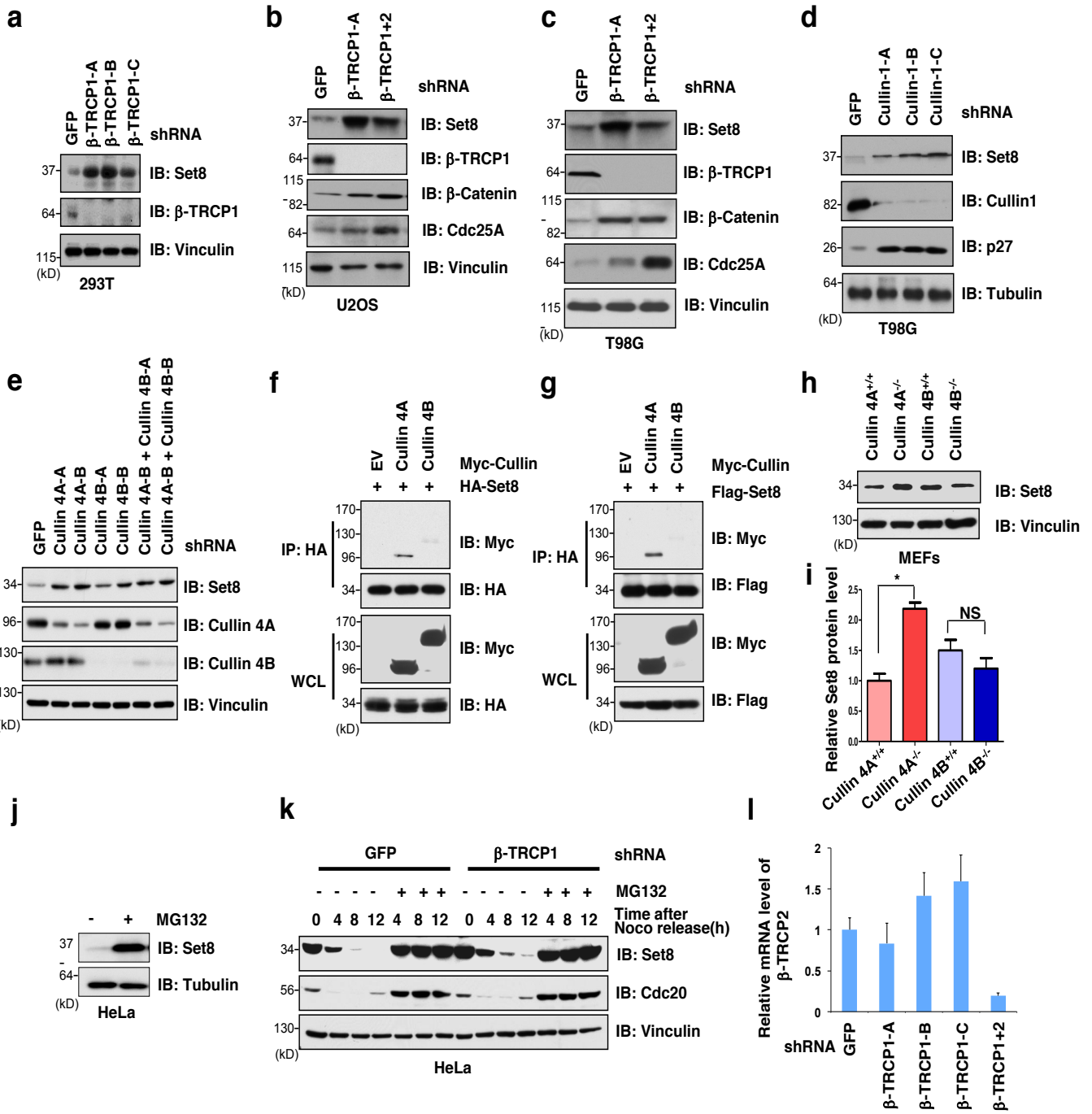


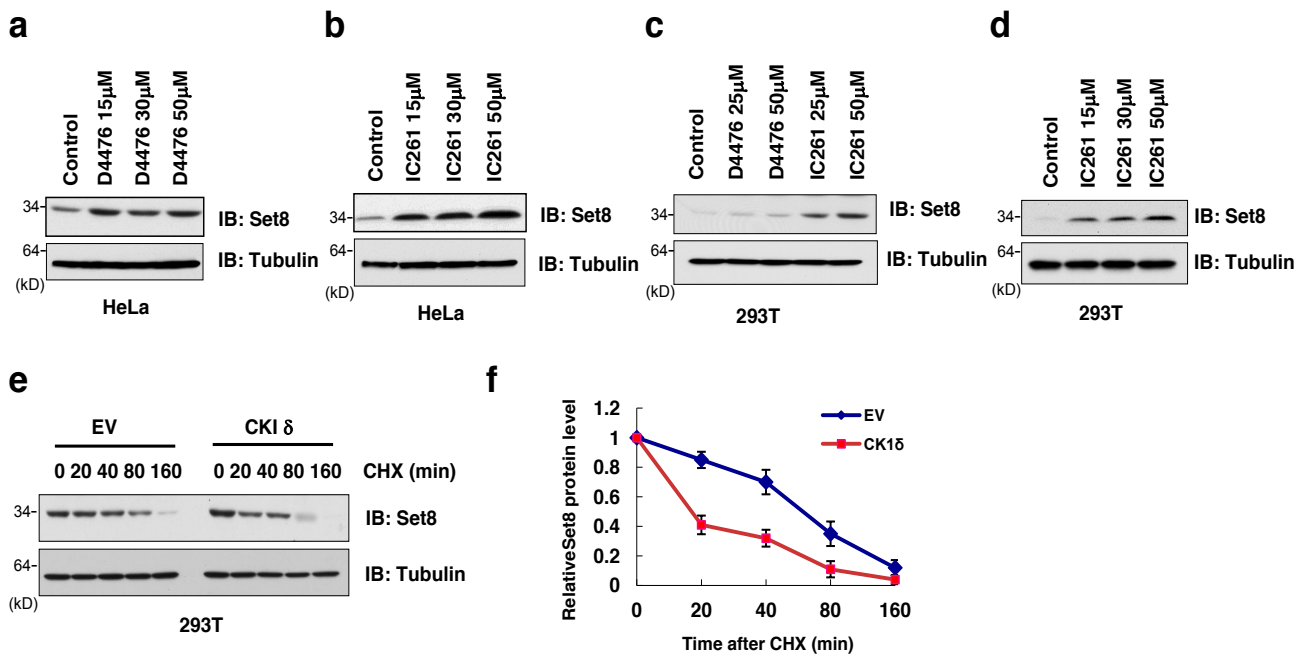
Supplementary Figure 1. Set8 interacts with the SCF ^{β -TRCP} complex.

