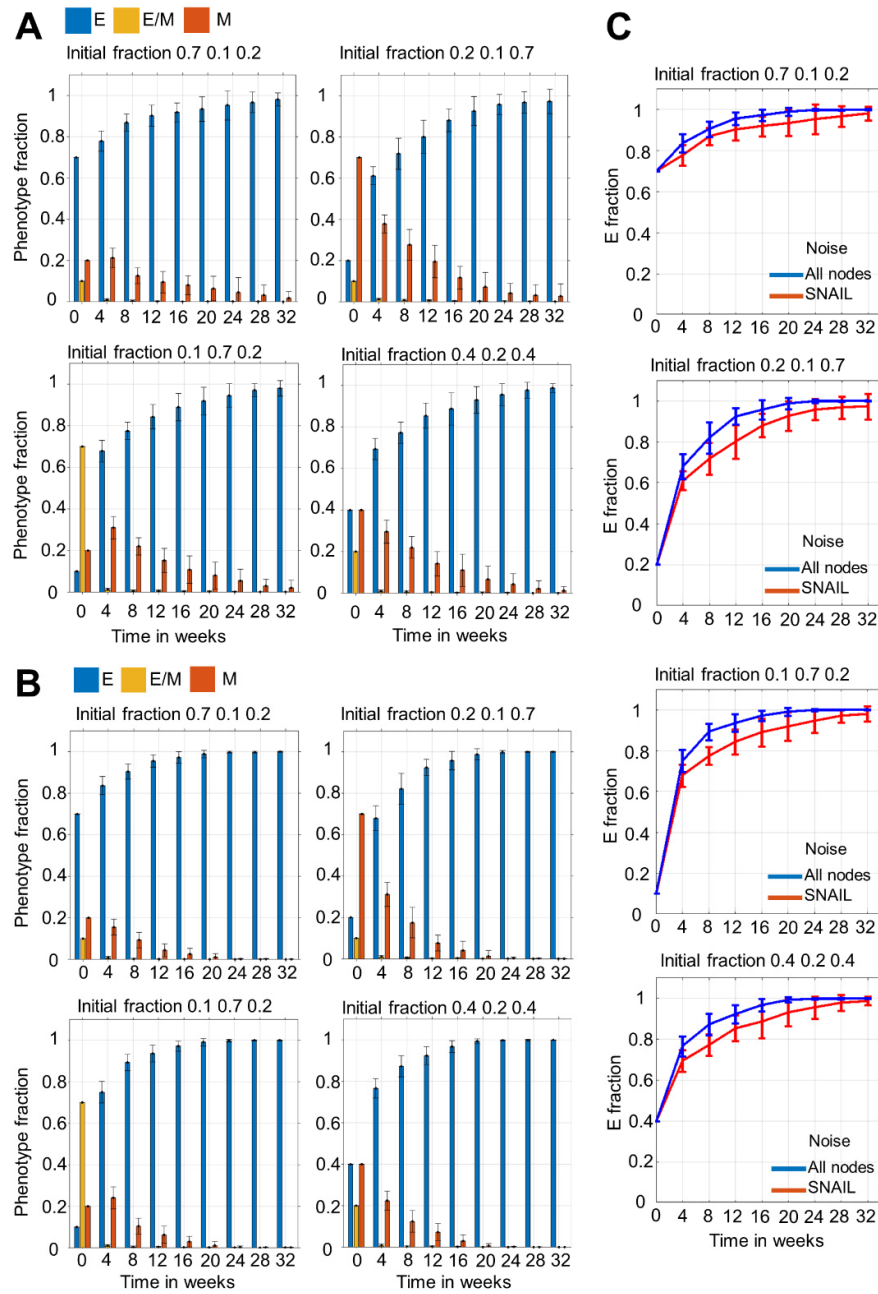
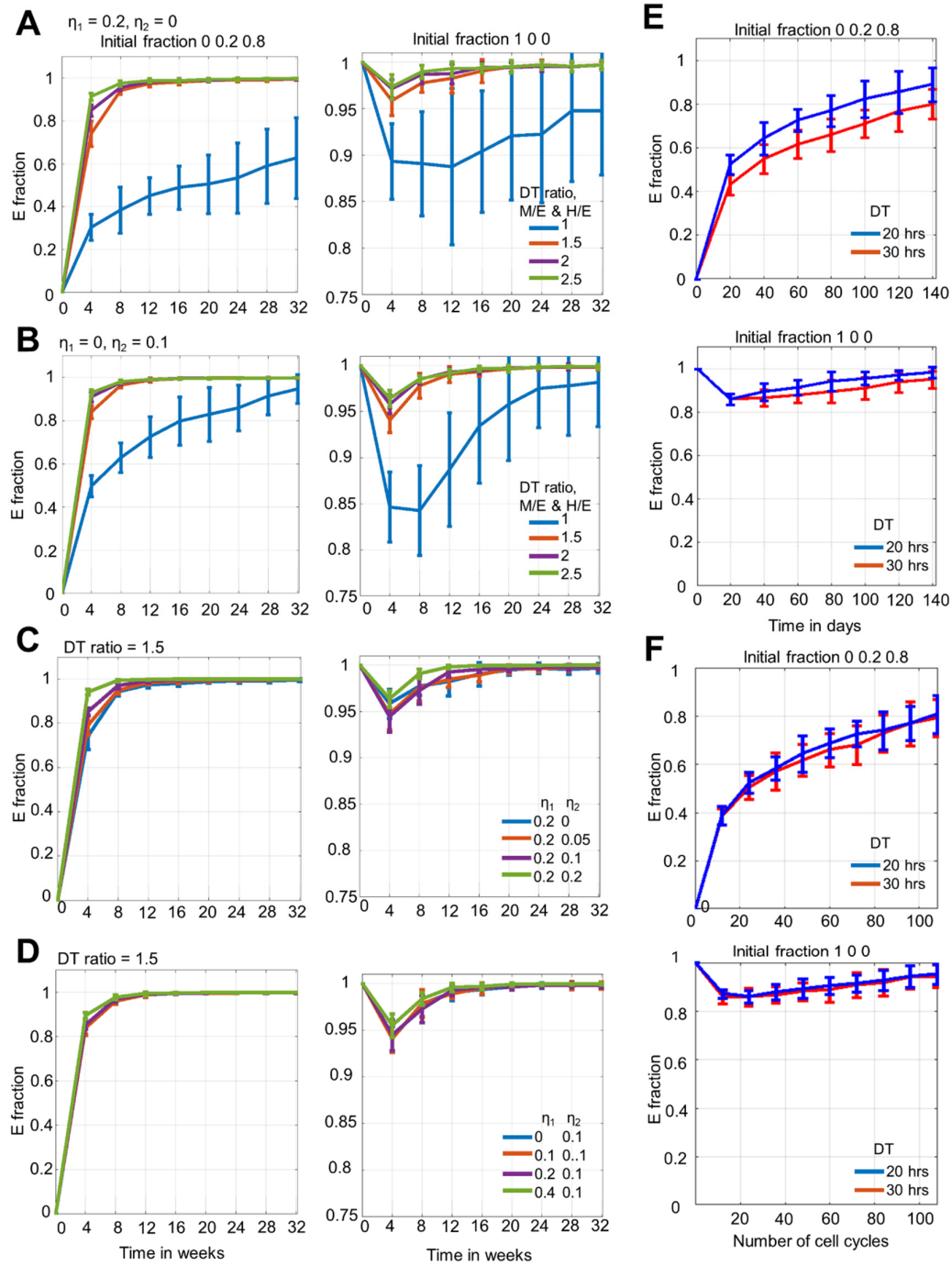


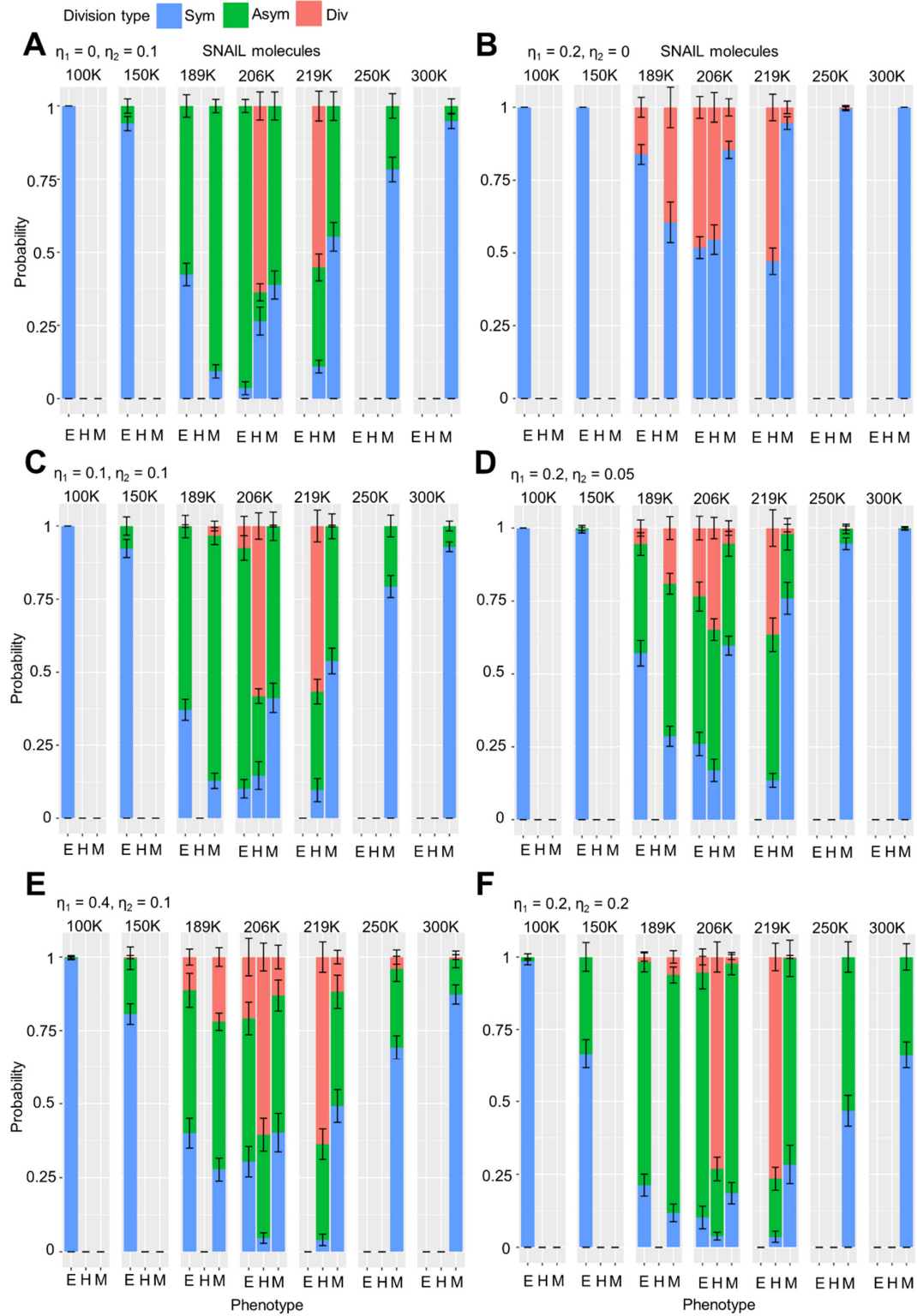
## Supplementary figures



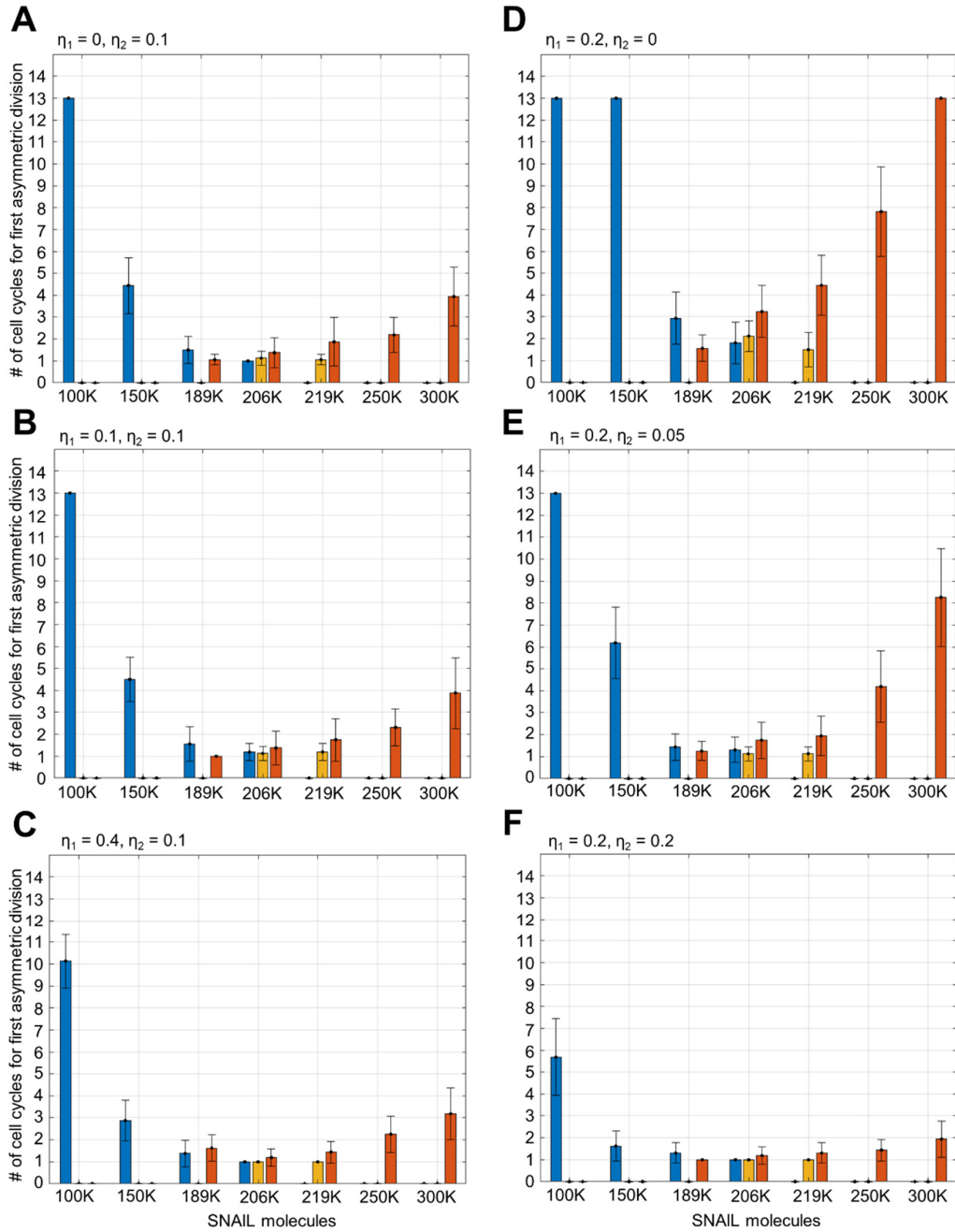
**Figure S1. Longer time simulations and similarities between effects of fluctuation in SNAIL and all players in core EMT network during cell division.** (A) Extension of simulation of results shown in Fig1C to 32 