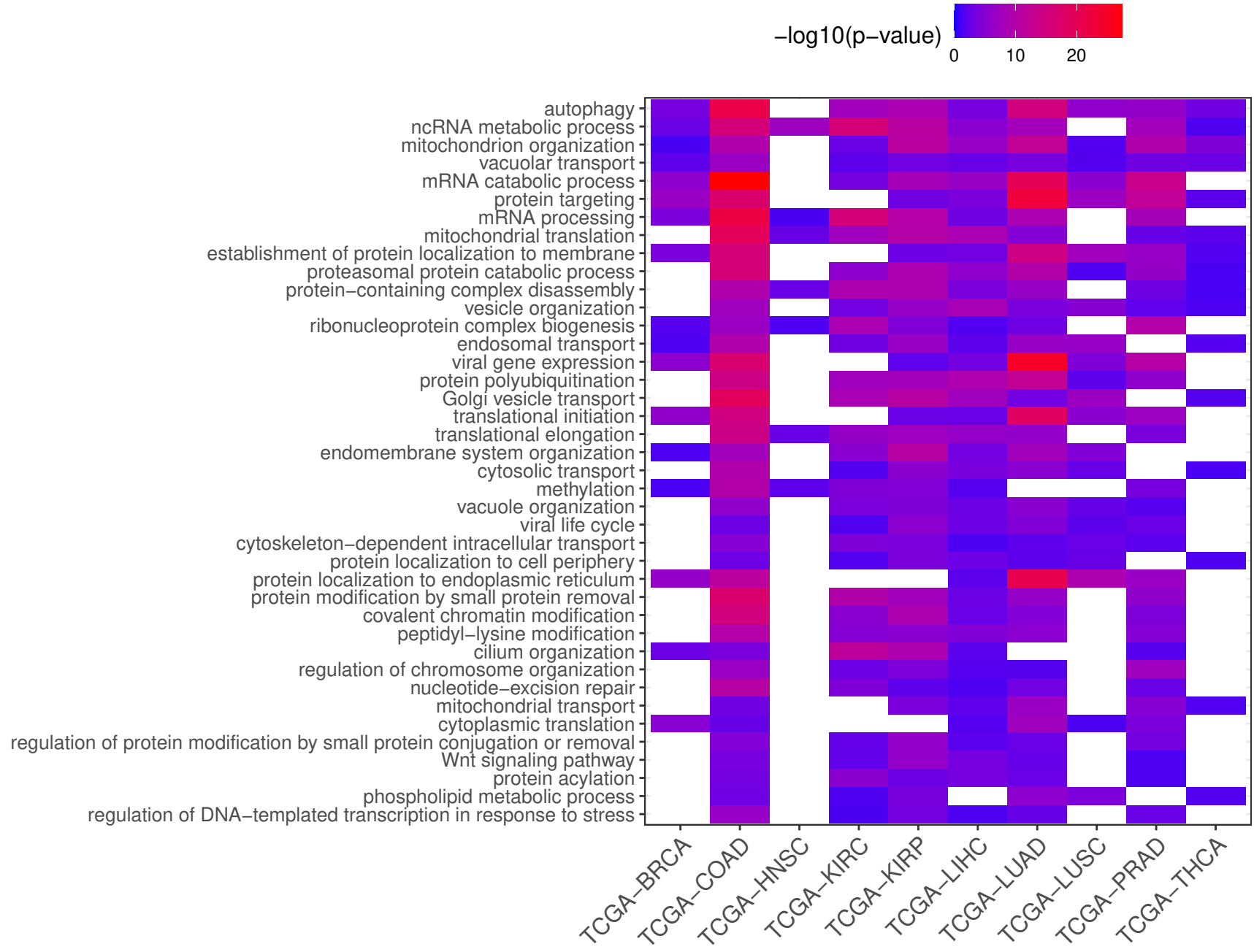
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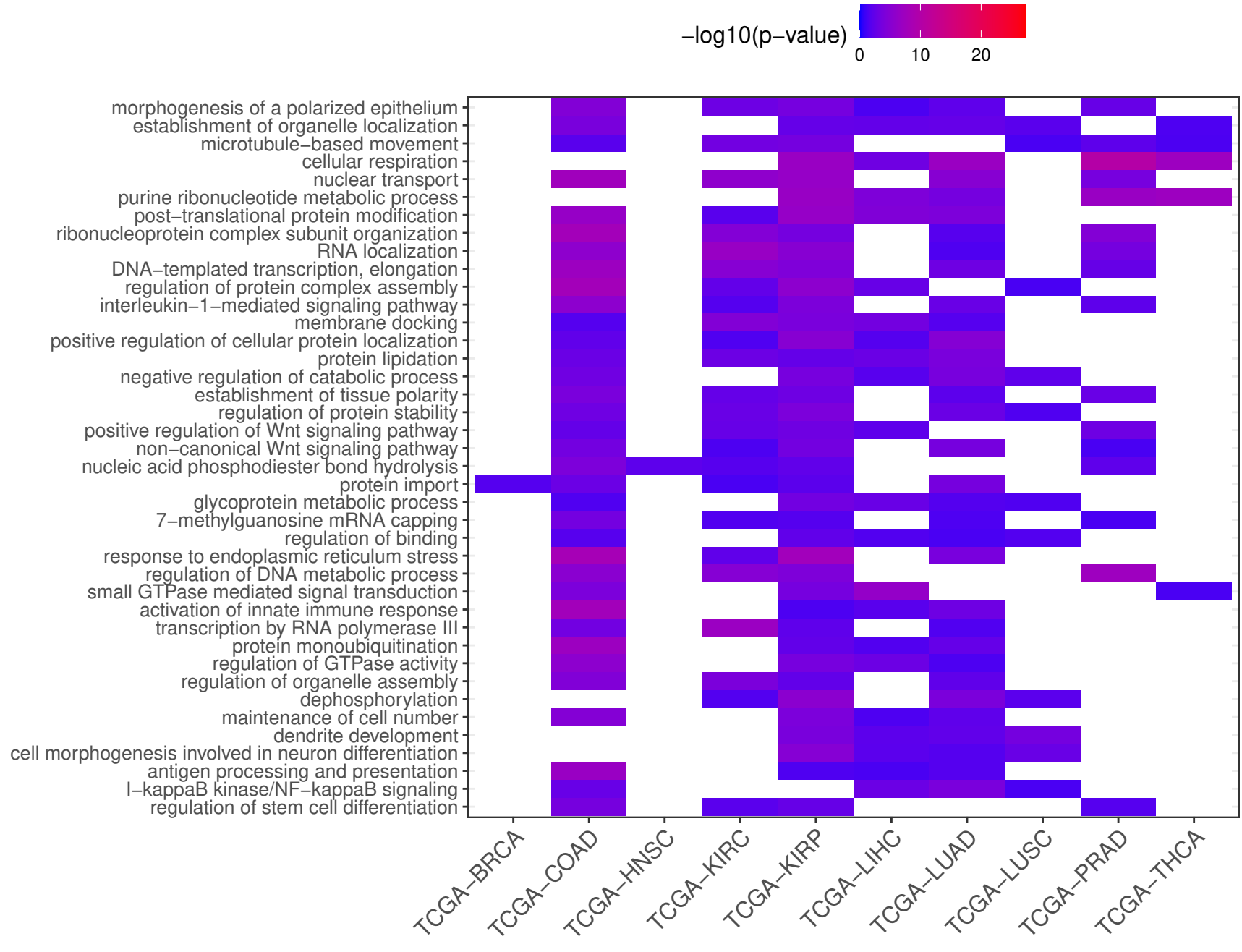
autophagy
ncRNA metabolic process
mitochondrion organization
vacuolar transport
mRNA catabolic process
protein targeting
mRNA processing
mitochondrial translation
establishment of protein localization to membrane
proteasomal protein catabolic process
protein−containing complex disassembly
vesicle organization
ribonucleoprotein complex biogenesis
endosomal transport
viral gene expression
protein polyubiquitination
Golgi vesicle transport
translational initiation
translational elongation
endomembrane system organization
cytosolic transport
methylation
vacuole organization
viral life cycle
cytoskeleton−dependent intracellular transport
protein localization to cell periphery
protein localization to endoplasmic reticulum
protein modification by small protein removal
covalent chromatin modification
peptidyl−lysine modification
cilium organization
regulation of chromosome organization
nucleotide−excision repair
mitochondrial transport
cytoplasmic translation
regulation of protein modification by small protein conjugation or removal
Wnt signaling pathway
protein acylation
phospholipid metabolic process
regulation of DNA−templated transcription in response to stress
