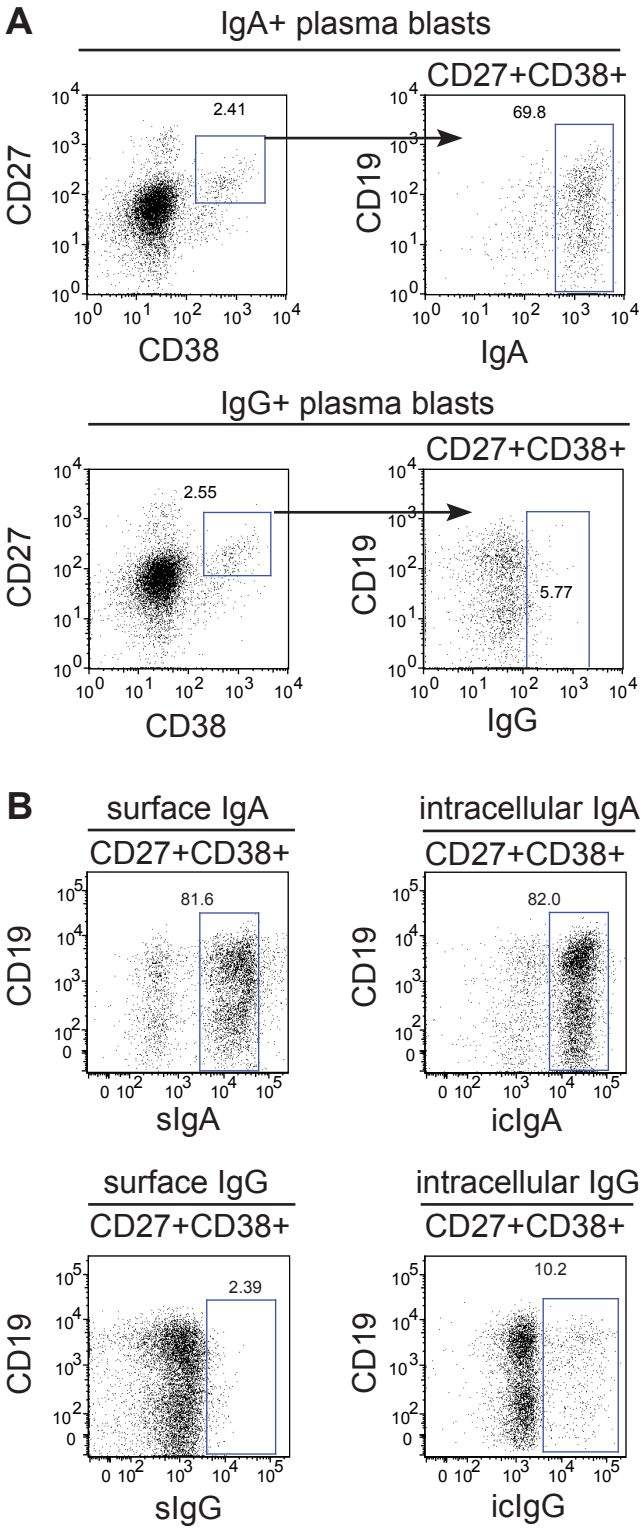

Figure S1: FACS-based isolation strategy of single intestinal IgA+ and IgG+ plasma blasts Purified intestinal lymphocytes from healthy donors were (A) surface labeled with fluorochrome-coupled anti-CD27, anti-CD38, anti-CD19 and anti-IgA or anti-IgG antibodies, respectively. CD27+CD38+ cells were gated and analyzed for CD19 and Ig isotype expression. Sort gates for FACS single cell isolation of CD27+CD38+CD19+/-IgA+ and CD27+CD38+CD19+/-IgG+ B cells are shown. (B) Comparison of surface (s) and intracellular (ic) IgA and IgG staining for purified intestinal CD27+CD38+CD19+/- lymphocytes.

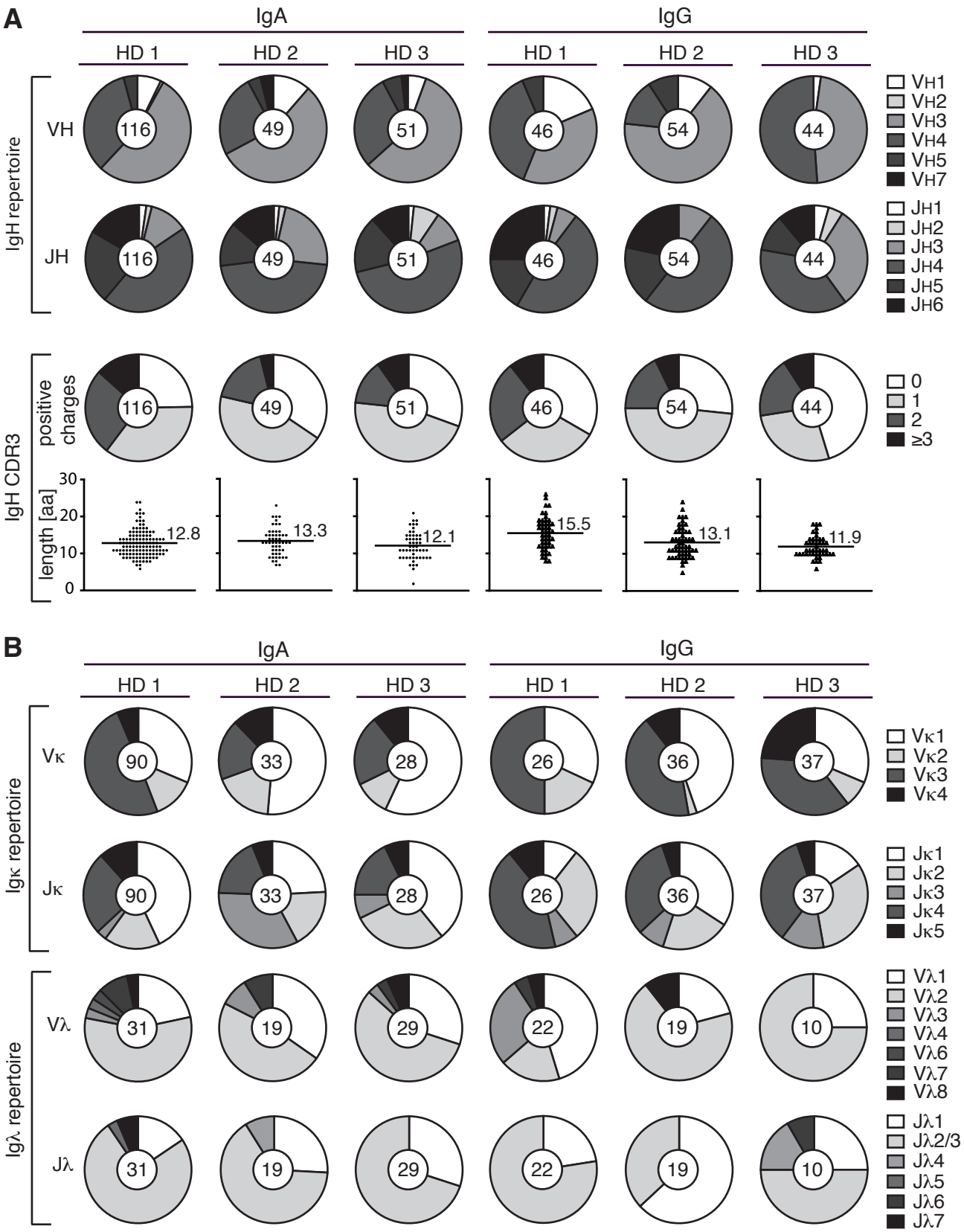

Figure S2: *Ig* gene repertoire and *Ig* gene features of IgA+ and IgG+ intestinal plasma blasts in three donors.

(A) The *Igh* gene sequences of IgA+ and IgG+ plasma blasts from terminal ileum of three donors were analyzed for *Igh* V family and J gene usage, absolute and average CDR3 aa length and CDR3 positive charges. The absolute number of sequences analyzed is indicated. (B), *Igκ* and *Igλ* V family and J gene usage. The absolute number of sequences analyzed is indicated in each pie chart center.