weeks. (B) Temporal changes in phenotypic distribution for same initial fractions as in Fig1A but with stochastic fluctuations considered in all players of core EMT network during cell division. (C) Overlap in temporal changes in E fraction when SNAIL (red), and all players of core EMT network (blue) had fluctuations in their levels during cell division. Avg. doubling time (DT) of each phenotype is set to 20 hrs and scaling factors  $\eta_1$  and  $\eta_2$  to 0.2 and 0.1, respectively. The initial population size was 200 cells. Mean and standard deviation calculated from 16 independent runs.



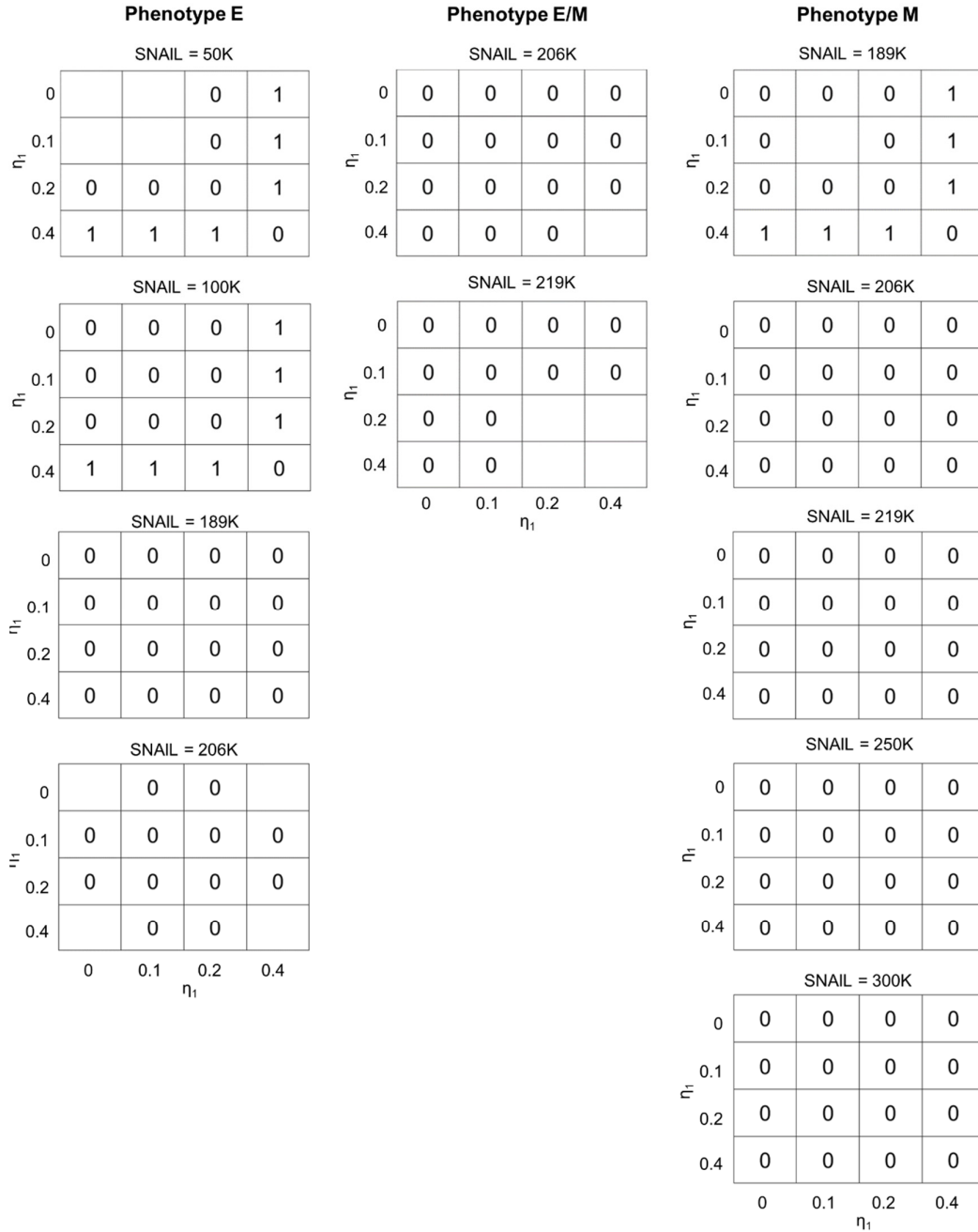
**Figure S2. Temporal changes in E fraction for combinations of avg. doubling time (DT) ratio,  $\eta_1$ , and  $\eta_2$  values; and higher cell doubling time.** Temporal E fraction changes for different DT ratios when (A)  $\eta_1 = 0.2$  and  $\eta_2 = 0$ , and (B)  $\eta_1 = 0$  and  $\eta_2 = 0.1$ . Temporal E fraction changes for different  $\eta_1$  and  $\eta_2$  values when (C)  $\eta_1 = 0.2$  and  $\eta_2$  varying, and (D)  $\eta_1$  = varying and  $\eta_2 = 0.1$ . Here, the DT(E, E/M, M) = 20 hrs. (E) Overlap in E fraction changes for DT(E, E/M, M) = 20 hrs and DT(E, E/M, M) = 30 hrs when plotted against time in days. (F) Overlap in E fraction changes for DT(E, E/M, M) = 20 hrs and DT(E, E/M, M) = 30 hrs when plotted against number of cell cycles, determined by DT. In all, initial fractions of 1) Mix of E/M and M, and 2) pure E phenotypes are considered. The initial population size was 200 cells. Mean and standard deviation calculated from 16 independent runs.



