

Supplementary Figure Legends

Supplementary Figure 1. FANCI depleted U2OS cells exhibit sensitivity to MMC (A) that can be rescued with expression of shRNA resistant wtFANCI (B). Inside panel A; FANCI protein levels were assessed after depletion with two shRNA constructs using FANCI specific antibodies. Inside panel B; Ectopic expression of HA-6xHis-FANCI was measured by HA specific antibody. (C) Relative protein levels of endogenous FANCI and HA-6xHis-FANCI. Western blotting was carried out using FANCI specific antibody. (D) FANCI depleted cells accumulate in G2/M phase of the cell cycle in response to MMC induced damage.

Supplementary Figure 2. FACS analysis of control and FANCI depleted U2OS SCR35S cells after transfection with control plasmid (spontaneous) or I-SceI plasmid. Frequency of I-SceI induced GFP⁺ cells (A) and absolute frequency of I-SceI induced GFP⁺ RFP⁺ cells (B) from control and FANCI depleted U2OS SCR35S cells. (C) Ratio of I-SceI-induced RFP⁺GFP⁺/Total GFP⁺ frequencies (LTGC/overall GC, expressed as a percentage) from the experiment whose results are shown in panels A and B.

Supplementary Figure 3. Protein sequence alignment of FANCI helicase from human (*Homo sapiens*), mouse (*Mus musculus*) and Chinese hamster (*Cricetulus griseus*) using ClustalW2. Red boxes indicate conserved helicase signature motifs. NLS motif is indicated by green box. The four conserved cysteine residues that form Fe-S domain are shown in pink boxes. The C-terminal BRCA1 interacting domain is indicated in blue dotted box. The S990 residues responsible for FANCI interaction with BRCA1 upon phosphorylation is shown in orange box.

Supplementary Figure 4. Hamster FANCI controls SCR and suppresses LTGC. (A)

FANCI deficiency cause MMC induced sensitivity in hamster cells. Western blot of FANCI

depletion is shown inside the graph. (B) I-SceI induced GFP⁺ frequencies in control and FANCI depleted V79B SCR55 cells. (C) I-SceI induced BsdR⁺ frequencies for the same experiment shown in panel A. (D) Ratio of I-SceI-induced LTGC/overall GC (expressed as a percentage) from the experiment whose results are shown in panels B and C.

Supplementary Figure 5. (A) I-SceI induced GFP⁺ frequencies in control and FANCI depleted U2OS SCR18 cells. (B) Frequencies of I-SceI induced BsdR⁺ colonies for the same experiment shown in panel A. (C) Ratio of I-SceI-induced BsdR⁺/GFP⁺ frequencies (LTGC/overall GC, expressed as a percentage) from the experiment whose results are shown in panels A and B.

Supplementary Figure 6. Southern blot analysis of I-SceI induced BsdR⁺GFP⁺ colonies from control and FANCI depleted U2OS SCR18 cells. Genomic DNA was isolated and 5 µg of DNA was digested with EcoRI (A), SacI (B) and PstI (C) and DNA samples were resolved on 0.8% agarose gel and subjected to Southern hybridization using *GFP* cDNA specific probe. “L” and “R” indicate left and right arms of the reporter, respectively.

Supplementary Figure 7. Analysis of Fe-S cluster mutants of FANCI helicase. (A)

