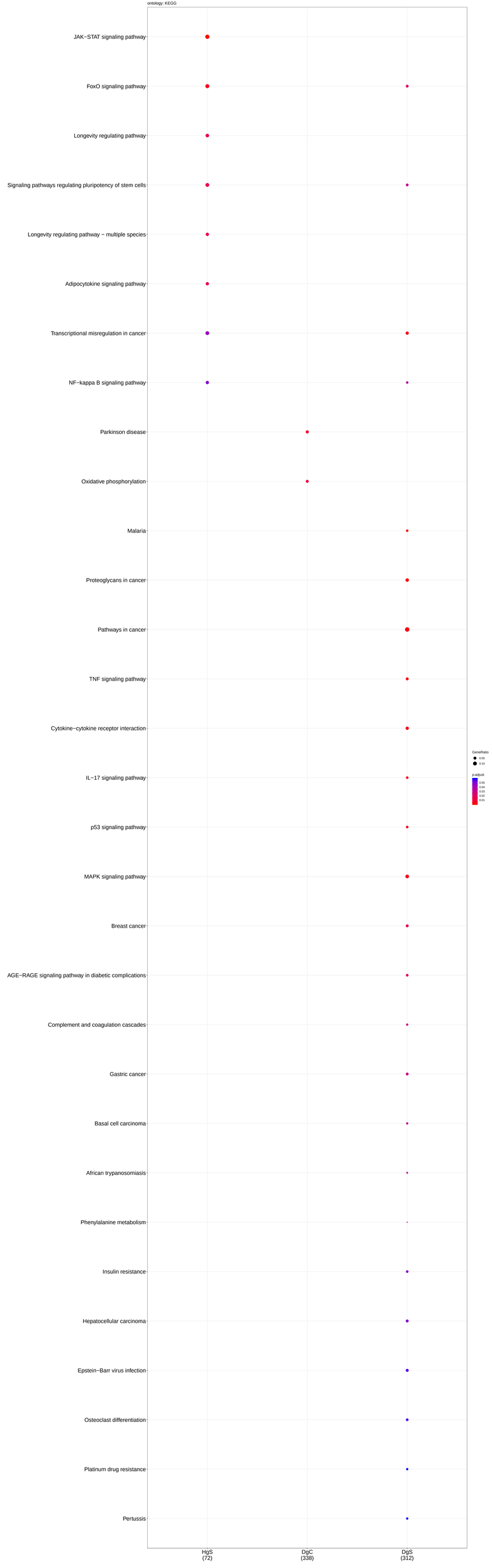

ontology: BP
purine ribonucleotide transport
purine nucleotide transport
nucleotide transport
cellular response to organic cyclic compound
negative regulation of intracellular signal transduction
negative regulation of T cell differentiation
negative regulation of CD4−positive, alpha−beta T cell differentiation
regulation of DNA−binding transcription factor activity
negative regulation of lymphocyte differentiation
negative regulation of alpha−beta T cell differentiation
negative regulation of CD4−positive, alpha−beta T cell activation
regulation of MAP kinase activity
intracellular receptor signaling pathway
positive regulation of vasculature development
regulation of cytokine−mediated signaling pathway
cellular response to peptide
cellular response to peptide hormone stimulus
regulation of T cell differentiation
cellular response to interleukin−1
negative regulation of leukocyte differentiation
positive regulation of cellular component movement
positive regulation of DNA−binding transcription factor activity
alpha−beta T cell differentiation
regulation of alpha−beta T cell differentiation
regulation of response to cytokine stimulus
maternal behavior
regulation of JAK−STAT cascade
cellular response to steroid hormone stimulus
tyrosine phosphorylation of STAT protein
regulation of STAT cascade
positive regulation of angiogenesis
cellular response to organonitrogen compound
negative regulation of T cell activation
parental behavior
negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
negative regulation of alpha−beta T cell activation
CD4−positive, alpha−beta T cell differentiation
positive regulation of cell migration
response to steroid hormone
negative regulation of phosphorylation
negative regulation of hemopoiesis
response to interleukin−6
response to leukemia inhibitory factor
cellular response to leukemia inhibitory factor
response to interleukin−1
negative regulation of adaptive immune response
protein autophosphorylation
negative regulation of T−helper cell differentiation
positive regulation of cell motility
regulation of leukocyte differentiation
T−helper 1 type immune response
response to peptide hormone
regulation of lymphocyte differentiation
JAK−STAT cascade
leukocyte cell−cell adhesion
regulation of CD4−positive, alpha−beta T cell differentiation
response to peptide
negative regulation of leukocyte cell−cell adhesion
negative regulation of kinase activity
STAT cascade
negative regulation of cell−cell adhesion
negative regulation of viral entry into host cell
growth hormone receptor signaling pathway
interleukin−6−mediated signaling pathway
regulation of cytokine production involved in immune response
negative regulation of cell adhesion
CD4−positive, alpha−beta T cell activation
T cell differentiation
negative regulation of immune response
positive regulation of locomotion
JNK cascade
cellular response to growth hormone stimulus
regulation of leukocyte cell−cell adhesion
alpha−beta T cell activation
regulation of leukocyte activation
response to leptin
positive regulation of mRNA catabolic process
negative regulation of lymphocyte activation
temperature homeostasis
regulation of alpha−beta T cell activation
negative regulation of cytokine production involved in immune response
nuclear−transcribed mRNA catabolic process, deadenylation−dependent decay
regulation of innate immune response
regulation of T cell activation
regulation of CD4−positive, alpha−beta T cell activation
positive regulation of leukocyte activation
