

## Clonal heterogeneity in chronic lymphocytic leukemia cells: superior response to surface IgM cross-linking in CD38, ZAP-70-positive cells

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Citation: Cutrona G, Colombo M, Matis S, Fabbi M, Spriano M, Callea V, Vigna E, Gentile M, Zupo S, Chiorazzi N, Morabito F, and Ferrarini M. Clonal heterogeneity in chronic lymphocytic leukemia cells: superior response to surface IgM cross-linking in CD38, ZAP-70 positive cells. Haematologica 2008 Mar; 93(3):413-422. doi: 10.3324/haematol.11646

ID	% increase of spontaneous apoptosis induced by aµ-Ab	CD38	% VH mutations	ZAP70		ID	% increase of spontaneous apoptosis induced by aμ-Ab	CD38	% VH mutations	ZAP70
GE129	84	9	5.3	weak		GE104	20	2	6.1	neg
RC18*	79	42	0	strong		GE98	19	2	8.6	weak
RC19*	68	55	0	strong		GE107	18	80	0	strong
RC24	64	37	0	strong		GE186	17	2	8.4	neg
GE171	62	3	0	strong		GE99	17	10	0	weak
RC2	58	1	7.5	neg		GE149*	16	2	0	strong
RC5*	57	74	0	strong		RC7*	16	23	0	Weak
GF182	56	15	9.2	neg		GF145	16	17	1.3	Strong
GF134	55	6	61	neø	-	GE88	16	76	0	Strong
GF80	55	97	ND	ND	8	GF106	15	12	0.3	strong
GF162*	52	99	0	strong	10	GF122	14	10	33	weak
GF118	52	86	24	weak	9	RC21*	14	58	0.0	strong
PC12*	51	10	7 1	non		GF156*	13	1	11 /	nor
CE02	51	70	0	ctrond		GF1//	10	05	0	etrono
DC20*	51	2	4.7	nor		CE125	11	0	27	nor
DC11*	50	0/	4.7 5.0	nor			0	5	2.1	woold
CE106	50	04	0.0	ctrond		CE00	9	20	16	ND
GE120	49	0/	0	strong		0E90	9	30 10	4.0	otrond
GE104	40	94 40	0	strong		GE110 CE120	9	20	U E 1	Strong
R622	40	49	0	Strong		0E120	1	20	0.1	Weak
	47	11	0	strong		PZ1 0F106	1	30	4	weak
RU23	40	95	0	Strong		GE130	1	2	9.5	neg
RU4*	40	18	3	weak		GE103*	4	8	U	strong
GE143	42	35	1	strong		GE133	4	10	ND	neg
GE100	41	6	0	weak		GE101*	2	8/	0	strong
GE1/3*	40	14	0	strong		GE124	1	5	1	neg
RC15*	40	58	0	strong		GE146	1	90	6.6	weak
GE95	38	4	1.1	weak		RC16	0	1	1.8	weak
GE115*	37	40	5	weak		CU2	0	15	0	neg
GE91	34	68	0	ND		RC13*	0	8	1.4	neg
GE131	34	/3	0	strong		GE110	0	0	12.6	neg
RC1*	34	3	0	strong		GE93	0	5	2.7	neg
GE94	34	99	1.3	strong		GE137	0	97	0	strong
RC17	33	4	5.6	weak		GE165	0	1	3	strong
GE111	33	90	0	strong						
GE141	33	1	ND	weak		RC10	-10	9	8	neg
GE178	32	4	7.8	weak		CU1	-11	91	0	strong
GE117	31	73	4.2	neg		RC9	-13	1	4.9	neg
GE114	28	73	0	strong	3	GE89	-14	50	0	ND
GE130	27	64	0	strong	ē	GE140	-18	46	2.3	neg
GE128	27	7	7	strong	2	GE142	-25	96	3.7	weak
					9	GE175*	-35	1	5.8	weak
						RC3	-46	3	2.6	strong
						0007	E0	EO	0	

H

## В 30 50 p=0.035 p=0.017 40 number of cases 10 30 20 🗖 group B 10 0 🔳 group A positive negative negative positive CD38 CD38 D 24 38 36. p=0.17 p=0.3 22 34 32 number of cases 20 30. 28. 18. 26, 24 16 22 🔲 group B 20 14 group A Ň unmutated unmutated mutated mutated VH mutational status VH mutational status F 40 30 p=0.26 p=0.18 number of cases 01 30

0

neg

weak

ZAP-70

strong

A

% aμ-Ab induced apoptosis (mean±sem)

% aµ-Ab induced apoptosis (mean±sem)

E

% aµ-Ab induced apoptosis (mean±sem)

20

10

18

neg

18

weak

ZAP-70

34

strong

**Supplementary Figure 1** 

🔲 group B

🔳 group A

Figure 1. Correlation between aµ-Ab induced apoptosis *in vitro* and expression of prognostic markers by CLL cells. Cases classified in Group A and B in Table 1 were considered for the analysis. (A, C, E) percentage of aµ-Ab induced apoptosis relative to the expression of the indicated apoptosis relative to the expression of the indicated prognostic marker. (B, D, F) CLL cases were classified as group A (apoptosis > 20%) or group B (apoptosis  $\leq$  20%) and subsequently classified as positive or negative for the indicated marker. Statistical analyses: Mann-Whitney non para-metric test in A and C; Kruskal-Wallis non para-metric test in E; Chi-square test in B, D, F.