Supporting Information

CRISPR/Cas13a-assisted amplification-free miRNA biosensor via dark-field imaging and magnetic gold nanoparticles

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SUPPLEMENTARY FIGURES



Figure S1. Dynamic Light Scattering (DLS) measurement results for mixture of magnetic beads (MBs) and gold nanoparticles (AuNPs) without (A) or with (B) a linker.



Figure S2. Dark-field (DF) images of gold nanoparticles (AuNPs) of different sizes (50 nm, 60 nm, and 80 nm) captured using a portable DF imaging system. Scale bar, 100 μm.







Figure S4. Calculation of the limit of the detection. A. Signal values for different concentrations of miR-21-5p and negative control (mock) to determine the limit of detection (LOD) threshold by the mean + 3 times the standard deviation. Based on the threshold value (510.9), we determined the LOD as 0.5 fmole (25 pM). **B.** Bar graph showing the signal values from different miR-21-5p concentrations and the LOD threshold value.

Name	Sequence (5' to 3') ^{abc}
miR-21-5p-F	TAGCTTATCAGACTGATGTTGA
U6 snRNA-F	CAAATTCGTGAAGCGTTC CA
universal-R	AGGCAGTGGTATCAACGCAGA
miR-RT-adaptor	AGGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT
T7-univeral upper	TAATACGACTCACTATAG
T7-bottom miR-21-5p	TAGCTTATCAGACTGATGTTGAGTTTTAGTCCCCTTCATTTTTGGGGTGGTCTAAATCTATAGTGAGTCGTATTA
miR-21-5p (WT)	phospho-uagcuuaucagacugauguuga
miR-21-5p (SM)	phospho-uagcuuaucggacugauguuga
miR-21-5p (DM)	phospho-uugcuuaucggacugauguuga
miR-9-5p	phospho-ucuuugguuaucuagcuguauga
miR-421	phospho-aucaacagacauuaauugggcgc
DRD probe	FAM-TAuuGC-Quencher
Linker only	biotin-GATGGGCAGACAGGGTTAAGTTTTTTTuuTAGGACTCGTGCAGCTAAGG-thiol
MB linker	biotin-TTTTTTTGATGGGCAGACAGGGTTAAG
AuNP linker	TAGGACTCGTGCAGCTAAGGTTTTTTTT-thiol
Bridge without poly-T	CCTTAGCTGCACGAGTCCTATuuCCTTAACCCTGTCTGCCCATC
Bridge with poly-T	CCTTAGCTGCACGAGTCCTATTTTTTTTTUUTTTTTTTCCTTAACCCTGTCTGCCCATC
Capture probe	CCTTAGCTGCACGAGTCCTATTTTTTTTTTTTTT-biotin

Supplemental Table S1. Sequences of oligomers used in this study.

 a V = A, C, or G; N = A, C, G, or T

^b Lower case letters denote RNA.

° Underline letters indicate mismatch.