Table S1. Related to Figure 2. Molecular characteristics of the identified VRC01-class antibodies. Antibodies encoded by the same kappa V-gene allele are grouped together. Synthesized antibodies for further characterization are in red letters. CDR L3 encoded by V genes are in blue letters. Sequence ID, CDR L3 and H3 of the antibodies derived from the same clonal family are highlighted in yellow, and CDR L3 of antibodies sharing the same lineage are highlighted in orange.

Sequence ID	Kappa chain							Heavy chain						
	Mouse V-GENE and allele	V-REGION identity % (nt)	V-REGION mutation % (aa)	Mouse J-GENE and allele	CDR-IMGT lengths	CDR1 aa	AA JUNCTION	Human V-GENE and allele	V-REGION identity % (nt)	V-REGION mutation % (aa)	Mouse J-GENE and allele	Mouse D-GENE and allele	CDR-IMGT lengths	AA JUNCTION
3181-GT6-E1	IGKV4-57-1*01 F	98	3	IGKJ4*01 F	[7.3.5]	SSVSSSY	CQQYSAF	IGHV1-2*02 F	100	0	IGHJ2*01 F	IGHD2-3*01 F	[8.8.14]	CARVPAYDGYYSFDYW
3181-GT6-A1		97	3	IGKJ4*01 F	[7.3.5]	SSVSSSY	CQQYSAF		100	0	IGHJ2*02 F	IGHD2-3*01 F	[8.8.14]	CARVPAYDGYYSFDYW
3180-A4	IGKV4-61*01 F	95	4	IGKJ1*01 F, or 02 F	[5.3.5]	SSVSY	CQQYQTF	IGHV1-2*02 F	94	9	IGHJ2*01 F	IGHD2-4*01 F	[8.8.11]	CARNDYDSYFDYW
3182-C2		96	3	IGKJ1*02 F(c)	[5.3.5]	SSVSY	CQQYETF		93	10	IGHJ2*01 F	IGHD2-4*01 F	[8.8.10]	CATMTTGYFDYW
3181-E7		96	4	IGKJ1*01 F	[5.3.5]	SSVSY	CQLYQTF		99	3	IGHJ1*01 F	IGHD3-3*01 F	[8.8.10]	CARDGTGYFDVW
3181-P2–E1		96	7	IGKJ1*01 F, or 02 F	[5.3.5]	SSVSY	CQRYQTF		99	2	IGHJ2*01 F	IGHD3-3*01 F	[8.8.12]	CAKRDWDGNYFDYW
3183-G10		96	8	IGKJ2*01 F	[5.3.5]	SSISY	CQQYQSF		98	6	IGHJ2*01 F	IGHD1-1*02 F	[8.8.9]	CARDGGYYDYW
3181-GT6-B7	IGKV4-86*01 F	97	7	IGKJ4*01 F	[5.3.5]	SSVNY	CQQWSYF	IGHV1-2*02 F	98	5	IGHJ3*01 F	IGHD1-1*02 F	[8.8.13]	CARRDDYDGGWFAYW
3181-A11		97	7	IGKJ4*01 F	[5.3.5]	SSVNY	CQQWSYF		98	5	IGHJ3*01 F		[8.8.13]	CARRDDYDGGWFAYW
3185-P2-A6	IGKV6-23*01 F	96	7	IGKJ2*01 F	[6.3.5]	QDVGTA	CQQYSTF	IGHV1-2*02 F	99	3	IGHJ1*01 F	IGHD4-1*01 F	[8.8.13]	CALLPAGTGCFFDGW
3185-P1-H3		97	5	IGKJ2*01 F	[6.3.5]	QDVGTA	CQQYSTF		98	4	IGHJ1*01 F	IGHD4-1*02 F	[8.8.13]	CARVPTGTGWHFDVW
3184_P1-A1	IGKV8-30*01 F	97	3	IGKJ1*01 F	[12.3.5]	QSLLYSSNQKNY	CQQYYTF	IGHV1-2*02 F	98	3	IGHJ2*01 F	IGHD1-3*01 F	[8.8.10]	CARKGGSYFDYW
3184_P1-F11		96	6	IGKJ1*01 F	[12.3.5]	QSLLYSSNQKNY	CQQYNTF		99	3	IGHJ2*01 F	IGHD3-2*02 F	[8.8.10]	CARQGGSYFDYW
3184-P2_B12		98	1	IGKJ4*01 F	[12.3.5]	QSLLYSSNQKNY	CQQYYTF		100	0	IGHJ2*01 F	IGHD4-1*01 F	[8.8.10]	CAREIGTYFDYW
3185-P1-G1	IGKV10-96*01 F	96	5	IGKJ1*01 F	[6.3.5]	QDISNY	CQQDNTF	IGHV1-2*02 F	99	2	IGHJ4*01 F	IGHD5-7*01 ORF	[8.8.11]	CARQFDRGSMDYW
3181-F12	IGKV17-121*01 F	95	9	IGKJ2*01 F	[6.3.5]	TDIDDD	CLHMYTF	IGHV1-2*02 F	100	0	IGHJ1*01 F	IGHD2-2*01 F	[8.8.14]	CARWIYYGYDKYFDVW

