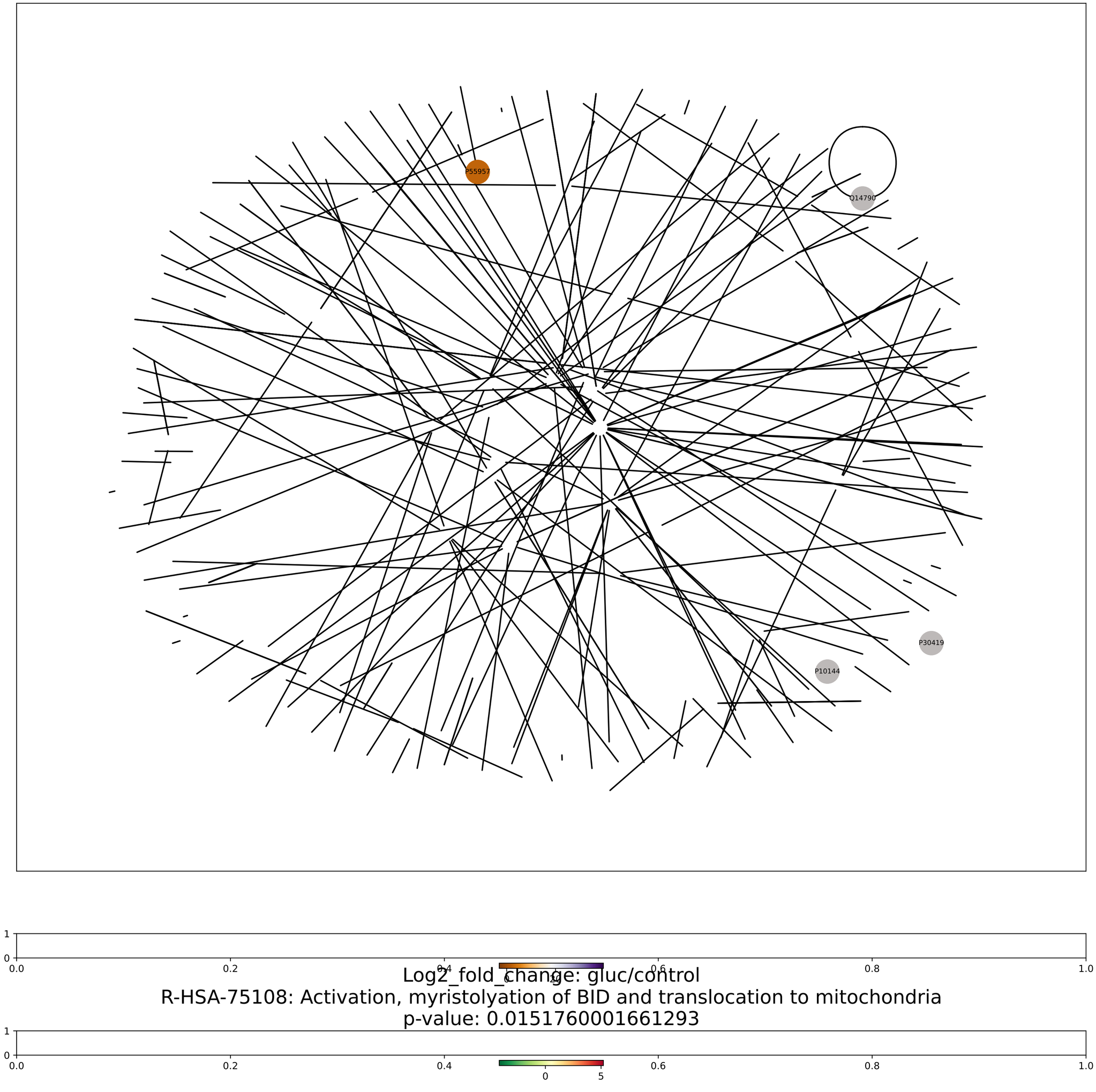
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Q14790
P30419
P10144
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0.2
0.4
0.6
0.8
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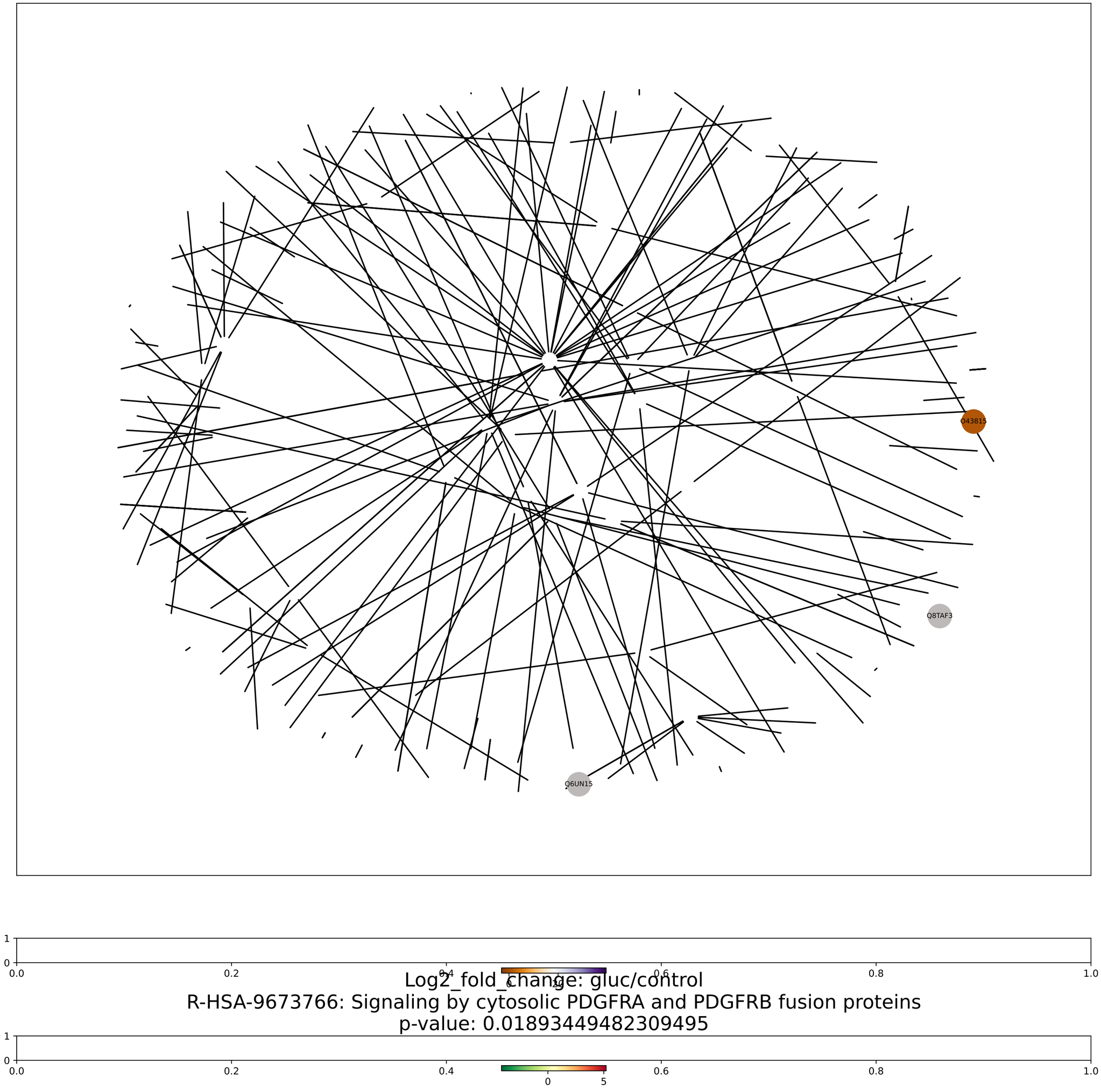
Log2_fold_change: gluc/control
R-HSA-75108: Activation, myristolyation of BID and translocation to mitochondria
p-value: 0.0151760001661293
0
5


