Supporting Information

Controllable DNA nanodevices regulated by logic gates for multi-stimulus recognition

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S1: DNA sequences

The length and sequence(strand A,B,M,F,Q) in the sensing module of the nanodevices were adopted from reference ^{1,2}. The length and sequence of other strands were designed and analyzed by NUPACK³ to decrease the unexpected secondary structure and minimize crosstalk between strands.

Name	Sequence $(5' \rightarrow 3')$	Length (nt)
A	FAM-TCATGTTTGTTTGTTGGCCCCCCTTCTTTCTTA	33
В	ACAAACATGA-BHQ	10
L6	GTGAGATAAGAAAGAAGGGGGGGCCAACAA	29
L7	CGCGCAATAAGAAAGAAGGGGGGGGCCAACAA	30
L8	TAAGTGCATAAGAAAGAAGGGGGGGGCCAACAA	31
L9	CCAGCACAATAAGAAAGAAGGGGGGGCCAACAA	32
К	TTGTTGGCCCCCCTTCTTTCTTATGCACTTA	31
G1	TAAGAAAGAAGGGGGGGCCAACAAGTCCGG	29
I1	CCGGACTTGTTGGCCCCCCTTCTTTCTTA	29
G2	CGCCCATAAGTGCATAAGGGGGGGCCAACAAGTCCGG	36
I2	TTGTTGGCCCCCCTTATGCACTTATGGGCG	30
I3	CCGGACTTGTTGGCCCCCCTTATGCACTTA	30
G3	TAAGTGCATAAGGGGGGGCCAACAAGCGCGTGCCGATATCG	40
Т	AGTCAGATTACGATATCGGCACGCGC	26
I4	GCGCGTGCCGATATCGTAATCTGACT	26
15	ACGCGCTTGTTGGCCCCCCTTATGCACTTA	30
М	CCTGCCACGCTCCGCTCACTGACCTGGGGGGAGTATTGCGGAGGAA GGT	48

Table S1. Sequences of the Oligonucleotides (5' to 3')

F	FAM-GCGGAGCGTGGCAGG	15
Q	CCCAGGTCAGTG-BHQ	12
Ll	CCATCTACCTTCCTCCGCAATACTCC	26
K1	GGAGTATTGCGGAGGAAGGTAGATGG	26

S2: Optimization for repressing the sensor



Figure S1. PAGE gel analysis of different lengths and concentrations of strand 'L'. Lane 1 and lane 10: (A/B); Lane 2-5: the sensor (A/B) with addition of different concentrations of 'L8' (31nt) as 1 μ M, 2 μ M, 3 μ M and 4 μ M; Lane 6-9: the sensor (A/B) with addition of different concentrations of 'L9' (32nt) as 1 μ M, 2 μ M, 3 μ M and 4 μ M; Lane 11-13: the sensor (A/B) with addition of different concentrations of 'L6' (29nt) as 2 μ M, 3 μ M and 4 μ M; Lane 14-16: the sensor (A/B) with addition of different concentrations of 'L7' (30nt) as 2 μ M, 3 μ M and 4 μ M. [A]=1 μ M and [B] =4 μ M.

To obtain better performance, the control experiments of PAGE analysis were carried out to choose the appropriate length and concentration of lock strand 'L' (Figure S1). A series of different lengths of strand 'L' and different concentrations of each length were introduced to suppress the sensor as 29-nt to 32-nt (Lanes 11-13, 14 -16, 2-5, 6-9). It is noted that although some unexpected secondary structure was produced, the remained complex (A/B) was the least when the length of 'L' was 31-nt and the corresponding concentration was 4 times higher than the sensor in lane 5. Therefore 31-nt strand 'L8' was chosen as the lock strand to avoid unexpected background signals.

