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**Supporting Information**

**for**

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**Scarcity of autoreactive human blood IgA<sup>+</sup> memory  
B cells**

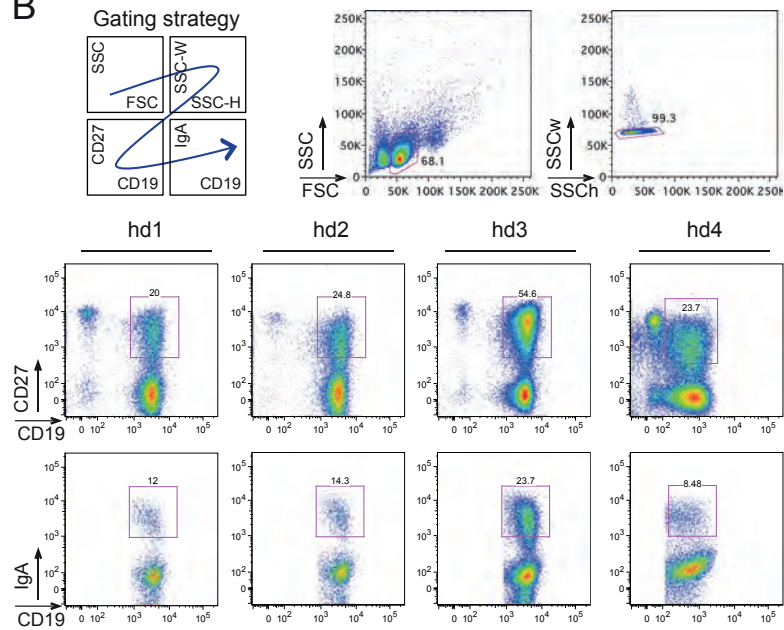
# Supporting Information Fig. 1

A

Donor	Gender	Age	ANA	ANCA	HIV	DTP	HBV	MMR	Flu
hd1	M	42	/	/	/	X	X	X	nd
hd2	M	51	/	/	/	X	X	nd	nd
hd3	F	51	/	/	/	X	X	nd	nd
hd4	F	25	/	/	/	X	X	X	nd

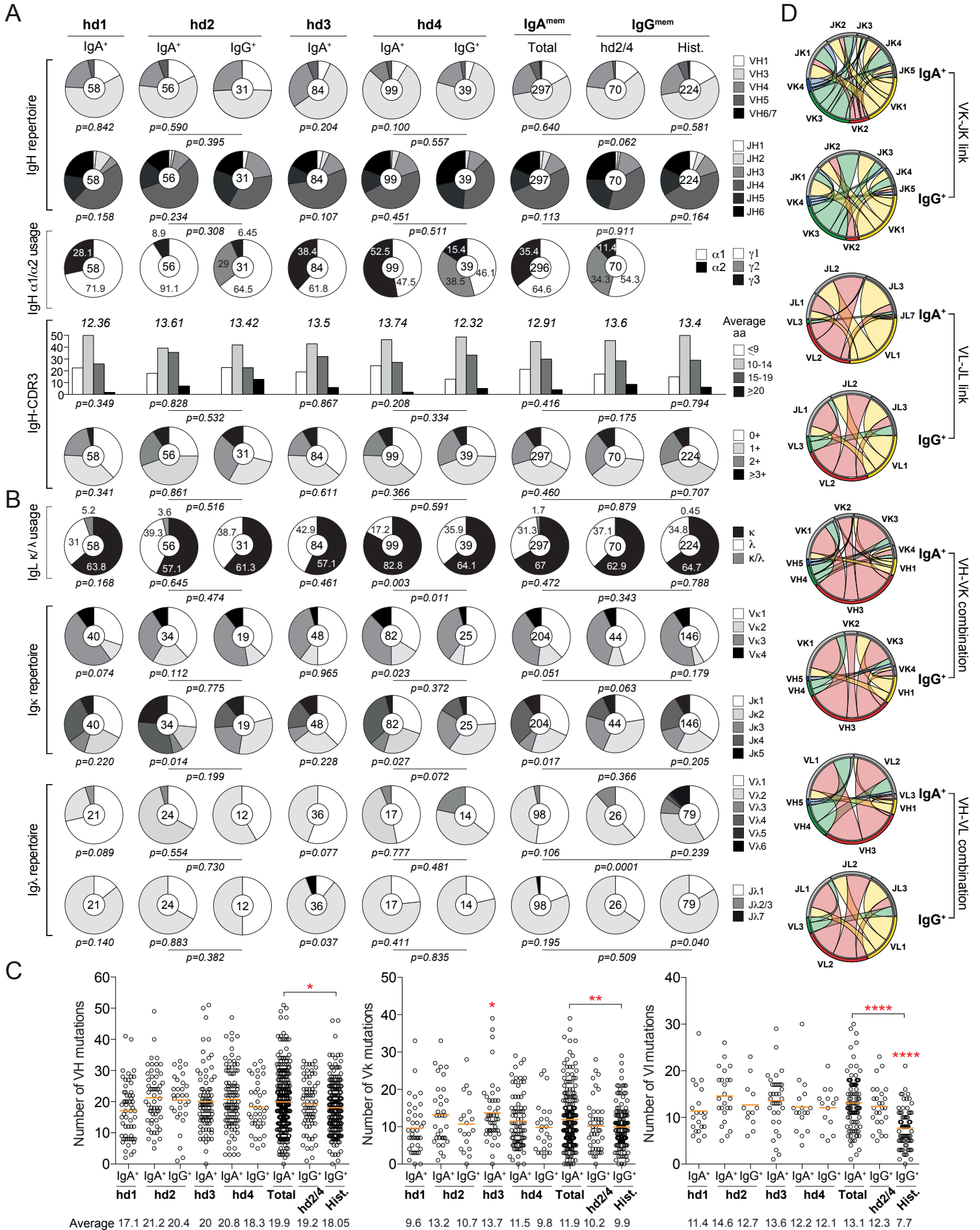
M, male; F, female; ANA, antinuclear antibodies; ANCA, anti-neutrophil cytoplasmic antibodies; HIV, human immunodeficiency virus status; DTP, diphtheria-tetanus-pertussis vaccine; HBV, hepatitis B virus vaccine MMR, measles-mumps-rubella vaccine; Flu, influenzae vaccine; nd, not determined.

