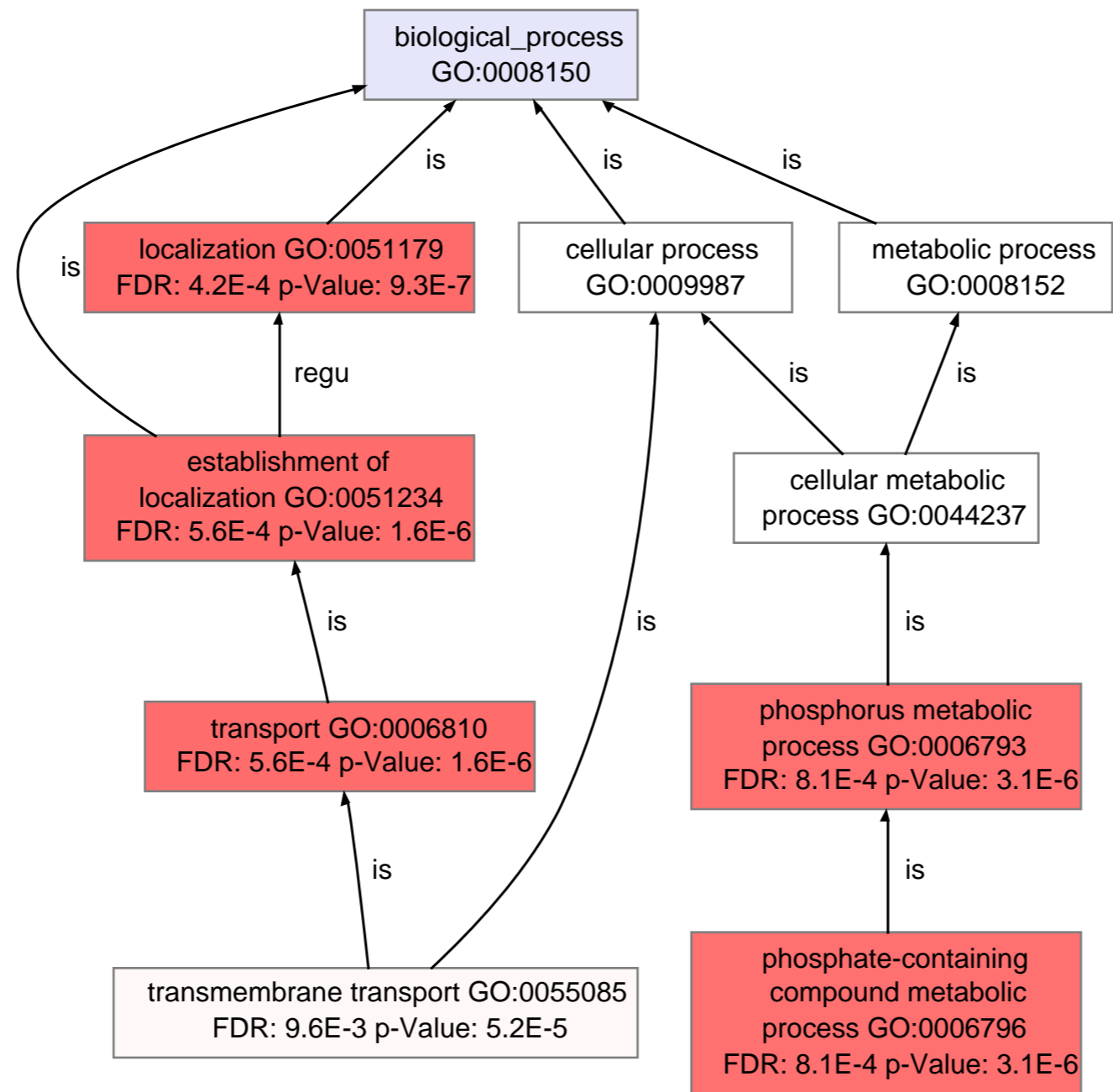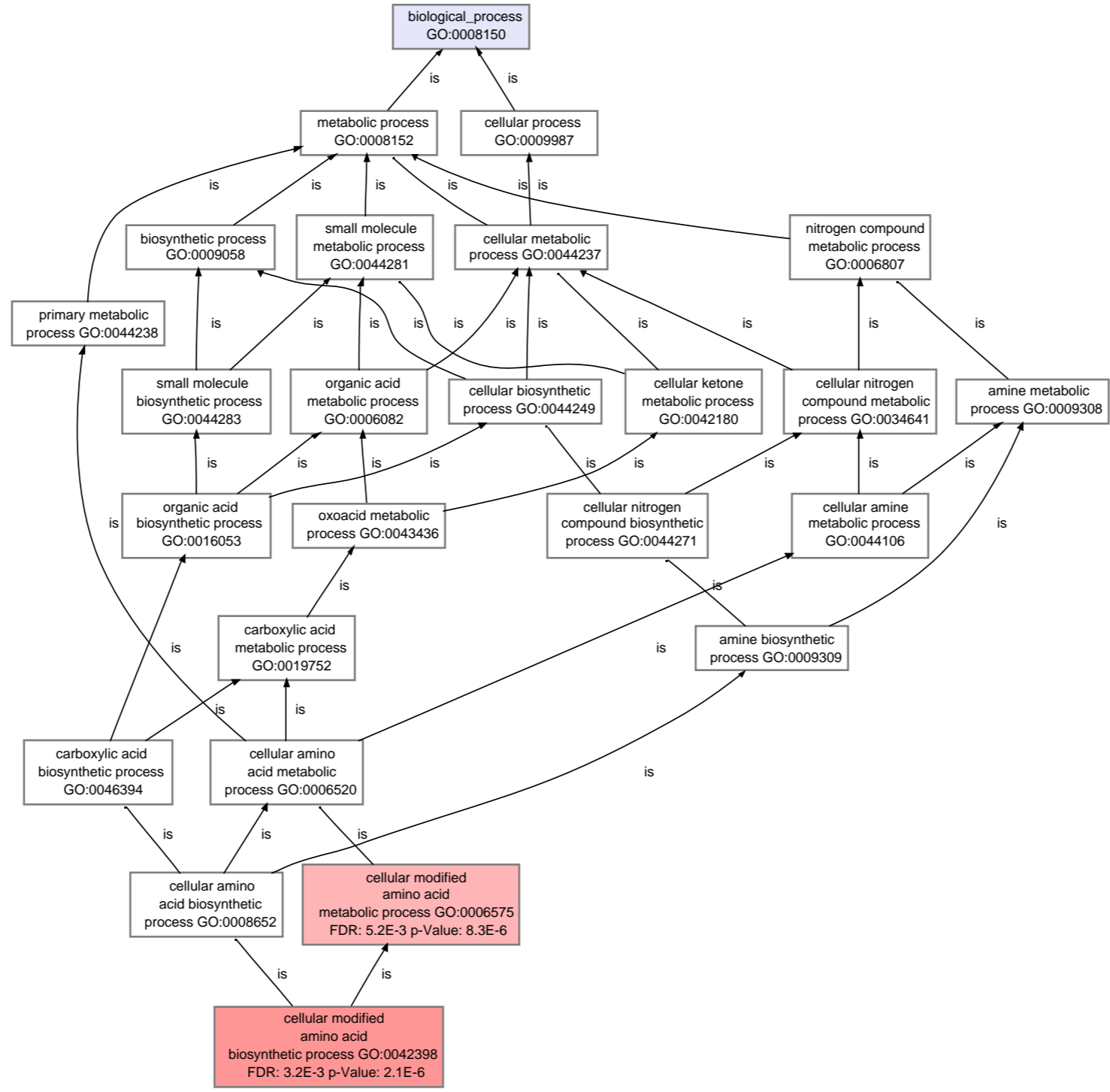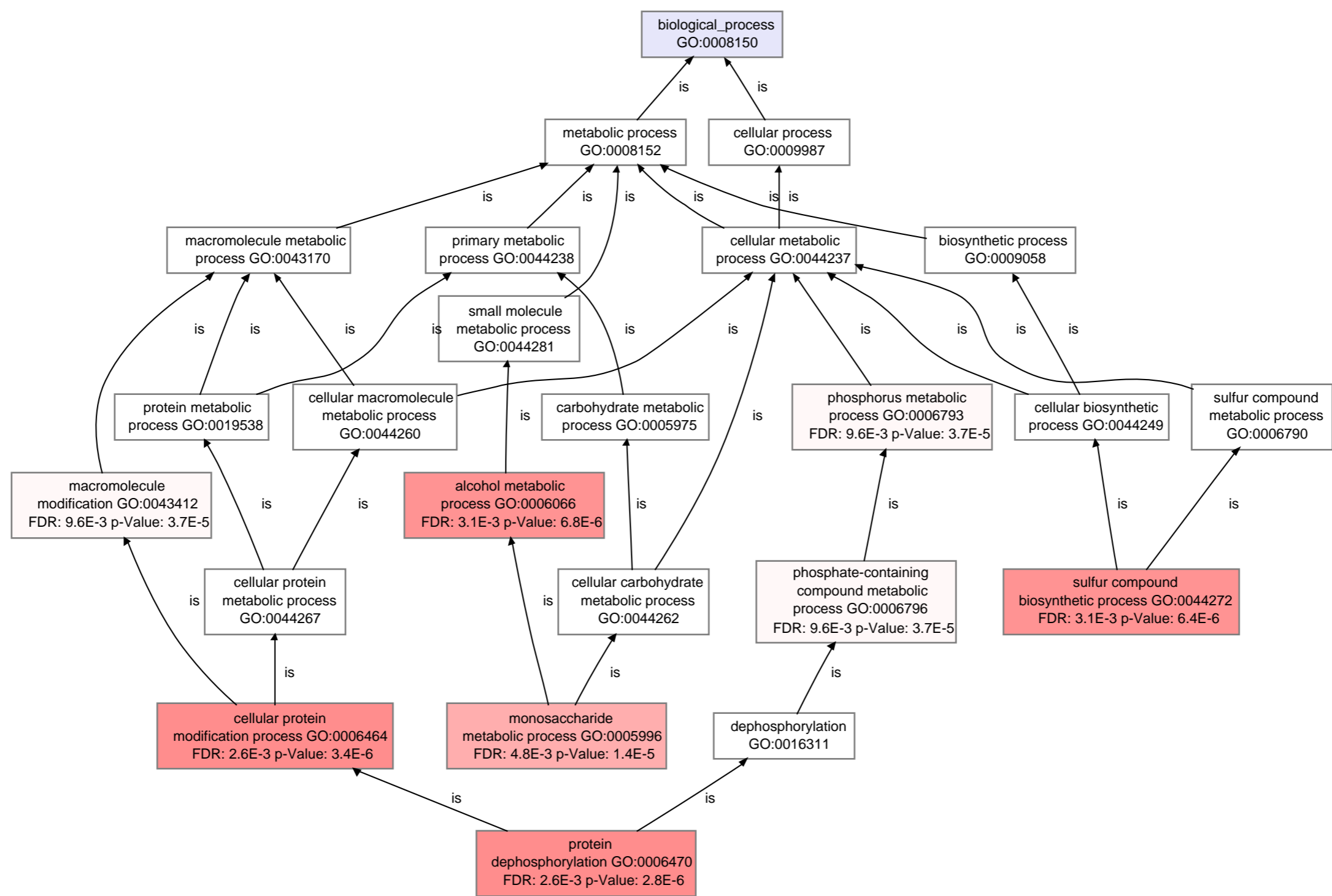**Figure