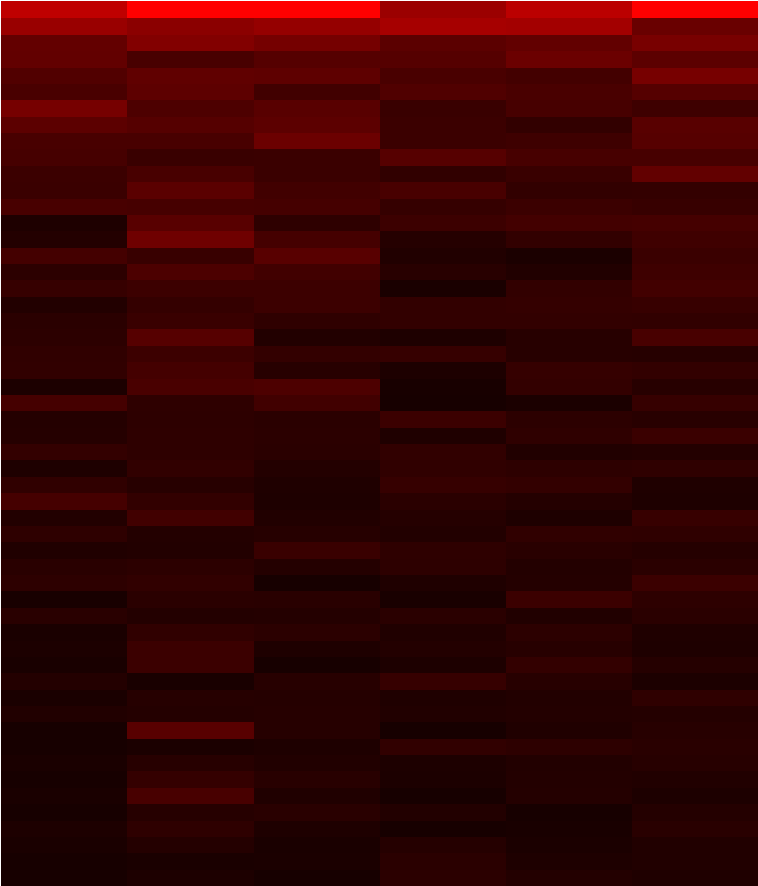


GAGE Up-test: $-\log_{10}(\text{p-value})$



- hsa04630 Jak-STAT signaling pathway
- hsa04623 Cytosolic DNA-sensing pathway
- hsa04972 Pancreatic secretion
- hsa04062 Chemokine signaling pathway
- hsa04672 Intestinal immune network
- hsa00532 Glycosaminoglycan biosynthesis
- hsa00564 Glycerophospholipid metabolism
- hsa04622 RIG-I-like receptor signaling pathway
- hsa04514 Cell adhesion molecules
- hsa04971 Gastric acid secretion
- hsa00910 Nitrogen metabolism
- hsa04141 Protein processing in endoplasmic reticulum
- hsa04380 Osteoclast differentiation
- hsa04662 B cell receptor signaling pathway
- hsa04973 Carbohydrate digestion and absorption
- hsa00511 Other glycan degradation
- hsa04614 Renin-angiotensin system
- hsa04666 Fc gamma R-mediated phagocytosis
- hsa04964 Proximal tubule bicarbonate reabsorption
- hsa00565 Ether lipid metabolism
- hsa04640 Hematopoietic cell lineage
- hsa00533 Glycosaminoglycan biosynthesis
- hsa04150 mTOR signaling pathway
- hsa00534 Glycosaminoglycan biosynthesis
- hsa04210 Apoptosis
- hsa00601 Glycosphingolipid biosynthesis
- hsa04920 Adipocytokine signaling pathway