- Mass spectrometry analysis of β -TRCP1-associated proteins.
- Immunoblot (IB) analysis of whole cell lysates (WCL) and immunoprecipitation (IP) derived from 293T cells transfected with HA-Set8 or empty vector (EV) as a negative control.
- U2OS cells harboring inducible Flag-tagged Set8^{WT} were treated with 0.1 μ g ml⁻¹ doxycycline (Dox) to induce the ectopic expression of Flag-WT-Set8. The cells were then treated with 15 μ M MG132 for 12 hr and harvested for anti-Flag immunoprecipitation (IP). Mouse normal IgG was used as a control.
- IB analysis of WCL and IP derived from 293T cells transfected with HA-Set8 and Flag-tagged wild-type (WT) or R474A mutant β -TRCP1 constructs, or EV.
- IB analysis of WCL and IP derived from 293T cells transfected with Flag-Set8 and Myc-Cullin 1, 2, 3, 4A or 5 expressing plasmids.



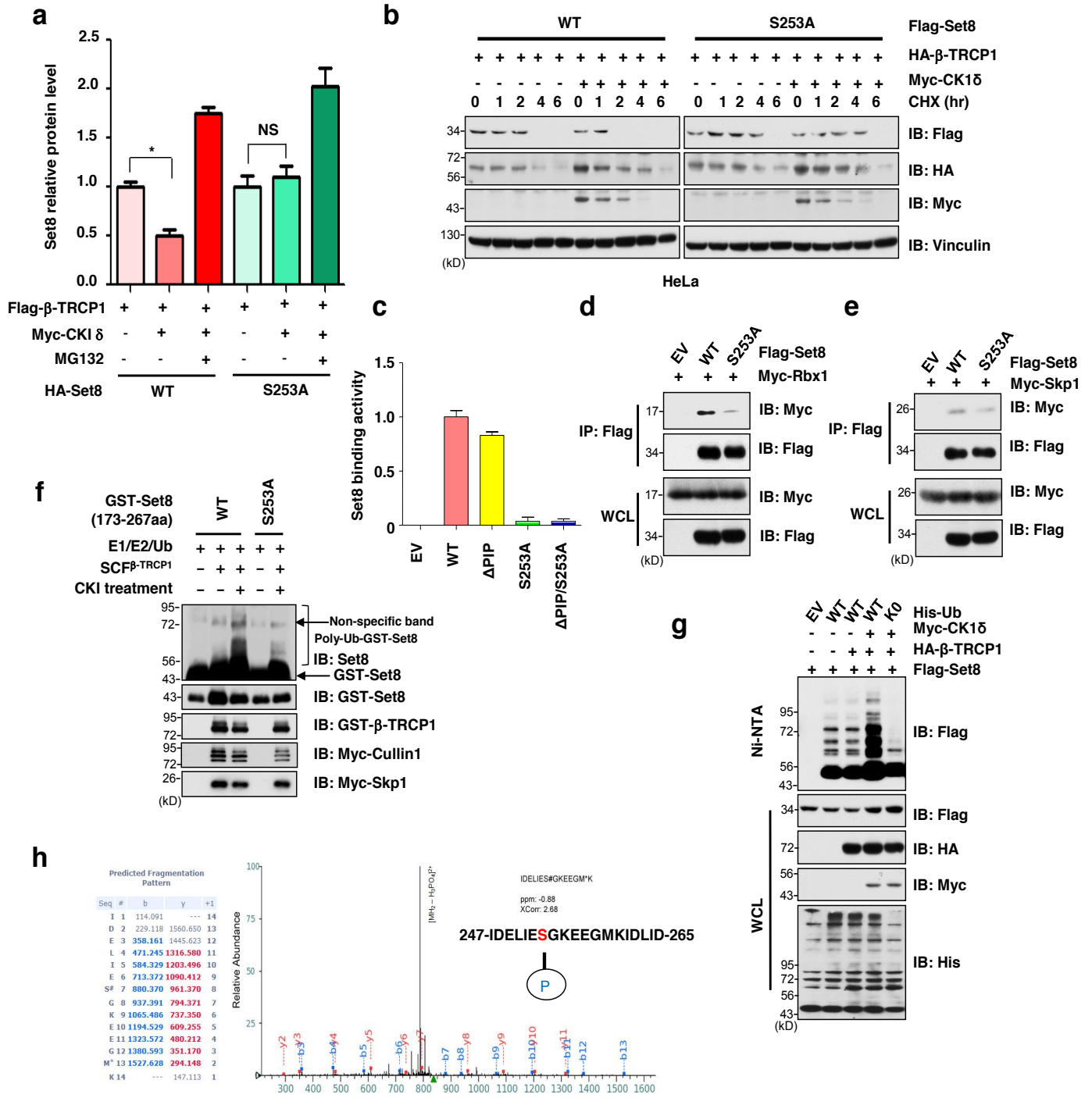
Supplementary Figure 2. Depletion of endogenous β -TRCP or *Cullin 1* increases Set8 protein levels.

- a-c. Immunoblot (IB) analysis of whole cell lysates (WCL) derived from 293T (a), U2OS (b), and T98G (c) infected with shRNA constructs specific for *GFP*, β -TRCP1 (three independent shRNAs, namely -A, -B and -C), or β -TRCP1+2, followed by selection with 1 μ g ml⁻¹ puromycin for three days to eliminate non-infected cells.
- d. IB analysis of WCL from T98G cells infected with shRNA specific for *GFP*, or several shRNA constructs against *Cullin 1* (three independent lentiviral *Cullin 1*-targeting shRNA constructs namely, -A, -B, -C) followed by selection with 1 μ g ml⁻¹ puromycin for three days to eliminate non-infected cells.
- e. IB analysis of WCL from HeLa cells infected with shRNA construct specific for *GFP*, or several shRNA constructs against *Cullin 4* (two independent lentiviral *Cullin 4A*-targeting shRNA constructs namely, -A, -B, and two independent lentiviral *Cullin 4B*-targeting shRNA constructs namely, -A, -B) followed by selection with 1 μ g ml⁻¹ puromycin for three days to eliminate non-infected cells.
- f. IB analysis of WCL and IP derived from 293T cells transfected with HA-Set8 and Myc-tagged *Cullin 4A* and *Cullin 4B*.
- g. IB analysis of WCL and IP derived from 293T cells transfected with Flag-Set8 and Myc-tagged *Cullin 4A* and *Cullin 4B*.
- h. IB analysis of WCL derived from *Cullin 4A*^{fl/fl} and *Cullin 4B*^{fl/fl} MEFs that are retrovirally infected with the Cre-recombinase encoding vectors to delete endogenous *Cullin 4A* or *Cullin 4B*, respectively.
- i. Quantification of the Set8 band intensities in (h). Set8 band intensity was normalized to Vinculin. Data are shown as mean \pm s.d. of three independent experiments. *p<0.05, Student's t-test
- j. IB analysis of WCL derived from HeLa cells with or without MG132 treatment.
- k. HeLa cells were infected with the shGFP or sh β -TRCP1 followed by selection with 1 μ g ml⁻¹ puromycin for three days to eliminate non-infected cells. The generated stable cell lines were then treated with nocodazole. At the indicated time points, WCL were prepared and immunoblots were probed with the indicated antibodies.
- l. mRNA levels of β -TRCP2 in HeLa cells infected with the indicated shRNA constructs. β -TRCP2 mRNA levels were normalized to *GAPDH*, and then normalized to the control cells (shGFP), n=3.



