

## Supplemental Tables

**Supplemental Table 1: Single cell PCR efficiency.**

	MG-AChR-1		MG-AChR-2		MG-AChR-3		MG-MuSK-1		MG-MuSK-2		HD-1		HD-2	
	10+	10-	10+	10-	10+	10-	10+	10-	10+	10-	10+	10-	10+	10-
<b>Sorted cells</b>	96	96	96	96	96	96	48	48	48	48	144	304	96	144
<b>Amplified VH</b>	80	50	67	54	54	43	40	41	34	37	46	79	56	42
<b>Amplified VL</b>	65	57	99	88	67	52	39	36	36	37	43	45	47	33
<b>Sequenced VH</b>	39	29	55	39	47	38	24	27	24	27	18	21	31	21
<b>Sequenced VL</b>	32	26	48	35	41	33	19	22	19	22	18	21	31	21

New emigrant B cells are identified as 10+, referring to their expression of CD10. Mature naive B cells are identified as 10-, referring to their lack of CD10 expression. Amplified VH and VL refer to the quantity of single sorted cells for which a detectable (by gel electrophoresis) VH or VL PCR product was generated (The VL count includes both kappa and lambda for instances for which both products were found). Sequenced VH and VL refer to the number of PCR amplified VH and VLs for which complete sequences were generated. For MG-AChR-3, HD-1 and HD-2 only the light chains that had a successfully amplified matching heavy chain were subsequently amplified and sequenced. All matched VH and VLs were selected for expression of recombinant IgG. Sequence data that revealed stop codons, reading frame shifts or harbored greater than 3 replacement mutations or a single replacement mutation in the CDR3 were discarded from the recombinant IgG expression pipeline. B cells that yielded both a kappa and lambda light chain were both expressed, and then tested on the ELISAs (these clones are indicated on Supplemental Table 2 *below*).

## Supplemental Table 2: Sequence and reactivity tables for the MG and HD study subjects.

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject MG-AChR-1

Ig	HEAVY					MG-AChR-1, 10+				LIGHT					Reactivity
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vκ	Jκ	CDR3(aa)	Length	Mutations	Poly
H2	3-48	3-22	2	5	3	CARDSYDSSGGYGFYNWFDPW	1	21	0	1-12	4	CQQANSFPFTF	11	0	-
H8	3-23	1-26	3	6	2	CAKGPESGSFPYYYYGMDVW	1	21	0	2-28	1	CMQALQTPRTF	11	0	+
H9	3-21	6-6	2	4	2	CARDIAARYFDYW	2	13	0	1-9	3	CQQLNSYPRFTF	12	0	-
H18	3-33	2-15	2	5	1	CARRGGYCSGGSCNHLPEW	3	19	0	1-12	4	CQQANSFPHTF	11	0	-
H19	3-30	5-12	2	4	3	CARDADSPRGYFDYW	2	15	0	3-11	4	CQQRSNWPQLTF	12	0	-
H20	3-33	6-13	1	6	4	CARDLSPEQYSSSWARDKYYYYGMDVW	3	27	0	1-39	4	CQQSYSTPLTF	11	0	-
H23	3-7	3-22	2	4	1	CARMVTGSSGYTAPKDYW	2	19	0	3-11	4	CQQRSNWPRELTF	13	0	-
H30	3-66	4-11	2	5	4	CARDQHDYSNYDAPRSRWFDPW	4	22	0	3-15	2	CQQYNNWPRTF	11	0	-
H39	4-61	2-15	2	4	3	CARGRPASVVGYSGGSCYPHEDYFDYW	3	28	0	1-9	3	CQQLNSYPRFTF	12	0	-
H43	4-59	4-17	2	3	5	CAREGGDYVDDAFDIW	1	16	0	3-20	3	CQQYGSSPFTF	11	0	-
H50	3-66	3-22	2	4	2	CARCACGYYSQNYFDYW	1	18	0	3-11	2	CQQRSNHTF	9	0	+
H53	3-30	2-8	2	4	3	CARDADSPRGYFDYW	2	15	0	3-20	2	CQQYGSSHELYTF	13	0	-
H59	3-30	5-5	1	6	2	CAKADTAMGNWRTSMDVW	2	18	0	1-5	2	CQQYNSYSYTF	11	0	-
H70	3-66	2-8	2	1	0	CARVGYPHPW	2	11	0	1-5	1	CQQLNSYPYTF	11	0	+
H86	3-21	2-15	2	4	1	CARGSAGGYFDYW	1	13	0	3-20	3	CQQYGSSPIFTF	12	0	-
H96	3-7	2-2	2	5	1	CARVKGLGYCSSTSCYTTGYNWFDPW	2	26	0	1-8	1	CQQYYSYPPTF	11	0	+

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vλ	Jλ	CDR3(aa)	Length	Mutations	Poly
H5	4-30	2-15	2	5	2	CARDAYCSGGSCYSGNWFDPW	1	21	0	2-23	1	CCSYAGSYVF	10	0	-
H33	3-30	3-16	3	4	1	CAKPRIMITFGGAYYFDYW	2	19	0	2-14	1	CSSYTSSSTLIF	12	0	-
H49	3-15	3-10	3	5	1	CATGGGVFRFDPW	1	13	0	3-25	2	CQSADSSGTYYVF	13	0	-
H55	1-18	3-10	2	4	1	CARRSPYYGSGSFDYW	2	17	0	2-14	2	CSSYTSSSTLGYVVF	15	0	+
H57	3-30	5-12	2	4	3	CAKDADSPRGYFDYW	2	15	0	2-14	2	CSSYTSSSTLLF	12	0	+
H58	1-2	3-10	3	4	2	CARGPRDRGDYW	3	12	0	2-14	2	CSSYTSSSTPVVF	13	0	+
H61	4-30	4-17	3	4	1	CALSAGGMTTIVDYW	0	15	0	3-1	2	CQAWDSSVVF	10	0	+
H63	3-33	4-17	2	4	4	CARECWAGDGDYACIDYW	1	18	0	2-14	2	CSSYTSSSTLVF	12	0	-
H67	3-30	5-12	3	4	3	CAKDRHSGYDHYKYYFDYW	5	18	1s CDR2	2-11	2	CCSYAGSYTLVF	12	0	-

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s : silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject MG-AChR-1