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA


−log10(p−value)
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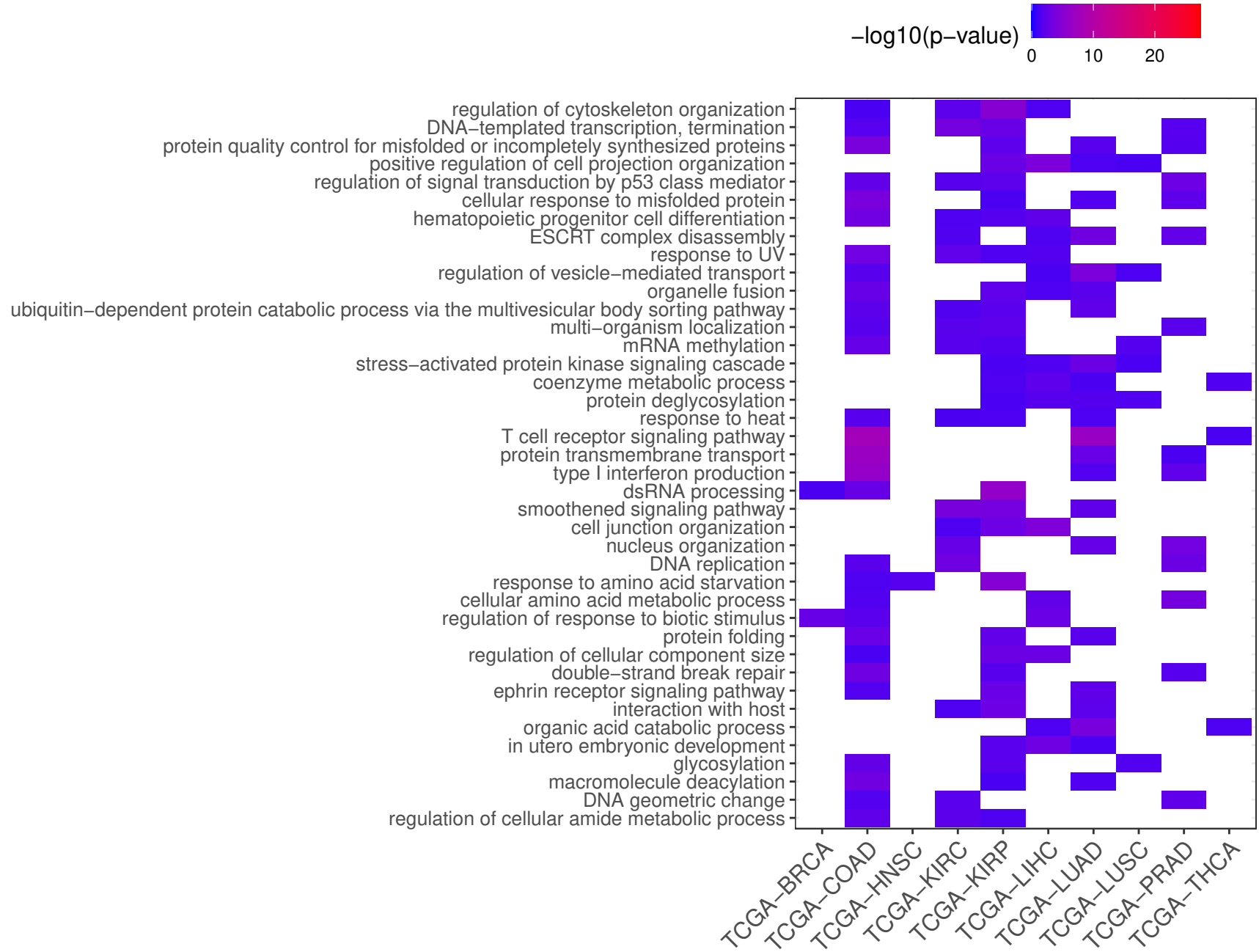
10
20
morphogenesis of a polarized epithelium
establishment of organelle localization
microtubule−based movement
cellular respiration
nuclear transport
purine ribonucleotide metabolic process
post−translational protein modification
ribonucleoprotein complex subunit organization
RNA localization
DNA−templated transcription, elongation
regulation of protein complex assembly
interleukin−1−mediated signaling pathway
membrane docking
positive regulation of cellular protein localization
protein lipidation
negative regulation of catabolic process
establishment of tissue polarity
regulation of protein stability
positive regulation of Wnt signaling pathway
non−canonical Wnt signaling pathway
nucleic acid phosphodiester bond hydrolysis
protein import
glycoprotein metabolic process
7−methylguanosine mRNA capping
regulation of binding
response to endoplasmic reticulum stress
regulation of DNA metabolic process
small GTPase mediated signal transduction
activation of innate immune response
transcription by RNA polymerase III
protein monoubiquitination
regulation of GTPase activity
regulation of organelle assembly
dephosphorylation
