Online Figure Legends:

FIG E1. CD19^{hi}CD21$^{-/lo}$CD10^{-}CD27^{-} B cell frequencies in CVID patients with and without AICs. Dot plots from representative subjects and pooled subset frequencies. Dark bars represent average group values. Statistically significant differences are indicated, ****P <0.0001 (Mann-Whitney U tests).

FIG E2. The IgG heavy chain repertoire of CVID+AIC patients is skewed toward VH4 gene usage. Pooled VH gene segment usage frequencies of the indicated subjects are represented. Light bars indicate standard error of the mean. Statistically significant differences are indicated, **P <0.01, *P <0.05 (Mann-Whitney U tests).

FIG E3. CVID-AIC patients display germinal centers hypoplasia. A hematoxylin and eosin (H&E) stained excisional axillary (left) and cervical (right) lymph node biopsies from two additional CVID-AIC patients. GCs are outlined with white dashed lines. Original magnification, 12.5X.

FIG E4. Asymmetric, enlarged germinal centers (GCs) predominate in lymph nodes from eleven additional CVID+AIC patients. Hematoxylin and eosin (H&E) stained excisional inguinal lymph node biopsies from (starting at top, from left to right) CVIDC14, CVIDC78, CVIDC6 and CVIDC3. An H&E iliac lymph node biopsy from CVIDMS1. H&E stained axillary lymph node biopsies from CVIDMS2, CVIDY43, CVIDY12, CVIDC76 and CVIDCA1. A H&E stained cervical lymph node removed during the autopsy of CVIDYA1. GCs are outlined with white dashed lines. Original magnification, 12.5X.

FIG E5. Immunohistochemical staining of an excisional axillary lymph node biopsy from CVID+AIC patient CVIDC6. Follicular structures are revealed by staining sequential lymph node sections with hematoxylin and eosin, anti-BCL-6, anti-CD20, anti-CD3 and (E) anti-CD21.

FIG E6. Hyperplastic but circular GCs predominate in excised bacterial lymphadenitis (BL) lymph nodes. (A) A representative hematoxylin and eosin stained cervical lymph node from an immune competent 3-year-old male with Moraxella lymphadenitis but not AICs. GCs are outlined (white dashed line). (B) The percentage of each analyzed lymph node's total 2-dimensional cellular area comprised of follicular structures is displayed. (C) The average circularity quotient of identified follicular structures is displayed. Dark bars represent group average values. Statistically significant differences are indicated, *P <0.05 (Mann-Whitney U tests)

Table E1- Demographic and clinical information on CVID patients with and without autoimmune cytopenias

	age[a]	sex	Freiburg classification[b]	*VH* mutation analysis?	genotype	lymph node	AIC	other inflammatory diseases
CVIDC18	10	F	II	-	-	-	-	AS
CVIDC1	16	M	Ib	-	-	-	-	DM1
CVIDC31	17	M	II	Y	-	-	-	-
CVIDC48	18	M	Ib	-	-	-	-	-
CVIDY39	19	F	II	Y	-	-	-	-
C12A[c]	20	F	Ib	Y	TACI wt/C104R	-	-	-
CVIDC17	21	F	II	-	-	-	-	AS
CVIDC32	22	M	II	-	-	-	-	-
CVIDC67	28	F	II	-	-	-	-	ILD
CVIDC83	28	F	Ib	-	CTLA4 wt/G146R	-	-	AIE, AIR
CVIDC41	36	F	Ib	-	-	-	-	RA
CVIDCA2	51	F	-	-	-	AN	-	BC
CVID170	53	F	Ib	Y	-	-	-	-
CVIDY11	54	M	II	-	-	-	-	PM
CVIDCA3	56	M	-	-	-	CN	-	TC
CVIDC63	60	F	Ib	Y	-	AN	-	BC
CVIDY37	63	F	II	Y	-	AN	-	BC
CVIDY41	63	M	Ib	-	-	-	-	-
CVIDY33	65	F	II	-	-	-	-	-
CVIDY34	67	F	Ia	-	-	-	-	CD
CVIDCA1	7	M	-	-	CTLA4 wt/A86fs[§]	AN	ES	AIE, LA
CVIDC9	12	F	Ia	-	-	-	ES	EC, GR
CVIDC76	14	M	Ib	-	-	INN	ES	LA
CVIDC14	15	M	Ib	-	-	INN	ES	LA, SP
CVIDC44	15	M	Ia	-	-	-	ES	-
CVIDC11	18	F	Ia	-	-	-	ES	LA, SP
CVIDC6	19	M	Ia	Y	CTLA4 wt/R70Q	INN	ES	LA, SP

CVIDC22	19	M	Ib	-	-	-	ITP	-
CVIDC10	23	F	Ib	-	-	-	AIHA	-
CVIDC39	23	F	Ib	-	-	-	ITP	BOOP
CVIDC3	23	M	II	-	-	INN	ITP	-
CVIDC23	26	M	II	-	NFKB1 wt/W783X	-	ITP	-
CVIDC78	30	M	Ia	-	TACI wt/C172Y	INN	ES	ILD, PN
CVIDY42	39	M	Ib	-	-	-	ITP	G
CVIDY12	40	F	Ib	-	-	AN	ITP	GR, LA, SP
CVIDY15	40	M	Ia	-	TACI wt/C104R	-	ITP	B, G, SP
CVIDY40	45	F	Ib	-	-	AN	ITP	-
CVID292[d]	45	F	Ia	Y	TACI wt/C104R	-	ITP	LA, SP
CVIDC59	47	F	-	-	-	-	ITP	-
CVIDY17	48	F	Ib	-	TACI wt/C104R	-	ES	B, SP
CVIDY28	48	F	Ib	Y	-	AN	ITP	LA, PN, SP
CVIDY43	50	F	Ia	Y	-	AN	ITP	-
CVIDMS2	53	M	-	-	-	CN	ITP	LA
CVIDC49	57	F	Ia	-	-	-	ITP	-
CVIDY45	59	F	Ia	Y	-	AN	ITP	BC, LA, SP
CVIDY20	62	M	Ia	-	-	-	ITP	SP
CVIDMS1	63	F	Ia	Y	-	ILN	ITP	EMC
CVIDYA1	67	M	-	-	-	CN[e]	ITP	-
CVIDY8	68	F	Ia	-	-	-	AIHA	-

AIE, autoimmune enteropathy; AIHA, autoimmune hemolytic anemia; AIR, autoimmune retinopathy; AN, axillary lymph node; AS, asthma; B, bronchiectasis; BC, breast cancer; BOOP, bronchiolitis obliterans with organizing pneumonia; CD, Crohn's disease; CN, cervical lymph node; DM1, diabetes mellitus type 1; EC, enterocolitis; EMC, endometrial cancer; ES, Evan's syndrome; F, female; G, giardiasis; GR, granulomas; INN, inguinal lymph node; ILN, iliac lymph node; ILD, interstitial lung disease; ITP, immune thrombocytopenia; LA, lymophadenopathy; M, male; ND, not determined; PM, polymyositis; PN, pulmonary nodules; RA, rheumatoid arthritis; SA, sarcoidosis; SP, splenomegaly; TC, thyroid cancer; UC, ulcerative colitis; wt, wild type; Y, yes

[a] Age (years) at time of study enrollment, [b] classification described in Warnatz et al. Blood (2002), [c] as described in Castigli et al. Nat Genet. (2005), [d] as described in Romberg et al. J Clin Invest. (2013), [e] specimen obtained at autopsy, § patient has received hematopoietic stem cell transplantation