Ig	HEAVY					MG-AChR-1, 10-				LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vκ	Jκ	CDR3(aa)	Length	Mutations	Poly	Hep2
H60	3-74	6-19	1	6	1	CASGYSSGWPNNYYYYGMDVW	0	21	0	1-39	1	CQQSYSTPRTF	11	0	+	+
H62	3-30	3-10	2	5	1	CAGSVRGPNSKGGWFDPW	2	18	0	1-39	3	CQQSYSTPLFTF	12	0	+	+
H6	3-30	3-22	2	3	4	CAKVLMEVIGYYDSSGYPDAFDIW	1	24	0	1-39	4	CQQSYSTPLTF	11	0	-	+
H19	3-23	3-3	3	4	1	CAKVRRGQRAIFGVGKYYFDYW	5	22	0	1-5	1	CQQYNSYSHTF	11	0	+	+
H22	3-7	3-9	3	4	1	CAGSSGLVSFDYW	0	13	0	1-39	3	CQQSYSTPFTF	11	0	-	-
H30	3-53	3-3	2	6	3	CARDRYDFWSGLVGMVDVW	2	18	0	1-39	2	CQQSYSTPPNTF	12	0	-	+
H32	3-53	6-13	2	4	1	CARVYGRGAAAGTIDYW	2	17	0	3-15	1	CQQYNNWPWTF	11	0	-	+
H45	3-23	1-20	2	6	4	CAKQDMEGNQMDVW	1	15	0	1D-8	4	CQQYYSFPLTF	11	0	-	-

	Vλ	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vλ	Jλ	CDR3(aa)	Length	Mutations	Poly	HeP2
H69	3-53	6-13	2	4	1	CARGGPTSGIAAVDYW	1	16	0	2-14	2	CSSYTSSSTLVF	12	0	+	+
H71	5-51	5-5	3	4	1	CARANGGYSYGWPYYFDYW	1	19	0	2-14	7	CSSYTSSSTAVF	12	0	-	+
H87	3-15	3-22	2	1	2	CTTDQWPTYYYDSSGFQHW	1	19	0	3-21	3	CQVWDSSTPSWVF	14	0	-	-
H89	3-48	3-22	2	4	1	CARGQGSYSSASSAVDYW	1	20	0	3-1	2	CQAWDSSTVVF	11	0	-	-
H5	4-31	2-21	2	1	2	CARILAYCGGDCHEYFQHW	3	19	0	1-40	3	CQSYDSSLGGSVF	13	0	-	-
H12	4-31	2-15	2	4	1	CARWGYCSGGSCRGDYW	2	17	0	1-36	2	CAAWDDSLNGVVF	13	0	-	-
H14	4-31	3-22	2	6	2	CARGYDSSGYSSYYGMDVW	1	19	0	2-23	1	CCSYAGSSTFNYYVF	14	0	-	-
H27	4-30	3-22	3	4	5	CARAYRSPWDYYDSSGYDDGFDYW	2	26	0	1-44	3	CAAWDDSLNGPVF	13	0	-	-
H39	3-30	2-2	2	6	1	CAKPAQYCSSTSCYHLKPYYYGMDVW	3	27	0	2-14	2	CSSYTSSSTKVF	12	0	+	+

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s : silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject MG-AChR-2

Ig	HEAVY					MG-AChR-2, 10+					LIGHT					Reactivity
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vκ	Jκ	CDR3(aa)	Length	Mutations	Poly	
H4	1-18	1-26	3	6	0	CARSYSGPYGMDVW	0	10	0	1-39	1	CQQSYSTPRTF	9	0	-	
H7	4-59	2-2	2	5	1	CARGGSSTSCYHGGQCANWFDPW	1	19	0	3-15	2	CQQYNNWPYTF	9	0	-	
H8	4-34	2-15	2	6	2	CARASPPPLWDCSGGSCYSKGYGMDVW	1	23	0	1-5	1	CQQYNSYPWTF	9	0	-	
H9	3-30	5-12	3	4	2	CARDYDYW	0	4	0	1-17	3	CLQHNSYPFTF	9	0	-	
H10	4-59	6-13	1	4	1	CARLSGSSWYPYFDYW	0	13	0	3-15	2	CQQYNNWPPYTF	12	0	-	
H12	3-23	3-9	2	4	2	CAKSRGVYDILTGGGDIW	1	14	0	1-39	4	CQQSYSTPLTF	9	0	+	
H20	3-33	3-3	1	5	3	CARDLDGINWFDPW	0	10	0	1-5	1	CQQYNSYPTWTF	10	0	-	
H27	4-31	3-10	2	4	3	CARDRPGPTMVRGVSDWGGYYFDYW	3	25	0	1-39	1	CQQSYSTPVTF	9	0	-	
H36	3-11	6-6	3	4	2	CARDMVLGSSGSQNDYW	0	13	0	1-5	1	CQQYNSYSRTF	9	0	-	
H37	1-69	2-15	3	6	1	CARVGGVVGARGGLYYYYGMDVW	1	19	0	1-39	3	CQQSYSTPFTF	9	0	+	
H38	4-39	2-8	1	5	3	CARLREVKESGPGNWFDPW	2	15	0	3-11	4	CQQRSNWPLTF	9	0	-	
H42	4-59	6-19	2	3	1	CARVQQWLAQWGAFDIW	0	13	0	1-8	1	CQQYYSYPWTF	11	0	+	
H22	3-64	1-26	2	4	3	CARGGIEWELYNDYW	0	11	0	3-15	2	CQQYNNWPPYTF	11	0	-	
H29	4-31	3-10	1	4	1	CATGRKAGFFDYW	2	9	0	4-1	1	CQQYSTLTWTF	11	0	+	
H48	4-39	3-22	3	4	1	CARHYSPMIVVINPFDYW	1	17	0	3-20	4	CQQYGSPLAF	10	0	+	