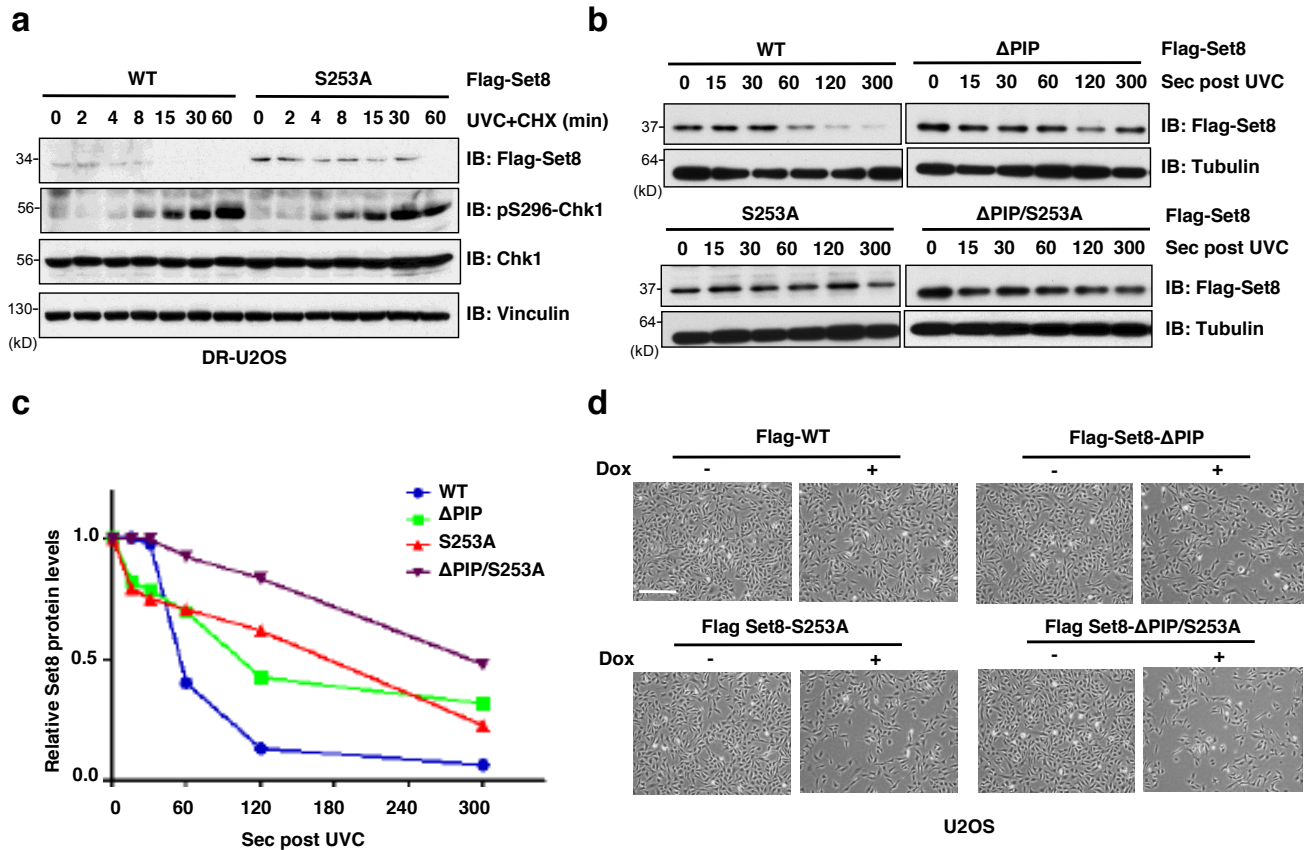
Supplementary Figure 3. Casein Kinase I δ (CKI δ) controls Set8 stability.

- a-b.** Immunoblot (IB) analysis of WCL from HeLa cells treated with the CKI inhibitor D4476 (**a**) or IC261 (**b**) at the indicated concentrations for 12 hours.
- c-d.** IB analysis of WCL from 293T cells treated with the CKI inhibitor D4476 (**c**) or IC261 (**d**) at the indicated concentrations for 12 hours.
- e.** 293T cells were transfected with EV or CKI δ expression plasmid. The transfected cells were then split into 60-mm dishes. Cells were treated with 20 μ g ml⁻¹ CHX after 20 hours. At the indicated time points, WCL were prepared, and immunoblots were probed with the indicated antibodies.
- f.** Quantification of the Set8 band intensities in (e). Set8 band intensity was normalized to tubulin, and then normalized to the t=0 controls, n=3.



