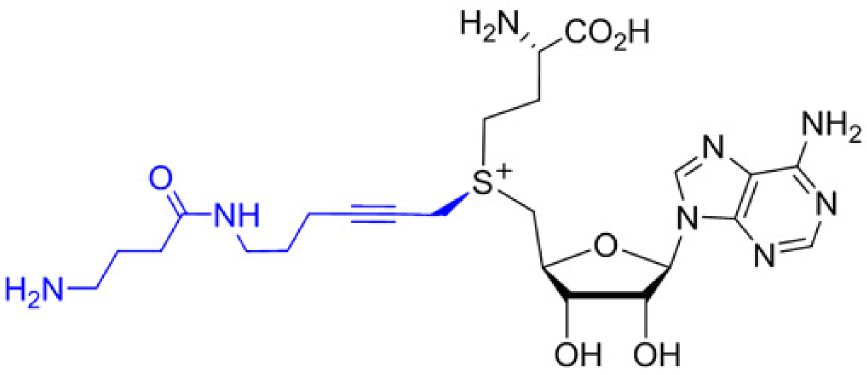
Video S1- Deposition of labeled DNA onto a surface by an evaporating droplet. Exposure time is 1s and each frame is 41.5µm by 41.5µm in size. DNA is deposited onto a PMMA-coated surface at the air/ droplet interface. Bright, blurred spots at the edge of the droplet are DNA molecules diffusing in solution.



Ado-11-amino

Figure S1- Chemical structure of the Ado-11-amino cofactor. The transferable group is shown in blue.

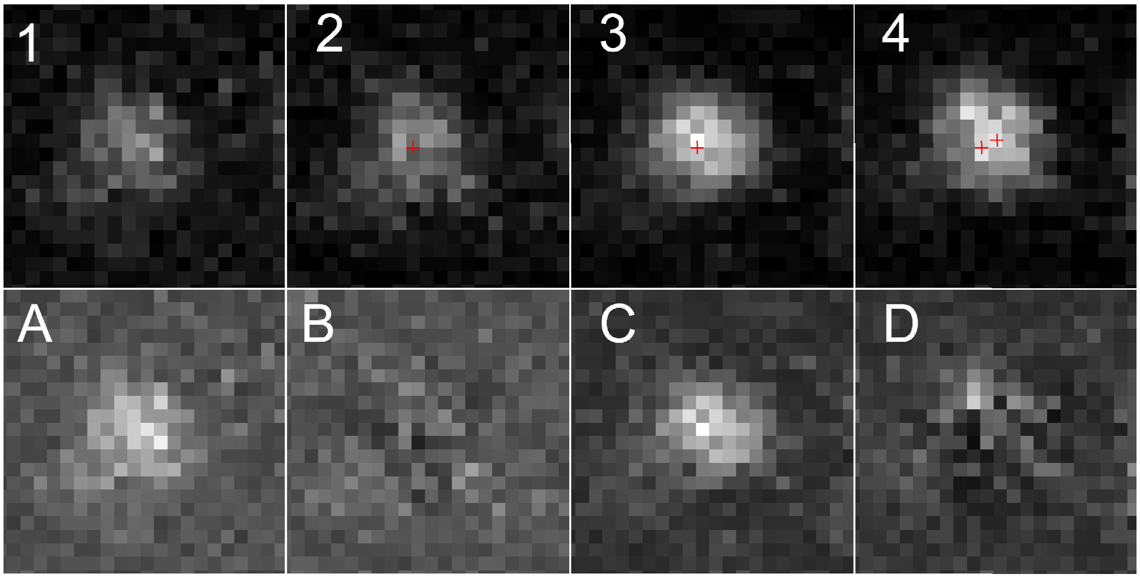


Figure S2- Fluorophore localization using photobleaching to identify individual emitters. Here, movie frames are shown in reverse chronological order, just as in our analytical procedure. Frames 1-4 show the observed intensity changes as two spatially close emitters are switched 'on' (there are many frames between 2 and 3). Frames A-D show emitters switching 'on' and, in the next frame and following localization of the emitter, their signal being subtracted from the remainder of the movie. The positions of the localized chromophores are indicated by the red crosses in frames 2-4.

