

Table S2. Predicted results of all possible mutations to all codons of the FW1 region for the 1,919 genes analyzed

Codon	Count ¹	Amino acid	Exchanges ²												Hotspots ³			Colspots ⁴		
			C to T	C to A	C to G	A to T	A to C	A to G	T to C	T to A	T to G	G to C	G to T	G to A	Pos.	Count	Proportion	Pos.	Count	Proportion
CAG	6602	Q	X	R	R	R	R	R	R	R	R	R	S	S	P1	4324	65%	P1	388	6%
CTG	4928	L	S	R	R	R	R	R	R	R	R	S	S	S	P1	1386	28%	P1	3542	72%
TCC	3804	S	RS	RS	RS	R	R	R	R	R	R	S	S	S	P2	41	1%	P2	3804	100%
ACC	3657	T	RS	RS	RS	R	R	R	R	R	R	S	S	S	P2	3617	99%	P2	3617	99%
GTG	3042	V	R	R	R	R	R	R	R	R	R	RS	RS	RS	P3	2783	100%			
GGC	2783	G	S	S	S	R	R	R	R	R	R	RR	RR	RR	P2	2222	100%			
GAG	2494	E	R	X	R	R	R	R	R	R	R	RR	XR	RS	P1	1910	100%	P1	3	0%
TCG	2222	S	R	X	R	R	R	R	R	R	R	S	S	S	P3	1745	100%	P3	1910	100%
GGA	2102	G	R	X	R	S	S	S	R	R	R	RR	XR	RR	P1	1838	100%	P1	1838	100%
AAG	2015	K	R	X	R	RR	RR	RR	S	S	S	R	R	S	P2	2222	100%			
CCT	1913	P	RR	RR	RR	RR	S	S	S	S	S	R	R	R	P3	1047	100%	P1	7	1%
GTC	1910	V	S	S	S	R	R	R	S	S	S	R	R	R	P2	900	89%	P2	115	11%
CTC	1838	L	RS	RS	RS	R	R	R	R	R	R	R	R	R	P2	903	99%	P2	7	1%
TGC	1745	C	S	X	R	R	R	R	R	R	R	R	R	R	P3	411,	52%,	P1,2	899	100%
GGT	1717	G	R	R	R	R	R	R	S	S	S	R	R	R	P2	1420	99%			
TCT	1429	S	R	R	R	R	R	R	RS	RS	RS	RR	RR	RR	P1	744	100%			
GGG	1291	G	R	R	R	R	R	R	R	R	R	RR	RR	RR	P2	455	100%			
AGT	1109	S	R	R	R	R	R	R	S	R	R	R	R	R	P2	73,212	34,100%			
TTC	1047	F	S	R	R	R	R	R	S	R	R	R	R	R	P1	8	1%	P1,2	899	100%
GCT	1015	A	R	R	R	R	R	R	S	S	S	R	R	R	P2	5	1%	P2	818	99%
GCA	910	A	R	R	R	R	R	R	R	R	R	R	R	R	P3	6602	100%			
CCA	899	P	RR	RR	RR	RR	S	S	S	S	S	R	R	R	P1	103	100%			
ATC	872	I	S	S	R	R	R	R	R	R	R	R	R	R	P3	90	100%			
TTG	844	L	R	R	R	R	R	R	R	R	R	R	R	R	P2	52	100%			
ACT	823	T	R	R	R	R	R	R	S	S	S	R	R	R	P1	44	100%			
TAT	744	Y	R	R	R	R	R	R	RS	RX	RX	R	R	R	P2	176	100%			
TGG	744	W	R	R	R	R	R	R	R	R	R	R	R	R	P3	744	100%			
CTA	741	L	S	R	R	R	S	S	S	S	S	R	R	R	P1	741	100%			
AGC	693	S	S	R	R	R	S	S	S	S	S	R	R	R	P2	455	100%			
TCA	455	S	R	X	X	R	S	S	S	S	S	R	R	R	P2	140	66%	P2,3	73,212	34,100%
GCC	212	A	RS	RS	RS	R	R	R	RS	RX	RR	R	R	R	P1	1	25%	P1,2	5	15%
TGT	176	C	R	X	S	R	R	R	RS	RR	RR	R	R	R	P3	103	100%			
AGA	171	R	R	X	S	R	R	R	R	R	R	R	R	R	P1	103	100%			
TTT	112	F	R	X	S	R	R	R	RR	RR	RR	R	R	R	P3	90	100%			
CAA	103	Q	X	R	R	R	R	R	R	R	R	R	R	R	P1	1	100%			
AGG	102	R	R	R	R	R	R	R	R	R	R	R	R	R	P2	8	100%			
TAC	90	Y	S	X	X	R	R	R	R	R	R	R	R	R	P1	1	100%			
GTA	65	V	S	R	R	R	R	R	R	R	R	R	R	R	P2	8	100%			
GTT	52	V	R	R	R	R	R	R	R	R	R	R	R	R	P2	5	100%			
CGG	44	R	R	S	R	R	R	R	R	R	R	R	R	R	P1	5	100%			
GAT	38	D	R	S	R	R	R	R	R	R	R	R	R	R	P3	1	100%			
GAA	36	E	D	R	R	R	R	R	R	R	R	R	R	R	P2	24	100%			
GCG	24	A	R	R	R	R	R	R	R	R	R	R	R	R	P2	8	100%	P1,2	5	100%
ACA	8	T	R	R	R	R	R	R	R	R	R	R	R	R	P3	5	100%	P3	3	75%
CCG	5	P	RR	RR	RR	R	R	R	R	R	R	R	R	R	P1	1	100%			
GAC	5	D	S	R	R	R	R	R	R	R	R	R	R	R	P1	1	100%			
CTT	4	L	R	R	R	R	R	R	R	R	R	R	R	R	P1	1	100%			
TTA	2	L	R	R	R	R	R	R	R	R	R	R	R	R	P2	1	100%			
AAT	1	N	R	R	R	R	R	R	R	R	R	R	R	R	P3	1	100%			
ATT	1	I	R	R	R	R	R	R	R	R	R	R	R	R	P1	1	100%			
CAT	1	H	R	RR	RR	RR	RR	RR	R	R	R	R	R	R	P1	1	100%			
CCC	1	P	RRS	RRS	RRS	RRS	R	R	R	R	R	R	R	R	P1,2	1,1	100%			
CGC	1	R	RS	RS	RS	RS	R	R	R	R	R	R	R	R	P1,3	1	100%			
Sums: 57640																				

