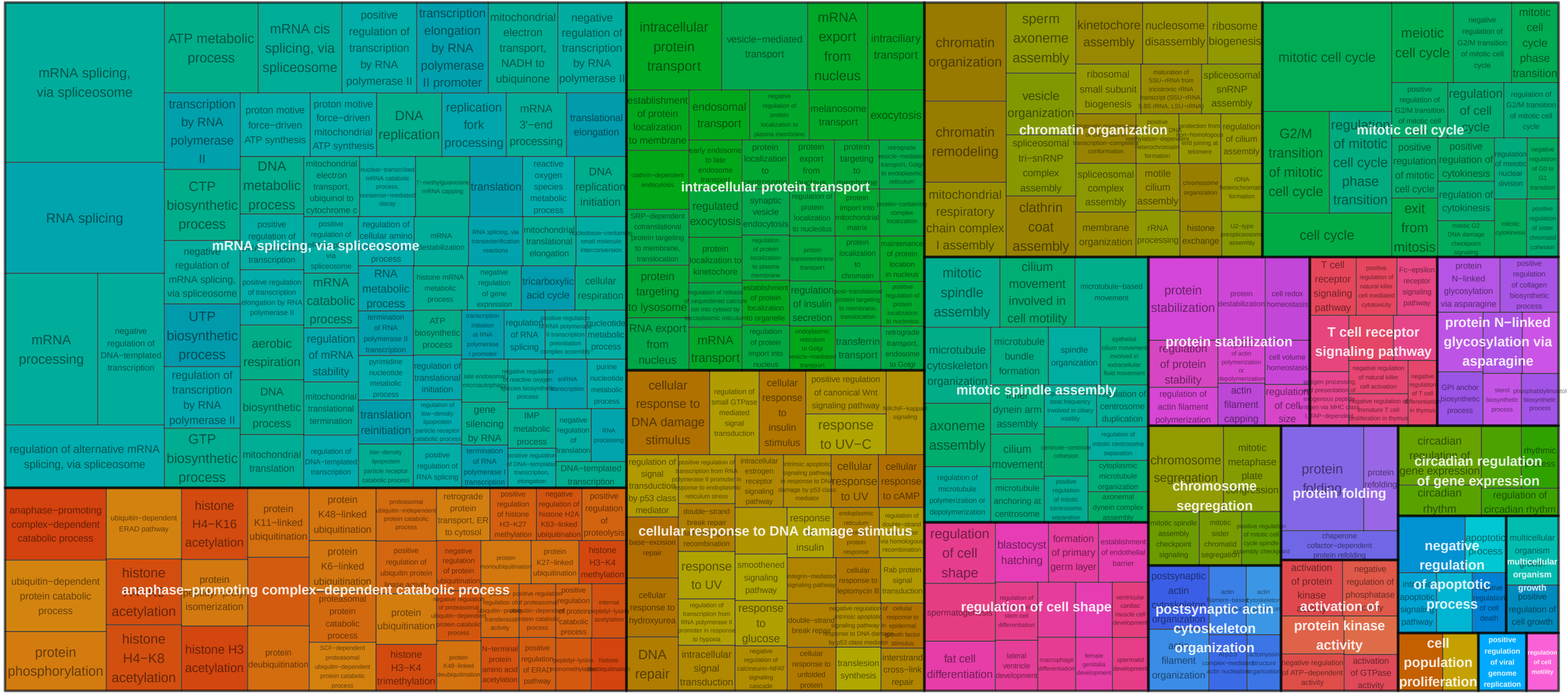
mRNA splicing, via spliceosome
ATP metabolic process
mRNA cis splicing, via spliceosome
positive regulation of transcription by RNA polymerase II
transcription elongation by RNA polymerase II promoter
mitochondrial electron transport, NADH to ubiquinone
negative regulation of transcription by RNA polymerase II
RNA splicing
transcription by RNA polymerase II
proton motive force−driven ATP synthesis
proton motive force−driven mitochondrial ATP synthesis
DNA replication
replication fork processing
mRNA 3'−end processing
translational elongation
CTP biosynthetic process
DNA metabolic process
mitochondrial electron transport, ubiquinol to cytochrome c
nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
7−methylguanosine mRNA capping
translation
reactive oxygen species metabolic process
DNA replication initiation
mRNA processing
negative regulation of DNA−templated transcription
negative regulation of mRNA splicing, via spliceosome
positive regulation of transcription
positive regulation of mRNA splicing, via spliceosome
regulation of cellular amino acid metabolic process
mRNA destabilization
RNA splicing, via transesterification reactions
mitochondrial translational elongation
nucleobase−containing small molecule interconversion
positive regulation of transcription elongation by RNA polymerase II
UTP biosynthetic process
mRNA catabolic process
RNA metabolic process
histone mRNA metabolic process
negative regulation of gene expression
tricarboxylic acid cycle
cellular respiration
aerobic respiration
regulation of mRNA stability
termination of RNA polymerase II transcription
ATP biosynthetic process
transcription initiation at RNA polymerase I promoter
regulation of RNA splicing
positive regulation of RNA polymerase II transcription preinitiation complex assembly
nucleotide metabolic process
regulation of transcription by RNA polymerase II
DNA biosynthetic process
pyrimidine nucleotide metabolic process
regulation of translational initiation
late endosomal microautophagy
negative regulation of reactive oxygen species biosynthetic process
snRNA transcription
purine nucleotide metabolic process
regulation of alternative mRNA splicing, via spliceosome
GTP biosynthetic process
mitochondrial translational termination
translation reinitiation
regulation of low−density lipoprotein particle receptor catabolic process
gene silencing by RNA
IMP metabolic process
negative regulation of translation
RNA processing
mitochondrial translation
regulation of DNA−templated transcription
low−density lipoprotein particle receptor catabolic process
positive regulation of RNA splicing
termination of RNA polymerase I transcription
positive regulation of DNA−templated transcription, elongation
DNA−templated transcription
intracellular protein transport
vesicle−mediated transport
mRNA export from nucleus
intraciliary transport
establishment of protein localization to membrane
endosomal transport
negative regulation of protein localization to plasma membrane
melanosome transport
exocytosis
clathrin−dependent endocytosis
early endosome to late endosome transport
protein localization to centrosome
protein export from nucleus
protein targeting to membrane
retrograde vesicle−mediated transport, Golgi to endoplasmic reticulum
SRP−dependent cotranslational protein targeting to membrane, translocation
regulated exocytosis
synaptic vesicle endocytosis
regulation of protein localization to nucleolus
protein import into mitochondrial matrix
protein−containing complex localization
protein localization to kinetochore
regulation of protein localization to plasma membrane
proton transmembrane transport