Localized Emitters	Matched Emitters	Standard Deviation/ bases	Stretching Factor
83	78	68	1.6162
88	75	65	1.6603
91	79	76	1.6581
108	94	73	1.6522
95	75	73	1.6030
68	64	69	1.6093
64	57	78	1.6292
77	71	73	1.6198
109	90	65	1.5672
75	63	70	1.5632
85	81	75	1.5789
88	72	76	1.6485
86	74	84	1.6674
64	58	65	1.6543
64	54	60	1.6036
109	80	75	1.6522
97	80	75	1.6700
79	68	68	1.6237
108	94	73	1.5887
94	77	66	1.5269

Table S1- The number of localized and matched emitters and the standard deviation derived from the difference between the experimentally determined labelling sites and their matches for each DNA molecule. Also shown are the stretching factors applied to each molecule (derived by comparison to the HhaI map where the distance between base pairs (step) is fixed at 0.34nm).

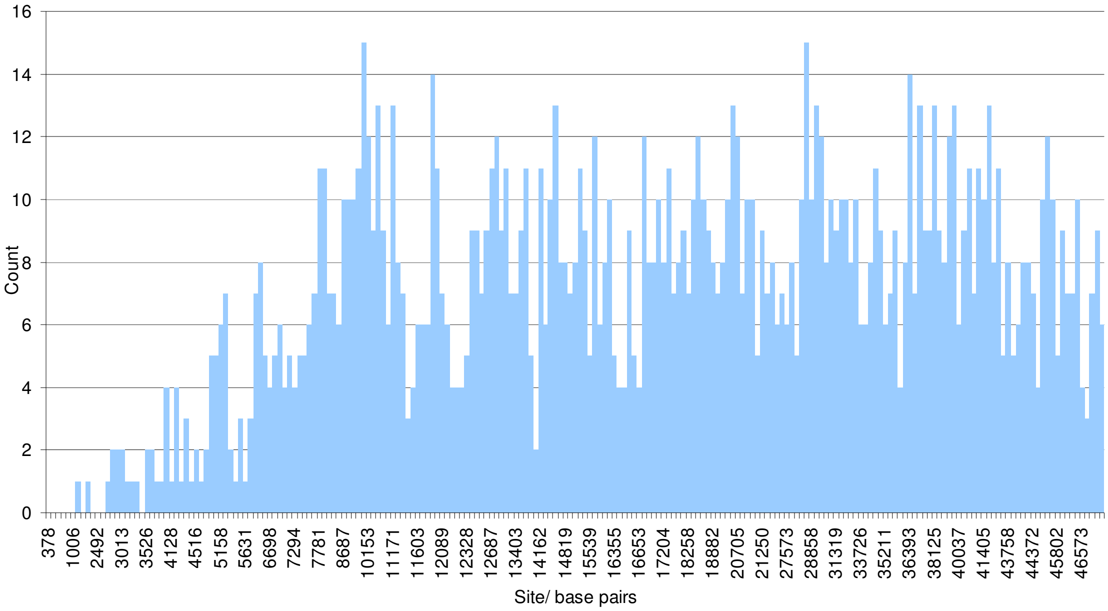


Figure S3- Histogram showing the number of experimentally derived, matched HhaI sites and their location on the lambda DNA molecule in base pairs. Sites below 5000 base pairs appear underrepresented in the data possibly due to breakage of the DNA at this end of the molecule.