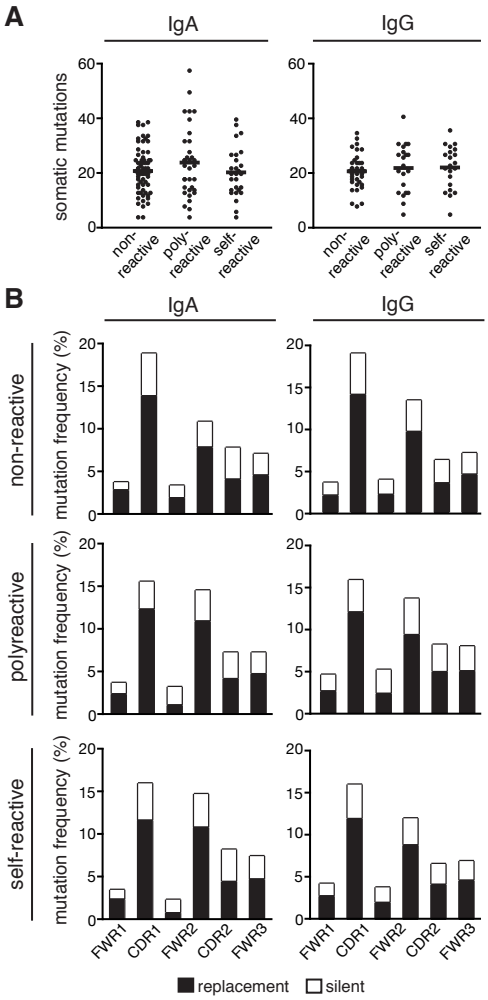

Figure S3: Somatic mutations of intestinal plasma blast antibodies
The *Igh* gene sequences of non-reactive, polyreactive and self-reactive IgA+ and IgG+ plasma blasts from terminal ileum of HD1-HD3 were analyzed for (A) absolute number of somatic mutations in V genes and (B) frequency of replacement (black) and silent (white) mutations in FWR and CDR. Horizontal lines in A indicate average means of V gene somatic mutations.

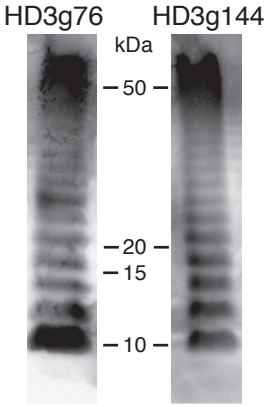

Figure S4: LPS reactivity of intestinal antibodies.
Western blot of extracted LPS from *E. coli* after separation by SDS page using *E. coli* reactive recombinant monoclonal antibodies HD3g76 and HD3g144 identifies LPS as cognate antigen. The molecular weight marker is indicated for comparison.

Table S1: Ig gene analysis and antibody reactivity of IgA+ and IgG+ intestinal plasma blasts form HD1

