

Supplementary Table 1. Individual clinical and biomolecular features of the 77 CLL patients included in the study

Name	Age	Gender ^a	del(11q22.3)	del(13q14) ^b	del(17p13.1)	+12	IgVH mutation ^c	IgVH gene usage	CD38+	ZAP-70+	Alu ^d	LINE-1 ^d	SAT- α ^d
AS0012	59	M	-	+ (99.5%)	-	-	mut	VH4-34	-	-	21.0	65.3	82.6
BC0035	64	F	-	+ (100%)	-	-	mut	VH3-7	-	-	22.4	66.8	84.1
CD0018	69	F	-	+ (29%)	-	-	mut	VH3-30	-	+	24.4	76.0	85.2
CG0037	47	M	-	-	-	-	unmut	VH3-15	-	+	24.6	78.7	86.1
CS0030	60	M	-	-	-	+ (99%)	unmut	VH1-18	-	+	23.2	75.1	86.9
CS0100	70	M	-	+ (12.5%) ++ (83.5%)	-	-	mut	VH4*02	-	-	22.5	69.1	85.4
CS12	68	M	-	-	-	+ (80,5%)	unmut	VH3-30	+	-	23.1	60.7	87.0
CS17	66	F	-	-	-	-	unmut	VH3-23	+	-	na	61.9	61.8
CS18	57	M	-	-	-	-	unmut	VH3-49	+	+	12.6	39.6	42.1
CS3	78	F	-	+ (40%) ++(58%)	-	-	mut	VH4-59	-	+	16.4	46.4	36.0
CZ26	66	F	-	-	-	-	mut	VH6-1	-	-	23.4	60.5	85.7
CZ36	70	M	-	+ (96%)	-	-	unmut	VH3-53	-	-	20.4	76.5	90.1
CZ41	66	M	-	-	-	-	mut	VH4-34	-	-	21.8	75.2	na
CZ78	70	F	-	-	-	-	unmut	VH1-69	-	-	25.0	70.9	87.4
DC0017	65	M	+ (13%)	+ (38%)	-	-	mut	VH3-53	-	-	22.1	58.6	85.6
EB0042	72	M	-	-	-	-	mut	VH3-7	+	-	21.9	66.4	na
FT0019	69	F	-	+ (90%)	-	-	mut	VH4*02	-	-	24.8	83.7	85.1
GC0015	58	M	-	-	-	+ (94%)	unmut	VH4-39	-	+	24.7	76.3	86.8
GE101	63	M	+ (100%)	+ (99%)	-	-	unmut	VH3-53	+	-	18.9	74.2	na
GE110	52	F	-	+ (66%) ++ (33%)	+ (96%)	-	mut	VH3-23	-	-	17.1	59.6	66.5
GE111	67	M	+ (61%)	+ (47%)	-	-	unmut	VH1-2	+	-	25.1	61.1	86.5
GE114	81	M	-	-	-	-	unmut	VH1-69	+	+	24.5	67.3	86.7
GE117	70	M	-	-	-	-	mut	VH3-23	+	-	22.2	75.2	82.6
GE118	68	M	-	+ (89%)	-	-	mut	VH3-66	+	+	20.4	72.7	83.9
GE126	64	M	+ (99%)	+ (100%)	+ (100%)	-	unmut	VH3-7	-	+	17.7	56.4	66.6
GE225	66	M	-	-	-	+	mut	VH4-34	-	-	22.6	73.0	84.9
GE87	76	M	-	-	+ (100%)	-	unmut	VH3-11	+	-	14.8	53.3	64.3