regulation of T−helper 1 type immune response
regulation of platelet−derived growth factor receptor signaling pathway
stress−activated MAPK cascade
regulation of stress−activated MAPK cascade
negative regulation of MAPK cascade
regulation of JNK cascade
T−helper cell differentiation
regulation of stress−activated protein kinase signaling cascade
regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
positive regulation of hemopoiesis
regulation of hemopoiesis
negative regulation of immune system process
negative regulation of transferase activity
CD4−positive, alpha−beta T cell differentiation involved in immune response
cytokine production involved in immune response
regulation of cellular carbohydrate metabolic process
positive regulation of cell activation
alpha−beta T cell activation involved in immune response
alpha−beta T cell differentiation involved in immune response
regulation of antigen receptor−mediated signaling pathway
regulation of cell activation
regulation of cell−cell adhesion
negative regulation of cytokine production
regulation of vasculature development
regulation of tyrosine phosphorylation of STAT protein
connective tissue development
cold−induced thermogenesis
regulation of cold−induced thermogenesis
positive T cell selection
positive regulation of pri−miRNA transcription by RNA polymerase II
T cell differentiation involved in immune response
regulation of NIK/NF−kappaB signaling
positive regulation of JAK−STAT cascade
platelet−derived growth factor receptor signaling pathway
regulation of lymphocyte activation
negative regulation of leukocyte activation
regulation of adaptive immune response
peptidyl−tyrosine phosphorylation
regulation of stem cell differentiation
steroid hormone mediated signaling pathway
stress−activated protein kinase signaling cascade
peptidyl−tyrosine modification
positive regulation of STAT cascade
reproductive behavior
interleukin−7−mediated signaling pathway
regulation of viral entry into host cell
negative regulation of lymphocyte apoptotic process
interleukin−1−mediated signaling pathway
cellular response to glucocorticoid stimulus
adaptive thermogenesis
regulation of mRNA catabolic process
negative regulation of production of molecular mediator of immune response
regulation of T−helper cell differentiation
response to interleukin−7
cellular response to interleukin−7
positive regulation of NF−kappaB transcription factor activity
regulation of protein serine/threonine kinase activity
cytokine biosynthetic process
cytokine metabolic process
oxidative phosphorylation
regulation of cytokine biosynthetic process
respiratory electron transport chain
positive regulation of cytokine biosynthetic process
positive regulation of lymphocyte proliferation
positive regulation of mononuclear cell proliferation
positive regulation of T cell proliferation
phagocytosis, engulfment
positive regulation of leukocyte proliferation
positive regulation of leukocyte cell−cell adhesion
cell chemotaxis
leukocyte migration
mitochondrial ATP synthesis coupled electron transport
positive regulation of lymphocyte activation
ATP synthesis coupled electron transport
regulation of chemotaxis
lymphocyte proliferation
positive regulation of leukocyte migration
positive regulation of cytokine production
mononuclear cell proliferation
cellular respiration
electron transport chain
positive regulation of T cell activation
regulation of leukocyte migration
plasma membrane invagination
regulation of lymphocyte proliferation
positive regulation of response to external stimulus