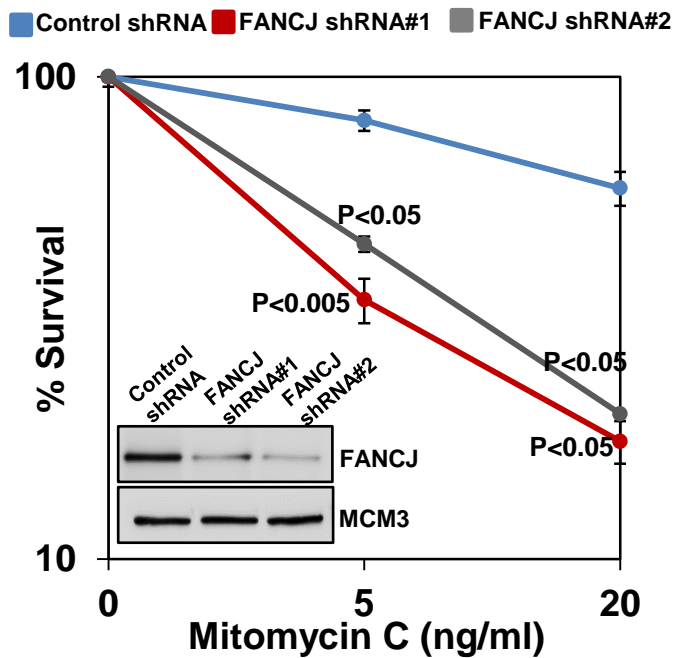
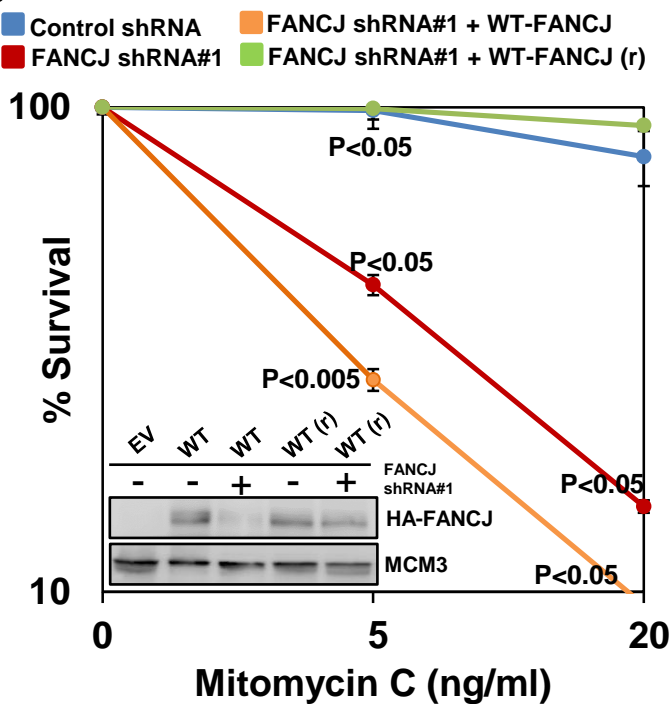
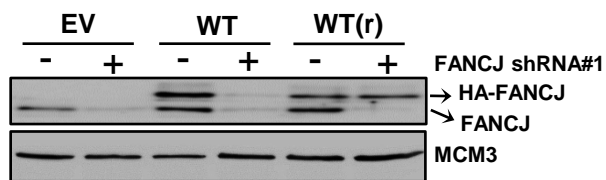
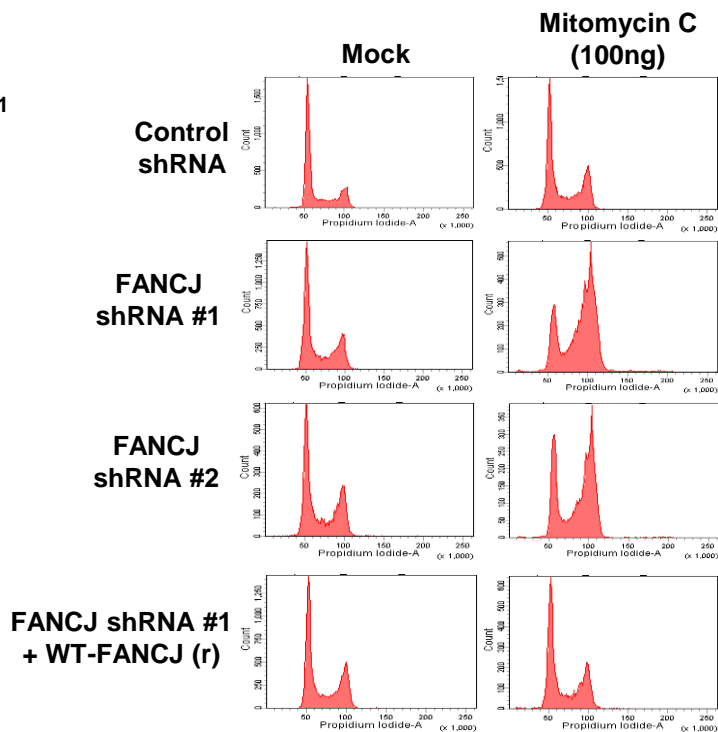
Schematic diagram of FANCI depicting the conserved helicase domains and Fe-S cluster.

