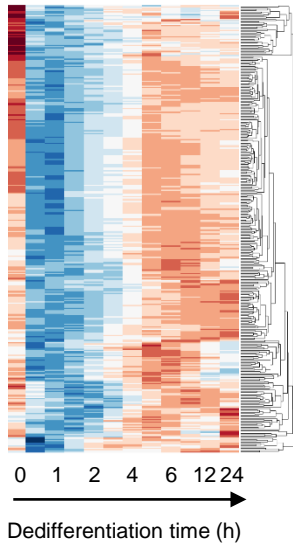


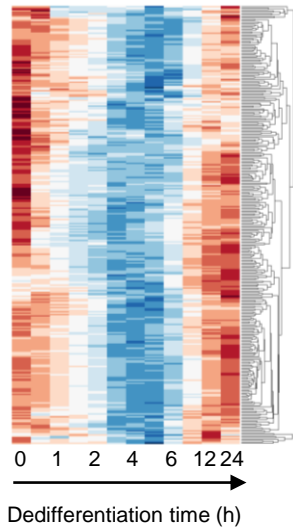
A



## GO biological process complete

DNA strand elongation involved in DNA replication	30.06	1.3·10 <sup>-14</sup>
mitotic DNA replication initiation	36.5	3.2·10 <sup>-5</sup>
pre-replicative complex assembly involved in DNA replication	36.5	2.6·10 <sup>-8</sup>
chromosome condensation	24.33	2.3·10 <sup>-8</sup>
microtubule polymerization	22.81	1.4·10 <sup>-5</sup>
replication fork arrest	36.5	0.00035
lagging strand elongation	29.2	5.6·10 <sup>-5</sup>
mitotic sister chromatid segregation	18.84	3.3·10 <sup>-14</sup>
DNA repair	8.05	8.7·10 <sup>-23</sup>
pyrimidine deoxyribonucleotide biosynthetic process	27.37	0.00061
establishment of chromosome localization	21.9	0.00095
mitotic spindle assembly	20.86	0.00014
DNA unwinding involved in DNA replication	20.28	2.2·10 <sup>-5</sup>
DNA replication checkpoint	18.25	3.2·10 <sup>-5</sup>
cytoplasmic microtubule organization	18.25	3.2·10 <sup>-5</sup>
mitotic spindle assembly checkpoint	18.25	0.00021
maintenance of DNA repeat elements	18.25	0.00140
double-strand break repair via homologous recombination	7.87	6.2·10 <sup>-7</sup>
'de novo' IMP biosynthetic process	15.64	0.00196
mismatch repair	15.03	2.1·10 <sup>-6</sup>
DNA synthesis involved in DNA repair	13.69	0.00265
regulation of cell cycle G2/M phase transition	12.17	0.00070
sister chromatid cohesion	18.25	1.2·10 <sup>-7</sup>
microtubule-based movement	13.27	8.3·10 <sup>-7</sup>
base-excision repair	13.04	0.00011
chromosome separation	12.88	2.4·10 <sup>-5</sup>
centrosome cycle	12.17	0.00015
chromatin silencing	11.23	0.00090
mitotic DNA integrity checkpoint	8.11	0.00249
telomere maintenance	8.11	0.00249
protein import into nucleus	7.1	0.00013
cell division	6.48	2.3·10 <sup>-13</sup>
protein export from nucleus	6.08	0.00030
proton transmembrane transport	5.84	0.00014
protein-containing complex localization	4.87	0.00226
mRNA splicing, via spliceosome	3.39	0.00208

B



## GO biological process complete

proteasomal protein catabolic process	12.49	3.8·10 <sup>-25</sup>
positive regulation of transcription initiation from RNA pol. II promoter	25.44	8.4·10 <sup>-6</sup>
fructose 1,6-bisphosphate metabolic process	40.7	0.00026
COPII-coated vesicle cargo loading	40.7	0.00026
attachment of GPI anchor to protein	33.91	3.2·10 <sup>-6</sup>
arginine biosynthetic process	32.56	3.7·10 <sup>-5</sup>
oxaloacetate metabolic process	24.42	0.00070
NADH metabolic process	24.42	0.00070
signal peptide processing	23.26	9.4·10 <sup>-5</sup>
proteasome assembly	23.26	2.4·10 <sup>-8</sup>
NADPH regeneration	20.35	0.00014
peptide catabolic process	20.35	0.00014
glyoxylate cycle	20.35	0.00103
hydrogen peroxide catabolic process	17.44	0.00145
glycolytic process	16.28	2.1·10 <sup>-7</sup>
gluconeogenesis	16.28	0.00027
endoplasmic reticulum organization	14.8	0.00036
ubiquitin-dependent ERAD pathway	11.63	1.7·10 <sup>-6</sup>
retrograde vesicle-mediated transport, Golgi to ER	9.69	0.00033
protein localization to endoplasmic reticulum	9.04	0.00012
regulation of protein catabolic process	8.14	0.00019
intra-Golgi vesicle-mediated transport	8.14	0.00067
cellular response to oxidative stress	7.94	1.9·10 <sup>-5</sup>
tricarboxylic acid cycle	7.54	0.00091
fatty acid beta-oxidation	7.54	0.00091
cellular oxidant detoxification	6.78	0.00046
regulation of proteolysis	5.81	0.00095
cell redox homeostasis	5.68	0.00106
negative regulation of gene expression	3.13	0.00074
intracellular protein transport	2.44	0.00035