Figure S9.—Summaries varying the binding specificity of the TF binding functions. These panels summarize simulations for enhancers A-D, which correspond closely to enhancers 1-4 (respectively) but employ TFs with binding specificities (PWMs) over a range of information content levels. (A) Scatter plot illustrating how correlated the selective (horizontal axis) and functional (vertical axis) patterns of the final haplotype are to the corresponding patterns of the first haplotype for each of the simulations. Although some regulatory problems show a noticeable effect of the PWM information content on the number of substitutions, there is still much variation among regulatory problems and among replicates, suggesting the dynamics of turnover described are not driven primarily by the information content of the PWMs. (B) Cumulative distribution function for the distribution of selection coefficients for mutations arising on the ancestral haplotypes (replicates are pooled). Absolute fitness (horizontal axis) is shown on a log scale. Since the populations of all simulations stay very near the global maximum absolute fitness (=1), these absolute fitnesses can be converted into approximate selection coefficients by subtracting 1. Colors indicate PWM information content as in (A). (C) Number of substitutions as a function of PWM information content. Shown are the numbers of substitutions along the lineages leading to the most common haplotype at the end of the simulations for six replicates of four distinct regulatory problems at 10 levels of PWM information content. The Pearson correlation between PWM information content and number of substitutions is shown for each regulatory problem.