Supplementary Information

Determining Relative Dynamic Stability of Cell States Using Boolean Network Model

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Supplementary Table S1. Derived logic tables for Boolean network model for EMT.

Snail(t+1) = Input*(t)* AND NOT (*Snail(t)* AND *μ34(t)*)

Input(*t*)	Snail(*t*)	μ34(*t*)	Snail(*t*+1)
0	0	0	**0**
0	0	1	**0**
0	1	0	**0**
0	1	1	**0**
1	0	0	**1**
1	0	1	**1**
1	1	0	**1**
1	1	1	**0**

μ34(t+1) = NOT *Snail(t)* AND NOT *Zeb(t)*

Snail(t)	Zeb(t)	μ34(t+1)
0	0	**1**
0	1	**0**
1	0	**0**
1	1	**0**

Zeb(t+1) = NOT *μ200(t)* OR (*Snail(t)* AND *Zeb(t)*)

Snail(t)	Zeb(t)	μ200(t)	Zeb(t+1)
0	0	0	**1**
0	0	1	**0**
0	1	0	**1**
0	1	1	**0**
1	0	0	**1**
1	0	1	**0**
1	1	0	**1**
1	1	1	**1**

μ200(t+1) = NOT *Snail(t)* OR (*Zeb(t)* AND *μ200(t)*)

