## Architecture of Dual Emissive Three Dimensional Nanostructures Composite Containing Graphitic 2D Sheets and Iron Oxide Nanoparticles: Detecting Short Single-Stranded DNA Sequences

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**Figure S1**. Energy dispersive X-ray analysis (EDX) spectrum of 3D nanostructure composite of 5<sup>th</sup> cycle. In inset elements and their atomic percentage table. Corresponding TEM image, from where area scan done during EDX, (red square area).



**Figure S2**. (a),The TEM image of after the 1<sup>st</sup> cycle's produced materials. (b) HRTEM of the 1<sup>st</sup> cycle's produced materials where amorphous carbon dots (CDs) and crystalline  $Fe_3O_4$  nanoparticles (NPs) presence. (c) Lattice pattern of  $Fe_3O_4$  nanoparticles.



**Figure S3.** Fluorescence spectra of blank 3D nanostructure composite (without ssDNA probe) at the 350 nm and 450 nm excitation wavelength.



**Figure S4.** Linearity curve of target DNA detection with the presence of 3D nanostructure. The excitation wavelength is 450 nm, and the monitored emission wavelength is 500 nm. The detection limit of T (Sudan Ebola Virus DNA in this study) using 3D nanostructure nano sensor is determined from the following equation:  $LOD = K \times SD/S$ , where K = 3, SD is the standard deviation of the blank solution, and S is the slope of the calibration curve.  $LOD = K \times SD/S = 3 \times 0.02/0.12545$  nM =  $0.47 \times 10^{-9}$  M (therefore, finally limit of detection=0.47 nM).

		1 <sup>st</sup> Cycle	2 <sup>nd</sup> Cycle	3 <sup>rd</sup> Cycle	4 <sup>th</sup> Cycle	5 <sup>th</sup> Cycle
Fe2p	(%)	0.8	1.01	1.62	1.72	1.84
01s	(%)	33.76	30.85	24.98	24.11	28.99
N1s	(%)	6.66	4.64	3.6	4.18	5.54
C1s	(%)	50.04	54.89	62.37	62.26	56.18
P2p	(%)	8.75	7.95	5.67	6.3	7.45

Table S1. Peak table of different cycles of 3D nanostructures materials atomic percentages is provided

Table S2. The empirical DNA sequences are summarizes.

Name Sequence 5' to 3'						
ssDNA or (P)	GCATTAGCTTCCGTTCTCTC					
SudZai Ebola virus DNA or Target DNA (T)	GAGACAACGGAAGCTAATGC					
Single base mismatch DNA or (SM)	GAGACAACGG <u>G</u> AGCTAATGC					
Random DNA or (R)	$\underline{\mathbf{A}} \mathbf{A} \mathbf{G} \mathbf{A} \underline{\mathbf{T}} \mathbf{A} \underline{\mathbf{C}} \mathbf{C} \mathbf{G} \mathbf{G} \underline{\mathbf{T}} \mathbf{A} \mathbf{G} \mathbf{C} \mathbf{C} \mathbf{A} \mathbf{A} \mathbf{T} \underline{\mathbf{C}} \mathbf{C}$					

\* The mutation base is indicated by underline and **bold**