Table E2: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDC31

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDC31 IgG+ mem 04	3-72	3-10	2	4	AVNYYDSNGHYNVLSD	16	9	0	1	1	1	0	0	2	1	2	1
CVIDC31 IgG+ mem 09	3-20	/	/	4	ARGIRFVYGQDLDY	14	15	2	1	3	0	0	0	1	3	5	0
CVIDC31 IgG+ mem 11	3-23	3-3	3	4	ARDEAIFGVFPFDY	14	20	3	0	1	0	1	1	7	1	5	1
CVIDC31 IgG+ mem 21	3-30	3-10	2	4	ARDMFSGAPDFFDY	14	21	0	0	2	0	0	2	11	0	3	3
CVIDC31 IgG+ mem 22	3-33	2-15	3	4	ARDAVVGSPGAHFDY	15	14	0	0	3	0	2	0	4	0	2	3
CVIDC31 IgG+ mem 24	3-9	6-13	3	4	VKVDIPAAGTFFED	14	21	2	0	4	0	1	1	1	3	5	4
CVIDC31 IgG+ mem 33	4-31	5-5	2	4	ARSTIHKYDRNGYFIPLLWNFND	23	15	1	1	3	0	1	0	1	0	7	1
CVIDC31 IgG+ mem 40	1-46	/	/	5	TRDSRIQNWFDP	12	7	0	0	2	0	2	0	0	1	2	0
CVIDC31 IgG+ mem 48	4-59	/	/	2	ARAGSDWYFDL	11	25	2	1	5	0	4	1	3	2	4	3
CVIDC31 IgG+ mem 49	3-30	/	/	6	AKALISAHYYYAMDV	15	9	0	0	3	0	1	0	1	1	3	0
CVIDC31 IgG+ mem 60	1-18	3-9	3	5	ARDLVMSDSGFDP	13	21	1	0	3	0	0	1	4	0	8	4
CVIDC31 IgG+ mem 61	3-7	2-2	2	6	AREGCSGTSCMDV	13	12	1	1	1	1	2	1	4	1	0	0
CVIDC31 IgG+ mem 69	4-31	1-26	3	4	ASGMAGKVGAFDY	13	7	1	0	1	0	0	0	0	0	5	0
CVIDC31 IgG+ mem 72	3-23	2-15	2	4	AKGSLGRCSGVRCYHFDS	18	11	1	0	1	0	1	0	4	0	3	1
CVIDC31 IgG+ mem 84	3-15	2-2	3	4	TTDRPDIVVVPAVIRIYRLGIDY	23	8	1	0	1	0	0	0	3	1	2	0
CVIDC31 IgG+ mem 93	4-30	/	/	4	ARDSGRAATDY	11	17	2	0	1	0	1	0	3	0	6	4
CVIDC31 IgG+ mem 98	3-23	4-11	2	4	AKDSDFHYSAFDY	13	14	0	1	1	0	1	0	7	1	2	1
CVIDC31 IgG+ mem 120	3-11	/	/	4	ARGPGRY	7	3	1	0	0	0	0	0	0	0	2	0
CVIDC31 IgG+ mem 136	4-31	4-23	3	6	ARDNTVVITSNYGMDV	16	9	3	0	0	0	1	1	2	0	1	1
CVIDC31 IgG+ mem 138	3-73	3-16	3	5	VEVIRDTFGGALES	14	20	4	1	0	0	3	0	3	0	6	3
CVIDC31 IgG+ mem 139	4-31	3-3	2	6	ARDRERFWSGYFYYYGLDV	19	31	3	2	4	1	1	1	4	2	9	4
CVIDC31 IgG+ mem 143	3-11	/	/	6	ARAGEVEQPYYNYYGMDV	18	12	0	1	0	0	1	0	4	0	5	1
CVIDC31 IgG+ mem 149	3-9	2-15	2	6	AKDRCSGGTCYSGMDV	16	10	1	2	0	1	1	0	0	1	2	2
CVIDC31 IgG+ mem 160	1-2	6-13	3	6	ARLNLRTLAAAATNRDGLRYGLDV	24	4	0	0	0	0	0	0	1	0	2	1
CVIDC31 IgG+ mem 170	3-23	2-15	2	4	AKGSLGRCSGVRCYHFDS	18	11	1	0	1	0	1	0	4	0	3	1
CVIDC31 IgG+ mem 180	1-8	6-13	3	6	ARESPRHMAAAGSYYYGMDV	20	7	0	0	0	0	2	0	0	1	4	0
CVIDC31 IgG+ mem 185	3-48	2-2	3	6	ARDRWDIVVVPAAIYMDV	18	4	0	0	1	0	0	0	3	0	0	0

R, amino acid replacement mutation; S, silent mutation

Table E3: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDY39

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDY39 IgG+ mem 49	3-15	3-22	2	5	DGFGYYPNGFDP	12	16	1	0	1	3	0	0	3	0	4	4
CVIDY39 IgG+ mem 51	3-30	/	/	6	DPPNNEGFDYYDMDV	15	5	0	0	1	1	1	0	0	0	0	2
CVIDY39 IgG+ mem 54	3-30	6-6	3	4	AARTADRPSYFDY	13	14	4	2	3	1	1	0	1	0	2	0
CVIDY39 IgG+ mem 57	3-30	2-2	2	4	CEGYCQVSGIDY	12	13	0	1	4	0	0	2	3	0	2	1
CVIDY39 IgG+ mem 58	3-23	5-24	3	3	EATWTTIDAFDI	12	5	0	0	1	0	1	0	2	0	1	0
CVIDY39 IgG+ mem 61	3-33	3-22	2	4	GPYYDDGGPLTDF	13	16	1	0	2	0	2	0	3	1	4	3
CVIDY39 IgG+ mem 63	1-18	/	/	6	DHSAYYESIDGPLRV	15	10	0	1	0	0	1	0	3	0	3	2
CVIDY39 IgG+ mem 65	7-4	3-22	2	6	DYYDYRAYGMDV	12	32	2	1	4	0	4	3	5	1	7	5
CVIDY39 IgG+ mem 66	3-23	3-10	3	6	VVIRGVDYYFQALDV	15	26	1	0	3	1	2	1	6	1	8	3
CVIDY39 IgG+ mem 68	4-39	4-17	2	5	QFDYANSPLQT	11	33	1	1	7	0	4	0	6	1	6	7
CVIDY39 IgG+ mem 70	3-23	3-3	1	4	IQFLEWLLLDY	11	8	0	1	1	1	1	0	1	1	0	2
CVIDY39 IgG+ mem 71	4-31	3-3	3	2	GRVVTTNMGPYWYFDL	16	13	1	1	3	1	2	0	0	0	4	1
CVIDY39 IgG+ mem 72	3-30	6-19	2	1	DRGGYSSLTSYFQH	14	9	0	0	1	0	4	2	0	0	2	0
CVIDY39 IgG+ mem 73	4-59	/	/	4	HLGYDFHS	8	24	0	0	3	0	0	1	15	1	2	2
CVIDY39 IgG+ mem 74	3-23	/	/	4	DSSRYGRTGYFDY	13	8	0	1	2	0	2	1	0	0	1	1
CVIDY39 IgG+ mem 82	3-23	3-10	3	4	DRDIRLPYAVLRGVY	15	6	0	0	1	0	2	0	0	0	3	0
CVIDY39 IgG+ mem 84	3-23	/	/	4	RGGGTRLMVYDIHFFDY	17	17	2	0	2	0	3	1	5	0	2	2
CVIDY39 IgG+ mem 85	5-51	3-22	2	4	MQGYYNSSAFSYYFDY	16	16	2	1	3	3	1	0	0	0	4	2
CVIDY39 IgG+ mem 86	3-30	6-19	2	6	DRDHYSSGWWGVDFYYYVMDV	21	24	0	0	1	0	2	1	16	0	1	3
CVIDY39 IgG+ mem 90	3-9	3-9	2	4	DEDYWTGHSNTRFDQ	15	19	1	0	2	1	1	0	4	0	6	4
CVIDY39 IgG+ mem 92	7-4	/	/	6	GGPLQAYYYDMDV	13	6	0	0	1	0	0	0	0	0	5	0
CVIDY39 IgG+ mem 93	3-30	/	/	4	SHSQYTPSDVYFDY	14	16	0	1	2	0	2	3	3	0	2	3
CVIDY39 IgG+ mem 96	3-23	3-3	2	1	VGYYYDSSGYYPSSEYFQH	19	11	0	0	0	2	2	1	1	1	2	2

R, amino acid replacement mutation; S, silent mutation

Table E4: IgH repertoire and VH mutations of IgG+ memory B cells from 12A

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
12A IgG+ mem 08	3-43	3-10	1	4	DSTGGFGELYPVRPRRRFDY	20	14	0	0	2	1	1	0	2	0	5	3
12A IgG+ mem 12	4-39	4-17	2	4	HLSDYPVGY	9	20	0	0	2	3	1	0	6	0	4	4
12A IgG+ mem 19	4-59	/	/	4	QEEGFDS	7	15	0	0	1	2	1	1	2	1	5	2
12A IgG+ mem 26	3-53	3-3	2	5	ADGWSGYKAFDL	12	32	0	2	4	1	2	2	5	3	6	7
12A IgG+ mem 29	4-39	4-17	2	4	RNLHGDYLFWHY	12	6	0	0	0	0	0	0	2	0	4	0
12A IgG+ mem 31	3-48	/	/	6	DILADYYYYGWDV	13	16	0	0	0	1	2	0	5	3	4	1
12A IgG+ mem 47	3-23	3-10	2	4	EQFNAPLYYLDH	12	16	0	1	0	0	4	0	6	1	2	2

