

Table S1: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa483-499)-binding memory B cells from patient SR-1.

IG	HEAVY CHAIN						LIGHT CHAIN				REACTIVITY		
SR-1	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin	
C-029	3-74	5-5/18	2	ARGYGEYVYFDL	6	1-27	4	QKYDSAPFT	2				
C-041	1-18	6-19	6	ARRAGWPDYVGMVD	5	1-5	4	QQFNITYS	3				
C-051	4-59	2-8	6	ARHVPHYCNSGVCSAFGMVDV	11	1-39	nd	nd	nd				
C-055	5-51	2-21/6-6	4	ARPMVAASAPGY	4	3-20	1	LOYGSSPPWT	nd				
C-086	3-64	3-3	3	AREGCTYDWSWGYGEDTFDI	9	3-20	2	QOYGNAPMAMT	4				
C-116	4-59	1-7/3-10/3-9	4/5/6	GRLRVDDLWFFPY	nd	1-5	1	HRYNSHRT	nd				
C-118	1-46	3-10	5	ARAGSNWFDP	9	1-39	1	QQTNYIPWIT	4	R	R	R	
C-132	1-18	6-19	6	ARPLEASGWYPPPGMVDV	10	3-15	2	QOYDNWPSYT	4	R	R	R	
C-140	3-23	3-10/6-13	4	AENGSTSLAGIVY	9	2-28	4	MQALTRPPT	2				
C-152	4-34	3-3/3-9	4/5/6	AASRGYAAWQV	6	1-39	1	QOSYTPRT	0	NR	NR	NR	
C-175	4-34	1-26/6-19/3-3	4	ARLRTAFSRSGFSYFRGNNLFD	3	3-15	4	QOYNWPPPLT	3	NR	R	R	
C-188	3-33	3-1	2	ARAQLAVGLWFFDL	9	2-40	4	MQHIOFPF	nd				
C-206	1-69	3-3	6	ARVANKFFGVAQNYFFVHMDV	5	2-28	5	MQALQTLPT	2				
C-207	3-15	3-16	4	TTRLRVVDTRPDY	7	1-27	3	QKYDSVPFT	5				
C-214	3-15	3-16	4	TTLRPSDY	6	3-11	2	QORSNLGY	4	NR	NR	R	
C-216	4-34	3-22	4	ARGLDTSGYYPDFDS	5	3-11	4	QERNWWRVT	0				
C-226	4-38-2	4-11/4-4	5	ARVGSNYYGGWFDP	8	1-39	4	QQTSSPLT	8	NR	NR	NR	
C-228	4-34	3-22	5	ARGRVVRWLLRQWFPD	3	3-15	1	QOYYSSPPT	4	NR	R	R	
C-229	3-7	3-10/3-16	4/5	TSSGAGSTFAF	11	1-8	1	QOYYNVPWT	5				
C-230	3-33	3-3/3-9	6	ARELTPVYGLAWGPKNTRLTYGMVDV	9	3-11	4	QORRSWPLT	5	NR	NR	NR	
C-237	4-39	1-7	5	ARHSNPNYNWYVWFPD	nd	1-39	1	QOSYTPPA	2	NR	NR	NR	
C-241	1-3	1-20/1-1	4	ARDPNWVKGEFDY	9	1-5	2	QOYESVPCD	4				
C-244	4-31	3-3/2-15/2-21	4	ARAIGNHFFDS	nd	3-15	4	QOYNWPPPLT	3				
C-248	3-30	2-15	6	ARSDYCSGEAARSPLYAMVDV	12	1D-33	4	QOYENLPLT	4				
C-249	5-51	3-22	6	ARSLYYDSSGYRGLDV	6	3-11	3	QORSNWPLFT	1				
C-252	3-33	6-19	5	ARDAVYTSIGWFRWVFPD	4	1-12	4	QOQHIFPLT	2	R	R	R	
C-253	4-38-2	5-5/18	3	VGSGYTYGDHYFDM	6	2D-40	4	MORLQFPRT	2				
C-254	1-3	3-9	4/5	nd	nd	1-5	1	LHYNYSYGT	3				
C-259	4-59	3-16/5-12/3-3	5	AREGHMLRPYDSWGGWFDP	10	1-5	2	QOYNSFSPT	7	R	R	R	
C-260	4-59	2-2	6	ARVDCSSSCYWAPLGMNV	2	1-39	4	QOSYSTPLTFTG	0				
C-263	3-48	1-7/1-20	6	RRATLSLNOYGMVDV	nd	2-28	1	MQALHTPPWT	2				
C-265	3-23	1-26	3	AKDWASGSYFADFND	5	3-NL4	4	QORSSL	nd				
C-266	3-74	2-2	4	VRESSDEYNTRTFFDS	9	4-1	2	QOYYTPRT	5				
C-267	3-15	5-24	6	STADDSRWSLVY	14	4-1	2	HOYYPFMFMA	7	NR	NR	NR	
C-268	1-69	3-16	4	ANIDGRVPCFLFDN	15	3-15	1	QOYNWPT	3				
C-272	4-34	6-19	5	AKHPPTYSGRRRNMVVDL	9	1-12	nd	nd	nd				
C-276	4-59	3-22	4	ARGEYVYDGNSTDMRYLDY	nd	1-39	1	EQSYTTPWT	10				
C-281	4-59	1-26/3-3	4	ARHLWEFGPFDY	10	1-12	4	QOAGDFPLT	4				
C-283	4-59	6-19/6-6/25	5	AVGYSRWIDS	10	3-15	2	QOYNNVLYT	1	NR	NR	NR	
C-287	3-73	2-2/3-3	6	TRSRGGMVDV	10	1-39	5	QOSLITPFT	7				
C-291	3-15	3-22	4/5	TTWPGSIRWVGH	nd	1-5	1	QOYNSWY	1				
C-302	3-43D	6-19	4	GKDVGTSAIAGTIDF	12	3-11	1	QOHSNWRPT	2				
C-303	1-46	2-15	4	AREEVFGCSGSCYEDY	9	3-20	4	QOYGISPLT	3	R	R	R	
C-307	3-15	6-19/6-6/25	2	STRNATREYVYVYGMVDV	2	1-39	2	QOSYSTPH	3	R	R	R	
C-311	4-4	2-15/3-16	6	AREKRLGQYYNSGMVDV	nd	3-20	2	QOYSSPPYT	2				
C-315	3-53	4-17/4-23	3	AKNDYGVKGIWAFDM	10	2-28	3	MOGLQTT	5				
C-317	4-59	2-8	5	ARHVSARWVFDH	5	3-20	5	QOYNSPPIT	6	R	R	R	
C-326	4-39	6-19	4	ATSPGTVH	nd	2-28	3	MHALQPT	nd				
C-328	3-20	2-2/2-15	4	ARVLEDSNCDY	6	4-1	2	QOYYSPYT	2				
C-330	3-15	3-16	4	TTDGGAGEFARSFDH	nd	4-1	1	QOYITPRT	4				
C-411	3-30	5-12	6	AKDDTRWFSGIVGGVYHGMVDV	6	1-5	1	QOYNSWY	6	R	R	R	
C-417	3-7	3-10/3-16	6	ARWEEPSTYSMFYHYGLDV	5	1-9	1	QQLNYPRT	2				
C-422	1-46	2-21	2	ARGFCGGDCYSDWYFDS	8	3-20	4	QOYGSLLT	3	NR	NR	NR	
C-427	3-48	2-21	3	VVGATGGIAY	6	1D-33	4	QOYDNLPPIT	2				
C-428	3-33	3-3/3-9	4	ARGPFAEGHYLDY	9	4-1	4	QOYYSFPLT	6				
C-430	1-18	3-10	4	ARESWFDDRKLDDH	7	1-5	4	QOYNSVLT	3				
C-432	3-53	3-10	3	ARDQGLDF	3	3-15	4	QOYNWPPKLT	1				