B



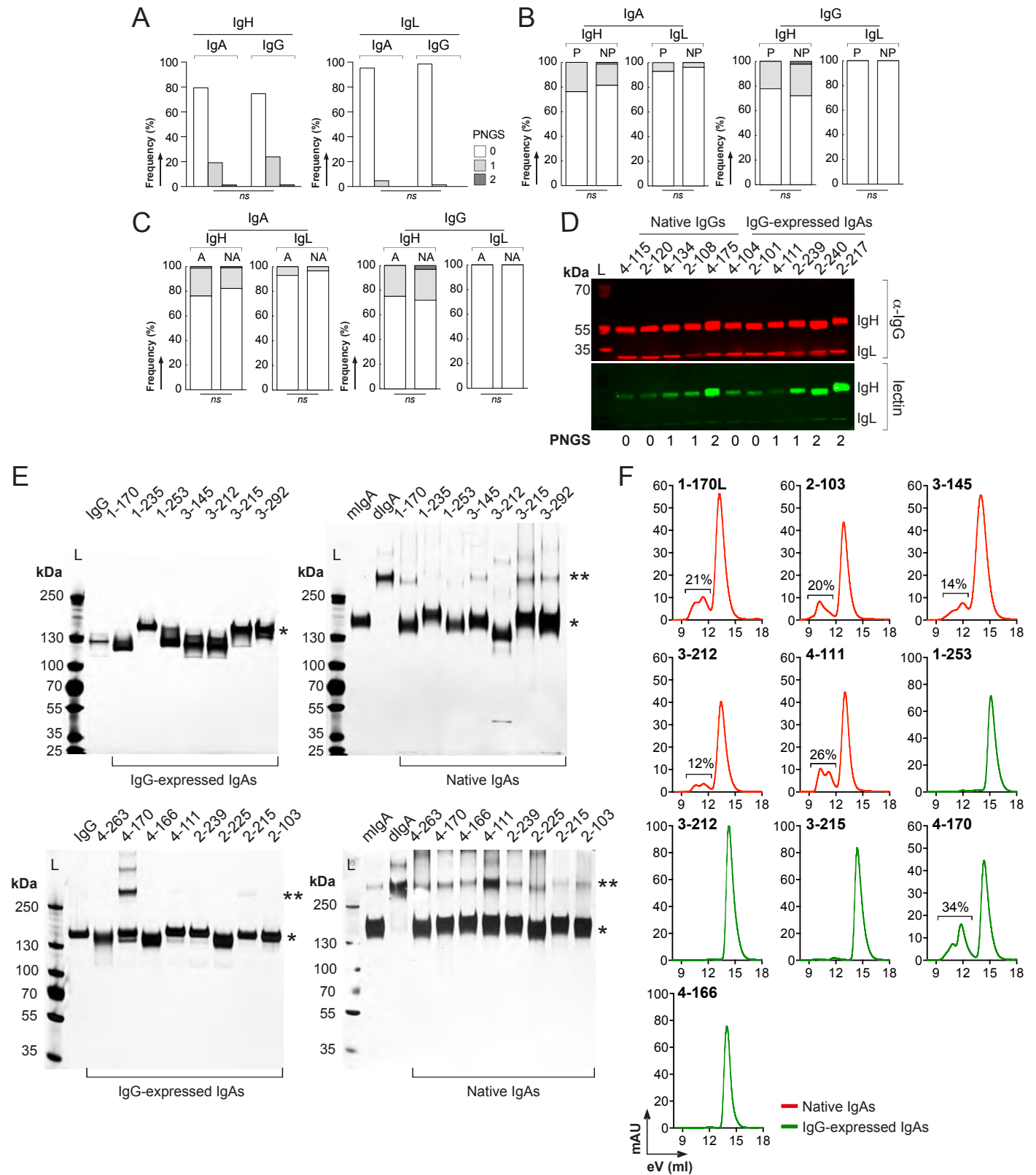
Supporting Information Fig. 1. Characteristics of healthy donors and memory B cells. (A) Table provides clinicobiological information for the four healthy donors. (B) Flow cytometry plots show the staining of donors' PBMC with anti-CD19, anti-CD27 and anti-IgA fluorescently labeled antibodies used for single B-cell sorting. IgA<sup>+</sup> memory B cells were identified as IgA<sup>+</sup>CD27<sup>+</sup>CD19<sup>+</sup> cells in the lymphocyte/singlet gate. IgG<sup>+</sup> memory B cells were identified as IgG<sup>+</sup>CD27<sup>+</sup>CD19<sup>+</sup> cells using the same strategy but with an anti-IgG antibody (data not shown).

# Supporting Information Fig. 2



Supporting Information Fig. 2. Immunoglobulin gene repertoire of IgA<sup>+</sup> and IgG<sup>+</sup> memory B-cell antibodies. (A) IgH V and J gene usages, CDR3 length and CDR3 positive charge numbers from IgA<sup>+</sup> memory B-cell antibodies in hd1 to hd4 compared to IgG<sup>+</sup> memory B-cell antibodies from hd2 and hd4 (hd2/4), and historical data (Hist.) [15, 17]. The number of antibody sequences analyzed is indicated in the center of each pie chart. The average of IgH CDR3 length is indicated above each histogram. p-values indicated below the pie charts or histograms and the lines were calculated by comparison to the total hd2/hd4 IgG<sup>+</sup> control antibodies (hd2/4) and IgG<sup>+</sup> antibodies from the same donor (for hd2 and hd4), respectively. (B) Same as in (A) but for IgL κ/λ usage, VL and JL gene usages for Igκ and Igλ. (C) Dot plots show the number of mutations in VH, Vκ and Vλ genes in IgA<sup>+</sup> memory B cell and IgG<sup>+</sup> control antibodies as shown in (A). The average number of mutations in VH, Vκ and Vλ genes is indicated below each dot plot. The p-values were determined by comparison to IgG<sup>+</sup> memory B-cell antibodies from hd-2 and hd4 (hd2/4), and from the same donor (for hd2 and hd4) using unpaired student's t-test with Welch's correction. All comparisons were statistically non significant unless indicated with a red star. The numbers of mutations in IgA<sup>+</sup> genes were also compared with the same statistical test to historical data for IgG<sup>+</sup> memory antibodies (Hist.) [15, 17]. \*, p<0.05; \*\*, p<0.01; \*\*\*, p<0.001; \*\*\*\*, p<0.0001. (D) Circos plots comparing the frequency of VκJκ and VλJλ rearrangements, and VH-VL associations between IgA<sup>+</sup> and IgG<sup>+</sup> memory B-cell antibodies from hd1-hd4 individuals.

