Electronic Supplementary Information

Nicking Endonuclease-assisted signal amplification of split molecular aptamer beacon for biomolecules detection using graphene oxide as sensing platform

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Table S1. List of the oligonucleotides used

Oligonucleotide	Sequences (from 5' to 3')
Apt 0	5'- DABCYL-GCA GCT ATG TGG GGG TGG ACG T↓***CC A***GC TGC-FAM-3'
Apt 1	5'-GCA GCT ATG TGG GGG TGG ACG T↓***CC A***GC TGC-FAM-3'
Apt 2	5'-TGG ATA CGG CCG GGT AGA TA-3'
Apt 3	5'-CGA CGA CCT GGG GGA GTA T↓***CC G***CG TCG-FAM -3'
Apt 4	5'-CGG AGC GGA GGA AGG T-3'.

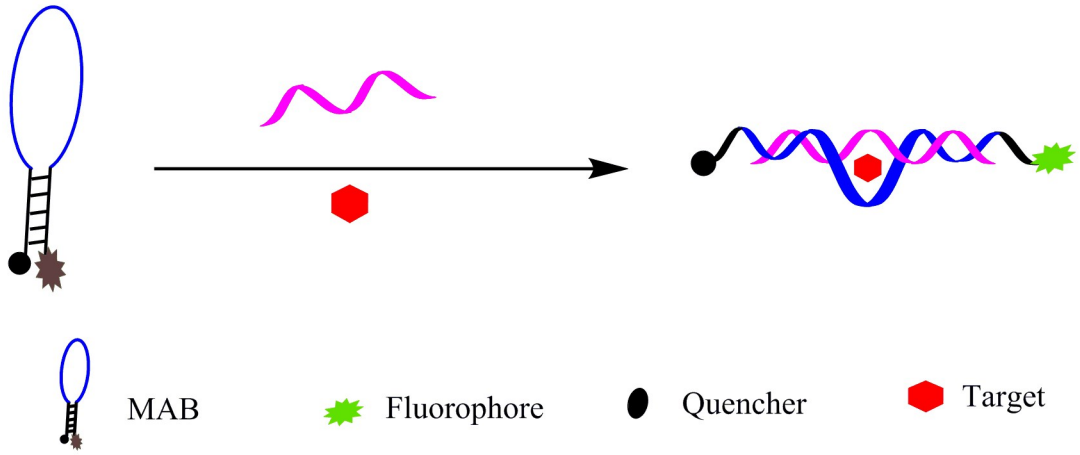
Table S2. Comparison of fluorescence methods for determination of $VEGF_{165}$

Technique and method	**LOD and linear range**	**ref**
fluorescent (peptide)	5 ng/mL, 0-52 nM	S1
chemiluminescence	19 ng/mL, 0-1 μM	S2
fluorescence	456 ng/mL, 0-300 nM	S3
fluorescence; Exo-III amplification	0.19 ng/mL, 0-500 pM	S3
fluorescence polarization	12.1 ng/mL, 0-5 nM	S4
fluorescence	9.5 ng/mL, 0-500 nM	S5
fluorescence; nicking-enzyme amplification	0.038 ng/mL, 0-200 pM	this study

It should be noted that 1 pM ≈ 38 pg/mL

Table S3. Sensing platforms for the detection of ATP

Technique and method	**LOD and linear range**	**real sample**	**ref**
fluorescence; carbon nanotubes	500 nM, 0.8-80 μM	No	S6
fluorescence; graphene oxide nanosheet	2000 nM, 5-2500 μM	cell extraction	S7
fluorescence; MoS_2 nanosheet	4000 nM, 10-2000 μM	cell extraction	S8
fluorescence; graphene oxide nanosheet	6000 nM, 20-1400 μM	serum sample	S9
fluorescence anisotropy; graphene oxide nanosheet	120 nM; 0.5-250 μM	human serum	S10
fluorescence Exo III- amplification	9.5 nM, 0.01-2 μM	No	S11
colorimetric; Exo III- amplification	0.3 nM, 0.001-0.1 μM	human serum	S12
fluorescence; DNase I- amplification	140 nM, 0.5-50 μM	No	S13
fluorescence; Exo III-amplification molecular aptamer beacon	250 nM, 0.25-20 μM	No	S14
fluorescence ; DNase I-amplification; graphene oxide nanosheet	40 nM, 0.1-1000 μM	No	S15
fluorescence; DNase I- amplification; carbon nanoparticle	0.2 nM, 0 -1000 μM	cell media	S16
fluorescence; nicking-enzyme amplification; graphene oxide nanosheet	4 nM, 10-1000 nM	cell extraction	this study



Scheme S1. Detection of biomolecules by the traditional molecular aptamer beacon method.

