTGGCCCTAGAGCAGACAGGGCGCAGGGGTGGCACCGGGCTGGGTGACATGG
GCTGGTCCTGGGGTGTCTCACTGAGCTCTTTGGGGAGGGGTTGGAGCCCTGGGGCAATCACAGCACACACAGAGG
AGGTGGGGGGATGCAGCCAG**CAGCTG**CCCTGCACTAAGAAAACCCCATCCGTGGGCTTT**CAGATG**GCCTTCCCATC
TCTCTGCAGCCTCTGCATGGGCTGAGCACAAGGTTTAAGTGTTTCTGCCATGTTTTTGGGCATGTTTGGAGGGGCAG
CGTGGGCCCGGGCATACGGGTACCGC**CACGTG**CTGCCAGCCCCA**CAGCTG**AGCCTGCACTCTCC**CAGATG**TGCTG
ACCGCAGCCACGGGGGCAACAGTTTCTCTTGCTAAAAATTGTAGCCGGGAAGAAAA**CACGTG**GCAACTTCGGCCAA
ACAG**CAGCTG**GAGGACAGGAATAGCCGTGGCCACGGCACGCTCTGCTTCCTCGGCACAAACATTCCAGTACGTGGC
ACCACGAGCGCCGCTGCCCGGCACAGCAGCAAGCAGAGCCAGGAGCAGGAAATGCTGATTTGGGCCCCATTTTGG
CCATGGCTGAGAGAAGAGGCTTCCAGGGAGCTGGTCAGCTTGGTCCCCAAGCTGTGGCTTGGGGAAATGATGGGG
AGGGGATTGCCACTGCCCACCCTGCAGAGCAGGCTCTGGTCCCATCTCACTGCAGGGCACCAGGGCGTTTGCACTG
CAGCAATTCACAGAAACATTGAAATGGCTCCT

Fig. S3. Sequences of key DIVAC fragments. (A) DIVAC 1703. (B) DIVAC 1928. In both, the F2 core is the 5’ underlined section and the F3 core is 3’ underlined section. E boxes are indicated in bold.

Table S1

A

Construct Name	Primer Sequence	Template DNA	Product Size (bp)
1	F: cccgctagcctgggaacagggggagttctg R: cccactagtccctgtggtcccgctgagt	DT40 Genomic	1493
2	F: cccgctagctgaggagcatgtgctgaatta R: cccactagtgggctgtttcggtcaggt	DT40 Genomic	1476
3	F: cccgctagcggcggagccccagctgtagg R: cccactagtgcggtgctccccaggatacca	DT40 Genomic	1633
2a	F: 2 F R: cccactagtctgctgatgccacgtc	2	590
2b	F: cccgctagcaacatcccaccagcacacg R: cccactagtcagagacacggatggagcagt	2	650
2c	F: cccgctagcccccccaggctgacccc R: 2 R	2	350
2b-1	F: 2b F R: cccactagtgaagggctgtgtggccctgggcc	2	227
2b-2	F: cccgctagcagccccgggagcaggcagggcct R: cccactagtcaaagctcagtctggcaaagccc	2	316
2b-3	F: cccgctagcagagcgagcgccgcgcaaaccggc R: 2b R	2	244
1-3	F: 1 F R: 3 R	DT40 Genomic	4384
2-3	F: 2 F R: 3 R	DT40 Genomic	2989
2-3Δ2a	F: 2b F R: 3 R	2-3	2452
2-3Δ2c	F: 2 F R: 2b R	2-3 (added to 3)	2640
2-3Δ2a/2c	Digested 2b vector and inserted into 3	--	2103
2-3ΔN	F: 2 F R: cccactagtacaagctcggggtctcagtttg	2-3	1610
2-3Δ3'N	F: 2 F R: cccactagtaacatggcagaaacacttaaac	2-3	2118
2-3Δ5'N	F1: 2 F R1: tccaaacatgcccaaagggctgtttcggtca F2: tgaccgaaacagccctttgggcatgtttgga R2: 3 R	2-3	2347
2-3ΔCR1	F: 2 F R: cccactagtaggagccatttcaatgtttctgtga	2-3	2626
2b-2 Δ1-50	F: cccgctagcagccccgggagcaggcag R: 2b-2 R	2b-2	265
2b-2 Δ51-100	F1: 2b-2 F R1: ctgcatggtggggctgactgggcctggtgcttgcc F2: tcagccccaccatgcagc R2: 2b-2 R	2b-2	266
2b-2 Δ101-150	F1: 2b-2 F R1: ctgattggagactgagaaggcgtgctgcaccctgac F2: cccgctagccttctcagtctccaatca R2: 2b-2 R	2b-2	266
2b-2	F1: 2b-2 F	2b-2	265