R, amino acid replacement mutation; S, silent mutation

Table E5: IgH repertoire and VH mutations of IgG+ memory B cells from CVID170

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVID170 IgG+ mem 04	3-30	2-8	2	4	DLGYCTGGICRMSYFLY	17	15	0	0	1	1	3	0	2	1	3	4
CVID170 IgG+ mem 05	3-21	6-6	2	6	SEYSSSNNHMDV	12	16	1	0	2	0	1	2	0	2	2	6
CVID170 IgG+ mem 06	3-13	1-26	1	6	GRLRWDV	7	18	1	1	0	2	3	0	2	0	6	3
CVID170 IgG+ mem 07	3-7	2-8	2	4	GSTGGAGY	8	1	0	0	0	0	1	0	0	0	0	0
CVID170 IgG+ mem 09	3-23	/	/	4	GGGAEFDY	8	13	0	1	2	1	0	0	4	1	3	1
CVID170 IgG+ mem 11	3-23	/	/	4	KKEVYESWGGRKSSFFDN	18	20	0	0	3	0	2	3	2	1	6	3
CVID170 IgG+ mem 13	5-51	/	/	4	RRGG	4	11	2	1	4	0	2	0	1	1	0	0
CVID170 IgG+ mem 14	3-21	3-3	2	4	GGTRSGLSGVSGTMDY	16	30	0	0	3	1	2	0	7	4	8	5
CVID170 IgG+ mem 15	1-3	1-20	2	4	DEWNVLVFSY	10	4	0	0	2	0	0	0	0	0	2	0
CVID170 IgG+ mem 16	3-7	/	/	4	EHWFRIDY	8	34	0	0	2	3	5	0	6	1	10	7
CVID170 IgG+ mem 18	5-51	/	/	6	IFVGGMDV	8	12	0	0	2	0	2	0	0	0	5	3
CVID170 IgG+ mem 22	5-51	6-19	2	6	QAYSSGWSGDYYYYAMDV	18	16	1	0	4	1	2	2	2	0	3	1
CVID170 IgG+ mem 23	3-48	3-22	2	3	EDYDTSYWYDSTGYYPDAFDV	21	19	0	0	0	0	1	2	4	4	6	2
CVID170 IgG+ mem 25	1-2	6-6	3	4	EGLKLAALPSYYFDY	15	9	0	0	1	0	2	0	0	0	3	3
CVID170 IgG+ mem 27	3-23	4-17	2	4	GGDYGEFDL	9	2	0	0	0	0	1	0	1	0	0	0
CVID170 IgG+ mem 28	3-9	1-26	2	3	TMSGTFTAADPFDV	14	18	3	0	4	0	0	2	2	1	6	0
CVID170 IgG+ mem 32	5-51	/	/	4	EATRGFDY	8	11	1	0	5	0	1	0	0	0	3	1
CVID170 IgG+ mem 36	3-30	3-3	3	4	VKTRVVTSGGFDLDY	15	5	0	0	1	0	1	0	1	0	2	0
CVID170 IgG+ mem 37	3-23	5-12	3	5	SRHGIVATTSDY	12	29	0	0	3	0	3	2	5	1	9	6
CVID170 IgG+ mem 38	7-4	3-10	1	4	DRRLLWFKEMGLADY	15	22	2	1	3	2	1	1	1	2	7	2
CVID170 IgG+ mem 42	3-11	/	/	6	SRDNFWGDYYYSMDV	15	21	0	0	1	0	1	4	5	0	6	4
CVID170 IgG+ mem 43	4-61	3-22	2	6	DRKGTGYYYGMDV	13	34	3	1	2	2	3	2	1	2	11	7
CVID170 IgG+ mem 45	4-30	6-6	2	4	SGSSGNFDY	9	16	1	0	4	1	0	0	2	0	5	3
CVID170 IgG+ mem 46	3-30	6-13	1	4	DPGQQLFYYFDY	12	5	0	0	0	0	1	0	2	0	1	1

R, amino acid replacement mutation; S, silent mutation

Table E6: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDC63

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDC63 IgG+ mem 02	4-4	3-10	2	4	ASSRRLYGSLLENYYKDVDFAY	22	22	0	0	3	0	0	2	7	1	6	3
CVIDC63 IgG+ mem 09	4-61	2-2	3	5	ARESQDIVVLPALNWFDP	18	14	1	0	4	1	3	1	1	0	2	1
CVIDC63 IgG+ mem 12	1-46	5-18	3	5	ARDHSDTFIEGIARRGSWWFDP	22	31	2	1	6	0	4	1	6	0	10	1
CVIDC63 IgG+ mem 14	1-2	1-1	2	4	TRVVGQNYDNNWAEKFDY	18	15	2	0	2	0	1	0	2	0	6	2
CVIDC63 IgG+ mem 15	4-59	3-9	2	6	ASLPYDILPRGPQRFYHYGMDV	22	12	0	0	0	1	3	3	1	0	2	2
CVIDC63 IgG+ mem 19	3-23	6-6	2	5	AKGWGSSFGDWFDP	14	12	1	0	2	0	0	0	5	1	2	1
CVIDC63 IgG+ mem 20	1-2	3-9	3	5	AREALRGLVNTFDP	14	14	2	2	1	1	1	1	1	0	4	1
CVIDC63 IgG+ mem 28	1-8	5-18	2	4	ARVGGYSYGGGIKY	14	0	0	0	0	0	0	0	0	0	0	0
CVIDC63 IgG+ mem 33	4-61	3-16	2	4	ARQAYAYVHWD	11	19	1	2	0	2	4	0	1	1	4	4
CVIDC63 IgG+ mem 34	4-39	/	/	4	AKEVAR	6	36	4	1	4	1	4	2	6	1	7	6
CVIDC63 IgG+ mem 37	3-15	3-22	2	4	TTDPTGGYYFDSSGSYRDY	19	18	2	0	2	0	2	0	3	1	7	1
CVIDC63 IgG+ mem 48	4-31	2-15	2	4	ARDRYGGKWEVDS	13	25	2	2	3	0	4	1	4	0	5	4
CVIDC63 IgG+ mem 52	3-33	/	/	6	ARDQGWRRLLDYHYGFDV	18	5	0	0	1	0	1	0	1	0	2	0
CVIDC63 IgG+ mem 63	4-59	1-26	2	4	ARDSNGSYLDY	11	5	1	0	0	0	0	0	0	0	3	1
CVIDC63 IgG+ mem 65	1-46	/	/	4	AKDFFGHWTIDY	12	14	1	0	4	1	0	1	2	0	3	2
CVIDC63 IgG+ mem 68	3-23	3-3	2	4	AKDPYYDFWSGP	12	19	1	1	2	1	0	1	6	1	3	3
CVIDC63 IgG+ mem 69	3-23	1-26	3	4	AKDRIVGTIMGAWHY	15	9	0	1	1	0	1	0	1	0	1	4
CVIDC63 IgG+ mem 70	1-2	3-22	2	4	ATDHDSGYYFDY	12	22	1	0	4	0	1	1	2	0	11	2
CVIDC63 IgG+ mem 71	4-39	3-22	2	5	ARQSANYYDSGTHYILVDNWFDP	23	6	1	1	0	0	0	0	3	0	1	0
CVIDC63 IgG+ mem 72	3-7	3-16	1	4	ARDLYIGTYGGLGY	14	6	0	1	3	0	1	0	0	0	0	1
CVIDC63 IgG+ mem 75	1-8	1-14	1	4	ARGLPRTETWEPYYFDN	17	5	0	0	0	0	0	0	1	2	2	0
CVIDC63 IgG+ mem 81	3-7	2-21	2	4	ARLGGRCHQGRDCYPYYFDY	20	8	1	0	1	0	1	1	0	1	1	2
CVIDC63 IgG+ mem 82	1-46	6-19	2	6	ARDQKYSSGWYLEAIYYYYYYGLDV	25	4	0	0	1	0	0	0	1	0	1	1
CVIDC63 IgG+ mem 87	3-20	1-1	3	4	ARISLPTTAGAFDY	14	8	0	0	0	2	0	1	0	1	3	1
CVIDC63 IgG+ mem 88	1-2	3-10	2	4	ARPTNYYDTSGSLNY	15	15	2	1	0	1	2	0	1	0	5	3
CVIDC63 IgG+ mem 95	3-30	6-19	3	4	GKDLSGIAVAD	11	12	0	0	3	1	1	0	2	0	3	2

R, amino acid replacement mutation; S, silent mutation

Table E7: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDY37

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDY37 IgG+ mem 10	3-23	6-19	1	3	GQQWPFDFFFI	11	16	0	1	2	2	2	0	1	0	4	4
CVIDY37 IgG+ mem 11	4-59	/	/	5	WDRGCFDP	8	22	0	0	3	2	2	4	1	1	7	2
CVIDY37 IgG+ mem 12	3-23	2-21	2	5	DQFGCGRPTCYDGIPYYLGN	20	24	0	1	3	1	2	1	4	3	5	4
CVIDY37 IgG+ mem 13	4-31	/	/	6	DVGGPGTYKGDYYYYGMDV	19	17	0	1	2	0	1	1	1	1	7	3
CVIDY37 IgG+ mem 14	3-48	4-17	2	5	DPFSDDDGDYLEFNWFDS	18	14	0	0	2	2	2	0	1	2	3	2
CVIDY37 IgG+ mem 15	4-61	1-26	2	6	SGWHILVAGRSYNYYMDV	18	33	1	0	4	3	1	1	4	0	10	9
CVIDY37 IgG+ mem 16	4-59	3-22	2	4	TSYYDSISYYFDY	13	20	1	0	2	0	2	1	1	1	7	5
CVIDY37 IgG+ mem 18	3-30	5-5	3	4	GGGRGPMVLWTLDY	14	4	0	0	0	0	1	1	0	0	2	0
CVIDY37 IgG+ mem 21	3-11	3-3	2	4	EHYDLLSGYYSWVGGGLGNYLDY	23	9	0	1	0	0	2	1	1	0	3	1
CVIDY37 IgG+ mem 22	1-18	3-3	1	5	TPPRFFRWFDP	11	31	0	0	1	2	5	2	3	3	10	5
CVIDY37 IgG+ mem 23	3-21	3-10	2	3	EIGYFGSESYYSDAFDI	17	14	1	0	5	0	1	1	2	1	0	3
CVIDY37 IgG+ mem 26	3-21	3-10	2	4	DSVRGSGNYYHYY	13	14	1	0	5	0	1	1	2	1	0	3
CVIDY37 IgG+ mem 27	4-31	3-3	2	4	VGYDFWSGWATYADY	15	20	0	0	4	0	1	1	3	0	6	5
CVIDY37 IgG+ mem 28	3-30	6-19	2	4	ELSSGWFFDY	10	7	0	0	0	1	1	0	2	0	3	0
CVIDY37 IgG+ mem 29	3-30	1-20	3	4	DLPLWITGTTLPETFDC	17	23	0	0	0	3	2	0	3	0	7	8
CVIDY37 IgG+ mem 30	3-30	6-19	2	4	ELNNSGWFEEYFDA	14	16	0	0	1	0	0	1	2	0	7	5
CVIDY37 IgG+ mem 31	4-4	3-10	3	5	VLFGPGTLYRGLMRK	15	24	1	2	1	2	2	1	1	0	7	7
CVIDY37 IgG+ mem 35	1-69	6-19	3	4	SGAVAGRGLDY	11	17	0	1	1	0	2	1	4	1	5	2