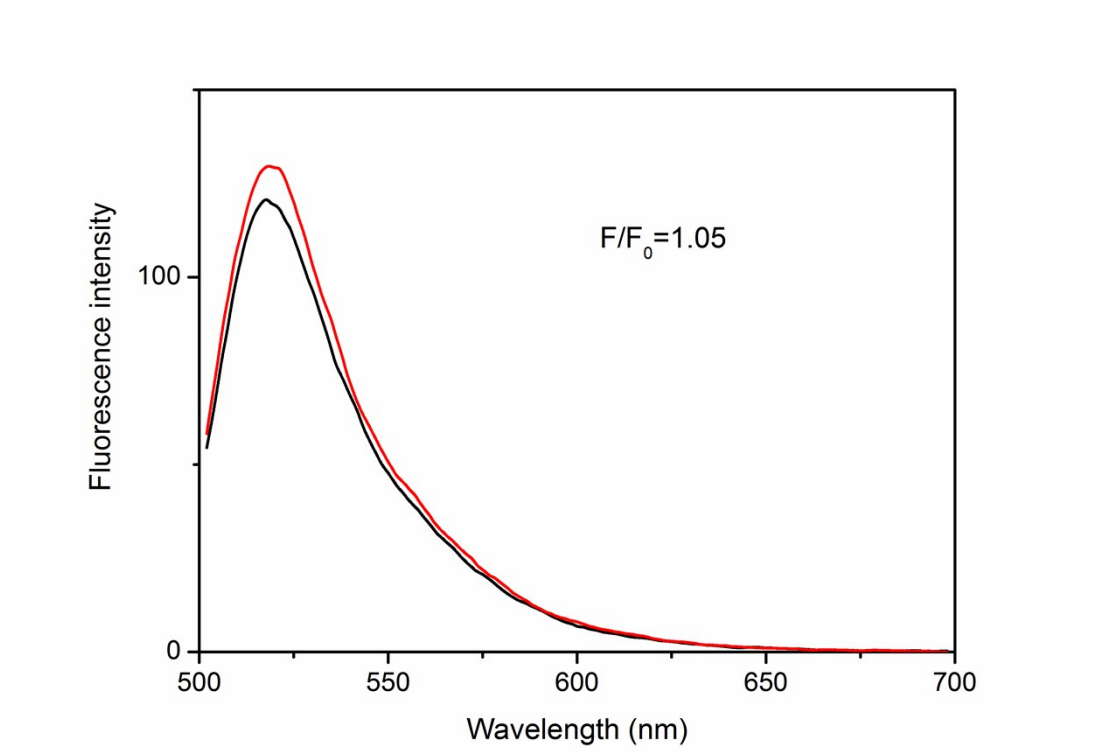


Figure S1. The fluorescence emission spectra of Apt 0 + Apt 2 in the absence (black line) and presence (red line) of $VEGF_{165}$. [Apt 0] = [Apt 2] = 20 nM, [$VEGF_{165}$] = 5 nM.

