Supplementary Information

Figure S1. Targeted ES cells by TALEN method. (**A**) Sequence alignment of BRCA1 for human, cow, rat and mouse. The marked fragment in mouse sequence is the deleted fragment, 421-701aa), (**B**) TALEN target sequences. An arrow shows the targeted site. (**C**) Donor BRCA1 targeting vector. (**D**) RT-PCR of gene-targeted BRCA1. WT: 3529bp, ΔDBR: 2713bp, Δ11:214bp (**E**) Western blot analysis of targeted mouse ES cells using antibodies for Flag and BRCA1. (**F**) MBP-tagged DBR of mouse BRCA1 (422-692aa) Left: Commassie staining of purified MBP-422-692aa, Right: EMSA using dsDNA. The concentration of labelled dsDNA and proteins are 40nM and 100nM, respectively.

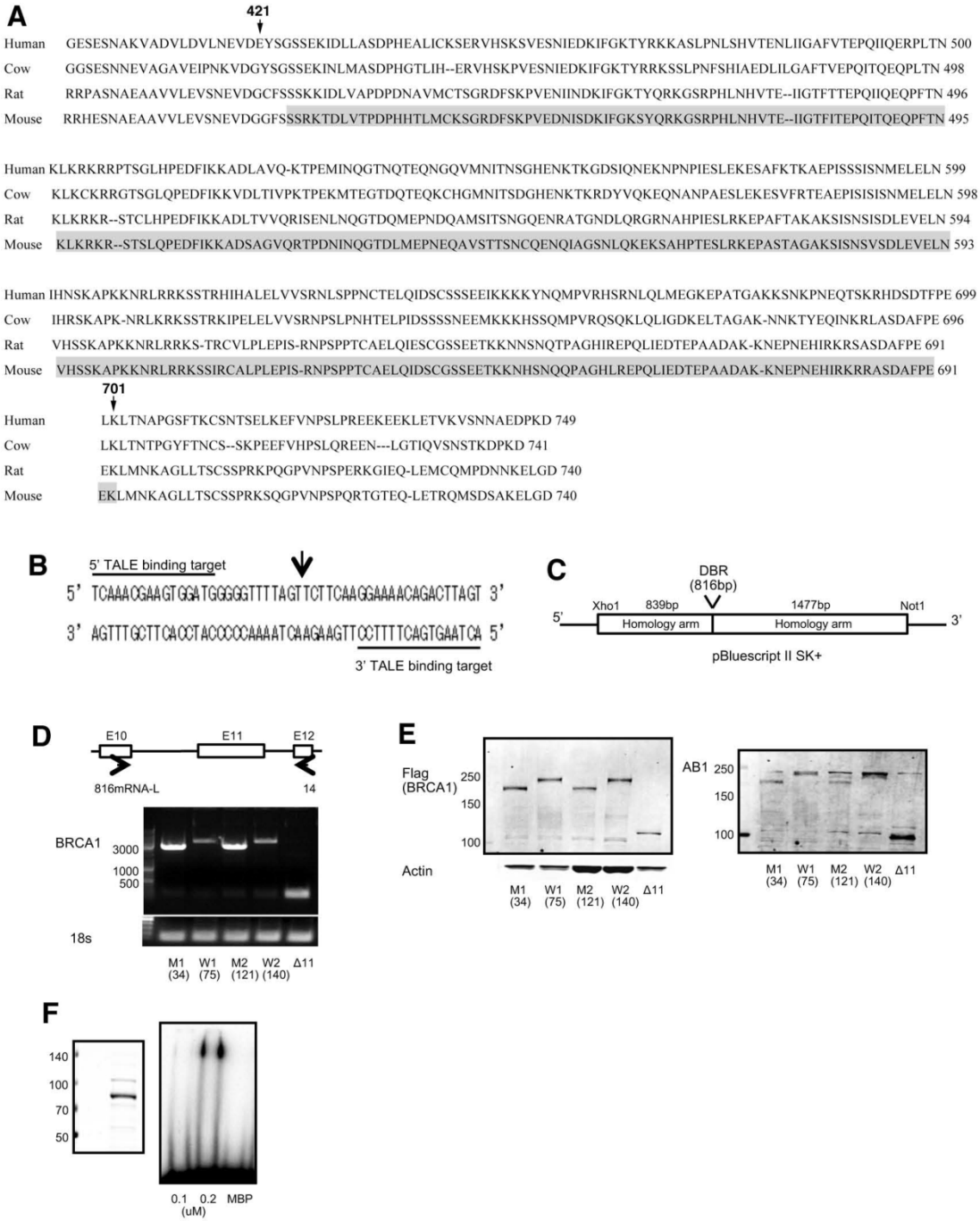


Figure S2. HR assay using HeLa cells in which BRCA1 is stably knocked down by shBRCA1 or the control. (**A**) Western blot analysis of HeLa cells for BRCA1 expression. (**B**) HR assay. *$P < 0.05$, $N = 3$ **$N.S.$, $N = 3$.

