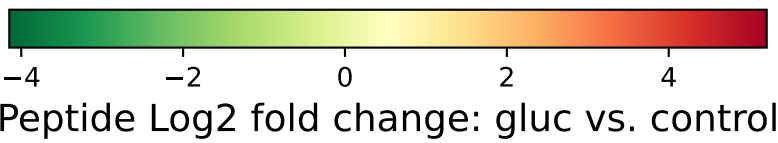
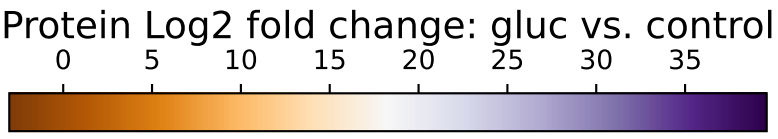
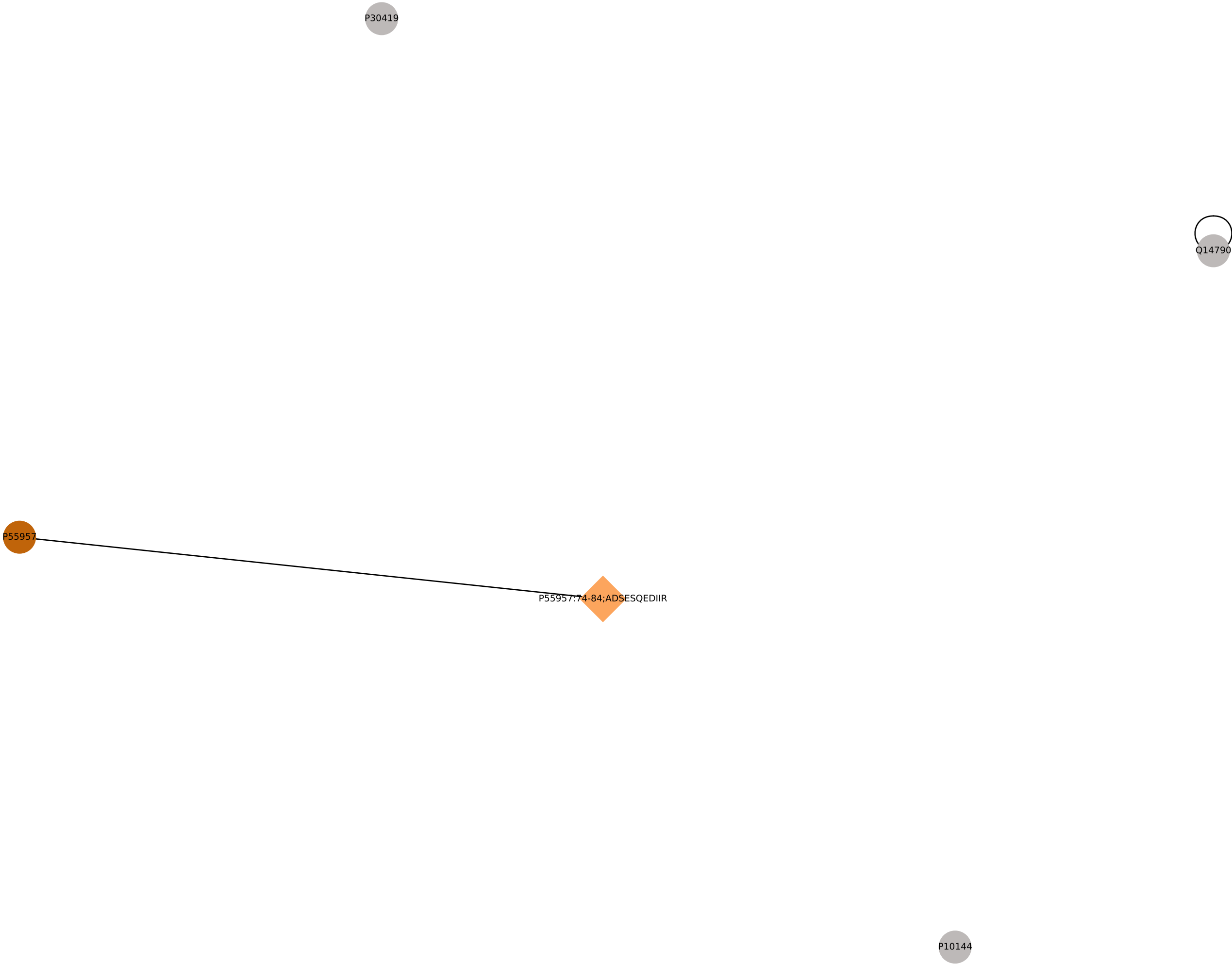
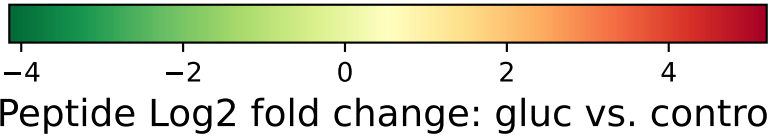
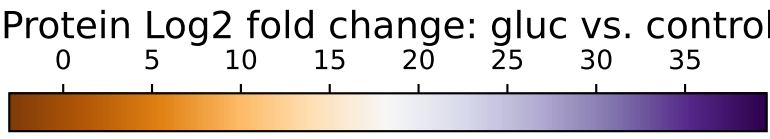
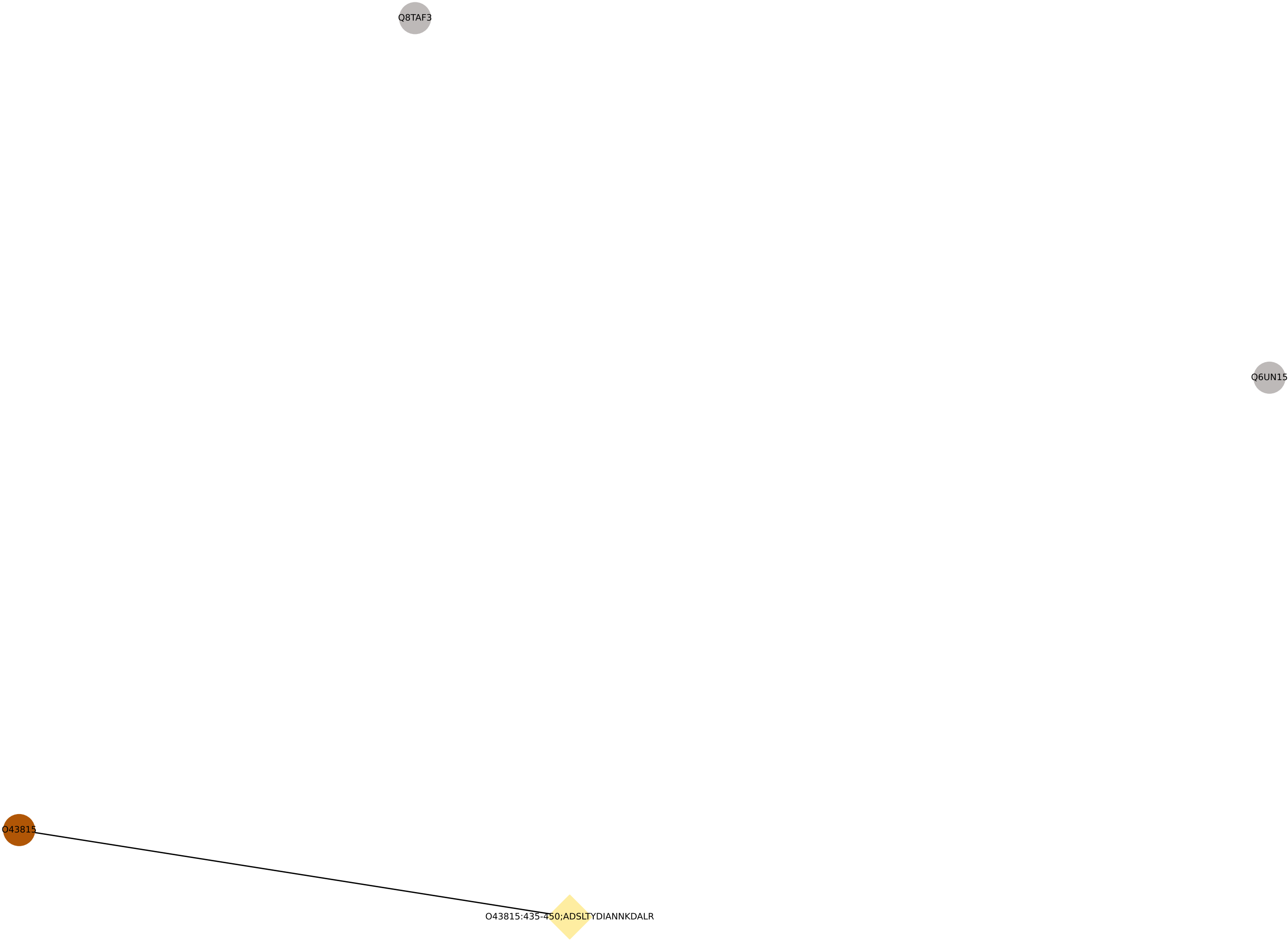


