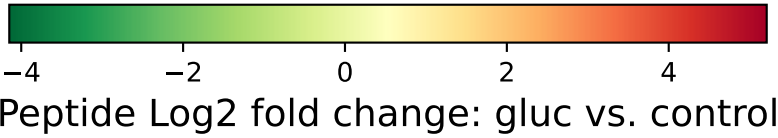
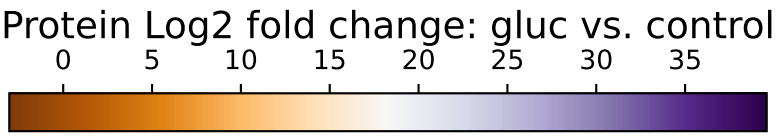
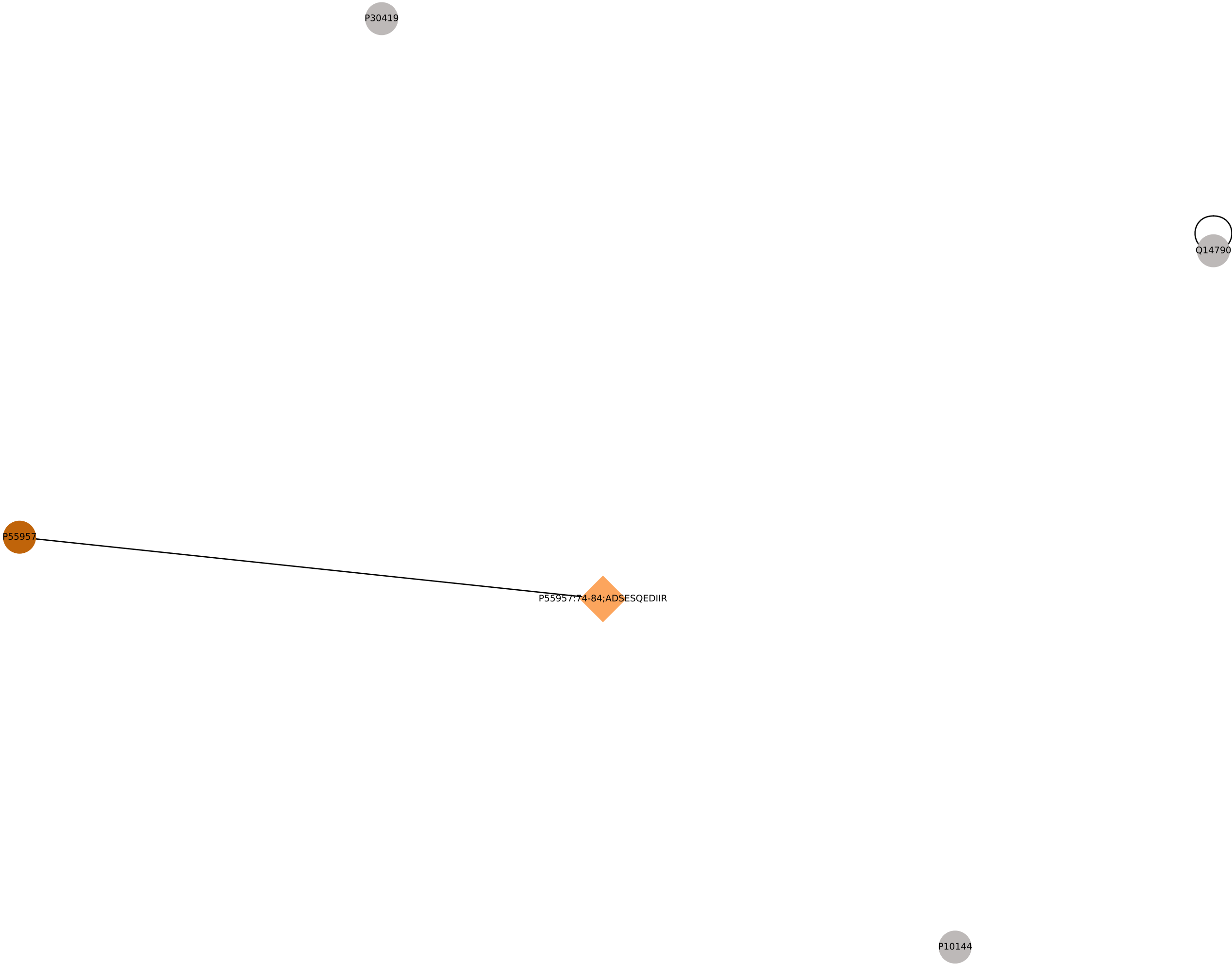
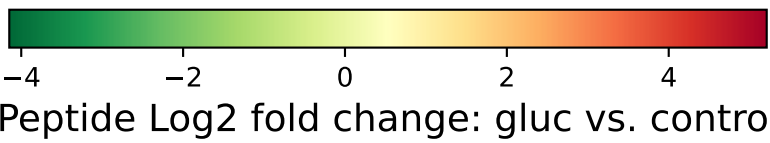
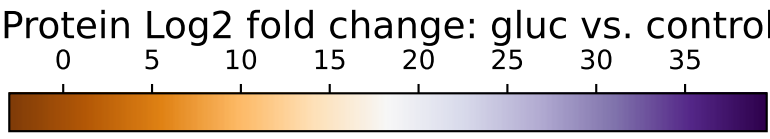
