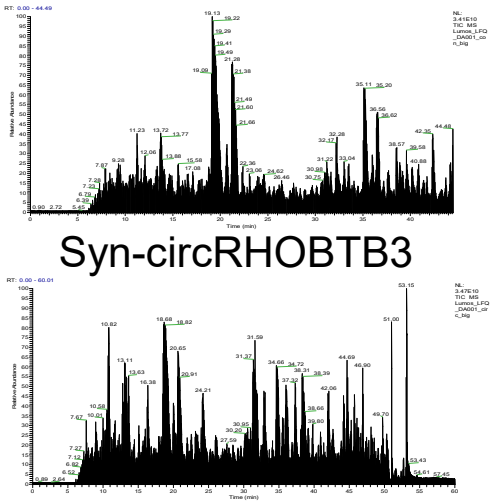
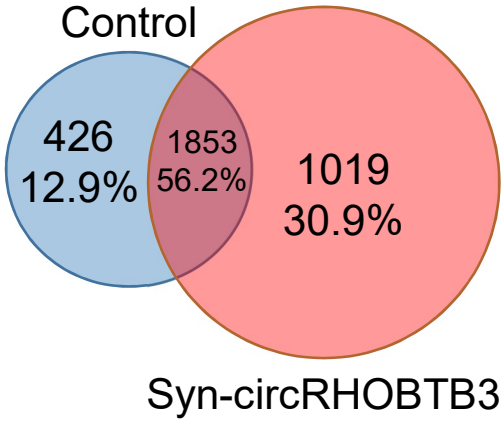
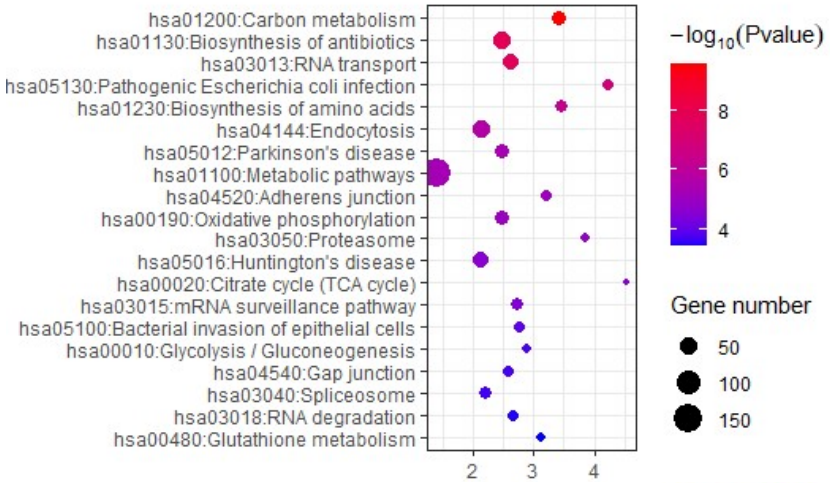
A

