

Dampened E2F1 and Myb activity in endocycles

| Table S3 Array values for genes regulated by the Myb-MuvB / dREAM complex (Georlette et al. 2007).¹ | | | | | | |
|---|-------------|-------------------------------|----------------|-------------------------------|----------------|--------------------------------|
| Class | Gene | Log₂ Sg/B-D | P-Value | Log₂ Fb/B-D | P-Value | Biological Process |
| A | Arp53D | nd | | 7.08 | 0.1222 | cytoskeleton organization |
| A | CG10157 | 3.15 | 0.1360 | 3.19 | 0.0897 | unknown |
| A | CG10383 | 0.84 | 0.1218 | 2.55 | 0.0020 | unknown |
| A | CG11089 | 3.07 | 0.1483 | nd | | IMP biosynthetic process |
| A | CG11760 | -0.14 | 0.6104 | 0.23 | 0.0172 | unknown |
| A | CG12643 | 0.36 | 0.5332 | 0.07 | 0.0877 | unknown |
| A | CG15829 | 1.68 | 0.4390 | 6.12 | 0.3952 | cellular acyl-CoA homeostasis |
| A | MCPH1 | -0.31 | 0.9742 | 2.01 | 0.0028 | mushroom body development |
| A | CG5080 | nd | | 2.03 | 0.1333 | unknown |
| A | CG7755 | nd | | 6.27 | 0.0029 | oxidation reduction |
| A | CG7997 | 2.60 | 0.0027 | 3.62 | 0.0088 | carbohydrate metabolic process |
| A | CG8316 | nd | | 4.29 | 0.0732 | unknown |
| A | Irc | 2.68 | 0.0048 | 3.84 | 0.0010 | response to oxidative stress |
| A | CG9427 | 0.10 | 0.5942 | -1.98 | 0.1157 | unknown |
| A | CG9577 | 1.43 | 0.0035 | 2.33 | 0.0268 | metabolic process |
| A | Cp1 | 1.14 | 0.2247 | -0.01 | 0.0880 | protein catabolic process |
| A | drongo | -0.37 | 0.8762 | -0.11 | 0.3009 | regulation of ARF GTPase |
| A | Fer1HCH | -0.02 | 0.2621 | 0.56 | 0.1913 | cellular iron homeostasis |
| A | Fer2LCH | -0.28 | 0.8570 | 0.05 | 0.2429 | cellular iron homeostasis |
| A | Myo31DF | 1.08 | 0.0994 | nd | | mesoderm development |
| A | NtR | 0.55 | 0.3749 | nd | | ion transport |
| A | Paip2 | 1.42 | 0.2593 | 1.23 | 0.2733 | regulation of cell growth |
| A | qtc | 1.08 | 0.2063 | 0.58 | 0.2043 | male courtship behavior |
| A | Rpt3R | nd | | 2.82 | 0.1279 | proteolysis |
| A | apt | -3.13 | 0.0017 | -2.20 | 0.0281 | branching tube morphogenesis |
| A | CG16953 | -0.44 | 0.6412 | -0.66 | 0.9109 | unknown |
| A | CG7628 | -2.97 | 0.0106 | -2.91 | 0.0625 | phosphate transport |
| A | CG7686 | -0.76 | 0.5595 | -0.11 | 0.4709 | unknown |
| A | CG9601 | -1.50 | 0.2815 | -1.03 | 0.5188 | unknown |
| A | how | -1.85 | 0.0980 | -0.83 | 0.7472 | cell differentiation |
| A | Jhl-21 | -1.46 | 0.1464 | -2.25 | 0.1862 | leucine import |
| A | Marf | nd | | 0.58 | 0.0213 | mitochondrion organization |
| A | shtd | -1.28 | 0.0588 | -2.25 | 0.0654 | unknown |
| A | CG2183 | -1.32 | 0.0561 | -0.37 | 0.6811 | mismatch repair |
| A | CG2264 | -1.59 | 0.1863 | nd | | signal transduction |
| B | CG10630 | nd | | 6.51 | 0.0289 | unknown |
| B | CG14864 | 2.66 | 0.0814 | nd | | unknown |
| B | CG17625 | nd | | 5.54 | 0.0231 | unknown |
| B | CG31100 | 4.45 | 0.2590 | nd | | monosaccharide transport |