Cysteine 350 and A349P missense mutation identified in FA patient are indicated. (B) Frequency of I-SceI induced GFP⁺ cells in U2OS SCR18 clone transfected with empty vector (EV) and the plasmids that express wtFANCI and its indicated mutant proteins. (C) Absolute frequencies of BsdR⁺ colonies for the experiment shown in panel B. (D) Ratio of LTGC:Overall GC obtained from the data shown in panels B and C. (E) Interaction of FANCI Fe-S cluster mutants with BRCA1.

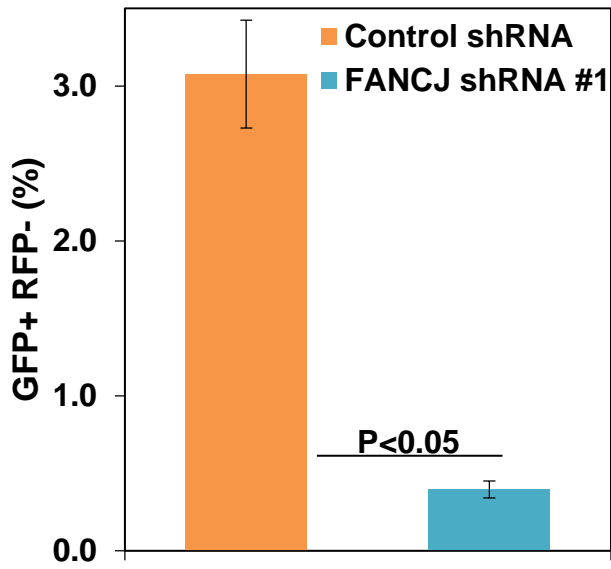
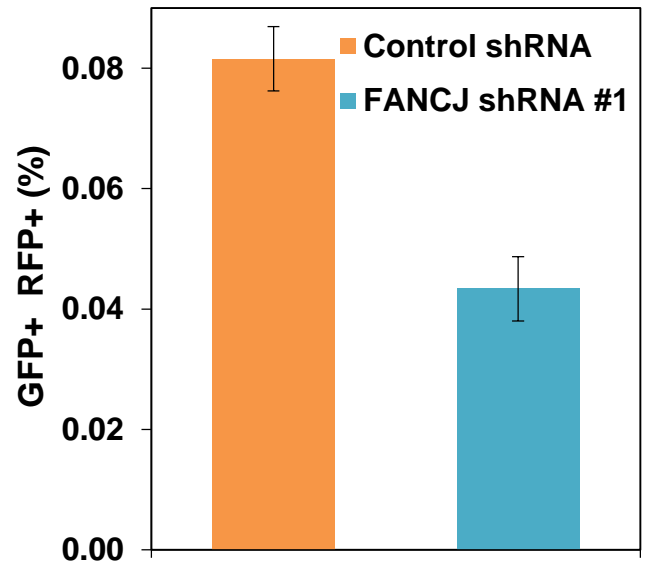
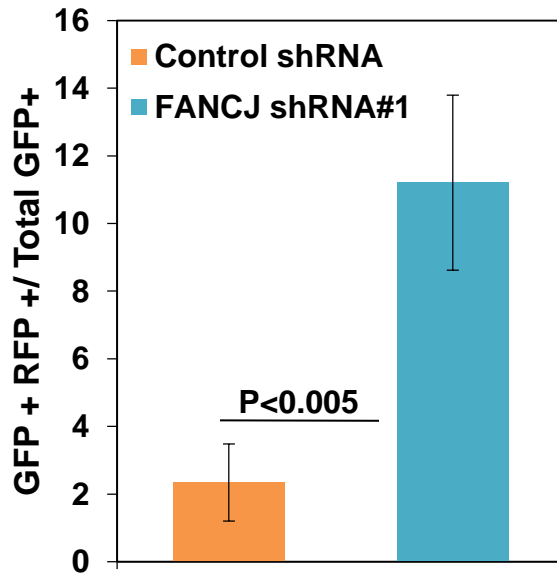
Supplementary Table 1. Oligo sequences used for generating shRNA constructs for depleting FANCI, FANCM, BRCA1 and also for generating shRNA resistant wt and FANCI mutants.