R, amino acid replacement mutation; S, silent mutation

TableE8: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDC6

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDC6 IgG+ mem 03	3-31	2-15	3	5	RDPGVVAATR	10	8	0	1	3	0	1	0	1	0	1	1
CVIDC6 IgG+ mem 04	1-69	3-10	2	6	RVEGSGSYYSTPYYYGMDV	19	1	1	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 06	4-34	2-15	2	5	RGPGYCSGGNCYSGWFDP	18	6	1	0	1	0	1	0	0	0	1	2
CVIDC6 IgG+ mem 07	3-30	6-13	1	6	RDLELVPQGYGLDV	14	5	0	0	0	0	1	0	1	1	1	1
CVIDC6 IgG+ mem 08	3-48	6-19	2	4	RDRFGGWQRFDY	12	3	2	0	0	1	0	0	0	0	0	0
CVIDC6 IgG+ mem 11	4-34	3-3	3	6	RGAPVTIFGVDSYYYGMDV	19	3	1	0	1	0	1	0	0	0	0	0
CVIDC6 IgG+ mem 12	3-15	3-9	2	4	RDRFGGWQRFDY	12	7	0	0	0	2	0	1	0	0	3	1
CVIDC6 IgG+ mem 13	4-30	5-5	2	5	RGAPVTIFGVDSYYYGMD	18	12	0	1	1	0	1	1	0	0	5	3
CVIDC6 IgG+ mem 14	1-69	6-19	2	6	TPTEYSNRPGGYYYGMDV	18	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 15	3-7	/	/	4	RGGYRRGFDY	10	2	0	0	0	0	0	0	0	0	0	2
CVIDC6 IgG+ mem 18	1-2	3-22	2	6	RGGWDSSGYYLRAGRGMDV	19	2	1	0	0	0	0	0	0	0	1	0
CVIDC6 IgG+ mem 19	3-21	/	/	4	REDVGSFDY	9	6	2	1	0	0	1	1	0	0	1	0
CVIDC6 IgG+ mem 20	3-23	/	/	6	KLSLTSGSPYYYYGMDV	17	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 29	1-46	6-19	2	4	GAGSGGY	7	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 31	4-34	/	/	5	RGYPTYYNDTSG	12	10	0	1	1	1	0	1	0	0	4	2
CVIDC6 IgG+ mem 32	3-30	2-21	2	4	KDTVAYCGGDCYSGFDY	17	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 33	4-34	2-2	2	4	RGSCSSTSCYRVKVIVPFD	19	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 36	4-39	2-2	2	4	GGNCSSTTCYGYYGSGSYIAY	21	4	0	0	1	0	0	0	1	0	0	2
CVIDC6 IgG+ mem 38	1-3	7-27	1	4	RGGLLSKLGY	10	3	1	0	0	1	0	0	0	0	0	1
CVIDC6 IgG+ mem 40	3-64	6-19	2	4	KDIGWSMARFDY	12	8	2	0	0	0	0	0	3	0	2	1
CVIDC6 IgG+ mem 43	3-33	6-19	2	4	REGSGWYVDY	10	1	0	1	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 44	4-4	6-13	2	4	RAKYSSSWFDY	11	12	3	1	0	1	0	4	0	3	0	0
CVIDC6 IgG+ mem 45	4-39	1-26	3	4	RLQGATLFDY	10	8	0	0	1	0	1	0	0	0	3	3
CVIDC6 IgG+ mem 46	4-34	2-2	2	4	RDCSSTSCSRYYFDY	15	2	0	1	1	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 47	4-30	5-5	2	4	RSGYSYGLRSGYSYGL	16	8	2	0	1	0	0	0	1	0	3	1
CVIDC6 IgG+ mem 48	4-34	3-22	3	4	RGGHKRIVVAAAHRFDY	17	5	0	1	1	0	0	0	0	1	2	0
CVIDC6 IgG+ mem 49	4-30	3-22	2	4	RERHYDSSGYYFDY	14	6	1	1	1	0	0	0	1	0	1	1
CVIDC6 IgG+ mem 51	4-39	3-16	1	5	GCQTGWFGELLVSLAFDP	18	3	0	0	3	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 52	1-2	3-3	3	5	RAHPRITIFGVVISSLTP	18	1	0	0	0	0	0	0	0	0	1	0
CVIDC6 IgG+ mem 55	3-30	5-12	2	5	RVKQRGYDGPYAF	13	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 61	4-61	6-13	3	4	SSPRPGIAAAGTSLPVY	17	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 62	3-7	2-2	3	4	RDPSNLVPAATFDY	14	9	0	1	2	2	0	1	2	0	1	0
CVIDC6 IgG+ mem 63	4-34	5-24	2	4	RGSGDGYNSHLGY	13	3	0	1	0	0	0	0	0	0	1	1
CVIDC6 IgG+ mem 66	4-59	3-3	1	6	GGGRFLEWPYYYYGMDV	17	11	2	1	1	0	0	2	1	0	2	2
CVIDC6 IgG+ mem 67	4-34	6-19	3	4	RGLPVAGDY	9	5	0	1	0	0	0	0	1	0	0	3
CVIDC6 IgG+ mem 68	1-2	2-2	3	6	REGHIVIPAASSPYYYYYAMDV	22	3	0	0	0	0	0	0	1	0	1	1
CVIDC6 IgG+ mem 69	1-18	2-2	3	6	REMGIVVVPAATHRRHPPLNLETP	24	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 70	3-33	5-12	3	2	REATITITMSTQWYFDL	17	16	1	1	1	1	1	0	3	1	5	2
CVIDC6 IgG+ mem 76	4-34	7-27	3	4	RHRSTGEIYFDH	12	7	1	1	0	0	1	0	0	0	4	0
CVIDC6 IgG+ mem 77	1-2	3-3	3	5	RAHPRITIFGVVISSLTPAKNWFDP	25	1	0	0	0	0	0	0	0	0	1	0
CVIDC6 IgG+ mem 78	3-30	5-5	3	4	RVFGGTAMVTDLDY	14	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 81	4-4	1-26	3	4	RGGVRVGAGGFDY	13	5	3	0	0	0	0	0	1	1	0	0
CVIDC6 IgG+ mem 85	1-46	6-6	3	4	RLGGPIAARPQSDY	14	1	1	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 87	4-39	2-15	2	5	RLSGHCGGSCLNWFDP	16	6	0	0	0	0	0	0	1	0	3	2
CVIDC6 IgG+ mem 89	3-30	5-5	3	4	RVFGGTAMVTDLDY	14	0	0	0	0	0	0	0	0	0	0	0
CVIDC6 IgG+ mem 90	4-59	/	/	5	RVGGFDWFDP	10	8	1	0	0	1	2	0	1	0	0	3
CVIDC6 IgG+ mem 92	3-64	6-19	2	4	KPHSSGWYGAFDY	13	4	0	0	0	0	1	0	2	1	0	0
CVIDC6 IgG+ mem 96	4-31	/	/	3	RDPLGPDAFDI	11	0	0	0	0	0	0	0	0	0	0	0

