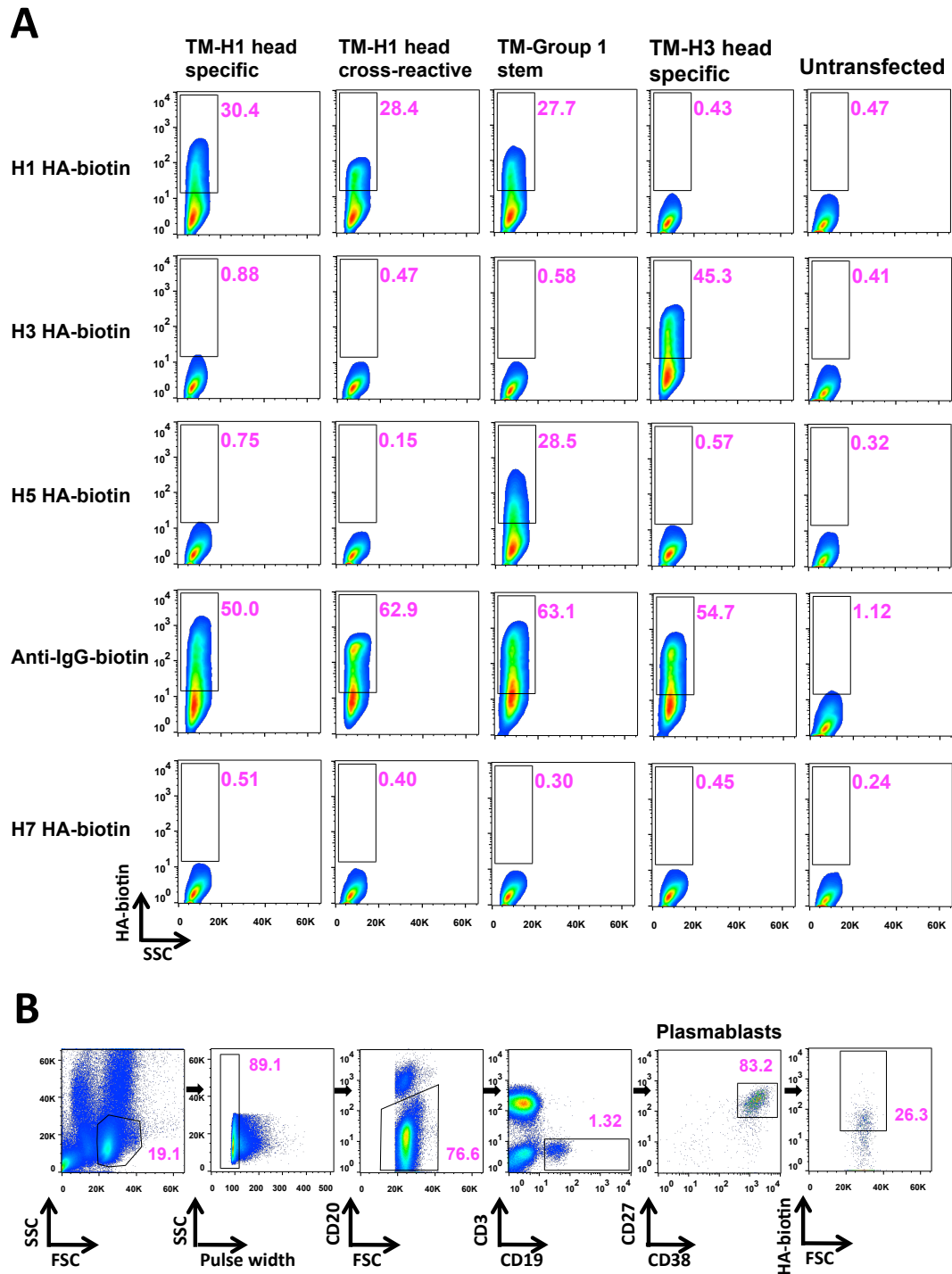


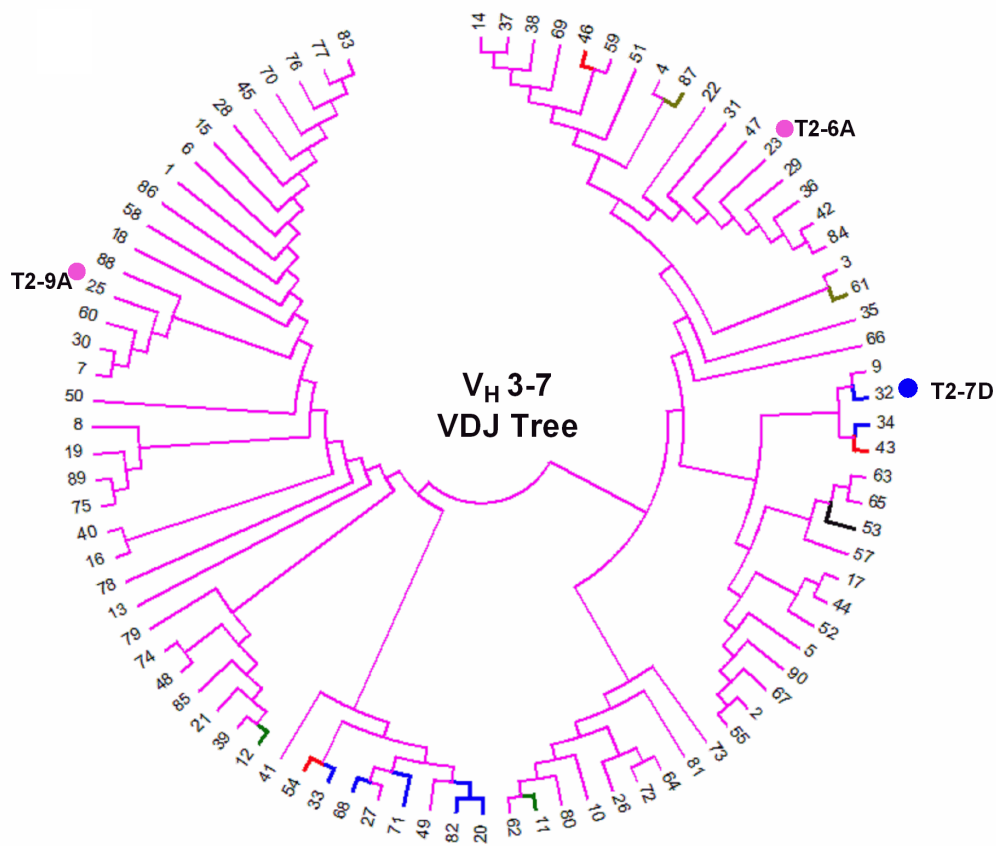
SUPPLEMENTAL DATA



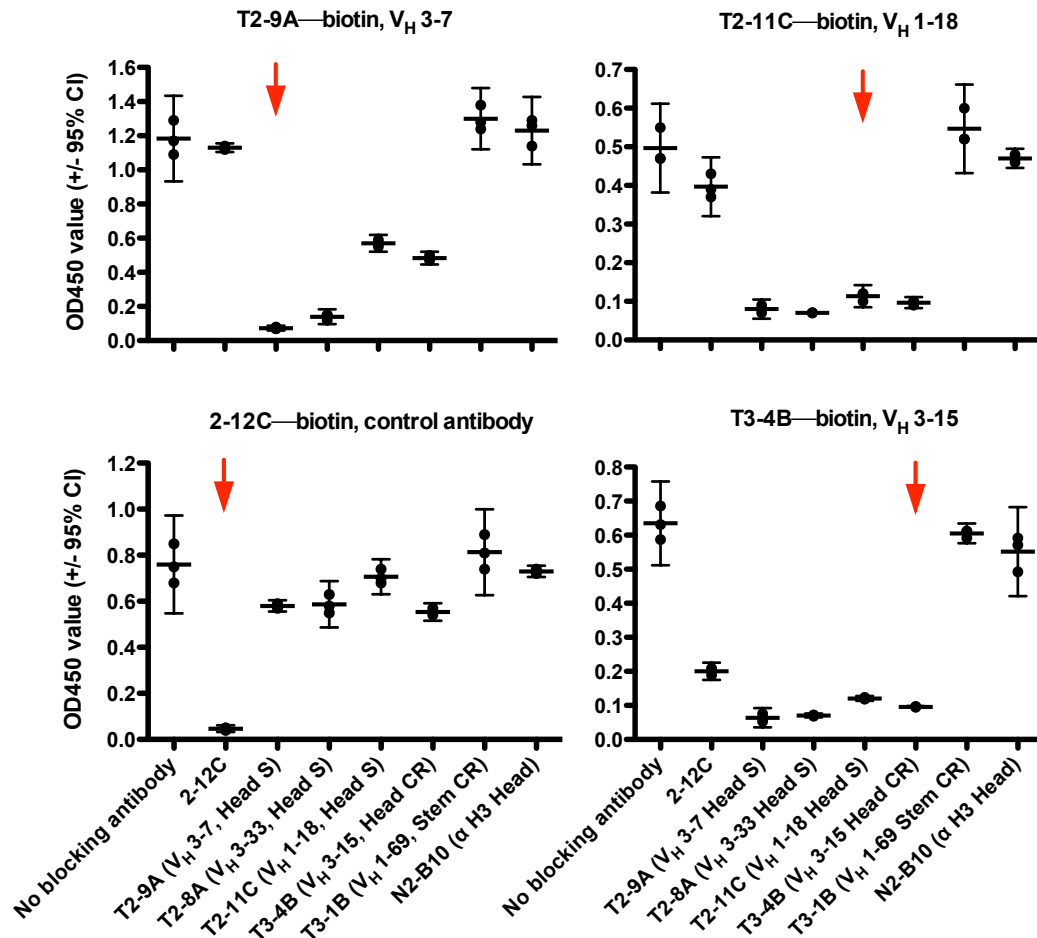
Supplemental Figure 1. Binding of recombinant HA to transmembrane expressed immunoglobulin G on 293T cells, and day 7 plasmablasts. (A) Staining

