

Supporting Information

Colorimetric detection of single-nucleotide mutation based on rolling circle amplification and G-quadruplex-based DNAzyme

Serge Yannick OUEDRAOGO^{a,b,1}, Moutanou Modeste Judes ZEYE^{c,1}, Xi Zhou^a,
Touwendpoulimdé Isabelle KIENDREBEOGO^b, Abdou Azaque ZOURE^{b,d}, Hanchun
Chen^a, Fangzhi Chen^{e,*}, Changbei Ma^{a,*}

^aDepartment of Biochemistry and Molecular Biology, School of Life Sciences, Central South University, Changsha 410013, Hunan, China

^bBiomolecular Research Center Pietro Annigoni (CERBA)/LABIOGENE, University of Ouaga 1 Pr Joseph KI ZERBO, UFR/SVT, Burkina Faso

^cDepartment of medical parasitology, School of Basic Medicine, Central South University, Changsha 410013, Hunan, China

^dInstitute of Health Sciences Research (IRSS/CNRST)/Department of Biomedical and Public Health, Burkina Faso

^eDepartment of Urology, The Second Xiangya Hospital of Central South University, Changsha 410007, Hunan, China

¹These authors have contributed equally to this work

*Corresponding authors: E-mail: macb2012@csu.edu.cn (C. Ma); fzc202@126.com (F. Chen)

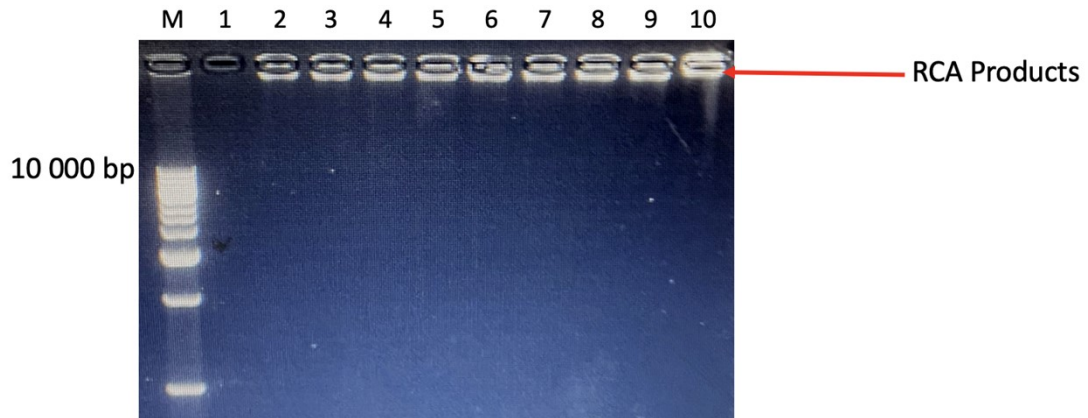


Fig. S1. Electrophoresis gel analysis of RCA products in the sensitivity assay. Lane 1 (0 nM of target DNA used), Lane 2 (0.01 nM), Lane 3 (0.1 nM), Lane 4 (0.5 nM), Lane 5 (1 nM), Lane 6 (10 nM), Lane 7 (50 nM), Lane 8 (100 nM), Lane 9 (500 nM), Lane 10 (1000 nM).