# Supporting Information Fig. 3



Supporting Information Fig. 3. Production of recombinant IgA and IgG memory antibodies. (A) Bar graphs comparing the frequency of putative N-glycosylation sites (PNGS) theoretically presents (defined as N-(X)-T/S) in immunoglobulin heavy- and light-chain (IgH and IgL) between IgA<sup>+</sup> and IgG<sup>+</sup> memory B-cell antibodies (n=297 and n=70, respectively). Groups were compared using Fisher's Exact test. ns, not significant. (B) same as in (A) but comparing polyreactive (P) and non polyreactive (NP) IgA<sup>+</sup> and IgG<sup>+</sup> memory B-cell antibodies (n=251 and n=61, respectively). (C) same as in (B) but comparing autoreactive (A) and non autoreactive (NA) IgA<sup>+</sup> and IgG<sup>+</sup> memory B-cell antibodies. (D) Infrared immunoblotting showing the reactivity of anti-human IgG antibodies ( $\alpha$ -IgG, red) and lectin from *Triticum vulgare* (wheat) (green) against native IgG (n=5) and IgG-expressed IgA (n=6) antibodies displaying different number of PNGS in IgH (from 0 to 2). L, protein ladder indicating molecular masses. (E) Silver-stained SDS-PAGE gel showing IgA memory antibodies produced as IgG (IgG-expressed IgAs) and native IgA molecules (n=15 for each). L, protein ladder indicating molecular masses. IgG, purified monomeric 10-1074 HIV-1 IgG antibody used as control; mIgA, purified monomeric 10-1074 HIV-1 IgA antibody used as control; dIgA, purified dimeric 10-1074 HIV-1 IgA antibody used as control [22]. \*, monomeric immunoglobulins; \*\*, dimeric immunoglobulins. (F) FPLC chromatogram showing the protein distribution (monomers and dimers) of the purified IgA memory antibodies produced as native IgA (red) and IgG (IgG-expressed IgAs, green) molecules (n=5 for each) after size exclusion chromatography (SEC). The x axis shows the elution volume (eV) required to obtain the values of absorption units at 280 nm (mAU) indicated on the y axis. The proportion of dimeric/multimeric immunoglobulins is indicated above the corresponding SEC pic.

Supplementary Table 1. Immunoglobulin gene repertoire and reactivity of IgA+ and IgG+ memory B-cell antibodies.

