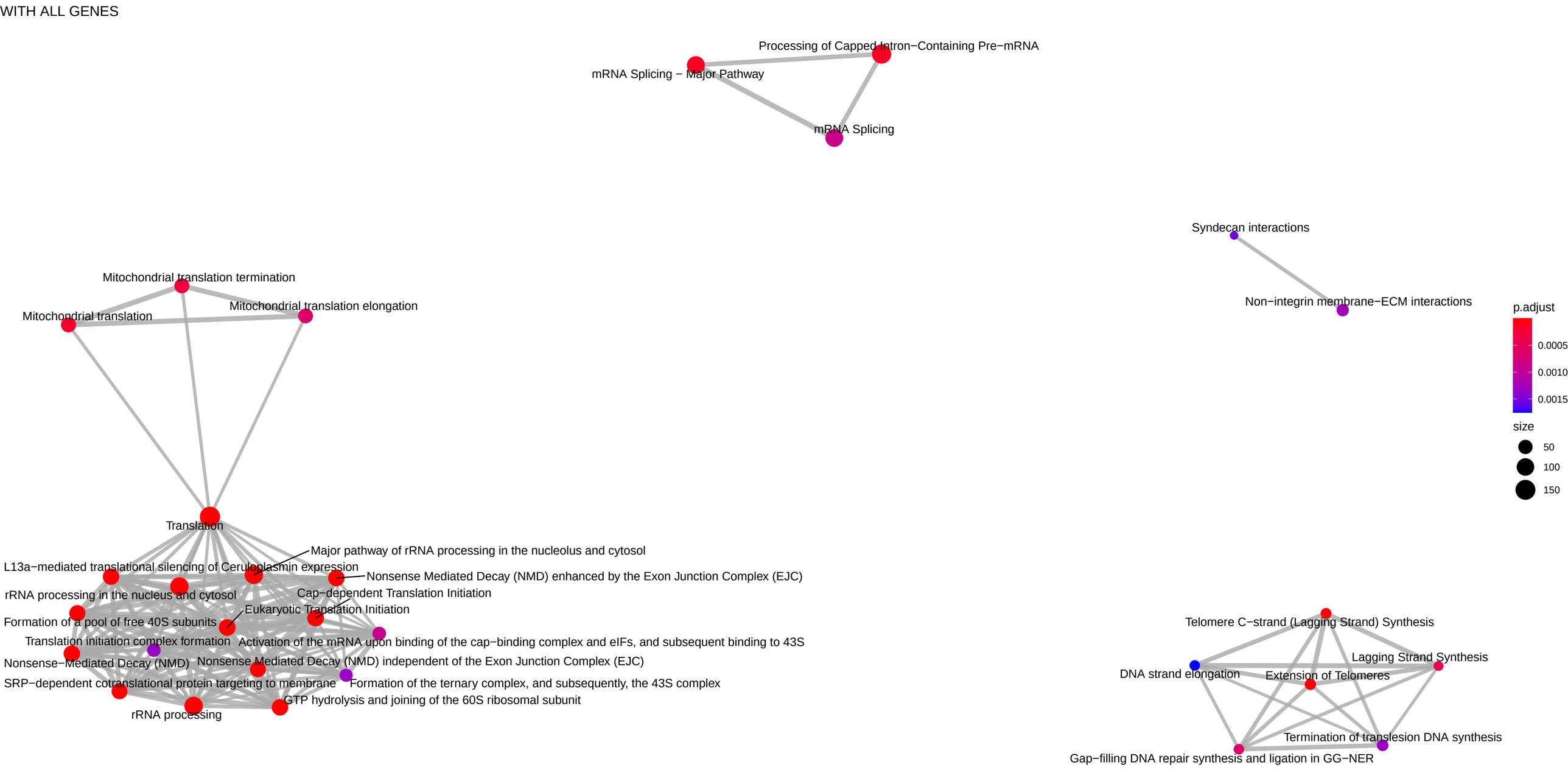
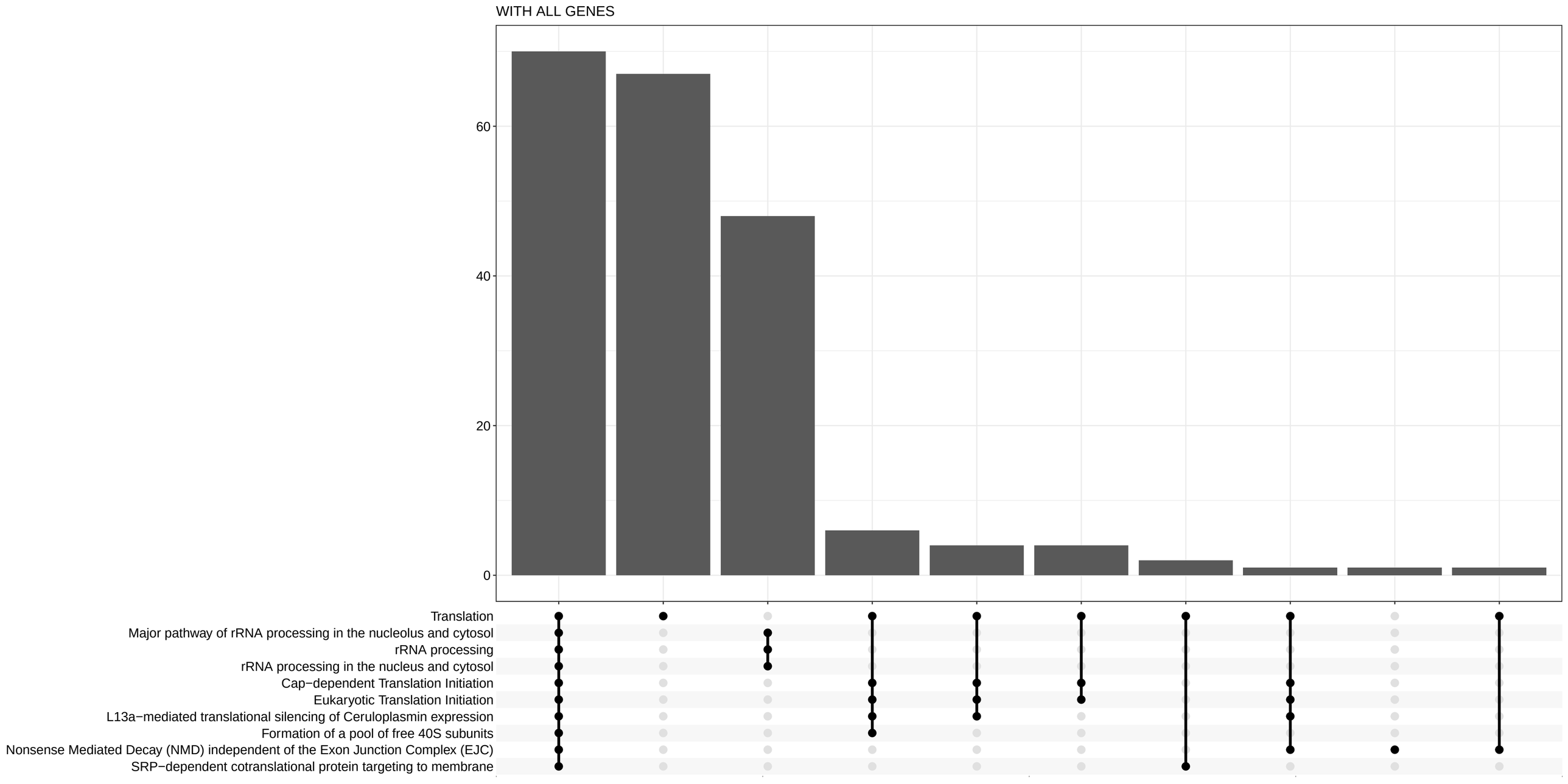
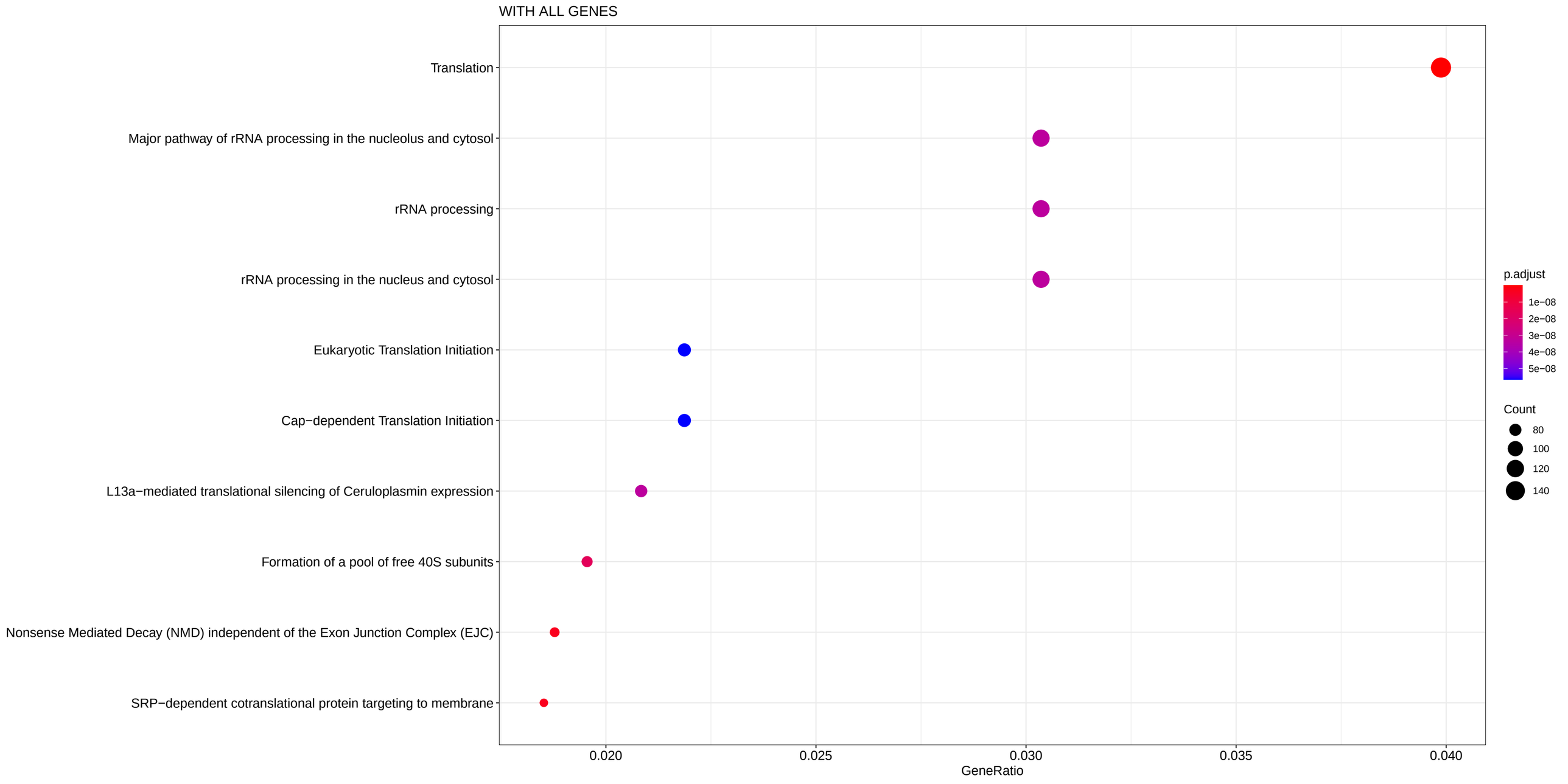