¹Codons are listed from the top by order of frequency in the 1,919 V genes analyzed.

²Results of all possible exchanges for each codon. Effects on identical nucleotides within a particular codon are listed respectively. R = amino acid replacement; S = Silent mutation; X = nonsense mutation.

³Hotspots refer to the number (count) and percentage (proportion) of cytidines associated with the particular codon that fall within a hotspot of AID activity in the various 1,919 V genes analyzed as described in the text. Position (Pos.) is the nucleotide position of the cytidine referred to within the codon where P1 is position 1, P2 is position 2, and P3 is position 3.

⁴Coldspots list the counts and proportions of cytidines in AID coldspots annotated similarly to comment 3 above.

Table S3. Predicted results of all possible mutations to all codons of the CDR1 region for the 1,919 genes analyzed

Codon	Count ¹	Amino acid	Exchanges ²												Hotspots ³			Colspots ⁴		
			C to T	C to A	C to G	A to T	A to C	A to G	T to C	T to A	T to G	G to C	G to T	G to A	Pos.	Count	Proportion	Pos.	Count	Proportion
TAC	3203	Y	S	X	X	R	R	R	R	R	R	RR	RR	XX	P3	3203	100%			
TGG	1786	W	S	X	X	R	R	R	R	R	R	R	R							
AGT	1664	S	S	R	R	R	R	R	S	R	R	R	R	R	P3	1594	100%			
AGC	1594	S	S	R	R	R	R	R	R	R	R	R	R	R						
GGT	1376	G	S	S	S	R	R	R	S	S	S	RR	RR	RR						
GGC	276	G	S	S	S	R	R	R	RS	RX	RX	RR	RR	RR	P3	276	100%			
TAT	236	Y	R	R	R	R	R	R	R	R	R	R	R	R						
ATG	193	M	H	R	R	R	R	R	R	R	R	R	R	R	P1	127	99%	P3	128	100%
CAC	128	H	R	R	R	R	R	R	R	R	R	R	R	R						
GAT	125	D	R	R	R	R	R	R	S	R	R	R	R	R						
AAC	94	N	S	R	R	R	R	R	R	R	R	R	R	R	P3	94	100%			
ATC	63	I	S	S	R	R	R	R	R	R	R	R	R	R						
GCC	47	A	R	S	R	S	R	S	R	R	R	R	R	R	P2	47	100%	P3	47	100%
GCT	47	A	R	R	R	S	R	S	S	R	R	R	R	R	P2	47	100%			
TCC	38	S	R	S	R	S	R	R	S	R	S	R	R	R	P2	38	100%			
GAC	10	D	R	S	R	S	R	R	R	R	R	R	R	R	P3	10	100%			
ACC	5	T	R	S	R	S	R	R	R	R	R	R	R	R	P2	4	80%	P2	1	20%
AAT	2	N	R	R	R	R	R	R	R	R	R	R	R	R	P2	1	100%			
CCT	2	P	RR	RR	RR	R	R	R	S	S	S	S	S	S	P1	1	100%			
ACT	1	T	R	R	R	R	R	R	S	S	S	S	S	S						
CAT	1	H	R	R	R	R	R	R	R	R	R	R	R	R						
GAA	1	E	R	R	R	R	R	R	R	R	R	R	X	R						
GGA	1	G	S	S	S	S	S	S	R	R	R	RR	RR	R						
TGC	1	C	S	X	R	S	S	S	R	R	R	R	R	R	P3	1	100%			
Total	10895																			

