

Supplementary Materials

# **The proteasomal deubiquitinating enzyme PSMD14 regulates macroautophagy by controlling Golgi-to-ER retrograde transport**

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**Figure S1. siRNA sequences directed against human PSMD14 used for Validation Stage.**

**Figure S2. Primer pairs sequences used for RT-qPCR.**

**Figure S3. The PSMD14 DUB inhibitor CZM increases the Golgi apparatus area.**

Immunofluorescence microscopy analysis of the Golgi area in parental H4 cells treated for 4 h either with the vehicle (DMSO; Control) or CZM. The Golgi marker GM130 was used to determine the region of interest in each condition. Statistical significance was determined by Student's t-test. Bars represent the mean ± SEM ( $n=43$  cells). \*\*\*P <0.001.

**Figure S4. CZM causes the accumulation of KDELR1-GFP at the Golgi apparatus.**

HeLa cells expressing KDELR1-GFP were either left untreated or treated with CZM for 30, 60 or 90 min. Cells were fixed and representative confocal images were acquired.

**Figure S5. Effect of CZM on proteasome activity.**

Parental H4 cells were treated either with the vehicle (DMSO; Control), CZM or MG132, for 90 min. Protein extracts were used to measure *in vitro* the Chymotrypsin-like peptidase activity of the proteasome. The enzymatic activity was quantified according to the cleavage of the fluorogenic substrate Suc-LLVY-AMC to AMC, and normalized to that of control cells. The statistical significance was determined by One-Way ANOVA, followed by Tukey's test. Bars represent the mean ± SD of biological replicates ( $n=3$ ). \*\*P <0.01; n.s., not significant.

**Figure S6. Effect of CZM and MG132 on basal macroautophagy.**

(A) Immunofluorescence microscopy analysis of the subcellular localization of LC3 in parental H4 cells treated with either with the vehicle (DMSO; Control), CZM for 4 h or MG132 for 6 h. Cells were fixed, permeabilized and stained with a rabbit polyclonal antibody to LC3B followed by Alexa-594-conjugated donkey anti-Rabbit IgG. Scale bar 10  $\mu$ m. (B) Parental H4 cells were treated as in (A) and the protein extracts were analyzed by western blot with a polyclonal antibody to LC3B. Densitometric quantification of the protein levels of LC3B were depicted as the Ratio LC3B-II/LC3B-I. The statistical significance was determined by One-Way ANOVA, followed by Tukey's test. Bars represent the mean ± SD of biological replicates ( $n=3$ ). \*\*\*P <0.001; n.s., not significant.

**Figure S7. Distribution of RAB1A upon CZM treatment.**

Immunofluorescence analysis of endogenous RAB1A in H4 parental cells treated either with vehicle (DMSO; Control) (A-C) or CZM for 4 h (D-F). Cells were fixed, permeabilized, and double stained with a rabbit

monoclonal antibody to RAB1A (clone D3X9S) (A and D) and a mouse monoclonal antibody to GM130 (clone35/GM130) (B and E), followed by Alexa-594-conjugated donkey anti-Rabbit IgG and Alexa-488-conjugated donkey anti-Mouse IgG. Merging of the images generated the third picture (C and F). Scale bar, 10  $\mu$ m. (G) Quantitative analysis of the fraction of RAB1A colocalizing with GM130 under CZM treatment and compared to control cells. The statistical significance was determined by Student's t-test. Bars represent the mean  $\pm$  SEM of the fluorescent signal per cell area (n=173 cells). \*P< 0.05.

