

**Table S1:** Different 3D diffusion simulation conditions that were tested

Box <sup>1</sup> x ( $\mu\text{m}$ )	Box y ( $\mu\text{m}$ )	Box z ( $\mu\text{m}$ )	Box vol. <sup>2</sup> (fL)	No. of molecules	Conc. <sup>3</sup> (pM)	D <sup>4</sup> ( $\mu\text{m}^2/\text{s}$ )	Time <sup>5</sup> (s)	PSF model <sup>6</sup> (G/N)
5.54	5.54	13.85	425	15	62	90.0	180	N
5.54	5.54	13.85	425	15	62	90.0	60	N
6.60	6.60	19.70	858	15	31	90.0	60	N
8.30	8.30	24.90	1715	15	15	90.0	60	N
5.54	5.54	13.85	425	15	62	22.5	60	N
5.54	5.54	13.85	425	15	62	5.6	180	N
5.54	5.54	13.85	425	15	62	5.6	60	N
5.54	5.54	13.85	425	15	62	90.0	180	G
5.54	5.54	13.85	425	15	62	90.0	60	G
6.60	6.60	19.70	858	15	31	90.0	60	G
8.30	8.30	24.90	1715	15	15	90.0	60	G
5.54	5.54	13.85	425	15	62	22.5	60	G
5.54	5.54	13.85	425	15	62	5.6	180	G
5.54	5.54	13.85	425	15	62	5.6	60	G

<sup>1</sup> The molecules diffuse inside a box having a length x, depth y & height z.

<sup>2</sup> The box volume is calculated from its dimensions

<sup>3</sup> The concentration is derived from the No. of molecules divided by Avogadro's number and then divided by the volume (in L units)

<sup>4</sup> The diffusion coefficient.

<sup>5</sup> The overall simulation time.

<sup>6</sup> The model of the point-spread-function (PSF) used in the simulation, either using the Gaussian approximation (G), or a numerically calculated PSF (N). See details in Materials and Methods.













**Table S4:** the values of all quantities assessed in this work from burst analyses of single-molecule FRET measurements of a mixture of two FRET subpopulations

Sample name	m <sup>1</sup>	f <sup>2</sup>	sz th <sup>3</sup>	Donor ch. BG rate <sup>4</sup> (Hz)	Acceptor ch. BG rate <sup>5</sup> (Hz)	$\mu_1^6$ ( $\times 10^3$ )	$\sigma_1^7$ ( $\times 10^3$ )	$\mu_2^8$ ( $\times 10^3$ )	$\sigma_2^9$ ( $\times 10^3$ )
(-8)TA-(+4)NTD <sup>10</sup>	10	6	10	176.6±1.4	121.7±1.0	679.9±8.3	128.1±8.3	- <sup>11</sup>	-
	10	11	10			683.3±7.7	133.8±7.7	-	-
	10	16	10			683.7±5.0	113.1±5.0	-	-
	10	21	10			686.1±4.2	117.3±4.2	-	-
(-15)TA-(+2)NTD	10	6	10	254.7±2.1	151.1±1.1	-	-	332.9±2.1	94.7±2.1
	10	11	10			-	-	336.6±2.1	96.6±2.1
	10	16	10			-	-	336.1±3.0	90.1±3.0
	10	21	10			-	-	335.1±3.1	92.9±3.1
Mixture <sup>12</sup>	10	6	10	339.0±6.4	201.3±3.8	640.3±23.3	135.6±20.6	327.6±4.2	100.8±3.4
	10	11	10			648.8±25.8	142.0±23.2	330.5±4.7	99.4±3.8
	10	16	10			667.9±19.9	117.2±19.6	337.4±4.5	104.3±4.2
	10	21	10			684.4±18.9	102.7±19.8	340.7±4.9	104.0±5.1

<sup>1</sup> – The burst search time window of  $m$  consecutive photons

<sup>2</sup> – A number setting the threshold on the minimal multiplier of the photon rate, relative to the BG rate, above which, photons are considered part of a burst

<sup>3</sup> – The minimal amount of photons in a burst (its minimal size)

<sup>4</sup> – The mean background (BG) rate in the donor detection channel, as was retrieved by from averaging over exponential function fitting the slow process in the inter-photon time histogram, for each 20 second period of the measurement. Errors were calculated as the standard error of all 20 second BG rates.

<sup>5</sup> The mean background (BG) rate in the acceptor detection channel, as was retrieved by from averaging over exponential function fitting the slow process in the inter-photon time histogram, for each 20 second period of the measurement. Errors were calculated as the standard error of all 20 second BG rates.

<sup>6</sup> – The best fit value of the mean FRET efficiency of the 1<sup>st</sup> population out of two (the simulated mean FRET efficiency was 0.75). The reported error values are the fitting error values.

<sup>7</sup> – The best fit value of the FRET efficiency standard deviation of the 1<sup>st</sup> population out of two. The reported error values are the fitting error values.

<sup>8</sup> – The best fit value of the mean FRET efficiency of the 2<sup>nd</sup> population out of two (the simulated mean FRET efficiency was 0.50). The reported error values are the fitting error values.

<sup>9</sup> - The best fit value of the FRET efficiency standard deviation of the 2<sup>nd</sup> population out of two. The reported error values are the fitting error values.

<sup>10</sup> – The nomenclature of the sample names refers to the positions of dye labeling a dsDNA with a sequence of the lacCONS promoter. (-X)TA-(+Y)NTD – an acceptor on the base X positions upstream to the transcription start site of the promoter, on the template strand, and a donor on the base Y positions downstream to the transcription start site of the promoter , on the nontemplate strand.

<sup>11</sup> – no values for this population, for fits to a single gaussian model

<sup>12</sup> – measurement of a mixture of both FRET constructs (-8)TA-(+4)NTD & (-15)TA-(+2)NTD