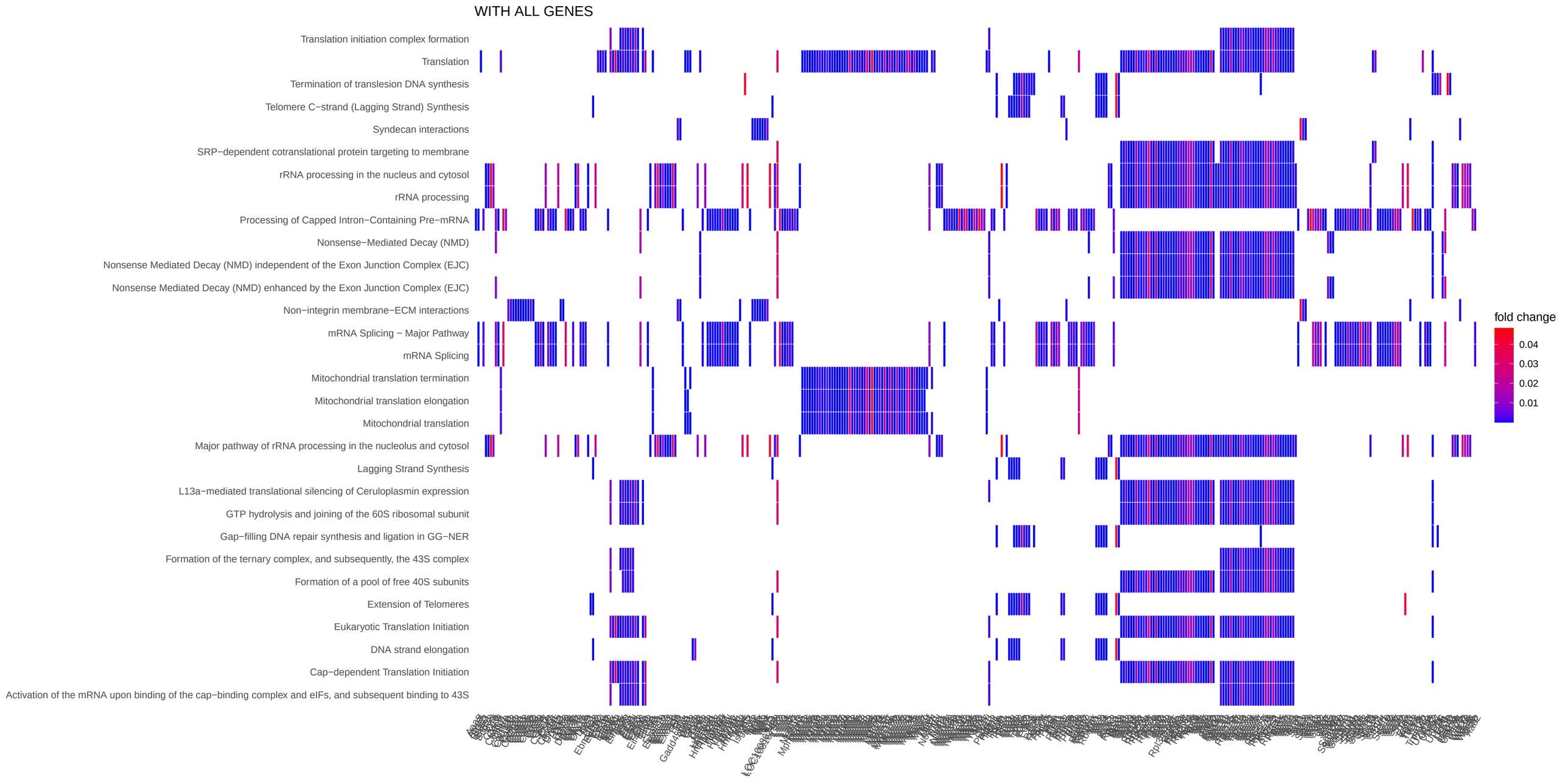
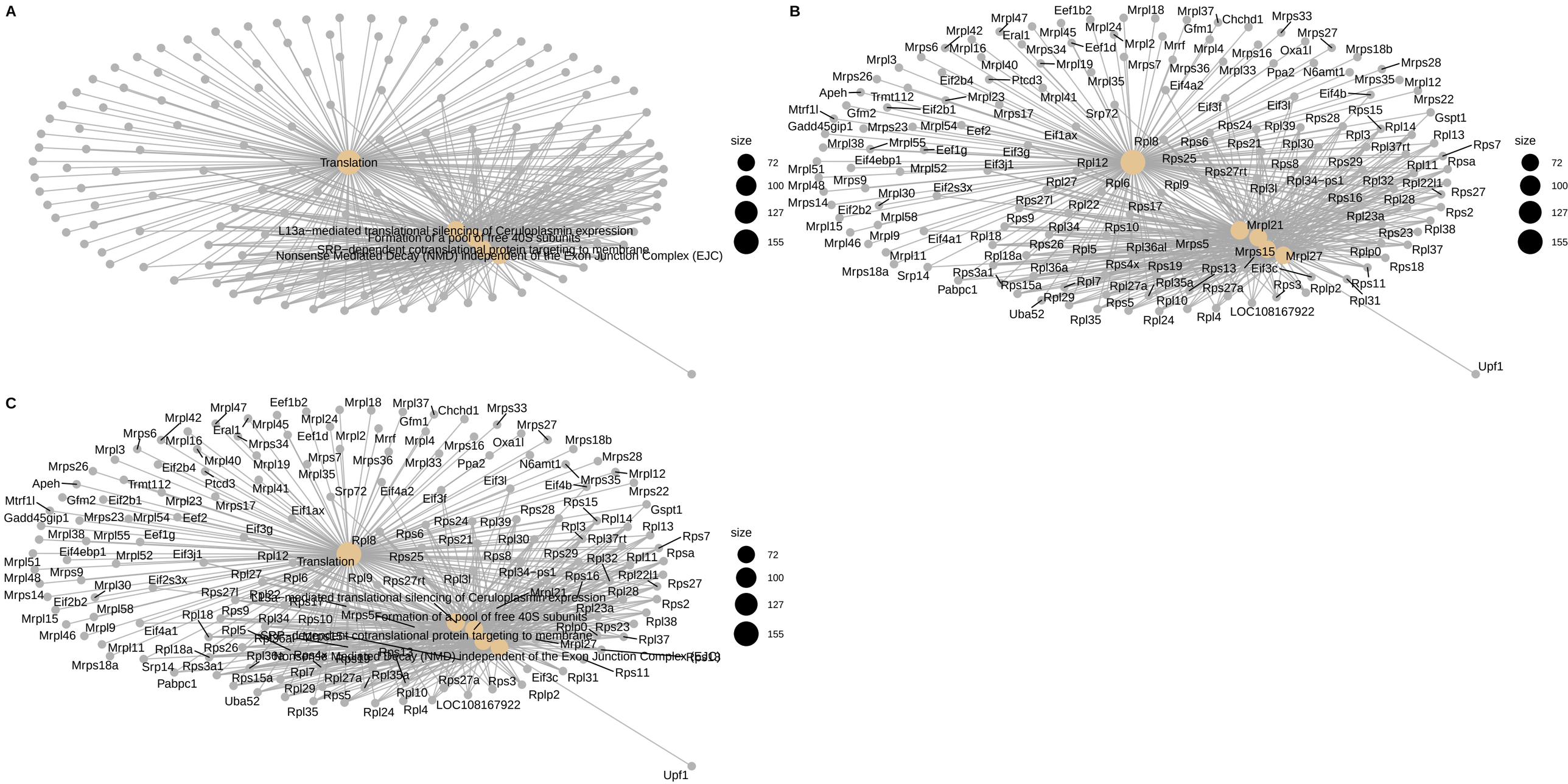
WITH ALL GENES



