SUPPLEMENTARY MATERIAL

Supplementary Table 1 Attractive forces of DNA binding determined by σ-factor (or transcription factor). Column headers represent bp-sharing (0-11 bps) between a random promoter and the consensus sequence. Entries within the table (0-1.0) indicate the population-level fitness coefficients, w, of genotypes that include a particular promoter; in practice the values are used as thresholds against the draw of a pseudorandom number, r, wherein the random promoter gains entry into the GPN provided that $r < w$. (A standardized composite measure was actually used which accounted for the three factors that influence likelihood of promoter entry with respect to similarity to the consensus – see Suppl. Table 4 which is a composite across Suppl. Tables 1-3.)

model \ bp-sharing	0.000	1.000	2.000	3.000	4.000	5.000	6.000	7.000	8.000	9.000	10.000	11.000
ATT-none	0.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
ATT-weak	0.000	0.091	0.182	0.273	0.364	0.455	0.545	0.636	0.727	0.818	0.909	1.000
ATT-strong	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.250	0.500	0.750	1.000

Supplementary Table 2 Repulsive forces arising from too tight a fit between σ-factor (or transcription factor) and promoter that is a close match to the optimal motif, resulting in failed promoter clearance.

model \ bp-sharing	0.000	1.000	2.000	3.000	4.000	5.000	6.000	7.000	8.000	9.000	10.000	11.000
REP-none	0.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
REP-weak	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.500	0.000
REP-strong	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.500	0.000	0.000	0.000

Supplementary Table 3 Intrinsic repulsion arising from random assembly of promoters in promoter space, where the distribution of matches to an 'optimal consensus' is heavily skewed to the left. Values in the table were determined empirically through the random generation of one million GPNs from a uniform base composition and the actual spacer distribution as observed in the σ^{54} regulon.

model \ bp-sharing	0.000	1.000	2.000	3.000	4.000	5.000	6.000	7.000	8.000	9.000	10.000	11.000
	0.113935	0.202643	0.258547	0.218363	0.129674	0.054951	0.017257	0.003908	0.00064	0.000077	0.000005	0.000000

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Supplementary Table 4 Composite fitness coefficients for the fitness and drift components of the DLA model: DNA-protein binding affinity (ATT), repulsion from failed promoter clearance (REP), and intrinsic repulsion. [com] = composite fitness coefficient, [std] = standardized to highest fitness of $w = \underline{1.0}$.

model \ bp-sharing	0.000	1.000	2.000	3.000	4.000	5.000	6.000	7.000	8.000	9.000	10.000	11.000
ATT-none/REP-none												
[com]	0.000000	0.202643	0.258547	0.218363	0.129674	0.054951	0.017257	0.003908	0.000640	0.000077	0.000005	0.000000
[com-std]	0.000000	0.783776	<u>1.000000</u>	0.844578	0.501549	0.212538	0.066746	0.015115	0.002475	0.000298	0.000019	0.000000
ATT-weak/REP-none												
[com]	0.000000	0.018441	0.047056	0.059613	0.047201	0.025003	0.009405	0.002485	0.000465	0.000063	0.000005	0.000000
[com-std]	0.000000	0.309337	0.789349	<u>1.000000</u>	0.791795	0.419416	0.157768	0.041694	0.007805	0.001057	0.000076	0.000000
ATT-strong/REP-none												
[com]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000160	0.000039	0.000004	0.000000
[com-std]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	<u>1.000000</u>	0.240625	0.023438	0.000000
ATT-none/REP-weak												
[com]	0.000000	0.202643	0.258547	0.218363	0.129674	0.054951	0.017257	0.003908	0.000640	0.000077	0.000003	0.000000
[com-std]	0.000000	0.783776	<u>1.000000</u>	0.844578	0.501549	0.212538	0.066746	0.015115	0.002475	0.000298	0.000010	0.000000
ATT-weak/REP-weak												
[com]	0.000000	0.018441	0.047056	0.059613	0.047201	0.025003	0.009405	0.002485	0.000465	0.000063	0.000002	0.000000
[com-std]	0.000000	0.309337	0.789349	<u>1.000000</u>	0.791795	0.419416	0.157768	0.041694	0.007805	0.001057	0.000038	0.000000
ATT-strong/REP-weak												
[com]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000160	0.000039	0.000002	0.000000
[com-std]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	<u>1.000000</u>	0.240625	0.011719	0.000000
ATT-none/REP-strong												
[com]	0.000000	0.202643	0.258547	0.218363	0.129674	0.054951	0.017257	0.003908	0.000320	0.000000	0.000000	0.000000
[com-std]	0.000000	0.783776	<u>1.000000</u>	0.844578	0.501549	0.212538	0.066746	0.015115	0.001238	0.000000	0.000000	0.000000
ATT-weak/REP-strong												
[com]	0.000000	0.018441	0.047056	0.059613	0.047201	0.025003	0.009405	0.002485	0.000233	0.000000	0.000000	0.000000
[com-std]	0.000000	0.309337	0.789349	<u>1.000000</u>	0.791795	0.419416	0.157768	0.041694	0.003908	0.000000	0.000000	0.000000
ATT-strong/REP-strong												
[com]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000080	0.000000	0.000000	0.000000
[com-std]	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	<u>1.000000</u>	0.000000	0.000000	0.000000