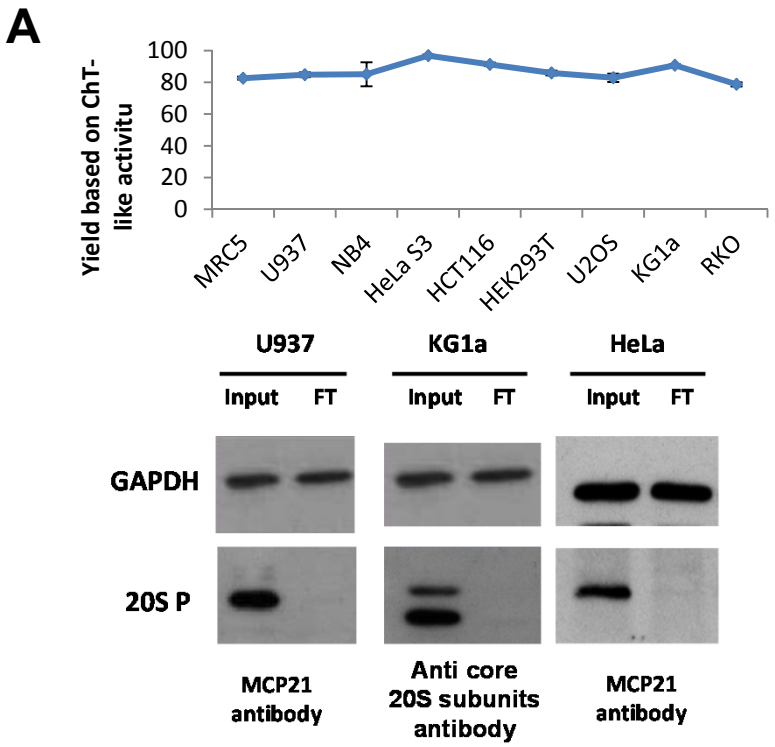
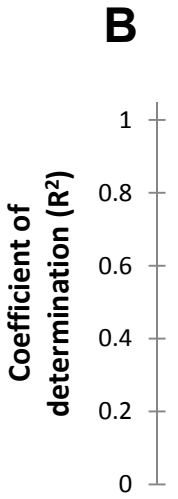
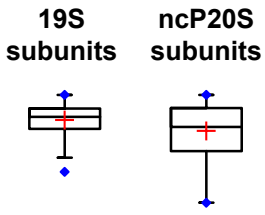
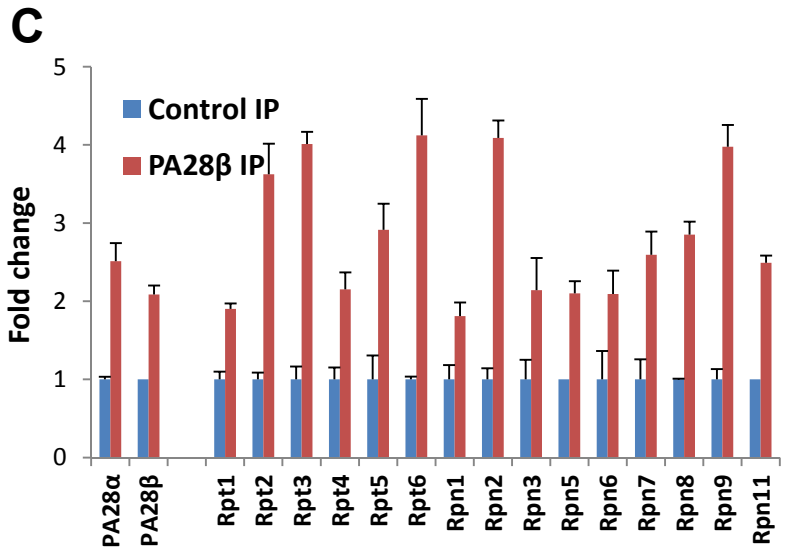
Figure S1

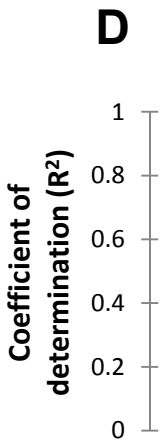


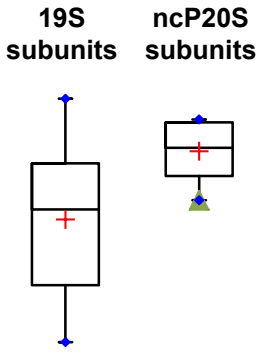




Statistics for R^2	19S subunits	20S subunits
No. of observations	324	122
Minimum	0.79	0.70
Maximum	1.00	1.00
1st Quartile	0.91	0.85
Median	0.94	0.91
3rd Quartile	0.96	0.96
Mean	0.93	0.90
Variance (n-1)	0.00	0.01
Standard deviation (n-1)	0.04	0.07







Statistic for R^2	19S subunits	20S subunits
No. of observations	324	122
Minimum	0.14	0.59
Maximum	0.91	0.84
1st Quartile	0.32	0.66
Median	0.56	0.75
3rd Quartile	0.70	0.83
Mean	0.53	0.74
Variance (n-1)	0.06	0.01
Standard deviation (n-1)	0.24	0.10

Figure S1: A- The total pool of 20S proteasome is immunopurified using the MCP21 antibody. Upper: Chymotrypsin-like (ChT-like) activity measured in the total cell lysate and in the flowthrough after immunopurification (n=3). Lower: Western-blot analyses in the total lysate (Input) and in the flowthrough after proteasome immunopurification (FT) using antibodies directed against GAPDH and 20S proteasome (MCP21 and anti-core alpha subunits). **B- Box-and-whisker plots showing the correlations of abundances, quantified with the R^2, between the different subunits of the 19S regulator and of the 20S proteasome in proteasome immuno-precipitates.** The R^2 are obtained from the pair wise comparison of protein abundances of core subunits of the 19S regulator (represented by Rpt1-6, Rpn1-3, 5-14) and of the non-catalytic 20S proteasome subunits (ncP20S) (represented by the 11 subunits constitutively found in the 20S CP, α1- α7, β3, β4, β6, and β7). Results were obtained from 324 (19S RP) and 122 (20S CP) observations. Red + and blue dots represent the mean values and the extreme values, respectively. In the table below the graph, detailed statistics for R^2 values are indicated. **C- Detection of hybrid proteasome in U937 cells.** Proteins were purified using an antibody directed the PA28β subunit (Cell signaling) and analyzed using quantitative label-free mass spectrometry. The contents of PA28β, PA28α, and 19S RP subunits in the immunopurification with the anti-PA28β antibody were compared with the ones in the control experiment (immunopurification with pre-immunized rabbits antibodies) to obtain a fold change relative to the control. **D- Box-and-whisker plots showing the correlations of abundances, quantified with the R^2, between the different subunits of the 19S regulator and of the 20S proteasome non catalytic subunits in the total cell lysates.** The same method as for B- was used.