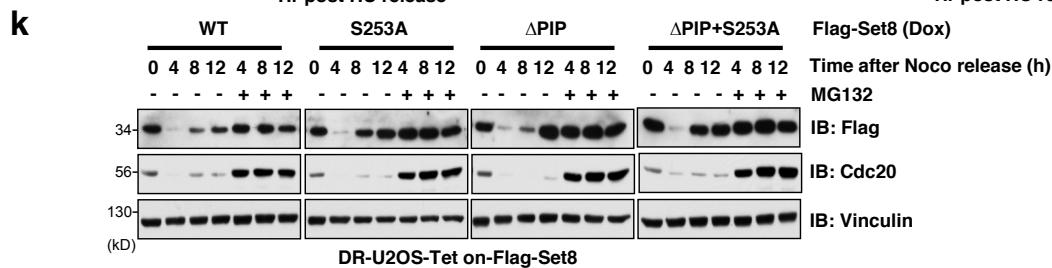
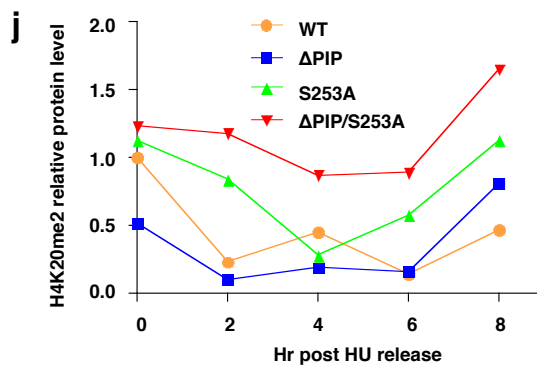
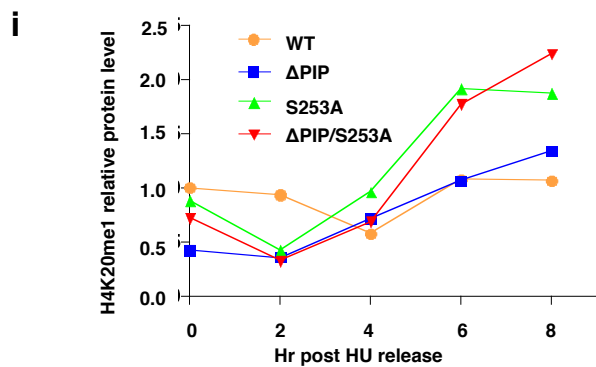
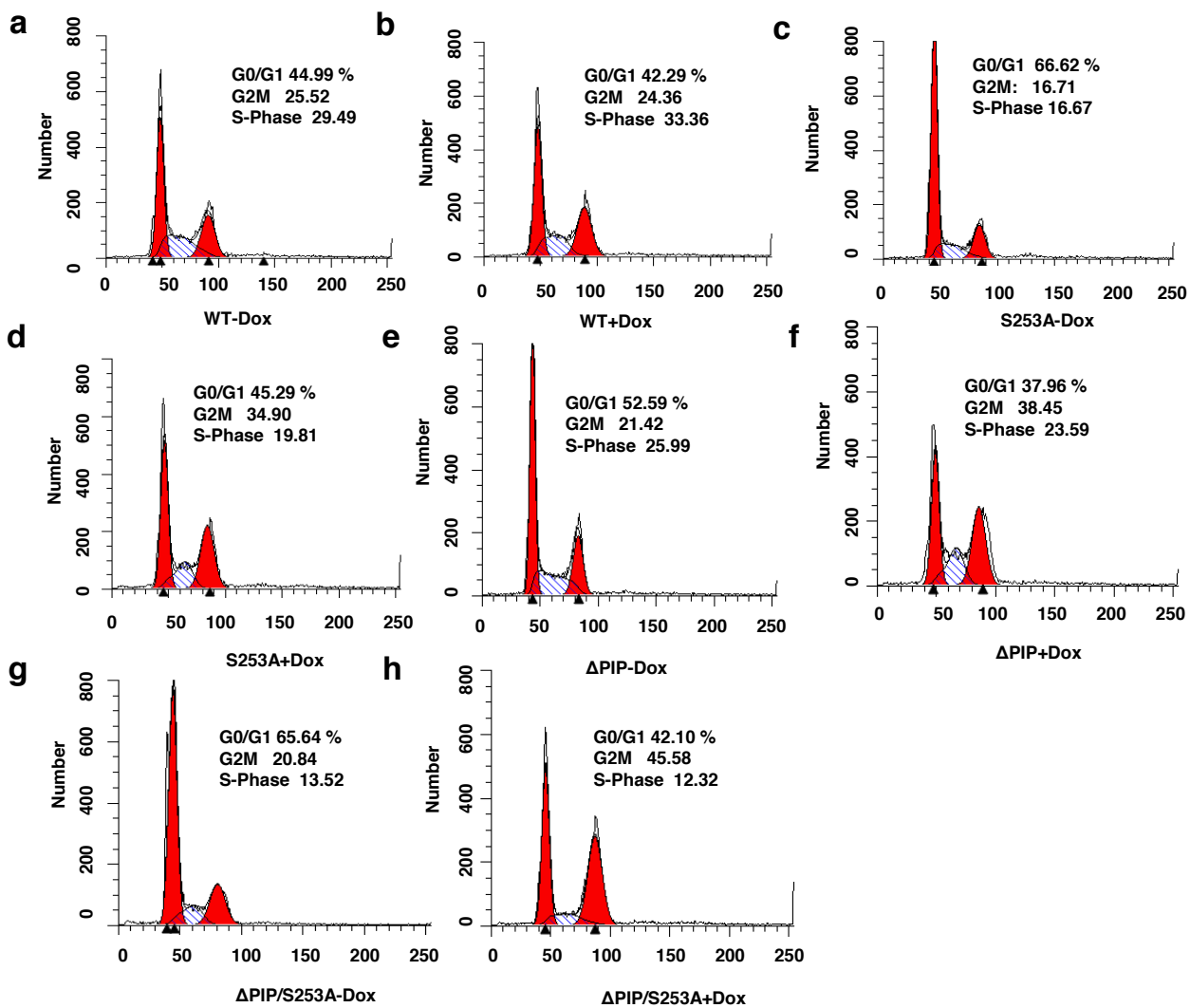
Supplementary Figure 4. Phosphorylation-dependent ubiquitination of Set8 by SCF ^{β -TRCP}.

- a. Quantification of the Set8 band intensities in Fig. 4b. Set8 band intensity was normalized to tubulin. Data are shown as mean \pm s.d. of three independent experiments. * $p < 0.05$, Student's t-test
- b. HeLa cells were transfected with the indicated plasmids. The transfected cells were treated with 20 $\mu\text{g ml}^{-1}$ CHX after 20 hours. At indicated time points, whole cell lysates (WCL) were prepared and the immunoblots were probed with the indicated antibodies.
- c. Quantification of the Set8 band intensities in Fig. 4h. Set8 band intensity was normalized to Set8 in WCL,
- d-e. IB analysis of WCL and immunoprecipitation (IP) derived from 293T cells transfected with Flag-Set8 and Myc-tagged Rbx1 or Skp1.
- f. Purified CKI δ protein was incubated with 5 μg of the indicated GST-Set8 (173-267aa) proteins in the presence of ATP. The kinase reaction products were incubated with purified E1, E2, ubiquitin, and the SCF ^{β -TRCP} complex for 45 min. Afterwards, the products were analyzed by IB with anti-Set8 antibody.
- g. *In vivo* ubiquitination assays to demonstrate that SCF ^{β -TRCP} promotes Set8 ubiquitination using the WT and K-0 mutant ubiquitin as indicated. His-pull-down products of ubiquitinated Set8 and WCL were subjected to IB analysis with indicated antibodies.
- h. Mass spectrometry analysis to identify the Ser253 phosphorylation event in Set8.