C-433	4-61	6-19	4	ARDLGGNSGWNOSYFDY	nd	3-20	4	QOYSSPFT	1				
C-435	3-30	2-15	6	ARDWLGYSGDCTCSYNGMVDV	9	1-39	2	QOQSTPHT	5				
C-436	4-61	7-27	4	ARKKVALVGTDFY	nd	2D-30	3	MODTHNPI	4				
C-438	4-31	3-16/5-5	6	ARGWGSYDSGSYGLDV	nd	3-20	2	QOYSSPFT	3				
C-439	3-11	3-3	2	ARETTYDFGTWVHFDV	10	1-16	4	QOYNSVPPFS	1				
C-441	4-38-2	3-3	4	ARGGGDFWGSYSHYFFD	3	1-39	5	QOSYTPPIT	2				
C-443	4-59	2-2/3-10	6	ASLPRSSAWNYHGDV	7	1-17	2	LOHNSPYT	4				
C-447	3-7	6-19/6-13	5	ARDARRSPWYVFPD	7	2D-29	1/4	MQSIGSLFEA	nd				
C-455	3-30	3-16	6	ARDKEGEDYFYGMVDV	4	4-1	4	QOYSLPH	nd	NR	NR	NR	
C-458	1-69	6-6	6	AVWAYHYGMVDV	5	1-9	4	QGRSARTRK	nd				
C-463	3-7	3-22	4/5	GREGFKDHYDSMGYYITQ	4	3-11	1	QORSRVPVPT	nd				
C-472	3-30	3-22	4	AKDRGPPYDFSTSYHPSDY	7	1-9	3	QLLNIYPPT	4				
C-473	3-30	3-3/3-22	4/5	AVWGGYSIGFG	11	2-30	1	PRDQEI	4				
C-481	3-30-3	4-17	4	ARGAIDVYASWRSYFDY	11	3-20	1	QHVSPIPT	nd				
C-486	4-34	6-13	1	ARRHSTSWYNLGMVFOE	nd	4-1	1	QOYFNPWT	8				
C-489	1-18	3-22	6	ARDSFYDRSYNAYYGMVDV	nd	2-24	1	MOATQFPRT	1				
C-490	3-33	6-19/6-6/25	4/5	TRDSOYSRSQTPFRY	4	4-1	2	QOYYGPPYT	2				
C-492	3-30	2-21/3-10/3-16	4	AKDLFYGGGEVFDY	9	3-11	4	QOYWIPLT	4				
SR-1	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _L	J _L	Igk-CDR3 (aa)	V _L -Mut	LPS	dsDNA	Insulin	
C-005	1-3	3-10	6	ARDGGAMVRGLPYHYGMVDV	1	1-36	3	AAWDDSLNGWV	1				
C-007	1-69	2-2	6	ARDRYCSGTTCQNYHYNYMVDV	2	3-21	2/3	AWDTSDDHPV	2				
C-040	1-46	1-26	3	ARERGSYVGRAPGI	9	1-51	3	GTWDNSLSAPWV	5				
C-063	3-33	1-20/1-1	6	AGOGSGTATFYFHGIDV	9	1-51	2/3	GTWDSSRAVAV	nd				
C-071	3-33	1-7/3-16/3-3	6	ARELLRDGMVDV	8	1-51	2/3	GTSDNSRRSVI	nd				
C-090	4-5	2-8	5	ARVNIWGNWVFPD	6	1-47	2/3	ATWDSGSVGV	4	R	R	R	
C-119	3-30	3-10	6	ANYYYYYGMDV	1	2-11	1	CSYAGSYV	0	R	R	R	
C-209	4-39	3-10	6	VRHNEWRGTAGTFYHYAMVDV	nd	2-14	2/3	TSYTTDSTL	7				
C-227	1-69	3-9/3-10	4	ARNKPTTFDTIGSYHFDV	6	2-23	3	CSYAGSNWV	2	NR	NR	NR	
C-231	3-48	3-3	6	ARDNPVGYDFWVMDV	5	1-44	3	ASWDDSLNGV	2				
C-235	3-33	3-3	6	ARDRLALRLEWFRVFMVDV	2	6-57	2/3	QSYDSSYHHV	nd				
C-246	4-59	5-24	6	ARHLPFRNYYFYGMVDV	9	7-43	2/3	LHYGGAQLV	2				
C-251	5-51	2-2	4	ARRIFCSSTRCYFYFDY	1	2-5	2/3	LLYNHCHLTV	nd				
C-270	3-23	3-3/2-21	6	AKDLNNVVIAPAVNYYYHGMVDV	5	1-44	3	AAWDDSLNGSWM	2				
C-277	3-64	1-7	4	VIRGAYRGNVPEY	11	1-47	3	AAWDDSLSGV	2				
C-288	3-48	3-3/3-10	6	ASVGLPSLIYHGMVDV	8	1-40	1	QSYDSSLSGV	2				
C-289	3-30	2-8/5-24	5	ARDMASTANNWFEP	14	2-14	1	SSYTSNVY	2				
C-292	1-69	3-3	4	ARVENALRTLDDY	6	2-14	2/3	SSYTRSTLEVL	3				
C-294	3-73	3-16	6	TROGGDSLSSLYYGMVDV	3	1-44	1	AAWDDLSAVY	3				
C-310	1-46	3-22	4	ARGEVDGTGHYDITDYYPYLYFEY	7	2-8	1	NSYAGRNNY	3	R	R	R	
C-318	1-2	3-10/2-8	6	ARARITPAGVNGMVDV	nd	3-1	2/3	QAWDSTVW	4				
C-319	3-7	3-10/5-12/3-3	4	ARDVFGITRSAHRY	8	1-44	3	AAWDDSLNGWV	2				
C-320	4-34	3-16	6	ARGPRTYSSROFYFYNYAMVDV	7	2-23	3	CSYAGSTFL	4				
C-329	1-2	4-4/4-11	6	ARAWGLODYGMVDV	nd	2-14	2/3	SSYTSSTLV	2				
C-406	1-3	3-3/3-10/3-16	6	AKGAKGSYVGVVDV	17	2-23	3	LSYAGSKWV	3				
C-413	5-51	4-23	4	VRRPPDYGNSGIDY	7	2-14	1	SSFSSGSLVY	4	R	R	R	
C-419	3-15	3-9	6	TTVGTYSDLTCHRYYYNYMVDV	11	1-51	1	GTWDSTLNIFY	6	R	R	R	
C-431	4-34	3-3	6	ARGRYRWFVSDLQSEADYFGLDV	5	1-47	3	AAWDDSLSGFQV	2				
C-437	3-23	1-26	4	AKERVFGSFSYFDY	7	2-11	2/3	CSFATVNLV	8	NR	NR	R	
C-444	3-23	3-10/5-12	4/5	IKDRGMMPTRADF	14	6-57	3	QSYDNNFNWV	2				
C-445	3-15	6-19	4	TTDGLAVAFDY	8	3-25	2/3	QASDSSGTYL	4				
C-462	5-51	6-6/2-21/6-25	5	ARRIAAQGDWLDV	7	1-44	2/3	AGWDDSLNGPV	nd				
C-477	4-39	3-10	4	ARPHSGMTRTEVGFAY	nd	2-23	3	CAHAGSTWV	7				
C-479	3-7	3-9/6-19	4	ASLEGSYFDY	9	1-40	3	QSYDRLSASNWV	nd				
C-482	5-51	4-11/4-4	4	AROYDYFNHFDL	12	1-47	3	AAWDTLRSGV	4				
C-484	3-73	3-3	6	SRSVTTFVGTTRSHNGMDI	5	3-1	2/3	QAWDYSTAY	4				
C-485	4-59	3-22	6	AREGGVYGGYGMVDV	nd	9-49	2/3	GADHSGSNNFV	4				
C-487	3-33	3-10	6	ARGYSVMVRGVIHSDNYGLDF	6	1-40	3	QSYDSSLSGWL	nd				
C-491	1-46												

