

Supplementary Information

**A multiplex and fast detection platform for
microRNA based on self-priming microfluidic
chip and duplex specific nuclease**

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The specificity of the assay between single-base and double-bases mismatch

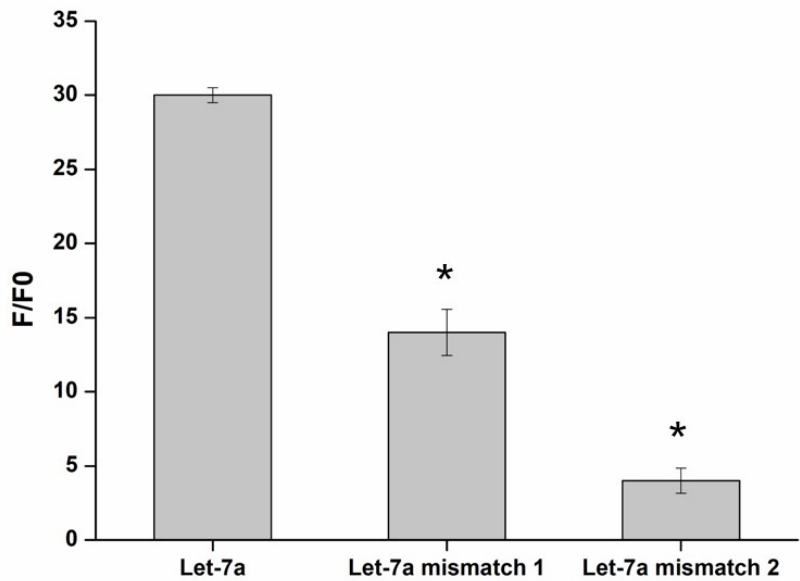


Figure S1 Discrimination power between perfectly matched and mismatched targets.

The probe used in three experiments was Probe Let-7a, and the concentration was 100 nM. The concentration of each template was 10 nM. The error bars are the standard deviations for three replicates. *p < 0.05 vs. Let-7a

Table S1 Sequences of perfectly matched and mismatched templates

Name	Sequence 5` - 3`
Let-7a	UGAGGUAGUAGGUUGUAUAGUU
Let-7a mismatch 1	UGAGGU ^C GUAGGUUGUAUAGUU
Let-7a mismatch 2	UGAGGU ^C GUAGGU ^G GUAUAGUU
Probe Let-7a	FAM-AACTATACAACCTACTACCTCA-BHQ

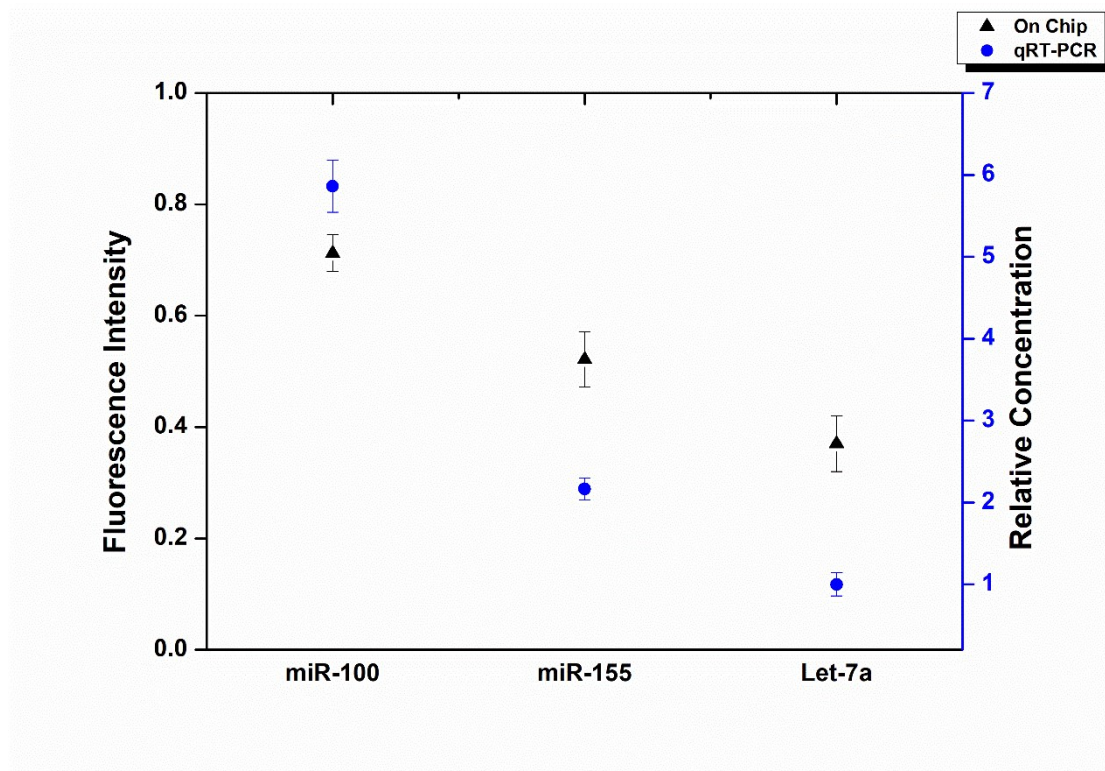


Figure S2 Quantification of different microRNA in MDA-MB-468 using different methods.

The figure showed the concentrations of three kinds of microRNA in MDA-MB-468 tested by our chip (Black triangle ▲) and qRT-PCR(Blue circle ●). The fluorescence intensity was obtained by imaging. The relative concentration was converted from ΔC_t . The error bars are the standard deviations for three replicates.

Table S2 Primers designed for qRT-PCR

miR-100 stem-loop RT primer	CCTGTTGTCTCCAGCCACAAAAGAGCACAATATTTTCAGGA GACAACAGGCACAAGT
miR-100 forward primer	CGGGCAACCCGTAGATCCGA
miR-100 reverse primer	CAGCCACAAAAGAGCACAAT
miR-155 stem-loop RT primer	CCTGTTGTCTCCAGCCACAAAAGAGCACAATATTTTCAGGA GACAACAGGCCCTAT
miR-155 forward primer	CGGGCTTAATGCTAATCGTG
miR-155 reverse primer	CAGCCACAAAAGAGCACAAT
Let-7a stem-loop RT primer	CCTGTTGTCTCCAGCCACAAAAGAGCACAATATTTTCAGGA GACAACAGGAACTATA
Let-7a forward primer	CGGGCTGAGGTAGTAGGTTG
Let-7a reverse primer	CAGCCACAAAAGAGCACAAT