of 293T cells transfected with TMlgG1 with soluble HAs. The percentage of positive cells is shown in the pink boxes. **(B)** Day 7 plasmablasts from donor H following 2011-12 influenza vaccination were stained with biotinylated H1N1pdm09 (A/England/195/2009) HA for single cell sorting. The percentage of cells selected in each gate is shown in pink.

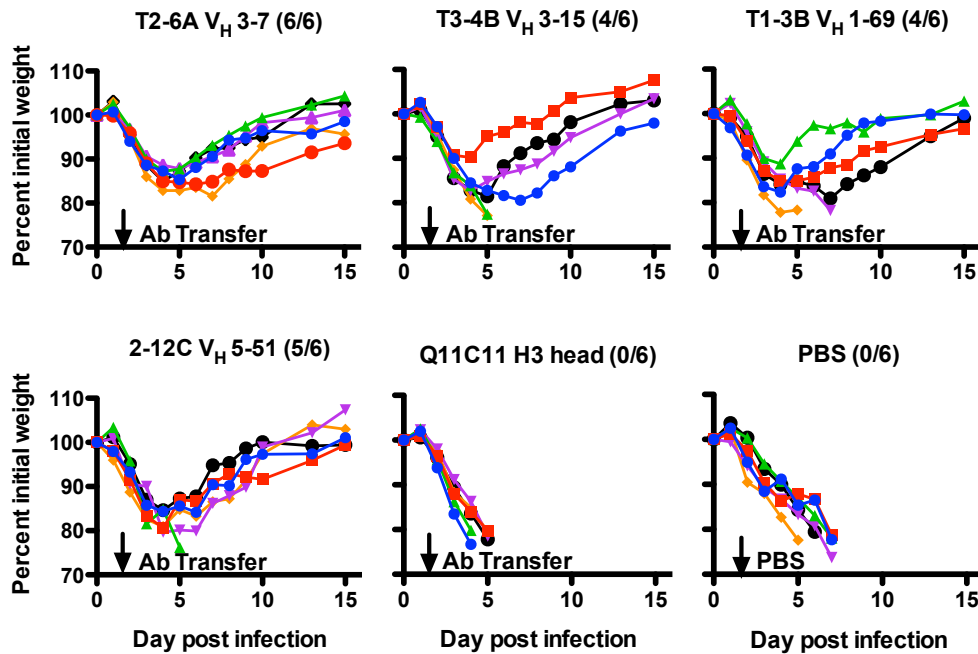
Color code	V _H	D _H	J _H	Reading frame	Size of the clone
	3-7*01	3-16*01	6*02	2	73
	3-7*03	3-16*01	6*02	2	2
	3-7*01	3-3*01	6*02	3	7
	3-7*01	3-3*01	6*02	2	3
	3-7*01	3-3*02	6*02	3	2
	3-7*01	3-16*01	6*01	2	1