Table S2: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa483-499)-binding memory B cells from patient SR-2.

IG	HEAVY CHAIN					LIGHT CHAIN				REACTIVITY		
	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin
J-021	3-30	3-3	4	AKDRGGGGGAIFGVVFPMTIDY	5	1-39	4	QOSYSVPLT	4	R	R	R
J-026	3-73	6-19	4	TRLOWDTSGWYRAGDY	5	4-1	4	HOYYITPLT	1	R	R	R
J-027	3-33	3-22	3	ARIHNYDSIGYSSDAFDI	3	1-39	1	QOSSNFPRT	3	R	R	R
J-029	3-48	1-14	6	ARRANVRYMVIPIPVITGSMVDV	13	3-20	2	QRSGGSPGT	7			
J-030	4-4	6-19	5	CCSGGRLRLHS	nd	1D-33	5	QOYYNPLPT	5			
J-036	3-23	5-5/18	6	AKGNTAMWYYALDV	7	2-28	4	MOSLQTLPT	3			
J-037	1-18	6-19	6	ARDGLADYYGLDV	nd	2-28	4	MAAQOTLT	2			
J-040	1-46	3-9	4	ARARHPKRDSIDWLLSPSSMGY	13	4-1	2	QOYHSTPYT	6			
J-050	1-2	3-10/3-16	6	ARENLTFTFHGMVDV	16	1-39	1	QOYNSPPWT	7			
J-059	3-30	3-10	6	AKEGDSRGLGPFDI	6	3-15	1	QOYNNWPLWT	3			
J-062	4-31	3-10	3	VRDASRIPVVRGNKADTFDI	11	1-9	2	QOLSNNPYT	7			
J-082	3-11	5-12	3	ASRTYSYGDAFDI	17	1-9	3	QYLNTPSFT	4	R	R	R
J-089	4-30-4	3-10	5	ARLLFRGVNWFDP	nd	1D-33	4	QOYLNPLPT	3			
J-094	3-23	5-5/18	4	AKDRYGFATFEF	8	1-12	2	QQAQSPPYT	4			
J-101	3-15	3-22	6	THYYESGGHYWGMVDV	7	2D-29	2	MOSSQLMYT	nd			
J-110	4-61	2-2/15	5	ARGYCSGSNCGEGDKWFDP	nd	1-39	3	QOSYGFPT	12			
J-122	1-58	1-26	4	ATDGGVGFDFY	2	1-39	1	QORYSTPWT	4			
J-123	3-21	7-27	4	AREISWGNFDL	7	2D-29	2	SOSTHVPT	nd			
J-124	3-21	6-13/6-19/6-25	4	ARVLGIAVGPIDY	9	3-15	1	QOSNNTSSA	nd			
J-127	1-69	3-3	3	ARDORRHIFDSSGGGAFDF	13	3-20	1	QYGNDSRPT	2	NR	NR	NR
J-133	3-30-3	3-3	4	ARGGRSGYSGY	5	4-1	3	QOYYTPT	2			
J-135	4-61	5-24	4	ARFCRDGYAEYFDY	7	3-20	4	QOYASSLT	4			
J-138	1-69	6-19/6-25	4/5	GYRYSYGAFDK	6	3-20	1	QOYGSPT	1	R	R	R
J-139	1-46	1-7/1-20/3-9	4/5	ARTSMGSONQDWLNHDAFDL	16	4-1	2	QOYFRTPYT	6			
J-142	3-30	3-22	3	AKDLNYYDSSGYFGGAFDI	3	1-8	1	QOYYTPT	2			
J-145	3-11	3-3	4	ARGPWVSPFEY	7	3-20	2	QOYSSAPT	4	R	R	R
J-146	3-48	3-22	6	ARGSPFNKYLVPDITGSMVDV	11	3-20	2	QOYSSPWT	4	NR	NR	NR
J-148	1-69	3-9	4	ATGDLLTYGYSFFDD	10	1-5	1	QOYKSWT	5			
J-150	4-34	3-16/6-19	4	ARGSGSHYHRRARWVFDY	nd	2-28	3	MOSLHTPFT	4	NR	NR	NR
J-151	3-15	2-21	3	TTSWACGGDCNDVFDI	5	1-5	4	QOYNTPLT	4	R	R	R
J-153	3-53	3-16	6	ARDLGYGMDV	3	3-11	1	QORTNWLGT	0			
J-157	4-34	2-21/3-3	4	ARGLELWLVSYGY	9	3-15	1	QOYHFWPRT	9			
J-165	4-61	3-22	3	ARKATFYSDFSGFSVFDI	nd	1-9	4	QQLNRYPT	3			
J-166	3-30	1-7/6-6	4	VSVGTKLWAY	5	1-9	2	QQLNGPYT	3			
J-168	3-11	4-17/4-23/5-12	2	ARGRYGAYFDL	13	3-20	3	QOYSSPFT	3	NR	NR	NR
J-171	1-69	5-24	6	ARIVRDYVPEVYFYAMVDV	4	3-20	2	QOYSSPOYT	1			
J-183	3-15	3-3/5-5	4/6	VRQGGYEFRL	20	3-20	4	QOYNSPLT	6			
J-193	3-9	3-16	5	VKAPRAWGGFDP	5	1-39	4	QOYSTRPT	5			
J-202	4-61	2-15	6	GRGSCNCGSCYPNFNVDV	nd	1-39	2	QOYSSRPT	2			
J-205	3-73	6-19	4/5	TRLEWNTNHWYRAGDF	7	4-1	4	HYYIVPLT	2			
J-216	3-9	3-9	5	AKDQNDLITGDNWDFP	3	1-5	1	QOYNSWT	2			
J-222	3-30	3-10/6-19	6	AKDFGKGYAYHYMDV	nd	3-15	1	QOYKRRPA	9			
J-236	4-59	2-21/3-16	4	GTNTAIGDCDHYFDY	nd	3-11	3	HRTNWLPLFT	2			
J-238	4-31	3-3/3-9	4	AKNKGSGVPLQY	10	3-15	1	QOYNSPPWT	3			
J-252	3-48	5-12	4	ARDQWASVDMYYEY	9	1-39	2	QOYSPYT	7			
J-253	1-69	3-22	4	ARVGYDSDNGYLLDQFDQ	nd	1-39	4	QOYSTPRCT	3			
J-269	3-23	7-27	4/5	AKLGVYRDIET	nd	1-39	3	LQSYSPFT	5			
J-271	3-49	3-10	4	AGANYGSGSAPFDY	8	1-5	1	QOYSTFFA	5			
J-272	4-31	6-6	6	AREEWGKYSARGLDV	10	1-39	1	QOYSTSPRT	8			
J-274	3-73	3-16	4	VREERYDYGGMVDV	nd	1-39	4	nd	9			
J-276	5-51	5-24/6-19	4	ARLREVAIAISHGDY	nd	1-9	1	QRDYSYPPWT	2	R	R	R
J-282	3-33	2-21	4	AKFGAYSLESSFDG	nd	1-16	4	QOYSSPFT	3			
J-284	3-21	3-16/4-4/4-11	6	ARCLQYYAMVDV	3	2-28	4	MALQTLPT	0	R	R	R
J-287	3-48	1-14/2-21/5-24	6	TTEIPNR	8	1-27	1	QKYDASLWT	4			
J-288	1-46	3-10	4	ALMDYESSRY	8	3-11	4	QOYNSPST	1	R	R	R
J-294	4-39	3-22	4	ARHDRYNSAYHH	7	1-5	1	QOYNDLWT	5	NR	NR	NR
SR-2	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin
J-002	1-2	4-4/4-11	4/5	ARGHYSTWYG	nd	1-44	1	AAWDASLNGPVLGTGTR	5			
J-014	4-34	3-22	4	ARRSHITMIVLSDYIDY	7	2-23	nd	nd	6			
J-015	3-23	2-15	4/5	AKDTSSRCSSGTCYLSIDF	3	4-69	2/3	OTWGTGIYVV	2			
J-028	1-3	4-4/4-11	6	ARTSNYYWFDV	30	3-21	1	QWDTSSDHYV	0			
J-064	3-48	3-16	4	AREGTYYDWFAY	12	2-23	nd	nd	6			
J-067	4-30-4	3-10	4	ARVNGDAFDY	14	3-21	1	QVWDPNSDHLVY	2			
J-068	3-23	6-13	4	AKRIGIAAGSRGLDY	8	2-14	1	SSFTNSRSVY	5			
J-069	3-30	2-15	6	AKDFREWWYAYHYMDV	7	1-51	1	GTWDSLSSEYV	7			
J-078	3-71	4-4/4-11	4	TSNYGYVYFDY	21	1-40	2/3	QSYDRTLIGYVV	5			
J-091	3-30	5-12	3	AKDYSYDFDPAFDI	nd	1-40	2/3	QSYDRTLSHVVH	2			
J-095	4-61	3-3	5	ARRISIGVDNWFDP	nd	2-23	2/3	CSYAGRLV	5			
J-103	3-30	nd	4	ARSVGGHFDY	6	3-21	3	QVWYSSDHPGV	1			
J-116	1-69	3-3	6	ARDPPVITTTGVIYGMVDV	3	2-23	2/3	CSYAGFSTI	3	R	R	R
J-140	4-31	4-17	3	AREGNFGDYMFAFDI	nd	2-8	3	TSYAGYHTGV	4	R	R	R
J-141	3-53	5-24	4	ASOKMANAALDY	9	2-8	2/3	SSYAGSNLV	3			
J-144	3-72	3-3/5-5	4	VRQGGYEFAY	20	2-14	2/3	SSYTNSPVT	2			
J-147	3-23	1-26	4	TKSPGWELMYFDY	3	1-47	3	APWDSLSGPG	0			
J-156	4-30-2	3-9	4	ARGMDTAGFDTTISHYFDY	12	2-5	2/3	nd	nd			
J-161	3-7	3-10	4/5	AMFGLAETLDS	6	2-11	1	CSSAGLHSHVY	6			
J-176	3-30	1-26	4	AKERVRYRGGYSYFDY	6	1-51	3	GTWDSLSRAWV	1			
J-181	3-48	2-2	4	ASWYQLPGDY	3	1-44	2/3	VTWDSLSNGPV	4			
J-182	3-9	3-10	4	ARDMRHFFGSGTYGFDY	5	1-47	2/3	ATWDSLSGVV	nd			
J-186	1-2	6-19	4	SRGRRWSSGWYDDY	7	1-44	3	AAWDSLSNGWV	3			
J-214	4-31	3-3	6	ARAPYDWTGDRSYGMDV	10	2-8	2/3	SSFSGNNHVV	2			
J-235	5-51	1-26	5	AKRSFGSFRGNWFHP	nd	1-40	2/3	QSYDRSLASAI	4			
J-241	5-51	5-24	5	AGVGPRIVATMLRDGGFGP	7	1-47	1	AAWDSLSDDV	4	NR	NR	NR
J-247	3-30	2-15	6	AKDFREWWYAYHYMDV	nd	2-23	nd	nd	nd			
J-249	5-8	4-17	5	ARRSGYGDYKRGWFDV	14	1-51	2/3	SVSDNNLRVV	4			
J-250	3-23	2-21	4	AKFLGAYSLESSFDG	nd	6-57	3	QSYDTTKRGEV	1			
J-289	5-51	5-24	4	ARSGLGYNPGDY	2	1-47	2/3	EAWDSLSSTVV	nd			

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined; R: reactive in ELISA; NR: not reactive in ELISA; clonally related antibodies are indicate in the same color

Table S3: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa 483-499)-binding memory B cells from patient SR-4.

