

TABLE S2

Ig L Chain V Region Characteristics of non-IgM⁺ B-CLL Cases

Non-IgM ⁺ CLL No.	GenBank AC Number	V _L Family	Most Homologous Germline V _L Gene	% V _L Gene Difference	Probability that R Mutations Occurred by Chance ^A			J _L Gene ^E	LCDR3 Length	LCDR3 Sequence and Charged Residues ^B	Number of Charged Residues in LCDR3			LCDR3 Estimated pI ^C	
					CDR	FR	±				=	Total			
030	X84341	κI	IGKV1-5	L12	6.4	0.0051 ^D	1.05E-05 ^D	Jκ4	9	QQYLNYP	VT	0	0	0	5.50
039	X84343	κI	IGKV1-39	O12	0.0	-	-	Jκ2	9	QQSYSTP	<u>RS</u>	1	0	1	9.05
040	X84344	κI	IGKV1-8	L9	0.0	-	-	Jκ1	10	QQYYSYPQ	TF	0	0	0	5.50
055	X84345	κI	IGKV1D-12	L19	6.3	0.1491	0.0623	Jκ4	10	QQANSFPI	TF	0	0	0	5.50
057	X84346	κI	IGKV1-39	O12	0.0	-	-	Jκ1	9	QQSYSTP	<u>RT</u>	1	0	1	9.05
097	AY043086	κI	IGKV1-39	O12	0.0	-	-	Jκ2	10	QQSYSTPP	YS	0	0	0	5.50
109	AY043092	κI	IGKV1-27	A20	3.9	0.2212	0.0457 ^D	Jκ4	9	<u>QRYNSAP</u>	VT	1	0	1	9.05
111	AY043093	κI	IGKV1-17	A30	3.8	0.0411 ^D	0.0116 ^D	Jκ3	11	LQ <u>HNNYPPG</u>	FT	1	0	1	7.00
114	AY043094	κI	IGKV1-39	O12	0.0	-	-	Jκ1	9	QQSYSTP	<u>RT</u>	1	0	1	9.05
132	AY043096	κI	IGKV1-5	L12	6.3	0.0981	0.0120 ^D	Jκ4	9	QQYDTYP	FT	0	1	1	3.43
202	AY043101	κI	IGKV1-39	O12	0.0	-	-	Jκ1	9	QQSYSTP	<u>RT</u>	1	0	1	9.05
GN01	AJ388640	κI	IGKV1-5	L12	4.5	0.0832	0.0148 ^D	Jκ1	9	QQY <u>N</u> RFS	WT	1	0	1	9.05
183	AY043097	κII	IGKV2-30	A17	1.6	-	-	Jκ2	10	MQGT <u>H</u> WPP	YT	1	0	1	7.00
240	AY574937	κII	IGKV2-30	A17	2.3	0.3065	0.0054 ^D	Jκ2	10	MQGT <u>H</u> WPP	YT	0	1	1	7.00
342	AY574944	κII	IGKV2-30	A17	3.7	0.0655	0.0171 ^D	Jκ1	9	MQGT <u>H</u> WP	WT	0	1	1	7.00
033	X84342	κIII	IGKV3-20	A27	4.8	0.2503	0.0170 ^D	Jκ1	9	QQYGS LP	ST	0	0	0	5.50
128	AY043095	κIII	IGKV3-20	A27	4.8	0.2492	0.0055 ^D	Jκ3	11	QQYGTSPPL	FT	0	0	0	5.50
158	AY043087	κIII	IGKV3-15	L2	0.0	-	-	Jκ2	10	QQYNNWPP	YT	0	0	0	5.50
185	AY043098	κIII	IGKV3-11	L6	0.0	-	-	Jκ4	10	QQ <u>RS</u> NWPA	LT	1	0	1	10.24
186	AY043099	κIII	IGKV3-20	A27	3.1	0.2121	0.0238 ^D	Jκ2	9	QQYGN SL	CS	0	0	0	5.50
196	AY043100	κIII	IGKV3-11	L6	3.1	0.2894	0.2112	Jκ5	10	QQASN WPP	IT	0	0	0	5.50
001	X84340	λI	IGLV1-44	1e	5.1	0.0584	0.1594	Jλ3	11	QTY <u>D</u> SRLNI	CV	1	1	2	5.96
089	AY043091	λI	IGLV1-47	1g	1.7	-	-	Jλ3	11	ATW <u>D</u> DSL SG	PV	2	0	2	3.22
005	AY043088	λII	IGLV2-23	2b2	8.4	0.0106 ^D	0.0002 ^D	Jλ2/3	12	CSYVTEGTFG	VV	0	1	1	3.62
078	AY043090	λII	IGLV2-14	2a2	4.4	0.2549	0.0266 ^D	Jλ2/3	11	SSYT <u>S</u> SRTL	GV	1	0	1	9.05
GN15	AJ388658	λII	IGLV2-8	2c	4.1	0.1495	0.0687	Jλ2/3	12	CSYVTEGTFG	VV	1	0	1	3.62
075	AY043089	λIII	IGLV3-19	31	8.0	0.0654	8.07E-06 ^D	Jλ3	11	<u>KS</u> <u>FVN</u> <u>R</u> GTQ	GV	3	0	3	12.48

^A Calculated according to Chang and Casali using a binomial probability model to evaluate whether the excess of R mutations in CDR or the scarcity in FR was due to chance (26).

^B Amino acids on left contributed by V_L segment; those on right by J_L segment. Positively charged aa are italicized and underlined; negatively charged residues are represented in bold type.

^C Calculated from the deduced aa sequence using MacVector software, version 7.0.

^D Denotes statistically significant difference (P<0.05).

^E Jλ3 indicates the use of the Jλ3*02 allele, Jλ2/3 indicates the use of gene Jλ3*01 or Jλ2*01 since they are identical.