R, amino acid replacement mutation; S, silent mutation

Table E9: IgH repertoire and VH mutations of IgG+ memory B cells from CVID292

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVID292 IgG+ mem 04	3-48	3-22	3	4	VSKDTTMMDDGFHI	14	19	0	0	5	2	2	2	0	2	1	5
CVID292 IgG+ mem 06	3-23	3-22	2	4	GDDSSGWGCFDY	12	17	2	0	1	0	1	1	3	1	4	4
CVID292 IgG+ mem 09	4-59	3-3	2	4	GLGTLYNSDFWSGDPGYFDY	20	15	2	1	4	0	0	2	1	1	3	1
CVID292 IgG+ mem 13	3-9	6-19	2	4	DQDSSGWGEFDY	12	3	0	0	0	0	0	0	0	0	2	1
CVID292 IgG+ mem 15	4-59	3-10	3	6	LLLVRGVIPYYYGMDN	16	21	2	0	0	0	1	2	3	2	6	5
CVID292 IgG+ mem 16	3-23	5-5	2	4	GYSYGYGWFDY	11	4	0	0	0	0	0	0	0	0	3	1
CVID292 IgG+ mem 17	3-30	6-6	2	4	SDSSSSSGSDY	11	2	0	0	0	0	1	0	0	0	0	1
CVID292 IgG+ mem 18	3-21	2-15	2	4	VPDCSGGSCYPRGYFDY	17	13	1	0	2	0	0	0	6	1	1	2
CVID292 IgG+ mem 19	4-4	/	/	5	VIRDSAVLEGLVGFDP	16	11	0	0	0	0	1	1	2	0	4	3
CVID292 IgG+ mem 20	3-49	5-5	2	6	DWHRYGYYHGMDV	13	11	0	0	1	2	1	1	3	2	1	0
CVID292 IgG+ mem 22	3-21	3-3	2	4	DAFNSAYNNFWSGYYENPFDY	21	8	1	0	2	0	0	0	1	0	2	2
CVID292 IgG+ mem 30	4-39	/	/	3	RLIVGDDAFDI	11	11	0	0	0	0	1	0	3	0	3	4
CVID292 IgG+ mem 33	4-39	5-5	2	2	GGYSYGKWYFDL	12	7	0	0	2	0	0	0	1	0	3	1
CVID292 IgG+ mem 34	4-34	1-1	2	6	ARYEASNYNYNGMNV	15	21	2	0	1	1	2	2	3	1	6	3
CVID292 IgG+ mem 35	4-59	3-9	2	2	LGLHDILTGYSFYWFFDL	18	22	1	0	3	0	4	2	2	1	6	3
CVID292 IgG+ mem 41	4-39	2-2	1	6	GPLTQQLPLLPLDDMDV	17	7	0	0	0	0	0	0	3	0	3	1
CVID292 IgG+ mem 42	1-69	4-17	2	4	TADYGDASCFDF	12	7	1	0	1	0	0	0	1	0	3	1
CVID292 IgG+ mem 44	4-34	/	/	6	VARYYYMDV	9	8	0	0	0	0	2	0	1	1	2	2
CVID292 IgG+ mem 45	3-15	5-12	2	4	VAYSGYD	8	12	0	0	1	0	2	0	2	1	5	1
CVID292 IgG+ mem 46	3-23	6-13	2	4	PHSGDTSSWFLFALDS	16	15	2	1	1	0	2	1	4	0	2	2
CVID292 IgG+ mem 47	3-15	3-16	2	4	DTVAARV	7	4	0	1	0	0	0	0	0	0	3	0
CVID292 IgG+ mem 49	4-59	5-5	2	4	LSRGYSANDPKSALDY	16	9	0	0	2	0	0	1	2	0	3	1
CVID292 IgG+ mem 50	4-59	6-13	2	5	LGSSTWHWFDP	11	12	1	0	1	0	1	0	2	0	4	3
CVID292 IgG+ mem 51	3-23	3-3	2	4	DVGGDFWSGPPLSDFDY	17	11	0	0	2	0	2	0	2	2	2	1
CVID292 IgG+ mem 52	3-21	6-19	2	4	GACGSGFDCSDY	12	12	0	1	3	0	2	0	1	1	2	2
CVID292 IgG+ mem 53	3-23	6-13	2	4	PHSGDTSSWFLFALDS	16	12	0	0	1	0	2	1	3	1	2	2
CVID292 IgG+ mem 55	3-23	2-8	2	3	VLVGSYVGSAFDI	13	1	0	0	0	0	0	0	1	0	0	0
CVID292 IgG+ mem 56	4-4	5-5	3	4	DRVDTKPPYYFDY	13	12	1	0	1	0	0	1	2	1	5	1
CVID292 IgG+ mem 58	4-4	/	/	5	ASFGILNP	8	10	1	0	0	2	1	1	1	1	2	1
CVID292 IgG+ mem 60	4-59	5-12	2	4	GPFHGYSGYTYFDS	14	8	0	0	2	0	0	0	2	1	3	0
CVID292 IgG+ mem 61	4-39	/	/	4	RFYITSSFDY	10	19	0	0	4	0	0	2	3	1	6	3
CVID292 IgG+ mem 62	4-59	5-5	2	4	LRGGYSYGYSLDY	13	6	0	0	2	2	0	1	1	0	0	0
CVID292 IgG+ mem 63	4-61	/	/	6	TPMGLTTVSRGLYDYYYYDV	20	15	0	0	0	0	2	1	0	2	6	4
CVID292 IgG+ mem 64	4-39	6-19	2	4	AGGTHSAGYSRGFDY	15	9	1	0	1	0	1	1	0	0	2	3
CVID292 IgG+ mem 66	4-59	4-17	3	5	QTTVTVDWFDP	11	0	0	0	0	0	0	0	0	0	0	0
CVID292 IgG+ mem 68	1-69	6-19	1	5	AVLRLWQWPLSAPFDP	16	18	2	1	1	2	2	1	1	1	4	3
CVID292 IgG+ mem 69	3-21	3-3	2	4	SGYHIFDS	8	11	1	0	1	3	0	1	0	1	2	2
CVID292 IgG+ mem 70	1-2	2-2	1	4	GTSQLLLFFDY	11	1	0	0	0	0	0	1	0	0	0	0
CVID292 IgG+ mem 71	1-18	/	/	5	VAAGDWFDP	9	4	1	0	1	0	1	0	0	0	1	0
CVID292 IgG+ mem 72	3-23	3-22	2	4	DEWGGRGSGYLFDH	14	13	1	0	1	0	1	0	4	1	3	2
CVID292 IgG+ mem 73	3-23	6-19	2	3	DHALYSSGWYSAFDI	15	2	0	0	0	0	2	0	0	0	0	0
CVID292 IgG+ mem 74	4-59	4-17	2	2	RGFGDYGDFYWYFDL	15	5	1	1	0	0	0	0	0	0	2	1
CVID292 IgG+ mem 75	4-39	5-24	2	4	DGVITSFDY	9	5	1	0	2	0	1	0	0	0	0	1

R, amino acid replacement mutation; S, silent mutation

Table E10: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDY28

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDY28 IgG+ mem 49	4-34	3-10	2	6	GFEVKYGSGSYYNSHYGLDV	20	12	1	0	1	0	1	0	2	1	4	2
CVIDY28 IgG+ mem 50	1-18	6-19	2	4	RSSSGNLDY	9	8	0	1	0	1	0	2	1	3	0	0
CVIDY28 IgG+ mem 51	4-59	3-3	2	4	HGGRNYDFWSGFLSAFDY	18	9	1	0	2	0	0	1	0	2	2	1
CVIDY28 IgG+ mem 53	3-9	6-19	2	1	GSDTGTYRTAEYFHH	15	1	0	0	0	0	1	0	0	0	0	0
CVIDY28 IgG+ mem 55	1-3	4-11	3	5	DRTTVTTINWFDP	13	1	0	0	0	0	0	0	0	0	1	0
CVIDY28 IgG+ mem 58	3-9	2-2	2	3	ATCSSTSCLPLDAFDI	16	8	0	2	0	1	0	0	1	0	3	1
CVIDY28 IgG+ mem 60	3-30	2-15	2	4	DGRKYCSGGGCYSPDY	16	5	0	0	1	0	1	0	0	0	0	3
CVIDY28 IgG+ mem 62	4-39	/	/	3	RKAGRTAFDI	10	4	1	0	0	0	2	0	0	0	1	0
CVIDY28 IgG+ mem 63	4-30	3-10	2	4	RRRGYYLPGFDY	12	3	0	0	0	0	0	0	0	0	3	0
CVIDY28 IgG+ mem 64	1-18	2-15	2	4	DRYCSGGTCYSSY	13	4	0	0	0	0	0	1	2	0	1	0
CVIDY28 IgG+ mem 70	3-11	3-10	3	5	DRGSIAVVRGVVIISTWFDP	20	12	0	0	1	1	3	0	5	0	1	1
CVIDY28 IgG+ mem 71	3-23	3-22	3	4	DHRRIVVSATVEYFDY	16	3	0	0	1	0	1	0	0	0	1	0
CVIDY28 IgG+ mem 74	4-31	5-12	1	4	EGNGYDYNPFDF	12	17	0	0	2	0	4	1	2	0	4	4
CVIDY28 IgG+ mem 78	3-30	/	/	6	NRDSWYTGSDSWGYYYYGMDV	21	10	0	0	1	0	1	0	1	2	1	4
CVIDY28 IgG+ mem 79	4-39	3-3	2	4	HALATSYDVWSGYLVDN	17	20	0	0	3	1	2	2	0	1	5	6
CVIDY28 IgG+ mem 81	3-15	3-3	1	4	VLRFFEWVRGGSDN	14	14	0	0	1	0	2	0	3	2	5	1
CVIDY28 IgG+ mem 82	4-59	5-12	2	4	ADSGYDGDFDY	11	16	0	1	1	0	2	1	6	0	4	1
CVIDY28 IgG+ mem 84	3-30	3-9	1	4	DRRRGYFDWLSIDY	14	3	0	0	0	0	0	0	1	0	1	1
CVIDY28 IgG+ mem 85	3-53	1-14	3	4	GITGNFDF	8	24	0	0	3	1	3	1	3	1	10	2
CVIDY28 IgG+ mem 88	4-31	/	/	4	EEAMTGDYFDY	11	1	0	0	0	0	0	0	0	0	0	1
CVIDY28 IgG+ mem 91	1-3	4-11	3	5	DRTTVTTINWFDP	13	0	0	0	0	0	0	0	0	0	0	0
CVIDY28 IgG+ mem 92	1-46	/	/	4	DAGMTGFGTIGLPDDY	16	9	1	0	0	2	0	0	1	0	2	3
CVIDY28 IgG+ mem 95	3-15	6-19	2	4	SGWTSKFDQ	9	4	1	1	0	0	0	0	0	0	1	1

