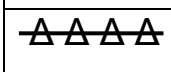
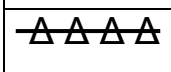
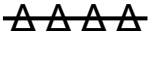
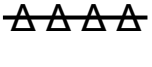
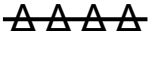
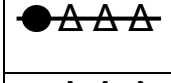
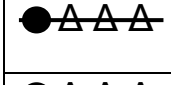
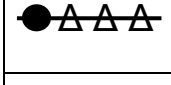
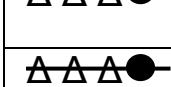
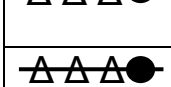
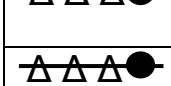
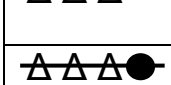
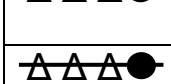
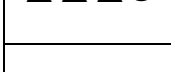
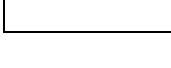
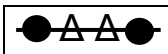
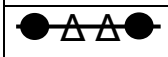
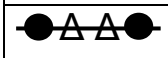
Supplemental Tables

Antibody	Transgene	Transgene	p =
IgG2a, CD40L	Δ HS1,2 + HS3B	Intact	0.0435
	Δ HS1,2 + HS3B (without 522)	Intact	0.123
	Δ HS1,2 + HS3B	NTg	0.061
	Δ HS1,2 + HS3B (without 522)	NTg	0.028
	Δ HS1,2 + HS3B	Δ HS3A + HS1,2 + HS3B	0.00025
	Δ HS3A + HS1,2 + HS3B	Intact	0.0001
	Δ HS3A + HS1,2 + HS3B	NTg	0.115
	Δ HS1,2 + HS3B + HS4	Intact	0.0028
	Δ HS1,2 + HS3B + HS4	NTg	0.044
	Δ HS3A + HS1,2 + HS3B +HS4	Intact	0.0007
	Δ HS3A + HS1,2 + HS3B + HS4	NTg	0.57
	Intact	NTg	0.0182
IgG2a, LPS	Δ HS1,2 + HS3B	Intact	0.066
	Δ HS1,2 + HS3B	NTg	0.21
	Δ HS1,2 + HS3B (without 522)	NTg	0.141
	Δ HS1,2 + HS3B	Δ HS3A + HS1,2 + HS3B	0.07
	Δ HS3A + HS1,2 + HS3B	Intact	<0.0001
	Δ HS3A + HS1,2 + HS3B	NTg	0.48
	Δ HS1,2 + HS3B + HS4	Intact	0.0039
	Δ HS1,2 + HS3B + HS4	NTg	0.047

	Δ HS3A + HS1,2 + HS3B +HS4	Intact	0.0004
	Δ HS3A + HS1,2 + HS3B + HS4	NTg	0.84
	Intact	NTg	0.0053
IgG1[a]	Δ HS1,2 + HS3B	Intact	0.48
	Δ HS1,2 + HS3B	NTg	0.066
	Δ HS1,2 + HS3B (without 522)	NTg	0.04
	Δ HS1,2 + HS3B	Δ HS3A + HS1,2 + HS3B	0.036
	Δ HS3A + HS1,2 + HS3B	Intact	0.0011
	Δ HS3A + HS1,2 + HS3B	NTg	0.0082
	Δ HS1,2 + HS3B + HS4	Intact	0.003
	Δ HS1,2 + HS3B + HS4	NTg	0.03
	Δ HS3A + HS1,2 + HS3B +HS4	Intact	0.0005
	Δ HS3A + HS1,2 + HS3B + HS4	NTg	0.46
	Intact	NTg	0.01

Supplementary Table I. Probabilities (two-tailed T test) that the Ig secretion data from the two groups of transgenes are different. Data from Fig. 2 were used for this analysis.

		Fig. 3A1	Fig. 3B1	Fig. 3C1	Fig. 3D1	Fig. 6A1	Fig. 6B1
3' enhancer composition	Transgenic Line--lane number	γ2a	γ2b	γ3	α	γ1	ε
28 kb Δ	820Δ—21	0.09	0.12	0.01	0.82	0.08	0.05
	934Δ—1	0.13	0.11	0.01	0.04	0.03	0.01
	923Δ--2	0.1	0.4	0.03	0.03	0.09	0.01
	842Δ--3	0.1	0.05	0.01	0	0.17	0.16
	835Δ--4	0.12	0.19	0.01	0.01	0.09	0.01
	925Δ--5	0.11	0.25	0.01	0.15	0.04	0.02
	501Δ—6	0.21	1.21	0.01	0.79	0.06	0.01
	522Δ—7	0.18	0.93	0.02	0.16	0.05	0.01
	410Δ—8	0.13	1.36	0.06	0.86	0.03	0.01
	934—9	5.3	0.3	0.03	3.19	0.07	0.04
	912—10	2.47	0.38	0.03	2.2	0.08	0.04
	923—11	5.72	1.18	0.25	0.59	1.02	0.17
	842—12	2.06	0.5	0.07	0.8	0.04	0.06
	835—13	5.92	1.2	0.25	2.17	0.89	0.09
	925--14	5.3	0.2	0.03	8.45	0.32	0.02
	501—15	4.97	0.41	0.2	3.4	0.19	0.08