Δ151-201	R1: actgtttcgtttcctttttaaatttagcttggggat F2: cccgctagcaaaaggaaacgaaacagt R2: 2b-2 R		
2b-2 Δ202-254	F1: 2b-2 F R1: gcggccggtttgcgcggctttggccggcgtgggccc F2: cccgctagcgccgcgcaaaccggccgc R2: 2b-2 R	2b-2	263
2b-2 Δ255-316	F: 2b-2 F R: cccactagtgctcgctctgcttcacac	2b-2	253
2b-2 154	F1: cccgctagctcagccccaccatgcagc R1: cccactagtgctcgctctgcttcacac	2b-2	154
3a	F: 3 F R: cccactagttgtcagtgctttgtggccctc	3	456
3b	F: cccgctagcccatgtttcccgatgcagg R: cccactagtgagaaactgttgcccccgtg	3	471
3c	F: cccgctagcccacagctgagcctgcactc R: cccactagtttgaacaaggcaggagccat	3	455
3Δa	F: cccgctagcccatgtttcccgatgcagg R: 3 R	3	888
3Δb	F1: 3 F R1: gctcagctgtggtgtcagtgctttg F2: caaagcactgacaccacagctgagc R2: 3 R	3	1262
3a+b	F: 3 F R: 3b R	3	1216
3c3	F: 3c F R: 3 R	3	807
PG	F1: cccgctagctcagccccaccatgcagc R1: cccactagttgttcagatggaacttcttatgttc	W	700
DIVAC 1703	F1: cccgctagcagcaggccgcatggtac R1: ctcctctttgcaagcggggtcagcctgggggg F2: ccccccaggctgaccccgcttgcaaagaggag R2: 2-3ΔCR1 R	DIVAC 2-3	1703
DIVAC 1703 Δ1-200	F: cccgctagccagcacgctcagccc R: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC 1703 Δ201-400	F1: DIVAC 1703 F1 R1: tctggcaaagcccccaccctgacagcgctg F2: cagcgctgtcagggtgggggctttgccagac R2: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC 1703 Δ401-600	F1: DIVAC 1703 F1 R1: cagctgcacaacaggcaacctgaggtgtgtgacatg F2: cacacacctcaggttgcctgttgtgcagct R2: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC 1703 Δ601-800	F1: DIVAC 1703 F1 R1: ctgcttcccttccaaggttgctgttttgcc F2: ggcaaaacagcaaccttggaagggaagcag R2: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC	F1: DIVAC 1703 F1	DIVAC 1703	1503

