These are the simulation results for most selection conditions that are presented in the paper. Simulation results under "no selection" are not included but they can be easily reproduced using the program (explained later).

The sub-folders in each selection condition correspond to replicates, and the name of a sub-folder is the random number seed of the replicate. For each replicate, we provide *accepted_mutation_x.txt*, which can be used to reproduce the genotype at a specific evolutionary step (see readme of the program for instructions), and *evo_summary_x.txt*, which records the fitness of the genotype at each evolutionary step. These two files are sufficient to reproduce all the analysis, except for Table S3, in the paper. Other output files are not included due to their large size, and are availabe at request.

To reproduce results under "no selection", set the program to neutral evolution mode and specifiy whether enabling direct regulation (see instructions in the program readme). We used 1, 2, 3,… 30 as the random number seeds for simulations under direction regulation and those under indirect regulation in the paper.