S3: Upstream 'AND' logic gate for actuation of the Hg²⁺ sensor

Figure S2. PGAE analysis of the components of 'AND' logic gate and operation upon addition of inputs. Lane 1: T, Lane 2: K, Lane 3: I4, Lane 4: I5, Lane 5: 20-bp DNA ladder, Lane 6: (G3/T), Lane 7: (G3/K), Lane 8: (T/I4), Lane 9: (I5/G3), Lane 10: (T/G3/K), Lane 11: (T/G3/K)+I4, Lane 12: (T/G3/K)+I5, Lane 13: (T/G3/K) +I4+I5.

As shown in Figure S2, gel results confirmed that only both inputs 'I4' and 'I5' were present strand 'K' could be released. Specifically, in lane 11, the band of the complex (T/G3/K) disappeared and yielded the waste (T/I4) and (G3/K) upon addition of 'I4'; in lane 12, the band of the complex (T/G3/K) did not disappear. However, in lane 13, when both 'I4' and 'I5' were added, the band of the complex (T/G3/K) disappeared and yielded the waste (T/I4) and (I5/G3). It is noted that the DNA complex used in this gate had some unexpected secondary structure, but this did not influence the downstream experiment.



Figure S3. PGAE analysis of the mixture of (T/G3/K) and (A/B/L) upon addition of inputs. Lane 1: 20bp ladder, Lane 2: (T/G3/K), Lane 3: (A/B/L), Lane 4: (T/G3/K)+ (A/B/L), Lane 5: (T/G3/K)+ (A/B/L)+I4, Lane 6: (T/G3/K)+ (A/B/L)+I5, Lane 7: (T/G3/K)+ (A/B/L)+I4+I5.

Further gel analysis shown in Figure S3 confirmed that both inputs 'I4' and 'I5' could activate the sensor. In lane 6, the band of gate complex (T/G3/K) and the locked sensor (A/B/L) disappeared and yielded the waste upon the addition of both inputs.

S4: NUPACK and Visual DSD simulation results

The state change of the nanodevice in this work utilized the strand displacement reaction between the lock strand and key strand. The sequence of each strand was specially designed according to the hybridization and displacement reaction. Thus, the sequence of a randomly designed oligonucleotide didn't satisfy the above requirement and couldn't react with the strands in the nanodevice. Take the reaction between the complex A/B/L and the key strand as an example, a random oligonucleotide 5'-AACTTCCATCCACCACCACCAACTTAACCA-3' was designed by NUPACK³. From the NUPACK simulation result in Figure S4, when the above randomly designed oligonucleotide mixed with strand A, B, L, K, it hardly affected the reaction product.

В			
		0.3 µM	
L-K			
	0.1 μM		
Random			
	0.1 μM		
A-B			
	0.098 µM		
A			
0.0013 µM			

Figure S4. (a) NUPACK simulation results of the reaction of strand A, B, L, and K. [A] = 0.1μ M, [B] = 0.4μ M, [L] = 0.1μ M, [K] = 0.1μ M.

The results could also be confirm by Visual DSD⁴. As can be seen in Figure S5, when the complex ABL(A/B/L) was mixed with the key strand K, they reacted and the complex ABL (red curve) was exhausted quickly. Howerver, in Figure S6, when the complex ABL(A/B/L) was mixed with the random strand, they didn't react and the complex ABL (red curve) was remained unchanged.



Figure S5. Visual DSD simulation results of the reaction between the complex ABL and the key strand K.



Figure S6. Visual DSD simulation results of the reaction between the complex ABL and the random strand.

References

- 1. Z. Wang, J. H. Lee and Y. Lu, *Chem. Commun.*, 2008, 6005-6007.
- 2. R. Nutiu and Y. Li, J. Am. Chem. Soc., 2003, 125, 4771.
- 3. J. N. Zadeh, C. D. Steenberg, J. S. Bois, B. R. Wolfe, M. B. Pierce, A. R. Khan, R. M. Dirks and N. A. Pierce, *J. Comput. Chem.*, 2011, **32**, 170-173.
- 4. M. R. Lakin, S. Youssef, F. Polo, S. Emmott and A. Phillips, *Bioinformatics*, 2011, **27**, 3211-3213.