1703 Δ801-1000	R1: cagtgagacaccccaagcaggtgtgtagctc F2: gagctacacacctgcttggggtgtctcactg R2: 2-3ΔCR1 R		
DIVAC 1703 Δ1001-1200	F1: DIVAC 1703 F1 R1: gcccctccaaacatgcggaccagcccatgtc F2: gacatgggctggtccgcatgtttggaggggc R2: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC 1703 Δ1201-1400	F1: DIVAC 1703 F1 R1: agcagagcgtgccgtgccaaaaacatggcag F2: ctgccatgtttttggcacggcacgctctgct R2: 2-3ΔCR1 R	DIVAC 1703	1503
DIVAC 1703 Δ1401-1703	F: DIVAC 1703 F1 R: cccactagtgccacggctattcct	DIVAC 1703	1400
DIVAC 1928	F: 2b F R: 2-3ΔCR1 R	2-3Δ2a/2c	1928
DIVAC 1928 Δ1	F1: 2b F R1: cctttttttggccggcaccctgacagcgctgtg F2: agcgctgtcagggtgccggccaaaaaaaggaaac R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ2	F1: 2b F R1: cctttttttggccgggcttggggatgccccggc F2: ggggcatccccaagcccggccaaaaaaaggaaac R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ3	F1: 2b F R1: ggcgctcgctctgctcgtgggcccctcagcttc F2: gctgaggggcccacgagcagagcgagcgccgcg R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ4	F1: 2b F R1: gtctggcaaagcccctcacacgtcagtgctttc F2: agcactgacgtgtgaggggctttgccagactga R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ5	F1: 2b F R1: cctgtgtgtgctgtgggaccagcccatgtcac F2: acatgggctggtcccacagcacacacaggagg R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ6	F1: 2b F R1: ggatggggttttcttattgccccagggctcca F2: agccctggggcaataagaaaaccccatccgtg R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ7	F1: 2b F R1: ctcagcccatgcagaggagtgcagggcagctgctg F2: cagctgccctgcactcctctgcatgggctgagcac R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ8	F1: 2b F R1: cccctccaaacatgcctgcagagagatgggaag F2: cccatctctctgcaggcatgtttggaggggcag R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ9	F1: 2b F R1: tggggctggcggccaaaaacatggcagaaa F2: ctgccatgtttttggccgccagccccacag R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928	F1: 2b F R1: ctgttgcccccgtggcacgtggcggtacccgta	DIVAC 1928	1878

Δ10	F2: gggtaccgccacgtgccacgggggcaacagtttc R2: 2-3ΔCR1 R		
DIVAC 1928 Δ11	F1: 2b F R1: tggccgaagttgccacgtctgcggtcagcacatctg F2: atgtgctgaccgcagacgtggcaacttcggcca R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ12	F1: 2b F R1: gaagcagagcgtgccgtggttttcttcccggctac F2: gccgggaagaaaaccacggcacgctctgcttc R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ13	F1: 2b F R1: ccgggcagcggcgctgccacggctattcctgtc F2: aggaatagccgtggcagcgccgctgcccggcac R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ14	F1: 2b F R1: aaatggggcccaaatccgtggtgccacatactgg F2: gtatgtggcaccacggatttgggccccattttgg R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ15	F1: 2b F R1: tggggaccaagctgaccaagcatttcctgctcctgg F2: gagcaggaaatgcttggtcagcttggtcccca R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ16	F1: 2b F R1: gtgggcagtggcaagctccctggaagcctcttc F2: aggcttccagggagcttgccactgcccaccctg R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ17	F1: 2b F R1: caaacgccctggtgctcccctccccatcatttc F2: tgatggggaggggagcaccagggcgtttgcac R2: 2-3ΔCR1 R	DIVAC 1928	1878
DIVAC 1928 Δ18	F: 2b F R: cccactagtcctgcagtgagatgggac	DIVAC 1928	1878
1-3 ΔF2 core	F1: 1 F R1: tctggcaaagcccccaccctgacagcgctg F2: cagcgctgtcagggtgggggctttgccagac R2: 3 R	DIVAC 1-3	4184
1-3 ΔF3 core	F1: 1 F F2: cgggtaccgccacgtgttgccactgcccaccctgcag R1: ggtgggcagtggcaacacgtggcggtacccgtat R2: 3 R	DIVAC 1-3	4034
1-3 ΔF2/F3 core	F1: 1 F R1: tctggcaaagcccccaccctgacagcgctg F2: cagcgctgtcagggtgggggctttgccagac R2: 3 R	DIVAC 1-3 ΔF3 core	3834
2-3 ΔF2 core	F1: 2 F R1: tctggcaaagcccccaccctgacagcgctg F2: cagcgctgtcagggtgggggctttgccagac R2: 3 R	DIVAC 2-3	2789
2-3 ΔF3 core	F1: 2 F F2: cgggtaccgccacgtgttgccactgcccaccctgcag R1: ggtgggcagtggcaacacgtggcggtacccgtat R2: 3 R	DIVAC 2-3	2639
2-3 ΔF2/F3	F1: 2 F R1: tctggcaaagcccccaccctgacagcgctg	DIVAC 2-3 ΔF2	2439

