

Specificity Improvement of Invader Assay by Introducing an Artificially Mismatched Base into the  
Probe

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## Supplementary

**Table S1** Comparison between Invader assay and other close-tube techniques for SNP detection.

Methods	Experiment set-up *	Specificity	Dye-labelled reporter
Invader assay	++	+++++	Universal
Real-time PCR (TaqMan™)	+++++	+++	SNP-specific
Allele-specific amplification	++++	++++	SNP-specific
Allele-specific ligation	+++++	+++++	SNP-specific

\*The number of “+” means the difficulty for setting up an experiment for detecting SNPs.

**Table S2** Oligonucleotides used for PCR or Invader reaction.

Name	Sequence (5'-3')	T <sub>m</sub> (°C)
FRET-1	VIC-TCT T (BHQ1) AG CCG GTT TTC CGG CTA AGA CCT CGG CGC G-C6-NH <sub>2</sub>	
FRET-2	FAM-TCT T (BHQ1) AG CCG GTT TTC CGG CTA AGA CTC CGC GTC CGT-C6-NH <sub>2</sub>	
<i>ALDH2*2-F</i>	CCG GGA GTT GGG CGA GTA C	70.1
<i>ALDH2*2-R</i>	GCC CCC AGC AGG TCC C	71.6
<i>ALDH2*2-UP</i>	GGG CTG CAG GCA TAC ACT T	69.0
<i>ALDH2*2-WP-1</i>	<u>CGC GCC GAG GGA</u> AGT GAA AAC TGT GAG TG- PO <sub>3</sub>	62.3
<i>ALDH2*2-WP-2</i>	<u>CGC GCC GAG GGg</u> AGT GAA AAC TGT GAG TG-PO <sub>3</sub>	59.6
<i>ALDH2*2-WP-3</i>	<u>CGC GCC GAG GGA</u> gGT GAA AAC TGT GAG TG-PO <sub>3</sub>	58.8
<i>ALDH2*2-WP-4</i>	<u>CGC GCC GAG GGA</u> AaT GAA AAC TGT GAG TG-PO <sub>3</sub>	56.9
<i>ALDH2*2-WP-5</i>	<u>CGC GCC GAG GGA</u> AGT GAA AAC TGT GAG gG - PO <sub>3</sub>	60.1
<i>ALDH2*2-WP-6</i>	<u>CGC GCC GAG GGc</u> AGT GAA AAC TGT GAG TG-PO <sub>3</sub>	57.4
<i>ALDH2*2-WP-7</i>	<u>CGC GCC GAG GGt</u> AGT GAA AAC TGT GAG TG-PO <sub>3</sub>	57.2
<i>ALDH2*2-MP</i>	<u>ACG GAC GCG GAG</u> AAA GTG AAA ACT GTG AGT G-PO <sub>3</sub>	62.6

Notes: FRET-1, 2 are fluorescence resonance energy transfer (FRET) probes used for reporting wild-type and mutant in Invader reactions, respectively. *ALDH2\*2-F*, *R* are paired PCR primers. *ALDH2\*2-UP* is an invasive oligo used for Invader reactions. *ALDH2\*2-WP* (Wild Probe), *MP* (Mutant Probe) are detection probes for wild-type and mutant respectively. Underlined nucleotides are sequence-tags for different alleles. Italic lowercase are artificially mismatched bases.

## Supplementary Figure Captions

**Fig. S1** Fluorescence signals of *ALDH2*\*2 polymorphisms assay. A: Fluorescence intensities of three genotypes detected by end-point Invader Plus assay. The signal of VIC was specific to allele \*1 and the signal of FAM was specific to allele \*2. B: Fluorescence intensity curves of an *ALDH2* \*2\*2 homozygote by real-time Invader Plus assay.

**Fig. S2** The real-time fluorescence intensity curves of *ALDH2* \*2\*2 homozygotes by using different concentrations of *Afu* flap endonuclease. a-e were specific signals detected by using 6.68, 2.67, 1.34, 0.89, 0.67 ng/μL *Afu* flap endonuclease, respectively. a'-e' were non-specific signals detected by allele\*1-specific probes when using 6.68, 2.67, 1.34, 0.89, 0.67 ng/μL *Afu* flap endonuclease, respectively. f and f' were blank controls.

