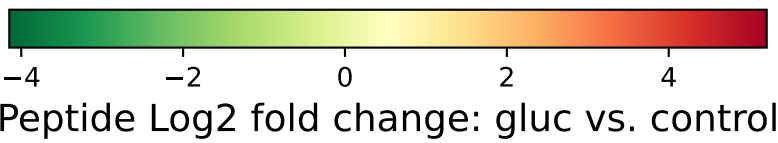
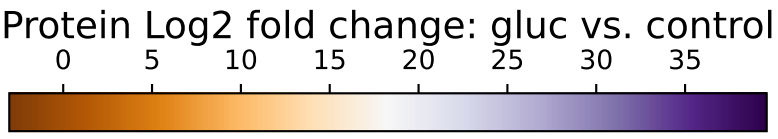
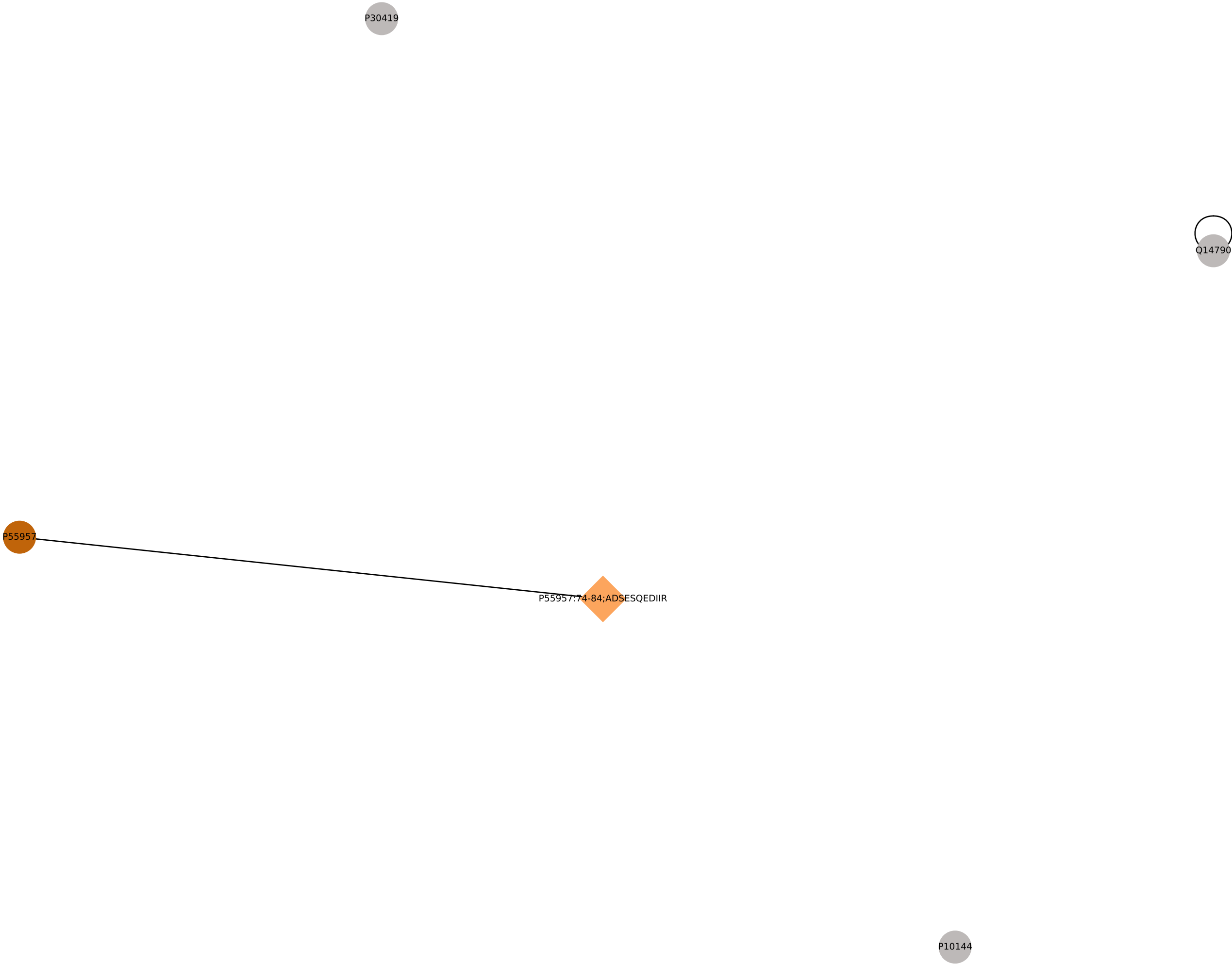
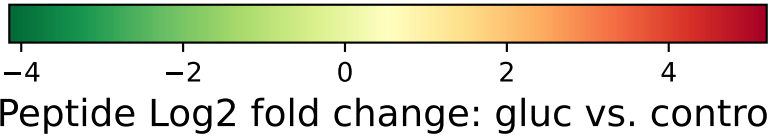
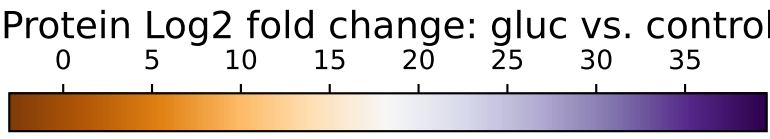
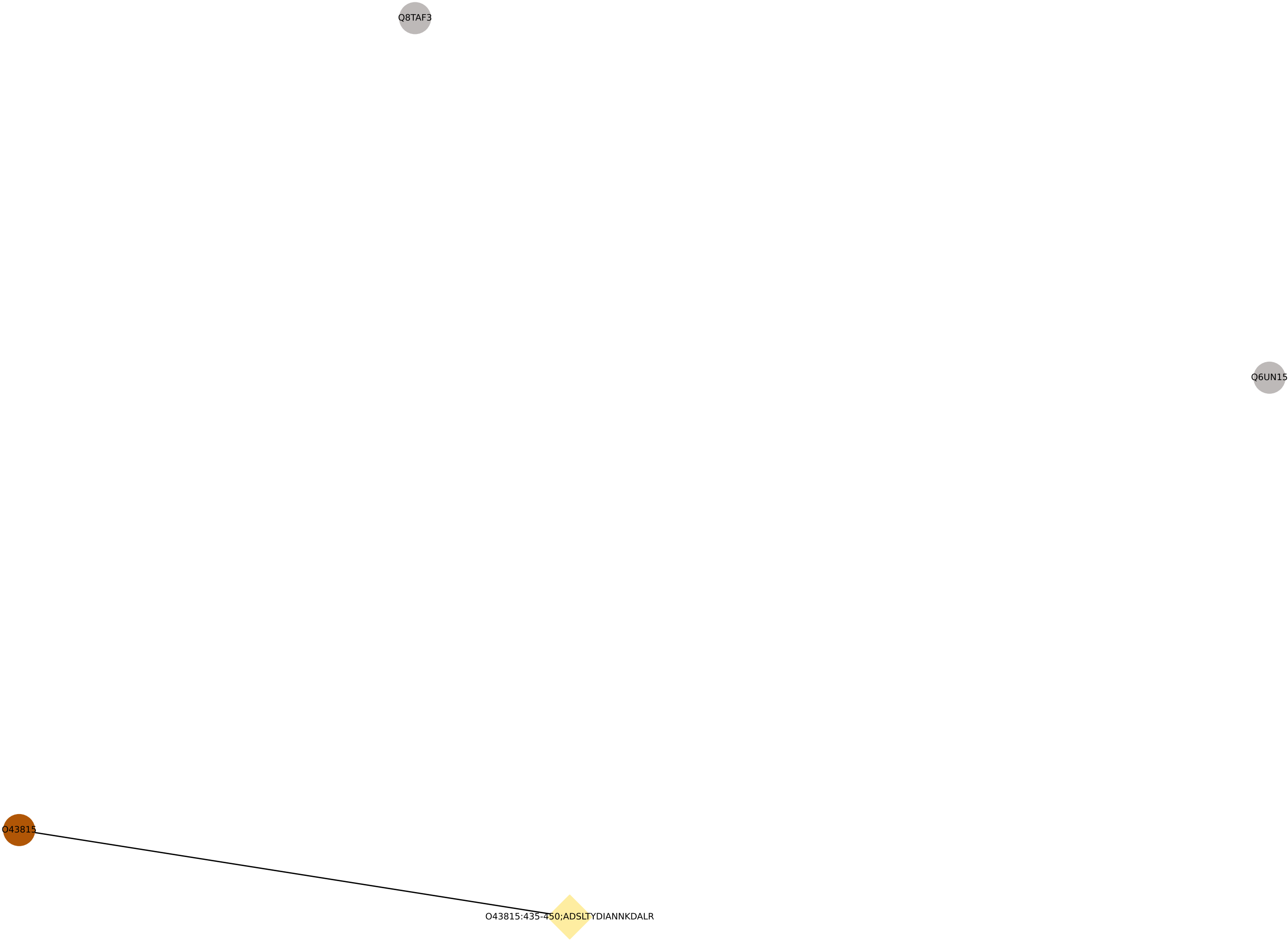