protein localization to chromatin
maintenance of protein location in nucleus
protein targeting to lysosome
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
establishment of protein localization to organelle
regulation of insulin secretion
post−translational protein targeting to membrane, translocation
positive regulation of protein localization to nucleolus
RNA export from nucleus
mRNA transport
regulation of protein import into nucleus
endoplasmic reticulum to Golgi vesicle−mediated transport
transferrin transport
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
NIK/NF−kappaB signaling
regulation of signal transduction by p53 class mediator
positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress
intracellular estrogen receptor signaling pathway
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
cellular response to UV
cellular response to cAMP
double−strand break repair
base−excision repair
recombination
response to UV
response to insulin
endoplasmic reticulum
protein response
regulation of double−strand break repair via homologous recombination
smoothened signaling pathway
integrin−mediated signaling pathway
cellular response to leptomycin B
Rab protein signal transduction
response to glucose
double−strand break repair
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
cellular response to epidermal growth factor stimulus
cellular response to hydroxyurea
regulation of transcription from RNA polymerase II promoter in response to hypoxia
DNA repair
intracellular signal transduction
negative regulation of calcineurin−NFAT signaling cascade
cellular response to unfolded protein
translesion synthesis
interstrand cross−link repair
chromatin organization
sperm axoneme assembly
kinetochore assembly
nucleosome disassembly
ribosome biogenesis
chromatin remodeling
vesicle organization
ribosomal small subunit biogenesis
maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
spliceosomal snRNP assembly
spliceosomal tri−snRNP complex assembly
positive regulation of DNA transcription−dependent heterochromatin formation
protection from non−homologous end joining at telomere
regulation of cilium assembly
mitochondrial respiratory chain complex I assembly
clathrin coat assembly
spliceosomal complex assembly
motile cilium assembly
chromosome organization
rDNA heterochromatin formation
membrane organization
rRNA processing
histone exchange
U2−type prespliceosome assembly
mitotic cell cycle
meiotic cell cycle
negative regulation of G2/M transition of mitotic cell cycle
mitotic cell cycle phase transition
positive regulation of G2/M transition of mitotic cell cycle
regulation of cell cycle
regulation of G2/M transition of mitotic cell cycle
G2/M transition of mitotic cell cycle
regulation of mitotic cell cycle phase transition
positive regulation of mitotic cell cycle
positive regulation of cytokinesis
regulation of meiotic nuclear division
negative regulation of G0 to G1 transition
regulation of cytokinesis
exit from mitosis
cell cycle
mitotic G2 DNA damage checkpoint signaling
mitotic cytokinesis
positive regulation of sister chromatid cohesion
mitotic spindle assembly
cilium movement involved in cell motility
microtubule−based movement
microtubule cytoskeleton organization
microtubule bundle formation
spindle organization
epithelial cilium movement involved in extracellular fluid movement
axoneme assembly
dynein arm assembly
beat frequency involved in ciliary motility
regulation of centrosome duplication
cilium movement
centriole−centriole cohesion
regulation of mitotic centrosome separation
cytoplasmic microtubule organization
microtubule anchoring at centrosome
positive regulation of mitotic centrosome separation