O43815
Q8TAF3
Q6UN15
1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5
Log2_fold_change: gluc/control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.01893449482309495
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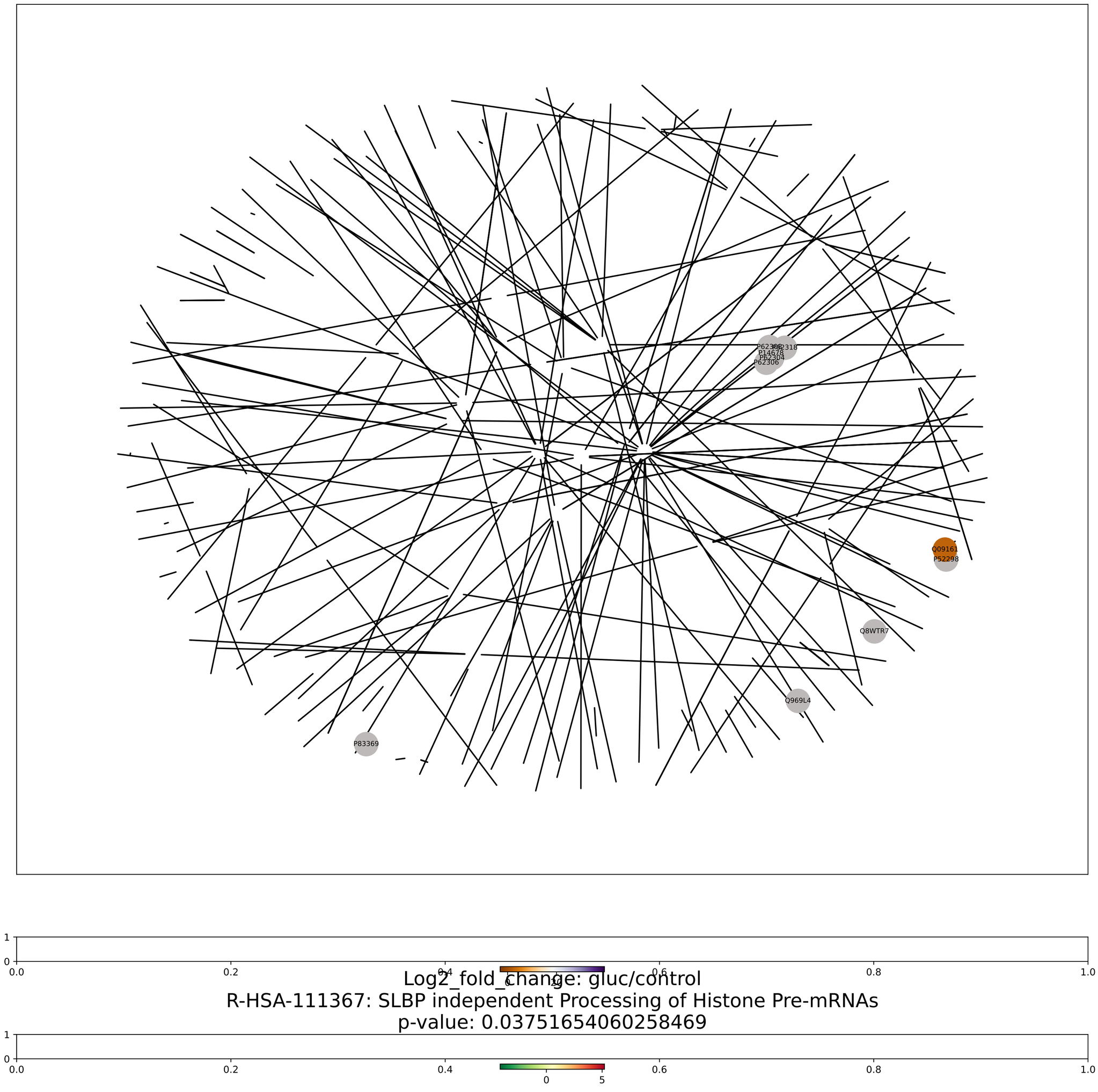
0.6
0.8
1.0
0
5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P62304
P62306
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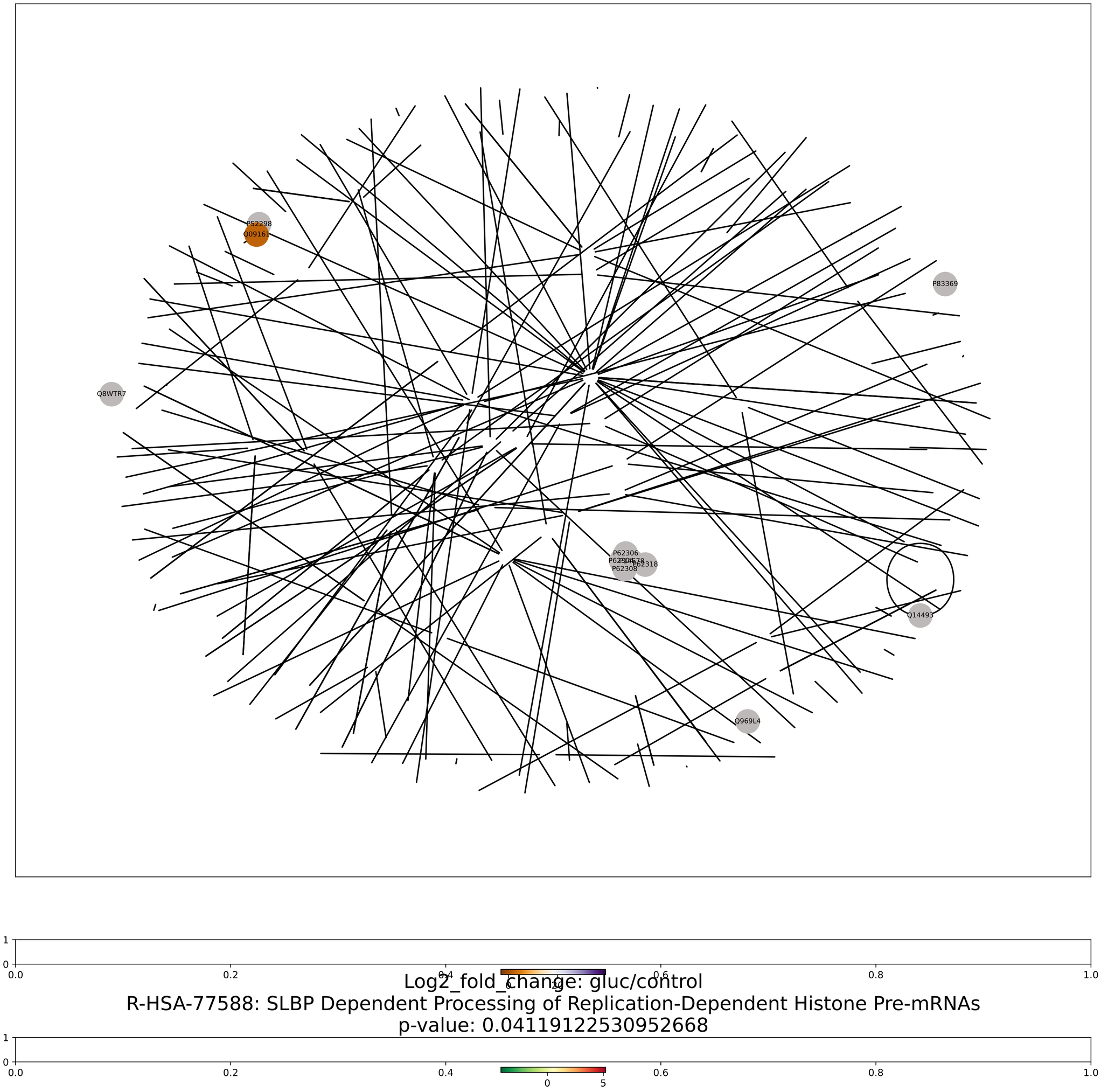
P52298
Q8WTR7
Q969L4
P83369
1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5
Log2_fold_change: gluc/control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03751654060258469
1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5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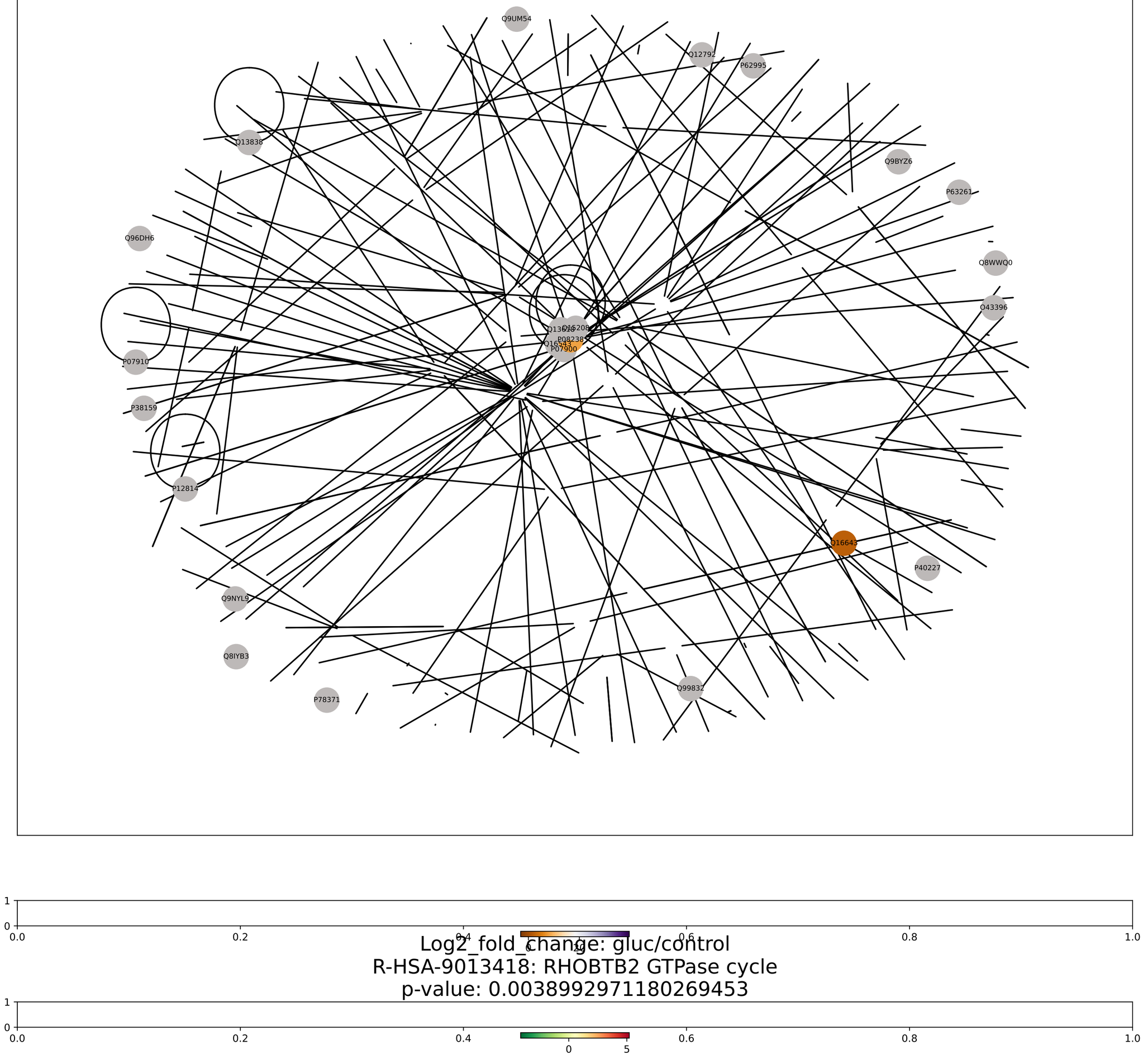
O09161
P83369
Q8WTR7
P62306
P62318
P62308
O14493
O969L4
0.0
0.2
0.4
0.6
0.8
1.0
0
5
Log2_fold_change: gluc/control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04119122530952668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Q12792
P62995
Q13838
Q9BYZ6
P63261
Q96DH6
Q8WWQ0
O43396
Q13618
P08238
P07900
P07910
P38159
P12814
Q16643
P40227
Q9NYL9
Q8IYB3
Q99832
P78371
