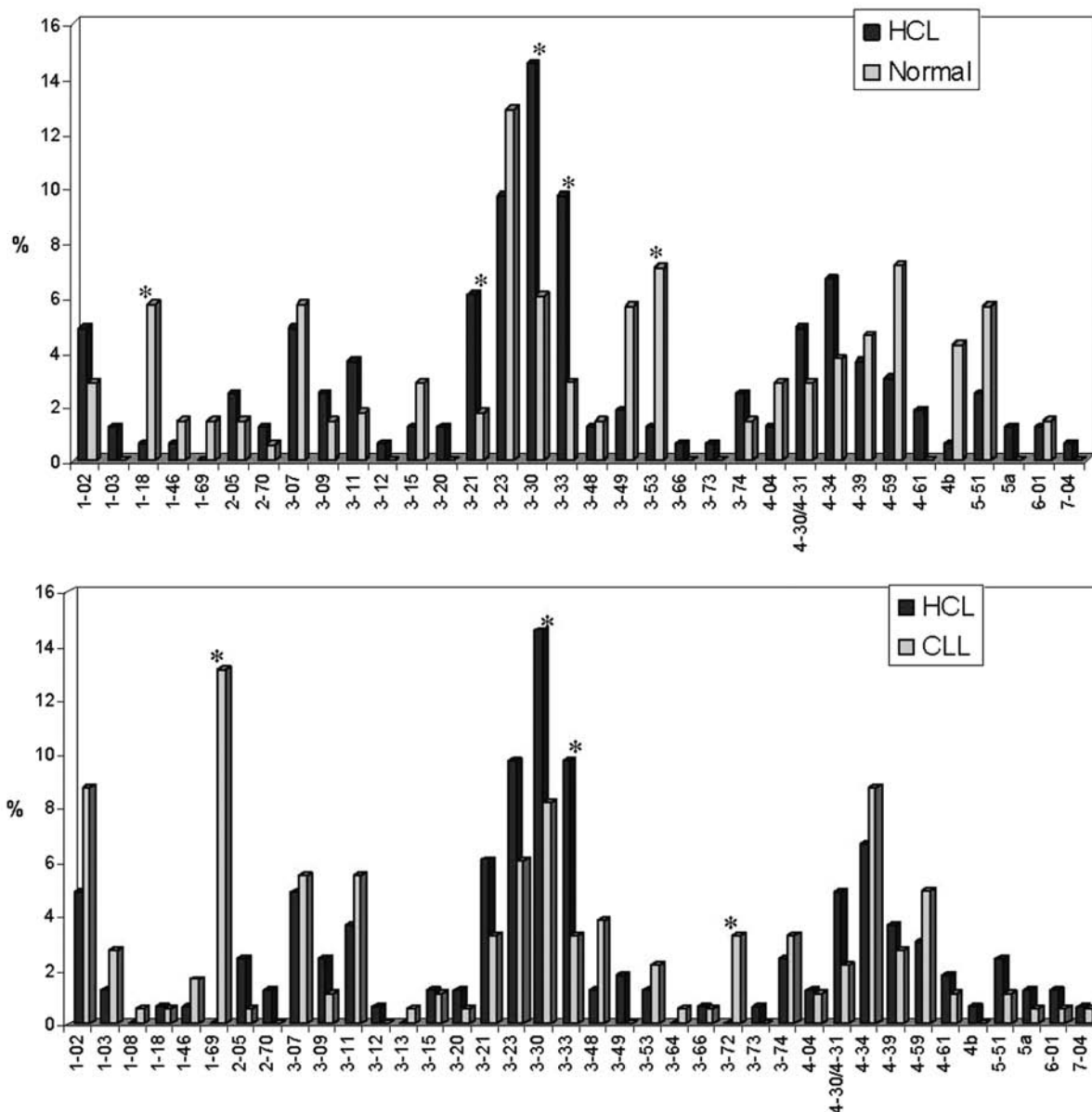


Selective influences in the expressed immunoglobulin heavy and light chain gene repertoire in hairy cell leukemia

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Supplementary Figure S1. IGHV region repertoire in HCL. Use of IGHV segments from our HCL database and from the literature (total 164 HCL cases) 2,7,8,21,22,37 was compared to that of (A) the normal B-cell repertoire, 20 or (B) the CLL repertoire (total 184 CLL cases from our internal database). Dark gray columns: HCL. Light gray columns: (A) normal B-cell repertoire, (B) CLL repertoire. (*) Asterisks indicate regions with significant differences between HCL and the normal B-cell repertoire or CLL repertoire.