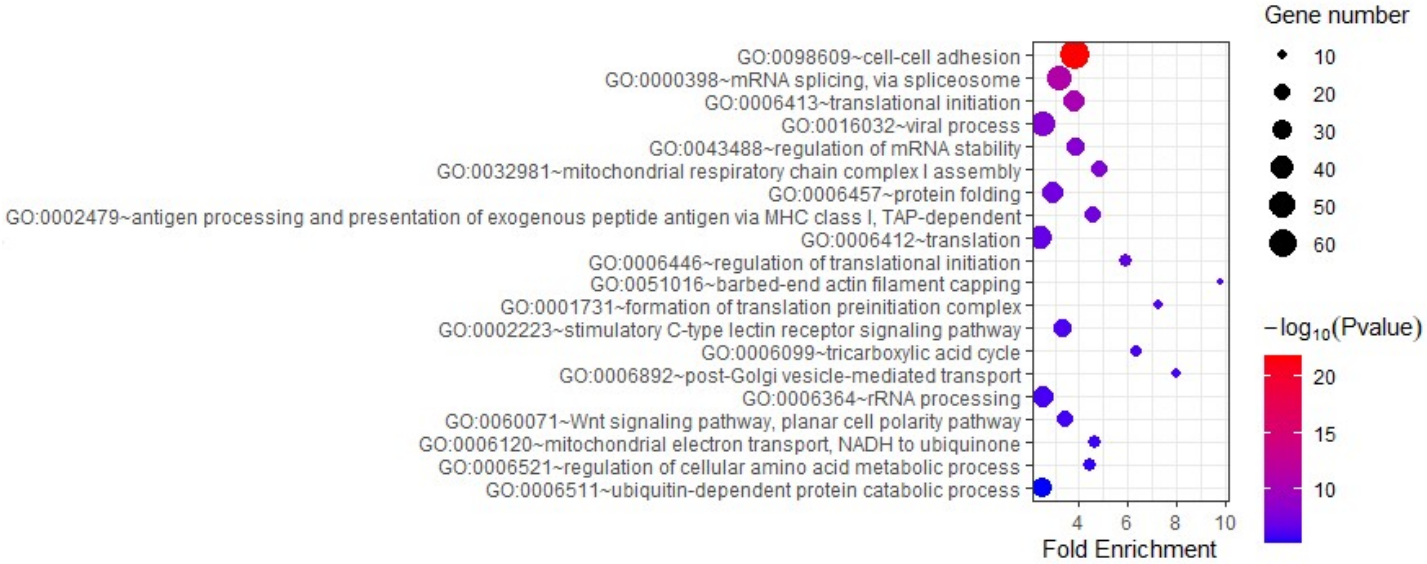

Control
Syn-circRHOBTB3

B


Control
426
12.9%
1853
56.2%
1019
30.9%
Syn-circRHOBTB3

C


hsa01200:Carbon metabolism
hsa01130:Biosynthesis of antibiotics
hsa03013:RNA transport
hsa05130:Pathogenic Escherichia coli infection
hsa01230:Biosynthesis of amino acids
hsa04144:Endocytosis
hsa05012:Parkinson's disease
hsa01100:Metabolic pathways
hsa04520:Adherens junction
hsa00190:Oxidative phosphorylation
hsa03050:Proteasome
hsa05016:Huntington's disease
hsa00020:Citrate cycle (TCA cycle)
hsa03015:mRNA surveillance pathway
hsa05100:Bacterial invasion of epithelial cells
hsa00010:Glycolysis / Gluconeogenesis
hsa04540:Gap junction
hsa03040:Spliceosome
hsa03018:RNA degradation
hsa00480:Glutathione metabolism
2
3
4
−log10(Pvalue)
8
6
4
Gene number
50
100
150


GO:0098609~cell-cell adhesion
GO:0000398~mRNA splicing, via spliceosome
GO:0006413~translational initiation
GO:0016032~viral process
GO:0043488~regulation of mRNA stability
GO:0032981~mitochondrial respiratory chain complex I assembly
GO:0006457~protein folding
GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent
GO:0006412~translation
GO:0006446~regulation of translational initiation
GO:0051016~barbed-end actin filament capping
GO:0001731~formation of translation preinitiation complex
GO:0002223~stimulatory C-type lectin receptor signaling pathway
GO:0006099~tricarboxylic acid cycle
GO:0006892~post-Golgi vesicle-mediated transport
GO:0006364~rRNA processing
GO:0060071~Wnt signaling pathway, planar cell polarity pathway
GO:0006120~mitochondrial electron transport, NADH to ubiquinone
GO:0006521~regulation of cellular amino acid metabolic process
GO:0006511~ubiquitin-dependent protein catabolic process
4
6
8
10
Fold Enrichment
Gene number
10
20
30
40
50
60
−log10(Pvalue)
20
15
10