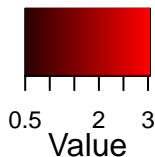
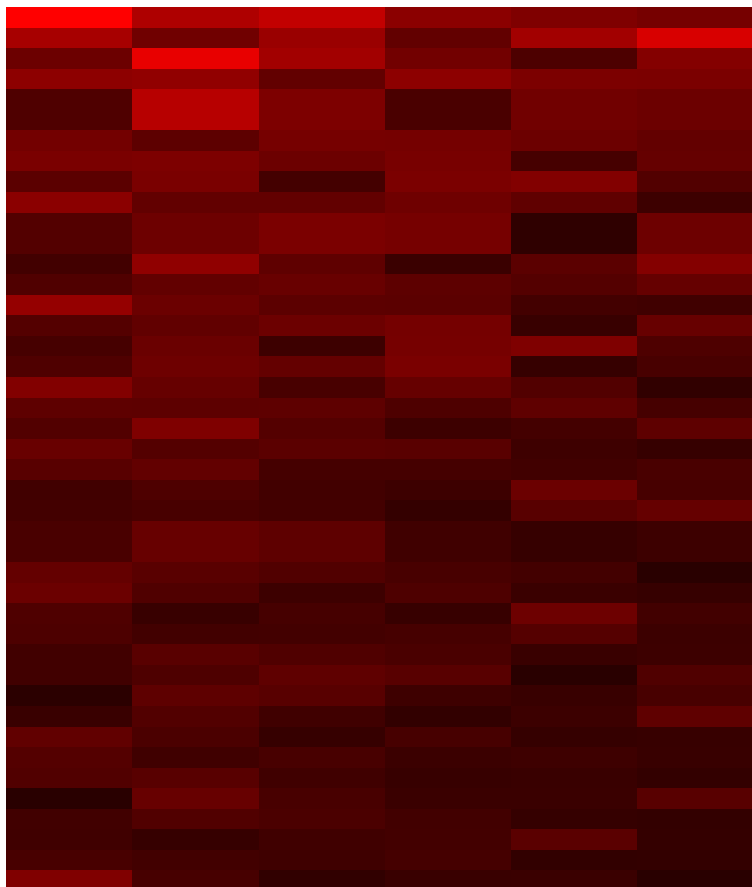


Color Key



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



GO:0001775 cell activation
GO:0002474 antigen processing
GO:0006022 aminoglycan meta
GO:0006029 proteoglycan meta
GO:0006505 GPI anchor metab
GO:0006506 GPI anchor biosyn
GO:0002237 response to molec
GO:0002520 immune system de
GO:0001822 kidney developme
GO:0002682 regulation of immu
GO:0002263 cell activation durin
GO:0002366 leukocyte activation
GO:0005975 carbohydrate meta
GO:0001990 regulation of syste
GO:0002684 positive regulation
GO:0002286 T cell activation du
GO:0001655 urogenital system m
GO:0002521 leukocyte differenti
GO:0003018 vascular process in
GO:0006486 protein amino acid
GO:0006516 glycoprotein catab
GO:0002696 positive regulation
GO:0001836 release of cytochro
GO:0006458 'de novo' protein fo
GO:0006487 protein amino acid
GO:0006023 aminoglycan biosyn
GO:0006024 glycosaminoglycan
GO:0002694 regulation of leuko
GO:0002250 adaptive immune r
GO:0006470 protein amino acid
GO:0003006 reproductive devel
GO:0003044 regulation of syste
GO:0002285 lymphocyte activat
GO:0001570 vasculogenesis
GO:0005976 polysaccharide me
GO:0002460 adaptive immune r
GO:0002685 regulation of leuko
GO:0006509 membrane protein
GO:0006497 protein amino acid
GO:0003073 regulation of syste
GO:0002377 immunoglobulin pr
GO:0001763 morphogenesis of
GO:0002443 leukocyte mediate

