

Supplemental Materials

Figure S1. Colocalization of endogenous Nrf2 and endogenous Crif1. (A) Immunocytochemistry for Nrf2 and Crif1 localization before and after *t*-BHQ treatment. Cells (DU-145) treated with DMSO or *t*-BHQ (100 μ M, for 30 min or 1 h) were stained with anti-Nrf2 or anti-Crif1 antibody as described in Experimental Procedures. (B-C) Whole cell lysates (B) and both cytosolic and nuclear fractions (C) of cells treated with 100 μ M of *t*-BHQ for the indicated times were extracted and then analyzed on WBs with the designated antibodies. The anti- α/β -tubulin (cytosolic maker) and anti-Lamin B1 (nuclear maker) antibodies were used as loading controls and to monitor the quality of the cytosol/nuclear fractionation method.

Figure S2. Crif1 partially interacts with Neh1 (bZIP) domain (DNA binding domain) of Nrf2. (A) A schematic drawing of Nrf2 deletion mutants containing a bZIP domain used for interaction studies. (B) *In vitro* synthesized (IVT) 35 S-labeled FLAG-Crif1 and 35 S-labeled Nrf2 containing bZIP domains interact. 35 S-labeled proteins were mixed, immunoprecipitated with an anti-FLAG antibody, subjected to SDS-PAGE, and exposed to X-ray film. These experiments were repeated three times and yielded similar results; a representative result is shown. Control antibody (mouse IgG) was used as a control for IP.

Figure S3. Crif1 regulates Nrf2 protein half-life. (A) Over-expressed Crif1 reduces Nrf2 half-life. HEK293 cells co-transfected with FLAG-Crif1, FLAG-Nrf2 or pCDNA3 (empty vector) for 24 h were incubated with CHX (10 μ g/ml) for the times indicated before WB analysis. Anti-FLAG antibody was used to detect both exogenously expressed Nrf2 (130 kDa) and Crif1 (30 kDa). The FLAG-Nrf2 band densities were quantified and then normalized to the total FLAG-Nrf2 protein level found at the zero time point (before adding CHX) in the pCDNA3-transfected group and demonstrated as a linear graph (see below WB image). (B) Down-regulated Crif1 effects on the half-life of endogenous Nrf2 protein in the presence of SFN. Total lysates of MCF-7 cells pre-treated with siRNA (control or Crif1-3 and -4) for 72 h, then incubated with SFN (5 μ M for 4h) and then treated with CHX (10 μ g/ml) for the times indicated were analyzed on WBs with anti-Nrf2 and anti-Crif1 mouse monoclonal antibodies. The intensities of the Nrf2-containing bands in the presence of control-siRNA were normalized to the total endogenous Nrf2 protein in the presence of Crif1-siRNA (without CHX treatment) and demonstrated as a linear graph (below WB image).

Figure S4. Interactions between Crif1 and quadruple point mutants (lysine to arginine) of Nrf2. Wild-type or a quadruple point mutant protein fragment (from 4 lysine [K] residues to 4 arginine [R] residues) of (A) N-terminal or (B) C-terminal Nrf2 deletion mutant constructs (see Figure 4B for the diagram) co-transfected with either FLAG-Crif1 or FLAG-Keap1 in HEK293 cells were immunoprecipitated with anti-His (Nrf2) antibody and then subjected to WB analysis as indicated. One-tenth of the total cell lysates was also used for WB analysis to determine the amount of protein expressed.

Figure S5. Over-expression of Crif1 reduced SFN (or *t*-BHQ)-stimulated Nrf2 protein level. (A) Over-expression of Crif1 reduced endogenous Nrf2 protein levels after SFN treatment. Cells (MCF-7) infected with Ad-GFP or Ad-GFP-Crif1 were treated with SFN (5 μ M) and harvested at the indicated times. (B) Over-expression of Crif1 reduced Nrf2 induction following *t*-BHQ (100 μ M). Cells (MCF-7) infected overnight with Ad-GFP or Ad-GFP-Crif1 were treated with *t*-BHQ and harvested at 0, 8, 16 and 24 h. Anti-Nrf2 and anti-GFP antibodies were used to monitor the expression of Nrf2 and Crif1.