SR-4	HEAVY CHAIN					LIGHT CHAIN					REACTIVITY		
	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin	
M-003	3-30	2-2/ 4-17/ 6-6	nd	AKSQLHLKR	8	1-5	1	QRVNSYSSWT	nd				
M-101	3-15	1-7	2	nd	nd	2-28	1	MGALQTWT	1				
M-118	3-23	6-19	4	AKDPGRSGSGTWDY	11	3-11	2	QRSDWPRYT	nd				
M-145	1-3	5-5/ 5-18	6	ASPVGYCYRYHYHYGMDV	nd	2-28	2	MKRIQSEH	nd				
M-164	1-69	3-22	x	ARGNQHYESSNY	14	3-15	2	QOYNDWPGT	nd				
M-167	3-23	3-10	2	AKDRGLYLIVL	nd	1-27	4	QTYHGAPK	nd				
M-201	3-9	3-3	4	ARQLRLTSTYRKYDSTPGVYFDY	11	1-39	4	QOQYTSLT	4	R	R	R	
M-211	4-39	4-23	4	ARDRRGGWARFDY	9	3-20	2	QOQYTSPPYIT	5	NR	R	R	
M-238	3-21	3-10	4	ARWKSVYLAIVAFYD	10	4-1	3	QOQYTSPPA	7				
M-240	1-69	3-22	6	ARGRYHDSSDHYLEVPPYYGMDV	5	1-9	3	QHLNTYLLFT	3	NR	NR	NR	
M-243	3-48	5-5	1/4	ARESDSYGVGDH	8	3-20	1	QOQYSSPPWT	3				
M-254	4-31	1-7	4	ARESVGWNYWGHDC	12	3-11	2	QORDNWPRT	6				
M-286	3-15	6-19	4	TTDGEQWLDYVFDY	6	1-17	1	LOHNNYPPWT	2	R	R	R	
M-292	4-30-4	3-3/ 3-22	6	ARDLGHYDSWGGYPLRMGMDV	nd	1-39	1	QOYSTPWT	4				
M-313	3-49	6-6	5	AKGRIGRRLHWFDP	11	3-15	2	QOYNNWPPY	5				
M-317	3-48	2-2/ 2-21	4/ 5	ARGSSSTSSYIDH	12	3-15	4	QOYNNWRIG	nd				
M-322	1-2	4-17	4	ARGVYDGFSDY	14	1-17	3	LQHSYDPT	2				
M-330	3-7	3-16	4	VGWGGVAHY	7	3-11	2	QORSNWPPY	0				
M-332	4-30-4	3-9	4	AGGNDFSTGLDY	14	3-11	5	QORSNWPGFT	5				
M-333	3-30	3-9	4	AKESVLRFFDWFSSKFFYDS	5	3-15	1	QOYNNWPLA	2				
M-334	3-9	5-5/ 5-18	4	AKDRHRYPSMVFYD	4	1D-33	2	QHYDHLPT	3				
M-336	4-30-4	3-3/ 3-9	4	AGGDHDFSTGLDY	11	3-11	5	QORSNWPGFT	5				
M-339	3-23	1-26/ 5-24	4	VKSSRGVVRDGGDGIY	9	1-5	1	QOYDAYSWT	8				
M-343	3-23	2-21	4	VKDCGGGSCY	12	1-6	nd	nd	nd				
M-345	4-31	3-10	4	ARGLYVYGGSYFDH	3	3-15	1	QOYNNWPLW	0				
M-363	1-2	2-15	4	ARDVNLGYCSGVSCYVFDY	6	2-30	1	MQGTHWPT	2				
M-369	5-51	nd	4	AKGKEGFDY	nd	2-28	2	MQALQTPYT	1				
M-389	4-30-4	3-22	5	AAEAGASDYHISGYFF	6	1-39	4	QOYSTPOT	7	NR	R	R	
M-407	1-69	3-3/ 3-9	4	ATDILRDLPS	12	2-30	1	MQGTHWPT	4	NR	NR	NR	
M-409	3-66	3-10	6	WGFELGGIRYGR	0	3-15	2	QOYNNWPF	0				
M-410	4-39	2-15/ 2-21	4	ARRWVSSFFDY	nd	3-15	4	QOYNDWPLT	5				
M-426	3-49	4-4/ 4-11	4	STLTWPTGRDY	7	3-11	3	QORSNWPPY	2				
M-429	3-23	3-10	4	AKFRPYGSSGSDY	6	1-39	4	QOYSTPSS	nd	R	R	R	
M-430	1-46	3-9/ 4-4/ 4-11	5	ASDDFRSNCFDL	nd	3-20	3	QOYSSPLT	4				
M-435	3-30-3	3-3/ 5-12	4	ARDEEVPVGNAYDFEY	6	1-39	1	QOYSLGT	2				
M-437	3-23	1-7	4	ATDNWNYCLGDY	7	2-24	4	MQTTQLPRS	4				
M-441	4-31	6-19	5	nd	9	3-15	1	HOYNNWGT	3				
M-448	1-69	1-26	5	AKPPVATGGFDI	10	1D-33	3	QOYNSPLFTT	5	NR	NR	NR	
M-449	3-23	6-19	4	AKGDKAVAGTAGFDY	9	1D-33	2	LOYDHLVPMY	5				
M-457	3-23	2-21/ 5-12	4/ 5	VKDVWVQLF	10	1-27	4	QSYTVPPVLS	5				
M-463	3-23	5-24	4/ 5	AKGSSRGVARDYAGNC	8	1-5	1	QOYNDYVIT	3	NR	R	R	
M-490	3-30	3-3	5	AKDLLFFSKNSRSVGSFDS	15	1-39	5	QOYSLPIT	22	R	R	R	
M-507	1-2	3-16	6	ARVLVITGAGKYFYDYGMDV	4	1-13	2	QOYSTFPYT	nd				
M-514	3-11	2-21/ 3-3/ 6-19	4/ 5	ARASVLF	5	3D-15	3	QOYDSWPF	3	R	R	R	
M-519	4-30-4	3-10/ 5-12/ 6-19	4/ 5	TRDVLRGWDDQ	15	3-15	2	QOYNNWPPG	10	NR	NR	NR	
M-529	4-b	5-24	4	AKSLTKTNYFDY	4	1-5	1	QOYNSFGT	5				
M-530	1-69	3-3	4	ARSLNYDFWGSYYFDY	nd	1-5	1	QOYNSFSKT	12				
M-533	4-4	3-10	5	TRDRGATGDDH	17	3-11	3	QORFIWPR	4				
M-535	3-23	3-22	4	AKRDYSDGSDYVPLDF	5	1-5	2	QOYNNVLT	6	NR	NR	NR	
M-703	3-23	3-16	4	nd	nd	2-28	1/3	MQALQSPRT	4				
M-705	4-61	1-26	5	SRVFGELDR	8	1-5	2	QOYNSLHT	3	NR	NR	R	
M-713	4-30-4	5-5/ 5-18	4	ARRRGVNYGYGALFDY	10	1D-33	3	QOYDHLPPFT	2				
M-802	3-15	3-3	6	nd	nd	2-30	3	MQGAHWPPGFT	3				
M-824	1-46	3-16	4	ARNDFGDYGRVSGY	nd	3-20	2	QOYSSSTGYT	3	R	R	R	
M-825	4-39	2-21/ 5-24	3/ 6	nd	nd	1-5	2	QOYNSLYI	2				
M-834	4-61	3-10/ 3-16/ 3-22	6	SRDGRADFGGYYA	8	1-39	2	QOYSTPRT	4	NR	NR	NR	
M-840	4-59	nd	6	ARGASVYDYHYAMDV	11	3-20	2	HOYGGSPYT	6				
M-841	5-51	2-21/ 5-5/ 5-18	4	VRLDGFDDY	9	1-39	1	VANFSD	8				
M-847	4-61	5-5/ 5-18	4	ARYRLVETFDS	nd	1-12	4	QOYNTFPPT	6				
M-855	3-33	4-4/ 4-11/ 7-24	4/ 5	nd	nd	2D-24	4	TOPTQFPRSL	2				
M-859	1-69	3-10/ 3-16/ 4-17	6	nd	nd	1-17	3	LOHNS	nd				
M-862	3-30	3-22	6	AKDLVYSSPSLGPYYHYGMDV	7	1-9	2	QOYNSNPT	4	R	R	R	
M-867	3-23	2-2/ 3-16	3	nd	nd	3-20	2	QHFSTSRAT	4				
M-868	3-15	2-21	4/ 5	VTAQCGDCHASTGSP	nd	3-11	5	QORRNWPI	1				
M-869	3-30-3	7-24	6	ARDYKVENWGGRYYYYGMDV	5	2-28	3	MQALQTPFT	2	R	R	NR	
M-872	3-53	4-2	4	AGRLATAAYDY	4	2-28	1	MQVOTPWT	2	R	R	NR	
M-877	1-2	5-5/ 5-18/ 6-19	1/ 4/ 5	MRGVAPGSGYSGPQNVH	9	3-20	3	QOYVSPGFT	6	NR	NR	R	
M-879	4-59	4-4/ 4-11/ 4-17	6	ARDGTSKYHYGMDV	nd	1-39	2	QOYSTHT	nd				
M-882	1-8	3-3/ 3-10/ 3-16	4/ 5	TRGLPTYVAFWDC	11	1-39	1	QOYSGVPT	7	R	R	R	
M-885	3-23	3-10/ 3-16	4/ 5	nd	nd	2D-40	4	DOGGDO	4				
M-886	4-39	2-15/ 3-22	4	ARIDRRRPFDSGSGFPDY	nd	3-20	1	HOYDPSPT	4				
M-888	5-a	1-1/ 1-20	6	nd	nd	3-20	1	QOYKTPWT	11				
SR-4	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _L	J _L	Igk-CDR3 (aa)	V _L -Mut	LPS	dsDNA	Insulin	
M-230	4-39	5-5/ 5-18	4	ARRGNSFGPPSAPFDY	2	2-14	2/3	SSYTSSTLV	3				
M-261	3-30	3-10	6	ATTRDFYSGRNGGMDV	12	8-61	1	VLYMSSGWT	3	R	R	R	
M-306	3-49	3-9	6	TRDGFVWLSITV	3	2-14	1	SSYTGNNTRPYV	2				
M-312	3-72	3-10	4	TTEGAYAGPDFDH	8	1-44	3	nd	nd				
M-318	3-9	1-1/ 1-20	6	VKDSATLLYYNMDV	9	1-47	nd	nd	nd				
M-358	3-h	3-16/ 6-12/ 6-19	4	ARGEWLFLGRANDY	nd	2-11	2/3	nd	nd				
M-413	3-23	3-10	4	AKWGSLSLWFGVLLD	10	1-47	3	AAWDDSLSVW	1				
M-422	3-74	2-2/ 2-15	4/ 5	TTTLATEAA	5	1-51	1	GTWDDSLSAV	1	NR	NR	NR	
M-433	1-69	nd	4	ARIGHSYTESENFY	15	1-47	3	AAWDDSLNGW	4				
M-458	3-15	2-21/ 4-23	3	IRNSPYDAFI	4	2-23	1	CSYAGTSTYV	0	R	R	R	
M-460	1-69	3-3	6	ARAERHSISVGVGPPSSVQYAMDV	12	1-40	3	QSYDRSLGASV	3				
M-463	4-59	1-26	3	ARVISGRGRAFI	5	1-47	2/3	AAWDDSLSVL	3				
M-493	3-53	1-7/ 4-11	4/ 5	ARNVPTGTWVNF	5	2-14	3	KSYTSSL	6				
M-494	3-30	5-12	4	AKENSQWRFOYFDC	7	1-44	1	AGWDDSLNRV	nd				
M-512	3-15	3-10	4	VTDSSGEWOPFFHY	nd	3-21	1	QVWDISENVY	4				
M-724	3-30	6-19	4	AKCGQWLPSEYFDC	13	1-44	1	AAWDDSLNGV	5	NR	NR	NR	
M-801	1-46	3-10	5	nd	nd	1-51	2/3	VPEEASLNSVL	nd				
M-805	4-4	6-6/ 6-13	4/ 5	ASSNEYVGLHY	10	2-8	1	SSYAGNSV	4				
M-806	4-59	3-10/ 3-16	5	ARGGYSRIODFNWFD	8	9-49	3	GADHSGTGKFWV	3				
M-808	3-53	6-19	6	AAVSAIWAQYHYGMDV	nd	2-23	3	CSNAASNETW	4				
M-811	4-39	4-17	6	ARVDVDDYDGYSLTSGMNV	6	2-23	1	CSYAGSSTYV	5				
M-814	1-69	3-10	4	ARGASGTLFFDY	nd	3-21	1	QVCDVTDHYV	nd				
M-818	1-46	2-21	5	GRGEVVAITODHLD	4	2-23	2/3	CSYAGSSTLV	2	R	R	R	
M-819	3-15	3-9	6	TTDEILTYGSLD	nd	1-44	3	APLGDLSNGR	nd				
M-822	3-23	6-6	2	AKFAWEAYSSSGDFDL	9	2-11	1	CSYAGSYTYV	0				
M-826	3-11	3-3	4	ARVDFWGSYYLDY	8	1-40	3	HSYDNRQSGTW	4	R	R	R	
M-851	3-23	5-12	4	AKDLRGGQNNIVAATDY	nd	2-14	1	SSYTTSTLV	7				
M-871	4-31	3-10/ 3-16	4	ARRSYNFDI	4	1-51	3	GTWDRSLPGW	2				
M-875	3-9	3-16	6	ARGASVITGLTYHYGMDV	4	2-11	2/3	CSYAGSYTLV	3	NR	NR	NR	