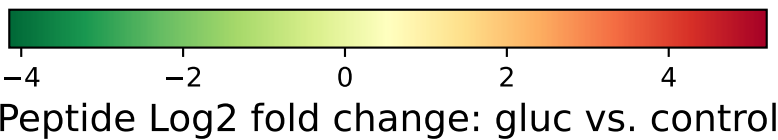
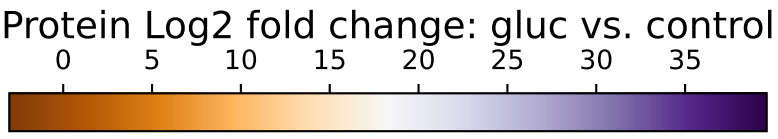
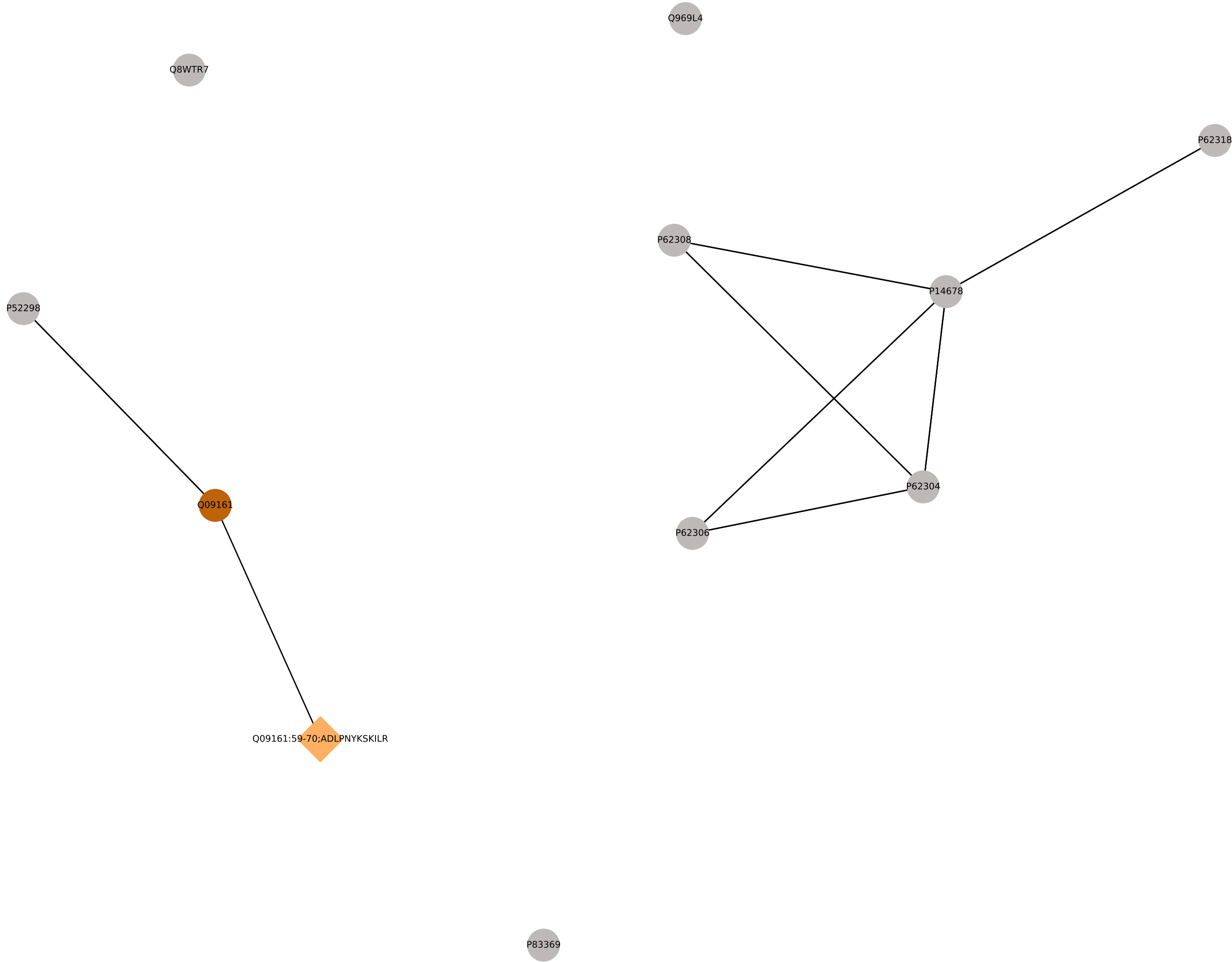
Log2 fold change: gluc vs. control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.015117656007649471



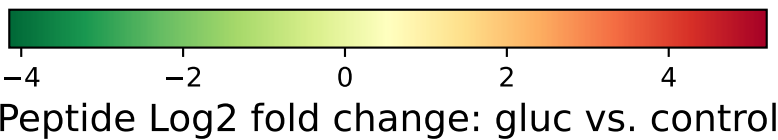
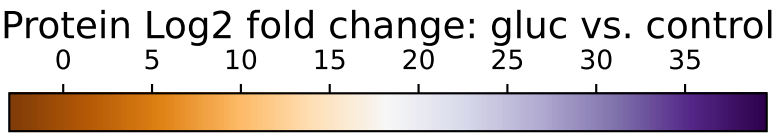
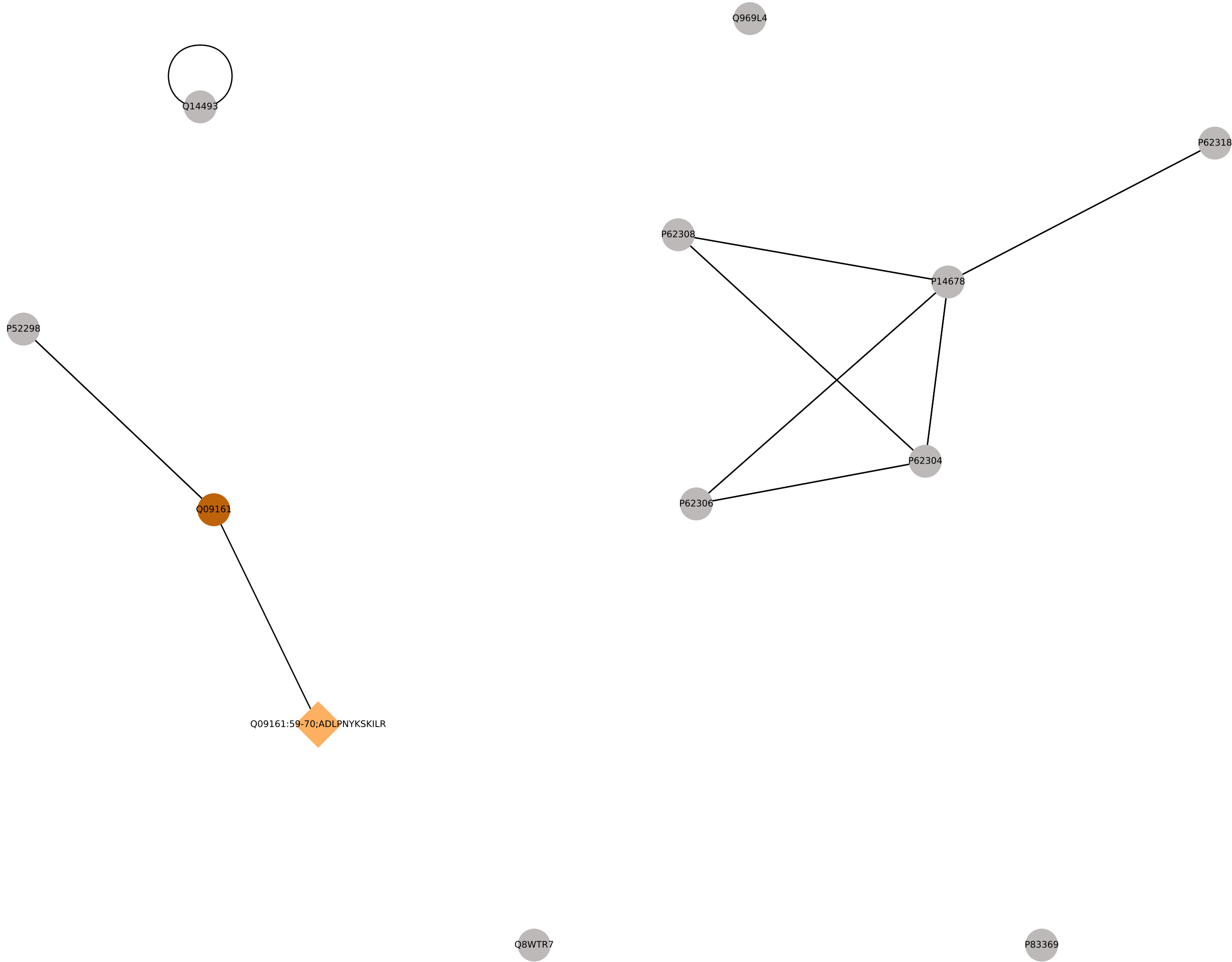
Log2 fold change: gluc vs. control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.018861837637962453