Antibody		IgH					IgL								Antibody reactivity												
patient	antibody	VH	JH	Isotype	CDR3	VH mutations	Vκ	Jκ	CDR3	Vκ mutations	Vλ	Jλ	CDR3	Vλ mutations	polyreactive	*Escherichia coli*	*Escherichia coli Nissle*	*Enterococcus faecalis*	*Enterobacter cloacae*	*Morganella morganii*	*Salmonella typhimurium*	*Lactobacillus reuteri*	*Bacteroides thetaiotaomicron*	rotavirus like particle	intestine	HEp-2
HD1a	7#	4-59	5	IgA2	KINSGGPIRR	37	3-15	1	HHYNNWPQTFG	16																	
HD1a	8κ	5-51	5	IgA2	WHRSNWFDY	28	1-5	2	QQYNTYSKT	5					+	+	+	+	/	+	/	/	/	/	+	C+N
HD1a	8λ										2-11	3	CSYAGSCL	0	/	+	+	+	+	/	/	/	/	/	/	/
HD1a	10#	4-39	3	IgA2	HSEKTLDTTVVQAFDV	24	3-20	1	QQYGSSPRT	18																	
HD1a	11	4-b	5	IgA2	EDHGSGSSYKYCWFDS	22	3-15	1	QQYHNWPRT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	12#	4-39	4	IgA2	ARGGYVDQNGVNYEDYYLDK	36	1-16	5	QQYFSYPIT	12																	
HD1a	17	4-59	2	IgA2	TRERDTWYFDL	22	3-20	2	QLYVVSSYT	17					/	/	/	/	/	/	/	/	/	/	/	N
HD1a	23	3-23	3	IgA2	NRREAYYDNNAYYDAPDALDI	13	1-5	1	QQYNSYTWT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	25#	3-7	3	IgA2	EAVEDLRDDAFDI	18	3-20	2	QQYGGSPLYT	17																	
HD1a	32	3-7	5	IgA2	DPDFHAWDS	26	3-20	1	QQYDKSPWT	10					+	+	+	+	+	+	/	/	/	/	/	/
HD1a	39#	4-39	4	IgA2	GHGTYYISTGYYSFDD	25	1-5	2	QQYHTYFYT	16																	
HD1a	40	5-a	5	IgA2	RGDCSSGSCYLGDH	14	3-20	1	QQYGPSSGGT	8					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	49#	1-46	3	IgA2	ARSGYNDRDYVSDI	30					8-61	3	VLYMGSGIWV	15												
HD1a	50	3-30	6	IgA1	GSPMTTVTRGNYYYYGMDV	25	1-33	5	QQYDTLPPT	6					+	/	/	+	+	+	/	/	/	/	/	/
HD1a	52	3-7	6	IgA2	ILRGWYGMDV	11	3-20	4	QQYGSSPSLA	23					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	57	4-59	5	IgA2	NGGSGYFIE	14	1-39	1	QQTYRTPLT	7					/	/	/	/	+	/	/	/	/	/	/	/
HD1a	59	4-34	4	IgA1	GGPRLEPFGY	32	1-12	1	LQTNNFPWT	11					+	+	+	+	+	/	/	/	/	/	/	/
HD1a	71#	5-51	5	IgA2	GFDRNSVDY	17	1-5	1	QQYSTYWT	37																	
HD1a	84	4-59	4	IgA2	DGRLTY	18	3-20	1	QQYGSSPPT	19					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	89	4-b	4	IgA1	DYYDSGGYYVDY	4					7-46	2/3	LLSYSGVVV	10	+	+	+	+	+	+	/	/	+	/	+	C+N
HD1a	93#	3-7	6	IgA2	GIKDTSGYWRYYYAVDV	17					2-14	1	SSYTTISSWV	15												
HD1a	95#	4-30-4	4	IgA2	RFWSGPTLFDY	25					1-40	3	HSFDSSLNEGV	19												
HD1a	102#	3-7	4	IgA2	GGDSYVEAQY	29					7-43	3	LLFYGATRLWV	12												
HD1a	103#	1-46	5	IgA2	RIVTGTTAGLVP	14	1-6	1	LQDYNYPRK	nd																
HD1a	104#	1-3	5	IgA2	AISPGAYITDY	24	4-1	4	QQYSAPIT	23																
HD1a	105	4-39	3	IgA1	VLVPPTMPASHAFDV	25	3-11	5	QQRSSWPPTIT	9					+	+	+	+	+	/	/	/	/	/	/	/
HD1a	116	3-72	3	IgA1	GYSGIHRYAFDI	25	3-20	1	QQYDISPRT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	117#	3-30	4	IgA1	VRGVLRSFDWLLSDV	23	4-1	2	QQNYIPPCS	nd																
HD1a	120	3-33	4	IgA2	DGYNGDLDY	33	2-24	1	MQATQFPWT	4					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	124	4-34	6	IgA1	GLVENDKWNYGAFAYMSYYHAMDV	25	3-20	1	QQYGDSPRT	10					+	+	+	+	+	+	+	+	+	/	+	C
HD1a	127#	3-30	6	IgA1	DVAVNHGSSSYLDFLQSVYIV	21					2-14	3	SSYISGSTPTVV	20												
HD1a	128	3-74	6	IgA2	DPAAMLVDGLDV	16	1-39	2	QESYSIPYR	10					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	131	4-4	4	IgA1	GVTQQGDFDY	21	1-39	1	QQNNRPPWK	21					/	/	/	/	/	/	/	/	/	/	+	/
HD1a	132	3-7	3	IgA1	ARAILGVIIPISIRCTFRGAAVAV	20	3-20	2	QQYADPPPYT	13					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	133#	3-23	5	IgA2	SEGPDRWGVV	20	3-11	5	QQRYSWPPIT	7																
HD1a	136#	3-15	3	IgA1	SLSPYGDYGPVDVFDI	46	3-11	1	QQRIHWPRT	20																
HD1a	138	4-39	4	IgA2	HEMEVVITVFVH	32	1-5	1	QQYYSYLT	7					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	141	5-51	4	IgA2	TFGTTIVFDY	24	3-15	1	QHYNIWPLA	23					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	143κ#	3-23	5	IgA2	TIANSYGIGDR	nd	1-5	2	QEYNTYLYT	25																
HD1a	143λ#										1-51	2/3	GTWEKSLSPGE	nd												
HD1a	144	3-74	4	IgA2	DYDWSIDY	34	2-30	1	MQGAHWPWT	8					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	145#	4-59	3	IgA1	RGSMPKENSFDV	23					2-11	3	CSYAGSYRWL	12												
HD1a	146	3-30	4	IgA2	GCGSGECFYTDY	13	4-1	1	QQSYSTPT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	150#	3-30	4	IgA2	DEDSGWYNSPRPFIY	23	3-15	1	QQYNTWPRT	nd																
HD1a	151#	2-5	4	IgA2	TYSNWETKTLHFYDY	31	3-15	1	QQYHNWWT	28																
HD1a	152#	5-51	4	IgA2	HVTGSPFDS	18	3-15	1	QHSNNWPQGT	12																
HD1a	154	3-23	4	IgA2	WGVQSWCQRTTEAR	22	3-20	1	QYFDVSTGT	14					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	160	3-7	5	IgA2	PAIAATGS	13	2-28	4	MQTLQAPFT	7					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	162#	3-72	5	IgA2	DPLGFEVVAAGVQ	9	1-16	4	QQYKDYRLT	nd																
HD1a	163#	4-39	4	IgA2	EAYGSGTSFAPFDY	29	3-11	1	HQRADWRSWS	nd																
HD1a	165	4-59	3	IgA1	SKTFCGAAVGV	13	3-20	4	QQYGSSPRT	3					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	168	4-31	4	IgA1	STDYSHFYFDD	18	3-15	1	QQYNDWPPGS	16					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	172#	3-23	5	IgA2	EEGSYGSGID	36	2-29	4	MQHIHLPLS	nd																
HD1a	175	3-23	5	IgA2	GYDLLVAGIS	34	4-1	1	QQYFDTRWT	15					/	/	/	/	/	/	/	/	/	/	/	C
HD1a	176	3-48	6	IgA1	GRLCETTSCQIYYHHGLAV	24	3-11	1	QQRDQWRVK	23					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	178	4-39	5	IgA2	RIHLYTHNRATE	21	2-28	4	LQVLDNPLT	4					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	181	3-20	4	IgA2	GVVSDIRVFEY	22					7-43	3	LLYYGAAQVGL	16	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	188	3-48	4	IgA2	DSDYYCSSAGCNAPYLDY	24	1-39	1	QKSHTAPWA	33					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	190	3-15	5	IgA2	DWPRTEK	24	2-28	2	MPGLPAPYT	8					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	192	3-74	5	IgA2	HCALDACFVNSYP	39	3-20	4	QQYTSSPLT	21					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	201κ#	3-30	4	IgA2	EVEITPPGVAAFDY	14	3-15	4	QQHYDWPLT	14																
HD1a	201λ#										2-14	2/3	SSYTTSSTVV	nd												
HD1a	203#	3-72	4	IgA2	AMTRGYYVDY	17	1-39	4	QQSYSMPT	9																
HD1a	206#	3-48	6	IgA2	DFRAGFVMDP	17					2-8	2/3	SSCAGGNNLL	nd												
HD1a	207#	4-39	5	IgA1	HSSLTRGGFDP	20					1-51	3	ATWDSSVGTPNWV	nd												
HD1a	219#	3-30	6	IgA2	DQGSGWSNQVYGLD	24					3-21	2	QVWDSNNDQSGVI	14												
HD1a	227#	4-39	3	IgA2	EAAVRAFDI	23	3-15	1	QEYSNWPRGT	37																
HD1a	229#	3-33	4	IgA1	SYRDTRVSSIWYYYYEF	nd					1-40	1	QSYDSGLSAPYV	nd												
HD1a	236#	3-23	4	IgA2	HLRGHGEGYSDTTRFDY	20					6-57	2/3	QANDSSNRGS	nd												
HD1a	242#	1-18	6	IgA1	DKHWNDFAHYYYFSMDV	20	3-20	5	QQYGSSPIT	15																
HD1a	245	4-39	4	IgA1	GAYGSSWQPNYYFDS	21	3-11	4	QQRSSGLT	19					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	252#	4-31	4	IgA2	TSSLAARRGYYFDS	21	1D-39	2	QQSYSPPYT	35																
HD1a	256#	4-59	5	IgA2	RQRSDIVMSADNWLDS	41	3-11	4	QQRSDWPLT	20																
HD1a	261#	4-59	6	IgA1	HRKVSYGMDV	47	1-12	4	QQASSFPLT	nd																
HD1a	262κ#	3-66	4	IgA1	GRGWYRVDY	16	1-6	1	LQDYSYPWT	11																
HD1a	262λ#										2-14	2/3	NSYTSNFAPYVV	nd												
HD1a	267#	4-b	6	IgA2	AMRNYYGSGGPFPYGMDV	nd	2-28	4	MQALQSPPT	12																
HD1a	272#	3-49	6	IgA2	DFWSGYYSPNGLEV	15	2-24	4	MQGSQFPHT	nd																
HD1a	276#	4-39	5	IgA1	GLMTYYYDVSGALKRGHKWFDP	22	3-15	2	QQYNNWPNT	17																
HD1a	279#	3-74	4	IgA1	DFREADY	24					2-14	3	TSFTTGEIHV	nd												
HD1a	301	3-15	2	IgA1	GGDYYFDL	16					2-11	7	CSYAAGFSVGV	8	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	311	3-30	4	IgA2	ELTERANDRRLDY	29	1-39	2	QQSYSFPYT	17					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	312#	3-30	4	IgA2	DLKIGPAGYYFDY	35	3-15	5	QQYNSWPLIT	12																
HD1a	314#	4-31	4	IgA2	GPGMTFGGVIALDY	27					1-47	2/3	PSDCDLGVV	nd												
HD1a	315#	3-30	6	IgA2	QGNCTGTSCNRDYYYYFGMDV	30	1-9	4	QQYITYPLT	33																
HD1a	319	3-33	4	IgA2	DSKPFPSDDVAGISGIFDS	33	4-1	1	HQYYGLYPWT	21					/	/	/	+	+	+	/	/	/	/	/	/
HD1a	323#	3-23	4	IgA2	GSRTSGYYFDY	26					4-60	1	ETWDTNIYV	6												
HD1a	330	3-73	4	IgA2	HGSGWYPDY	7					2-14	2/3	SSYRSRCFLV	4	/	/	+	+	/	+	/	/	/	/	/	/
HD1a	333	4-34	1	IgA1	RRGGIRNGVHSQVQLQ	28	2-30	5	WLILPFPPT	38					/	+	+	+	+	+	/	/	/	/	/	/
HD1a	342#	3-21	5	IgA2	GNGIYDNV	14	2-28	5	CKLHKIL	nd																
HD1a	345	1-46	1	IgA2	TGLRATDREYFRL	25	2-30	5	MQFTHWPI	18					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	346	4-39	4	IgA1	HRGYCSSSTCAVFFDY	32	3-20	4	QQYGTSPHT	22					/	/	/	/	/	/	/	/	/	/	/	/

