Local DAG for enriched terms in GO Biological Process
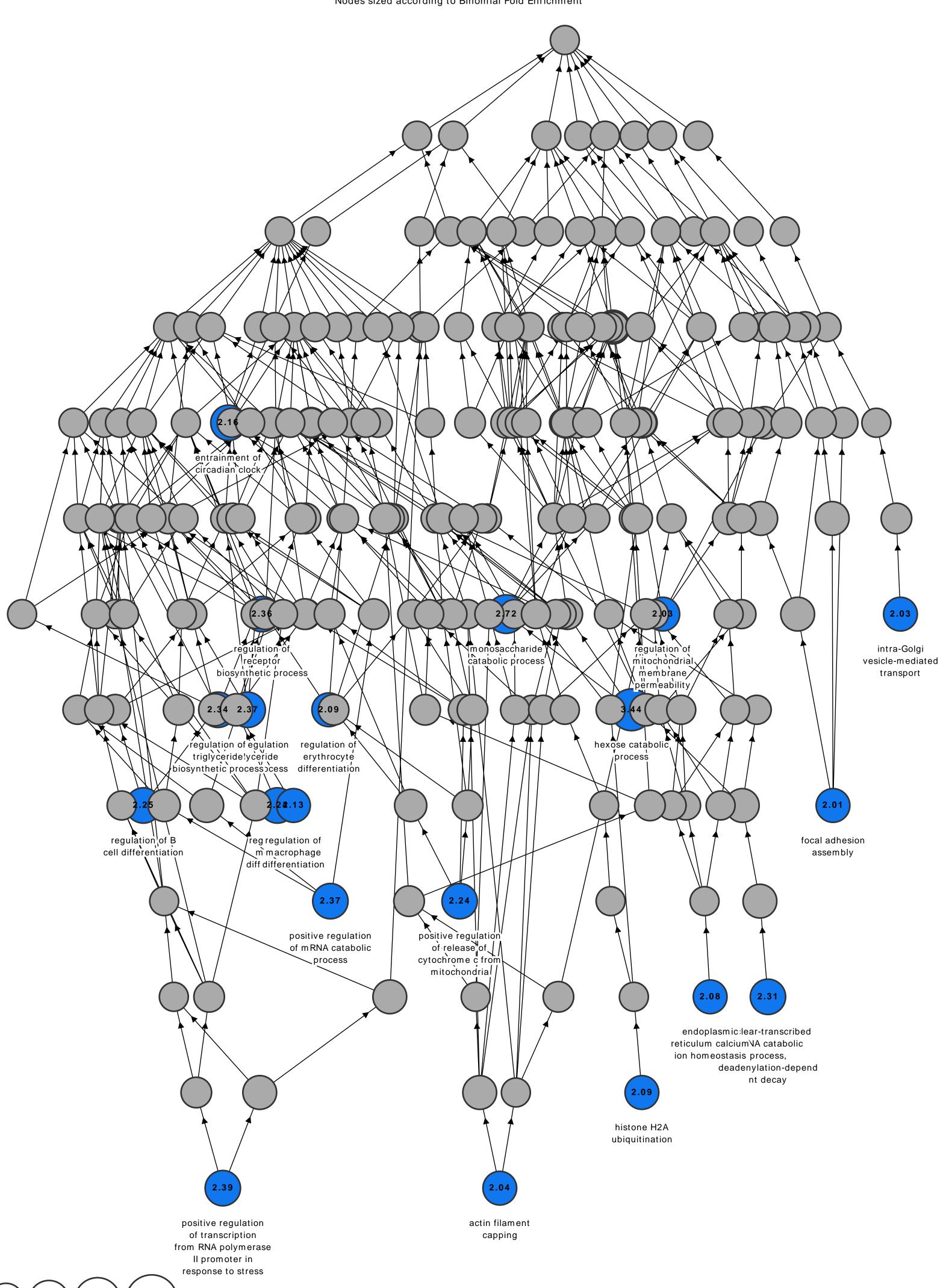
Nodes sized according to Binomial Fold Enrichment

entrainment of circadian clock

regulation of receptor biosynthetic process

monosaccharide catabolic process

regulation of mitochondrial membrane permeability

intra-Golgi vesicle-mediated transport

regulation of triglyceride biosynthetic process

regulation of glyceride biosynthetic process

regulation of erythrocyte differentiation

hexose catabolic process

regulation of B cell differentiation

regulation of macrophage differentiation

positive regulation of mRNA catabolic process

positive regulation of release of cytochrome c from mitochondrial

focal adhesion assembly

endoplasmic reticulum calcium ion homeostasis

nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay

histone H2A ubiquitination

positive regulation of transcription from RNA polymerase II promoter in response to stress

actin filament capping

Node size legend: < 1   2   3   4   > 5