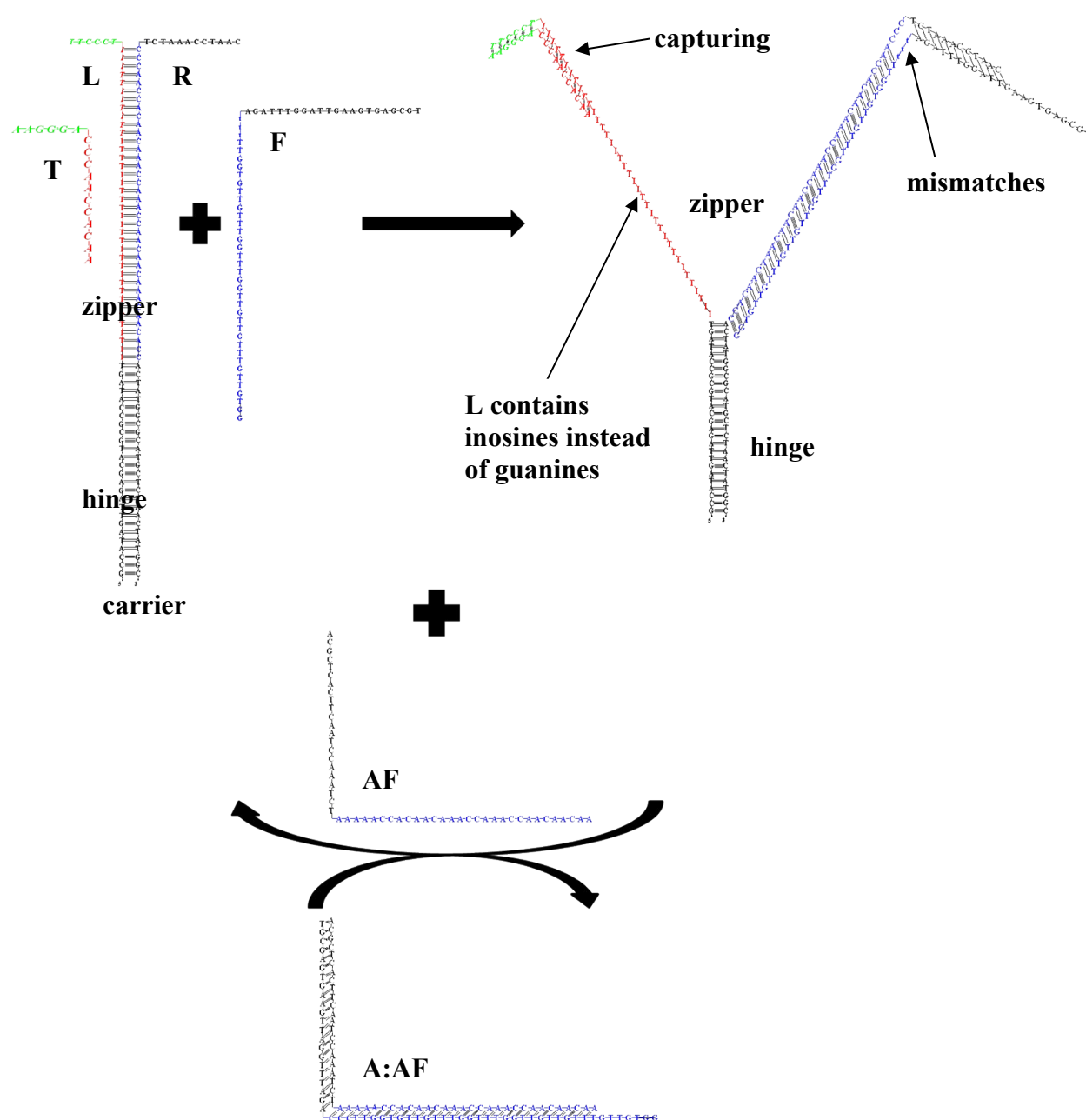