1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5
Log2_fold_change: gluc/control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.0038992971180269453
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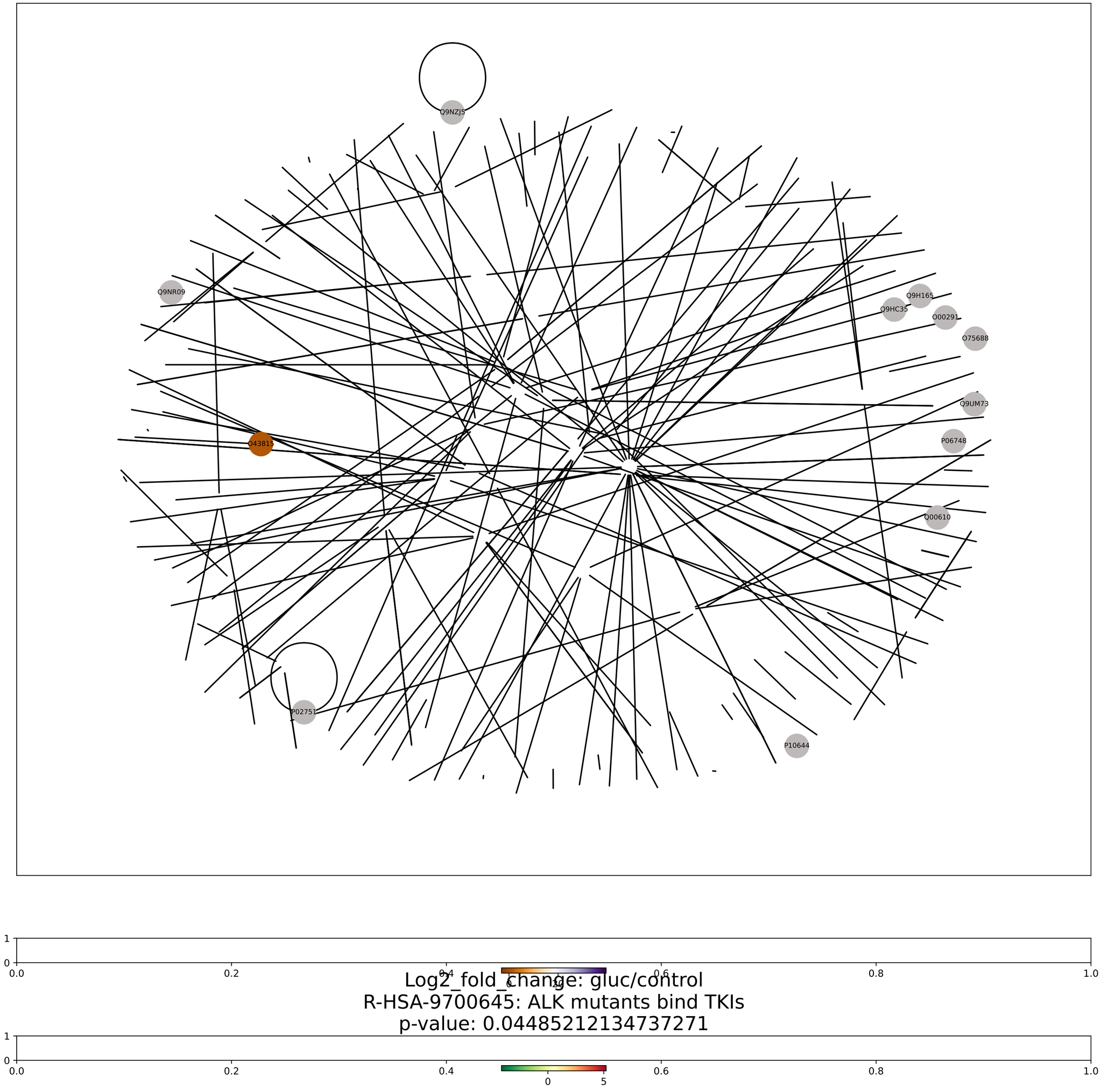
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5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Q9NR09
Q9H165
Q9HC35
O00291
O75688
Q9UM73
O43815
P06748
O00610
P02751
P10644
1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
20
Log2_fold_change: gluc/control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04485212134737271
1
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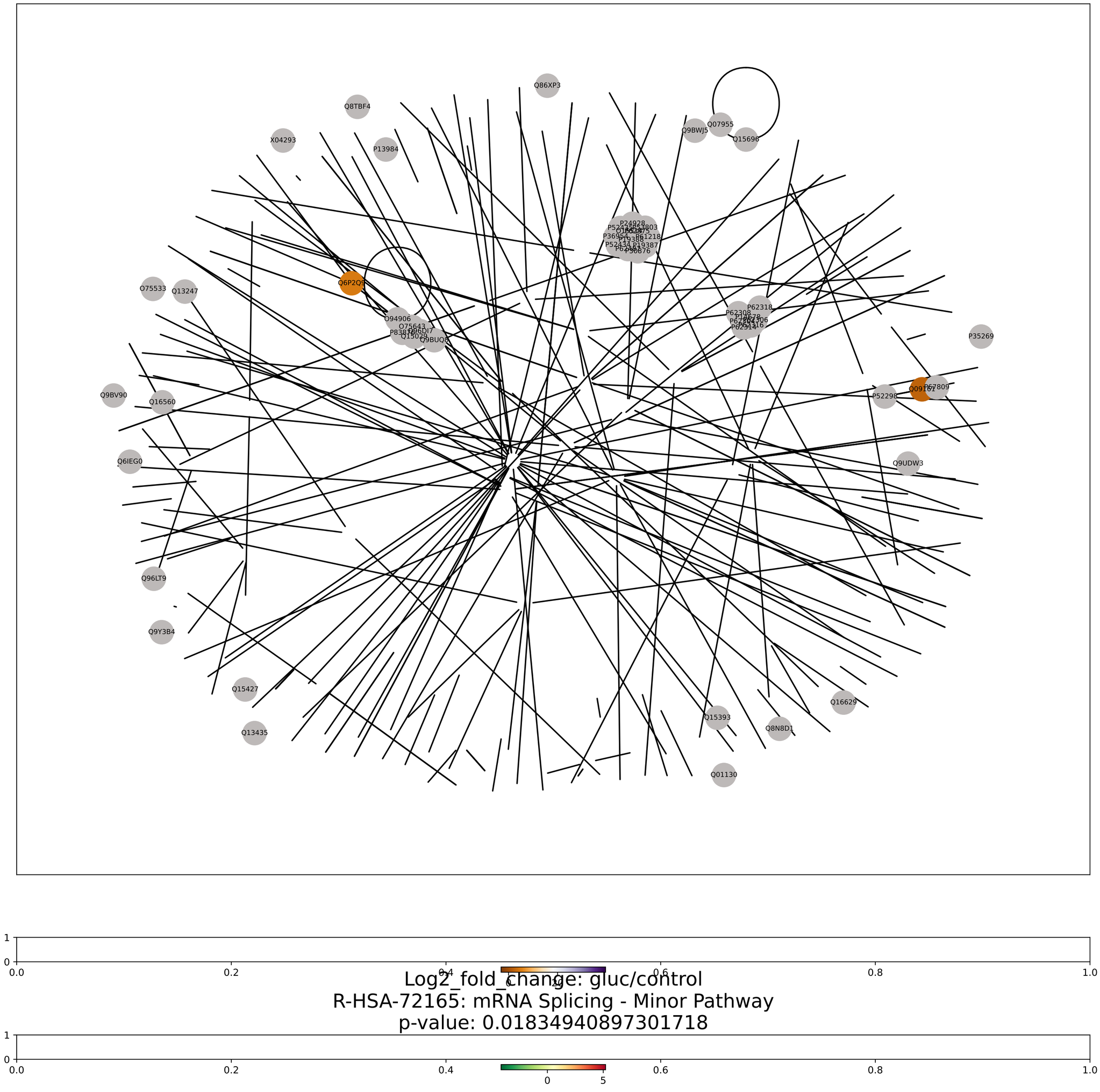
0.0
0.2
0.4
0.6
0.8
1.0
0
5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Q15029
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P35269
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Q9UDW3
Q96LT9
Q9Y3B4
Q15427
Q13435
Q16629
Q15393
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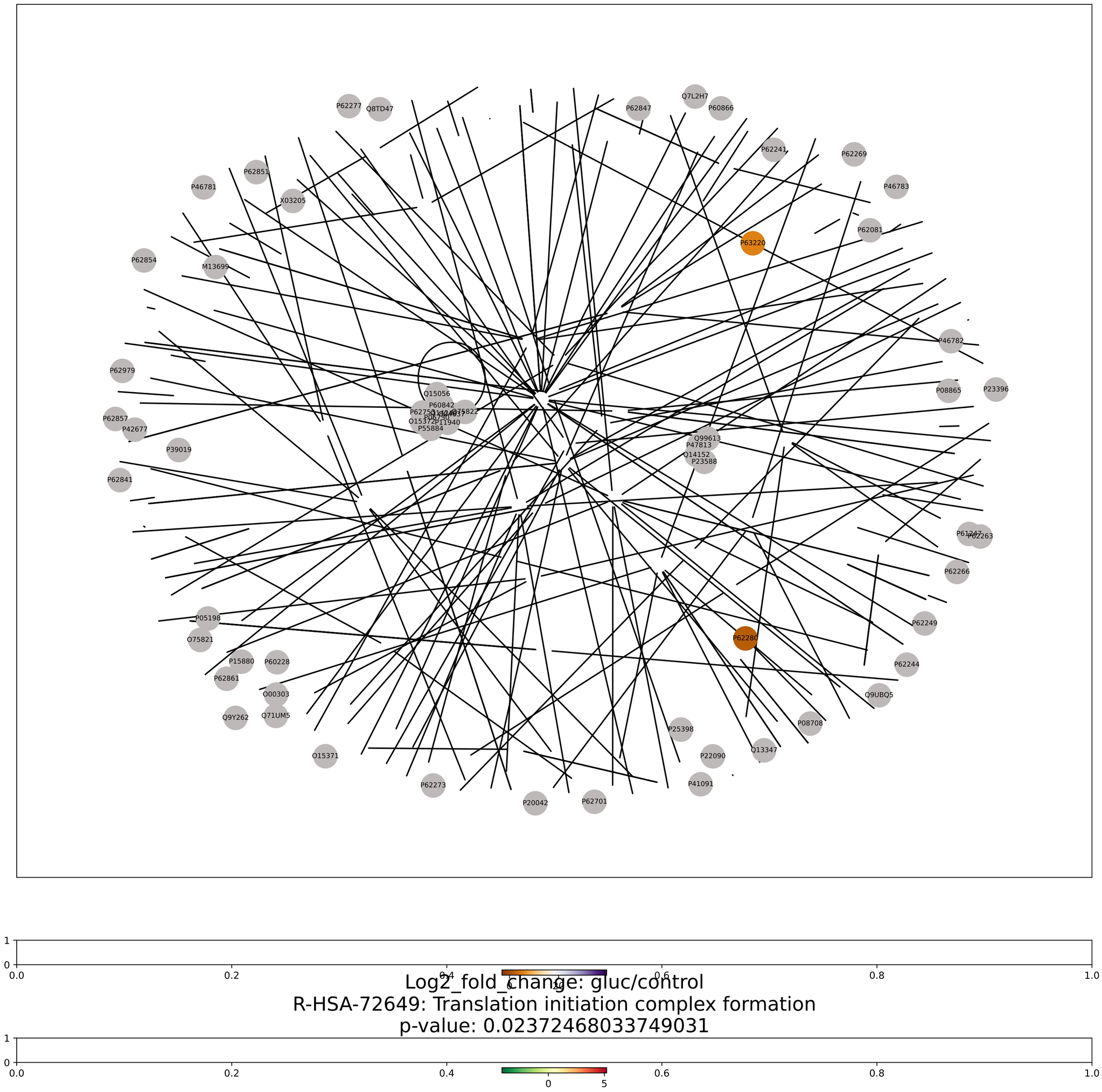
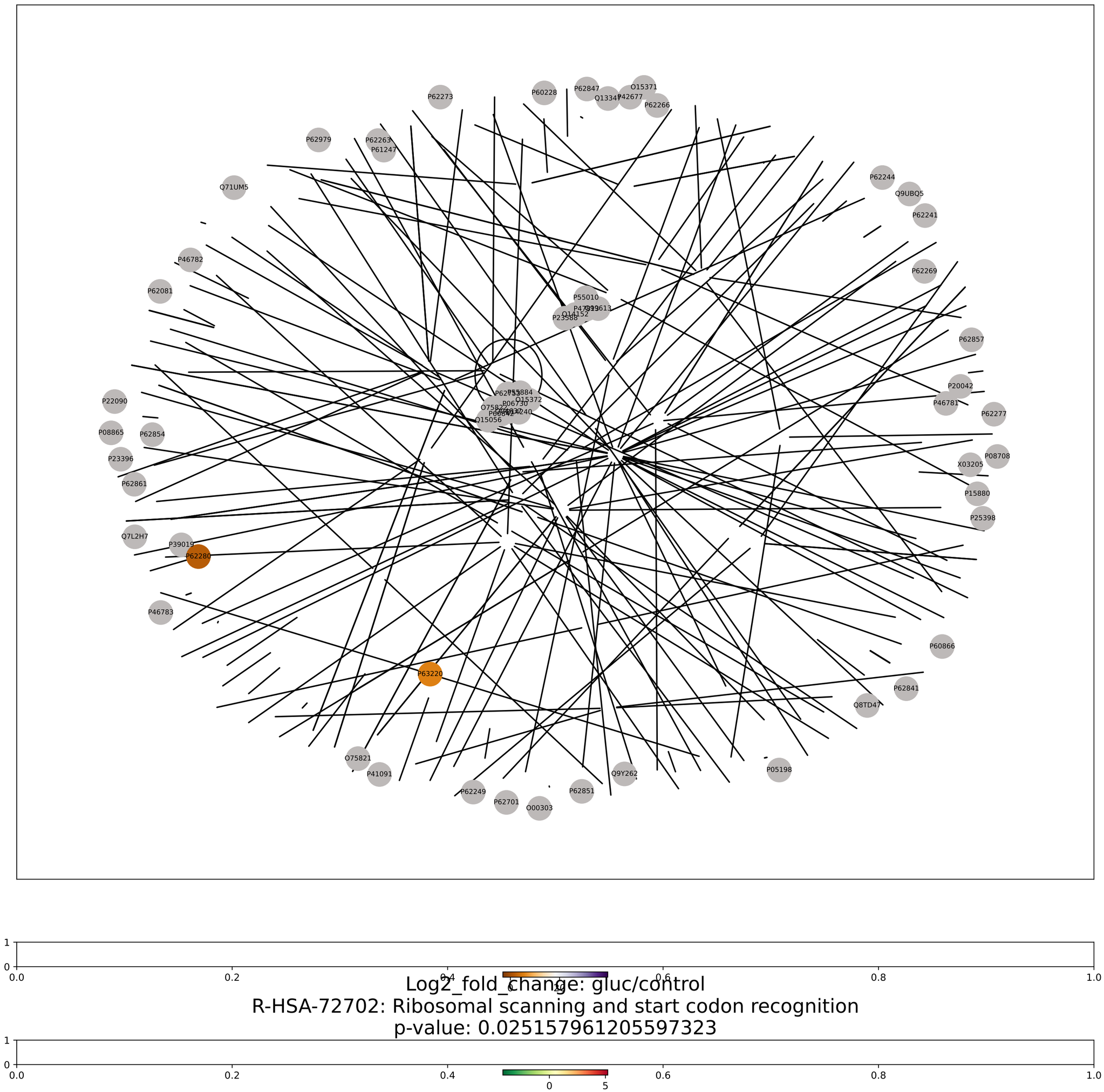
Q01130
Log2_fold_change: gluc/control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.01834940897301718