Figure S6. Crif1 reduces Nrf2 accumulation at ARE-containing enhancer regions of Nrf2 target gene (HO-1). MCF-7 cells were transfected for 24 h with expression vectors for FLAG-Crif1, His-V5-Nrf2 or both vectors and then fixed in formaldehyde and prepared for ChIP assays using mouse IgG (control), anti-His and anti-FLAG antibodies as described in Experimental Procedures. (A) A diagram of

ARE-containing and non-ARE-containing DNA sequence regions of the HO-1 enhancer region. (B-C) ARE-containing HO-1 enhancer genomic DNA sequence (B) and non-ARE-containing genomic DNA sequence regions (C) were PCR-amplified by using appropriate HO-1 primers. Mouse IgG was used as the negative, non-specific antibody control. DNA sequences, locations and primers are described in Experimental Procedures. (D) Quantitative real-time PCR confirms ChIP assay results of the ARE-containing HO-1 enhancer region (B).

Figure S1

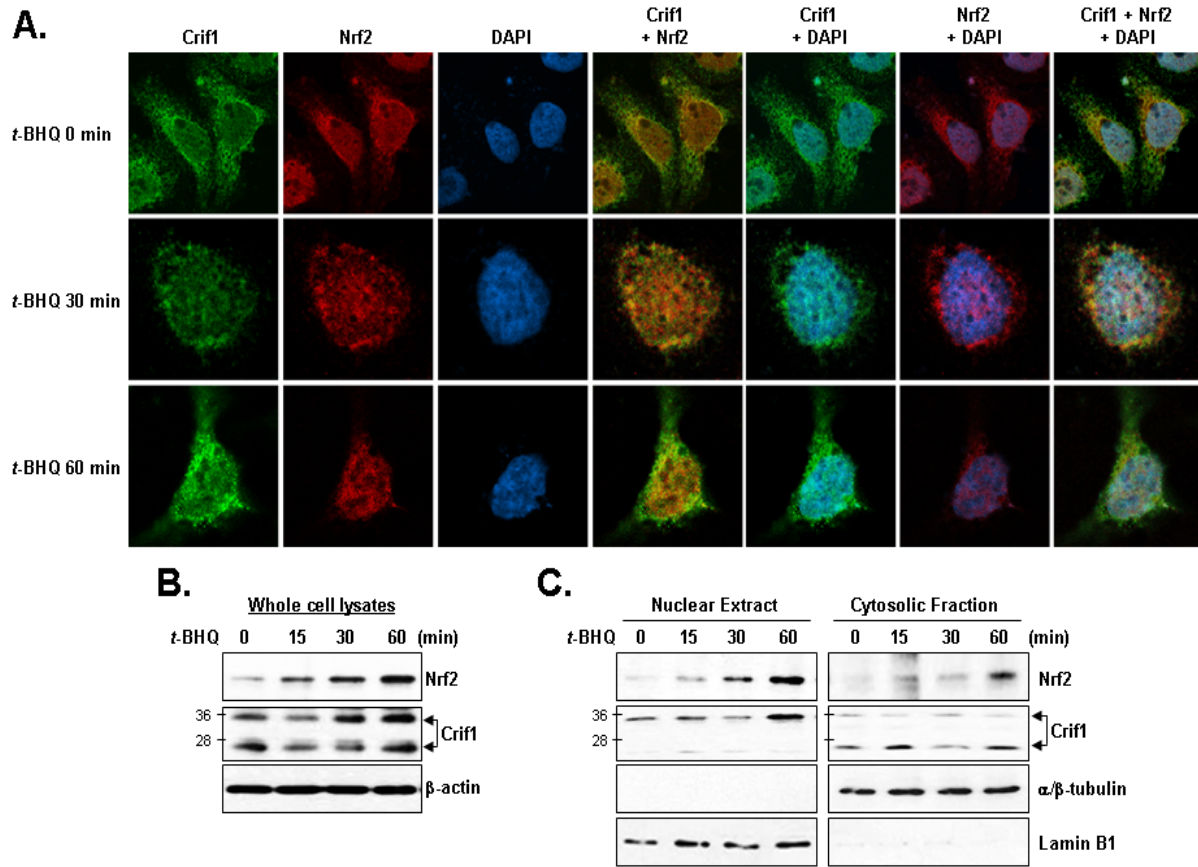
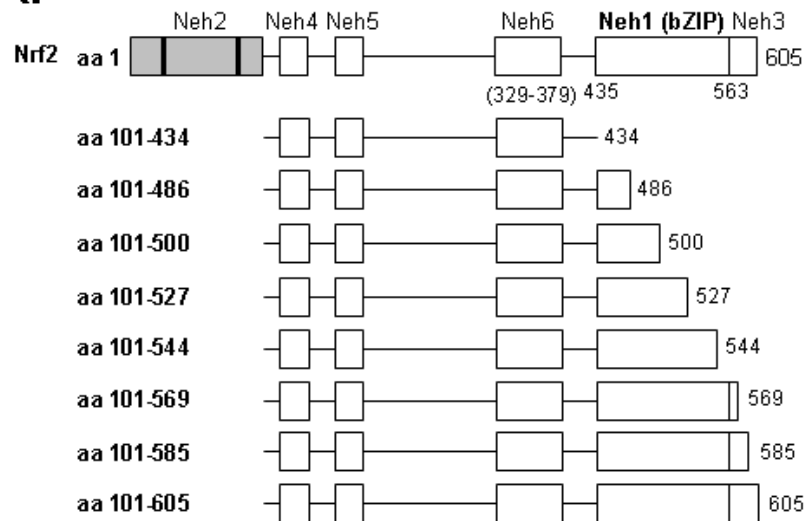