Table S2. Related to Figure 2. Summary of immunization studies performed on heterozygous V_H1-2 mice using VRC01-class germline-binding immunogens other than eOD-GT8 60mer. CD4 binding site-specific IgG$^+$ memory B cells were sorted using the eOD-GT6 and ΔeOD-GT6 probes as described in experimental procedures. IgH and IgL chains were amplified and the number of V_H1-2 HCs and 5aa CDR L3 LCs were listed.

Study	Immunization method	Number of Mice	Total B cells for sorting	Number of Sorted B cells	Number of V_H1-2 HCs	Number of 5aa CDRL3 LCs
eOD-GT6 60mer x4	eOD-GT6 60mer 4 times	3	1.16E+06	171	29	0
eOD-GT6 60mer x3	eOD-GT6 60mer 3 times	4	9.64E+05	66	10	0
Sequential	eOD-GT6 60mer 2 times /426C-Ferritin core/C13-Ferritin	3	5.35E+05	66	12	0
	eOD-GT6 60mer 2 times /C13-Ferritin/426C-Ferritin core	3	2.77E+05	50	13	0
	426C-Ferritin core 2 times /eOD-GT6 60mer/C13-Ferritin	3	3.09E+05	60	14	0
	C13-Ferritin 2 times /eOD-GT6 60mer/426C-Ferritin core	3	1.45E+05	13	7	0
	Mixture of eOD-GT6 60mer, 426C-Ferritin core and C13-Ferrtin 4 times	3	4.37E+05	47	4	0
Total		22	3.83E+06	473	89	0

Table S3. Related to Figure 2. Summary of paired HC-LC sequencing.

