High-density screening reveals a different spectrum of genomic aberrations in chronic lymphocytic leukemia patients with 'stereotyped' IGHV3-21 and IGHV4-34 B-cell receptors

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Online Supplementary Table S1. Overview of copy-number aberration number and size in *IGHV3-21* and *IGHV4-34* subgroups compared to in a general CLL cohort.

Subgroup: Subsets: (number)	IGHV3-21 Subset #2 (n=29)	Non-subset #2 (n=13)	Subset #4 (n=17)	IGHV4-34 Subset #16 (n=8)	Non-subset #4/16 (n=34)	General CLL cohort* All (n=203)
Average number of copy-number aberrations/sample	2.6	2.3	1.3	1.5	2.1	2.3
Median size of all copy-number aberrations (average)	1.39 (6.09)	1.8 (22.3)	0.74 (0.85)	0.64 (14.9)	0.95 (12.6)	1.46 (16.2)
Copy-number aberrations excluding the known recurrent aberrations						
Average number of copy-number aberrations/sample	1.5	1.5	0.9	1.3	1.5	1.4
Median size of copy-number aberrations (average)	0.51 (2.53)	0.82 (7.2)	0.55 (0.65)	0.61 (1.63)	0.54 (8.4)	0.9 (9.9)
Average number of copy-number aberrations/sample <1 Mbp	0.9	0.8	0.8	0.9	1.0	0.7
Median size of copy-number aberrations <1Mbp (average)	0.35 (0.42)	0.43 (0.46)	0.54 (0.51)	0.59 (0.50)	0.43 (0.46)	0.44 (0.48)
Average number of copy-number aberrations/sample >1 Mbp	0.6	0.7	0.2	0.4	0.5	0.7
Median size of copy-number aberrations >1Mbp (average)	2.37 (6.08)	13.39 (15.48)	1.16 (1.27)	1.53 (4.26)	4.02 (23.81)	5.9 (19.8)

*Median and average size are presented in Mbp. The copy-number aberration regions used for these calculations were in all cases >200 Mbp, and when divided according to size either 0.2-1 Mbp (small copy-number aberrations) or > 1 Mbp (large copy-number aberrations). *The CLL general cohort refers to the study by Gunnarsson* et al.[23] *Samples from the current study that overlapped with our recent array based Swedish CLL cohort study[26] were not removed from the analysis, as the overlap between studies was limited.*

Online Supplementary Table S2. Genomic aberrations excluding known recurrent aberrations.

	# losses	# gains	% losses	% gains
All IGHV3-21	40/63	23/63	63.5%	36.5%
Subset #2	26/43	17/43	60.5%	39.5%
Non-subset #2	14/20	6/20	70%	30%
All IGHV4-34	42/76	34/76	55.2%	44.8%
Subset #4	10/16	6/16	62.5%	37.5%
Subset #16	4/10	6/10	40%	60%
Non-subset #4/16	28/50	22/50	56%	44%

Online Supplementary Table S3. Genomic aberrations >1 Mbp in *IGHV3-21* and *IGHV4-34* subsets.