Log2_fold_change: gluc/control
R-HSA-72649: Translation initiation complex formation
p-value: 0.02372468033749031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Q9UBQ5
P62241
P46782
P62269
P62081
P55010
P47929
P19613
Q14152
P23588
P62857
P20042
P62753
P53884
O15372
P06730
O75822
P60842
P62240
Q15056
P46781
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P22090
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P62854
P23396
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P15880
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Q9Y262
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P62851
P62701
O00303

1
0
0.0
0.2
0.4
0.6
0.8
1.0
0
5
Log2_fold_change: gluc/control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.025157961205597323
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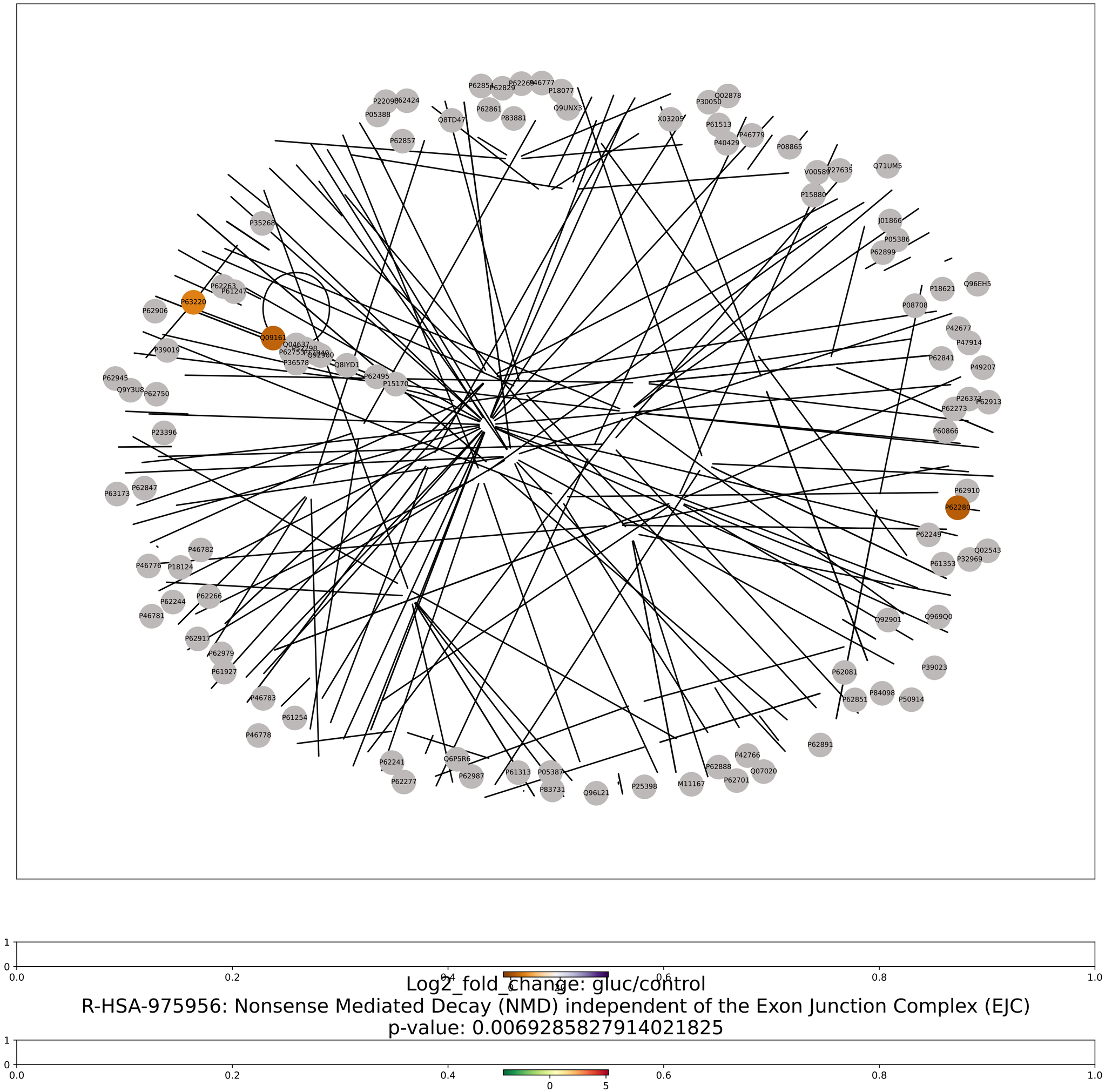
1.0
0
5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M11167

