

Figure S5: Four ways in which misregulation can affect adaptive gene expression in a new state or environment. (Analogous to Figure 3 but for $p_{B}=0.05, f^{O}=G_{o n} / G=0.5$.) The four panels show contour plots of four different quantities as a function of the fraction $f^{N}$ of genes that must be expressed for optimal adaptation in the new state (horizontal axes), and as a function of the expression correlation $c$ between the old and new state (vertical axes). These quantities are $\mathbf{A}$ ) the change in the fraction $\Delta f_{11}^{m}$ (eq. 2) of correctly 'on' genes under misregulation; $\mathbf{B}$ ) the change in the fraction $\Delta f_{00}^{m}$ (eq. 3) of correctly 'off' genes under misregulation; $\mathbf{C}$ ) the change in the fraction $\Delta f_{00}^{m}+\Delta f_{00}^{m}$ (eq. 4) of all correctly expressed genes under of misregulation; D) the change in mean fitness in the new state under misregulation, expressed as $r_{w}-1=\left(w^{N} /\left.w^{N}\right|_{m^{-}}\right)-1$ (eq. 5). These quantities do not only depend on $f^{N}$ and $c$, but also on the excess $\Delta_{m}=f_{01}^{O}-f_{10}^{O}$ of incorrectly on genes in the old state, which I obtained through computer simulations of the evolutionary dynamics of misregulation (Methods). These simulations are based on populations with $N_{e}=10^{3}$ individuals, $G=1500$ loci, $G_{o n}=750$ and thus $f^{O}=G_{o n} / G=0.5, p_{B}=0.05, s_{01}=0.1 / N_{e}, s_{10}=10 / N_{e}$, as estimated from empirical data (Kim et al. 2009; Mustonen and Lassig 2005; Mustonen et al. 2008; Hahn et al. 2003), a mutation rate per nucleotide of $\mu=10^{-5}$, and an incidence of mutations leading to the destruction or creation of binding sites estimated from mouse PBM data, as described in Methods. I initialized populations with no misregulation for each individual ( $f_{01}=f_{10}=0$ ), and continued the simulations for $1 / \mu$ generations, because preliminary simulations (not shown) had indicated that populations reach equilibrium by then. After $1 / \mu$ generations, I calculated the population average of $f_{01}$ and $f_{10}$ over 100 generations. I used this average to compute $\Delta_{m}=f_{01}^{O}-f_{10}^{O}$ for all panels.