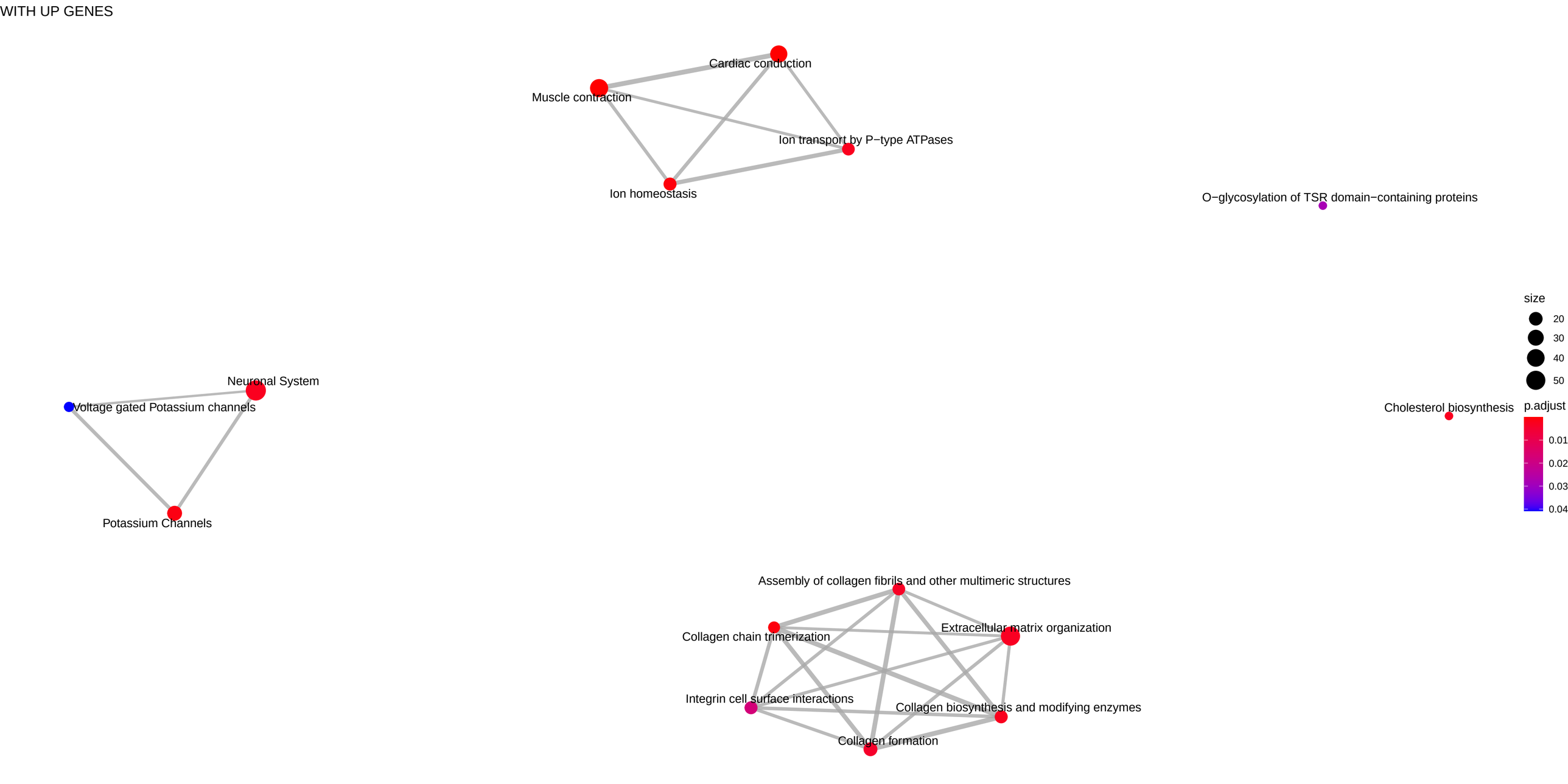

WITH ALL GENES
60
40
20
0
Translation
Major pathway of rRNA processing in the nucleolus and cytosol
rRNA processing
rRNA processing in the nucleus and cytosol
Cap−dependent Translation Initiation
Eukaryotic Translation Initiation
L13a−mediated translational silencing of Ceruloplasmin expression
Formation of a pool of free 40S subunits
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
SRP−dependent cotranslational protein targeting to membrane

