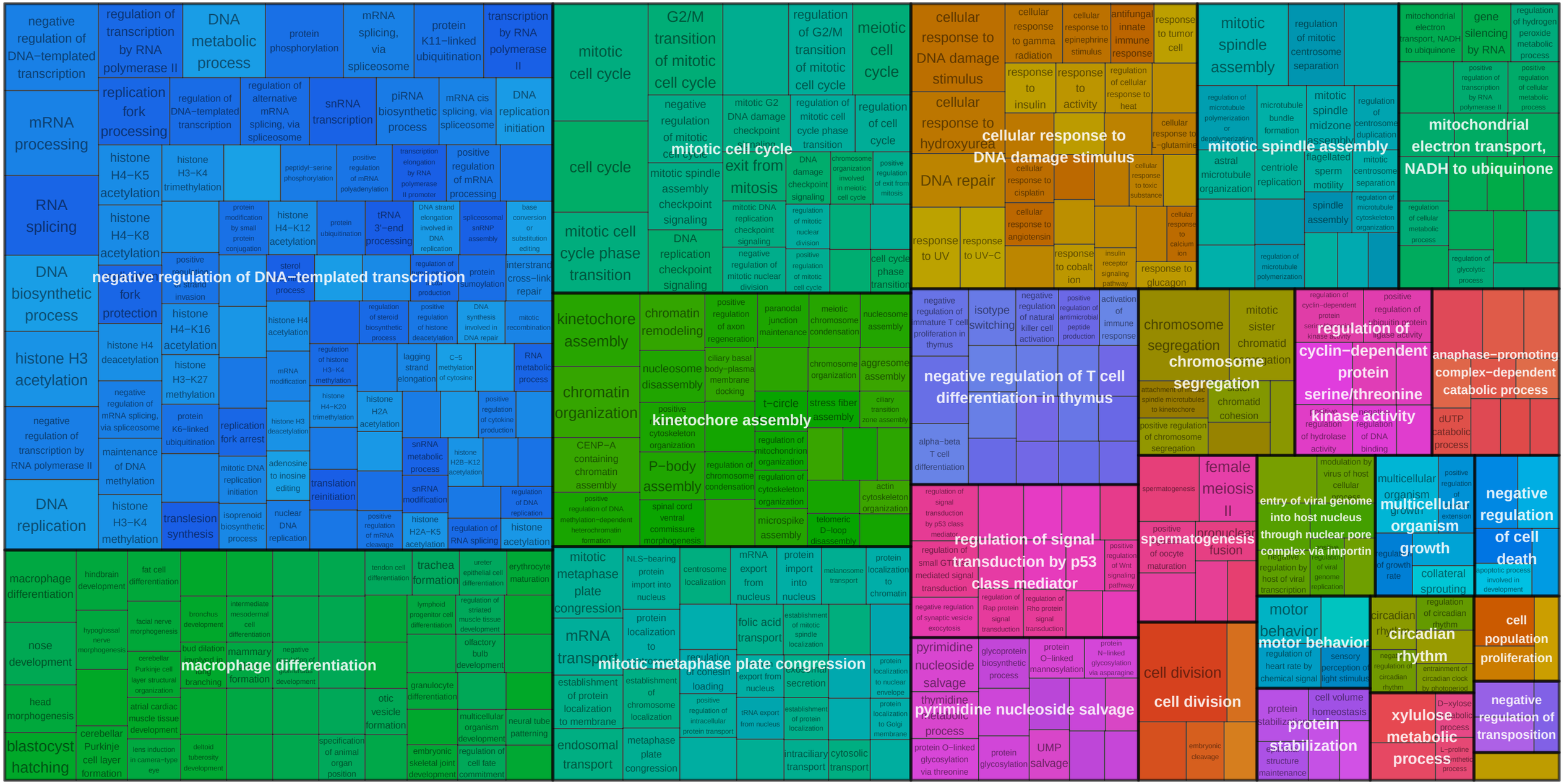
negative regulation of DNA−templated transcription
regulation of transcription by RNA polymerase II
DNA metabolic process
protein phosphorylation
mRNA splicing, via spliceosome
protein K11−linked ubiquitination
transcription by RNA polymerase II
mRNA processing
replication fork processing
regulation of DNA−templated transcription
regulation of alternative mRNA splicing, via spliceosome
snRNA transcription
piRNA biosynthetic process
mRNA cis splicing, via spliceosome
DNA replication initiation
RNA splicing
histone H4−K5 acetylation
histone H3−K4 trimethylation
peptidyl−serine phosphorylation
positive regulation of mRNA polyadenylation
transcription elongation by RNA polymerase II promoter
positive regulation of mRNA processing
DNA biosynthetic process
histone H4−K8 acetylation
protein modification by small protein conjugation
histone H4−K12 acetylation
protein ubiquitination
tRNA 3'−end processing
DNA strand elongation involved in DNA replication
spliceosomal snRNP assembly
base conversion or substitution editing
histone H4 acetylation
histone H4−K16 acetylation
histone H3−K27 methylation
protein K6−linked ubiquitination
histone H4 deacetylation
negative regulation of mRNA splicing, via spliceosome
maintenance of DNA methylation
histone H3−K4 methylation
DNA replication
translesion synthesis
isoprenoid biosynthetic process
nuclear DNA replication
replication fork arrest
mitotic DNA replication initiation
translation reinitiation
sterol metabolic process
protein sumoylation
interstrand cross−link repair
mitotic recombination
regulation of steroid biosynthetic process
positive regulation of histone deacetylation
DNA synthesis involved in DNA repair
regulation of histone H3−K4 methylation
lagging strand elongation
C−5 methylation of cytosine
RNA metabolic process
mRNA modification
histone H4−K20 trimethylation
histone H2A acetylation
positive regulation of cytokine production
histone H3 deacetylation
adenosine to inosine editing
snRNA metabolic process
histone H2B−K12 acetylation
snRNA modification
histone H2A−K5 acetylation
regulation of DNA replication
regulation of RNA splicing
histone acetylation
positive regulation of mRNA cleavage
mitotic cell cycle
G2/M transition of mitotic cell cycle
regulation of G2/M transition of mitotic cell cycle
meiotic cell cycle
cell cycle
negative regulation of mitotic cell cycle
mitotic G2 DNA damage checkpoint signaling
regulation of mitotic cell cycle phase transition
regulation of cell cycle
mitotic cell cycle phase transition
mitotic spindle assembly checkpoint signaling
exit from mitosis
DNA damage checkpoint signaling
chromosome organization involved in meiotic cell cycle
positive regulation of exit from mitosis
DNA replication checkpoint signaling
mitotic DNA replication checkpoint signaling
regulation of mitotic nuclear division
cell cycle phase transition
negative regulation of mitotic nuclear division
positive regulation of mitotic cell cycle
cellular response to DNA damage stimulus
cellular response to gamma radiation
cellular response to epinephrine stimulus
antifungal innate immune response
response to tumor cell
cellular response to hydroxyurea
response to insulin
response to activity
regulation of cellular response to heat
DNA repair
cellular response to L−glutamine
cellular response to cisplatin
cellular response to toxic substance
response to UV
response to UV−C
cellular response to angiotensin
cellular response to calcium ion
response to cobalt ion
insulin receptor signaling pathway
response to glucagon
mitotic spindle assembly
regulation of microtubule polymerization or depolymerization
microtubule bundle formation
regulation of mitotic centrosome separation
mitotic spindle midzone assembly
regulation of centrosome duplication
astral microtubule organization
centriole replication
flagellated sperm motility
mitotic centrosome separation
spindle assembly
regulation of microtubule cytoskeleton organization
regulation of microtubule polymerization
mitochondrial electron transport, NADH to ubiquinone
gene silencing by RNA