Figure S2

A.



B.

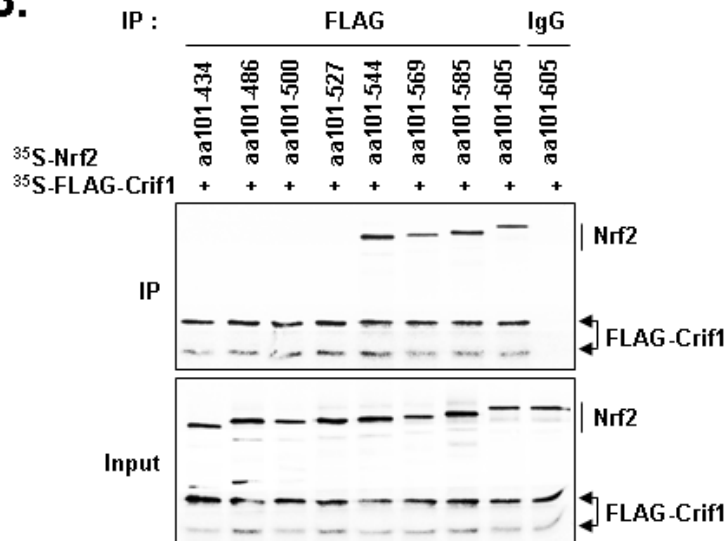


Figure S3

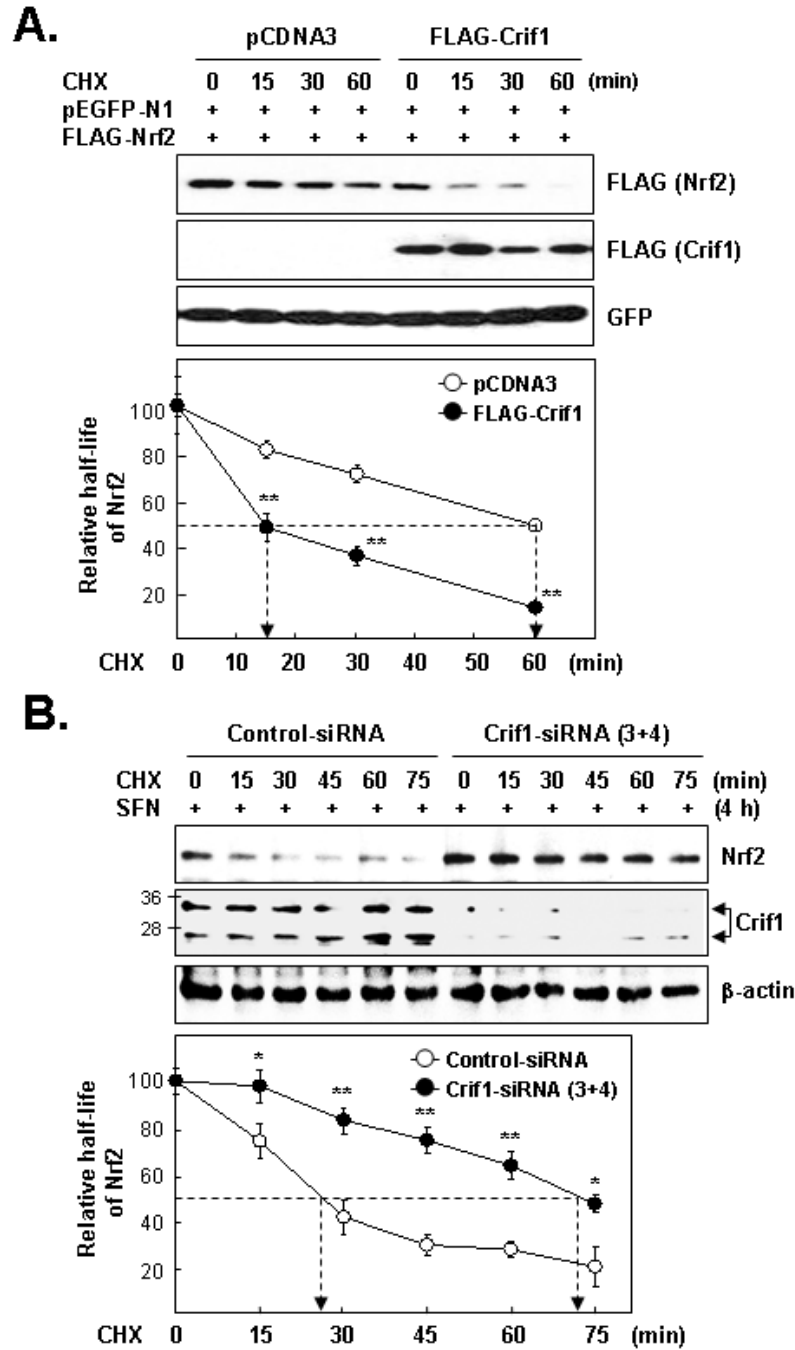