HD1a	347#	3-72	4	IgA2	DRRYDAHSYFDY	nd	1-9	4	EQLDNYPLT	nd																		
HD1a	350	3-33	5	IgA2	DRSFGAYDH	25					2-14	3	SSYTNRNTLV	5	/	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	353#	1-46	6	IgA2	GTLTGAAGGV	nd	1-6	1	LQDYRYPWA	nd																		
HD1a	355	4-39	4	IgA1	EWSGYDYYFDY	5	3-20	2	QQYGSSLCS	2					/	+	+	+	+	+	+	/	/	+	/	/
HD1a	356	3-74	6	IgA2	IRENGGSLRLQ	11	1-27	1	QKHQMVRGK	5					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	357	3-48	4	IgA2	DTRTDGWFDPPFDS	38	1-39	2	QQTYVNHYT	45					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	358#	3-23	1	IgA2	GGPVGNQYFLH	nd	3-15	1	LQPDVCPPLP	nd																		
HD1a	360	4-59	4	IgA2	SSEDFWIGHKYFDY	26	3-20	2	QQYNRSPKT	14					+	+	+	+	+	+	/	/	/	/	/	/
HD1a	361	3-74	4	IgA2	LSGDYKNYFDY	18					2-14	3	SSYTTRRTWV	26	+	+	+	+	+	/	+	/	nd	nd	/	/
HD1a	362#	4-34	6	IgA2	WNYFYGIDV	nd					2-11	3	CSYAAGYTFWV	nd												
HD1a	364	1-46	4	IgA2	EPPEKYYFDY	32					2-14	1	CSYTSSFTYV	28	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	365	3-48	5	IgA2	EDGGNTAGLDH	48	3-20	1	QGDGGALLWA	30					/	+	+	+	+	/	/	/	/	/	/	/
HD1a	368	4-31	4	IgA1	EHGYCRGECLTY	10	3-20	1	QQYGSSPRT	6					+	+	+	+	+	+	+	/	nd	nd	+	C+N
HD1a	369	3-30	3	IgA1	DSWPFAEHDAFEI	39					1-44	7	CSYTSSFTYV	23	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	371	3-74	5	IgA2	TSPDFSGG	24	3-11	4	QQRYNWLS	13					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	372	4-39	4	IgA1	RRHDGGSHHYFDS	22	3-20	4	HQYTSAPLT	20					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	374#	1-46	4	IgA2	DRSKVFSSSYYILDY	nd	3-20	3	QHYDFYTKSVF	nd																
HD1a	375#	3-66	4	IgA1	PHSGSFYVAPFDY	nd	3-20	2	QQFGSSLLGS	nd																
HD1a	377	3-74	4	IgA2	GGPRSWSPFDY	4					2-14	2/3	SSYTSSSTYVV	0	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	380	1-69	6	IgA1	DGEDRLLSHKYSYAMEV	18	3-20	5	QQHGTSPIT	13					+	+	+	+	+	+	+	+	/	+	/	/
HD1a	381#	3-23	4	IgA1	DLIAGDGKWVFDS	nd	1-6	4	LQDYNLPLT	nd																
HD1a	383	4-39	4	IgA2	RLYNTNWYHPIDF	25	3-15	1	QQHYDWPPWT	14					/	/	/	/	/	/	/	/	/	/	/	/
HD1a	385#	3-23	4	IgA2	DRGNCGSPGCYFDY	nd	4-1	4	QQYHIAPLF	nd																
HD1a	386	4-39	4	IgA2	AQPERWLQFFDH	33					2-14	2/3	SSYRSNSLAV	20	/	/	/	/	/	/	/	/	/	/	/	/
HD1a	388#	4-61	5	IgA2	GRRRNSDSSGYYDH	nd	1-39	3	QQSYSTPFT	nd																
HD1a	389#	3-21	3	IgA1	PQSGSTGTFDT	nd	3-15	2	HQYNYWVNS	nd																
HD1a	391	4-59	6	IgA2	QVGGWDWRFYNGLDV	18					2-14	3	SSYTSTNTL	12	+	+	+	+	+	+	/	+	+	/	/	/
HD1a	394#	3-33	4	IgA2	DEWGDDYKRLDY	nd					1-44	1	AAFEDSMDVYV	nd												
HD1g	2	3-23	4	nd	IDSRVATGSVPILRHAVDY	27	3-11	4	QQRHSWPLT	11					+	+	+	+	+	+	+	/	+	/	/	/
HD1g	4	1-3	4	IgG1	EYWGSYYYDF	15					3-21	2/3	QVWDSNNDVV	12	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	6	3-23	6	IgG1	SHIPLRPYWYGFDV	30					2-14	2/3	SSFTNRMTVI	16	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	13κ	3-23	6	IgG1	EIGAKQQLIPFSRSTRNYYYYGMDV	27	1-5	4	QQYNAYPLT	11					+	+	+	+	+	+	+	+	+	/	+	C
HD1g	13λ										3-25	2/3	QSVDSSKTYVI	20	+	+	+	+	+	+	/	/	+	+	C
HD1g	21#	4-39	4	IgG1	DLHTGYDFPSPSTDYFDY	nd					1-44	3	AAWDDSLNGRV	nd												
HD1g	23	1-18	6	IgG1	DPYFYDSSGYSPLHYYYGMDV	22					1-51	2/3	GTWDSSLSAGV	9	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	30	4-59	6	IgG1	GRGGNSRLPFG	26	3-20	2	QQCGSSPMYT	18					+	+	+	+	+	+	+	+	/	+	C
HD1g	37	4-39	5	nd	NSTTVMTADGRTANPGYKSFDP	17	1-39	4	QESYSSPLS	17					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	38	4-34	4	IgG3	GGRGQLVRRRSFDQ	21					3-21	2/3	QVWDRSSDHPVV	20	+	+	+	+	+	+	/	+	/	+	C
HD1g	44	3-23	4	IgG1	NLPLRPVGDSSKYFFDY	16					2-14	2/3	SSYTTSSTVV	8	+	+	+	+	+	+	/	+	+	/	+	C+N
HD1g	52	4-b	4	IgG1	VIYCGGGSCNLYLFDH	19	3-20	4	HQHGNSLLP	19					/	/	+	+	+	+	+	/	/	/	/	/
HD1g	53#	4-61	3	nd	WWRSGPTGTTFSYIGYDAFDI	nd					1-47	3	AAWDDSLSVWV	nd												
HD1g	54	4-34	5	IgG2	ELFGFKGRDL	35	3-20	2	QQYVTSPRMYI	15					/	/	/	/	/	/	/	/	+	/	/	/
HD1g	59	3-30	4	IgG1	DKKQWELLGFFDN	18	3-20	4	QQYGGSPRALT	10					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	62	3-74	5	IgG2	GGATAPGS	22					8-61	3	LLYMGGGIVL	12	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	74#	4-16	1	IgG1	GIPLRPAHQ	nd	3-15	2	QQTNSTPPKS	nd																
HD1g	83	4-39	4	IgG2	GWATSASIDF	29					1-51	2/3	GTWDSSLSAGV	15	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	85	3-30	4	IgG1	DRDIAAAGVGGFFDL	9	1-39	1	QQSYRIPRT	11					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	86	3-23	6	IgG1	EIEAKQQLIPFSRSTRNYYYYGMDV	28					3-25	2/3	QSVDSSKTYVI	20	+	+	+	+	+	+	+	/	+	+	+	C+N
HD1g	88	3-23	4	IgG1	PGYHFYDGNGFYAYFEF	13	3-15	2	QQFNDWPPMCS	20					+	+	+	+	+	+	+	/	+	+	+	C
HD1g	89#	1-46	3	nd	DLMIVEGGAFDF	nd					3-19	1	DSRDRSGNRL	nd												
HD1g	91	3-23	5	IgG1	IKTNPLMLYAIGGWFDP	12					2-14	1	SSYTSTSTYV	10	+	+	+	+	+	+	+	/	+	+	+	/
HD1g	94#	5-51	5	IgG1	LNSSGWNQ	nd	2-30	2	MQGTHWPPCS	20																
HD1g	96κ	3-30	4	IgG1	KAGYLAILSGSYYFDF	31	3-20	3	QEYGGSFT	nd					+	+	+	+	+	+	+	+	+	/	/	
HD1g	96λ.#										1-40	1	QSFDGSLNTYV	nd												
HD1g	102	4-59	6	IgG1	QGYSNWVNYYYAMDV	21	3-20	2	QQYGSSPCS	11					+	+	+	+	+	+	+	+	+	+	/	
HD1g	107	4-39	4	IgG1	DLHTGYDFPSPSTDYFDY	22					1-44	3	AAWDDSLNGRV	14	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	116	5-a	5	IgG1	CFNPTGYSYFDS	26	1-39	2	QQSYTTPFT	15					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	119	1-69	6	IgG1	ELTYYYDSSGYVLADGMDV	13					1-51	2/3	GTWDSSLRGKV	9	+	+	+	+	+	+	+	/	/	+	/	/
HD1g	123#	4-34	4	IgG2	ELFGFKRRA	nd					1-51	2/3	GTWDSSLSNEGV	nd												
HD1g	125#	1-46	5	IgG1	DSRKTESSSSVYWFDP	nd	1-39	4	QQTYMTPLT	nd																
HD1g	127	4-59	6	IgG1	HLYSAPSGDLYYYGVDV	18	2-28	1	MQALQTAWT	11					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	136	5-51	4	nd	PSMADAQMFDY	20					1-47	1	AWDDSLSGPV	8	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	138	3-11	5	IgG1	TGDSGFDYWFAP	21					2-14	1	SSYTSSTTLV	7	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	141	3-74	4	IgG2	RAVMSGPPK	19	2-28	5	MQAVQTPLT	12					/	/	/	/	/	/	/	/	/	/	/	C
HD1g	153	4-34	4	IgG1	GRLVDTSRLISFDG	30	2-28	4	MQTLEAPRT	19					+	+	+	+	+	+	+	/	+	+	/	/
HD1g	155	3-23	4	IgG1	VDDIADFWAGYVY	11	1D-12	4	QQANSFPPLT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	158#	3-21	4	nd	DTEMASIPYYFDS	nd					3-9	2/3	QVWDSSTACVI	nd												
HD1g	164#	3-64	4	IgG1	DRYDSSGYWYYFDY	nd	3-20	4	QQYGTSVT	nd																
HD1g	168#	4-59	6	IgG1	DSVRGGFLEWGSDSDYYYGMSV	nd					7-46	3	LLSYSGIRV	nd												
HD1g	169	4-59	6	IgG1	DIVPHFSGSDYYGMDV	18	1-39	4	QQSYTTPART	13					/	+	+	+	+	+	/	/	/	/	/	/
HD1g	172	4-59	4	nd	HKLGYCTGGSCYADDYYFDY	21	1-39	4	QQSYNPPAT	16					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	180	3-48	4	nd	GLIHDYNLDYFDY	19	3-11	5	QQRSDWPPIT	3					/	/	/	/	/	/	/	/	/	/	/	/
HD1g	181	4-39	2	IgG1	VLPAALLGTRGWFDP	23	3-20	2	QQYGTSLYT	7					+	+	+	+	+	+	+	/	+	+	+	C
HD1g	183#	1-3	3	nd	TYDGTGYSYSALDL	nd	3-20	3	QQYGSLPFT	17																
HD1g	194	1-18	4	nd	VFGDYVYYFDY	nd					1-44	2/3	AGWDDILRGLV	23	/	/	/	/	/	/	/	/	/	/	/	/
HD1g	195#	3-23	6	IgG1	ENGGGSGTYIYYYGVDV	nd	2-28	5	MQVLQIPIT	nd																