Mouse ID	*2890*	*2725*	*3994*	*3181*	*3182*
	Naïve 1	**Naïve 2**	**Naïve 3**	**eOD-GT8-30µg-1**	**eOD-GT8-30 µg-2**
B cells emulsified (million)	2.0	1.9	1.4	2.5	0.8
Total sequencing reads	563,227	1,105,376	1,557,620	5,568,478	5,725,480
Reads after quality-filtering*	289,522	429,267	1,017,553	3,098,129	2,717,338
Est. antibody lineages**	5,523	6,586	11,026	4,609	8,251
hu_VH1-2 reads	63,232	102,011	128,414	384,713	329,154
5aa CDR-L3 reads	5	77	157	7,469	4,046
hu_VH1-2+5aa_CDR-L3 reads	0	12	30	6,792	1,419
Class-switched reads after quality filtering*	72,542	315,436	582,883	1,366,695	1,327,508
Class-switched est. antibody lineages**	1,146	2,383	3,137	2,060	3,528
Class-switched hu_VH1-2 reads	15,895	84,008	86,059	368,817	292,251
Class-switched 5aa CDR-L3 reads	3	70	88	7,465	4,029
Class-switched hu_VH1-2+5aa_CDR-L3 reads	0	10	9	6,788	1,414
IgG reads after quality filtering*	44,297	303,710	464,108	1,195,909	1,184,144
IgG est. antibody lineages**	472	1,809	1,232	834	1,954
IgG hu_VH1-2 reads	11,527	81,292	71,959	337,430	251,865
IgG 5aa CDR-L3 reads	3	70	84	7,402	3,482
IgG hu_VH1-2+5aa_CDR-L3 reads	0	10	9	6,750	1,168
IgA reads after quality filtering*	28,245	11,726	118,775	170,786	143,364
IgA est. antibody lineages**	674	574	1,905	1,226	1,574
IgA hu_VH1-2 reads	4,368	2,716	14,100	31,387	40,386
IgA 5aa CDR-L3 reads	0	0	4	63	547
IgA hu_VH1-2+5aa_CDR-L3 reads	0	0	0	38	246
IgM reads after quality filtering*	187,373	90,735	338,867	74,651	206,313
IgM est. antibody lineages**	4,377	4,203	7,889	2,549	4,723
IgM hu_VH1-2 reads	47,337	18,003	42,355	15,896	36,903
IgM 5aa CDR-L3 reads	2	7	69	4	17
IgM hu_VH1-2+5aa_CDR-L3 reads	0	2	21	4	5

*R1/R2 filtered (Q-score 20 over 50% of the read), productive junction, and same VH:VL sequence (CDR H3:CDR-L3 nuclotide seq_gene ID_isotype) observed ≥2 times

**Estimated by 96% identity clustering of CDR-H3 nucleotide sequences

Table S4. Related to Figure 4. Summary of single-cell RT-PCR results for the V_H1-2/LC knock-in mouse study. V_H1-2 HCs and Vκ3-20 LCs were amplified with gene-specific primers from sorted eODGT6$^+$/ΔeODGT6$^-$/IgG$^+$ B cells by single cell RT-PCR and sequenced. The number of sorted B cells used for single cell PCR, the number of confirmed V_H1-2 (H) and Vκ3-20 (L) chains from the PCR, the number of V_H1-2/Vκ3-20 paired IgGs, the average nucleotide mutation rates and the mutation range (in parentheses) in all paired V_H1-2 and Vκ3-20 are listed for each sample in the table.

	naïve	**G1**			**G2**				
Mouse ID (sacrifice time)	**#1531 (wk0)**	**#1532 (wk2)**	**#1533 (wk22)**	**#1534 (wk22)**	**#1540 (wk2)**	**#1536 (wk6)**	**#1539 (wk10)**	**#1537 (wK14)**	**#1538 (wk22)**
Cells used for single cell PCR	80	103	96	96	88	156	96	95	96
Verified VH1-2, VK3-20	50H, 56L	28H, 67L	63H, 71L	50H, 75L	38H, 58L	63H, 61L	58H, 77L	50H, 50L	60H, 78L
Paired VH1-2/VK3-20	43	24	55	46	37	57	53	50	56
Paired VH1-2 mutation rate (nt)	0.48% (0-3.82%)	0.55% (0-3.47%)	0.34% (0-3.13%)	0.40% (0-3.12%)	0.67% (0-3.82%)	1.30% (0-4.90%)	1.99% (0-6.60%)	1.56% (0-9.38%)	2.03% (0-8.68%)
Paired VK3-20 mutation rate (nt)	0.16% (0-1.06%)	0.31% (0-1.77%)	0.21% (0-2.13%)	0.21% (0-1.77%)	0.45% (0-3.19%)	0.69% (0-3.60%)	0.98% (0-3.90%)	0.72% (0-4.25%)	0.89% (0-4.96%)

Table S5. Related to Figure 5. IgGs with neutralizing activities among the 27 synthesized antibodies identified from the V_H1-2/LC mice use mouse IGJH1*01, the ortholog of human IGHJ2*01. The 27 IgGs were grouped based on whether they neutralize 426c.N276D virus. The mouse IGHJ1*01 are highlighted in yellow and the conserved W (Trp) in CDRH3s is in bold.