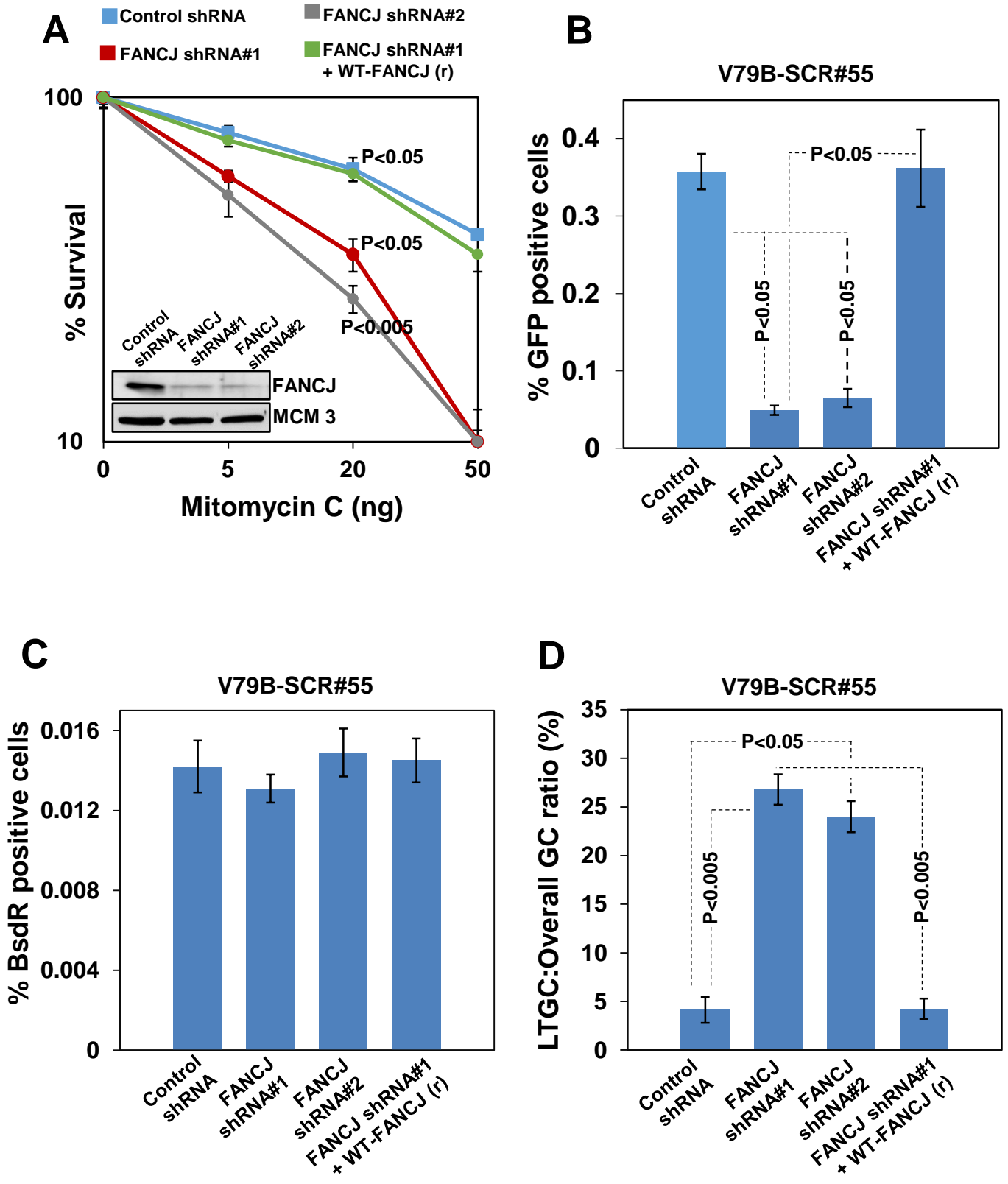
The sequences corresponding to the mRNAs of respective genes are underlined. Modified bases that were designed for constructing shRNA resistant FANCI are in bold and underlined.

