

## Supplementary Information

### Sensitive mutant DNA biomarkers detection based on magnetic nanoparticles and nicking endonuclease assisted fluorescence signal amplification

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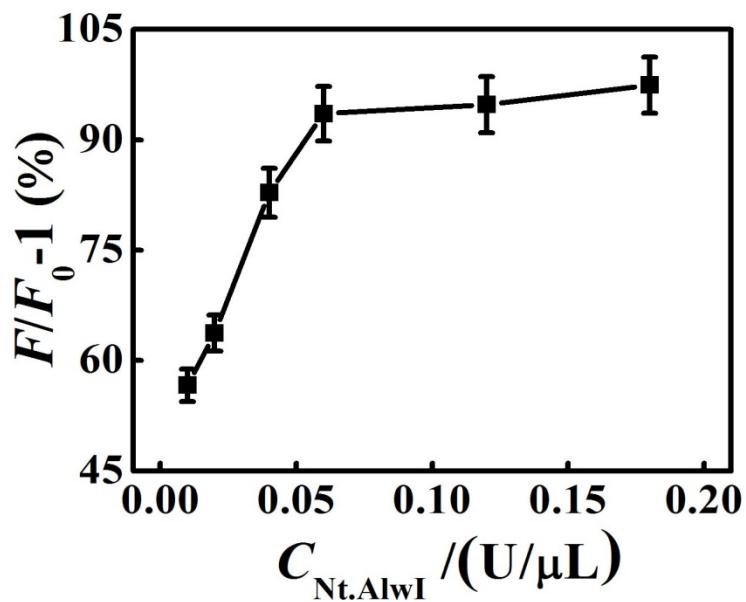
## **Contents**

<b>Sequence of oligomers (Table S1).....</b>	<b>S-3</b>
<b>Fig. S1.....</b>	<b>S-4</b>
<b>Fig. S2.....</b>	<b>S-5</b>
<b>Fig. S3.....</b>	<b>S-6</b>

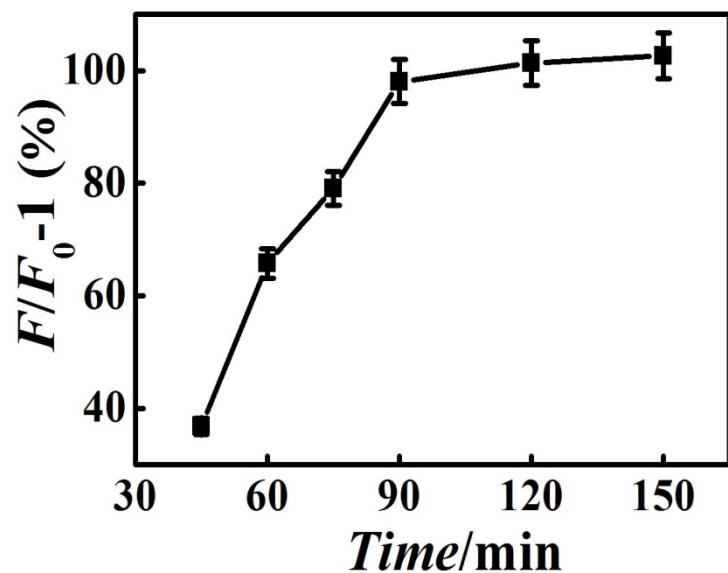
**Table S1 Sequence of oligomers used in this study**

Oligonucleotide	Sequence (5' to 3') description <sup>a</sup>
Hairpin capture probe (HP)	biotin-CCACGG <b>GGAT</b> CTGAC↓TGTCGTGG-FITC
Mutant human p53 gene target (T)	ACAGTCAGATCC
Single-base mismatched sequence (T1)	ACAGTCAAATCC
Three-base mismatched sequence (T3)	GCAGTCTGAACC
Five-base mismatched sequence (T5)	GCATTCTGAGCT
Non-complementary sequence (nDNA)	GGTTCTGACAGA

<sup>a</sup> The HP contains three functional regions: (1) two italic parts at the ends represent the complementary sequences of the stem arm; (2) the bold sequence is complementary to the target DNA; (3) GGATC is the recognition sequence of Nt.AlwI enzyme, and the arrow indicates the nicking position.

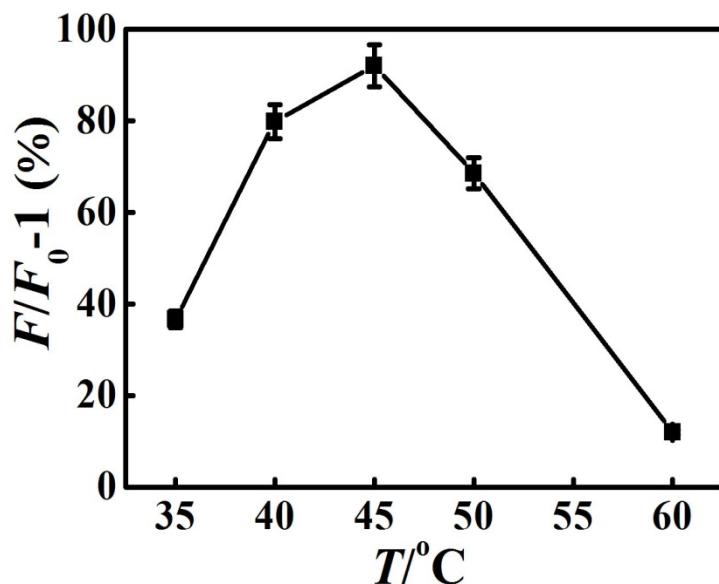


**Fig. S1** Effect of the Nt.AlwI enzyme concentration,  $C_{\text{Nt.AlwI}}$ , on fluorescence signal increase percentage ( $F/F_0 - 1$ ). Concentrations: MNPs (0.4 mg/mL), hairpin DNA (7.0  $\times$  10<sup>-8</sup> mol/L), the mutant target DNA (8.0  $\times$  10<sup>-12</sup> mol/L).



**Fig. S2** Effect of incubation time on fluorescence signal increase percentage ( $F/F_0 - 1$ ).

Concentrations: MNPs (0.4 mg/mL), hairpin DNA ( $7.0 \times 10^{-8}$  mol/L), the mutant target DNA ( $8.0 \times 10^{-12}$  mol/L), Nt.AlwI enzyme (0.06 U/ $\mu$ L).



**Fig. S3** Effect of incubation temperature on fluorescence signal increase percentage ( $F/F_0 - 1$ ). Concentrations: MNPs (0.4 mg/mL), hairpin DNA ( $7.0 \times 10^{-8}$  mol/L), the mutant target DNA ( $8.0 \times 10^{-12}$  mol/L), Nt.AlwI enzyme (0.06 U/ $\mu$ L).