maintenance of cell number
dendrite development
cell morphogenesis involved in neuron differentiation
antigen processing and presentation
I−kappaB kinase/NF−kappaB signaling
regulation of stem cell differentiation
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA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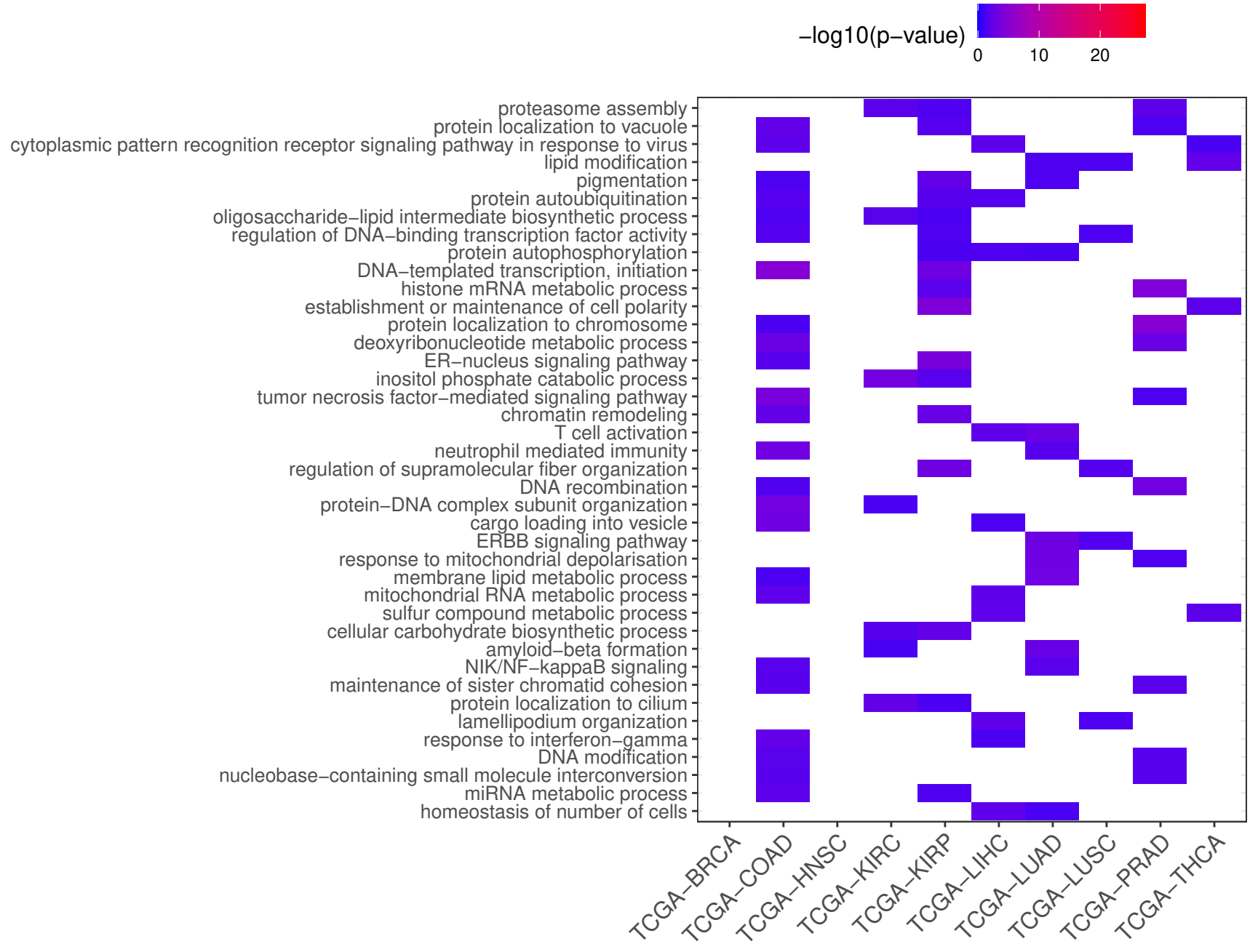
10
20
regulation of cytoskeleton organization
DNA−templated transcription, termination
protein quality control for misfolded or incompletely synthesized proteins
positive regulation of cell projection organization
regulation of signal transduction by p53 class mediator
cellular response to misfolded protein
hematopoietic progenitor cell differentiation
ESCRT complex disassembly
response to UV
regulation of vesicle−mediated transport
organelle fusion
ubiquitin−dependent protein catabolic process via the multivesicular body sorting pathway
multi−organism localization
mRNA methylation
stress−activated protein kinase signaling cascade
coenzyme metabolic process
protein deglycosylation
response to heat
T cell receptor signaling pathway
protein transmembrane transport
type I interferon production
dsRNA processing
smoothened signaling pathway
cell junction organization
nucleus organization
DNA replication
response to amino acid starvation