S1. Color-coded gene ontology (GO) graph showing significantly enriched GO terms describing biological processes.** Predicted targets of miRNAs within each cluster (Figure 4) were analyzed separately. A false discovery rate (FDR) of 0.01 was used as the threshold. For each GO term, a brief description, GO number, FDR and P value were shown.
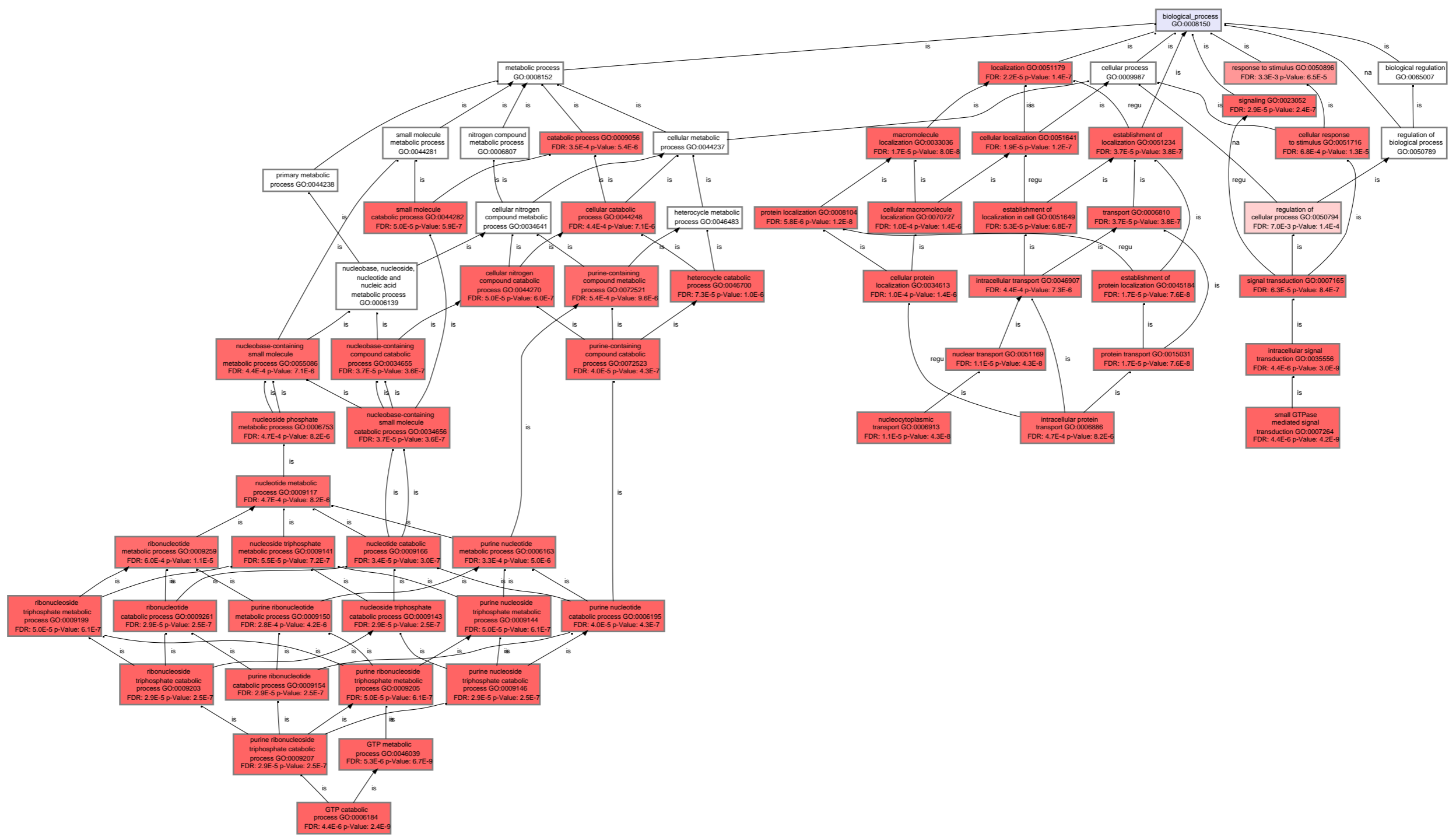
biological_process GO:0008150