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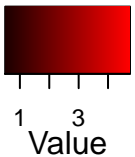
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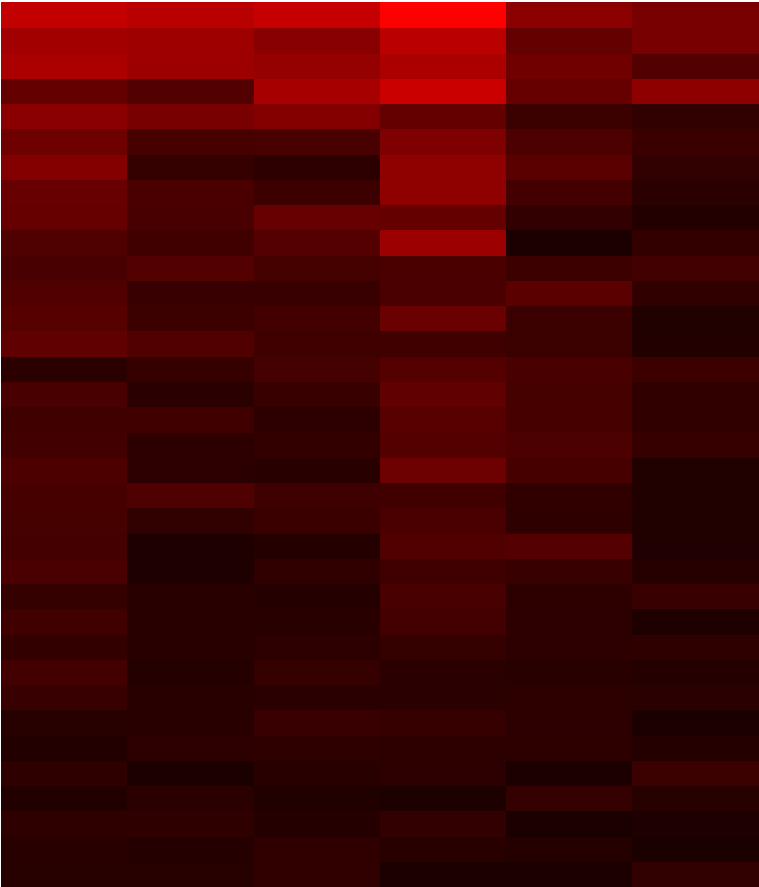
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Color Key



GAGE Down-test: $-\log_{10}(\text{p-value})$



- hsa03040 Spliceosome
- hsa04110 Cell cycle
- hsa03420 Nucleotide excision re
- hsa03010 Ribosome
- hsa03030 DNA replication
- hsa00620 Pyruvate metabolism
- hsa00280 Valine, leucine and iso
- hsa03013 RNA transport
- hsa03410 Base excision repair
- hsa00190 Oxidative phosphoryla
- hsa00290 Valine, leucine and iso
- hsa00380 Tryptophan metabolism
- hsa00630 Glyoxylate and dicarb
- hsa03430 Mismatch repair
- hsa04530 Tight junction
- hsa00071 Fatty acid metabolism
- hsa00650 Butanoate metabolism
- hsa00310 Lysine degradation
- hsa00640 Propanoate metabolism
- hsa00970 Aminoacyl-tRNA bios
- hsa03008 Ribosome biogenesis
- hsa04520 Adherens junction
- hsa04350 TGF-beta signaling p
- hsa04115 p53 signaling pathway
- hsa00020 Citrate cycle (TCA cyc
- hsa04310 Wnt signaling pathway
- hsa00040 Pentose and glucuron
- hsa04512 ECM-receptor interac
- hsa00980 Metabolism of xenobio
- hsa00350 Tyrosine metabolism
- hsa03022 Basal transcription fac
- hsa00120 Primary bile acid bios
- hsa00670 One carbon pool by fo
- hsa03020 RNA polymerase
- hsa00140 Steroid hormone bios

