S1A





S1B



72h

S1C



96h















S1 (A-C). Modfit histogram analysis of data summarized in Fig. 2B. All UbcH7 depletions are on the left, corresponding NS siRNA from the same experiment on the right. In some experiments 7-AAD (FL-3) was used instead of PI (FL-2) for cell cycle analysis. (A) Histograms for 48 h knockdown. (B) 72 h (C) 96 h. (D) Knockdown of UbcH7 with three different siRNAs results in S phase increase. Upper panel: summary of FACS analysis. Lower panel: immunoblot showing remaining UbcH7 expression. (E) Immunoblot analysis of UbcH7 expression for experiment shown in Fig. 2C.

S2 (**A**) Quantitative RT-PCR of UbcH7 from HLE cells synchronized by contact inhibition. mRNA was isolated from cells immediately after release from contact inhibition (cells in G0/G1), 18h after release (S phase) 32h after release (G2/M) and 40h (asynchronous). The amount of UbcH7 mRNA compared to GAPDH immediately after release was set to 1 and the ratio of UbcH7 to GAPDH at other time points were compared to this value. (**B**) HeLa cells were treated with cycloheximide in the presence or absence of MG132 for 1 or 2 hours as indicated. Levels of UbcH7 protein were determined by immunoblot and compared to the level in untreated cells. (**C**) Degradation of E2s. ¹²⁵I labeled E2s were added to reticulocyte lysates supplemented with Ubc4 and ATP. Degradation was performed as in (4C). (**D**) Cells synchronized using HU as in Fig. 1A, were lysed and the resulting extracts were used for degradation of β -B crystallin in the presence of

Ubc4, ATP and ubiquitin.

S3 Long term knockdown of UbcH7 results in S phase delay. Upper panel: immunoblot analysis of UbcH7 knockdown. Lower panel: cell cycle profile.