HD, Healthy donor; a, IgA; g, IgG; κ, Igκ; λ, Igλ; clonally related antibodies are indicated by the same color; #, antibody not expressed; nd, not determined; /, not reactive; +, reactive; **+**, high reactivity; C, cytoplasmic staining pattern; N, nuclear staining pattern; C+N, cytoplasmic and nuclear staining pattern

Table S2: Ig gene analysis and antibody reactivity of IgA+ and IgG+ intestinal plasma blasts form HD2

Antibody		IgH					IgL								Antibody reactivity												
patient	antibody	VH	JH	Isotype	CDR3	VH mutations	Vκ	Jκ	CDR3	Vκ mutations	Vλ	Jλ	CDR3	Vλ mutations	polyreactive	*Escherichia coli*	*Escherichia coli Nissle*	*Enterococcus faecalis*	*Enterobacter cloacae*	*Morganella morganii*	*Salmonella typhimurium*	*Lactobacillus reuteri*	*Bacteroidesthetaiotaomicron*	rotavirus like particle	intestine	HEp-2
HD2a	5	1-18	4	IgA1	GATNYYGSGRFYY	28	2D-28	4	MQALHILT	15					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	6	3-48	4	nd	GIVGTTTY	19	3-15	1	HHSNMWPWT	17					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	7	4-59	5	IgA1	APYLATADTLWFGT	58	3-20	4	QQYGASPVT	16					+	+	+	+	+	+	+	nd	nd	+	/	/
HD2a	8	3-23	3	IgA1	DDKHYATSTLEAMGYLYYYGLDV	40					3-10	3	YSTDSSGDQRV	23	+	+	+	+	+	+	+	nd	nd	+	+	N
HD2a	10	3-49	4	IgA1	WYGTSVLDY	15	1D-39	4	QQSFNTLS	12					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	15	4-39	3	IgA2	HRTDAYGGGVFDI	20					1-51	3	GTWDTSLNAAV	9	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	18	3-53	4	nd	GTDYAKGGY	17	4-1	1	QHYYSTPPWT	6					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	20	3-23	5	IgA2	GGHDDFASH	15	2-30	3	MQATHWPPAT	7					+	+	+	+	+	+	+	+	+	+	+	C
HD2a	21κ	5-51	3	IgA1	YPPSLRYLPTQQGDDGGFDI	38	1D-33	3	QQYDHLPIS	18					/	/	/	/	/	/	/	/	/	/	/	C
HD2a	21λ										2-11	3	CSYAGTYTWV	8	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	22	3-7	4	IgA2	DIDYIDY	23	1D-39	4	QQSYSNPPT	16					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	23	1-3	4	IgA2	ALVGATPCDY	0	1D-39	4	QQSYSTPQLT	0					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	25	3-72	4	nd	GEMGPTVPLLFDS	13					2-14	2/3	TSFSTGSAYVV	21	/	/	/	/	/	/	/	/	/	/	/	C
HD2a	27#	3-23	4	IgA2	DLDYSSLWIAGGGFDY	19	4-1	2	QQYSTTPPT	21																
HD2a	31	3-9	3	IgA1	DRGRLWSGYYNAFDI	13	3-20	3	QHYGPSPPFT	4					+	+	/	/	+	+	+	/	/	+	/	/
HD2a	34	4-39	4	IgA2	GTSQQLVEFYFDS	18					1-44	1	AAWDDNVNGL	nd	/	/	/	/	/	/	/	/	/	/	/	C
HD2a	35	4-39	3	IgA1	HRTSAYGGDVFDI	20					1-47	2/3	AAWDDTLSGLI	19	/	/	/	/	/	/	/	/	/	/	/	C
HD2a	36	1-69	3	IgA1	DAGQYCGGGSCRTFFGGFEI	32					2-14	1	ISCATSSTPCV	33	+	+	+	+	+	/	+	/	/	+	/	/
HD2a	39	3-48	4	IgA2	GNHGDHPHY	25	2D-28	3	LQTLKGPLT	nd					+	+	+	+	+	+	+	/	/	+	/	/
HD2a	41	3-23	4	IgA2	DLCFGASYCSTNVY	9	4-1	2	QQYYSPPCT	2					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	43	4-39	4	nd	GWSGYYYYFDY	6	1-27	1	QKYDSAPWT	13					/	+	+	+	/	/	/	/	/	/	/	C
HD2a	46	7-4-1	4	IgA2	DLRRSDTSGYLNY	10					2-8	1	ISYAGSNNFV	6	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	50	4-61	4	IgA2	GAFMTTVSL	21	1-16	2	QQYTFYPYT	11					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	51	4-4	3	IgA2	DLGGTSVKALNL	38					2-8	1	SSNRGANNYV	24	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	53	4-59	6	IgA1	STIAAWNYYYYYIDV	15					2-14	2/3	SSYTRLSSLHVL	8	/	/	/	/	/	/	/	/	/	+	/	/
HD2a	54κ	3-23	4	IgA2	ELCFGAGYCSTKVY	13	4-1	2	QQYYRLPST	9					/	/	+	+	+	+	+	+	/	/	/	C
HD2a	54λ										3-12	3	CSYAGTYTWV	15	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	56	3-11	3	IgA2	QKGVVYVISSFDI	12	1-5	2	QQFQSYSRT	10					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	57	4-59	4	nd	GRNTMFPGVILPASL	13					7-46	4	FLSFGGLV	20	+	+	+	+	+	+	+	+	+	+	+	C
HD2a	59	4-59	6	IgA2	SLYYSTSGSQYTGGFYYMDV	22	3-20	4	QQYAGSPLT	8					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	62	1-3	4	IgA1	DLGLRYCTHGVCQLAY	35	1-5	1	QQYNLFPVT	18					+	+	/	/	+	+	+	+	+	+	+	C
HD2a	63	1-46	3	nd	LEYDYVWGNSRHEGAFTL	11	1-27	5	QKYNTAPIT	4					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	64	4-59	4	IgA2	VGESGLTFDS	43	2D-28	1	MQDQKTPPT	9					+	/	+	+	+	+	+	+	+	+	/	/
HD2a	66	3-23	4	IgA2	HYSHFEN	43	1D-39	2	QQSYSFPYT	18					+	+	/	+	+	+	/	/	+	/	/
HD2a	67#	3-48	4	IgA2	EREEPGAPLAY	11	1D-37	5	QRTYNAPIA	nd																
HD2a	68	3-73	6	IgA2	YGLIPGTSDHSGMAV	25					1-51	3	GVWDHSLNEEV	18	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	69	3-23	2	IgA2	DQTPPGTIGWHAVWYFDL	15	3-20	3	QQYGSSPRVT	6					+	+	+	+	+	+	+	+	/	/	/	/
HD2a	70	3-15	4	IgA2	GGWMGALSRGYYFDY	18	1D-39	3	QQSISTPFT	20					+	+	+	+	+	+	+	+	+	+	+	C
HD2a	73κ	3-30	5	IgA2	DASLYGGKSGWFDP	12	3-11	1	QHRSNLVWT	3					/	/	/	/	/	/	/	/	/	+	/	/
HD2a	73λ#										2-11	3	CSYAGTYTWV	nd												
HD2a	74	3-23	1	IgA1	CNIHCQEGYFQY	20	1-9	3	LQLNLYPLT	9					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	75	3-23	5	IgA2	CYTDCYNKCFDS	27	1-9	3	QHLHSYPFT	11					/	/	/	/	/	/	/	/	/	/	/	C
HD2a	77	3-48	3	IgA2	DDTPPGMTGSKDAFDL	20	1D-39	3	QQSYTFPFT	18					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	79	3-15	5	nd	DGKYDFVTGSYWFDP	16	2D-28	1	MQSLQIPRT	9					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	82#	4-61	5	IgA1	SPLSTDWTPHSWFAP	39					2-23	2/3	CSFHEVPTYVV	nd												
HD2a	83	3-74	4	nd	GTSDWNGIDY	12	2-24	1	MQATQFPHT	5					/	/	/	/	/	/	/	/	/	/	/	/
HD2a	84	5-51	3	nd	PGGVCPFSSTWCGYTFDM	22	1-5	3	QQYGT	1					+	+	+	+	+	+	+	+	/	+	+	C
HD2a	87#	3-74	6	nd	GLEGSKPYYYMDL	26					2-23	3	CSKAGSSTLV	26												
HD2a	88	3-30	6	IgA2	AGATGLDV	26					1-51	3	GTWDNSMSAEV	10	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	91#	3-48	3	IgA2	RPSRQQLVLREGAWYAFDI	16					2-14	3	CSSTSSNTLGV	nd												
HD2a	94	7-4-1	6	IgA2	GGRTSFLDV	20					1-40	3	QSYDSSLRAWI	16	/	/	/	/	/	/	/	/	/	/	/	/
HD2a	96#	4-30-2	6	IgA2	DLYVDSGRYLAFGFDL	30	1-16	3	LHYEAFPLT	nd																
HD2g	1#	3-7	4	nd	SSNWGFDY	8					2-8	3	SSYAGSNNWV	nd												
HD2g	3#	3-23	4	IgG2	DRPNWGSFRYDSYYFDS	nd	1-5	1	QQYFTYGG	nd																
HD2g	4	3-7	4	nd	VGYEGWNHEY	14					1-44	1	GTWDDSLNGYV	19	/	/	/	/	/	/	/	/	/	/	/	/
HD2g	7	4-59	4	IgG1	RRSGSYWGFDY	17	1-39	1	QQSFSTPLT	17					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	11	1-3	5	nd	VPESVAGTLGL	22	4-1	1	HQYYDSWT	12					/	/	/	/	/	/	/	/	/	/	/	C
HD2g	12#	3-21	6	IgG4	ENSGHDVGYSYYGMDV	nd	3-11	5	QQRNEWPRT	21																
HD2g	24#	1-24	3	IgG1	KIWDVAASFNTFDL	22	3-20	4	QQYRDSTLT	nd																
HD2g	26	5-51	6	nd	PRYSTSYYGMDV	25	1-27	4	QQCDSPPLT	16					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	32	3-7	4	IgG2	EYDVGYYYYFDY	8	1-39	1	QQSYSIPRT	19					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	33	4-4	5	IgG4	IPGNQLLTPFSSSAWLDP	9					1-40	2/3	QSNDLSGSVV	13	+	+	+	+	+	+	+	+	+	+	/	/
HD2g	36	3-74	6	nd	AGPRVSSLDV	17					2-14	1	SSFVYTHTYV	15	/	+	/	/	/	/	/	/	/	/	/	/
HD2g	39	1-3	4	IgG1	RAAGVDEVYDY	30	3-20	4	QQYGGSRT	9					/	/	/	/	/	/	/	/	/	/	/	C
HD2g	42#	4-39	5	nd	HPVTLVGAAGS	nd	3-15	2	QHYNWPPMYT	19																
HD2g	43	3-30	3	nd	VWREKDDDALDV	19	3-11	4	QQRMYWPPLT	11					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	50#	1-69	6	IgG2	EGFRPHGLDV	59	3-11	3	QQLFP	17																
HD2g	52	3-30	5	IgG1	SDRLSDVWTGL	29	3-11	5	QQRYSWPPIT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	55#	3-30	4	nd	LVDLSGAPRAGDF	nd	3-11	3	QQRSNWPMYT	11																
HD2g	56	3-30	6	IgG1	GHDYLAAAAVRYYGMDV	16					2-14	1	SSFTTTRTLV	12	/	/	/	/	/	/	/	/	/	/	/	/
HD2g	62#	3-74	4	nd	DLGWSYSNYEASAGTHDY	nd					2-23	1	YSYAGSGTFLYV	nd												
HD2g	70	3-64	6	IgG1	VGGRDTVVAPAAVGFSYMDV	17	1-5	2	QQYSSFSS	9					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	72#	3-7	4	IgG2	KGFSSGPEY	24	1-17	1	LQHNSYPWT	5																
HD2g	73	4-30-2	4	nd	VVIDQTQQLVLNPSRYYFDY	9					3-1	1	QSWDSSTSFV	6	/	/	/	/	/	/	/	/	/	/	/	/
HD2g	76#	3-23	3	nd	VMAWPNQNFDVSPL	25	1-5	1	QQYESYPVT	28																
HD2g	77#	3-23	4	IgG1	ERSPHIVIGVVFDY	21	1-39	1	CRSHSMPWT	30																
HD2g	79#	5-51	6	IgG1	YGLEGCDGNGGKCYTSYYYYGMDV	19	3-20	2	QLASYT	nd																
HD2g	85#	3-7	3	nd	VRILGGHSVFDF	12	4-1	1	QQYYSFPPT	nd																
HD2g	88	3-7	4	nd	DFLGCNGYCYRGAIDY	21	1-5	4	HQYDTYSFS	20					/	/	/	/	/	/	/	/	/	/	+	/
HD2g	95#	3-7	5	nd	MGCSGCRRSHNFFDT	15	1-13	4	QQFNGFPQT	17																
HD2g	96	1-46	6	IgG2	GFEDIAAAGPPYYFYYYMDV	13	3-20	2	HQYGSPPYT	13					+	+	+	+	+	+	+	+	+	+	+	C
HD2g	134	4-34	4	nd	GGWVGYCSGGSCHYDY	5	1-5	2	QHYNSYPYT	nd					+	+	+	+	+	+	+	+	+	+	+	C
HD2g	155κ	3-15	3	nd	EGYSYGYHALGV	20	1-39	1	QQSYNTPRT	7					+	+	+	+	+	+	+	+	+	+	/	/
HD2g	155λ										3-1	1	QAWDSRTFV	13	/	/	/	/	/	/	/	/	/	/	/	/
HD2g	161#	5-51	4	nd	LAAAGGHTFDC	19	4-1	1	QQHYSTPRT	13																
HD2g	301	3-49	5	nd	DFLGAGSLEGWTGYQASHS	31	3-11	4	QQRDSWPLT	13					/	/	/	/	/	/	/	/	/	/	+	/
HD2g	312	3-74	5	nd	VVTWFDP	20					2-14	1	SSYTSRKSYV	3	/	/	/	/	/	/	/	/	/	/	/	/
HD2g	316#	3-74	4	nd	DRDWLLFDY	nd					1-47	2/3	ATWDDSLTDVV	nd												