Sample	Chromosomal aberration	Start (bp)	Stop (bp)	Length Mbp	Group	Known recurrent aberrations
			Subset #2			
SCAN243	del(2)(p14)	64009993	69181808	5.2	*IGHV3-21*	del(13q)
SCAN 12	dup(2)(p14p15)	62869883	64744629	1.9	*IGHV3-21*	del(11q)
SCAN243	del(2)(q36.1q36.3)	224509215	228513887	4	*IGHV3-21*	del(13q)
SWE 90	del(3)(p21.1p21.2)	51533155	54020380	2.5	*IGHV3-21*	del(13q)
SWE 196	del(3)(p21.31)	45202312	49211362	4	*IGHV3-21*	del(13q)
SWE 196	del(3)(p21.1p21.31)	51329164	53568451	2.2	*IGHV3-21*	del(13q)
SWE 196	del(3)(q29)	195805379	198076166	2.3	*IGHV3-21*	del(13q)
FRA 6	del(4)(p14p16.2)	3273890	38890474	35.6	*IGHV3-21*	del(13q)
SWE 393	del(10)(q22.3q23.1)	80620111	82334587	1.7	*IGHV3-21*	del(13q)
3293	del(10)(q24.32q25.1)	103739905	106427297	2.7	*IGHV3-21*	del(13q)
SCAN243	del(12)(q21.2q21.31)	77864705	80444582	2.6	*IGHV3-21*	del(13q)
SWE 169	del(13)(q14.11)	40364390	41919766	1.6	*IGHV3-21*	del(11q), del(13q)
SCAN 120	dup(14)(q23.3)	65434350	66507181	1	*IGHV3-21*	del(13q)
SWE 196	del(15)(q11.2)	38495266	39995543	1.5	*IGHV3-21*	del(13q)
FRA 2	dup(15)(q15.1q15.3)	40381970	41864641	1.5	*IGHV3-21*	del(13q)
SWE 54	dup(21)(q21.1q22.3)	19785302	46944323	27.2	*IGHV3-21*	del(13q)
			Non-subset #2			
3167	dup(2)(p15p16.1)	60037423	61614928	1.6	*IGHV3-21*	No
SCAN 140	del(3)(p12.3)	74823479	76087261	1.3	*IGHV3-21*	+12
13343	del(4)(q13.1q22.3)	62095761	97650386	35.6	*IGHV3-21*	No
SCAN303	del(5)(q14.3q21.3)	85108748	105299015	20.2	*IGHV3-21*	del(13q)
18246	del(6)(q21)	107756068	109611824	1.9	*IGHV3-21*	del(11q), del(13q)
18246	del(6)(q25.1q25.3)	155230471	158862598	3.6	*IGHV3-21*	del(11q), del(13q)
SWE 58	del(14)(q24.1q32.33)	68331711	106193423	37.8	*IGHV3-21*	+12
FRA 10	del(14)(q31.1q32.33)	82308607	106368585	24	*IGHV3-21*	No
SCAN368	del(16)(q11.2q21)	45065445	58461486	13.4	*IGHV3-21*	del(17p), +12
			Subset #4			
P4813	dup(4)(q35.2)	189177158	190335660	1.2	*IGHV4-34*	No
3309	del(6)(p22.2)	24990803	25994135	1	*IGHV4-34*	No
3226	dup(18)(q23)	74478925	76117153	1.6	*IGHV4-34*	No
			Subset #16			
Swe607H_II	del(6)(p11.2p12.13)	47236688	57270277	10	*IGHV4-34*	del(11q)
SCAN362	dup(8)(p11.1p11.21)	42592291	43820269	1.2	*IGHV4-34*	No
FRA105	dup(11)(p15.5)	0	1529449	1.5	*IGHV4-34*	No
			Non-subset #4/16			
4736	del(1)(p35.3p36.11)	25985121	29490451	3.5	*IGHV4-34*	del(11q)
SCAN311	del(1)(q12q21.1)	141510591	145121245	3.6	*IGHV4-34*	No
SCAN21	dup(2)(q12.2q12.3)	106240265	107911722	1.7	*IGHV4-34*	No
FRA102	del(2)(q32.3)	193037742	194084341	1	*IGHV4-34*	del(13q)
P5443	+3	0	199501827	200	*IGHV4-34*	No
SCAN311	del(4)(q31.3)	153577335	154818740	1.2	*IGHV4-34*	No
FRA032	del(6)(q15q22.1)	89834711	117000888	27.1	*IGHV4-34*	del(13q)
5998	dup(8)(p21.3p22)	18890869	20035408	1.1	*IGHV4-34*	+12, del(13q)
Swe603H	dup(8)(q24.13q24.3)	122765681	146274826	23.5	*IGHV4-34*	del(11q), del(13q)
FRA032	del(10)(q23.31q23.33)	90532620	94553632	4	*IGHV4-34*	del(13q)
4692	del(11)(p12p14.2)	26107585	42215178	16.1	*IGHV4-34*	No
Swe603H	dup(13)(q13.3q14.2)	37082407	46514472	9.4	*IGHV4-34*	del(11q), del(13q)
4522	dup(13)(q21.1q34)	56805245	114142980	57.3	*IGHV4-34*	del(13q)
4692	del(14)(q24.3q32.31)	75119925	101621949	26.5	*IGHV4-34*	No
FRA102	del(14)(q32.12)	90910859	91987193	1	*IGHV4-34*	del(13q)
FRA327	dup(22)(q11.21)	17275764	19785014	2.5	*IGHV4-34*	No
Swe603H	dup(22)(q11.23q13.33)	24236638	49691432	25.5	*IGHV4-34*	del(11q), del(13q)