Table S1.

	3UTR	5UTR	Exons	introns
184A1	52	5	1	7
MCF10A	9	4	1	4
MCF12	44	19	2	37

Table S2.

Target ID	r	P (two-tailed)
POLH	0.301	< 0.0001
ATM	0.244	0.0002
GINS4	0.0516	0.4442

Table S3.

LumA	TOTAL CASES	DECEASED	MEDIAN MONTHS SURVIVAL
Cases with Alteration(s) in Query Gene(s)	97	9	129.61
Cases without Alteration(s) in Query Gene(s)	138	17	113.74
			Logrank Test P: 0.630

LumB	TOTAL CASES	DECEASED	MEDIAN MONTHS SURVIVAL
Cases with Alteration(s) in Query Gene(s)	67	10	81.58
Cases without Alteration(s) in Query Gene(s)	64	7	79.57
			Logrank Test P: 0.894

Table S1. Significative comparisons (Wilcoxon Test p<0.05) between BC cells and interrogated immortalized cell line for those shared variants located in different transcript regions.

Table S2. Pearson Correlation for *ATM, GINS4* and *POLH* expression and editing counts.

Table S3. Survival proportions for LumA and LumB BRCA TCGA patients based on ADAR1 expression. Data obtained from The Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumors. Nature 490, 61–70 (2012).