

Dampened E2F1 and Myb activity in endocycles

Table S2. Array values for genes regulated by the E2F and Rb family (Dimova et al. 2003)¹.

| Class | Gene | Log ₂ Sg/B-D | P-Value | Log ₂ Fb/B-D | P-Value | Biological Process |
|-------|-----------|-------------------------|---------|-------------------------|---------|------------------------------------|
| A | dnk | -0.45 | 0.7617 | nd | | nucleotide metabolism |
| A | mus209 | -2.78 | 0.0012 | -2.53 | 0.0545 | DNA replication |
| A | Df31 | -4.32 | 0.0420 | nd | | nucleosome assembly |
| A | CG4924 | -2.73 | 0.0076 | -1.26 | 0.2809 | cellular homeostasis |
| A | glob1 | 2.00 | 0.0095 | 3.63 | 0.0696 | oxygen transport |
| A | Klp67A | -2.99 | 0.2751 | nd | | chromosome segregation; cytokinesi |
| A | CycE | -2.60 | 0.0873 | -3.98 | 0.0051 | G1/S transition |
| A | Mcm7 | -2.11 | 0.0063 | -2.35 | 0.1269 | DNA replication |
| A | RfC3 | -2.42 | 0.1193 | nd | | DNA replication |
| A | FK506-bp1 | -2.41 | 0.0957 | -1.89 | 0.0439 | protein folding |
| A | CG32436 | nd | | 6.03 | 0.0283 | unknown |
| A | CG12819 | -2.78 | 0.0169 | 0.07 | 0.1754 | brain development |
| A | Mcm2 | -2.76 | 0.0156 | nd | | DNA replication |
| A | Mcm5 | -2.13 | 0.2816 | -1.65 | 0.0608 | DNA replication |
| A | CG4584 | -3.45 | 0.0378 | -2.64 | 0.0041 | unknown |
| A | HmgZ | 1.06 | 0.0519 | 0.03 | 0.1877 | chromatin remodeling |
| A | Cap-G | -2.48 | 0.0108 | nd | | cytokinesis |
| A | Pvr | 1.69 | 0.0237 | nd | | actin cytoskeleton |
| A | mRpL20 | -2.07 | 0.0182 | -0.83 | 0.9174 | translation |
| A | Ote | -1.79 | 0.3553 | nd | | nuclear envelope reassembly |
| A | Nnf1a | -2.03 | 0.1299 | -1.50 | 0.0275 | chromosome segregation |
| A | tum | -3.78 | 0.0052 | -2.47 | 0.1225 | cytokinesis |
| A | WRNexo | -1.29 | 0.2681 | -1.92 | 0.0037 | WRN DNA exonuclease |
| A | CG3961 | 1.61 | 0.0048 | 3.41 | 0.0666 | metabolic process |
| A | nod | -2.09 | 0.0859 | nd | | chromosome segregation |
| A | Hrb87F | -0.84 | 0.3700 | -1.33 | 0.0393 | alternative mRNA splicing |
| A | mod(mdg4) | -2.18 | 0.0331 | -1.81 | 0.1283 | chromatin organization |
| A | Chro | -1.00 | 0.3763 | nd | | chromatin organization |
| A | CG11943 | -1.61 | 0.0378 | nd | | unknown |
| A | cdc2c | -1.52 | 0.0510 | nd | | kinase, G1/S transition |
| A | pav | -3.45 | 0.122 | -2.10 | 0.0087 | cytokinesis |
| A | CG1888 | 1.83 | 0.0413 | nd | | unknown |
| A | Map60 | -2.44 | 0.0206 | nd | | microtubule-based process |
| A | polo | -4.80 | 0.00001 | -1.01 | 0.7406 | mitotic kinase |
| A | l(3)neo26 | -2.80 | 0.1290 | nd | | unknown |
| A | RPA2 | -1.91 | 0.0039 | -0.91 | 0.7912 | DNA replication |
| A | Chrac-14 | -2.00 | 0.00009 | -1.49 | 0.4293 | nucleosome remodeling |
| A | Hel25E | -1.44 | 0.2044 | -1.90 | 0.2415 | mitotic spindle |