localization GO:0051179 FDR: 4.2E-3 p-Value: 4.5E-5

response to stimulus GO:0050896 FDR: 7.0E-4 p-Value: 3.1E-6

cellular process GO:0009987 FDR: 2.2E-3 p-Value: 1.6E-5

biological regulation GO:0065007 FDR: 4.5E-5 p-Value: 5.7E-8

metabolic process GO:0008152

signaling GO:0023052 FDR: 5.3E-7 p-Value: 1.7E-10

establishment of localization GO:0051234 FDR: 2.9E-3 p-Value: 2.5E-5

cellular response to stimulus GO:0051716 FDR: 4.2E-4 p-Value: 1.5E-6

regulation of biological process GO:0050789 FDR: 1.8E-4 p-Value: 4.4E-7

biosynthetic process GO:0009058

small molecule metabolic process GO:0044281

cellular metabolic process GO:0044237

nitrogen compound metabolic process GO:0006807

primary metabolic process GO:0044238

macromolecule metabolic process GO:0043170

transport GO:0006810 FDR: 2.9E-3 p-Value: 2.5E-5

regulation of cellular process GO:0050794 FDR: 2.6E-4 p-Value: 8.1E-7

cellular biosynthetic process GO:0044249

small molecule biosynthetic process GO:0044283

organic acid metabolic process GO:0006082

sulfur compound metabolic process GO:0006790

cellular ketone metabolic process GO:0042180

cellular nitrogen compound metabolic process GO:0034641

amine metabolic process GO:0009308

phosphorus metabolic process GO:0006793 FDR: 1.1E-3 p-Value: 6.7E-6

cellular macromolecule metabolic process GO:0044260

protein metabolic process GO:0019538

macromolecule modification GO:0043412 FDR: 1.6E-3 p-Value: 1.1E-5

signal transduction GO:0007165 FDR: 1.0E-6 p-Value: 6.6E-10

sulfur compound biosynthetic process GO:0044272 FDR: 3.0E-3 p-Value: 2.9E-5

organic acid biosynthetic process GO:0016053

cellular nitrogen compound biosynthetic process GO:0044271

oxoacid metabolic process GO:0043436

cellular amine metabolic process GO:0044106

phosphate-containing compound metabolic process GO:0006796 FDR: 1.1E-3 p-Value: 6.7E-6

cellular protein metabolic process GO:0044267

cellular protein modification process GO:0006464 FDR: 1.8E-4 p-Value: 5.1E-7

carboxylic acid metabolic process GO:0019752

amine biosynthetic process GO:0009309

phosphorylation GO:0016310 FDR: 9.4E-3 p-Value: 1.7E-4

carboxylic acid biosynthetic process GO:0046394

cellular amino acid metabolic process GO:0006520

protein phosphorylation GO:0006468 FDR: 2.3E-3 p-Value: 1.7E-5

cellular amino acid biosynthetic process GO:0008652

sulfur amino acid metabolic process GO:0000096

aspartate family amino acid metabolic process GO:0009066

sulfur amino acid biosynthetic process GO:0000097

aspartate family amino acid biosynthetic process GO:0009067

methionine metabolic process GO:0006555

methionine biosynthetic process GO:0009086

L-methionine biosynthetic process GO:0071265 FDR: 6.3E-3 p-Value: 9.9E-5

L-methionine salvage GO:0071267 FDR: 6.3E-3 p-Value: 9.9E-5

Enriched Graph

biological_process
GO:0008150

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localization GO:0051179
FDR: 4.2E-4 p-Value: 9.3E-7

cellular process
GO:0009987

metabolic process
GO:0008152

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establishment of
localization GO:0051234
FDR: 5.6E-4 p-Value: 1.6E-6

cellular metabolic
process GO:0044237

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transport GO:0006810
FDR: 5.6E-4 p-Value: 1.6E-6

phosphorus metabolic
process GO:0006793
FDR: 8.1E-4 p-Value: 3.1E-6

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transmembrane transport GO:0055085
FDR: 9.6E-3 p-Value: 5.2E-5

phosphate-containing
compound metabolic
process GO:0006796
FDR: 8.1E-4 p-Value: 3.1E-6

Enriched Graph

Enriched Graph

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