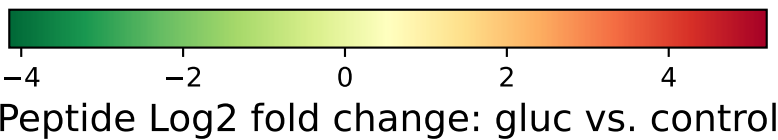
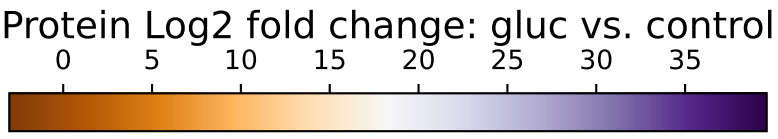
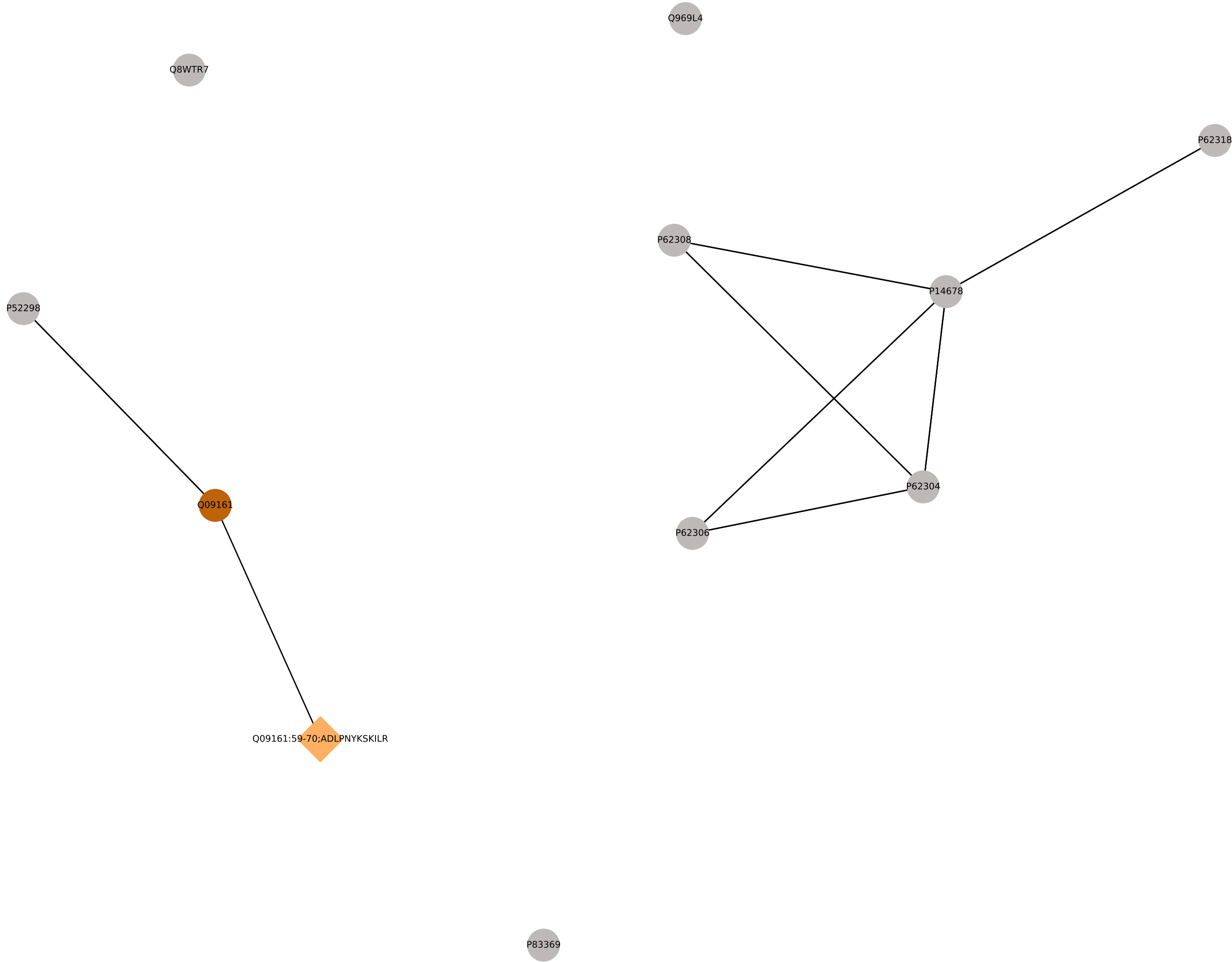
Log2 fold change: gluc vs. control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.015117656007649471



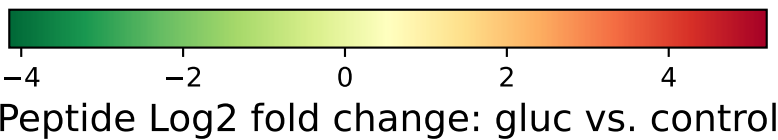
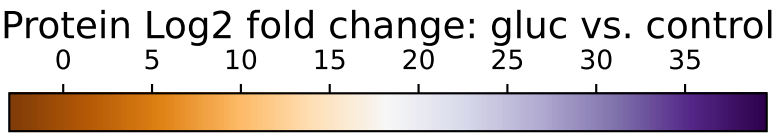
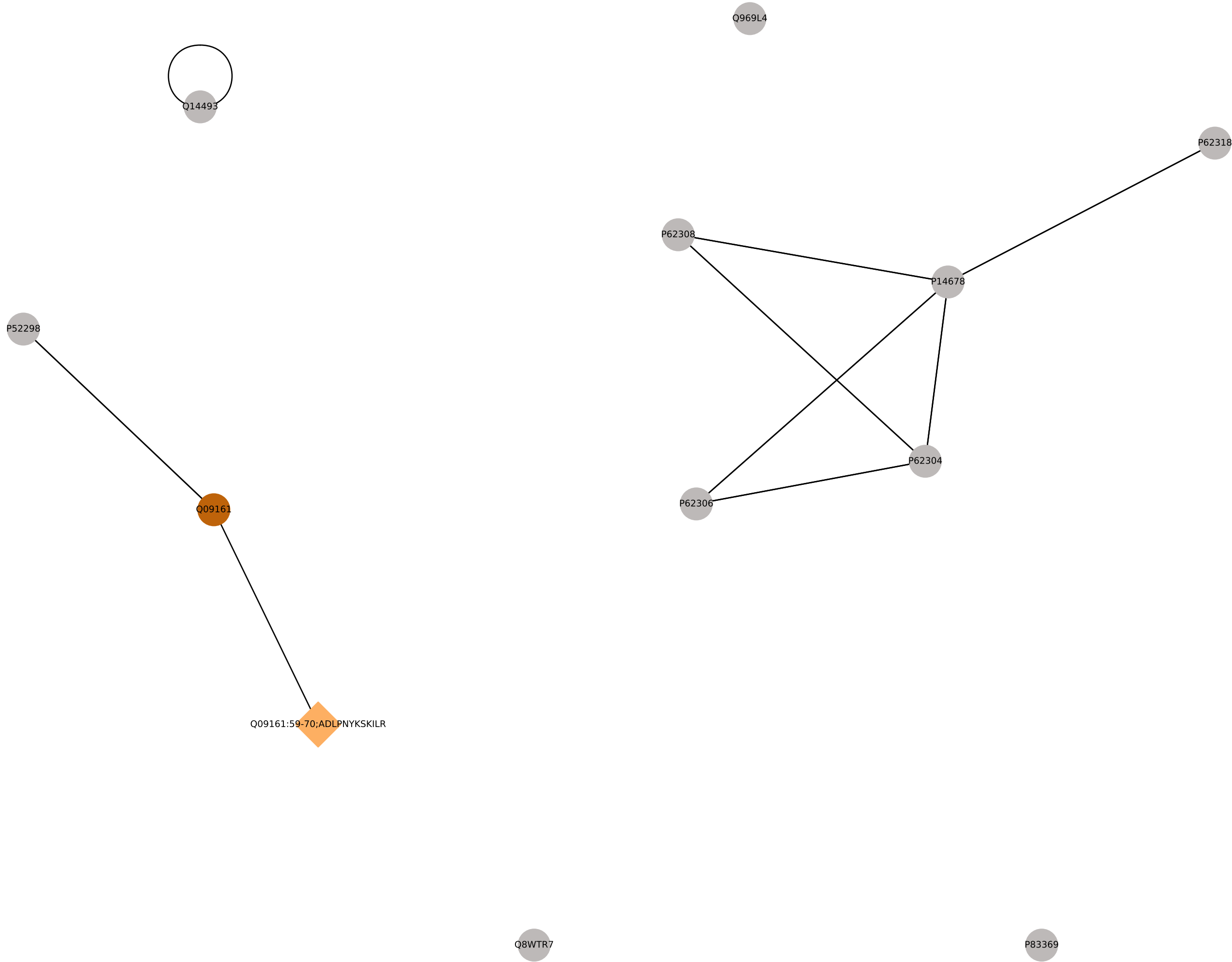
Log2 fold change: gluc vs. control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.018861837637962453



