These are the simulation results that are sufficient to reproduce the figures and tables in our paper. Each zip file contains the simulation replicates under a given condition; the name of the zip file indicates the selection condition and whether the signal is allowed to directly regulate the effector. In each zip file, the names of sub-folders are the random number seeds used to initialize simulation.

For each simulation replicate, we provide <code>accepted\_mutation\_x.txt</code>, which can be used to reproduce the genotype at any evolutionary step (see readme of the program for instructions). Except for the selection condition "no selection", we also provide <code>evo\_summary\_x.txt</code>, which records the fitness of the genotype at each evolutionary step. We have found that, in <code>evo\_summary\_x.txt</code>, the standard error of fitness under environment 1 and 2 is the same as the standard error of the average fitness, which is caused by an error in the code (now fixed). The zip file <code>spurious\_signal\_direct\_regulation.7z</code> contains an extra file <code>all\_mutations.txt</code>, which can be used to reproduce Table S3 of our paper.

Other output files, e.g.  $N_{motifs.txt}$  and networks.txt, are not included due to their large size, and are availabe at request.