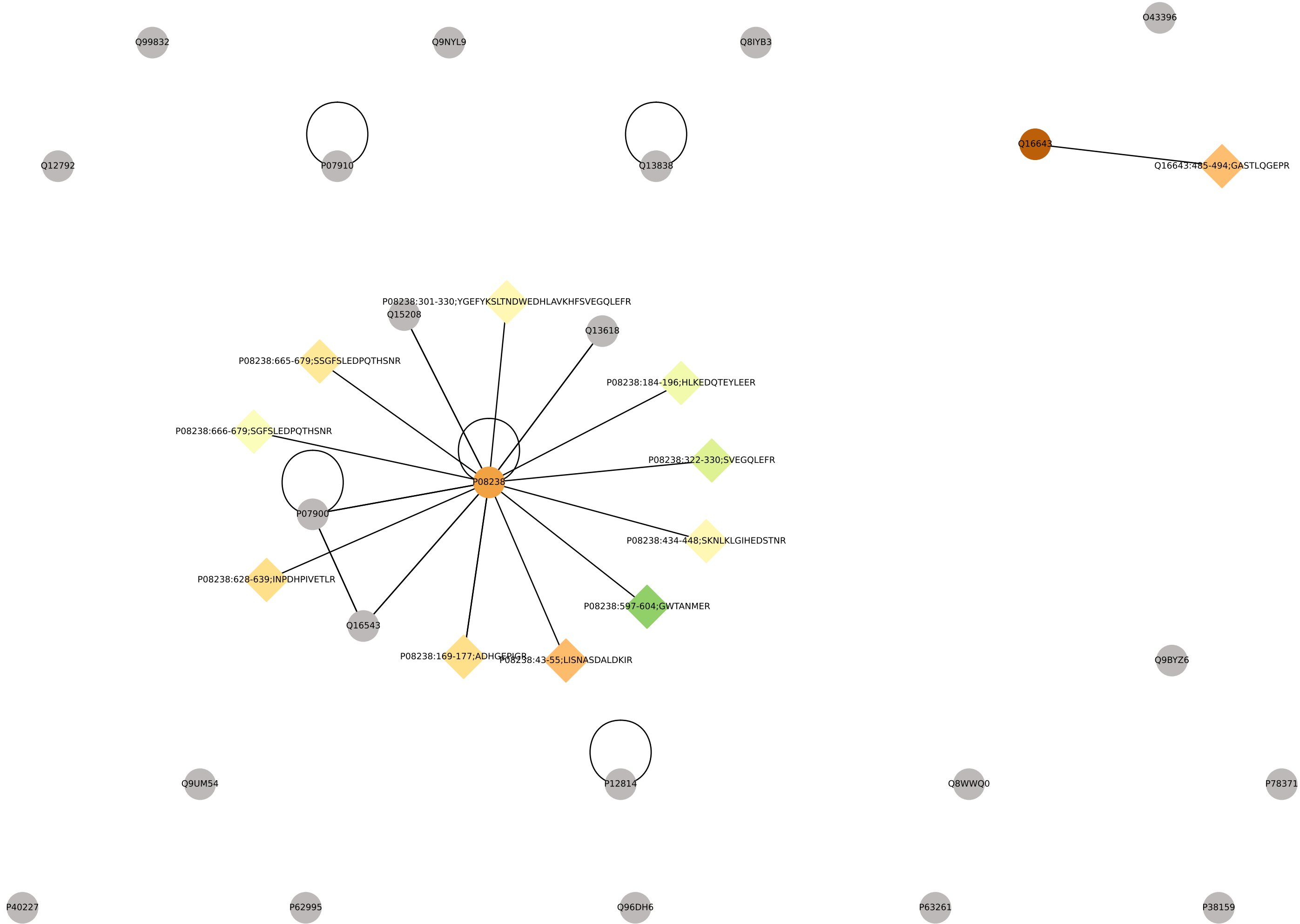
Log2 fold change: gluc vs. control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03737392638204595



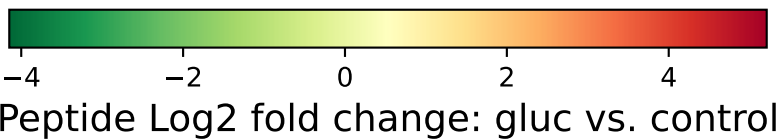
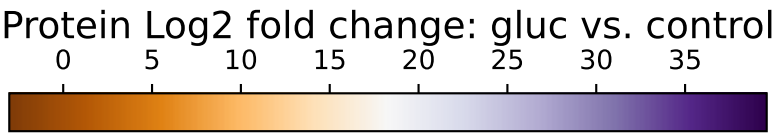
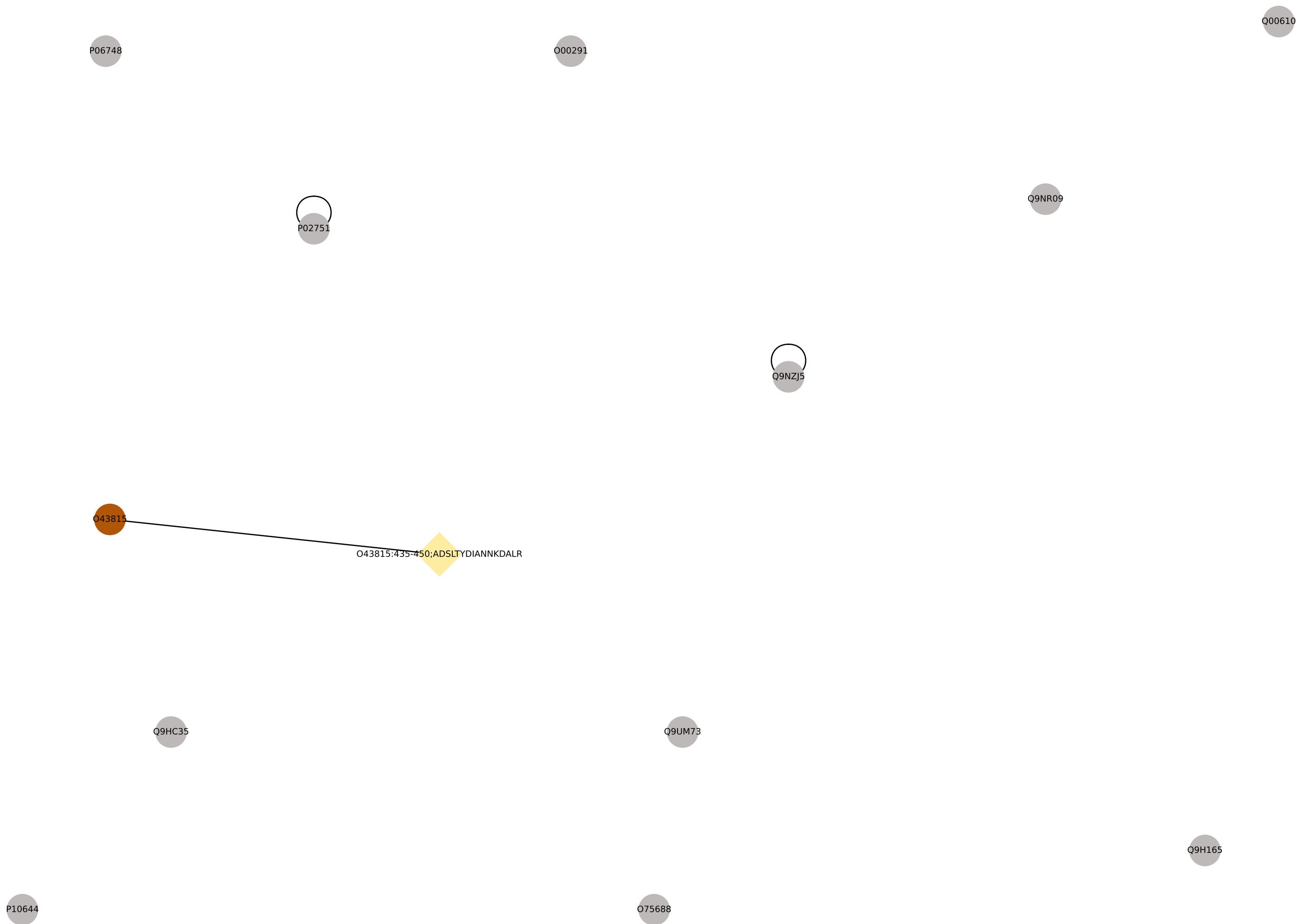
Log2 fold change: gluc vs. control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04103493715974438



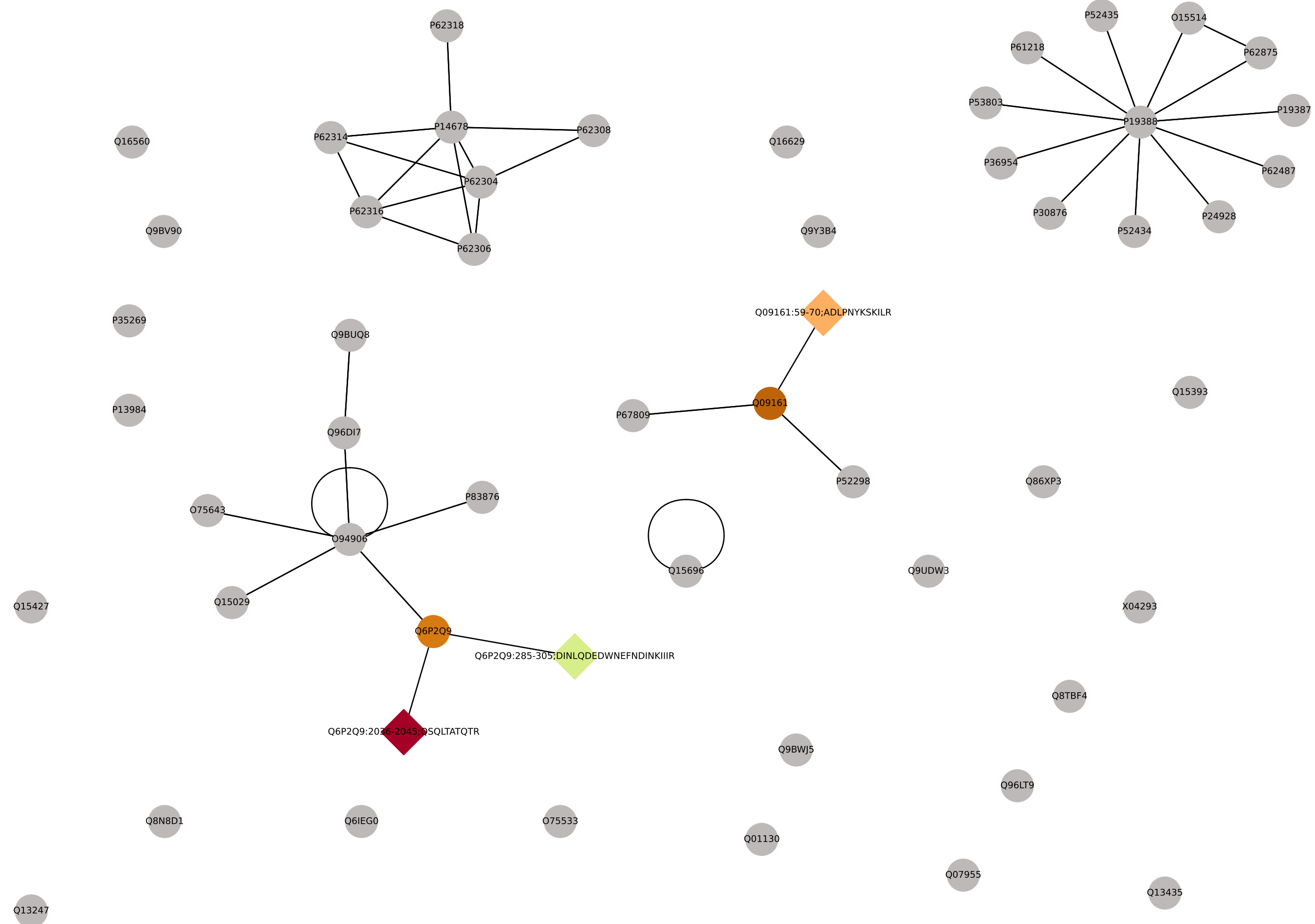
Log2 fold change: gluc vs. control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.003870027935771292



