Supplementary Table 2. F test results. *F* values for the data sets that were fit to the double exponential equation. The *F* test comparison of fits was performed to determine whether the greater number of variables in the double exponential equation was responsible for the better fit compared with the single exponential equation (for details see section "Data analysis"). The *F* values corresponding to the 95 % and 99 % confidence levels are shown. If the *F* value for a given data set is greater than its 95 % confidence level, for example, it means that there is at most a 5% probability that the scatter in the data could result in a better fit to the simpler model (a single exponential); therefore, we can say with a 95 % confidence level that a double exponential results in a better fit of the data. This analysis was performed by using the software PRISM (GraphPad, San Diego).

Wild type T7A1 promoter, 37°C, Template strand					
Tymine position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m12	2	63	21.029	3.143	4.959
m10	2	63	28.168	3.143	4.959
m6	2	63	33.012	3.143	4.959
m4	2	62	45.060	3.145	4.965
p1	2	60	49.261	3.150	4.977

Table 2A. F test results for the fits to the time-resolved permanganate data on the template strand of the wild type T7A1 promoter at 37°C.

Mutant T7A1 promoter (consensus -10 region), 37°C, Template strand					
Tymine position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m12	2	27	16.244	3.354	5.488
m4	2	27	15.411	3.354	5.488

Table 2B. F test results for the fits to the time-resolved permanganate data on the template strand of the consensus-10 T7A1 mutant promoter at 37°C.

Wild type T7A1 promoter, 37°C, Template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m55-m53	2	74	75.893	3.120	4.904
m45-m42	2	68	19.259	3.132	4.932
m34-m31	2	99	34.043	3.088	4.826
m23-m20	2	97	22.707	3.090	4.831
m19-m13	2	146	23.097	3.058	4.754
m12-m9	2	98	42.788	3.089	4.829
m8-m6	2	83	17.634	3.107	4.870
m5-m3	2	80	5,687	3.111	4.881
m2-p2	2	103	18.434	3.085	4.817
p3-p6	2	118	27.051	3.073	4.790
p7-p9	2	76	4.490	3.117	4.896
p10-p13	2	107	10.109	3.081	4.809
p14-p20	2	94	15.370	3.093	4.838

Wild type T7A1 promoter, 37°C, Non–template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m73-m70	2	64	17.884	3.140	4.953
m62-m58	2	70	60.452	3.128	4.922
m52-m48	2	88	15.403	3.100	4.855
m41-m38	2	64	14.317	3.140	4.953
m31-m27	2	73	12.761	3.122	4.908
m20-m14	2	137	64.407	3.062	4,763
m12-m11, m9-m5	2	154	32.927	3.055	4.746
m4-p2	2	121	22.419	3.071	4.785
p3-p6	2	89	21.235	3.099	4.852
p7-p12	2	126	4.824	3.068	4.778
p15-p20	2	99	13.600	3.088	4.826

Table 2C. F Test results for the fits to the time-resolved X-ray footprinting data of the wild type T7A1 promoter at 37°C.

Mutant T7A1 promoter (consensus -10 region), 37°C, Template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m55-m53	2	54	12.555	3.186	5.021
m45-m42	2	74	17.846	3.120	4.904
m33-m31	2	59	7.353	3.153	4.984
m23-m20	2	76	15.305	3.117	4.896
m18-m14	2	84	4.665	3.105	4.867
m13-m10	2	93	20.368	3.094	4.841
m9-m6	2	95	19.986	3.092	4.836
m5-m3	2	71	31.351	3.126	4.917
m2-p1	2	73	24.333	3.122	4.908
p2-p4	2	82	13.959	3.108	4.874
p5-p9	2	144	34.030	3.059	4.756
p10-p13	2	116	18.635	3.074	4.793
p14-p20	2	175	8.188	3.048	4.729

Mutant T7A1 promoter (consensus -10 region), 37°C, Non–template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m72-m68	2	51	19.976	3.179	5.047
m63-m58	2	68	29.175	3.132	4.932
m53-m48	2	149	39.591	3.057	4.750
m42-m38	2	137	25.188	3.062	4.763
m31-m26	2	145	24.896	3.058	4.755
m20-m17	2	108	56.127	3.080	4.807
m16-m15	2	53	17.047	3.172	5.030
m14-m13	2	49	8.068	3.187	5.066
m12-m11	2	54	27.334	3.168	5.021
m9-m4	2	157	48.806	3.054	4.743
m3-p2	2	142	46.723	3.060	4.758
p3-p7	2	144	41.355	3.059	4.756
p8-p13	2	127	23.687	3.068	4.776
p14-p20	2	172	29.996	3.049	4.731

Table 2D. F Test results for the fits to the time-resolved X-ray footprinting data of the consensus-10 T7A1 mutant promoter at 37°C.

Wild type T7A1 promoter, 20°C, Template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m46-m42	2	160	11.132	3.053	4.740
m34-m29	2	77	15.907	3.115	4.892
m23-m19	2	159	56.896	3.053	4.741
m18-m16	2	101	18.817	3.086	4.822
m15-m8	2	219	85.754	3.037	4.703
m7-m6	2	76	39.588	3.117	4.896
m5-m3	2	130	32.854	3.066	4.772
m2-p3	2	163	40.505	3.051	4.738
p4-p9	2	253	73.947	3.073	4.790
p10-p17	2	228	45.596	3.035	4.699

Wild type T7A1 promoter, 20°C, Non–template strand					
Nucleotide position	**DFn**	**DFd**	***F* value**	***F* value for P=0.05 (95%)**	***F* value for P=0.01 (99%)**
m72-m70	2	50	5.626	3.183	5.057
m63-m57	2	98	37.377	3.089	4.829
m53,m52,m48	2	70	15.116	3.128	4.922
m51-m49	2	70	24.653	3.128	4.922
m43,m42,m38	2	59	5.186	3.153	4.984
m41-m39	2	63	16.808	3.143	4.959
m32-m30,m26	2	81	23.493	3.109	4.877
m29-m27	2	68	18.414	3.132	4.932
m20-m18	2	68	13.554	3.132	4.932
m17-m14	2	95	31.069	3.092	4.836
m9-m7	2	69	8.069	3.130	4.927
m6-m3	2	98	32.205	3.089	4.829
m2-p2	2	105	18.951	3.083	4.813
p3-p6	2	98	24.810	3.089	4.829

Table 2E. F Test results for the fits to the time-resolved X-ray footprinting data of the wild type T7A1 promoter at 20°C.