Supplemental Figure 2. The amino acid sequence dendrogram of the largest set of HA head specific-binding antibodies, encoded by V_H 3-7 gene segment. The largest set V_H 3-7 dominated by a clone (pink) encoded by VDJ: 3-7*01/3-16*01/6*02 and reading frame 2. The dendrogram was generated based on the protein sequence with MEGA software version 6.06 using neighbor-joining tree.



Supplemental Figure 3. Competitive binding to purified A/England/195/2009 HA by the various sets of antibodies that are sensitive to K163E/Q. The head-specific antibody 2-12C recognizing K130, G155, a typical V_H 1-69 stem reactive antibody and an anti-H3 antibody were included as controls. Arrows indicate self-inhibition by the unlabeled version of each antibody. Measurements were in triplicate. Means and 95% confidence intervals are shown. The assay was done twice with equivalent results.



Supplemental Figure 4. Protection against influenza challenge with the antibodies described in the text. The *in vivo* therapeutic effect of antibodies: head-specific V_H 3-7, head cross-reactive V_H 3-15, stem cross-reactive V_H 1-69, head-specific V_H 5-51, and H3 head-specific Q11C11 in X179A challenged mice (n=6 per group). Twenty-four hours after intranasal infection with 150 MD₅₀ X179A virus, DBA/2 mice were treated with a single dose of 10 mg/kg antibody or PBS administered to the peritoneal space.

Supplemental Table 1. Details of the 157 antibody heavy and light chain sequences isolated from Donor H

Antibody	V _H	D _H	J _H	rf	Heavy Junction Sequence	V _k /V _λ	J _k /J _λ	λ/k	Light Junction Sequence
T1-1A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T1-7A	3-7*01	3-16*01	6*02	2	CARQGSYANTYFYY YAIDVW	1-40*03	2*01 or 3*01	λ	CQSYDTTSLGLD VVF
T1-8A	3-7*01	3-16*01	6*02	2	CARQDSFANTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSDLK VVF
T1-9A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLK VVF
T1-11A	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDNTPSGLH VVF
T1-12A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL NVVF
T1-2B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-51*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T1-4B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T1-5B	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSVSGLD VVF
T1-7B	3-7*03	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDNLNLSGLN VVF
T1-1C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDNLNLSGLN VVF
T1-2C	3-7*03	3-16*01	6*02	2	CARQGSYADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDNLNLSGLN VVF
T1-3C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDNLNLSGLN VVF
T1-5C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLK VVF
T1-7C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL NVVF
T1-9C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDNLNLSGLN VVF
T1-11C	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLSGLH VIF
T1-12C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL NVVF
T1-6D	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDNNLNGL DVVF
T1-10D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYYSD YGMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGSV VVF
T1-11D	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLSGLD VVF
T2-2A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDTGLSGLE VVF