Log2 fold change: gluc vs. control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04468226372702311

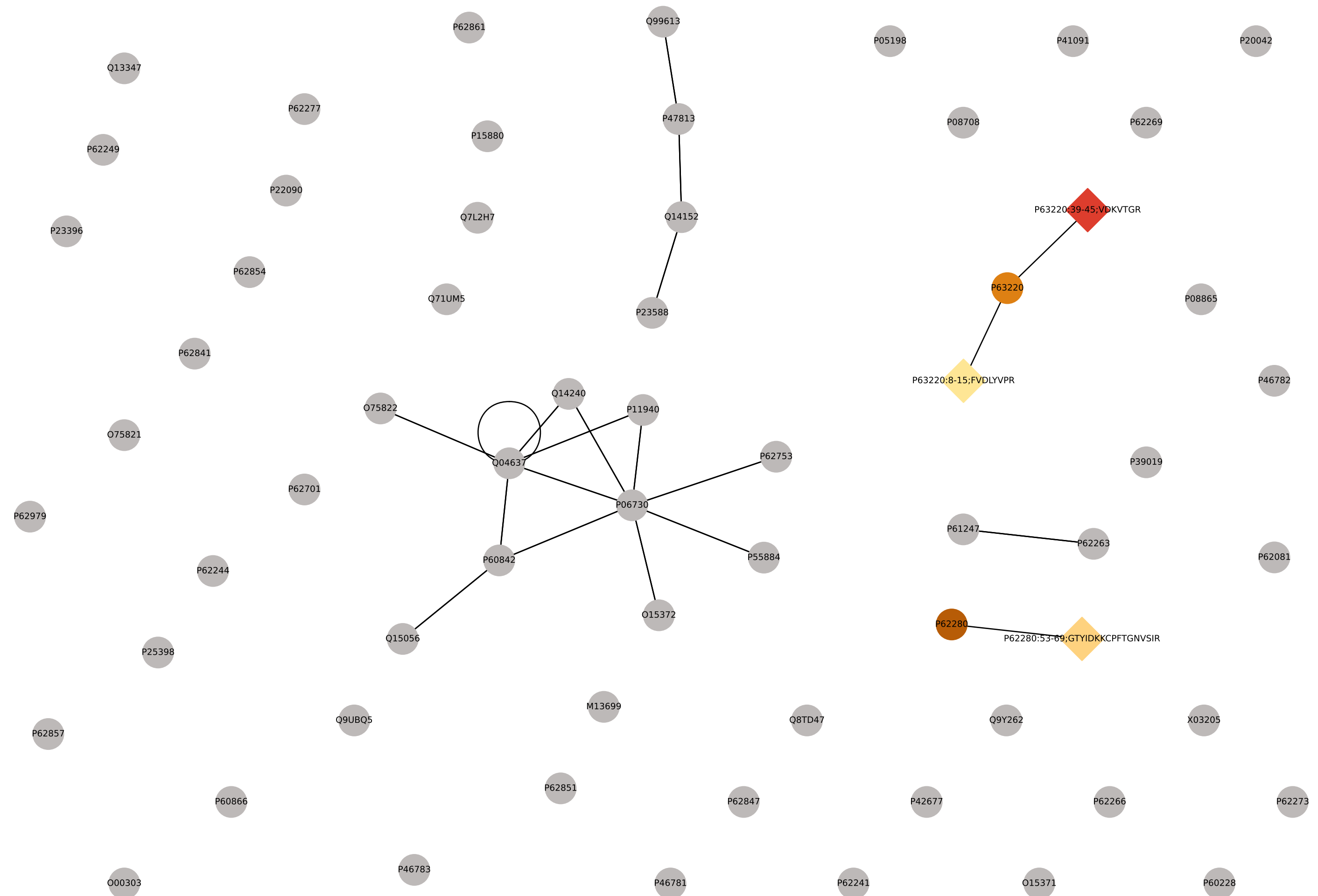


Log2 fold change: gluc vs. control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.018216773752471993



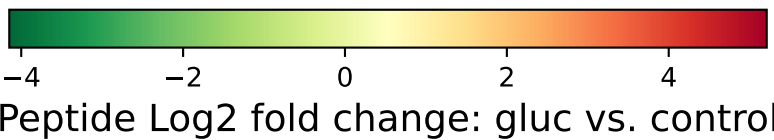
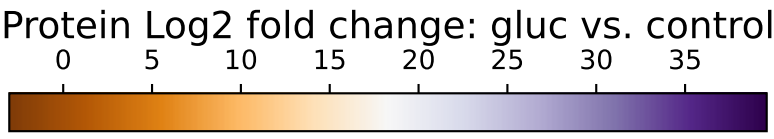
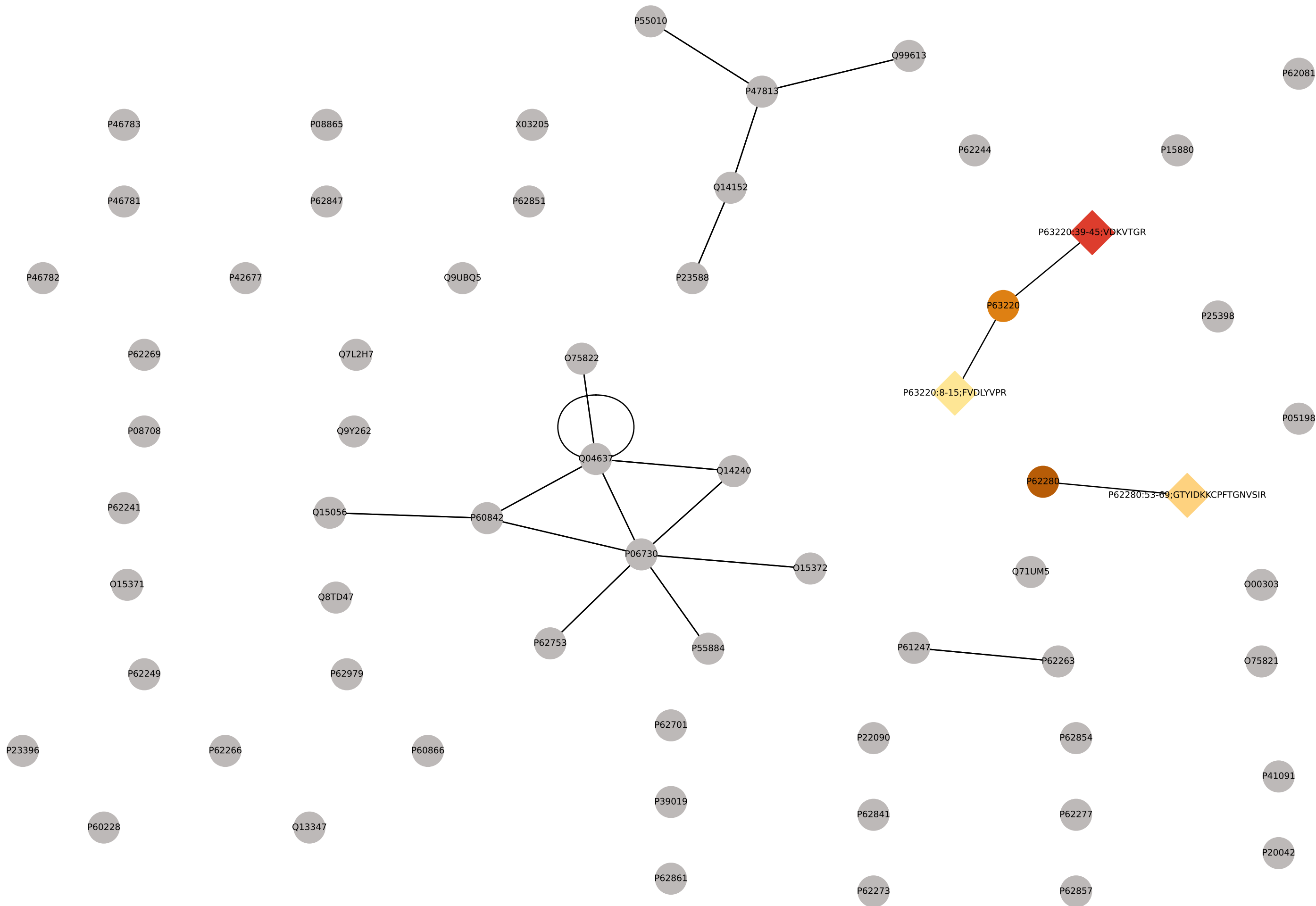
Peptide Log2 fold change: gluc vs. control

