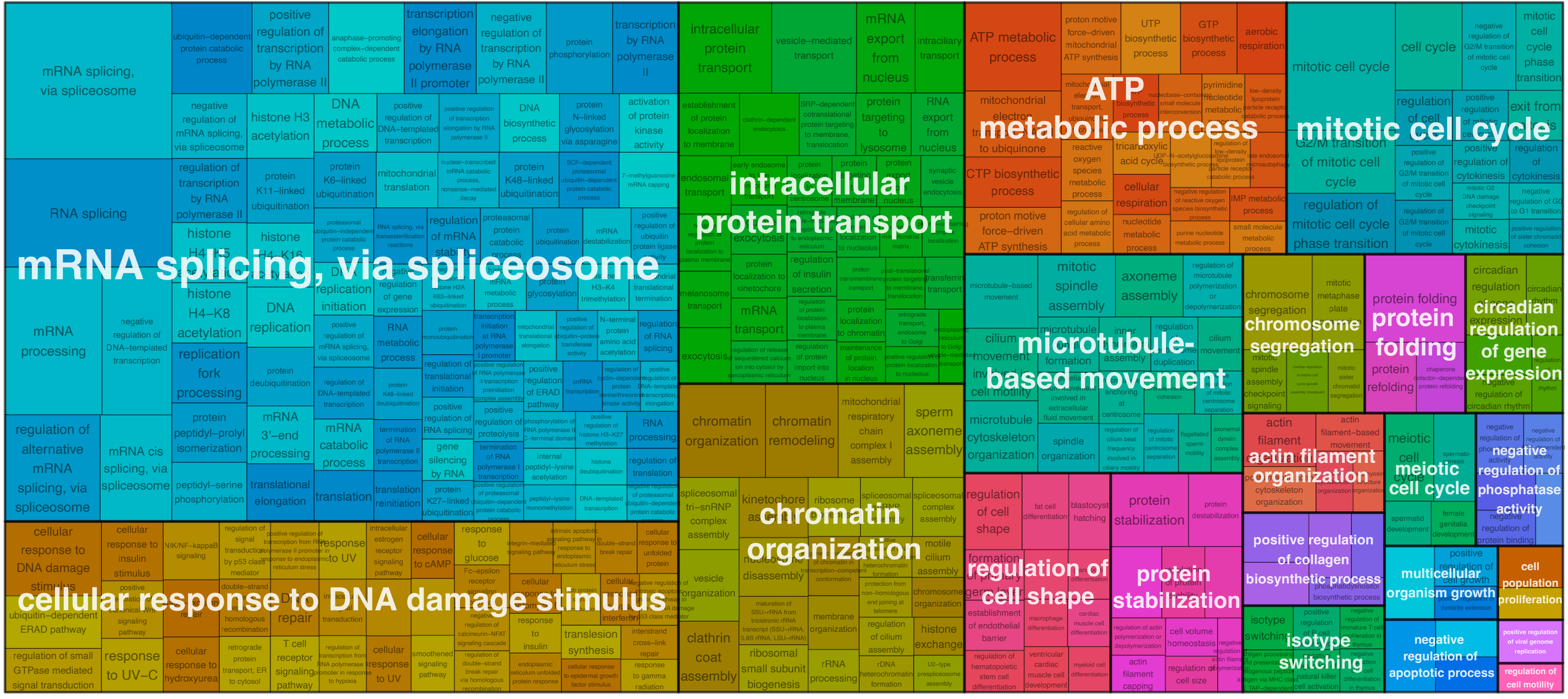
mRNA splicing, via spliceosome
cellular response to DNA damage stimulus
chromatin organization
intracellular protein transport
ATP metabolic process
mitotic cell cycle
microtubule-based movement
protein folding
chromosome segregation
actin filament organization
meiotic cell cycle
negative regulation of phosphatase activity
regulation of cell shape
protein stabilization
isotype switching
multicellular organism growth
cell population proliferation
negative regulation of apoptotic process
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
transcription by RNA polymerase II
RNA splicing
mRNA processing
negative regulation of DNA–templated transcription
regulation of alternative mRNA splicing, via spliceosome
mRNA cis splicing, via spliceosome
negative regulation of mRNA splicing, via spliceosome
histone H3 acetylation
DNA metabolic process
positive regulation of DNA–templated transcription
positive regulation of transcription elongation by RNA polymerase II
DNA biosynthetic process
protein N–linked glycosylation via asparagine
activation of protein kinase activity
regulation of transcription by RNA polymerase II
protein K11–linked ubiquitination
protein K6–linked ubiquitination
mitochondrial translation
nuclear–transcribed mRNA catabolic process, nonsense–mediated decay
protein K48–linked ubiquitination
SCF–dependent proteasomal ubiquitin–dependent protein catabolic process
7–methylguanosine mRNA capping
histone H4–K5 acetylation
histone H4–K16 acetylation
histone H4–K8 acetylation
DNA replication
proteasomal ubiquitin–independent protein catabolic process
RNA splicing, via transesterification reactions
regulation of mRNA stability
proteasomal protein catabolic process
protein ubiquitination
mRNA destabilization
positive regulation of ubiquitin protein ligase activity
DNA replication initiation
regulation of gene expression
histone H2A K63–linked ubiquitination
mRNA metabolic process
protein glycosylation
histone H3–K4 trimethylation
mitochondrial translational termination
RNA metabolic process
protein monoubiquitination
transcription initiation at RNA polymerase I promoter
mitochondrial translational elongation
positive regulation of ubiquitin–protein transferase activity
N–terminal protein amino acid acetylation
regulation of RNA splicing
regulation of translational initiation
positive regulation of RNA polymerase II transcription preinitiation complex assembly
snRNA transcription
regulation of cyclin–dependent protein serine/threonine kinase activity
positive regulation of DNA–template transcription, elongation
positive regulation of ERAD pathway
positive regulation of RNA splicing
positive regulation of proteolysis
phosphorylation of RNA polymerase II C–terminal domain
positive regulation of histone H3–K27 methylation
RNA processing
gene silencing by RNA
termination of RNA polymerase I transcription
internal peptidyl–lysine acetylation
histone deubiquitination
regulation of translation
protein K27–linked ubiquitination
positive regulation of proteasomal ubiquitin–dependent protein catabolic process
peptidyl–lysine monomethylation
DNA–templated transcription
negative regulation of proteasomal ubiquitin–dependent protein catabolic process
protein peptidyl–prolyl isomerization
mRNA 3'–end processing
peptidyl–serine phosphorylation
translational elongation
translation
translation reinitiation
protein deubiquitination
mRNA catabolic process