axonemal dynein complex assembly
regulation of microtubule polymerization or depolymerization
protein stabilization
protein destabilization
cell redox homeostasis
regulation of protein stability
regulation of actin filament polymerization
regulation of actin polymerization or depolymerization
actin filament capping
cell volume homeostasis
regulation of cell size
T cell receptor signaling pathway
positive regulation of natural killer cell mediated cytotoxicity
Fc−epsilon receptor signaling pathway
negative regulation of natural killer cell activation
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
negative regulation of immature T cell proliferation in thymus
negative regulation of T cell differentiation in thymus
protein N−linked glycosylation via asparagine
positive regulation of collagen biosynthetic process
GPI anchor biosynthetic process
sterol biosynthetic process
phosphatidylinositol biosynthetic process
regulation of cell shape
blastocyst hatching
formation of primary germ layer
establishment of endothelial barrier
spermatogenesis
regulation of stem cell differentiation
ventricular cardiac muscle cell development
fat cell differentiation
lateral ventricle development
macrophage differentiation
female genitalia development
spermatid development
chromosome segregation
mitotic metaphase plate congression
mitotic spindle assembly checkpoint signaling
mitotic sister chromatid segregation
positive regulation of mitotic cell cycle spindle assembly checkpoint
protein folding
protein refolding
chaperone cofactor−dependent protein refolding
circadian regulation of gene expression
circadian rhythm
regulation of circadian rhythm
postsynaptic actin cytoskeleton organization
actin filament−based process
actin cytoskeleton organization
actin filament organization
Arp2/3 complex−mediated actin nucleation
actomyosin structure organization
activation of protein kinase activity
negative regulation of phosphatase activity
negative regulation of ATP−dependent activity
activation of GTPase activity
negative regulation of apoptotic process
apoptotic process
multicellular organism growth
multicellular organism
positive regulation of cell growth
cell population proliferation
positive regulation of viral genome replication
regulation of cell motility
anaphase−promoting complex−dependent catabolic process
ubiquitin−dependent ERAD pathway
histone H4−K16 acetylation
protein K11−linked ubiquitination
protein K48−linked ubiquitination
proteasome−independent protein catabolic process
retrograde protein transport, ER to cytosol
positive regulation of histone H3−K27 methylation
negative regulation of histone H2A K63−linked ubiquitination
positive regulation of proteolysis
ubiquitin−dependent protein catabolic process
histone acetylation
protein K6−linked ubiquitination
positive regulation of ubiquitin protein ligase activity
negative regulation of protein ubiquitination
protein monoubiquitination
protein K27−linked ubiquitination
histone H3−K4 methylation
proteasomal protein catabolic process
protein ubiquitination
positive regulation of proteasomal ubiquitin−dependent protein catabolic process
positive regulation of ubiquitin−protein transferase activity
positive regulation of ubiquitin−dependent protein catabolic process
internal peptidyl−lysine acetylation
protein phosphorylation
histone H4−K8 acetylation
histone H3 acetylation
protein deubiquitination
SCF−dependent proteasomal ubiquitin−dependent protein catabolic process
histone H3−K4 trimethylation
protein K48−linked deubiquitination
N−terminal protein amino acid acetylation
positive regulation of ERAD pathway
peptidyl−lysine monomethylation
histone deubiquitination