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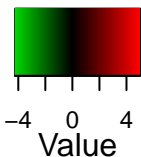
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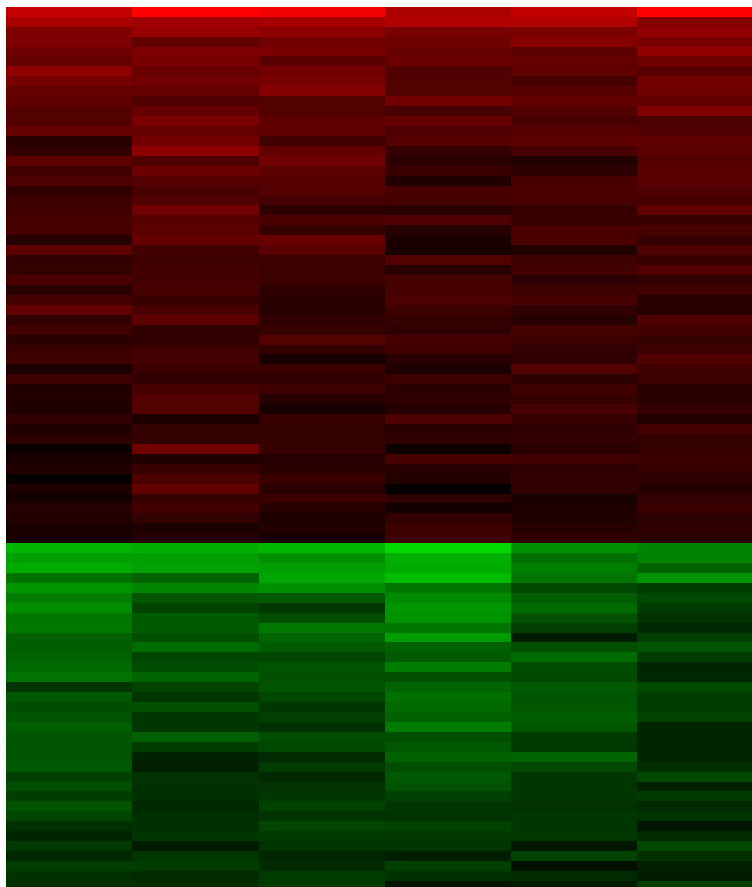
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Color Key



GAGE test statistics



hsa04142 Lysosome
hsa04670 Leukocyte transendothelial migration
hsa04612 Antigen processing and presentation
hsa04650 Natural killer cell mediated cytotoxicity
hsa04620 Toll-like receptor signaling pathway
hsa00600 Sphingolipid metabolism
hsa04320 Dorso-ventral axis formation
hsa00563 Glycosylphosphatidylinositol signaling system
hsa00531 Glycosaminoglycan degradation
hsa00561 Glycerolipid metabolism
hsa04664 Fc epsilon RI signaling pathway
hsa04145 Phagosome
hsa04621 NOD-like receptor signaling pathway
hsa04722 Neurotrophin signaling pathway
hsa04740 Olfactory transduction
hsa04610 Complement and coagulation cascades
hsa04966 Collecting duct acid secretion
hsa04976 Bile secretion
hsa00510 N-Glycan biosynthesis
hsa04070 Phosphatidylinositol signaling system
hsa04370 VEGF signaling pathway
hsa04710 Circadian rhythm - mammal
hsa04912 GnRH signaling pathway
hsa04910 Insulin signaling pathway
hsa04730 Long-term depression
hsa04916 Melanogenesis
hsa00603 Glycosphingolipid biosynthesis - lactosylceramide
hsa03040 Spliceosome
hsa03420 Nucleotide excision repair
hsa03030 DNA replication
hsa00280 Valine, leucine and isoleucine degradation
hsa03410 Base excision repair
hsa00290 Valine, leucine and isoleucine biosynthesis
hsa00630 Glyoxylate and dicarboxylate metabolism
hsa04530 Tight junction
hsa00650 Butanoate metabolism
hsa00640 Propanoate metabolism
hsa03008 Ribosome biogenesis in eukaryotes
hsa04350 TGF-beta signaling pathway
hsa00020 Citrate cycle (TCA cycle)
hsa00040 Pentose and glucuronate interconversions
hsa00980 Metabolism of xenobiotics by cytochrome P450
hsa03022 Basal transcription factors
hsa00670 One carbon pool by folate
hsa00140 Steroid hormone biosynthesis

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