**Figure S8. ATG9A is distributed in the swollen Golgi apparatus upon CZM treatment.**

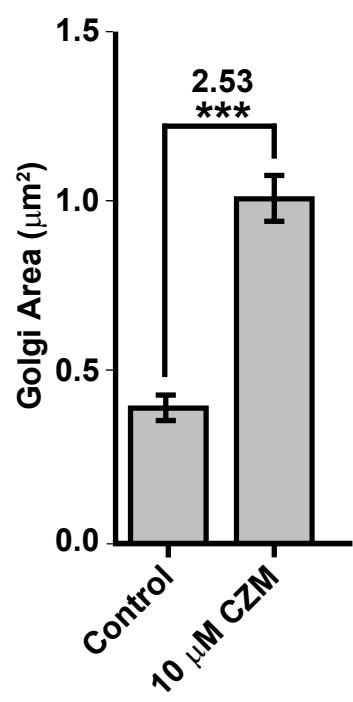
Immunofluorescence analysis of endogenous ATG9A in H4 parental cells treated either with the vehicle (DMSO; Control) (A-C) or CZM for 4 h (D-F). Cells were fixed, permeabilized, and double stained with a rabbit monoclonal antibody to ATG9A (clone EPR2450(2)) (A and D) and a mouse monoclonal antibody to GM130 (clone35/GM130) (B and E), followed by Alexa-594-conjugated donkey anti-Rabbit IgG and Alexa-488-conjugated donkey anti-Mouse IgG. Merging of the images generated the third picture (C and F). Scale bar, 10  $\mu$ m. (G) Quantitative analysis of the fraction of ATG9A colocalizing with GM130 under CZM treatment and compared to control cells. The statistical significance was determined by Student's t-test. Bars represent the mean  $\pm$  SEM of the fluorescent signal per cell area (n=93 cells). \*\*P <0.01.

	<b>Sequence</b>
<b>siRNA #1</b>	(5'-GAACAAGUCUAUAUCUCUU-3')
<b>siRNA #2</b>	(5'-GGCAUUAUUCAUGGACUA-3')
<b>siRNA #3</b>	(5'-AGAGUUGGAUGGAAGGUUU-3')
<b>siRNA #4</b>	(5'-GAUGGUUGGUUGGUUGGUAU-3')

**Figure S1**

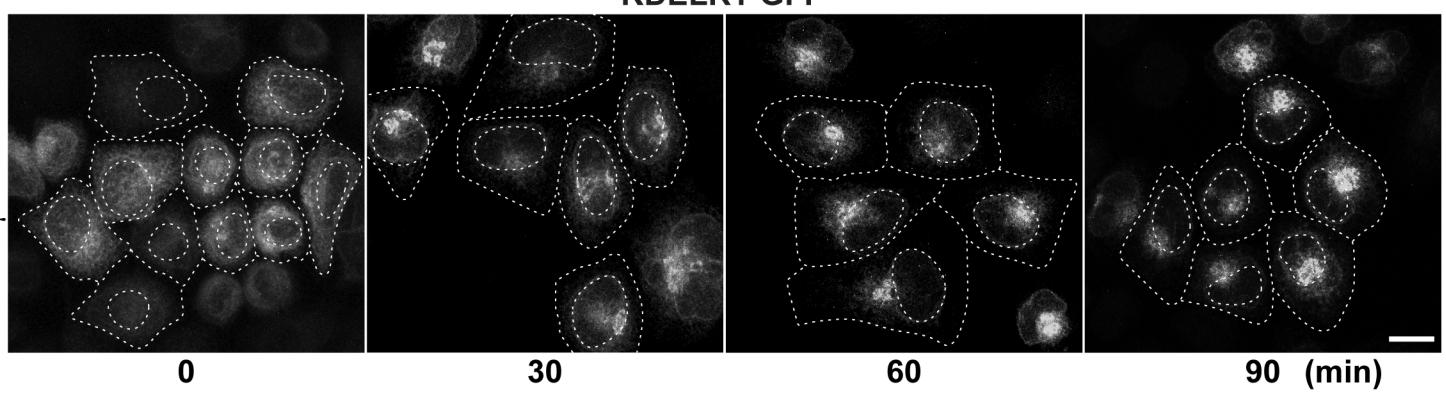
<b>Target</b>	<b>Sequence</b>
<b>hTBP1</b>	f(5'-TAGTCCAATGATGCCTTACG-3') r(5'-TGGTCAGAGTTGAGAATGG-3')
<b>hPSMD14</b>	f(5'-ACCTTAAGAGTTGTAGTTACTGACC-3') r(5'-TTAACAGTGCCAGGGAAGAG-3')
<b>hAPP</b>	f(5'-CCTAAAGCATTGAGCATG-3') r(5'-GTTTCCGTAACTGATCCTTG-3')

