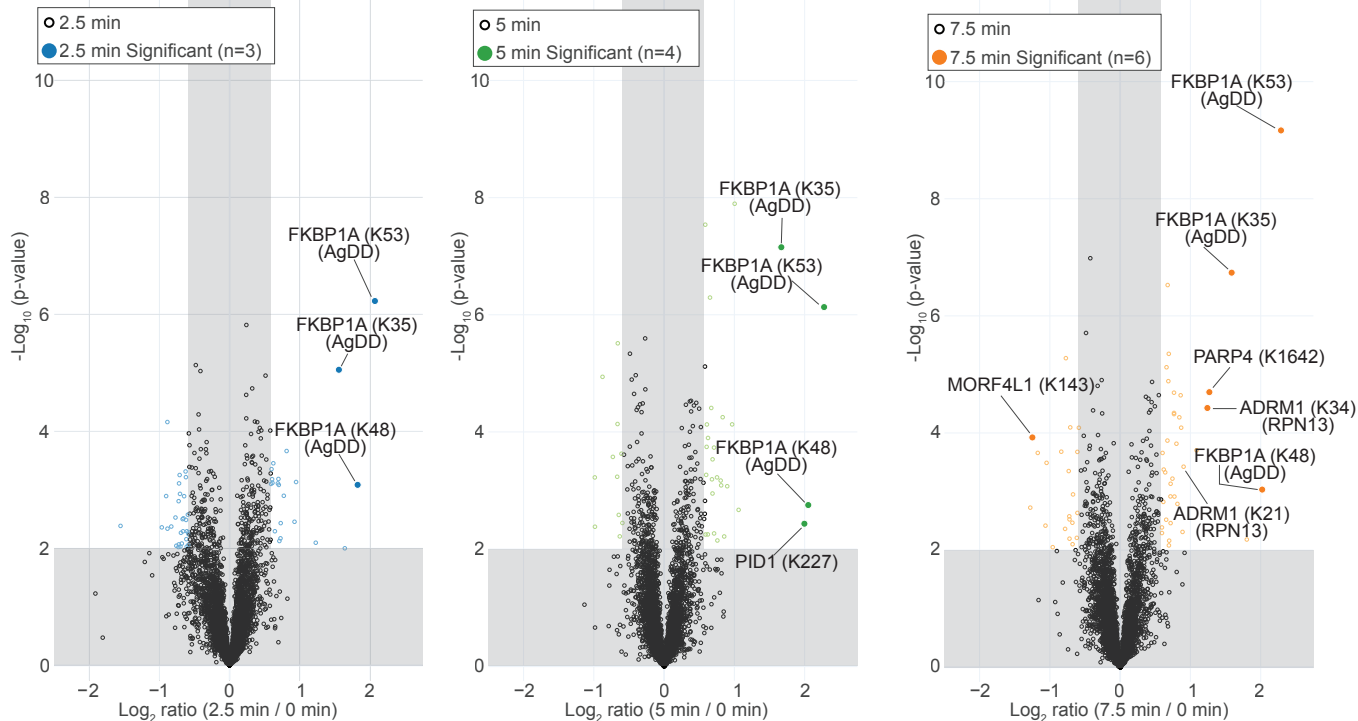


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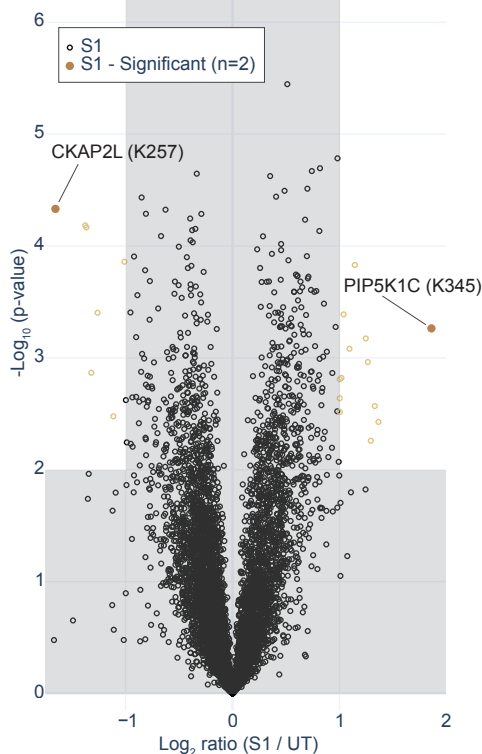
A

19986 total quantified Kgg in combined experiments
8623 unique quantified Kgg in combined experiments
4549 unique quantified sites common across both experiments