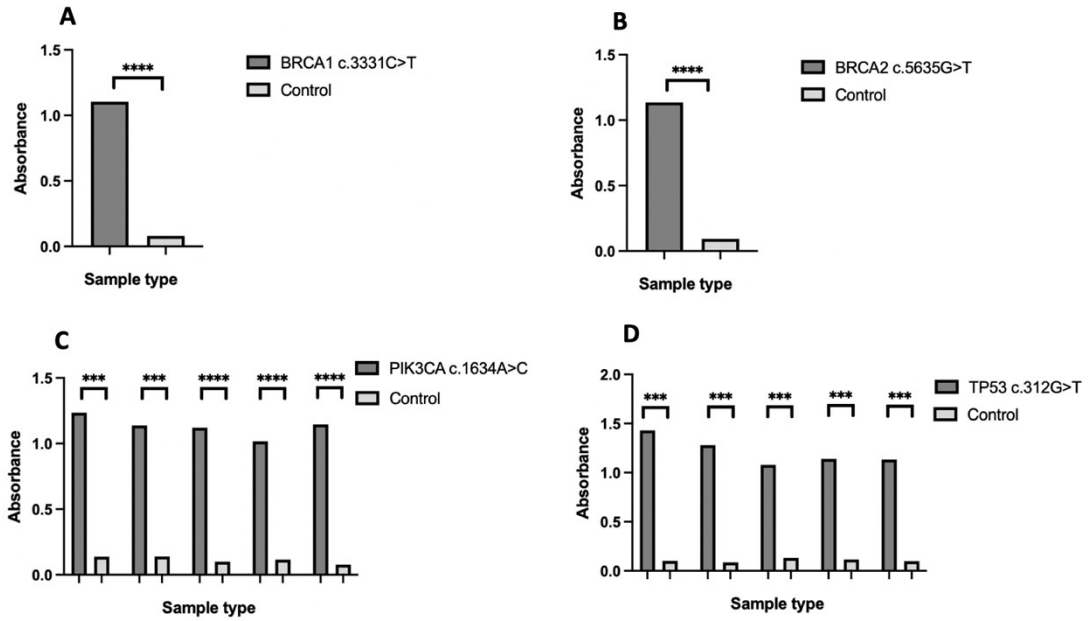


Fig.S2. Absorbance graphs for the mutation detection in breast cancer samples. (A) Graph showing the absorbance values of the mutant BRCA1 c.331C>T sample and a control WT sample. (B) Graph showing the absorbance values of the mutant BRCA2 c.5635G>T sample and a control WT sample. (C) Graph showing the absorbance values of mutant PIK3CA c.1634A>C samples and control WT samples. (D) Graph showing the absorbance values of mutant TP53 c.312G>T samples and control WT samples. All *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001. The data are presented as the average and the error bars show the SD of 3 replicated experiments.

Table S1. Oligonucleotide sequences (5' to 3')

Targeted Mutation	Sequence* (5' → 3')	Size (nt)
BRCA1 (c.3331C>T)	p <i>TTCTTATACTTCTCCCTAACCCCTAACCCCTAACCCGACT</i> TTATTTTTTCA	49
BRCA2 (c.5635G>T)	p <i>TCTTATTAGTTTTCCCTAACCCCTAACCCCTAACCCATT</i> CCTTTTGTGA	49
PIK3CA (c.1634A>C)	p <i>CAGTGATTTCCCCTAACCCCTAACCCCTAACCCCTTCTCC</i> TGCG	41
TP53 (c.312G>T)	p <i>CCGTCGATGCCAAACCCTAACCCCTAACCCCTAACCCCTC</i> TTTTGGATGGTA	49
BRCA1 (c.3331C>T)	TAGGGAGAAGTATAAGAA	18
BRCA2 (c.5635G>T)	TAGGGAAAACCTAAATAAGA	19
PIK3CA (c.1634A>C)	TAGGGGAAATCACTG	15
TP53 (c.312G>T)	TAGGGTTTGGCATCGACGG	19
BRCA1 (c.3331C>T)	CTGAAATAAAAAAGC/ <u>TAAGAATATGAAGA</u>	29/29
BRCA2 (c.5635G>T)	TAAGGAAAACAACG/ <u>TAGAATAAATCAAAA</u>	29/29
PIK3CA (c.1634A>C)	GAAATCACTGA/ <u>CGCAGGAGAA</u>	21/21
TP53 (c.312G>T)	AGAAAACCTACCAG/ <u>TGGCAGCTACGGTTT</u>	29/29
BRCA1 (c.3331C>T)	Forward primer: pTTAGGGGTTTTGCAACCTGAG Reverse primer: TAAGTTATCTGAAATCAGATAT	21 22
BRCA2 (c.5635G>T)	Forward primer: pTTTGTGTTTCACATGAAACAATT Reverse primer: ATCTAGAGAGTTATGAAGAATATC	23 24
PIK3CA (c.1634A>C)	Forward primer: pTGAATTAAGGGAAAATGA Reverse primer: CTGTGACTCCATAGAAAAT	18 19
TP53 (c.312G>T)	Forward primer: pTGCACCAGCCCCCTCCTGGC Reverse primer: GTGCAAGTCACAGACTTGGCT	20 21

*Red segment, C-rich region; Italic segment, RCA primer binding site; Bold segment, mutant recognition site; p, phosphorylation; nt, nucleotides; Underline, wild-type and mutant type sequence, respectively.

Table S2. Mutations and real BC samples number detected

Genes	Variants	BC samples detected
BRCA1^a	c.3331C>T	1
BRCA2^b	c.5635G>T	1
PIK3CA^c	c.1634A>C	5
TP53^d	c.312G>T	5
Control_BRCA1	-	5
Control_BRCA2	-	5
Control_PIK3CA	-	5
Control_TP53	-	5

^aBRCA1 reference sequence NCBI RefSeq NM_007294.3 (mRNA) and NP_009225.1 (protein)

^bBRCA2 reference sequence NCBI RefSeq NM_000059.3 (mRNA) and NP_000050.2 (protein)

^cPIK3CA reference sequence NCBI RefSeq NM_006218.2 (mRNA) and NP_006209.2 (protein)

^dTP53 reference sequence NCBI RefSeq NM_000546.5 (mRNA) and NP_000537.3 (protein)

Controls: Samples obtained from patients who did not harbor any of the mutations mentioned above.