

Down-regulated genes overlapped with De-Rubeis et al. (FDR<0.1)

Network Stats

number of nodes:

8

number of edges:

2

average node degree:

0.5

avg. local clustering coefficient:

0.5

expected number of edges:

0

PPI enrichment p-value:

0.0263

Functional enrichments in your network

Biological Process (GO)

pathway ID

pathway description

count in gene set

false discovery rate

GO:0008306

associative learning

3

0.0295

Down-regulated genes overlapped with De-Rubeis et al. (FDR<0.3)

Network Stats

number of nodes:

17

number of edges:

5

average node degree:

0.588

avg. local clustering coefficient:

0.412

expected number of edges:

1

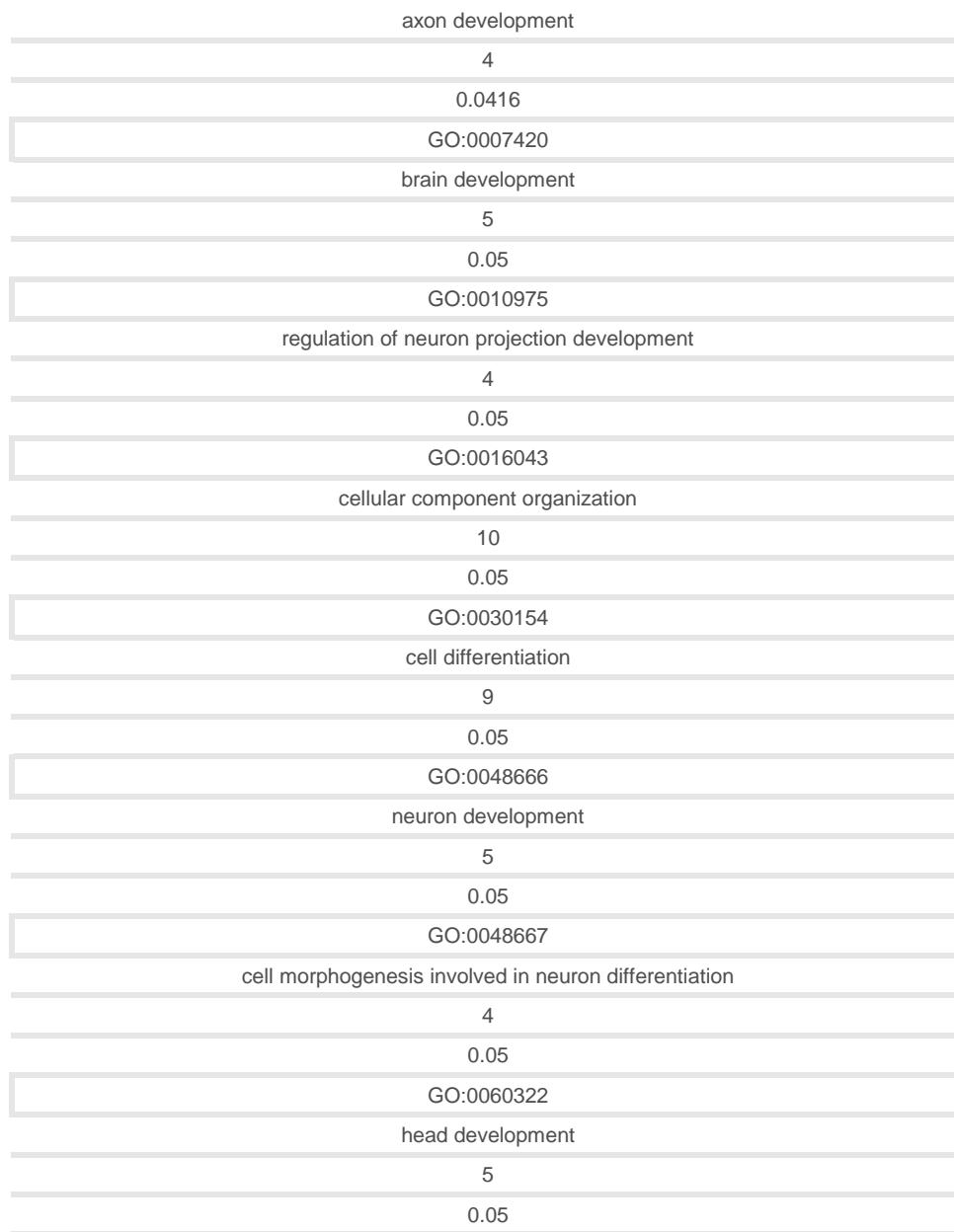
PPI enrichment p-value:

0.00647

Functional enrichments in your network

Biological Process (GO)

<i>pathway ID</i>
<i>pathway description</i>
<i>count in gene set</i>
<i>false discovery rate</i>
GO:0007399
nervous system development
9
0.0132
GO:0048731
system development
11
0.0206
GO:0007275
multicellular organismal development
11
0.0231
GO:0022603
regulation of anatomical structure morphogenesis
6
0.0231
GO:0022604
regulation of cell morphogenesis
5
0.0231
GO:0030182
neuron differentiation
6
0.0231
GO:0048699
generation of neurons
7
0.0231
GO:0031175
neuron projection development
5
0.0232
GO:0008306
associative learning
3
0.0318
GO:0007409
axonogenesis
4
0.0354
GO:0061564



Down-regulated genes overlapped with SFARI-GENE dataset

Network Stats

number of nodes:

125

number of edges:

176

average node degree:

2.82

avg. local clustering coefficient:

0.336

expected number of edges:

60

PPI enrichment p-value:

<1E-16

Functional enrichments in your network

Biological Process (GO)