^Previously published HCL cases were added the original code after the slash.^{2,7,29} % homol: % homology to closest germline IgHV gene segment. AA: amino acid. MM: molecular mass of HCDR3 amino acid sequence. pI: isoelectric point. Ngc: ratio of the number of g+c nucleotides to the total number of N region nucleotides. NGS: Novel N-glycosylation motifs (NXS/T, X any amino acid except D,E,P) introduced by somatic mutation. *HCL63 and HCL64 lost the natural NGS site by SM.

Supplement Table S2. Ig light chain (IgK and IgL) gene analysis in HCL

Code	IgH			Surface IgL	IgK/L								
	V	% homol.	κ		V	% homol.	J	CDR3					NGS
								AA length	MM	pl	Ngc	AA sequence	
HCL19	3-21	95,56	κ	KV1-17(A30) [^]	99,24	KJ1	9	1,365.54	9.25	2/2	CLQHNSYPRTF	no	
HCL37/G13	3-30	100	κ	KV1-5(L12)	94,98	KJ4	7	1,185.28	13.00	0/1	CQQYNGYYF	no	
HCL60	4-30.4	94,94	κ	KV1-9(L8)	95,69	KJ4	9	1,297.5	13.00	0/0	CQQLNAYPLTF	no	
HCL75	5a	97,79	κ	KV1-9(L8)	98,56	KJ3	9	1,271.42	7.5	0/0	CQQLNSHPPTF	no	
HCL63	4-34	95,83	κ	KV1D-17(L14)	98,48	KJ2	9	1,372.52	7.48	1/1	CLQHNSYPYTF	no	
HCL28	3-23	97,42	κ	KV1D-33(018/08)	95,69	KJ4	9	1,341.51	13.00	0/0	CQQYDNLPLTF	no	
HCL2	1-02	95,45	κ	KV1D-33(018/08)	96,62	KJ1	9	1,384.54	6.44	0/0	CQQYDNLPRTF	no	
HCL56	3-74	96,56	κ	KV1-D39(012/02)	94,32	KJ1	9	1,347.47	13.00	0/0	CQQSYSTPWTF	no	
HCL46	3-33	95,97	κ	KV1-D39(012/02)	96,77	KJ4	9	1,288.44	13.00	0/0	CQQSYTTLPTF	no	
HCL31	3-30	94,67	κ	KV1-D39(012/02)	97,26	KJ4	9	1,307.41	7.66	0/0	CHQSYSTHPTF	no	
HCL9	3-07	92,45	κ	KV1-D39(012/02)	97,49	KJ1	9	1,385.61	13.00	0/0	CQQSYIIPWTF	no	
HCL14	3-11	88,54	κ	KV1-D39(012/02)	95,69	KJ4	10	1,325.51	13.00	4/9	CQQSYSSPVTL	no	
HCL81	3-11	94,79	κ	KV1-D39(012/02)	100,00	KJ3	9	1,308.43	13	0/0	CQQSYSTPFTF	no	
HCL25/206	3-23	91,31	κ	KV3-11(L6)	97,13	KJ5	10	1,466.64	10.25	1/3	CQQRSNWPSTF	no	
HCL77	-	-	κ	KV3-15(L2)	97,13	KJ2	10	1,560.71	13.00	0/0	CQQYNNWPLYTF	no	
HCL78	-	-	κ	KV3-20(A27)	93,61	KJ2	9	1,416.58	7.49	1/2	CQHYDRALYTF	1 in CDR1	
HCL7/330	2-05	98,96	κ	KV3-20(A27)	96,90	KJ1	9	1,314.44	9.25	0/1	CQQYGRSPQTF	no	
HCL66	4-34	98,43	κ	KV3-20(A27)	98,22	-	-	-	-	-	-	no	
HCL67	4-34	100	κ	KV3-20(A27)	100	KJ2	9	1,349.49	9.07	6/8	CQQYGRSPYTF	no	
HCL59	4-30.1/4-31	96,01	κ	KV4-1(B3)	98,86	KJ1	9	1,361.5	13.00	0/1	CQQYYSPQTF	no	
HCL11	3-09	97,40	κ	KV6D-21(A26/A10)	99,28	KJ1	9	1,292.44	7.5	0/0	CHQSSSLPWTF	no	
HCL 84	2-70	nd	κ	KVI	98,92	KJ5	9	1,337.43	13.00	1/3	CQQYNSYPSTF	no	