cellular amino acid metabolic process
regulation of response to biotic stimulus
protein folding
regulation of cellular component size
double−strand break repair
ephrin receptor signaling pathway
interaction with host
organic acid catabolic process
in utero embryonic development
glycosylation
macromolecule deacylation
DNA geometric change
regulation of cellular amide metabolic process
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA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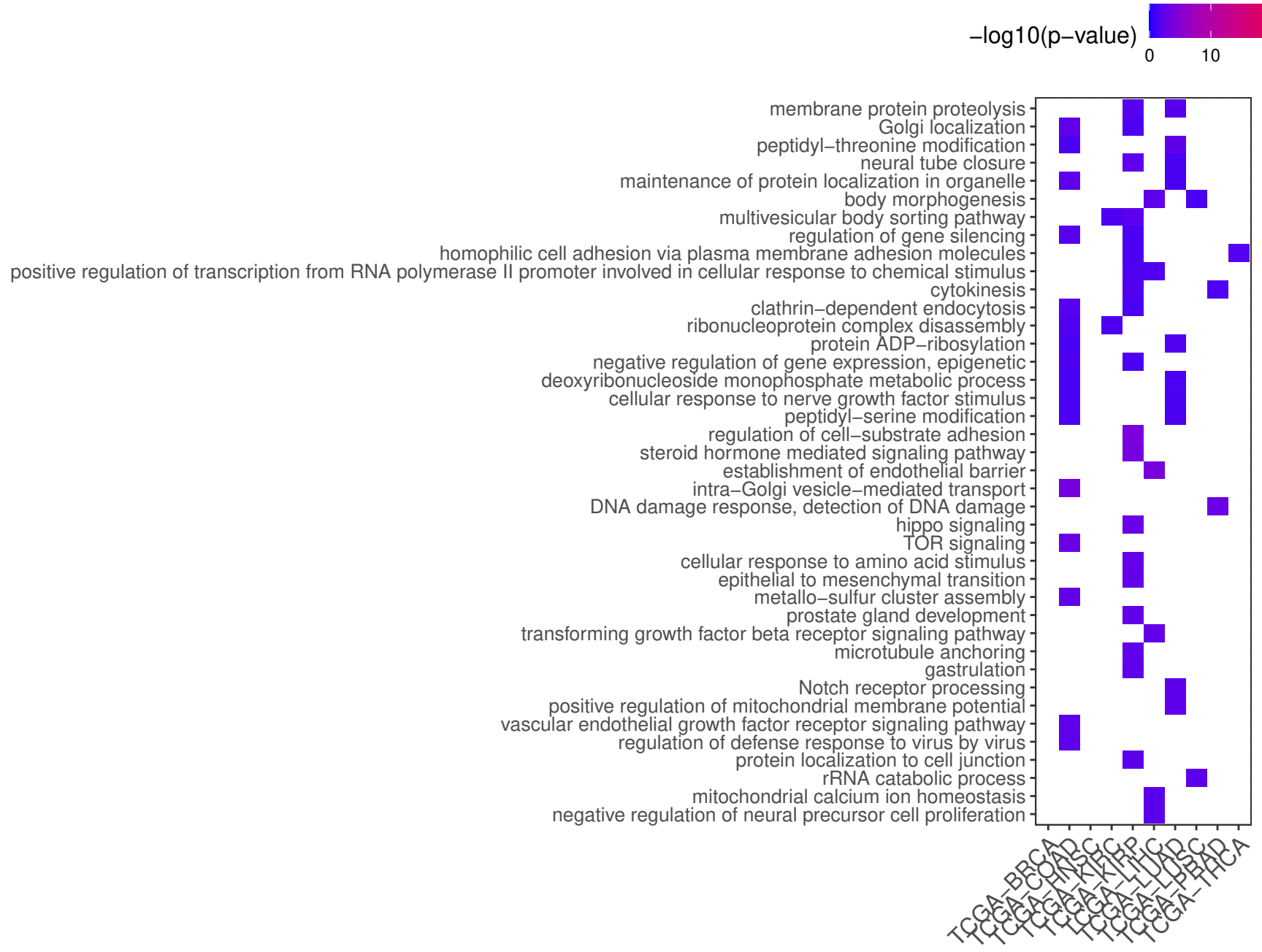
10
20
proteasome assembly
protein localization to vacuole
cytoplasmic pattern recognition receptor signaling pathway in response to virus
lipid modification
pigmentation
protein autoubiquitination
oligosaccharide−lipid intermediate biosynthetic process
regulation of DNA−binding transcription factor activity
protein autophosphorylation
DNA−templated transcription, initiation
histone mRNA metabolic process
establishment or maintenance of cell polarity
protein localization to chromosome
deoxyribonucleotide metabolic process
ER−nucleus signaling pathway
inositol phosphate catabolic process
tumor necrosis factor−mediated signaling pathway
chromatin remodeling
T cell activation
neutrophil mediated immunity
regulation of supramolecular fiber organization