pathway ID

pathway description

count in gene set

false discovery rate

GO:0007399

nervous system development

44

5.84E-15

GO:0007610

behavior

25

2.14E-13

GO:0044700

single organism signaling

56

6.24E-13

GO:0050794

regulation of cellular process

84

1.24E-12

GO:0007154

cell communication

56

1.99E-12

GO:0022008

neurogenesis

34

2.99E-12

GO:0044708

single-organism behavior

21

4.09E-12

GO:0065007

biological regulation

87

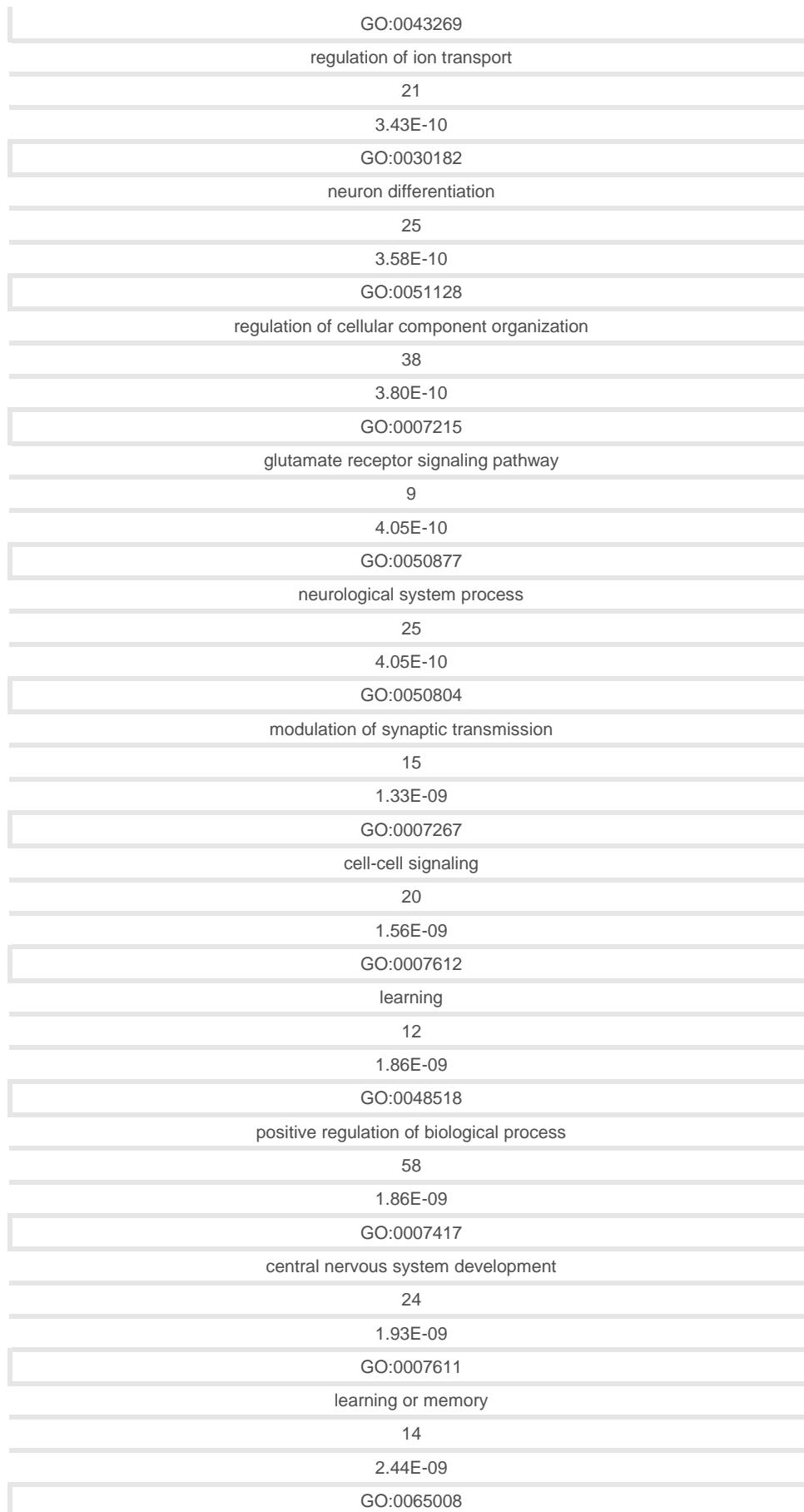
4.74E-12

GO:0007268

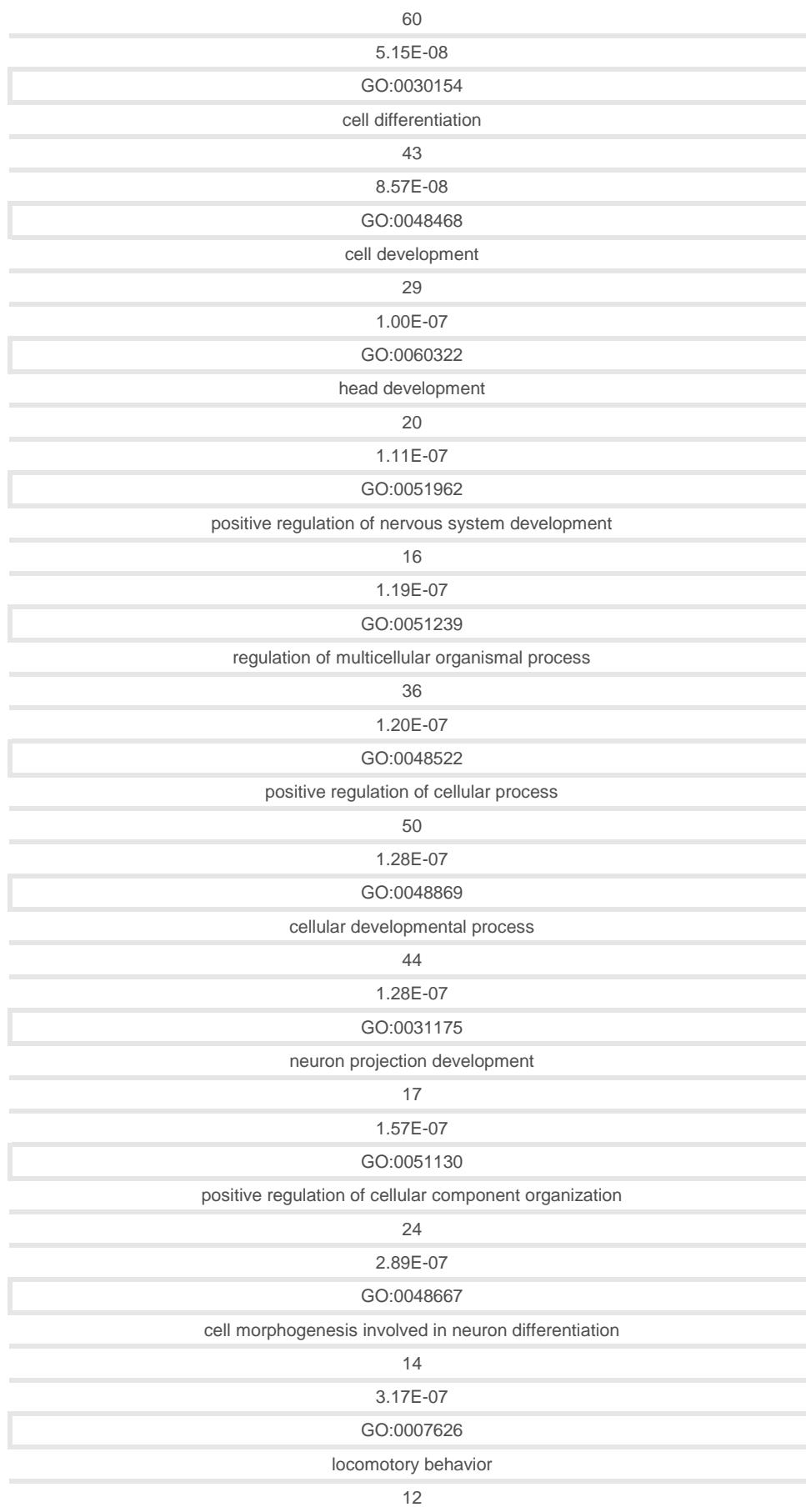
synaptic transmission

19

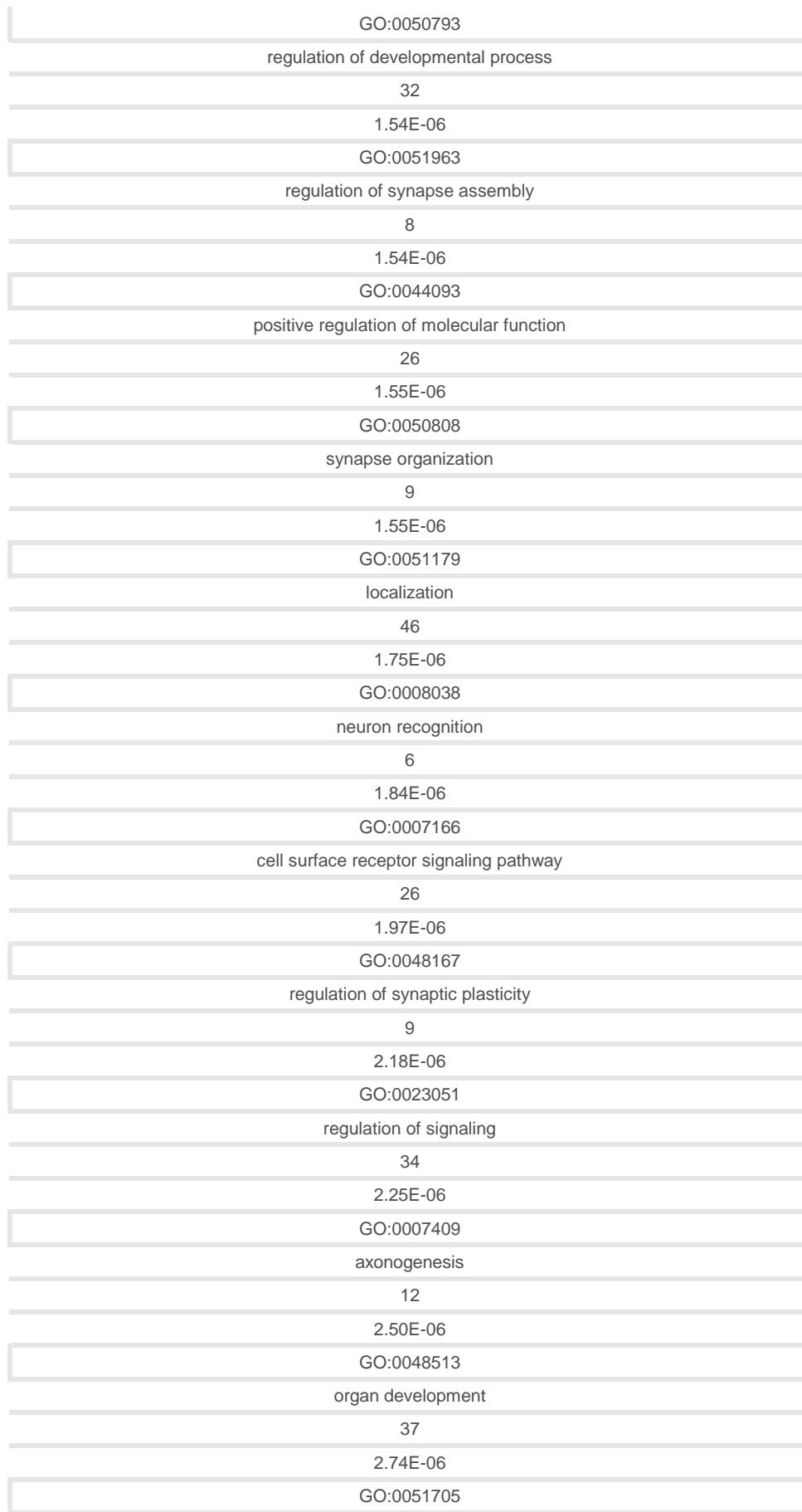














cell morphogenesis	1.30E-05
establishment of localization	1.51E-05
transport	1.67E-05
ionotropic glutamate receptor signaling pathway	1.89E-05
regulation of cell communication	1.95E-05
regulation of neuron projection development	2.21E-05
single-organism transport	2.21E-05
regulation of neuron differentiation	2.21E-05
axon guidance	2.55E-05
positive regulation of developmental process	2.56E-05
associative learning	2.77E-05

GO:0000902

cell morphogenesis

1.51E-05

GO:0051234

establishment of localization

1.67E-05

GO:0006810

transport

1.89E-05

GO:0035235

ionotropic glutamate receptor signaling pathway

1.95E-05

GO:0010646

regulation of cell communication

2.21E-05

GO:0010975

regulation of neuron projection development

2.21E-05

GO:0044765

single-organism transport

2.21E-05

GO:0045664

regulation of neuron differentiation

2.55E-05

GO:0007411

axon guidance

2.56E-05

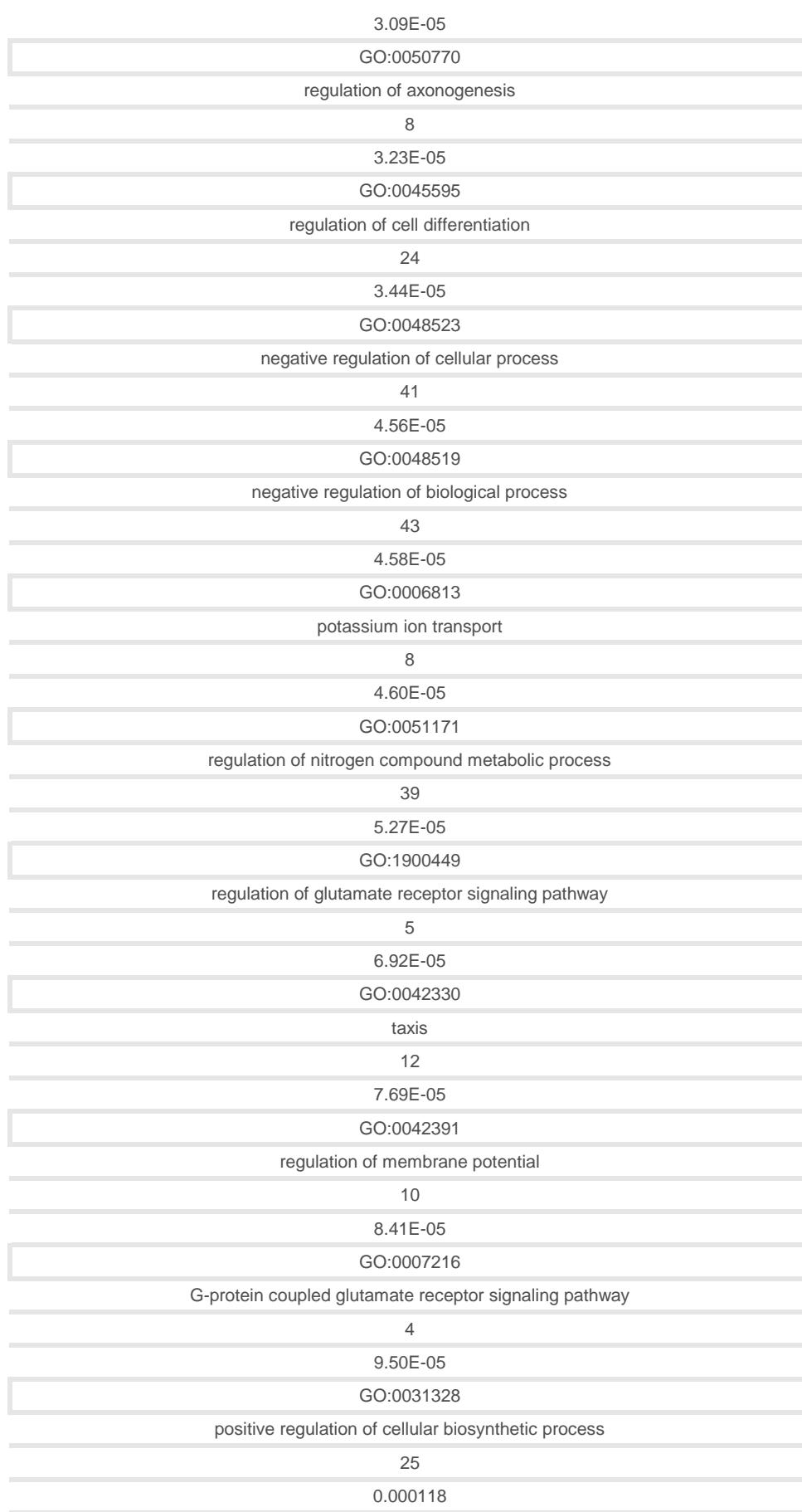
GO:0051094

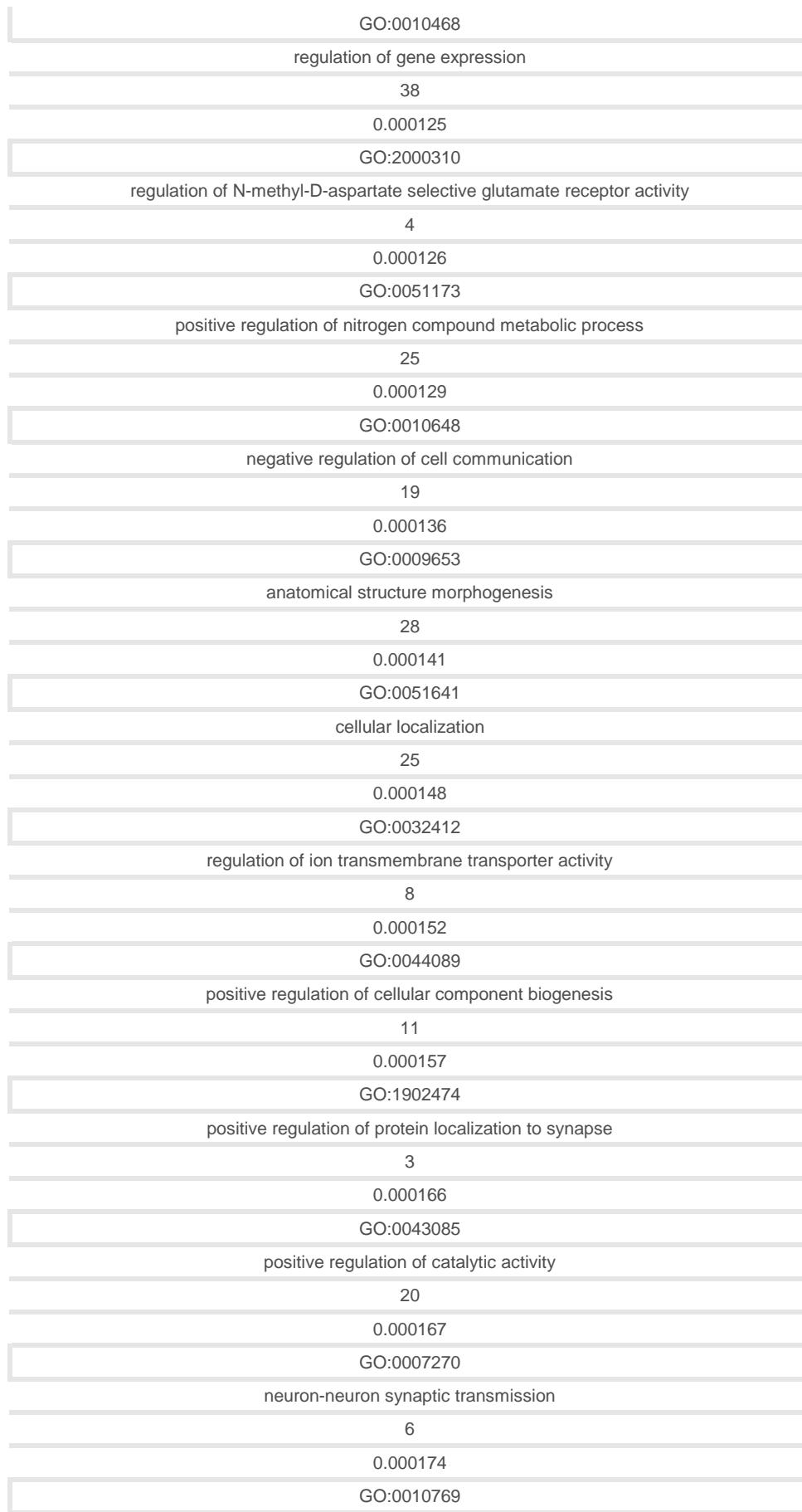
positive regulation of developmental process