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|---|-------------|-------|--------|-------|---------|---|
| B | CG9542 | 2.80 | 0.1481 | nd | | unknown |
| B | crb | 0.59 | 0.2460 | nd | | organ morphogenesis |
| B | hdm | 0.30 | 0.0639 | 0.68 | 0.1276 | reciprocal meiotic recombination |
| B | Lsd-1 | 4.84 | 0.0123 | 5.84 | 0.0029 | lipid storage |
| B | Pfk | -1.13 | 0.1106 | 0.32 | 0.0878 | glycolysis |
| B | CG14312 | -3.64 | 0.0224 | -1.24 | 0.4652 | unknown |
| B | CG5191 | -1.64 | 0.0873 | -1.07 | 0.7100 | unknown |
| B | Sas | -3.43 | 0.0035 | -1.88 | 0.0710 | carbohydrate biosynthetic process |
| B | Vha68-1 | -3.09 | 0.1509 | -1.06 | 0.1607 | proton transport |
| B | drpr | 0.37 | 0.1355 | -0.89 | 0.8601 | cell adhesion |
| | | | | | | |
| C | CG12161 | nd | | 6.20 | 0.00031 | proteolysis |
| C | CG14995 | nd | | 4.57 | 0.00111 | autophagic cell death |
| C | CG32436 | nd | | 6.03 | 0.02828 | unknown |
| C | CG6737 | nd | | 6.52 | 0.08096 | ATP synthesis coupled proton transport |
| C | CG6980 | nd | | 5.18 | 0.23645 | unknown |
| C | CG7045 | nd | | 8.32 | 0.03977 | unknown |
| C | CG7208 | nd | | 5.49 | 0.11213 | unknown |
| C | CG9875 | nd | | 6.65 | 0.00187 | metabolic process |
| C | skpB | 4.09 | 0.0335 | 5.17 | 0.02433 | ubiquitin-dependent protein catabolic process |
| C | CG31751 | 2.75 | 0.0058 | nd | | unknown |
| C | CG6330 | 2.56 | 0.0002 | nd | | nucleoside metabolic process |
| C | Cyp4e2 | 2.54 | 0.0026 | 3.83 | 0.19713 | unknown |
| C | ldgf1 | 2.30 | 0.0016 | 4.53 | 0.05829 | imaginal disc development |
| C | CG9989 | 2.55 | 0.0004 | nd | | unknown |
| C | CG7966 | 2.41 | 0.0801 | 3.63 | 0.00224 | unknown |
| C | CG8206 | 1.43 | 0.0554 | 2.78 | 0.21008 | unknown |
| C | CG8788 | 1.11 | 0.0179 | 2.02 | 0.02450 | unknown |
| C | CG5059 | 0.94 | 0.0174 | 0.72 | 0.04047 | positive regulation of apoptosis |
| C | CG11686 | 0.83 | 0.2417 | 0.64 | 0.02192 | unknown |
| C | CG17090 | 0.23 | 0.1492 | 0.36 | 0.19974 | protein amino acid phosphorylation |
| C | CG6115 | 0.21 | 0.4345 | 0.70 | 0.05265 | unknown |
| C | egr | -0.07 | 0.4177 | 0.76 | 0.26034 | JNK cascade; induction of apoptosis |
| C | Rbf2 | 0.46 | 0.0171 | -0.33 | 0.08957 | regulation of cell cycle |
| C | tok | -1.33 | 0.0644 | 0.09 | 0.32888 | imaginal disc-derived wing vein morphogenesis |
| C | CG5281 | -1.63 | 0.2039 | 0.45 | 0.18795 | unknown |
| C | CG1998 | -1.95 | 0.2235 | -1.16 | 0.44774 | oxidation reduction |
| C | CG3508 | -1.55 | 0.1384 | -0.49 | 0.30569 | unknown |
| C | ea | -1.78 | 0.0525 | -1.99 | 0.33110 | toll signaling pathway |
| C | lectin-24Db | -1.60 | 0.0050 | 0.12 | 0.22301 | unknown |

