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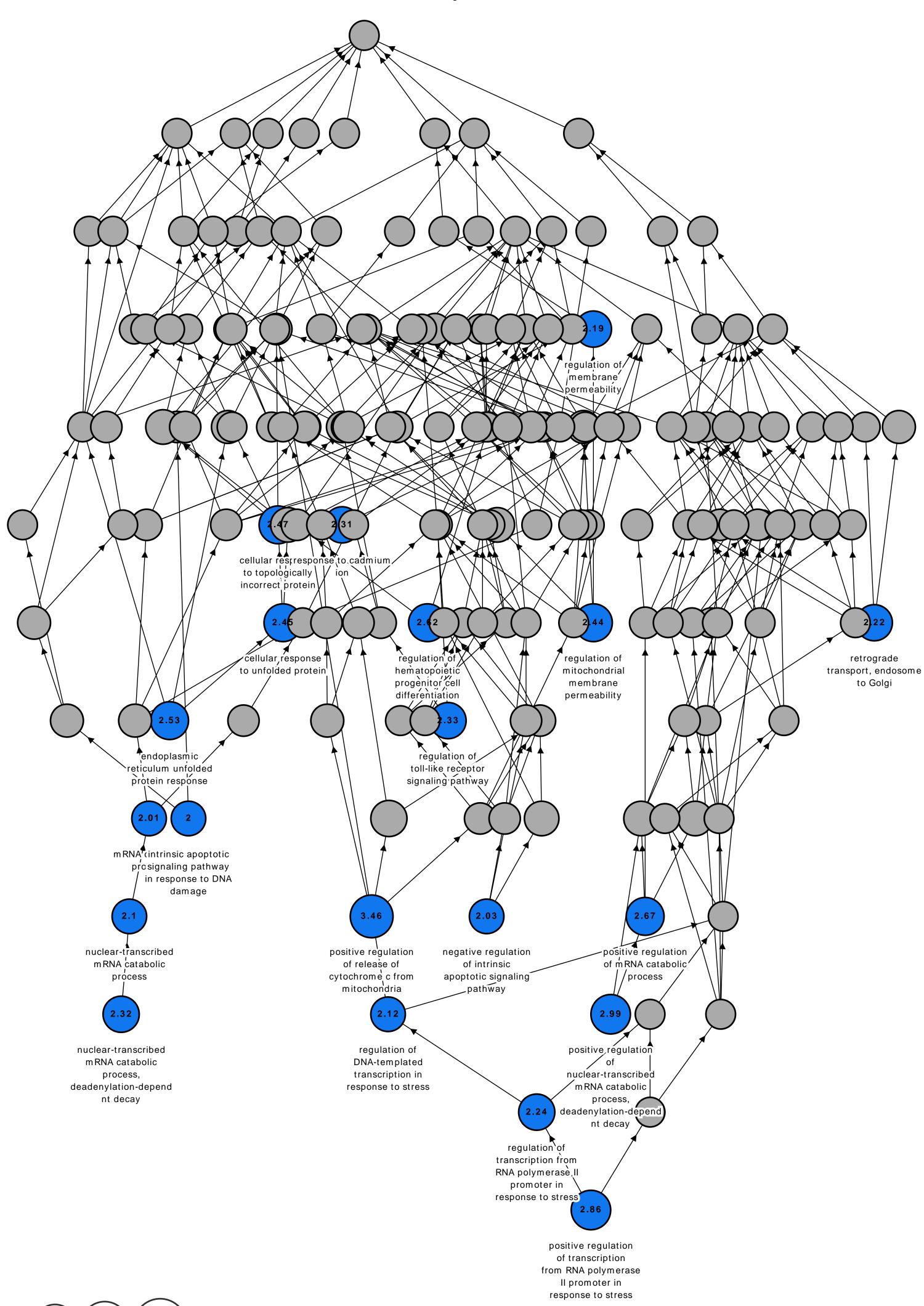
Nodes sized according to Binomial Fold Enrichment

2.19 regulation of membrane permeability

2.47 cellular response to topologically incorrect protein

2.31 cellular response to cadmium ion

2.45 cellular response to unfolded protein

2.62 regulation of hematopoietic progenitor cell differentiation

2.44 regulation of mitochondrial membrane permeability

2.22 retrograde transport, endosome to Golgi

2.53 endoplasmic reticulum unfolded protein response

2.33 regulation of toll-like receptor signaling pathway

2.01 **2** mRNA intrinsic apoptotic prosignaling pathway in response to DNA damage

2.1 nuclear-transcribed mRNA catabolic process

3.46 positive regulation of release of cytochrome c from mitochondria

2.03 negative regulation of intrinsic apoptotic signaling pathway

2.67 positive regulation of mRNA catabolic process

2.32 nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay

2.12 regulation of DNA-templated transcription in response to stress

2.99 positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay

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

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

Node size legend: **< 1** **2** **3** **4** **> 5**