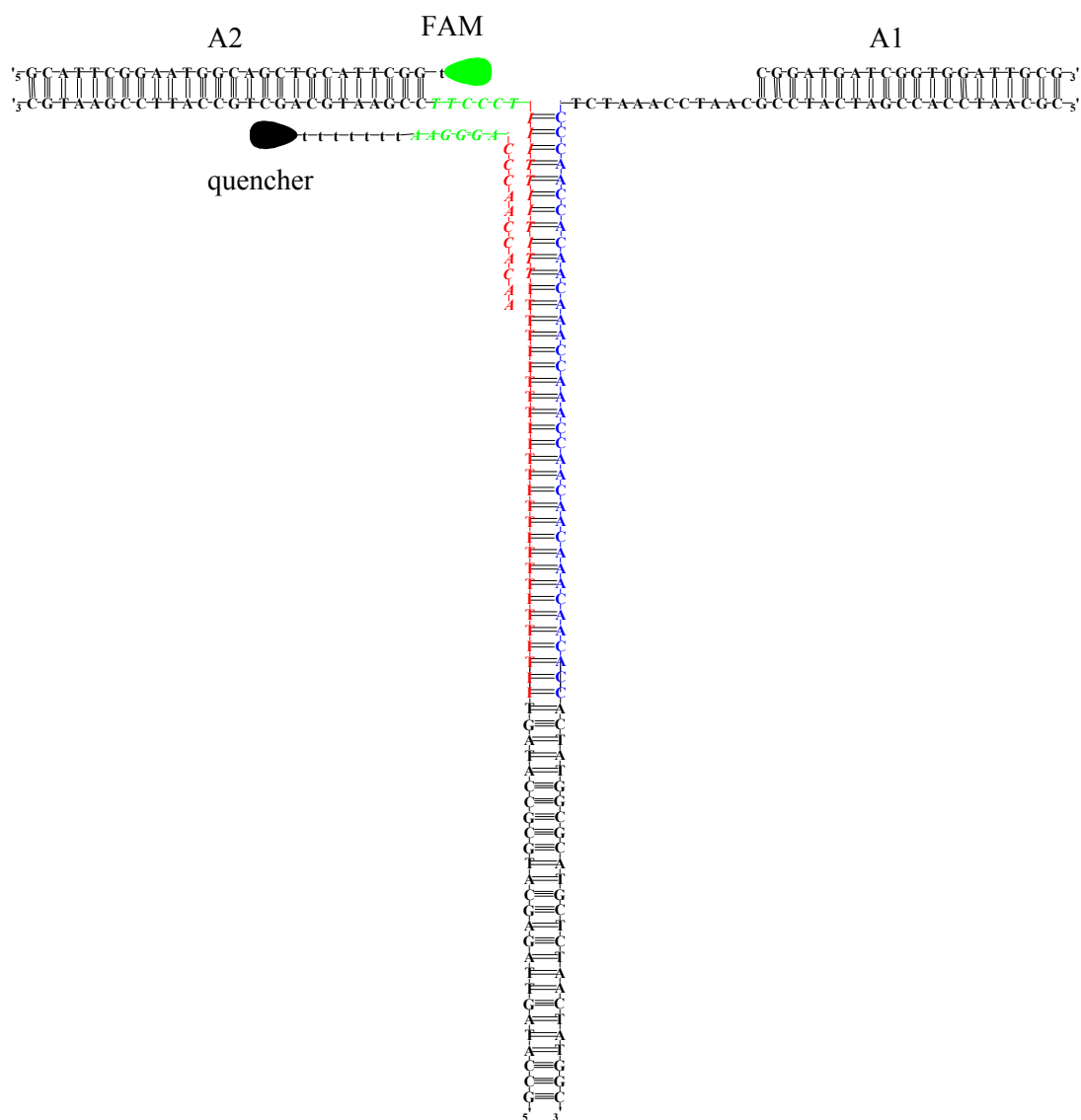