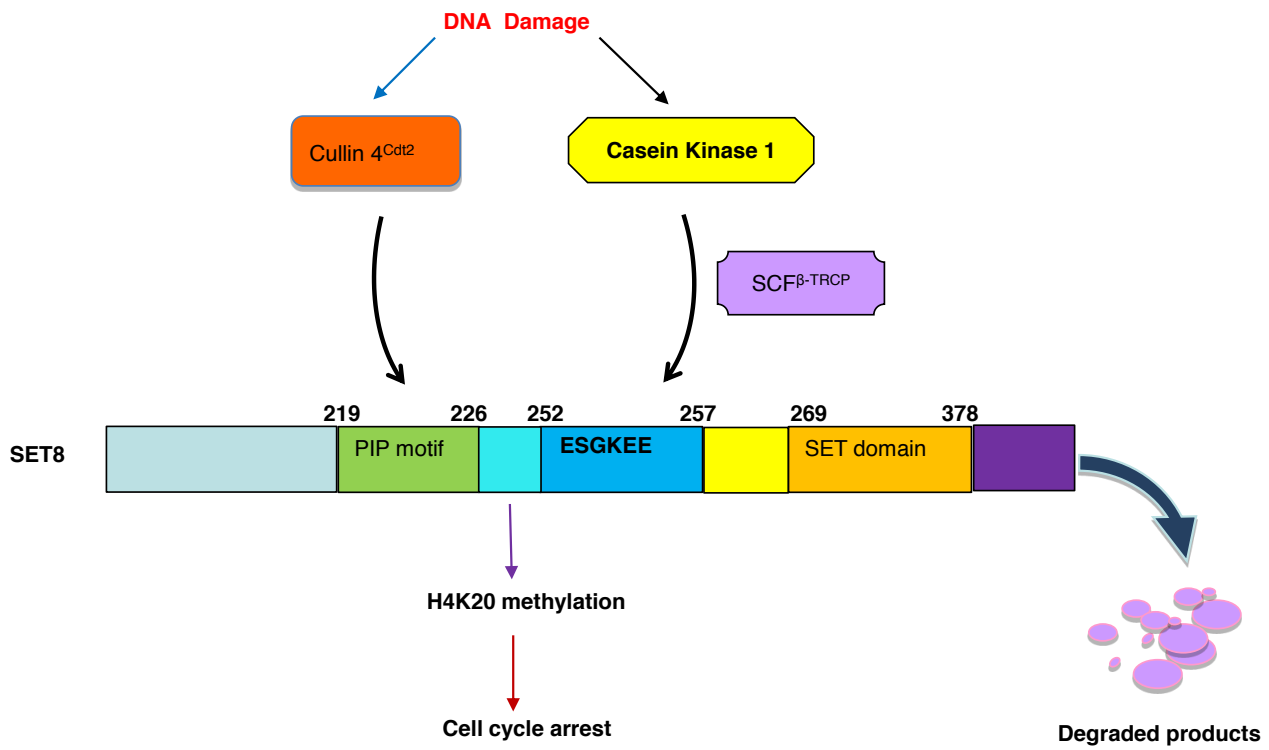
Supplementary Figure 5. Effects of β -TRCP-mediated degradation of Set8 on cell growth.

- U2OS cells were treated with doxycycline to induce the Set8 WT or S253A expression and then treated with UVC and $20 \mu\text{g ml}^{-1}$ CHX for different time periods. At the indicated time points, WCL were prepared, and immunoblots were probed with the indicated antibodies.
- U2OS cells with induced Flag-Set8^{WT}, Set8 ^{Δ PIP}, Set8^{S253A} or Set8 ^{Δ PIP/S253A} were treated with UV (50 J m^{-2}), IB analysis was performed to analyze the levels of Flag-Set8 and tubulin.
- Quantification of the Set8 band intensities in (b). Set8 band intensity was normalized to tubulin.
- U2OS cells harboring Flag-Set8^{WT}, Set8 ^{Δ PIP}, Set8^{S253A}, or Set8 ^{Δ PIP/S253A} were cultured in the absence or presence of $0.1 \mu\text{g ml}^{-1}$ doxycycline (Dox). The images were taken by microscopy to show a representative image of cell proliferation status. Scale bar: $100 \mu\text{m}$



Supplementary Figure 6. β -TRCP-mediated degradation of Set8 affects cell cycle.

- a-h.** U2OS cells harboring Flag-Set8^{WT} (**a, b**), Set8^{S253A} (**c, d**), Set8 ^{Δ PIP} (**e, f**), or Set8 ^{Δ PIP/S253A} (**g, h**) were cultured in the absence or presence of 0.1 $\mu\text{g ml}^{-1}$ doxycycline (Dox). Cell cycle was analyzed by PI staining using FACS.
- i-j.** Quantification of the H4K20me1 (**i**) and H4K20me2 (**j**) bands intensities in Fig. 6b. The band intensity was normalized to Vinculin.
- k.** U2OS cells harboring inducible Flag-Set8^{WT}, Set8^{S253A}, Set8 ^{Δ PIP}, or Set8 ^{Δ PIP/S253A} were synchronized in M phase with nocodazole for 18 hours. During the last 4 hours in nocodazole, expression of Set8 was induced by doxycycline (Dox). Then, cells with or without MG132 treatment were released from nocodazole in the presence of Dox, and IB analysis was performed to detect the indicated proteins.



Supplementary Figure 7. A schematic model showing mechanistically how both β -TRCP and Cdt2 regulate Set8 during the cell cycle progression.