T2-6A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T2-9A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGLD VVF
T2-10A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGLD VVF
T2-5B	3-7*01	3-16*01	6*02	2	CARQGSYGDYYYYD YAVD VW	1-40*01	2*01 or 3*01	λ	CQSYGSTLSGSV VIF
T2-1C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T2-2C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T2-10C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMD VW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQTYDSNLNGL DVVF
T2-6D	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T2-7D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGLD VVF
T2-8D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYYHD YGMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSMSGSV VVF
T2-10D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYFYY YALD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGLH VVF
T2-11D	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLGLD VVF
T3-3A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T3-8A	3-7*01	3-16*01	6*02	2	CARQGSFANTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T3-2B	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLNNLE VVF
T3-3B	3-7*03	3-16*01	6*02	2	CARQGSYADTYYYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDNSLGLD VVF
T3-5B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSNLGLD VVF
T3-7B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYD YGMD VW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLGLD VVF
T3-9B	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T3-11B	3-7*01	3-3*01	6*02	2	CARQGSFGDTYFYY YALD VW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGLH VVF
T3-6C	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY Y AID VW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T3-8C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
T3-9C	3-7*01	3-3*02	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
T3-12C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMD VW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDTGLSGLE VVF

T3-1D	3-7*01	3-16*01	6*02	2	CVRQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDRSLSGLD VVF
T3-2D	3-7*01	3-3*01	6*02	2	CARQGSFGDTYYSD YGMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLSGSV VVF
T3-3D	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL NVVF
T3-4D	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLK VVF
T3-6D	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YGIDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGLH VIF
T3-9D	3-7*01	3-16*01	6*01	2	CARQGSYADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDISLSRTD VVF
T3-10D	3-7*01	3-3*01	6*02	2	CARQGSFGDTYFYD YGMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSMSGSV VVF
T3-11D	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDTTLGDLN VIF
mbc T1-8A	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDISLSRSD VVF
mbc T1-9A	3-7*01	3-16*01	6*02	2	CARQGSFADTYHYH YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T1-7B	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
mbc T1-10B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T1-5C	3-7*01	3-3*02	6*02	3	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLG VVF
mbc T1-7C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDNSLSGLD VVF
mbc T1-8C	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDISLSRSD VVF
mbc T1-9C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSRSGLD VVF
mbc T1-10C	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDISLSRSD VVF
mbc T1-1D	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGLD VVF
mbc T1-5D	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDTTLSGLD VVF
mbc T1-10D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYYDYD YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGSV VVF
mbc T1-12D	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLNNLE VVF
mbc T2-2A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQPYDSNLNGL DVVF
mbc T2-7A	3-7*01	3-3*01	6*02	3	CARQGSFGDTYYDYD YGMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGSV VVF
mbc T2-8A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGLD VVF

mbc T2-10A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGSLD VVF
mbc T2-11A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGSLD VVF
mbc T2-2B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T2-3B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T2-5B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CRSYDSNLNGLD VVF
mbc T2-6B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGSLD VVF
mbc T2-9B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLGSLD VVF
mbc T2-5C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDNSLSGLD VVF
mbc T2-11C	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGSLD VVF
mbc T2-2D	3-7*01	3-3*01	6*02	3	CARQGSFGDTYYSD YGMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSSLGSV VVF
mbc T3-4A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T3-7A	3-7*01	3-16*01	6*02	2	CARQGSFADTYFYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
mbc T3-11A	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01 or 1-40*02	2*01 or 3*01	λ	CQSYDSSLGSLN VVF
mbc T3-2B	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T3-7B	3-7*01	3-3*02	6*02	3	CARQGSFADTYFYY YALDVW	1-40*01	2*01 or 3*01	λ	CQSYDTGLSGLE VVF
mbc T3-3C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	1-40*01	2*01 or 3*01	λ	CQSYDSNLNGL DVVF
mbc T3-12C	3-7*01	3-16*01	6*02	2	CARQGSFADTYYYY YAMDVW	2-28*01 or 2D- 28*01	2*01	κ	CMQTLETPQTF
mbc T3-5D	3-7*01	3-16*01	6*02	2	CARQGSYADTYFYY YAIDVW	1-40*01	2*01 or 3*01	λ	CQSYDTALSGLD VVF
T1-5A	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQRSNWQSSF
T1-10A	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQRSNWHSSF
T1-8D	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQRSNWQSSF
T2-8A	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQR TNWHSSF
T2-1B	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQR SNWHSSF
T2-3D	3- 33*01or05o r06	1-26*01	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	κ	CQQR SNWQSSF

