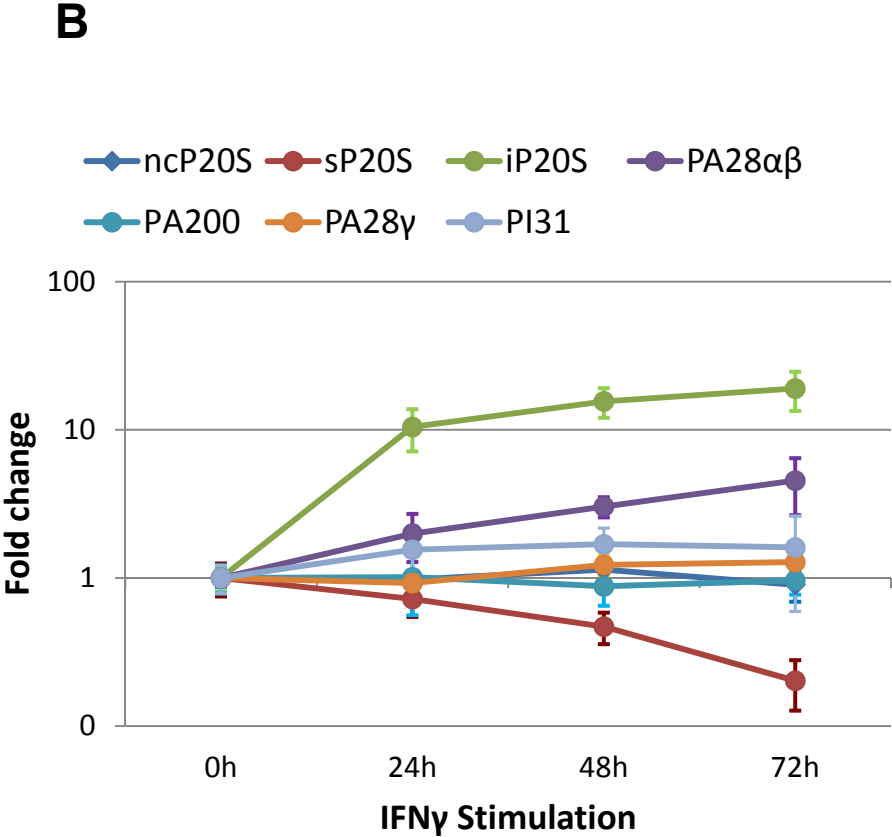
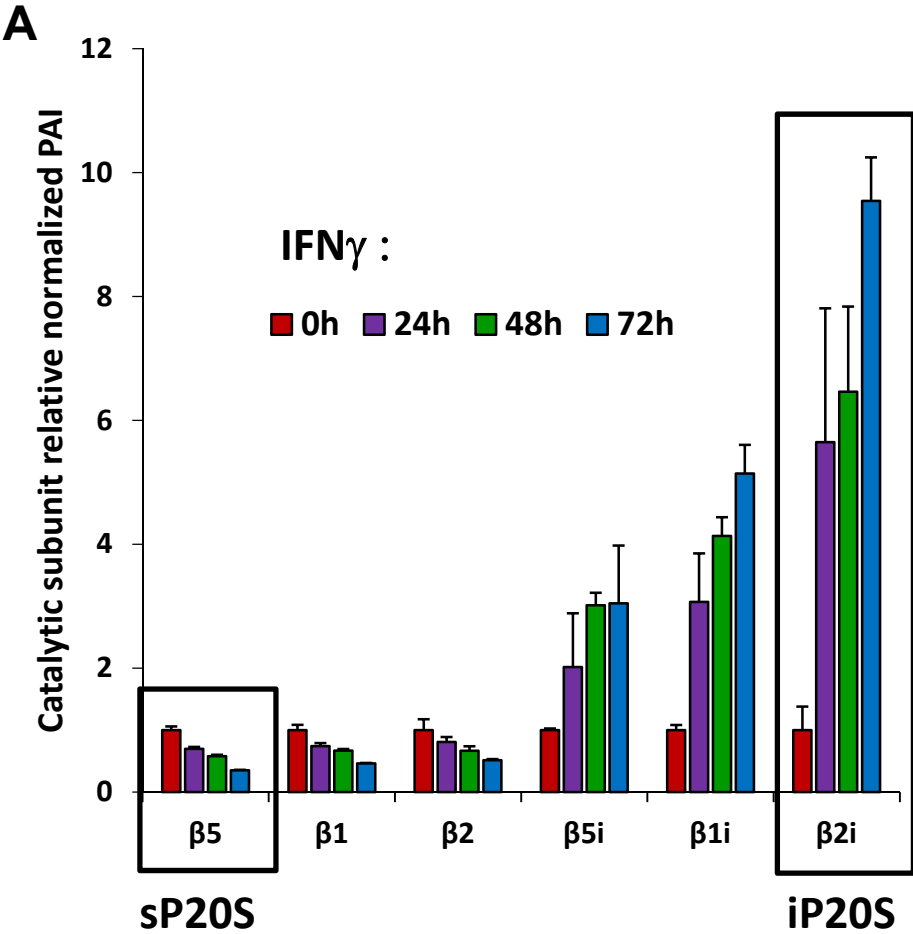


Figure S7



**Figure S7: sP20S and iP20S associate with a different subset of regulators**

A) 20S proteasome subunits dynamics upon IFN- $\gamma$  kinetic in proteasome immunoprecipitates was measured by label free quantitative proteomic. The normalized abundance index of each catalytic 20S subunit at each time point was compared to the one obtained at the 0h time point to obtain a catalytic subunit relative normalized PAI. The kinetics results for  $\beta 5$  and  $\beta 2i$ , representing the sP20S and the iP20S, respectively, are black framed (n=3 per condition).

B) Variations of the expression level of the different proteasome sub-complexes in the total cell lysate and during the IFN- $\gamma$  kinetic (n=3 per condition). The abundances of ncP20S subunits (median abundance of  $\alpha 2$ ,  $\alpha 7$ ,  $\alpha 4$  and  $\beta 6$ ), sP20S (abundance of  $\beta 5$ ), iP20S (abundance of  $\beta 2i$ ), PA28 $\alpha\beta$  (median abundance of PA28 $\alpha$  and PA28 $\beta$ ), PA200, PA28 $\gamma$ , and PI31 were obtained by SRM and normalized with the median abundance of histones H1.2 and H2A type 1-B. The abundances of the 19S subunits (Rpt1-6, Rpn1-3, 5-14) were obtained from label free MS quantification and normalized with the median abundance of all the detected histones.