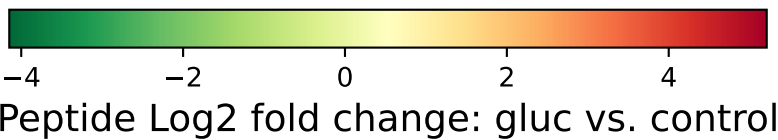
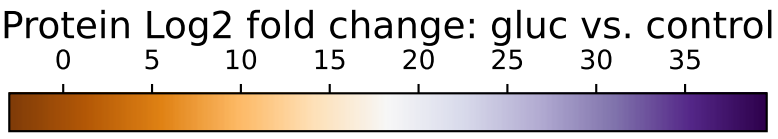
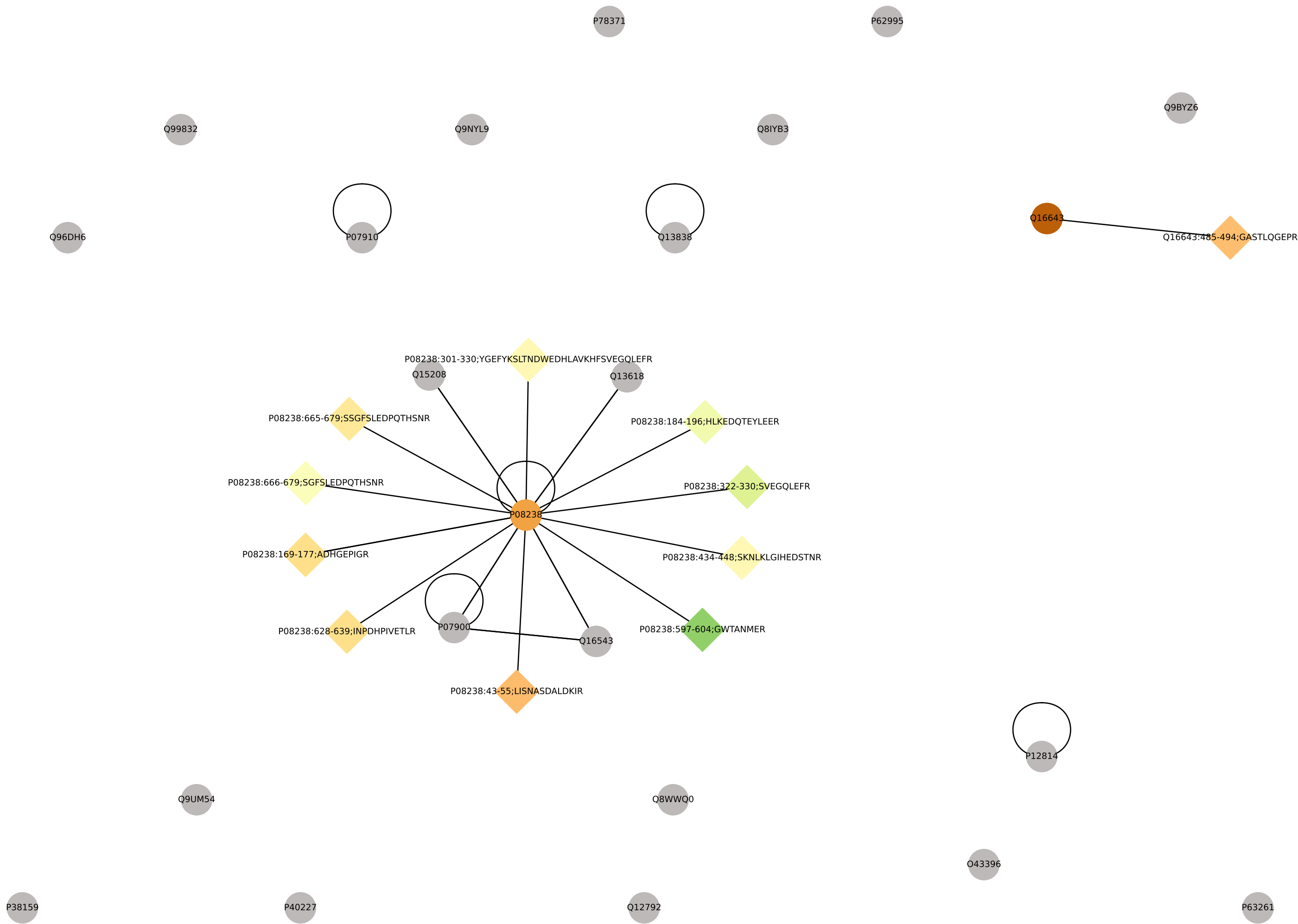
Log2 fold change: gluc vs. control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03737392638204595



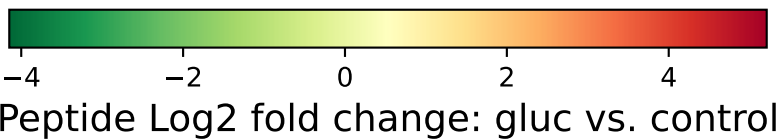
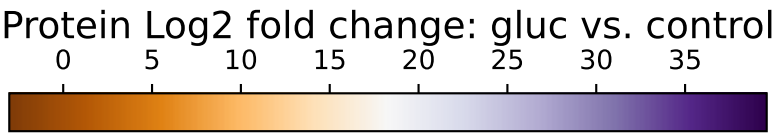
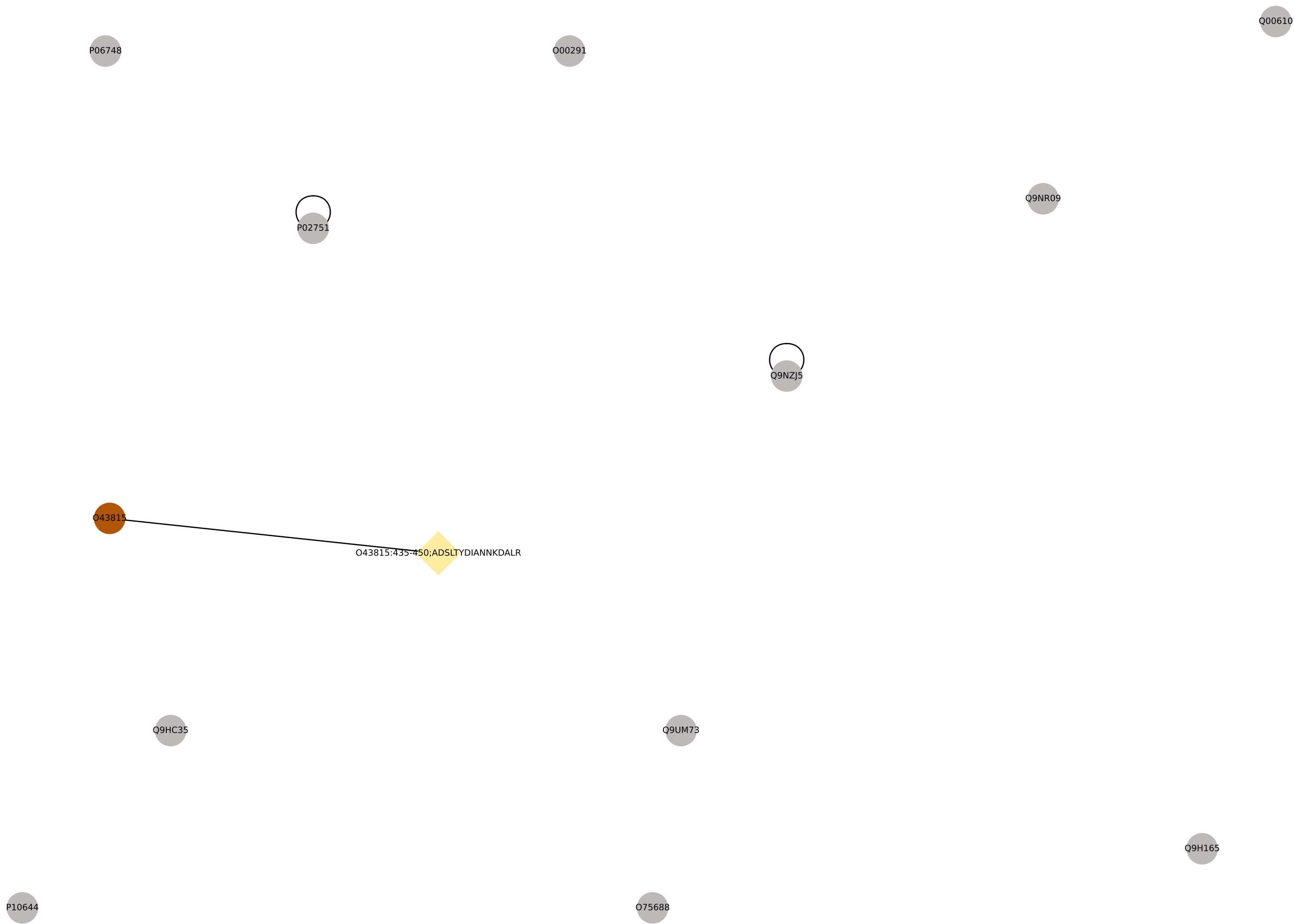
Log2 fold change: gluc vs. control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04103493715974438



