



Figure S1 Independent effects on the genotype-phenotype (G-P) map of bioenergetic parameters ΔG_1 , E_{diff} and N_{TF} . Horizontal axis: the number of mismatched bits between the binding site and the transcription factor's binding motif. Vertical axis: the phenotype, which in this case is the expression level normalized to a scale of zero to one. ΔG_1 and E_{diff} are in units of $k_b T$. (A) effect of ΔG_1 , the unit of change in the free energy of formation contributed by a single bit for binding between transcription factor and target binding site, in steps of $0.0825 k_b T$. (B) effect of E_{diff} , the free energy of formation for general nonspecific binding relative to specific binding, in steps of $1 k_b T$. (C) effect of exponential increase in N_{TF} , the number of transcription factor molecules, stepping the exponent 1.25 units and rounding to the nearest integer. N_{TF} on the exponential scale has the same effect on the G-P map as does E_{diff} on the linear scale, and values for N_{TF} can be chosen for panel C's condition of $E_{diff} = 0$ that match, to the nearest integer, the curves of panel B. To avoid redundancy, we therefore varied only E_{diff} in the analyses.