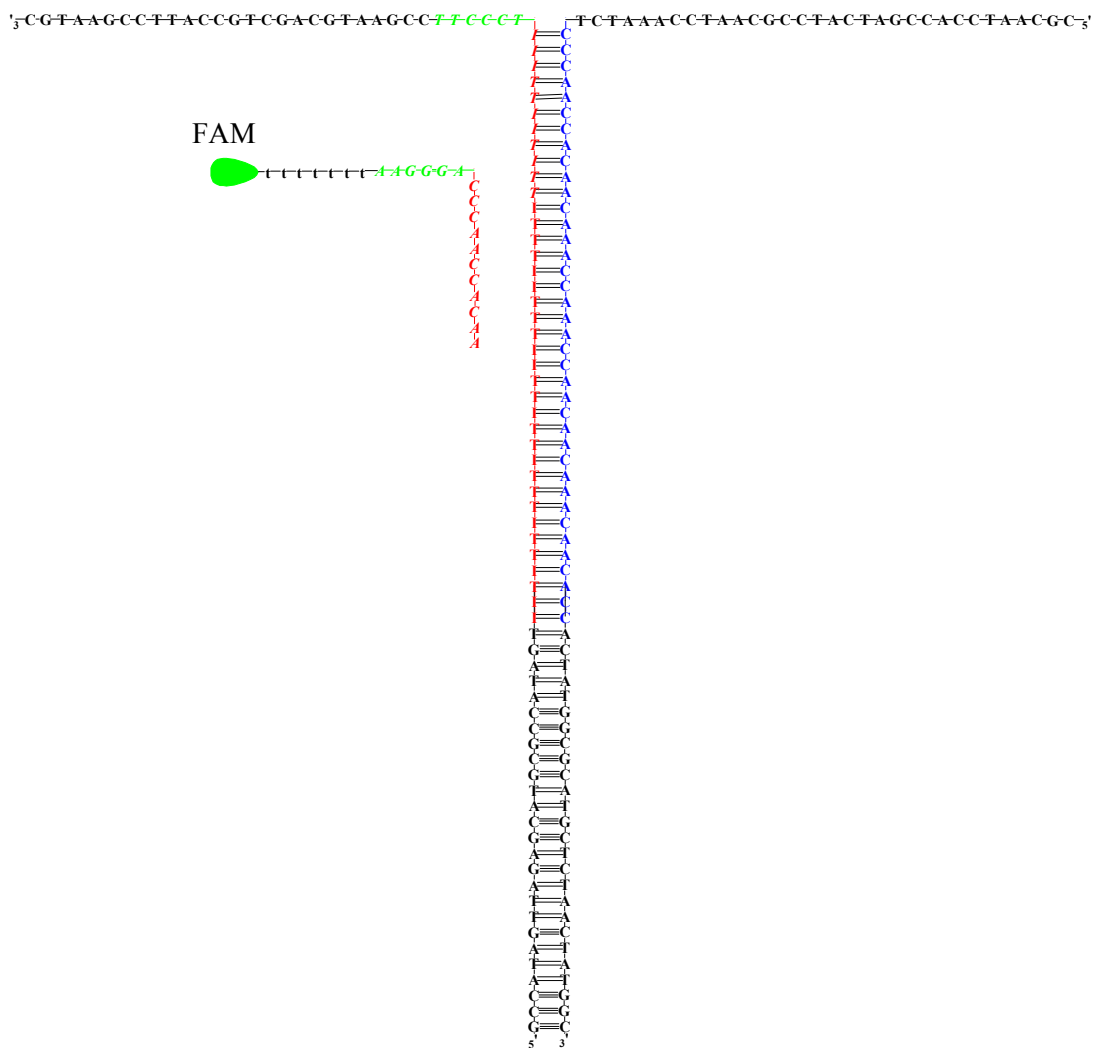
## Supporting Information



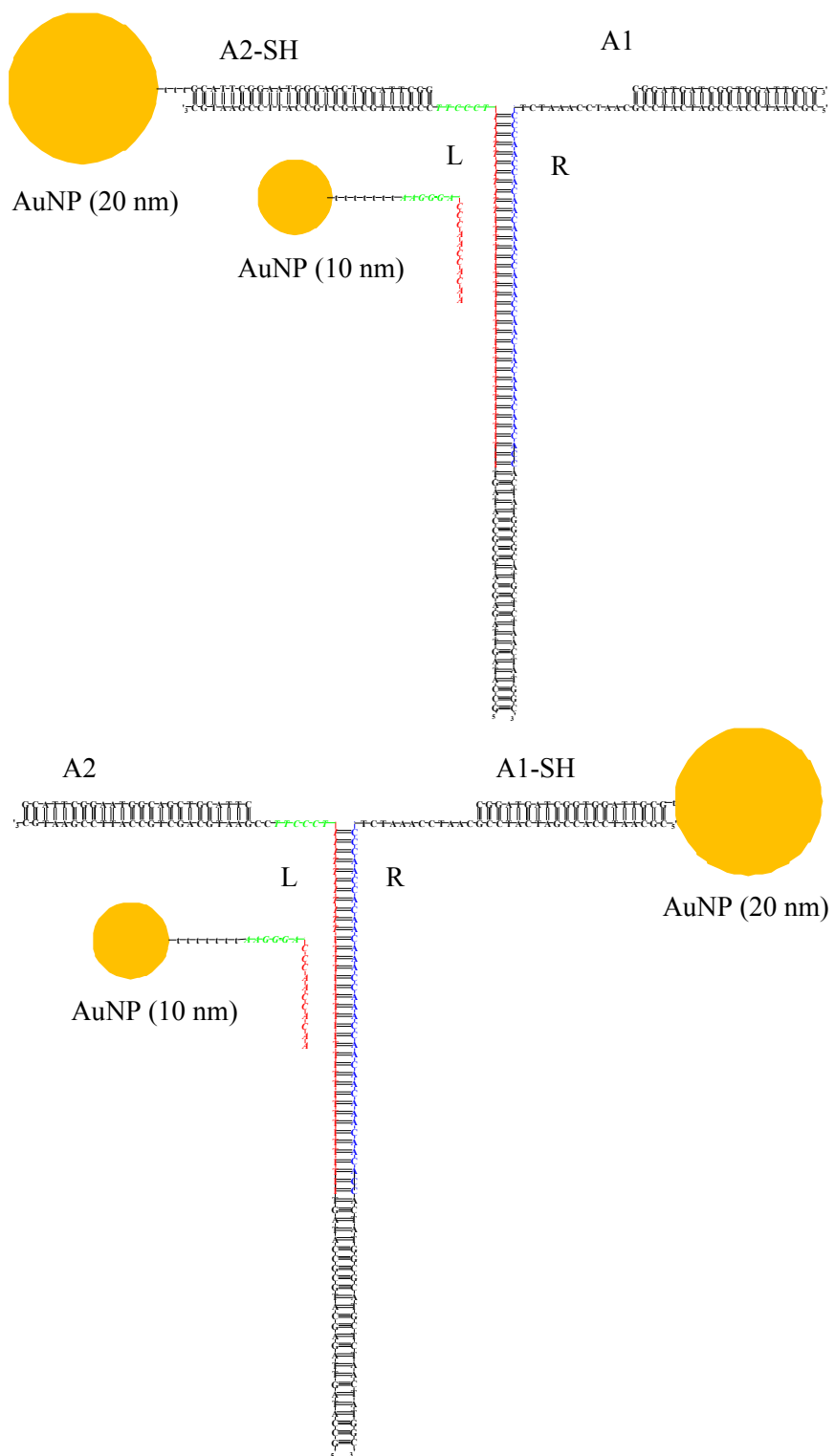
**Figure S1.** Specific sequences and schematic of the DNA strands used in the capture and release device.