hd1 - IgA memory antibodies

mAb name	VH	DH	JH (-)	Heavy chain							Light chain					Polyreactivity							
				CDR3 (aa)	(+)	Length	Vmut	PNGS	α1/α2	k/λ	Vk/λ	Jk/λ	CDR3	Length	Vk/λmut	PNGS	κH	dsDNA	Insulin	LPS	Poly	HEP-2	
1-117	3-23	2-15/-21	6	1	RVAIRLGGNAYGMVD	2	15	30	0	α2	k	2-28	5	MQALKGFPIT	9	10	1	X	/	X	X	X	X
1-122	3-23	2-15/5-12/3-22	4	2	RDVRSQGHTFDY	3	12	13	0	α1	k	3-11	4	QQRSSWPTT	9	7	0	/	/	/	/	/	/
1-134	4-31	2-2	4	1	RTSRYFFDY	2	10	12	1	α1	λ	1-40	2/3	QSYDSSLSGPPV	12	11	0	/	/	/	/	/	/
1-143	3-23	1-26	6	3	EVGGGRWYVMDV	1	14	25	0	α1	λ	1-47	2/3	AWDDRLSLVVA	11	17	0	/	/	/	/	/	/
1-145	3-48	6-6/-13	4	2	DAMVVKFDS	0	9	23	0	α2	λ	2-14	2	TSYTRSLVI	10	8	0	/	/	/	/	/	X
1-146	1-8	3-3/-10	6	1	AGVSYVGMVD	0	11	30	0	α1	λ	3-21	3	QVWDSSTELRV	11	11	0	/	/	/	/	/	/
1-155	4-61	4-11/3-3	4	1	GVGTTNFEY	0	9	18	0	α2	k	1-39	4	QCSYGLPIT	9	13	0	/	/	/	/	/	X
1-160	1-2	6-13	4	1	GRAVLTIPACTPLFDY	1	17	6	0	α2	k	3-20	4	QHYGSSPLT	9	5	0	/	/	/	/	/	/
1-168	3-23	1-26	4	1	SQGLILGATFLPVPFDS	0	15	19	0	α1	λ	1-51	3	GTWDTLSLWVM	11	10	0	X	/	/	/	/	X
1-170k	3-23	3-3	6	3	WALLEWVVDGMDV	0	13	19	0	ND	k/λ	1-39	2	QCSYSPFTT	9	0	0	X	X	X	X	X	X
1-170A																							
1-171	1-46	6-13/2-2	6	2	DPFRGAAAPTGHYYVGMVD	2	19	9	1	α1	k	3-20	2	QQYGSQPTT	9	13	0	/	/	/	/	/	/
1-180	3-23	3-22	2	4	DMVDYSSGLAYWFDL	0	17	15	0	α1	k	1-9	3	QQLNTYPP	8	9	0	/	/	/	/	/	/
1-182	3-23	1-7	4	1	GGSTGNYLPHFDS	1	13	26	0	α2	k	3-15	4	QQYNDWPLT	9	11	0	/	/	/	/	/	/
1-193	4-59	3-16	5	3	AEADYLSGGLDR	1	12	15	1	α1	k	4-1	1	HQYKGSPPRT	9	12	0	/	/	/	/	/	/
1-194	1-2	3-3/2-15/2-21	4	2	EAFIAQGIKISDY	1	13	22	0	α1	k	1-39/1D-39	1	QQYVGFPPIT	9	25	0	X	X	X	X	X	X
1-205	3-23	3-22	5	2	KYYSDTRHYGNWFDV	3	16	9	0	α2	k	3-15	1	QQYNNWPLA	9	3	0	/	/	/	/	/	/
1-208	1-69	2-8	3	1	YQITVGLNADFV	0	13	28	1	α2	k	1-27	3	QKYDMAFFT	9	18	0	X	X	X	X	X	X
1-211	3-53	3-3/-16	4	1	HYRGNLLEF	2	10	40	0	α1	k	1-39/1D-39	4	QQSFRTPLT	9	33	0	X	X	X	X	X	X
1-212	1-18	2-2/3-3/3-16	4	1	ALLAYTTSRVFDY	1	13	8	0	α1	k	1-39/1D-39	3	QCSYSPFTT	9	8	0	/	/	/	/	/	/
1-215	3-30	3-3	6	1	PSLAYGGTYYYAMVDV	0	15	20	0	α1	λ	1-40	1	QSYDSSLSGPFV	11	5	0	/	/	/	/	/	/
1-217	3-23	5-5/-18	5	1	TGPRGGYVDS	1	10	17	0	α1	k	3-15	1	HQYNNWPLT	9	3	0	/	/	/	/	/	/
1-219	4-59	6-13	5	1	GPAAGWFDV	0	10	3	1	α1	k	3-11	4	HQRSNWPLT	9	7	0	/	/	/	/	/	/
1-221	3-23	5-5/-18	4	0	VWAMVFHY	1	8	28	0	α1	k	3-20	4	QQYGSLSFT	9	15	0	/	/	/	/	/	/
1-227	3-23	3-10	4	1	PGSRYPAPFDY	2	12	9	0	α2	k	3-20	4	QQYGSPLT	9	7	0	/	/	/	/	/	X
1-228	1-2	3-3	1	2	GSAEWSYWGAEHFQH	2	18	7	0	α1	λ	1-44	2/3	AAWDDLSGSSVV	12	6	0	/	/	/	/	/	/
1-231k	3-48	5-24	4	2	GGPKWQYNEIDY	1	13	7	0	α2	k/λ	3-15	1	QQYNNRHW	9	0	1	/	/	/	/	/	X
1-231A																							
1-232	3-23	5-12/-5/-18	4	1	VLWTFLFDY	0	9	22	0	α1	k	3-15	4	QQYNNWPLT	9	19	1	ND	ND	ND	ND	ND	ND
1-234	5-51	3-3	6	2	LDWSGYHMDV	1	10	8	0	α1	λ	1-40	3	QSYDSSLSGSRV	12	6	0	/	/	/	/	/	/
1-235	5-51	5-5/-18	6	2	REGYNGFGMDV	1	12	8	0	α1	k	1-12	2	QQSSSFPQN	9	7	0	X	X	X	X	X	X
1-239	3-74	1-26	5	0	GGTPGA	0	6	22	0	α2	k	3-15	2	QQYNDWPLY	9	7	0	X	X	X	X	X	X
1-242	3-33	2-2	5	2	DFPSRIGGYCGSINCYPYFNLFDP	1	22	12	0	α1	λ	1-51	3	GTWDDLSLVPV	11	11	0	/	/	/	/	/	/
1-244	1-46	3-16	4	4	DVYNSDELNFDY	0	12	29	0	α1	k	2-28/2D-28	1	MQSLQTPWT	9	5	0	/	/	/	/	/	/
1-249	3-9	4-11/-4	5	3	DKDNSNFVSAWFDV	1	14	14	0	α1	k	3-11	3	QQRSSWPTT	9	7	0	/	/	/	/	/	/
1-250	4-61	1-7	2	3	DQLELRFPRSYWFDL	2	15	8	1	α2	k	1-39	2	QQSYTKPYT	9	3	0	/	/	/	/	/	/
1-253	3-48	3-16	6	1	GGGLYVYVGMVDV	0	12	20	0	α1	k	3-20	2	QQYGNSPLYT	10	3	0	X	X	X	X	X	X
1-258k	3-30	6-13	4	2	DGAMGRSWYGFYD	1	13	28	1	α1	k/λ	1D-8	1	QQYYSFPR	8	ND	0	ND	ND	ND	ND	ND	ND
1-258A																							
1-259	1-46	6-6/-13/-19	6	2	GGTYSRPEGFYVGMVDV	1	17	16	0	α1	k	4-1	2	QQYYSAPYT	9	9	0	/	/	/	/	/	/
1-266	3-53	3-10	3	2	LLGEGAFDI	0	9	15	0	α1	k	2-28/2D-28	2	MQALQTPYI	9	4	0	/	/	/	/	/	/
1-270	1-2	2-21	5	2	VAYCATDCSRPLNWFDP	1	17	17	0	α2	λ	2-11	2/3	CSYAGSSFFW	10	8	0	/	/	/	/	/	/
1-276	3-23	2-8	4	2	DRWTTVAVMVQPAHDY	2	16	23	0	α1	λ	1-44	1	AAWDDLSGLYV	12	8	0	X	/	/	/	/	/
1-281	4-31	2-21	4	2	DCAGDCHYV	1	9	41	1	α1	k	3-20	1	QQYDSSPQT	9	19	0	/	/	/	/	/	/
1-282	3-15	6-19/-25	4	2	EBAAGVGH	1	9	20	0	α2	k	1-5	1	QEYNTYWT	8	14	0	/	/	/	/	/	/
1-284	3-30	6-13/19/-10	6	3	DDSSVYQYGMVDV	0	14	27	0	α1	λ	1-51	3	GRWRDLSLWVI	11	18	0	/	/	/	/	/	/
1-288	3-21	1-1	4	1	VGINWSSDY	0	9	20	1	α1	k	1-9	1	QQVNTYPTW	9	11	0	/	/	/	/	/	/
1-334	3-33	6-13	5	2	DWQYSSWFDS	0	11	8	0	α1	λ	2-23	2/3	CSYAGSSHMV	10	9	1	/	/	/	/	/	/
1-340	3-48	3-10	6	2	NVDRFYNGMDV	1	12	27	0	α1	k	2-28/2D-28	5	MQALQTPSIT	9	11	0	/	/	/	/	/	/
1-342	4-61	5-24	2	2	WQLSDWYFDL	0	10	12	1	α1	λ	1-44	3	AAWDDLSGWL	11	12	0	X	/	/	/	/	/
1-345	3-7	6-6	4	0	SRGRPY	2	6	2	0	α2	k	3-20	1	QQYGSFPWT	9	1	0	/	/	/	/	/	/
1-348	4-34	1-26	4	1	GPDRAKQGY	2	9	17	0	α1	k	4-1	2	QQYTYLPT	9	16	0	/	/	/	/	/	/
1-351	4-4	2-8/3-16	4	2	GDRNGFFDY	1	9	23	1	α1	k	4-1	1	QQYTYTPT	9	9	0	/	/	/	/	/	X
1-356	4-59	3-16	2	3	DQVGGDWYFDL	0	11	21	1	α1	λ	1-44	3	AAWDDLSLGHV	12	16	0	/	/	/	/	/	/
1-357	4-61	2-21	4	1	WDAYCGGACYPSRPH	1	15	20	1	α2	k	3-20	1	QQYGSFPWT	9	16	0	/	/	/	/	/	/
1-365	3-33	1-26	2	3	GLWBERGFDL	1	10	8	0	α1	λ	2-14	3	SSYVSSSTLWV	11	10	0	/	/	/	/	/	X
1-369	3-30	3-10/3-16	4	2	DKGVRYFDY	2	9	19	0	α2	k	3-11	4	QQRSNWPTT	9	4	0	/	/	/	/	/	/
1-384	4-59	2-15/2-21	4	2	LYDPWFFDY	0	10	8	1	α1	k	3-20	4	QQYDSSPQLT	10	3	0	/	/	/	/	/	/
1-392	3-53	1-7/1-20/1-1	3	1	HAPMNNHALDI	2	11	12	0	α2	λ	1-40	1	QSYDSSVLNGYV	12	18	0	/	/	/	/	/	/
1-393	3-23	1-26	6	1	PIVGAAGSANYGLDV	0	16	4	0	α1	k	3-15/3D-15	5	QQYNNWPTT	10	7	0	/	/	/	/	/	/
1-396	3-9	6-19/6-25	4	3	DILSWGYSSSSGDFYD	0	16	4	0	α1	λ	2-14	2/3	SSYTSNTVTV	10	7	0	/	/	/	/	/	/