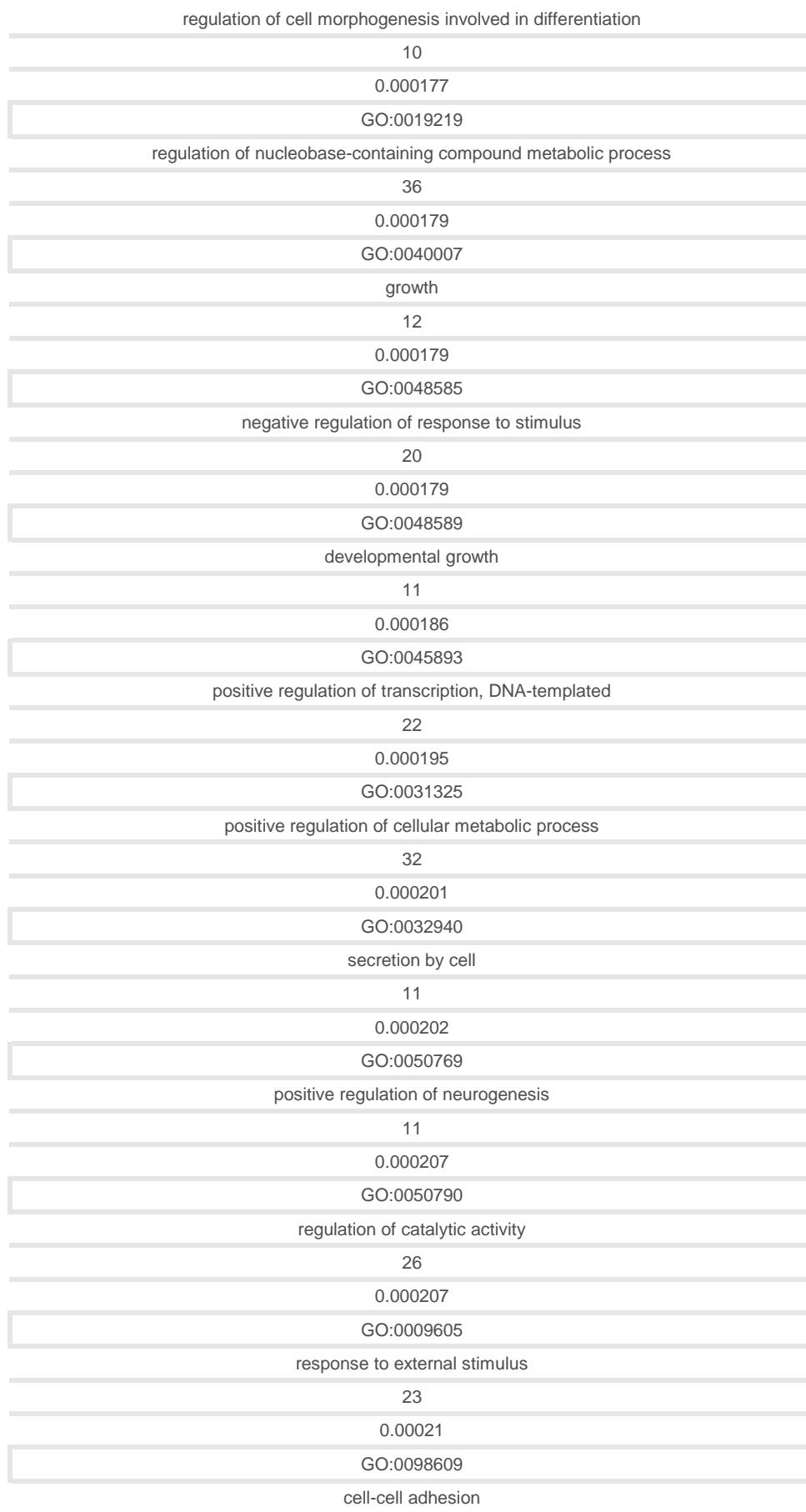
2.77E-05

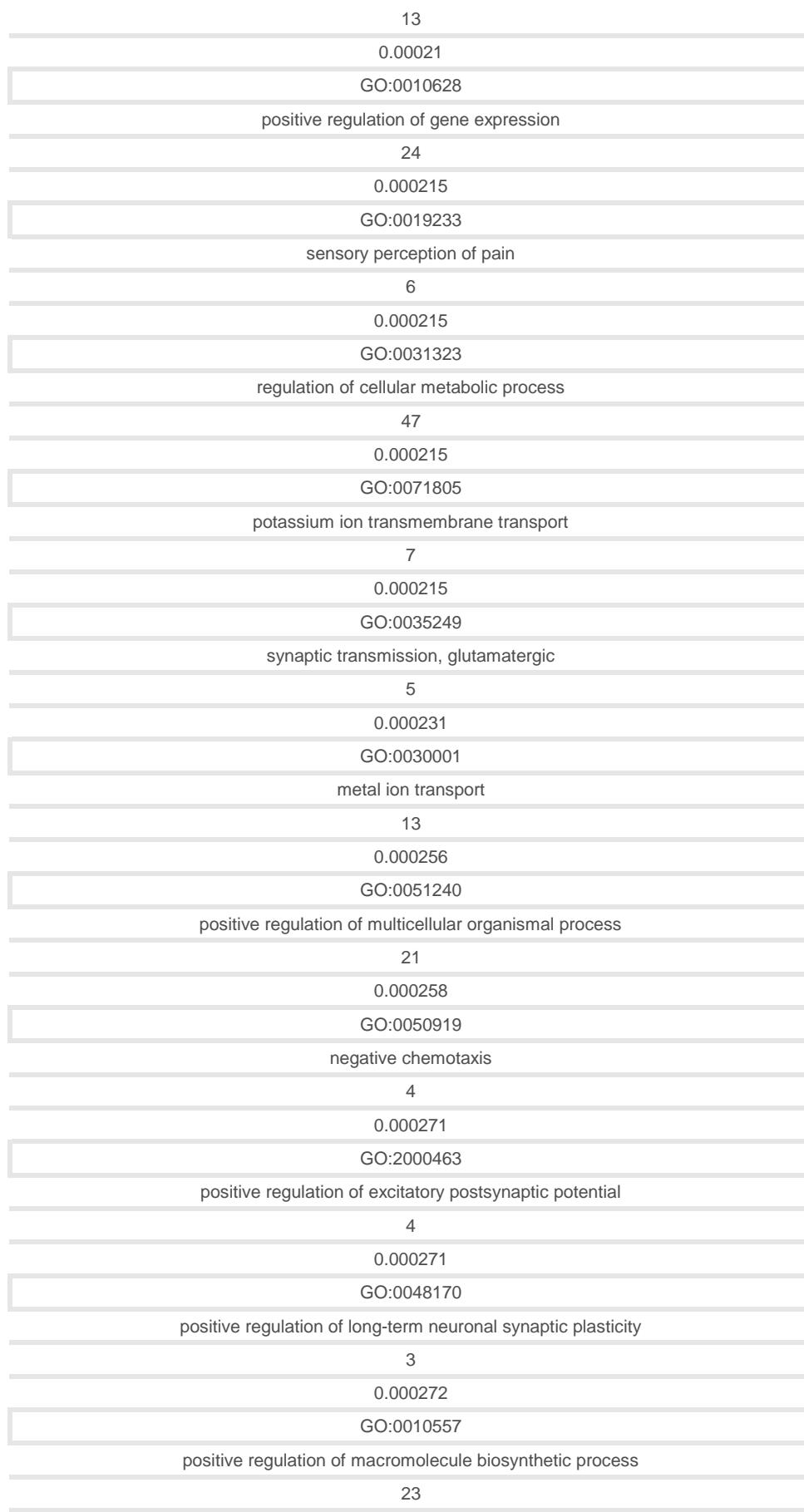
GO:0008306

associative learning

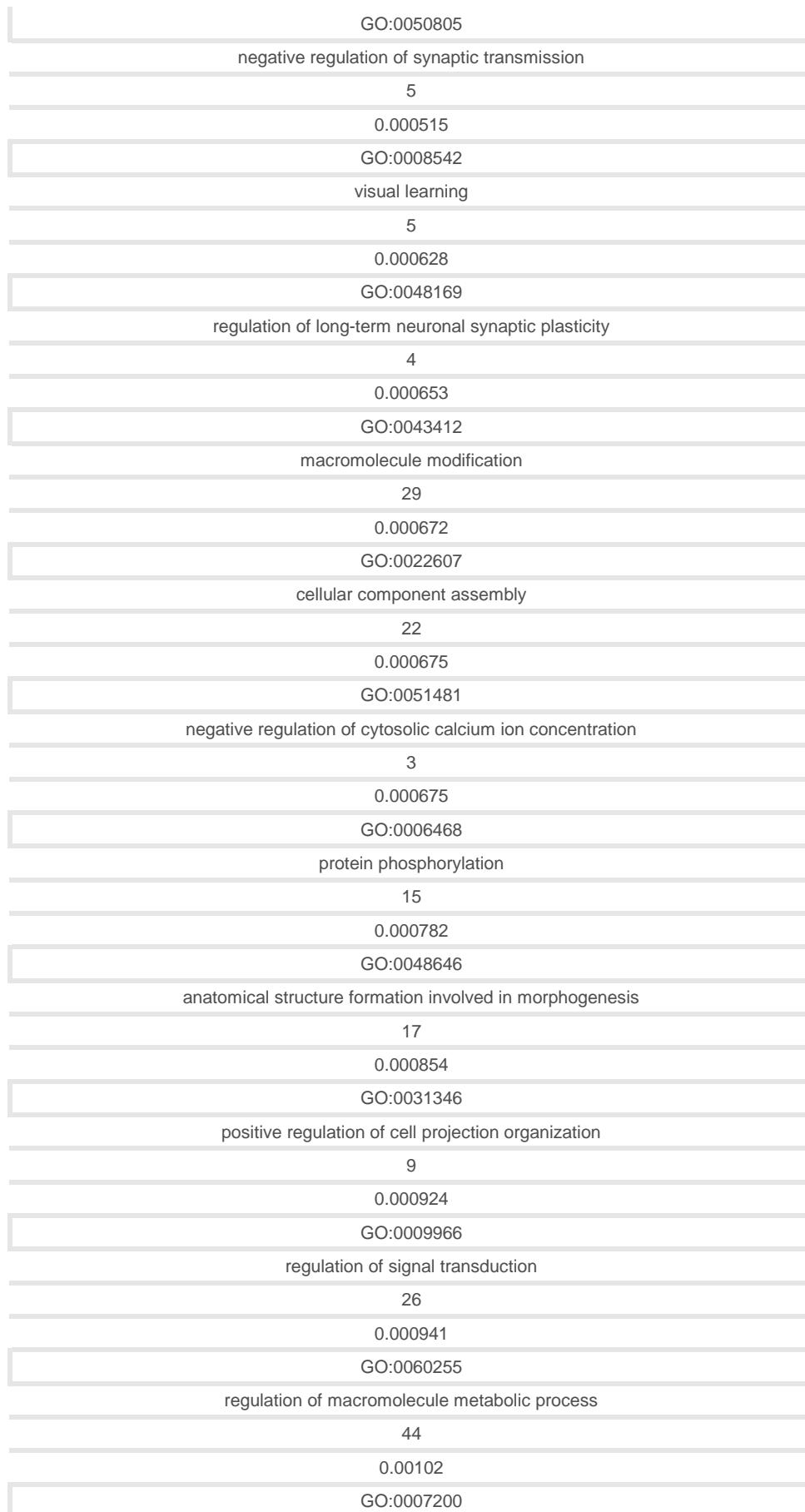


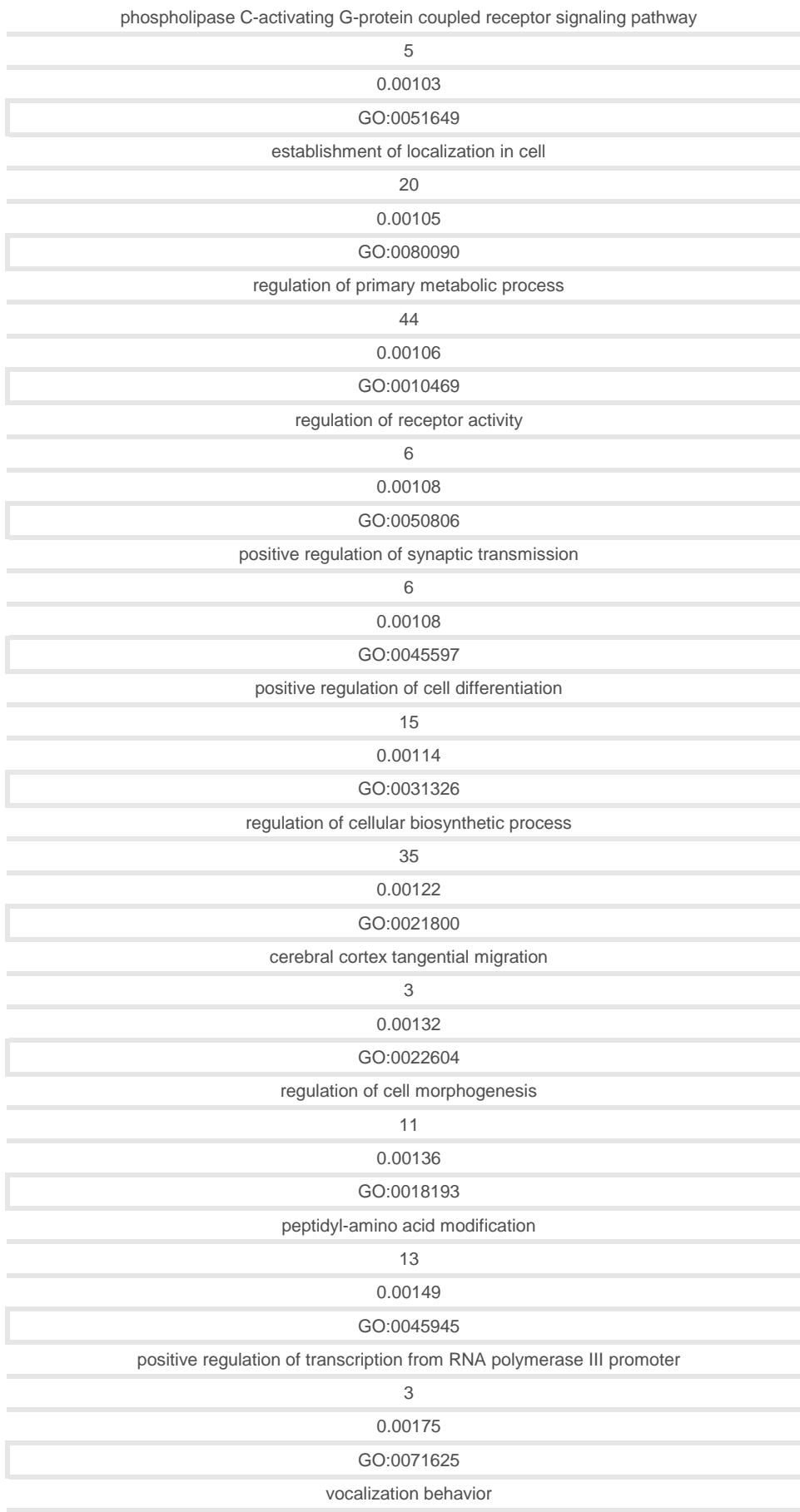


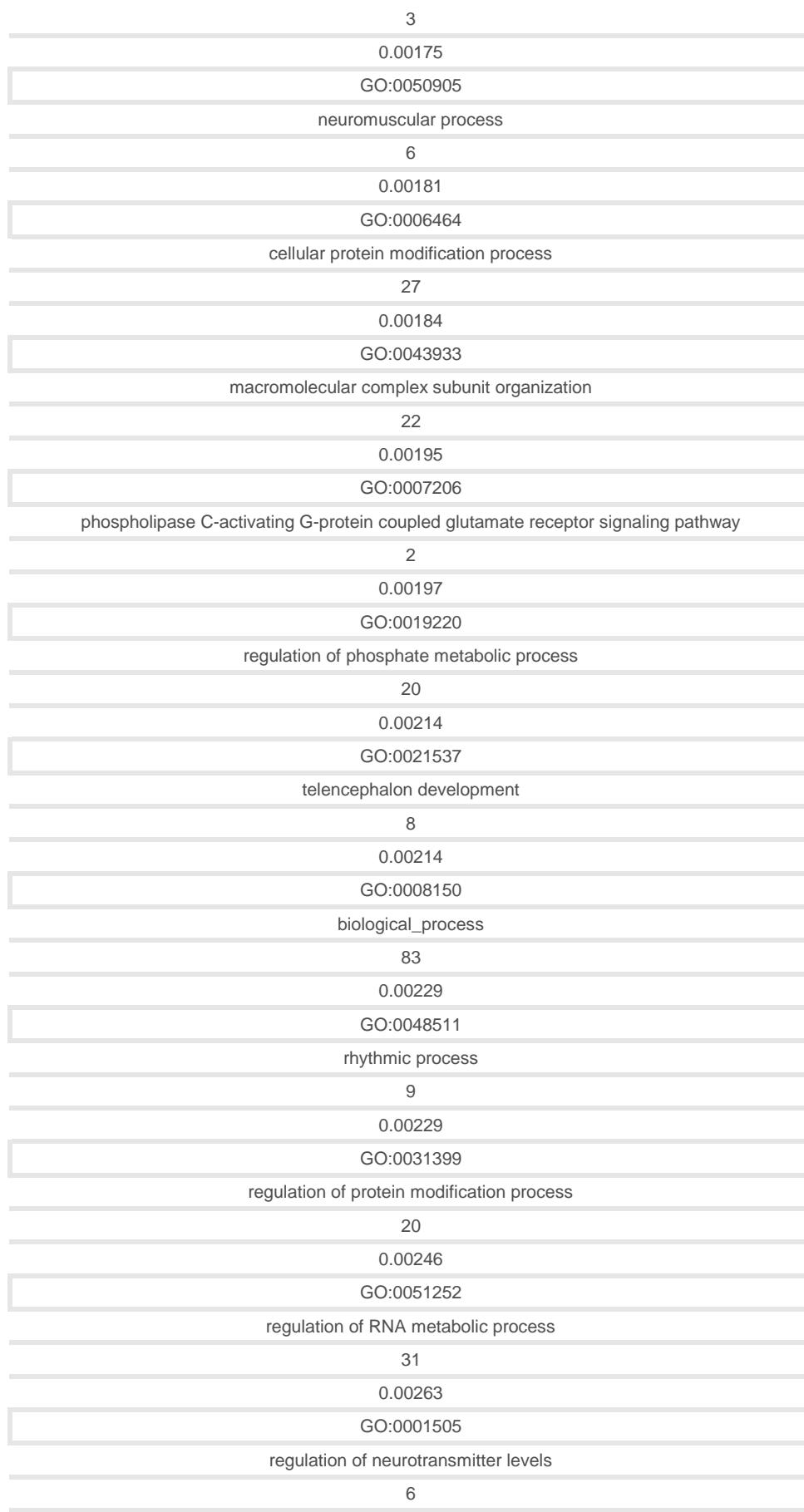


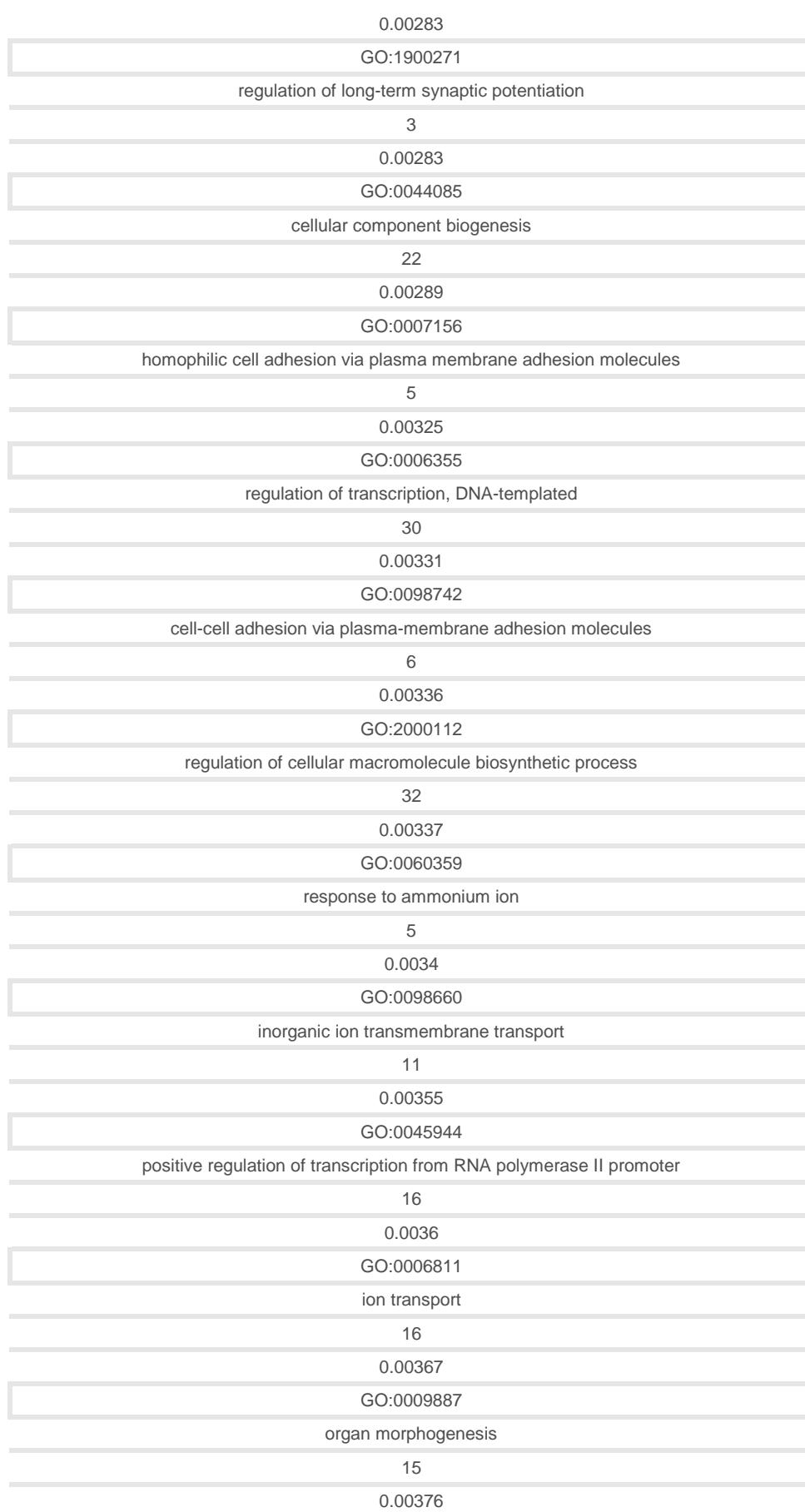