HCL 45	3-33	94,44	κ	KVII (A19/A3)	97,27	KJ4	9	1,252.52	13.00	0/0	CMQALQTLPTF	no	
HCL64	4-34	96,90	λ	LV1-40(1e)	97,08	LJ3	12	1,436.52	13.00	1/2	CQSYDSSLSGSGVVF	no	
HCL23	3-21	98,90	λ	LV1-40(1e)	98,83	LJ3	12	1,576.71	6.44	3/5	CQSYDNSLSGTRVVF	no	
HCL35	3-30	98,49	λ	LV1-44(1c)	97,16	LJ3	11	1,352.53	13.00	0/0	CAAWDASLNGVVF	no	
HCL22	3-21	97,05	λ	LV1-44(1c)	98,43	LJ1	12	1,597.73	4.39	2/2	CAAWDSSLNGHYVF	no	
HCL44/42	3-33	93,50	λ	LV1-47(1g)	94,68	LJ3	11	1,456.6	13.00	0/0	CAAWDSSLGWWVF	no	
HCL49	3-33	97,27	λ	LV1-47(1g)	98,40	LJ3	11	1,327.44	13.00	3/4	CAAWDSSLGGVVF	no	
HCL40	3-30	97,61	λ	LV1-47(1g)	98,93	LJ3	10	1,339.49	4.4	0/0	CAAWDSSLRGVVF	no	
HCL79	-	-	λ	LV1-51(1b)	95,73	LJ3	12	1,613.81	13.00	1/2	CGTWDDTSLALWVVF	no	
HCL36	3-30	98,95	λ	LV1-51(1b)	97,51	LJ3	11	1,329.45	13.00	0/0	CGTWDSLSAGVVF	no	
HCL 30*	3-23	98,29	λ	LV2 (2 a1)	91,22	LJ1	11	1,324.5	8.47	3/5	CCSYTSAT*RVF	no	
HCL20	3-21	95,92	λ	LV2-11(2e)	98,38	LJ3	10	1,347.53	13.00	0/1	CCSYAGSYTFVF	no	
HCL38/283	3-30	100	λ	LV2-11(2e)	100	LJ3	10	1,365.56	8.47	3/5	CCSYAGSRWVVF	no	
HCL3/266	1-02	96,18	λ	LV2-14(2a2)	95,43	LJ3	11	1,373.55	13.00	0/0	CSSYTSNPLVVF	no	
HCL8	3-07	92,70	λ	LV2-14(2a2)	96,09	LJ3	11	1,403.69	8.47	8/14	CCSYARAATLVVF	no	
HCL34	3-30	98,26	λ	LV2-14(2a2)	97,46	LJ3	10	1,324.5	13	0/2	CCSYTSSNTLVF	no	
HCL52	3-33	98,16	λ	LV2-14(2a2)	89,92	LJ3	10	1,265.41	13.00	0/0	CSSYASSTLVF	no	
HCL68	4-39	93,84	λ	LV2-8(2c)	96,84	LJ3	9	1,118.28	13.00	2/4	CSAYAGSTVLF	no	
HCL32	3-30	95,83	λ	LV3-21(3h)	96,01	LJ3	11	1,508.63	4.39	0/0	CQVWDSSSDHWVVF	no	
HCL27	3-23	96,52	λ	LV3-21(3h)	98,18	LJ3	11	1,595.71	4.39	0/0	CQVWDSSSDHWVVF	no	
HCL26/216	3-23	91,66	λ	LV4-69(4b)	95,87	LJ3	9	1,327.53	13.00	0/0	CQWTWGPWFVVF	no	
HCL80	-	-	λ	LV6-57(6a)	95,48	LJ3	9	1,303.46	13.00	5/12	CQSYDSEVIIF	no	
HCL33*	3-30	96,90	λ	LV6-57(6a)*	98,95	LJ6	10	1,187.21	13.00	0/1	CQSSDSSN#NVF	1 in CDR3	
HCL55	3-66	96,12	λ	LV7-43(7a)	95,31	LJ3	9	1,319.59	13.00	0/1	CLLYYGGVWVVF	no	
HCL6	1-46	94,75	λ	LV9-49(9a)	98,43	LJ3	13	1,451.54	5.45	3/4	CGADHGSGSNFPGVVF	no	

*the amplified transcript was non functional as a result of a stop codon (HCL30) and an out-of-frame deletion (HCL33) introduced by somatic mutation in the CDR3. [^]Kawasaki nomenclature is indicated in parentheses to facilitate comparison with data from the literature. KV1D-39: cases aligning to KV1D-39 showed similar homology to KV1-39 and only the distal segment is indicated for simplicity. Also refer to supplement table S1.