R, amino acid replacement mutation; S, silent mutation

Table E11: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDY43

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDY43 IgG+ mem 01	3-21	3-22	/	6	DFHQWGTEFTLTVVAKRYYYYGMDV	25	12	0	0	2	1	1	1	3	2	2	0
CVIDY43 IgG+ mem 03	3-30	4-17	/	6	GFQYGDFVLWYYGVDV	16	3	0	0	0	0	0	0	1	0	2	0
CVIDY43 IgG+ mem 07	4-59	/	/	3	LSSSDAFDI	9	10	0	0	0	0	1	2	1	0	3	3
CVIDY43 IgG+ mem 10	1-69	3-22	/	4	DYHHYDNRGYSFLDY	15	10	0	0	3	1	1	0	2	0	1	2
CVIDY43 IgG+ mem 11	3-23	6-19	/	1	DVDDQWLRPEYFHH	14	15	2	0	1	1	3	0	1	0	3	4
CVIDY43 IgG+ mem 12	5-10	6-6	2	6	HRAPGSSSPYYYGMDV	16	1	0	0	1	0	0	0	0	0	0	0
CVIDY43 IgG+ mem 13	4-31	3-22	3	3	GDTMIVVADDAFDI	14	4	0	0	2	0	0	0	0	1	1	0
CVIDY43 IgG+ mem 14	4-34	3-10	2	1	GFDYYGSGTYYMRPWYFQY	19	19	1	2	0	1	1	3	3	0	4	4
CVIDY43 IgG+ mem 16	3-30	4-17	2	6	GRSPPHDSADYDSQNYYYGMDV	22	11	0	0	2	0	1	0	2	0	3	3
CVIDY43 IgG+ mem 17	3-30	2-21	2	4	DSRMWVNWSYCLGGVCYWDYFDY	23	5	0	0	1	0	0	0	2	0	1	1
CVIDY43 IgG+ mem 18	1-69	3-3	2	4	GSWYYDFWSGYSDAFDY	17	0	0	0	0	0	0	0	0	0	0	0
CVIDY43 IgG+ mem 20	3-30	3-3	1	6	ARLSTLLSPNYYYYGMDV	18	2	0	0	0	0	1	0	0	0	0	1
CVIDY43 IgG+ mem 21	3-23	3-3	3	6	VQGVTMIFGVVIISDYYYYGMDV	23	8	0	0	2	1	3	1	1	0	0	0
CVIDY43 IgG+ mem 22	4-34	6-13	1	6	DSREQQLVAGKHYDYYYGLDV	21	6	0	0	0	1	0	1	0	0	0	4
CVIDY43 IgG+ mem 23	4-39	/	/	5	VVESSSGLTGDWFDP	15	18	1	0	4	0	1	2	2	1	3	4
CVIDY43 IgG+ mem 24	4-59	/	/	6	LSGPLGTGDYYYGMDV	16	10	0	1	2	0	0	0	2	0	2	3
CVIDY43 IgG+ mem 25	3-7	6-19	2	4	VRGSGWYGDY	10	3	1	0	0	0	1	0	0	0	1	0
CVIDY43 IgG+ mem 27	1-69	2-2	2	6	TYCSHTSCGKYGLDV	15	11	0	0	3	0	0	1	1	0	3	3
CVIDY43 IgG+ mem 28	3-73	3-3	2	5	DLYDFLEAVAFDP	13	2	0	0	0	0	1	0	0	0	0	1
CVIDY43 IgG+ mem 29	1-3	6-19	2	4	VGSGWYQY	8	6	0	1	1	1	0	1	0	0	1	1
CVIDY43 IgG+ mem 30	3-23	2-2	2	4	RVYGCSNTSCSVGSFDY	17	7	0	1	1	0	2	1	0	0	1	1
CVIDY43 IgG+ mem 31	4-61	2-15	1	4	DLLPHMGLDY	10	9	0	0	4	0	1	1	0	0	1	2
CVIDY43 IgG+ mem 32	3-30	2-15	3	4	EVVAVWVFDY	10	9	0	0	2	0	1	3	1	0	1	1
CVIDY43 IgG+ mem 34	3-23	/	/	3	ENRIGDAFDI	10	25	1	0	6	0	0	1	6	4	5	2
CVIDY43 IgG+ mem 35	4-39	5-24	2	4	HRIGYNGYDY	10	4	0	1	1	0	1	0	0	0	1	0
CVIDY43 IgG+ mem 36	1-69	3-10	2	6	VITLEINYVRYYYAMDV	17	9	0	1	1	1	1	0	1	0	3	1
CVIDY43 IgG+ mem 39	1-69	/	/	4	GGRPNSPIYYFDYWGQGTLVTVSS	24	1	0	0	0	0	0	0	0	0	1	0
CVIDY43 IgG+ mem 40	1-3	6-13	3	4	SRAAALRPWDY	11	6	1	0	2	0	0	0	2	0	1	0
CVIDY43 IgG+ mem 41	4-39	2-15	2	4	ATPFHCSGGTCYDY	14	21	1	0	7	0	1	5	1	0	4	2
CVIDY43 IgG+ mem 42	1-2	/	/	5	VRQHLSNWFDP	11	7	0	1	0	0	1	2	0	0	2	1
CVIDY43 IgG+ mem 43	4-59	3-3	2	6	GTTKDYDFWSGYSSPYYYGMDV	22	12	0	0	0	1	1	1	2	1	3	3
CVIDY43 IgG+ mem 44	3-48	3-10	3	4	DDSLIQGVRY	10	3	1	0	0	0	0	0	1	0	1	0
CVIDY43 IgG+ mem 45	1-69	2-8	2	2	HYPPDSRYCTSGASCQNRYFHL	22	7	0	0	1	0	0	0	0	1	4	1
CVIDY43 IgG+ mem 46	3-30	2-15	2	5	GEGNYFDGSGTHF	13	14	0	0	1	0	2	0	2	1	7	1
CVIDY43 IgG+ mem 47	4-34	2-15	3	6	GRMPTGIVVVVAALRNYGVGMDV	23	14	1	0	4	2	0	0	0	0	4	3

R, amino acid replacement mutation; S, silent mutation

Table E12: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDY45

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVID Y45 IgG+ mem 03	1-69	2-2	2	6	EFYSLGYCSSSSCRPGYGMDV	21	3	0	0	1	0	0	0	0	0	1	1
CVID Y45 IgG+ mem 05	3-30	2-21	2	4	VNCGGDCYSRDYFDY	15	2	0	0	0	0	0	0	0	0	0	2
CVID Y45 IgG+ mem 06	3-64D	5-24	1	4	HERWLQLGAY	10	5	0	0	0	0	2	0	2	0	0	1
CVID Y45 IgG+ mem 09	4-59	3-22	2	4	SRGYDGSVFDY	11	5	0	0	1	1	2	0	0	0	1	0
CVID Y45 IgG+ mem 11	1-69	3-22	2	3	EGGHYYGRSGYSAFDI	16	11	2	0	1	1	0	0	0	0	2	5
CVID Y45 IgG+ mem 13	4-30	2-8	2	4	ALRYCTNDVCFGYFDY	16	6	0	0	1	0	1	3	0	1	0	0
CVID Y45 IgG+ mem 15	3-30-3	5-12	/	4	GLWTIDY	7	4	0	0	1	0	1	0	0	0	1	1
CVID Y45 IgG+ mem 16	4-39	6-19	2	4	HDMVGSGWESRFDY	14	8	1	0	1	1	0	0	1	0	3	1
CVID Y45 IgG+ mem 17	3-53	3-22	2	4	EGLDSSGYHYFDY	13	2	0	0	0	0	0	0	1	0	0	1
CVID Y45 IgG+ mem 19	4-59	4-23	2	4	GDWTYGGLFDY	11	4	0	0	2	0	0	2	0	0	0	0
CVID Y45 IgG+ mem 20	4-59	2-21	2	4	APQAYCGGDCYYFDY	15	1	0	0	1	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 21	1-69	2-15	3	5	CIALAATPFES	11	5	0	0	0	0	0	0	1	0	1	3
CVID Y45 IgG+ mem 22	1-18	4-11	3	5	DSTVTPVDNWFDP	13	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 26	1-18	2-2	2	1	SSSRHCSSTSCYANEYFQH	19	1	0	0	0	0	0	0	0	0	0	1
CVID Y45 IgG+ mem 29	4-39	6-6	3	4	HIAADYFDY	9	1	1	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 31	4-4	6-19	/	4	EGSGANPRFDF	11	4	0	0	0	0	0	0	0	0	3	1
CVID Y45 IgG+ mem 33	1-69	3-3	3	3	ALRITIFGVVRQKSAFDI	18	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 35	4-30-4	3-9	2	4	VAPFHYDILKESGNLIFDY	19	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 36	3-64D	6-19	3	4	GIAVSGSPTTRHPPGDY	17	1	0	0	0	0	0	0	1	0	0	0
CVID Y45 IgG+ mem 37	4-61	3-3	2	4	GEADYDFWSGYFSPRGGAFDY	21	2	0	0	0	0	1	0	0	1	0	0
CVID Y45 IgG+ mem 38	4-59	2-2	/	6	EVIGYSAASGDFSFYYGMDV	20	14	1	1	3	0	0	2	0	1	5	1
CVID Y45 IgG+ mem 40	4-34	6-19	1	4	GWSEQWLIWSDYFDY	15	11	0	0	2	1	1	1	1	0	4	1
CVID Y45 IgG+ mem 45	3-30-3	3-22	3	6	DESIVVVLKYYGMDV	15	2	0	0	0	0	1	0	0	0	1	0
CVID Y45 IgG+ mem 46	3-21	3-3	/	6	DQSSPGFFYYYGMDV	15	4	0	0	2	0	0	0	0	0	2	0
CVID Y45 IgG+ mem 48	4-34	5-12	/	2	GPRYERPTWYFDL	13	6	0	0	1	0	0	1	0	0	2	2
CVID Y45 IgG+ mem 50	1-69	3-3	2	6	GSRGFWSSYYPLYYYYDMDV	20	3	1	0	0	0	0	0	1	0	0	1
CVID Y45 IgG+ mem 51	1-69	3-3	3	3	ALRITIFGVVRQKSAFDI	18	1	1	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 52	4-34	4-23	3	1	GCGVTPCHFQH	11	3	0	0	1	0	0	0	1	0	1	0
CVID Y45 IgG+ mem 54	1-69	2-21	3	6	DLVVTATYGMDV	12	9	1	0	2	0	0	0	1	0	4	1
CVID Y45 IgG+ mem 55	1-69	3-3	3	3	GLRITIFGVVRQKSAFDI	18	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 56	4-59	5-12	1	4	DKGDRWLRFFDY	12	4	0	0	2	0	1	0	0	0	0	1
CVID Y45 IgG+ mem 57	3-30-3	5-24	/	4	DDGGSGGWVGSPFDY	15	6	0	0	2	0	2	0	0	0	2	0
CVID Y45 IgG+ mem 60	3-21	2-2	2	4	RRDPGYCSSTSCYVFDY	17	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 61	4-34	1-7	/	5	GWNHWFDP	8	5	0	0	1	0	0	0	0	0	2	2
CVID Y45 IgG+ mem 62	3-23	4-17	2	4	DPGNYGALPPHFDY	14	7	1	0	0	1	1	0	1	0	2	1
CVID Y45 IgG+ mem 64	1-46	5-12	/	6	DLYSLVLGHYYYYAPDV	17	12	1	2	1	1	1	0	0	2	2	2
CVID Y45 IgG+ mem 66	4-39	6-6	2	6	TYSSLPHGMDV	11	3	3	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 67	3-21	6-13	2	4	EGDSSSWPPPPWY	13	0	0	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 69	3-23	4-23	3	5	IPFPTVVANHMYNWFDP	17	3	0	0	0	0	1	1	1	0	0	0
CVID Y45 IgG+ mem 70	4-30-2	6-13		4	GLGHFDY	7	12	5	0	1	0	1	1	0	0	3	1
CVID Y45 IgG+ mem 71	3-21	1-26	3	6	AVGATEEVKKYYYGMDV	17	1	0	0	0	0	1	0	0	0	0	0
CVID Y45 IgG+ mem 72	1-69	3-22	2	6	EGATYYYDSSGYLASVYYGMDV	22	6	2	0	1	0	0	0	0	0	3	0
CVID Y45 IgG+ mem 77	4-34	1-7	/	5	ISERAAELTHSGWGFDP	17	9	0	0	0	0	1	1	0	0	5	2
CVID Y45 IgG+ mem 78	3-15	3-9	1	4	VVRYFDLGAPYFDY	14	1	0	0	1	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 84	1-18	6-6	1	4	DVELVRAPIFDY	12	5	0	0	1	2	0	0	0	0	1	1
CVID Y45 IgG+ mem 86	3-23	6-19	/	4	WPGWLEYFDF	10	8	0	0	0	0	2	0	2	0	2	2
CVID Y45 IgG+ mem 90	1-69	6-19	1	5	DRSRQWPDWFDP	12	1	1	0	0	0	0	0	0	0	0	0
CVID Y45 IgG+ mem 91	1-69	3-16	1	4	GMDLGELSLGDY	12	5	2	1	0	0	0	0	0	0	2	0
CVID Y45 IgG+ mem 92	3-33	3-10	2	4	DIPLKGLSGSVDY	13	5	0	0	1	0	1	0	0	1	1	1
CVID Y45 IgG+ mem 94	1-69	3-10	2	4	GYYGSGSYGSFDY	13	12	2	0	1	0	2	0	2	0	3	2