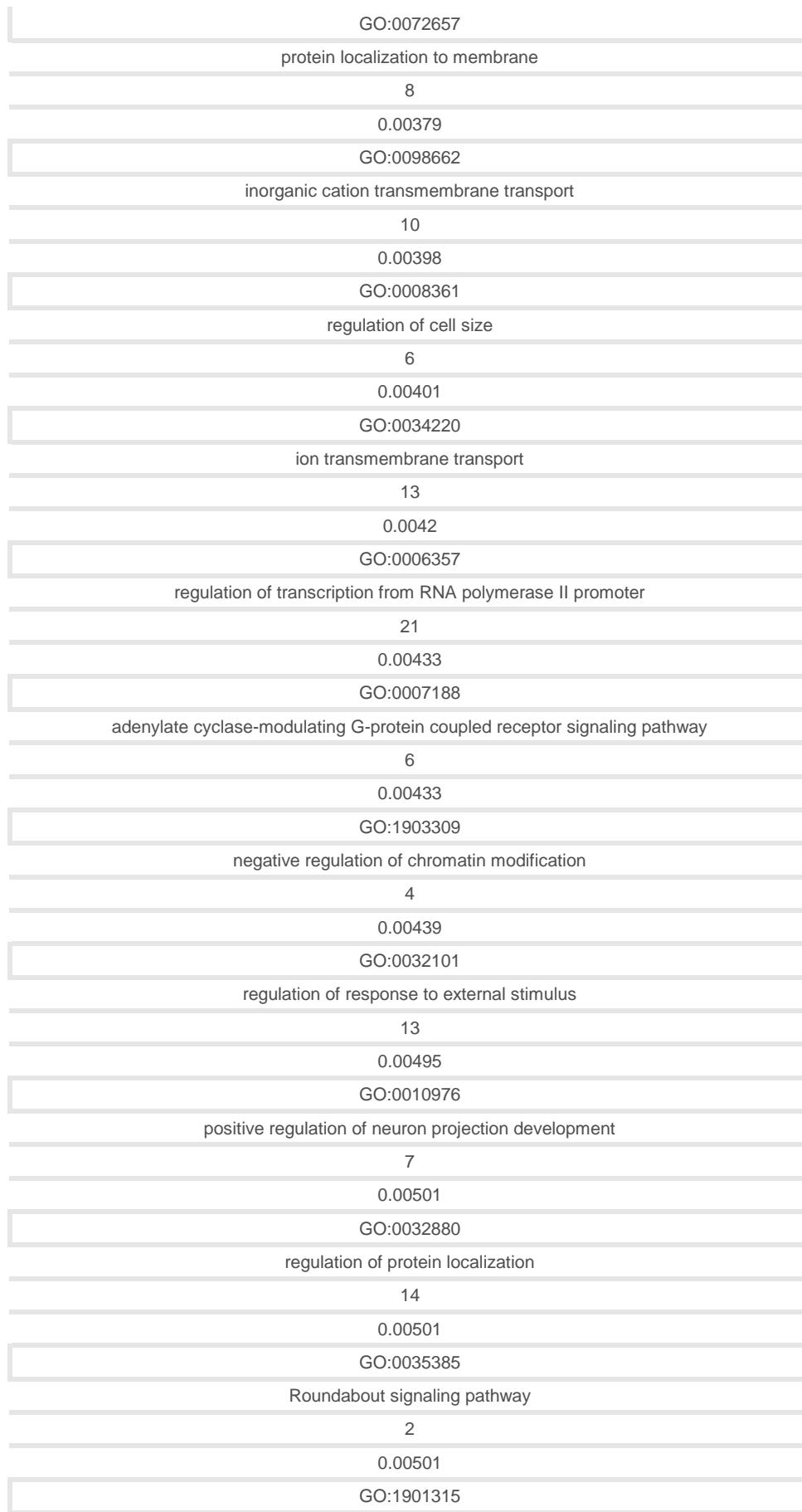


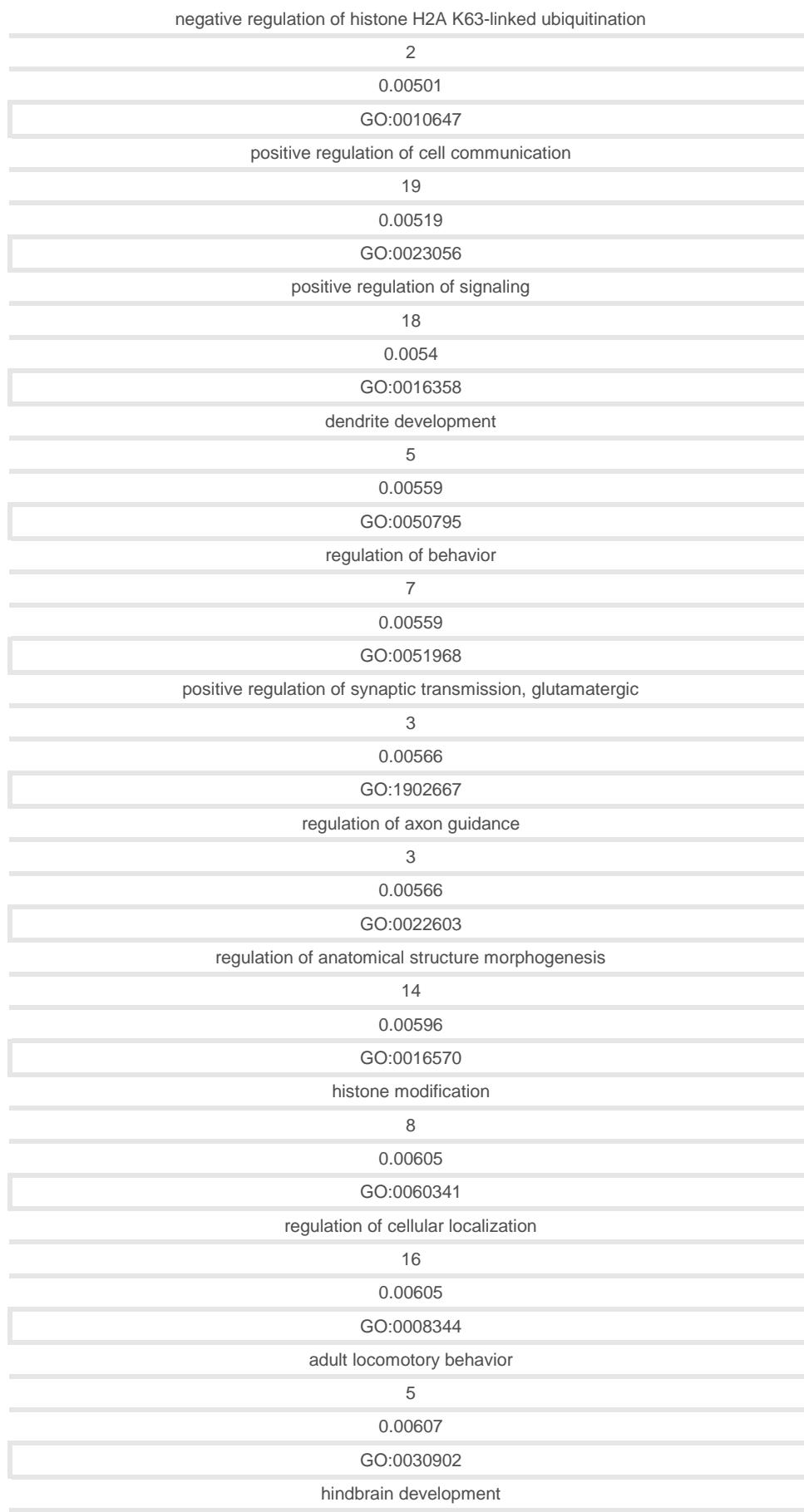




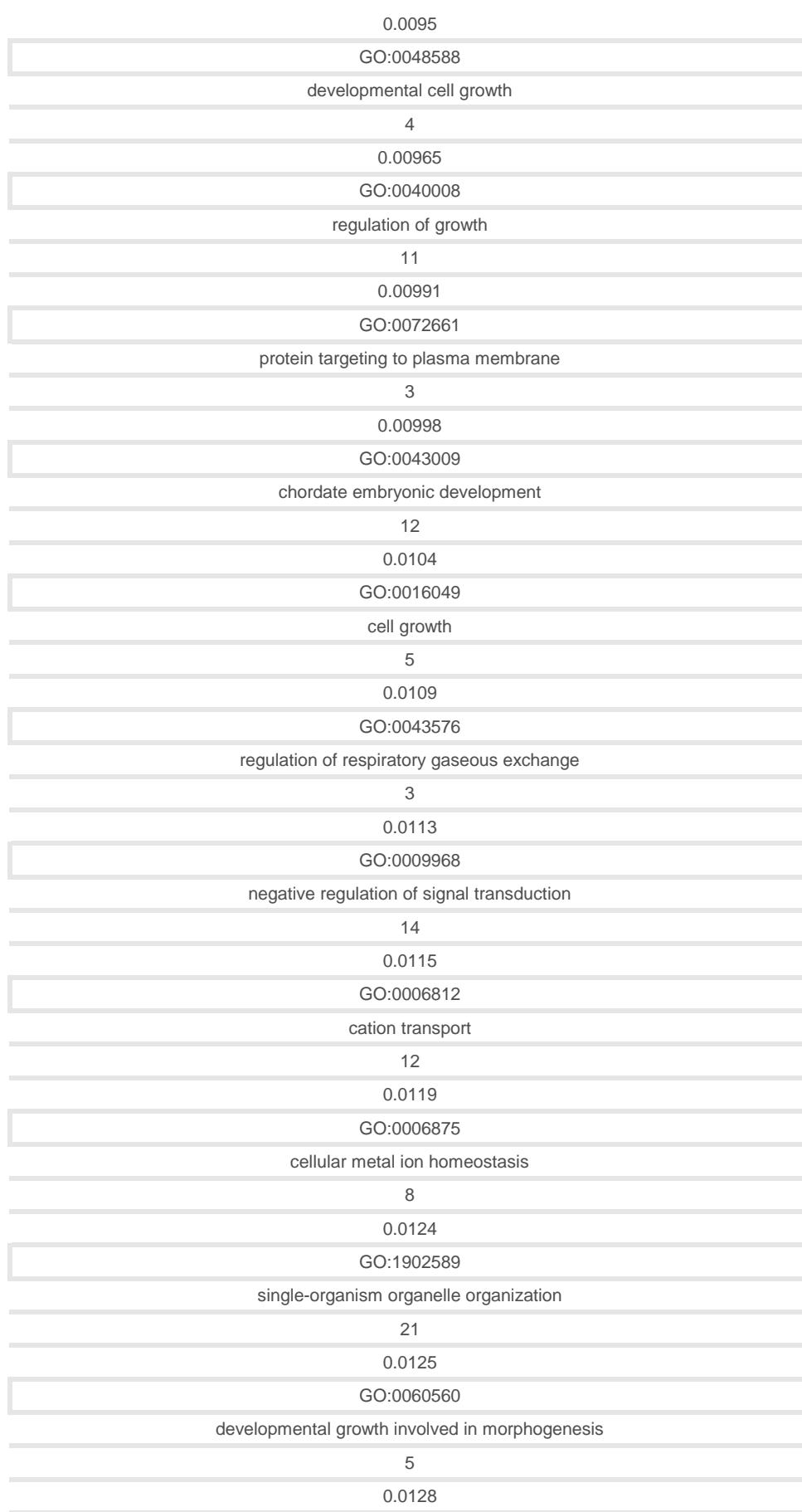


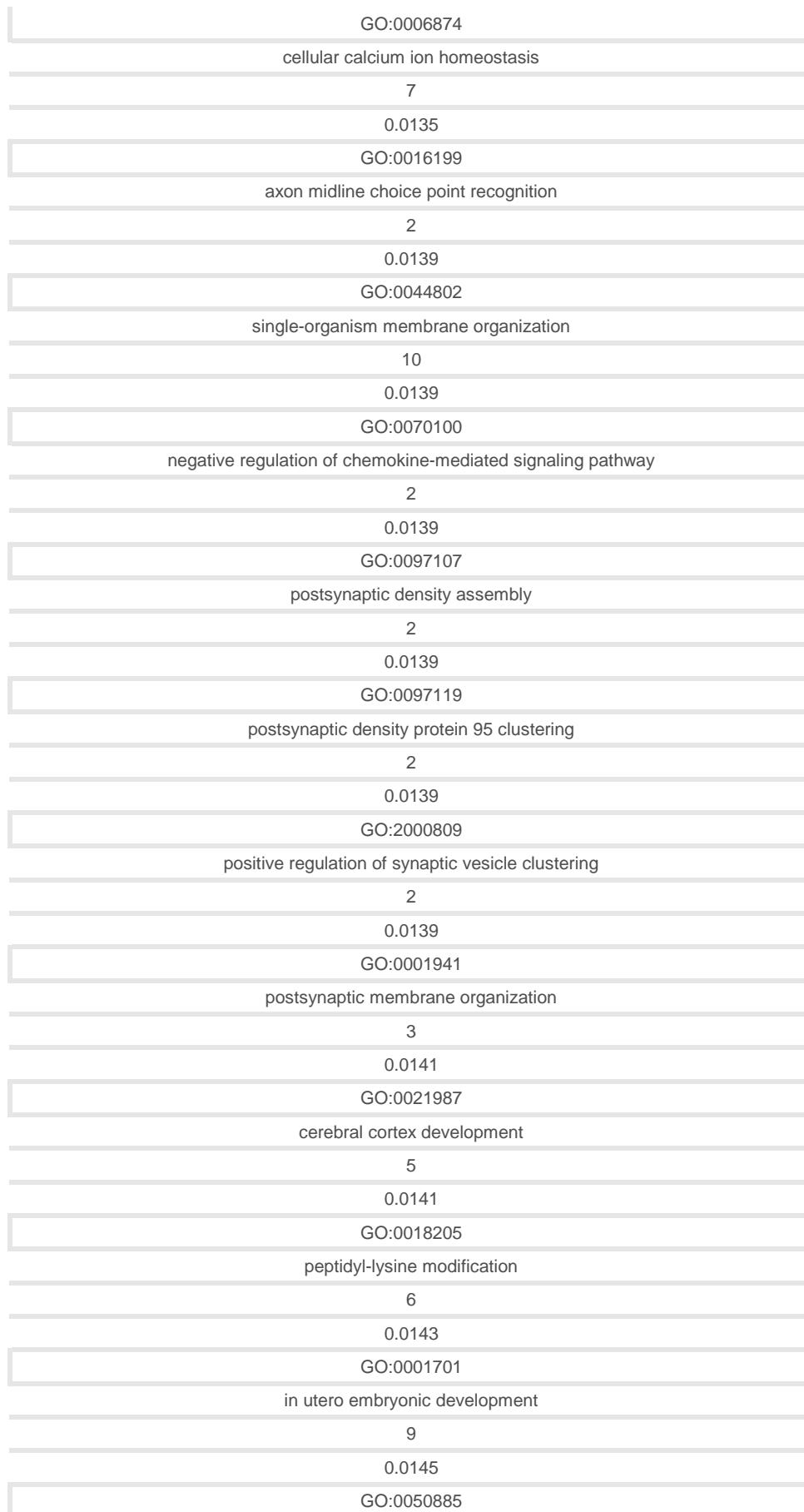




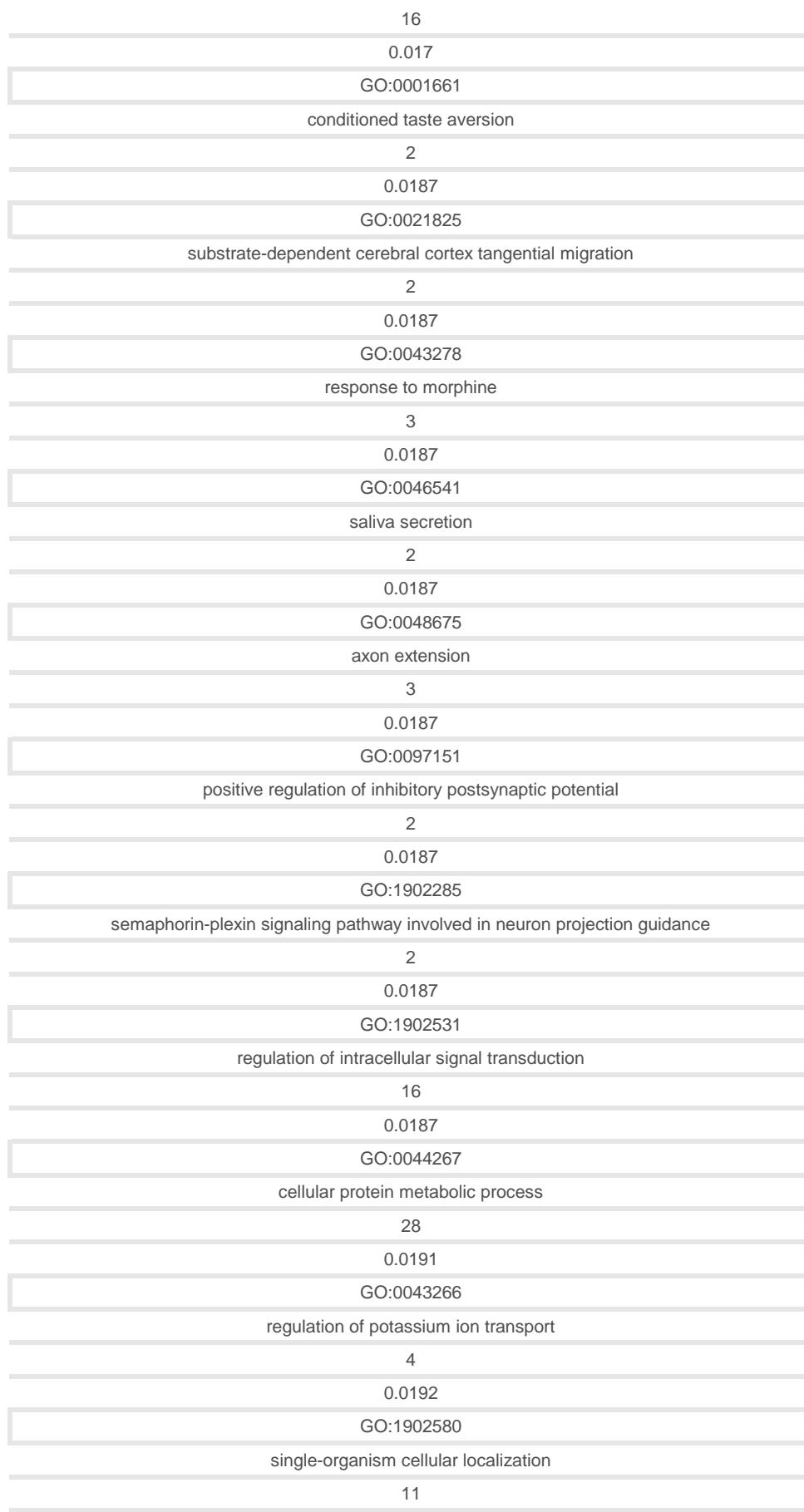


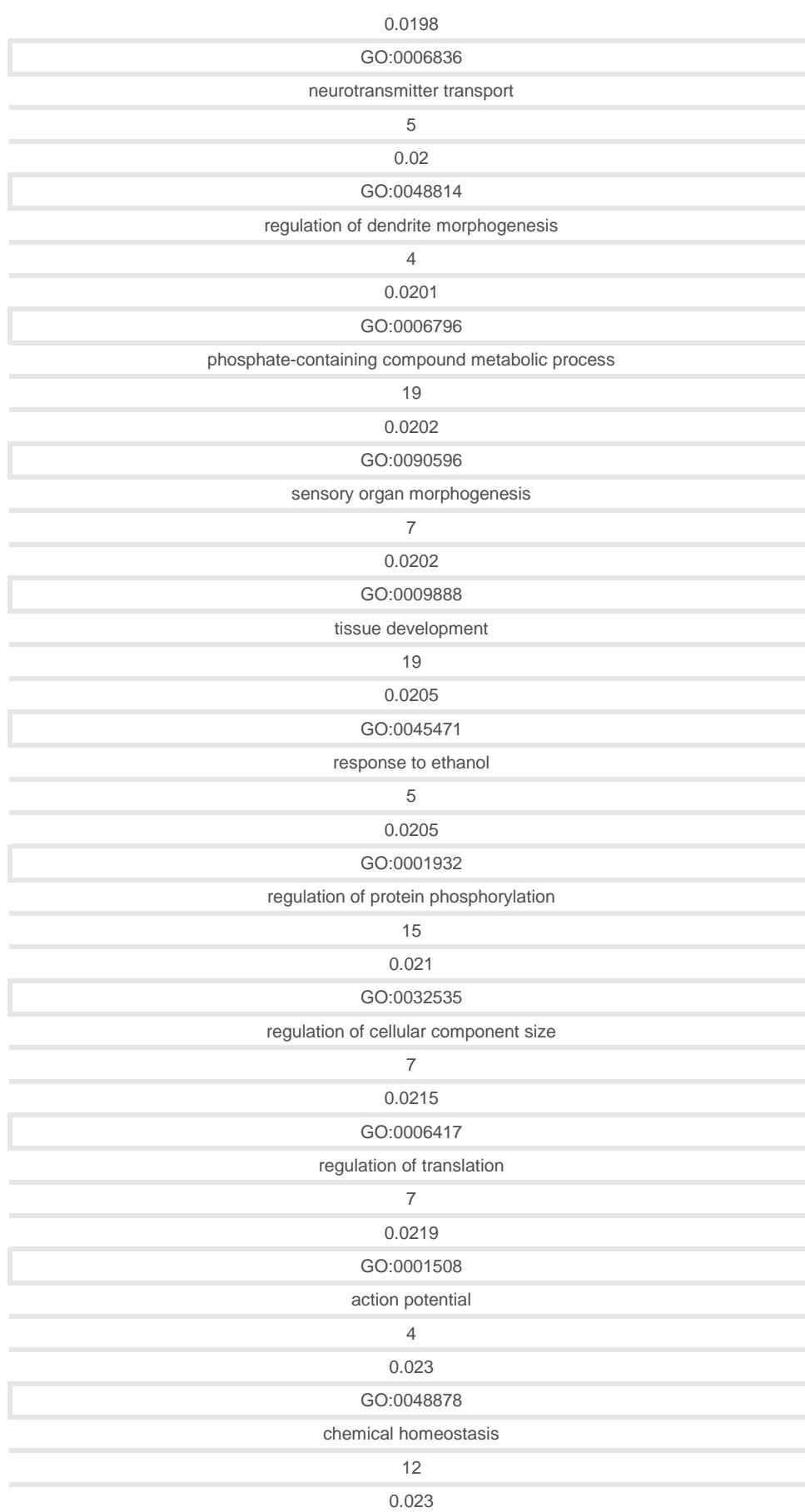


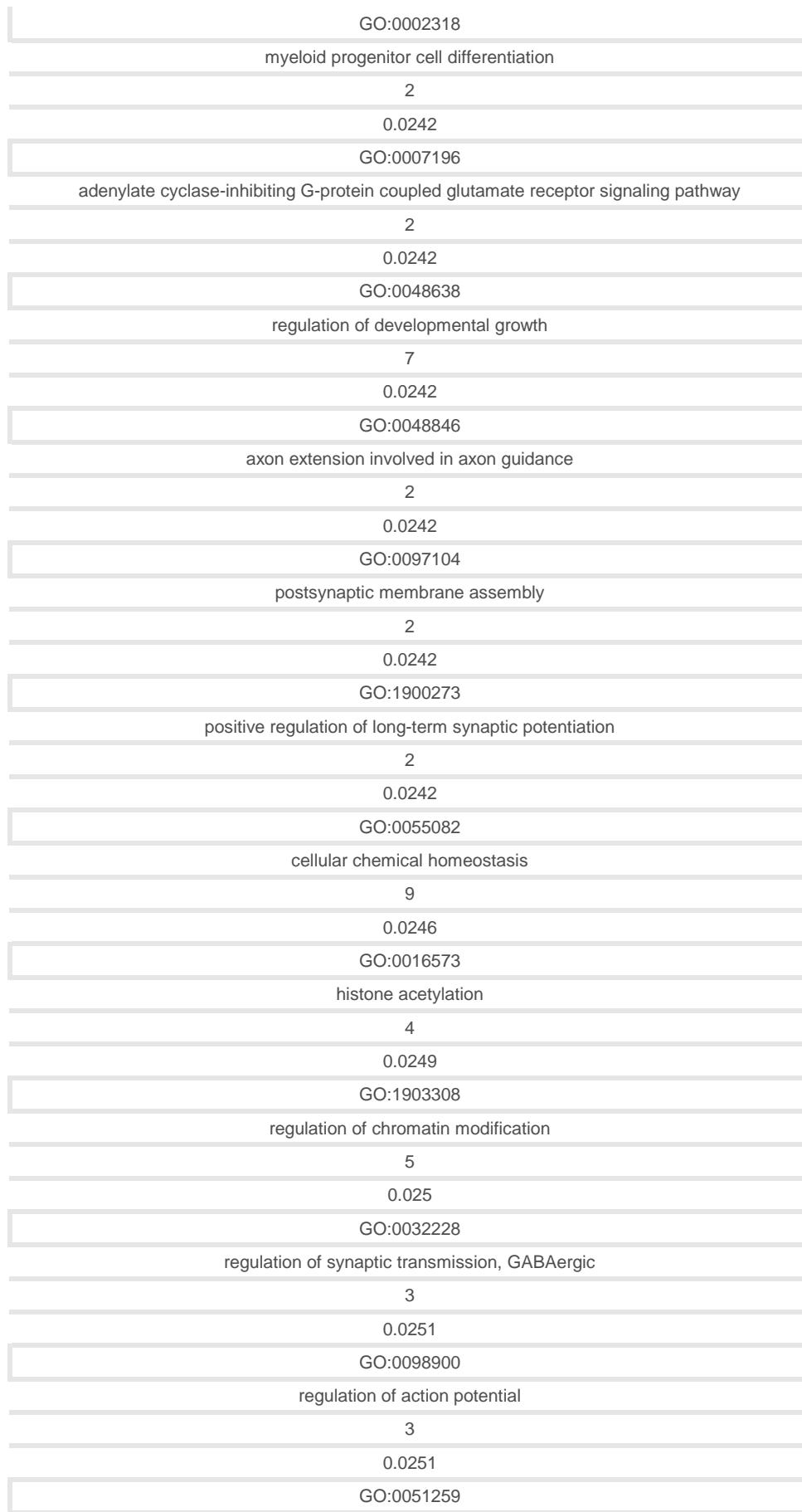


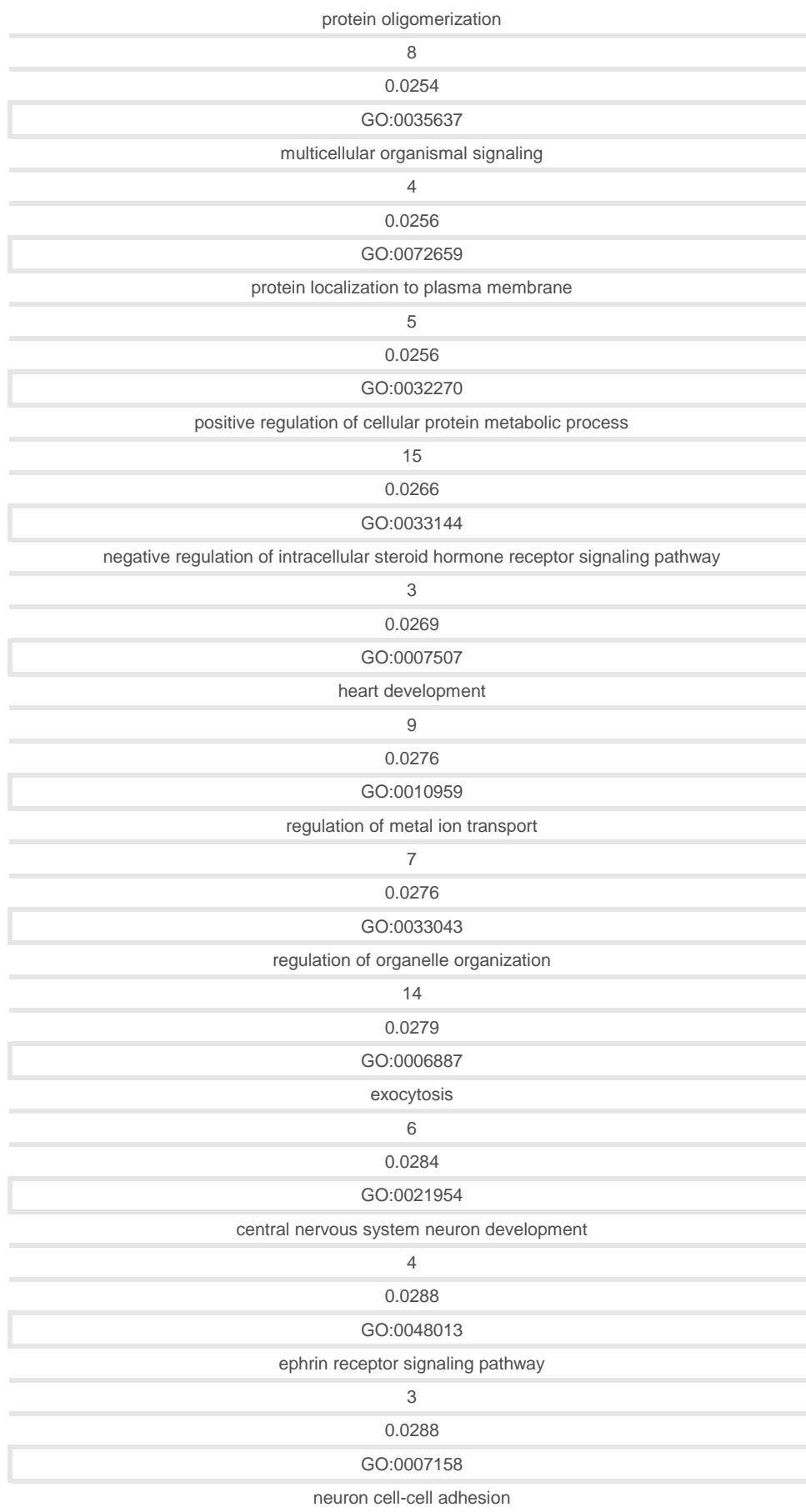