Log2 fold change: gluc vs. control
R-HSA-72649: Translation initiation complex formation
p-value: 0.023554931232115828

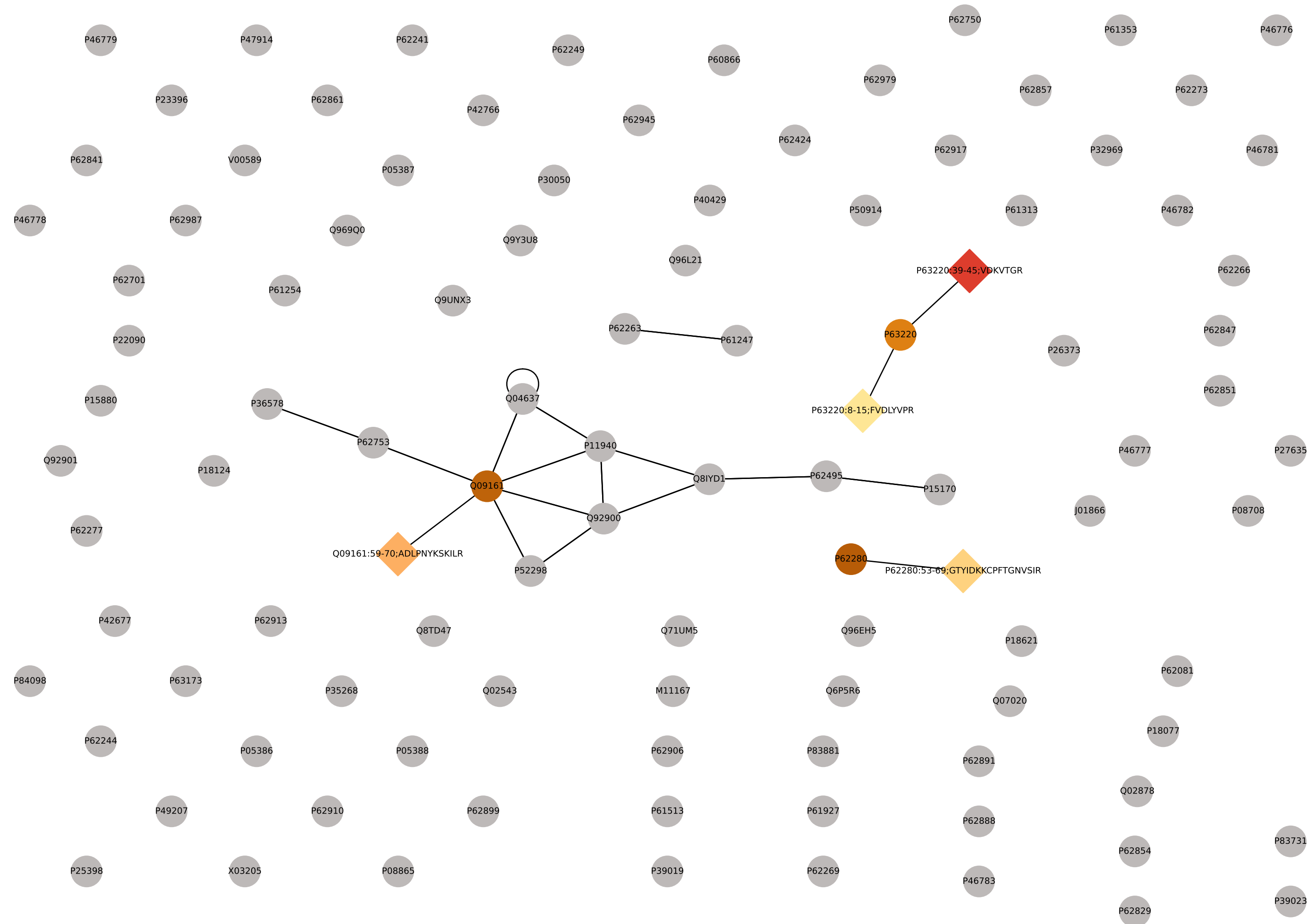


Peptide Log2 fold change: gluc vs. control

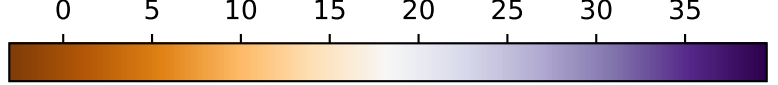
Log2 fold change: gluc vs. control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.024978417082091475



Log2 fold change: gluc vs. control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.006855569728165922



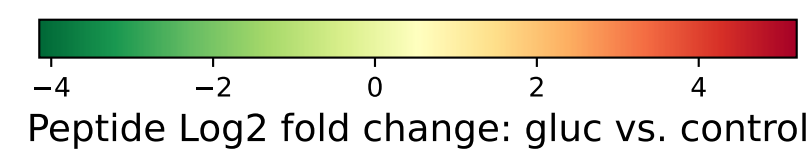
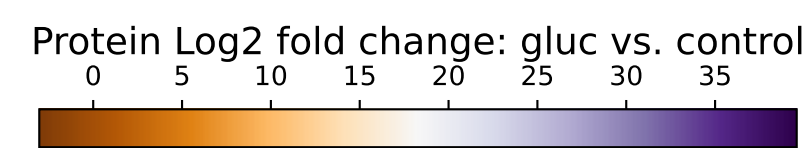
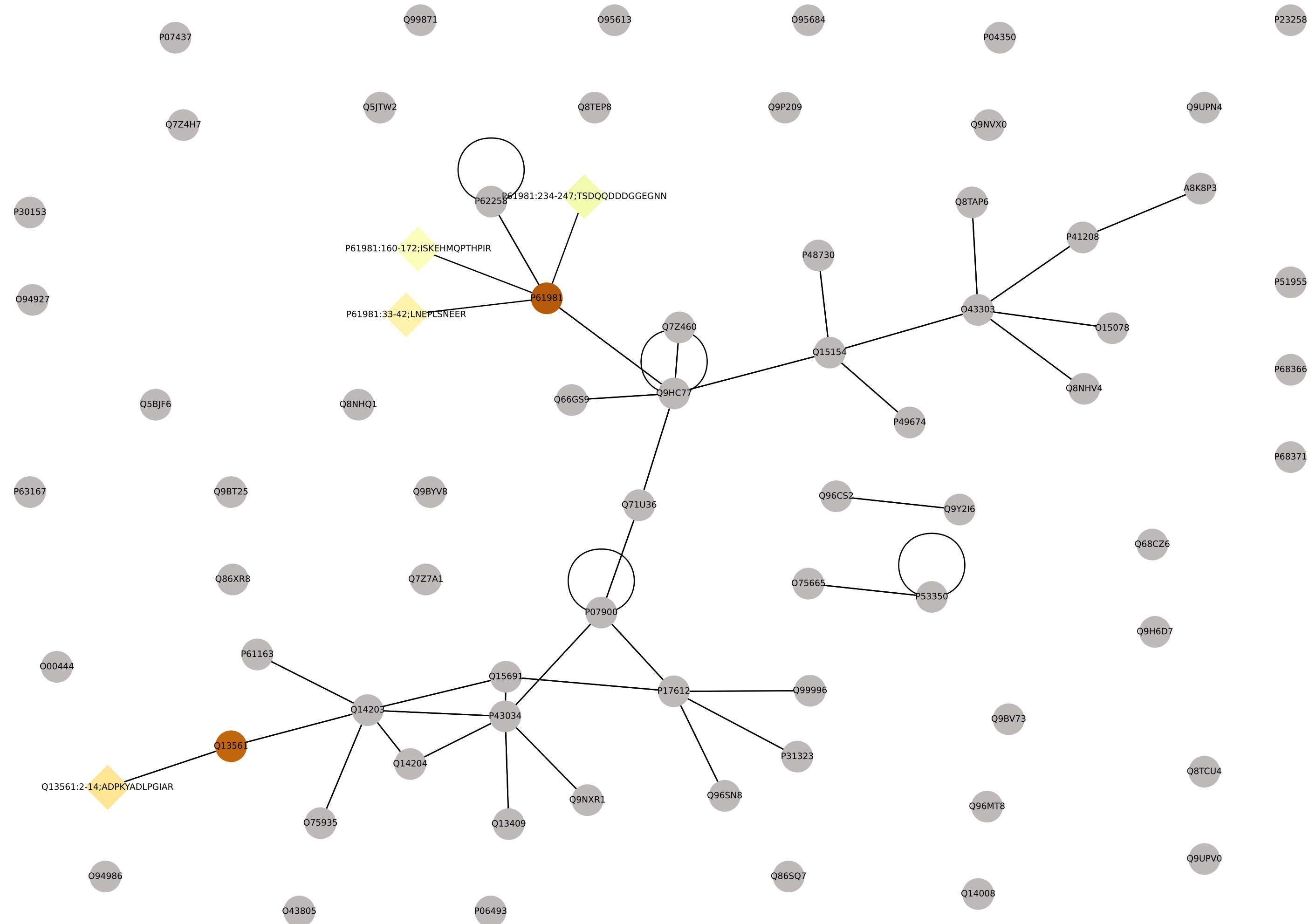
Protein Log2 fold change: gluc vs. control