regulation of hydrogen peroxide metabolic process
positive regulation of transcription by RNA polymerase II
positive regulation of cellular metabolic process
mitochondrial electron transport, NADH to ubiquinone
regulation of cellular metabolic process
regulation of glycolytic process
kinetochore assembly
chromatin remodeling
positive regulation of axon regeneration
paranodal junction maintenance
meiotic chromosome condensation
nucleosome assembly
chromatin organization
nucleosome disassembly
ciliary basal body−plasma membrane docking
chromosome organization
aggresome assembly
positive regulation of cytoskeleton organization
t−circle formation
stress fiber assembly
ciliary transition zone assembly
CENP−A containing chromatin assembly
regulation of mitochondrion organization
P−body assembly
regulation of chromosome condensation
regulation of cytoskeleton organization
actin cytoskeleton organization
spinal cord ventral commissure morphogenesis
microspike assembly
telomeric D−loop disassembly
positive regulation of DNA methylation−dependent heterochromatin formation
negative regulation of T cell differentiation in thymus
negative regulation of immature T cell proliferation in thymus
isotype switching
negative regulation of natural killer cell activation
positive regulation of antimicrobial peptide production
activation of immune response
alpha−beta T cell differentiation
chromosome segregation
mitotic sister chromatid segregation
attachment of spindle microtubules to kinetochore
chromatid cohesion
positive regulation of chromosome segregation
regulation of cyclin−dependent protein serine/threonine kinase activity
positive regulation of ubiquitin protein ligase activity
regulation of cyclin−dependent protein serine/threonine kinase activity
anaphase−promoting complex−dependent catabolic process
regulation of hydrolase activity
regulation of DNA binding
dUTP catabolic process
macrophage differentiation
hindbrain development
fat cell differentiation
tendon cell differentiation
trachea formation
ureter epithelial cell differentiation
erythrocyte maturation
nose development
hypoglossal nerve morphogenesis
facial nerve morphogenesis
bronchus development
intermediate mesodermal cell differentiation
lymphoid progenitor cell differentiation
regulation of striated muscle tissue development
olfactory bulb development
bud dilation involved in lung branching
mammary gland duct formation
granulocyte differentiation
head morphogenesis
cerebellar Purkinje cell layer structural organization
otic vesicle formation
multicellular organism development
neural tube patterning
atrial cardiac muscle tissue development
blastocyst hatching
cerebellar Purkinje cell layer formation
lens induction in camera−type eye
deltoid tuberosity development
specification of animal organ position
embryonic skeletal joint development
regulation of cell fate commitment
mitotic metaphase plate congression
NLS−bearing protein import into nucleus
centrosome localization
mRNA export from nucleus
protein import into nucleus
melanosome transport
protein localization to chromatin
mRNA transport
protein localization to centrosome
folic acid transport
establishment of mitotic spindle localization
establishment of protein localization to membrane
establishment of chromosome localization
sister chromatid cohesion
export from nucleus
exocytosis
protein localization to nuclear envelope
endosomal transport
metaphase plate congression
positive regulation of intracellular protein transport
tRNA export from nucleus
establishment of protein localization
protein localization to Golgi membrane
intracellular transport
cytosolic transport
regulation of signal transduction by p53 class mediator
positive regulation of Wnt signaling pathway
regulation of small GTPase mediated signal transduction
regulation of Rap protein signal transduction
regulation of Rho protein signal transduction
negative regulation of synaptic vesicle exocytosis
pyrimidine nucleoside salvage
glycoprotein biosynthetic process
protein O−linked mannosylation
protein N−linked glycosylation via asparagine
