

Table S1 Nucleotide sequence

Name	Sequence (5'-3')
Padlock	p-GGG CCC TTG TAT AGC CCC CCC GGG CCC TAG TTC CTC CAG GCC CAA CTA TAC CTG GAG GAA
miRNA-326	CCU CUG GGC CCU UCC UCC AG
Complementary	CCC TAG TTC CTC CAG GCC CAA
Complementary (with fluorescence)	FAM- CCC TAG TTC CTC CAG GCC CAA-BHQ
sgRNA	CCU CUG GGC CCU UCC UCC AGU GUA GAU CAU CUU CCU CGA U
Trigger	TTC CTC CAG GTA TAG ATA TTA AAT
H2 probe	FAM-GTT GGG CCT CTG GGC CCT TAT AAT CTA CAG AGG CCC-BHQ
Mismatch 1	CCU CUG <u>AGC</u> CCU UCC UCC AG
Mismatch 2	CCU CUG <u>ATC</u> CCU UCC UCC AG
Mismatch 3	CCU CUG <u>ATG</u> CCU UCC UCC AG

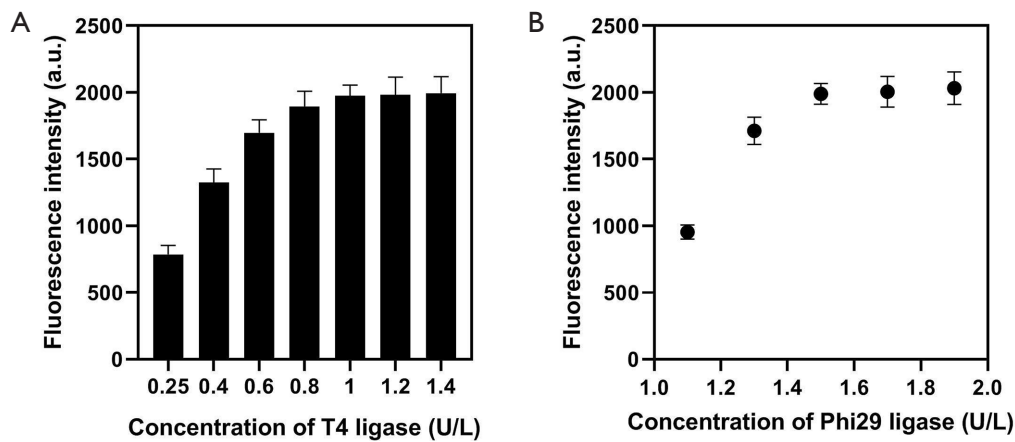


Figure S1 Optimization of enzyme concentration. (A) Fluorescence signal expression of the CRISPR/Cas9 system after adding different concentrations of T4 ligase; (B) fluorescence signal expression of the CRISPR/Cas9 system after adding different concentrations of phi29 polymerase. a.u., absorbance unit; CRISPR, clustered regularly interspaced short palindromic repeats; Cas9, CRISPR-associated nucleases 9.