shRNA		Sequence (5'→ 3')
FANCI #1	Oligo 1	GATCC <u>G</u> TACAGTACCCACCTTATTTCAAGAGA ATAAGGTGGGGTACTGTACTTTTTA
	Oligo 2	AGCTTAAAAAGTACAGTACCCACCTTATCTCTTGAA ATAAGGTGGGGTACTGTACG
FANCI #2	Oligo 1	GATCCAGCTTACCCGTCACATTCAAGAGA TGTGACGGGTAAGCTTTTTA
	Oligo 2	AGCTTAAAAA <u>AGCTTACCCGTCACAT</u> TCTCTTGAA TGTGACGGGTAAGCTG
FANCM	Oligo 1	GATCCAGACATCGCTGAATTTAAATTCAAGAGA TTTAAATTCAGCGATGTCTTTTTA
	Oligo2	AGCTTAAAAA <u>AGACATCGCTGAATTTAAAT</u> TCTCTTGAA TTTAAATTCAGCGATGTCTG
BRCA1	Oligo 1	GATCC <u>G</u> TGTGCAGCTGAGAGGCATTCAAGAGA TGCCTCTCAGCTGCACACTTTTTA
	Oligo 2	AGCTTAAAAAGTGTGCAGCTGAGAGGCATCTCTTGAA TGCCTCTCAGCTGCACACG
FANCI shRNA#1 resistant primers	Oligo 1	ACCTCTTTAAA <u>A</u> T <u>A</u> T <u>A</u> G <u>C</u> A <u>C</u> A <u>T</u> C <u>C</u> C <u>C</u> T <u>A</u> C <u>T</u> TACTGGAA
	Oligo 2	TTCCAGTAA <u>G</u> T <u>A</u> G <u>G</u> G <u>G</u> G <u>A</u> T <u>G</u> T <u>G</u> C <u>T</u> A <u>T</u> A <u>T</u> TTTAAAGAGGT

