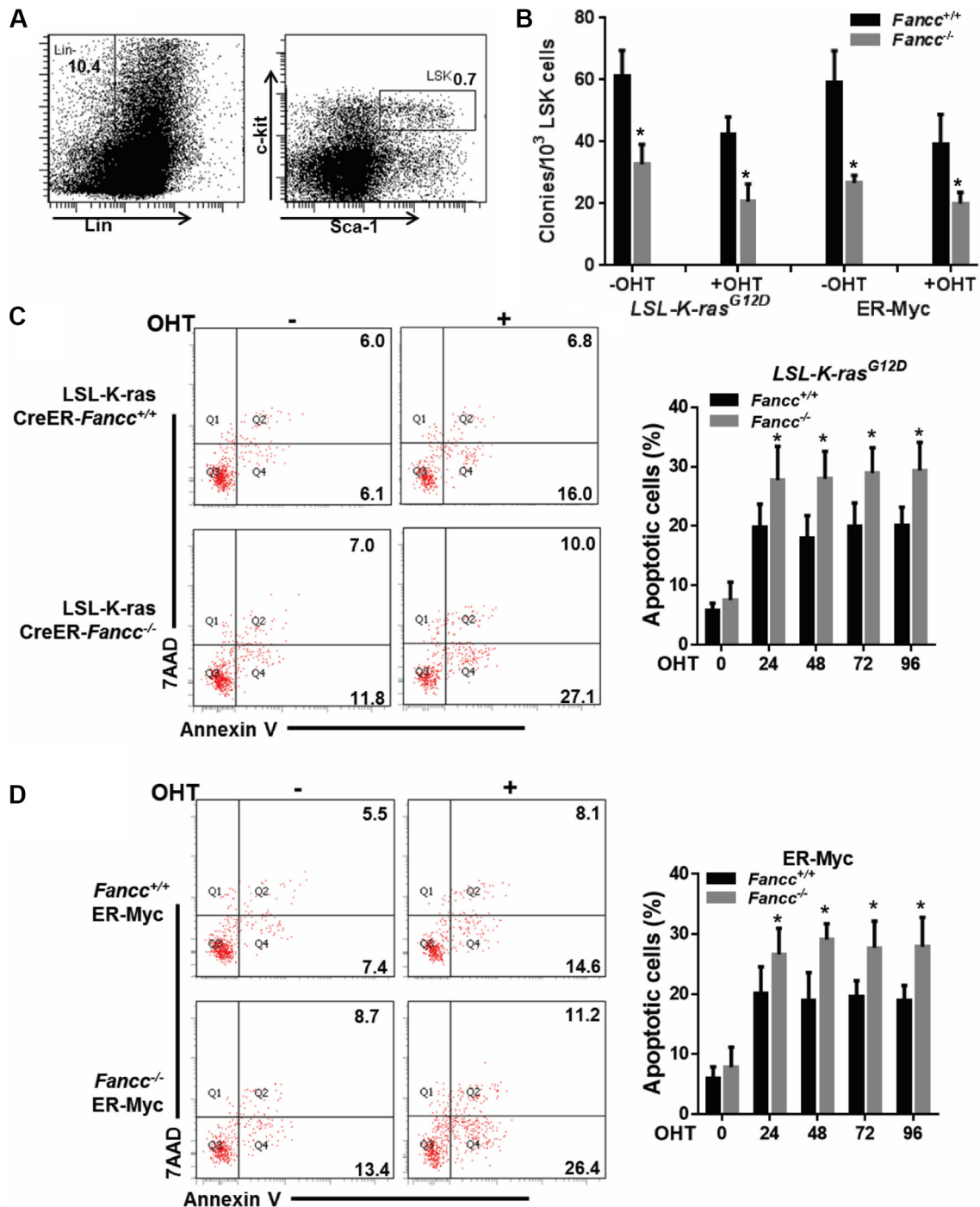
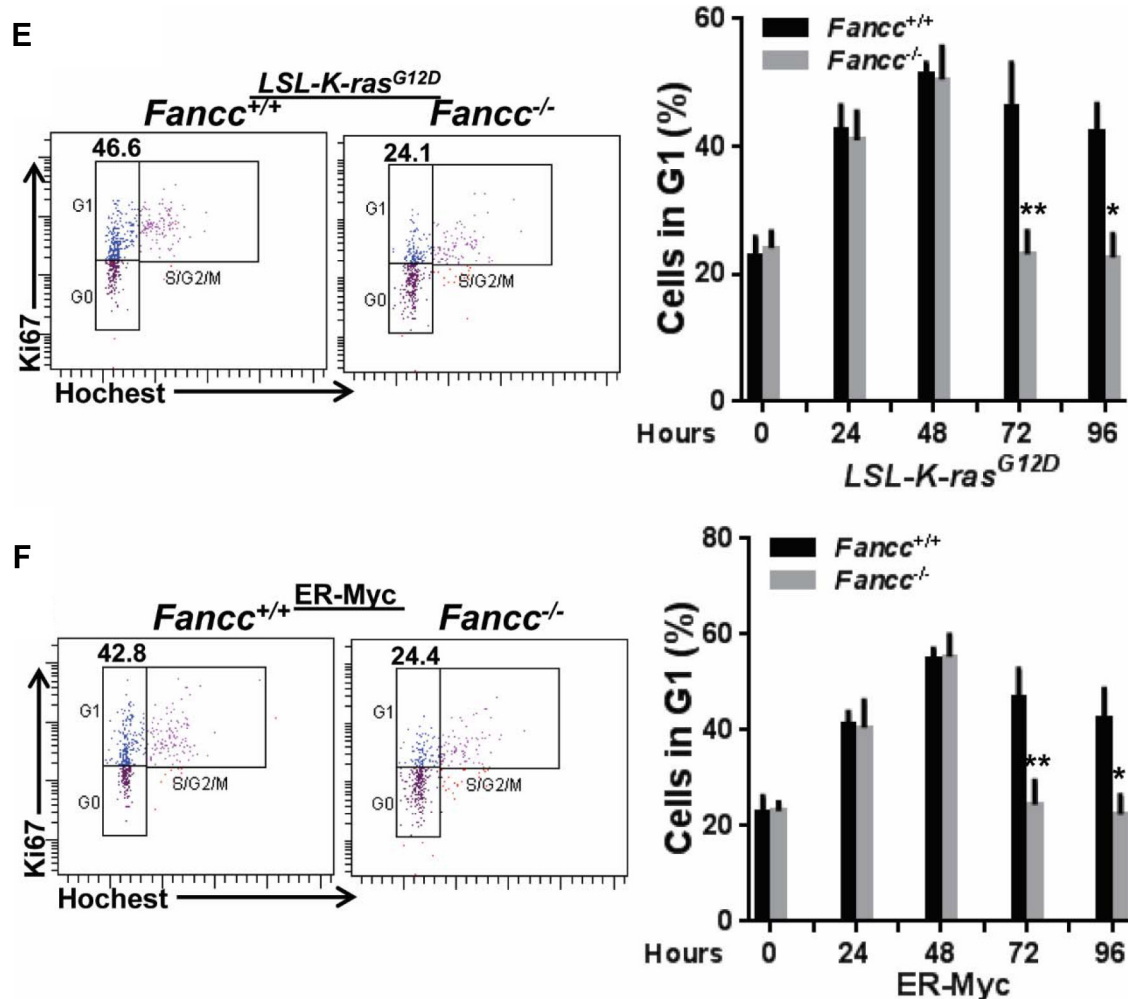


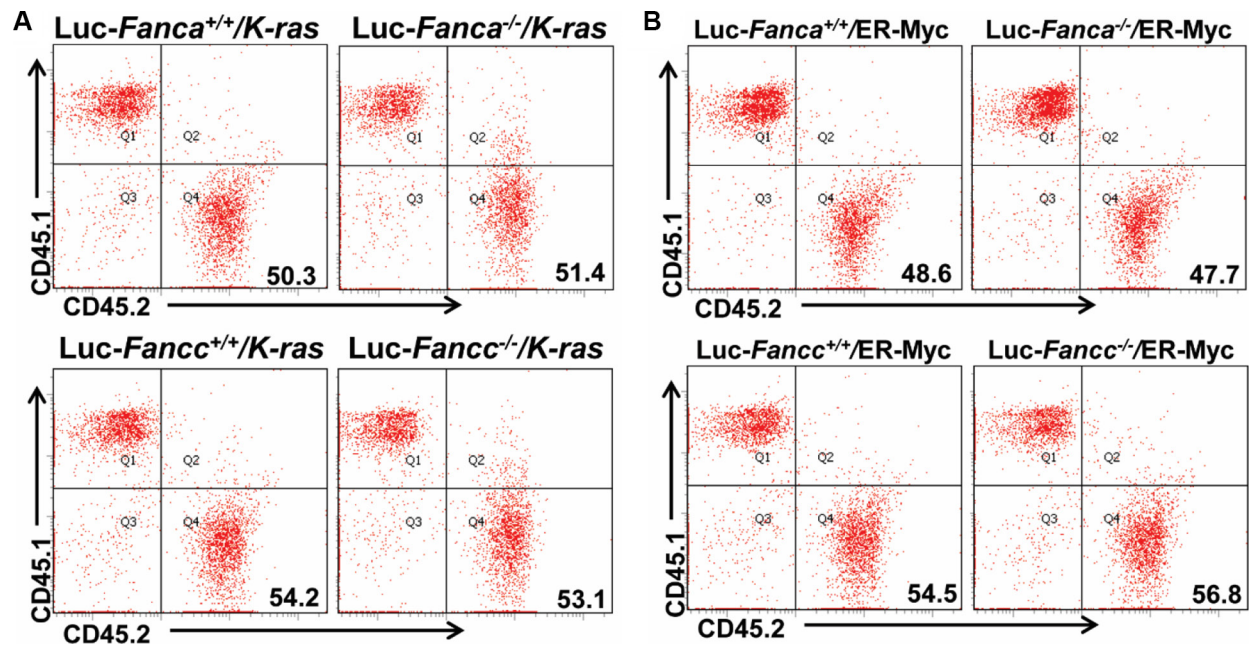
The Fanconi anemia pathway controls oncogenic response in hematopoietic stem and progenitor cells by regulating PRMT5-mediated p53 arginine methylation

Supplementary Materials

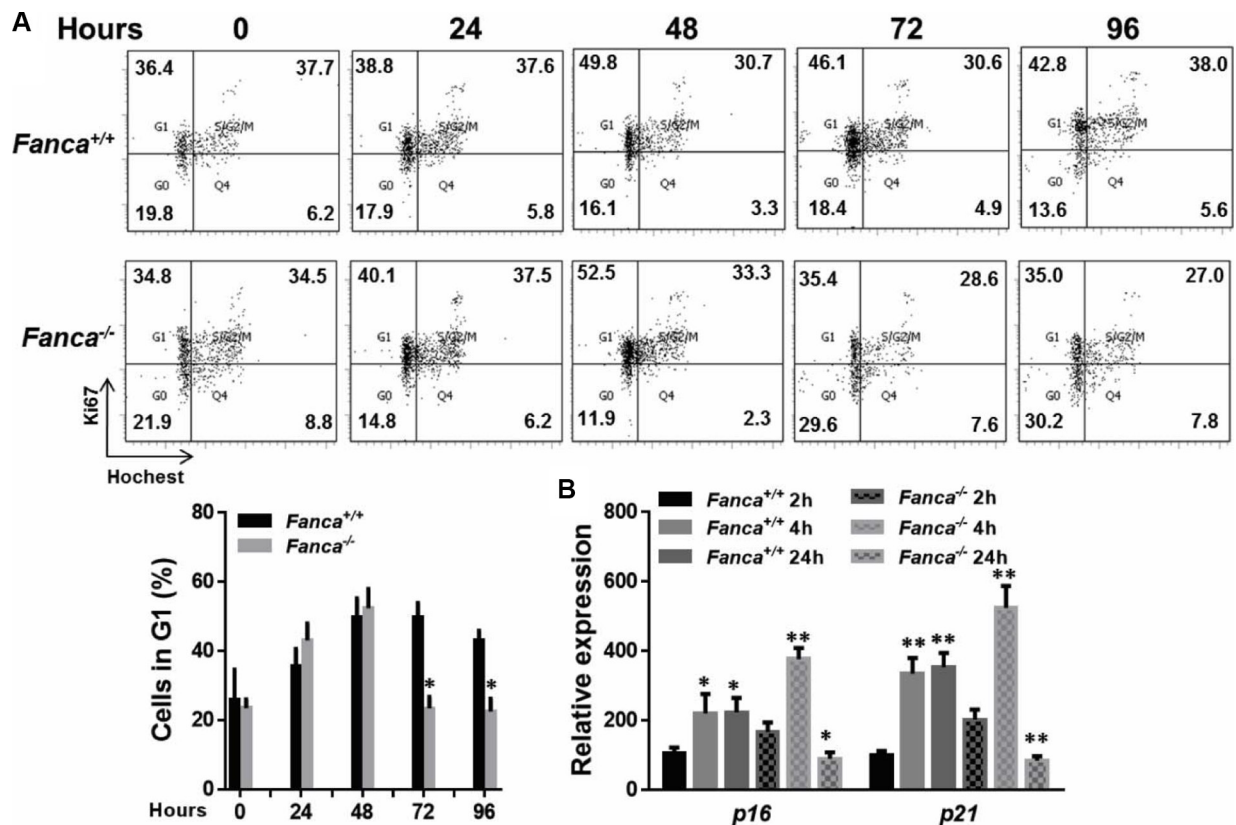




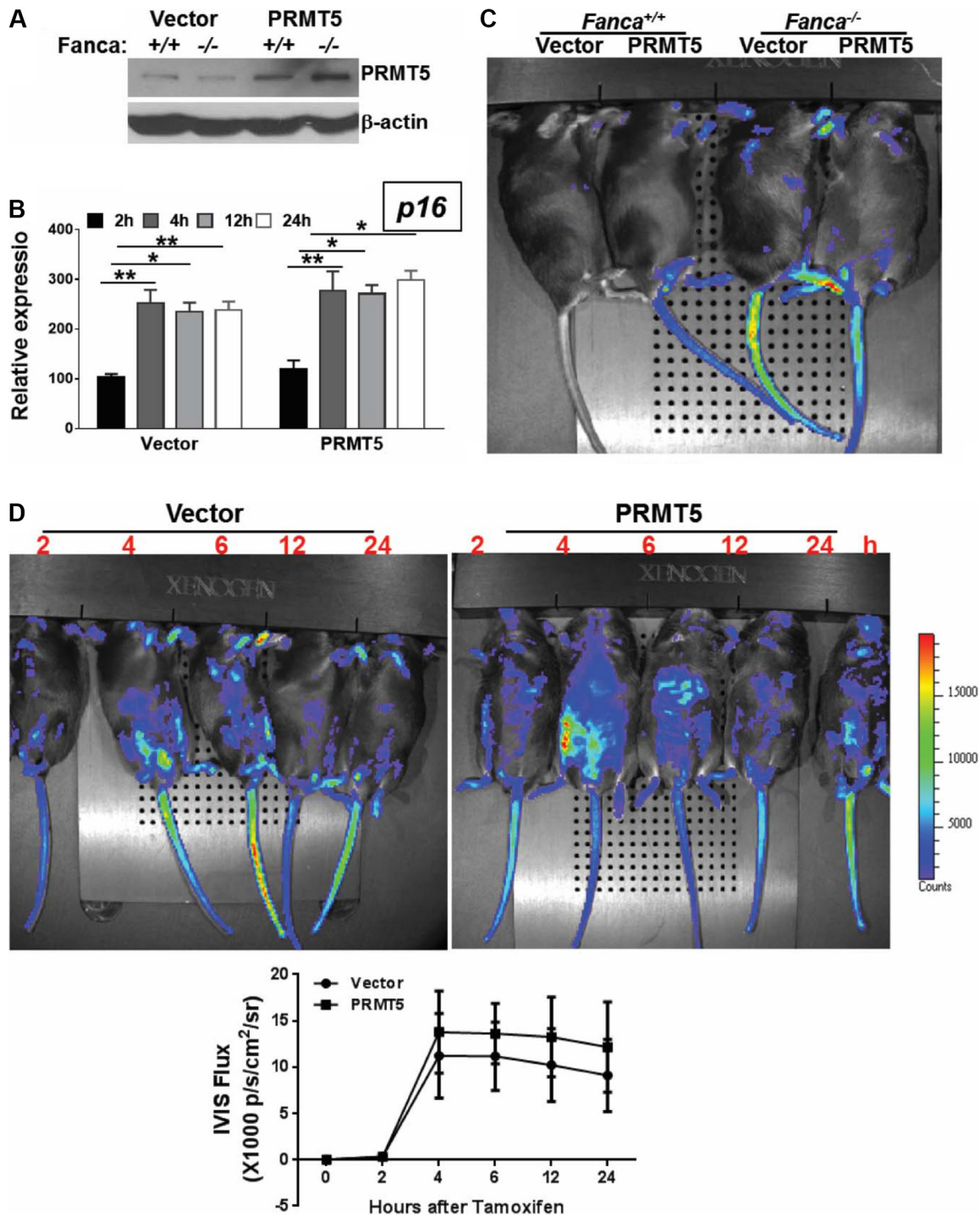
Supplementary Figure S1: *Fancc* deficiency induces a short-lived response to oncogenic stress *in vitro*. (A) Gating strategy