core	F2: cagcgctgtcagggtgggggctttgccagac R2: 3 R		
DIVAC 1928 ΔF2 core	F1: 2b F R1: tctggcaaagcccccaccctgacagcgctg F2: cagcgctgtcagggtgggggctttgccagac R2: 2-3ΔCR1 R	DIVAC 1928	1728
DIVAC 1928 Δ1201-1400	F1: 2b F R1: agcagagcgtgccgtgccaaaaacatggcag F2: ctgccatgtttttggcacggcacgctctgct R2: 2-3ΔCR1 R	DIVAC 1928	1728
DIVAC 751	F1: cccgctagccagcacgctcagccc R1: gcccctccaaacatgcgtcagcctgggggcacc F2: ggtgcccccaggctgacgcatgtttggaggggc R2: cccactagttcccctccccatcatttc	DIVAC 1928	751
Murine iEκ	F: cccgctagccaaggaaagggtgacttatt R: cccactagtacacaagcacataaggtaaga	C57BL/6 Genomic DNA	1001
Murine 3'Eκ	F: cccgctagcagctcaaaccagcttaggctac R: cccactagttgtctgggccccatgaaacatc	C57BL/6 Genomic DNA	801
Murine Eλ2-4	F: cccgctagctggggatactcagtaatcttc R: cccactagttgctctacccaagttgct	C57BL/6 Genomic DNA	724
Murine Eλ3-1	F: cccgctagctctagtttccactatcatctc R: cccactagtcttactcctttgtgctct	C57BL/6 Genomic DNA	682

B

Gene	PCR Fragment	Primer	Ta	Product Size (bp)
γ-actin	--	**F:** acagcattcgggtggagt **R:** ttgagcatcctccttcacac **Probe:** cctcagccctcacctgcacg	60	127
RSV Promoter (in IgLGFP2)	**a**	**F:** ttcttcatgcaattgtcggt **R:** ctgctccctgcttgtgtg **Probe:** tgctcgcgcactactcagcg	60	95
GFP2 (in IgLGFP2)	**b**	**F:** tgaccctgaagttcatctgc **R:** gaagtcgtgctgcttcatgt **Probe:** cccaccctcgtgaccaccct	60	125
IRES (in IgLGFP2)	**c**	**F:** ccctaggaatgctcgtcaag **R:** cctaacgttactggccgaag **Probe:** tttccgggccctcacattgc	60	139
BSR (in IgLGFP2)	**d**	**F:** aatggcttctgcacaaacag **R:** gcgacagagaagattacaatgc **Probe:** cgaattgccgctcccacatg	60	141
2b	**e**	**F:** tccaatcagaaactgaagctg **R:** cgctctgcttcacacgtc **Probe:** aggaaacgaaacagtctccagaaagca	60	80
3	**f**	**F:** agctggaggacaggaatagc **R:** ctctgcttgctgctgtgc **Probe:** cgctctgcttcctcggcaca	60	109
W fragment, upstream of cores (DIVAC 1)	**g**	**F:** gatctgctacagccactcca **R:** gctggatggagacatagggt **Probe:** cagcacctccagccatccca	60	113

W fragment, between cores (Δ601-800)	**h**	**F:** aaacagctccaaactgagacc **R:** cacggcacaaaggtgtttat **Probe:** ccgagcttgtccacaggttgtaaaca	60	74
18S	**--**	**F:** taaaggaattgacggaaggg **R:** tgtcaatcctgtccgtgtc **Probe:** cgcaggctccactcctggtg	60	102

Table S1. Primer and probe sequences for experiments. (A) Primers for the creation of all tested DIVAC fragments. (B) qPCR primer pairs and probes for gene expression and ChIP. All sequences are written 5' to 3'.