Sequence ID	V-GENE and allele	V-REGION identity % (nt)	J-GENE and allele	D-GENE and allele	CDR-IMGT lengths	AA JUNCTION	Neutralize 426c.N276 virus
1538-67_H	Homsap IGHV1-2*02 F	99.65% (287/288 nt)	Musmus IGHJ4*01 F	Musmus IGHD2-4*01 F	[8.8.17]	CARVDYDYDGRDYYAMDYW	No
1538-91_H	Homsap IGHV1-2*02 F	100.00% (288/288 nt)	Musmus IGHJ3*01 F	Musmus IGHD4-1*01 F	[8.8.11]	CARELGLAWFAYW	
1538-93_H	Homsap IGHV1-2*02 F	100.00% (288/288 nt)	Musmus IGHJ3*01 F	Musmus IGHD3-2*01 F	[8.8.12]	CARDSSGSAWFAYW	
1539-B10_H	Homsap IGHV1-2*02 F	100.00% (288/288 nt)	Musmus IGHJ3*01 F	Musmus IGHD2-1*01 F	[8.8.12]	CARRVYGNYDWAYW	
1539-B9_H	Homsap IGHV1-2*02 F	94.79% (273/288 nt)	Musmus IGHJ3*01 F	Musmus IGHD2-12*01 F	[8.8.13]	CARRRYNYD**W**EFVYW	
1540-E9_H	Homsap IGHV1-2*02 F	99.65% (287/288 nt)	Musmus IGHJ2*01 F	Musmus IGHD2-2*01 F	[8.8.10]	CARKTTMVFDYW	
1536-hvk-E6_H	Homsap IGHV1-2*02 F	98.61% (284/288 nt)	Musmus IGHJ1*02 F	Musmus IGHD2-1*01 F	[8.8.14]	CARPGYGNYG**W**YFDVW	
1539-A1_H	Homsap IGHV1-2*02 F	96.88% (279/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-14*01 F	[8.8.18]	CAAAYYNYDAESFD**W**YFDVW	
1539-B5_H	Homsap IGHV1-2*02 F	95.83% (276/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD1-2*01 F	[8.8.13]	CAVYYGYGD**W**YFDVW	
1538-1_H	Homsap IGHV1-2*02 F	96.18% (277/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDVDG**W**YFDVW	Yes
1538-12_H	Homsap IGHV1-2*02 F	94.79% (273/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.16]	CARYRNSYDDDG**W**KFDIW	
1538-17_H	Homsap IGHV1-2*02 F	94.44% (272/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDDDG**W**SFDVW	
1538-19_H	Homsap IGHV1-2*02 F	95.14% (274/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDGDG**W**SFDVW	
1538-20_H	Homsap IGHV1-2*02 F	95.83% (276/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDADG**W**FFDVW	
1538-26_H	Homsap IGHV1-2*02 F	91.67% (264/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD1-3*01 F	[8.8.14]	CARYNNEEDG**W**YFDVW	
1538-4_H	Homsap IGHV1-2*02 F	94.79% (273/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDHDGPG**W**YFDVW	
1538-65_H	Homsap IGHV1-2*02 F	94.44% (272/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-3*01 F	[8.8.14]	CARYDSDGEG**W**YFDVW	
1538-69_H	Homsap IGHV1-2*02 F	94.44% (272/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD4-1*01 F	[8.8.13]	CARDRTGND**W**NFDVW	
1538-76_H	Homsap IGHV1-2*02 F	96.18% (277/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDGEG**W**YFDVW	
1538-79_H	Homsap IGHV1-2*02 F	91.32% (263/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD4-1*01 F	[8.8.13]	CARDRTGND**W**YFDVW	
1538-86_H	Homsap IGHV1-2*02 F	96.18% (277/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.14]	CARYDNDADG**W**YFDVW	
1539-B3_H	Homsap IGHV1-2*02 F	96.18% (277/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-2*01 F	[8.8.13]	CAIYYVYGD**W**YFDVW	
1539-C8_H	Homsap IGHV1-2*02 F	94.79% (273/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.15]	CARRGDYDEGD**W**YFHVW	
1539-E6_H	Homsap IGHV1-2*02 F	93.40% (269/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD3-1*01 F	[8.8.13]	CARHIFDSH**W**YFDVW	
1539-G2_H	Homsap IGHV1-2*02 F	96.88% (279/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.15]	CARPSTYDDYD**W**YFDVW	
1539-G5_H	Homsap IGHV1-2*02 F	95.49% (275/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD3-3*01 F	[8.8.13]	CAKDMSGTD**W**HLDVW	
1539-G6_H	Homsap IGHV1-2*02 F	94.79% (273/288 nt)	Musmus IGHJ1*01 F	Musmus IGHD2-4*01 F	[8.8.15]	CARPSYDYDHD**W**YFDVW	

