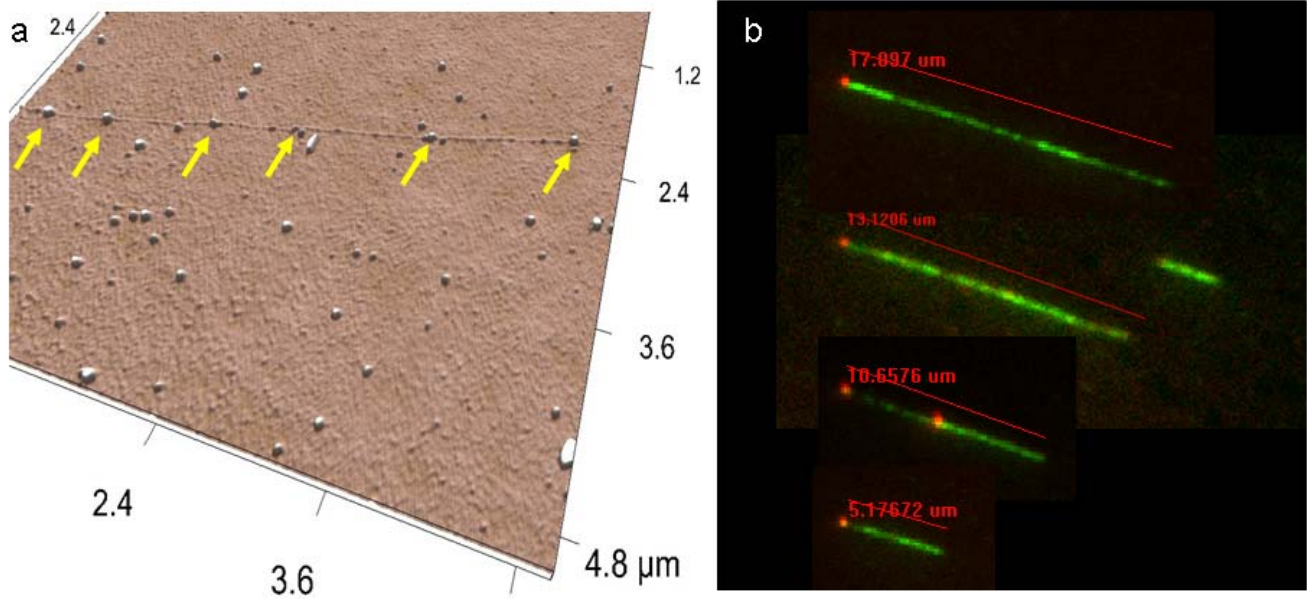
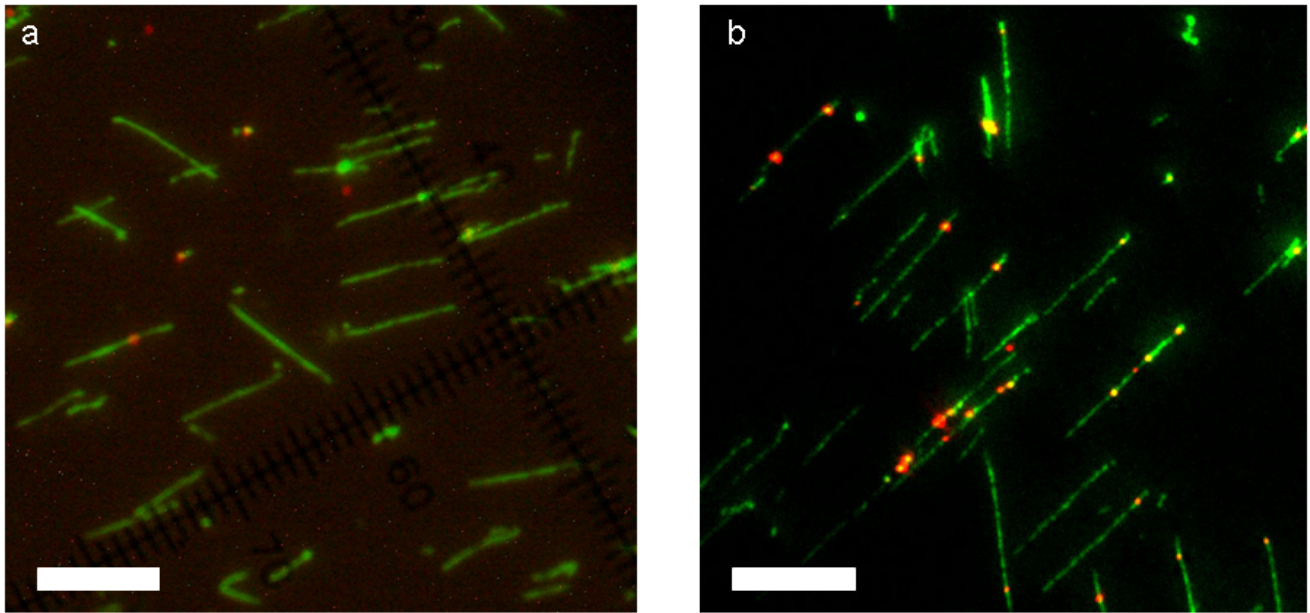


Supporting Figure 1. High-resolution localization of quantum dots. a, Localization principle; a point source produces a quasi Gaussian point spread function (PSF) with dimensions comparable to the emission wavelength. The peak position, representing the point source location, may be found by fitting a 2D Gaussian to the point spread function. Precision is a function of the number of photons collected. b, A typical QD point spread function imaged with a 100 ms integration time by a CCD camera (Coolsnap HQ, Roper scientific) may be localized with 1 nm precision (inset). The localization along the X axis of a QD observed for 500 successive frames is represented in the histogram. The typical width is about 10 nm (this width contains all system instabilities such as drift, vibrations and intensity fluctuations due to blinking).



Supporting Figure 2. Molecular combing of DNA-TF-QD complexes on polystyrene coated glass. a, 3D AFM image of Lambda-phage DNA with crosslinked RNAP. Yellow arrows indicate RNAP enzymes bound to the DNA. b, Cropped fluorescence images of T7-phage DNA (green) with crosslinked RNAP, tagged with qdot 655-streptavidin (red). Extended DNA length is indicated in red. Only the end QD survives the combing process.



Supporting Figure 3. Typical $50 \mu\text{m}^2$ field of view for the T7-phage sample described in the text. a, Full color image acquired through the microscope eyepiece with a home grade digital camera (C-60 Zoom, Olympus). b, overlaid green and red images acquired with an EMCCD (DU897, Andor). (Scale bar $10 \mu\text{m}$).

	# Sequence Specific Flags	Distance from nearest promoter (bp)				
		QD1	QD2	QD3	QD4	QD5
Genome 1	none	1390	832	1761	1619	-
	1	fixed	583	341	52	-
	2	fixed	635	289	fixed	-
Genome 2	none	2091	1187	1538	589	909
	1	1289	414	644	1015	fixed
	2	fixed	376	4	829	fixed
Genome 3	none	997	618	2639	1454	-
	1	fixed	303	1436	503	-
	2	fixed	229	326	fixed	-

Supporting Table 1. Evaluation of the resolution improvement expected from sequence specific flags. 3 genomes are analyzed as if they contained 2,1 or no flag QDs, and the measured distance (bp) between detected QDs and promoters is reported for each case.