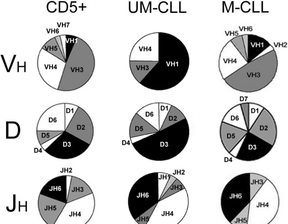
Supplemental Figure S1



Supplemental Figure S1 UM-CLL B cells display a unique Ig repertoire. V_H (top), D (middle), and J_H (bottom) gene segment usage in control $CD5^+$ (left), UM-CLL (middle), and M-CLL (right) B cells. V_H1 usage was significantly increased to 60.7% in UM-CLL B cells compared to 6.5% in control $CD5^+$ ($P < 0.0001$) and 13.8% in M-CLL B cells ($P = 0.0003$). Although D3 family usage was increased up to 50% in UM-CLL B cells it didn’t reach statistical significance. J_H6 usage was also increased in both UM- and M-CLL B cells without reaching statistical significance.

CLL No.	**HEAVY CHAIN**							**LIGHT CHAIN**					**REACTIVITY**				
	VH	D	RF	JH	CDR3 (aa)	Length	Mutations	Vκ	Jκ	CDR3 (aa)	Length	Mutations	ssDNA	dsDNA	Insulin	LPS	HEp-2 ELISA
64	4-39	3-22	2	2	ARPLIYYDSSGPDWYFDL	18	0	3-11	1	QQRSNWPPWT	10	0	-	-	-	-	+
68	1-69	3-16	2	3	ARGGDYDYVWGSYRSNDAFDI	21	0	3-20	4	QQYGSSPT	8	0	+	+	+	+	+
141	4-34	5-5	3	5	ARGDWRIVRLPAAVDTAMAANWFDP	25	1	1-27	2	QKYNSAPRMYT	11	2	+	+	+	+	+
185	3-13	5-24	3	4	ARGPRELVATIPYYFDY	17	2	3-11	4	QQRSNWPALT	10	0	-	-	-	-	+
246	1-69	3-3	2	6	ARSDQNYDFWSGYFRYYGMDV	21	0	3-20	1	QQYGSSPET	9	0	+	+	+	+	+
249	3-23	2-21	3	4	AKDRIVVVTAILQD	14	3	1-8	1	QQYYSYPRT	9	0	+	+	+	+	+
258	1-69	3-16	2	3	ARGGIYDYVWGSYRPNDAFDI	21	0	3-20	1	QQYGSSPGT	9	0	+	+	+	+	+
260	4-39	2-2	3	6	ARAEIVVVPAAYYYYYGMDV	20	0	1-27	3	QKYNSAPQVT	10	0	+	+	+	+	-
266	1-2	6-19	1	4	AREQWLGAENFDY	13	0	1-39	2	QQSYSTPPKT	10	0	-	-	-	-	+
270	1-2	6-19	1	4	ARVQWLGLRHFDY	13	0	1-39	2	QQSYSTPPYT	10	0	+	+	+	+	+
321	4-34	3-3	2	6	ASAKGPIWSGIYYYYYYGMDV	21	0	2-24	2	MQATQFPYT	9	0	-	-	-	-	-
340	1-2	6-19	1	4	AREQWLVLKNFDY	13	0	1-39	2	QQSYSTPPYT	10	0	+	+	+	+	+
355	1-69	3-3	2	6	ARADLPYYDFWSGMYYYGMDV	21	0	1-5	1	QQYNSYQT	8	0	+	+	+	+	+
360	1-3	6-19	1	4	AREQWLVLNYFDY	13	1	1-39	2	QQSYSTPPYT	10	0	+	+	+	+	+
376	1-24	4-17	3	1	ATSAFTVTHAEYFQH	15	0	3-11	1	QQRSNWPWT	9	0	-	-	-	-	+
394	1-69	3-16	3	4	ASTQRVPIMITFGGVIVMGNLTGPKYYFDY	30	0	1-33	3	QQYDNLPSFT	10	0	+	+	+	+	+
403	4-4	5-5	2	6	ARAHSYGLRYYYYYGMDV	18	0	1-39	2	QQSYSTLPRCS	11	0	+	+	+	+	+
408	4-28	2-2	3	6	ARGSRRSDIVVVPAAKARYYGMDV	24	0	3-20	1	QQYGSSPPWT	10	0	+	+	+	+	+