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined; R: reactive in ELISA; NR: not reactive in ELISA; clonally related antibodies are indicate in the same color

Table S4: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa 483-499)-binding memory B cells from patient SR-5.

IG	HEAVY CHAIN					LIGHT CHAIN				REACTIVITY		
	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin
Z-034	1-2	6-19	4/5	ARLQWLSNAGFG	9	1-5	1	QOYNSYGVWT	6			
Z-036	4-61	2-2/ 2-8	3	ARDRRLRYHAFDM	9	3-20	1	QOYGSSLWVT	1	NR	NR	NR
Z-037	1-18	3-16	4	ARDLGLTDYELWLKRYRPPPYDY	10	4-1	2	QOYHTTPOYT	4			
Z-038	3-23	2-8/ 3-16/ 6-6	5	ARQVNRILDP	9	3-15	2	QOQDDNWPVYT	1			
Z-203	3-74	6-19	6	VRDSPVAGMKGDKYYGMDV	6	1-39	4	QOQSYTPR	2	R	R	R
Z-205	3-33	3-10	3	ARSGPDVAFDI	3	3-20	3	QOYSGPFGT	nd	R	R	R
Z-207	4-59	6-6	4	ARWEARLDY	6	4-1	1	QOYYTIPWT	2			
Z-208	4-59	6-21	3	AARNVVPATNGRPIDV	8	4-1	2	QOYYSTPYT	4	R	R	R
Z-211	4-39	2-21	3	AGAHAYFSMDV	16	3-15	2	QOYNTWPS	4			
Z-212	3-30	3-22	3	AKTYYSATSGYFFYQH	7	3-15	3	QOYNNWPPFT	4			
Z-221	4-59	2-21	3	AGRNWVPAATDGRPIDI	9	4-1	nd	nd	nd			
Z-222	4-59	2-21/ 3-16	4/5	ATTDF	6	2-30	nd	nd	nd			
Z-233	4-39	6-13	6	AROSAIVGAYYYFMDV	9	3-15	1	LOYNEWPPWT	6	NR	NR	NR
Z-302	4-59	2-21	3	AGRNWVPAATDGRPIDI	7	4-1	2	QOYYSTPYT	4	R	R	R
Z-306	4-39	2-21	6	VRLAISGYYHYMDV	10	3-15	1	LOYNEWPPWT	nd			
Z-313	5-51	6-19	3	VRFRLSGGDAFDI	4	1-16	3	QOYDNFPFT	3			
Z-315	4-39	1-26	4	ARRYSGSHSYFDY	5	1-39	3	QOQSFLLT	4			
Z-318	3-15	3-16	4	ALPMLRGVPY	8	3-11	4	QORSDWPPPLT	4			
Z-319	3-49	3-10/ 3-22	4	TKDVSDMTEPPYFDS	13	3-11	3	QORGNWPPPL	9			
Z-335	1-18	1-26	4	ARSGSPSYGGILSDS	9	1-39	1	QOSHSPSWT	5			
Z-336	4-59	4-4/ 4-11	6	AGTRTENNSSGMDV	nd	4-1	nd	nd	nd			
Z-337	3-48	3-3	4	ARGWNYDLWSGYSAPFDY	3	1-17	4	LOHNSYPLT	1			
Z-339	4-34	1-26	6	ARVKGAYLYFYHYMDV	3	3-11	5	QPRSNWPT	6			
Z-341	3-11	3-9	4/5	VVIPTGYKSGTFSF	12	1-33	4	QOYDTPPT	0			
Z-345	4-59	2-21	3	AGRNWVPAATDGRPIDI	7	4-1	2	QOYYSTPYT	4			
Z-350	4-4	2-15	6	AGSSFYHGLDV	11	3-20	3	QOYSSPFT	4			
Z-352	4-59	3-10	4	ARHLHYSSGIFHYLDS	11	2-24	4	MOQKFPPLT	3			
Z-353	3-23	3-3	6	AKVGGDFWRGATFYFYFMDV	6	3-15	1	QOYNNLWLT	4			
Z-356	3-43	3-10/ 5-5/ 5-18	6	AKDKNIWSPMDV	3	3-11	4	QORSNWPRVT	2			
Z-357	4-59	3-10	4	AGFRFRASDGRPIDI	6	4-1	2	QOYYSPYT	1			
Z-363	4-4	2-2	4	ATRLGYCDDTCKNPLFDH	4	3-20	2	QOYSSPMPYT	3			
Z-367	3-9	2-21	3	AILVVATARDVHDF	8	3-15	2	QOHNYYWT	4			
Z-368	4-31	3-10	4	ARERGYHDF	15	3-15	2	QOYDNWLYT	7			
Z-376	4-61	3-22	4	ASRSTSDSSGYPFDY	4	3-15	2	QOYYSPYT	1			
Z-377	3-30-3	3-22	6	VRKAANYGMDV	6	1-6	3	LDQYSHPT	6			
Z-381	4-61	3-16	6	GGTRTKVNNSSGMDV	nd	4-1	1	QOYYSPWT	4			
Z-382	4-39	3-3	4	ARTTVFGGVIHPAFDS	12	3-15	1	QOYNNWPPWT	2			
Z-401	4-61	2-2	6	ARHAGSTSAWSDRPNRYKYIDV	nd	3-15	1	QOYNNWPT	5			
Z-406	3-48	3-16	6	ARAGLNTNYDYTKRYRNYHYMDV	7	3-15	1	QOYNIWPT	2			
Z-407	3-20	5-24	4	ARDGRDEGHDY	6	3-11	2	QOLFKNPYT	4			
Z-415	4-59	6-25	3	ARVLESSVAFDI	5	2-28	3	MOALGTPT	0			
Z-417	5-51	3-9/ 3-10/ 6-19	3	TGVLFRNDWAPGVYGFDI	5	3-15	1	QOYNNWPPWT	3			
Z-446	4-49	3-10/ 3-16	6	VSRTLPTSHSPGGY	nd	2-28	2	MOALGTWST	5			
Z-448	4-39	6-13	6	GRHRAIGHYHYFMDV	10	3-15	2	LOYNEWPPCT	3			
Z-451	3-11	3-3	4	ARSFCSGNRCSYFYFDY	6	1-5	1	QOYNSYWT	0			
Z-452	4-59	2-21	3	AGRNWVPAAHGWGLIDI	9	4-1	2	QOYYSTPYT	4			
Z-461	4-39	2-15/ 3-16	4	ARRNLVGTTFDFY	nd	1-39	1	QOQSLAPWT	6			
Z-471	4-4	2-15	2	ARDLEYCSGGRCSWFFDL	9	3-20	nd	nd	4			
Z-474	3-33	3-3	4	AREGIGDSWGLYD	5	3-15	2	QOYNNWPHPT	2			