Figure 1d

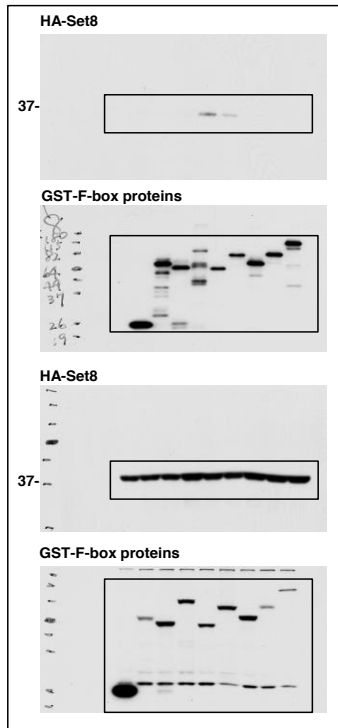


Figure 1f

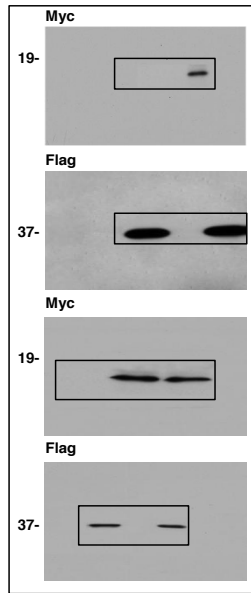


Figure 1g

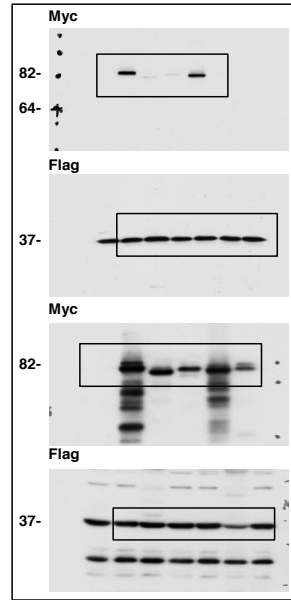


Figure 2b

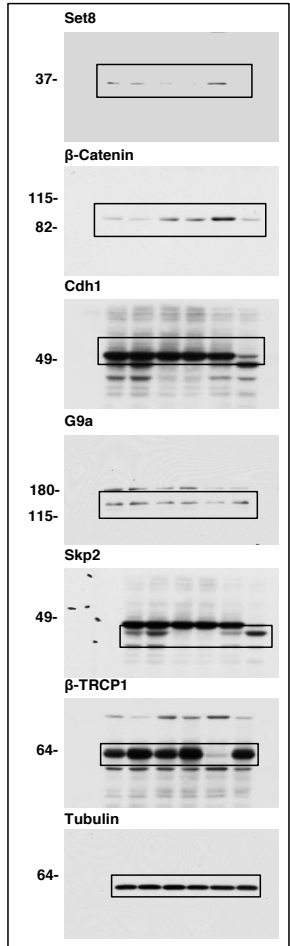


Figure 2c

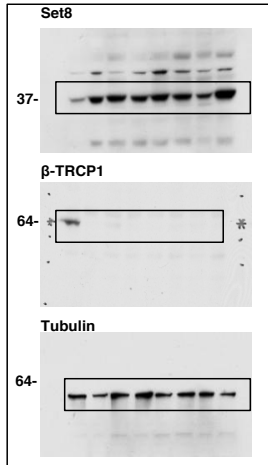


Figure 2f

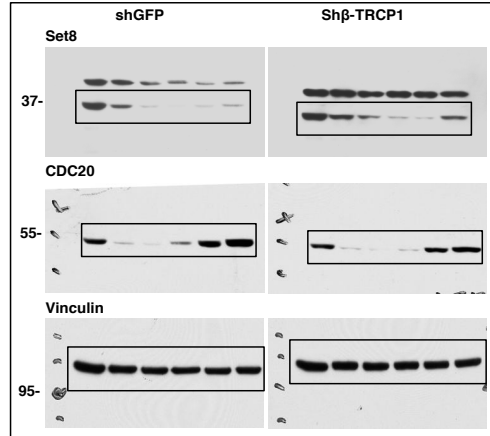


Figure 2d

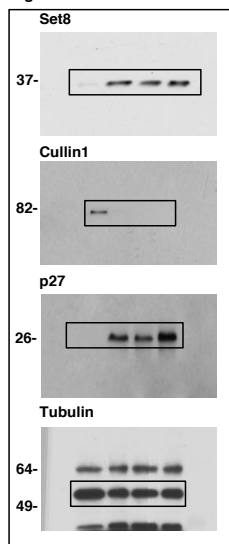
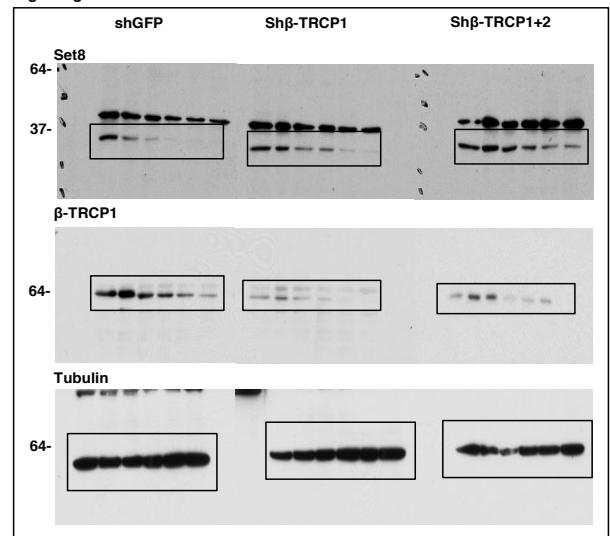


Figure 2g



Supplementary Figure 8a. Full images of the most important immunoblots in Figure 1 and 2. Small black boxes show approximate image used for presentation.

