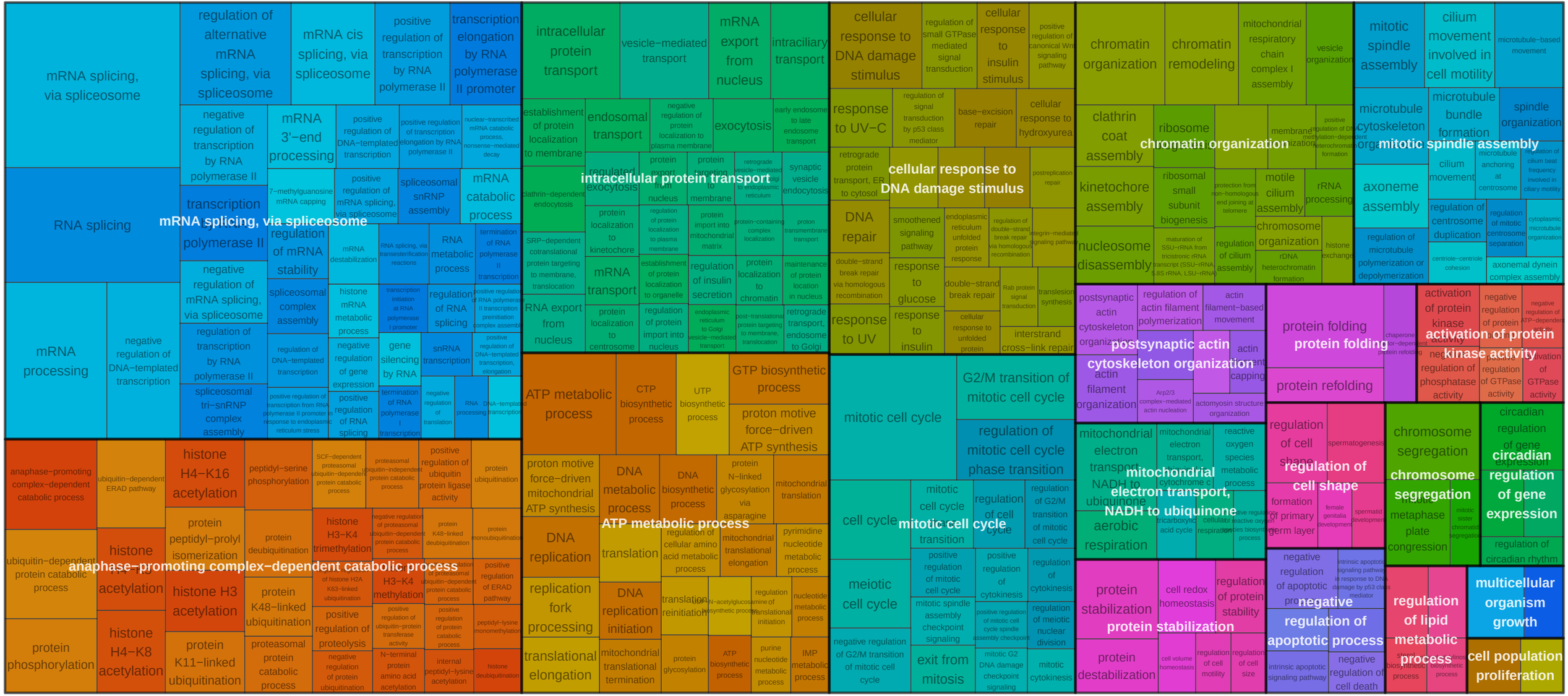
mRNA splicing, via spliceosome
regulation of alternative mRNA splicing, via spliceosome
mRNA cis splicing, via spliceosome
positive regulation of transcription by RNA polymerase II
transcription elongation by RNA polymerase II promoter
RNA splicing
negative regulation of transcription by RNA polymerase II
mRNA 3'−end processing
positive regulation of DNA−templated transcription
positive regulation of transcription elongation by RNA polymerase II
nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
transcription by RNA polymerase II
7−methylguanosine mRNA capping
positive regulation of mRNA splicing, via spliceosome
spliceosomal snRNP assembly
mRNA catabolic process
mRNA processing
negative regulation of DNA−templated transcription
negative regulation of mRNA splicing, via spliceosome
regulation of mRNA stability
mRNA destabilization
RNA splicing, via transesterification reactions
RNA metabolic process
termination of RNA polymerase II transcription
regulation of transcription by RNA polymerase II
spliceosomal complex assembly
histone mRNA metabolic process
transcription initiation at RNA polymerase I promoter
regulation of RNA splicing
positive regulation of RNA polymerase II transcription preinitiation complex assembly
spliceosomal tri−snRNP complex assembly
regulation of DNA−templated transcription
negative regulation of gene expression
gene silencing by RNA
snRNA transcription
positive regulation of DNA−templated transcription, elongation
positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress
positive regulation of RNA splicing
termination of RNA polymerase I transcription
negative regulation of translation
RNA processing
DNA−templated transcription
intracellular protein transport
vesicle−mediated transport
mRNA export from nucleus
intracellular transport
establishment of protein localization to membrane
endosomal transport
negative regulation of protein localization to plasma membrane
exocytosis
early endosome to late endosome transport
regulated exocytosis
protein export from nucleus
protein targeting to membrane
retrograde vesicle−mediated transport, Golgi to endoplasmic reticulum
synaptic vesicle endocytosis
clathrin−dependent endocytosis
protein localization to kinetochore
regulation of protein localization to plasma membrane
protein import into mitochondrial matrix
protein−containing complex localization
proton transmembrane transport
SRP−dependent cotranslational protein targeting to membrane, translocation
mRNA transport
establishment of protein localization to organelle
regulation of insulin secretion
protein localization to chromatin
maintenance of protein location in nucleus
RNA export from nucleus
protein localization to centrosome
regulation of protein import into nucleus
endoplasmic reticulum to Golgi vesicle−mediated transport
post−translational protein targeting to membrane, translocation
retrograde transport, endosome to Golgi
cellular response to DNA damage stimulus
regulation of small GTPase mediated signal transduction
cellular response to insulin stimulus
positive regulation of canonical Wnt signaling pathway