HD2g	319#	5-51	4	nd	LSPRRLGFCASVGCPLDS	16	1-5	2	QQYNGPET	nd																
HD2g	320#	3-7	4	nd	DRRVGTVHFDY	nd					2-11	3	CSYAGRYTEV	3												
HD2g	325#	3-21	4	nd	REEIY	nd	3-20	2	QQYVNPMYT	nd																
HD2g	328#	3-33	4	nd	DLGMGKYFDY	nd					2-8	3	RSYVNNTGVV	nd												
HD2g	338#	3-48	6	nd	EGESPYWYFDV	nd	3-15	1	QQYNNWPPWT	nd																
HD2g	344#	5-51	5	nd	LGNWGSYIYNWFDP	nd					2-8	1	SSYGGGIYL	nd												
HD2g	347	3-23	4	nd	NSSWYAFDH	36					2-11	1	SSYSGGYV	35	/	/	/	/	/	/	/	/	/	/	/	C
HD2g	348	3-7	4	nd	DFLGCNGMCYRGAIDY	24	1-5	4	HQYSDYPFS	17					/	/	+	+	+	+	+	/	/	/	+	/
HD2g	349#	3-23	4	nd	NSTWFDIDY	nd					2-11	1	SSYSHYYV	nd												
HD2g	351	3-30	5	nd	RERTYCTSSSCNMLDH	14	1-16	4	QQYNTFPLT	5					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	353#	3-23	4	nd	NITHSDLDS	nd					2-11	1	CSYVGGLVGGYV	nd												
HD2g	354	3-23	4	nd	TDCYGGRCYYVDSRDGYNRFDY	31	1-39	2	QQSFVIPYT	28					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	358#	1-69	5	nd	AGIAAAGIGVWFDP	nd					1-40	3	QSFDSSVSGSYVV	nd												
HD2g	365#	4-34	6	nd	ERSAYNSFYYFMDV	nd	3-20	4	QQYGSSPVT	nd																
HD2g	367#	3-23	4	nd	NSTNYALQY	nd	3-11	1	QQRNDQWT	nd																
HD2g	370#	4-59	6	nd	EEGGYMDV	nd					2-14	3	SSYTSGSTLL	nd												
HD2g	373	3-74	4	nd	NRFGDYVKF	22	4-1	1	QQYYNTPWT	18					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	377	4-59	6	nd	LSPDFYYYMDV	16	1-39	3	QQSYSTLFT	19					/	/	/	/	/	/	/	/	/	/	/	/
HD2g	383	3-23	4	nd	NITYSDLDS	41					2-11	1	CSYIGGYVGGYV	25	+	+	+	+	+	+	+	+	/	+	+	/