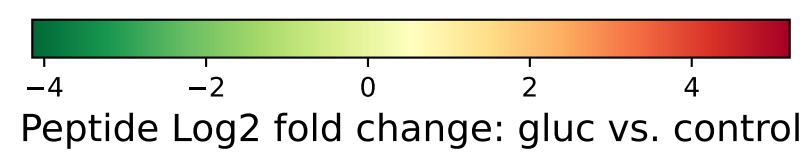
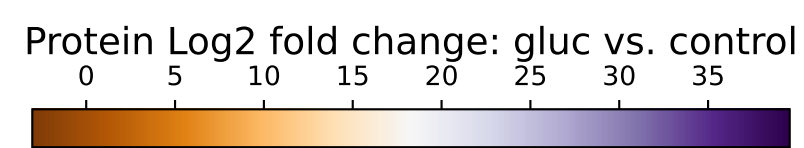
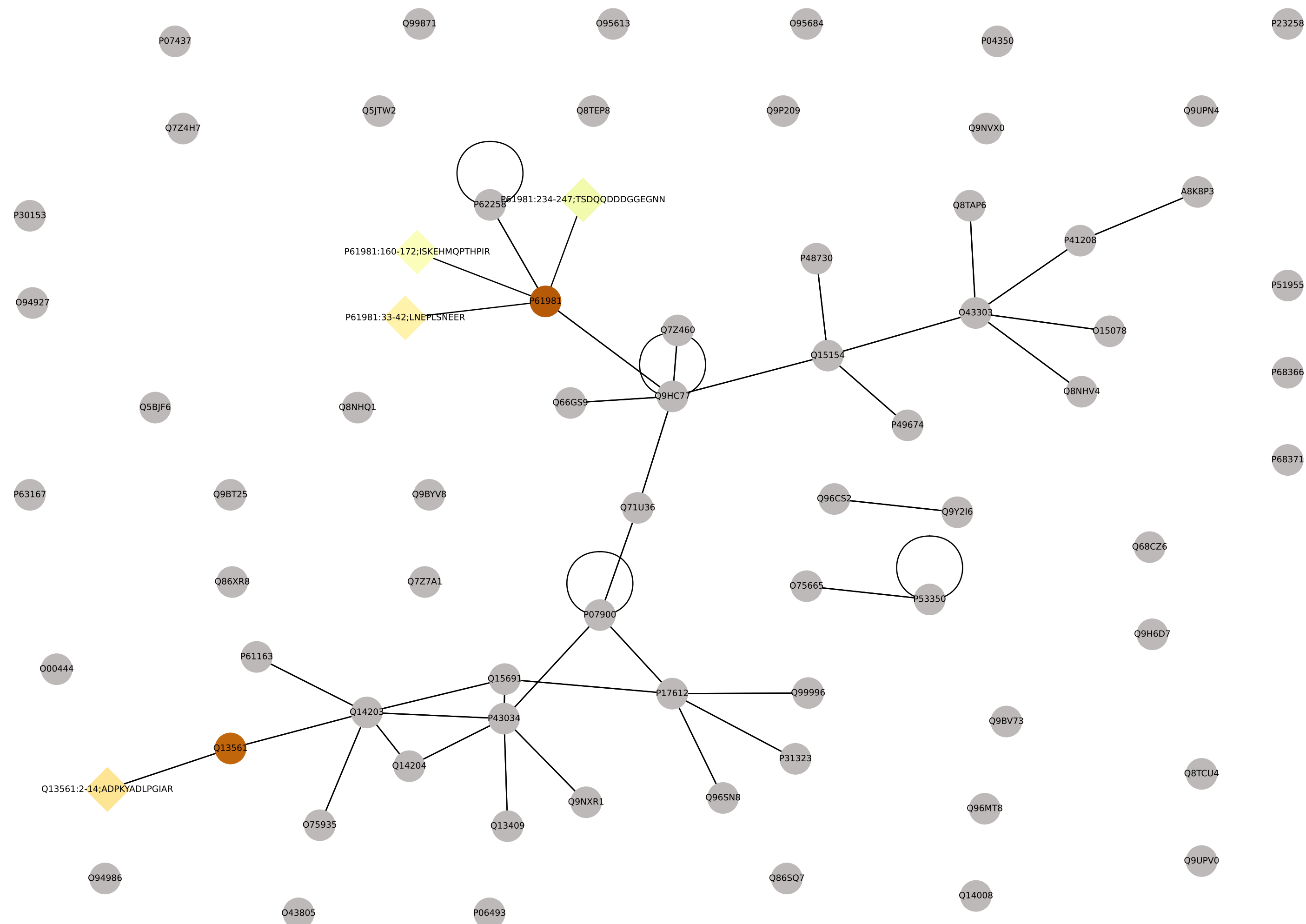
Peptide Log2 fold change: gluc vs. control



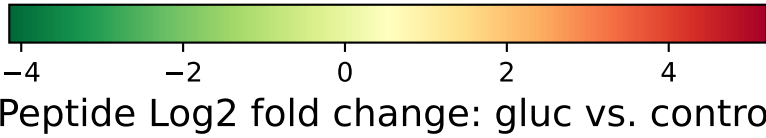
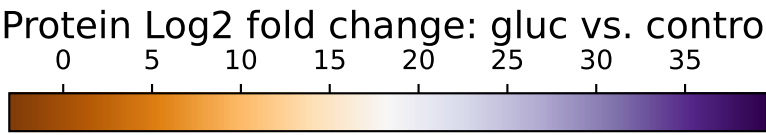
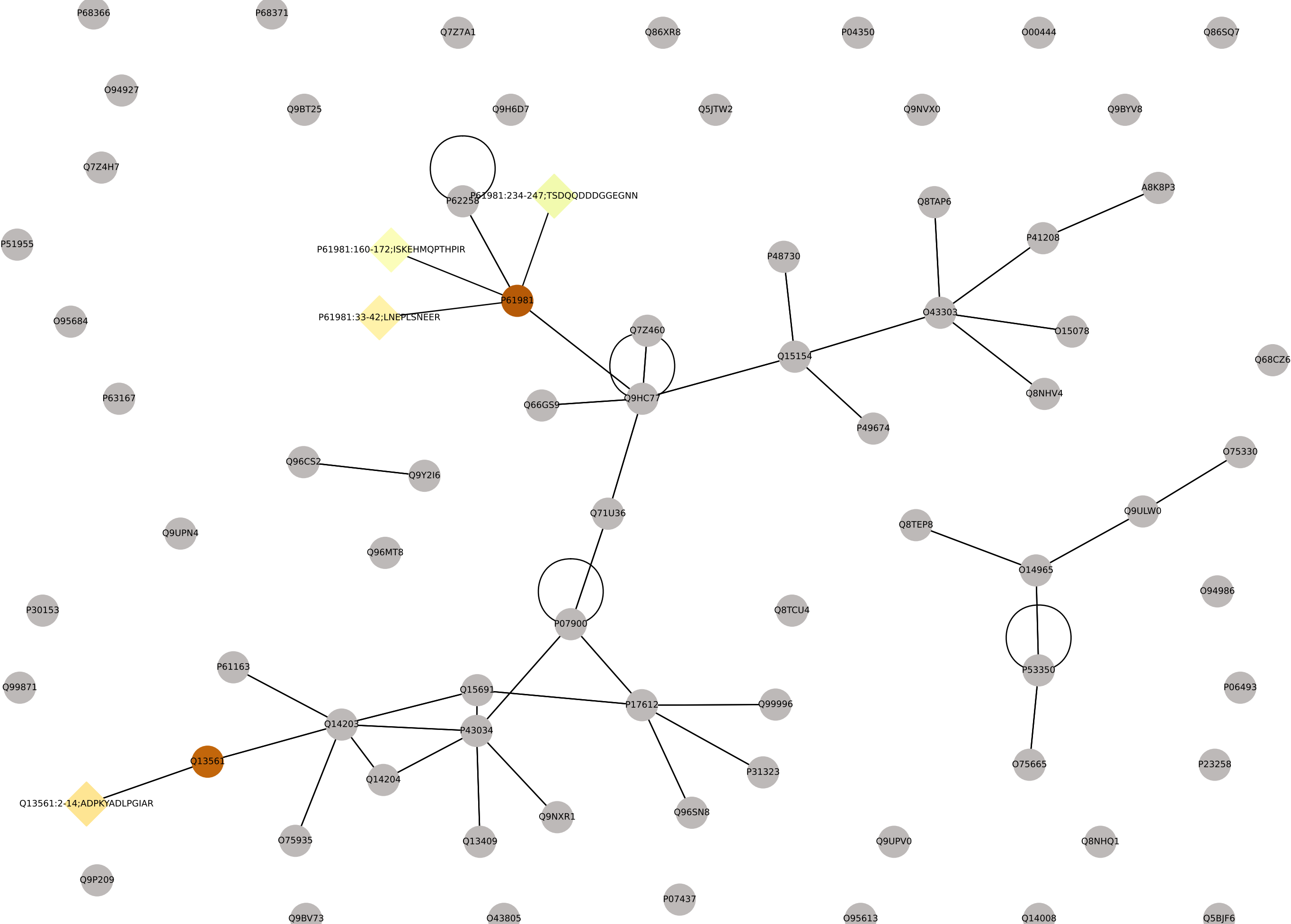
Log2 fold change: gluc vs. control
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome
p-value: 0.030227589686308676