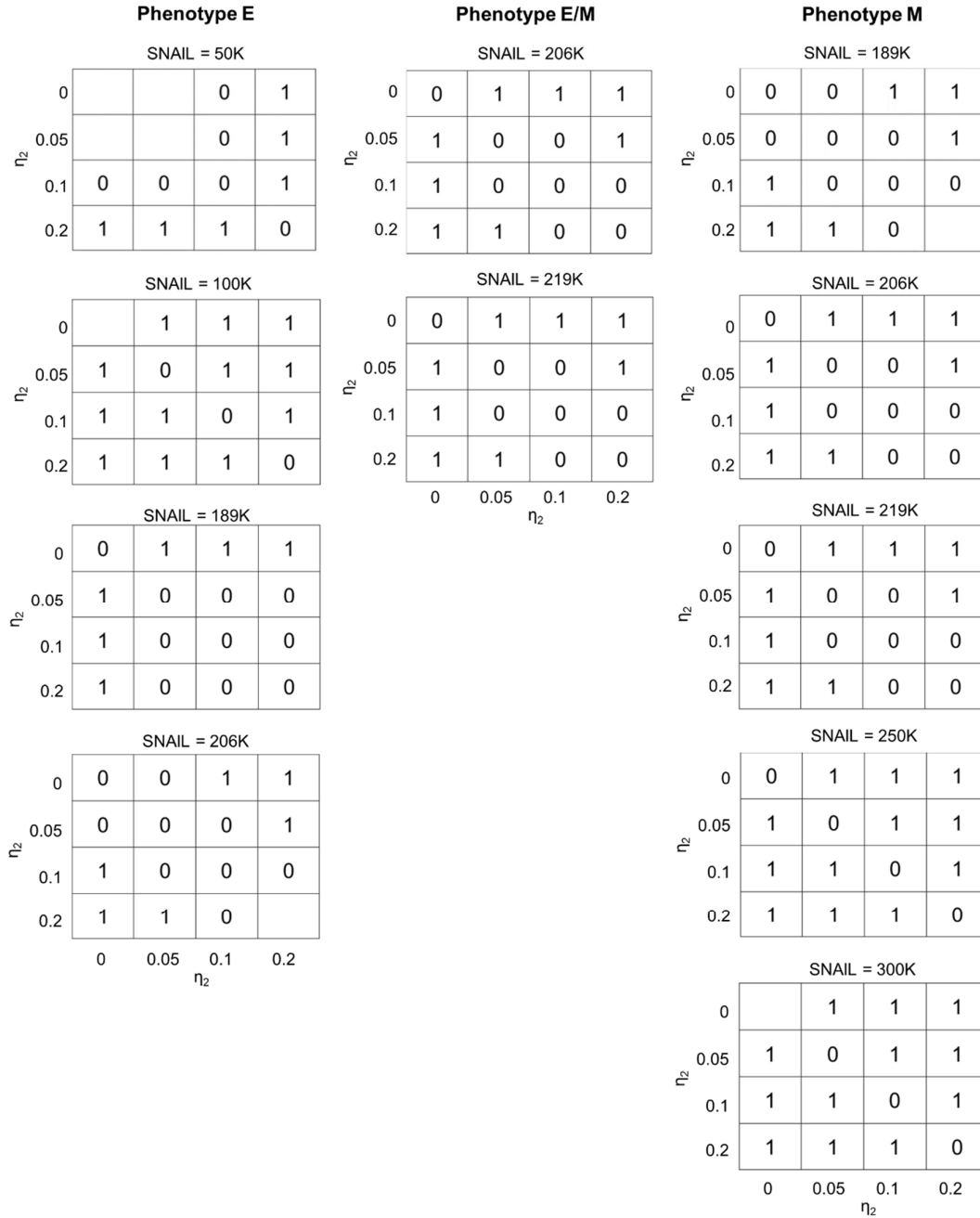
**Figure S3. Phenotypic switching probability for various scaling factors ( $\eta_1$  and  $\eta_2$ ) values across SNAIL levels.** Mean, and standard deviation are calculated from 10 independent runs of 100 iterations each.



**Figure S4. Average cell cycles/generations required for first asymmetric switching for various scaling factors ( $\eta_1$  and  $\eta_2$ ) values across SNAIL levels. Progeny up to 12 generations/cell cycles were observed for phenotypic switching. Mean, and standard deviation are calculated from 16 independent runs.**



**Figure S5. Statistical analysis of differences in minimum cell cycles for required asymmetric division by a cell of given phenotype and SNAIL level on varying  $\eta_1$  and keeping  $\eta_2$  fixed (0.1).** Here, 1 represents a statistically significant difference, while 0 denotes insignificance, according to p-value of 0.05. The blank space corresponds to nan (not-a-number) values resulted as an outcome of non-variability in data in and across pair of observations.



**Figure S6. Statistical analysis of differences in minimum cell cycles required for asymmetric division for a cell of given phenotype and SNAIL level on keeping  $\eta_1$  fixed (0.2) and varying  $\eta_2$ .** Here, 1 represents a statistically significant difference, while 0 denotes insignificance, according to p-value of 0.05. The blank space corresponds to nan (not-a-number) values resulted as an outcome of non-variability in data in and across pair of observations.