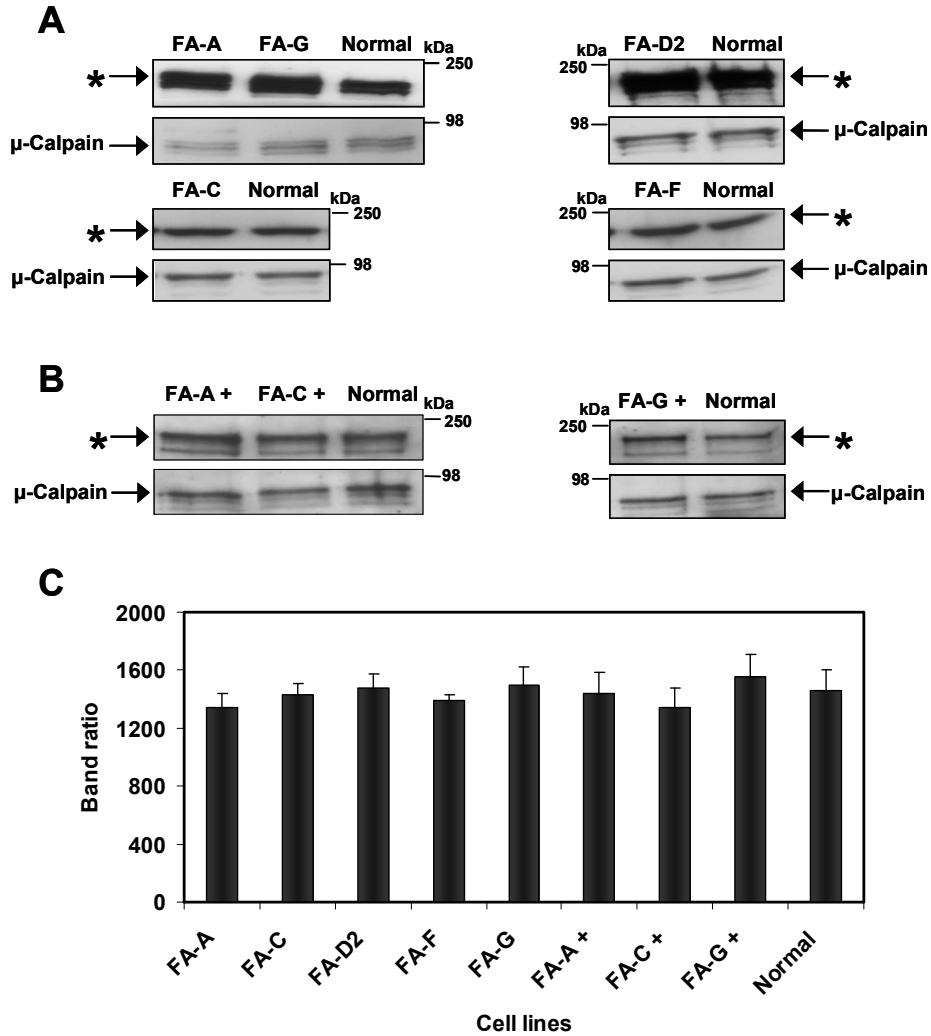


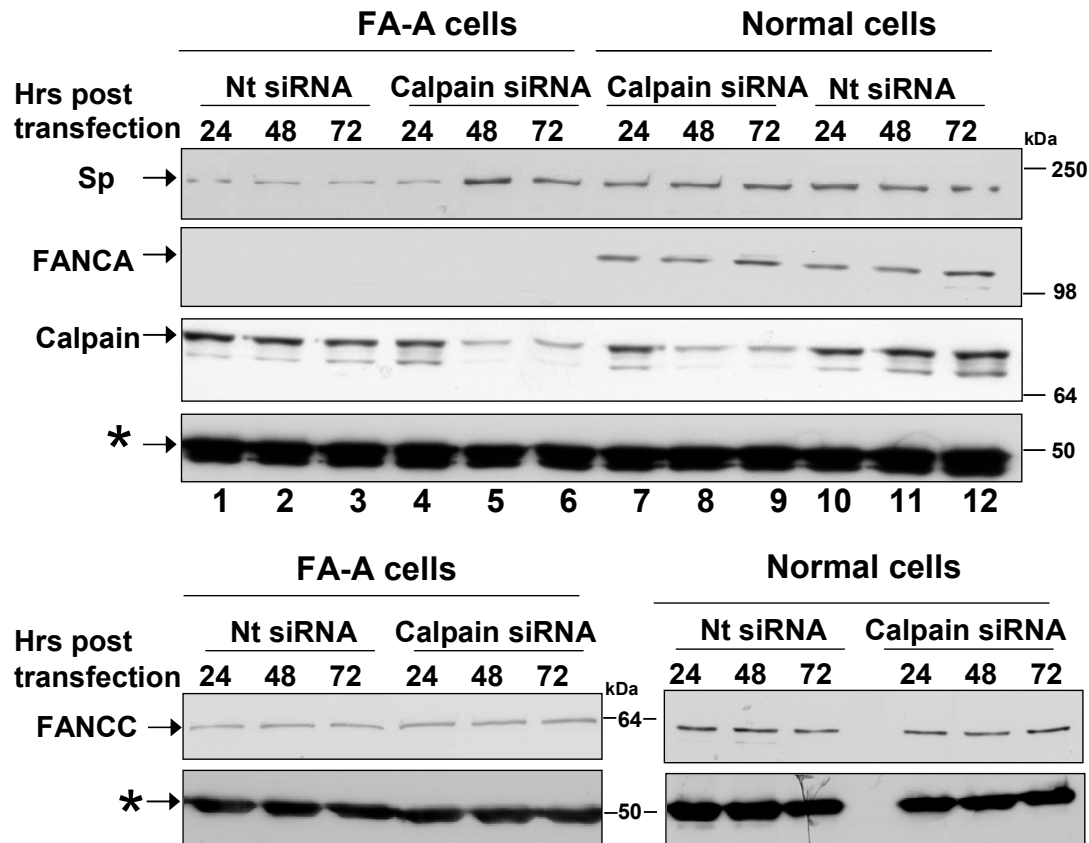
## SUPPORTING INFORMATION

### Knockdown of $\mu$ -calpain in Fanconi Anemia, FA-A, cells by siRNA Restores $\alpha$ II Spectrin levels and Corrects Chromosomal Instability and Defective DNA Interstrand Cross-link Repair

Pan Zhang, Deepa Sridharan, and Muriel W. Lambert



**FIGURE S1.** Levels of  $\mu$ -calpain protein in FA cells are the same as those in corrected FA cells and normal cells. Chromatin-associated protein extracts from (A) FA-A, FA-G, FA-C, FA-D2, and FA-F and (B) corrected FA-A+, FA-C+ and FA-G+ cells were examined for levels of  $\mu$ -calpain using western blot analysis and compared with  $\mu$ -calpain levels found in these extracts from normal cells. Blots were probed with anti- $\mu$ -calpain. Topoisomerase (\*) was used as a loading control. Molecular weight markers are as indicated. (C) These immunoblots were scanned and levels of  $\mu$ -calpain quantitated. Vertical lines represent  $\pm$  s.e.m. for 4-6 experiments.



**FIGURE S2.** Knocking down  $\mu$ -calpain in FA-A cells by siRNA leads to restoration of levels of  $\alpha$ IISp to normal 48 hours post transfection and has no effect on levels of FANCA or FANCC. FA-A and normal cells