Supplementary information

Multiple regulatory mechanisms of the biological function of NRF3 (NFE2L3) control cancer cell proliferation

A M Masudul Azad Chowdhury¹, Hiroki Katoh¹, Atsushi Hatanaka¹, Hiroko Iwanari², Nanami Nakamura¹, Takao Hamakubo², Tohru Natsume³, Tsuyoshi Waku¹, Akira Kobayashi¹*

¹Laboratory for Genetic Code, Graduate School of Life and Medical Sciences, Doshisha University, Kyotanabe, Kyoto, Japan, ²Department of Quantitative Biology and Medicine, Research Center for Advanced Science and Technology, The University of Tokyo, Tokyo, Japan, ³National Institutes of Advanced Industrial Science and Technology, Biological Information Research Center (JBIRC), Tokyo, Japan.

Address correspondence to: Akira Kobayashi Laboratory for Genetic Code, Graduate School of Life and Medical Sciences, Doshisha University, 1-3 Tatara Miyakodani, Kyotanabe 610-0394, Japan Phone: +81-774-65-6273, Fax +81-774-65-6274 E-mail: akobayas@mail.doshisha.ac.jp



Figure S1. HRD1 and β -TRCP also regulate the NRF3 degradation in HCT116 cells. (A and B) *VCP* and *HRD1* siRNA stabilized the endogenous NRF3 in HCT116 cells (A). The knockdown efficiency of *HRD1* and *VCP* siRNA was determined using qRT-PCR analysis (B). The values were normalized to β -actin data. These experiments were performed as described in the legend of Figures 1. (C and D) β -TRCP promotes the degradation of the endogenous NRF3 in HCT116 cells (C). The knockdown efficiencies of β -TRCP1 and β -TRCP2 siRNA were determined using qRT-PCR analysis (D). The values were normalized to β -actin data. These experiments were performed as described in the legend of the statistical analysis. ** *P* < 0.01 and *** *P* < 0.001 compared to the Control data.



Figure S2. Additional NRF3 siRNA also reduces the UHMK1 expression in DLD-1 cells. (A and B) The effects of additional *NRF3* siRNA (NRF3 (A)) on the mRNA and protein expression levels were determined by qRT-PCR and immunoblot analyses, respectively. The detailed experimental procedure was described in the legend of Figures 5. The error bars (A) represent data from three independent experiments (mean \pm standard deviation). The two-tailed Student's t-test was used for the statistical analysis. **P* < 0.05 and *** *P* < 0.001 compared to the Control data.



Figure S3. NRF3 also regulates the expression of *UHMK1* in HCT116 cell. (A and B) Reduction of the NRF3-mediated *UHMK1* expression was observed by introducing two distinct *NRF3* siRNAs into HCT116 cells. The mRNA and protein expression levels of UHMK1 were determined by qRT-PCR and immunoblot analyses, respectively. The detailed experimental procedure was described in the legend of Figures 5. The error bars (A) represent data from three independent experiments (mean \pm standard deviation). The two-tailed Student's t-test was used for the statistical analysis. * *P* < 0.05, ** *P* < 0.01 and *** *P* < 0.001 compared to the Control data.



Figure S4. UHMK1 promotes the proliferation of colon cancer cells. (A) *UHMK1* knockdown significantly reduced the proliferation of DLD-1 cells. The cells were transfected with Control, *UHMK1 or UHMK1(A)* siRNA. At 36 and 72 hr after transfection, the cell numbers were counted using a hemocytometer. The initial cell numbers at the time of transfection were 1 x 10⁵. (B) *UHMK1* siRNAs significantly reduces mRNA and protein levels of UHMK1 in DLD-1 cells. At 48 hr after transfection with Control, *UHMK1* or *UHMK1(A)* siRNA, the mRNA expression levels of *UHMK1* was determined by qRT-PCR analysis. The values were normalized to 18S rRNA data (top). Immunoblotting of the whole-cell extracts with the anti-UHMK1 antibodies was performed (bottom). α -Tubulin was used as an internal control. The error bars (A, B) represent data from two independent experiments in duplicate (n=4, mean ± standard deviation). The two-tailed Student's t-test was used for the statistical analysis. *** *P* < 0.001 (A, B) compared to the Control data.