415	1-3	3-3	2	4	ARRPESGYSFVTPFDY	16	0	1-39	2	QQSYSTPPHT	10	0	+	+	+	+	+
472	1-69	3-22	2	1	ARGGYYDSSGYYRAPH	16	0	4-1	4	QQYYSTPRT	9	0	+	+	+	+	+
GO13	1-69	2-2	3	6	ARGGDIVVVPAAMRYYYYGMDV	22	0	3-11	3	QQRSNT	6	0	+	+	+	+	+
	VH	D	RF	JH	CDR3 (aa)	Length		Vλ	Jλ	CDR3 (aa)	Length	Mutations	ssDNA	dsDNA	Insulin	LPS	HEp-2 ELISA
14	1-69	3-3	2	6	ATKNDFWSGYYEGYYYYYYMDV	22	0	3-1	1	QAWDSSTCYV	10	0	+	+	+	+	+
20	1-58	1-26	3	4	AAPPLVGATTIGY	13	0	3-1	2	QAWDSSTVV	9	3	+	+	+	+	+
58	3-15	3-9	1	4	TALLRYFDWLLSPYYFDY	18	0	1-44	1	AAWDDSLNGPFYV	13	0	+	+	+	+	+
152	1-2	3-16	3	5	ARGGESRAPIVTYNWFDP	18	0	2-11	3	CSYAGSYIWV	10	0	-	-	-	-	-
258					See 258 kappa			2-8	1	SSYAGSNNLL	10	6	+	+	+	+	+
259	3-11	5-5	2	6	ARDRGVLNSYGYFYYYYGMDV	21	0	2-14	1	SSYTSSSTLYV	11	0	+	+	+	+	+
400	4-39	3-10	1	4	ASTRGGLLWFGESLNFDY	18	0	2-14	1	SSYTSSSTLGV	11	0	+	+	+	+	+
RF22	1-69	3-10	3	6	ARGMVRGVIIYYYYYYYMDV	20	0	1-44	3	AAWDDSLNGRV	11	0	+	+	+	+	+

CLL No.	HEAVY CHAIN								LIGHT CHAIN					REACTIVITY				
	VH	D	RF	JH	(-)	CDR3 (aa)	Length	Mutations	Vκ	Jκ	CDR3 (aa)	Length	Mutations	ssDNA	dsDNA	Insulin	LPS	HEp-2 ELISA
33	4-34	2-15	2	6	2	ASRFYCSGETCHSSQFYYYHGLDA	24	24	3-20	1	QQYGSLPST	9	11	-	-	-	-	-
38	3-7	/	/	6	3	ARDGGPPDYGMDV	13	21	1-5	2	QQYNSYSGYT	10	22	-	-	-	-	-
88	5-51	6-19	2	4	1	AKSGYYNAWYGSLDS	15	28	1-27	1	QKYNSAPWT	9	14	-	-	-	-	+
109	1-18	/	/	4	1	ARGGVQVWANDY	12	20	1-27	4	QRYNSAPVT	9	9	-	-	-	-	+
124	3-7	3-22	2	3	4	ARVDAYFEDSGYRSFDI	17	22	1-39	2	HQSCTTPYT	9	26	-	-	-	-	-
127	6-1	/	/	6	3	ARDRADYGMDV	11	26	4-1	1	QQYFGTPWT	9	13	-	-	-	-	-
153	3-53	2-15	2	3	3	ARDRNADGSTFDI	13	13	1D-13	5	QQINNSPA	8	16	-	-	-	-	+
153-2	3-11	3-22	3	4	1	ARVKVVVITSSWFDY	15	4	1D-13	5	QQINNSPA	8	16	-	-	-	-	+
154	1-18	6-19	1	4	2	AREQWLVLSHFDY	13	4	1-39	1	QQSYSTPPWT	10	0	-	-	-	-	+
165	3-15	1-26	1	6	3	TTDNNKWEVTSAGGMDV	17	16	2-28	1	MQALQTPWT	9	3	-	-	-	-	-
169	3-33	3-9	2	4	2	AREGGVTGQGGFDY	14	25	4-1	4	QQYYSTPLT	9	0	-	-	-	-	-
183	4-34	5-5	3	6	2	ARGYGDTPTIRRYYYYGMDV	20	10	2-30	2	MQGTHWPPYT	10	5	-	-	-	-	+
215	3-7	/	/	6	2	ARAPSAVFGVTRDYNFYGLDV	21	27	3-15	1	QQYSNWPPWT	10	15	-	-	-	-	+
240	4-34	5-5	3	6	2	ARGYADTPVFRRYYYYGMDV	20	10	2-30	2	MQGTHWPPYT	10	7	-	-	-	-	+
261	3-33	5-12	3	4	2	ARDPVVATAYYFDY	14	11	1-39	3	QQSYSAPRT	9	22	-	-	-	-	+
265	3-23	2-8	2	4	1	AKNPYCTYGLCYGLEY	16	26	1-D16	2	QQYNTYPYT	9	7	+	+	+	+	+