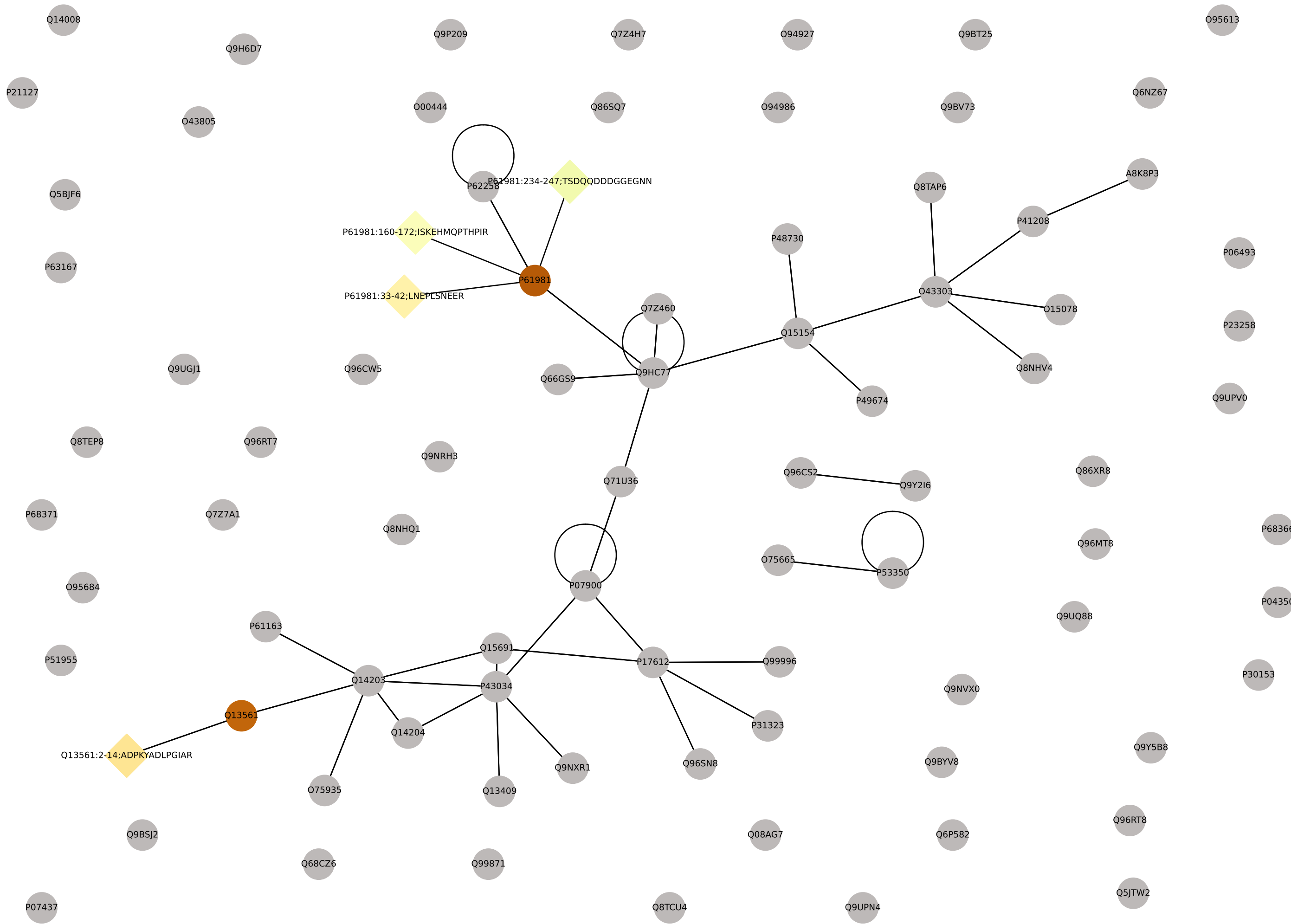
Log2 fold change: gluc vs. control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030227589686308676



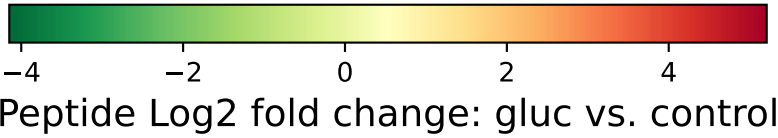
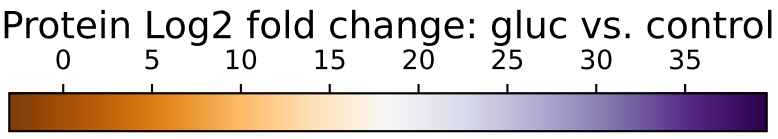
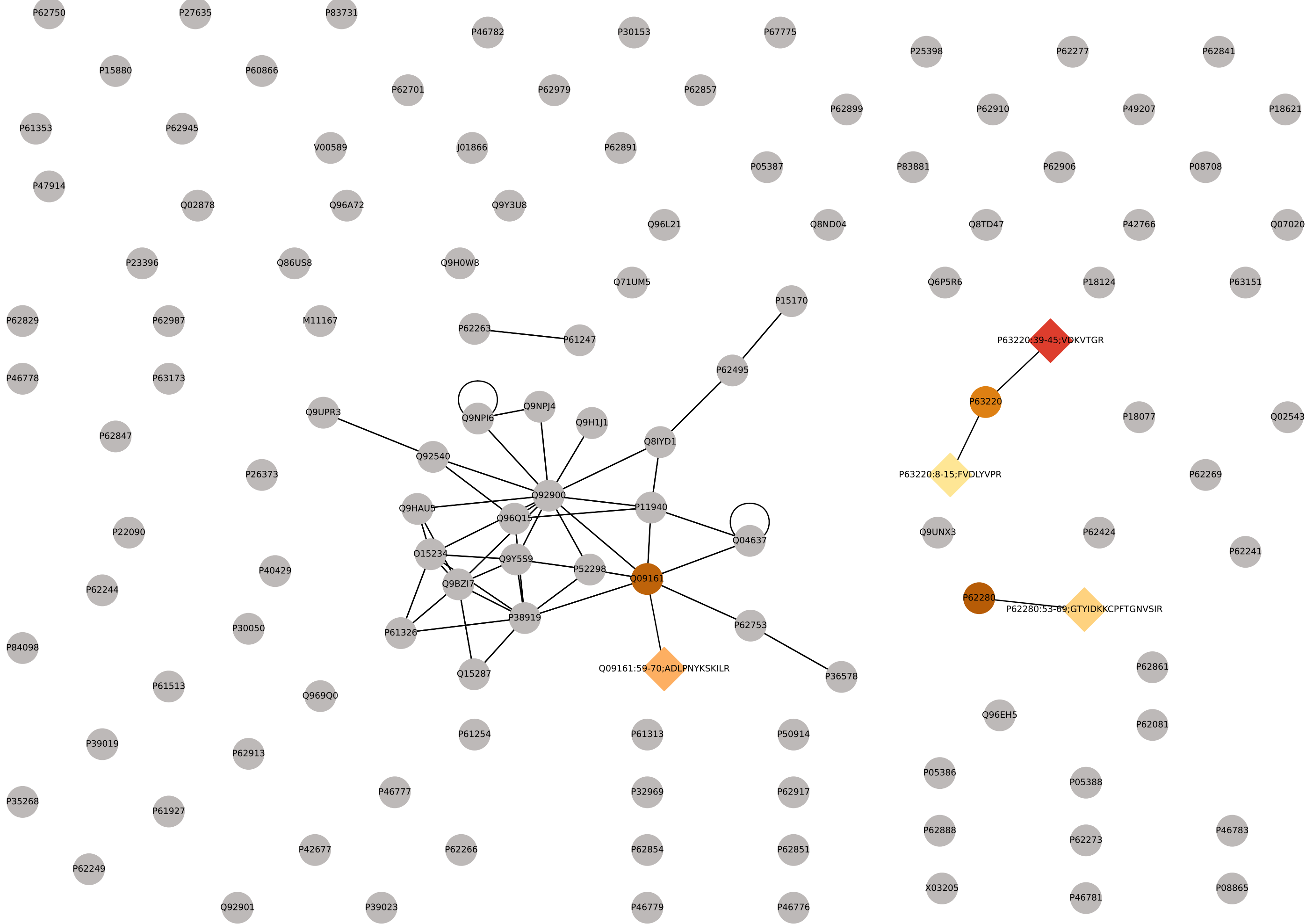
Log2 fold change: gluc vs. control
R-HSA-8854518: AURKA Activation by TPX2
p-value: 0.032600049302680456