¹Codons are listed from the top by order of frequency in the 1,919 V genes analyzed.

²Results of all possible exchanges for each codon. Effects on identical nucleotides within a particular codon are listed respectively. R = amino acid replacement; S = Silent mutation; X = nonsense mutation.

³Hotspots refer to the number (count) and percentage (proportion) of cytidines associated with the particular codon that fall within a hotspot of AID activity in the various 1,919 V genes analyzed as described in the text. Position (Pos.) is the nucleotide position of the cytidine referred to within the codon where P1 is position 1, P2 is position 2, and P3 is position 3.

⁴Coldspots list the counts and proportions of cytidines in AID coldspots annotated similarly to comment 3 above.

Table S4. Predicted results of all possible mutations to all codons of the FW2 region for the 1,919 V genes analyzed

Codon	Count ¹	Amino acid	Exchanges ²												Pos.	Hotspots ³	Colspots ⁴	
			C to T	C to A	C to G	A to T	A to C	A to G	T to C	T to A	T to G	G to C	G to T	G to A				
GGG	4659	G	W									R	R	R	R			
TGG	3799	W																
GAG	1915	E														P1	1879	100%
CAG	1879	Q	X	R	R	R	R	R	R	R	R	R	R	R				
AAG	1837	K		X	R	R	R	R	R	R	R	R	R	R	S			
CTG	1830	L	S	R	R	R	R	R	R	R	R	S	S	S		P1	1830	100%
																	1556,	
CCA	1755	P	RR	RR	RR	RR	S	S	S	S	S	RS	RS	RS		P1	38	2%
ATT	1663	I					R	R	R	RS	RS	RS	RR			P1,2	1551	89, 88%
ATC	1647	I	S	S	R	R	R	R	R	R	R	R	R	R				
CCC	1468	P	RR	RR	RR	RR	RS		P1	1466	100%							
															P1,3	1372	0, 100%	
CGC	1372	R	RS	RS	RS	RS						R	R	R				
GGA	547	G					S	S	S							P3	377	100%
CGG	462	R	R	S	S	R										P3	282	100%
GGC	377	G	S	S	S	S										P2	95,	46,
GTC	282	V	S	S	S	S										P2	130	76%
GCC	209	A	RS	RS	RS	RS										P2	113	54%
GCT	171	A	R	R	R	R										P2	41	24%
GTG	167	V																
CAC	161	H	RS	RR	RR	RR	R	R	R	R	R	R	R	R		P1	161	100%
CAA	122	Q	X	R	R	R	R	R	R	R	R	R	R	R		P1	122	100%
ATG	82	M																
CGA	82	R	X	S	S	S	S	S	S	S	S	S	S	S		P1	81	99%
CTT	82	L	R	R	R	R	R	R	R	R	R	R	R	R		P1	1	1%
																P1	82	100%
CCT	71	P	RR	RR	RR	RR						S	S	S		P1,2	71, 71	100%
GCA	71	A	R	R	R	R	S	S	S	S	S					P2	71	100%
TCA	70	S	R	X	X	R	S	S	S	S	S	R	R	R		P2	69	99%
GAA	63	E					RR	RR	RS	S	S	S	S	S				
CGT	42	R	R	R	R	R	R	R	R	R	R	R	R	R		P1	38	91%
GTT	16	V																
GGT	12	G																
AGT	11	S																
ACT	10	T	R	R	R	R	R	R	R	R	R	R	R	R		P2	10	100%
GTA	9	V																0%
CTA	8	L	S	R	R	R	R	R	R	R	R	R	R	R		P1	8	100%
TCT	7	S	R	R	R	R	R	R	R	R	R	R	R	R		P2	7	100%
TTC	7	F	S	R	R	R	R	R	R	R	R	R	R	R		P3	7	100%
TAC	5	Y	S	X	X	R	R	R	R	R	R	R	R	R				0%
CCG	4	P	RR	RR	RR	R	R	R	R	R	R	S	S	S		P1	4	100%
TAT	2	Y																
AAC	1	N	S	R	R	R	R	R	R	R	R	R	R	R		P3	1	100%
ACC	1	T	RS	RS	RS	R	R	R	R	R	R	R	R	R		P2	1	100%
ACG	1	T	R	R	R	R	R	R	R	R	R	R	R	R		P2	1	100%
AGC	1	S	S	R	R	R	R	R	R	R	R	R	R	R				
AGG	1	R																
ATA	1	I														P1,P3	1, 1	100%,
CTC	1	L	RS	RS	RS	R	R	R	R	R	R	R	R	R		P3	1	100%
GAC	1	D	S	R	R	R	R	R	R	R	R	R	R	R		P2	1	100%
TCC	1	S	RS	RS	RS	R	R	R	R	R	R	R	R	R		P2	1	100%
	Sums 26983																	