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vλ	Jλ	CDR3(aa)	Length	Mutations	Poly
H5	3-30	6-6	1	6	2	CARDRNLYSSSSAGYYYYGMDVW	1	20	0	3-1	3	CQAWDSSTVVF	9	0	-
H13	3-30	6-13	2	3	2	CARDRRAAAGTVRYAFDIW	3	15	0	2-23	2	CCSYAGSSTVVF	10	0	+
H24	3-15	3-22	2	4	4	CTTDGDYDSSGYYYGIPRNFYDW	1	23	0	1-51	3	CGTWDSLSADVVF	12	0	-
H30	3-7	5-12	1	4	3	CAREDIVATSADYW	0	10	0	1-44	3	CAAWDDSLNGWVF	11	0	-
H31	4-4	3-10	2	2	2	CARTYYYGSGSYEGALPRGHWFYDLW	3	26	0	3-1	2	CQAWDSSTAVF	11	0	-
H35	4-34	4-17	2	5	2	CARGGSRGDYHNWFDPW	2	13	0	1-51	3	CGTWDSLSAVVF	11	0	-
H45	4-39	3-10	1	4	2	CARRLWFGELLYYYLDYW	2	15	0	3-1	3	CQAWDSTVVF	8	0	+
H46	4-39	6-13	2	4	1	CARLVAAAGTLNFDYW	0	12	0	3-25	3	CQSADSSGTLVF	10	0	-
H48	3-30	2-15	2	4	2	CARAESCSCYSPVFDYW	0	14	0	3-21	3	CQVWDSSTHVVVF	11	0	-
H7	4-39	3-9	3	3	4	CARWVYDIEHNPDADFIDW	1	14	0	1-51	2	CGTWDSLSAVVF	13	0	-
H28	4-4	3-10	2	4	1	CARVRGGYSGSSSDYW	1	13	0	1-47	3	CAAWDDSLSGRGF	13	0	-
H31	4-30	2-15	3	2	3	CARSFGGDDVVVAASRWYFDLW	1	19	0	2-14	2	CSSYTSSTLVF	12	0	-
H35	3-40	3-22	2	4	2	CARNHRGRTYYYDSSGYLPDYW	3	18	0	1-44	2	CAAWDDSLNGPVVF	14	0	-
H36	3-30	3-10	2	5	2	CARDQAYYSGSYGTDFDPW	0	16	0	1-51	3	CGTWDSLSAGVF	13	0	-
H43	3-53	6-25	2	4	4	CASGGGIAAAEGDEFDYW	0	14	0	3-1	3	CQAWDSSTAWF	11	0	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject MG-AChR-2

Ig	HEAVY						MG-AChR-2, 10-				LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2	
H49	3-30	3-22	3	4	2	CARDITMIVVPGDYW	0	11	0	4-1	1	CQQYYSTPWTF	11	0	+	+	
H52	3-30	2-2	3	4	1	CATSNPPVPAQYYFDYW	0	15	0	3-20	2	CQQYGSSPPVYTF	13	0	-	-	
H54*	4-59	1-26	3	4	2	CARDLSGSYHFDYW	1	10	0	1-12	3	CQQANSFPFSF	11	0	-	+	
H55	1-2	6-19	1	4	0	CARRHSSGWRGLNYW	3	11	0	1-17	4	CLQHNSYPFSF	11	0	+	-	
H70	5-1	6-13	1	4	1	CASPGYSSSWYDYW	0	10	0	3-15	1	CQQYNNWPRTF	11	0	+	+	
H75	3-7	5-5	3	4	1	CATFRGYSYGFNDYW	1	11	0	2-28	3	CQQYGSSSYTF	11	0	-	-	
H77	1-58	3-22	2	4	3	CAAFNHDIYDSSGYQPHFDYW	2	20	0	3-20	2	CQQYGSSSYTF	11	0	-	-	
H89	3-23	6-13	3	4	1	CAKVQQLGPFDYW	0	9	0	1-5	1	CQQYNSYWTF	10	0	-	+	
H92	3-48	4-17	2	1	2	CARGKADYGDYVRYFQHW	3	14	0	1-5	4	CQQYNSYSSTF	11	0	-	+	
H56	3-64	3-22	2	4	3	CVKSPLVGYDSSGYEDYW	0	15	0	1-39	3	CQQSYSTLTF	10	0	-	+	
H62	4-31	5-19	1	6	2	CARDRHGGSSGPKSQVGFDPW	3	17	0	1-33	1	CQQYDNLPRTF	11	0	-	+	
H66	3-30	3-9	2	4	2	CAKQIYDILTYSPFDYW	1	14	0	2-28	4	CMQALQTPPTF	11	0	-	-	
H74	3-23	3-10	1	1	1	CAKGVLLWFGELLGGFQHW	5	15	0	1-33	3	CQQYDNLPTF	11	0	+	-	

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly	HeP2
H50	4-30	3-3	3	5	1	CARGVHGPPERRITIFAKGVPPSYRPW	5	23	0	1-36	7	CAAWDDSLNGPVF	11	0	+	+
H54*	4-59	1-26	3	4	2	CARDLSGSYHFDYW	1	10	0	1-12	1	CQQANSFPFSF	11	0	-	+
H63	4-59	6-19	1	2	2	CARDQVASRFDLW	1	9	0	1-44	3	CAAWDDSLNGPVF	11	0	-	-
H87	1-18	3-10	2	5	2	CARVPPGDYGGSSIRFDPW	1	16	0	1-47	3	CAAWDDSLSGVVF	11	0	-	-
H95	3-23	1-17	3	4	2	CAKGDRWNYVSVPTTNDYW	1	15	0	2-14	3	CSSYTSSSVVF	9	0	+	-
H76	3-30	3-9	2	4	2	CARAGLYDILTYFDYW	0	12	0	3-21	2	CQVWDSSSHVVVF	13	0	-	-
H77	1-2	6-19	2	4	2	CARDIAVAGLFDYW	0	10	0	1-44	3	CAAWDDSLNGPVF	13	0	-	-
H78	3-21	2-15	2	3	2	CARESGYCSCSYSGTAFDIW	0	18	0	2-8	1	CSSYAGSNNYVF	12	0	-	-

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s : silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject MG-AChR-3

