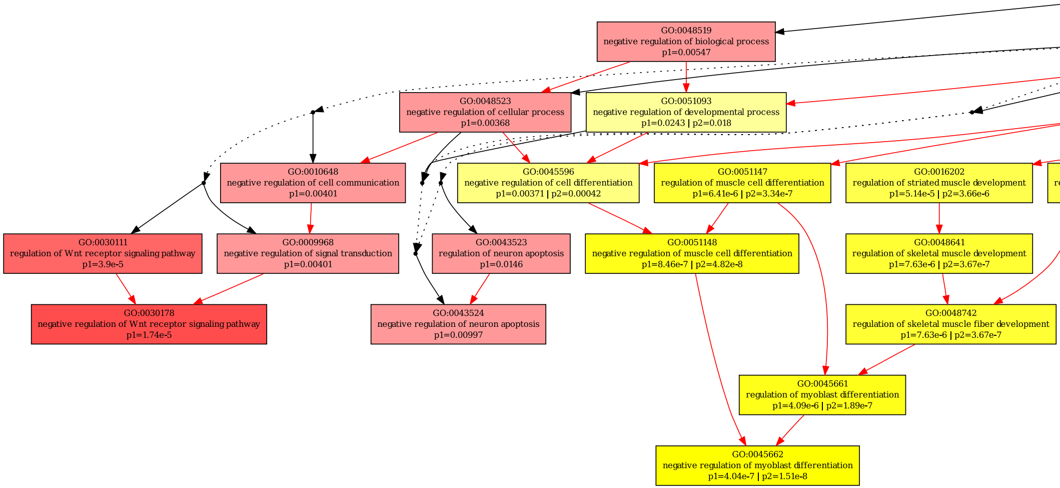
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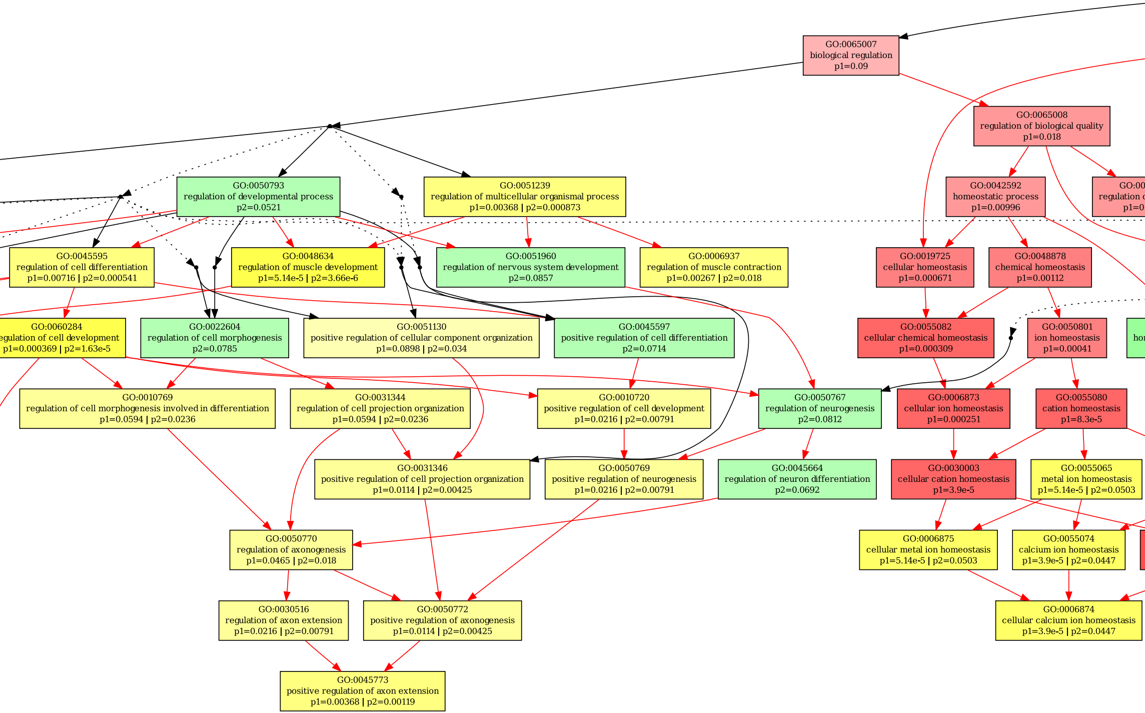
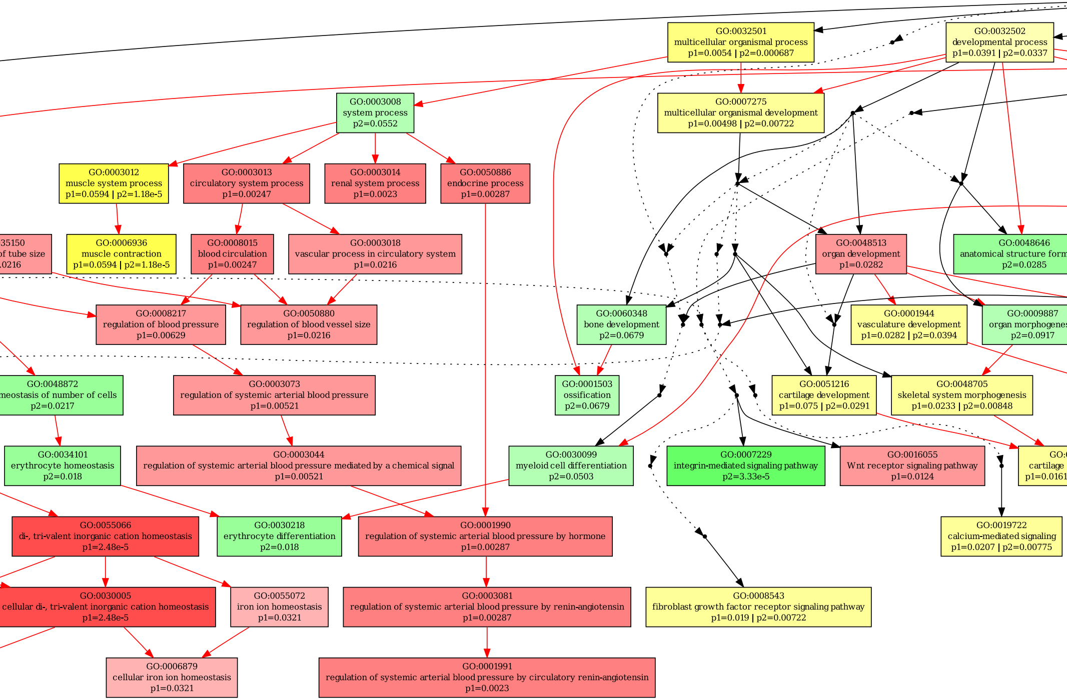
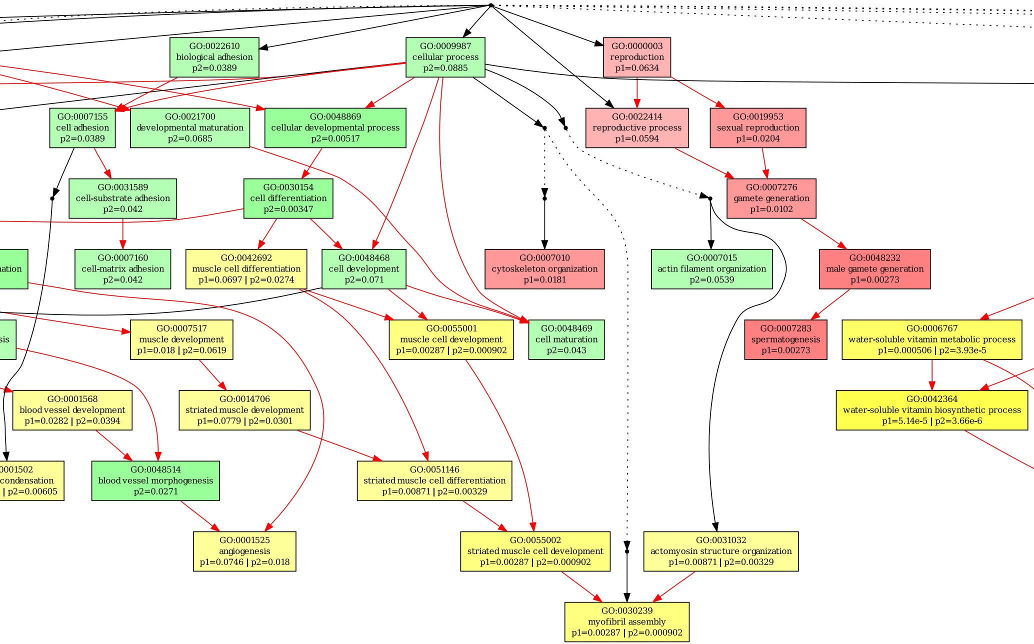
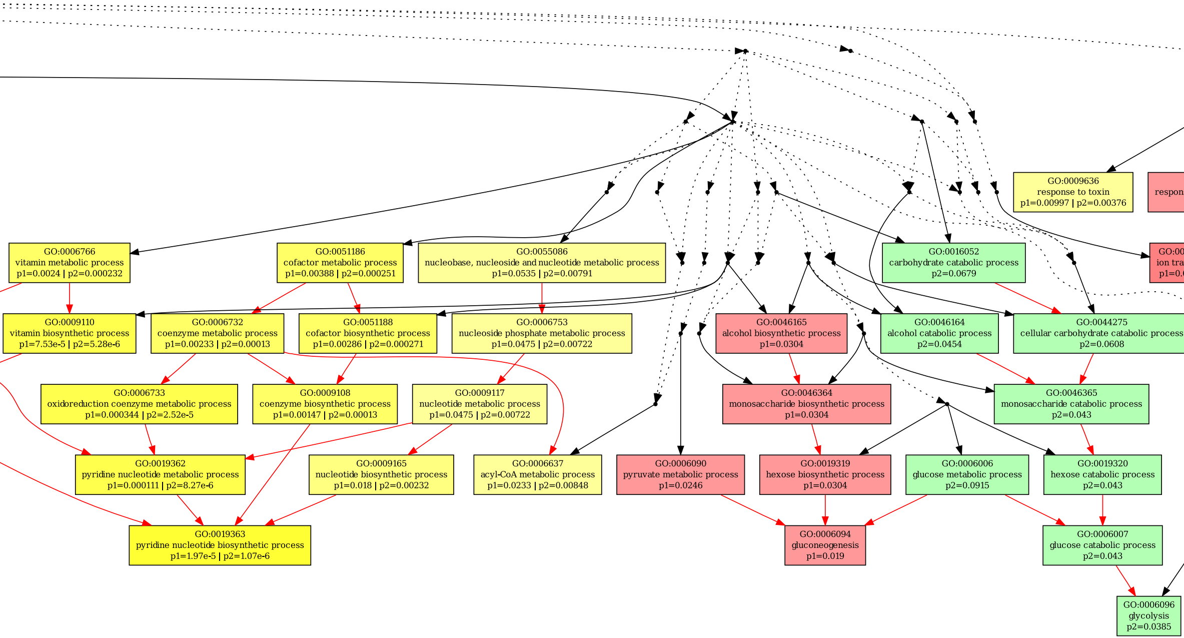
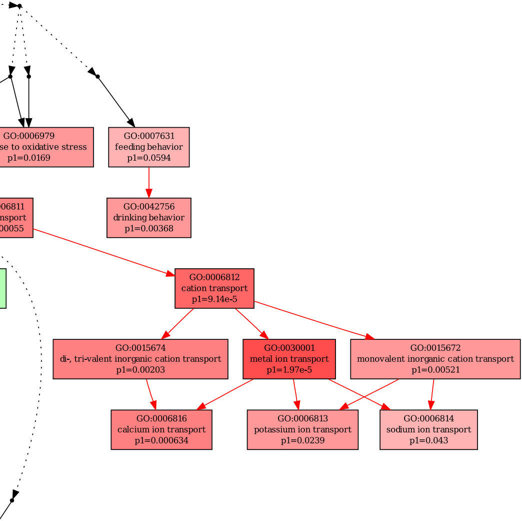
p1=0.00547
GO:0048523
negative regulation of cellular process
p1=0.00368
GO:0051093
negative regulation of developmental process
p1=0.0243 | p2=0.018
GO:0010648
negative regulation of cell communication
p1=0.00401
GO:0045596
negative regulation of cell differentiation
p1=0.00371 | p2=0.00042
GO:0051147
regulation of muscle cell differentiation
p1=6.41e-6 | p2=3.34e-7
GO:0016202
regulation of striated muscle development
p1=5.14e-5 | p2=3.66e-6
GO:0030111
regulation of Wnt receptor signaling pathway
p1=3.9e-5
GO:0009968
negative regulation of signal transduction
p1=0.00401
GO:0043523
regulation of neuron apoptosis
p1=0.0146
GO:0051148
negative regulation of muscle cell differentiation
p1=8.46e-7 | p2=4.82e-8
GO:0048641
regulation of skeletal muscle development
p1=7.63e-6 | p2=3.67e-7
GO:0030178
negative regulation of Wnt receptor signaling pathway
p1=1.74e-5
GO:0043524
negative regulation of neuron apoptosis
p1=0.00997
GO:0048742
regulation of skeletal muscle fiber development
p1=7.63e-6 | p2=3.67e-7
GO:0045661
regulation of myoblast differentiation
p1=4.09e-6 | p2=1.89e-7
GO:0045662
negative regulation of myoblast differentiation
p1=4.04e-7 | p2=1.51e-8


GO:0065007
biological regulation
p1=0.09
GO:0065008
regulation of biological quality
p1=0.018
GO:0050793
regulation of developmental process