1
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0.4
0.6
0.8
1.0
0
2
Log2_fold_change: gluc/control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.0069285827914021825
1
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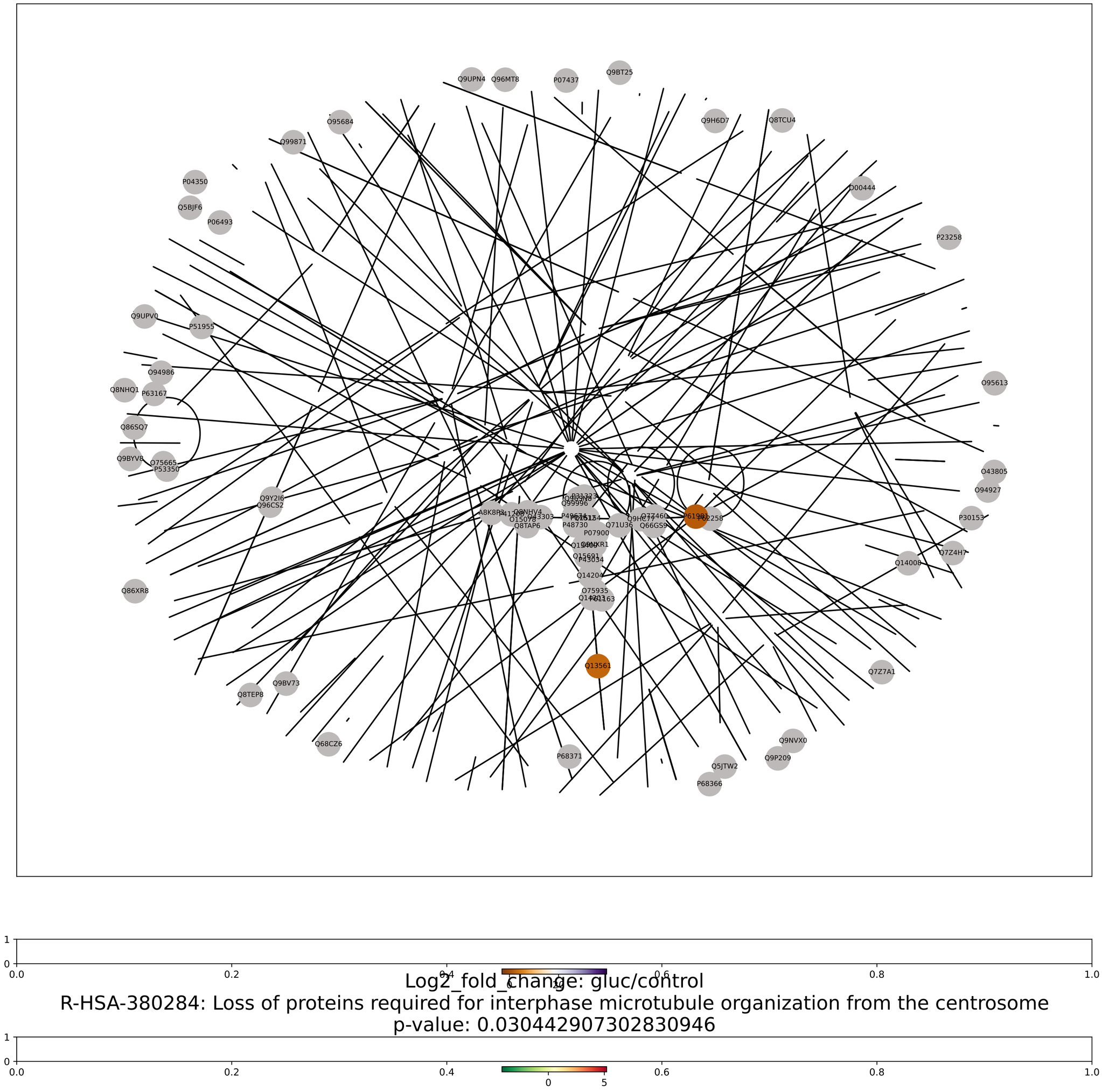
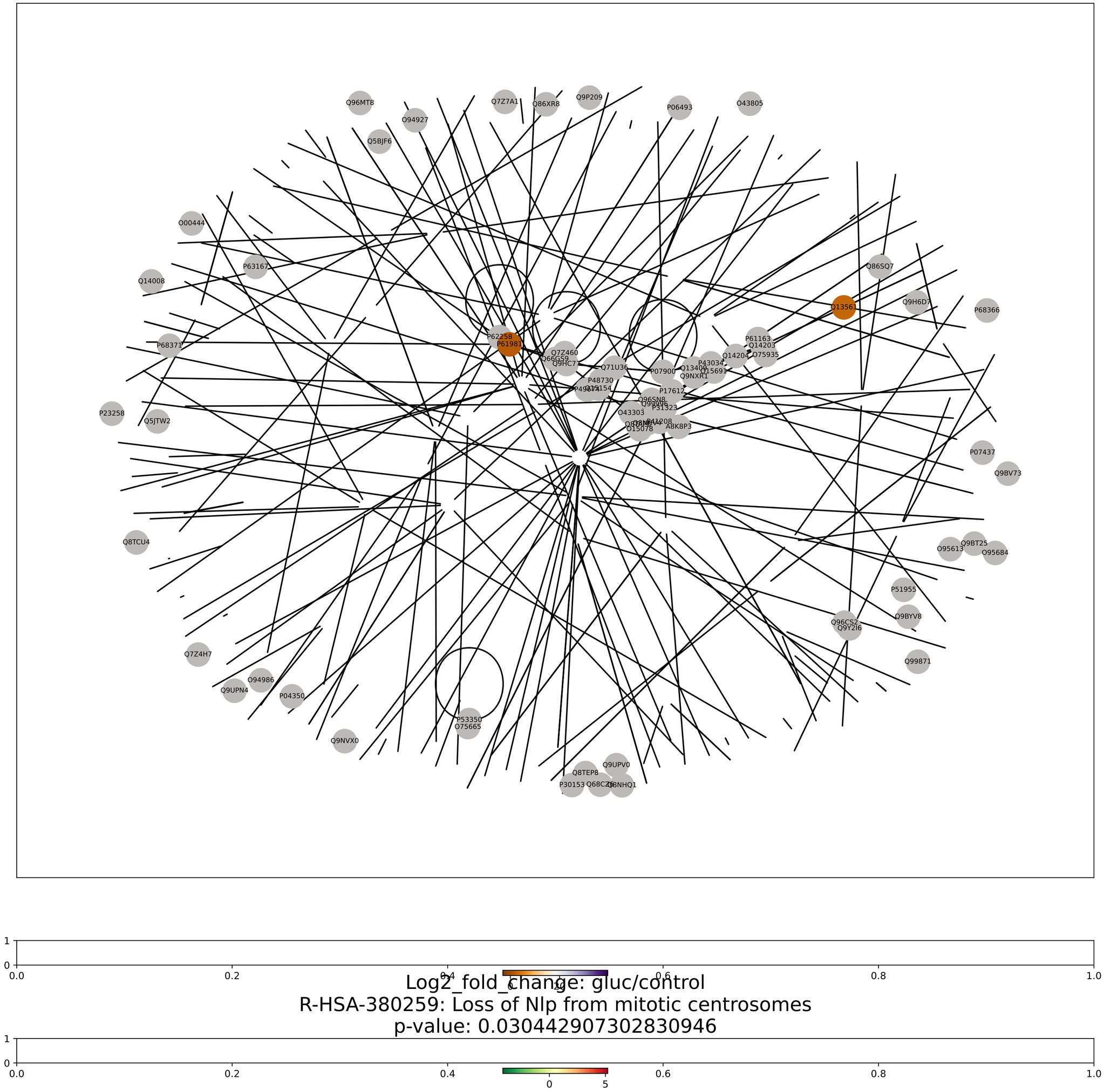
0.4
0.6
0.8
1.0
0
5