**Figure S2**

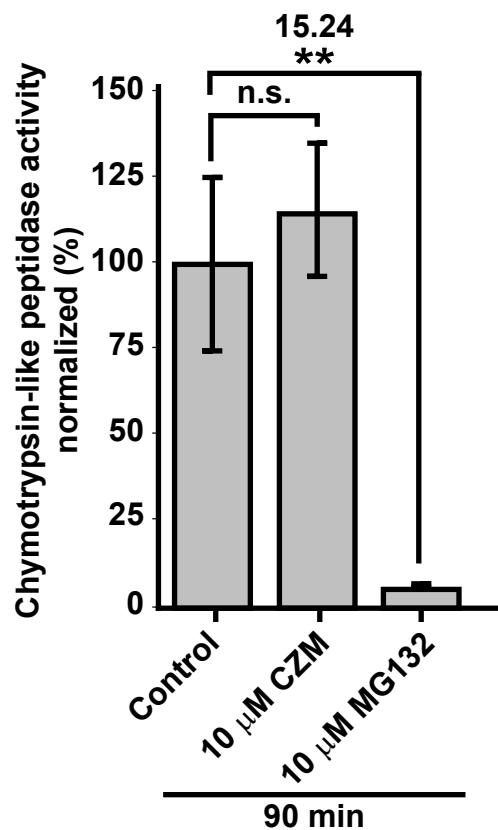


**Figure S3**

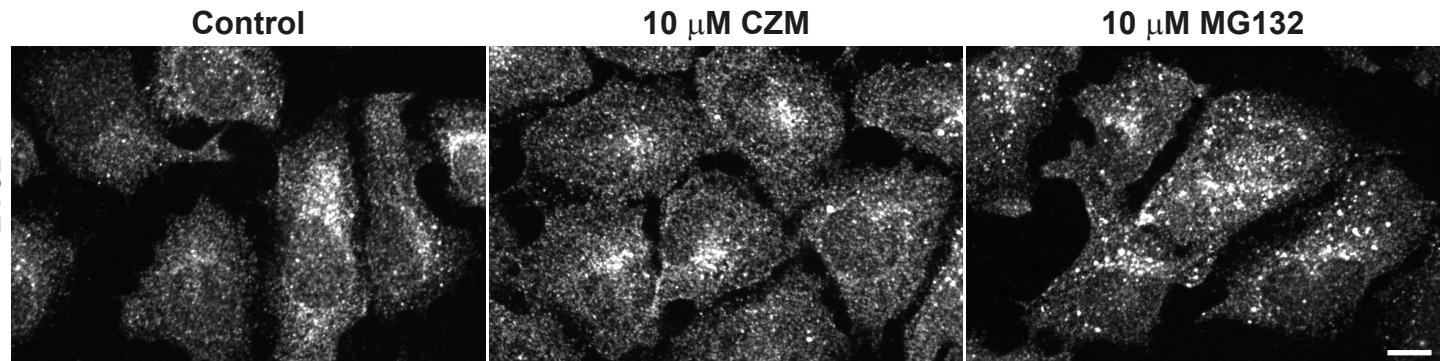
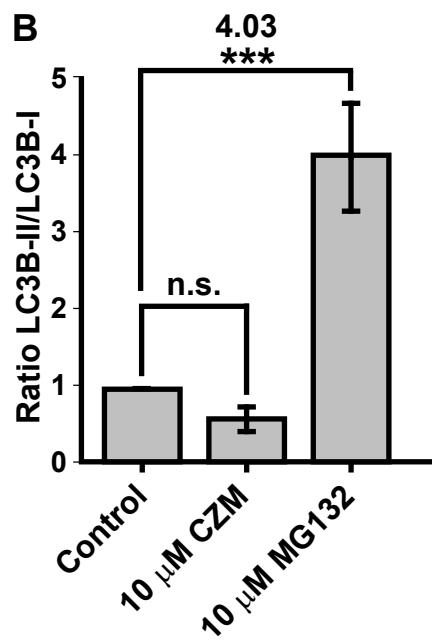
10  $\mu$ M CZM