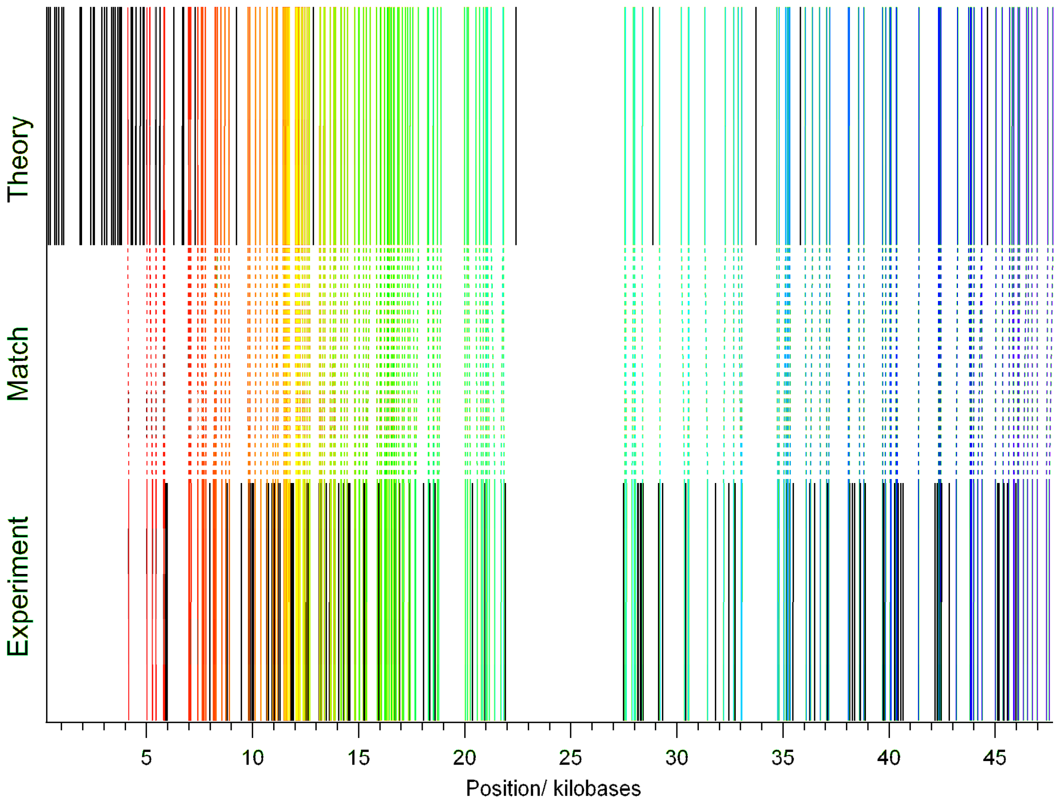


Figure S4- Matching the consensus fluorocode to the map of HhaI sites. Matched sites are shown in rainbow colors with the unmatched sites shown in black. Each time more than one count falls into a 33-base bin, an HhaI site is added to the consensus fluorocode. 163 of 215 sites in the HhaI map are matched to 163 of 248 experimentally determined sites.