R, amino acid replacement mutation; S, silent mutation

Table E13: IgH repertoire and VH mutations of IgG+ memory B cells from CVIDMS1

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
CVIDMS1 IgG+ mem 02	1-3	4-11	3	5	DRTTVTTINWFDP	13	2	1	0	1	0	0	0	0	0	0	0
CVIDMS1 IgG+ mem 05	3-30-3	3-22	2	4	DLDRTAGYYDSSGYYRNVGY	20	4	0	0	0	0	1	0	1	1	1	0
CVIDMS1 IgG+ mem 08	3-33	3-22	2	5	DLNYDSEPPIN	11	4	0	0	1	0	1	0	0	0	1	1
CVIDMS1 IgG+ mem 09	4-30-4	2-15	2	5	GPKTYCSGGSCYFGWFDP	18	3	0	0	1	0	0	0	0	0	1	1
CVIDMS1 IgG+ mem 10	1-18	2-15	2	4	GPADCSRGACYFTSYFDY	18	12	0	0	1	1	2	0	5	1	0	2
CVIDMS1 IgG+ mem 11	3-66	2-21	2	4	IRGGGGDCYRCFDY	14	1	0	0	0	0	0	1	0	0	0	0
CVIDMS1 IgG+ mem 16	3-23	3-10	2	4	VGYIGNDPQLYYFDY	15	17	1	0	1	4	3	1	2	1	1	3
CVIDMS1 IgG+ mem 17	3-33	6-19	2	4	DLSSGWYIDY	10	5	0	0	1	1	0	0	0	0	2	1
CVIDMS1 IgG+ mem 18	3-15	3-16	3	4	SLRMITFGGLIVPPFDY	17	10	0	0	2	0	1	1	2	0	1	3
CVIDMS1 IgG+ mem 19	3-23	3-22	2	4	WRTDYDSAGYYGDYFDY	17	17	1	0	2	1	2	1	0	2	3	5
CVIDMS1 IgG+ mem 27	3-33	1-7	1	6	VPGLWELSEKYMDV	14	7	0	0	0	0	1	0	2	0	3	1
CVIDMS1 IgG+ mem 28	3-23	3-22	2	4	DRNEYDFDSSGYISAADY	18	7	0	0	1	0	2	0	1	0	2	1
CVIDMS1 IgG+ mem 32	3-30-3	1-26	3	4	CRAKTRVGADRFDY	14	4	0	0	0	0	0	0	1	1	1	1
CVIDMS1 IgG+ mem 33	4-61	3-3	2	2	GHYDADYYGMDV	12	3	0	0	0	1	0	0	1	0	0	1
CVIDMS1 IgG+ mem 34	4-59	/	/	5	HGTFEGWFDP	10	9	1	0	0	2	0	0	1	0	2	3
CVIDMS1 IgG+ mem 35	3-73	/	/	6	QREDDAGYYYYYMDV	15	11	0	0	0	0	1	0	3	1	4	2
CVIDMS1 IgG+ mem 39	3-15	6-19	2	4	ERYSSELDY	9	7	0	0	2	0	1	0	0	1	1	2
CVIDMS1 IgG+ mem 42	4-61	3-22	2	2	GSRVDHYDSSGYQKDWYFDL	20	9	0	0	1	0	0	0	3	1	2	2
CVIDMS1 IgG+ mem 43	4-59	2-8	2	3	SPEYGVPFGAFDI	13	10	0	0	3	0	0	0	1	0	6	0
CVIDMS1 IgG+ mem 45	3-23	/	/	4	GYFDSLDGKYFSY	13	8	0	0	1	0	1	0	3	0	2	1
CVIDMS1 IgG+ mem 46	4-39	3-3	3	6	QETTIFGVVITHTHYYYGMDV	21	4	0	0	2	0	0	0	0	0	2	0
CVIDMS1 IgG+ mem 51	3-30	3-3	2	4	IREGGYDFWSGIDY	14	2	0	0	0	0	0	0	1	0	1	0
CVIDMS1 IgG+ mem 54	3-15	3-3	2	4	GDFWSGNYRNFDH	13	9	1	1	0	0	0	1	1	0	3	2
CVIDMS1 IgG+ mem 55	3-15	6-19	3	4	DGIEVAGNGVGFDY	14	15	0	0	2	0	0	3	2	0	6	2
CVIDMS1 IgG+ mem 58	1-18	3-22	2	4	VSDRYYDTSVYYWAGDY	17	2	0	0	1	0	0	0	0	0	0	1
CVIDMS1 IgG+ mem 59	3-33	6-19	2	4	DAEAYISGWYGNFDY	15	5	0	0	1	0	1	0	1	0	1	1
CVIDMS1 IgG+ mem 60	4-59	3-16	3	4	FTFGEMWYDY	10	10	1	0	2	0	0	1	0	0	3	3
CVIDMS1 IgG+ mem 61	4-59	3-10	1	6	HQLWPRYYYYYYMDV	15	4	0	0	1	0	1	0	2	0	0	0
CVIDMS1 IgG+ mem 62	3-49	5-12	2	4	GGGYGSFDWEVDF	13	14	1	1	0	0	1	2	3	1	4	1
CVIDMS1 IgG+ mem 63	4-61	5-12	2	6	GLYSGYDWPPTVGMDV	16	1	0	0	0	0	0	0	0	0	0	1
CVIDMS1 IgG+ mem 64	3-33	6-19	2	3	DRHSSGWDAFDI	12	5	0	0	2	0	0	0	1	0	1	1
CVIDMS1 IgG+ mem 65	3-23	3-22	2	5	PYYYDSSDYYNGY	13	13	0	0	3	0	1	2	2	0	2	3
CVIDMS1 IgG+ mem 67	3-53	2-21	3	4	QVHIPMVTGFDF	12	29	1	1	1	2	4	1	2	2	8	7
CVIDMS1 IgG+ mem 74	4-61	6-19	/	5	EGRVFSSGGGQGA	13	20	0	0	2	1	2	2	3	0	6	4
CVIDMS1 IgG+ mem 75	3-73	3-22	2	5	RLYSYDSGGYRGDWFDP	17	9	0	0	1	2	2	0	0	0	2	2
CVIDMS1 IgG+ mem 79	4-39	3-10	2	5	SNYFASGNFRPFDP	14	16	0	0	4	1	1	0	3	2	3	2
CVIDMS1 IgG+ mem 80	3-23	3-22	2	6	GKESSTSWDPFFAYYYMDV	19	10	0	0	0	1	2	1	1	1	1	3
CVIDMS1 IgG+ mem 83	4-34	6-13	1	4	VGEQLGVDH	9	5	0	0	0	0	1	0	1	0	1	2
CVIDMS1 IgG+ mem 84	3-53	4-17	3	4	QVHTPTVTGFDY	12	24	1	0	3	1	3	2	2	1	7	4
CVIDMS1 IgG+ mem 85	4-4	3-9	/	4	AGGYFLSRRGTPFDY	15	24	1	0	1	1	1	3	3	1	7	6
CVIDMS1 IgG+ mem 90	3-30-3	3-16	1	6	TTLGGGYDYSYYYMDV	16	10	0	0	0	1	0	0	1	1	4	3
CVIDMS1 IgG+ mem 94	3-30	6-13	3	6	DRGAAAGTGDGMDV	14	6	0	0	0	0	1	0	0	0	2	3
CVIDMS1 IgG+ mem 95	4-31	5-24	2	4	VGWDGYNSGHFDY	13	1	0	0	1	0	0	0	0	0	0	0