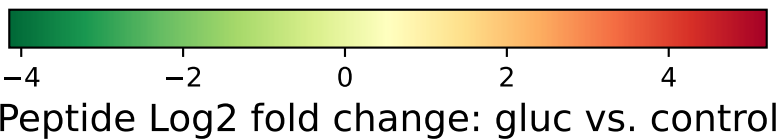
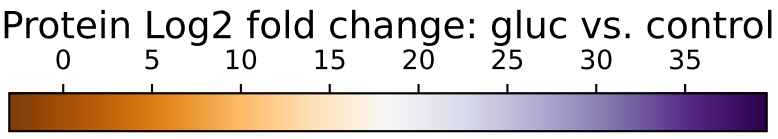
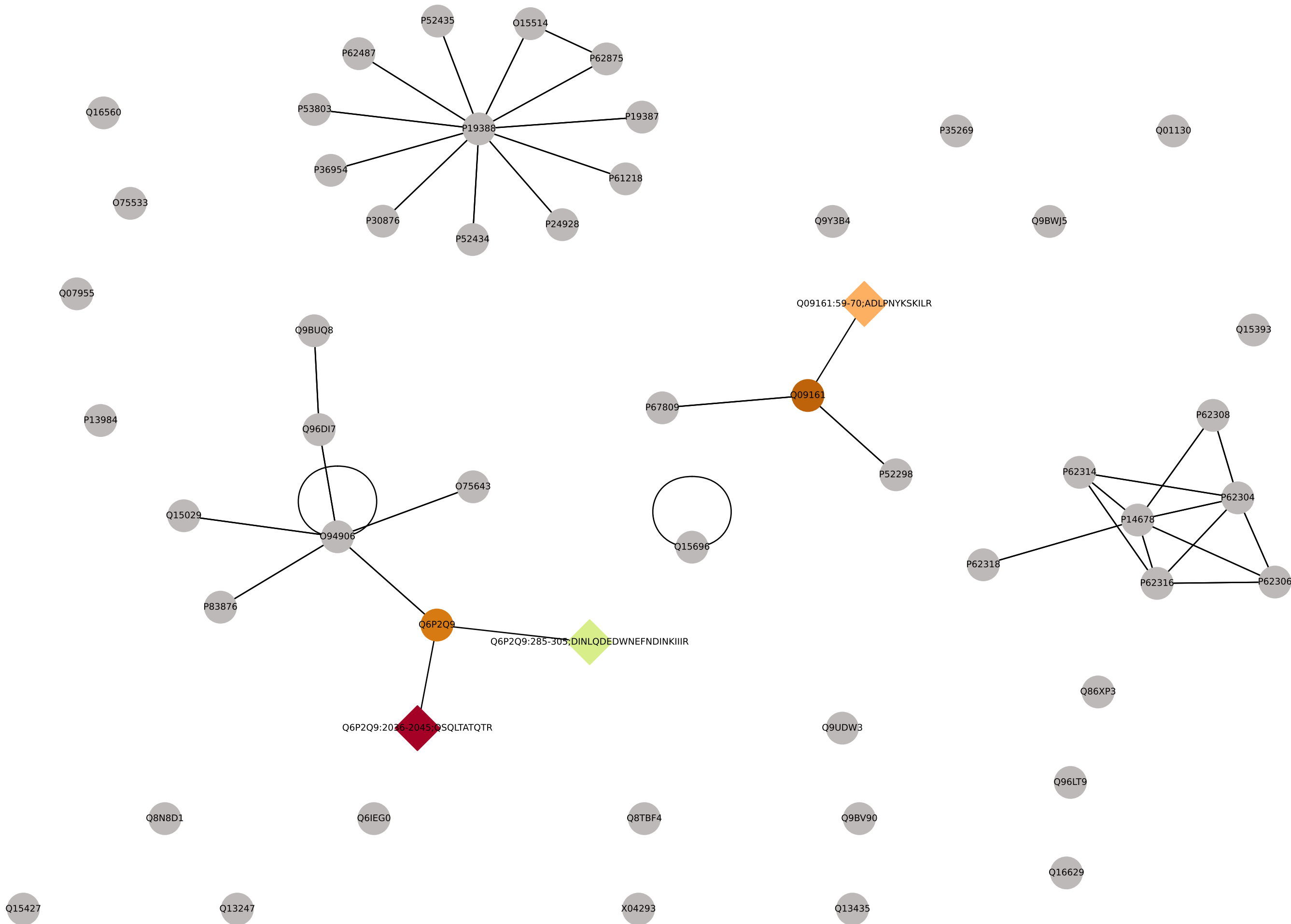
Log2 fold change: gluc vs. control
R-HSA-9013418: RHOBTB2 GTPase cycle
p-value: 0.003870027935771292



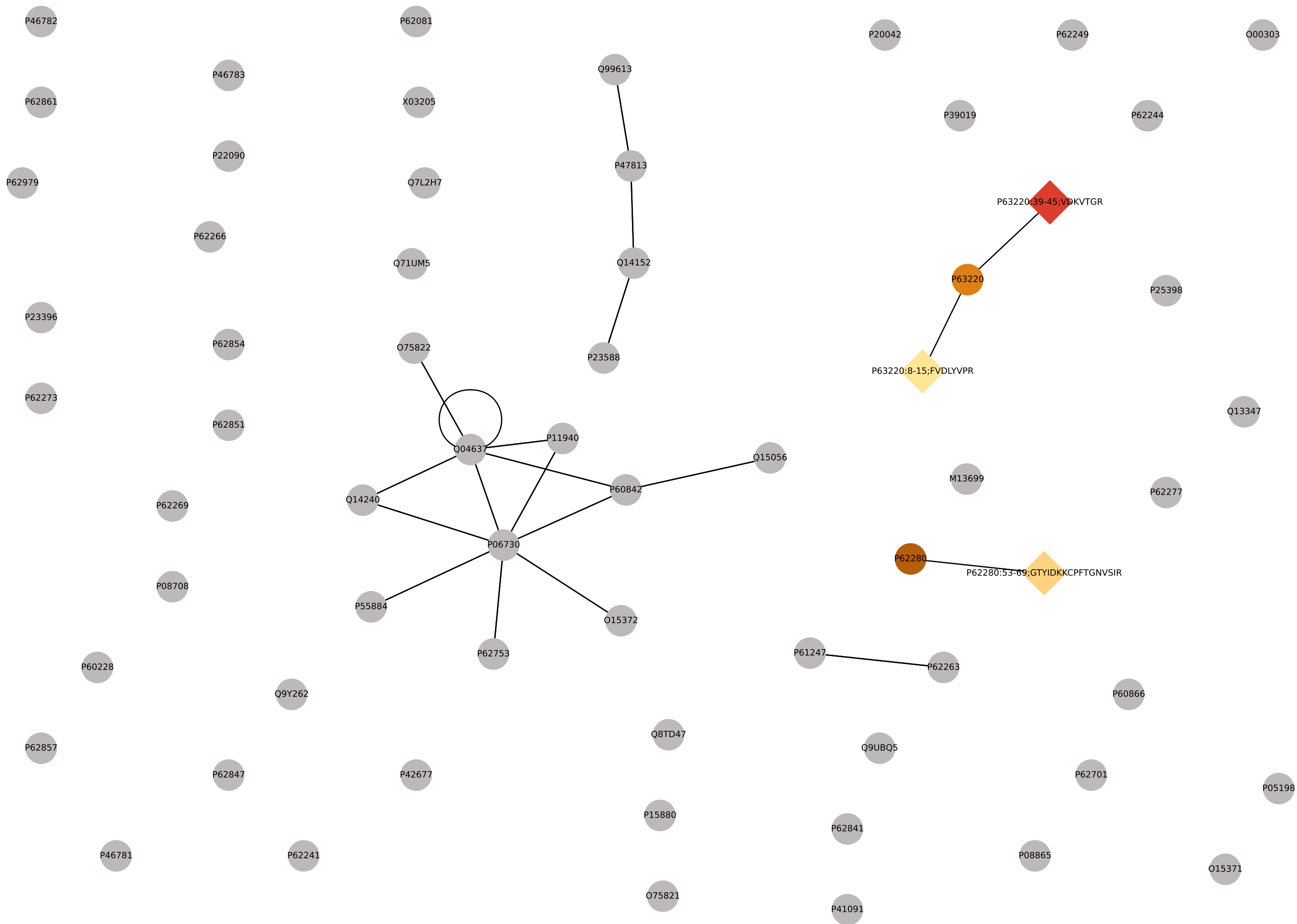
Log2 fold change: gluc vs. control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04468226372702311