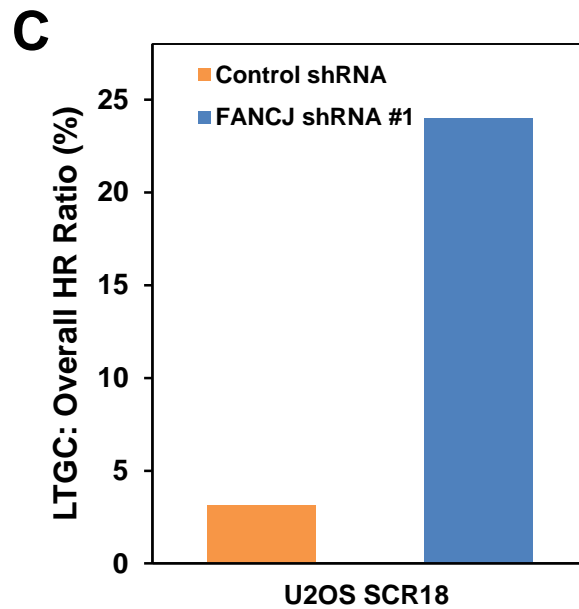
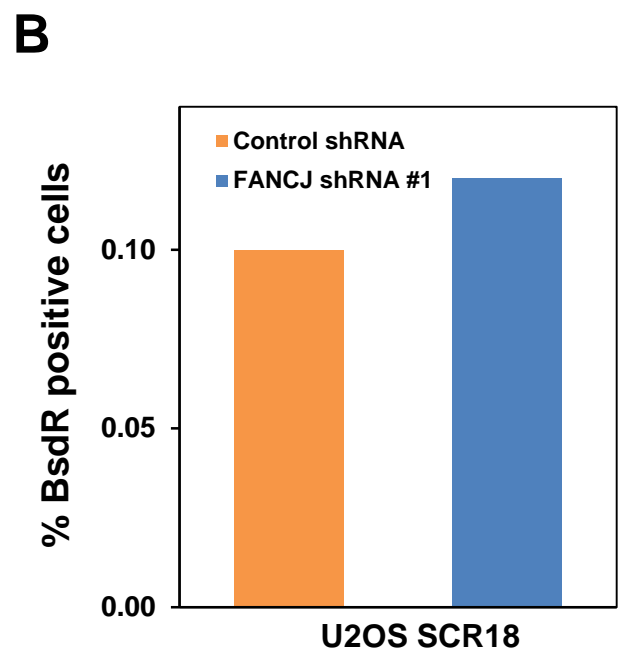
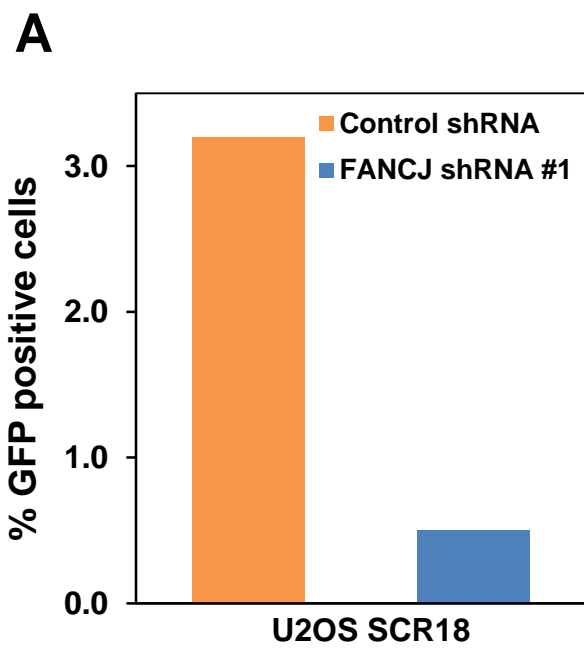
A**B****C****D**