Ig	HEAVY					MG-AChR-3, 10+					LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>K</sub>	J <sub>K</sub>	CDR3(aa)	Length	Mutations	Poly		
H18	3-23	1-26	3	4	1	CATDRGSYW	1	9	0	1-5	2	CQQYNSYSQTF	11	0	+		
H26	4-34	6-6	2	4	1	CARIKSSIAARNFDYW	3	16	0	3-20	2	CQQYGSSQYTF	11	0	-		
H27*	4-59	6-19	2	2	2	CARAMGAVAGMRDYSFDYW	2	19	0	3-15	3	CQQYNNWPPEFTF	13	0	-		
H31	1-69	3-22	2	3	3	CARTVRRYDSSEYAFDIW	3	18	0	3-11	4	CQQRNSLTF	10	0	-		
H39*	3-23	3-10	2	4	2	CAKDQSNYYDPVSHW	2	15	0	4-1	4	CQQYYSTPLTF	11	1s FR3/ 1s CDR3	-		
H4	4-31	3-16	2	4	1	CARDRFGSGSYGYW	2	15	0	3-11	3	CQQRSTLTF	10	0	-		
H6*	4-31	3-10	3	4	1	CARLVMVRGVIISRFDYW	3	18	0	3-11	1	CQQRSNWPPWTF	12	0	+		
H20	3-11	3-22	2	4	3	CASGPYYDSSGYEFPDYW	0	19	1r Fr2	1-39	4	CQQSYSTPPLTF	12	0	-		
H21	4-30	1-26	1	4	1	CARGVVGATKGGYFDYW	2	17	0	1-39	1	CQQSYSTPRTF	11	0	-		
H39	3-7	2-21	3	4	2	CAREGRTLVTATPSDYW	2	18	0	3-20	2	CQQYGSSPYTF	11	0	-		
H41	1-3	3-22	2	6	2	CAMSYYYDSSGRGKPYYYGMDVW	2	23	0	2-28	2	CMQALQTPYTF	11	0	-		

Ig	VH	D	RF	JH	(-)	HEAVY				LIGHT		Poly			
						CDR3(aa)	(+)	Length	Mutations	V <sub>L</sub>	J <sub>L</sub>				
H15	4-31	3-22	2	2	4	CARDSKKDYDSSGHPKPWFYDLW	5	24	0	3-21	3	CQVWDDSSDPQGVF	14	0	-
H27*	4-59	6-19	2	2	2	CARAMGAVAGMRDYSFDYW	2	19	0	3-1	2	CQAWDSSPYVVF	12	0	-
H33	4-61	1-7	1	4	1	CARGGITGTTFFVDYW	2	16	0	1-44	2	CAAWDDSLKAVF	12	0	-
H35	1-69	3-3	2	4	3	CARDRERWNFDYW	3	13	0	2-14	3	CSSYTSSSTRVVF	12	1r FR3	+
H39*	3-23	3-10	2	4	2	CAKDQSNYYDPVSHW	2	15	0	1-47	3	CAAWDDSLSGRFF	13	0	-
H40	4-31	5-18	3	6	1	CARGGYSYGTYYYYGMDVW	1	19	0	2-8	2	CSSYAGSNNLVF	12	0	-
H47	4-34	4-23	3	4	1	CARGVATPGDYW	1	12	0	2-14	2	CSSYTSSSTLVF	12	1r FR3	-
H1	1-3	3-10	1	4	2	CVPELWYGAHYFDYW	1	15	0	2-14	1	CSSYTSSSTPYVF	13	1r FR3	+
H6*	4-31	3-10	3	4	1	CARLVMVRGVIISRFDYW	3	18	0	2-14	2	CSSYTSSSTPYVF	13	1r FR3	+
H9	3-15	5-18	3	6	1	CTTVYSNYYGMDVW	0	15	0	7-46	1	CLLSYSGAHYVF	12	0	-
H13	3-30	3-10	1	4	3	CAKDRSWGGLDYW	2	14	0	3-25	1	CQSADSSGTYVF	12	0	-
H15	1-2	6-13	1	6	2	CARDQPIYGRYSSSWYYYGMDVW	2	23	0	1-44	2	CAAWDDSLNVVF	12	0	-
H17	3-66	1-26	1	4	1	CARGFIGGFYDW	1	12	0	2-14	2	CSSYTSSSTPYVVF	14	1r CDR2/1r FR3	-
H19	1-18	3-10	1	1	1	CARTVLLWFGVGSHPDPW	2	18	0	2-11	1	CCSYAGSYTPLVF	13	0	+
H37	3-21	5-12	3	6	1	CARIGGYAYYYYGMDVW	1	17	0	1-51	3	CGTWDDSSLSAGVF	13	0	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject MG-AChR-3

Ig	HEAVY					MG-AChR-3, 10-				LIGHT				Reactivity		
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>K</sub>	J <sub>K</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H58	3-23	6-19	2	1	1	CAKESGVIAVAGTSGYW	1	17	0	3-11	1	CQQRSNWPPWTF	12	0	+	+
H59*	3-23	4-23	3	4	3	CAKAPGVTPEDFFDYW	1	16	0	3-20	1	CQQYGSSPRTF	11	0	-	-
H64	1-69	1-20	3	5	3	CARDTDNWNPNPGKNWFDPW	2	19	0	3-11	2	CQQRSNWPPYTF	12	0	+	-
H72	5-51	5-12	3	4	2	CARLDGGPMDYW	1	12	0	1-27	1	CQKYNSAPRTF	11	0	-	+
H75	4-34	3-16	2	4	2	CARYSRAPYDYVWGSYRYSFDYW	3	23	0	4-1	4	CQQYYSTPPLTF	12	0	+	-
H87*	4-4	1-26	1	4	1	CARGAILGIFYW	1	13	0	1-33	4	CQQYDNLPRTF	11	0	-	+
H89	3-21	2-2	3	4	3	CAREGEKSVVPAARTRDYW	4	19	0	1-16	2	CQQYNSYPLTF	11	0	+	+
H61	1-46	1-7	2	4	2	CARARWNYKDFDYW	3	14	1r CDR1/2r FR3	1-39	3	CQQSYSTPLTF	11	0	-	+
H62	1-18	2-21	1	4	3	CARDYQLYCGGDCYYDYW	1	18	0	3-15	2	CQQYNNWPRTF	11	0	-	-

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly	HeP2
H59*	3-23	4-23	3	4	3	CAKAPGVTPEDFFDYW	1	16	0	1-40	1	CQSYDSSLGYSYVF	13	0	-	-
H65	1-69	3-22	2	6	2	CASPYTLTDSSGYPSSPLYGMDVW	0	24	0	3-21	3	CQVWDSSSDHWVF	13	0	+	+
H71	5-51	3-10	2	4	3	CARRGRSWELWGDPFDYW	3	18	0	1-44	2	CAAWDDSLNGPVF	13	0	-	-
H87*	4-4	1-26	1	4	1	CARGAILGIFYW	1	13	0	1-40	3	CQSYDSSLRVF	11	0	-	+
H94	4-30	3-10	1	4	3	CAREGGLLWFGERYFDYW	2	19	0	1-44	3	CAAWDDSLNGYWVF	14	0	+	+
H65	4-30	3-10	2	5	1	CARNYGSGSRNWFDPW	2	16	0	1-40	3	CQSYDSSLGYSYVF	12	0	-	+
H93	4-34	5-18	3	5	1	CARLGYRPPTVGFDPW	2	16	0	2-14	3	CSSYSSSTRVF	12	1r FR3	-	+