¹Codons are listed from the top by order of frequency in the 1,919 V genes analyzed.

²Results of all possible exchanges for each codon. Effects on identical nucleotides within a particular codon are listed respectively. R = amino acid replacement; S = Silent mutation; X = nonsense mutation.

³Hotspots refer to the number (count) and percentage (proportion) of cytidines associated with the particular codon that fall within a hotspot of AID activity in the various 1,919 V genes analyzed as described in the text. Position (Pos.) is the nucleotide position of the cytidine referred to within the codon where P1 is position 1, P2 is position 2, and P3 is position 3

⁴Coldspots list the counts and proportions of cytidines in AID coldspots annotated similarly to comment 3 above.

Table S5. Predicted results of all possible mutations to all codons of the CDR2 region from the 1,919 V genes analyzed

Codon	Count ¹	Amino acid	Exchanges ²												Hotspots ³			Colspots ⁴			
			C to T	C to A	C to G	T to A	A to C	A to G	T to C	T to A	T to G	G to C	G to T	G to A	Pos.	Count	Proportion	Pos.	Count	Proportion	
AGT	3799	S				R	R	R	S	R	R	R	R	R	P3	3178	100%				
TAC	3178	Y	S	X	X	R	R	R	R	R	R	R	R	R	P3	3048	100%				
AAC	3048	N	S	R	R	R	R	R	R	R	R	R	R	R							
AAG	1912	K				X	R	R	R	R	R	R	R	R							
AGC	1809	S	S	R	R	R	R	R	R	R	R	R	R	R	P3	1809	100%				
ACC	1798	T	RS	RS	RS	R	R	R	R	R	R	R	R	R	P2	123	7%	P2	1676	93%	
TCC	1762	S	RS	RS	RS	R	R	R	R	R	R	R	R	R	P2	1756	100%				
ATC	1717	I	S	S	R	R	R	R	R	R	R	R	R	R							
CTC	1705	L	RS	RS	RS	R	R	R	R	R	R	R	R	R	P1	41	2%	P1,3	1705	98,	
TAT	1631	Y				R	R	R	RS	R	R	R	R	R				P1,3	1664	100%	
CCG	1289	P	RR	RR	RR										P2	1289	100%				
GGG	953	G																			
AAT	870	N																			
CAT	850	H	R	R	R	R	R	R	R	R	R	R	R	R							
GGA	823	G	S	S	S	R	R	R	R	R	R	R	R	R							
GAA	749	E																			
CCC	379	P	RRS	RRS	RRS																
GGC	301	G	S	S	S																
GGT	234	G																			
GCA	203	A	R	R	R	S	S	S	S	R	R	R	R	R	P2	203	100%				
GTC	180	V								R	R	R	R	R							
CAG	163	Q	X	R	R	R	R	R	R	R	R	R	R	R				P1	94	58%	
GAC	159	D	S	R	R	R	R	R	R	R	R	R	R	R				P3	159	100%	
ACA	135	T	R	R	R	R	R	R	R	R	R	R	R	R				P2	115	85%	
ATA	133	I																			
TGG	121	W																			
CGA	117	R	X	S	R	S	S	S	R	R	R	R	R	R				P1	117	100%	
AAA	110	K		XRRRRRRRRR	S																
ATT	109	I																			
GAT	90	D																			
CGT	81	R	R	R	R	R	R	R	R	R	R	R	R	R				P1	81	100%	
GTT	75	V																			
TCT	70	S	R	R	R	R	R	R	R	R	R	R	R	R	P2	70	100%				
GCT	68	A	R	X	X	S	S	S	S	S	S	S	S	S	P2	68	100%	P2	7	11%	
TCA	59	S	R	R	R	S	S	S	R	R	R	R	R	R	P2	41	100%	P3	39	100%	
GCG	41	A	R	R	R	R	R	R	R	R	R	R	R	R				P3	39	100%	
CCT	39	P	RR	R	R	R	R	R	R	R	R	R	R	R				P3	39	100%	
GTC	39	V	S	S	S	R	R	R	R	R	R	R	R	R				P3	39	100%	
TTC	39	F	S	R	R	R	R	R	R	R	R	R	R	R				P3	39	100%	
TTT	21	F																			
CAA	12	Q	X	R	R	RR	RR	RR	RS	R	R	R	R	R							
GAG	12	E																			
ATG	10	M																			
AGA	9	R																			
ACT	6	T	R	S	R	R	R	R	S	S	S	S	R	R		P2	4	67%	P2	2	33%
GCC	6	A	R	R	R	R	R	R	R	R	R	R	R	R		P3	6	100%			
CTT	5	L	R	R	R	R	R	R	RS	RS	RS	S	S	S		P1	4	80%			
ACG	3	T	R	R	R	R	R	R	R	R	R	S	S	S		P2	3	100%			
CCA	2	P	RR	R	R	R	R	R	S	S	S					P2	2	100%			
CTG	2	L	S	R	R	R	R	R	R	R	R	S	S	S		P1	1	50%	P1	1	50%
AGG	1	R																			
Sums:			30924																		