protein K48–linked deubiquitination
termination of RNA polymerase II transcription
intracellular protein transport
vesicle–mediated transport
mRNA export from nucleus
intraciliary transport
establishment of protein localization to membrane
clathrin–dependent endocytosis
SRP–dependent cotranslational protein targeting to membrane, translocation
protein targeting to lysosome
RNA export from nucleus
endosomal transport
early endosome to late endosome transport
protein localization to centrosome
protein localization to membrane
protein export from nucleus
synaptic vesicle endocytosis
exocytosis
protein localization to nucleolus
mitochondrial matrix
protein localization to plasma membrane
protein localization to kinetochore
regulation of insulin secretion
proton transmembrane transport
post–translational protein targeting to membrane, translocation
transferrin transport
melanosome transport
mRNA transport
regulation of protein localization to plasma membrane
protein localization to chromatin
retrograde transport, endosome to Golgi
exocytosis
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
regulation of protein import into nucleus
maintenance of protein location in nucleus
positive regulation of protein localization to nucleolus
chromatin organization
chromatin remodeling
mitochondrial respiratory chain complex I assembly
sperm axoneme assembly
spliceosomal tri–snRNP complex assembly
kinetochore assembly
ribosome biogenesis
spliceosomal complex assembly
vesicle organization
nucleosome disassembly
motile cilium assembly
clathrin coat assembly
maturation of SSU–rRNA from tricistronic rRNA transcript (SSU–rRNA, 5.8S rRNA, LSU–rRNA)
chromosome organization
membrane organization
histone exchange
ribosomal small subunit biogenesis
rRNA processing
regulation of cilium assembly
rDNA heterochromatin formation
U2–type prespliceosome assembly
ATP metabolic process
proton motive force–driven mitochondrial ATP synthesis
UTP biosynthetic process
GTP biosynthetic process
aerobic respiration
mitochondrial electron transport, ubiquinol to cytochrome c
nucleobase–containing small molecule interconversion
pyrimidine nucleotide metabolic process
low–density lipoprotein particle receptor catabolic process
CTP biosynthetic process
reactive oxygen species metabolic process
tricarboxylic acid cycle
UDP–N–acetylglucosamine biosynthetic process
regulation of low–density lipoprotein particle receptor catabolic process
proton motive force–driven ATP synthesis
regulation of cellular amino acid metabolic process
cellular respiration
negative regulation of reactive oxygen species biosynthetic process
IMP metabolic process
nucleotide metabolic process
purine nucleotide metabolic process
small molecule metabolic process
mitotic cell cycle
cell cycle
negative regulation of G2/M transition of mitotic cell cycle
mitotic cell cycle phase transition
regulation of cell cycle
positive regulation of G2/M transition of mitotic cell cycle
exit from mitosis
G2/M transition of mitotic cell cycle
positive regulation of cytokinesis
regulation of cytokinesis
regulation of mitotic cell cycle phase transition
mitotic G2 DNA damage checkpoint signaling
negative regulation of G0 to G1 transition
regulation of G2/M transition of mitotic cell cycle
mitotic cytokinesis
positive regulation of sister chromatid cohesion
microtubule–based movement
mitotic spindle assembly
axoneme assembly
regulation of microtubule polymerization or depolymerization