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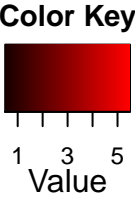
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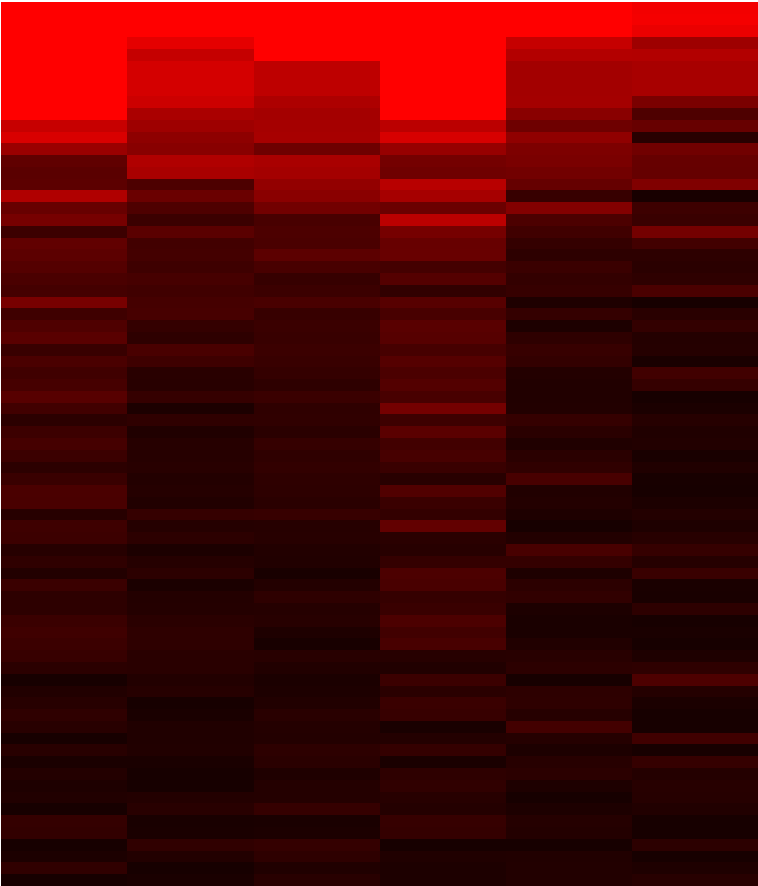
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GAGE Down-test: $-\log_{10}(\text{p-value})$



- GO:0000087 M phase of mitotic cell cycle
- GO:0000279 M phase
- GO:0006412 translation
- GO:0000377 RNA splicing, via trans-splicing
- GO:0006397 mRNA processing
- GO:0006289 nucleotide-excision repair
- GO:0000226 microtubule cytoskeleton organization
- GO:0000819 sister chromatid segregation
- GO:0006259 DNA metabolic process
- GO:0006325 establishment or maintenance of transcription
- GO:0006457 protein folding
- GO:0006297 nucleotide-excision repair
- GO:0001756 somitogenesis
- GO:0006268 DNA unwinding during replication
- GO:0006354 RNA elongation
- GO:0006284 base-excision repair
- GO:0000387 spliceosomal snRNP biogenesis
- GO:0006091 generation of precursor
- GO:0000245 spliceosome assembly
- GO:0006413 translational initiation
- GO:0001707 mesoderm formation
- GO:0000075 cell cycle checkpoint
- GO:0006119 oxidative phosphorylation
- GO:0000187 activation of MAPK activity
- GO:0006333 chromatin assembly or reorganization
- GO:0006082 organic acid metabolic process
- GO:0006338 chromatin remodeling
- GO:0006403 RNA localization
- GO:0001502 cartilage condensation
- GO:0001933 negative regulation of protein
- GO:0006446 regulation of translation
- GO:0002228 natural killer cell mediated cytotoxicity
- GO:0003015 heart process
- GO:0000041 transition metal ion transport
- GO:0001523 retinoid metabolic process
- GO:0006099 tricarboxylic acid cycle
- GO:0006520 amino acid metabolic process
- GO:0003012 muscle system process