DNA recombination
protein−DNA complex subunit organization
cargo loading into vesicle
ERBB signaling pathway
response to mitochondrial depolarisation
membrane lipid metabolic process
mitochondrial RNA metabolic process
sulfur compound metabolic process
cellular carbohydrate biosynthetic process
amyloid−beta formation
NIK/NF−kappaB signaling
maintenance of sister chromatid cohesion
protein localization to cilium
lamellipodium organization
response to interferon−gamma
DNA modification
nucleobase−containing small molecule interconversion
miRNA metabolic process
homeostasis of number of cells
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA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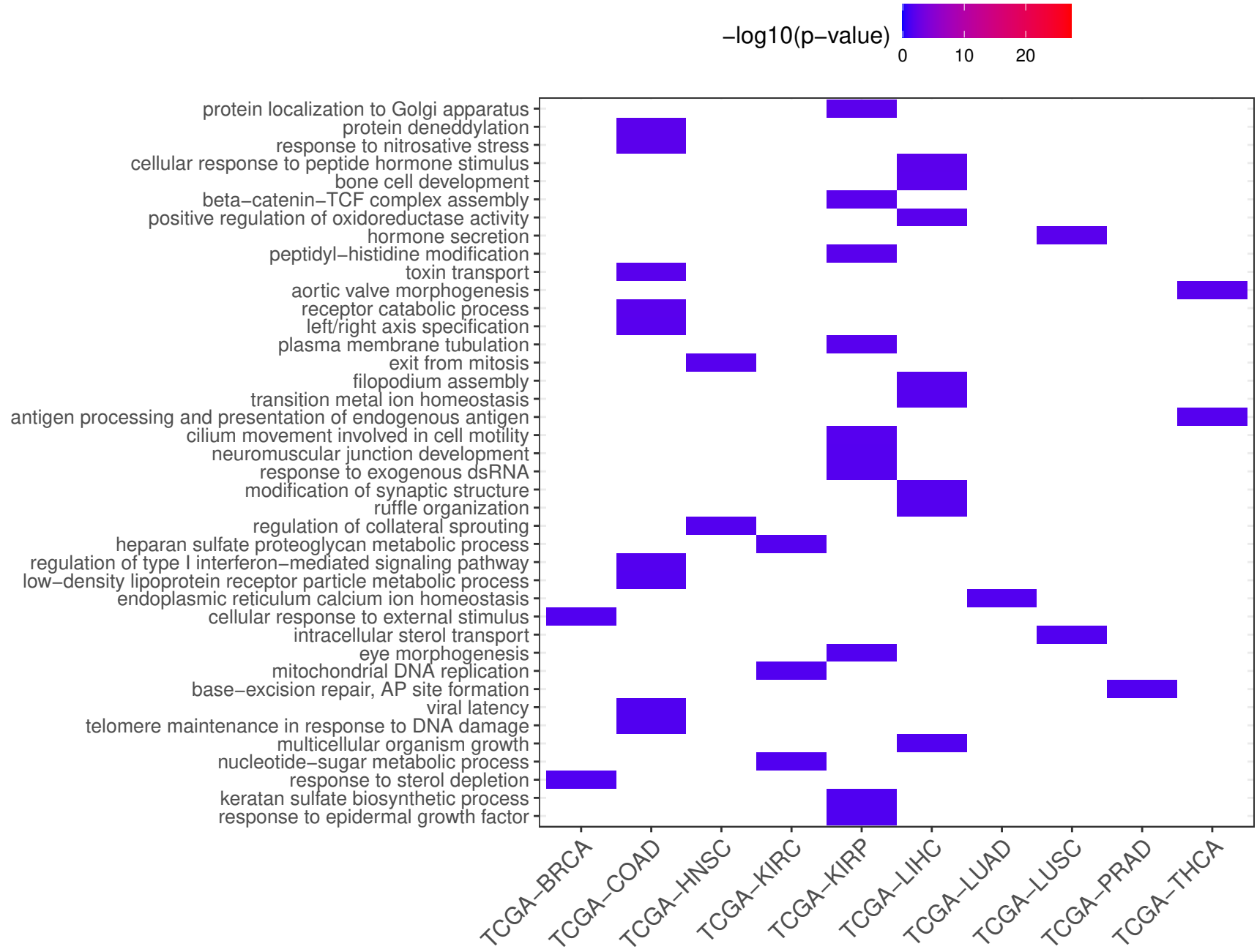
membrane protein proteolysis
Golgi localization
peptidyl−threonine modification
neural tube closure
maintenance of protein localization in organelle
body morphogenesis
multivesicular body sorting pathway
regulation of gene silencing
homophilic cell adhesion via plasma membrane adhesion molecules
positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus
cytokinesis
clathrin−dependent endocytosis
ribonucleoprotein complex disassembly
protein ADP−ribosylation
negative regulation of gene expression, epigenetic
deoxyribonucleoside monophosphate metabolic process