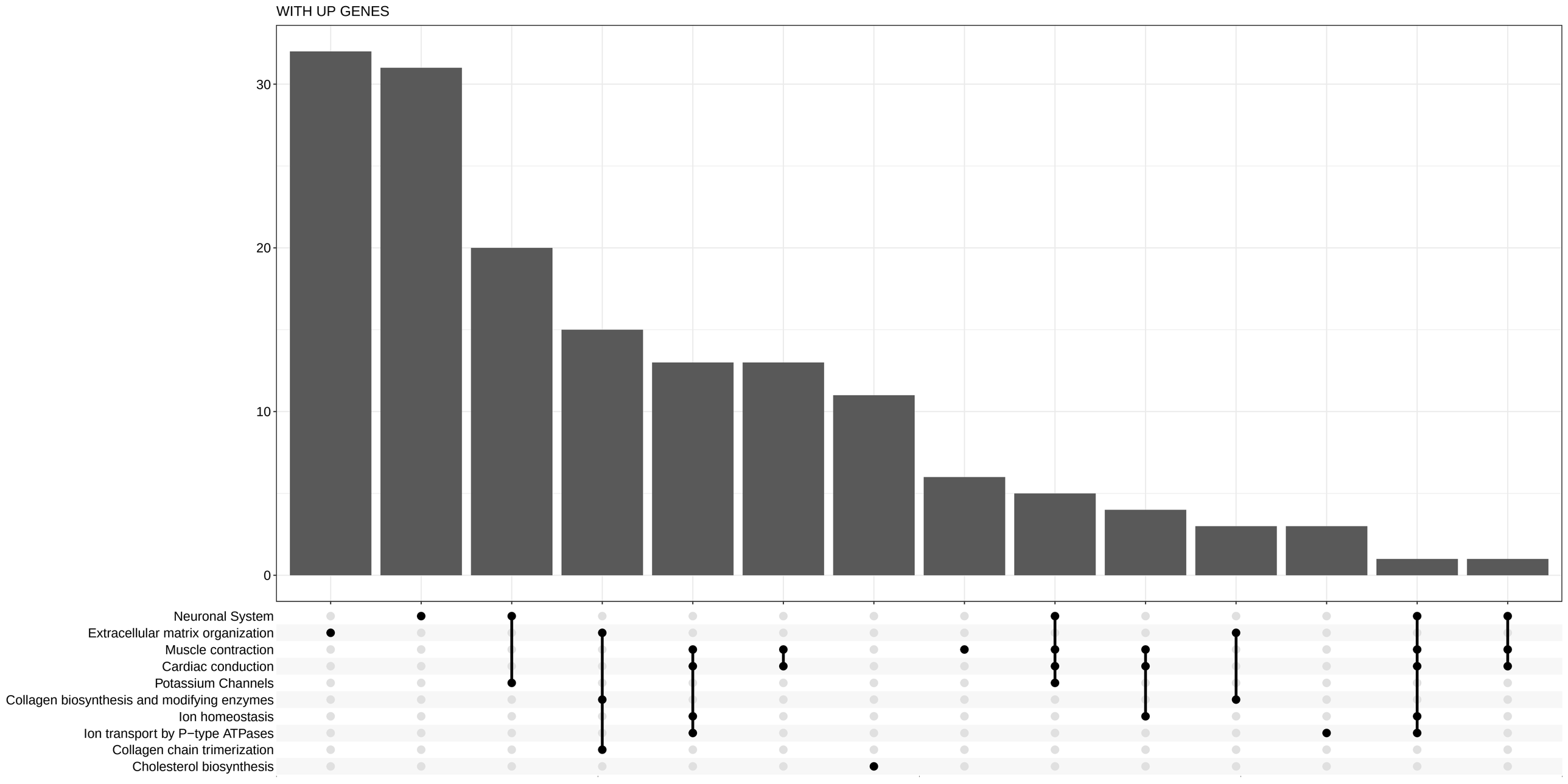

WITH ALL GENES
Translation
Major pathway of rRNA processing in the nucleolus and cytosol
rRNA processing
rRNA processing in the nucleus and cytosol
Eukaryotic Translation Initiation
Cap−dependent Translation Initiation
L13a−mediated translational silencing of Ceruloplasmin expression
Formation of a pool of free 40S subunits
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
SRP−dependent cotranslational protein targeting to membrane
0.020
0.025
0.030
0.035
0.040
GeneRatio
p.adjust
1e−08
2e−08
3e−08
4e−08
5e−08
Count
80
100
120
140

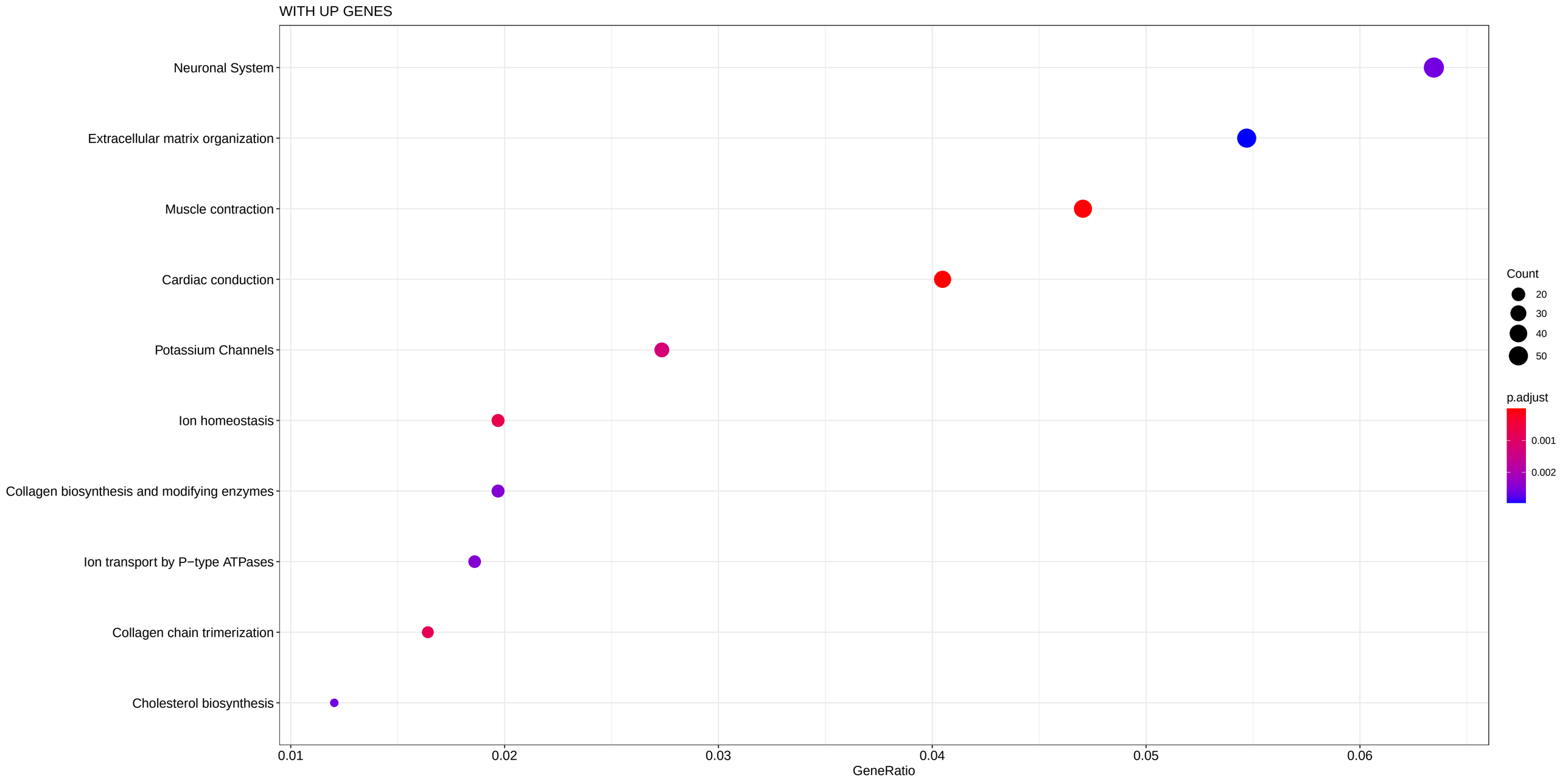

WITH ALL GENES
Translation initiation complex formation
Translation
Termination of translesion DNA synthesis
Telomere C−strand (Lagging Strand) Synthesis
Syndecan interactions
SRP−dependent cotranslational protein targeting to membrane
rRNA processing in the nucleus and cytosol
rRNA processing
Processing of Capped Intron−Containing Pre−mRNA
Nonsense−Mediated Decay (NMD)
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
Non−integrin membrane−ECM interactions
mRNA Splicing − Major Pathway
mRNA Splicing
Mitochondrial translation termination
Mitochondrial translation elongation
Mitochondrial translation
Major pathway of rRNA processing in the nucleolus and cytosol
Lagging Strand Synthesis
L13a−mediated translational silencing of Ceruloplasmin expression
GTP hydrolysis and joining of the 60S ribosomal subunit
Gap−filling DNA repair synthesis and ligation in GG−NER
Formation of the ternary complex, and subsequently, the 43S complex
Formation of a pool of free 40S subunits
Extension of Telomeres
Eukaryotic Translation Initiation
DNA strand elongation
Cap−dependent Translation Initiation
Activation of the mRNA upon binding of the cap−binding complex and eIFs, and subsequent binding to 43S
fold change
0.04
0.03
0.02
0.01