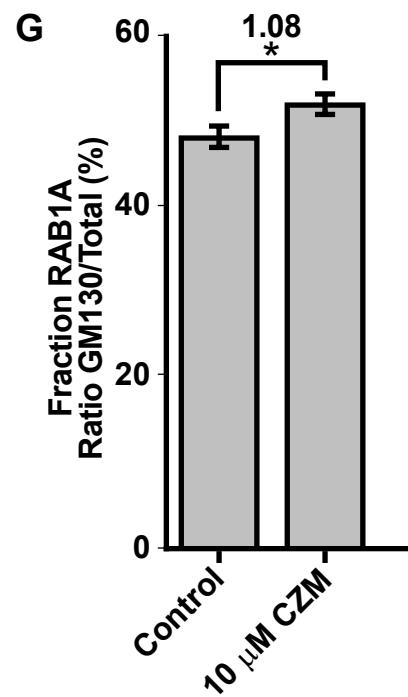
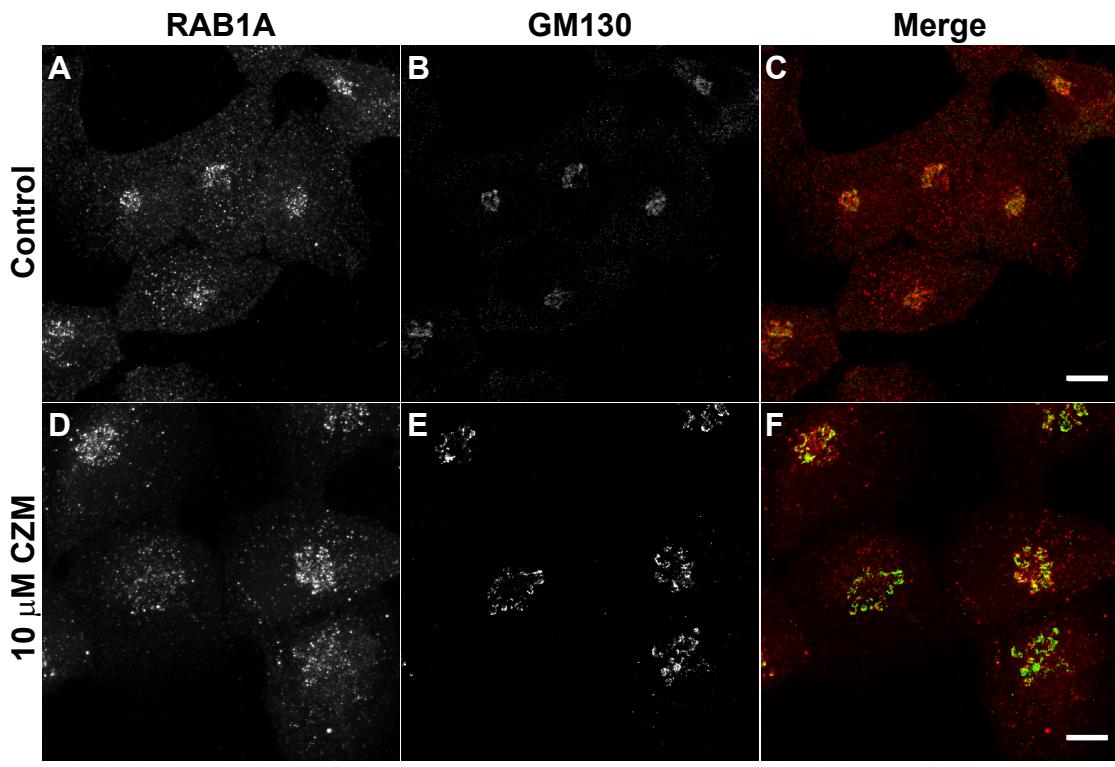