	522—16	0.37	1.32	0.01	0.8	0.17	0.01
	418—17	8.97	1.5	0.15	4.47	0.26	0.30
	410—18	14.8	2.07	0.95	9.14	1.08	0.14
	518—19	11.0	0.99	0.14	7.43	0.21	0.15
	820--20	7.36	0.48	0.3	9.8	0.44	0.37

Supplementary Table II. Quantification of germline transcripts. For each heavy chain gene listed in the second row of the Table, the ratio of transgenic band density to endogenous band density is shown. These ratios are calculated from Phosphorimager files from Figs. 3 and 6, subparts 1, as indicated in the top row of the Table. Transgenic lines (and lane number in the corresponding Figure, after the dashes), listed in the second column from the left, are grouped according to the 3' enhancer composition of the transgene.

Supplemental Figures

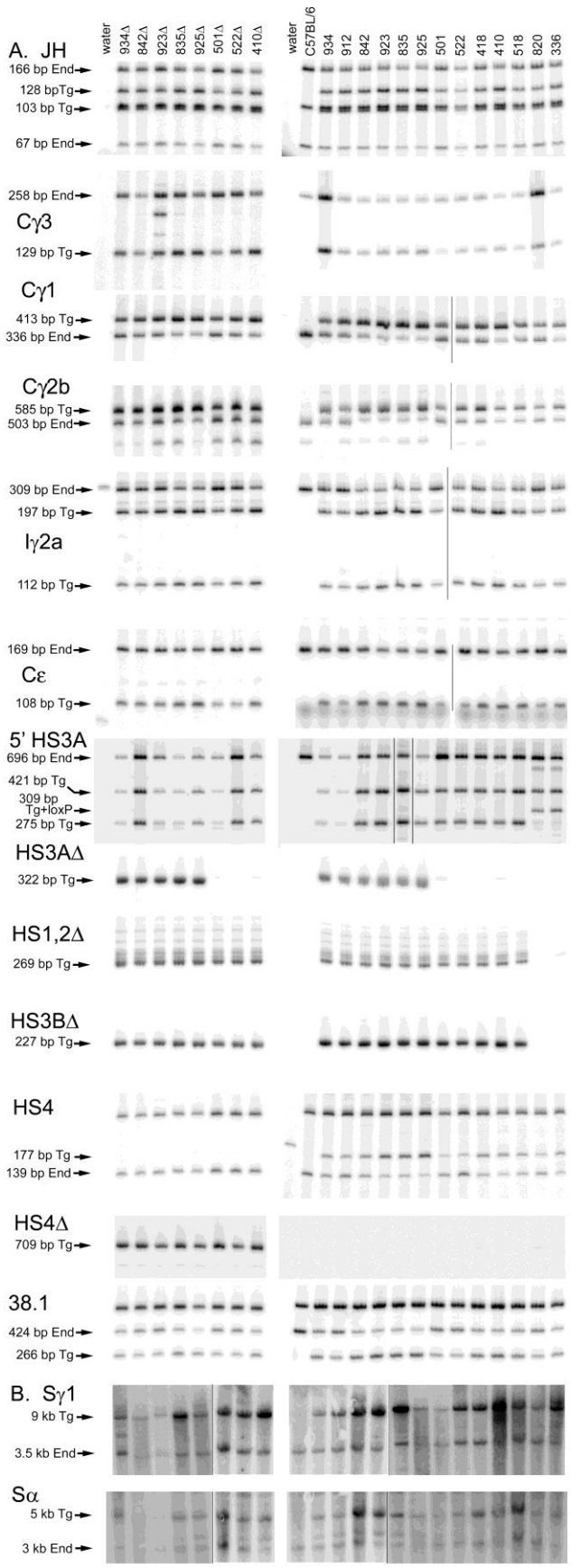


FIGURE S1. Gene composition of transgenic lines. A. PCR amplification and restriction enzyme digestion for the indicated gene segments. Note that lines 912 and 923 are reversed in this Figure compared to the presentation in Figures 2, 3, and 6. These analyses were completed in two sets of experiments, as indicated by the break between the 410Δ and water samples in the middle of each set of gel images. For some gene segments, the grey line indicates that the experiment for samples C57BL/6, 934, etc. was fractionated on two gels. The grey lines around the 835 sample in the analysis for the 5' HS3A gene segment indicates that this sample was analyzed in a separate experiment from the other samples. B. Southern hybridization analysis for the γ1 and α switch regions (digestion with *Sst*I). These data were generated in two experiments. One experiment included 14 samples, 934Δ to 835Δ and 925 to 336; the second experiment included 8 samples, 501Δ to 835Δ.