for apoptosis and cell-cycle analysis. Low density bone marrow cells (LDBMCs) isolated from experimental mice were subjected to Flow cytometric analysis. (B) Oncogenic stress compromises colony formation capacity of FA HSPCs. LSK cells (Lin⁻Sca1⁺c-kit⁺ cells) isolated from LSL-*Fancc*^{+/+}/K-ras/CreER and LSL-*Fancc*^{-/-}/K-ras/CreER mice, or retroviral vector MSCV-IRES-Myc^{ER} transduced LSK cells from *Fancc*^{+/+} or *Fancc*^{-/-} mice were *in vitro* culture in the presence of 4-OHT for 48 hours followed by plating in cytokine-supplemented methycellulose medium. Colonies were enumerated on day 7 after plating. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 9$ per group). (C) K-ras activation induces apoptosis in FA HSCs. LSK cells (Lin⁻Sca1⁺c-kit⁺ cells) isolated from LSL-*Fancc*^{+/+}/K-ras/CreER and LSL-*Fancc*^{-/-}/K-ras/CreER mice were subjected to Flow cytometric analysis for apoptosis by Annexin V/7AAD staining at different time points. Representative images (left) and quantification (right) were shown. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 6$ per group). (D) Myc activation induces apoptosis in FA HSCs. Retroviral vector MSCV-IRES-Myc^{ER} transduced LSK cells from *Fancc*^{+/+} or *Fancc*^{-/-} mice were subjected to Flow cytometric analysis for apoptosis by Annexin V/7AAD staining. Representative images (left) and quantification (right) were shown. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 9$ per group). (E) Activation of K-ras leads to short-lived G₁ arrest in FA cells. Cells described in (C) were subjected to cell cycle profiling by Hochest33324/Ki67 staining. Representative images (left) and quantification (right) were shown. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 6$ per group). (F) Activation of Myc leads to short-lived G₁ arrest in FA cells. Cells described in (D) were subjected to cell cycle profiling by Hochest33324/Ki67 staining. Representative images (left) and quantification (right) were shown. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 9$ per group).



