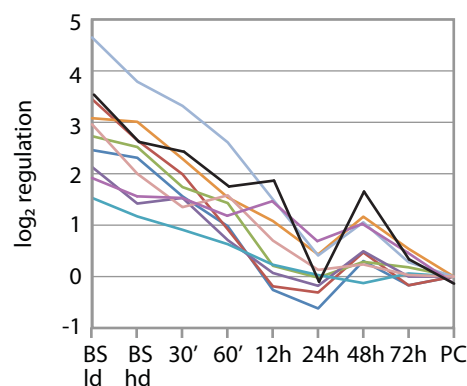
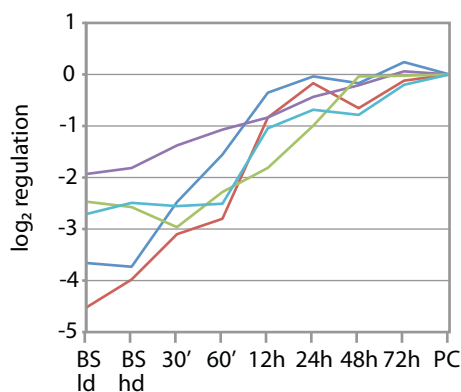
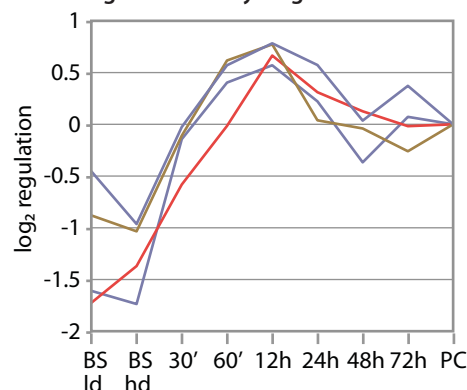


A. Glycolysis

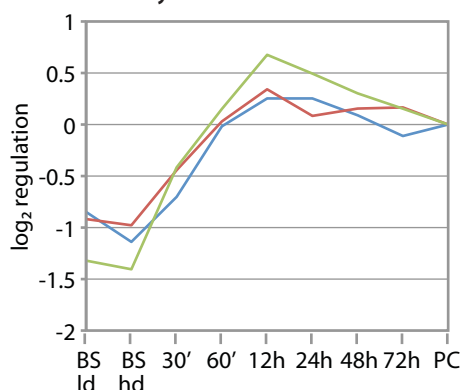
- Tb927.3.3270 Phosphofructokinase (PFK)
- Tb10.61.2680 Pyruvate kinase (PYK)
- Tb927.1.3830 Glucosylphosphate isomerase (PGI)
- Tb10.70.1370 Aldolase (ALD)
- Tb11.02.5280 Glyceraldehyde -3-phosphate dehydrogenase (G3PDH)
- Tb10.6k15.2030 Hexose transporter THT1E
- Tb927.1.700 Glycosomal phosphoglycerate kinase (PGKC)
- Tb10.61.2650 aquaglyceroporin
- Tb10.6k15.3640 Alternative oxidase (AOX)
- Tb927.8.2780 RNA-binding protein RBP10

B. Glycosomal pyruvate metabolism

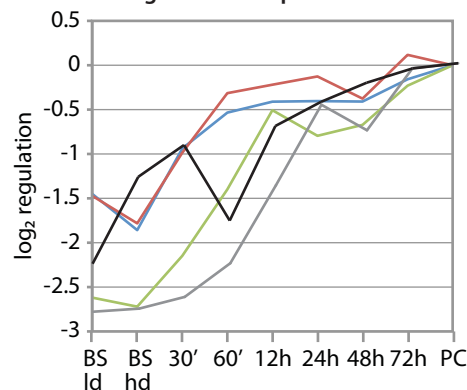
- Tb11.02.4150 Pyruvate phosphate dikinase (PPDK)
- Tb10.61.0980 Glycosomal malate dehydrogenase (MDH)
- Tb927.5.930 Glycosomal fumarate reductase
- Tb927.2.4210 Phosphoenol pyruvate carboxykinase
- Tb927.3.4500 Fumarate hydratase (fumarase)

C. 2-Oxoglutarate dehydrogenase

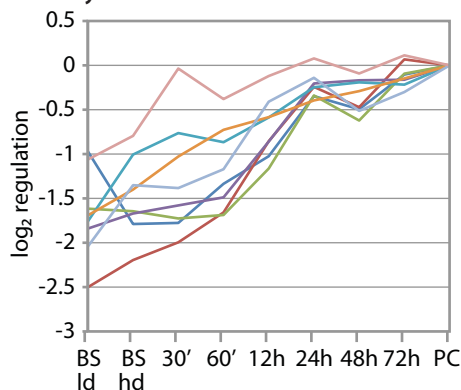
- Tb11.01.1740 E1 subunit
- Tb11.01.3550 E2 subunit
- Tb11.47.0004 E1 subunit
- Tb11.01.8470 Dihydrolipoyl dehydrogenase

D. Succinyl CoA metabolism

- Tb11.02.0290 acetyl:succinate coA transferase
- Tb10.6k15.3250 succinyl coA synthetase beta chain
- Tb927.3.2230 succinyl coA synthetase alpha chain

E. Proline degradation/import

- Tb927.7.210 proline oxidase
- Tb10.70.4280 Δpyrrol deHase
- Tb09.160.4310 glutamate deHase
- Tb927.5.1060 proc. peptidase beta s.u.
- Tb11.02.1480 proc. peptidase alpha s.u.

F. Cytochrome c oxidase

- Tb927.8.5120 cytochrome c
- Tb927.1.4100 oxidase IV
- Tb09.160.1820 oxidase V
- Tb10.6k15.2180 oxidase IX
- Tb10.100.0160 oxidase VI
- Tb927.3.1410 oxidase VII
- Tb11.01.4702 oxidase X
- Tb10.70.4380 assembly