regulation of mononuclear cell proliferation
leukocyte proliferation
energy derivation by oxidation of organic compounds
positive regulation of cell−cell adhesion
purinergic nucleotide receptor signaling pathway
generation of precursor metabolites and energy
regulation of leukocyte proliferation
membrane invagination
alcohol metabolic process
purinergic receptor signaling pathway
positive regulation of cell adhesion
positive regulation of chemotaxis
phagocytosis
positive regulation of myeloid leukocyte mediated immunity
ATP metabolic process
hyperosmotic response
B cell activation
positive regulation of leukocyte chemotaxis
regulation of leukocyte chemotaxis
B cell differentiation
ribonucleoside monophosphate metabolic process
positive regulation of calcium−mediated signaling
purine ribonucleoside monophosphate metabolic process
B cell proliferation
mitochondrial electron transport, NADH to ubiquinone
purine nucleoside monophosphate metabolic process
nucleoside monophosphate metabolic process
regulation of B cell activation
positive regulation of B cell activation
mitochondrial transmembrane transport
T cell proliferation
purine ribonucleoside triphosphate metabolic process
rhythmic behavior
cristae formation
regulation of T cell proliferation
regulation of B cell differentiation
lymphocyte activation involved in immune response
NADH dehydrogenase complex assembly
mitochondrial respiratory chain complex I assembly
ribonucleoside triphosphate metabolic process
leukocyte differentiation
purine nucleoside triphosphate metabolic process
leukocyte chemotaxis
interleukin−6 production
regulation of interleukin−6 biosynthetic process
T cell activation
circadian sleep/wake cycle process
myeloid leukocyte migration
organic hydroxy compound metabolic process
nucleoside triphosphate metabolic process
regulation of peptide secretion
positive regulation of lymphocyte migration
cellular zinc ion homeostasis
acute inflammatory response
zinc ion homeostasis
epithelial cell differentiation
detoxification
fibrinolysis
membrane raft assembly
wound healing
cellular transition metal ion homeostasis
detoxification of copper ion
stress response to copper ion
cellular response to transforming growth factor beta stimulus
transmembrane receptor protein serine/threonine kinase signaling pathway
cellular response to retinoic acid
positive regulation of MAP kinase activity
detoxification of inorganic compound
positive regulation of organ growth
positive regulation of MAPK cascade
response to transforming growth factor beta
negative regulation of blood coagulation
negative regulation of hemostasis
protein activation cascade
blood coagulation
stress response to metal ion
coagulation
regulation of blood coagulation
regulation of hemostasis
actin−mediated cell contraction
transforming growth factor beta receptor signaling pathway
negative regulation of coagulation
hemostasis
development of primary sexual characteristics
regulation of protein processing
regulation of inflammatory response
response to oxygen levels
reactive oxygen species metabolic process
regulation of coagulation
granulocyte migration
granulocyte chemotaxis
regulation of protein maturation
regulation of signaling receptor activity
positive regulation of protein kinase activity
response to interferon−gamma
positive regulation of cardiac muscle tissue growth
positive regulation of stress−activated MAPK cascade
gonad development
protein processing
negative regulation of wound healing
muscle cell proliferation
positive regulation of JNK cascade
