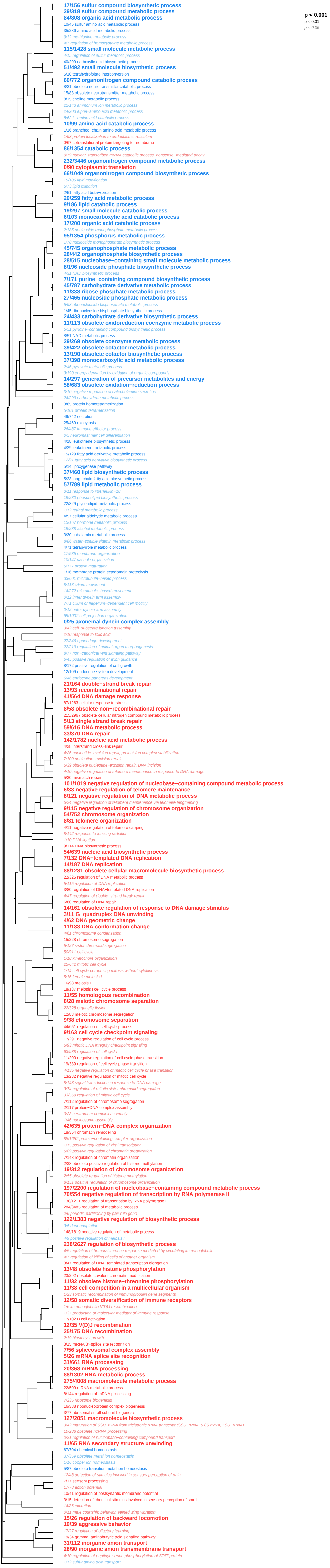
p < 0.001
p < 0.01
p < 0.05
17/156 sulfur compound biosynthetic process
29/318 sulfur compound metabolic process
84/808 organic acid metabolic process
10/45 sulfur amino acid metabolic process
35/286 amino acid metabolic process
9/32 methionine metabolic process
4/7 regulation of homocysteine metabolic process
115/1428 small molecule metabolic process
4/15 regulation of sulfur metabolic process
40/299 carboxylic acid biosynthetic process
51/492 small molecule biosynthetic process
5/10 tetrahydrofolate interconversion
60/772 organonitrogen compound catabolic process
8/21 obsolete neurotransmitter catabolic process
15/83 obsolete neurotransmitter metabolic process
8/15 choline metabolic process
22/143 ammonium ion metabolic process
24/203 alpha−amino acid metabolic process
8/62 L−amino acid catabolic process
10/99 amino acid catabolic process
1/16 branched−chain amino acid metabolic process
1/93 protein localization to endoplasmic reticulum
0/67 cotranslational protein targeting to membrane
86/1354 catabolic process
0/79 nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
232/3446 organonitrogen compound metabolic process
0/90 cytoplasmic translation
66/1049 organonitrogen compound biosynthetic process
15/186 lipid modification
5/73 lipid oxidation
2/51 fatty acid beta−oxidation
29/259 fatty acid metabolic process
9/186 lipid catabolic process
19/297 small molecule catabolic process
6/103 monocarboxylic acid catabolic process
17/200 organic acid catabolic process
2/185 nucleoside monophosphate metabolic process
95/1354 phosphorus metabolic process
1/78 nucleoside monophosphate biosynthetic process
45/745 organophosphate metabolic process
28/442 organophosphate biosynthetic process
28/515 nucleobase−containing small molecule metabolic process
8/196 nucleoside phosphate biosynthetic process
4/31 NAD biosynthetic process
7/171 purine−containing compound biosynthetic process
45/787 carbohydrate derivative metabolic process
11/338 ribose phosphate metabolic process
27/465 nucleoside phosphate metabolic process
5/93 ribonucleoside bisphosphate metabolic process
1/45 ribonucleoside bisphosphate biosynthetic process
24/433 carbohydrate derivative biosynthetic process
11/113 obsolete oxidoreduction coenzyme metabolic process
5/51 pyridine−containing compound biosynthetic process
8/51 NAD metabolic process
29/269 obsolete coenzyme metabolic process
39/422 obsolete cofactor metabolic process
13/190 obsolete cofactor biosynthetic process
37/398 monocarboxylic acid metabolic process
2/46 pyruvate metabolic process
3/190 energy derivation by oxidation of organic compounds
14/297 generation of precursor metabolites and energy
58/683 obsolete oxidation−reduction process
3/10 negative regulation of catecholamine secretion
24/299 carbohydrate metabolic process
3/65 protein homotetramerization
5/101 protein tetramerization
49/742 secretion
25/469 exocytosis
26/487 immune effector process
0/5 neuromast hair cell differentiation
4/18 leukotriene biosynthetic process
4/29 leukotriene metabolic process
15/129 fatty acid derivative metabolic process
12/91 fatty acid derivative biosynthetic process
5/14 lipoxygenase pathway
37/460 lipid biosynthetic process
5/23 long−chain fatty acid biosynthetic process
57/789 lipid metabolic process
3/11 response to interleukin−18
19/230 phospholipid biosynthetic process
22/329 glycerolipid metabolic process