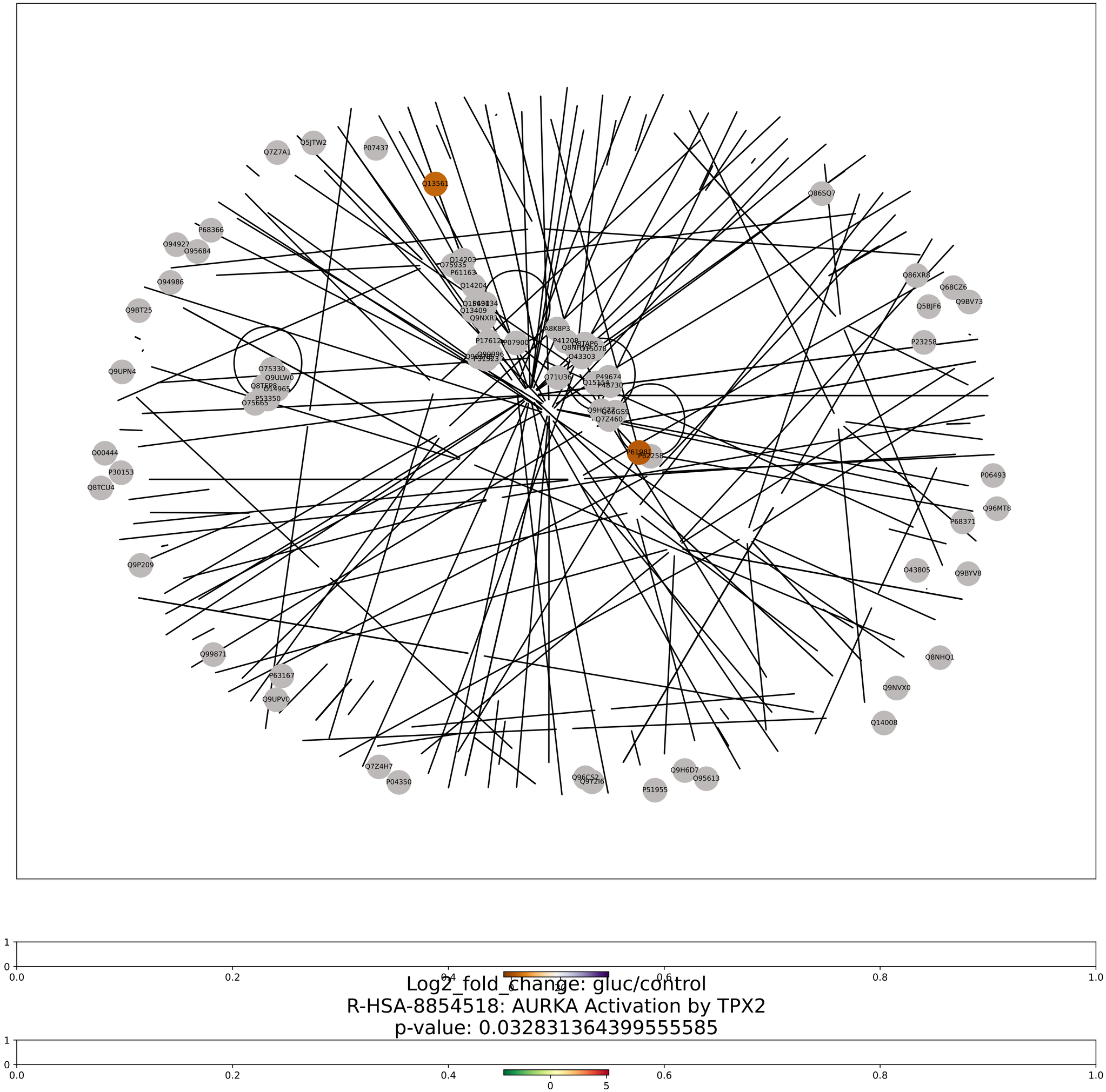
Log2_fold_change: gluc/control

R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome

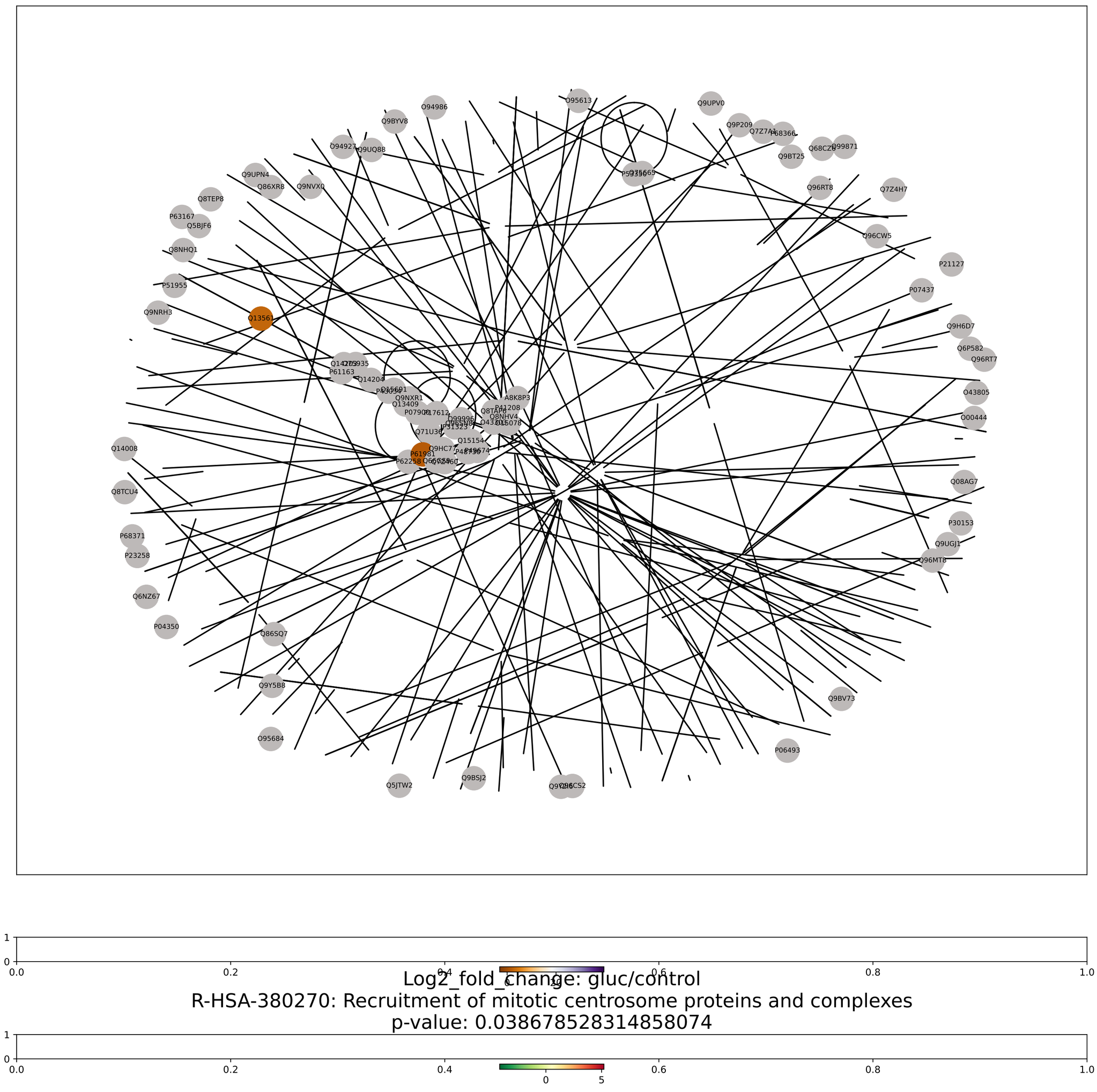
p-value: 0.030442907302830946



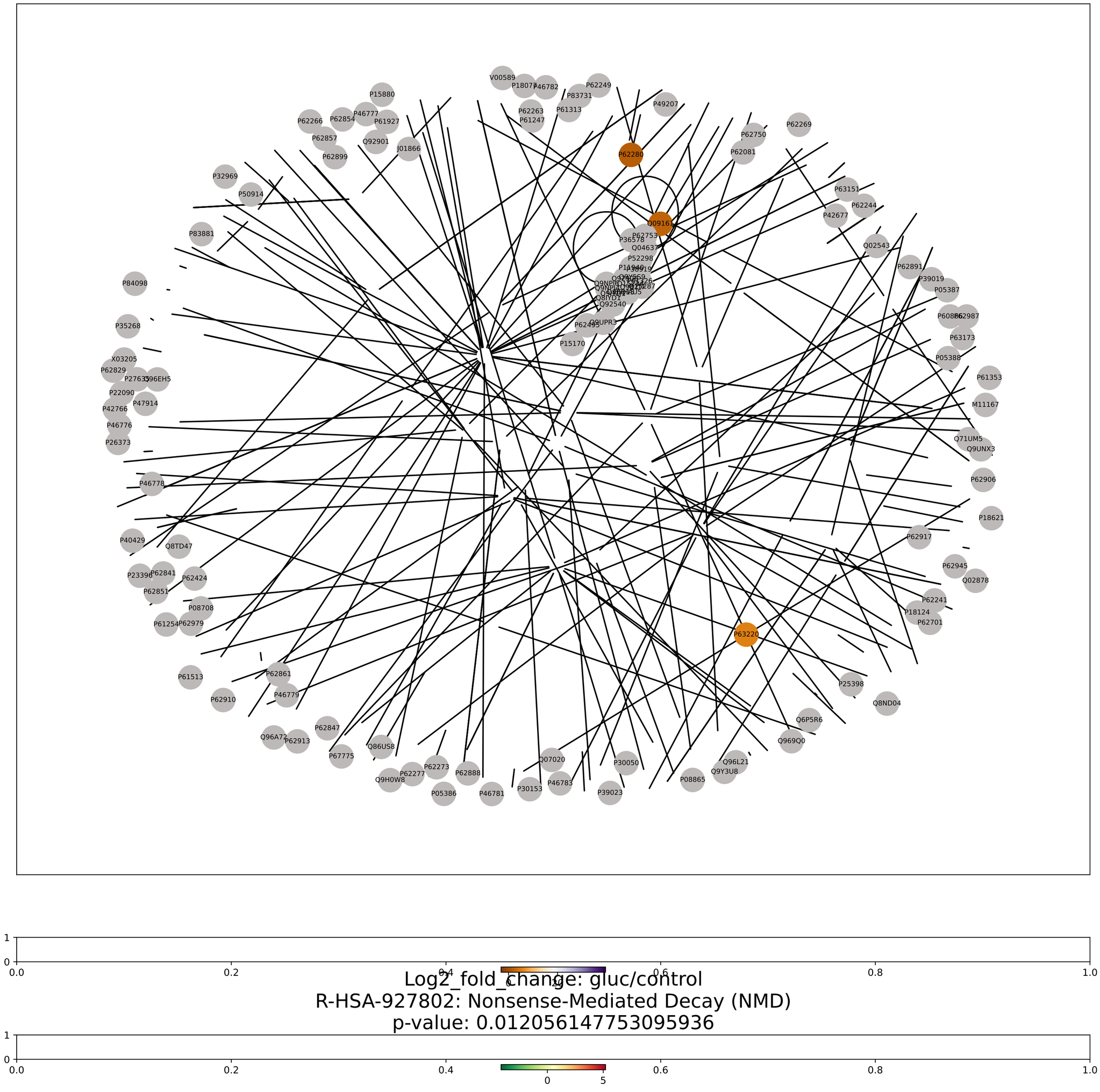
Log2_fold_change: gluc/control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030442907302830946



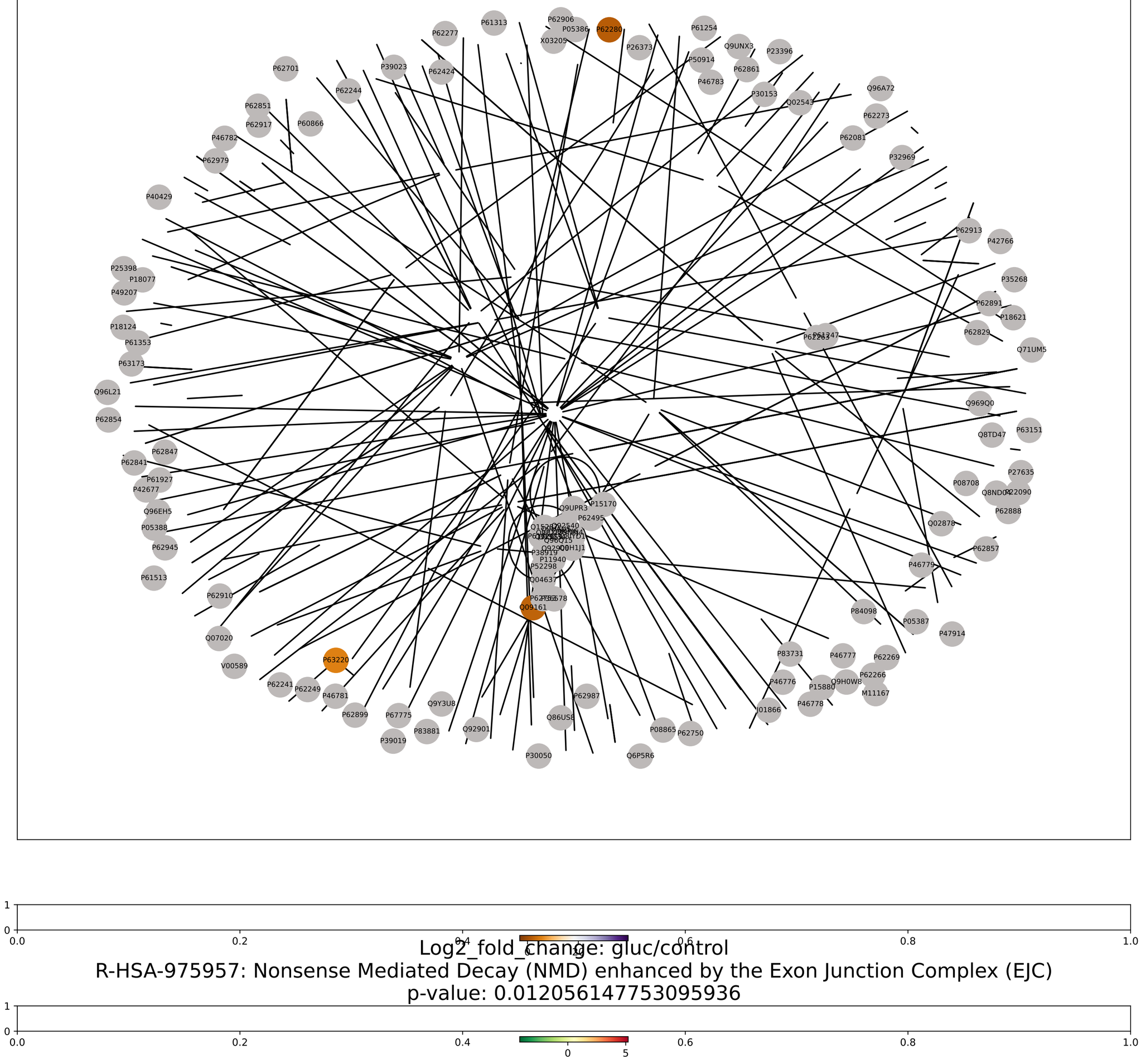