p2=0.0521
GO:0051239
regulation of multicellular organismal process
p1=0.00368 | p2=0.000873
GO:0042592
homeostatic process
p1=0.00996
GO:00
regulation o
p1=0
GO:0045595
regulation of cell differentiation
p1=0.00716 | p2=0.000541
GO:0048634
regulation of muscle development
p1=5.14e-5 | p2=3.66e-6
GO:0051960
regulation of nervous system development
p2=0.0857
GO:0006937
regulation of muscle contraction
p1=0.00267 | p2=0.018
GO:0019725
cellular homeostasis
p1=0.000671
GO:0048878
chemical homeostasis
p1=0.00112
GO:0060284
egulation of cell development
p1=0.000369 | p2=1.63e-5
GO:0022604
regulation of cell morphogenesis
p2=0.0785
GO:0051130
positive regulation of cellular component organization
p1=0.0898 | p2=0.034
GO:0045597
positive regulation of cell differentiation
p2=0.0714
GO:0055082
cellular chemical homeostasis
p1=0.000309
GO:0050801
ion homeostasis
p1=0.00041
hor
GO:0010769
regulation of cell morphogenesis involved in differentiation
p1=0.0594 | p2=0.0236
GO:0031344
regulation of cell projection organization
p1=0.0594 | p2=0.0236
GO:0010720
positive regulation of cell development
p1=0.0216 | p2=0.00791
GO:0050767
regulation of neurogenesis
p2=0.0812
GO:0006873
cellular ion homeostasis
p1=0.000251
GO:0055080
cation homeostasis
p1=8.3e-5
GO:0031346
positive regulation of cell projection organization
p1=0.0114 | p2=0.00425
GO:0050769
positive regulation of neurogenesis
p1=0.0216 | p2=0.00791
GO:0045664
regulation of neuron differentiation
p2=0.0692
GO:0030003
cellular cation homeostasis
p1=3.9e-5
GO:0055065
metal ion homeostasis
p1=5.14e-5 | p2=0.0503
GO:0050770
