

A simplified pyrosequencing protocol based on linear-after-the-exponential (LATE)-PCR using
whole blood as starting material directly

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Supplementary Table

Supplementary Table S1. Sequences of LATE-PCR primers

Name ^a	Sequence (5'-3')	Conc. (μ M)	T _m value (°C)	T _m ^L - T _m ^X ^b (°C)	T _m ^A ^c (°C)
677-PX	TGTCATCCCTATTGGCAGGTTAC	1	65.9	5.8	77.0
677-PL	AGATCCCGGGGACGATGGGGCAAG	0.1	71.7		
1298-PX	GGACTACTACCTCTTCTACCTGA	1	63.5	6.5	75.7
1298-PL	GGGTCCCCACTCCAGCATCACTCAC	0.1	70.0		
DPYD-PX	<u>GGG</u> ^d TATAAGCCTATGAATTGGATG	1	62.7	7.2	73.8
DPYD-PL	TGGCCCTGGACAAAGCTCCTTTCTGA	0.1	69.9		

^a PX mean excess primer, PL mean limiting primer; ^b T_m^L and T_m^X mean the T_m value of limiting primer and excess primer, respectively; ^c T_m^A mean the T_m value of amplicons; ^d: underlined letters were artificially mismatched bases.

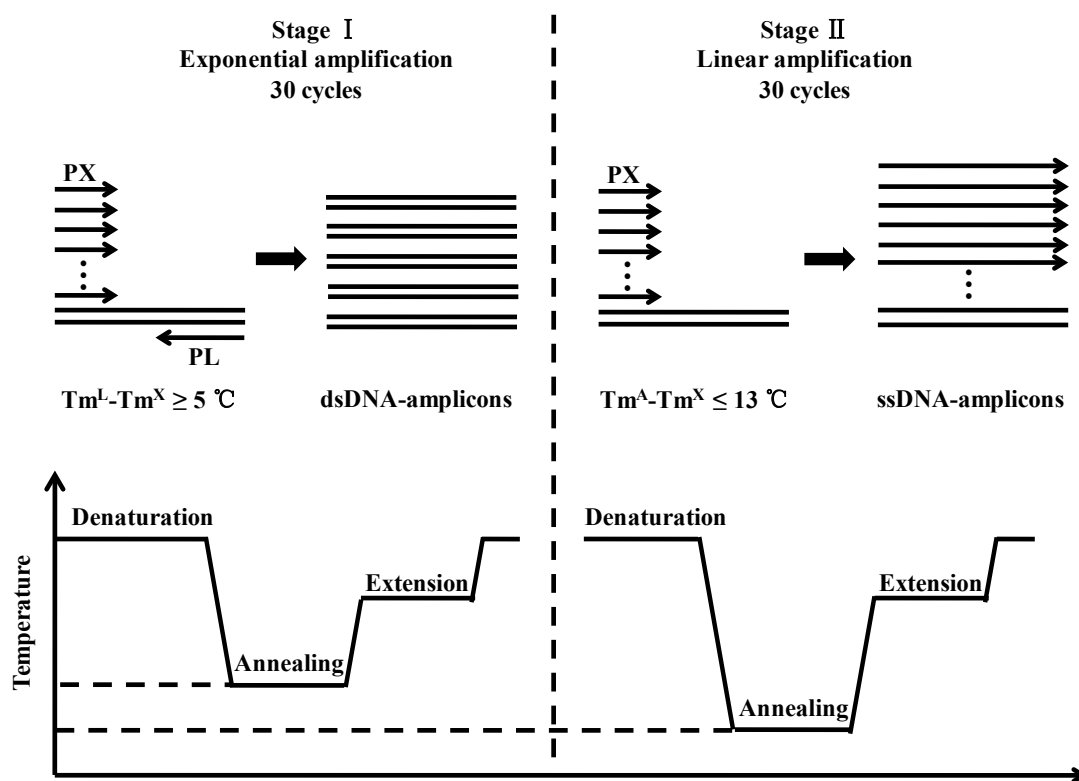
Supplementary Figure Captions

Supplementary Fig. S1. The principle of linear-after-the-exponential (LATE)-PCR.