Z-475	3-11	2-15/ 2-21	6	ARHVNYSNYHYIDV	6	3-15	1	LOYNNWPPWT	3			
Z-478	4-39	3-9	4	VRSARRDLTYGRNKEKNHFDI	13	3-20	5	QOYGTST	2			
Z-487	4-59	5-5/ 5-18	4	ARVNSRPLAHFDY	10	1-39	2	QHSYITPY	6			
Z-491	4-59	1-1/ 1-7/ 1-20	4	ARKKSAGQPRGLDY	10	1-39	1	QOYNSYKPT	14			
Z-492	1-8	3-22	4/5	ARDVSRROYDSTGYYPWF	8	3-15	3	QOYNDWPPFT	6			
SR-5	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igk-CDR3 (aa)	V _K -Mut	LPS	dsDNA	Insulin
Z-204	3-33	nd	6	ARDISLNHYYYGLDV	5	2-14	3	SSYTTNNTMM	2	R	R	R
Z-229	5-51	7-27	6	ARHTGVQGMWNSRPNRSTYYYMDI	10	2-14	2/3	NSYANNIVV	nd			
Z-231	3-11	1-26	4	ARDRIVGVSASVDY	4	1-40	3	QSFDRSPRV	5			
Z-303	3-74	3-3	5	ARGRGDSWGGYPPDS	7	2-14	2/3	SSYTTNTFVL	nd			
Z-307	3-9	4-17	4	VKEDIQEDYDGIHFDH	8	1-40	1	QSYDNRLRAYV	4	R	NR	NR
Z-309	5-51	4-17	5	ARSSOITVYDS	13	2-14	1	ASLTSDDTL	7			
Z-316	3-21	1-26/ 1-15/ 6-19	4	TRALVRGTGWGDY	9	2-14	3	CSYTSITTPWV	4			
Z-320	4-4	1-1/ 1-20	4	ARESLNWNDFGNFDY	3	2-14	1	SSYSSLLFV	1	NR	NR	NR
Z-325	3-43	4-4/ 4-11	6	AKNNYESRYSFRNYHYNGLDV	14	1-44	2/3	ATWDDSLNGPV	5			
Z-328	4-34	6-6/ 6-19/ 6-25	6	ARGSLRIAYHYGMDV	8	1-51	3	GTWDDSLSAGV	5			
Z-330	4-59	2-8	4	AROVQHTGFSYLLFDY	7	7-43	3	LIYGVAVQV	2			
Z-331	4-39	3-22	4	ARHPVQSYPLLYFDY	5	2-11	1	CSYAGGYTFWV	3	R	R	R
Z-342	3-74	3-3	6	ARLYDFWVSGYSRVD	6	2-8	1	SSYAGSNPV	2			
Z-344	3-11	3-9/ 3-16	4/5	ARDLWGTGVTGTRFDI	13	2-14	3	CSYDTSARRV	5			
Z-347	4-59	3-22	4	ARGSYDDTSGQPRGLFDH	10	1-40	1	HSYDNTLRGSNV	3			
Z-348	4-59	2-2	3	ARHLPASGGDAFDI	3	2-23	1	CSYAGTSTV	0	R	R	R
Z-349	1-18	3-16	6	ARSLGFRGSYGMVD	4	1-44	3	AAWDDSLNGYVW	0			
Z-362	1-2	2-8/ 3-16	6	ARDKGTVMNYAMDV	3	1-51	3	GTWDDSLSAGV	2			
Z-366	3-64	3-3	4	AREGGRRLSGVIGKHFDFY	7	2-23	3	CSYAGPYTSWV	6			
Z-370	3-21	1-26/ 2-15/ 6-19	4	TRALVRGTGWGDY	9	2-14	3	CSYTSITTPWV	4			
Z-378	3-33	3-22	3	ARAEYDSSGYPPDAFDI	1	2-14	1	SSYTSSTLTV	0			
Z-380	3-33	2-15	6	ARPSTPCSLTSCNPDV	4	2-23	1	CSYAGTSTV	0			
Z-416	4-30-2	6-13	5	ARCHPTSRYSRSPDFD	4	2-14	1	SSYTSSTLTV	3			
Z-420	3-11	5-5/ 5-18	4	VRYSSSTIQIGSRNFDI	8	2-14	nd	SSYTSNT	4			
Z-424	3-33	4-17/ 4-23	4	AREPDYLDIY	4	4-69	3	QTYWSDIHGV	3			
Z-425	1-18	3-22/ 6-19	5	ARNSSWDVENWVDP	7	2-23	1	YSYAGYSTV	6			
Z-429	4-59	1-26	4	ARRRSGLHTGSFHLDS	9	6-57	3	QSYDRTNWV	3			
Z-430	3-23	6-19	6	AKGVSSGWVNGMDV	3	2-14	1	SSYTSSTHYV	0			
Z-436	4-59	6-13	4	ARRQLATHEFDY	10	2-23	3	CSYAGGPTV	5			
Z-438	4-49	4-17	4	ARLTHYGDYFDY	13	1-44	nd	AARDDSL	4			
Z-441	3-20	2-2	4/5	AKYPCRYCSSTRSGLDK	11	1-44	3	AAWDDSLNGPV	3			
Z-443	3-23	3-22	4	AKDFSSFMYSNDSGYCQGLDY	4	1-40	3	QSYDSSLSCSV	1			
Z-445	3-33	4-23/ 5-12/ 5-24	4	ARDGSYEVYD	10	2-18	3	SSFTTGGTYFRV	5			
Z-447	4-59	2-2/ 3-9	4	AROVQSCAGYCYVHFDY	nd	7-43	3	LLYHGAQV	3			
Z-449	4-59	5-24	3	ARWRSDAHVFHALDV	11	2-11	1	CSYAGSYTV	0			
Z-450	3-21	6-15/ 6-19	4/5	ASHLSGDSGGYD	4	4-69	3	QTYWGTIIV	3			
Z-454	3-33	4-17	6	ARGPASTVTKPGWYHYHYGMDV	2	1-40	3	QSYDTSLSGWV	4			
Z-456	4-59	5-24	5	ARFRDGYDSYWFDP	5	3-25	nd	QOYADSSGY	nd			
Z-457	1-2	1-7/ 1-20	5	ARADNWNPSNWFDP	0	2-23	1	CSYAGSYRVV	4			
Z-458	4-59	2-2	4	AREVQSCSTNCLYHFDY	11	7-43	2	LLYSGHTQV	3			
Z-466	1-18	3-3	4	ARVNYDFSNGSHAPYSLDY	14	2-14	3	SSYTTSSSLE	4			
Z-467	4-59	2-2	4	AREVQSCSTNCLYHFDI	10	7-43	2/3	LLYSGHTQV	3			
Z-477	3-48	4-17	4	ARDGLGTVSPLEFDY	4	1-44	1	AAWDDSLNGV	5			
Z-486	3-74	3-3	5	ARGRGDSWGGYPPDS	10	2-14	nd	nd	4			
Z-488	4-39	3-22	4	ARGTYNSDNGYPLGYFDY	8	1-40	nd	nd	nd			
Z-494	3-9	5-12	4	AKDIAGDDIVIASDY	6	2-14	1	SSYTSNTKV	3			