**Fig. S3** The real-time fluorescence signal curves of an *ALDH2* \*1\*1 homozygotes and a \*2\*2 homozygotes with different concentrations of probe 1 for allele \*1. a-c were specific signals of a \*1\*1 homozygotes with 500, 250, 125 nmol/L probe 1, respectively. a'-c' were non-specific signals of a \*2\*2 homozygotes with 500, 250, 125 nmol/L probe 1, respectively.

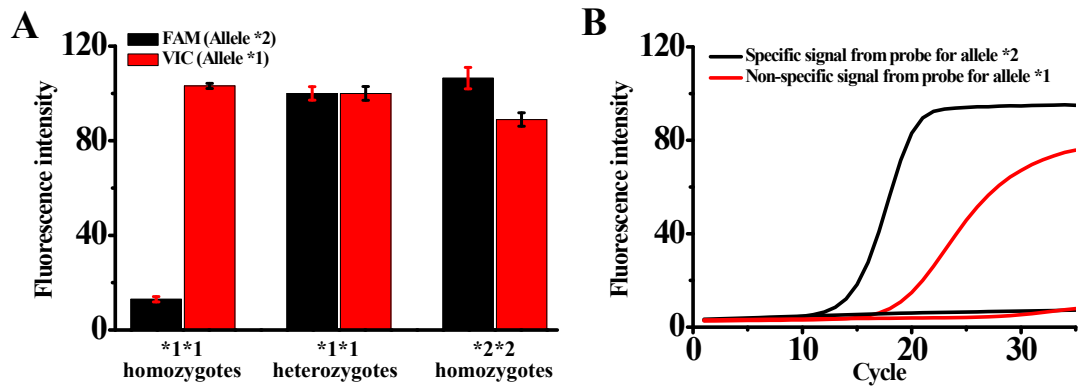
**Fig. S4** The distribution of Allele\*1 : Allele\*2 ratios using the complementary probe of WP-1 (A) and the mismatched probe of WP-2 (B). The FOZ value and the ratio can be calculated as following

formulas:  $FOZ = \frac{\text{Raw counts from sample}}{\text{Raw counts from No Template Control}}$ ,  $Ratio = \frac{(\text{Net Allele * 1 FOZ})}{(\text{Net Allele * 2 FOZ})}$ . The Net

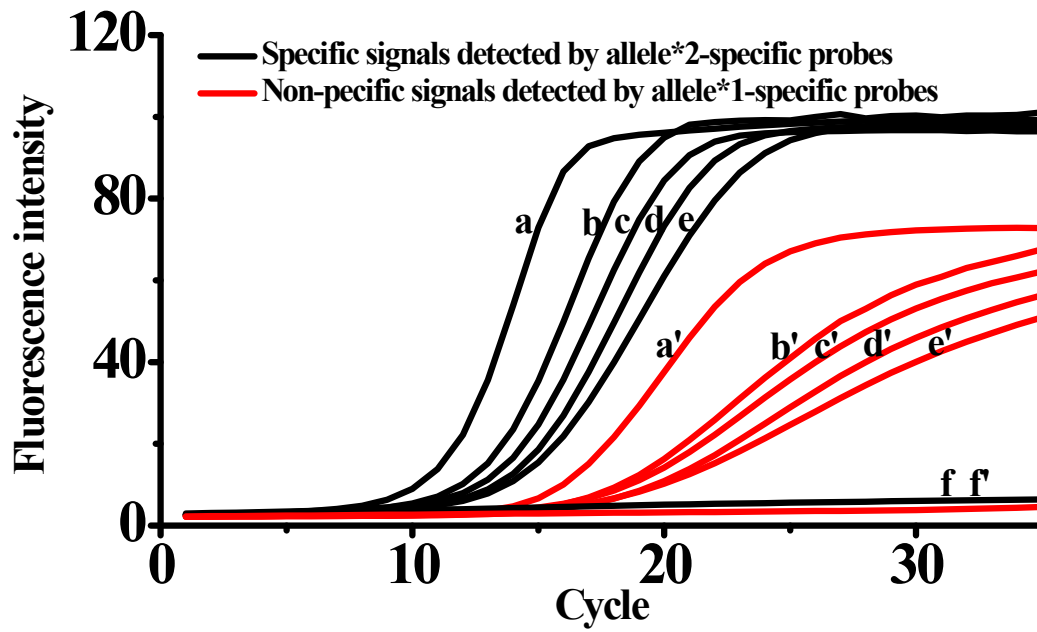
Allele FOZ=FOZ-1.

