

Electronic Supplementary Information

High-throughput ultra-selective discrimination of single nucleotide polymorphism via click chemical ligation

Qian-Yu Zhou,^a Xin-Ying Zhong,^a Ling-Li Zhao,^a Li-Juan Wang,^{ab} Ying-Lin Zhou, *^a and Xin-Xiang Zhang ^a

a. Beijing National Laboratory for Molecular Sciences (BNLMS), MOE Key Laboratory of Bioorganic Chemistry and Molecular Engineering, College of Chemistry and Molecular Engineering, Peking University, Beijing 100871, China.

b. Key Laboratory of Medical Chemistry and Molecular Diagnosis, Ministry of Education, Hebei University, Baoding 071002, Hebei, China

*Corresponding author, E-mail address: zhouyl@pku.edu.cn.

Table S1. The oligonucleotides used in the exploring performance of SNP discrimination experiments (5'-3')

| Name | Sequence |
|--|--|
| P1 | NH ₂ C ₁₂ -AAAAAGAGGTCTCG-CHCH |
| P2 | N ₃ -CGATGTCCAA-Biotin |
| Perfectly matched target (T) | TTGGACATCGCGAGGACCTC |
| Mismatch-1-C (M ₁ =C) target (M1) | TTGGACAT <u>CCC</u> GAGGACCTC |
| Mismatch-2-G (M ₂ =G) target (M2) | TTGGACAT <u>GGC</u> GAGGACCTC |
| Mismatch-3-A (M ₃ =A) target (M3) | TTGGACA <u>ACG</u> CGAGGACCTC |
| Mismatch-4-T (M ₄ =T) target (M4) | TTGGACT <u>T</u> CGCGAGGACCTC |
| Mismatch-5-G (M ₅ =G) target (M5) | TTGGAG <u>A</u> TCGCGAGGACCTC |
| Mismatch-6-T (M ₆ =T) target (M6) | TTGG <u>T</u> CATCGCGAGGACCTC |
| Mismatch-7-G (M ₇ =G) target (M7) | TTGGAC <u>G</u> TCGCGAGGACCTC |
| Mismatch-8-C (M ₈ =C) target (M8) | TTGGAC <u>CT</u> CGCGAGGACCTC |

Note: The underlined bases are mutant bases.

Table S2. Comparison between the proposed CuAAC-LA based SNP detection strategy with other SNP detection approaches reported since 2015.

| Methods | Selectivity | DNA enzyme | reference |
|---|-------------|--|-----------|
| CuAAC-LA based SNP detection | 0.05-0.1% | No | This work |
| Dynamic sandwich assay (DSA) | 0.1–0.5% | No | 1 |
| Using CCP to probe the hybridization equilibrium of short duplex | 0.1% | No | 2 |
| Simulation-guided DNA probe and sink design | 1% | No | 3 |
| Sequestration-assisted molecular beacon | 0.5% | No | 4 |
| Combining cooperativity with sequestration | 0.2% | No | 5 |
| Hairpin masking with FNP counting | 0.05%-0.1% | No | 6 |
| One-step isothermal detection | 1% | Taq DNA ligase | 7 |
| Isothermal ligase reaction combined with a modified cycling probe assay | 1% | E.coli DNA ligase, RNase H | 8 |
| Real-time fluorescence LCR-based detection | 0.1% | Ampligase | 9 |
| Rolling circle amplification (RCA)-responsive G-quadruplex and thioflavin T | 0.13% | Taq DNA ligase, phi29 DNA polymerase | 10 |
| Mismatched ligation triggered cascade strand displacement amplification | 0.2% | Taq DNA ligase, Klenow fragment, Nb.BbvC | 11 |
| A genotyping–microarray by ligating a universal fluorescence-probe with SNP-encoded flaps cleaved from invasive reactions | NA | DNA Ligase, flap endonuclease | 12 |
| Mass spectrometry-based method allele-specific ligation and strand displacement amplification | NA | 9°N™ DNA ligase, Vent (exo-) polymerase, and Nt. BstNBI nicking enzyme | 13 |
| Toehold strand displacement (TSD) and endonuclease IV (Endo IV) | 0.5% | Endonuclease IV | 14 |
| Strand displacement and selective digestion | 0.2% | lambda exonuclease | 15 |
| Nucleic Acid Self-Assembly Circuitry Aided by Exonuclease III | 1% | exonuclease III | 16 |
| Ligase-based analysis with modified base-end downstream ligation fragments | NA | T4 DNA ligase | 17 |

| | | | |
|--|------------|--------------------|----|
| Lambda exonuclease and a chemically modified DNA substrate structure | 0.5% | lambda exonuclease | 18 |
| Abasic site modified fluorescent probe and lambda exonuclease | 0.02-0.05% | lambda exonuclease | 19 |

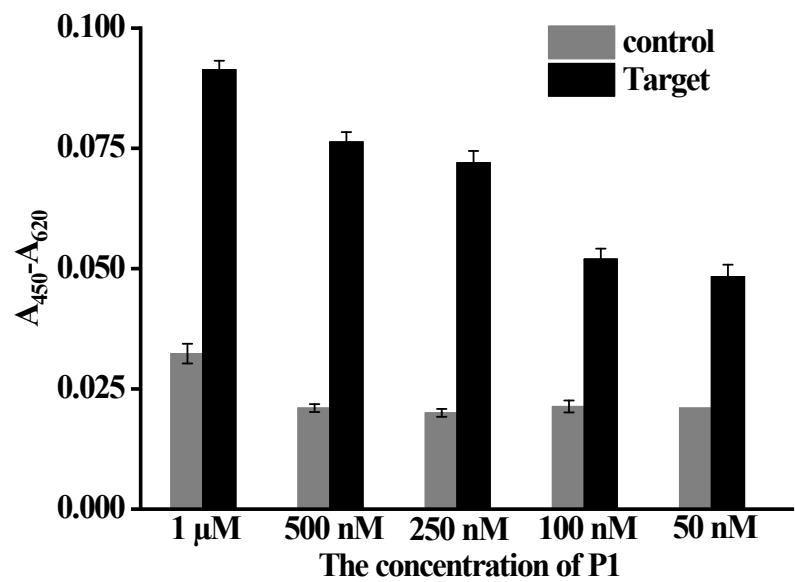


Fig. S1. The effect of the concentration of P1 for DNA detection. Experimental conditions: 50 nM P2 ,1 nM T with different concentration of P1 incubated at 25°C for 2 h.