hd2 - IgA memory antibodies

mAb name	VH	DH	JH (-)	Heavy chain							Light chain					Polyreactivity							
				CDR3 (aa)	(+)	Length	Vmut	PNGS	α1/α2	k/λ	Vk/λ	Jk/λ	CDR3	Length	Vk/λmut	PNGS	κH	dsDNA	Insulin	LPS	Poly	HEP-2	
2-101	3-30	6-6	4	2	DPFHIAARTPTFFDY	2	16	8	0	α1	λ	2-14	1	SSYTSSTDFIV	11	6	0	/	/	/	/	/	/
2-102	3-30	4-23	4	2	DRSPHTQTYGNSVMDA	2	17	14	0	α1	k	1-39	3	QQSFNTPQT	9	13	0	/	/	/	/	/	/
2-103	1-2	1-1	5	1	LIYTTSKLLGWFDV	1	14	32	0	α1	k	4-1	1	QQYDTPPT	9	10	0	X	X	X	X	X	X
2-104	3-30	2-2/6-6/3-16	4	2	EKLSRGLIRGYFDY	3	15	26	0	α1	k	3-20	1	QQYGSFPWT	9	8	0	ND	ND	ND	ND	ND	ND
2-110k	3-74	3-3/22	4	2	DVSGSIDY	0	8	16	0	α1	k/λ	2-30	2	MQGSHWPT	9	1	0	/	/	/	/	/	/
2-110A																							
2-111	3-30	1-26	4	0	GMGGILY	0	7	17	1	α1	λ	2-14	2/3	QVWDDSSDHVV	11	5	0	/	/	/	/	/	/
2-115	3-64	3-10/5-12	4	1	VFGYNSGTRWRYFDY	1	16	25	0	α2	k	3-11	4	ASYSDDNSVI	10	21	1	ND	ND	ND	ND	ND	ND
2-120																							





