**S1 Table.** **Ranges of the parameters for randomization**

|  |  |
| --- | --- |
| Parameter | Range# |
| Maximum production rate () | 1-100 |
| Degradation rate () | 0.1-1 |
| Fold change ()\* | 1-100 |
| Threshold () | Depend on inward regulations |
| Cooperativity of the regulation () | 1, 2, 3, 4, 5, 6 |

#Units: the range of values for each parameter may have different meanings/units for different organisms. For example, the maximum production rate (G) can be 102 – 104 copies per hour per cell for E. *Coli*, and it can be 103 - 105 copies per hour per cell for H. *sapiens*. The degradation rate (k) can be 0.1 – 1 hour-1 for E. *Coli*, and it can be 0.01 – 0.1 hour-1 for H. *sapiens* (data inferred from bionumbers.org[1]). In the current RACIPE method, the exact unit is not crucial to the results, because the gene expression data for all the RACIPE models were normalized before further analysis.

\*For inhibition, fold change ranges from 0.01 to 1, but a uniform distribution is sampled for the inverse of .

**References**

1. Milo R, Jorgensen P, Moran U, Weber G, Springer M. BioNumbers—the database of key numbers in molecular and cell biology. Nucleic Acids Res. 2010;38: D750–D753. doi:10.1093/nar/gkp889