1/12 retinal metabolic process
4/57 cellular aldehyde metabolic process
15/167 hormone metabolic process
19/238 alcohol metabolic process
3/30 cobalamin metabolic process
8/86 water−soluble vitamin metabolic process
4/71 tetrapyrrole metabolic process
17/535 membrane organization
10/147 vacuole organization
5/177 protein maturation
1/16 membrane protein ectodomain proteolysis
33/601 microtubule−based process
8/113 cilium movement
14/272 microtubule−based movement
0/12 inner dynein arm assembly
7/71 cilium or flagellum−dependent cell motility
0/12 outer dynein arm assembly
69/1007 cell projection organization
0/25 axonemal dynein complex assembly
3/42 cell−substrate junction assembly
2/10 response to folic acid
27/346 appendage development
22/219 regulation of animal organ morphogenesis
8/77 non−canonical Wnt signaling pathway
6/45 positive regulation of axon guidance
8/172 positive regulation of cell growth
12/109 endocrine system development
6/46 endocrine pancreas development
21/164 double−strand break repair
13/93 recombinational repair
41/564 DNA damage response
87/1263 cellular response to stress
8/58 obsolete non−recombinational repair
215/2967 obsolete cellular nitrogen compound metabolic process
5/13 single strand break repair
59/616 DNA metabolic process
33/370 DNA repair
142/1782 nucleic acid metabolic process
4/38 interstrand cross−link repair
4/26 nucleotide−excision repair, preincision complex stabilization
7/100 nucleotide−excision repair
5/39 obsolete nucleotide−excision repair, DNA incision
4/10 negative regulation of telomere maintenance in response to DNA damage
5/30 mismatch repair
101/1019 negative regulation of nucleobase−containing compound metabolic process
6/33 negative regulation of telomere maintenance
8/121 negative regulation of DNA metabolic process
6/24 negative regulation of telomere maintenance via telomere lengthening
9/115 negative regulation of chromosome organization
54/752 chromosome organization
8/81 telomere organization
4/11 negative regulation of telomere capping
8/142 response to ionizing radiation
1/10 DNA ligation
9/114 DNA biosynthetic process
54/639 nucleic acid biosynthetic process
7/132 DNA−templated DNA replication
14/187 DNA replication
88/1281 obsolete cellular macromolecule biosynthetic process
22/325 regulation of DNA metabolic process
5/115 regulation of DNA replication
3/80 regulation of DNA−templated DNA replication
4/47 regulation of double−strand break repair
6/80 regulation of DNA repair
14/161 obsolete regulation of response to DNA damage stimulus
3/11 G−quadruplex DNA unwinding
4/62 DNA geometric change
11/183 DNA conformation change
4/61 chromosome condensation
15/228 chromosome segregation
5/127 sister chromatid segregation
50/911 cell cycle
1/18 kinetochore organization
25/642 mitotic cell cycle
1/14 cell cycle comprising mitosis without cytokinesis
5/16 female meiosis I
16/98 meiosis I
18/137 meiosis I cell cycle process
11/55 homologous recombination
8/28 meiotic chromosome separation
22/328 organelle fission
12/83 meiotic chromosome segregation
9/38 chromosome separation
44/651 regulation of cell cycle process
9/163 cell cycle checkpoint signaling
17/291 negative regulation of cell cycle process
5/93 mitotic DNA integrity checkpoint signaling
63/938 regulation of cell cycle
11/200 negative regulation of cell cycle phase transition
19/389 regulation of cell cycle phase transition