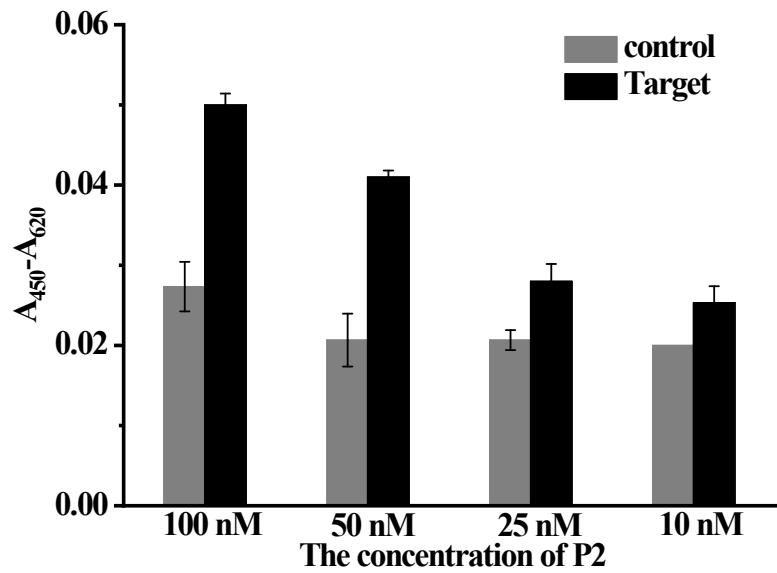


Fig S2. The effect of the concentration of P2 for DNA detection. Experimental conditions: 250 nM P1

,1 nM T with different concentration of P2 incubated at 25°C for 2 h.

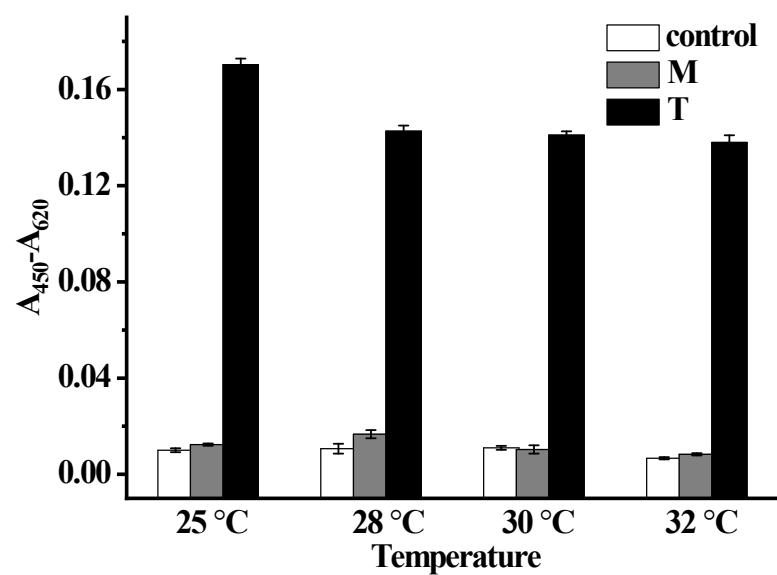


Fig S3. The effect of temperature for SNP detection. Experimental conditions: 250 nM P1, 50 nM P2 with 10 nM T or M incubated at different temperature for 2 h.

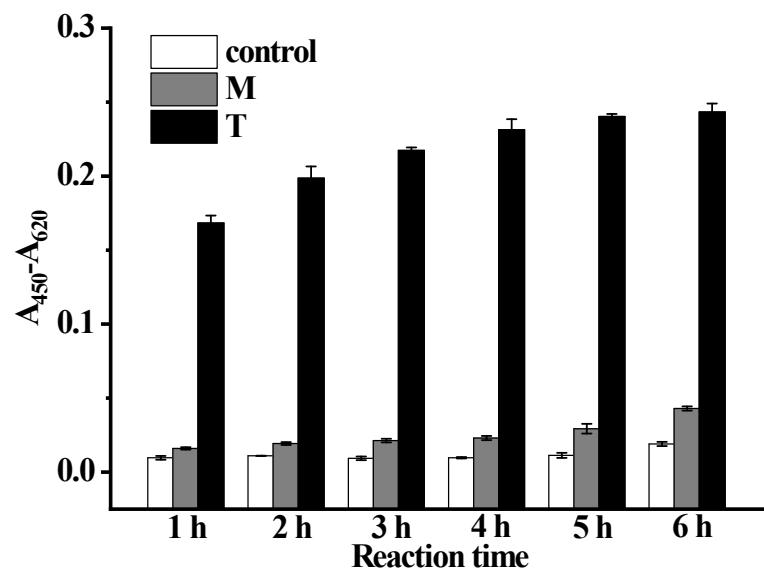


Fig S4. The effect of reaction time for DNA detection. Experimental conditions: 250 nM P1, 50 nM P2 with 10 nM T or M incubated at 25°C for different reaction time.

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