

Table S5. Ig characteristics of IgM memory B cells of healthy donors

Clone #	VH	DH	JH	V # of mut	% mut	CDR3 (aa)	Length	Net Charge
6491C2H	3-23	2-15	4	5	1.7	DLIVGGY	7	-1
6491C3H	3-49	3-21	3	0	0.0	EMLGSTF	7	-1
6491D2H	3-30	4-19	6	2	0.7	ADEEL	5	-3
6491D10H	3-15	6-19	4	3	1.0	DTVRGGQCEL	10	-1
6491B3H	4-34	6-13	4	4	1.0	GTVSSQYY	9	0
6491B6H	4-34	2-15	3	4	1.0	GTVRLDD	7	-1
6491C3H	3-15	6-19	3	3	1.7	DTVRGGQCV	9	0
6492B3H	4-61	6-19	3	3	1.7	DGPGGG	6	-1
6492D2H	3-7	5-12	3	1	0.3	GNYDFWS	7	-1
6492E9H	1-69	3-3	4	10	2.0	SPGAYDDFWSGYYAY	15	-2
50591B5H	3-48	3-3	3	1	0.3	GRGFCSGHT	9	+2
50591B8H	3-23	2-2	6	3	1.0	DTVGIL	6	-1
50591C4H	4-59	5-16	3	5	1.7	GLSGLPY	7	0
50591C7H	4-61	6-19	3	4	1.0	WAGRWLVVCF	10	+1
50591D4H	3-48	3-16	4	6	2.4	DEWGETTEASGY	12	-4
50591E9H	3-33	2-21	3	2	0.7	DTVGGQCSL	9	-1
50591E10H	1-69	3-22	4	2	1.0	ETIEITVL	8	-2
50591F11H	3-74	6-14	5	3	1.0	SPVLGLTNAAA	11	0
50591G9H	5-51	6-19	4	3	1.0	IQLQISC	8	+1
50591G8H	5-a	4-17	3	2	0.7	QTSPAA	6	0
51531D5H	3-30	2-21	4	1	0.3	DPQVGGSPDY	11	-2
51531D6H	3-23	3-15	5	0	0.0	DTVRGSCEPEG	11	-2
51531E3H	4-34	3-23	4	2	0.7	GTVRAPRAD	9	+1
51531F6H	4-61	2-21	3	2	0.7	DTMHQGPGLPPGA	14	-1
51532B5H	3-53	3-15	4	0	0.0	RPWAA	5	+1
51532C9H	4-34	4-17	5	2	0.7	SGALLQEHL	9	0
51531G6H	3-30	2-15	4	5	1.7	DGC	3	-1
51531G7H	5-1	5-16	3	1	0.3	FWRSAPGAED	10	-1
WH102E2H	3-33	2-15	4	0	0.0	DLALD	5	-2
WH102E4H	3-11	2-21	3	3	1.0	GGTRTLRSAFDI	13	+1
WH103C3H	3-33	3-3	3	3	1.0	DTVRGGYNT	9	0
WH103D4H	1-18	1-26	4	3	1.0	DAGKRSSGVTSGSYYRD	17	+1
WH104B3H	4-59	1-26	5	3	1.0	YLLQWENTG	9	-1
WH104B4H	3-33	2-21	3	5	1.7	DLALD	5	-2
WH104B8H	4-59	2-21	3	2	0.7	GLVLEDYYSLV	11	-2
WH104D7H	3-15	3-3	6	4	1.4	DPPNFWSGYYGEYYYYYGMDV	21	-3
WH104E4H	3-11	6-13	4	7	2.4	VGSIAAAGTYDY	12	-1
WH104G2H	3-48	4-11	6	1	0.3	DTVVDG	5	-2
WH104G8H	3-23	2-21	4	8	2.0	MQLTGRDWFYD	11	-1
17WH1B8H	3-33	2-21	3	2	0.7	DLALDAFDI	9	-3
17WH1B9H	3-33	4-17	5	5	1.7	DTDYADSWSSL	11	-3
17WH1C3H	3-23	2-21	4	2	0.7	MQLTGW	6	0
17WH1C10H	3-30	2-21	4	3	1.0	DPQVGGSPDY	11	-2
17WH1D3H	4-34	4-23	2	2	1.0	GRYYTVV	7	+1
17WH1D5H	1-69	5-15	1	5	1.4	VFGAGDRSSALCTS	15	0
17WH1D6H	4-61	6-19	5	2	0.7	DGPGGGWFKSA	11	0
17WH1E6H	3-7	3-16	3	0	0.0	LGEAIQA	7	-1
17WH1F8H	4-30	3-16	4	1	0.3	TPGAGSGSW	9	0
17WH1G9H	4-61	3-15	4	2	0.7	DTQPLPRS	8	0
51312C3H	4-59	3-15	1	2	0.7	TGAGSGEAF	9	-1
51312C6H	3-1	4-15	4	5	1.7	DTVEGRS	7	-1
51312C8H	3-11	6-13	4	1	0.3	VGSIAAAGTYDY	12	-1
51312C9H	3-23	5-16	2	2	0.7	DLIVGGYGSG	10	-1
51312D5H	4-30	7-15	1	3	1.0	YNPGYSSTHYLI	13	+1
51312G2H	3-48	3-9	3	3	1.0	GHC GGSTCDSLERTFDI	17	-1
51312G4H	3-74	4-17	4	6	1.7	HSPSVAKLV	9	+2