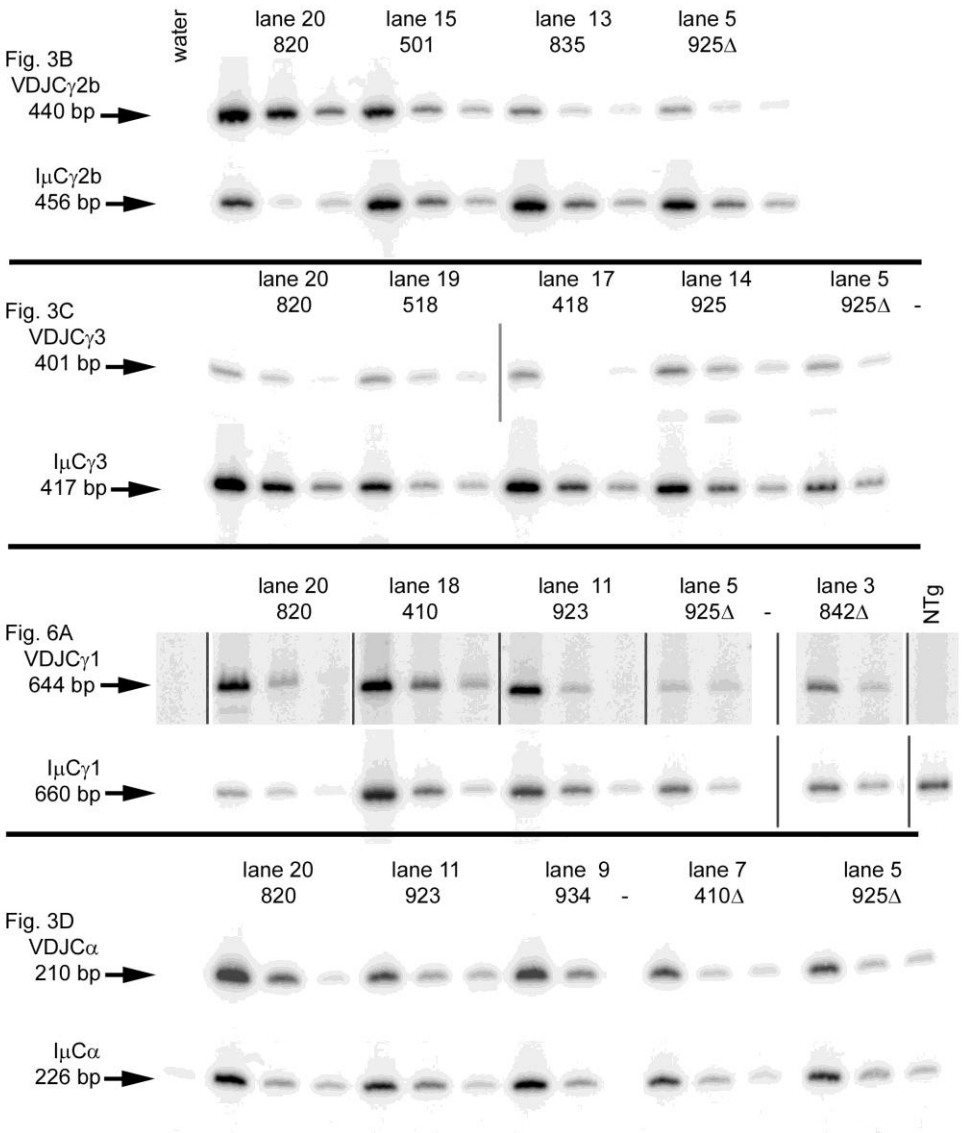


FIGURE S2. Semi-quantitative RT-PCR analysis of post-switch transcripts. cDNA samples from the original experiment (indicated as a Figure number and Part to the left of the gel images) were amplified using the same cDNA concentration as the original experiment, and one or two additional five-fold dilutions. Lane numbers corresponding to the original Figure and transgenic line founder numbers are listed at the top of each gel image. Grey lines indicate a change in the order of samples from the original gel image. Empty lanes are indicated by dashes.