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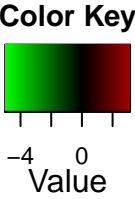
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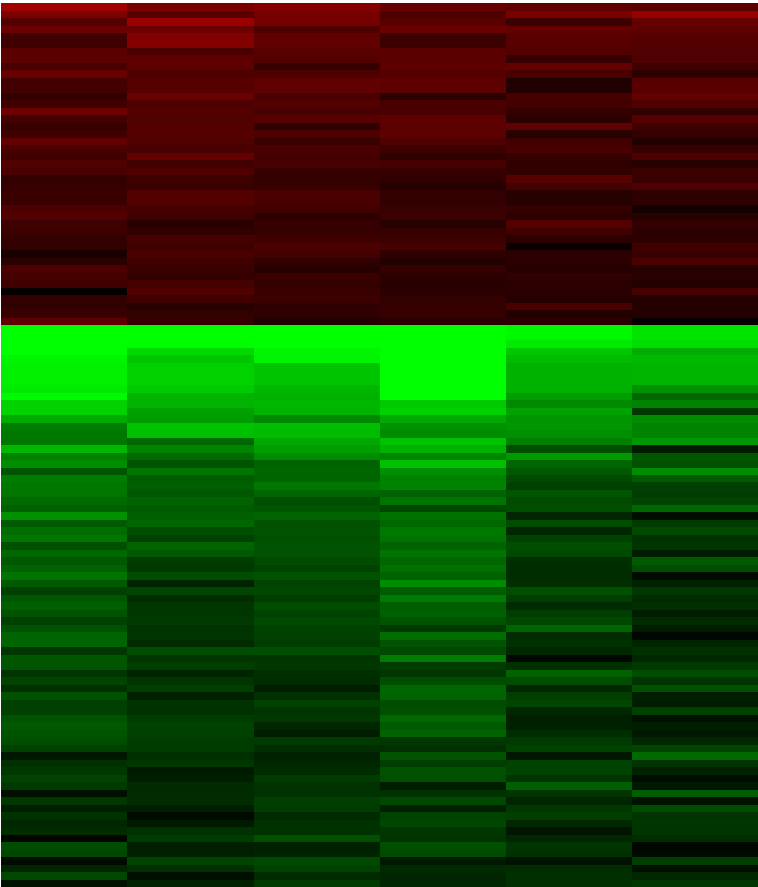
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GAGE test statistics



- GO:0001775 cell activation
- GO:0006029 proteoglycan metabolism
- GO:0002237 response to molecule of
- GO:0002682 regulation of immune s
- GO:0005975 carbohydrate metabolic
- GO:0002286 T cell activation during
- GO:0003018 vascular process in circ
- GO:0002696 positive regulation of le
- GO:0006487 protein amino acid N-li
- GO:0002694 regulation of leukocyte
- GO:0003006 reproductive developme
- GO:0001570 vasculogenesis
- GO:0002685 regulation of leukocyte
- GO:0003073 regulation of systemic a
- GO:0002443 leukocyte mediated imm
- GO:0000279 M phase
- GO:0000375 RNA splicing, via trans
- GO:0006397 mRNA processing
- GO:0006281 DNA repair
- GO:0000819 sister chromatid segreg
- GO:0001654 eye development
- GO:0006457 protein folding
- GO:0000718 nucleotide-excision rep
- GO:0006268 DNA unwinding during
- GO:0006418 tRNA aminoacylation fo
- GO:0000387 spliceosomal snRNP bi
- GO:0002088 lens development in ca
- GO:0006413 translational initiation
- GO:0006399 tRNA metabolic proces
- GO:0006119 oxidative phosphorylati
- GO:0000059 protein import into nucl
- GO:0006082 organic acid metabolic
- GO:0006310 DNA recombination
- GO:0001502 cartilage condensation
- GO:0006461 protein complex assem
- GO:0002228 natural killer cell media
- GO:0002027 regulation of heart rate
- GO:0001523 retinoid metabolic proc
- GO:0003001 generation of a signal in
- GO:0003012 muscle system process

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