Quantification of cyclin D1 and D2 proteins in multiple myeloma identifies different expression patterns from those revealed by gene expression profiling

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SUPPLEMENTARY INFORMATION.

Supplementary Table 1 Patient characteristics (n = 165).

Characteristics	Patients (n)=165
Age, median (range)	59 (31-65)
Group, n (%)	
Grupo A - Melphalan 200 mg/m^2	80 (49)
Grupo B - Busulfan/Melphalan	85 (51)
Sex, n(%)	
Male	87 (52)
Female	78 (48)
M-protein type, n (%)	
IgG	105 (64)
IgA	37 (22)
Light chain	21 (13)
IgD	0 (0)
Non-secretory	2 (1)
ISS stage, n (%)	
I	52 (31)
II	67 (41)
III	43 (26)
Missing	3 (2)
ISS-R stage, n (%)	
I	74 (45)
II	65 (39)
III	12 (7)
Missing	14 (9)
ECOG performance status, n (%)	
0	67 (41)
1	66 (40)
2	21 (12)
3	8 (5)
Missing	3 (2)
Hemoglobin (g/dL), median (range)	10.7 (6.7-15.5)
Creatinine (mg/dL), median (range)	0.9 (0.4-2)
B2-microglobulin (mg/L), median (range)	3.9 (1.5-17.4)
Elevated lactate dehydrogenase, n (%)	
Yes	19 (12)
No	141 (85)
Missing	5 (3)
Plasmacytoma, n(%)	
Yes	33 (20)
No	132 (80)
Cytogenetics, n (%)	
t(11;14)	23 (17)
11q13 gain	38 (51)
t(4;14)	17 (13)
t(14;16)	4 (3)
del(17p)	18 (12)
del(1p)	21 (14)
1q gain	77 (49)
Follow-up (months): median (range)	69 (9.4-88.5)

ECOG, Eastern Cooperative Oncology Group; ISS, International Staging System; ISS-R, Revised International Staging System.

Supplementary Figure 1. A) Distribution of cyclin D2 protein expression in the groups generated after dichotomizing the samples. Patients with cyclin D2 expression ≤ 0.058 and > 0.058 were classified as "Low" and "High", respectively (***, $p < 0.001$). B) Percentage of patients with chromosomal abnormalities by cyclin D2 protein-expression groups. None of the contrasts between low and high levels of Cyclin D2 within the cytogenetic groups were statistically significant ($p > 0.05$), as demonstrated by the Mann-Whitney U test or Fisher's exact test, as appropriate.
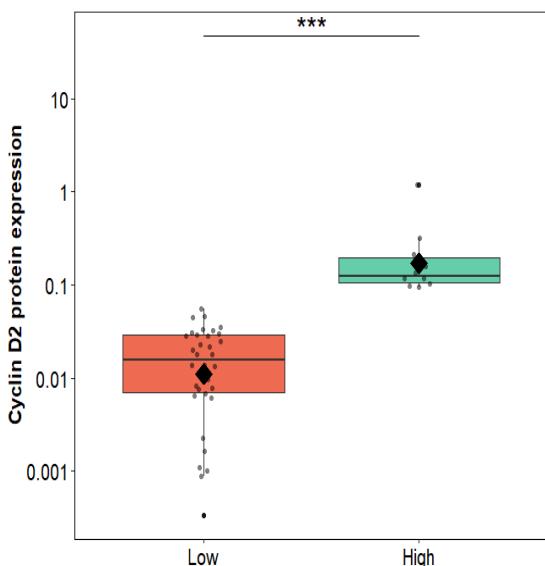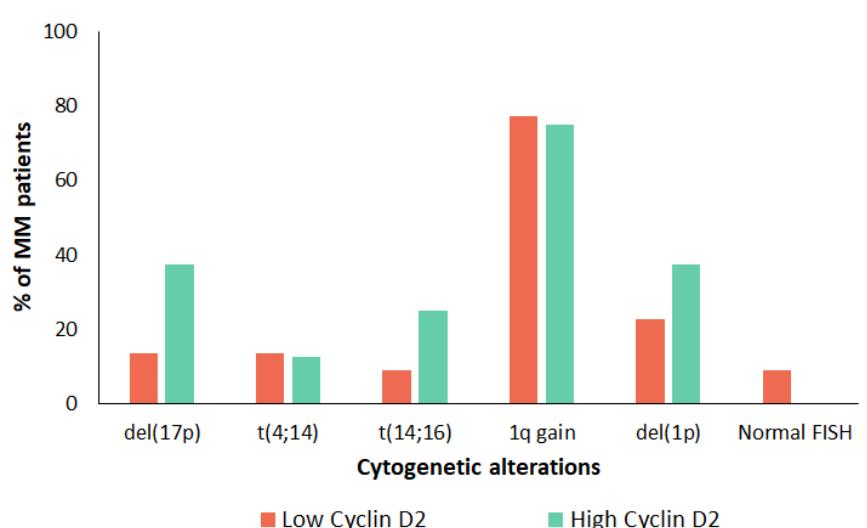
Supplementary Table 2. Distribution of cytogenetic abnormalities by cyclin D-expression groups.