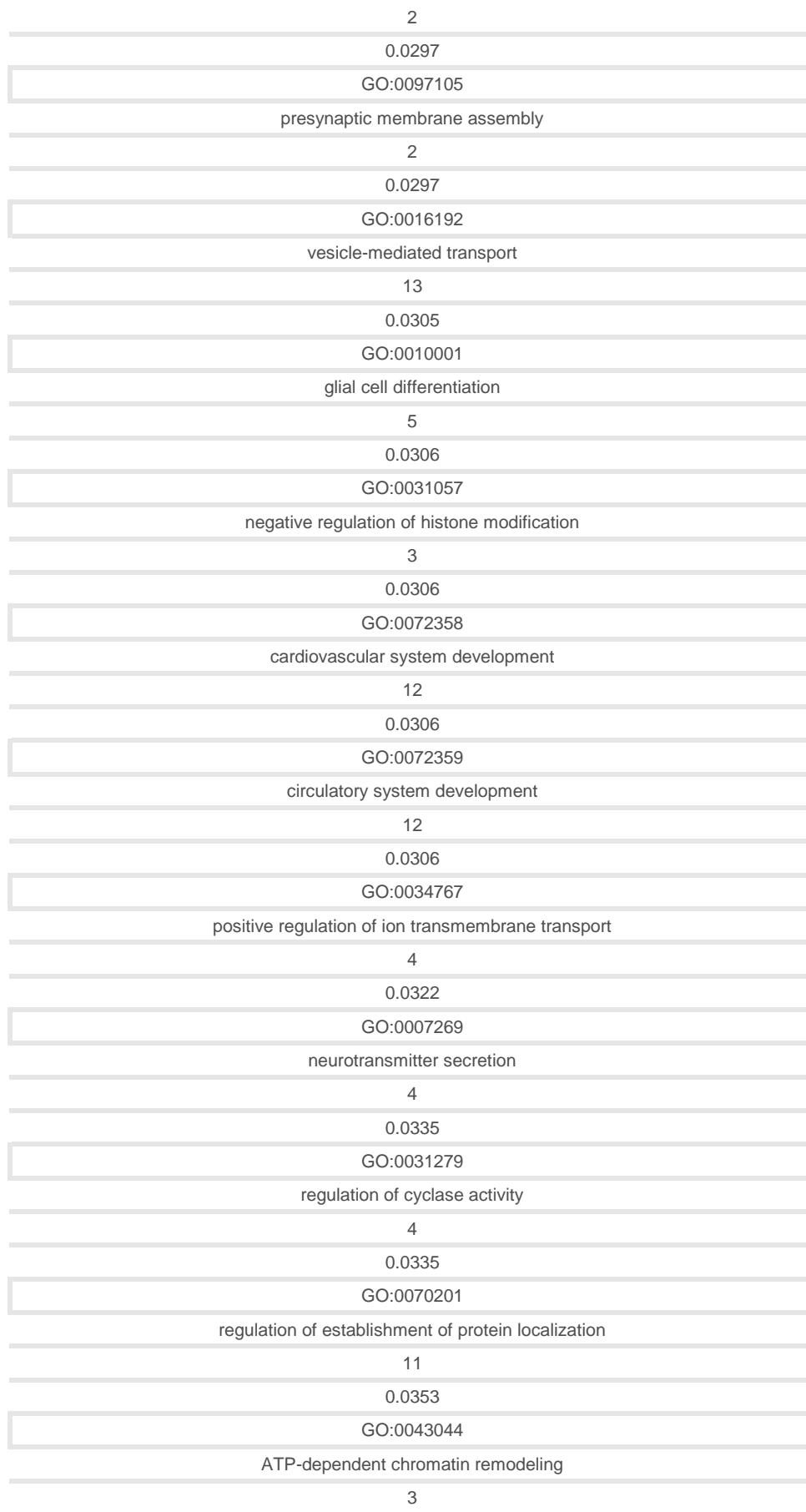


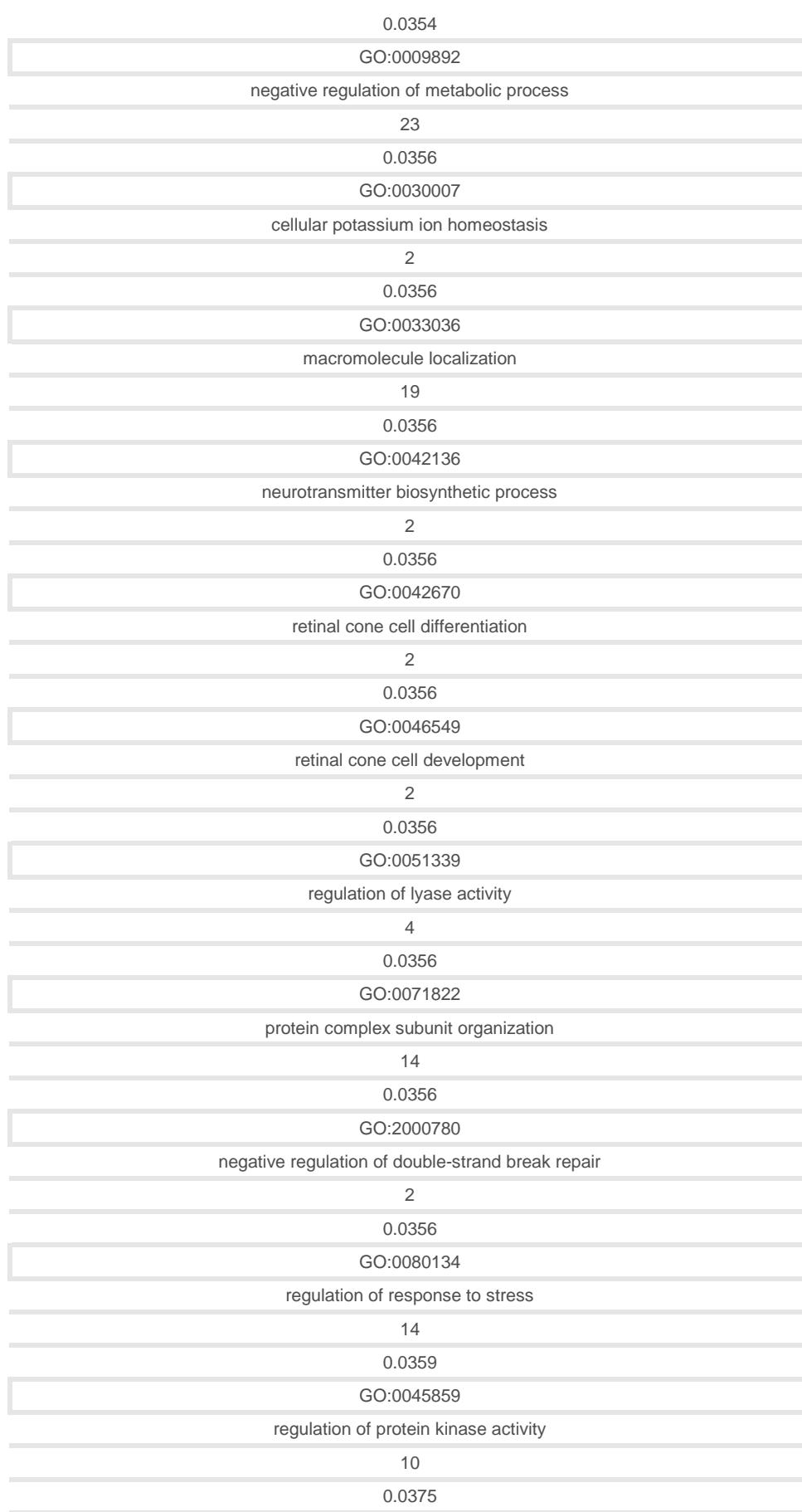


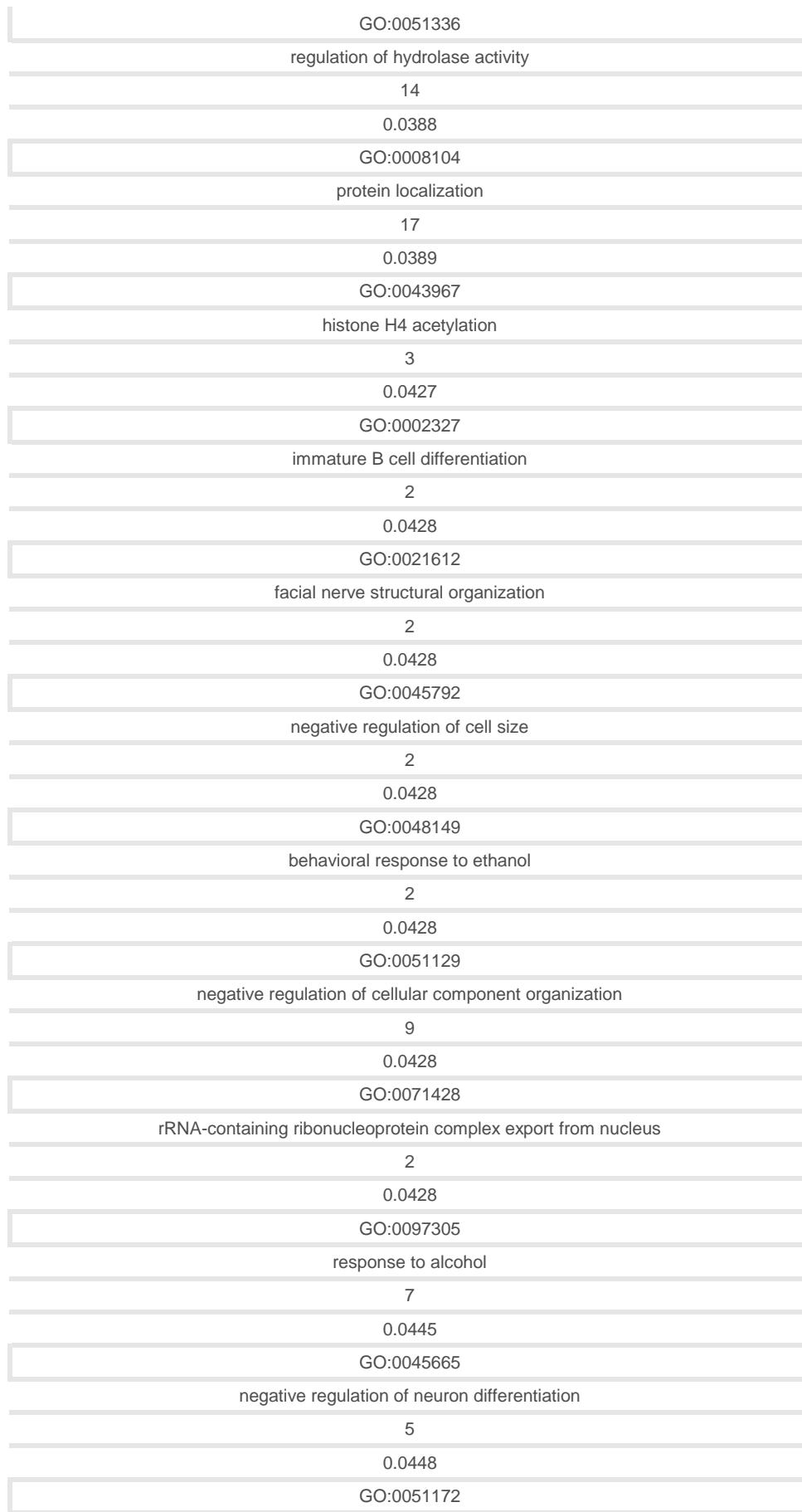




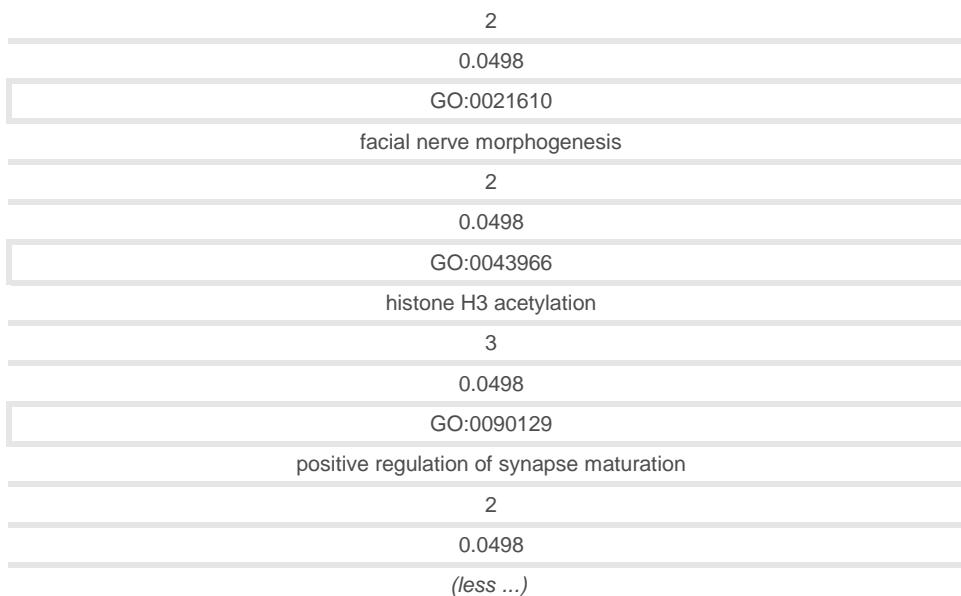




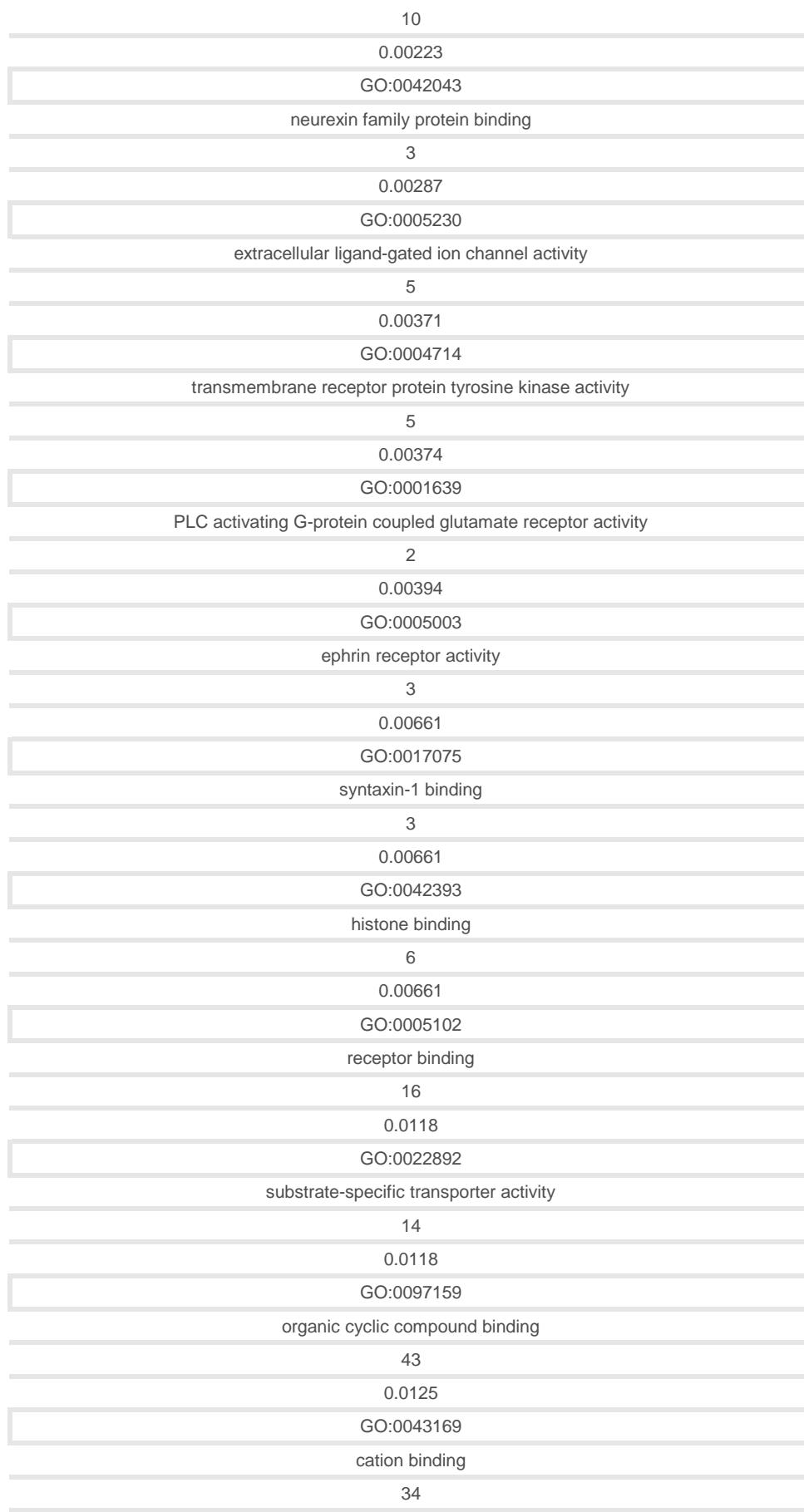


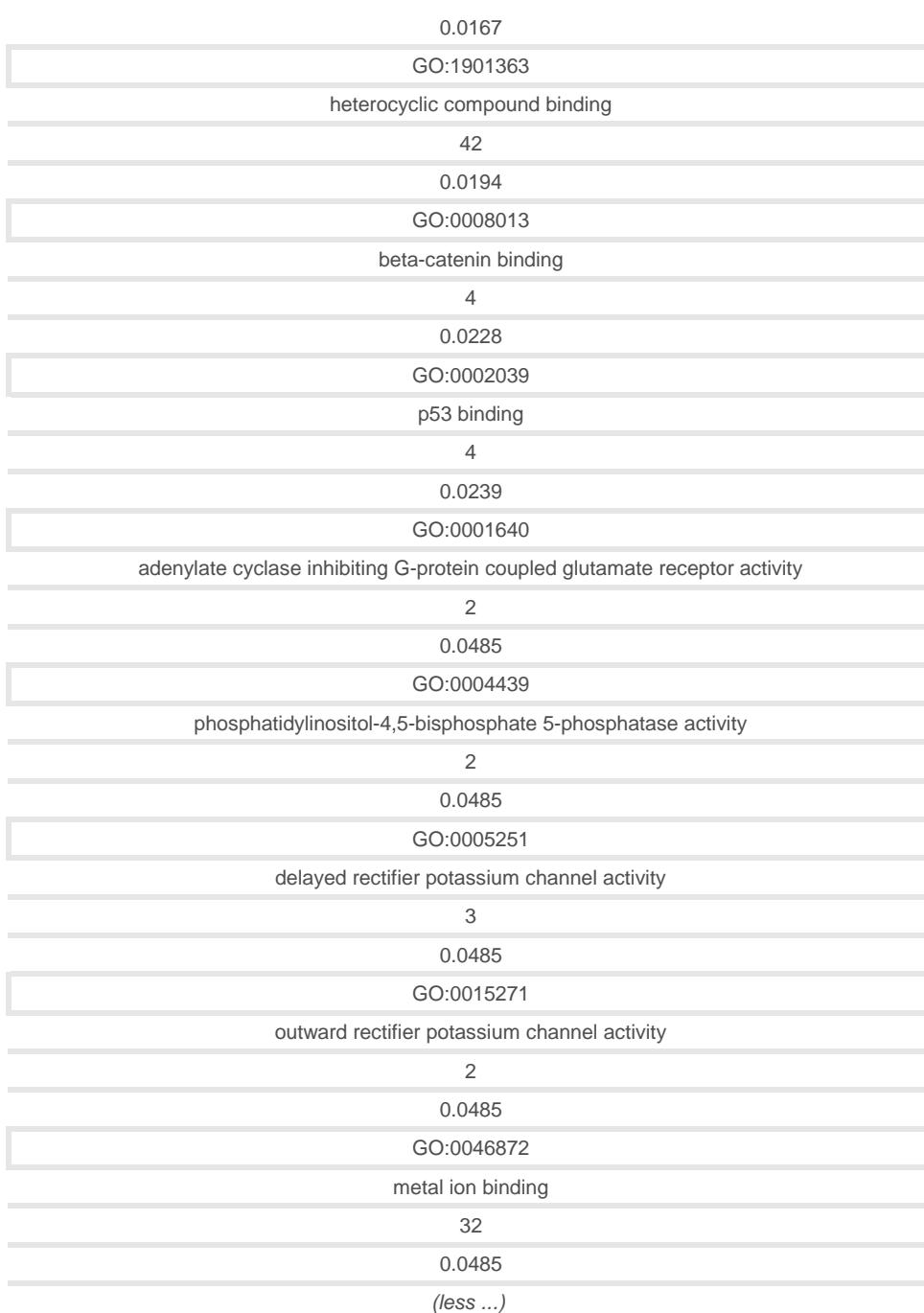












Cellular Component (GO)

pathway ID