4-165	3-23	6-19/-25/-13	4	2	VWYSTQDY	0	9	25	0	α2	λ	1-44	3	AAWDDSLNVVW	11	4	0	/	/	/	/	/	/	/
4-166*	3-72	5-12	3	1	GYSVSVYAFDL	0	12	24	0	α1	κ	1-17	1	LQHNXPWT	9	0	0	X	X	X	X	X	X	X
4-169	3-72	2-21	4	0	ANSGN	0	5	8	0	α2	κ	1-17	4	LQHNXPWT	9	5	0	ND	ND	ND	ND	ND	ND	ND
4-170	4-39	2-2	4	1	IPLCSTVSCYIGNFDY	0	16	5	1	α1	κ	1-5	1	QQYNSYRST	9	0	0	X	X	X	X	X	X	X
4-174	3-23	5-24	4	2	SRDVSRYGFYD	2	12	11	0	α2	κ	3-15	4	QHYDKWFLP	9	11	0	X	X	X	X	X	X	X
4-175	3-23	3-10	6	2	AGGSGPYTLEGGYFGLDV	0	18	31	0	α2	κ	1-39	2	QESYVVPYT	9	11	0	ND	ND	ND	ND	ND	ND	ND
4-176	4-39	6-6/-25/2-8	3	2	LKIAFDADFV	1	10	19	1	α1	λ	2-8	2/3	SSYADNKRKRV	9	11	0	/	/	/	/	/	/	/
4-178	3-23	3-9/5/2-18	3	3	DRVNHKLFDFGLDV	3	14	30	0	α1	κ	1D-33	4	QQSGSLPPLT	10	27	0	/	/	/	/	/	/	/
4-180	1-2	6-6/2-8/-2	4	3	DPVIVSDHFDY	1	12	26	0	α2	κ	2-28	3	MQSLRFPPT	9	18	0	/	/	/	/	/	/	/
4-181	5-51	6-19/-13	5	1	QQGYLAGSCHWFLD	1	15	30	0	α2	κ	1-9	3	QHLSSYPT	8	22	0	ND	ND	ND	ND	ND	ND	ND
4-183	3-7	3-9	4	2	LPAIDWFLGGFDC	0	13	17	0	α2	κ	3-11	1	QHRLDWFWPT	9	14	0	/	/	/	/	/	/	/
4-184	3-7	7-27	5	1	ALGLFDP	0	7	12	0	α1	κ	3-15	2	QQYNNPFT	9	6	0	/	/	/	/	/	/	/
4-187	5-51	3-10	3	3	QDGGSHDAFDI	1	12	29	0	α2	κ	3-15	2	QQYNNPFT	10	18	1	/	/	/	/	/	/	/
4-188	4-4	2-8/4-23	4	1	NGKFSLEH	2	8	25	1	α1	κ	3-20	2	QRFSGEYPT	9	5	0	X	X	X	X	X	X	X
4-192	4-39	6-19	4	1	HAHGWVDY	3	9	29	1	α2	λ	1-51	2/3	ATWDSNLASHL	11	18	1	ND	ND	ND	ND	ND	ND	ND
4-193	3-33	3-22	4	3	DIYDSSGYRFDY	1	13	13	0	α2	κ	3-20	1	QQYSSSPRWT	10	4	0	/	/	/	/	/	/	/
4-196	3-30	3-10	4	1	DLYGSGSYHTGMVY	1	14	10	0	α2	λ	2-14	3	STYTTSSTWV	10	7	0	/	/	/	/	/	/	/
4-203	3-9	3-3	6	2	DRGNGFSGSLFVGHFNSLDA	2	20	32	0	α2	κ	1D-33	4	QQYKRVPLT	9	29	0	X	X	X	X	X	X	X
4-204	3-21	3-9	5	1	YFEA	4	4	9	0	α1	κ	3-20	2	QQYSSPFT	9	7	0	/	/	/	/	/	/	/
4-205	3-48	7-27	3	2	DLHWAFDI	1	8	17	0	α1	λ	2-14	3	SSPASI	6	7	0	/	/	/	/	/	/	/
4-206	3-7	6-13	4	1	SRVAVAGRYFDY	2	13	13	0	α2	κ	4-1	3	QQYVTSHH	8	7	0	ND	ND	ND	ND	ND	ND	ND
4-208	3-7	2-21/6-6/5-12	4	2	VWGSYDLIEY	0	10	14	0	α2	κ	3-11	4	QHSST	5	12	0	ND	ND	ND	ND	ND	ND	ND
4-210	3-23	1-26	4	1	GLNPSYGGYSHRVLDY	2	16	14	0	α2	κ	3-15	4	QQYINWPLT	9	4	0	/	/	/	/	/	/	/
4-211	3-74	1-1	4	2	DPGTGTSFRPFDY	1	12	3	0	α1	κ	4-1	2	QQYVTSPT	9	5	0	/	/	/	/	/	/	/
4-212	5-51	2-21/4-17	4	5	LLRNSDFDDFDY	1	13	16	0	α2	κ	2-30	1	MQGTHWPKT	9	4	0	/	/	/	/	/	/	/
4-215	3-23	4-11/-4/2-21	4	4	GAYDYHESIGLAFDD	1	16	25	0	α1	κ	3-11	5	QQRDSWPT	9	11	0	/	/	/	/	/	/	/
4-216	3-7	1-7/1-20	5	1	IGRNWPEA	1	10	15	0	α2	κ	1-5	1	QQHNDYLWT	9	7	0	/	/	/	/	/	/	/
4-217	3-23	3-3/5-12	4	2	VAGNNKCLDY	1	11	18	0	α2	κ	3-15	2	QQCNPWPT	9	5	0	/	/	/	/	/	/	/
4-219*	3-72	5-12	3	1	GYSVSVYAFDI	0	12	13	0	α1	κ	3-20	4	QQYGRSPRT	9	7	0	/	/	/	/	/	/	/
4-221	3-30	3-22	4	3	DASGYIYDFYD	0	13	18	0	α2	κ	4-1	3	QQHNSPPT	9	18	0	/	/	/	/	/	/	/
4-225	3-21	5-24/1-1	6	2	GLYNRAEPPYFGMDV	1	16	23	0	α2	κ	1-5	1	QQYNNVPLT	9	22	0	ND	ND	ND	ND	ND	ND	ND
4-228	3-9	6-13	4	2	GGNSNRQMSALPTELDH	2	18	15	0	α1	κ	3-11	4	QQRSATLT	8	3	0	/	/	/	/	/	/	/
4-229	3-7	3-16	2	2	RGKDLSPHSFFDL	3	13	23	0	α2	κ	3-20	4	QQYGGSPLT	9	8	0	/	/	/	/	/	/	/