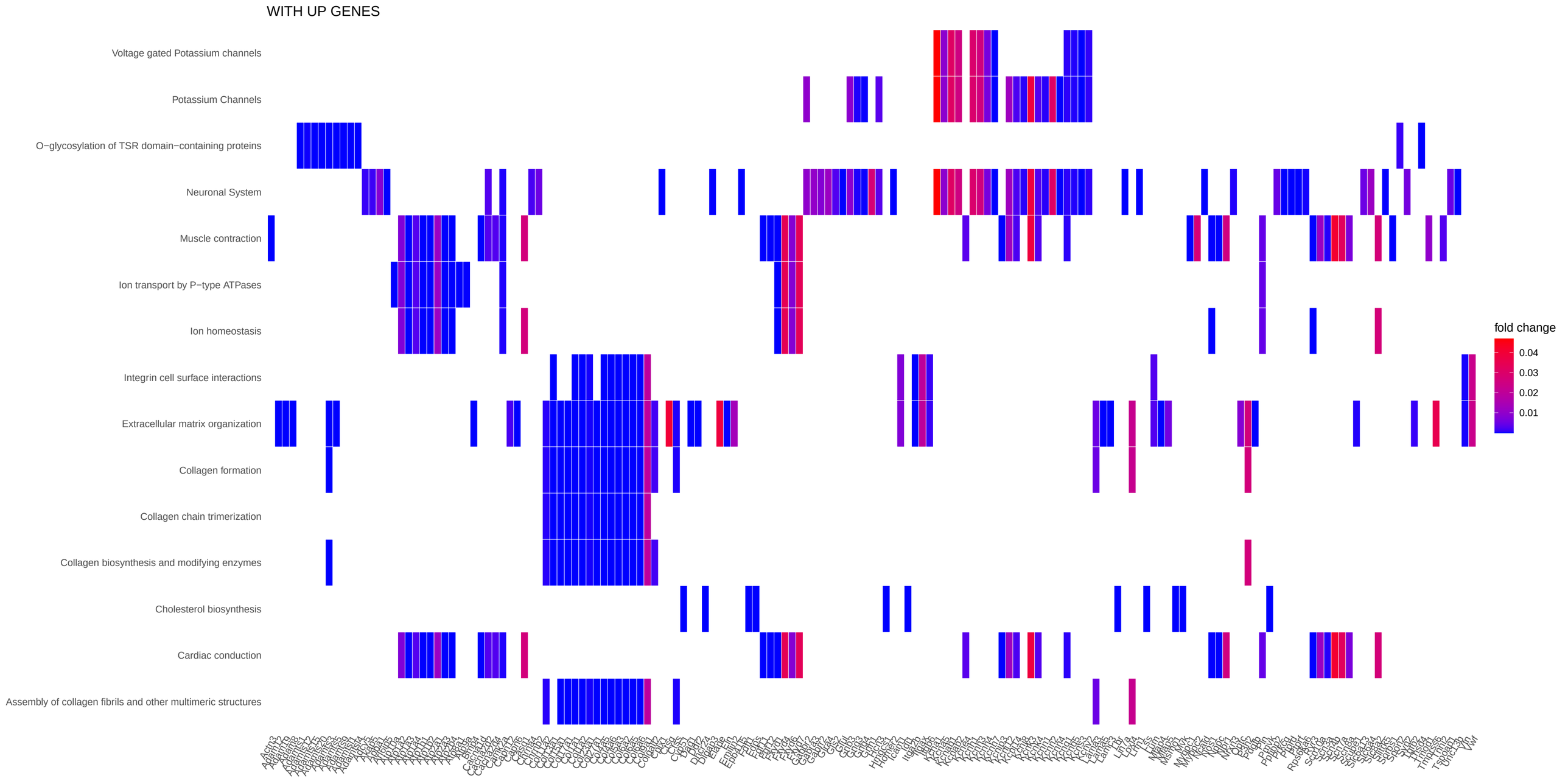

A
Translation
L13a−mediated translational silencing of Ceruloplasmin expression
Formation of a pool of free 40S subunits
SRP−dependent cotranslational protein targeting to membrane
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
size
72
100
127
155
B
Upf1
C
Upf1