HD, Healthy donor; a, IgA; g, IgG; κ, Igκ; λ, Igλ; clonally related antibodies are indicated by the same color; #, antibody not expressed; nd, not determined; /, not reactive; +, reactive; **+**, high reactivity; C, cytoplasmic staining pattern; N, nuclear staining pattern; C+N, cytoplasmic and nuclear staining pattern

Table S3: Ig gene analysis and antibody reactivity of IgA+ and IgG+ intestinal plasma blasts form HD3

Antibody		IgH					IgL								Antibody reactivity												
patient	antibody	VH	JH	Isotype	CDR3	VH mutations	Vκ	Jκ	CDR3	Vκ mutations	Vλ	Jλ	CDR3	Vλ mutations	polyreactive	*Escherichia coli*	*Escherichia coli Nissle*	*Enterococcus faecalis*	*Enterobacter cloacae*	*Morganella morganii*	*Salmonella typhimurium*	*Lactobacillus reuteri*	*Bacteroides thetaiotaomicron*	rotavirus like particle	intestine	HEp-2
HD3a	1	3-21	2	IgA2	PYYGSGNLGDWYFDL	4					1-40	2/3	QSYDSSLSAVV	nd	/	/	/	/	/	/	/	/	/	/	/	/
HD3a	2#	3-7	3	IgA1	RTLVRANAFDI	14					2-8	3	SSYAGRNNWV	nd												
HD3a	6	3-23	5	IgA2	GGYGSSWF	7	1-16	5	QQYNSYPIT	3					+	+	+	+	+	+	+	nd	nd	+	/	/
HD3a	10#	3-74	6	IgA2	DWRNGGMDV	28					2-14	1	SSKRISSTLAPYV	12												
HD3a	14κ	1-8	4	IgA1	SGFGAPVNFDH	8	1-39	1	QQSFETRA	14					/	/	/	/	/	/	/	/	/	/	/	/
HD3a	14λ										2-11	1	SSYAGSPYV	20	+	+	+	+	+	+	+	+	+	/	/	/
HD3a	18	3-30	5	IgA2	DLYQMLYGEVMDS	17	3-11	4	QQRSHWPPLT	9					/	/	/	/	/	/	/	/	/	/	/	/
HD3a	33#	3-74	4	IgA2	RFDYYAD	25	4-1	4	QQYSTTPLT	13																
HD3a	35#	4-34	4	IgA2	GRSGTVAEN	21					1-44	3	SAWHISLNFWV	nd												
HD3a	41	1-3	4	IgA2	GFGWGHFDY	14	1-5	1	QQYDSFPRT	17					+	+	+	+	+	+	+	/	/	+	+	C
HD3a	43#	5-51	3	IgA2	SAYSSTWYGAFDI	9	3-20	2	LQYGRHPGT	14																
HD3a	47#	4-61	5	IgA2	QLVYHRLGNSYAHIWFDS	nd					2-14	2/3	SSYTTSGAYVL	8												
HD3a	53	3-74	6	IgA2	DWRNGGMDV	27					2-14	1	SSKRISSTLAPYV	12	/	/	/	/	/	/	/	/	/	/	/	C
HD3a	55	3-7	3	IgA1	DLTPETSGHYFDALDI	20	1-6	1	LQDYNYPRT	10					/	/	/	/	+	/	/	/	/	/	+	/
HD3a	62#	3-7	4	IgA2	APSPGTLDY	16					2-14	2/3	GCHTSRIPVL	9												
HD3a	67#	4-59	4	IgA1	WGSRSSVFVPGAIDN	nd					2-14	3	TSWRGTTTFELEV	23												
HD3a	72#	4-59	4	IgA2	LLGDRTACLDS	29					1-44	3	AAWDEILNGPWV	nd												
HD3a	75	1-8	4	IgA1	SGFGAPVNFDH	9	1-39	1	QQSFETRA	14					/	/	/	/	/	/	/	/	/	/	/	/
HD3a	78#	7-4-1	4	IgA2	LLRATAPSDN	nd					2-14	1	STYTTTNRV													
HD3a	83	4-59	2	IgA1	VRTTSYYPNWYFDL	14					2-11	2/3	CSYGGSHTMPVR	12	+	+	+	+	+	+	+	+	+	+	+	C
HD3a	84	5-51	4	IgA1	HLAAHCSGNSCSYYFDY	20					1-44	2/3	AAWDDSRNGVV	8	/	/	/	/	/	/	/	/	/	/	/	N
HD3a	86#	3-23	2	IgA2	DLTTVYWYLDV	17	4-1	2	QQYFSTPRT	17																
HD3a	87	4-b	5	IgA1	TVPAPSLGAIAAAGASSS	50	1-5	1	QHYNSYWWT	19					+	+	+	+	+	+	+	+	+	/	/	
HD3a	92#	3-23	4	IgA2	APSGCTGECFLMDY	nd	1-5	1	QQCNTYLRT	6																
HD3a	94κ	4-39	5	IgA2	DGDLAATGNGLNS	36	1-5	1	QQYKTYKT	18					/	/	/	/	/	/	/	/	/	/	+	/
HD3a	94λ#										2-14	3	TSYSFSSTVV	nd												
HD3a	96#	3-7	4	IgA2	GWGLDQ	nd	2-29	4	METTHVPPV	4																
HD3a	101	3-23	4	IgA2	GSSIIDY	27	2-30	2	MQGSHWPFT	12					/	/	/	/	/	/	/	/	/	/	/	/
HD3a	103	3-15	5	IgA2	HPGGSCPGATCLRS	21	3-20	3	QHYGSSPPQLT	10					/	/	/	/	/	/	/	/	/	/	/	C
HD3a	111#	3-7	4	IgA2	VGHSTTWFGGYYFDS	12					2-11	3	CSYAGGYTYWV	10												
HD3a	113	4-28	3	IgA2	TRSNPSIDAFDV	23					8-61	3	VLYMGSGIWV	4	+	+	+	+	+	+	+	/	+	+	+	N
HD3a	119	3-23	4	IgA2	RSASGTFYFDY	21					2-11	3	CSYAGSYTWV	9	+	+	+	+	+	+	+	nd	nd	+	/	/
HD3a	125#	4-39	4	IgA1	DWRQSGGWYSGS	41	3-11	4	QQRSAWPLI	15																
HD3a	130	5-51	1	IgA2	SGGLGYCGDRNCYPENFHH	20	2-30	1	MQGIQWPWT	19					/	/	/	/	/	/	/	/	/	/	/	N
HD3a	132	4-39	6	IgA2	GHVSGTYGLDV	43					2-14	2/3	SSYSSTTTVL	nd	+	+	+	+	+	+	+	+	+	/	/	
HD3a	133	3-23	4	IgA2	HRAGNDY	22	1-9	5	QQVNSYPRT	21					/	+	+	/	+	/	/	/	/	/	/	
HD3a	134	3-30	4	IgA2	RAESGSHKSIEY	34					2-14	1	CSYTTSGTFV	nd	/	/	/	/	/	/	/	/	/	/	/	
HD3a	135#	3-23	4	IgA2	EPTVTTWRGYLDS	20	1-39	2	QQSYNSPQYT	23																
HD3a	139	4-61	4	IgA1	DQVPYYDIFTASYKEQYFLDS	23					1-44	3	AAWDDNLNGL	15	+	+	+	+	+	+	+	/	+	+	/	/
HD3a	140	3-7	4	IgA2	GRAVTATDY	12	1-6	1	LQDNDKPLT	26					+	+	+	+	+	+	+	/	+	+	/	/
HD3a	143	3-30	4	IgA2	EIRGYYSAL	19	1-9	2	QQLNTYPYT	8					/	/	/	/	/	/	/	/	/	/	/	N
HD3a	144	3-66	6	IgA2	FV	22					7-46	3	AFSHNGHWT	30	+	+	+	+	+	+	+	+	+	+	+	C+N
HD3a	146	3-74	6	IgA2	DWRNGGMDV	28					2-14	1	SSKRISSTLAPYV	12	/	/	/	/	/	/	/	/	/	/	/	/
HD3a	147	3-23	4	IgA1	DLWRRDGGGLGPFDY	15					2-14	2/3	MSSTSSSTVL	14	/	/	/	/	/	/	/	/	/	/	/	C
HD3a	153#	3-23	2	IgA2	DVSDIIALVVPPRGDYLDL	24					3-1	3	QTWGSGTAV	nd												
HD3a	157κ	4-30-4	4	IgA1	GAVPGRGSALHFDS	44	1-9	4	QQLSSYPLT	26					/	/	/	/	/	/	/	/	/	/	/	/
HD3a	157λ#										2-14	2/3	SSYSSTTTVL	19												
HD3a	158#	4-39	4	IgA2	YDGRWALDQ	39	1-39	1	HQSSNEAWT	11																
HD3a	159	3-7	4	IgA2	AVIAAALDY	22	1-6	1	LQDNGYPKT	20					/	/	/	/	/	+	/	/	/	/	/	/
HD3a	162#	3-11	5	IgA2	AVGPGVGASIS	24	4-1	2	QQYFNTPYT	25																
HD3a	163κ	3-23	5	IgA2	GSVTALGILDN	19	3-11	2	QQRSSWPYT	9					/	+	+	/	+	+	/	/	/	/	/	/
HD3a	163λ										1-36	1	AVWDDTLDGYV	18	/	/	/	/	/	/	/	/	/	/	/	/
HD3a	165κ#	3-48	4	IgA2	DDAYYYDNTNYYSLDY	16	1-39	2	QQSYSTHPYT	13																
HD3a	165λ										1-40	1	QSYDTSLNGRV	10	/	/	/	/	/	/	/	/	/	/	/	/
HD3a	169κ#	4-34	6	IgA1	REKKRTRVRYDLDV	19	3-20	3	QHYVGSSLFT	9																
HD3a	169λ#										1-44	1	AAWDDGLRSYL	nd												
HD3a	171#	4-59	5	IgA1	NRLPHDNDSKTYYNWFDP	nd					1-44	3	AVWDDSLNGCWL	12												
HD3g	7	3-66	6	IgG1	EQVREPMSGVIQAEAMDV	24	3-15	1	HQYNNWWT	15					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	10	4-59	3	IgG4	NSTSTSPLDI	22	4-1	4	QQYCTTPFT	16					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	13	4-59	3	IgG4	NSTSSSPLDI	24	4-1	4	QQYCTNPFT	16					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	16	4-30-4	3	IgG2	EVLSPVDSDAFDV	33	3-15	4	QHYNNLPLT	10					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	19	4-59	3	IgG4	NSSSSSPLDV	22	4-1	4	QQYCTPPFT	21					/	/	/	/	/	/	/	/	/	/	/	C
HD3g	26	1-46	5	IgG2	DPSLRDRSSGRGWLDP	21					2-11	3	CSYAGRYTWV	12	/	/	/	/	/	/	/	/	+	+	/	/
HD3g	28	4-4	5	IgG2	REYRLGYVGWFDP	20	3-15	2	QQYANWPPGYT	21					/	+	+	+	+	+	+	/	/	/	/	/
HD3g	31#	3-21	4	IgG1	GFSSSRYAFDY	29	3-20	3	QQYGTSPFT	7																
HD3g	32#	3-48	6	IgG2	DRHYYDAGRDHNYYGMDV	20	1D-39	2	QQSYSTRPYT	15																
HD3g	34	4-39	5	IgG2	TGGRRYTLGA	21	2D-28	4	MQALQTPLT	9					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	37	3-23	4	IgG2	DRGGLISKFDY	12					2-14	1	NSHTRKNTPGCV	13	/	/	/	/	/	/	/	/	/	/	/	C
HD3g	38#	4-39	2	IgG2	GPYIFGTFWYFDL	25					1-44	3	ATWDDSLNGFWV	nd												
HD3g	39	4-39	3	IgG4	NSTSTSPLDI	20	4-1	4	QQYCTTPFT	15					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	41	4-59	3	IgG2	HAYTGTEGHDAFDI	36	1-39	1	QQSHSLPWT	24					/	/	/	/	/	/	/	/	/	/	+	/
HD3g	44#	3-7	6	IgG2	GEDLVATTEYLYGLDV	35	1-6	3	LQDYAYPYT	15																
HD3g	50	3-23	4	IgG1	TGFGESSFDH	27	1-16	3	QQYSTYPFT	18					+	+	+	+	+	+	+	+	+	+	+	C
HD3g	53	3-74	5	IgG2	DFDYPTSV	24					2-14	1	SACTTSNTYV	17	/	+	+	+	+	+	/	/	/	/	/	/
HD3g	54	3-23	6	nd	PIGYQWHQYGLDV	24	2-28	2	MQALQTVYT	8					/	/	/	/	/	/	/	/	/	/	/	/
HD3g	55#	3-15	4	IgG2	DVANPMSQIDY	26	2-28	2	MQVLETPPGCT	23																
HD3g	70	4-4	5	IgG2	IRGGCSVHSCFIDP	31	3-20	2	QLYVTPTMYI	14					+	+	+	+	+	+	+	nd	nd	+	/	C
HD3g	71	3-23	4	IgG2	GSAAPTYQFDH	31	1-16	4	QQYHTYPPT	15					/	/	/	/	/	+	/	/	/	/	/	/
HD3g	72#	3-21	4	IgG2	IPVLPGSFPDDY	18	3-20	5	QHYNSMPPNT	18																
HD3g	73	4-30-4	3	IgG2	EVNRPAPDSDAFDI	29	3-15	4	QQYGKRPLT	17					/	/	/	/	/	/	/	/	/	/	/	C
HD3g	75#	4-39	3	IgG1	GTWYNDNSGYYRQMPFDI	25	1-5	1	QQYNGYSRT	9																
HD3g	76	4-61	6	IgG4	AVHGRGGLDA	31	1-5	1	QHFGAYSPWT	19					+	+	+	+	/	/	/	/	+	/	/	/
HD3g	77	3-23	2	IgG4	TRENWYFAL	24	3-11	4	QHRDNLPLT	14					/	/	/	/	/	/	/	/	/	/	/	N
HD3g	78#	4-59	3	IgG4	NSSRTSPLDI	39	4-1	4	HQHCSLPFT	28																
HD3g	80#	4-34	4	IgG1	GWASSGYYFYFDY	22	3-20	2	QQYSSSPPMYA	21																
HD3g	81#	3-48	4	IgG1	AKPEGRWELRFYFDY	26	3-15	2	QQYNHWPGT	15																
HD3g	87#	3-48	4	IgG1	VYRQVLTPRAEFDY	27	3-15	2	QQYNIWPPFT	18																
HD3g	89#	3-43	4	IgG3	EMDTMFFDY	41	3-15	5	QQYNNWPPIT	26																