Supplementary Figure S2: Establishment of Luc-Fanc/Kras or Luc-Fanc/MyER chimera. (A) 1,000 LSK cells from *Luc-LSL-K-ras/CreER-Fanca*^{+/+} or 2,000 LSK cell from *Luc-LSL-K-ras/CreER-Fanca*^{-/-} mice along with 3×10^5 BM cells from congenic BoyJ mice were transplanted into lethally irradiated BoyJ recipients. Donor-derived hematopoiesis was determined by Flow Cytometry at 4-month post BMT (Upper). Similar experiments were conducted using *Luc-LSL-K-ras/CreER-Fancc*^{+/+} or *Luc-LSL-K-ras/CreER-Fancc*^{-/-} cells (Lower). (B) LSK cells from *Luc-Fanca*^{+/+} or *Luc-Fanca*^{-/-} mice were transduced with retroviral vector MSCV-IRES-MyER. 1,500 transduced *Luc-Fanca*^{+/+} cells or 3,000 transduced *Luc-Fanca*^{-/-} cells along with 3×10^5 BM cells from congenic BoyJ mice were transplanted into lethally irradiated BoyJ recipients. Donor-derived hematopoiesis was determined by Flow Cytometry at 4-month post BMT (Upper). Similar experiments were conducted using *Luc-Fancc*^{+/+} or *Luc-Fancc*^{-/-} cells (Lower).



Supplementary Figure S3: Altered oncogenic response in *Fanca*^{-/-} MEF cells. (A) Activation of K-ras leads to short-lived G₁ arrest in *Fanca*^{-/-} MEF cells. Primary mouse embryonic fibroblasts (MEFs) isolated from Luc-LSL-K-ras/CreER-*Fanca*^{+/+} and Luc-LSL-K-ras/CreER-*Fanca*^{-/-} mice, were cultured in the presence of 4-OHT for 2 hours then released in fresh medium for the indicated time intervals, followed by cell cycle profiling by Hoechst33324/Ki67 staining. Representative flow plots (left) and quantification (right) are shown. Results are means ± standard deviation (SD) of 3 independent experiments (*n* = 6 per group). (B) Expression of cell cycle regulators. RNA extracted from MEFs described in (A) at different time points were subjected to qPCR analysis using primers for *p16* and *p21*. Levels of the expression in each sample were normalized to the level of *GAPDH* mRNA, and the expression levels of the *Fanca*^{+/+} samples at 2 h were normalized as 100.



Supplementary Figure S4: Ectopic expression of PRMT5 augments stress response. (A) Ectopic expression of PRMT5 in *Fanca*^{+/+} and *Fanca*^{-/-} cells. BM Lin⁺ cells from Luc-LSL-*Fanca*^{+/+}/K-ras/CreER or Luc-LSL-*Fanca*^{-/-}/K-ras/CreER mice were transduced with lentiviral vector expressing PRMT5. Sorted Venus⁺ cells were then subjected to immunoblotting using antibodies against PRMT5 or β -actin. (B) Forced expression of PRMT5 does not affect *p16* expression in WT cells. LSK cells from WT mice were transduced with lentiviral vector expressing PRMT5. Sorted Venus⁺ cells were cultured in the presence of 4-OHT for 2, 4, 12 and 24 hours followed by RNA extraction and qPCR analysis using primers for *p16*. Samples were normalized to the level of *GAPDH* mRNA, and the expression level of the sample at 2h was normalized as 100. (C) Minimum bioluminescence of Luc mice without Tamoxifen injection. LSK cells from Luc-LSL-*Fanca*^{+/+}/K-ras/CreER mice were transduced with lentiviral vector expressing PRMT5. Sorted Venus⁺ cells were used for BMT to lethally irradiated BoyJ recipients. 4-month post BMT, live images of the recipient mice were taken right before tamoxifen injection. Luminescence scale is in p/s/cm²/sr. (D) Ectopic expression of PRMT5 augmented K-ras-induced luciferase expression in WT donor cells. Single dose of 4-OHT was administered to the recipient mice described in (C) and live images were taken at indicated time after 4-OHT induction. The bioluminescent image signals were quantified using LiveImage Pro. 2.0 software. Results are means \pm standard deviation (SD) of 3 independent experiments ($n = 6$ per group).

Supplementary Table S1: Primers used for qPCR

Gene	Forward	Reverse
p15	AGATCCCAACGCCCTGAACCG	TGCTCTTCAGCCAAGTCTACC
p16	CGAACTCTTTCGGTCGTACCC	TTGAGCAGAAGAGCTGCTACG
p19	CGGAATCCTGGACCAGGTG	ACCAGCGTGTCCAGGAAGC
p21	GGCCCGGAACATCTCAGG	AAATCTGTCAGGCTGGTCTGC