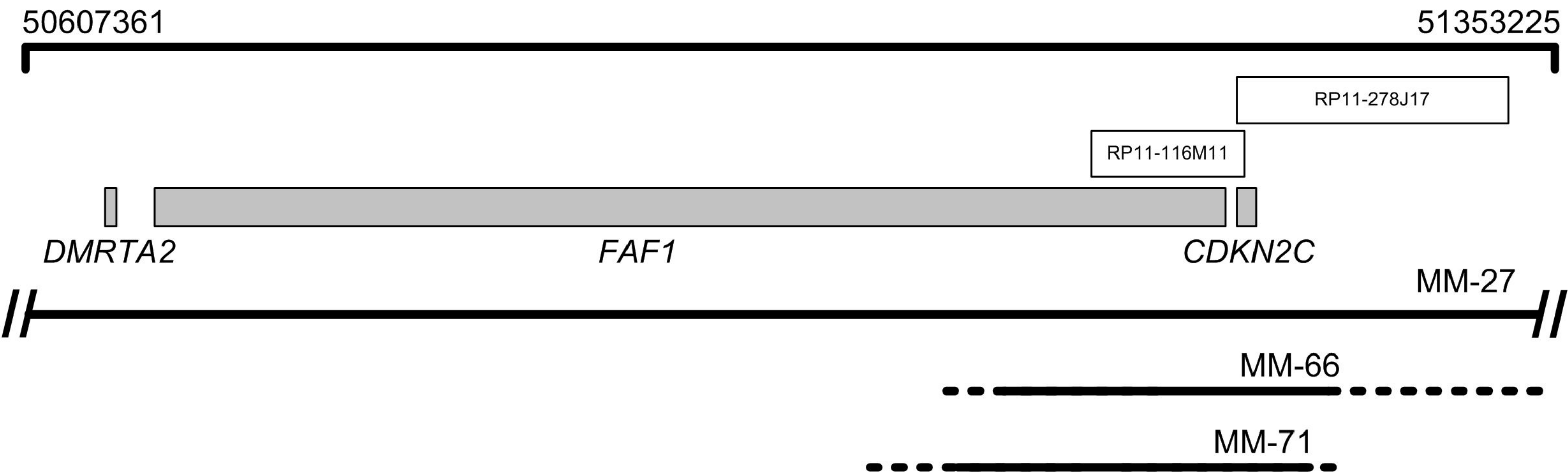


## Supplementary Figure Legends

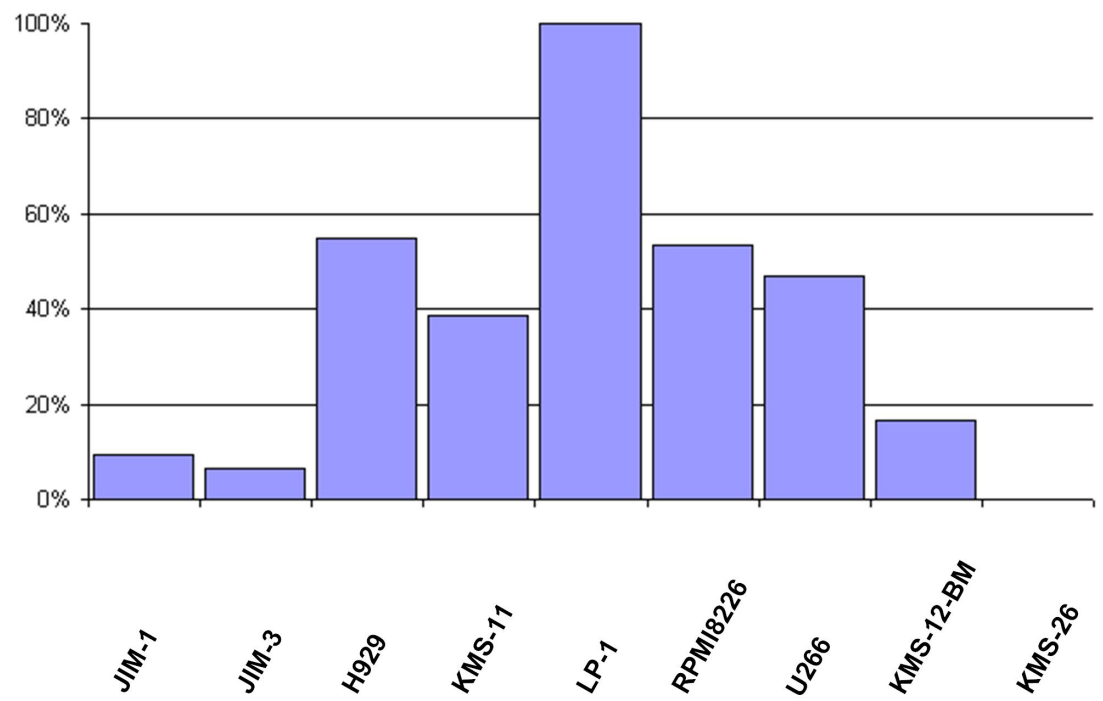
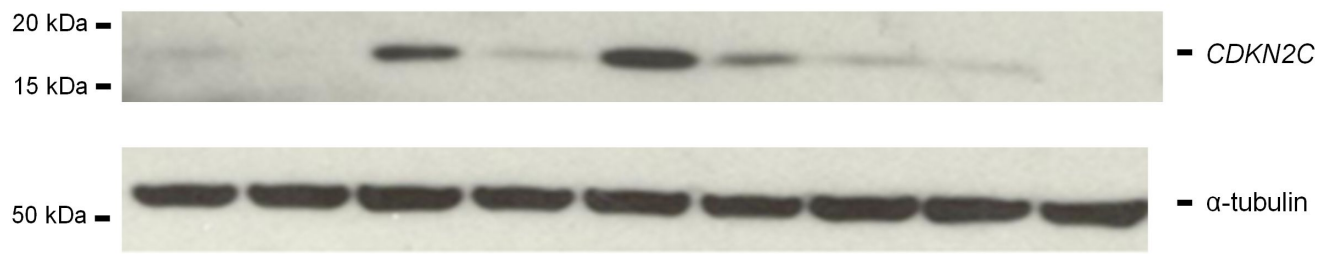
**Supplementary Figure 1.** Schematic of the region of interest surrounding *CDKN2C*. The map is drawn to scale. The white boxes represent the two probes used to determine the status of 1p32.3. The grey boxes represent the genes located in the region between 50607361 and 51353225 bp. The black lines indicate the regions of homozygous deletion in each case. In the cases MM-66 and MM-71 the dashed lines indicate the regions between SNPs for which no mapping data are known, and which are potentially homozygously deleted. In the case of MM-27, the deletion extends beyond the boundary of the figure, as indicated by the slashes.