T3-8B	3- 33*01or05o 1-26*01 r06	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	ℳ	CQQRSNWQSSF
mbc T1-4A	3- 33*01or05o 1-26*01 r06	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	ℳ	CQQRSNWHSSF
mbc T2-1A	3- 33*01or05o 3-16*02 r06	6*02	3	CARDEWAVNDSYYY GMDVW	3-11*01	5*01	ℳ	CQQRSNWQVTF
mbc T2-4A	3- 33*01or05o 1-26*01 r06	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	ℳ	CQQRSNWQSSF
mbc T2-9A	3- 33*01or05o 1-26*01 r06	6*02	2	CARDEWAVHDSYYY GMDVW	3-11*01	5*01	ℳ	CQQRSNWQSSF
mbc T3-9D	3- 33*01or05o 3-16*02 r06	6*02	3	CARDEWAVNDSYYY GMDVW	3-11*01	5*01	ℳ	CQHRSNWQVTF
T1-3A	1-18*01 2-21*02	6*02	2	CAREDWSYGDTYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T1-2D	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T2-3B	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T2-11C	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPASF
T2-12C	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T2-4D	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T3-4A	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T3-7A	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T3-10B	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
T3-7D	1-18*01 4-17*01	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T1-1A	1-18*01 4-17*01	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T1-3A	1-18*01 4-17*01	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T1-6A	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T1-6D	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T2-8B	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T3-2A	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T3-6A	1-18*01 2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F
mbc T3-3B	1-18*01 3-16*01	6*02	2	CAREDWSYGDTYYY GMDVW	3-11*01	4*01	ℳ	CQQRTNWPPAT F

mbc T3-4B	1-18*04	2-21*02	6*02	2	CAREDWSYGDSYYN GMDVW	3-11*01	4*01	⌘	CQQR TNWPPAT F
mbc T3-9A	1-18*01	1-14*01	4*02	1	CARDSDSGTSLENW	3-20*01	1*01	⌘	CHHYGSSPQTF
T1-9B	3- 15*01or02	3-22*01	4*02	2	CFTAATNDYYDTYG YCDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLHTPQTF
T1-10C	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSDFW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
T1-1D	3- 15*01or02	3-22*01	4*02	2	CVTSATNDYYDTYG YSDFW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
T1-4D	3- 15*01or02	3-22*01	4*02	2	CVTAATHDYYDTYG YSNYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
T2-12B	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
T2-5D	3- 15*01or02	3-22*01	4*02	2	CVTAATHDYYDTYG YSNYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
T2-4A	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
T2-11A	3- 15*01or02	4-23*01	4*02	2	CVTAATKDYYDTSG YSDHW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
T2-12A	3- 15*01or02	3-22*01	4*02	2	CFTAAQNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
T2-8B	3- 15*01or02	3-22*01	4*02	2	CVTAATHDYYDTYG YSNYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
T2-1D	3-15*04	3-22*01	4*02	2	CSTAATDYYDTYG YSVYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTRQSPQTF
T3-11A	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLHTPQTF
T3-4B	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
T3-3C	3- 15*01or02	3-22*01	4*02	2	CVTAATHDYYDTYG YSNYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
mbc T1-2A	3- 15*01or02	3-22*01	4*02	2	CFTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
mbc T1-12C	3- 15*01or02	3-22*01	4*02	2	CFTAATNDYYDTYG YSDYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLQTPQTF
mbc T3-1A	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTHG YSNYW	2-28*01 or 2D- 28*01	2*03	⌘	CMQTLETPQSF
mbc T3-11B	3- 15*01or02	3-22*01	4*02	2	CVTAATNDYYDTYG YSNYW	2-28*01 or 2D- 28*01	2*01	⌘	CMQTLETPQTF
mbc T2-7C	3-30-3*01	3-3*02	6*03	2	CTRSHFDSNFDHYYY YMDVW	2-28*01 or 2D- 28*01	2*02	⌘	CMQGLQTPCTF
mbc T2-10C	3-30-3*01	3-3*02	6*03	2	CTRSHFDSNFDHYYY YMDVW	2-28*01 or 2D- 28*01	2*02	⌘	CMQGLQTPCTF
mbc T2-6D	3-30*03 or 3-30*18	3-9*01	4*02	1	CAKESALRALRYFD WLSASNFDYW	1-16*02	5*01	⌘	CQQYN SHPITF
T1-3B	1-69*01 or 1-69D*01	2-2*02	6*03	2	CARGPNYYNSYMDV W	3-20*01	1*01	⌘	CQQYGTSPQTF