Table S6. Related to Figure 2. Primers for single cell RT-PCR in the V_H1-2 mouse model and the V_H1-2/LC mouse models (1: derived from Tiller et al, 2009. 2: derived from Wu el al, 2010. *: New design).

Mouse Model	PCR step	Primer name	5′–3′ sequence	Reference
VH1-2/IGCR1-single knock-in mice	IgH 1st PCR	Vh1-2 For1	ATGGACTGGACCTGGAGGATCCTCTTCTTGGTG	VRC design*
		ZR013-Outer-mCmu	AGGGGGCTCTCGCAGGAGACGAGG	1
		ZR0014-Outer-mCg1	GGAAGGTGTGCACACCGCTGGAC	1
		ZR015-Outer-mCg2c	GGAAGGTGTGCACACCACTGGAC	1
		ZR016-Outer-mCg2b	GGAAGGTGTGCACACTGCTGGAC	1
		ZR017-Outer-mCg3	AGACTGTGCGCACACCGCTGGAC	1
		ZR018-Outer--mCgA	GAAAGTTCACGGTGGTTATATCC	1
		ZR66-mIgD58	TTTCCTCTGGGGCTTTGCACT	JZ design*
	IgH 2nd PCR	Vh1-2 For3	ACAGGAGCCCACTCCCAGGTGCAGCTGGTGCAG	VRC design*
		ZR007-inner-mCmu	AGGGGGAAGACATTTGGGAAGGAC	1
		ZR008-inner-mCg1	GCTCAGGGAAATAGCCCTTGAC	1
		ZR009-inner-mCg2c	GCTCAGGGAAATAACCCTTGAC	1
		ZR010-inner-mCg2b	ACTCAGGGAAGTAGCCCTTGAC	1
		ZR011-inner-mCg3	GCTCAGGGAAGTAGCCTTTGAC	1
		ZR012-inner-mCgA	TGCCGAAAGGGAAGTAATCGTGAAT	1
		ZR038-Inner-mCd	TCTGAGAGGAGGAACATGTC	1
	IgK 1st PCR	ZF006-mLVk3	TGCTGCTGCTCTGGGTTCCAG	1
		ZF007-mLVk4	ATTWTCAGCTTCCTGCTAATC	1
		ZF008-mLVk5	TTTTGCTTTTCTGGATTYCAG	1
		ZF009-mLVk6	TCGTGTTKCTSTGGTTGTCTG	1
		ZF010-mLVk6-8-9	ATGGAATCACAGRCYCWGGT	1
		ZF011-mLVk14	TCTTGTTGCTCTGGTTYCCAG	1
		ZF012-mLVk19	CAGTTCCTGGGGCTCTTGTTGTTC	1
		ZF013-mLVk20	CTCACTAGCTCTTCTCCTC	1
		ZR003-mCK609	AGTTGATGTCTTGTGAGTGGCCTCA	JZ design*
	IgK 2nd PCR	ZF047-IgLmVK-Ratner	CTGGGTTCCAGGTTCCACTGGTGACGAYATTGTGMTSACMCARWCTMCA	1
		ZR006-mCK-Tiller	GATGGTGGGAAGATGGATACAGTT	1
VH1-2/VK3-20 double knock-in mice	IgH 1st PCR	VH1 LEADER-A	ATGGACTGGACCTGGAGGAT	2
		3'musCg-1st	CCCTTGACCAGGCATCCYAG	VRC design*
		3'musCm-1st	GGCAGCCCATGGCCACCAGA	
	IgH 2nd PCR	xj-VH1-1st:	ACAGGAGCCCACTCCCAGGTGCAG	
		3'musCg-2nd	CCAGGGGCCAGTGGATAGACHGATGG	
		3'musCm-2nd	AGACAGGGGGCTCTCGCAGGA	
	IgK 1st PCR	5' hVK3-20.6	CGCAGCTTCTCTTCCTCCTG	
		3'musCk-1st	ACTGGATGGTGGGAAGATGGA	
	IgK 2nd PCR	5' hVK3-20.4	ACTCTGGCTCCCAGATACCA	
		3'musCk-2nd	GGAAGATGGATACAGTTGGTG	