**Fig. S5** The typical results of the three genotypes using commercial Sanger sequencing (Left) and the real-time improved-Invader Plus method (Right). The arrows show the *ALDH2\*2* polymorphism site in Sanger sequencing.

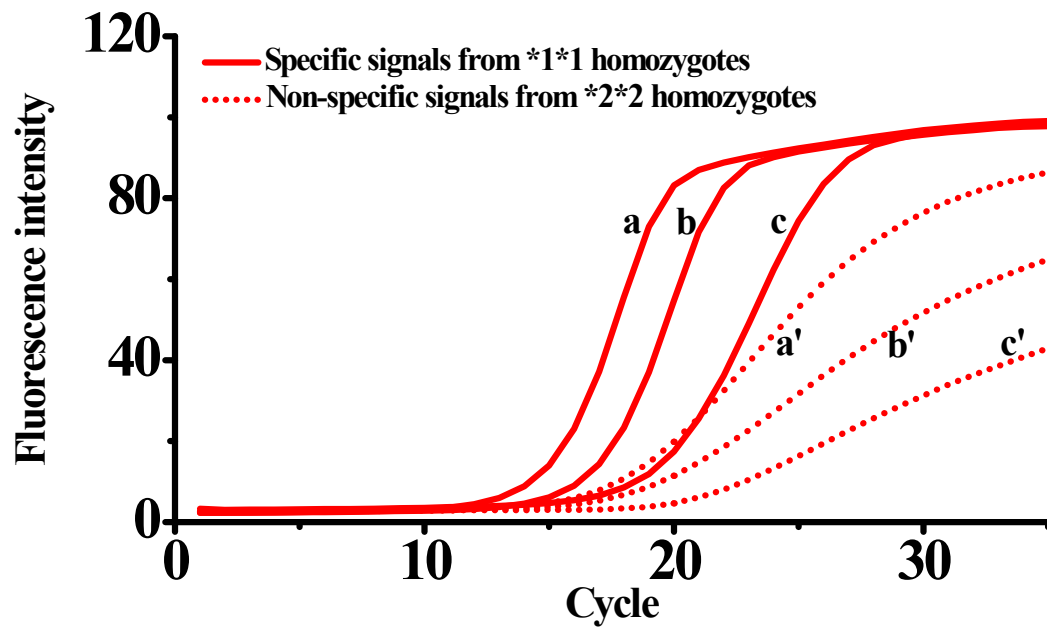
Supplementary Figures



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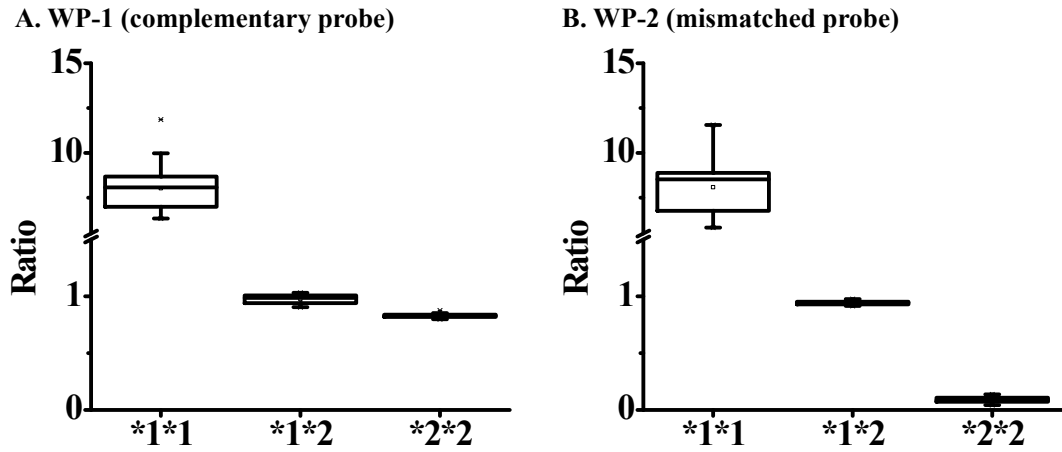