regulation of axonogenesis
p1=0.0465 | p2=0.018
GO:0006875
cellular metal ion homeostasis
p1=5.14e-5 | p2=0.0503
GO:0055074
calcium ion homeostasis
p1=3.9e-5 | p2=0.0447
GO:0030516
regulation of axon extension
p1=0.0216 | p2=0.00791
GO:0050772
positive regulation of axonogenesis
p1=0.0114 | p2=0.00425
GO:0006874
cellular calcium ion homeostasis
p1=3.9e-5 | p2=0.0447
GO:0045773
positive regulation of axon extension
p1=0.00368 | p2=0.00119


GO:0032501
multicellular organismal process
p1=0.0054 | p2=0.000687
GO:0032502
developmental process
p1=0.0391 | p2=0.0337
GO:0003008
system process
p2=0.0552
GO:0007275
multicellular organismal development
p1=0.00498 | p2=0.00722
GO:0003012
muscle system process
p1=0.0594 | p2=1.18e-5
GO:0003013
circulatory system process
p1=0.00247
GO:0003014
renal system process
p1=0.0023
GO:0050886
endocrine process
p1=0.00287
35150
f tube size
.0216
GO:0006936
muscle contraction
p1=0.0594 | p2=1.18e-5
GO:0008015
blood circulation
p1=0.00247
GO:0003018
vascular process in circulatory system
p1=0.0216
GO:0048513
organ development
p1=0.0282
GO:0048646
anatomical structure form
p2=0.0285
GO:0008217
regulation of blood pressure
p1=0.00629
GO:0050880
regulation of blood vessel size
p1=0.0216
GO:0060348
bone development
p2=0.0679
GO:0001944
vasculature development
p1=0.0282 | p2=0.0394
GO:0009887
organ morphogenes
p2=0.0917
GO:0048872
meostasis of number of cells
p2=0.0217
GO:0003073
regulation of systemic arterial blood pressure
p1=0.00521
GO:0001503
ossification
p2=0.0679
GO:0051216
cartilage development
p1=0.075 | p2=0.0291
GO:0048705
skeletal system morphogenesis