**Figure S4**

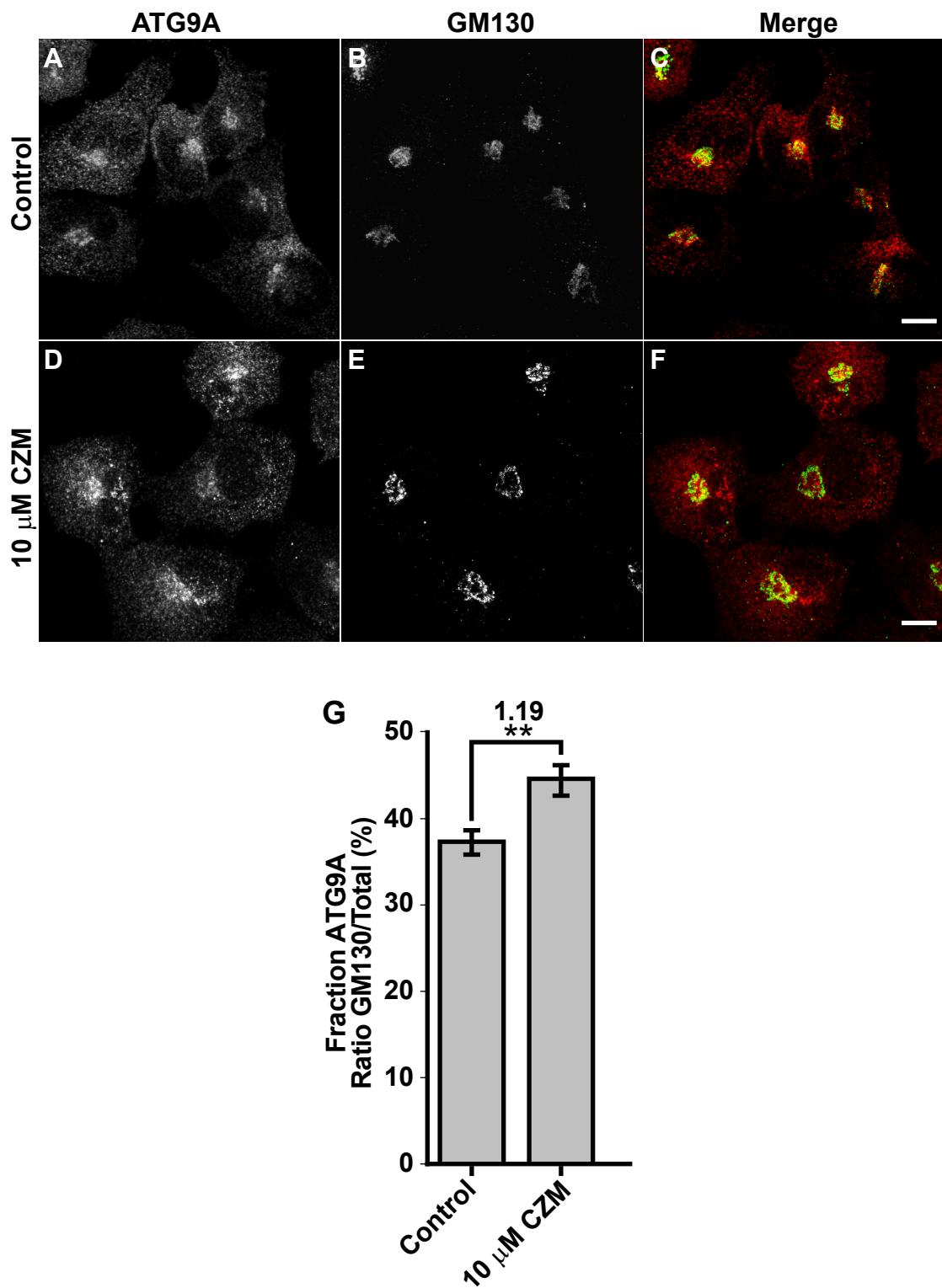


**Figure S5**

**A****B****Figure S6**



**Figure S7**



**Figure S8**

## Target List High-Content siRNA Screening "Ubiquitinome"

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PSMD7	NM_002811
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NACA	NM_005594
EPN1	NM_013333
SIAH2	NM_005067
UBA52	NM_003333
EIF3S5	NM_003754
MARK4	NM_031417
UBC	NM_021009
UBE2E3	NM_182678
RBM6	NM_005777
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PRPF8	NM_006445
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KIAA1536	NM_020898
WDR11	NM_018117
SH3RF2	NM_152550
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RNF141	NM_016422
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