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|---|------------|-------|---------|-------|---------|--|
| C | L | -1.74 | 0.0032 | -1.15 | 0.14797 | negative regulation of programmed cell death |
| C | Nrg | -1.89 | 0.0048 | -1.22 | 0.59819 | organ development |
| C | CG4502 | -1.79 | 0.4616 | nd | | regulation of protein metabolic process |
| C | plexB | -0.83 | 0.4098 | -2.82 | 0.05312 | signal transduction |
| C | ed | -2.59 | 0.1112 | -4.01 | 0.11519 | organ morphogenesis |
| C | CG3964 | -2.50 | 0.0594 | nd | | protein modification process |
| C | TM4SF | -2.51 | 0.0568 | -0.90 | 0.69724 | unknown |
| C | Rab23 | nd | | -1.86 | 0.00551 | small GTPase mediated signal transduction |
| C | CG9634 | -3.42 | 0.0024 | -3.91 | 0.05901 | proteolysis |
| C | BthD | -3.59 | 0.0010 | -3.04 | 0.05210 | redox signal response |
| C | DAAM | -5.18 | 0.0055 | -1.09 | 0.55658 | actin cytoskeleton organization |
| C | CG13320 | nd | | nd | | unknown |
| C | CG13848 | 0.12 | 0.4192 | nd | | rhodopsin biosynthetic process; phototransduction |
| C | CG6643 | 2.83 | 0.00017 | 1.70 | 0.21639 | unknown |
| C | CG8801 | -0.72 | 0.0721 | -0.62 | 0.77993 | unknown |
| C | CG9154 | -1.08 | 0.0592 | -0.35 | 0.23413 | methylation |
| C | TI | -0.76 | 0.5144 | nd | | response to stress |
| C | tor | -0.77 | 0.3712 | -1.14 | 0.67123 | torso signaling pathway |
| C | CG14117 | -0.07 | 0.1934 | nd | | unknown |
| | | | | | | |
| D | CG2930 | nd | | 4.10 | 0.3287 | oligopeptide transport |
| D | CG4822 | 3.26 | 0.0455 | 3.56 | 0.0012 | unknown |
| D | Gs1 | 3.41 | 0.0412 | 3.74 | 0.0006 | glutamine biosynthetic process |
| D | glob1 | 2.00 | 0.0095 | 3.63 | 0.0696 | oxygen transport |
| D | CG12428 | 1.64 | 0.0054 | 2.98 | 0.0327 | unknown |
| D | regucalcin | 2.18 | 0.1588 | 2.42 | 0.0025 | unknown |
| D | CG33969 | 0.60 | 0.0170 | 0.89 | 0.3469 | G-protein coupled receptor protein signaling pathway |
| D | CG10165 | -0.26 | 0.5745 | 0.83 | 0.2089 | unknown |
| D | CG13163 | nd | | 0.93 | 0.1713 | translational initiation |
| D | CG10424 | 0.90 | 0.0495 | 0.79 | 0.0004 | unknown |
| D | CG11455 | -0.62 | 0.7080 | 0.25 | 0.4154 | mitochondrial electron transport |
| D | Pxn | -1.33 | 0.0820 | -0.03 | 0.4373 | response to oxidative stress |
| D | CG4164 | 0.96 | 0.0033 | -0.34 | 0.6016 | response to heat; protein folding |
| D | CG31549 | -0.03 | 0.5820 | -0.46 | 0.7247 | metabolic process |
| D | CG18528 | -1.00 | 0.4708 | -1.00 | 0.3990 | tRNA modification |
| D | Pen | -3.84 | 0.0304 | -0.45 | 0.8925 | cytoplasmic transport |
| D | RacGAP50 | -3.78 | 0.0052 | -2.47 | 0.1225 | dendrite morphogenesis |
| D | CG13914 | -3.81 | 0.00002 | -0.23 | 0.5344 | mitotic spindle organization |
| D | CycB | -3.54 | 0.0547 | nd | | mitosis |
| D | pav | -3.45 | 0.1218 | -2.10 | 0.0087 | cytokinesis |

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|---|-----------|-------|--------|-------|--------|-------------------------------------|
| D | pim | -3.21 | 0.0012 | -0.77 | 0.8483 | mitotic chromosome segregation |
| D | sip2 | -3.11 | 0.1199 | 0.18 | 0.0146 | unknown |
| D | l(1)G0237 | -3.20 | 0.0112 | -3.21 | 0.1638 | chromosome segregation |
| D | Klp67A | -2.99 | 0.2751 | nd | | chromosome segregation |
| D | CG8173 | -3.00 | 0.0382 | -1.66 | 0.2294 | protein amino acid phosphorylation |
| D | feo | -3.28 | 0.0167 | -1.71 | 0.1802 | cytokinesis |
| D | sle | -2.78 | 0.0169 | 0.07 | 0.1754 | brain development |
| D | ial | -2.60 | 0.0759 | -2.10 | 0.0267 | cytokinesis |
| D | Klp61F | -2.73 | 0.0572 | -1.87 | 0.0260 | microtubule-based movement |
| D | CG2213 | -2.38 | 0.0445 | nd | | mitotic spindle organization |
| D | scra | -2.11 | 0.0128 | -2.30 | 0.0462 | cytokinesis |
| D | CG14896 | -2.08 | 0.0063 | -0.62 | 0.9306 | unknown |
| D | Nnf1a | -2.03 | 0.1299 | -1.50 | 0.0275 | mitotic metaphase plate congression |
| D | CG11454 | -0.40 | 0.9080 | -0.58 | 0.8832 | unknown |
| 1: Red and green font: 2 fold decreased and increased respectively. Red and green shading: 2 fold decreased and increased respectively with $p \leq 0.05$. nd: no data | | | | | | |