Figure S5

A

In the figure, we observe a series of scatter plots each illustrating the relationship between different proteins and other variables.

- **PA28αβ** with $R^2 = 0.33$ for β5
- **PA28αβ** with $R^2 = 0.37$ for β2i
- **Rpn11** with $R^2 = 0.7$ for α7
- **Rpn6** with $R^2 = 0.8$ for α6

B

The figure also includes a histogram showing the coefficient of determination ($R^2$) for different proteins, with blue and red bars representing different categories.
Figure S5: Correlations of proteins abundances in the total cell lysates of the 9 cell lines

A) Correlations of proteins abundances in the total cell lysates of the 9 cell lines. The abundances of the 5 main proteasome regulators (PA28, βα 19S, PA28 γPI31, and PA200) were plotted as a function of the abundances of the iP20S (represented by β2i) or the sP20S (represented by β5). Correlations of abundances of α7 and α6, Rpn6 and Rpn11, PA28β and PA28α, and Rpn1 with Rpt1, Rpn2, Rpn3, Rpn10, and Rpn12. PA28αβ abundance corresponds to the median of PA28α and PA28β abundances and the 19S abundance corresponds to the median of Rpt1-6, Rpn1-3, 5-14 abundances. Protein abundances were obtained by calculating the PAI from label free MS quantification (blue circles) or from MRM quantification (blue triangles), as detailed in the Supplementary Materials and Methods.

B) Plot of the R² values in the 24 cell total lysates between the iP20S or the sP20S and 193 proteins correlating (R² > 0.8) with the iP20S, the sP20S or the ncP20S in proteasome complexes.