cellular response to nerve growth factor stimulus
peptidyl−serine modification
regulation of cell−substrate adhesion
steroid hormone mediated signaling pathway
establishment of endothelial barrier
intra−Golgi vesicle−mediated transport
DNA damage response, detection of DNA damage
hippo signaling
TOR signaling
cellular response to amino acid stimulus
epithelial to mesenchymal transition
metallo−sulfur cluster assembly
prostate gland development
transforming growth factor beta receptor signaling pathway
microtubule anchoring
gastrulation
Notch receptor processing
positive regulation of mitochondrial membrane potential
vascular endothelial growth factor receptor signaling pathway
regulation of defense response to virus by virus
protein localization to cell junction
rRNA catabolic process
mitochondrial calcium ion homeostasis
negative regulation of neural precursor cell proliferation
TCGA−BRCA
TCGA−COAD
TCGA−CESC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA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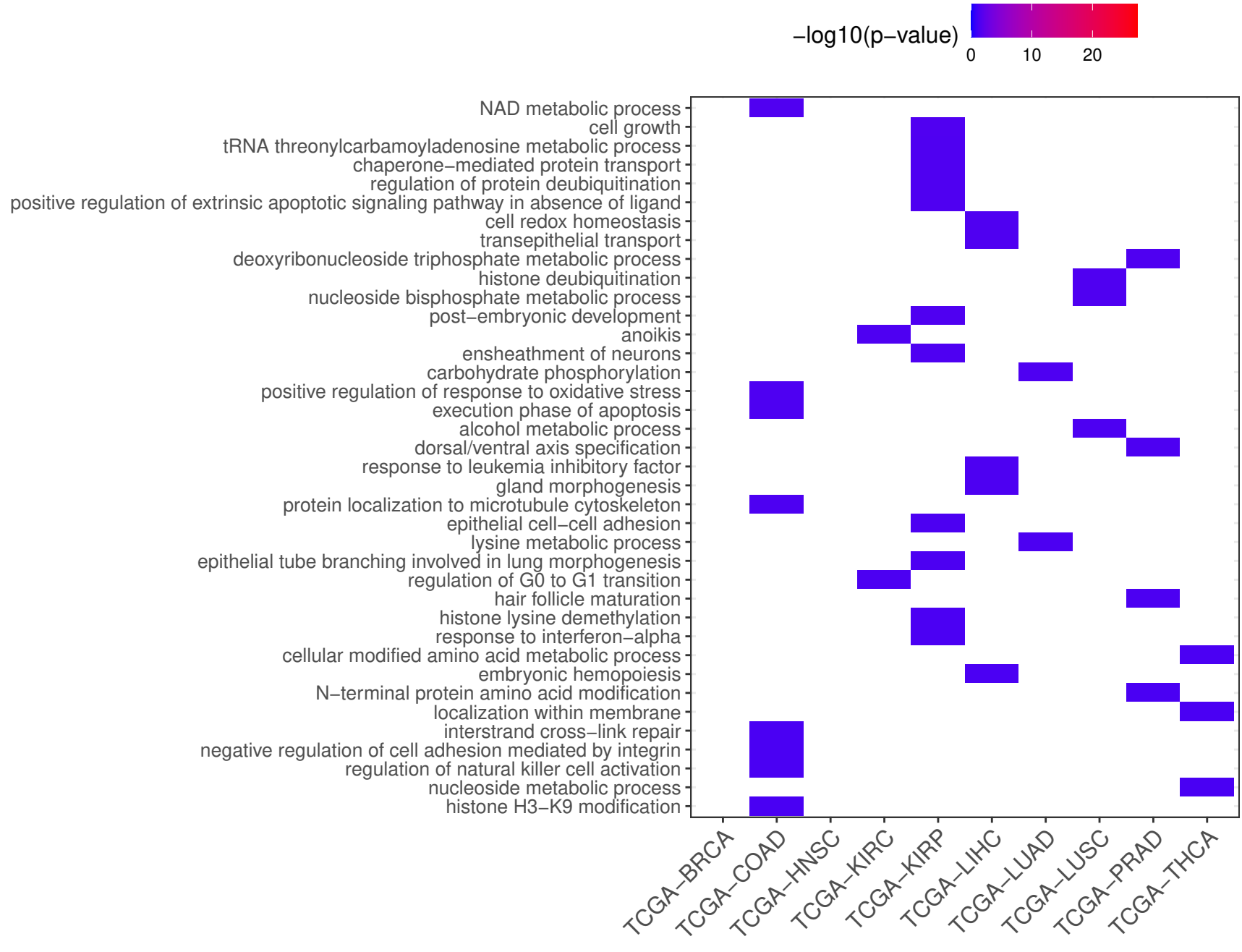
protein localization to Golgi apparatus
protein deneddylation
response to nitrosative stress
cellular response to peptide hormone stimulus
bone cell development
beta−catenin−TCF complex assembly
positive regulation of oxidoreductase activity