p1=0.0233 | p2=0.00848
GO:0034101
erythrocyte homeostasis
p2=0.018
GO:0003044
regulation of systemic arterial blood pressure mediated by a chemical signal
p1=0.00521
GO:0030099
myeloid cell differentiation
p2=0.0503
GO:0007229
integrin-mediated signaling pathway
p2=3.33e-5
GO:0016055
Wnt receptor signaling pathway
p1=0.0124
GO:
cartilage
p1=0.0161
GO:0055066
di-, tri-valent inorganic cation homeostasis
p1=2.48e-5
GO:0030218
erythrocyte differentiation
p2=0.018
GO:0001990
regulation of systemic arterial blood pressure by hormone
p1=0.00287
GO:0019722
calcium-mediated signaling
p1=0.0207 | p2=0.00775
GO:0030005
cellular di-, tri-valent inorganic cation homeostasis
p1=2.48e-5
GO:0055072
iron ion homeostasis
p1=0.0321
GO:0003081
regulation of systemic arterial blood pressure by renin-angiotensin
p1=0.00287
GO:0008543
fibroblast growth factor receptor signaling pathway
p1=0.019 | p2=0.00722
GO:0006879
cellular iron ion homeostasis
p1=0.0321
GO:0001991
regulation of systemic arterial blood pressure by circulatory renin-angiotensin
p1=0.0023


GO:0022610
biological adhesion
p2=0.0389
GO:0009987
cellular process
p2=0.0885
GO:0000003
reproduction
p1=0.0634
GO:0007155
cell adhesion
p2=0.0389
GO:0021700
developmental maturation
p2=0.0685
GO:0048869
cellular developmental process
p2=0.00517
GO:0022414
reproductive process
p1=0.0594
GO:0019953
sexual reproduction
p1=0.0204
GO:0031589
cell-substrate adhesion
p2=0.042
GO:0030154
cell differentiation
p2=0.00347
GO:0007276
gamete generation
p1=0.0102
nation
GO:0007160
cell-matrix adhesion
p2=0.042
GO:0042692
muscle cell differentiation