Log2_fold_change: gluc/control
R-HSA-8854518: AURKA Activation by TPX2
p-value: 0.032831364399555585



Log2_fold_change: gluc/control
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes
p-value: 0.038678528314858074



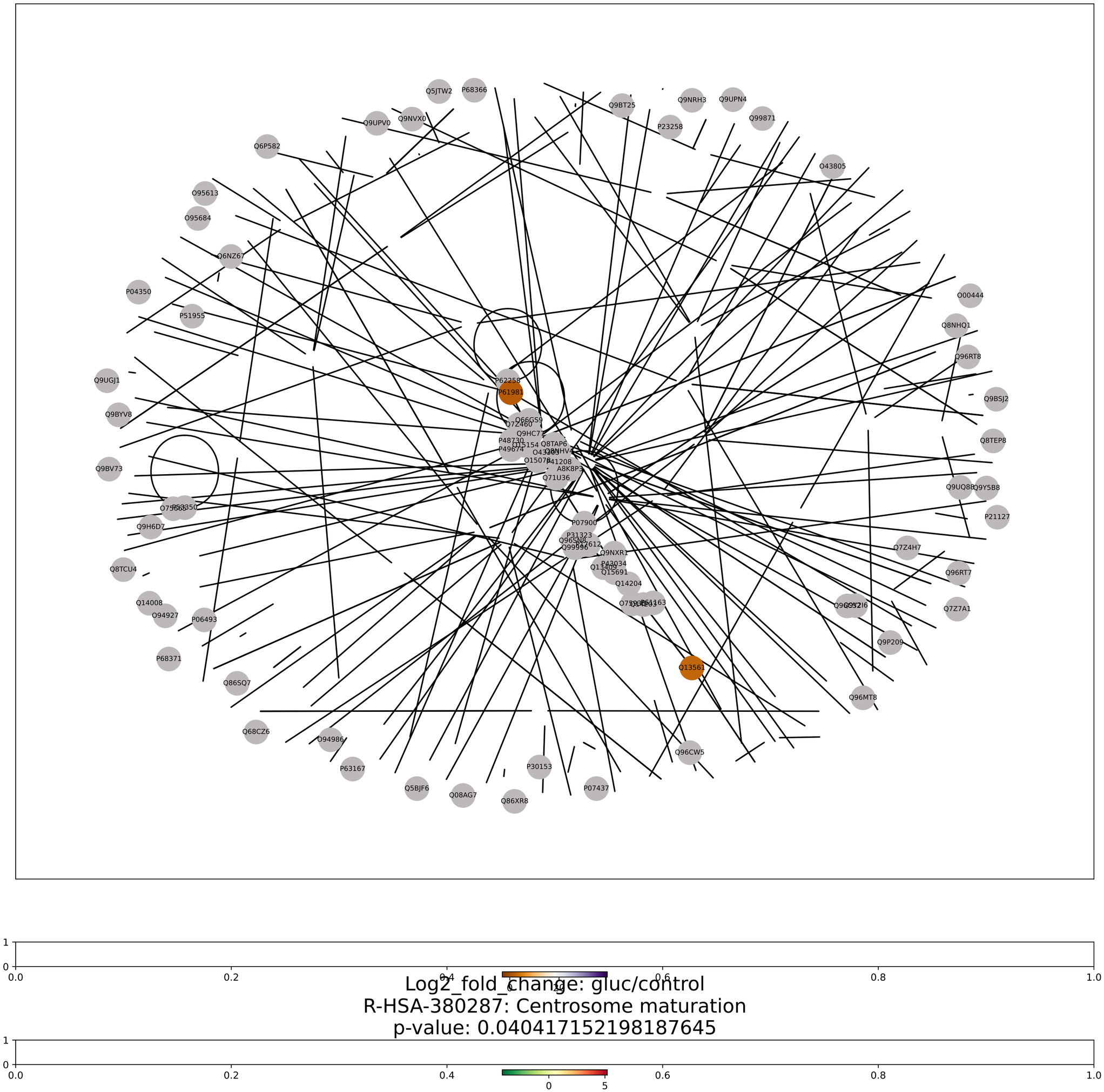
Log2_fold_change: gluc/control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.012056147753095936