positive regulation of stress−activated protein kinase signaling cascade
complement activation
epithelial cell development
actin filament−based movement
positive regulation of cardiac muscle cell proliferation
arginine transport
activation of protein kinase activity
extrinsic apoptotic signaling pathway via death domain receptors
regulation of endopeptidase activity
organ growth
regulation of necrotic cell death
divalent inorganic cation homeostasis
positive regulation of cold−induced thermogenesis
response to copper ion
positive regulation of heart growth
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
cellular divalent inorganic cation homeostasis
cellular response to acid chemical
regulation of peptidase activity
necrotic cell death
response to toxic substance
transition metal ion homeostasis
reproductive system development
cardiac muscle cell proliferation
activation of MAPK activity
humoral immune response
membrane raft organization
response to hyperoxia
pattern specification process
acute−phase response
response to growth hormone
GeneRatio
0.03
0.06
0.09
p.adjust
0.05
0.04
0.03
0.02
0.01
HgC (150)
HgS (154)
DgC (681)
DgS (661)


ontology: MF
DNA−binding transcription repressor activity, RNA polymerase II−specific
growth factor binding
regulatory RNA binding
cytokine binding
purinergic receptor activity
purinergic nucleotide receptor activity
nucleotide receptor activity
NADH dehydrogenase (ubiquinone) activity
NADH dehydrogenase (quinone) activity
NADH dehydrogenase activity
receptor ligand activity
receptor regulator activity
long−chain fatty acid binding
HgS
(153)
DgC
(671)
DgS
(665)
GeneRatio
0.02
0.04
0.06
p.adjust
0.04
0.03
0.02
0.01


ontology: CC
proteasome core complex, beta−subunit complex
mitochondrial membrane part
inner mitochondrial membrane protein complex
mitochondrial inner membrane
mitochondrial protein complex
organelle inner membrane
respiratory chain complex
oxidoreductase complex
mitochondrial respiratory chain
respiratory chain
mitochondrial respiratory chain complex I
NADH dehydrogenase complex
respiratory chain complex I
phagocytic cup
mitochondrial respiratory chain complex III
respiratory chain complex III
neuronal cell body
integral component of mitochondrial membrane
intrinsic component of mitochondrial membrane
extracellular matrix
collagen−containing extracellular matrix
blood microparticle
myofibril
contractile fiber
contractile fiber part
endoplasmic reticulum lumen
hemoglobin complex
platelet alpha granule lumen
I band
HgC
(154)
DgC
(707)
DgS
(687)
p.adjust
0.04
0.03
0.02
0.01
GeneRatio
0.02
0.04
0.06


ontology: KEGG
JAK−STAT signaling pathway
FoxO signaling pathway
Longevity regulating pathway
Signaling pathways regulating pluripotency of stem cells
Longevity regulating pathway − multiple species
Adipocytokine signaling pathway
Transcriptional misregulation in cancer
NF−kappa B signaling pathway
Parkinson disease
Oxidative phosphorylation
Malaria
Proteoglycans in cancer
Pathways in cancer
TNF signaling pathway
Cytokine−cytokine receptor interaction
IL−17 signaling pathway
p53 signaling pathway
MAPK signaling pathway
Breast cancer
AGE−RAGE signaling pathway in diabetic complications
Complement and coagulation cascades
Gastric cancer
Basal cell carcinoma
African trypanosomiasis
Phenylalanine metabolism
Insulin resistance
Hepatocellular carcinoma
Epstein−Barr virus infection
Osteoclast differentiation
Platinum drug resistance
Pertussis
HgS
(72)
DgC
(338)
DgS
(312)
GeneRatio
0.05
0.10
p.adjust
0.05
0.04
0.03
0.02
0.01