Figure S5 (Top) Sample paths for evolving binding site length and degeneracy. Populations started outside of the stable region evolve to values inside it. (Bottom) The distribution of $n$ and $r$ for $10^2$ binding sites after $n$ and $r$ have been allowed to evolve to equilibrium. Rates of mutations to $n$ and $r$ used in both plots are $u_n = u_r = 10^{-8}$. All other parameters are the default values given in Table 1.