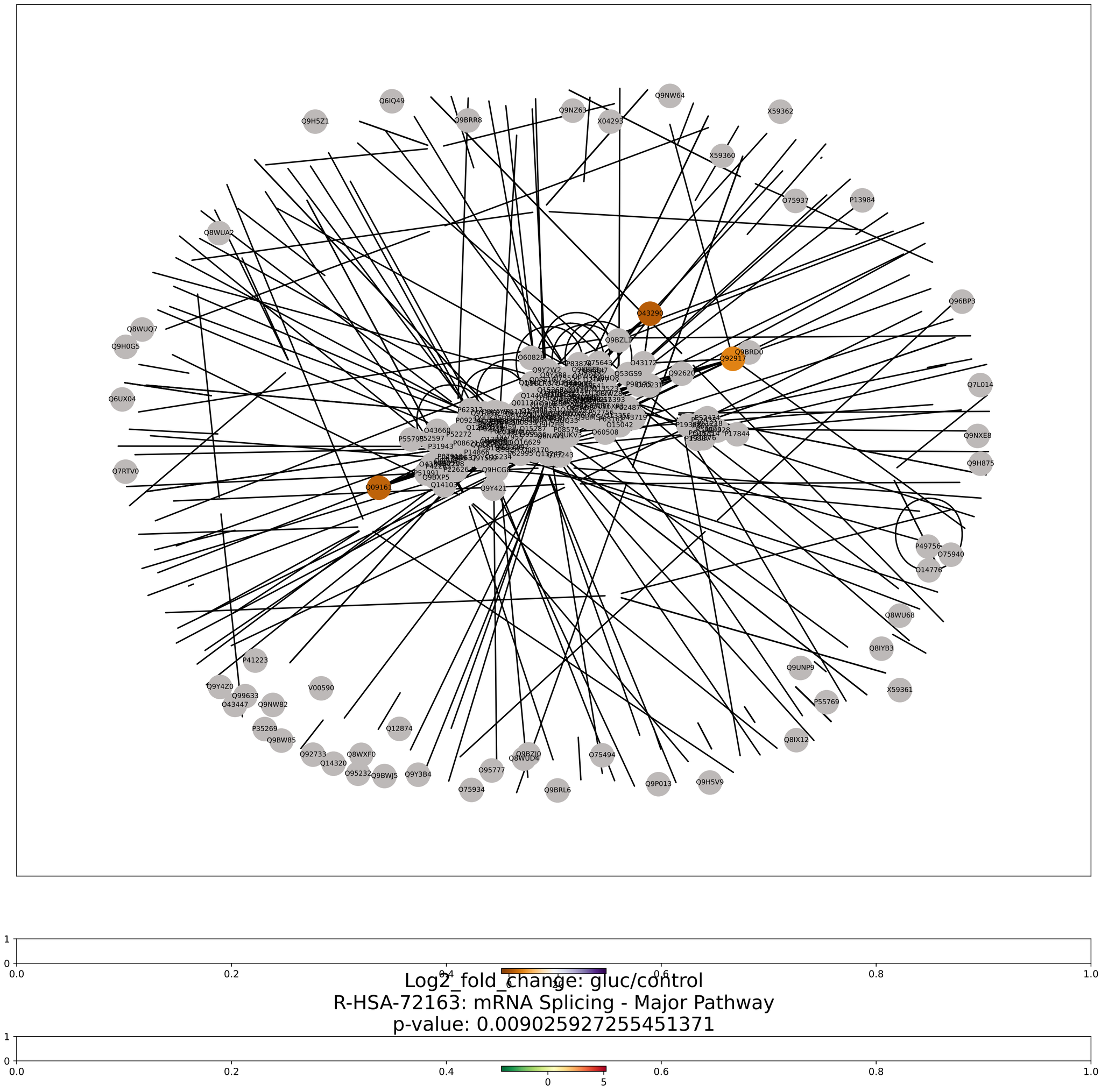
Log2_fold_change: gluc/control

R-HSA-975957: Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)

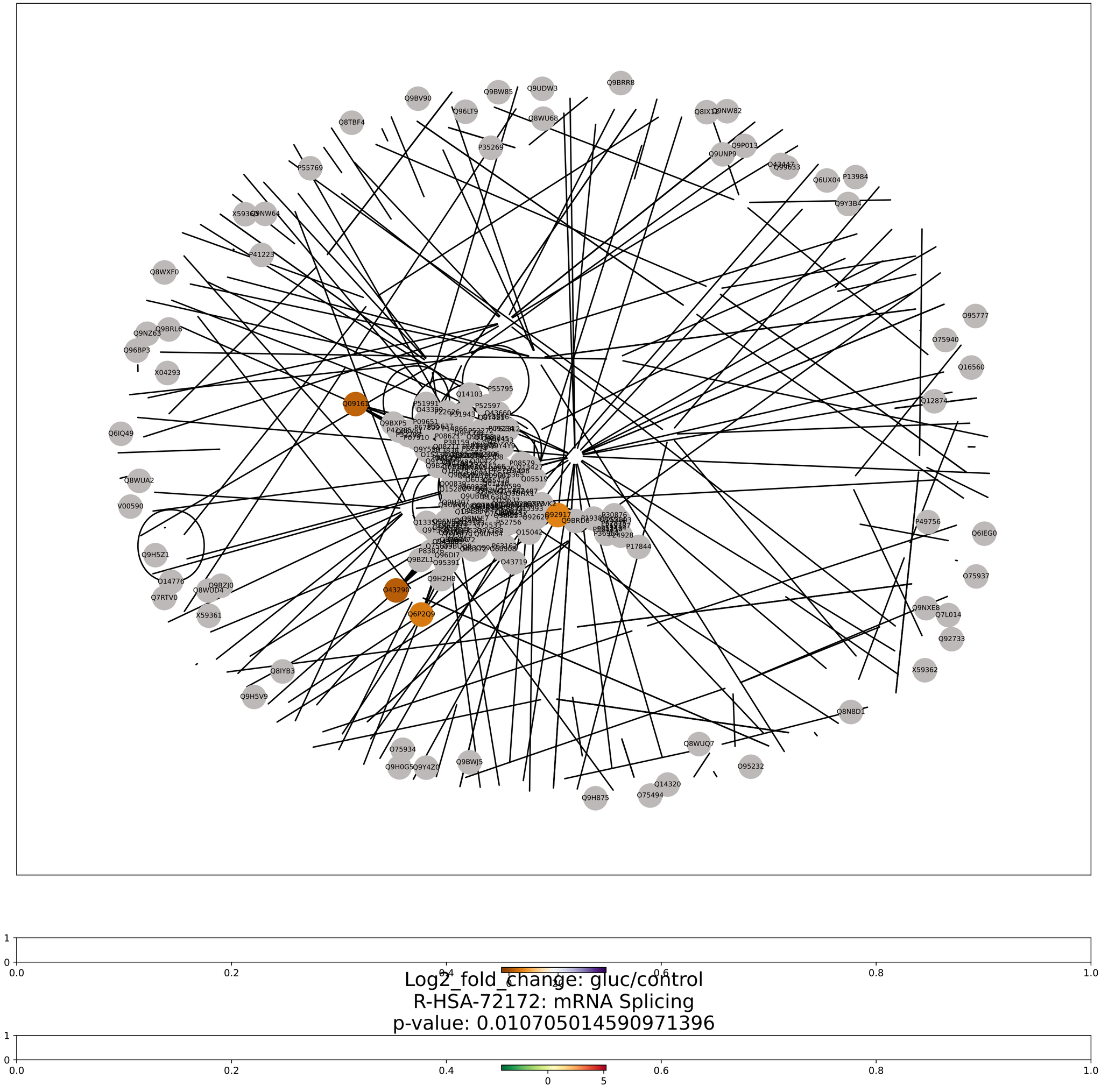
p-value: 0.012056147753095936



Log2_fold_change: gluc/control
R-HSA-380287: Centrosome maturation
p-value: 0.040417152198187645



Log2_fold_change: gluc/control
R-HSA-72163: mRNA Splicing - Major Pathway
p-value: 0.009025927255451371


Log2_fold_change: gluc/control
R-HSA-72172: mRNA Splicing
p-value: 0.010705014590971396