pathway description

count in gene set

false discovery rate

GO:0097458

neuron part

43

1.01E-23

GO:0043005

neuron projection

35

1.69E-19

GO:0042995

cell projection

44

4.86E-18

GO:0030425

dendrite

25

3.64E-17

GO:0044456

synapse part

25

5.33E-15

GO:0045202

synapse

27

8.00E-15

GO:0071944

cell periphery

60

9.69E-15

GO:0098794

postsynapse

21

1.86E-14

GO:0097060

synaptic membrane

18

1.57E-13

GO:0044463

cell projection part

28

2.59E-13

GO:0005886

plasma membrane

56

1.13E-12

GO:0045211

postsynaptic membrane

16

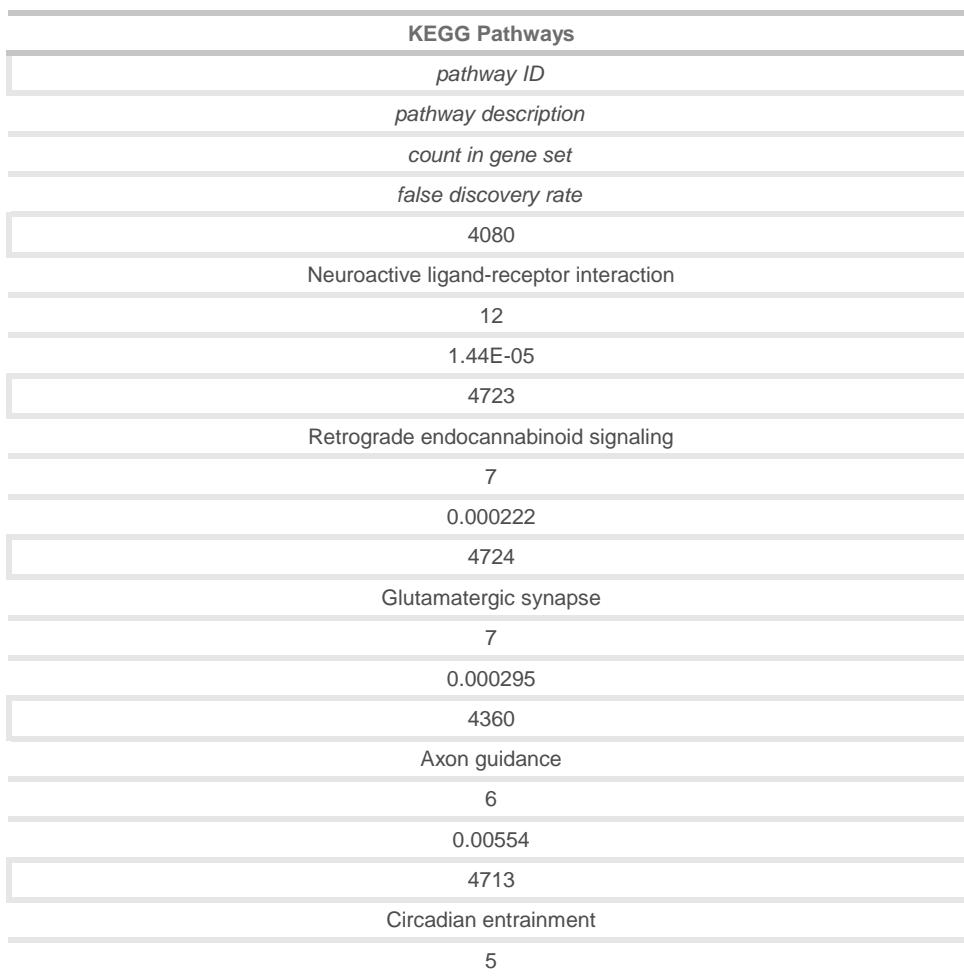
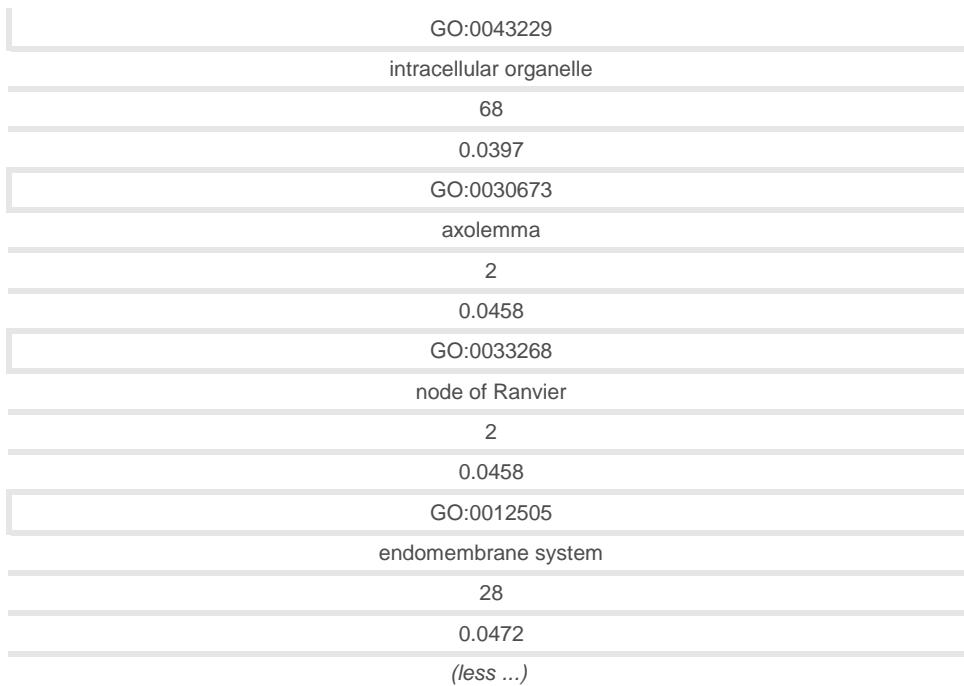