were transiently transfected with 300 pM  $\mu$ -calpain siRNA or nontarget (Nt) siRNA. Levels of  $\alpha$ IISp,  $\mu$ -calpain, FANCA and FANCC in the FA-A and normal cells were examined by western blot analysis at 24, 48 and 72 hours post transfection. Immunoblots were probed with anti- $\alpha$ IISp, anti- $\mu$ -calpain, anti-FANCA, and anti-FANCC antibodies. Tubulin (\*) was used as a loading control.

**Table S1. MMC-induced chromosomal aberrations in normal cells transfected with nontarget (Nt) siRNA and FA-A cells transfected with Nt siRNA or  $\mu$ -calpain siRNA**

	MMC (30 nM)	Cells with chromosomal aberrations <sup>a</sup>	Chromosomal aberrations <sup>b</sup>			Total chromosomal aberrations <sup>b</sup>
			Interchromatid exchanges	Fusions/ radials	Breaks	
Normal +	-	12	9	6	3	18
Nt siRNA	+	34	65	28	39	132
FA-A	-	14	15	5	5	25
	+	95	401	97	130	628
FA-A +	-	16	10	4	7	21
Nt siRNA	+	92	393	87	118	598
FA-A +	-	17	18	2	4	24
$\mu$ -calpain siRNA	+	48	80	11	55	146

<sup>a</sup> 100 cells in each group were counted to determine how many cells contained metaphase spreads with chromosomal aberrations (i.e. interchromatid exchanges, fusions/radials and breaks)

<sup>b</sup> Chromosomal aberrations found in metaphase spreads from 100 cells in each group