¹Codons are listed from the top by order of frequency in the 1,919 V genes analyzed.

²Results of all possible exchanges for each codon. Effects on identical nucleotides within a particular codon are listed respectively. R = amino acid replacement; S = Silent mutation; X = nonsense mutation.

³Hotspots refer to the number (count) and percentage (proportion) of cytidines associated with the particular codon that fall within a hotspot of AID activity in the various 1,919 V genes analyzed as described in the text. Position (Pos.) is the nucleotide position of the cytidine referred to within the codon where P1 is position 1, P2 is position 2, and P3 is position 3

⁴Coldspots list the counts and proportions of cytidines in AID coldspots annotated similarly to comment 3 above.

Table S6. Predicted results of all possible mutations to all codons of the FW3 region for the 1,919 V genes analyzed

Codon	Count ¹	Amino acid	Exchanges ²												Hotspots ³			Colspots ⁴		
			C to T	C to A	C to G	A to T	A to C	A to G	T to C	T to A	T to G	G to C	G to T	G to A	Pos.	Count	Proportion	Pos.	Count	Proportion
CTG	3969	L	S	R	R	R	R	R	R	R	R	S	S	S	P1	1942	46%	P1	1972	50%
GAC	3852	D	S	RS	RS	RS	R	R	R	R	R	S	R	R	P3	3852	100%	P3	3852	100%
TCC	3669	S	R	RS	RS	RS	R	R	R	R	R	R	S	R	P2	3449	94%	P2	3449	94%
ACG	3631	T	R	RS	RS	RS	R	R	R	R	R	S	S	S	P2	3631	100%	P2	3631	100%
AAG	3546	K	X	RR	RR	RR	R	R	R	R	R	S	R	S						
GTG	3527	V	R	RS	RS	RS	R	R	R	R	R	RS	RS	RS						
ACC	3441	T	RS	RS	RS	R	R	R	R	R	R	RS	RS	RS	P2	271	7%	P2	3185	93%
GCG	2900	A	R	RS	RS	RS	R	R	R	R	R	RS	RS	RS	P2	3072	100%			
GCC	2638	A	RS	RS	RS	R	R	R	R	R	R	RS	RS	RS	P2	1839	66%			
TAT	2077	Y	R	RS	RS	RS	R	R	R	R	R	RS	RS	RS	P2,3	902,	34,	P2,3	2638	100%
AAC	2065	N	S	R	R	R	RR	RR	RR	RR	RR	R	R	R	P3	2187	100%			
AGC	1998	S	S	RS	RS	RS	R	R	R	R	R	R	R	R	P3	2116	100%			
TAC	1982	Y	S	X	X	R	R	R	R	R	R	R	R	R	P3	2100	100%			
TCT	1904	S	R	R	R	R	R	R	RS	RS	RS	R	R	R	P2	1824	96%			
TGT	1873	C	S	R	R	R	R	R	RS	RS	RS	R	R	R						
TTC	1832	F	S	R	R	R	R	R	RS	RS	RS	R	R	R	P3	1832	100%			
CGA	1679	R	X	S	R	S	S	S	S	S	S	R	R	R	P1	1679	100%			
GTA	1677	V	R	S	S	S	S	S	S	S	S	R	R	R						