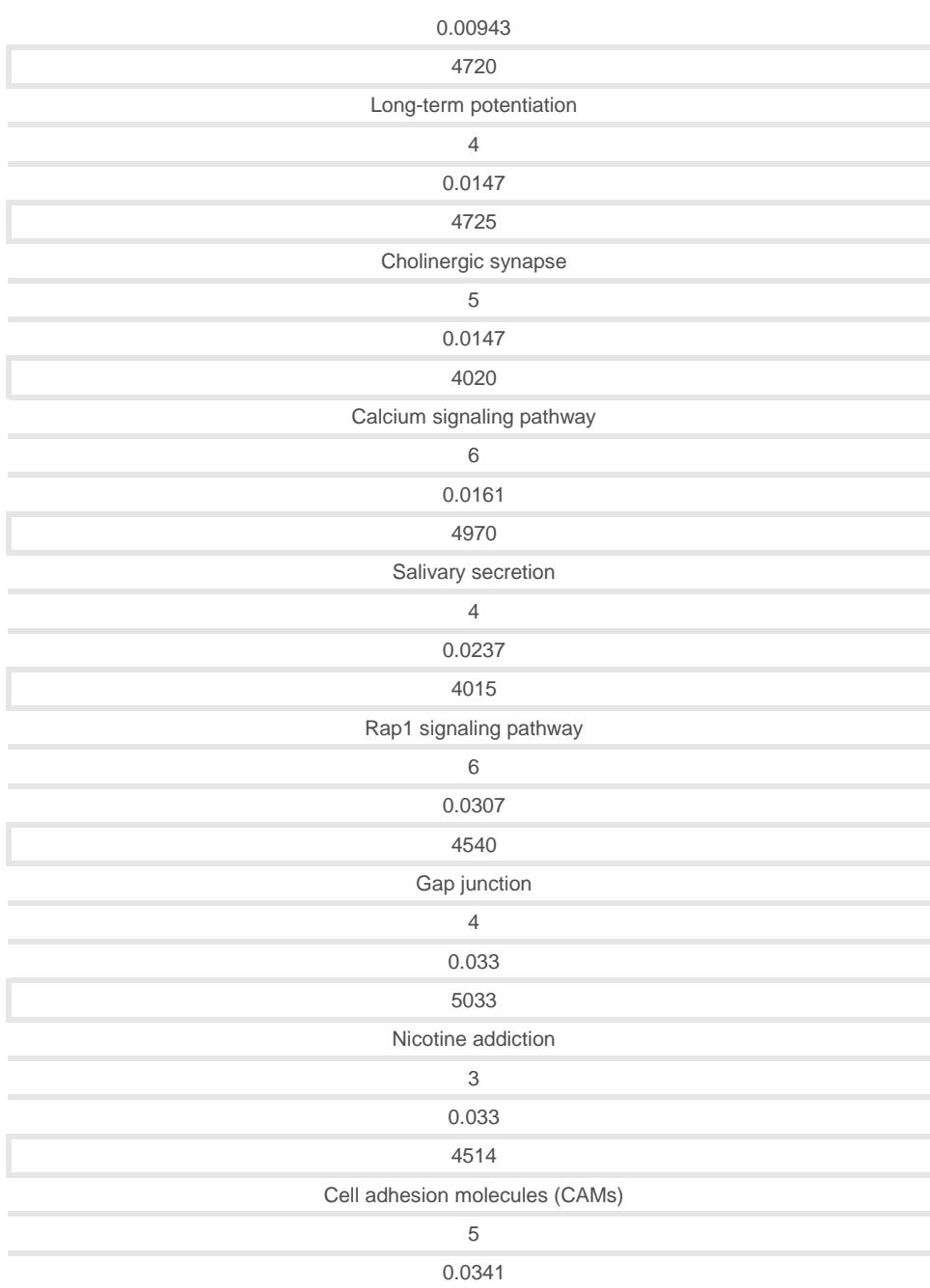












Up-regulated genes overlapped with SFARI-GENE dataset

Network Stats

number of nodes:

44

number of edges:

14

average node degree:

0.636

avg. local clustering coefficient:

0.348

expected number of edges:

6

PPI enrichment p-value:

0.00559

Functional enrichments in your network

Biological Process (GO)

pathway ID

pathway description

count in gene set

false discovery rate

GO:0060997

dendritic spine morphogenesis

3

0.00162

GO:0098815

modulation of excitatory postsynaptic potential

4

0.00162

GO:0071625

vocalization behavior

3

0.00505

GO:0044710

single-organism metabolic process

19

0.00579

GO:0003008

system process

11

0.0088

GO:0019725

cellular homeostasis

8

0.0088

GO:0060996

dendritic spine development

3

0.0088

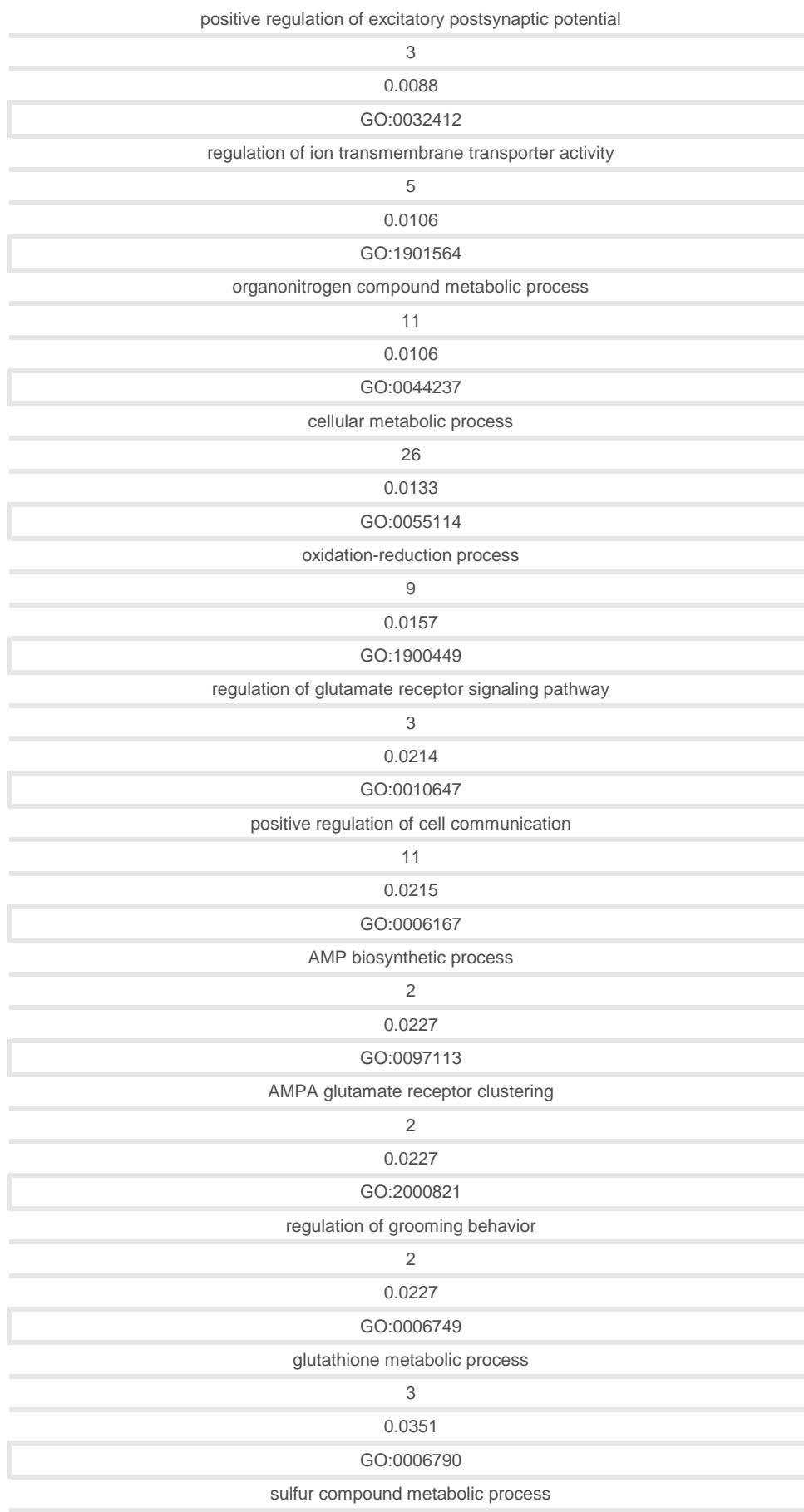
GO:0065008

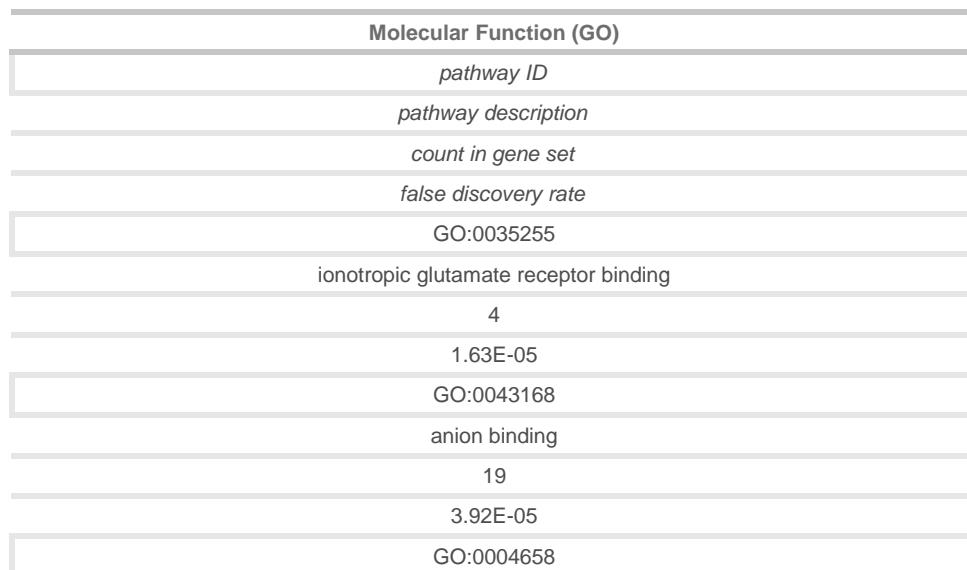
regulation of biological quality

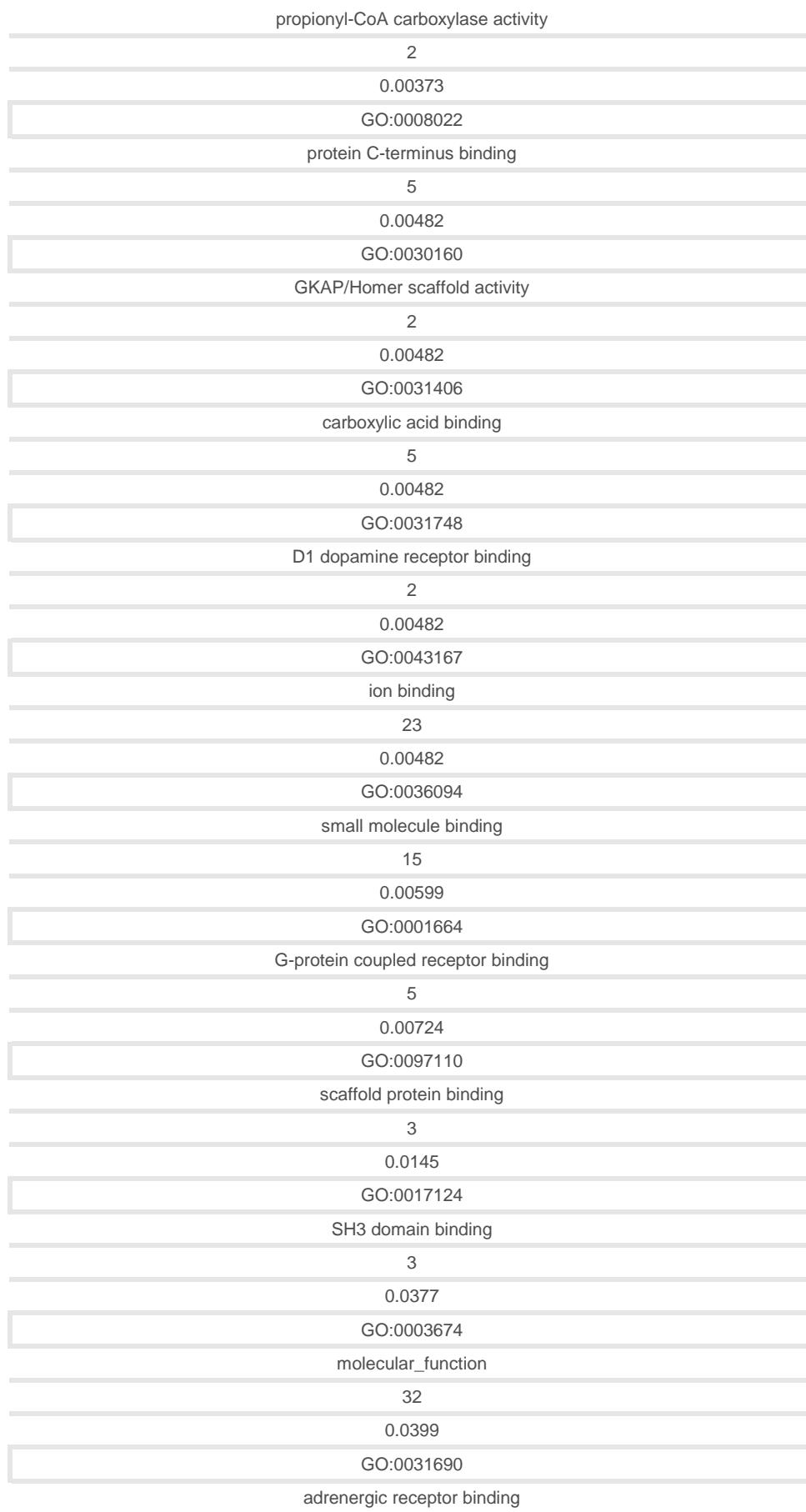
16

0.0088

GO:2000463







2

0.0486

(less ...)

Cellular Component (GO)

pathway ID

pathway description

count in gene set

false discovery rate

GO:0005737

cytoplasm

32

0.00364

GO:0005829

cytosol

13

0.00364

GO:0030425

dendrite

7

0.00364

GO:0060076

excitatory synapse

3

0.00364

GO:0044429

mitochondrial part

8

0.0221

GO:0036477

somatodendritic compartment

7

0.0228

GO:0005739

mitochondrion

11

0.0242

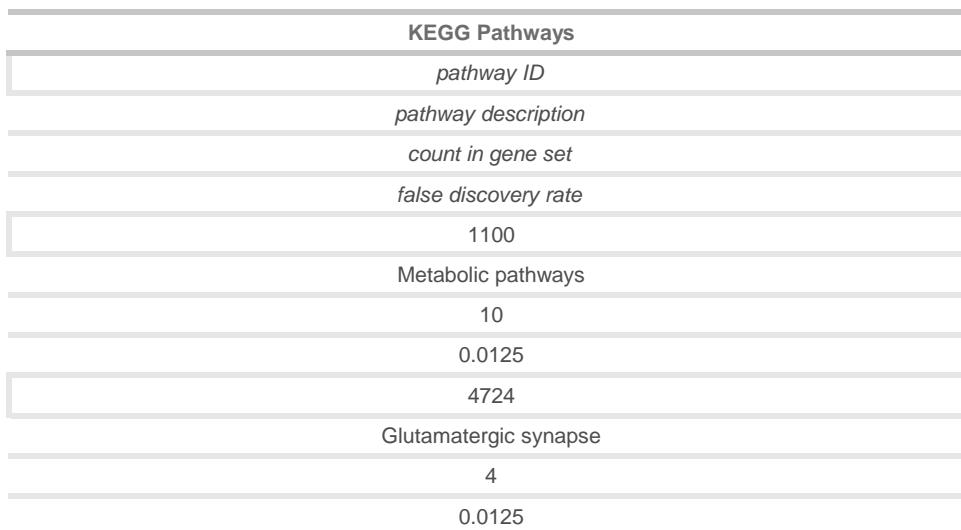
GO:0043005

neuron projection

8

0.0242

GO:0005759



5016
Huntington s disease
4
0.0347
4146
Peroxisome
3
0.0372