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| | | | | | | |
|---|----------------------|-------|---------|-------|--------|---|
| A | Hel25E | -1.44 | 0.2044 | -1.90 | 0.2415 | mitotic spindle organization |
| A | Spc105R | -3.63 | 0.00002 | -0.74 | 0.9577 | mitotic spindle organization |
| A | CG8289 | -1.47 | 0.0120 | -3.11 | 0.1242 | chromatin assembly or disassembly |
| A | sti | -3.89 | 0.0681 | -2.38 | 0.0525 | chromatin organization |
| A | dap | -3.10 | 0.0081 | nd | | CKi, negative regulation of G1/S transition |
| A | Sd | -2.08 | 0.0128 | -2.40 | 0.0856 | compound eye morphogenesis |
| A | Kmn1 | -3.20 | 0.0112 | -3.21 | 0.1638 | chromosome segregation |
| A | Nup107 | -1.12 | 0.2143 | nd | | nuclear transport |
| A | RnrS | -0.65 | 0.4419 | -1.27 | 0.0187 | nucleotide metabolism |
| | | | | | | |
| B | DNAprim | -1.90 | 0.0050 | -3.05 | 0.1949 | DNA replication |
| B | His2Av | -2.14 | 0.0005 | -2.45 | 0.1477 | histone variant |
| B | CG9752 | -0.60 | 0.5822 | -2.48 | 0.0706 | unknown |
| B | HmgD | -2.99 | 0.1190 | nd | | chromatin organization |
| B | Mcm3 | -3.16 | 0.0001 | -2.77 | 0.0145 | DNA replication |
| B | DNAPol- α 180 | -0.88 | 0.8236 | nd | | DNA replication |
| B | UK114 | 4.46 | 0.0007 | 5.17 | 0.0267 | negative regulation of translation |
| B | Mes4 | -0.45 | 0.6878 | -1.02 | 0.7546 | DNA replication |
| B | CG13350 | -1.56 | 0.0978 | nd | | unknown |
| B | geminin | -2.42 | 0.0054 | -1.55 | 0.2598 | negative regulation of DNA replication |
| B | CG3430 | -1.99 | 0.0132 | -1.96 | 0.3639 | unknown |
| B | Rfc40 | -1.84 | 0.0479 | -1.80 | 0.1518 | DNA replication |
| B | Orc5 | -0.84 | 0.4995 | nd | | DNA replication |
| B | CDC45L | -1.01 | 0.2253 | nd | | DNA replication |
| B | msd5 | -2.38 | 0.0445 | nd | | mitotic spindle organization |
| B | CG9740 | -1.89 | 0.1557 | -0.43 | 0.5707 | unknown |
| B | CG10336 | -1.54 | 0.0033 | nd | | cell cycle |
| B | SMC2 | nd | | -2.00 | 0.1569 | mitotic chromosome condensation |
| B | CG30457 | 1.40 | 0.1607 | -0.69 | 0.5564 | unknown |
| B | spd-2 | -1.84 | 0.0349 | -0.94 | 0.6324 | mitotic spindle organization |
| B | DNAPol- δ | -1.57 | 0.0749 | nd | | DNA replication |
| B | CG5602 | -2.23 | 0.0450 | -1.52 | 0.4504 | DNA replication |
| B | Fen1 | nd | | -1.29 | 0.3118 | DNA replication |
| B | mad2 | -4.95 | 0.0081 | -0.71 | 0.8494 | spindle checkpoint |
| B | DNAPol- α 50 | -1.06 | 0.0418 | nd | | DNA replication |
| B | CG13690 | -1.81 | 0.0045 | nd | | RNA metabolic process |
| B | CG8142 | -2.61 | 0.0573 | -1.64 | 0.2327 | DNA replication |
| B | Rrp1 | -3.42 | 0.1855 | -5.11 | 0.1151 | DNA repair |

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| | | | | | | |
|--|---------|-------|---------|-------|--------|----------------------------------|
| C | mars | -2.91 | 0.1376 | nd | | regulation of mitotic cell cycle |
| C | msd1 | -3.81 | 0.00002 | -0.23 | 0.5344 | mitotic spindle organization |
| C | Sep5 | nd | | -0.88 | 0.9559 | cytokinesis |
| C | BthD | -3.59 | 0.0010 | -3.04 | 0.0521 | redox signal response |
| D | Ndc80 | -1.31 | 0.7789 | nd | | chromosome segregation |
| D | CG14434 | -2.16 | 0.0976 | -2.05 | 0.2180 | cAMP metabolic process |
| D | CG8447 | nd | | 0.14 | 0.3477 | unknown |
| D | CG8399 | -2.25 | 0.0091 | -0.84 | 0.8459 | histidine catabolic process |
| D | CG8316 | nd | | 4.29 | 0.0732 | unknown |
| D | CG9427 | 1.06 | 0.5942 | -1.98 | 0.1157 | unknown |
| E | Rpt3R | nd | | 2.82 | 0.1279 | proteolysis |
| E | NtR | -0.80 | 0.3749 | nd | | ion transport |
| E | qtc | 1.08 | 0.2063 | 0.58 | 0.2043 | male courtship behavior |
| E | CG6845 | -1.00 | 0.1112 | -1.41 | 0.4532 | unknown |
| E | CG6790 | nd | | 6.91 | 0.0072 | GPI anchor biosynthetic process |
| E | CG7997 | 2.72 | 0.0027 | 3.62 | 0.0088 | carbohydrate metabolic process |
| E | Arp53D | nd | | 7.08 | 0.1222 | cytoskeleton organization |
| E | CG3505 | 2.60 | 0.0280 | 3.68 | 0.0106 | proteolysis |
| E | CG7628 | -2.97 | 0.0106 | -2.91 | 0.0625 | phosphate transport |
| ¹ Red and green font: Twofold decreased and increased, respectively. Red and green shading: Twofold decreased and increased, respectively, with $P \leq 0.05$. nd: no data | | | | | | |