Table S2: DSB% at DSB1 and DSB2 sites				
Figure no.		**Treatment**	**DSB% at DSB1**	**DSB% at DSB2**
Fig 1J		shControl	28.5 ± 1.9	19.5 ± 3.1
		shBRCA1	18.3 ± 2.5	7.95 ± 2.3
		shMRE11	19.7 ± 5.03	7.57 ± 2.7
		shCtIP	19.5 ± 4.3	8.47 ± 2.3
		shFANCJ # 1	23.5 ± 2.88	15.7 ± 4.24
		shFANCJ # 2	23.3 ± 5.05	16.5 ± 2.1
		shDNA2	23.7 ± 4.76	16.8 ± 3.7
		sh53BP1	25.3 ±4.5	17.9 ± 2.28
Fig. 2G		shControl	22.3 ± 5.3	15.8 ± 2.01
		shFANCJ # 1	26.7 ± 3.05	17.3 ± 3.07
		shCtIP	27.7 ± 2.08	17.9 ± 3.19
		shFANCJ # 1+ shCtIP	21.6 ± 7.6	12.22 ± 1.03
Fig. 3D		shControl	24.3 ± 3.05	13.7 ± 1.16
		shFANCJ # 1	16.7 ± 0.57	9.45 ± 0.79
		shFANCJ # 1 + WT-FANCJ	18.3 ± 5.77	10.4 ± 0.87
		shFANCJ # 1 + 1-881 FANCJ	26.7 ± 3.5	15.11 ± 1.3
Fig. 4C		shControl	22.7 ± 6.6	12.8 ± 1.08
		shFANCJ # 1	20.0 ± 4.58	11.3 ± 0.95
		shFANCJ # 1 + WT-FANCJ	21.0 ± 1.26	11.8 ± 1.00
		shFANCJ # 1 + S990A-FANCJ	24.3 ± 2.52	13.8 ± 1.16
		shFANCJ # 1 + S990E-FANCJ	28.5 ± 1.28	16.13 ± 1.36
Fig. 5C		shControl	19.7 ± 5.5	11.15 ± 0.94
		shFANCJ # 1	19.3 ± 0.6	10.95 ± 0.92
		shFANCJ # 1 + WT-FANCJ	21.0 ± 1.8	11.9 ± 1.00
		shFANCJ # 1 + K1249R-FANCJ	19.3 ± 3.78	15.01 ± 2.84
		shFANCJ # 1 + K1249Q-FANCJ	23.6 ± 4.6	18.3 ± 3.46
Fig. 8C	shControl	shCtIP + EV	22.0 ± 2.2	
		shCtIP + WT-CtIP (R)	21.4 ± 3.7	
		shCtIP + S327A-CtIP (R)	24.0 ± 1.9	
		shCtIP + T847A-CtIP (R)	19.8 ± 5.6	
	shFANCJ	shCtIP + EV	18.5 ± 6.2	
		shCtIP + WT-CtIP (R)	21.0 ± 3.1	
		shCtIP + S327A-CtIP (R)	17.6 ± 4.2	
		shCtIP + T847A-CtIP (R)	15.6.0 ± 3.2	
Fig.8D		shControl	20.7 ± 1.43	9.54 ± 0.81
		shFANCJ # 1	15.1 ± 0.62	10.14 ± 1.13
		shBRCA1	17.3 ± 1.5	11.37 ± 2.71
		shFANCJ # 1+ shBRCA1	18.5 ± 3.3	7 ± 0.68
Fig. 9E		shControl	20.0 ± 5.2	9.04 ± 1.89
		shFANCJ # 1	21.3 ± 3.78	9.5 ± 1.95

Figure no.	Treatment	DSB% at DSB1	DSB% at DSB2
	shFANCJ # 1 + WT-FANCJ	23.3 ± 4.7	10.5 ± 2.17
	shFANCJ # 1 + K52A-FANCJ	28.3 ± 2.08	12.8 ± 2.6
	shFANCJ # 1 + K52R-FANCJ	20.6 ± 1.38	9.3 ± 1.9

* **Summary of the % DSBs at the two selected AsiSI sites after 4 h of 4-OHT treatment**.

  % DSB values were measured by qPCR using undigested gDNA samples and two sets of primers across the two AsiSI sites (Fig. 1A). The 'No DSB' primers were used to normalize the amount of gDNA in the qPCR reaction. DSB percentages at DSB1 and DSB2 sites in mock-treated cells were both set to zero.