Figure S4

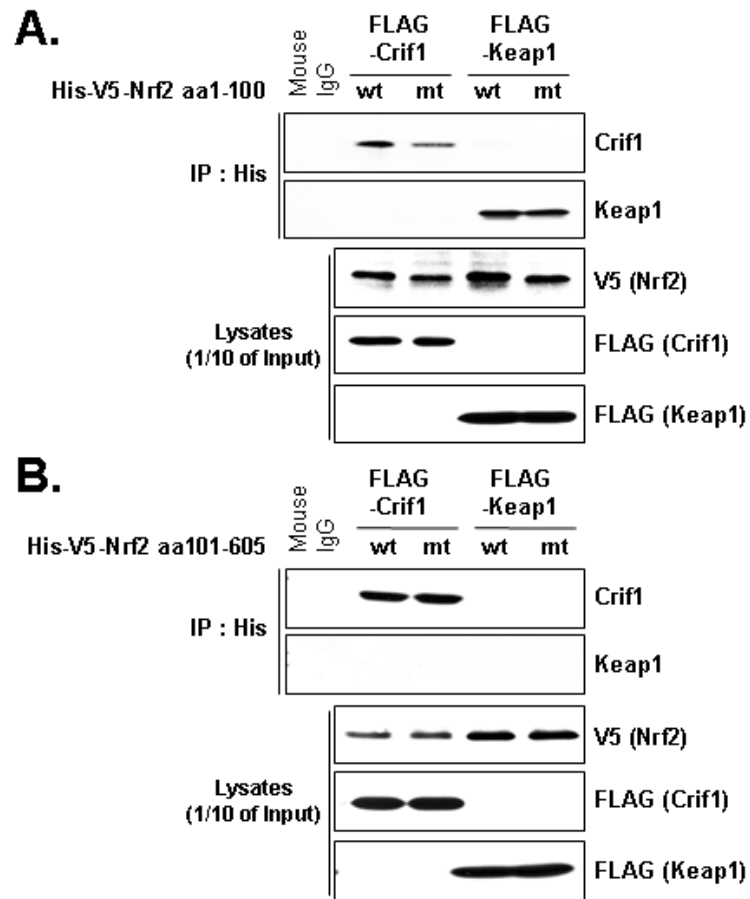


Figure S5

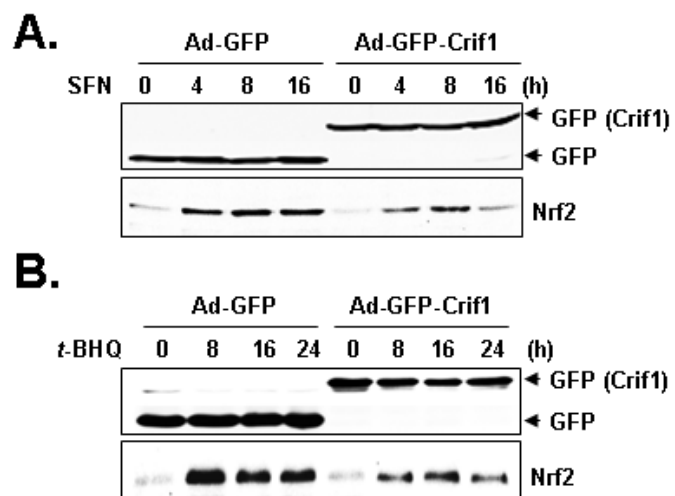


Figure S6