Figure S5. NRF1 and NRF2 also regulate the *UHMK1* gene expression. *NRF1 or NRF2* knockdown significantly reduce mRNA and protein levels of UHMK1 in DLD-1 cells. At 48 hr after transfection with Control, *NRF1* or *NRF2* siRNA, the mRNA expression levels of *UHMK1*, *NRF1 and NRF2* were determined by qRT-PCR analysis. The values were normalized to 18S rRNA data (top). Immunoblotting of the whole-cell extracts with the anti-UHMK1 antibodies was performed (bottom). α -Tubulin was used as an internal control. The error bars represent data from two independent experiments in duplicate (n=4, mean ± standard deviation). The two-tailed Student's t-test was used for the statistical analysis. *** *P* < 0.001 compared to the Control data.

А









Figure S6 (A) Full-length western blots for figure 1 A, C, D and E. The line box regions are the cropped portion of the blot shown in the main figure.

В



Figure S6 (B) Full-length western blots for figure 2A, C and D. The line box regions are the cropped portion of the blot shown in the main figure.

70

50

С



Figure S6 (C) Full-length western blots for figure 3A, C and E. The line box regions are the cropped portion of the blot shown in the main figure.

D



Figure S6 (D) Full-length western blots for figure 4 A and B. The line box regions are the cropped portion of the blot shown in the main figure.



Figure S6 (E) Full-length western blots for figure 4 D and E. The line box regions are the cropped portion of the blot shown in the main figure.

Е



Figure S6 (F) Full-length western blots for figure 5C. The line box regions are the cropped portion of the blot shown in the main figure.

F



Figure S6 (G) Full-length western blots for figure S1 A and C. The line box regions are the cropped portion of the blot shown in the main figure.



Figure S6 (H) Full-length western blots for figure S2 B. The line box regions are the cropped portion of the blot shown in the main figure.

Н



I

Figure S6 (I) Full-length western blots for figure S3 B. The line box regions are the cropped portion of the blot shown in the main figure.



Figure S6 (J) Full-length western blots for figure S4 B. The line box regions are the cropped portion of the blot shown in the main figure.





Figure S6 (K) Full-length western blots for figure S5. The line box regions are the cropped portion of the blot shown in the main figure.



Supplementary	Table	1.	Identification	of	NRF3-associated	proteins	by	mass
spectrometry.								

Gene Symbol	Score	Protein Name/Description
SKP1	3	S-phase kinase-associated protein 1
VCP	4	transitional endoplasmic reticulum ATPase
USP15	4	ubiquitin carboxyl-terminal hydrolase 15
HCFC1	4	host cell factor 1
PSMA1	4	Proteasome subunit alpha type-1
PSMA2	4	Proteasome subunit alpha type-2
PSMA4	4	Proteasome subunit alpha type-4
PSMA6	4	Proteasome subunit alpha type-6
PSMA7	3	Proteasome subunit alpha type-7
PSMC1	4	26S Proteasome regulatory subunit 4
PSMC2	4	26S Proteasome regulatory subunit 7
PSMC3	4	26S Proteasome regulatory subunit 6A
PSMC6	4	26S Proteasome regulatory subunit 10B
PSMD11	4	26S Proteasome non-ATPase regulatory subunit 11
PSMD12	4	26S Proteasome non-ATPase regulatory subunit 12
PSMD2	3	26S Proteasome non-ATPase regulatory subunit 2
PSMD6	4	26S Proteasome non-ATPase regulatory subunit 6
PSMD8	4	26S Proteasome non-ATPase regulatory subunit 8