T2-5A	1-69*01 or 1-69D*01	2-2*02	6*03	2	CARGPTYYNsyMDV W	3-20*01	1*01	κ	CQQYGSSPQTF
T2-5C	1-69*01 or 1-69D*01	2-2*02	6*03	2	CARGPTYYNsyMDV W	3-20*01	1*01	κ	CQQYGTSPQTF
T3-1B	1-69*06	2-2*02	6*03	2	CARGPTYYNsyMDV W	3-20*01	1*01	κ	CQQYGSSPQTF
mbc T2-4C	1-69*01 or 1-69D*01	2-2*02	6*03	2	CAKGPTYYNsyMDV W	3-20*01	1*01	κ	CQQYGTSPQTF
mbc T3-8A	1-69*01 or 1-69D*01	2-2*01	6*03	2	CARGPTYHYNyMDV W	2-28*01 or 2D- 28*01	1*01	κ	CMQALQTPRAC
T2-8C	1-69*09	1-1*01	5*01 or 5*02	3	CARHKTTSDLTMDs W	3-15*01	5*01	κ	CQQYNswLLSF
mbc T1-10A	1-69*04 or 1-69*09	4-23*01	4*02	2	CANINRDYGDNSLY YW	3-20*01	2*01	κ	CQQYGTfMYTF
T2-10B	3-23*01 or 3-23D*01	3-3*01	6*03	2	CAKHGPNDFWsgY FFPSHMDVW	1-9*01	4*01	κ	CQQLNSYPPVTF
T2-6C	3-23*01 or 3-23D*01	3-22*01	4*02	2	CAKSAETQYfyDSN GYAYW	3-15*01	2*02	κ	CQQYNDWPRTF
T3-5D	3-23*04	3-22*01	4*02	2	CAKSVETQYfyDSN GYAYW	3-15*01	2*02	κ	CQQYNDWPRTF
mbc T3-1B	3-23*04	3-22*01	4*02	2	CARFSYYLDSSGYVG GNDYW	1-44*01	3*02	λ	CAAWDDRLNGR VF
T1-2A	4-39*01	6-13*01	2*01	2	CARHVSkgFLIAVAG MVAPYFDLW	1-51*01	2*01 or 3*01	λ	CGTWDSGLSAH VVF
T2-4C	4-59*08	1-26*01	3*01 or 3*02	3	CARQFTEKLYSGNy GAFDFW	1-39*01 or 1D- 39*01	1*01	κ	CQqSYNTLWTF
T1-9D	3-9*01	2-2*02	6*02	3	CAKASLDASAAINE IRGYGLDVW	2-11*01	1*01	λ	CCSYAGTYTYVF
mbc T1-4C	3-21*01	1*01	6-6*01	2	CAPLATRPQRTEYFQ HW	1-40*01	2*01 or 3*01	λ	CQSYDSSLSGLH VIF

V_H, heavy chain variable region; D_H, heavy chain diversity region; J_H, heavy chain joining region; rf, reading frame.