Supplementary Figure 1

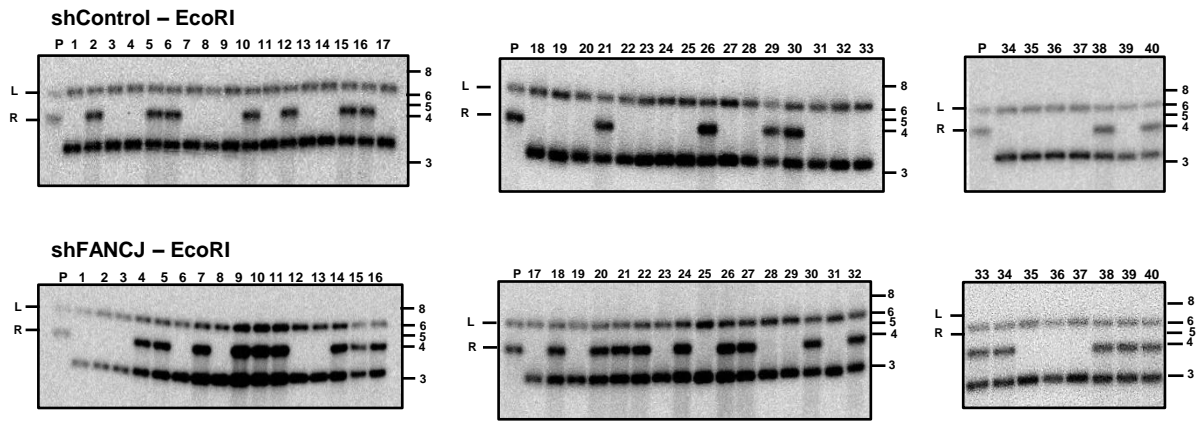
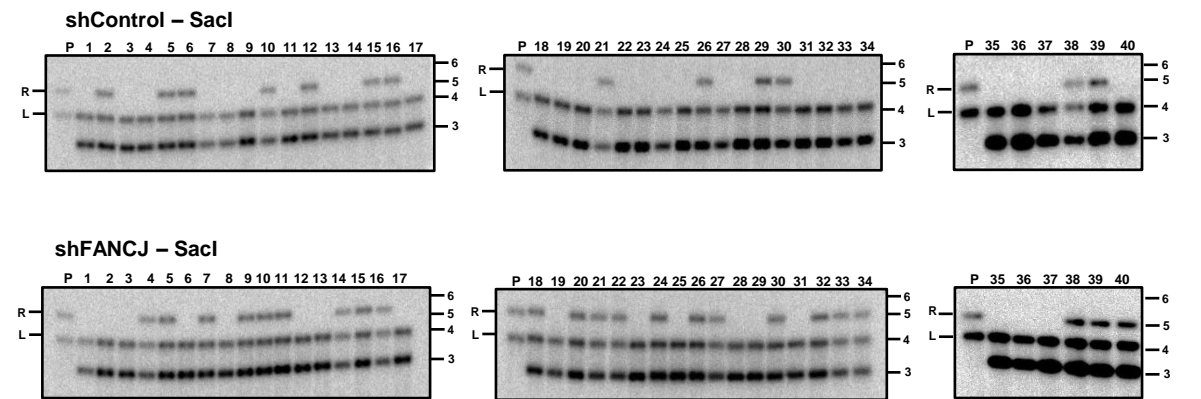
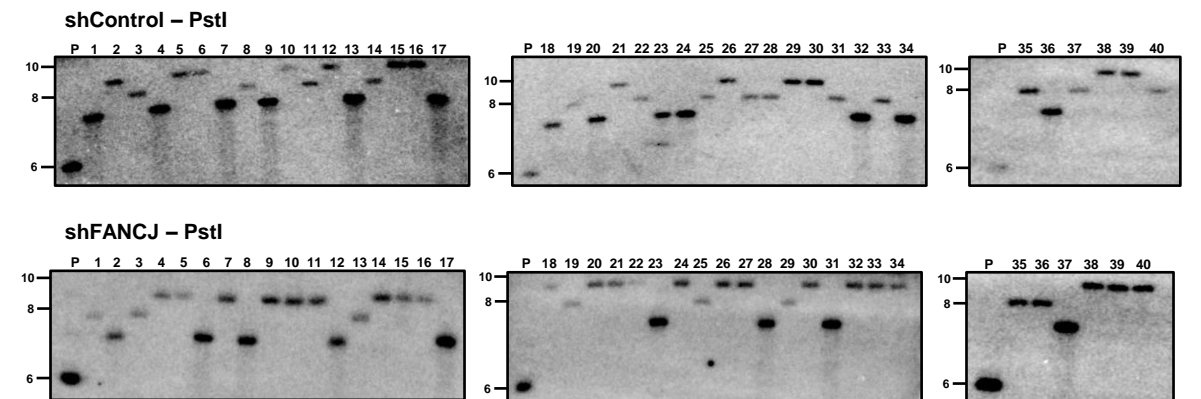
A**B****C****Supplementary Figure 2**