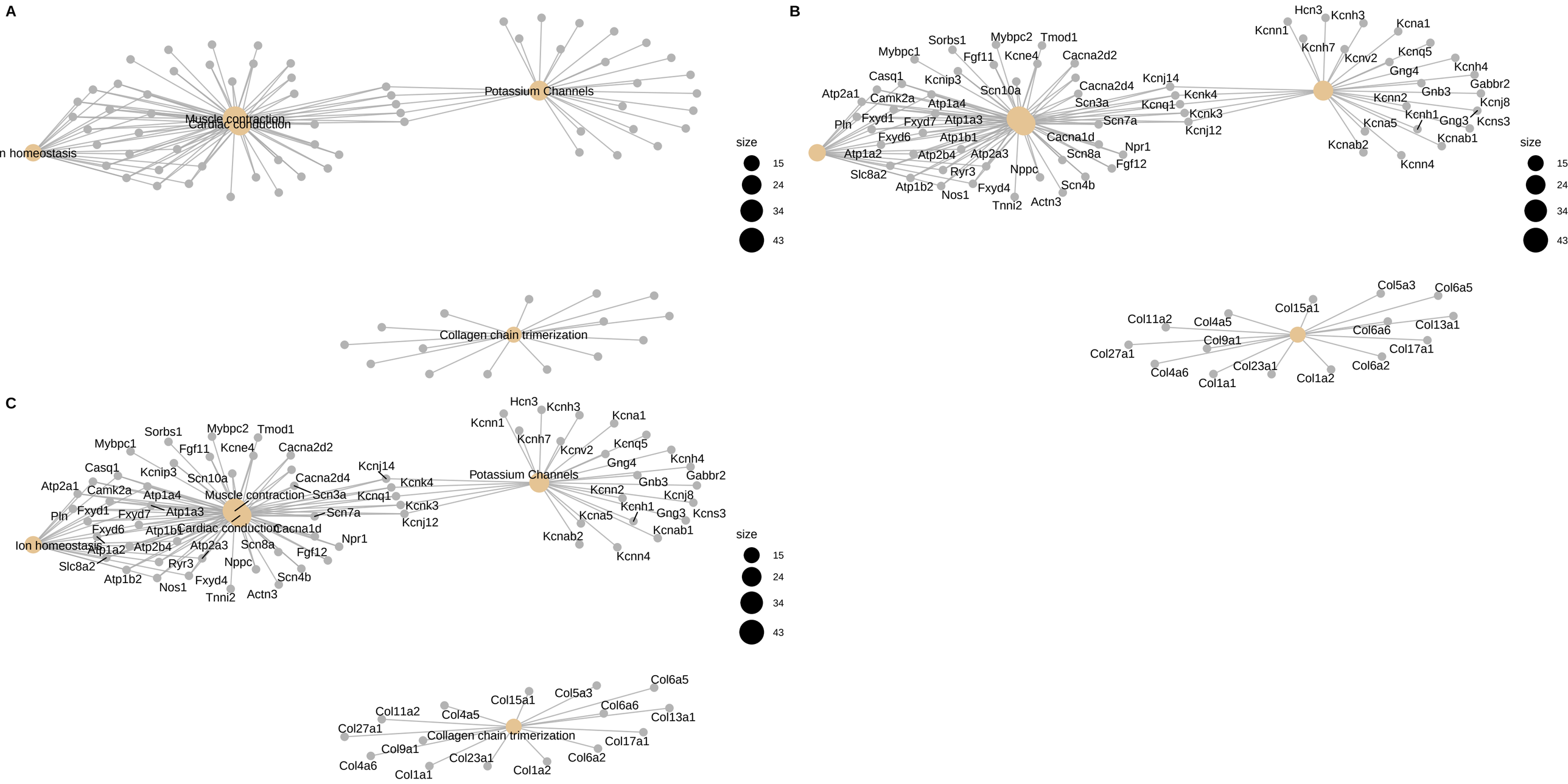
WITH UP GENES



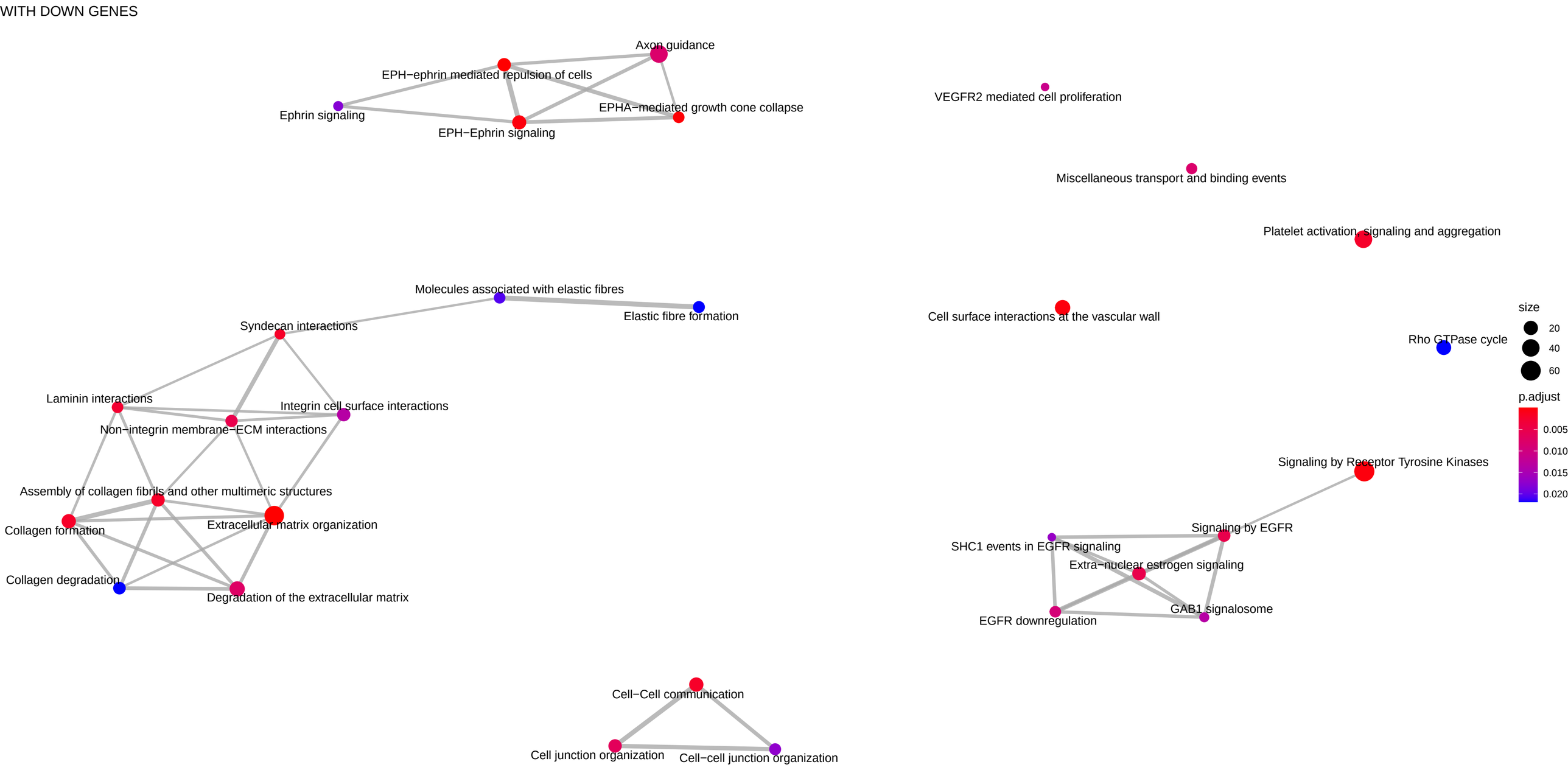

WITH UP GENES
30
20
10
0
Neuronal System
Extracellular matrix organization
Muscle contraction
Cardiac conduction
Potassium Channels
Collagen biosynthesis and modifying enzymes
Ion homeostasis
Ion transport by P−type ATPases
Collagen chain trimerization
Cholesterol biosynthesis

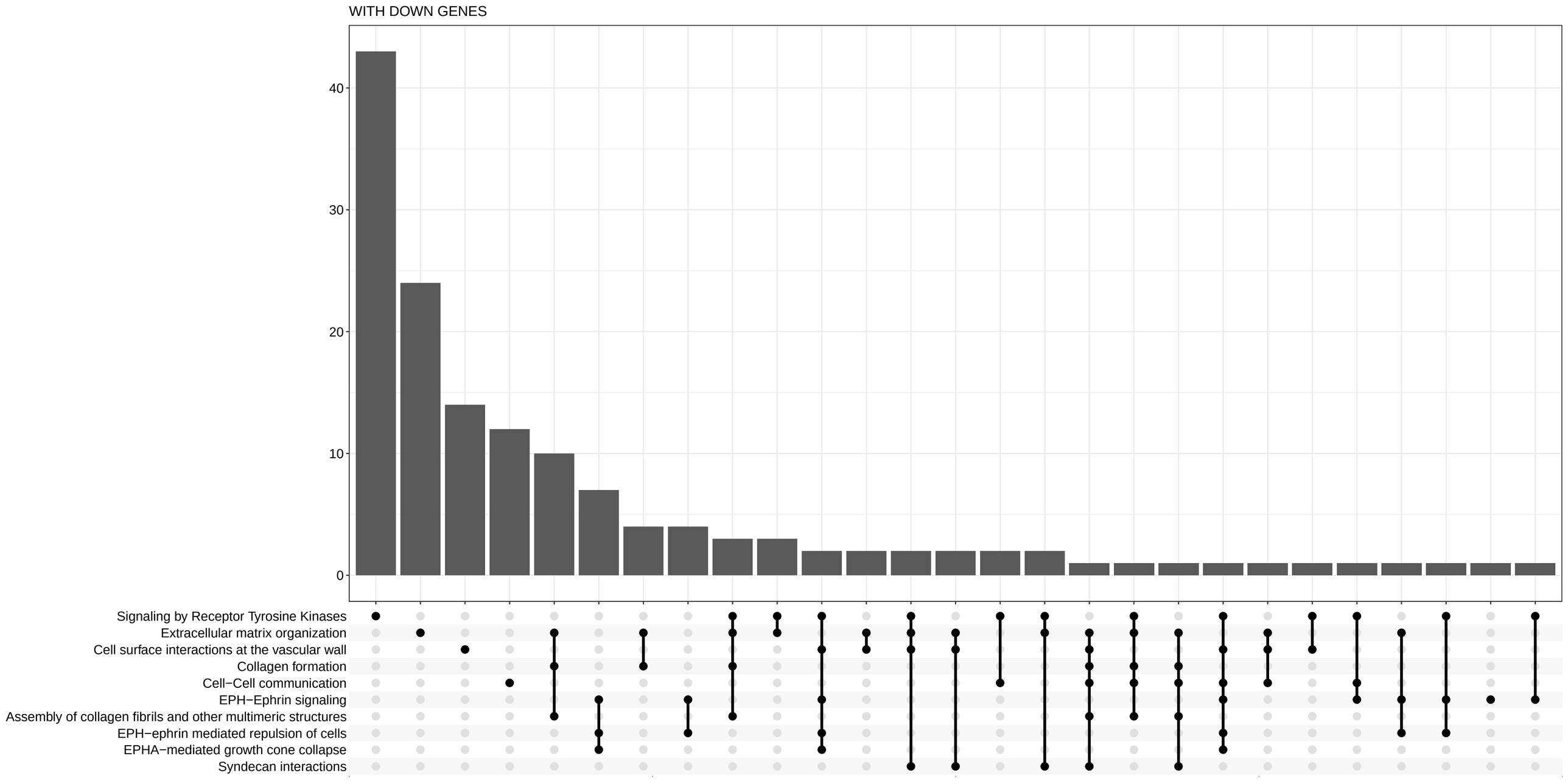

WITH UP GENES
Neuronal System
Extracellular matrix organization
Muscle contraction
Cardiac conduction
Potassium Channels
Ion homeostasis
Collagen biosynthesis and modifying enzymes
Ion transport by P−type ATPases
Collagen chain trimerization
Cholesterol biosynthesis
0.01
0.02
0.03
0.04
0.05
0.06
GeneRatio
Count
20
30
40
50
p.adjust
0.001
0.002

