



**Figure S7** The more complex biophysical model produces stable regions that show good qualitative agreement with those produced by the more simple model (Fig. 2). Points show invasibility criteria for mutations that change binding site length  $n$ , with fixed  $r = 1.6$ . Above the black points a mutation that decreases  $n$  is advantageous. Below it is disadvantageous. Below the red points a mutation that increases  $n$  is advantageous. Above it is disadvantageous. In the region between the two sets of points neither increasing or decreasing  $n$  is advantageous. Binding sites with lengths in this region are stable. Parameter values are the default values given in Table 1, with  $\epsilon = 2$  and  $P = 10^2$ . Results show averages from  $10^5$  Monte-Carlo simulations.