Supporting Information

White et al. 10.1073/pnas.1116776109

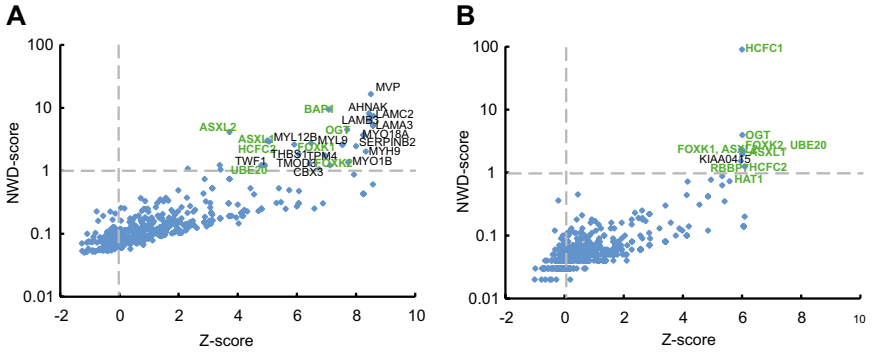

Fig. S1. CompPASS analysis of N/Tert-1 HA-BAP1 immunoprecipitation-MS/MS data analyzed by using a statistics table generated in 293 cells (*A*) or in N/Tert-1 cells (*B*). Green marks known BAP1 high-confidence interacting proteins as described by Sowa et al. (1). Black marks other proteins passing HCIP cutoff values. The NMD-score refers to the normalized weighted D-score, a metric that incorporates the uniqueness, abundance, and reproducibility of a given interactor.

1. Sowa ME, Bennett EJ, Gygi SP, Harper JW (2009) Defining the human deubiquitinating enzyme interaction landscape. *Cell* 138:389–403.

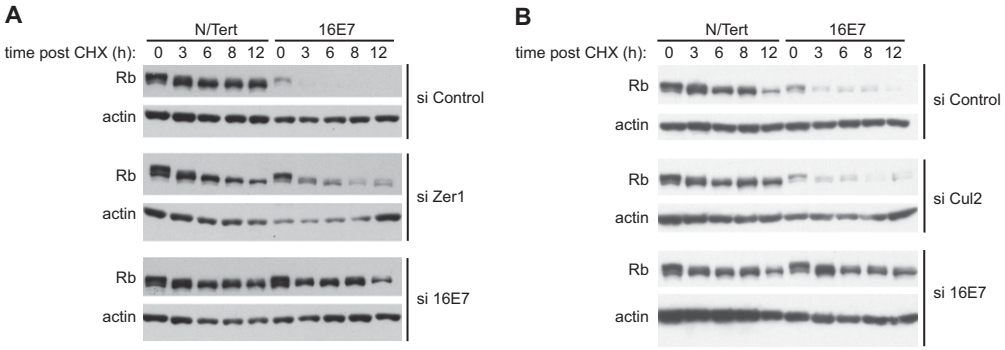

Fig. S2. Proteins required for the destabilization of RB1 by HPV16 E7. Control cells or N/Tert-1 cells stably expressing HPV16 E7-Flag HA were transfected with control, Zer1, and 16E7 siRNAs (*A*) or control, cullin 2 (Cul2), and 16E7 siRNAs (*B*) as indicated, then, 72 h later, treated with 40 μg/mL cycloheximide (CHX) and harvested at the indicated time points. Lysates were separated by SDS/PAGE and Western blotted by using antibodies to RB1 and actin.

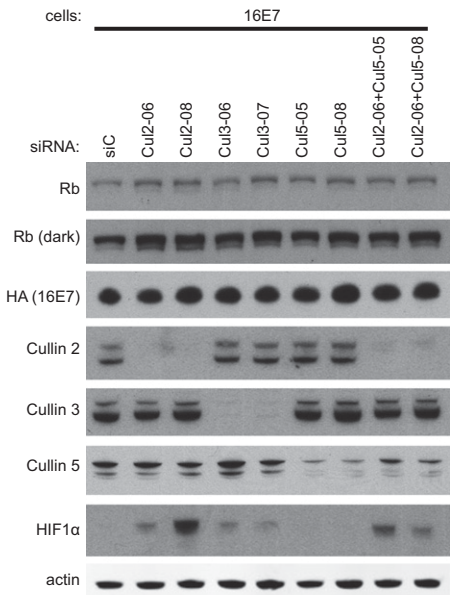

Fig. S3. Depletion of cullin 3 (Cul3) or cullin 5 (Cul5) does not affect RB1 levels in N/Tert-16E7 cells. N/Tert-1 cells stably expressing HPV16 E7-Flag HA were transfected with siRNAs as indicated and harvested for Western blots at 72 h after transfection. Lysates were separated by SDS/PAGE and Western blotted by using antibodies to RB1, HA, Cul2, Cul3, Cul5, HIF1α, and actin.

Other Supporting Information Files

Dataset S1 (XLS)
Dataset S2 (XLS)
Dataset S3 (XLS)
Dataset S4 (XLS)
Dataset S5 (XLS)
Dataset S6 (XLS)
Dataset S7 (XLS)