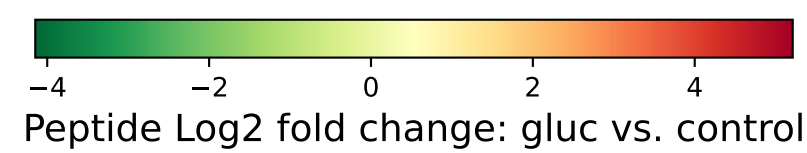
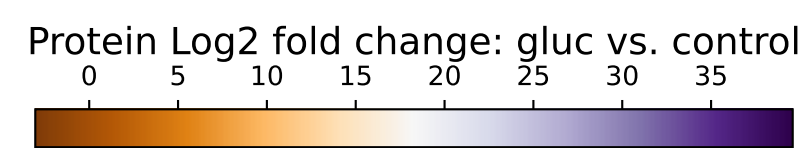
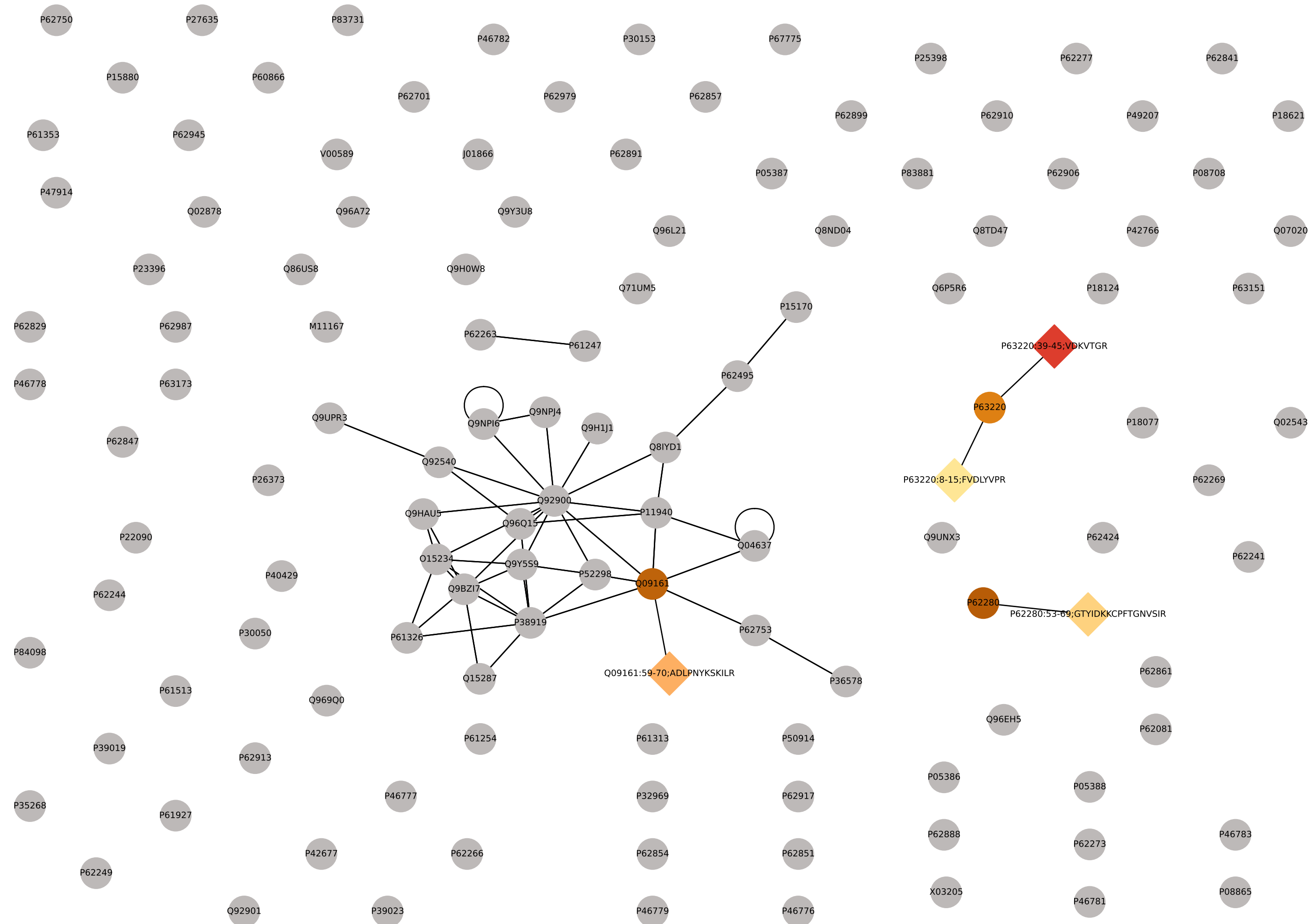
Log2 fold change: gluc vs. control
R-HSA-380270: Recruitment of mitotic centrosome proteins and complexes
p-value: 0.0384084717376354



Log2 fold change: gluc vs. control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.011931898374331729



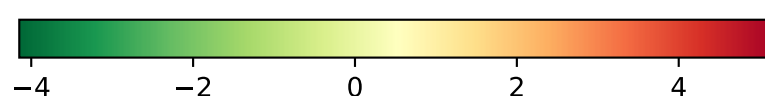
Log2 fold change: gluc vs. control
R-HSA-975957: Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
p-value: 0.011931898374331729



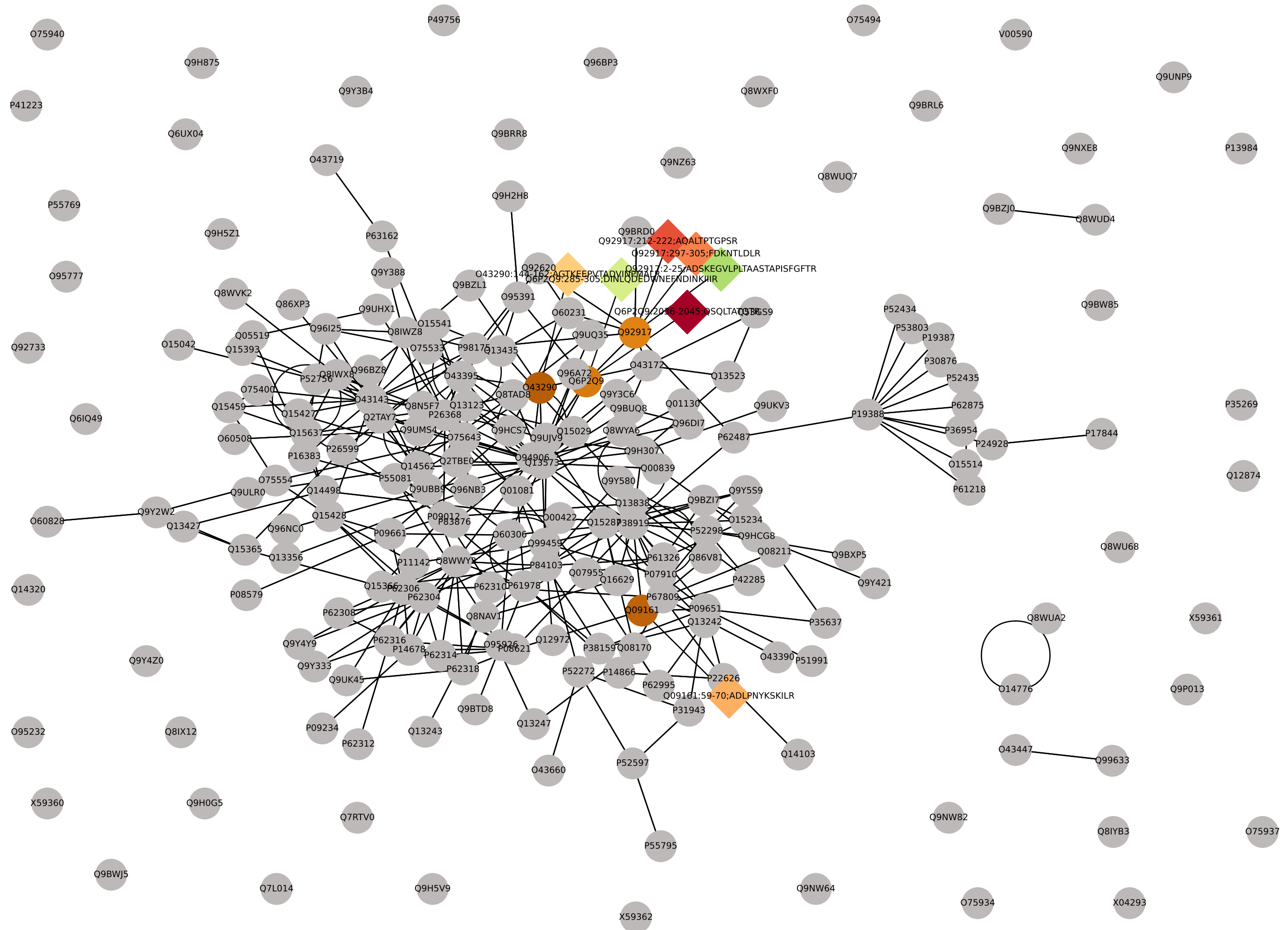
The diagram illustrates a network of protein interactions. Nodes are represented by grey circles, each labeled with a UniProt ID. Two nodes are highlighted in orange: P61981 (top center) and Q13561 (bottom left). Several nodes are represented by yellow diamonds, indicating specific protein names: P61981:234-247:TSQQDDDGEGNN (top center), P61981:160-172:ISKEHMQPTHPIR (top left), P61981:33-42:LNEPLSNEER (top left), Q13561:2-14:ADPKYADLPGIAR (bottom left), and P53350 (middle right). The network includes numerous connections between nodes, with some nodes having self-loops. The background is white with a light grey grid.

Key nodes and their connections include:

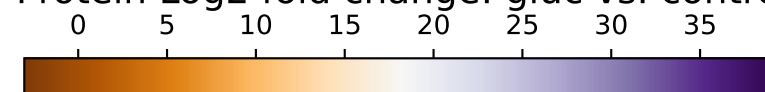
- P61981** (orange) is connected to P62258, P61981:234-247:TSQQDDDGEGNN, P61981:160-172:ISKEHMQPTHPIR, P61981:33-42:LNEPLSNEER, Q9HC77, Q72460, Q66G59, Q71U36, Q8NHQ1, Q96CW5, Q9NVX0, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8, Q9P209, Q7Z4H7, Q94927, Q865Q7, Q9B5J2, Q8TCU4, P68366, P07437, Q9UPV0, Q98V73, Q86XR8, Q96MT8, Q6N267, Q8AG7, Q5JTW2, P06493, Q9UPN4, Q9BT25, Q99871, Q9H6D7, P21127, P68371, Q14008, P04350, Q96RT8, Q96RT7, Q7Z7A1, Q95613, Q94986, Q5BJF6, P30153, Q95684, Q68CZ6, Q8TEP8,



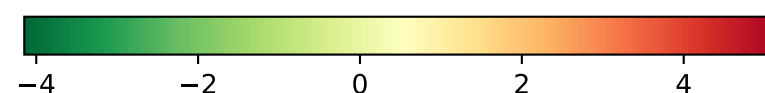
Log2 fold change: gluc vs. control
R-HSA-72163: mRNA Splicing - Major Pathway
p-value: 0.008907459881584257



Protein Log2 fold change: gluc vs. control



Peptide Log2 fold change: gluc vs. control



0 5 10 15 20 25 30 35