Figure 3a

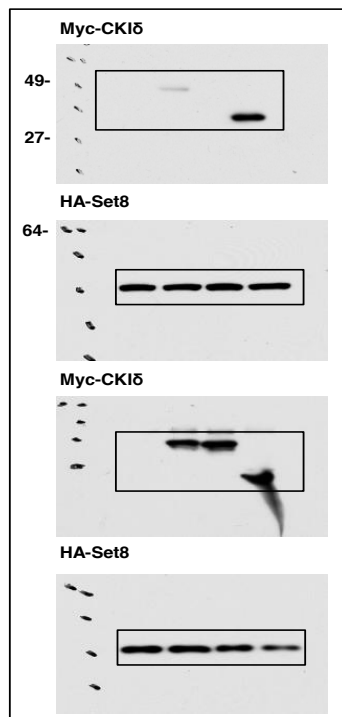


Figure 3b

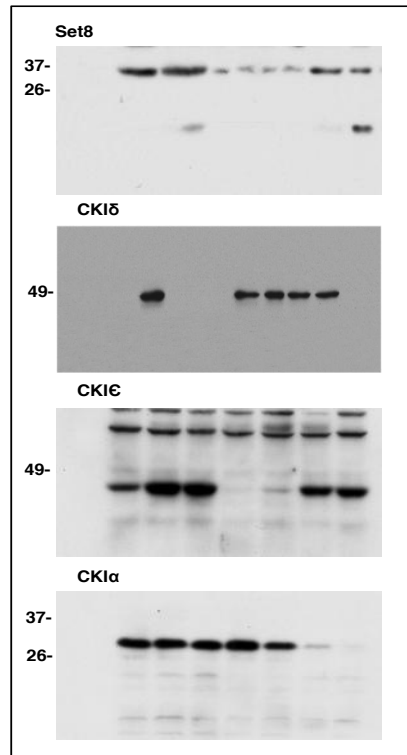


Figure 3c

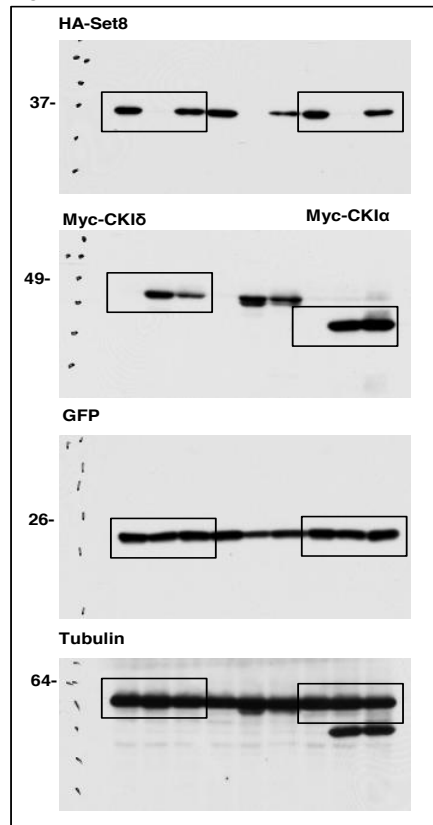


Figure 3d

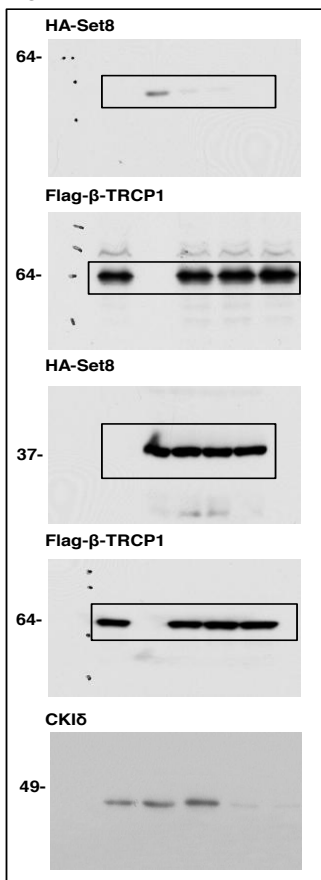


Figure 3f

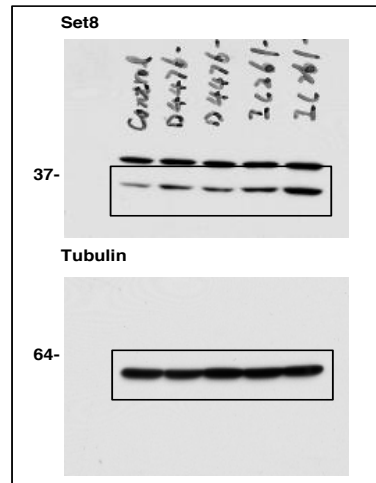
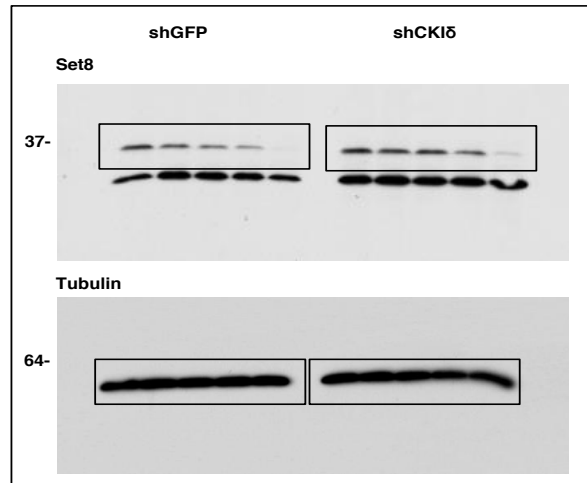


Figure 3g



Supplementary Figure 8b. Full images of most important immunoblots in Figure 3. Small black boxes show approximate image used for presentation.