cilium movement involved in cell motility
microtubule cytoskeleton organization
microtubule formation
inner dynein arm assembly
cilium movement
spindle organization
cilium or flagellum–dependent cell motility
regulation of cilium movement involved in extracellular fluid movement
anchoring at centrosome
centriole duplication
regulation of mitotic centrosome separation
regulation of cilium beat frequency involved in ciliary motility
regulation of mitotic centrosome separation
flagellated sperm motility
axonemal dynein complex assembly
chromosome segregation
mitotic metaphase plate congression
mitotic spindle assembly checkpoint signaling
positive regulation of mitotic cell cycle spindle assembly checkpoint
mitotic sister chromatid segregation
protein folding
protein refolding
chaperone cofactor–dependent protein refolding
circadian regulation of gene expression
negative regulation of circadian rhythm
actin filament organization
actin filament–based movement
cytoskeleton organization
actin cytoskeleton organization
meiotic cell cycle
spermatogenesis
spermatid development
female genitalia development
negative regulation of phosphatase activity
negative regulation of protein binding
positive regulation of collagen biosynthetic process
phosphatidylinositol biosynthetic process
regulation of cell shape
fat cell differentiation
blastocyst hatching
formation of primary germ layer
establishment of endothelial barrier
macrophage differentiation
cardiac muscle cell differentiation
regulation of hematopoietic stem cell differentiation
ventricular cardiac muscle cell development
myeloid cell differentiation
protein stabilization
protein destabilization
regulation of protein stability
regulation of actin polymerization or depolymerization
cell volume homeostasis
actin filament capping
regulation of cell size
isotype switching
positive regulation of B cell activation
negative regulation of immature T cell proliferation in thymus
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP–dependent
natural killer cell activation
negative regulation of cell differentiation in thymus
multicellular organism growth
positive regulation of cell growth
positive regulation of dendrite extension
cell population proliferation
negative regulation of apoptotic process
positive regulation of viral genome replication
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
positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress
response to UV
intracellular estrogen receptor signaling pathway
cellular response to cAMP
response to glucose
Fc–epsilon receptor signaling pathway
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
double–strand break repair
cellular response to unfolded protein
integrin–mediated signaling pathway
ubiquitin–dependent ERAD pathway
DNA repair
double–strand break repair via homologous recombination
interferon–gamma–mediated signaling pathway
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
regulation of transcription from RNA polymerase II promoter in response to hypoxia
cellular response to UV
smoothened signaling pathway
regulation of double–strand break repair via homologous recombination
negative regulation of calcineurin–NFAT signaling cascade
response to insulin
endoplasmic reticulum unfolded protein response
translesion synthesis
interstrand cross–link repair
cellular response to epidermal growth factor stimulus
response to gamma radiation