CAG	1642	Q	X	R	R	R	R	R	R	R	R	R	R	R						
ATA	1628	I	R	RS	RS	RS	R	R	R	R	R	R	R	R						
TCA	1541	S	R	X	X	S	S	S	S	S	S	R	R	R	P2	92	6%			
GTC	1466	V	S	S	S	S	S	S	S	S	S	R	R	R	P3	1466	100%			
GCT	1334	A	R	R	R	R	R	R	S	S	S	R	R	R	P2	361	26%	P2	993	74%
AGA	476	R	R	X	R	RS	RS	RS	R	R	R	R	R	R						
ATG	363	M	R	R	R	R	R	R	R	R	R	R	R	R						
GCA	346	A	R	R	R	R	R	R	R	R	R	R	R	R	P2	364	99%	P2	2	1%
GAG	274	E	R	R	R	R	R	R	R	R	R	X	RS	RS	P2	6	2%	P2	232	98%
ACT	238	T	R	R	R	R	R	R	R	S	S	S	S	S						
GTT	232	V	R	R	R	R	R	R	R	S	S	S	S	S						
ATC	192	I	S	S	R	R	R	R	R	R	R	R	R	R						
ACA	174	T	R	R	R	R	R	R	R	R	R	R	R	R	P1	174	100%			
CAA	174	Q	X	R	R	R	R	R	R	R	R	R	R	R	P1	8	4%			
AGG	142	R	R	R	R	R	R	R	R	R	R	R	R	R						
AAT	88	N	R	R	R	R	R	R	R	R	R	R	R	R						
AGT	39	S	R	R	R	R	R	R	R	R	R	R	R	R						
TTG	35	L	R	R	R	R	R	R	R	R	R	R	R	R						
CCC	32	P	RRS	RRS	RRS	RS	P2,3	32, 32	100%											
AAA	30	K	XRR	RRR	RRR	RRR	RRR	RRR	RS	RS	RS	RS	RS	RS	P3	20	100%			
CAC	20	H	RS	RR	RR	RR	RR	RR	R	R	R	R	R	R						
GAT	18	D	R	R	R	R	R	R	R	R	R	R	R	R						
CGG	15	R	R	S	R	R	R	R	R	R	R	R	R	R	P1	15	100%			
ATT	10	I	R	R	R	R	R	R	R	R	R	R	R	R						
CTA	10	L	S	R	R	R	S	S	S	R	R	R	R	R						
CTT	8	L	R	R	R	R	R	R	R	R	R	R	R	R						
GAA	8	E	RR	RR	RR	RS	RS	RS	RS	RS	RS	R	R	R						
GGT	7	G	S	S	S	S	S	S	S	S	S	R	R	R						
GGC	2	G	S	S	S	S	S	S	S	S	S	RR	RR	RR	P3	2	100%			
TTT	2	F	RRS	RRR																
	Sum:	58801																		

¹Codons are listed from the top by order of frequency in the 1,919 V genes analyzed.

²Results of all possible exchanges for each codon. Effects on identical nucleotides within a particular codon are listed respectively. R = amino acid replacement; S = Silent mutation; X = nonsense mutation.

³Hotspots refer to the number (count) and percentage (proportion) of cytidines associate with the particular codon that fall within a hotspot of AID activity in the various 1,919 V g analyzed as described in the text. Position (Pos.) is the nucleotide position of the cytidine referred to within the codon where P1 is position 1, P2 is position 2, and P3 is position 3

⁴Coldspots list the counts and proportions of cytidines in AID coldspots annotated similarly comment 3 above.