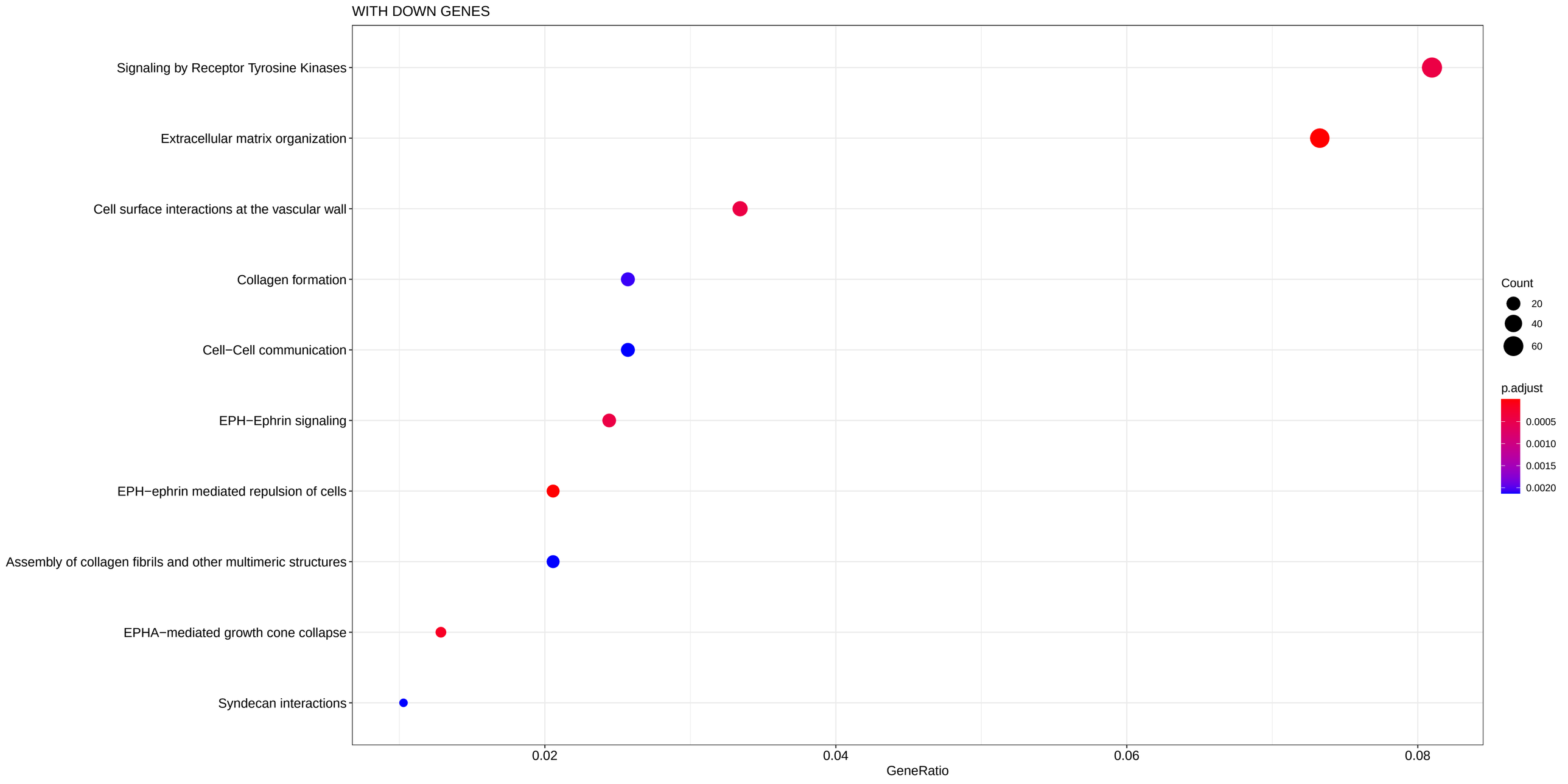

WITH UP GENES
Voltage gated Potassium channels
Potassium Channels
O−glycosylation of TSR domain−containing proteins
Neuronal System
Muscle contraction
Ion transport by P−type ATPases
Ion homeostasis
Integrin cell surface interactions
Extracellular matrix organization
Collagen formation
Collagen chain trimerization
Collagen biosynthesis and modifying enzymes
Cholesterol biosynthesis
Cardiac conduction
Assembly of collagen fibrils and other multimeric structures
fold change
0.04
0.03
0.02
0.01