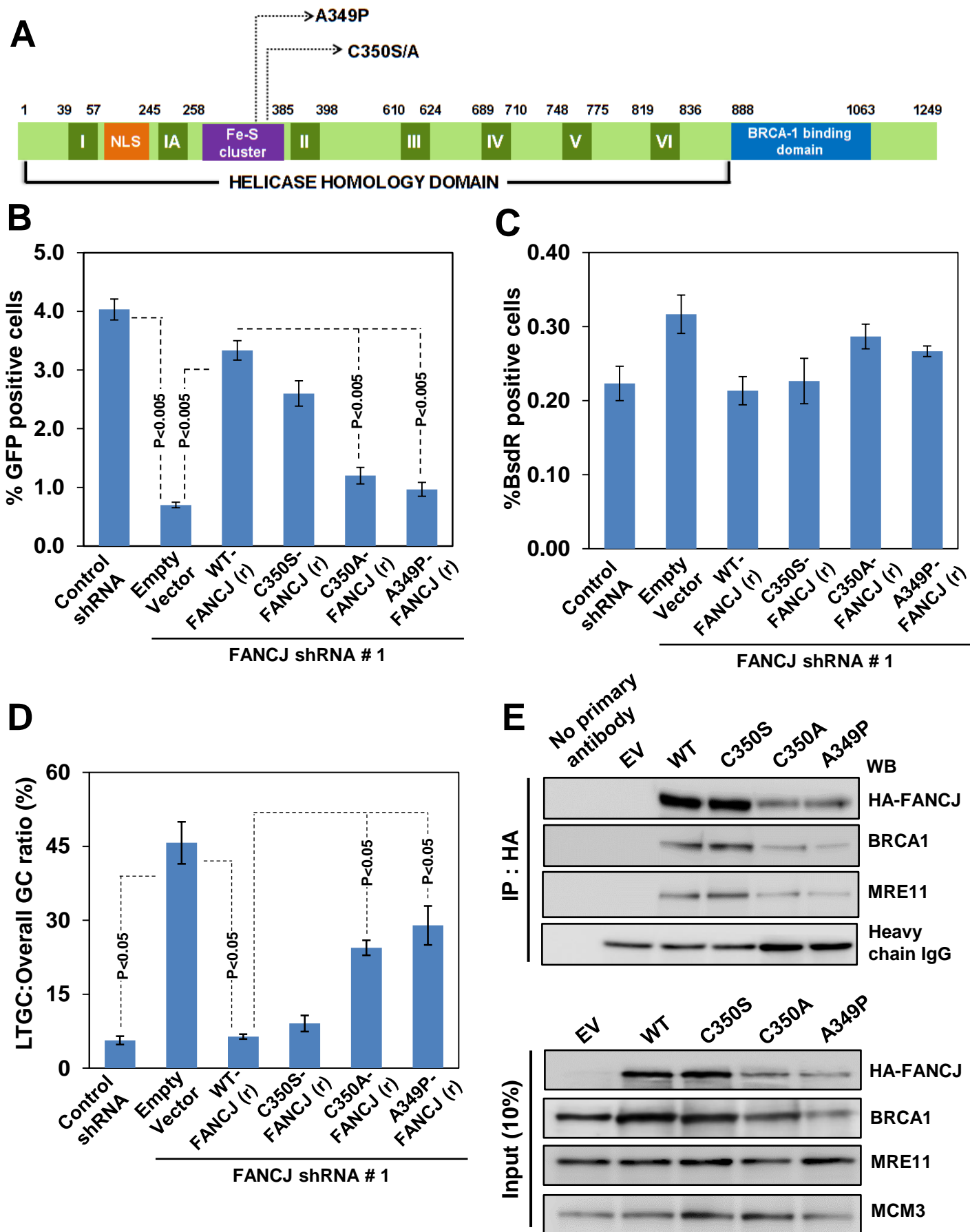


Supplementary Figure 4



Supplementary Figure 5

A**B****C****Supplementary Figure 6**



Supplementary Figure 7