response to UV−C
regulation of signal transduction by p53 class mediator
base−excision repair
cellular response to hydroxyurea
retrograde protein transport, ER to cytosol
postreplication repair
DNA repair
smoothened signaling pathway
endoplasmic reticulum unfolded protein response
regulation of double−strand break repair via homologous recombination
integrin−mediated signaling pathway
double−strand break repair via homologous recombination
response to glucose
double−strand break repair
Rab protein signal transduction
translesion synthesis
response to UV
response to insulin
cellular response to unfolded protein
interstrand cross−link repair
chromatin organization
chromatin remodeling
mitochondrial respiratory chain complex I assembly
vesicle organization
clathrin coat assembly
ribosome biogenesis
membrane organization
positive regulation of DNA methylation−dependent heterochromatin formation
kinetochore assembly
ribosomal small subunit biogenesis
protection from non−homologous end joining at telomere
motile cilium assembly
rRNA processing
nucleosome disassembly
maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
regulation of cilium assembly
chromosome organization
histone exchange
rDNA heterochromatin formation
mitotic spindle assembly
cilium movement involved in cell motility
microtubule−based movement
microtubule cytoskeleton organization
microtubule bundle formation
spindle organization
cilium movement
microtubule anchoring at centrosome
regulation of cilium beat frequency involved in ciliary motility
axoneme assembly
regulation of centrosome duplication
regulation of mitotic centrosome separation
cytoplasmic microtubule organization
regulation of microtubule polymerization or depolymerization
centriole−centriole cohesion
axonemal dynein complex assembly
ATP metabolic process
CTP biosynthetic process
UTP biosynthetic process
GTP biosynthetic process
proton motive force−driven ATP synthesis
proton motive force−driven mitochondrial ATP synthesis
DNA metabolic process
DNA biosynthetic process
protein N−linked glycosylation via asparagine
mitochondrial translation
DNA replication
translation
regulation of cellular amino acid metabolic process
mitochondrial translational elongation
pyrimidine nucleotide metabolic process
replication fork processing
DNA replication initiation
translation reinitiation
UDP−N−acetylglucosamine biosynthetic process
regulation of translational initiation
nucleotide metabolic process
translational elongation
mitochondrial translational termination
protein glycosylation
ATP biosynthetic process
purine nucleotide metabolic process
IMP metabolic process
mitotic cell cycle
G2/M transition of mitotic cell cycle
regulation of mitotic cell cycle phase transition
cell cycle
mitotic cell cycle
mitotic cell cycle transition
regulation of cell cycle
regulation of G2/M transition of mitotic cell cycle
meiotic cell cycle
positive regulation of mitotic cell cycle
positive regulation of cytokinesis
regulation of cytokinesis
negative regulation of G2/M transition of mitotic cell cycle
mitotic spindle assembly checkpoint signaling