Snail(t)	Zeb(t)	μ200(t)	μ200(t+1)
0	0	0	**1**
0	0	1	**1**
0	1	0	**1**
0	1	1	**1**
1	0	0	**0**
1	0	1	**0**
1	1	0	**0**
1	1	1	**1**
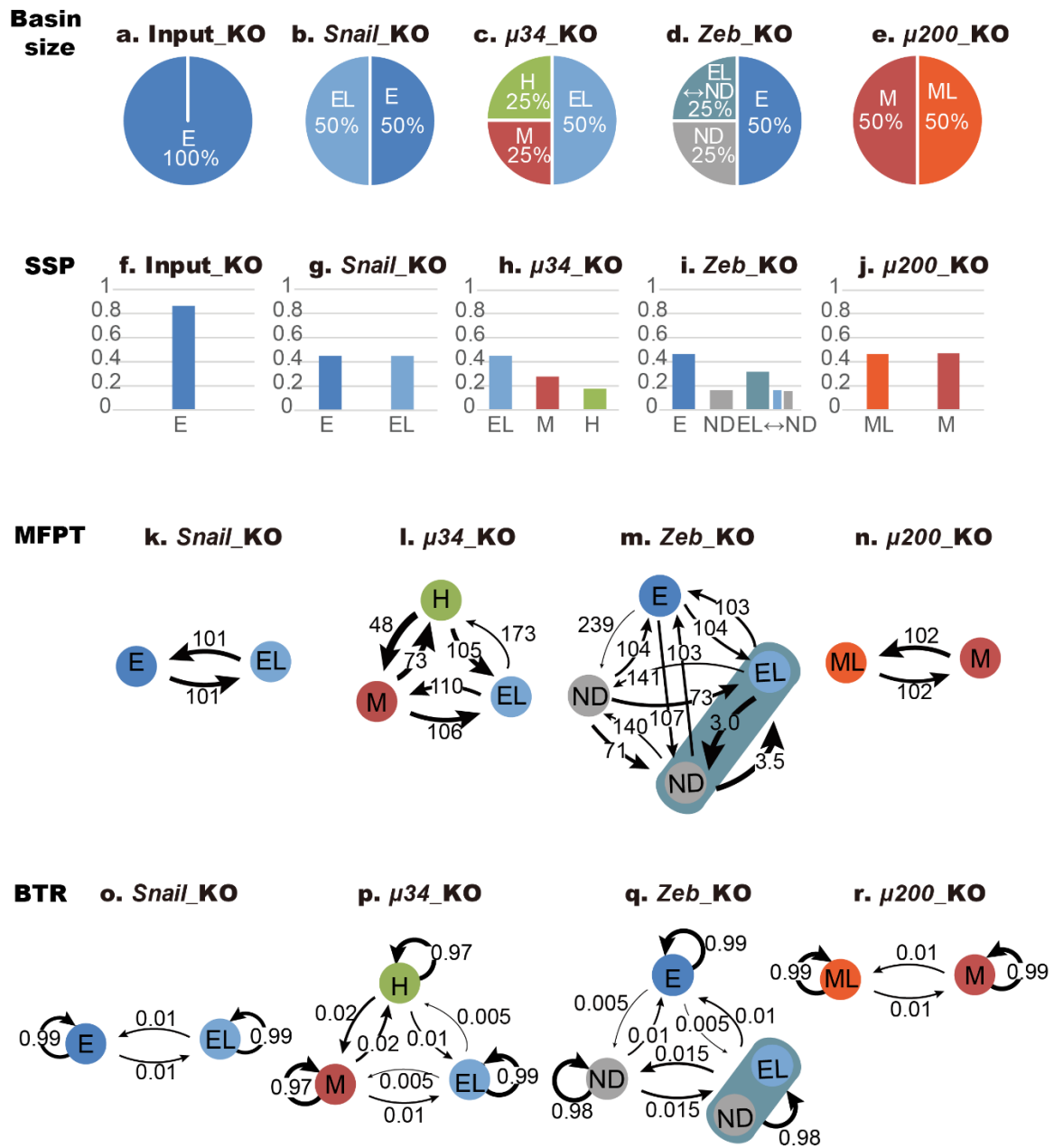
Supplementary Figure S1. **The relative dynamic stabilities of attractors in EMT Boolean model with single KO mutation.**
(**a-e**) The attracting basin size ratio of three attractors for each single gene knock-out. (**f-j**) The steady state probability distribution of three attractors for each single gene knock-out. For cyclic attractors, narrow bars represent steady state probability distribution of each state consisting the cyclic attractor and thick bar represent summed probability of them. (**k-n**) The mean first passage time between three attractors for each single gene knock-out. (**o-r**) The basin transition rates between three attractors for each single gene knock-out. States of cyclic attractor are grouped within the same color block. Note that we cannot analyze MFPT and BTR of the "Input node knock-out" case because the case had only one cell attractor.
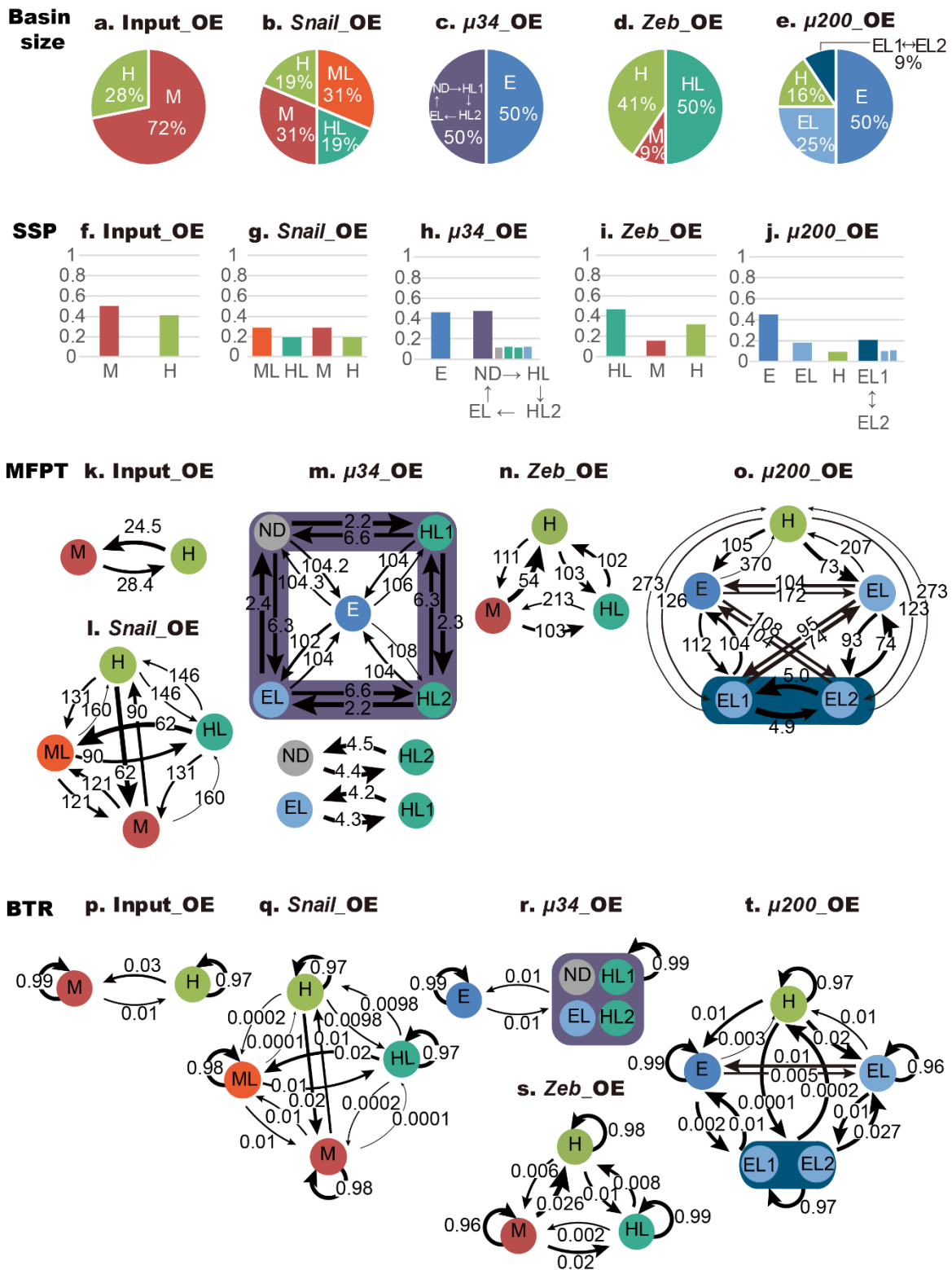
Supplementary Figure S2. **The dynamic stability of EMT Boolean model with a single gene over-expression**

(a-e) The attracting basin size ratio of three attractors for each single gene over-expression. **(f-j)** The steady state probability distribution of three attractors for each single gene over-expression. **(k-n)** The mean first passage time between three attractors for each single gene over-expression. **(o-r)** The basin

transition rates between three attractors for each single gene over-expression. States of cyclic attractor are grouped within one color block.

Supplementary File. SBML-qual format of EMT Boolean model (sbml).

Supplementary Table S2. Data for the relative dynamic stability of EMT Boolean model with single mutation (xlsx).

Supplementary Table S3. 1-degree neighbor of wild type and mutated EMT network (xlsx).