



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.