p1=0.0697 | p2=0.0274
GO:0048468
cell development
p2=0.071
GO:0007010
cytoskeleton organization
p1=0.0181
GO:0007015
actin filament organization
p2=0.0539
GO:0048232
male gamete generation
p1=0.00273
sis
GO:0007517
muscle development
p1=0.018 | p2=0.0619
GO:0055001
muscle cell development
p1=0.00287 | p2=0.000902
GO:0048469
cell maturation
p2=0.043
GO:0007283
spermatogenesis
p1=0.00273
GO:0006767
water-soluble vitamin metabolic process
p1=0.000506 | p2=3.93e-5
GO:0001568
blood vessel development
p1=0.0282 | p2=0.0394
GO:0014706
striated muscle development
p1=0.0779 | p2=0.0301
GO:0042364
water-soluble vitamin biosynthetic process
p1=5.14e-5 | p2=3.66e-6
0001502
condensation
| p2=0.00605
GO:0048514
blood vessel morphogenesis
p2=0.0271
GO:0051146
striated muscle cell differentiation
p1=0.00871 | p2=0.00329
GO:0001525
angiogenesis
p1=0.0746 | p2=0.018
GO:0055002
striated muscle cell development
p1=0.00287 | p2=0.000902
GO:0031032
actomyosin structure organization
p1=0.00871 | p2=0.00329
GO:0030239
myofibril assembly
p1=0.00287 | p2=0.000902


GO:0009636
response to toxin
p1=0.00997 | p2=0.00376
respon
GO:0006766
vitamin metabolic process
p1=0.0024 | p2=0.000232
GO:0051186
cofactor metabolic process
p1=0.00388 | p2=0.000251
GO:0055086
nucleobase, nucleoside and nucleotide metabolic process
p1=0.0535 | p2=0.00791
GO:0016052
carbohydrate catabolic process
p2=0.0679
GO:00
ion tra
p1=0.
GO:0009110
vitamin biosynthetic process
p1=7.53e-5 | p2=5.28e-6
GO:0006732
coenzyme metabolic process
p1=0.00233 | p2=0.00013
GO:0051188
cofactor biosynthetic process
p1=0.00286 | p2=0.000271