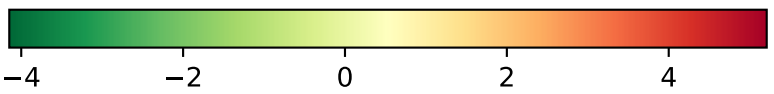
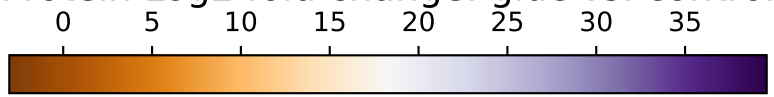
Log2 fold change: gluc vs. control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.018216773752471993



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

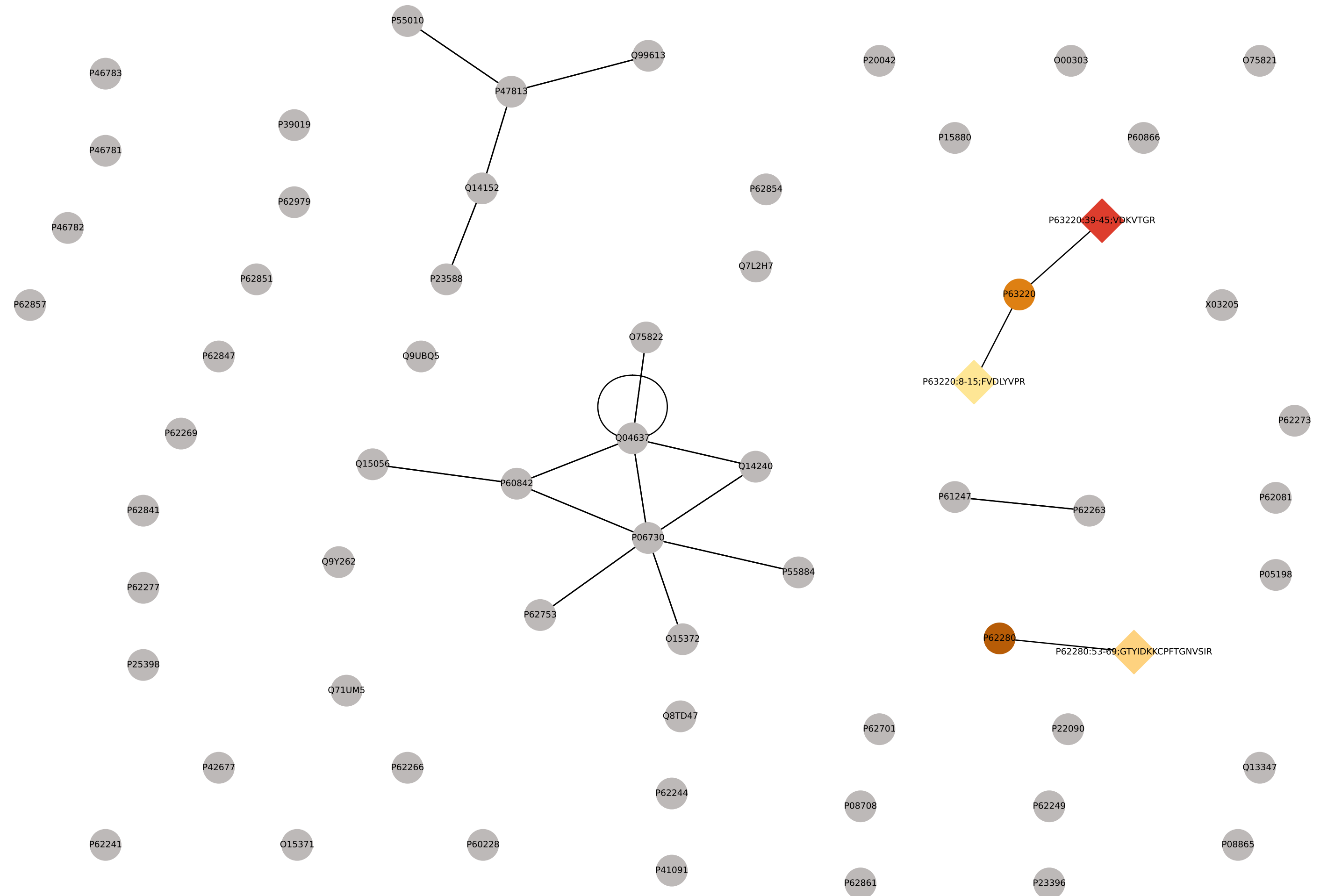


Protein Log2 fold change: gluc vs. control



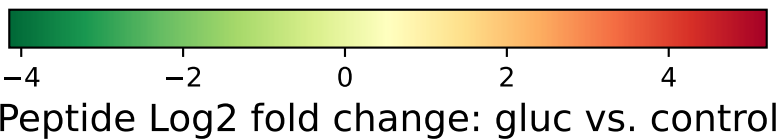
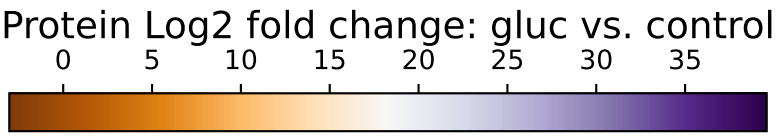
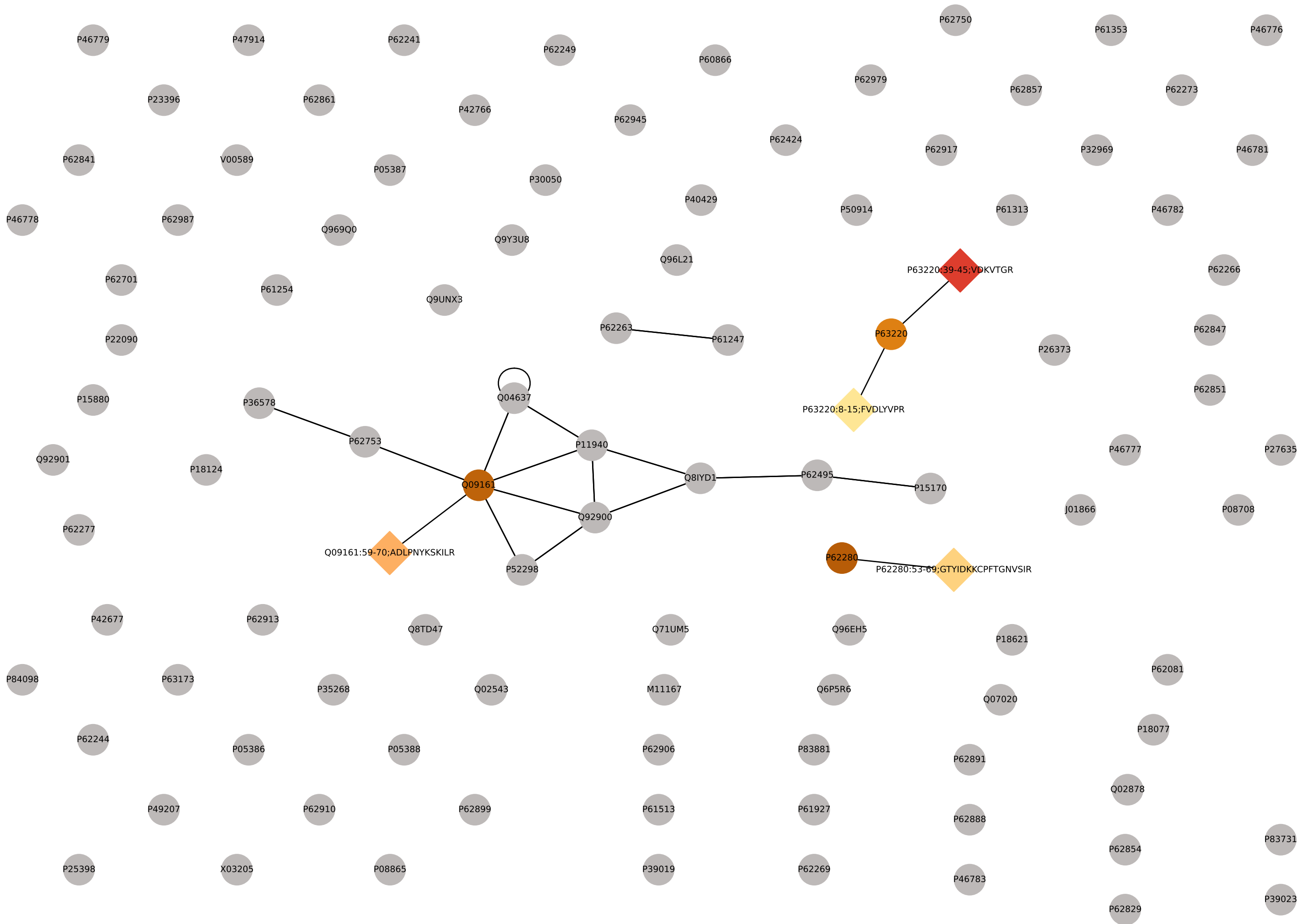
Peptide Log2 fold change: gluc vs. control