Cytogenetic alteration	Cyclin D1*	Cyclin D2*	Coexpression*	No expression*	Total**
t(11;14)	23 (100)	0 (0)	0 (0)	0 (0)	23
11q13 gain	21 (55)	3 (8)	3 (8)	11 (29)	38
t(4;14)	2 (12)	4 (24)	2 (12)	9 (53)	17
t(14;16)	0 (0)	4 (100)	0 (0)	0 (0)	4
del(17p)	3 (17)	6 (33)	1 (6)	8 (44)	18
del(1p)	4 (19)	8 (38)	3 (14)	6 (29)	21
1q gain	16 (21)	24 (31)	10 (13)	27 (35)	77

*n (%); **n

Supplementary Figure 2. Spearman's correlation between protein and mRNA. A and B) Scatter plot showing protein and mRNA expression for cyclin D1/*CCND1* and cyclin D2/*CCND2*, respectively. The mRNA cutoff (red) divides the samples into normal expression (to the left of this line) and overexpression (to the right). For proteins, the orange line indicates "no protein expression", while the blue line separates samples with low and high protein expression.
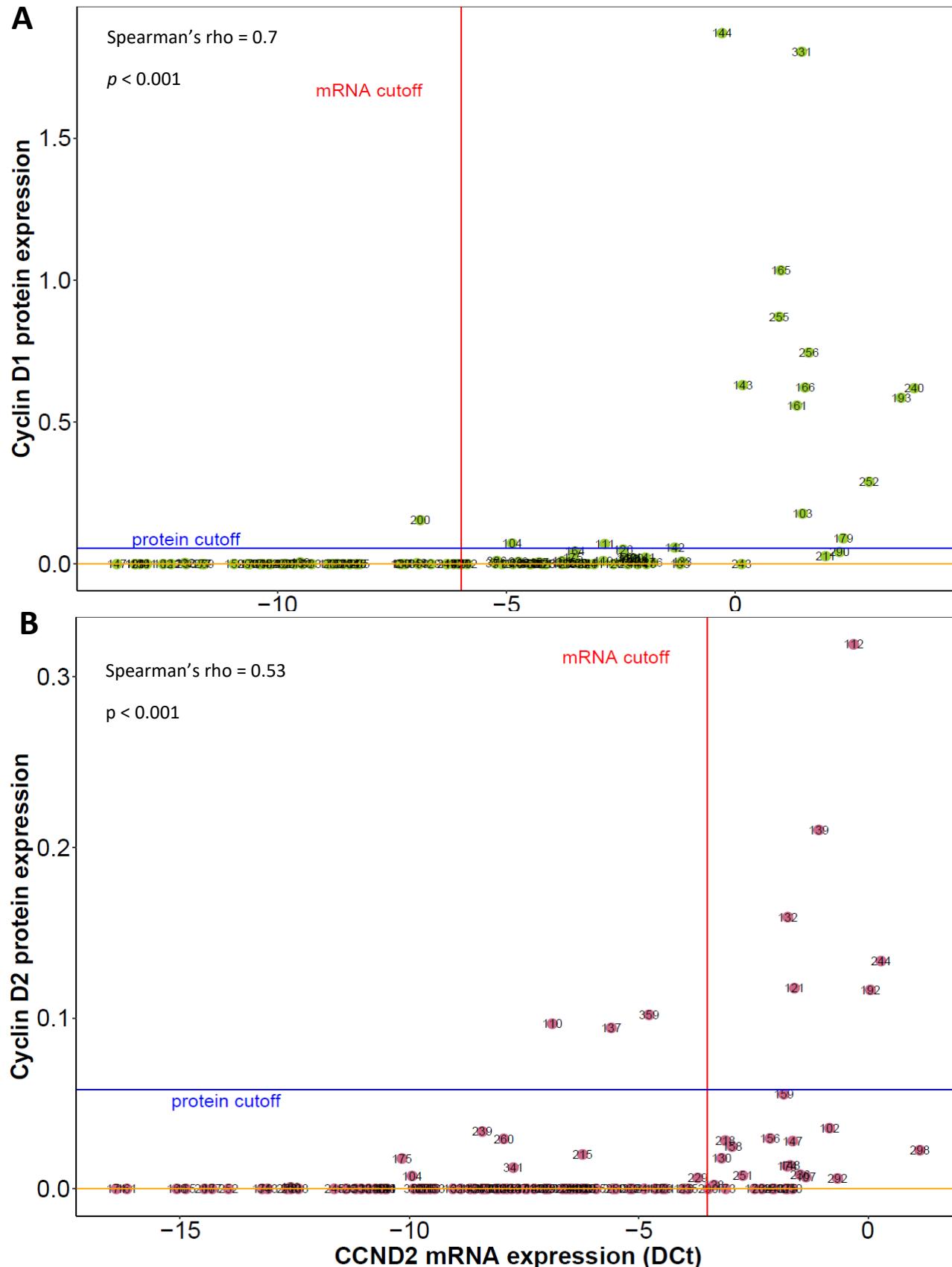
Supplementary Figure 3. Survival analysis of *CCND1* and *CCND2* mRNAs. A and B) Kaplan-Meier curves of OS and TTP, respectively, according to *CCND1* mRNA expression. Log-rank (Mantel-Cox) test *p* values are shown.