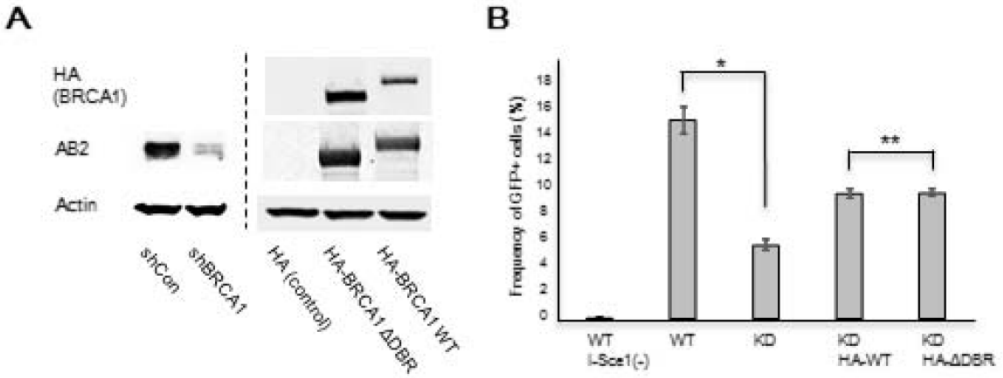


Figure S3. Purified BRCA1 proteins stained with Coomassie. (**A**) MBP, MBP-full-length BRCA1, MBP-BRCA1 deficient in DBR. (**B**) GST-BRCA1 fragments. (**C**) MBP-BRCA1 fragments.