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

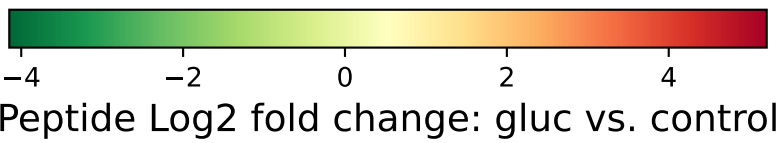
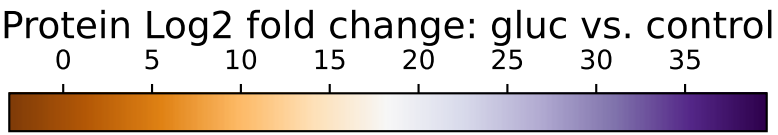
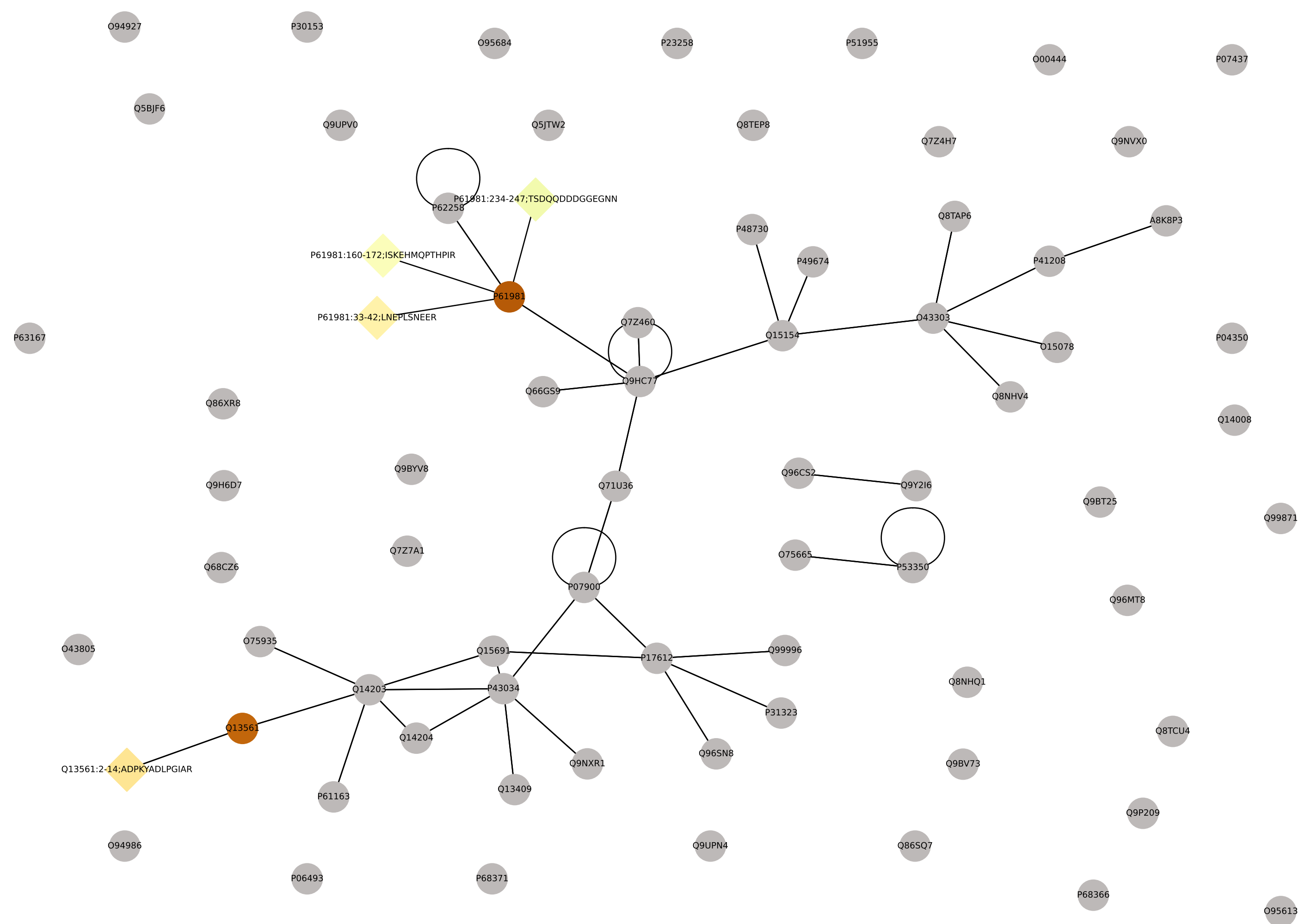


Peptide Log2 fold change: gluc vs. control

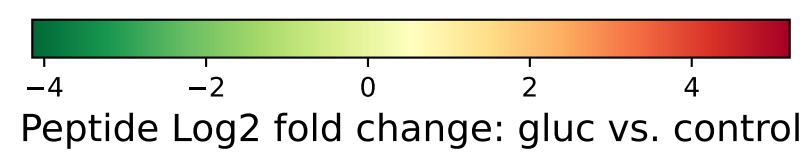
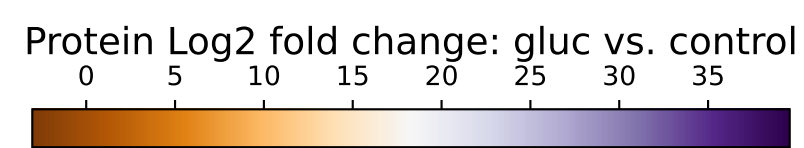
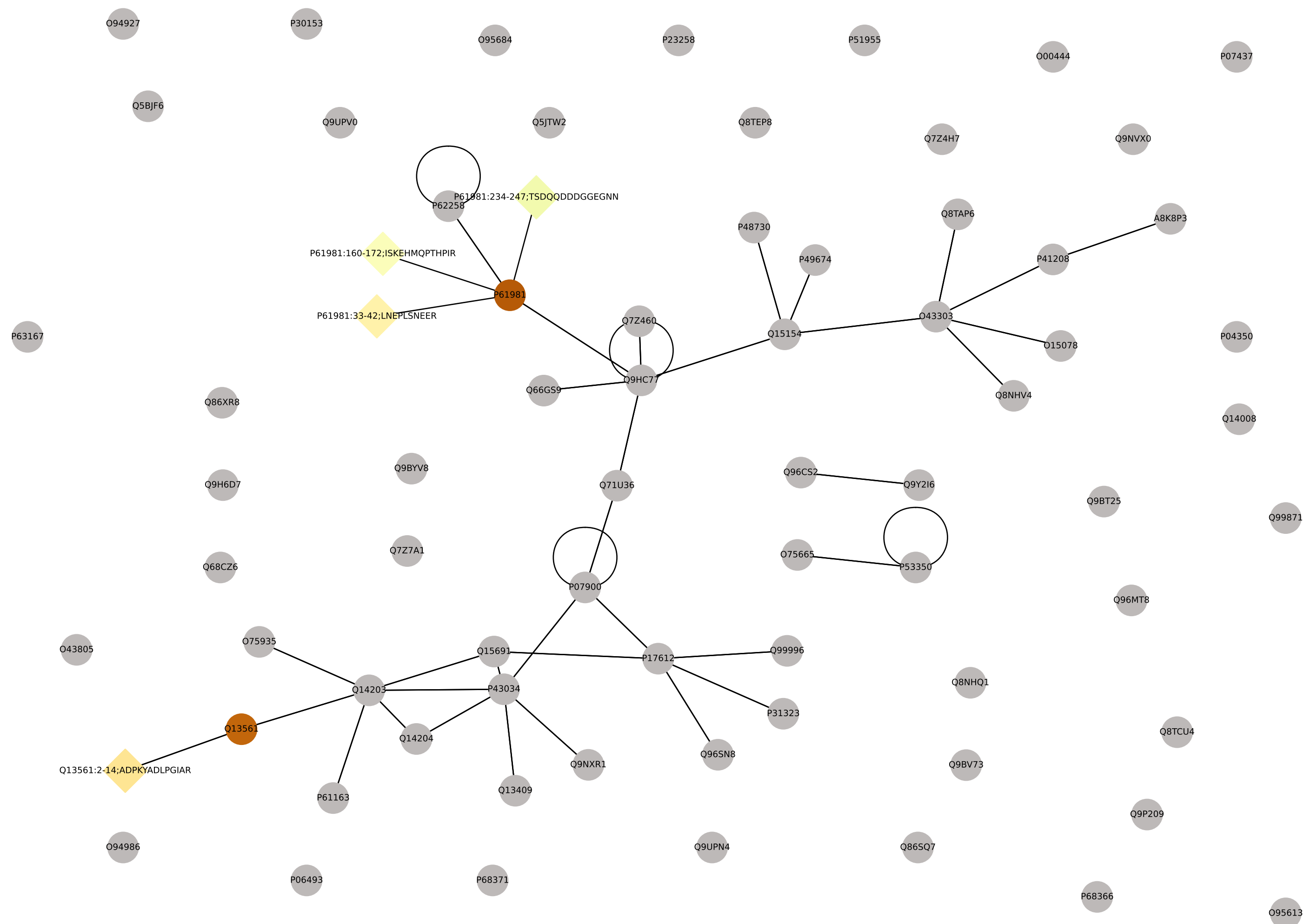
Log2 fold change: gluc vs. control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.006855569728165922