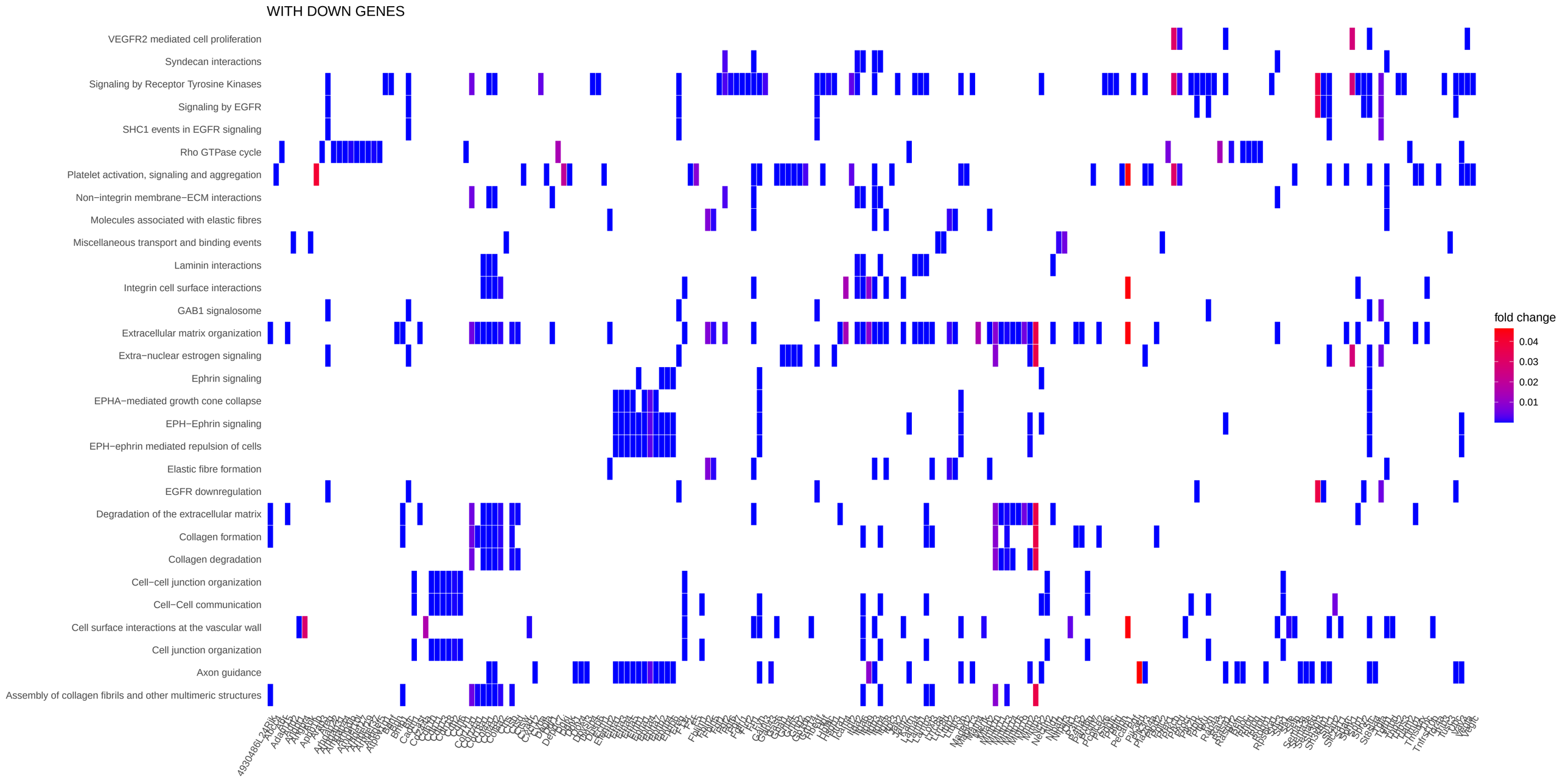

A
Muscle contraction
Cardiac conduction
Potassium Channels
n homeostasis
Collagen chain trimerization
size
15
24
34
43
B
Hcn3
Kcnh3
Kcna1
Kcnn1
Kcnh7
Kcnv2
Kcnq5
Gng4
Kcnh4
Gabbr2
Gnb3
Kcnn2
Kcnj8
Kcnh1
Gng3
Kcns3
Kcna5
Kcnab1
Kcnab2
Kcnn4
Mybpc1
Sorbs1
Mybpc2
Tmod1
Fgf11
Kcne4
Cacna2d2
Casq1
Kcnip3
Cacna2d4
Kcnj14
Atp2a1
Camk2a
Scn10a
Atp1a4
Scn3a
Kcnq1
Kcnk4
Kcnk3
Kcnj12
Pln
Fxyd1
Fxyd7
Atp1a3
Scn7a
Fxyd6
Atp1b1
Cacna1d
Atp1a2
Atp2b4
Atp2a3
Scn8a
Npr1
Fgf12
Slc8a2
Ryr3
Nppc
Scn4b
Atp1b2
Nos1
Fxyd4
Tnni2
Actn3
Col5a3
Col6a5
Col15a1
Col11a2
Col4a5
Col6a6
Col13a1
Col9a1
Col27a1
Col17a1
Col4a6
Col23a1
Col6a2
Col1a1
Col1a2
C
Hcn3
Kcnh3
Kcna1
Kcnn1
Kcnh7
Kcnv2
Kcnq5
Gng4
Kcnh4
Gabbr2
Gnb3
Kcnn2
Kcnj8
Kcnh1
Gng3
Kcns3
Kcna5
Kcnab1
Kcnab2
Kcnn4
Potassium Channels
Mybpc1
Sorbs1
Mybpc2
Tmod1
Fgf11
Kcne4
Cacna2d2
Casq1
Kcnip3
Cacna2d4
Kcnj14
Atp2a1
Camk2a
Scn10a
Atp1a4
Muscle contraction
Scn3a
Kcnq1
Kcnk4
Kcnk3
Kcnj12
Pln
Fxyd1
Fxyd7
Atp1a3
Scn7a
Fxyd6
Atp1b1
Cardiac conduction
Cacna1d
Ion homeostasis
Atp1a2
Atp2b4
Atp2a3
Scn8a
Npr1
Fgf12
Slc8a2
Ryr3
Nppc
Scn4b
Atp1b2
Nos1
Fxyd4
Tnni2
Actn3
size
15
24
34
43
Col6a5
Col5a3
Col15a1
Col11a2
Col4a5
Col6a6
Col13a1
Col27a1
Collagen chain trimerization
Col17a1
Col9a1
Col23a1
Col6a2
Col4a6
Col1a1
Col1a2

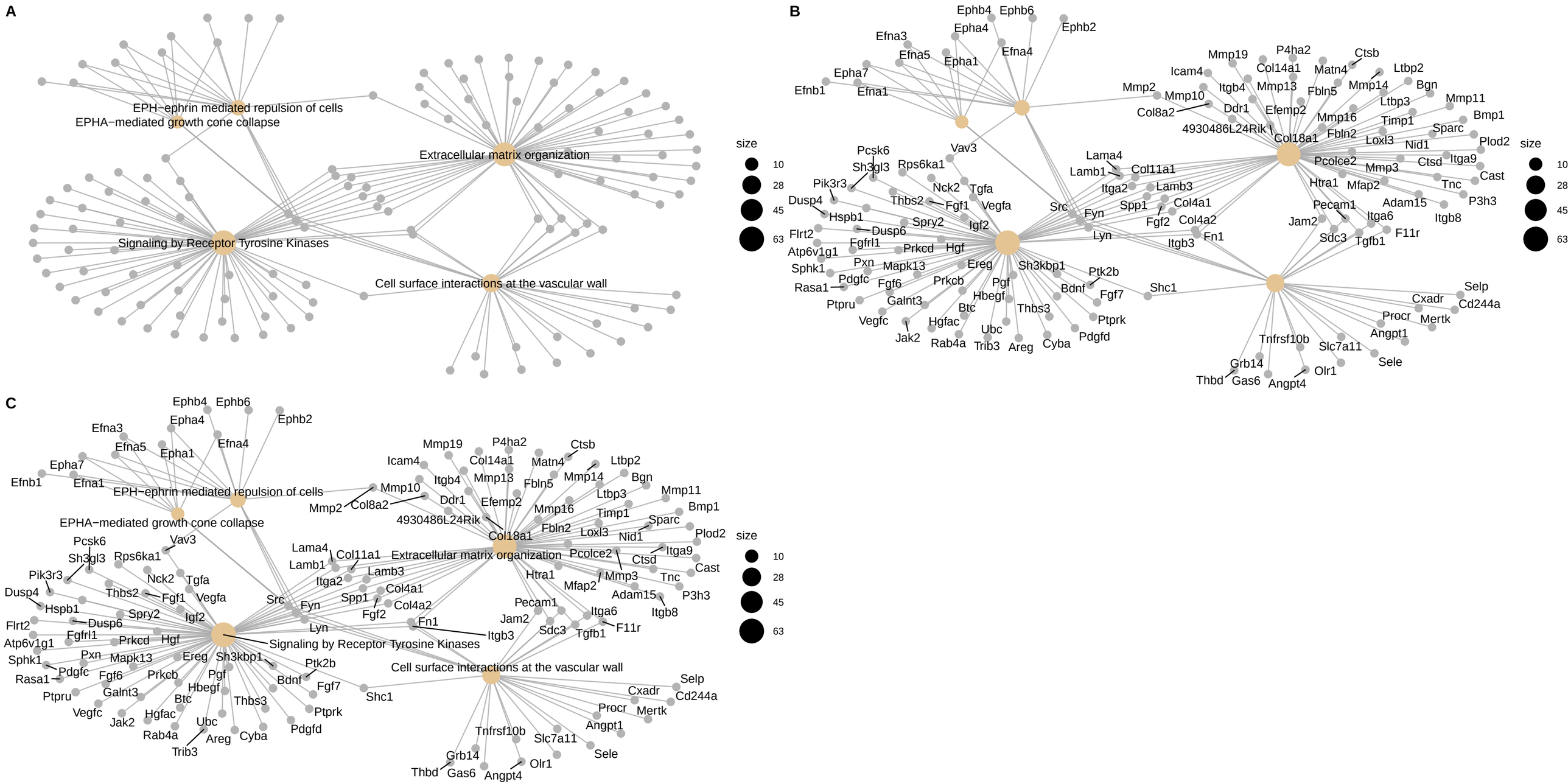
WITH DOWN GENES




WITH DOWN GENES
40
30
20
10
0
Signaling by Receptor Tyrosine Kinases
Extracellular matrix organization
Cell surface interactions at the vascular wall
Collagen formation
Cell−Cell communication
EPH−Ephrin signaling
Assembly of collagen fibrils and other multimeric structures
EPH−ephrin mediated repulsion of cells
EPHA−mediated growth cone collapse
Syndecan interactions


WITH DOWN GENES
Signaling by Receptor Tyrosine Kinases
Extracellular matrix organization
Cell surface interactions at the vascular wall
Collagen formation
Cell−Cell communication
EPH−Ephrin signaling
EPH−ephrin mediated repulsion of cells
Assembly of collagen fibrils and other multimeric structures
EPHA−mediated growth cone collapse
Syndecan interactions
0.02
0.04
0.06
0.08
GeneRatio
Count
20
40
60
p.adjust
0.0005
0.0010
0.0015
0.0020


WITH DOWN GENES
VEGFR2 mediated cell proliferation
Syndecan interactions
Signaling by Receptor Tyrosine Kinases
Signaling by EGFR
SHC1 events in EGFR signaling
Rho GTPase cycle
Platelet activation, signaling and aggregation
Non−integrin membrane−ECM interactions
Molecules associated with elastic fibres
Miscellaneous transport and binding events
Laminin interactions
Integrin cell surface interactions
GAB1 signalosome
Extracellular matrix organization
Extra−nuclear estrogen signaling
Ephrin signaling
EPHA−mediated growth cone collapse
EPH−Ephrin signaling
EPH−ephrin mediated repulsion of cells
Elastic fibre formation
EGFR downregulation
Degradation of the extracellular matrix
Collagen formation
Collagen degradation
Cell−cell junction organization
Cell−Cell communication
Cell surface interactions at the vascular wall
Cell junction organization
Axon guidance
Assembly of collagen fibrils and other multimeric structures
fold change
0.04
0.03
0.02
0.01


A
EPH−ephrin mediated repulsion of cells
EPHA−mediated growth cone collapse
Extracellular matrix organization
Signaling by Receptor Tyrosine Kinases
Cell surface interactions at the vascular wall
B
size
10
28
45
63
C