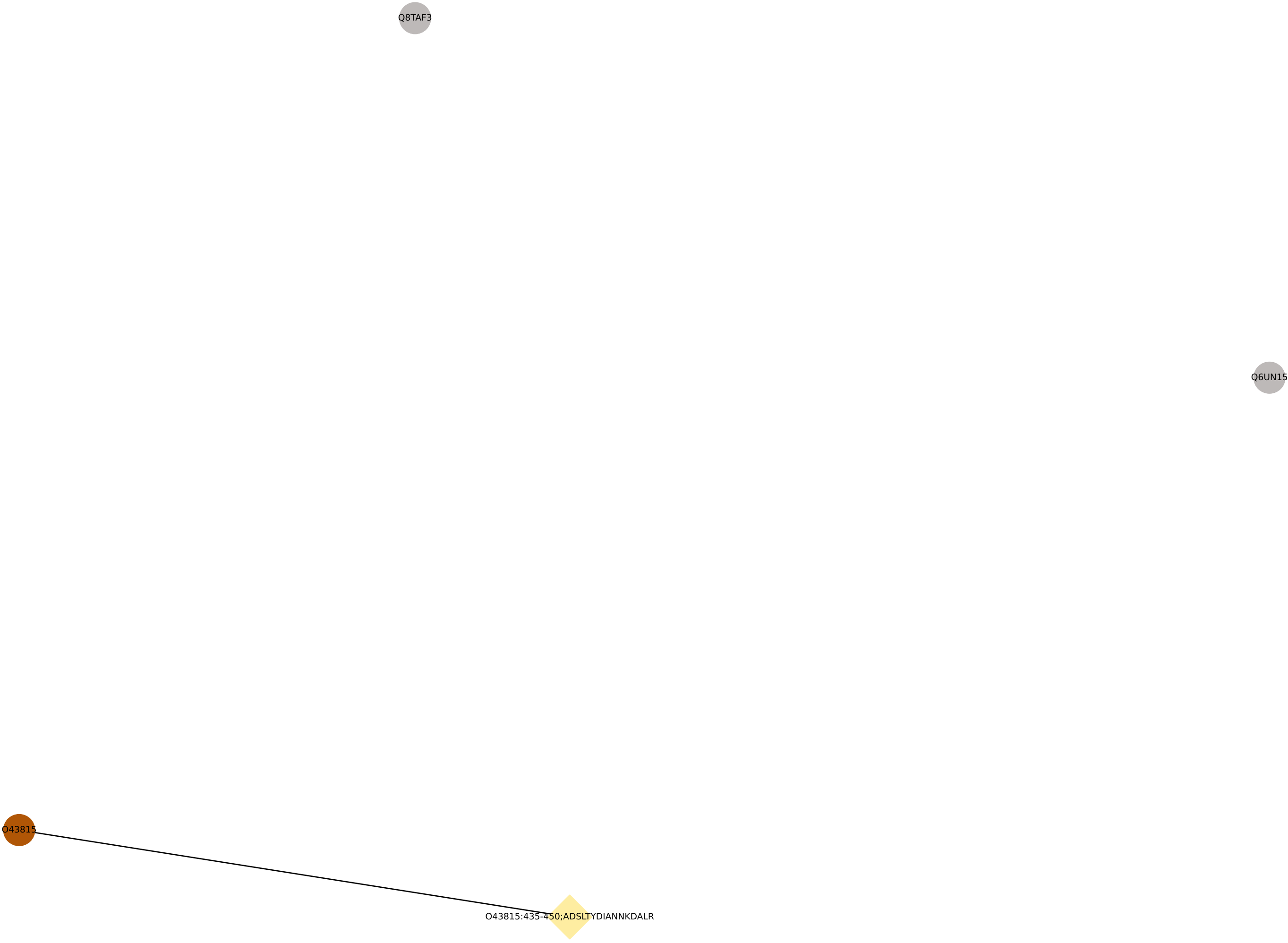


No interaction map found for pathway: R-HSA-9734195

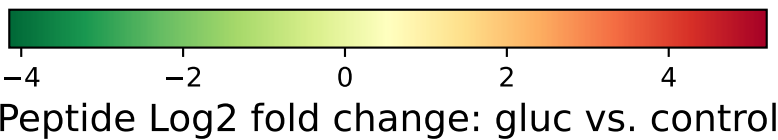
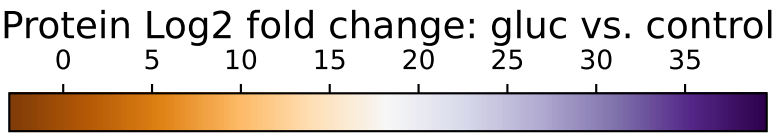
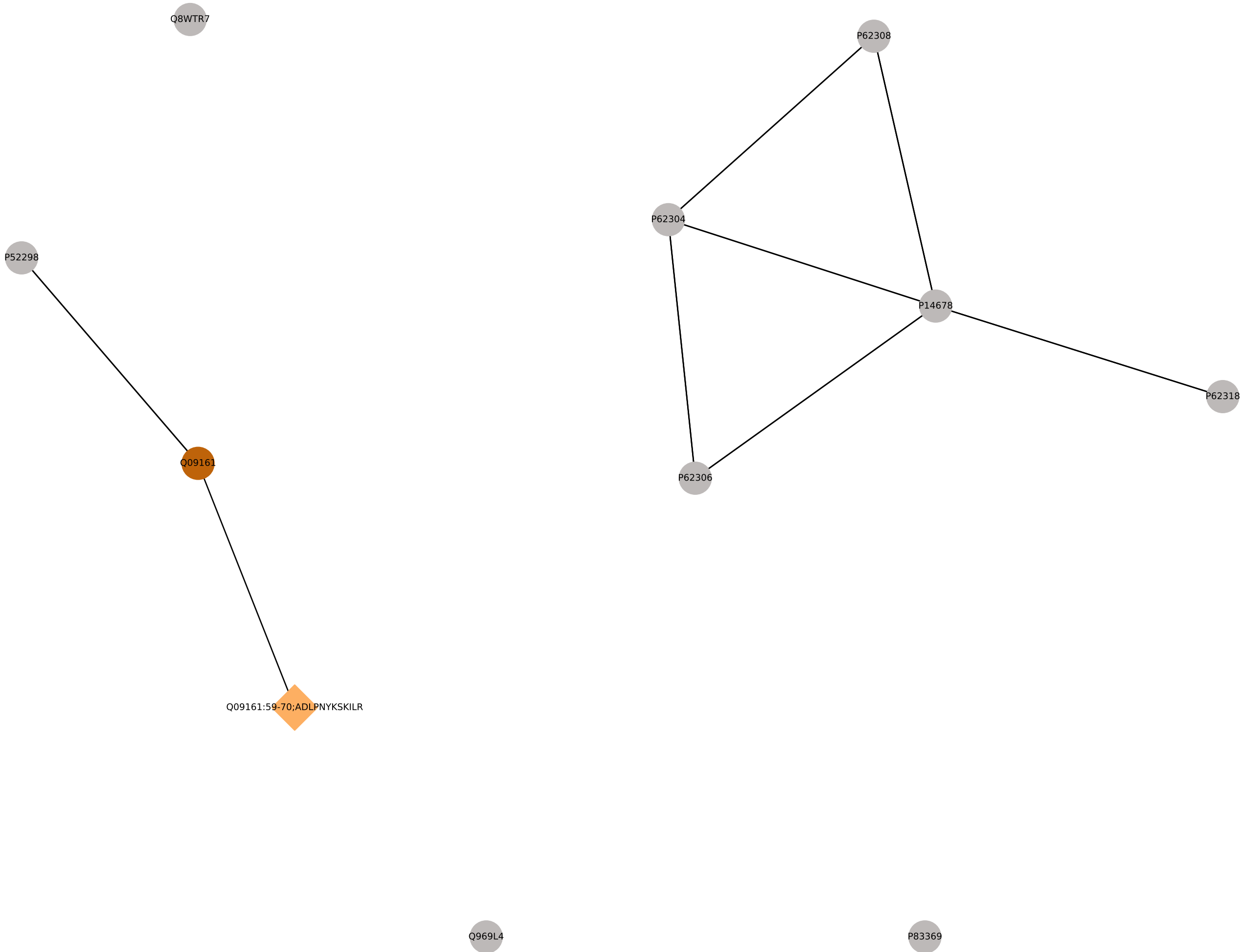