positive regulation of mitotic cell cycle spindle assembly checkpoint
regulation of meiotic nuclear division
exit from mitosis
mitotic G2 DNA damage checkpoint signaling
mitotic cytokinesis
postsynaptic actin cytoskeleton organization
regulation of actin filament polymerization
actin filament−based movement
actin filament organization
Arp2/3 complex−mediated actin nucleation
actomyosin structure organization
actin capping
protein folding
protein folding
chaperone−mediated protein folding
activation of protein kinase activity
negative regulation of protein kinase activity
negative regulation of phosphatase activity
positive regulation of GTPase activity
activation of GTPase activity
mitochondrial electron transport, NADH to ubiquinone
mitochondrial electron transport, cytochrome c to oxygen
reactive oxygen species metabolic process
aerobic respiration
tricarboxylic acid cycle
cellular respiration
regulation of reactive oxygen species biosynthetic process
regulation of cell shape
spermatogenesis
formation of primary germ layer
female gonad development
spermatid development
chromosome segregation
metaphase plate congression
mitotic sister chromatid segregation
circadian regulation of gene expression
regulation of circadian rhythm
protein stabilization
cell redox homeostasis
regulation of protein stability
protein destabilization
cell volume homeostasis
regulation of cell motility
regulation of cell size
negative regulation of apoptotic process
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
intrinsic apoptotic signaling pathway
negative regulation of cell death
regulation of lipid metabolic process
sphingolipid biosynthetic process
cholesterol biosynthetic process
multicellular organism growth
cell population proliferation
anaphase−promoting complex−dependent catabolic process
ubiquitin−dependent ERAD pathway
histone H4−K16 acetylation
peptidyl−serine phosphorylation
SCF−dependent proteasomal ubiquitin−dependent protein catabolic process
proteasomal ubiquitin−independent protein catabolic process
positive regulation of ubiquitin protein ligase activity
protein ubiquitination
ubiquitin−dependent protein catabolic process
histone H4−K5 acetylation
protein peptidyl−prolyl isomerization
protein deubiquitination
histone H3−K4 trimethylation
negative regulation of proteasomal ubiquitin−dependent protein catabolic process
protein K48−linked deubiquitination
protein monoubiquitination
protein phosphorylation
histone H4−K8 acetylation
histone H3 acetylation
protein K48−linked ubiquitination
histone H3−K4 methylation
positive regulation of histone H2A K63−linked ubiquitination
positive regulation of proteasomal ubiquitin−dependent protein catabolic process
positive regulation of ERAD pathway
protein K11−linked ubiquitination
proteasomal protein catabolic process
positive regulation of proteolysis
positive regulation of ubiquitin−protein transferase activity
positive regulation of protein catabolic process
peptidyl−lysine monomethylation
negative regulation of protein ubiquitination
N−terminal protein amino acid acetylation
internal peptidyl−lysine acetylation
histone deubiquitination