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s: silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject MG-MuSK-1

Ig	HEAVY					MG-MuSK-1, 10+				LIGHT					Reactivity
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly
H56*	3-30	3-10	3	4	3	CARARGVRGVIGYFDYW	0	17	0	3-20	4	CQQYGSSPRITF	12	0	-
H58	4-30	3-10	2	5	2	CARGRPLLAYGSGSYMPNWFDPW	0	24	0	4-1	4	CQQYYSTPLTF	11	0	+
H59	3-33	6-19	2	4	3	CAREQIAVAATRGRNYFDYW	0	20	0	1-39	1	CQQSYSTPTWTF	12	0	+
H60	4-61	5-5	3	4	1	CARGGGGYSYGWESSHEEHFDYW	0	23	0	1-5	1	CQQYNSYRTF	10	0	+
H61	4-61	3-10	3	4	1	CARGNKGTFDYW	1	12	0	1-39	1	CQQSYSTPRTF	11	0	+
H62	4-59	6-13	1	2	1	CARGYSSSYLLYWYFDLW	0	18	0	4-1	1	CQQYYSTPLTF	11	0	+
H69	1-3	3-10	3	5	2	CARGPMVRGVPSDIIPW	0	17	0	3-20	1	CQQYGSSPGTF	11	0	+
H72*	4-34	5-12	3	4	3	CARGWADRRYSGYDWQPGYYFDYW	0	24	0	4-1	1	CQQYYSTPQTF	11	0	-
H73	3-23	3-22	2	4	0	CAKSPYYYDSSGYPVYFDYW	1	20	0	3-20	3	CQQYGSSPFTF	11	0	-
H75	3-30	2-15	2	4	1	CARSQSSGKHWPDYW	1	16	0	1-9	1	CQQLNSYPRTF	11	0	+
H80	3-23	1-26	3	4	1	CAKRGSGSYEGFVDYW	1	17	0	4-1	2	CQQYYSTPCSF	11	0	+
H89	4-34	1-14	3	4	1	CARVRIHYFDYW	0	12	0	1-39	4	CQQSYSTPLTF	11	0	-
H90	3-9	3-16	2	6	1	CAKDAPRGDYARGYYYYGMDVW	0	22	0	3-20	1	CQQYGSSF	8	0	-
H91	4-34	6-13	2	4	3	CASSRIAAGSQDYW	0	15	0	1-39	1	CQQSYSTPLTF	11	0	-
H95	3-11	3-22	1	4	3	CARDKHYYDSSGVYSYW	0	17	0	1-9	2	CQQLNSYPPYTF	12	0	-

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly
H54	1-2	5-5	3	4	1	CAGSRGYSYGPFYDW	1	15	0	2-23	3	CCSYAGSSTMVF	12	0	-
H56*	3-30	3-10	3	4	1	CARARGVRGVIGYFDYW	3	17	0	1-40	2	CQSYDSSLGWDVVF	17	0	-
H72*	4-34	5-12	3	4	3	CARGWADRRYSGYDWQPGYYFDYW	3	24	0	2-11	2	CCSYAGSYTLVF	12	0	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation



Sequence and reactivity tables for mature naive B cells, (CD10-), from subject MG-MuSK-1

Ig	HEAVY					MG-MuSK-1, 10-				LIGHT				Reactivity		
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H3	1-69	5-12	3	4	3	CARAREGYSGYDPLTGGGYFDYW	2	23	0	3-11	2	CQQRSNWPPMYTF	13	0	-	-
H6	3-11	5-5	2	4	3	CARDLDPGIQLWPGGDYD	1	18	0	1-39	1	CQQSYSTPETF	11	0	-	+
H7	3-33	3-3	2	3	2	CARGGSGYYLDAFDIW	1	16	0	1-12	4	CQQANSFPHTF	11	0	-	-
H8	1-69	6-19	2	5	2	CARERRTGIPDPW	3	13	0	3-11	1	CQQRINWWTF	10	0	-	-
H10*	1-3	3-22	2	4	1	CARVSANYDSSGYFFGHW	2	19	0	3-20	3	CQQYGSSFTF	10	0	-	+
H14	3-21	5-24	2	3	5	CARDGDLDRPNSSGDAFDIW	2	20	0	1D-33	1	CQQYDNLPPTF	11	0	-	-
H19	3-23	3-10	2	4	3	CAKDCRRDYGGSGSFASDYW	3	22	0	3-15	1	CQQYNNWPLF	10	0	+	+
H24	3-48	3-10	1	6	1	CATLGGPGMDVW	0	12	0	3-20	1	CQQYGSSPDTF	11	0	-	-
H26	4-31	6-19	1	3	3	CARDLGYSSGWYKEDIW	2	18	0	3-11	1	CQQRSNWPVAF	11	0	-	+
H27	4-30	3-10	3	3	1	CARGLPMVLGVITLYAFDIC	1	20	0	1-39	4	CQQSYSTGRF	10	0	+	+
H30	3-7	3-3	2	4	3	CARSRNDPWYDFWSGYQYFDYW	2	24	0	1-5	1	CQQYNSYRWTF	11	0	+	+
H35	1-2	2-21	2	4	3	CARDPGAYCGGDCYSSGGIDYW	1	21	0	1-9	2	CQQLNSYPYTF	11	0	-	+
H39	1-69	3-22	2	5	2	CASISYYDSSGYSNWFDPW	0	19	0	3-20	1	CQQYGSSPWTF	11	0	+	-
H43	4-39	3-9	2	3	2	CASAYYDILTYGRTKHAFDIW	3	22	0	1-16	4	CQQYNSYPLTF	11	0	+	+
H47	3-30	7-27	3	4	1	CARVANWGYMYFDYW	1	16	0	3-20	4	CQQYGSSPLTF	11	0	-	+