Figure 4b

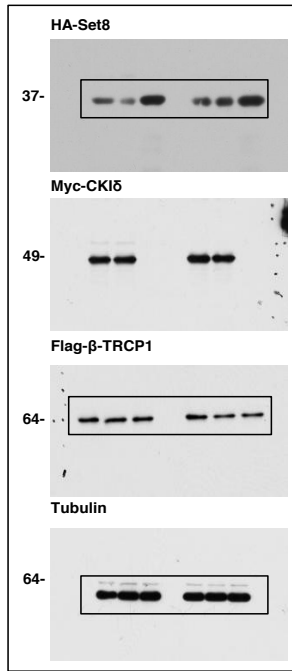


Figure 4e

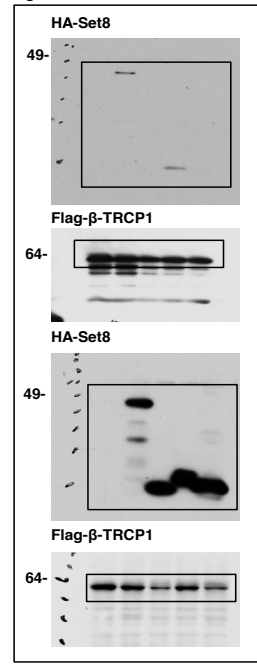


Figure 4g

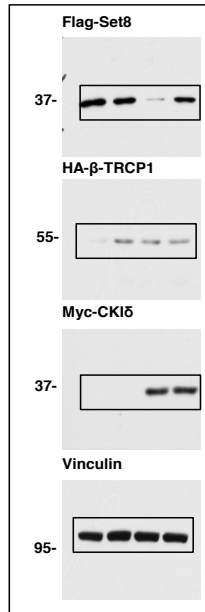


Figure 4h

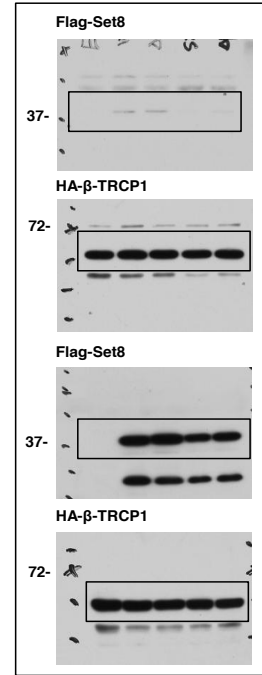


Figure 4i

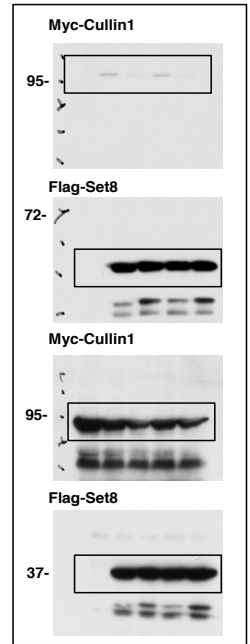


Figure 4j

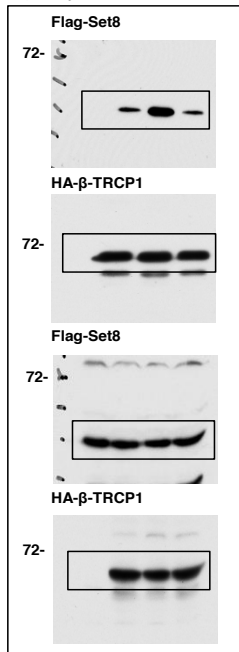


Figure 4k

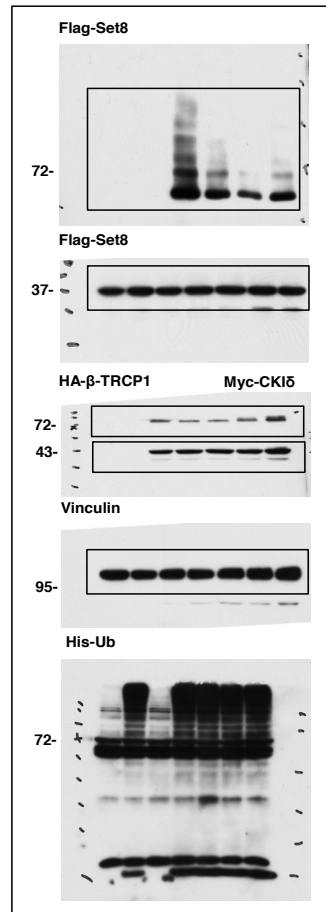
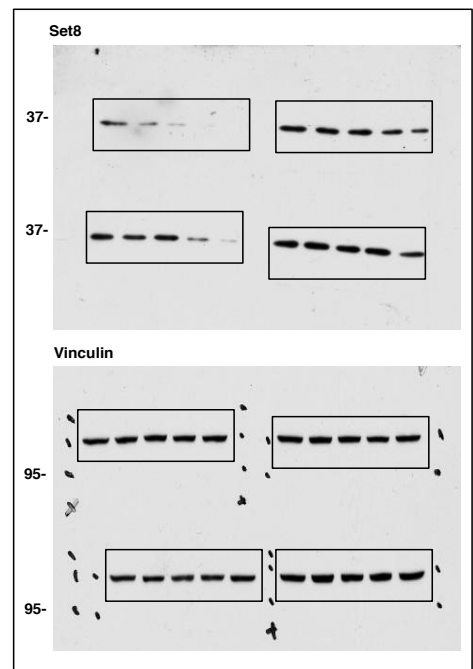


Figure 5a



Supplementary Figure 8c. Full images of most important immunoblots in Figure 4 and Figure 5. Small black boxes show approximate image used for presentation.

Figure 5c

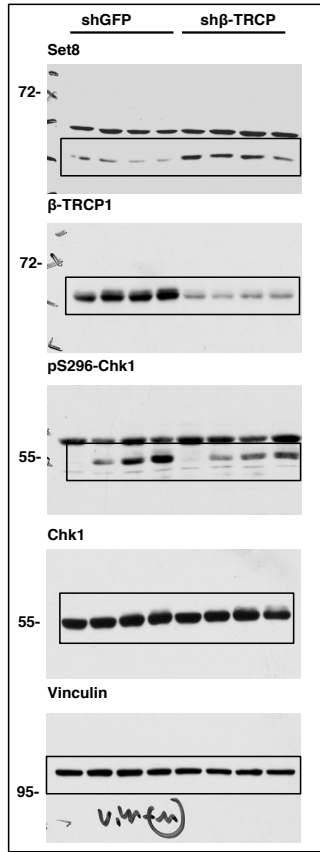
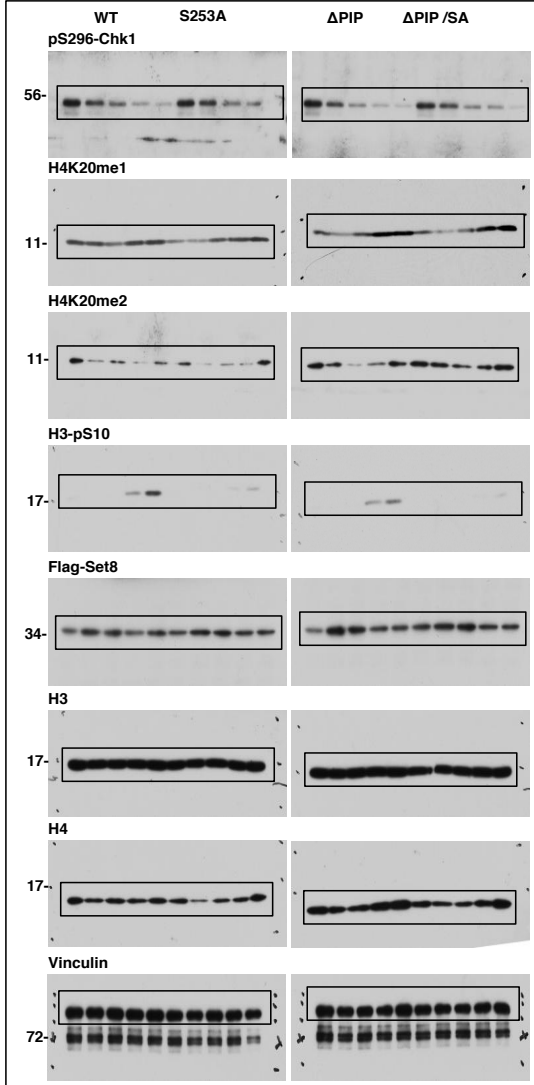
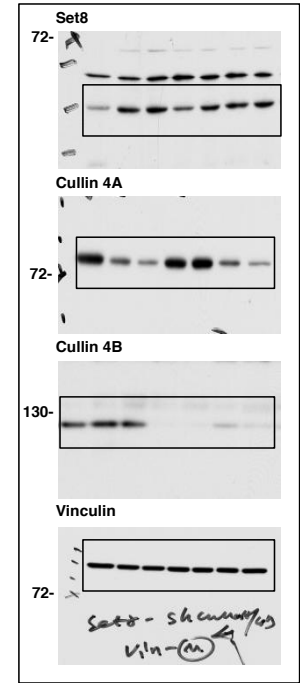


Figure 6b



Supplementary Figure 2e



Supplementary Figure 2h

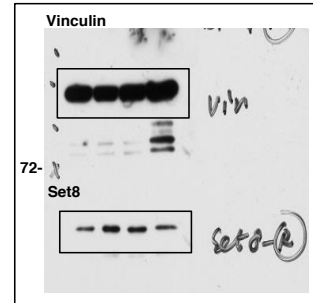
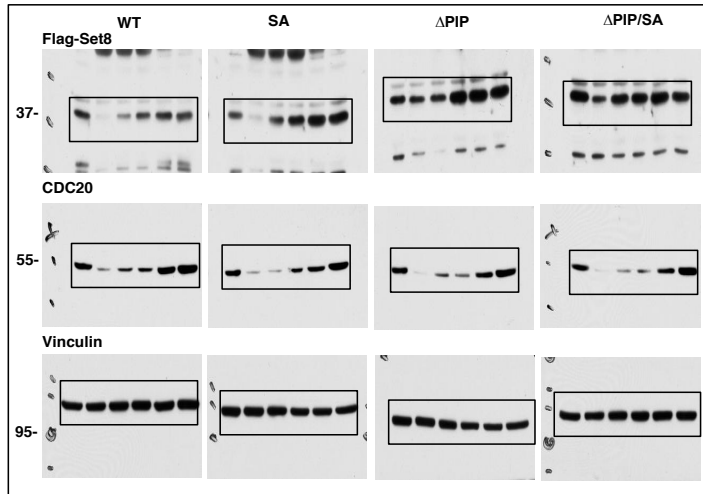


Figure 6c



Supplementary Figure 8d. Full images of most important immunoblots in Figure 5, Figure 6 and Supplementary Figure 2. Small black boxes show approximate image used for presentation.