## SUPPORTING INFORMATION

## Directional and Regioselective Hole injection in A/T-rich DNA Induced by Intercalated Spiropyran Photoswitches

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Figure S1. Comparison between computed and experimental spectra of 2a in water.<sup>1</sup>



**Figure S2** Comparison between computed and experimental spectra of **2b** in water<sup>2</sup> (**A**) and DNA environment<sup>2</sup> (**B**). We reproduced the lower energy absorption band in the limit of error of our method and the small red shift induced by DNA embedding.

State	Energy	f	CT number	electron hole	excited electron
S <sub>1</sub>	2.79	0.012	0.980	0.956 ( <b>t-A</b> )	0.897 ( <b>2a</b> )
S <sub>2</sub>	3.20	0.002	0.997	0.956 ( <b>t-A)</b>	0.896 ( <b>c-T</b> )
S <sub>3</sub>	3.24	0.907	0.057	0.877 ( <b>2b</b> )	0.980 ( <b>2b</b> )
S <sub>4</sub>	3.67	0.009	0.991	0.943 ( <b>t-T</b> )	0.924 ( <b>2a</b> )
S₅	3.71	0.004	0.982	0.935 ( <b>t-A</b> )	0.868 ( <b>2a</b> )

**Table S1**. Energy (eV), oscillator strength (*f*), CT number and excited electron/hole population (in parenthesis the fragment of e/h localization) for the first five excited singlet states of the minimum energy geometry of **2b**:DNA.

**Table S2**. Average distances (Å) between the center of mass (COM) of probes **2a** and **2b** and the COM of the four surrounding nucleobases on the coding (c-T,c-A) and on the template strand (t-T, t-A) along the QM/MM MD simulations. Distances computed with the *cpptraj* program of AMBER suite.

	distance between COMs (Å)				
	c-A	c-T	t-A	t-T	
<b>2a</b> :DNA	4.12	5.16	4.13	4.97	
2b:DNA	4.31	5.83	4.24	5.09	



**Figure S3.** HOMO of the photoprobe **2a** and the four surrounding nucleobases c-A, c-T (left, coding strand) and t-T and t-A (right, template strand) for the minimum energy geometry of the complex 2a:DNA.



**Figure S4.** Superimposition of complexes **2a**:DNA (C-atoms colored in pink) and **2b**:DNA (C-atoms colored in green) in their minimum energy geometries.

**Table S3.** HOMO energies (eV) and electronic delocalization on the c-A, t-A, c-T and t-T of the A-T nucleobases of the DNA duplex in the absence of the intercalative probes **2a** and **2b**. The representative structures were obtained by means of MD simulations and the values were calculated at the CAM-B3LYP/def2-SVP level.

Orbital	Δε (eV)	Delocalization
НОМО	0.00	<b>c-A</b> , <b>t-A</b>
HOMO-1	-0.34	t-A, c-A
HOMO-2	-0.76	t-T, c-T
HOMO-3	-0.78	c-T, t-T

## References

- 1. M. Hammarson, J. R. Nilsson, S. Li, T. Beke-Somfai and J. Andréasson, *J. Phys. Chem. B*, 2013, 117, 13561-13571.
- 2. M. Hammarson, J. R. Nilsson, S. Li, P. Lincoln and J. Andréasson, *Chem. Eur. J.*, 2014, 20, 15855-15862.