Table S7. Related to Figure 2. Paired heavy and light chain emulsion linkage RT-PCR primer mix (upper panel) and nested PCR primer mix for amplification of linked VH:VL constructs (lower panel).

Final conc. (nM)	Primer name	Sequence 5'-3'
400	CH-AHX89	CGCAGTAGCGGTAAACGGC
400	CL-BRH06	GCGGATAACAATTTCACACAGG
40	mIgG-OE-aPEX	CGCAGTAGCGGTAAACGGC GGACAGGGMTCCAKAGTTCCA
40	mIgA-OE-aPEX	CGCAGTAGCGGTAAACGGC TCAGGCAGCCGATTATCACG
40	mIgM-OE-aPEX	CGCAGTAGCGGTAAACGGC CCCCCTGTCCTCAGTGTTGG
40	mIgK-OE-aPEX	GCGGATAACAATTTCACACAGG GTTCAAGAAGCACACGACTGAGG
40	mIgL-OE-aPEX	GCGGATAACAATTTCACACAGG ATCRKACACACSAGTGTGGC
40	mH-RTL1	ccagcagctagcgttttagca GA KGT RMA GCT TCA GGA GTC
40	mH-RTL2	ccagcagctagcgttttagca GA GGT BCA GCT BCA GCA GTC
40	mH-RTL3	ccagcagctagcgttttagca CA GGT GCA GCT GAA GSA STC
40	mH-RTL4	ccagcagctagcgttttagca GA GGT CCA RCT GCA ACA RTC
40	mH-RTL5	ccagcagctagcgttttagca CA GGT YCA GCT BCA GCA RTC
40	mH-RTL6	ccagcagctagcgttttagca CA GGT YCA RCT GCA GCA GTC
40	mH-RTL7	ccagcagctagcgttttagca CA GGT CCA CGT GAA GCA GTC
40	mH-RTL8	ccagcagctagcgttttagca GA GGT GAA SST GGT GGA ATC
40	mH-RTL9	ccagcagctagcgttttagca GA VGT GAW GYT GGT GGA GTC
40	mH-RTL10	ccagcagctagcgttttagca GA GGT GCA GSK GGT GGA GTC
40	mH-RTL11	ccagcagctagcgttttagca GA KGT GCA MCT GGT GGA GTC
40	mH-RTL12	ccagcagctagcgttttagca GA GGT GAA GCT GAT GGA RTC
40	mH-RTL13	ccagcagctagcgttttagca GA GGT GCA RCT TGT TGA GTC
40	mH-RTL14	ccagcagctagcgttttagca GA RGT RAA GCT TCT CGA GTC
40	mH-RTL15	ccagcagctagcgttttagca GA AGT GAA RST TGA GGA GTC
40	mH-RTL16	ccagcagctagcgttttagca CA GGT TAC TCT RAA AGW GTS TG
40	mH-RTL17	ccagcagctagcgttttagca CA GGT CCA ACT VCA GCA RCC
40	mH-RTL18	ccagcagctagcgttttagca GA TGT GAA CTT GGA AGT GTC
40	mH-RTL19	ccagcagctagcgttttagca GA GGT GAA GGT CAT CGA GTC