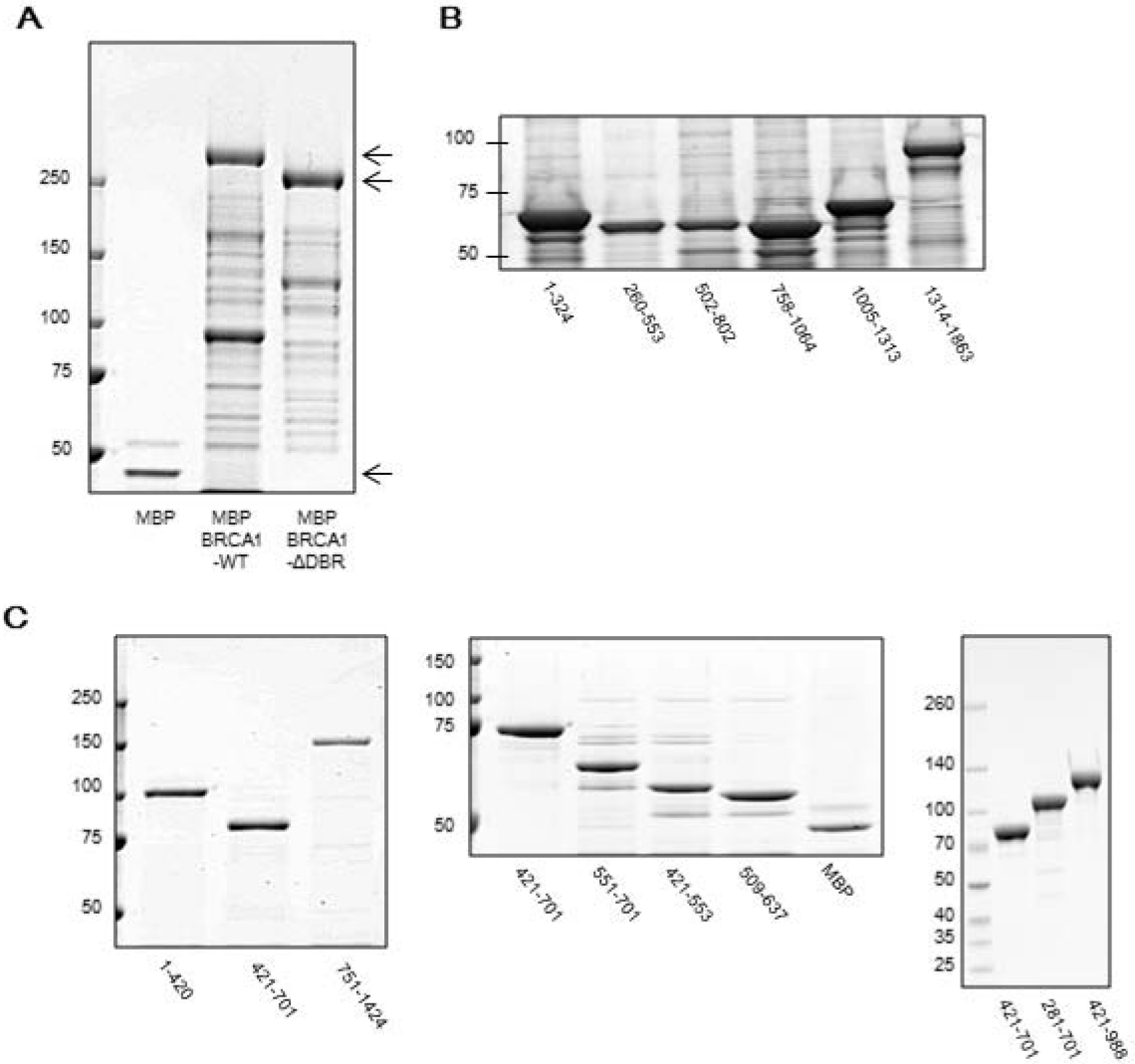
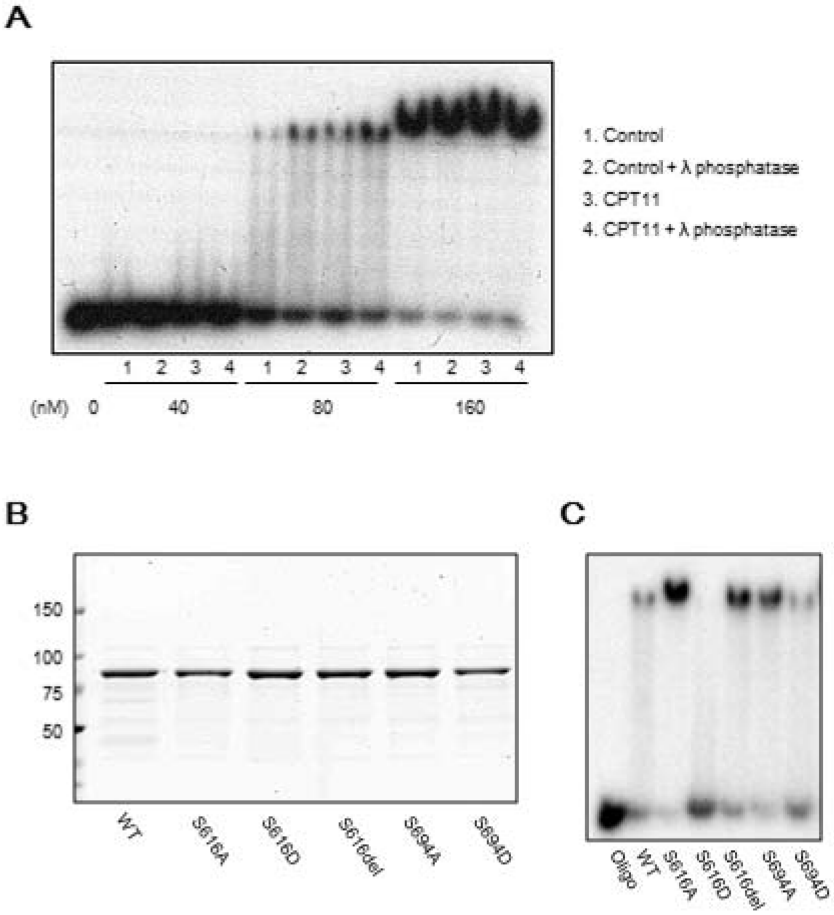


Figure S4. Phosphorylation status of BRCA1-DBR affects the binding affinity to dsDNA *in vitro*. (**A**) EMSA using CPT11-treated BRCA1-DBR or the control with or without incubation with λ protein phosphatase *in vitro*. The concentration of labelled dsDNA is 40nM. (**B**) Purified BRCA1 mimics with Coommasie staining. Mimics of phosphorylation (from serine (S) to aspartic acid (D)) and dephosphorylation (from serine (S) to alanine (A)) in S616 and S694, which are reported to be phosphorylation sites or mutations in breast cancer patients within DBR [31,32]. (**C**) EMSA using the dephosphorylation mimic. They bind to dsDNA better than the wild type or the phosphorylation mimic. The concentration of labelled dsDNA and proteins are 40nM and 100nM, respectively.



Legend for Illustration: The role of DBR in BRCA1 for genomic integrity.

The DBR in BRCA1 modulates genetic stability through intra-S-phase checkpoint by phosphorylation of Chk1 resulting from replication stress, although its role in HR repair is dispensable.

