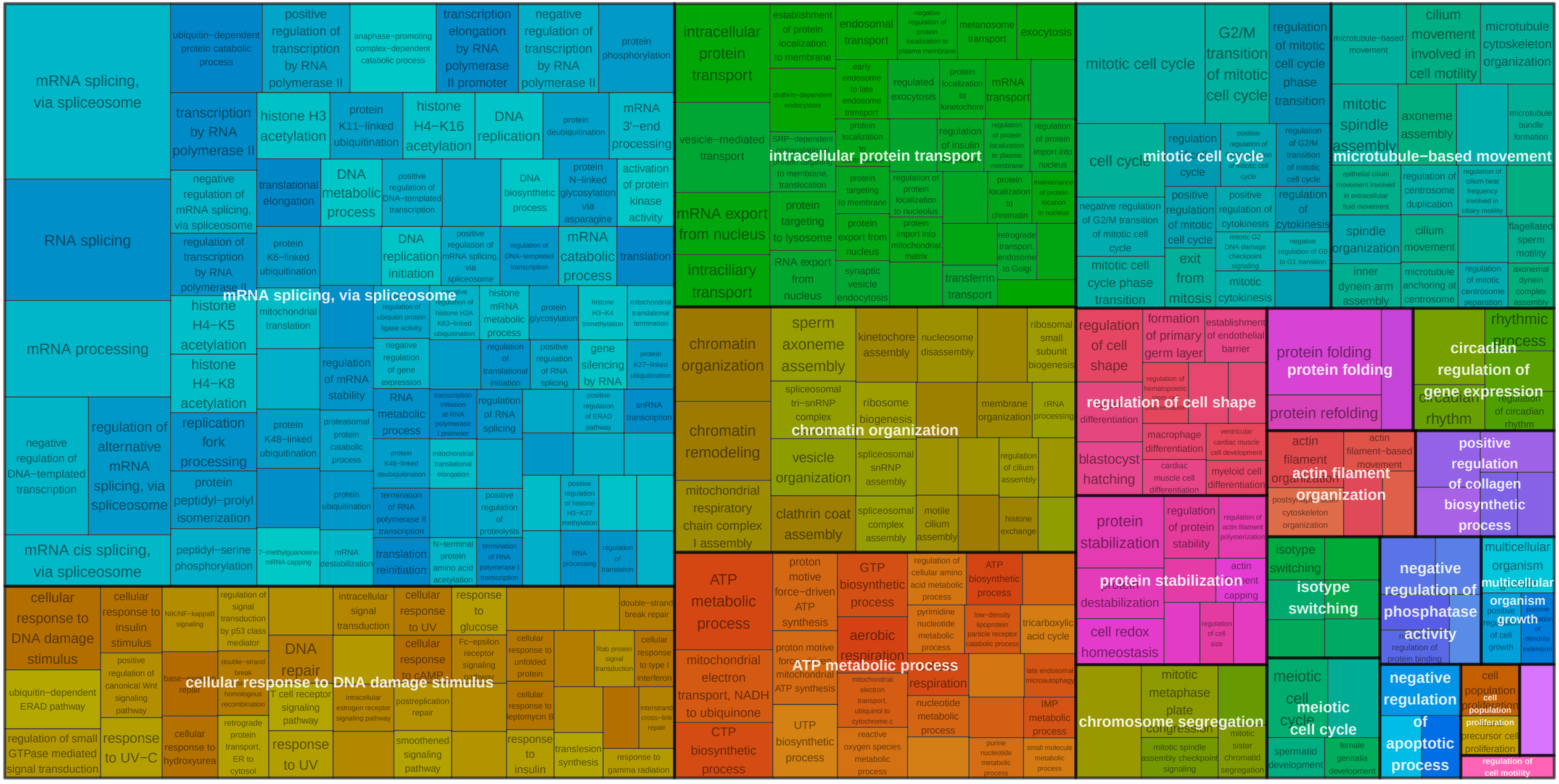
mRNA splicing, via spliceosome
ubiquitin−dependent protein catabolic process
positive regulation of transcription by RNA polymerase II
anaphase−promoting complex−dependent catabolic process
transcription elongation by RNA polymerase II promoter
negative regulation of transcription by RNA polymerase II
protein phosphorylation
RNA splicing
transcription by RNA polymerase II
histone H3 acetylation
protein K11−linked ubiquitination
histone H4−K16 acetylation
DNA replication
protein deubiquitination
mRNA 3'−end processing
negative regulation of mRNA splicing, via spliceosome
translational elongation
DNA metabolic process
positive regulation of DNA−templated transcription
DNA biosynthetic process
protein N−linked glycosylation via asparagine
activation of protein kinase activity
regulation of transcription by RNA polymerase II
protein K6−linked ubiquitination
DNA replication initiation
positive regulation of mRNA splicing, via spliceosome
regulation of DNA−templated transcription
mRNA catabolic process
translation
mRNA processing
histone H4−K5 acetylation
mitochondrial translation
regulation of ubiquitin protein ligase activity
regulation of histone H2A K63−linked ubiquitination
histone mRNA metabolic process
protein glycosylation
histone H3−K4 trimethylation
mitochondrial translational termination
histone H4−K8 acetylation
regulation of mRNA stability
negative regulation of gene expression
regulation of translational initiation
positive regulation of RNA splicing
gene silencing by RNA
protein K27−linked ubiquitination
replication fork processing
protein K48−linked ubiquitination
proteasomal protein catabolic process
RNA metabolic process
transcription initiation at RNA polymerase I promoter
regulation of RNA splicing
positive regulation of ERAD pathway
snRNA transcription
protein peptidyl−prolyl isomerization
protein K48−linked deubiquitination
mitochondrial translational elongation
negative regulation of DNA−templated transcription
regulation of alternative mRNA splicing, via spliceosome
protein ubiquitination
termination of RNA polymerase II transcription
positive regulation of histone H3−K27 methylation
peptidyl−serine phosphorylation
7−methylguanosine mRNA capping
mRNA destabilization
translation reinitiation
N−terminal protein amino acid acetylation
termination of RNA polymerase I transcription
RNA processing
regulation of translation
mRNA cis splicing, via spliceosome
intracellular protein transport
establishment of protein localization to membrane
endosomal transport
negative regulation of protein localization to plasma membrane
melanosome transport
exocytosis
vesicle−mediated transport
clathrin−dependent endocytosis
early endosome to late endosome transport
regulated exocytosis
protein localization to kinetochore
mRNA transport
SRP−dependent cotranslational protein targeting to membrane, translocation
protein localization to chromosome
regulation of insulin secretion
regulation of protein localization to plasma membrane
regulation of protein import into nucleus
mRNA export from nucleus
protein targeting to membrane
regulation of protein localization to nucleolus
protein localization to chromatin
maintenance of protein location in nucleus
protein targeting to lysosome
protein export from nucleus
protein import into mitochondrial matrix
intraciliary transport
RNA export from nucleus
synaptic vesicle endocytosis
retrograde transport, endosome to Golgi
transferrin transport
mitotic cell cycle
G2/M transition of mitotic cell cycle
regulation of mitotic cell cycle phase transition
cell cycle
regulation of cell cycle
positive regulation of cell cycle
regulation of G2/M transition of mitotic cell cycle
negative regulation of G2/M transition of mitotic cell cycle
positive regulation of mitotic cell cycle
positive regulation of cytokinesis
regulation of cytokinesis
mitotic cell cycle phase transition
exit from mitosis
mitotic G2 DNA damage checkpoint signaling
mitotic cytokinesis
negative regulation of G0 to G1 transition
microtubule−based movement
cilium movement involved in cell motility