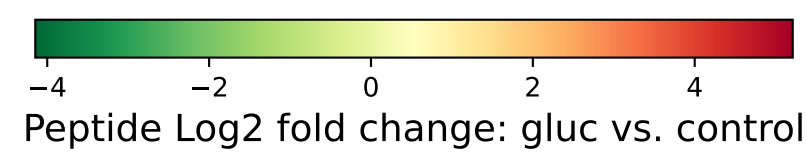
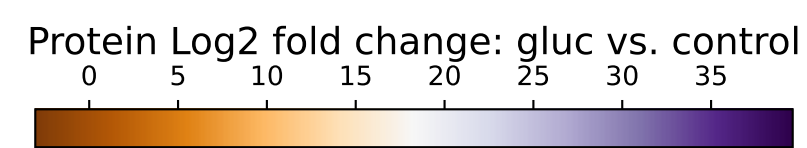
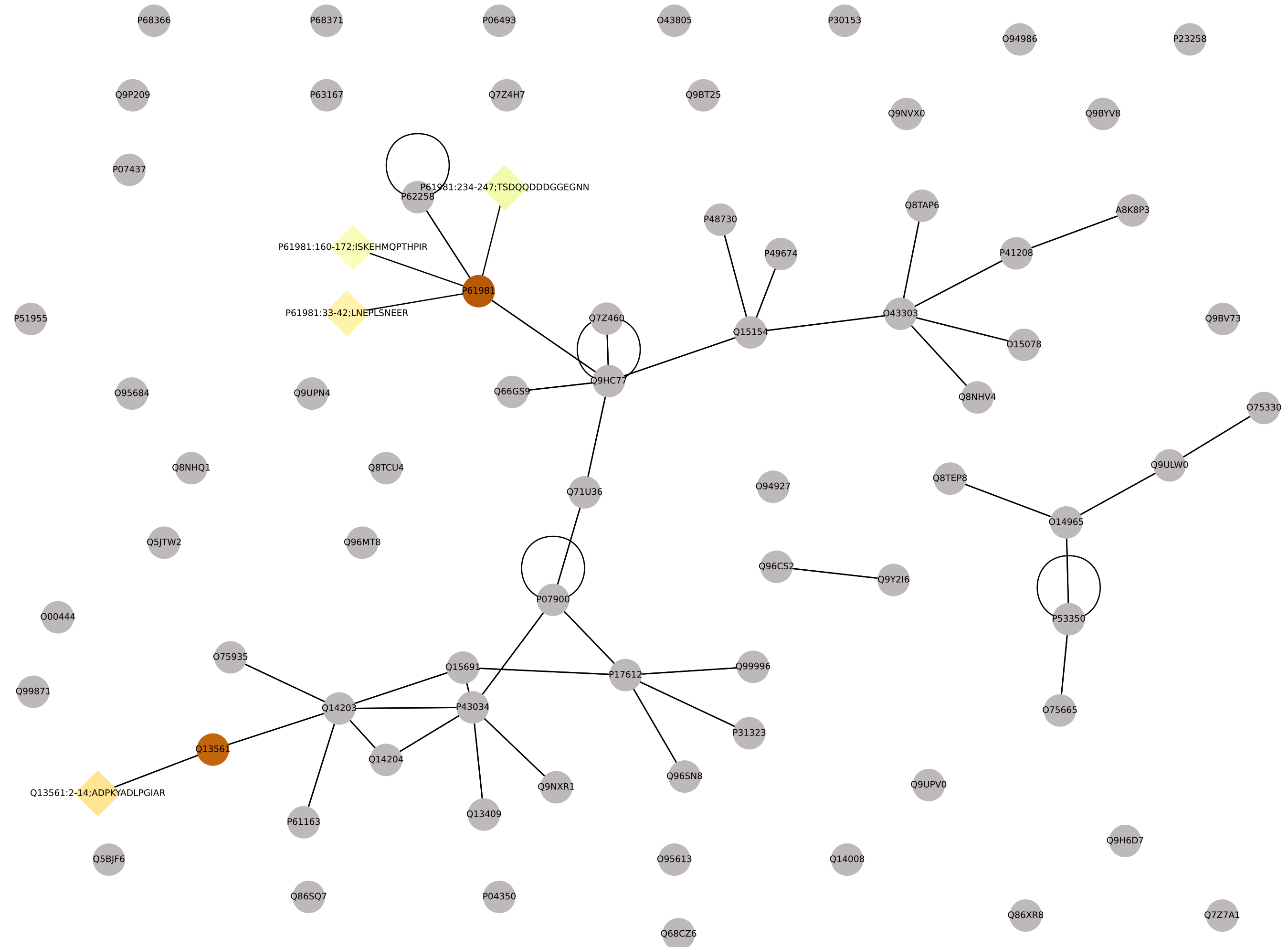
Log2 fold change: gluc vs. control
R-HSA-380284: Loss of proteins required for interphase microtubule organization from the centrosome
p-value: 0.030227589686308676



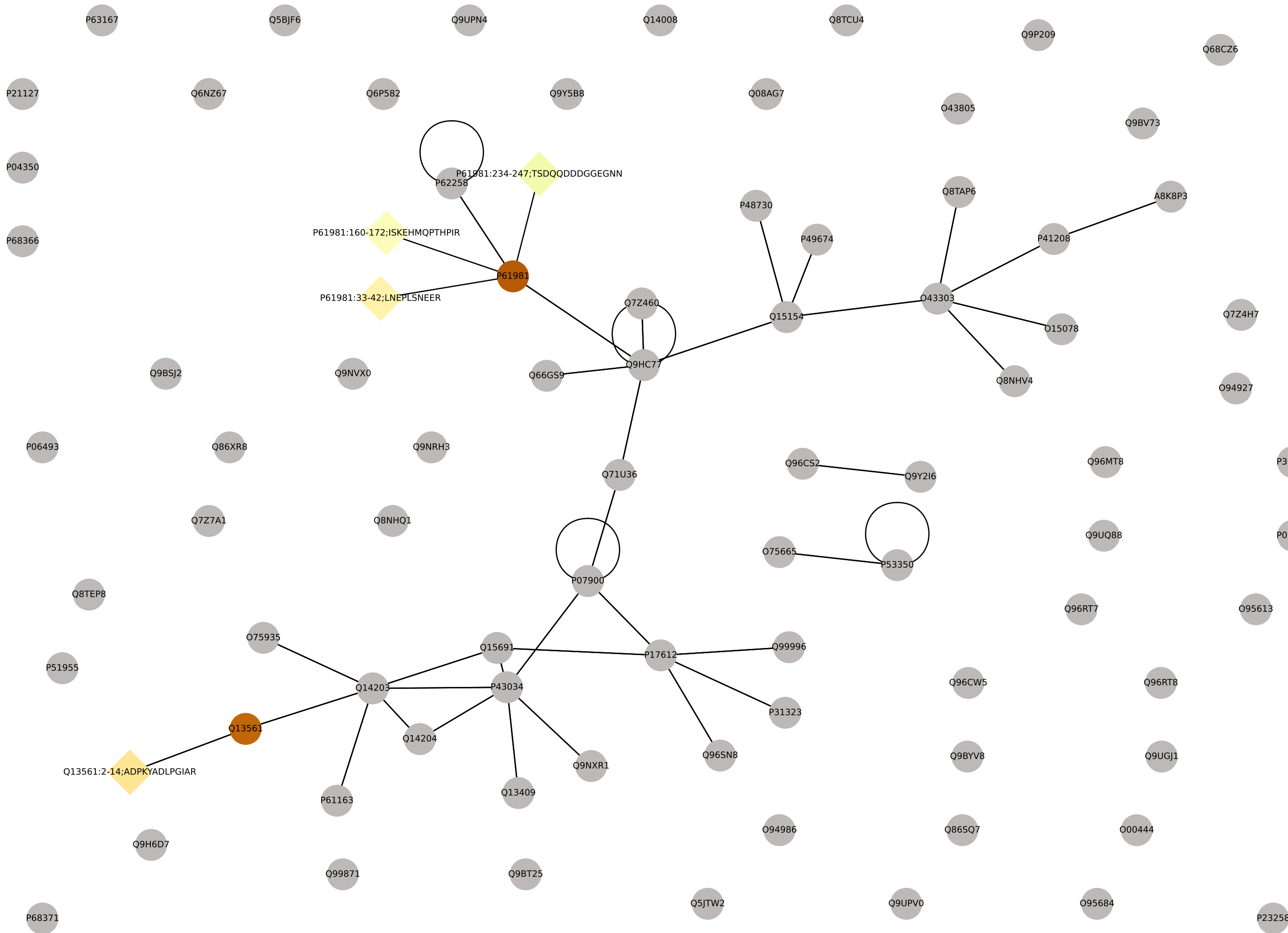
Log2 fold change: gluc vs. control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030227589686308676