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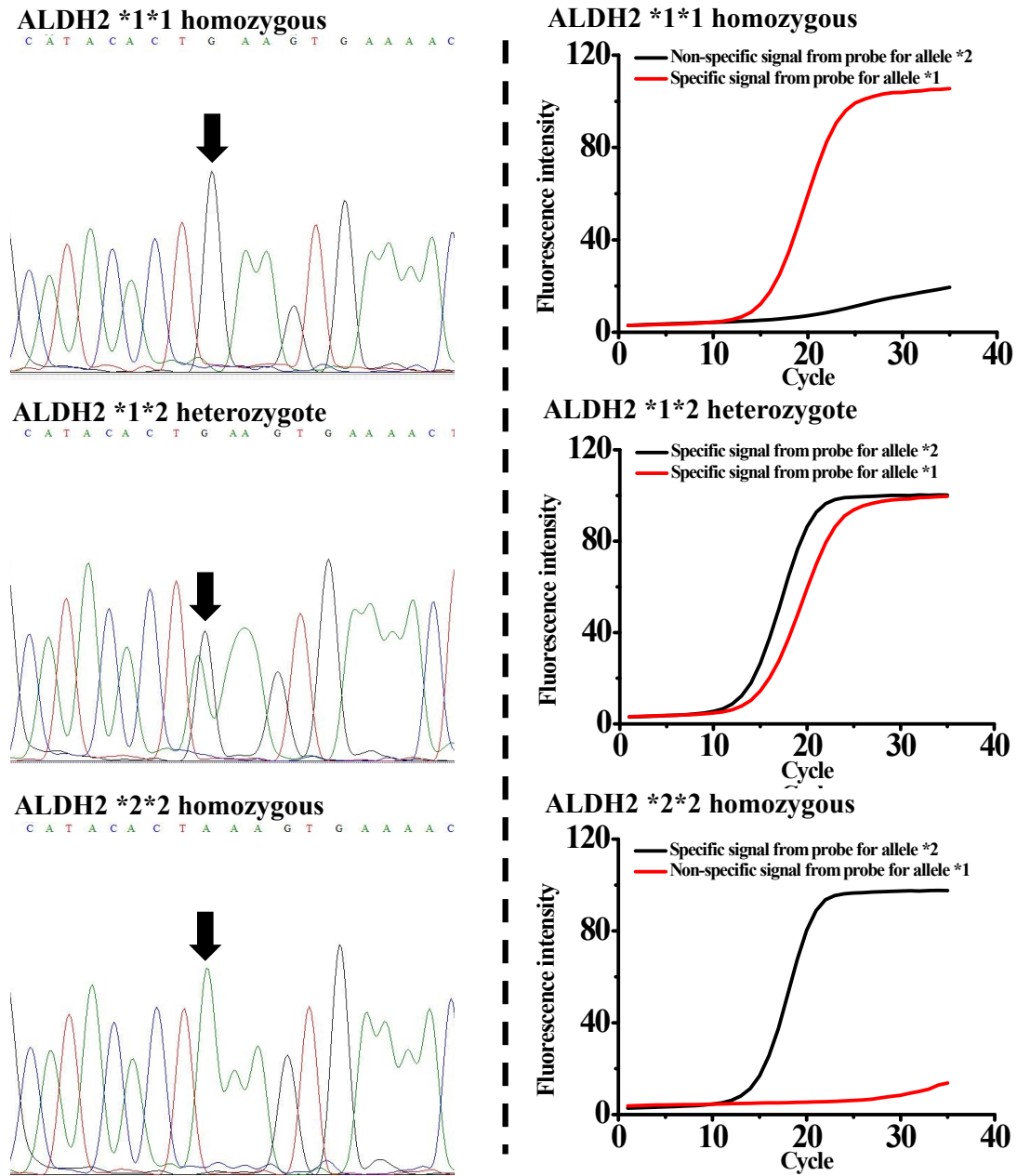
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$$FOZ = \frac{\text{Raw counts from sample}}{\text{Raw counts from No Template Control}}, \text{Ratio} = \frac{(\text{Net Allele * 1 FOZ})}{(\text{Net Allele * 2 FOZ})}. \text{The Net Allele}$$

FOZ=FOZ-1.



**Fig. S5** The typical results of the three genotypes using commercial Sanger sequencing (Left) and the real-time improved-Invader Plus method (Right). The arrows show the *ALDH2*\*2 polymorphism site in Sanger sequencing.