

Table S8. Summary of phenotypic values, variability thresholds and distribution of V_A/V_G ratios for the cell cycle model [22]. The first three columns list the phenotype abbreviations used in this study, a text description of the phenotypes and their units. The thresholds used to filter out dataset with very low relative and/or absolute variability are listed in the next two columns, followed by the number of Monte Carlo simulations (out of 1000) passing the threshold. The last 7 columns contain quantiles and means of the V_A/V_G values for the datasets passing the variability threshold.

Phenotype	Description	Units	Variability threshold		# of valid datasets	Quantiles and mean values of V_A/V_G						
			rel.	abs.		$Q_{0.05}$	$Q_{0.1}$	$Q_{0.2}$	$Q_{0.3}$	$Q_{0.5}$	$Q_{0.8}$	mean
APCP	Peak concentration (<i>PC</i>) of phosphorylated anaphase-promoting complex	au	0.01	1e-4	948	0.86	0.93	0.96	0.98	0.99	1	0.96
APCP(ttp)	Time to <i>PC</i> of APCP	min	0.01	0.5	726	0.92	0.95	0.97	0.98	0.99	1	0.98
Bud	Time of bud emergence	min	0.01	0.5	913	0.77	0.91	0.95	0.97	0.99	1	0.95
Cdc6	<i>PC</i> of Cdc6	au	0.01	1e-4	948	0.82	0.89	0.95	0.97	0.99	1	0.96
Cdc6(ttp)	Time to <i>PC</i> of Cdc6	min	0.01	0.5	836	0.83	0.86	0.92	0.94	0.97	0.99	0.95
Clb2	<i>PC</i> of B-type cyclin Clb2	au	0.01	1e-4	903	0.84	0.92	0.96	0.98	0.99	1	0.97
Clb2(ttp)	Time to <i>PC</i> of Clb2	min	0.01	0.5	749	0.94	0.96	0.97	0.98	0.99	1	0.98
Clb5	<i>PC</i> of B-type cyclin Clb5	au	0.01	1e-4	935	0.90	0.95	0.98	0.98	0.99	1	0.98
Clb5(ttp)	Time to <i>PC</i> of Clb5	min	0.01	0.5	779	0.90	0.93	0.96	0.97	0.99	1	0.97
Cln2	<i>PC</i> of cyclin Cln2	au	0.01	1e-4	914	0.78	0.90	0.95	0.97	0.99	1	0.96
Cln2(ttp)	Time to <i>PC</i> of Cln2	min	0.01	0.5	790	0.90	0.94	0.96	0.98	0.99	1	0.98
Rep	Start time of DNA replication	min	0.01	0.5	932	0.91	0.93	0.96	0.98	0.99	1	0.97
Sic1	<i>PC</i> of cyclin-dep. kinase inhibitor Sic1	au	0.01	1e-4	950	0.77	0.89	0.94	0.97	0.99	1	0.95
Sic1(ttp)	Time to <i>PC</i> of Sic1	min	0.01	0.5	751	0.82	0.84	0.89	0.92	0.96	0.99	0.93
Spn	Time of completed chromosome alignment	min	0.01	0.5	816	0.94	0.96	0.97	0.98	0.99	1	0.98