4/135 negative regulation of mitotic cell cycle phase transition
13/232 negative regulation of mitotic cell cycle
8/143 signal transduction in response to DNA damage
3/74 regulation of mitotic sister chromatid segregation
33/569 regulation of mitotic cell cycle
7/112 regulation of chromosome segregation
2/117 protein−DNA complex assembly
0/28 centromere complex assembly
1/46 nucleosome assembly
42/635 protein−DNA complex organization
18/354 chromatin remodeling
88/1657 protein−containing complex organization
1/15 positive regulation of viral transcription
5/89 positive regulation of chromatin organization
7/148 regulation of chromatin organization
2/38 obsolete positive regulation of histone methylation
19/312 regulation of chromosome organization
2/55 obsolete regulation of histone methylation
8/151 positive regulation of chromosome organization
197/2200 regulation of nucleobase−containing compound metabolic process
70/554 negative regulation of transcription by RNA polymerase II
138/1211 regulation of transcription by RNA polymerase II
284/3485 regulation of metabolic process
2/6 periodic partitioning by pair rule gene
122/1383 negative regulation of biosynthetic process
3/5 dark adaptation
148/1819 negative regulation of metabolic process
4/9 positive regulation of meiosis I
238/2627 regulation of biosynthetic process
4/5 regulation of humoral immune response mediated by circulating immunoglobulin
4/7 regulation of killing of cells of another organism
3/47 regulation of DNA−templated transcription elongation
13/48 obsolete histone phosphorylation
23/292 obsolete covalent chromatin modification
11/32 obsolete histone−threonine phosphorylation
11/38 cell competition in a multicellular organism
1/23 somatic recombination of immunoglobulin gene segments
12/58 somatic diversification of immune receptors
1/6 immunoglobulin V(D)J recombination
1/37 production of molecular mediator of immune response
17/102 B cell activation
12/35 V(D)J recombination
25/175 DNA recombination
2/19 blastocyst growth
3/15 mRNA 3'−splice site recognition
7/56 spliceosomal complex assembly
5/26 mRNA splice site recognition
31/661 RNA processing
20/368 mRNA processing
88/1302 RNA metabolic process
275/4008 macromolecule metabolic process
22/509 mRNA metabolic process
8/144 regulation of mRNA processing
7/235 ribosome biogenesis
16/388 ribonucleoprotein complex biogenesis
3/77 ribosomal small subunit biogenesis
127/2051 macromolecule biosynthetic process
3/42 maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)
10/288 obsolete ncRNA processing
0/21 regulation of nucleobase−containing compound transport
11/65 RNA secondary structure unwinding
67/704 chemical homeostasis
37/359 obsolete metal ion homeostasis
1/16 copper ion homeostasis
5/87 obsolete transition metal ion homeostasis
12/48 detection of stimulus involved in sensory perception of pain
7/17 sensory processing
17/78 action potential
10/41 regulation of postsynaptic membrane potential
3/15 detection of chemical stimulus involved in sensory perception of smell
14/86 excretion
0/11 male courtship behavior, veined wing vibration
15/26 regulation of backward locomotion
19/39 aggressive behavior
17/27 regulation of olfactory learning
19/34 gamma−aminobutyric acid signaling pathway
31/112 inorganic anion transport
28/90 inorganic anion transmembrane transport
4/10 regulation of peptidyl−serine phosphorylation of STAT protein
1/12 sulfur amino acid transport