280	5-51	1-26	3	3	1	ARPRIVGGTMGAFDM	15	12	1-27	4	QQYNSAPLT	9	19	-	-	-	-	-
331	3-48	/	/	5	2	ARGPYDVGGPLNWFDP	16	12	1D-8	2	QQYYNFPYT	9	13	-	-	-	-	+
336	1-3	6-19	1	4	2	AREQWLVLSYFDY	13	5	1-39	2	QQSYSSPPYT	10	1	+	+	+	+	+
342	4-34	5-5	3	6	2	ARGWGDTPMLKRYYYYGLDV	20	10	2-30	1	MQGTHWPWT	9	9	-	-	-	-	+
377	2-5	4-23	2	4	5	AHRRELNADWDYGDFDY	17	18	1-33	2	QQYDHRPMYT	10	13	-	-	-	-	-
	VH	D	RF	JH	(-)	CDR3 (aa)	Length		Vλ	Jλ	CDR3 (aa)	Length	Mutations	ssDNA	dsDNA	Insulin	LPS	HEp-2 ELISA
105	3-23	2-21	2	4	3	ARDQCGGDCPRLGGYFDY	18	4	3-21	1	QVWDSSSDLPYV	12	7	-	-	-	-	+
169						See Kappa			1-44	3	AAWDDSLNGWV	11	3	-	-	-	-	-
189	4-34	/	/	5	3	ARGTKEDFVPRGFDS	15	21	3-21	3	QVWDSSSDQWV	11	7	-	-	-	-	-
255	4-59	3-22	2	4	2	ARHRGYESSGYYSSYFDY	18	12	3-1	2	QAWDSSTVV	9	7	-	-	-	-	-
257	3-7	7-27	1	5	0	ARGQQLGS	8	14	8-61	3	LMHMGSGIWV	10	9	-	-	-	-	+
282	3-21	/	/	6	2	ARDANGMDV	9	7	3-21	3	QVWDSSSDHPWV	12	6	-	-	-	-	-
332	1-69	3-22	2	4	3	AREALYDSSGYYGVDY	16	6	2-23	1	CSYAGGGTFYV	11	0	+	+	+	+	+
374	4-34	2-2	3	6	2	ARGQQDIVVVSAATLVNSYNYMDV	24	16	3-19	1	NSRDSSGNHYV	11	4	+	+	+	+	+
412	3-21	/	/	6	2	ARDQNGMDV	9	6	3-21	3	QVWDSSSDHPWV	12	2	-	-	-	-	-

Ig	HEAVY CHAIN						LIGHT CHAIN				REACTIVITY				
	VH	D	RF	JH	CDR3 (aa)	Length	Vk	Jk	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2 ELISA
SY01	3-23	4-17	2	4	AKEGYGDYGLFDY	13	1-39	3	QQSYSTPFT	9	-	-	-	-	-
SY24	6-1			4	ARQPTASWEHRHNFDY	16	3-20	5	QQYGSSLSIT	10	-	-	-	-	-
SY37	3-30	1-26	1	6	ARDRLGELLLVYYGMDV	17	1-33	3	QQYDNLPFT	9	-	-	-	-	-
SY49	3-23			4	AKGSISHVFASINY	14	2-40	1	MQRIEFPWT	9	-	-	-	-	-
SY61	4-39	1-7	3	4	ARDAGTTPDVY	11	3-11	1	QQRSNWPWT	9	-	-	-	-	-
SY63	3-49			6	TREAWEDGPYYYYGMDV	17	1-39	2	QQSYSTPRT	9	-	-	-	-	-
HW01	3-73	6-19	2	4	TRGASSGDY	9	4-1	3	QQYYSTPFT	9	-	-	-	-	+
HW45	7-81	6-19+2-8	2+3	4	ARGPRYSSEEDIVLMVYAI	19	2-28	5	MQALQTPPT	9	-	-	-	-	+
HW63	3-21	3-3	1	3	ARADFEKRFLDAFDI	15	4-1	2	QQTYSTLYT	9	-	-	-	-	-
HW82	1-46	3-16	1	3	ARAFGGGEENDAFDI	14	1-8	4	QQYYSYPLT	9	-	-	-	-	-
HW88	4-34	3-22	3	3	ARGPITMIY	9	3-20	2	QQYGSSLYT	9	-	-	-	-	-
EM17	3-23			4	AKTPGQGEDY	10	4-1	2	QQYYSTRCS	9	-	-	-	-	-
EM20	4-31	2-15	2	2	ARVRSRCSGGSCYSIWYFDL	20	1-33	4	QQYDNLPS	8	-	-	-	-	-
EM49	4-34			3	ARPGAGGAFDI	11	1-27	1	QKYNSAPRT	9	-	-	-	-	-