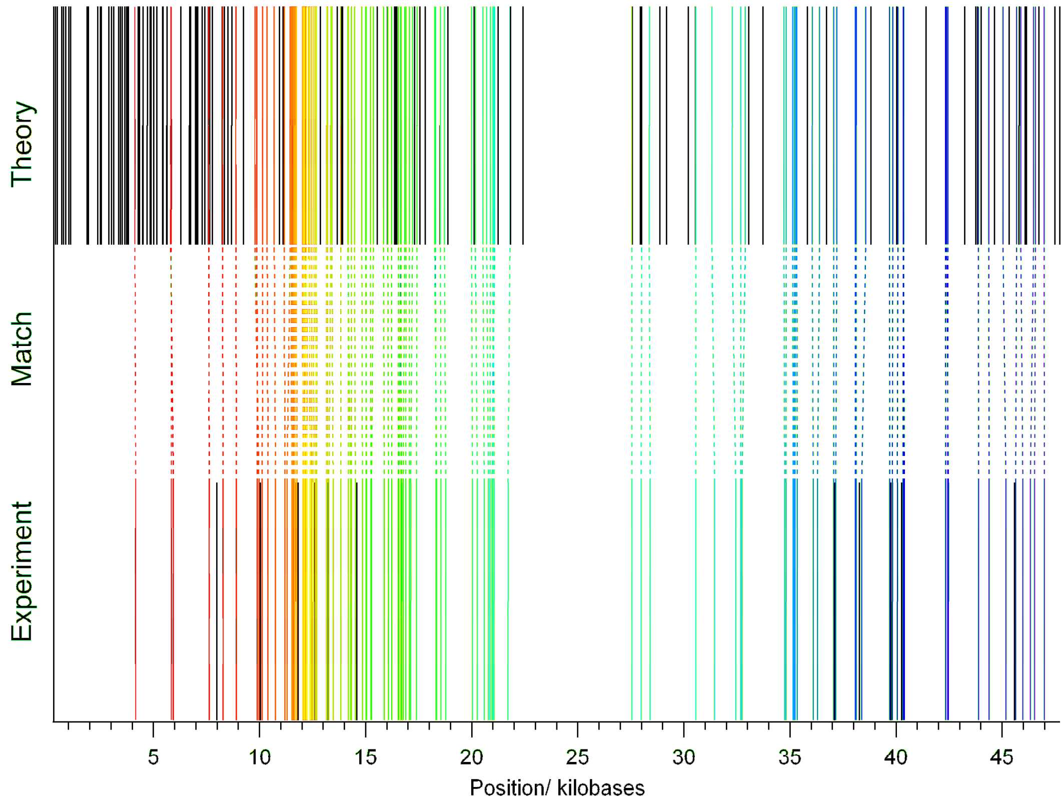


Figure S5- Matching the consensus fluorocode to the map of HhaI sites (high threshold). Matched sites are shown in rainbow colors with the unmatched sites shown in black. Each time more than two counts falls into a 33-base bin, an HhaI site is added to the consensus fluorocode. 109 of 215 sites in the HhaI map are matched to 109 of 120 experimentally determined sites.

33 base bins, threshold of 2 counts				33 base bins, threshold of 3 counts			
Matched Sites		Unmatched Sites		Matched Sites		Unmatched Sites	
Experiment	Map	Experiment	Map	Experiment	Map	Experiment	Map
4158	4129	5907	377	4158	4129	7986	377
5016	5019	5940	465	5841	5841	10032	465
5280	5157	5973	681	5940	5817	11814	681
5445	5442	7986	758	7623	7608	12606	758
5808	5817	8811	858	8283	8256	13233	858
5841	5841	9471	1005	8910	8882	14586	1005
6996	6981	9834	1102	9900	9878	37092	1102
7029	7017	9900	1870	9966	9783	38280	1870
7095	7078	9966	1938	10131	10152	39765	1938
7425	7410	10032	2380	10395	10358	40260	2380
7623	7608	10659	2491	10758	10696	45573	2491
7656	7653	10758	2500	11187	11170		2500
7722	7577	10923	2505	11286	11446		2505
7788	7780	11022	2542	11517	11503		2542
8151	8342	11220	2890	11550	11565		2890
8217	8239	11286	3012	11616	11602		3012
8283	8256	11814	3118	11649	11638		3118