40	huVH1fwd	ccagcagctagcgttttagca CAGGTCCAGCTKGTRCAGTCTGG
40	huVH157fwd	ccagcagctagcgttttagca CAGGTGCAGCTGGTGSARTCTGG
40	mL-RTL1	tgctaaaacgctagctgctggttcccatggca G AYA TCC AGC TGA CTC AGC C
40	mL-RTL2	tgctaaaacgctagctgctggttcccatggca G AYA TTG TTC TCW CCC AGT C
40	mL-RTL3	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGM TMA CTC AGT C
40	mL-RTL4	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGY TRA CAC AGT C
40	mL-RTL5	tgctaaaacgctagctgctggttcccatggca G AYA TTG TRA TGA CMC AGT C
40	mL-RTL6	tgctaaaacgctagctgctggttcccatggca G AYA TTM AGA TRA MCC AGT C
40	mL-RTL7	tgctaaaacgctagctgctggttcccatggca G AYA TTC AGA TGA YDC AGT C
40	mL-RTL8	tgctaaaacgctagctgctggttcccatggca G AYA TYC AGA TGA CAC AGA C
40	mL-RTL9	tgctaaaacgctagctgctggttcccatggca G AYA TTG TTC TCA WCC AGT C
40	mL-RTL10	tgctaaaacgctagctgctggttcccatggca G AYA TTG WGC TSA CCC AAT C
40	mL-RTL11	tgctaaaacgctagctgctggttcccatggca G AYA TTS TRA TGA CCC ART C
40	mL-RTL12	tgctaaaacgctagctgctggttcccatggca G AYR TTK TGA TGA CCC ARA C
40	mL-RTL13	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGA TGA CBC AGK C
40	mL-RTL14	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGA TAA CYC AGG A
40	mL-RTL15	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGA TGA CCC AGW T
40	mL-RTL16	tgctaaaacgctagctgctggttcccatggca G AYA TTG TGA TGA CAC AAC C
40	mL-RTL17	tgctaaaacgctagctgctggttcccatggca G AYA TTT TGC TGA CTC AGT C
40	mL-RT1Lambda	tgctaaaacgctagctgctggttcccatggca G ARG CTG TTG TGA CTC AGG AAT C
200	mIgG-OEnested-4N	NNNN ATGGGCCCTG CCARKGGATAGACHGATGGGG
200	mIgA-OEnested-4N	NNNN ATGGGCCCTG TGGTGGGATTTCTCGCAGAC
200	mIgM-OEnested-4N	NNNN ATGGGCCCTG GCAGGAGACGAGGGGGAAGA
200	mIgK-OEnested-4N	NNNN GTGCGGCCGC GGTGGGAAGATGGATACAGTTGGT
200	mIgL-OEnested-4N	NNNN GTGCGGCCGC TCAGRGGAAGGTGGRAACA