

Figure S4

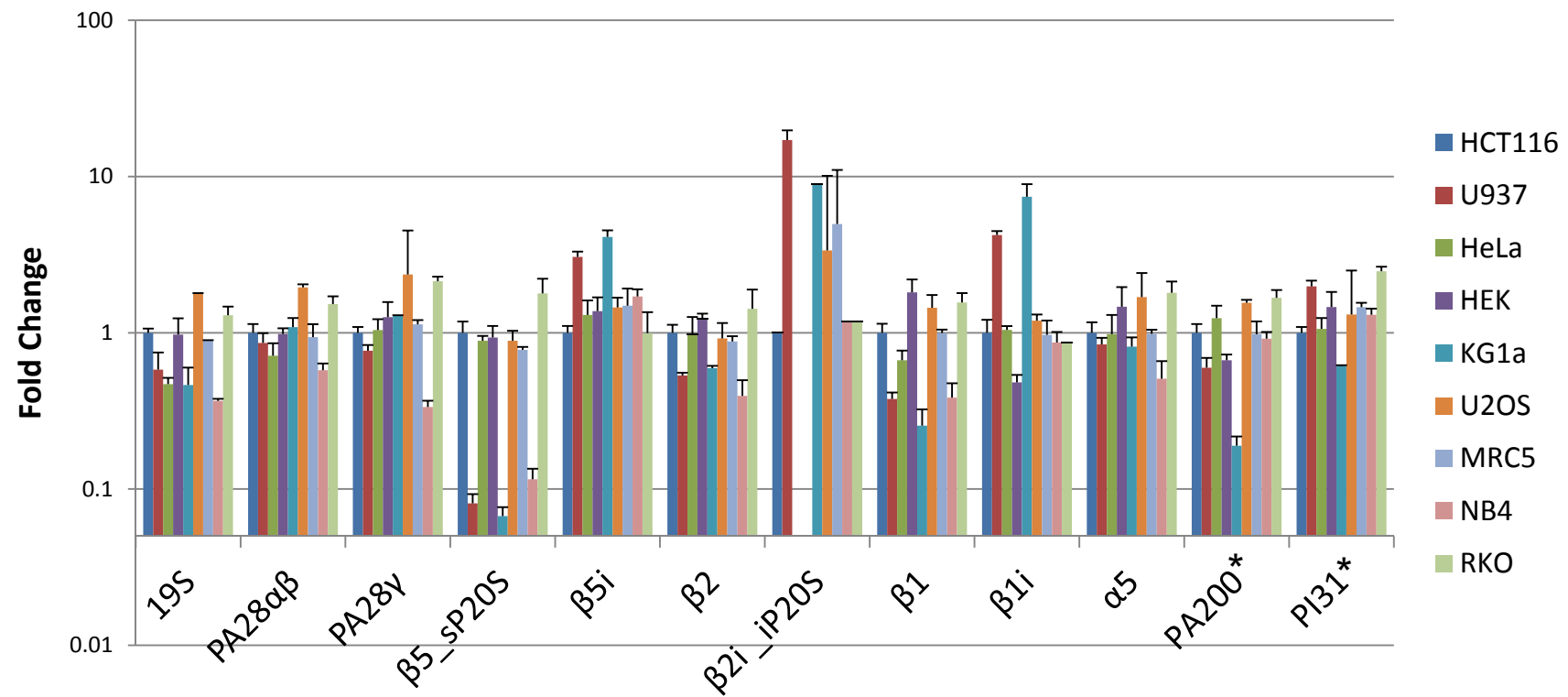


Figure S4: Expression levels of the different proteasome subunits and subcomplexes in the lysates of the nine cell lines. Protein abundances were obtained from label free MS quantification and normalized with the median abundance of all the detected histones. The abundances of 19S and PA28 $\alpha\beta$ are calculated by meaning the abundances of their corresponding subunits (Rpt1-6, Rpn1-3, 5-14 for the 19S and PA28 α , PA28 β for PA28 $\alpha\beta$). Fold changes compared with the HCT116 cell line are shown (n=3). Proteins with an asterisk were quantified by MRM and normalized with histone H2A type 1-B (as detailed in the Supplementary Materials and Methods). MRM transitions could be unambiguously assigned with the help of co-injected isotope-labeled peptides.