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H10*	1-3	3-22	2	4	1	CARVSANYDSSGYFFGHW	2	19	0	3-1	2	CQAWDSSTVVF	11	0	-	+
H21	1-46	4-17	4	2	7	CAREIADDDYGDQEAGGLDYW	1	21	0	2-23	1	CCSYAGSSTYVF	12	0	-	-
H38	3-11	2-15	3	4	1	CARGTPRDYW	2	11	0	1-47	3	CAAWDDSLSGWVF	13	0	-	+
H40	5-51	3-22	2	4	3	CARQGYDSSGVDPFDYW	1	18	0	1-40	3	CQSYDSSLRVF	11	0	-	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject MG-MuSK-2

Ig	HEAVY					MG-MuSK-2, 10+				LIGHT				Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>k</sub>	J <sub>k</sub>	CDR3(aa)	Length	Mutations	Poly
H59	4-59	3-10	3	3	4	CAREMTRFGELSGVSDAFDIW	2	21	1r FR3	1-5	1	CQQYNSYSPWTF	12	0	-
H62	1-2	5-24	3	4	2	CARSDGYPRWGFYDW	2	15	0	3-15	3	CQQYNNWLTF	10	0	-
H64	3-23	2-2	3	6	1	CAKSLTKPSIKAVVPAAILYYYGMDVW	3	28	0	1-39	1	CQQSYSTLSWTF	12	0	+
H65	1-18	6-19	1	2	1	CARPNLGSGWSIYQPNWYFDLW	1	22	0	3-20	2	CQQYGSSPPYTF	12	0	+
H68	4-31	6-6	2	1	1	CARNHFIAARPMAYFQHW	4	19	0	3-15	2	CQQYNNWPSYTF	12	0	-
H69	4-59	3-16	2	3	2	CARARSDVWGSYRMKGAFDIW	4	21	0	2-28	4	CMQALQTLTF	10	0	+
H74	3-30	3-3	2	6	3	CAKEAPLYDFWGSYRSYYYYYMDVW	2	26	0	2-28	1	CMQALQTPRTF	11	0	+
H77	3-30	5-5	3	4	1	CAKGLGYNYGYPYFDYDW	1	18	0	3-15	3	CQQYNNWPLTF	11	0	-
H80	4-34	3-22	2	6	2	CARARVYTYYYDRIMDVW	3	18	0	1-5	2	CQQYNSYPYTF	11	0	-
H81	3-33	3-10	1	6	3	CARDLIRLWFGESGGYYYYYMDVW	2	26	0	2-28	1	CMQALQTPTWTF	12	0	+
H83	3-9	3-3	2	4	2	CVKGGNPYYDFWSDHW	2	16	0	1-13	4	CQQFNSYPLTF	11	0	-
H89	4-61	4-23	2	6	2	CARDFQVGLRYYYYYMDVW	2	19	0	1-89	2	CQQSYSTPYTF	11	0	+
H91	3-30	2-2	3	5	2	CARDPNIVVRNWFDPW	2	17	0	3-20	2	CQQYGSSPYTF	11	0	+
H95	3-21	6-13	1	3	1	CARAGYSSSWYPWAFDIW	1	18	0	1-39	2	CQQSYSTPPYTF	12	0	+

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly
H96	3-30	3-22	3	5	3	CAREVRMIVVEGWDFPW	2	17	0	3-21	3	CQVWDSSSDHWVF	13	0	-

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s : silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject MG-MuSK-2

Ig	HEAVY					MG-MuSK-2, 10-					LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2	
H3	4-39	3-9	2	5	2	CARVPSYYDILTGYSQNWDFPW	1	22	0	1-5	2	CQQYNSYLYTF	11	0	+	+	
H5	4-39	2-15	2	5	1	CASPYCSGGSCYYGWDFPW	0	19	0	3-20	4	CQQYGSSPPGLTF	13	0	-	+	
H6	1-46	6-13	2	6	1	CASSSSLNGPSDVW	0	14	0	3-15	1	CQQYNNWPPWTF	12	0	-	+	
H7	4-39	4-17		4	3	CARDYGDYVLGVYFDYW	1	18	0	1-5	1	CQQYNSYSRTF	11	0	-	-	
H10	4-39	5-24	1	3	1	CARRSRMATAGKAFDIW	0	17	0	1-5	4	CQQYNSYLYTF	10	0	+	+	
H14	4-59	3-22	2	2	2	CARAPTYYYDSSGYPRSYWYFDLW	2	25	0	2-30	2	CMQGTWPLYTF	12	0	+	+	
H23	4-61	1-7	3	3	4	CAREGYNWNYRDQYDAFDIW	0	20	1r FR3	1-5	4	CQQYNSYSIF	10	0	-	+	
H24	3-30	1-26	3	4	5	CAREEYNWKYRDQYDAFDIW	3	20	0	3-11	4	CQQRSNWPKTF	11	0	-	+	
H25	4-61	2-2		6	2	CARGRLEPAAMHLNYYMDVW	3	20	1r FR3	1-5	4	CQQYDRWGLTF	11	0	+	+	
H26	1-18	2-2	3	6	2	CARDRGVVVPAAPLRGYYGMDVW	3	25	0	2-30	1	CMQGTWHPRTF	11	0	+	+	
H29	3-23	4-23	2	4	3	CAKDLTQGGEPYGPLDYW	1	18	0	3-20	1	CQQYGSSPRTF	11	0	-	-	
H30	3-30	5-12	1	4	0	CVLGVATMNW	0	10	0	1-5	1	CQQYNSYWTF	10	0	-	+	
H38*	1-46	4-75	2	6	5	CARVRDDYGDYARPDSSYYMDVW	0	22	0	3-11	1	CQQRSNWWTF	10	0	-	+	
H42	5-51	3-3	3	5	2	CARGARGGEGWDFPW	2	15	0	3-15	2	CQQYNNWPPMYTF	13	0	-	+	
H43	3-48	3-22	2	4	4	CARESSGYEGGPDYW	1	16	0	1-5	1	CQQYNSYLWTF	11	0	-	-	
H44	1-18	6-13	2	5	1	CARDDGIAAAGTGPW	0	15	0	1-39	4	CQQSYSTLSLTF	12	0	-	-	
H46	1-2	3-10	2	6	7	CAREYYYGSGSKVYYGMDVW	2	21	0	2-28	2	CMQALQTPNTF	11	0	-	+	