EM68	3-73	6-13	1	6	TRQPGEQQLVLGYYYYYMDV	20	1-39	1	QQSYSTPT	8	+	+	-	-	+
EM85	3-23			4	AKDKQGDYFDY	11	1-39	2	QQSYSTPCS	9	-	-	-	-	-
EM86	4-34	6-19	3	5	ARGLLAVAEESVWFDP	16	4-1	1	QQYYSTPPT	9	-	-	-	-	-
EM92	3-15	5-5/5-18	3	4	TTGAMVPSRSDY	12	3-11	4	QQRSNWPPLT	10	-	-	-	-	-
EM01	5-51	2-2	2	4	ARGCTSTSCYSLFEY	15	1-17	1	LQHNSYPRT	9	-	-	-	-	-
EM07	3-20	2-2	2	5	ARDKYGCSSTSCSLRWFDP	19	3-15	1	QQYNNWPRT	9	-	-	-	-	-
EM15	3-23	3-22	3	4	AKEHSAGMIAIPGD	14	4-1	1	QQYYSTPWT	9	-	-	-	-	-
EM19	3-30	5-5	1	4	AREMSQLYFREF	12	3-20	1	QQYVTSSGT	9	-	-	-	-	+
EM31	3-48	3-10	2	5	AGQNYPSGRGFDP	13	4-1	2	LQYYSVPYT	9	-	-	-	-	-
EM63	4-28	2-2	2	5	ARVRGGCSSTSCQLDP	16	3-20	2	QLYDNSPFYT	10	-	-	-	-	-
	VH	D	RF	JH	CDR3 (aa)	Length	Vl	J l	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	Hep-2 ELISA
SY13	5-51	2-2	3	5	ARHRRANIVVVPAAIYWFDP	20	1-40	3	QSYDSSLSPWV	11	-	-	-	-	+
HW38	5-51	6-13	3	5	ARLGAAAGVVSNWFDP	16	3-21	2	QVWDSSSDYVV	11	-	-	-	-	+
HW58	1-69	2-2	3	6	ASAELDIVVVPAAIQAYYYGMDV	23	3-10	1	QAWDSSTGV	9	-	-	-	-	-
HW65	4-39			6	AREGVGATGGGYYYYGMDV	19	3-1	1	QAWDSSTGV	9	-	-	-	-	-
EM06	4-59	3-22	2	3	ARHLPAPYYYDSSGYSDAFDI	21	1-51	2	GTWDSSLSAGV	11	-	-	-	-	-
EM18	4-39	3-3	1	6	ARDGRFLEWSSRADYYMDV	19	1-44	2	AAWDDSLNVV	10	-	-	-	-	-
EM87	3-30	6-19	2	5	ARGEGDSSGWHGQDTGFDP	19	1-17	3	AAWDDSLSGWV	11	-	-	-	-	-

Supplemental Table S4: Primers used to revert M-CLL antibodies

Primer	Sequence
109 Antisense	5'-CGATAACTCCCCCCCTCGCACAGTAATACACGG-3'
109 Sense	5'-GCGAGGGGTGGAGTTATCGTTTGGGCTAATGACTACTG-3'
183/240 Antisense	5'-CTCTCGCACAGTAGTATACAG-3'
183/240 Sense	5'-CTGTATACTACTGTGCGAGAGGATACGTGGATACAGCTATGGTTAGAAG-3'
189 Antisense	5'-CGAAGTCCACCGTAGTTCCTCTCGCACAGTAATACACAG-3'
189 Sense	5'-AGAGGAACTACGGTGGACTTCGTCCCGCGAGGCTTCGACCCCTG-3'
215 Antisense	5'-GAACCACTCCAAAAATCGCCGATGGAGCTCTCGCACAGTAATAC-3'
215 Sense	5'-GGCGATTTTTGGAGTGGTTCGGTACTACTACTACTACGGTATGGA-3'
261 Antisense	5'-CTCTCGCACAGTAATACACAG-3'
261 Sense	5'-GTGTATTACTGTGCGAGAGATCATATTGTGGCTACG-3'
342 Antisense	5'-GTTTGATTTCCACCTTGGTCCCTTGGCCGAACGTCCAAGGCCAGTG-3'
342 Sense	5'-CTGTATACTACTGTGCGAGAGGCTGGGTGGATACAGCTATGGTTAAAAG-3'
374 Antisense	5'-GCAGCTGGGACCACGACAATATCTTGTTGGCCTCTCGCACAGTAA-3'
374 Sense	5'-GTCGTGGTCCCAGCTGCTATTTTGGTCTACTACTACTACTACATG-3'