GO:0006753
nucleoside phosphate metabolic process
p1=0.0475 | p2=0.00722
GO:0046165
alcohol biosynthetic process
p1=0.0304
GO:0046164
alcohol catabolic process
p2=0.0454
GO:0044275
cellular carbohydrate catabolic process
p2=0.0608
GO:0006733
oxidoreduction coenzyme metabolic process
p1=0.000344 | p2=2.52e-5
GO:0009108
coenzyme biosynthetic process
p1=0.00147 | p2=0.00013
GO:0009117
nucleotide metabolic process
p1=0.0475 | p2=0.00722
GO:0046364
monosaccharide biosynthetic process
p1=0.0304
GO:0046365
monosaccharide catabolic process
p2=0.043
GO:0019362
pyridine nucleotide metabolic process
p1=0.000111 | p2=8.27e-6
GO:0009165
nucleotide biosynthetic process
p1=0.018 | p2=0.00232
GO:0006637
acyl-CoA metabolic process
p1=0.0233 | p2=0.00848
GO:0006090
pyruvate metabolic process
p1=0.0246
GO:0019319
hexose biosynthetic process
p1=0.0304
GO:0006006
glucose metabolic process
p2=0.0915
GO:0019320
hexose catabolic process
p2=0.043
GO:0019363
pyridine nucleotide biosynthetic process
p1=1.97e-5 | p2=1.07e-6
GO:0006094
gluconeogenesis
p1=0.019
GO:0006007
glucose catabolic process
p2=0.043
GO:0006096
glycolysis
p2=0.0385


GO:0006979
se to oxidative stress
p1=0.0169
GO:0007631
feeding behavior
p1=0.0594
06811
nsport
00055
GO:0042756
drinking behavior
p1=0.00368
GO:0006812
cation transport
p1=9.14e-5
GO:0015674
di-, tri-valent inorganic cation transport
p1=0.00203
GO:0030001
metal ion transport
p1=1.97e-5
GO:0015672
monovalent inorganic cation transport
p1=0.00521
GO:0006816
calcium ion transport
p1=0.000634
GO:0006813
potassium ion transport
p1=0.0239
GO:0006814
sodium ion transport
p1=0.043