R, amino acid replacement mutation; S, silent mutation

Table E14: IgH repertoire and VH mutations of IgG+ memory B cells from HD36

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
HD36 IgG+ mem 01	4-59	3-22	2	4	ETNNYGYYYFDY	12	9	1	0	1	0	0	1	1	1	4	0
HD36 IgG+ mem 06	4-59	5-12	2	4	NRETGYDELDY	11	19	2	2	1	0	1	1	2	1	7	2
HD36 IgG+ mem 09	4-34	2-15	2	6	GGRFCDGGRCYSRFYYPAMDV	21	29	3	1	7	2	1	2	2	0	7	4
HD36 IgG+ mem 13	3-30-3	6-13	3	1	LAAAGNFQE	9	4	0	0	1	1	1	0	0	0	0	1
HD36 IgG+ mem 15	3-9	1-7	3	6	SVTGAQKGDYYGMDV	15	4	0	0	0	0	1	0	0	0	2	1
HD36 IgG+ mem 17	1-2	/	/	4	VFERSFILGVDY	12	31	2	0	5	1	4	1	5	1	10	2
HD36 IgG+ mem 18	3-7	4-17	2	4	ARLGGGDYADRYFDN	15	22	2	0	2	1	2	0	5	0	8	2
HD36 IgG+ mem 20	3-48	3-10	2	4	SGSGSFVF	8	16	0	1	3	0	2	0	2	1	5	2
HD36 IgG+ mem 21	3-30-3	2-15	2	5	DGCSGFSCNVLGFDL	15	27	2	1	3	0	4	1	4	1	7	4
HD36 IgG+ mem 23	3-11	5-12	2	6	DSGGYDFASYYYYGVDV	17	14	0	0	0	0	1	0	5	0	5	3
HD36 IgG+ mem 24	3-23	3-16	2	6	DVWDDYFWGSYRYTDYYGLDV	21	26	0	0	2	1	3	0	5	3	7	5
HD36 IgG+ mem 26	3-23	3-10	1	3	DLETLWFGRRGAFDI	15	14	1	2	0	0	2	1	3	1	2	2
HD36 IgG+ mem 28	3-33	/	/	3	SVYGRDGLGDAFDV	14	20	2	0	1	3	1	0	3	3	4	3
HD36 IgG+ mem 30	3-23	3-10	1	6	DLWLNSAAGPMDV	13	9	0	0	1	0	2	1	1	0	4	0
HD36 IgG+ mem 31	4-59	3-10	2	5	SDDYGSGSRPFDP	13	14	0	0	4	1	1	1	0	0	3	4
HD36 IgG+ mem 32	3-33	3-3	2	4	DEGRSGSDY	9	10	0	1	2	0	0	0	0	0	6	1
HD36 IgG+ mem 33	4-31	4-23	2	4	DDGGNGDRYFDY	12	54	5	5	4	4	6	1	3	1	16	9
HD36 IgG+ mem 37	4-59	1-7	2	5	HRENYPHLADL	11	24	0	0	3	1	4	5	3	1	5	2
HD36 IgG+ mem 39	1-8	3-3	2	4	GGYTLFDF	8	32	3	0	1	1	4	2	5	3	9	4
HD36 IgG+ mem 40	1-18	6-19	2	4	DRGVYSSSWYDY	12	19	0	0	1	2	1	2	3	1	6	3
HD36 IgG+ mem 42	3-30-3	2-2	2	6	GGYCSSTSCSSYYHYGLDV	19	13	3	0	4	0	3	0	0	0	1	2
HD36 IgG+ mem 43	3-15	/	/	6	PDV	3	5	1	0	1	0	0	0	1	0	2	0
HD36 IgG+ mem 46	4-59	6-19	3	6	SLDVAVAPVPYYYGMDV	17	21	2	0	2	1	0	0	3	1	8	4

R, amino acid replacement mutation; S, silent mutation

Table E15: IgH repertoire and VH mutations of IgG+ memory B cells from HD37

								FWR1		CDR1		FWR2		CDR2		FWR3	
	VH	D	RF	JH	CDR3 (aa)	Length	VH Mutations	R	S	R	S	R	S	R	S	R	S
HD37 IgG+ mem 50	4-31	3-10	2	6	GITMVRGVITYYYYGLDV	18	13	0	0	3	0	4	0	1	0	4	1
HD37 IgG+ mem 51	3-23	5-24	1	4	WEKRWMMHDLGY	12	27	0	1	1	1	1	2	3	1	10	7
HD37 IgG+ mem 53	4-61	5-5	3	4	DTSMVTGYFDF	11	33	2	1	5	1	2	3	2	1	7	9
HD37 IgG+ mem 56	3-74	3-10	2	4	RASGSSDSCCKFDY	14	8	0	0	2	0	0	0	1	2	2	1
HD37 IgG+ mem 60	3-13	3-9	1	5	GTHVGWAGLHFDS	13	15	0	0	0	2	1	0	2	0	7	3
HD37 IgG+ mem 61	3-7	2-15	3	5	DRGGVDSAATPNWFDP	16	22	2	1	4	0	0	2	2	0	7	4
HD37 IgG+ mem 62	3-7	6-19	2	4	EVPLHSLSGWYFDY	14	11	0	0	1	0	0	1	1	0	5	3
HD37 IgG+ mem 63	3-30	4-17	2	4	EGPPYGDYVDFFDY	14	31	0	0	3	3	1	1	6	0	10	7
HD37 IgG+ mem 64	3-30	5-24	2	4	SSRDGYNPKY	10	0	0	0	0	0	0	0	0	0	0	0
HD37 IgG+ mem 65	3-73	/	/	6	HGVREEAQAQLYYYGMDV	18	43	1	3	5	4	4	1	6	1	7	11
HD37 IgG+ mem 67	4-59	/	/	3	EEQSLGTFDI	10	20	0	0	3	0	2	0	1	0	12	2
HD37 IgG+ mem 69	5-51	/	/	3	HPNSLDMGTEI	11	14	0	0	3	1	1	1	1	1	5	1
HD37 IgG+ mem 72	3-23	2-21	3	5	DVTVMLTADSFDP	13	13	0	0	0	0	2	1	2	2	4	2
HD37 IgG+ mem 73	3-13	1-26	3	6	GATIVNFYYFYGMDV	15	15	0	0	1	1	1	2	2	1	5	2
HD37 IgG+ mem 77	3-23	2-21	2	3	GAPCGGDCTSFDI	13	30	3	1	5	0	3	1	3	3	10	1
HD37 IgG+ mem 80	1-8	6-6	2	5	GQFLASSLLSP	11	37	2	1	6	2	2	1	2	1	14	6
HD37 IgG+ mem 85	1-2	3-10	2	3	VRSSRGSGTYFPNDSFDL	18	32	2	2	4	0	5	2	0	0	11	6
HD37 IgG+ mem 87	4-34	1-26	3	6	GRVGSIEYSITYYYYYGMDV	20	31	2	2	2	0	1	3	2	1	14	4
HD37 IgG+ mem 88	4-4	/	/	4	EGPNRATRELDH	12	18	0	1	3	0	2	0	4	0	4	4
HD37 IgG+ mem 90	4-59	1-26	2	4	GPYGGTYYDVASHGGFDF	18	33	1	0	3	2	1	2	4	1	9	10
HD37 IgG+ mem 91	1-46	/	/	4	GFYGYDS	7	23	0	1	4	0	1	2	3	3	6	3
HD37 IgG+ mem 94	4-39	/	/	6	TSWFSRVLDHYALDV	15	32	0	0	7	0	4	0	3	1	10	7
HD37 IgG+ mem 96	3-30	2-2	2	4	DQAPYPYCSRTSCYGGGFDY	20	4	0	0	0	0	1	0	2	0	0	1

R, amino acid replacement mutation; S, silent mutation