Description for the attached code:

1. Deterministic and stochastic simulation of WT and mutant phenotype (Figures 2B-G, 3B, 3C, 3G, S3B, S4B, and S9)

   File : run "**stochastic simulation.m**" in the folder: "./stochastic simulation/

   1.1 (stochastic simulation.m) switch "gene switch" to "0" for setting gene mutation

   1.2 (stochasticsim_mod27det.m and stochasticsim_mod27sc.m) switch the "noise tuning" to "0" for deterministic simulation

   1.3 (stochasticsim_mod27det.m and stochasticsim_mod27sc.m) Switch from 'LogicgeneX' to 'LogicgeneX_noAC' (in the regulatory function of gene X to exclude BLMP-1 activation of *lin-29* through regulating gene X.

2. nullcline_analysis (Figure 4)

   File : run "**nullcline_analysis.m**"

   2.1 generate the phase map by setting the ratio of maximum LIN-42, SCF-DRE-1, and DAF-12 ligand production

   2.2 Set the parameter 'neg_strength_BLMP1rpgeneX' to '0' to include BLMP-1 activation of *lin-29*, or set it to '1' to exclude BLMP-1 activation of *lin-29*.

3. SCF-DRE-1 activity variation (Figures 5Bii and 5Biii)

   File : run "**Dre1_activity_variation.m**" in the folder: "./ Dre-1 activity variation/

   3.1 (Dre1_activity_variation.m) Choose either 'K_Dre1_re_Blmp1_sc' or 'gama_Dre1_re_Blmp1_sc' for plotting the output when tuning either the threshold of BLMP-1 degradation or the degradation rate of BLMP-1 regulated by SCF-DRE-1, respectively.

   3.2 (para28.m) To tune either the threshold of BLMP-1 degradation or the degradation rate of BLMP-1 by SCF-DRE-1, multiply the scaling factor for either parameter 'K_Dre1_re_Blmp1_sc' or 'gama_Dre1_re_Blmp1_sc', respectively.

4. Dre-1 onset time variation (Figure 5Bii)

   File : run "**Dre1_onset_time_variation.m**" in the folder: "./ Dre-1_onset_time_variation /

5. noise induced switching test (using constant LIN-42 level as input) (Figures 6Ai and 6Bi) File : run "**noise induced switching_constant LIN-42.m**" in the folder: "./ noise induced switching constant LIN-42 /

5.1 (**n**oise induced switching_constant LIN-42.m) use the parameter "L42_sc" for setting the ratio of maximum LIN-42 production.

5.2 (**n**oise induced switching_constant LIN-42.m) switch "gene switch" to "0" for setting gene mutation

5.3 (stochasticsim_mod27det.m and stochasticsim_mod27sc.m) switch the "noise tuning" to "0" for deterministic simulation

5.4 Compare the simulation results by running "swithingplot.m"

6 noise induced switching test (using constant LIN-42 level as input) (Figure 6Aii-iii and 6Bii-iii) File : run "**noise_induced_switching_cyclicLIN42.m**" in the folder: "./ noise induced switching cyclic LIN-42 /

6.1 (**n**oise induced switching_constant LIN-42.m) switch "gene switch" to "0" for setting gene mutation

6.2 (stochasticsim_mod27det.m and stochasticsim_mod27sc.m) switch the "noise tuning" to "0" for deterministic simulation

6.3 (stochasticsim_mod27det.m and stochasticsim_mod27sc.m) Set gamma_L42 to 5 times its default value to increase the LIN-42 noise frequency by fivefold.

6.4 Run 'plotnetworkI.m' to compare the distribution of DTC turning times simulated with either 1X (default) or 5X LIN-42 noise frequency.

6.5 Run "plotnetworkII.m" to compare the heatmap of DTC turning time simulated with 1X (default) or 5X LIN-42 noise frequency.

7 Bistability analysis (Figures S7 and S8)

File : run "**bistability_analysis.m**" in the folder: "./bistability analysis/

7.1 (bistability_analysis.m) switch the "gene switch" to "0" for gene mutation

7.2 (bistability_analysis.m) run the "deterministic_mod30.m" and "deterministic_mod30_noAC.m" for simulating from a high UNC-5 level. The file with "_noAC" indicating the simulation of circuit excluding BLMP-1 activation of *lin-29*.

7.3 (bistability_analysis.m) run the "deterministic_mod30m.m" and "deterministic_mod30m_noAC.m" for simulating from a low UNC-5 level. The file with "_noAC" indicating the simulation of circuit excluding BLMP-1 activation of *lin-29*.

8 Simple regulation test (Figure S10)

File : run "**simple model.py**"

8.1 For stochastic simulation of the gene circuit with BLMP-1 activation of *lin-29*, use the regulatory function 'f_as_g' to simulate a 'low to

high' LIN-42 transition, or use 'f_de_r' to simulate a 'high to low' LIN-42 transition.

8.2   For stochastic simulation of the gene circuit excluding BLMP-1 activation of *lin-29*, use the regulatory function 'f_noAC_as_g' to simulate a 'low to high' LIN-42 transition, or use 'f_noAC_de_r' to simulate a 'high to low' LIN-42 transition.