



Table I. Characteristics of the study population (n=195)

Sex (M/F)	128/67 (66%-34%)
Age at diagnosis, median [range] (n=185*)	63 y [33-88]
Binet stage at diagnosis (n=169*)	
A	100 (59%)
B	48 (29%)
C	21 (12%)
<i>IGHV</i> unmutated (n=47*)	38 (81%)
<i>TP53</i> mutated (n=60*)	55 (92%)
Treated patients (n=182*)	158 (87%)
<i>TP53</i> deletion acquired after treatment (n=124*)	28 (23%)
Number of treatment lines, median [range] (n=179*)	2,5 [0-10]
Treatment-free survival, median (95% CI) (n=93*#)	18 mo (11-29)
Deaths (n=179*)	63 (35%)
Overall survival, median (95% CI) (n=183*)	179 mo (135-242)
Follow-up from diagnosis, median [range] (n=183*)	70 mo [0-401]

*: available data; y:years; mo: months; # analyzed on the 96 patients with 17p deletion before treatment

Table II. Karyotyping and FISH data (n=195)

Parameter	Median [range]	n (%)
Number of abnormalities, 17p included	4 [1-26]	
Complex karyotype (≥ 3 abnormalities)		141 (72%)
Highly complex karyotype (≥ 5 abnormalities)		89 (46%)
Monosomal karyotype		52 (27%)
Unbalanced translocations (all: involving 17p or not)		181 (93%)
Number of 17p abnormalities		
1		162 (83%)
2		25 (13%)
3 or more		8 (4%)
17p- alone by karyotype		28 (14%)
Clonal hierarchy for 17p abnormalities when not alone, n=167		
primary		43 (26%)
secondary		42 (25%)
same clone		64 (38%)
independant clone		18 (11%)
Types of 17p abnormalities^a		
Unbalanced translocation		158 (81%)
<i>Unbalanced translocation with identified partner</i>		123 (63%)
<i>arm-to-arm translocation</i>		62 (32%)
<i>der/dic(17;18)</i>		32 (16%)
<i>other unbalanced translocation</i>		61 (31%)
<i>Unbalanced translocation, add(17)(p)</i>		35 (18%)
17p deletion		45 (23%)
Monosomy 17		15 (8%)
Isochromosome 17q		9 (5%)
Ring 17		4 (2%)
% of cells with TP53 deletion (FISH)	70 [3-100]	
Additional abnormalities		
Unbalanced translocations (not 17p)		121 (63%)
8p deletion, n=189 ^b		40 (21%)
8q24 gain, n=112 ^c		14 (12.5%)
Trisomy 12, n=195		30 (15%)
13q14 deletion, n=118 ^d		71 (60%)
11q deletion (<i>ATM</i> gene), n=161 ^d		20 (12%)

a. The number of patients with the corresponding abnormality is given. The frequencies are related to the total cohort (n=195). The total is higher than 100% because 33 patients have more than one 17p abnormality.

b. The presence of a 8p deletion could not be determined in 6 patients with a complex karyotype including a monosomy 8 and addition(s) of chromosomal material of undermined origin.

c. the presence of a 8q24 gain could not be determined in 83 patients having a complex karyotype with addition(s) of chromosomal material of undermined origin, without FISH analysis with MYC probe

d. detected by FISH

Table III. Univariate and multivariate analyses of variables with a significant impact on TFS and OS.

Variable		n	Univariate HR (95%CI)	p-value	Multivariate HR (95%CI)	p-value
TFS						
Binet stage B/C at diagnosis	Yes/no	31/60	6.24 (2.89-13.47)	<0,0001	119.75 (14.53-986.65)	<0.0001
Monosomy 17	Yes/no	8/85	2.07 (0.76-5.61)	0,04	2.83 (0.63-12.71)	0.17
Highly CK ≥ 5 abnormalities	Yes/no	41/52	1.81 (1.10-2.97)	0,009	1.62 (0.77-3.38)	0.19
8q24 gain (involving MYC)	Yes/no	4/49	6.46 (0.59-71.23)	<0,0001	5.76 (1.18 – 28.05)	0.03
OS						
Age at diagnosis	$\geq 65y / < 65y$	80/97	1.85 (1.06-3.21)	0,01	2.65 (1.12-6.27)	0.03
Binet stage B/C at diagnosis	Yes/no	68/96	3.10 (1.78-6.40)	<0,001	10.01 (3.60-27.78)	<0.0001
IGHV unmutated	Yes/no	32/8	2.89(1.04-8.07)	0,04	-	
Isochromosome 17q	Yes/no	8/169	2.77 (0.55-14.01)	0,04	4.07 (0.59-27.97)	0.15
Unbalanced translocations (all: including 17p or not)	Yes/no	165/12	5.96 (2.49-14.29)	0.04	4.80 (0.61-37.50)	0.13
Unbalanced translocations (not 17p)	Yes/no	109/68	1.79 (1.09-2.96)	0,03	0.84 (0.39-1.80)	0.66
8q24 gain (involving MYC)	Yes/no	13/89	3.48 (0.93-13.07)	0,001	3.73 (1.32-10.54)	0.01

HR : hazard ratio, CI : confidence interval. There were too few data on *IGHV* mutational status for inclusion in the multivariate analysis.