8547	8518	11880	3361	11682	11692		3361
8745	8686	11913	3437	11748	11743		3437
8910	8882	12540	3523	12045	12036		3523
9801	9783	12606	3525	12078	12088		3525
9867	9878	12639	3648	12111	12201		3648
10131	10152	13134	3726	12144	12130		3726
10395	10358	13233	3797	12210	12211		3797
10692	10696	13464	3816	12243	12217		3816
10956	10942	13629	4127	12375	12361		4127
11088	11108	14058	4272	12408	12327		4272
11187	11170	14289	4333	12474	12470		4333
11484	11446	14520	4497	12540	12573		4497
11517	11503	14586	4515	12639	12659		4515
11550	11565	15246	4707	12705	12686		4707
11616	11602	15279	4846	13167	13169		4846
11649	11638	15939	4890	13200	13197		4890
11682	11692	16731	5437	13266	13357		5019
11748	11743	16929	5460	13464	13402		5157
12045	12036	17391	5628	13827	13834		5437
12078	12088	18051	5630	14190	14179		5442
12111	12201	18348	5643	14289	14161		5460
12144	12130	18612	6286	14322	14325		5628
12210	12211	20361	6697	14520	14468		5630
12243	12217	20955	6751	14850	14818		5643
12375	12361	21912	7293	15015	15027		6286
12408	12327	27489	9238	15048	14999		6697
12474	12470	28149	11596	15246	15227		6751
12573	12573	28182	12867	15279	15361		6981
12672	12659	28281	22406	15873	15841		7017
12705	12686	28314	28857	16071	16048		7078
13167	13169	28413	33725	16236	16219		7293
13200	13197	29139	35812	16533	16543		7410
13266	13357	29337	44635	16566	16650		7577
13398	13402	30426		16665	16674		7653
13662	13654	31812		16698	16652		7780
13695	13860	32439		16764	16842		8239
13827	13834	32736		16896	16905		8342
13893	13908	35178		17061	17060		8518
14157	14161	35310		17127	17203		8686
14190	14179	35475		17391	17420		9238
14322	14325	36267		18315	18298		10942
14454	14468	36498		18348	18257		11108
14817	14816	37092		18546	18523		11596
14850	14818	37125		18777	18717		12867
15015	15027	38148		20031	19990		13654
15048	14999	38280		20262	20165		13860
15213	15227	38379		20592	20522		13908
15345	15361	38643		20790	20704		14816
15378	15538	38874		20856	20880		15538
15873	15841	39732		20955	21078		16027
16005	16027	39765		20988	20997		16354
16071	16048	40260		21054	21039		16403

16236	16219	40293		21714	21807		16468
16269	16468	40425		27555	27548		17312
16335	16354	40557		27984	28009		17555
16434	16403	40656		28413	28375		17810
16533	16543	42174		30558	30567		18510
16566	16650	42273		31449	31318		18881
16665	16674	42405		32439	32281		20108
16698	16652	42471		32670	32685		21249
16764	16842	42834		32736	32889		21828
16896	16905	45111		34749	34718		22406
17061	17060	45177		34815	34823		27572
17127	17203	45408		35145	35134		27951
17358	17312	45573		35178	35122		28011
17424	17420	45969		35211	35210		28857
17655	17555			35244	35273		29184
17688	17810			35343	35327		30210
18282	18298			36102	36051		30546
18315	18257			36300	36392		33065
18513	18510			37059	37059		33725
18546	18523			37158	37204		35812
18711	18717			38082	38077		36723
18777	18881			38115	38124		38811
20031	19990			38379	38571		40036
20130	20108			39699	39691		41404
20262	20165			39831	39849		43227
20592	20522			40062	40084		43757
20790	20704			40326	40335		43835
20856	20880			40359	40360		44007
20988	20997			40392	40350		44359
21054	21039			42339	42325		44635
21153	21078			42438	42445		45338
21417	21249			42471	42382		45801
21714	21807			43890	43883		46074
21846	21828			44385	44371		46153
27555	27548			45177	45043		46726
27621	27572			45639	45681		47481
27885	27951			45969	45879		47722
27984	28009			46332	46480		
28050	28011			46530	46572		
28380	28375			46992	46977		
29205	29184						
30360	30210						
30525	30546						
30558	30567						
31449	31318						
32208	32281						
32670	32685						
33033	32889						
33066	33065						
34749	34718						
34815	34823						
35046	35122						

35145	35134						
35211	35210						
35244	35273						
35343	35327						
36102	36051						
36300	36392						
36762	36723						
37059	37059						
37158	37204						
38082	38077						
38115	38124						
38610	38571						
38808	38811						
39699	39691						
39831	39849						
40062	40036						
40095	40084						
40326	40335						
40359	40360						
40392	40350						
41382	41404						
42339	42325						
42372	42382						
42438	42445						
43164	43227						
43824	43835						
43857	43757						
43890	43883						
43989	44007						
44187	44359						
44385	44371						
45012	45043						
45375	45338						
45639	45681						
45870	45879						
45903	45801						
46068	46074						
46101	46153						
46332	46480						
46530	46572						
46761	46726						
46992	46977						
47421	47481						
47553	47722						

Table S2- Matched and unmatched fluorophore positions from the consensus fluorocode. Showing the bin in the consensus fluorocode and its match in the HhaI map of the lambda genome.