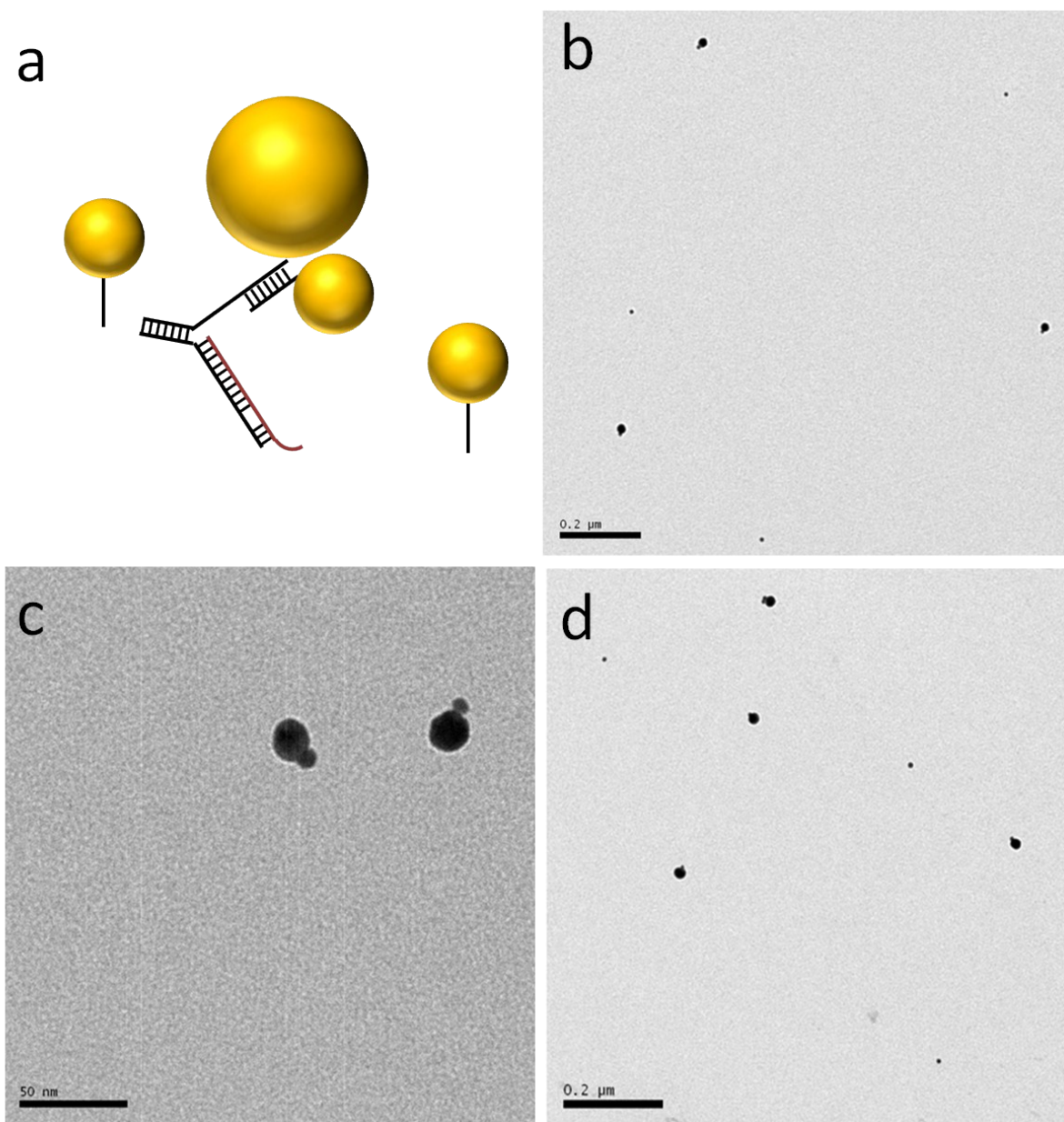
**Figure S2.** Schematic of the DNA strands used for the fluorescence experiments.