4-233	3-48	7-27/3-16	4	2	FRGGGPFY	1	8	20	0	α2	κ	1-9	4	QHLSTFPRLT	11	13	0	/	/	/	/	/	/	/
4-234	4-4	7-27	4	1	VSTVTGPEYFPY	0	13	31	1	α1	κ	4-1	4	QQYIITPLT	9	13	0	ND	ND	ND	ND	ND	ND	ND
4-235	3-11	1-14	3	1	GNRSPGASDI	1	10	15	1	α1	κ	1-5	4	QQYNSYPLT	9	9	0	/	/	/	/	/	/	/
4-242	3-23	-	4	2	EKPYFD	1	6	26	0	α2	λ	1-51	3	GAWDSLRGRV	11	11	0	/	/	/	/	/	/	/
4-243	3-7	6-6/3-16	6	2	VRVGYDGMV	1	11	19	0	α1	κ	1-5	4	QQYNSG	6	6	0	ND	ND	ND	ND	ND	ND	ND
4-245	3-9	6-19	4	2	GPPRLASELWLPAFFDF	1	17	33	0	α1	κ	3-20	3	QQYSSG	6	9	0	ND	ND	ND	ND	ND	ND	ND
4-247	3-23	5-12/-5/1-14	4	2	TNQWMEGRYRFDY	1	15	20	0	α2	κ	1-17	1	LQHNXPFT	9	15	0	/	/	/	/	/	/	/
4-252	4-39	3-16	5	3	QHSDELWVNGYRPFDD	2	16	34	1	α1	λ	2-8	2/3	SSYPGRNTVVV	11	14	0	/	/	/	/	/	/	/
4-253	1-18	6-13	4	4	EKGGDRSQWPELDY	2	14	22	0	α1	κ	1D-33	2	QQYDLSPLYT	9	14	0	/	/	/	/	/	/	/
4-255	1-18	4-17/-23	4	1	AGAAVTHPDS	1	11	16	0	α1	κ	3-20	1	QQYSSLWPT	9	6	0	/	/	/	/	/	/	/
4-257	4-59	6-25/-19	4	2	GERLGGDY	1	8	20	1	α2	κ	2-30	1	MQGTHWPT	9	13	0	/	/	/	/	/	/	/
4-258	3-11	6-6	4	1	LSGSSVEN	8	8	19	0	α2	κ	2-30	4	MQGTHWPLT	10	5	0	/	/	/	/	/	/	/
4-260	3-7	3-10	3	2	DRGQTFDL	1	9	24	0	α2	λ	2-8	1	GSYGGRI	8	11	0	/	/	/	/	/	/	/
4-262	3-72	2-21	4	3	TAYCGGGMCTEDYSEY	0	17	41	0	α1	κ	1-5	4	QQYQSPVT	9	22	0	/	/	/	/	/	/	/
4-263	3-30	3-22	3	3	ERYDRGGPSIGAAFDI	2	17	22	0	α1	λ	2-14	1	CSYKSGSSYV	10	15	0	X	X	X	X	X	X	X
4-265	3-15	2-8	6	2	EGYCTNSGSLVSGNSYGMV	0	22	18	0	α1	κ	3-20	1	QQYVTSPTWT	10	12	0	ND	ND	ND	ND	ND	ND	ND
4-266	3-74	3-9	6	2	DWRVGLDV	1	8	17	0	α1	λ	2-14	3	SSYTTNSNV	10	12	0	/	/	/	/	/	/	/
4-268	3-30	3-9	4	4	DLQDQDLWLVGFDS	0	15	40	0	α1	κ	3-11	2	QQRSNWPLT	10	18	0	/	/	/	/	/	/	/
4-269	3-23	2-21	6	4	DLYSDCGADCYPKVDV	1	17	22	0	α1	κ	1-17	4	LQHHDFPLT	9	5	0	/	/	/	/	/	/	/
4-273	3-74	5-24	4	3	DGEGILPWFY	0	10	19	0	α1	κ	3-15	1	QQHNVWPT	9	9	0	/	/	/	/	/	/	/
4-276	3-7	4-17	4	3	GNPYGRVDFLQK	2	13	15	0	α2	κ	2-28	2	MQPVRTPYT	9	16	0	ND	ND	ND	ND	ND	ND	ND
4-277	4-31	5-5/-18/2-2	3	3	EVNAPVTSDAFDI	0	13	25	0	α1	κ	3-15	4	QQYKRVPLT	9	7	0	/	/	/	/	/	/	/
4-279	3-49	5-12/3-3/1-20	6	2	ERFPYGMV	1	9	19	0	α2	κ	4-1	1	QQYGLIRT	9	14	0	/	/	/	/	/	/	/
4-281	3-30	3-16/1-1	6	2	DRQFQLQVRYGLDV	2	15	24	0	α1	λ	2-23	1	SSYVSLNTPYV	11	30	0	/	/	/	/	/	/	/
4-282	3-9	2-21	2	2	ASESYCSGDCPRFWYFAL	1	17	22	0	α1	κ	4-1	1	QQYFTPLA	11	10	0	/	/	/	/	/	/	/
4-283	3-48	2-21	4	2	GWDRSHGDY	2	10	10	0	α2	κ	2-30	1	MDGSRWT	7	8	0	/	/	/	/	/	/	/
4-284	1-3	3-16/-22	3	2	GAAGRVSDDGGGSYDI	1	16	22	0	α2	κ	4-1	1	QQYVSPWPT	9	14	0	ND	ND	ND	ND	ND	ND	ND
4-286	3-21	4-17	4	2	GTNGDYD	0	8	3	0	α2	κ	1-17	1	LQNNYRPT	9	4	1	/	/	/	/	/	/	/
4-289	3-30	5-12	3	3	SSAGDYAFDI	0	11	3	0	α2	κ	2-28	1	MQALQTPRT	9	5	0	/	/	/	/	/	/	/
4-293	3-30	3-22	4	3	DPSWFYETSSAYFDY	0	16	12	0	α1	λ	1-51	3	GTWDSLSVGV	11	10	0	/	/	/	/	/	/	/
4-294*	3-72	5-12	3	1	GYSVSVYAFDL	0	12	19	0	α2	κ	3-20	4	QQYATSPRT	9	21	0	ND	ND	ND	ND	ND	ND	ND
4-295	3-23	1-1	5	2	AGTSLDQIFTD	0	11	32	0	α2	κ	3-11	5	QQRYSWPPLT	10	11	0	ND	ND	ND	ND	ND	ND	ND