thymidine metabolic process
protein O−linked glycosylation via threonine
protein glycosylation
UMP salvage
spermatogenesis
female meiosis II
positive regulation of oocyte maturation
propulsean fusion
cell division
embryonic cleavage
entry of viral genome into host nucleus through nuclear pore complex via importin
modulation by virus of host cellular process
negative regulation by host of viral transcription
regulation of viral genome replication
multicellular organism growth
positive regulation of growth rate
collateral sprouting
negative regulation of cell death
apoptotic process involved in development
motor behavior
regulation of heart rate by chemical signal
sensory perception of light stimulus
circadian rhythm
negative regulation of circadian rhythm
regulation of circadian rhythm
entrainment of circadian clock by photoperiod
cell population proliferation
protein stabilization
cell volume homeostasis
establishment or maintenance of cell polarity
xylulose metabolic process
D−xylose metabolic process
L−proline biosynthetic process
negative regulation of transposition


translation
translational elongation
proteasomal protein catabolic process
formation of cytoplasmic translation initiation complex
mitochondrial translational elongation
protein deubiquitination
positive regulation of translational elongation
membrane protein ectodomain proteolysis
negative regulation of histone H3−K27 methylation
negative regulation of translation
signal peptide processing
translational initiation
regulation of cellular amino acid metabolic process
mitochondrial translation
protein K69−linked ufmylation
chondroitin sulfate metabolic process
proteolysis
rescue of stalled ribosome
chondroitin sulfate proteoglycan biosynthetic process
mitochondrial protein processing
protein methylation
protein N−linked glycosylation via asparagine
regulation of translation
protein−FAD linkage
cytoplasmic translation
choline catabolic process
ribosomal large subunit assembly
mitochondrial translational termination
extracellular matrix organization
ribosomal small subunit assembly
mitochondrial respiratory chain complex I assembly
protein insertion into mitochondrial inner membrane
proteasome assembly
rRNA processing
mature ribosome assembly
platelet dense granule organization
high−density lipoprotein particle assembly
ribosomal large subunit biogenesis
Golgi organization
positive regulation of lamellipodium assembly
negative regulation of collagen fibril organization
focal adhesion assembly
positive regulation of dendritic spine development
regulation of synapse organization
translocation of LSU−rRNA
eye pigment granule organization
iron−sulfur cluster assembly
cristae formation
cytoplasmic translational termination
cell junction assembly
telomerase holoenzyme complex assembly
translational termination
collagen fibril organization
stress granule assembly
Golgi vesicle budding
rRNA methylation
DNA geometric change
membrane organization
actin filament capping
regulation of hematopoietic stem cell differentiation
positive regulation of fat cell differentiation
aging
decidualization
limb bud formation
mesoderm formation
epithelial tube branching involved in lung morphogenesis
multicellular organism aging
regulation of epidermis development
abscission
Mullerian duct regression
bone mineralization
striated muscle cell differentiation
skin epidermis development
adrenal gland development
elevation formation
spermatid development
regulation of cell shape
epithelial cell differentiation
cartilage development
endodermal cell differentiation
hard palate development
pyramidal neuron development
epidermis development
regulation of transcription from RNA polymerase II promoter in response to hypoxia
endoplasmic reticulum unfolded protein response
response to endoplasmic reticulum stress
cellular response to unfolded protein
cellular response to glucose starvation
IRE1−mediated unfolded protein response
response to starvation
response to nutrient
regulation of cellular senescence
blood coagulation, intrinsic pathway
response to high light intensity