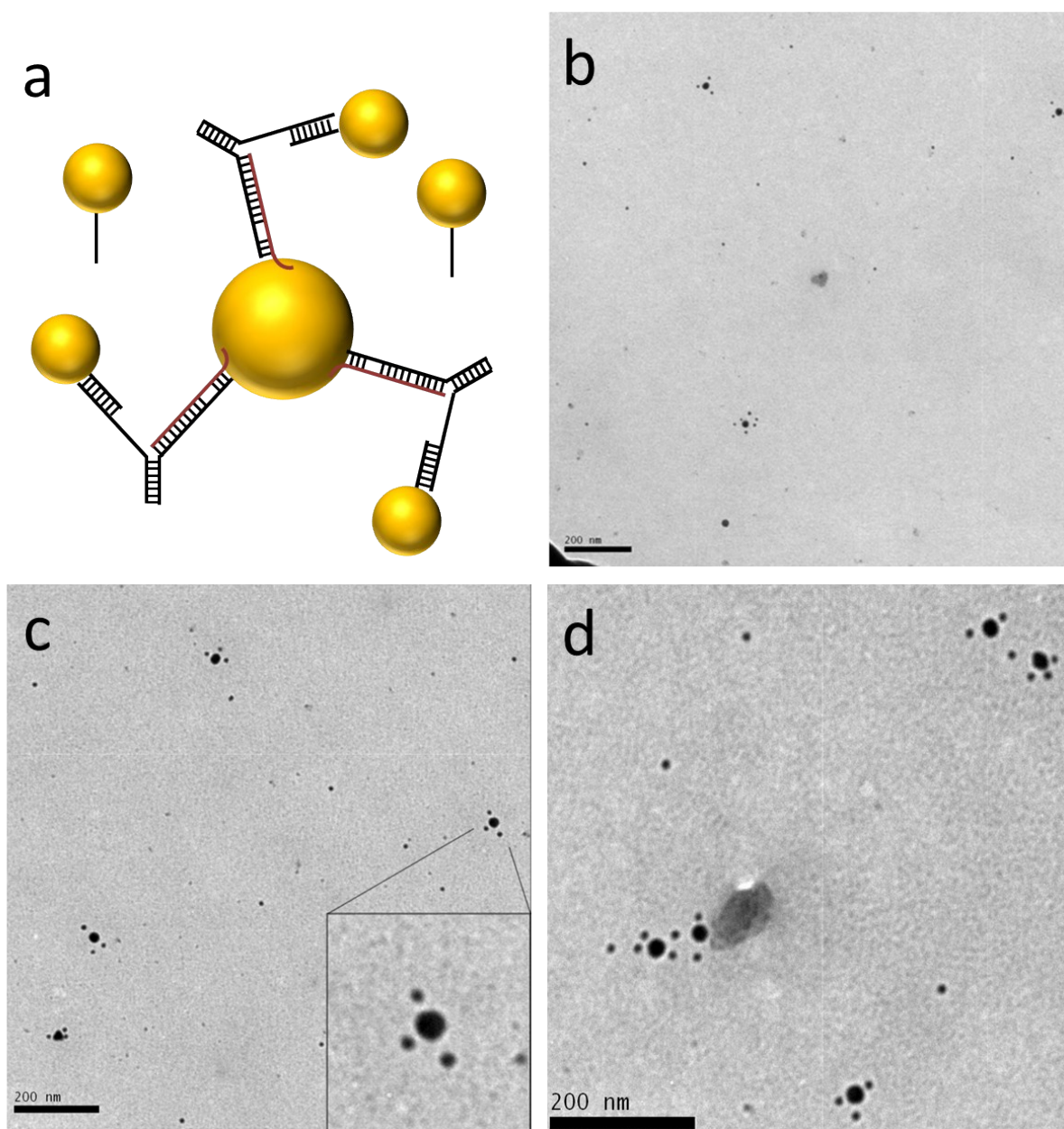
**Figure S3.** Schematic of the DNA strands used for the gel electrophoresis experiments.