#### hd2 - IgG memory antibodies

mAb name	VH	DH	JH (-)	Heavy chain				Light chain				Polyreactivity											
				CDR3 (aa)	(+) Length	VHmut	PNGS	γ1-γ4	κ/λ	Vκ/λ	Jκ/λ	CDR3	Length	Vκ/λmut	PNGS	κLH	dsDNA	Insulin	LPS	Poly	Hep-2		
2-106	1-46	1-1/5-24	4	3	DGQLEPADY	0	9	24	1	γ3	κ	3-11	3	QRHYDWLET	9	13	0	/	/	/	/	/	/
2-107	4-39	5-24	4	2	WERGTIRDY	2	9	22	1	γ2	λ	2-11	1	CSYAGTYAEV	10	12	0	/	/	/	/	/	/
2-108	3-9	6-19	3	2	ERSVAVAGPRSFDI	2	14	16	1	γ1	λ	2-11	1	CSYAGGFNLV	10	12	0						



4-141	3-11	3-10	6	2	GTMRGVDDYYGMDV	1	15	12	0	γ2	κ	3-15	2	QQYNNWLYT	9	7	0	/	/	/	/	/	/	X
4-145	3-7	3-16	4	0	WGALGSL	0	7	18	1	γ2	κ	2-30	2	MQRTHWPHT	9	14	0	ND	ND	ND	ND	ND	ND	ND
4-147	3-30	6-19/4-11/4-4	5	2	DAVAPATVGVLYNWFDV	0	17	18	0	γ2	κ	3-15	4	QQHNDWPLT	9	9	0	/	/	/	/	/	/	/
4-152	3-15	3-10	5	1	DRGVQWRPLFAT	2	12	30	0	γ2	κ	1D-39 / 1-3	2	QQSYSTPPYT	10	24	0	ND	ND	ND	ND	ND	ND	ND
4-155	3-11	3-3	6	2	GSPYDFWGYRPHGMDV	1	17	8	0	γ1	λ	2-8	2/3	SSFAGSIGV	9	6	0	/	/	/	/	/	/	/
4-156	3-23	1-26	4	2	LGGGDSWRLELTH	2	12	26	0	γ1	κ	4-1	5	QQYYSAP	7	10	0	ND	ND	ND	ND	ND	ND	ND
4-162	3-23	3-3/3-16/3-9	5	1	GGHLKNWLEDP	2	10	23	0	γ2	λ	2-14	1	SSYTKTSRYV	11	14	0	/	/	/	/	/	/	/
4-166	3-30	3-10	4	2	TLRRGQFGEFQTPFDV	2	16	6	0	γ2	κ	1D-39 / 1-3	4	QQSYRTHS	8	3	0	/	/	/	/	/	/	X
4-172	3-23	3-16	6	2	GYSGTNIILGDYQYYGMDV	0	21	9	0	γ1	κ	1D-8	1	QQYHSFPWT	9	15	0	X	X	X	X	X	X	/
4-175	4-34	6-19/6-25/6-13	5	1	LRGGYSSGWRHLSWFDV	3	16	24	2	γ1	λ	1-40	2/3	QSYDSSLGVL	11	14	0	/	/	/	X	/	/	/
4-176	4-61	3-3	2	1	NNVGSYGSGYFDEL	0	14	29	1	γ1	λ	3-21	1	QVWESLNDHYV	11	21	0	/	/	/	/	/	/	/
4-178	3-30-3	3-3	5	2	QFATYYDFWGSIGALDT	0	19	28	0	γ3	κ	3-20	2	QQYSSPYT	9	7	0	ND	ND	ND	ND	ND	ND	ND
4-182	3-48	3-3/3-16/3-9	3	2	ESLRGFDI	1	8	5	0	γ2	κ	1-5	1	QQYNNYPTWT	10	3	0	/	/	/	/	/	/	/
4-188	5-51	1-26	3	1	PRIVGARVYAAFDV	2	13	23	0	γ1	κ	3-11	3	QQGNNWPLT	9	12	0	/	/	/	/	/	/	X
4-191	3-48	6-6	6	2	GGTWRVYGMVDV	1	12	14	0	γ2	λ	1-44	2/3	AVWDDSLTGRVV	12	13	0	/	/	/	/	/	/	/
4-192	3-30/-3	3-22	4	2	PNYNYDSLTPFDS	0	14	16	0	γ1	κ	1-5	1	QQYDRWYT	8	12	0	ND	ND	ND	ND	ND	ND	ND
4-195	3-30/-3	7-27/3-9	6	2	GGSDWGLNSYHGMDV	1	15	32	0	γ3	κ	1D-39 / 1-3	1	QQSYGLLWT	9	25	0	X	X	X	X	X	X	X

(-) and (+) indicate the numbers of negatively and positively charged aminoacids in the IgH complementary determining region (CDR3), respectively. VHmut and Vc/7mut indicate the total number of mutations in the VH and VL Ig genes. PNGS, number of putative N-glycosylation sites (N(X)S/T).

Poly, polyreactivity. X, reactive; /, non reactive.

**Supporting Information Table 2. Gene features and reactivity of germline-reverted IgA+ memory B-cell antibodies.**

mAb name	Heavy chain										Light chain				Reactivity					
	VH	DH	JH	VH-mut	CDR3 (aa)	Reverted CDR3 (aa)	Length	κ/λ	Vκ/λ	Jκ/λ	VL-mut	CDR3 (aa)	Reverted CDR3 (aa)	Length	Mutated				Reverted	
															Poly	Hep-2	ELISA	HEp-2	IFA	Poly
1-170λ	3-23	3-3	6	19	WALLEWVFDGMDV	WALLEWVFDGMDV	13	λ	1-47	3	7	QSYDDSLGSWV	QSYDDSLGSWV	11	X	X	X	/	/	/
1-239	3-74	1-26	5	22	GGTPGA	GGTPGA	6	k	3-15	2	7	QQYNDWPTY	QQYNNWPTY	9	X	X	X	/	/	/
2-215	1-2	2-15	4	18	THGGYCSGGTCYGTWTFDY	THGGYCSGGTCYGTWTFDY	19	k	1-17	5	10	LQHNSYPLT	LQHNSYPLT	7	X	X	X	/	X	/
2-225	3-66	6-6/-19/-25	2	12	NKNIAGNAWGGNWFYFDL	NKNIAGNAWGGNWFYFDL	17	λ	2-8	2/3	9	SSYAGSRMV	SSYAGSRMV	9	X	X	X	/	/	/
2-239	4-39	3-3	4	17	ERDFWTGYWPDQ	ERDFWSGYWPDQ	12	k	1-17	1	13	LQHSHPWT	LQHNSYPWT	9	X	X	X	/	/	/
3-165	3-74	6-19/1-1/6-13	4	40	ESLPTGTRYFEY	ESLPTGTRYFDY	12	k	3-15	3	15	HQYNSWPVT	QQYNNWPVT	9	X	X	X	/	/	/
3-292	3-33	3-16	4	15	EIFSFGGLIARYFDN	EIFSFGGVIARYFDY	15	k	1-39/1D-39	2	11	QOSYGTPTY	QOSYSTPTY	9	X	X	X	/	X	/
4-170	4-39	2-2	4	5	IPLCSVTSCYIGNFDY	IPLCSVTSCYIGNFDY	16	k	1-5	1	0	QQYNSYSRT	QQSYSTPTY	9	X	X	X	X	X	X
4-263	3-30	3-22	3	22	ERYDRGGPSIGAADI	ERYDRGGPSIGAADI	17	λ	2-14	1	15	CSYKSGSSYV	SSYTSSTTYV	10	X	X	X	/	/	/

(-) and (+) indicate the numbers of negatively and positively charged aminoacids in the IgH complementary determining region (CDR3), respectively. VHmut and Vκ/λmut indicate the total number of mutations in the VH and VL Ig genes. Poly., polyreactivity. X, reactive; /, non reactive.