response to heat
response to oxidative stress
removal of superoxide radicals
fatty acid beta−oxidation using acyl−CoA dehydrogenase
ATP metabolic process
citrate metabolic process
D−xylose metabolic process
glyoxylate catabolic process
proton motive force−driven ATP synthesis
positive regulation of glycolytic process
regulation of glucose metabolic process
glycerol ether metabolic process
cholesterol metabolic process
glycerol biosynthetic process
CTP biosynthetic process
glyoxylate cycle
aspartate catabolic process
AMP salvage
D−amino acid metabolic process
ATP biosynthetic process
IMP metabolic process
SRP−dependent cotranslational protein targeting to membrane
amino acid transport
cholesterol efflux
vacuolar transport
toxin transport
reverse cholesterol transport
regulation of exocytosis
ribosomal large subunit export from nucleus
phospholipid efflux
retrograde transport, endosome to Golgi
intracellular cholesterol transport
regulation of protein transport
vesicle docking involved in exocytosis
intracellular protein transport
protein import into mitochondrial matrix
regulation of chloride transport
L−cystine transport
ion transport
iron ion transport
peptide secretion
nuclear migration
regulation of AMPA receptor activity
cobalt ion transport
retrograde vesicle−mediated transport, Golgi to endoplasmic reticulum
vesicle−mediated transport
protein targeting to lysosome
copper ion transport
endoplasmic reticulum to Golgi vesicle−mediated transport
protein targeting to ER
negative regulation of sodium ion transport
nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
proteasomal ubiquitin−independent protein catabolic process
regulation of mRNA stability
autophagosome maturation
mRNA splicing, via spliceosome
lipid biosynthetic process
negative regulation of transcription by RNA polymerase II
mRNA catabolic process
RNA splicing
positive regulation of autophagy
negative regulation of DNA repair
negative regulation of DNA−templated transcription
positive regulation of kinase activity
positive regulation of transcription by RNA polymerase II
regulation of protein catabolic process
autophagosome assembly
regulation of transcription by RNA polymerase II
late endosomal microautophagy
regulation of lipid metabolic process
miRNA catabolic process
GPI anchor biosynthetic process
fatty acid biosynthetic process
tRNA modification
mRNA cis splicing, via spliceosome
NIK/NF−kappaB signaling
stimulatory C−type lectin receptor signaling pathway
positive regulation of canonical Wnt signaling pathway
Fc−epsilon receptor signaling pathway
Rab protein signal transduction
nodal signaling pathway
regulation of long−term synaptic potentiation
integrin−mediated signaling pathway
T cell receptor signaling pathway
negative regulation of MAPK cascade
cellular response to antibiotic
cellular response to BMP stimulus
response to glucose
cellular response to glucose stimulus
response to TNF agonist
response to stilbenoid
cellular response to interleukin−1
response to lithium ion
cellular response to insulin stimulus
cellular response to fructose stimulus
response to mercury ion
cell redox homeostasis
fatty acid homeostasis
protein stabilization
regulation of peroxisome size
cellular copper ion homeostasis
hormone metabolic process
water homeostasis
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
viral transcription
modulation by virus of host process
viral release from host cell
positive regulation of viral process
protein folding
protein refolding
'de novo' post−translational protein folding
respiratory electron transport
tricarboxylic acid cycle
negative regulation of G2/M transition of mitotic cell cycle
regulation of cell cycle
vesicle transport along microtubule
microtubule
axonal transport
positive regulation of epithelial cell migration
negative regulation of apoptotic process
positive regulation of epithelial cell proliferation
negative regulation of cell growth
regulation of cell growth
negative regulation of focal adhesion assembly
positive regulation of DNA N−glycosylase activity
actin filament−based process