Table S1. Primer sequences for BRCA1 expression constructs.

Construct	PCR primers (5'-3')
human	
full length	ACCGGTCGCCTCCCTCGGATCCATGGA
	GGGCCCTCTAGATGCATGCTCGAGCC
full length del 421-701	GATTCCCAGGACCCACACTG
	CTGAGGGCTGGGATTGACAG
1-420	ACCGGTCATGGATTTATCTGCTCTTC
	CTCGAGTCAATCTACCTCATTTAGAACG
421-701	ACCGGTCGAATATTCTGGTTCTTCAGA
	CTCGAGTCACTTCAGCTCTGGGAAAGTA
751-1424	ACCGGTCATGTTAAGTGGAGAAAGGGT
	CTCGAGTCACTGGCTCCCATGCTGTTCT
421-553	ACCGGTCGAATATTCTGGTTCTTCAGA
	CTCGAGTCAATGACCACTATTAGTAATATTC
509-637	ACCGGTCACATCAGGCCTTCATCCTGAG
	CTCGAGTCAAGTACAATTAGGTGGGCTTAG
551-701	ACCGGTCGGTCATGAGAATAAAACAAAAGG
	CTCGAGTCACTTCAGCTCTGGGAAAGTA
281-701	ACCGGTCAGCTCATTACAGCATGAGAA
	CTCGAGTCACTTCAGCTCTGGGAAAGTA
421-988	ACCGGTCGAATATTCTGGTTCTTCAGA
	CTCGAGTCATGACTTGATGGGAAAAAG
421-701 S616A	AGGAGGAAGTCTGCTACCAGGCATATTC
	GAATATGCCTGGTAGCAGACTTCCTCCT
421-701 S616D	GAGGAGGAAGTCTGATACCAGGCATATTC
	GAATATGCCTGGTATCAGACTTCCTCCTC
421-701 S616del	ACCAGGCATATTCATGCGCTTG
	AGACTTCCTCCTCAGCCTATTC
421-701 S694A	ACCGGTCGAATATTCTGGTTCTTCAGA
	CTCGAGTCACTTCAGCTCTGGGAAAGTATCGGCGTCATG
421-701 S694D	ACCGGTCGAATATTCTGGTTCTTCAGA
	CTCGAGTCACTTCAGCTCTGGGAAAGTATCGTCGTCATG
mouse	
422-693	ACCGGTCTCTTCAAGGAAAACAGACTT
	CTCGAGTTATTTCTCTTCTGGGAAAGC

Table S2. Oligonucleotides used in EMSA.

Substrate	No	Sequence (5'-3')
Double strand	1	GAACCGGCCGCTCCCGCGACATCACAGGAAGGCTGAGAGA
		TCTCTCAGCCTTCCTGTGATGTCGCGGGAGCGGCCGGTTC
	2	CTGATTTGCATAGCCCAATGGCCAAGCTGCATGCAAATGAG
		CTCATTTGCATGCAGCTTGGCCATTGGGCTATGCAAATCAG
	3	GCTCCCGCGACATCACAGGAAGGCT
		AGCCTTCCTGTGATGTCGCGGGAGC
	4	TCTTTGACACGTTTATGGATTACAG
		CTGTAATCCATAAACGTGTCAAAGA
	5	GAAGTGGTGTATACGACAGAGACCG
		CGGTCTCTGTCGTATACACCACTTC
	6	CTCCCGCGACATCACAGGAA
		TTCCTGTGATGTCGCGGGAG
	7	GGCCGCTCCCGCGACATCACAGGAAGGCTG
		CAGCCTTCCTGTGATGTCGCGGGAGCGGCC
	8	GCGCCTGCGCGAACCGGCCGCTCCCGCGACATCACAGGAAGGCTGAGAGAAAGGGCAGGT
		ACCTGCCCTTTCTCTCAGCCTTCCTGTGATGTCGCGGGAGCGGCCGGTTCGCGCAGGCGC
Single strand	9	GAACCGGCCGCTCCCGCGACATCACAGGAAGGCTGAGAGA
Splayed-arm	10	GAACCGGCCGCTCCCGCGACTAGTGTCCTTCCGACTCTCT
		TCTCTCAGCCTTCCTGTGATGTCGCGGGAGCGGCCGGTTC
5' overhang	11	GAACCGGCCGCTCCCGCGAC
		TCTCTCAGCCTTCCTGTGATGTCGCGGGAGCGGCCGGTTC
3' overhang	12	ATCACAGGAAGGCTGAGAGA
		TCTCTCAGCCTTCCTGTGATGTCGCGGGAGCGGCCGGTTC