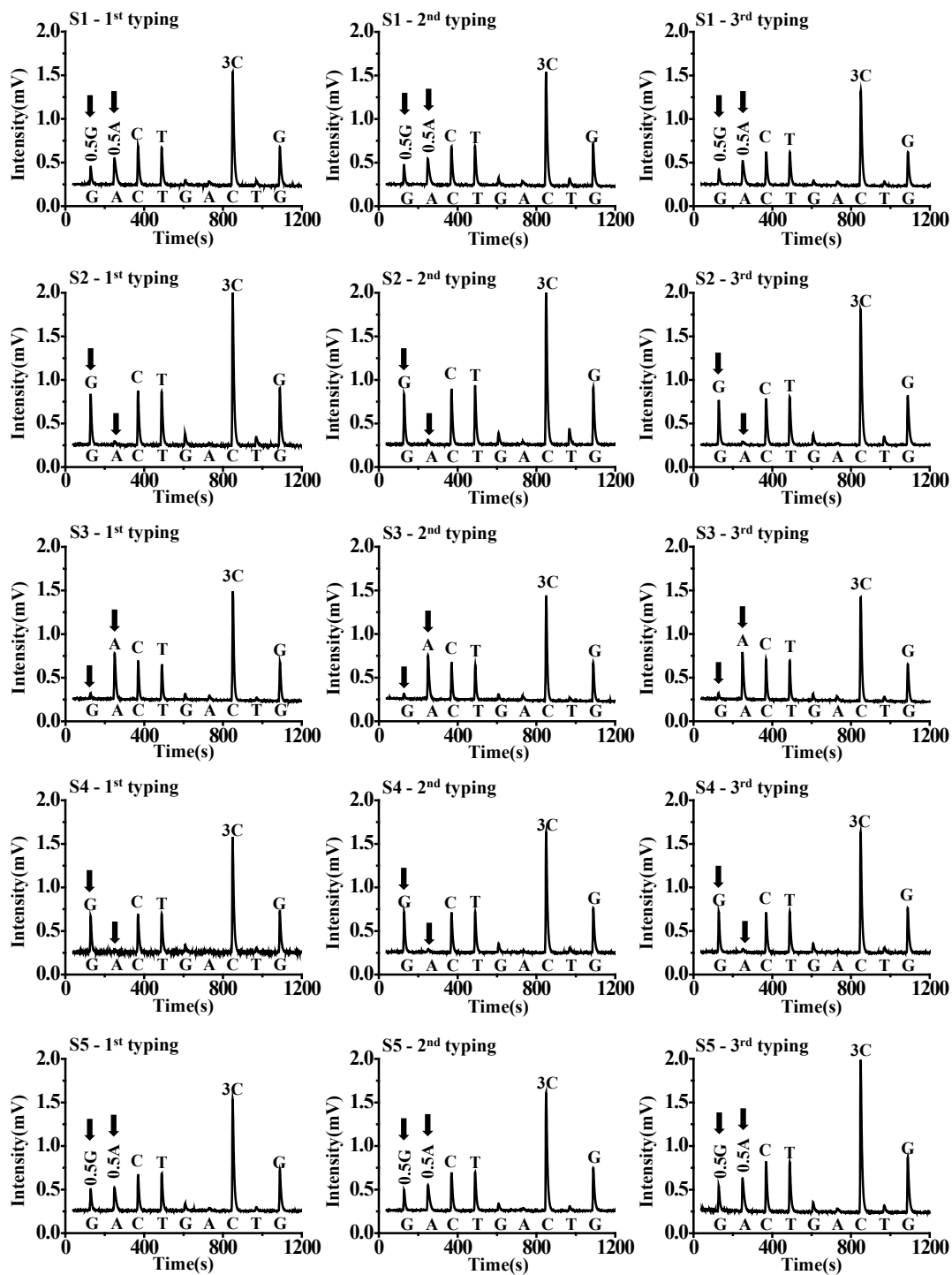
Supplementary Fig. S2. Pyrograms for genotyping MTHFR C677T in a set of five typical samples in triplicate.

Supplementary Fig. S3. The genotyping results of the 3 polymorphisms from the same sample using the whole blood LATE-PCR based pyrosequencing(A), conventional PCR based pyrosequencing(B) and commercial Sanger sequencing(C).

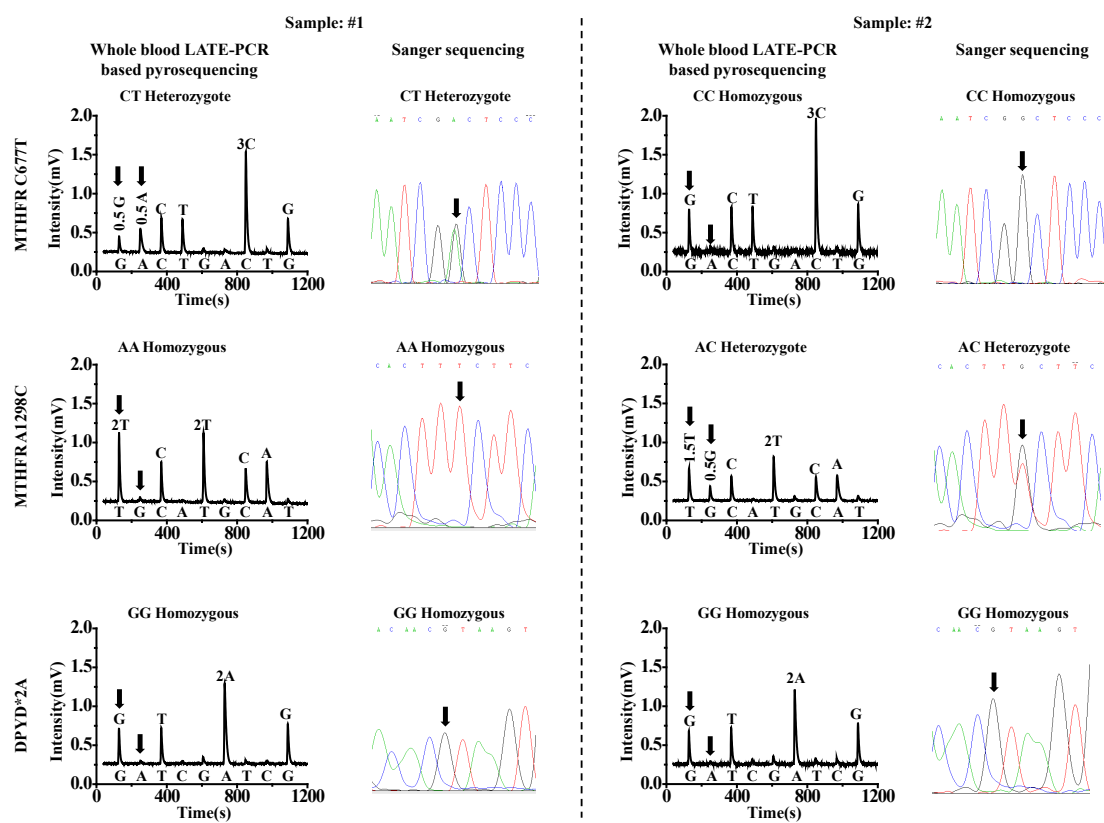
Supplementary Figures



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