B

7059 unique quantified Kgg sites
10071 total quantified Kgg sites



C

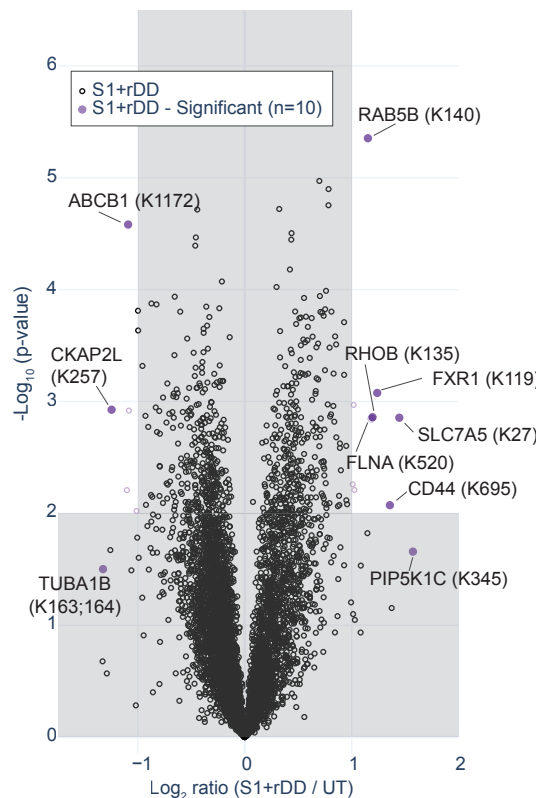


Fig. S1. S1 w/o in AgDD cells rapidly alters the ubiquitylation of PN components. (A) Volcano plots ($-\text{Log}_{10}$ p-value versus \log_2 ratio to untreated cells) of K-GG sites at 2.5, 5 and 7.5 min following S1 w/o. Proteins with $\log_2 < -0.585$ or > 0.585 ($p < 0.01$) are indicated as colored empty circles, and filled colored circles indicate statistically significant hits (Welch's t test [$S_0 = 0.5$], corrected for multiple comparison by permutation-based false discovery rate [FDR] [1%]) (B) Volcano plot ($-\text{Log}_{10}$ p-value versus \log_2 ratio to untreated cells) of K-GG sites in HEK293 WT cells grown in S1 vs vehicle. (C) Volcano plot ($-\text{Log}_{10}$ p-value versus \log_2 ratio to untreated cells) of K-GG sites in HEK293 cells grown in S1 and undergoing S1 w/o (S1+rDD). (B,C) Proteins with $\log_2 < -1$ or > 1 ($p < 0.01$) are indicated as colored empty circles, and filled colored circles indicate statistically significant hits (Welch's t test [$S_0 = 1.2$], corrected for multiple comparison by permutation-based false discovery rate [FDR] [1%]).

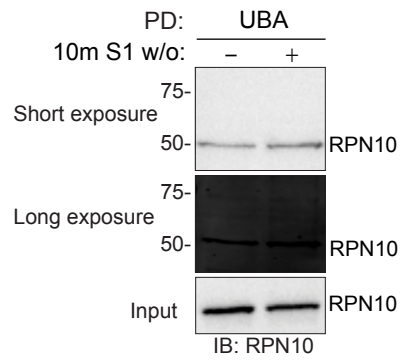


Fig S2. Ubiquitylation of RPN10 induced by S1 w/o is not detectable by immunoblotting. UBA capture of RPN10 did not reveal slower migrating bands that increased in intensity following S1 w/o.

PD: RPN11-HTBH (Input and flow through samples)

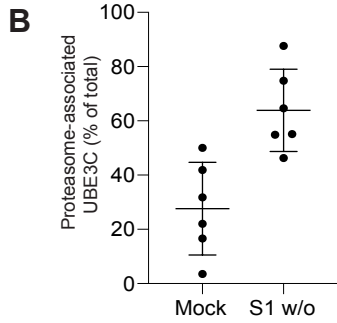
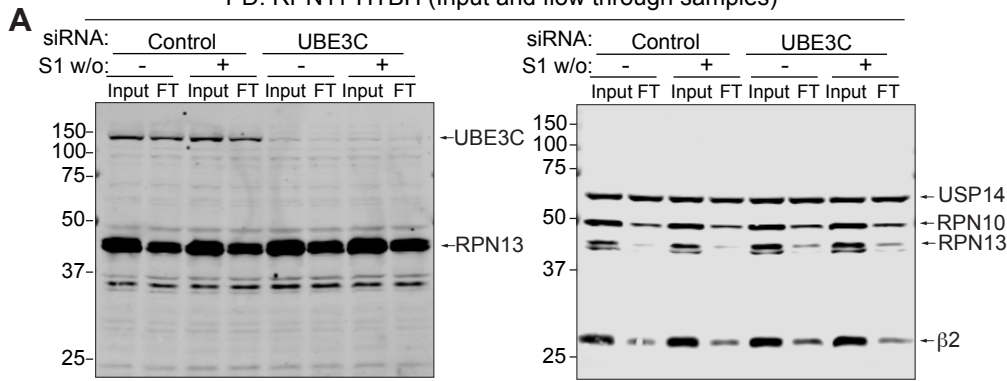


Fig S3. UBE3C-catalyzed ubiquitylation of RPN13 and AgDD at the proteasome following 10 min S1 w/o. (A) Input and flow through (FT) samples showing depletion of UBE3C and several other proteasome-associated proteins following proteasome affinity capture. (B) Increase in the fraction of total intracellular UBE3C that associates with proteasomes following S1 w/o. Error bars represent standard deviation.

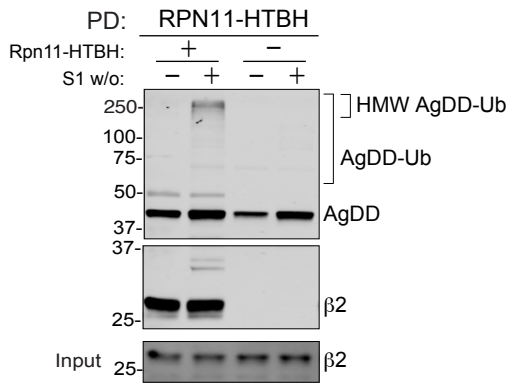


Fig S4. Ubiquitylated AgDD co-purifies with 26S proteasomes. HEK cells stably expressing AgDD alone or in combination with Rpn11-HTBH were subjected to either mock or S1 w/o for 10 min prior to harvest. Proteasomes were captured from Rpn11-HTBH expressing cells using streptavidin-coated magnetic beads. Immunodetection of the 20S subunit $\beta 2$ (middle panel) confirmed the capture of intact 26S proteasomes from AgDD Rpn11-HTBH cells. Immunodetection of GFP (upper panel) detected ubiquitylated AgDD in association with captured proteasomes.