GE88	62	F	-	-	-	+ (40%)	unmut	VH1-46	+	+	18.3	79.1	72.4
GE93	58	M	-	++ (98%)	+ (33.5%)	-	mut	VH4-74	-	-	17.9	49.6	49.3
GE98	47	M	+ (21%)	+ (82.5%)	-	-	mut	VH4-74	-	-	19.0	62.7	86.1
GG0027	66	M	-	+ (95%)	-	-	unmut	VH1-18	+	+	22.1	75.4	85.7
LL0130	52	M	+ (99%)	+ (100%)	-	-	unmut	VH1-69	+	+	22.4	83.3	86.5
LD0062	48	M	-	+ (13%) ++ (82%)	-	-	mut	VH4-34	-	-	23.4	80.8	84.1
LG0038	45	M	+ (100%)	-	-	-	unmut	VH1-2	+	+	24.9	80.8	85.4
MC0055	53	F	-	-	-	+ (73%)	unmut	VH1-69	+	+	22.5	68.8	84.3
CS103	51	F	-	-	+ (69%)	-	unmut	VH1-69	na	-	17.4	41.8	26.7
CS89	79	M	-	++ (23%)	+ (71%)	-	mut	VH5-5	na	na	13.7	40.4	36.2
CS26	67	F	-	+ (78%)	-	-	unmut	VH2-5	+	-	23.9	64.5	86.5
CS128	66	F	-	+ (37%)	+ (100%)	-	unmut	VH3-21	na	na	18.2	61.0	58.7
CS115	71	M	-	-	+ (43%)	-	unmut	VH1-69	na	-	15.4	42.9	24.3
CS71	68	M	-	-	+ (92%)	-	unmut	VH3-7	na	-	16.5	52.9	56.0
CS95	58	M	+ (97%)	+ (98%)	-	-	unmut	VH1-69	+	+	24.9	66.1	88.0
NG0068	62	F	-	-	-	+ (94%)	unmut	VH4-39	+	+	23.2	68.0	83.5
NI0099	69	F	-	-	-	+ (92%)	unmut	VH4-39	+	+	23.6	66.4	85.0
PF0024	61	M	+ (51%)	+ (38%)	-	-	unmut	VH3-20	+	-	24.0	71.0	86.9
PS0044	64	F	-	+ (100%)	-	-	mut	VH1-1	-	-	19.2	78.9	88.6
RA0023	61	F	-	-	-	+ (100%)	unmut	VH2-5	+	+	23.0	64.5	83.9
RF0116	70	F	-	-	-	+ (52.5%)	mut	VH3-7	-	-	23.8	75.1	87.4
RC1	65	F	-	+ (97.5%)	-	-	unmut	VH4-59	-	+	19.1	62.5	61.4
RC11	73	F	-	-	-	+ (56%)	mut	VH7-4	+	-	18.3	64.9	61.5
RC12	27	M	-	-	-	-	mut	VH4-34	-	-	23.7	81.0	85.0
RC14	87	F	-	-	+ (99,5%)	-	unmut	VH1-2	-	-	13.5	32.2	32.7
RC18	47	F	-	++ (96%)	-	-	unmut	VH3-21	+	+	19.4	51.7	59.2
RC19	57	M	+ (88%)	-	-	-	unmut	VH4-39	+	+	22.4	67.8	77.2
RC20	51	F	-	-	-	-	mut	VH4-34	-	-	17.7	61.5	82.5
RC21	80	M	-	+ (61.5%)	-	-	unmut	VH3-21	+	+	20.0	64.1	62.0
RC22	71	M	-	+ (98%)	-	-	unmut	VH1-2	+	+	16.7	68.5	86.9
RC24	55	M	+ (63%)	-	-	-	unmut	VH1-69	+	+	20.9	70.8	82.3
RC25	64	F	-	-	-	+ (92%)	na	na	na	na	18.2	48.9	56.3

RC33	68	F	-	-	-	+ (91%)	unmut	VH1-69	+	+	17.1	69.2	81.8
RC4	54	F	-	-	-	-	mut	VH3-30	-	-	17.5	50.5	73.8
RC5	61	M	+ (99%)	-	-	-	unmut	VH3-48	+	+	21.0	78.1	na
RC7	73	F	+ (99%)	-	-	-	unmut	VH1-69	-	-	24.0	76.3	na
RC75	78	F	-	-	-	+ (95.5%)	unmut	VH3-30	+	+	15.2	49.5	58.9
RC81	86	M	-	-	+ (98%)	-	unmut	VH1-3	-	-	18.3	62.2	63.5
RC84	65	M	-	-	-	+ (87.5%)	unmut	VH5-9	+	-	25.6	65.3	87.9
RC87	58	M	-	+ (100%)	-	-	unmut	VH1-69	+	-	24.6	57.3	85.4
RC88	60	M	-	-	-	-	unmut	VH6-1	-	-	19.7	68.3	85.5
RC92	64	M	-	+ (98%)	-	-	unmut	VH3-21	-	-	24.5	54.8	89.5
RC93	54	F	-	-	-	+ (97,5%)	mut	VH4-34	+	-	17.5	79.9	74.2
RC94	73	M	-	-	+ (96%)	-	unmut	VH1-69	-	-	10.8	31.0	19.8
SA0093	59	M	+ (73%)	-	-	-	unmut	VH3-33	-	+	23.6	73.6	90.2
TS12	68	F	-	+ (98%)	-	-	unmut	VH3-7	-	-	15.4	69.2	83.6
TS3	56	M	-	-	-	+ (96,5%)	unmut	VH1-69	+	-	25.7	74.9	87.1
VB0013	69	M	-	+ (72.5)	-	-	mut	VH3-23	-	-	20.5	66.7	81.7
VP0089	62	F	-	++ (99%)	-	-	mut	VH5-51	-	-	22.9	66.8	80.4
VS0016	64	M	-	-	-	-	mut	VH4-34	+	-	18.4	72.2	84.5

^a M, male; F, female; ^b -, negative;+, positive;++, positive for 13q14 biallelic deletion; ^c mut, mutated; unmut, unmutated; ^d median methylation levels; na, not available

Supplementary Table 2. Primers and PCR conditions for DNA methylation analyses of repetitive elements evaluated in the study.

ID	Type	Sequence	PCR conditions
Alu	F	b-TTTTTATTAAAAATATAAAAATT	96°C for 90'', 43°C for 60'', 72°C for 120'', (45 cycles)
	R	CCCAAAC TAAAATACAATAA	
	S	AATAACTAAAATTACAAAC	
LINE-1	F	TTTTGAGTTAGGTGTGGGATATA	95°C for 30'', 50°C for 30'', 72°C for 30'', (45 cycles)
	R	b-AAAATCAAAAAATCCCTTTC	
	S	AGTTAGGTGTGGGATATAGT	
SAT-α	F	b-TGTAAGTGGATATTTGGATTATTGG	95°C for 60'', 55°C for 60'', 72°C for 60'', (45 cycles)
	R	TTTCCAAAAAAATCTTCAAAAAAAT	
	S	CTCAAAAATTTCTAAAAATACTTCTC	

F, Forward primer (5' to 3'); R, Reverse primer (5' to 3'); S, Sequencing primer (5' to 3'); b, biotin