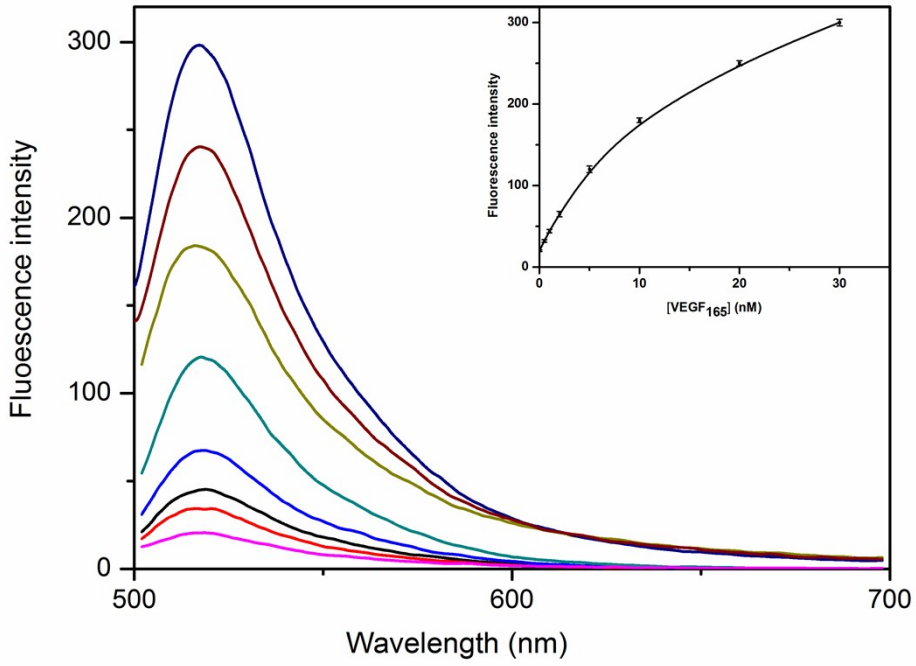


Figure S2. Fluorescence emission of Apt 1 + Apt 2-GO system upon addition of different concentrations of $VEGF_{165}$ in the absence of nicking enzyme. Inset is the relationship of the fluorescence enhancement with $VEGF_{165}$ concentration. The concentration of $VEGF_{165}$ from bottom to top is 0.5, 1.0, 2.0, 5.0, 10.0, 20.0, 30.0 nM. [Apt 1] = [Apt 2] = 20 nM, and [GO] = 15 μg/mL.

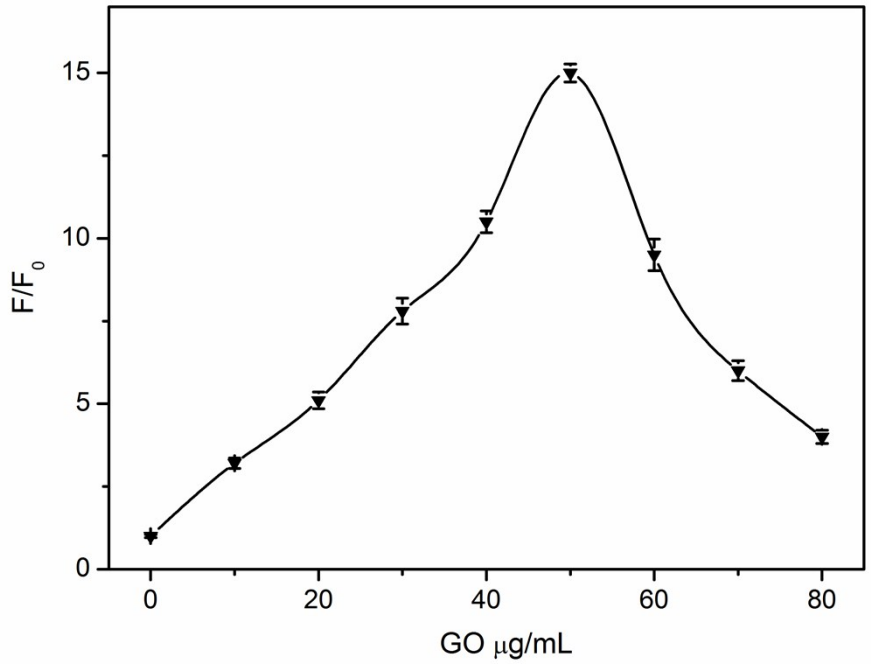


Figure S3. The effect of GO concentration on the fluorescence response of the sensing system. [Apt 3] = [Apt 4] = 100 nM, [Nt.CviPII] = 0.4 U/μL. F_0 and F are the fluorescence intensity in the absence and the presence of 1 μM of ATP, respectively. All experiments were performed in the 1×NEBufer 2.

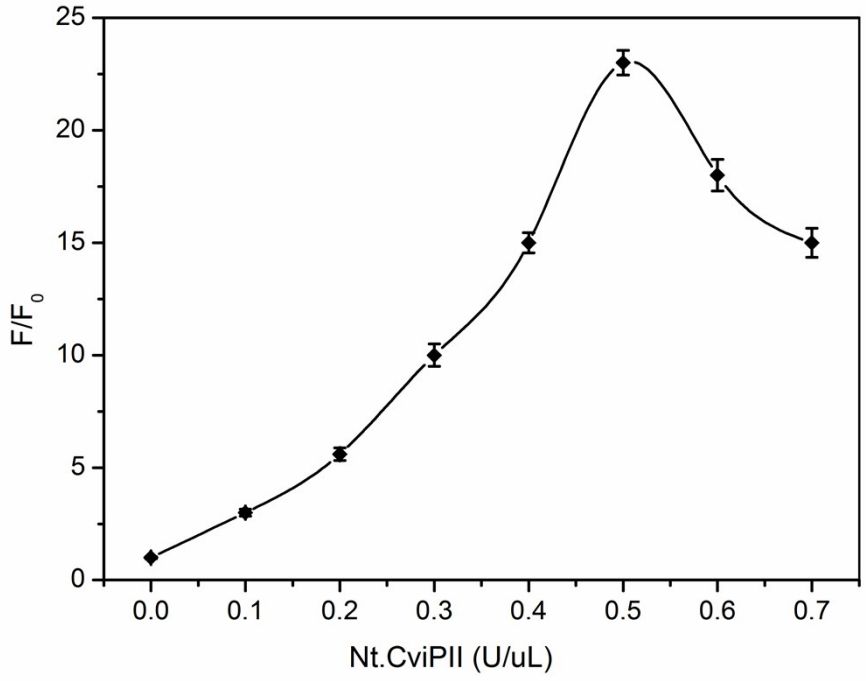


Figure S4. The effect of Nt.CviPII concentration on the signal-to-noise level of the detection system. [Apt 3] = [Apt 4] = 100 nM, [GO] =50 μg/mL. F and F_0 are the fluorescence intensity of the sensing system with and without 1 μM of ATP, respectively.