hormone secretion
peptidyl−histidine modification
toxin transport
aortic valve morphogenesis
receptor catabolic process
left/right axis specification
plasma membrane tubulation
exit from mitosis
filopodium assembly
transition metal ion homeostasis
antigen processing and presentation of endogenous antigen
cilium movement involved in cell motility
neuromuscular junction development
response to exogenous dsRNA
modification of synaptic structure
ruffle organization
regulation of collateral sprouting
heparan sulfate proteoglycan metabolic process
regulation of type I interferon−mediated signaling pathway
low−density lipoprotein receptor particle metabolic process
endoplasmic reticulum calcium ion homeostasis
cellular response to external stimulus
intracellular sterol transport
eye morphogenesis
mitochondrial DNA replication
base−excision repair, AP site formation
viral latency
telomere maintenance in response to DNA damage
multicellular organism growth
nucleotide−sugar metabolic process
response to sterol depletion
keratan sulfate biosynthetic process
response to epidermal growth factor
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA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10
20
NAD metabolic process
cell growth
tRNA threonylcarbamoyladenosine metabolic process
chaperone−mediated protein transport
regulation of protein deubiquitination
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand
cell redox homeostasis
transepithelial transport
deoxyribonucleoside triphosphate metabolic process
histone deubiquitination
nucleoside bisphosphate metabolic process
post−embryonic development
anoikis
ensheathment of neurons
carbohydrate phosphorylation
positive regulation of response to oxidative stress
execution phase of apoptosis
alcohol metabolic process
dorsal/ventral axis specification
response to leukemia inhibitory factor
gland morphogenesis
protein localization to microtubule cytoskeleton
epithelial cell−cell adhesion
lysine metabolic process
epithelial tube branching involved in lung morphogenesis
regulation of G0 to G1 transition
hair follicle maturation
histone lysine demethylation
response to interferon−alpha
cellular modified amino acid metabolic process
embryonic hemopoiesis
N−terminal protein amino acid modification
localization within membrane
interstrand cross−link repair
negative regulation of cell adhesion mediated by integrin
regulation of natural killer cell activation
nucleoside metabolic process
histone H3−K9 modification
TCGA−BRCA
TCGA−COAD
TCGA−HNSC
TCGA−KIRC
TCGA−KIRP
TCGA−LIHC
TCGA−LUAD
TCGA−LUSC
TCGA−PRAD
TCGA−THCA