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H15	4-39	3-9	3	4	2	CARQGSVDYFDYW	1	13	0	4-1	2	CQAWDSSSVVF	11	0	-	-
H34	4-39	5-12	1	5	2	CARKLVATNEAWDFPW	2	16	0	2-14	1	CSSYTSSSTLEYVF	14	1r CDR2	-	-
H38*	1-46	4-75	2	6	5	CARVRDDYGDYARPDSSYYMDVW	3	22	0	2-14	2	CSSYTSSSTLVF	12	0	-	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject HD-1

Ig	HEAVY					HD-1, 10+				LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly	
H1	4-34	6-6	1	4	1	CARFGGYSSSLFDYW	1	15	0	1-17	1	CLQHNSYPRTF	11	0	-	
H3	3-11	1-26	1	4	1	CARGRRWENPGGYW	3	14	0	1-5	1	CQQYNSYPWTF	11	0	+	
H4	1-69	3-10	1	2	4	CAREFSETREHRNWFYDLW	4	19	0	1-39	2	CQQSYSTPPYTF	12	0	-	
H5	3-21	6-13	3	3	3	CARDAAGGVAAAAYDAFDIW	1	20	0	1-39	5	CQQSYSTPITF	11	0	-	
H6	1-18	6-19	2	5	2	CARESSSGWLMGWFDPW	1	17	0	3-20	1	CQQYGSSLTWTF	12	0	-	
H7	4-39	4-17	3	5	2	CARGFGEWHTVTTFPTNWFDPW	2	23	0	1-8	3	CQQYYSYPPTF	11	0	-	
H8	3-11	1-26	1	3	4	CAREGAEWDLPAFDIW	1	17	0	3-15	1	CQQYNNWPRTF	11	0	-	
H9	4-31	2-2	2	5	0	CARGSSTSCYWATW	1	14	0	4-1	4	CQQYYSTPLTF	11	0	-	
H10	3-72	4-11	3	6	1	CARGMTTVTHPMDVW	1	15	0	2-28	1	CMQALQTATF	10	0	-	
H11	3-23	3-10	3	4	2	CAKDLGKPGVDYW	2	13	0	1-17	3	CLQHNSYPFTF	11	0	-	
H12	3-30	6-19	3	4	3	CARDGSRGDVAGTVGYFDYW	2	20	1r FR2/1r FR3	3-15	2	CQQYNNWPPYSF	12	0	-	
H13	3-9	6-19	2	6	3	CAKDILLSSDSSGWYYHRYYYGMDVW	3	26	1r FR2	1-12	4	CQQANSFPRVF	11	0	-	
H14	3-15	3-3	2	5	3	CTTDHSRDFWSAHRANWFDPW	4	21	0	1-27	4	CQKYNSAPLTF	11	0	+	
H15	3-30	4-11	2	6	3	CAREFDYAYSNYHSYYYGMDVW	2	22	0	1-39	3	CQQSYSTPFTF	11	0	-	
H16	3-23	3-9	2	4	3	CARGKRNDILTGSEFDYW	3	18	0	1-5	1	CQQYNSYWTF	10	0	-	

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly
H2	3-13	3-22	2	6	1	CARGVSSGYSGTYYYYGMDVW	1	22	0	1-51	3	CGTWDSLSAGVF	13	0	-
H17	3-9	2-2	2	6	2	CARDIRPRAGYCSSTSCYHHSYYYGMDVW	5	30	0	1-40	1	CQSYDSSLSGYVF	13	2r FR3	-
H18	3-21	3-22	2	4	3	CARDYDSSGLGSPYDYW	1	17	1r CDR2	2-23	2	CCSYAGSSTFGGVF	14	0	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s: silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject HD-1

Ig	HEAVY					HD-1, 10-				LIGHT					Reactivity	
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>κ</sub>	J <sub>κ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H3	3-21	5-12	2	4	2	CARDFGGYSGYDQGSYW	1	17	0	1-5	1	CQQYNSYWTF	10	0	-	+
H5	4-34	3-3	2	5	2	CARGCYDFWGSVRFDPW	2	19	0	3-15	2	CQQYNNWPPMYSF	13	0	+	-
H6	3-9	3-3	2	4	2	CAKAIRSLSTNDFWSGRGYFDYW	3	24	0	3-11	4	CQQRSNWPLTF	11	0	-	-
H7	4-61	3-10	1	2	4	CAREPNDLWFGELLPNHSYWYFDLW	2	25	0	3-20	1	CQQYGSSQRTF	11	0	-	+
H8	3-7	3-22	2	4	2	CAREYSSGYPLDYW	1	15	0	1-39	2	CQQSYSTPYSF	11	0	-	-
H10	3-9	3-10	2	4	3	CAKDKDYASGTYPPYFDYW	2	20	0	3-11	4	CQQRKGF	7	1r FR3	-	-
H11	69-42	3-22	2	6	2	CAGSRGRDSSGYYYGMDVW	2	21	0	3-15	1	CQQYNNWPPTWTF	13	0	-	-
H12	3-48	2-2	3	6	3	CARDQVVVPADLTYYYYGMDVW	1	24	0	2-28	2	CMQALQTPYTF	11	0	-	-
H13	4-61	4-11	2	3	4	CARDLSYMGDAFDIW	1	16	0	3-15	1	CQQYNNWPQTF	11	0	-	-
H14	3-30	2-15	3	4	3	CARDSATFDYW	1	12	0	1-39	1	CQQSYSTPPTF	11	0	-	+
H15	4-34	6-13	2	6	2	CARDPAAGRYPGFYYYGMDVW	2	22	0	1-12	4	CQQANSFPRTF	11	0	-	-
H16	4-31	3-10	2	4	2	CASRGDGVYDW	0	11	0	4-1	1	CQQYYSTPWTF	11	0	+	-
H17	3-33	3-22	2	3	3	CARDRYYYDSSGYVKSAFDIW	3	24	0	1-33	2	CQQYDNLYSF	10	0	-	-