HD3g	94	3-23	3	IgG2	GGKVTGYAFDM	14					2-8	3	SSYAGDNNYVV	5	/	/	/	/	/	/	/	/	/	+	/	C
HD3g	102κ#	4-59	3	IgG2	NSTSSSPLDI	25	4-1	2	HQYYSSPYT	22																	
HD3g	102λ#										2-23	1	CSYVRSGVV	13													
HD3g	108#	4-39	1	IgG2	QITPYVPADL	31					2-14	4	SSFTSSITYV	13													
HD3g	117#	3-23	4	IgG1	VGVRVLLYLGELKN	20	4-1	2	QQYHSRPQT	7																	
HD3g	132#	3-15	4	IgG2	HHWDSSGYFHLGN	29	1-39	2	QQSYSTRPYT	16																	
HD3g	144κ#	3-13	3	IgG2	SYCSGPGICYDIGSFDV	18	1-6	3	LQDYAYPYT	15																	
HD3g	144λ										2-8	3	SSYAGSNNWV	4	/	+	/	/	/	/	/	/	/	/	/	C+N
HD3g	149κ#	3-74	4	IgG2	GDYGLS	22	3-15	4	QQYNKWPLT	15																	
HD3g	149λ										2-8	2/3	CSYAPIIDLDI	16	/	+	/	/	/	/	/	/	/	/	+	/
HD3g	150#	4-59	4	IgG2	DKWGSLDY	22	1-16	3	RQYVTSTFT	nd																	
HD3g	161#	4-59	4	IgG2	DRKGNGYEYHFDF	31	1-5	4	LQYNSYPLT	12																	
HD3g	166#	4-61	1	IgG2	GGGTYTSDFQY	34	3-20	1	QQYGSSPRT	18																	
HD3g	176#	4-59	3	IgG2	NSTATSALDI	27	1-5	1	QHFGAYSPWT	21																	
HD3g	178#	4-59	3	IgG2	NSSSGSPLDI	31	4-1	4	HQHCSLPFT	25																	
HD3g	191	4-34	4	IgG3	GEFGEMED	31					1-44	3	SAWDSSLSGPV	25	/	/	/	/	/	/	/	/	/	/	/	C

HD, Healthy donor; a, IgA; g, IgG; κ, Igκ; λ, Igλ; clonally related antibodies are indicated by the same color; #, antibody not expressed; nd, not determined; /, not reactive; +, reactive; **+**, high reactivity; C, cytoplasmic staining pattern; N, nuclear staining pattern; C+N, cytoplasmic and nuclear staining pattern