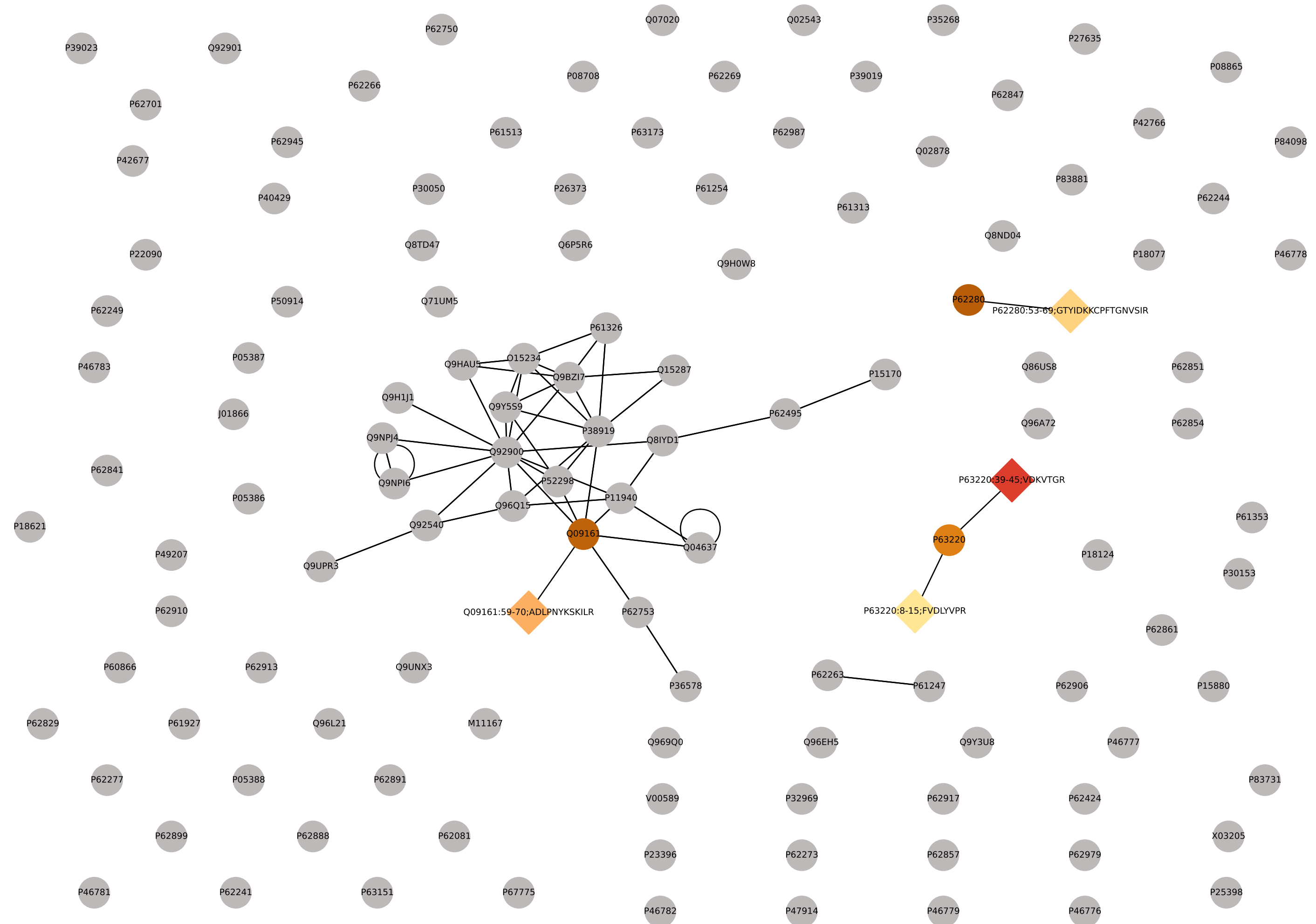
Log2 fold change: gluc vs. control
R-HSA-8854518: AURKA Activation by TPX2
p-value: 0.032600049302680456



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



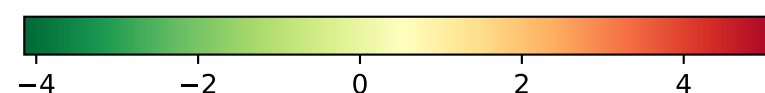
Log2 fold change: gluc vs. control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.011931898374331729



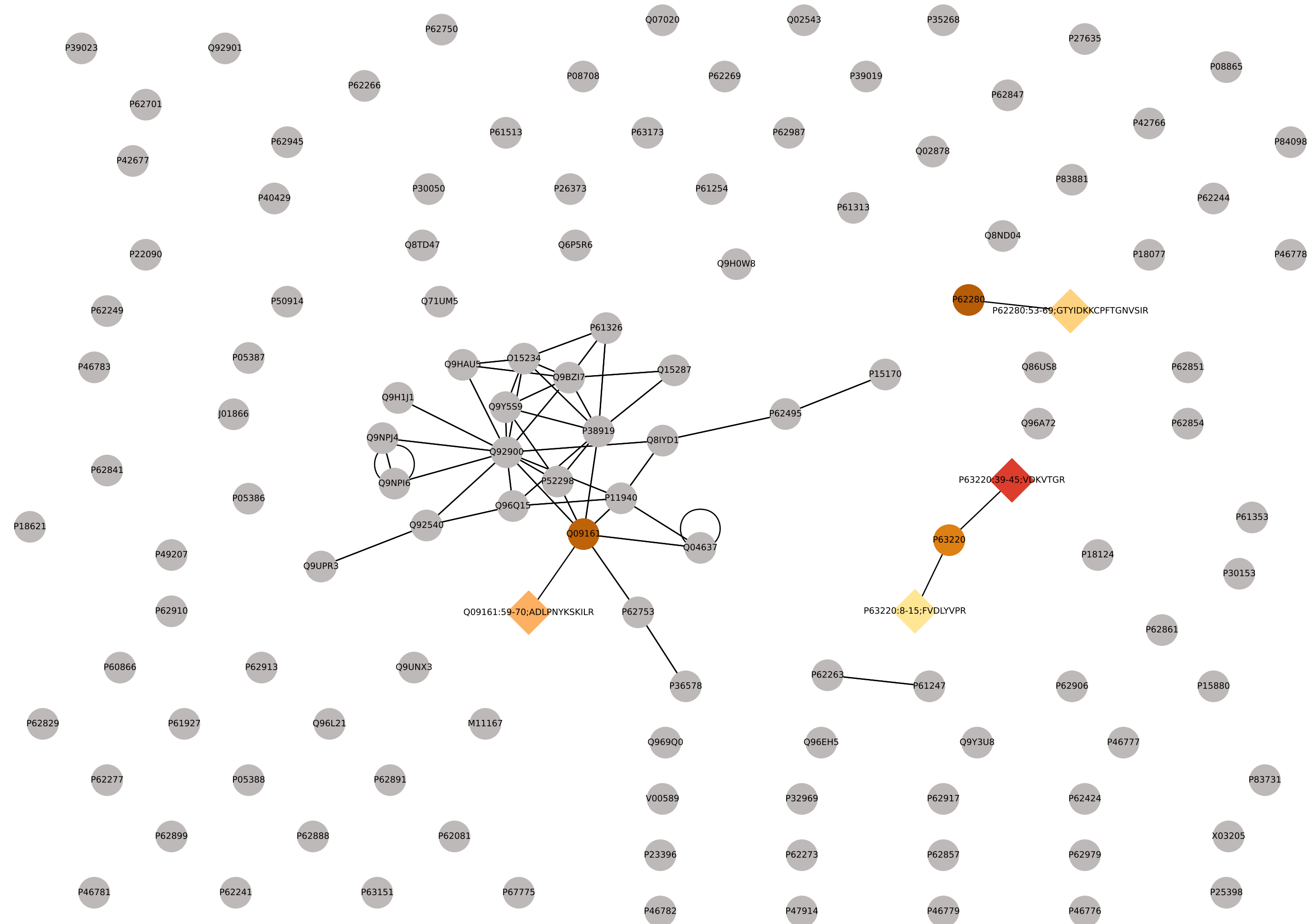
Protein Log2 fold change: gluc vs. control



Peptide Log2 fold change: gluc vs. control



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



Protein Log2 fold change: gluc vs. control



Peptide Log2 fold change: gluc vs. control

The diagram illustrates a network of protein-protein interactions. The nodes are represented by grey circles, with two nodes highlighted in orange (P61981 and Q13561) and three nodes highlighted in yellow (P61981:160-172, P61981:33-42, and Q13561:2-14). Edges represent interactions between nodes. The diagram is densely packed with nodes and edges, forming a complex web of connections. The nodes are labeled with protein IDs and some have associated domain names in brackets. The layout is circular, with nodes arranged around a central area.



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