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined; R: reactive in ELISA; NR: not reactive in ELISA; clonally related antibodies are indicate in the same color

Table S5: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa 483-499)-binding memory B cells from patient CHC-3.

IG	HEAVY CHAIN					LIGHT CHAIN			
	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _k	J _k	Igk-CDR3 (aa)	V _k -Mut
E-019	3-48	3-9	4	ARALEPDHILTYDYD	6	3-15	1	QQYNSWLT	2
E-021	4-30-4	3-16	4/5	ASGRIGVRLGGEFLQ	5	1-39	1	QQSDIIPWT	nd
E-040	3-53	3-16	4/5	ARVGLGELSLYYT	nd	2-28	3	MQALQTPQT	2
E-043	3-72	2-15	4	IRTYGCTGGTCEPYFES	3	1D-17	4	LQHKYSPLT	3
E-077	1-69	3-16/2-2	6	ASKPYTWIDRMVIQHYVMDV	nd	2-29	4	QQDKHLRT	nd
E-107	4-59	6-19	3	AGEWAVAGSDAFDI	nd	2-30	5	nd	6
E-206	3-33	3-3	3	ARVALGGWDAFDI	7	1-39	2	QQSSSTPGYT	5
E-209	4-31	3-10/2-15	4	ARESGDLLCSDY	nd	1-39	1	QQSYSTPRT	3
E-211	5-51	2-21	6	ARTKRDCGGDCYQYYGYMDV	1	2-28	4	MQALQTLT	nd
E-212	3-15	2-8	6	TTVGMAPPELLDCTSPPCPRYYGYMDV	1	1-39	2	QQSYNNPRT	7
E-215	3-21	4-17	6	ARANGDYVYHYHYMDV	6	3-15	2	QQYNNWPPYT	1
E-218	3-30	3-10	3	AKAPRLHRPHYGGSRDAFHI	1	3-20	1	QQYGSLLWT	1
E-220	4-39	3-9/5-24/6-25	6	ARESGNTISGFYYMMNV	nd	3-11	2	QQSINWPPSYT	2
E-221	3-23	6-19/5-12	6	AKDRKSGFQNYCYNNMAV	4	3D-20	5	QHCGRSPPT	5
E-222	1-69	2-2	4	ARGVFCSTSCCLFDY	11	3-15	1	HQYNNWWT	3
E-237	3-20	3-10/3-16	6	ARHRGYVGSQYMDV	9	3D-15	3	QQYNNGAT	4
E-241	3-15	4-17	6	TADYGNLGFYYGYMDV	2	3-20	5	QQYGSSSQIT	1
E-248	3-30-3	3-16	6	ARDAVPRYYDWSAYTPDYGYMDV	5	3-20	2	QQYGSPPHT	2
E-251	1-69	2-2/2-15/2-21	6	ARDPPPGRSSNYCSYMDL	8	3D-15	1	QQYTSRT	1
E-255	5-a	1-26/5-12/7-27	4	ARRRNSAWGSDH	10	3-20	2	HOSASSLYT	5
E-257	3-9	2-2/4-11	3	AKDNASALPRPSDAFDG	4	3-11	2	QQRRDWPT	3
E-260	3-48	3-22	6	ARTPYHYDSRSYNPRVGYFYGYMDV	nd	1-39	4	QQSYNSPLT	5
E-261	1-18	2-2	4	AREQGFCSTSCYRSLDF	nd	3-20	2	QQYVSSYT	3
E-267	4-34	2-2	4	ARPHYCSSTCTGPFHY	9	3-15	1	QQYNNW/PWT	5
E-271	3-30	3-10/3-16	5	VRDQFTYAVTGRFDP	nd	1-17	2	QQHNSPYT	6
E-272	3-30	2-2/2-15	5	ARTPNCRSSCYRLVRP	nd	1-39	1/4	QQSYTTPHT	3
E-282	1-69	2-2	6	ARDRYCSGTTCCQNYHYNYMDV	3	1-39	2	QQSYNSSPV	5
E-284	3-7	6-19/6-13	4	ARDGSRNWPYDIDY	6	1-16	2	QQYHTYPT	1
E-290	1-69	6-6	6	ARDPPPGRSSNYCSYMDL	6	3D-15	1	QQYHSRT	1
E-295	1-18	6-19	3	ARERDSSGWRSLAFDI	nd	3-11	5	QQRSFWPPT	2
E-318	4-4	3-10	4	ARDSLEGTDFD	nd	2-28	1	KQPIGTQ	nd
E-323	5-51	2-2	3	AAAIWVPAIPDAFDI	0	1-17	4	LQHNYSYPH	0
E-331	1-69	2-2	4	ARRADCCSPSCPYNY	5	3-20	2	QQYGSPPYT	1
E-334	4-39	3-3/3-22	6	ARERISSTVFVVYDYYMMNV	5	2-28	1	MQALQTPRT	0
E-412	3-9	4-23	6	AKDLLRTVDNNYYGMDV	7	1D-33	3	nd	3
E-415	1-2	1-26	5	ARVGVGALP	3	3-20	1	QQYGNSPGT	0
E-416	3-21	2-2	6	VRETTSYCRSTSCRGNYYMDV	3	2-28	5	VQALQTPLT	2
E-420	4-61	3-3	5	ARSPLYDFWSPRGGFDP	nd	1D-17	4	LQHNYSY	nd
E-421	1-18	3-3	6	ARIFGVIPVPIYYMDV	nd	1-39	2	QQTFSSPYT	5
E-423	4-31	3-10/6-6/6-19	5	ATSIAPRGGNFDDP	nd	1-12	4	QQANSFPLT	3
E-424	3-9	5-5/5-18	5	ARGYSYVYNWLDP	6	2-30	1	MQATHWWT	2
E-429	5-51	1-26	3	ARREGLVLPDGPDTFDI	10	1-6	2	LQDFNFPPT	7
E-431	1-69	2-2	6	AVGGSSGVYCRSSSRLTTPHYFYMDV	2	1-39	5	QQRYSTPIT	3
E-432	4-61	3-3	6	AREHGSWYGVDFYNGVDV	nd	3-20	1	QQHSSLPDT	4
E-435	1-8	6-19	6	ARGGSGWYDI	6	1-5	1	QQFNSPRT	3
E-516	3-66	3-10	6	AKESAMVRGVYGYGYMDV	3	1-39	2	QQSYNTPRT	7
E-520	3-30-3	3-3	5	ARPDYHFVWNYWFDP	6	3-15	1	QQYHNWPLT	2
E-522	4-31	2-21/3-10/6-19	5	AGDKGIAEGIDP	nd	1-17	3	LQHNYSYPT	3
E-523	3-23	3-22	3	AKNRTLILVDFRCFDI	nd	1-37	5	QRTYNAPR	nd
E-524	3-74	2-2	6	ARSGPAALDV	7	3-20	4	QQYGSNPLT	5
E-525	3-21	5-12	2	ARKRGKGGHDYGNWYFDL	8	1-39	3	QQSYSPLRT	8
E-526	1-8	6-19	4	ARGRNSGWSYNFDN	6	1-33	3	QHYDHWPSIFT	4
E-529	3-30-3	2-2	3	ARDRNWVPAAPDAFNI	3	1-39	4	QQSYTTPLT	3
E-530	1-2	6-19	4/5	AKDKVYGINLADF	10	4-1	2	QQYFRPPPT	nd
E-532	4-39	6-19	6	ARNSQWLFCFGGMNV	nd	1-9	3	QQILDNPFT	3
E-533	1-2	2-2	4	ARGQMVPAILPY	2	3-20	2	QHYGNSPNT	3
E-536	4-59	2-15/3-22	6	ARVYSPGSEGNFYGYMDV	6	1-39	1	QQSYSLPRT	6
E-540	1-2	2-15	5	VRGYCSDTTCVIGGALDP	10	2-28	3	LQALQTPRT	3
E-543	3-23	3-3	4	ATHGVVLPSDY	nd	3-15	1	HQYHDWPLT	2
E-545	1-18	6-13/6-19	4	AREFTGTWYFLDY	7	1-39	4	QQSYSAPTH	5
E-546	3-30	2-21/2-8	6	ASPGGGRTYDYGMDV	7	2-28	2	MQALQTPVT	2
E-548	4-34	2-2	3	ARRPIVIPARKRGAFDI	nd	1-39	1	QQSYFRT	3
E-549	4-39	3-3	6	ARTADFWSHGVIVPHSEYMDV	nd	4-1	4	QQYHSAPLS	8
E-550	3-53	3-16	4	ARGKPYDYWGGFDY	2	1D-16	4	QQSYSPRS	nd
E-551	3-30	3-16	4/5	AKDRLGSAEGLIWPDN	6	2-28	5	MQGLQTPIT	3
CHC-3	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _k	J _k	Igk-CDR3 (aa)	V _k -Mut
E-014	4-39	1-14	4	VTANQQY	16	3-21	1	QVWDSGSAHYV	nd
E-029	4-39	3-3	4	ARHGKALRYLEGSYPFDY	6	2-23	2/3	CSHAGSTPLRHVI	2
E-038	3-23	3-10	4	AKNTYTTFTSGFDC	nd	2-8	3	SSYAGNNIV	3
E-054	1-69	6-19	6	ARDTVAVPHNYGYMDV	4	7-46	2/3	LLSYTGGRV	5
E-085	4-39	5-24/6-6	4	GRGWPSAFY	nd	3-1	1	QAWDTNSYV	5
E-086	1-18	2-15	4	ARERGAVVVTTTFDS	6	1-40	1	QSYDSSLRGGV	nd
E-108	3-23	6-13	6	ANEQQLVTAYGMDV	7	1-51	1	GTWDSLRAGV	1
E-111	4-39	3-10	6	VSARGSVYYGYMDV	8	1-44	2/3	AAWDDSLNGYVL	2
E-121	3-23	3-16	4	AKDRGGLISKFDY	6	2-8	2/3	TSYAGITNVV	2
E-127	3-9	1-26/3-16/7-27	4	AKDSGGNGALHPDF	5	4-69	2/3	QTWGTGVRVL	5
E-214	1-18	2-2/2-15	4	ARSDIWA/VPTGIYSDYFDY	nd	1-51	2/3	GTWDSLSVVV	3
E-223	3-53	6-19	6	ARHQSSGWYGDGMVDV	7	1-40	1	QSYDSSLRGGV	4
E-247	4-59	3-3/3-16	4	ARMGVVWSSFLLELYFDL	nd	1-36	2/3	ATWDDSVNGPV	2
E-343	5-a	5-12	4	ARQNGAYDSGFY	3	3-21	3	QVWDSSTDHGV	0

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined

Table S6: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa 483-499)-binding memory B cells from patient CHC-6.