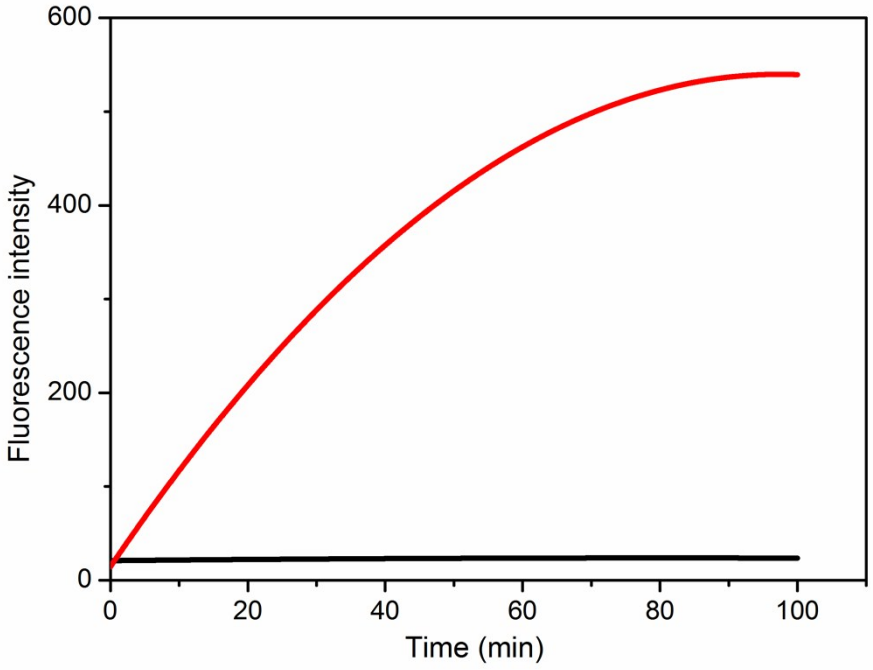


Figure S5. Time course of fluorescence intensities recorded before (black line) and after (red line) the addition of 1 μM of ATP into the system. [Apt 3] = [Apt 4] = 100 nM, [GO] =50 μg/mL, [Nt.CviPII] = 0.5 U/μL.

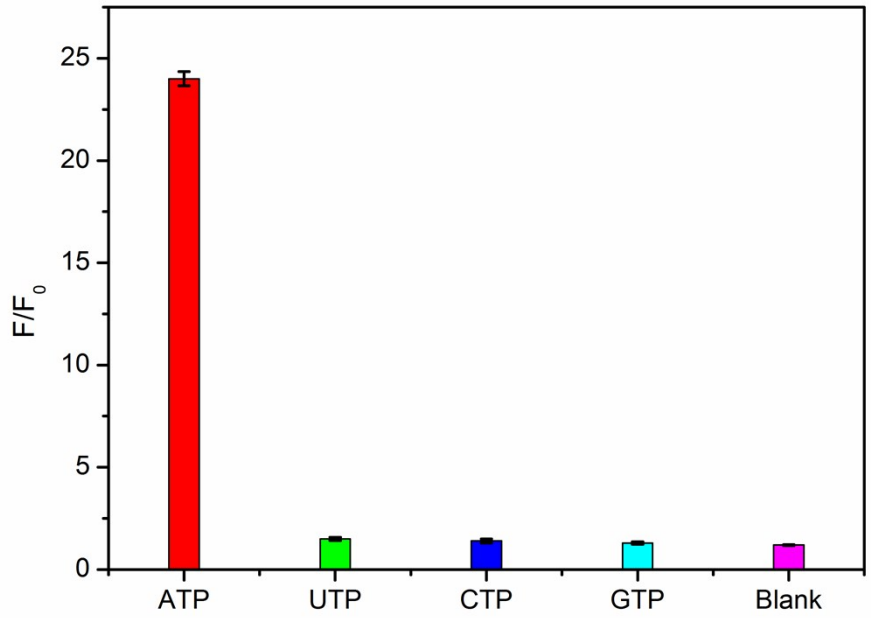


Figure S6. Selectivity of the developed sensing system for ATP(1 μM) against other interfering molecules: UTP, CTP and GTP at 100 μM. The error bar was calculated from three independent experiments.

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