microtubule cytoskeleton organization
mitotic spindle assembly
axoneme assembly
microtubule bundle formation
epithelial cilium movement involved in extracellular fluid movement
regulation of centrosome duplication
regulation of cilium beat frequency involved in ciliary motility
spindle organization
cilium movement
flagellated sperm motility
inner dynein arm assembly
microtubule anchoring at centrosome
regulation of mitotic centrosome separation
axonemal dynein complex assembly
chromatin organization
sperm axoneme assembly
kinetochore assembly
nucleosome disassembly
ribosomal small subunit biogenesis
chromatin remodeling
spliceosomal tri−snRNP complex
ribosome biogenesis
membrane organization
rRNA processing
vesicle organization
spliceosomal snRNP assembly
regulation of cilium assembly
mitochondrial respiratory chain complex I assembly
clathrin coat assembly
spliceosomal complex assembly
motile cilium assembly
histone exchange
regulation of cell shape
formation of primary germ layer
establishment of endothelial barrier
regulation of hematopoietic stem cell differentiation
differentiation
macrophage differentiation
ventricular cardiac muscle cell development
blastocyst hatching
cardiac muscle cell differentiation
myeloid cell differentiation
protein folding
protein refolding
circadian regulation of gene expression
rhythmic process
circadian rhythm
regulation of circadian rhythm
actin filament organization
actin filament−based movement
positive regulation of collagen biosynthetic process
protein stabilization
regulation of protein stability
regulation of actin filament polymerization
protein destabilization
actin filament capping
cell redox homeostasis
regulation of cell size
isotype switching
negative regulation of phosphatase activity
multicellular organism growth
multicellular organism
positive regulation of cell growth
positive regulation of dendrite extension
regulation of protein binding
ATP metabolic process
proton motive force−driven ATP synthesis
GTP biosynthetic process
regulation of cellular amino acid metabolic process
ATP biosynthetic process
pyrimidine nucleotide metabolic process
low−density lipoprotein particle receptor catabolic process
tricarboxylic acid cycle
proton motive force−driven mitochondrial ATP synthesis
aerobic respiration
mitochondrial electron transport, NADH to ubiquinone
late endosomal microautophagy
mitochondrial electron transport, ubiquinol to cytochrome c
respiration
nucleotide metabolic process
IMP metabolic process
CTP biosynthetic process
UTP biosynthetic process
reactive oxygen species metabolic process
purine nucleotide metabolic process
small molecule metabolic process
chromosome segregation
mitotic metaphase plate congression
mitotic spindle assembly checkpoint signaling
mitotic sister chromatid segregation
meiotic cell cycle
meiotic cell cycle
spermatid development
female genitalia development
negative regulation of apoptotic process
cell population proliferation
cell population proliferation
precursor cell proliferation
regulation of cell motility
cellular response to DNA damage stimulus
cellular response to insulin stimulus
NIK/NF−kappaB signaling
regulation of signal transduction by p53 class mediator
intracellular signal transduction
cellular response to UV
cellular response to glucose
double−strand break repair
ubiquitin−dependent ERAD pathway
positive regulation of canonical Wnt signaling pathway
base−excision repair
double−strand break repair via homologous recombination
DNA repair
cellular response to cAMP
Fc−epsilon receptor signaling pathway
cellular response to unfolded protein
Rab protein signal transduction
cellular response to type I interferon
regulation of small GTPase mediated signal transduction
response to UV−C
cellular response to hydroxyurea
retrograde protein transport, ER to cytosol
T cell receptor signaling pathway
intracellular estrogen receptor signaling pathway
postreplication repair
cellular response to leptomycin B
interstrand cross−link repair
response to UV
smoothened signaling pathway
response to insulin
translesion synthesis
response to gamma radiation