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	V <sub>λ</sub>	J <sub>λ</sub>	CDR3(aa)	Length	Mutations	Poly	Hep2
H1	3-9	2-15	2	6	2	CAKDSGCGGSCYSSYYYYYGMVW	1	25	0	3-21	2	CQVWDSSSHVVVF	13	0	-	-
H2	3-9	3-22	2	4	5	CAKDGAEGYDSSGFDYFDYW	1	22	0	3-21	2	CQVWDSSSHVVVF	13	0	-	-
H4	3-74	6-13	2	6	2	CARDVGAYSSWYYYGMDVW	1	21	0	3-25	2	CQSADSSGTYYVF	13	0	-	-
H9	1-3	6-19	3	6	2	CAREAIAVAGSYSSYYYGMDVW	1	22	0	3-21	3	CQVWDSSSHVVVF	13	0	-	-
H18	3-21	1-26	2	4	1	CARGRSYGSYYGRDYW	3	17	0	3-21	1	CQVWDSSSHVVVF	13	0	-	-
H19	4-31	5-24	2	4	2	CARGPPIRDGYNPYFDYW	2	18	0	2-14	3	CSSYTSSTLWVF	13	0	-	-
H20	4-34	3-10	2	4	1	CARAGSGSYFDYW	1	15	0	2-23	2	CCSYAGSSTWVF	12	0	-	+
H21	3-48	3-22	2	6	3	CARDYYDSSGYRHYGMDVW	3	19	0	2-14	2	CSSYTSSTLVVF	13	1r CDR2	-	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for new emigrant B cells, (CD10+), from subject HD-2

Ig	HEAVY					HD-2, 10+				LIGHT					Reactivity
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vκ	Jκ	CDR3(aa)	Length	Mutations	Poly
H1	3-21	7-27	3	4	1	CARNWGFGRGANDYW	2	17	0	3-20	2	CQQYGSSPETF	11	0	+
H4	3-43	2-15	2	5	2	CAREVYCSGGSCYTGWFDPW	1	20	0	3-20	2	CQQYGSSPPYTF	12	0	-
H5	3-21	5-12	1	4	3	CARDMEATIRNFDYW	2	15	0	3-11	4	CQQRSNWPRELTF	14	0	-
H7	3-21	3-16	2	5	1	CARTKGLGWFDPW	2	13	0	1-16	1	CQQYNSYPPTF	11	0	-
H11	1-18	3-9	2	6	2	CARGYDILTGSGLYYYYYYMDVW	1	24	0	2-28	4	CMQALQTRSF	10	0	-
H12	3-53	2-15	2	6	3	CARDRVLVDGYCSGGSCYGGYYYYMDVW	2	28	0	3-20	1	CQQYGSSPGWTF	12	0	-
H13	4-39	1-26	3	4	1	CARLGYSGSYHLPYYFDYW	2	19	0	1-5	2	CQQYNSYSTF	10	0	-

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vλ	Jλ	CDR3(aa)	Length	Mutations	Poly
H2	3-73	4-17	2	4	2	CTRLWVPYGDYAVDYW	1	16	0	1-44	3	CAAWDDSLNGWVF	13	0	-
H3	3-23	2-2	2	4	2	CAKFEGYCSSTSCYPGFYDW	1	20	0	3-25	2	CQSADSSGTYVVF	13	0	-
H6	3-73	2-15	2	4	2	CALRSECSGGSCYSFSNDYW	2	20	0	3-25	1	CQSADSSGTYVVF	12	0	-
H8	5-51	6-13	2	6	1	CARHLGLAAAGYYYYYYMDVW	2	20	0	1-47	2	CAAWDDSLSGVVF	13	0	-
H9	4-4	5-12	1	4	1	CARVDIVATGAFYW	1	14	0	2-11	1	CCSYAGSYVF	10	0	-
H10	3-74	5-12	3	4	2	CARARGYSGYDVDYDW	2	15	0	1-44	2	CAAWDDSLNGPRVVF	15	0	-
H14	5-51	6-19	1	5	1	CARAYSSGWYTNWFDPW	1	17	0	1-51	2	CGTWDDSLSAHVVF	14	0	-
H15	4-31	2-2	2	2	3	CARDTGYCSSTSCDWYFDLW	1	20	0	2-14	3	CSSYTSSTLVF	12	0	-

RF : reading frame - : non-reactive + : reactive \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures FR : framework CDR : complementarity determining r : replacement mutation s : silent mutation

Sequence and reactivity tables for mature naive B cells, (CD10-), from subject HD-2

Ig	HEAVY					HD-2, 10-				LIGHT				Reactivity		
	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vκ	Jκ	CDR3(aa)	Length	Mutations	Poly	Hep2
H2	1-69	3-10	2	3	3	CARVGIFKAETPGGSGSYNSESFAFDIW	2	29	0	4-1	1	CQQNNWPWTF	10	0	-	-
H7	1-46	3-22	2	4	3	CARGRYYYDSSAADGEYW	2	18	0	3-11	4	CQQRSNWPRELTF	13	0	-	-
H11	3-23	2-2	3	4	1	CAKELRIIVVPAAYTRYW	3	19	0	1-39	1	CQQSYSTRWTF	11	0	+	+
H12	3-23	1-24	1	6	3	CAEPEGDFDYW	1	11	0	3-15	1	CQQYNNWPRWTF	12	1r FR3	-	-

	VH	D	RF	JH	(-)	CDR3(aa)	(+)	Length	Mutations	Vλ	Jλ	CDR3(aa)	Length	Mutations	Poly	Hep2
	H1	4-39	6-19	3	4	3	CARQEQWLVGGEYYFDYW	1	18	0	1-47	3	CAAWDDSLSGRNWVF	15	0	-
H3	3-74	3-3	2	4	3	CARDDFWSGYLYYFDYW	1	17	0	8-61	2	CVLYMGSGIWVF	12	0	-	-
H4	3-73	2-8	2	6	1	CTRGMRYSTTYMDVW	2	16	0	1-47	3	CAAWDDSLSGWVF	13	0	-	-
H5	5-51	3-9	2	4	2	CARLPPHYDILTGGYRKGFDYW	4	22	0	3-21	2	CQVWSSSDPVF	12	0	-	-
H6	3-9	4-17	2	6	3	CAKSPGDYDYMDVW	1	14	0	3-21	2	CQVWSSSDVVF	12	0	-	-
H8	3-48	6-19	2	6	2	CARQPAPQYSSGWYYDYDYYY-MDVW	1	25	0	1-40	2	CQSYDSSLGSGNVVF	15	0	-	+
H10	4-4	5-5	2	3	3	CAREGRYGGPVDAFDIW	2	17	0	1-51	2	CGTWSSLSAVVF	13	0	-	+

RF : reading frame    - : non-reactive    + : reactive    \* : kappa<sup>+</sup> and lambda<sup>+</sup> (dual receptor), both were expressed and tested on ELISA, but only one receptor was plotted on graphed figures    FR : framework    CDR : complementarity determining    r : replacement mutation    s: silent mutation