IG		HEAVY CHAIN					LIGHT CHAIN			
CHC-6	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _κ	J _κ	Igκ-CDR3 (aa)	V _κ -Mut	
B-004	1-46	nd	3	VREGAREAFDV	9	3-11	5	QQRINWPT	3	
B-006	3-48	3-10	4/5	AFMSHNFRGGFSDV	6	3-20	2	QQYGSAPPYT	5	
B-008	1-46	2-2/ 2-15	4	ARDLHRSEYCSDDGCYPIDY	6	1-5	2	QQYDTYLYT	2	
B-011	4-34	3-3/ 6-19	3	TRGRSREWPTSDI	13	3-20	1	QYYGSPRPT	7	
B-023	4-61	3-16	6	ARESAGEGTPSGYGLDV	8	1-39	3	QQSYSTPQIT	6	
B-024	1-18	2-21/ 3-3	4	ARDSDNWIHYFDY	5	1-39	2	QQYSSSPRT	3	
B-028	3-23	2-2	6	AKDKSATYHFYNGMDV	8	3-11	4	QQRSNWPLT	2	
B-030	1-2	2-8/ 4-4/ 4-11	4	ARLNGDYTHFDY	8	2-28	4	MQALQTPHA	3	
B-031	4-59	3-9/ 3-16/ 6-13	6	ATTSWATDAFET	8	3-20	4	QQYSSSPLT	5	
B-043	3-21	3-22	4	ArEDSSGYSYFSDY	5	3-20	1	QQFDGSRWT	1	
B-051	3-9	2-6	5	AKDIRTRLGVCAGGICYNWFDP	5	3-15	2	QQYNNWPTY	1	
B-052	1-2	2-2/ 2-8/ 6-25	1/ 4/ 5	VTIPSARKDFRGY	16	1-9	5	VQLGRYPIT	10	
B-058	3-21	1-26	4	ARENSGTYHQADY	11	1-39	1	QQSLRTPRT	3	
B-064	4-4	3-22	6	ARSYYDDSSGYSSHYYYYYMDV	5	1-39	2	QQYSYYPYT	3	
B-065	4-59	2-21/ 3-3/ 7-27	3	ARATQASSNAFDI	11	3-20	1	QHYGSSSWT	4	
B-069	4-4	2-21	5	AKPGAYCGGDCYDEGG	7	3-11	4	QQRSDWPPKFT	0	
B-071	4-59	3-10/ 3-16/ 4-17	3	ATTGGLLTPDGSYLEGAFDV	9	1D-33	4	QHYDNLPTV	5	
B-073	3-66	6-19	5	ARDLAVAGTGNWFDP	7	3-20	1	QQFRT	2	
B-074	4-39	3-16	4	ATPVYDYVWGRSRPPRYFEY	9	3D-15	4	QQYNNWSPLT	3	
B-078	3-43	6-13	4	ARDIPHISISWFYLDL	8	3-11	4	QHRTNWPLT	3	
B-079	3-48	3-3	4/5	ARESTIFGGADH	3	3-11	5	QQRSNWPRIT	0	
B-084	5-51	3-16/ 5-12	1/ 4/ 5	ARHNLKGLLEH	7	1-5	1	QQYNSYRST	3	
B-090	3-23	4-4/ 4-11/ 6-13	4	AKDADYSSPYFDD	9	3-20	1	HOYGSST	4	
B-092	1-69	3-22	3	ARAADYYSRSGWVALDI	8	3-15	2	QQYNNWPPYT	2	
B-103	1-2	1-1/ 3-16	6	ATTLQRFTVLDGMDV	2	1-39	3	QQYSSPAT	4	
B-105	3-23	1-26/ 3-16/ 5-12	4	ARDLEYSADYLDGIYFDS	6	1-9	1	HQLNSYPRT	0	
B-106	3-30-3	6-13	4	ARDLKGYPYSTWYTMIFDY	3	3-11	2	QQRSNWPTY	3	
B-107	3-7	3-3/ 3-22	4/5	ATMDTIFYDSVGYEVLDH	6	1-9	4	QQLNSVPPT	3	
B-108	4-4	6-19	4	TSQYSSGIWHDY	9	4-1	2	QQYRSAPOT	3	
B-110	3-9	2-2/ 2-15/ 2-21	3	AKDTEILPNALVAFDN	nd	3-11	4	QQRSNWPLT	1	
B-117	3-30	2-15/ 6-19	6	ARAGGPISYFITSSTTI	11	1-39	3	QQSYSSPFT	5	
B-128	3-23	6-19/ 6-13	4	AKETSTWYYPIDY	5	1-6	3	LQDYDYPFT	3	
B-129	3-49	1-1/ 1-7/ 3-3	4	SRASTDGLDY	7	4-1	1	QQYDTPWWT	3	
B-130	3-66	2-15/ 3-16	4/5	ANGGHSAY	8	4-1	1	HQYITAPVT	2	
CHC-6	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _λ	J _λ	Igλ-CDR3 (aa)	V _λ -Mut	
B-005	4-59	3-22	3	ARARPLNYYDNSGVDAFDI	4	1-40	1	QSYDSSLASVY	2	
B-007	3-23	3-10/ 3-16	4	AKVVDNHGNSNFFDH	7	2-14	2/3	SSYTSISTVI	2	
B-010	1-69	3-3/ 3-9/ 3-16	3	TKDLHHRGQADYDGFVDV	14	1-40	3	QSFDSRLRGPV	5	
B-018	3-74	3-16	4	VRLSLGVGVANDY	6	1-47	1	AAWDDSLSGSYV	1	
B-026	4-39	3-10	6	ARREVGYSYGNVHMDV	4	2-23	3	CSYANSTTWW	3	
B-034	3-21	4-17/ 4-23	3/6	ARGMSTVYGVVHSGDI	6	2-14	2/3	SSYTTSTLTV	4	
B-047	3-66	3-22	4	ARGAYYDGPYQLEAFYFDY	nd	1-40	1	QSYDSSLNAFV	4	
B-049	3-23	4-17/ 4-23	2	AKDDYGTVDGVGVYFDL	9	3-1	2/3	QAWDSGTVI	4	
B-060	3-74	5-24	4	ARGWLPLDY	4	1-44	3	AAWDDSLNGWA	3	
B-067	3-15	3-16	6	MTDIGMEEFRGAIDTSRYSSYYMDV	7	4-69	3	QTWGTGIV	2	
B-077	3-33	3-3	4	ARDKTFWGFHDH	9	2-8	1	SSYVGGNFYV	3	
B-088	4-34	2-21/ 3-9/ 6-19	4	ARGVVDVAVTGLIAPYFFDY	8	1-40	2/3	QSYDRSLSVV	7	
B-089	3-7	3-16	4/5	AKEHWGPTSP	6	2-8	1	FSYAGSSYV	2	
B-091	1-2	3-10	6	ARDARFRELSGFIMDV	3	2-14	2/3	SSYTSSTTVV	5	
B-094	3-30	4-17/ 4-23	2	ARLIDYGNLTVTSNYDV	13	3-27	1	YSATDYTV	5	
B-095	3-23	3-10	6	AKLDGPTMQGVINYYAMDV	2	3-25		QSADSSDTY	2	
B-102	3-30-3	5-5/ 5-18	6	VTGRTAHYVYGMVDV	6	2-14	3	CSYTTISTWW	2	
B-121	3-21	3-22/ 3-3	5	ARRVPRLWSRFDS	7	1-40	2/3	QSYDTTHVI	3	
B-127	4-28	3-10	4	AGGLWFGSFDY	7	2-11	2/3	CSYAGTFRDVV	3	

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined

Table S7: Ig gene analysis and antibody reactivity of HCV E2 peptide (aa 483-499)-binding memory B cells from patient CHC-8.

IG	HEAVY CHAIN					LIGHT CHAIN				
	V _H	D	J _H	IgH-CDR3 (aa)	V _H -Mut	V _K	J _K	Igκ-CDR3 (aa)	V _K -Mut	
CHC-8										
S-007	5-51	2-21/ 6-25	4	ARRRAAPAYYLD	4	1-27	4	QKYNASPLT	2	
S-011	4-b	3-3	4	ARVEGTRTIFGVMDY	7	1-5	1	QQYNSYPWT	2	
S-013	3-72	4-17	4	ARLAYGDYFFDY	2	1-16	4	QQYNSYPLT	1	
S-016	3-9	2-21	6	AKDIDCSGGCCYSNFYGMDV	4	2D-29	4	MQTIQLPLT	9	
S-017	4-30-4	2-2	3	ARDGYCSSSTCYLRDVFDI	6	1D-33	1	QQFDDLPR	3	
S-021	4-39	6-19	4	AKPRDDYSGWYPPFDH	7	1-5	4	QQYKSNPEIT	2	
S-022	4-61	1-7	5	CREGYPIGILVELLSIF	nd	1-39	1	QQYSNPR	7	
S-027	3-21	2-2/ 2-15	6	VRDRDVLPGANFYAMDV	8	1-5	1	QQYNSYRRT	3	
S-028	5-51	5-12	4	ARRMDSGYDPQQYFDY	6	1-39	2	QQYSNRNT	6	
S-138	3-30	3-22	4	AKGNYYYDSSGYGDDY	2	4-1	4	QQYYSTPLT	0	
S-141	3-7	2-2	4/ 5	ARENRRGIPVSI	nd	2-30	2	MQATQWPFT	4	
S-146	1-18	4-4/ 4-11/ 4-17	6	VRDRHEVYGNYGDDYMDV	5	1D-17	2	LQHNSYPYT	1	
S-152	3-48	1-7/ 4-11	4/ 5	ATRKNKITY	9	1-39	1	QQIYTTWT	nd	
S-154	1-69	3-3	6	AAHHESTRYLFAGAGNYYMDV	8	1-5	1	QQYKTMGT	3	
S-155	3-30	4-11/ 4-17/ 4-23	4	ARNIDVVGDFD	11	1-5	1	QQYSTYST	5	
S-158	1-3	2-15/ 2-21/ 7-27	4/ 5	ARDWWGSYDC	10	3-15	2	QQYQRNT	0	
S-159	1-69	3-3	3	ARTYNFWSGYTYAFDI	7	2-28	4	MQTLQSLT	0	
S-165	3-23	7-27	4/ 5	AERGWNWGPFFHN	8	3-15	4	QQHSDWFLT	3	
S-176	4-59	2-15/ 2-21	6	ARQKEVVEGYYHYHGMDV	10	1-39	5	QQNYSIT	5	
S-188	3-74	3-9/ 5-5/ 6-13	4	ARDLSWLLFDY	8	2D-29	1	MQSIQFPWT	4	
S-190	3-21	3-16	3	ARDLGGRRRLRSDFDF	7	2-40	4	MORIEFLT	1	
CHC-8										
S-004	5-51	3-3/ 5-12	5	ARRVDVVMFMFGDNWFDS	10	1-40	2/ 3	QSYDTSLSASL	5	
S-005	4-39	2-2	4	TRLSSACATSCYDGYFDD	7	1-51	2/ 3	GTWDSRLSTVV	3	
S-010	3-7	3-10/ 3-16	4/ 5	ASYHGGFFSPY	9	2-14	1	CSYSSSTYV	4	
S-018	4-b	1-26/ 3-3	4/ 5	ARTGVGARVQFDS	11	2-14	2/ 3	LSYTLNNTLV	5	
S-142	4-4	2-2	5	nd	9	6-57	2/ 3	QSYDNNINLV	8	
S-153	7-4-1	3-9	4/ 5	ARDRYDFYFGS	7	1-36	1	STWDYSLSAPYV	nd	
S-177	1-69	3-3/ 3-16	6	ARGDRDRFTWFGNYYNMDV	6	2-23	2/ 3	CSYAGGPV	2	
S-183	3-23	4-17	3	GRDPNGDYLGAFD	9	3-1	2/ 3	QAWDSSTVV	0	
S-191	3-23	3-22	4/ 5/ 6	AKGANYYDNGGYLN	7	1-47	2/ 3	ATWDDSLSGVV	9	
S-194	1-3	3-3/ 3-9/ 6-13	1/ 4/ 5	VRDRRAGKDFEH	11	2-14	1	CSYTFSSARV	5	
S-415	4-b	1-7/ 1-26/ 6-19	5	ARIIGIWGNWFD	5	2-23	2/ 3	CSYVGSRRV	4	
S-437	1-69	3-10	4	ARTRAGIPFGSGSYKQYFFDY	7	2-14	1	CSYATSSFEV	3	
S-447	7-4-1	6-19	4/ 5/ 6	ARAPYSYSSGWLYN	3	2-11	1	CSYAGSYV	nd	
S-493	4-34	6-6	4	AREGPLFQPRIAARRRPKYFDY	11	1-40	2/ 3	QSYDSSSLTGYMV	4	

aa: amino acids; V-Mut: no. of mutations within V region; nd: not determined