

Supporting information

Comparison of chemiluminescent heterogeneous and homogeneous-heterogeneous assays coupled with isothermal circular strand-displacement polymerization reaction amplification for the quantification of miRNA-141

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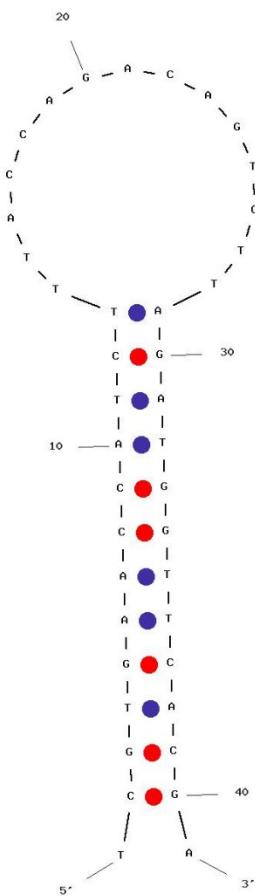
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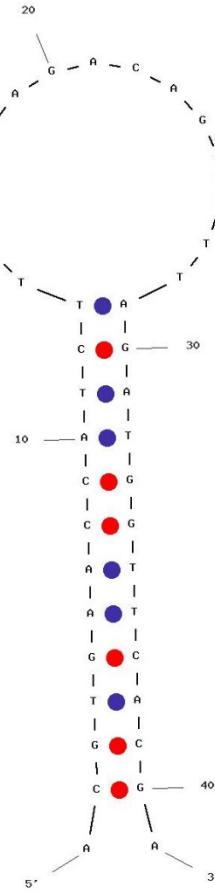
Table S1. Chemical structures of oligonucleotides used in this work

oligonucleotides	5'→3' sequence
miRNA-141	UAA CAC UGU CUG GUA AAG AUG G
fluorescein-labeled hairpin 1 (Flu-HP1)	FAM- TCG TGA ACC ATC TTT ACC AGA CAG TGT TAG ATG GTT CAC GA
fluorescein-labeled hairpin 2 (Flu-HP2)	FAM- ACG TGA ACC ATC TTT ACC AGA CAG TGT TAG ATG GTT CAC GA
fluorescein-labeled hairpin 3 (Flu-HP3)	FAM- AGG TGA ACC ATC TTT ACC AGA CAG TGT TAG ATG GTT CAC GA
biotinylated primer	Biotin – TCG TGA AC
biotinylated DNA analogue of miRNA-141	TAA CAC TGT CTG GTA AAG ATG G - Biotin
miRNA-39	UCA CCG GGU GUA AAU CAG CUU G
miRNA-429	UAA UAC UGU CUG GUA AAA CCG U
miRNA-200a	UAA CAC UGU CUG GUA ACG AUG U
miRNA-200b	UAA UAC UGC CUG GUA AUG AUG A
miRNA-200c	UAA UAC UGC CGG GUA AUG AUG GA

Flu-HP1



Flu-HP2



Flu-HP3

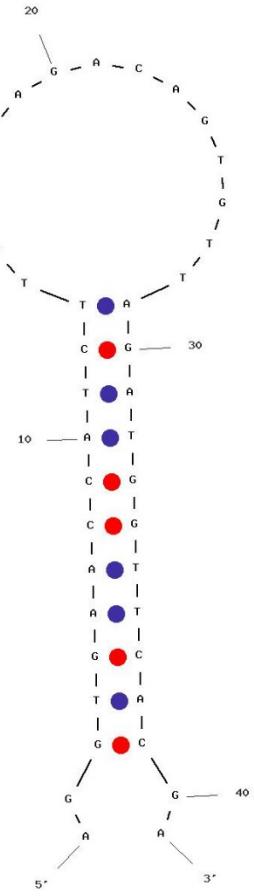


Figure S1. Secondary structures of Flu-labeled capture hairpin probes. Modeling of the hairpin structure was carried out using OligoAnalyzer 3.1 software.

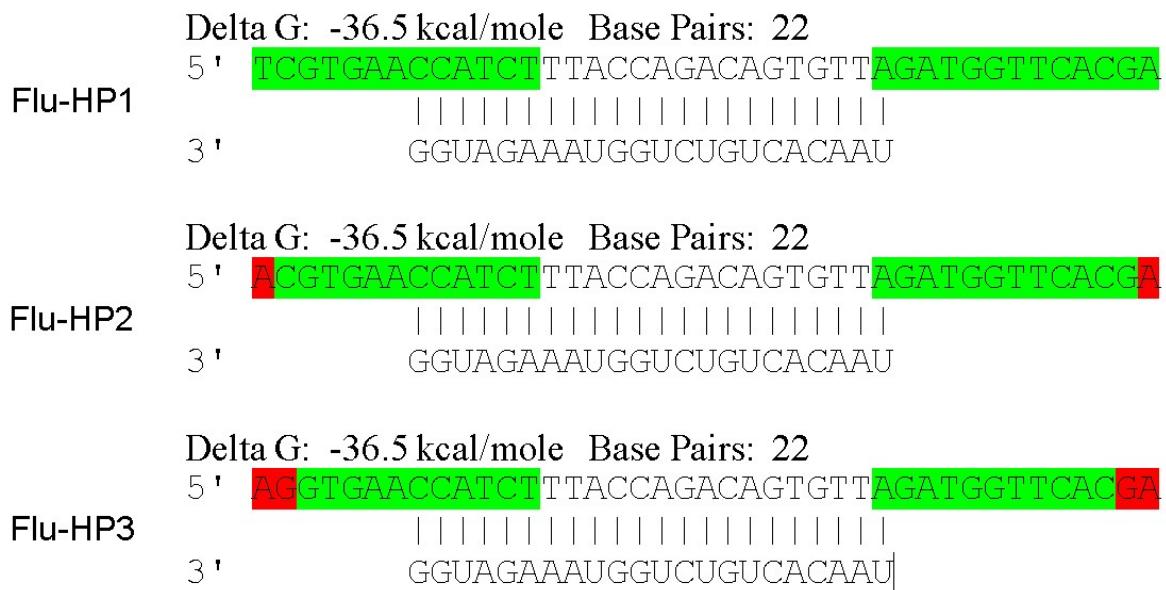


Figure S2. Interactions of Flu-labeled capture hairpin-probes with the target miRNA-141. Modeling of the hairpin structure was carried out using Oligo Analyzer 3.1 software.