**Figure S4.** Schematic of the DNA attachment to the AuNP used in the TEM experiments.



**Figure S5.** Additional TEM images of AuNP functionalized devices. The ratio of carrier and AuNPs are 1:1. (a) shows the model of assembly conformation. The blue line represents fuel strands.



**Figure S6.** Additional TEM images of AuNP functionalized devices. The ratio of carrier and AuNPs are 3:1. (a) shows the model of assembly conformation. The blue line represents fuel strands.

**Table S1.** Gibbs energy

R - F		R - L
Number of Mismatches	Gibbs Energy (kcal/mol)	
3	-38.18	<b>-21.00</b>
6	-27.46	
7	<b>-23.49</b>	
8	<b>-19.02</b>	
9	-16.81	
12	-6.24	

If the toehold on the fuel strand was long enough to assume that it was always hybridized to the device, then when the energy favoring the device to open and close are the same only 50 % of the device should be open. Our device displays 50 % efficiency when 6 mismatches in the fuel strand, however, thermodynamic calculation using the nearest neighbor model indicate this occurs when there are 7-8 mismatches.<sup>1</sup>

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<sup>1</sup> <http://biophysics.idtdna.com/>

**Table S2.** Sequences for the DNA devices

L	5'- GCC ATA GTT AGA GCA TGC GCC ATA GTI ITI TTI TTT ITT ITT IIT TTI ITT TIT TIT IIT TII ITC CCT TCC GAA TGC AGC TGC CAT TCC GAA TGC -3'
R	5'- CGC AAT CCA CCG ATC ATC CGC AAT CCA AAT CTC CCA ACC ACA ACA AAC CAA ACC AAC AAC AAA CAA CAC CAC TAT GGC GCA TGC TCT AAC TAT GGC -3'
F	5'- GGT GTT GTT TGT TGT TGG TTT GGT TTG TTG TGG TTT TTA GAT TTG GAT TGA AGT GAG CGT -3'
F- no mismatch	5'- GGT GTT GTT TGT TGT TGG TTT GGT TTG TTG TGG TTG GGA GAT TTG GAT TGA AGT GAG CGT -3'
F- 1 mismatch	5'- GGT GTT GTT TGT TGT TGG TTT GGT TTG TTG TGG TTG CGA GAT TTG GAT TGA AGT GAG CGT -3'
F- 6 mismatches	5'- GGT GTT GTT TGT TGT TGG TTT GGT TTG TT ATA ATT AAA A GA TTT G GAT TGA AGT GAG CGT -3'
F- 12 mismatches	5'- GGT GTT GTT TGT TAT TAA TTT AAT TTA TT ATA ATT AAA A GA TTT G GAT TGA AGT GAG CGT -3'
AF	5'- ACG CTC ACT TCA ATC CAA ATC TAA AAA CCA CAA CAA ACC AAA CCA ACA ACA A -3'
T	5'- AAG GGA CCC AAC CAC AA -3'
T-SH	5'- /5ThioMC6-D/TTT TTT TAA GGG ACC CAA CCA CAA -3'
T-FQ	5'- /FAM Q/TTT TTT TAA GGG ACC CAA CCA CAA -3'
T-FAM	5'- /FAM/TTT TTT TAA GGG ACC CAA CCA CAA -3'
A1	5'- CGG ATG ATC GGT GGA TTG CG -3'
A2	5'- GCA TTC GGA ATG GCA GCT GCA TTC -3'
A2-FAM	5'- GCA TTC GGA ATG GCA GCT GCA TTC GGT /FAM/ -3'
A1-SH	5'- CGG ATG ATC GGT GGA TTG CG TTT /3ThioMC3-D/ -3'
A2-SH	5'- /5ThioMC6-D/TGC ATT CGG AAT GGC AGC TGC ATT C -3'