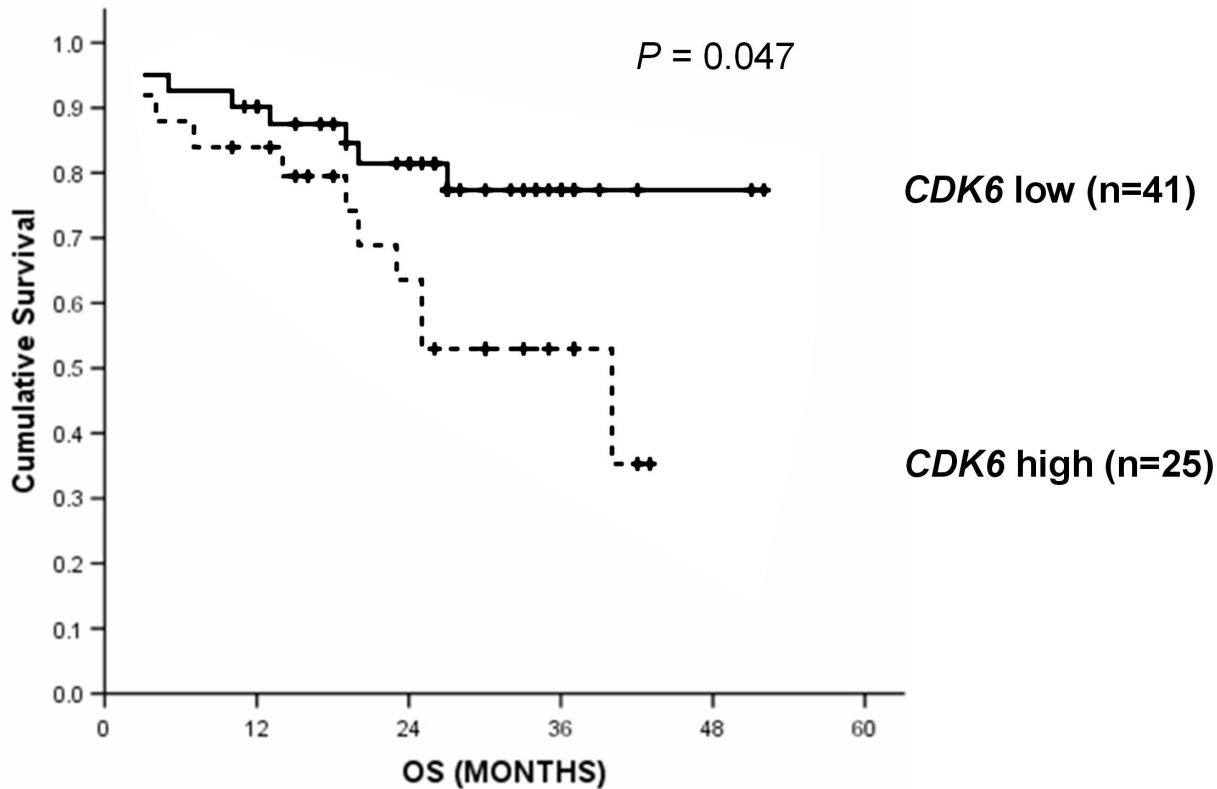
**Supplementary Figure 2.** Distribution of the status of *CDKN2C* in myeloma cell lines. (A) The level of expression of *CDKN2C* by expression array. (B) The protein level of *CDKN2C* by western blotting.

**Supplementary Figure 3.** Effect of the expression level of *CDK6* on overall survival. Kaplan-Meier estimates of overall survival in cases with high *CDK6* expression versus cases with low expression ( $P = 0.047$ ).



Supplementary Figure 1

**A.****B.****Supplementary Figure 2**



Supplementary Figure 3