Log2 fold change: gluc vs. control
R-HSA-75108: Activation, myristoylation of BID and translocation to mitochondria
p-value: 0.015117656007649471



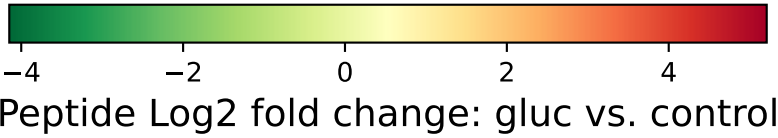
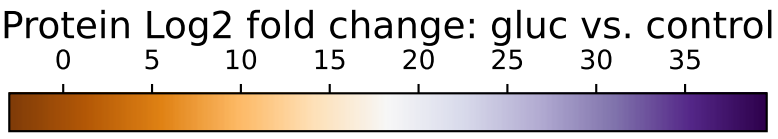
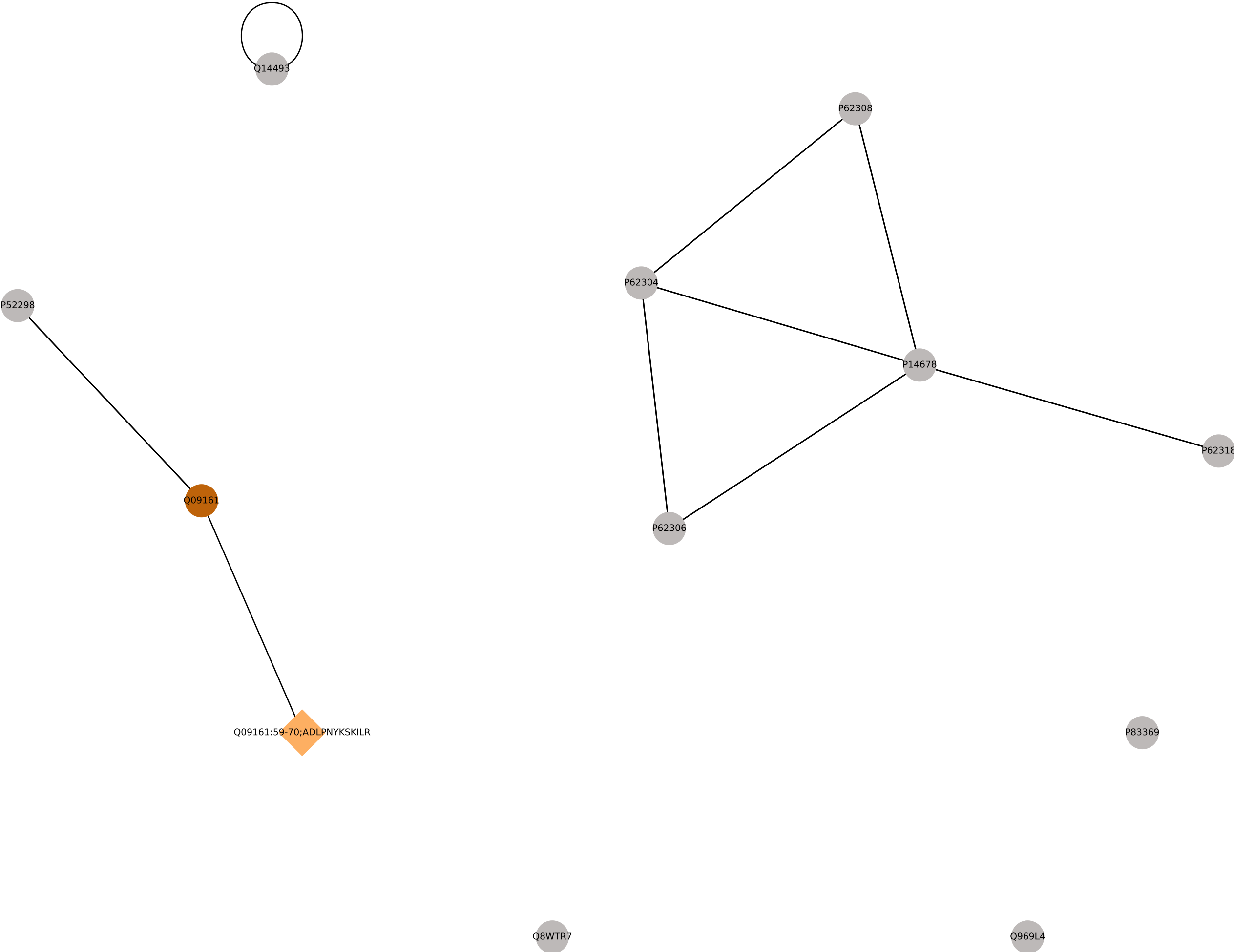
Log2 fold change: gluc vs. control
R-HSA-9673766: Signaling by cytosolic PDGFRA and PDGFRB fusion proteins
p-value: 0.018861837637962453



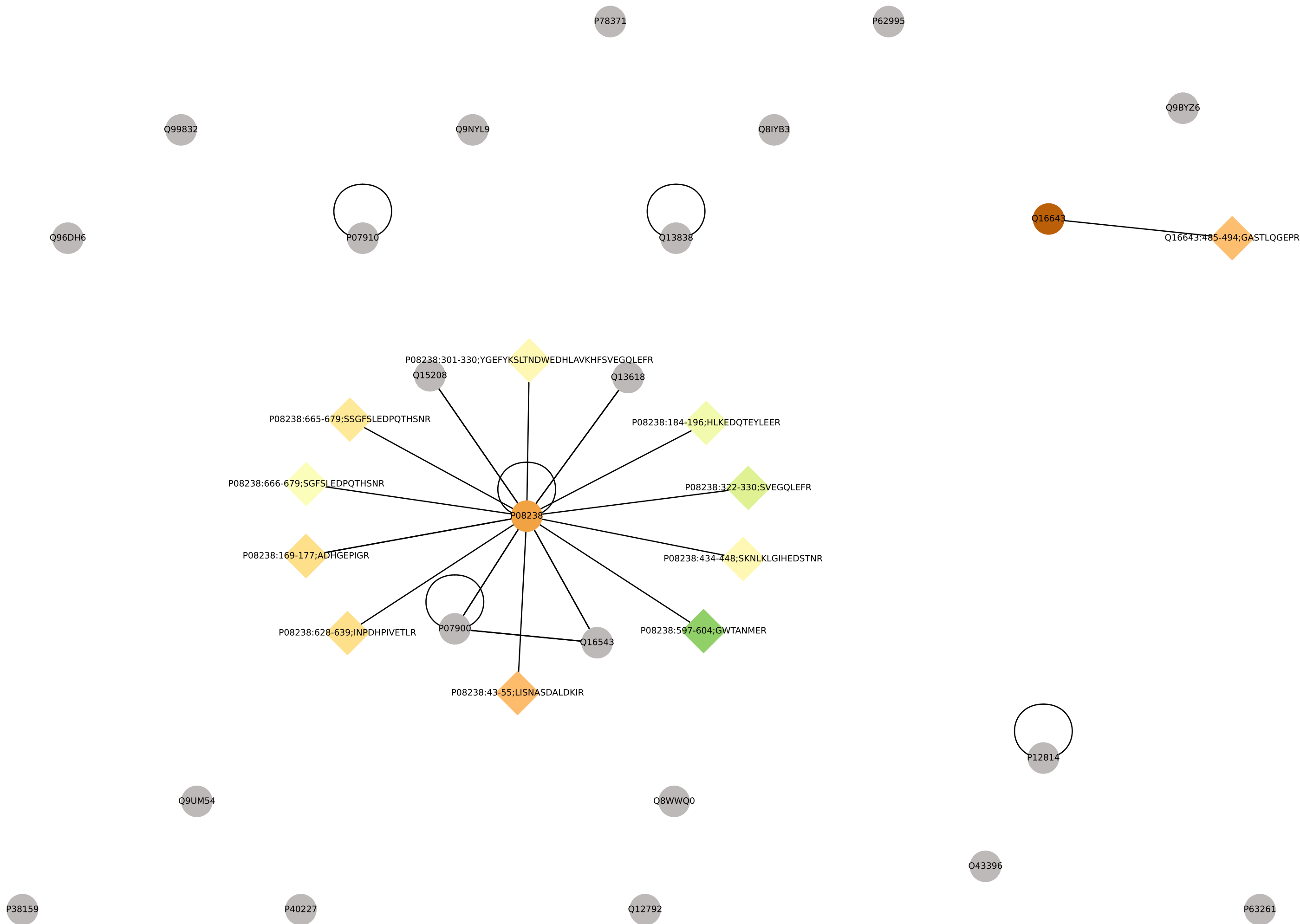
Log2 fold change: gluc vs. control
R-HSA-111367: SLBP independent Processing of Histone Pre-mRNAs
p-value: 0.03737392638204595



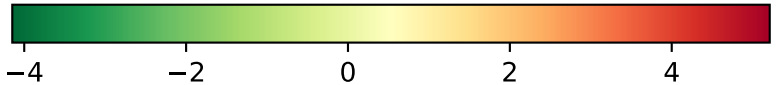
Log2 fold change: gluc vs. control
R-HSA-77588: SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs
p-value: 0.04103493715974438



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

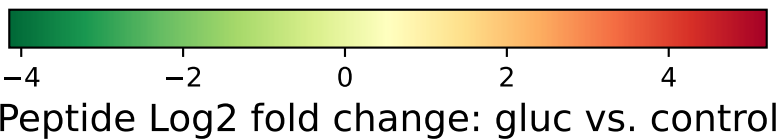
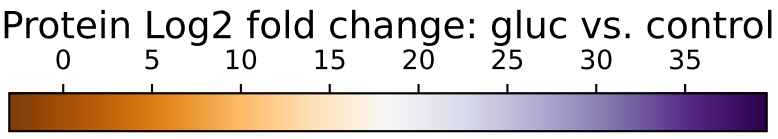
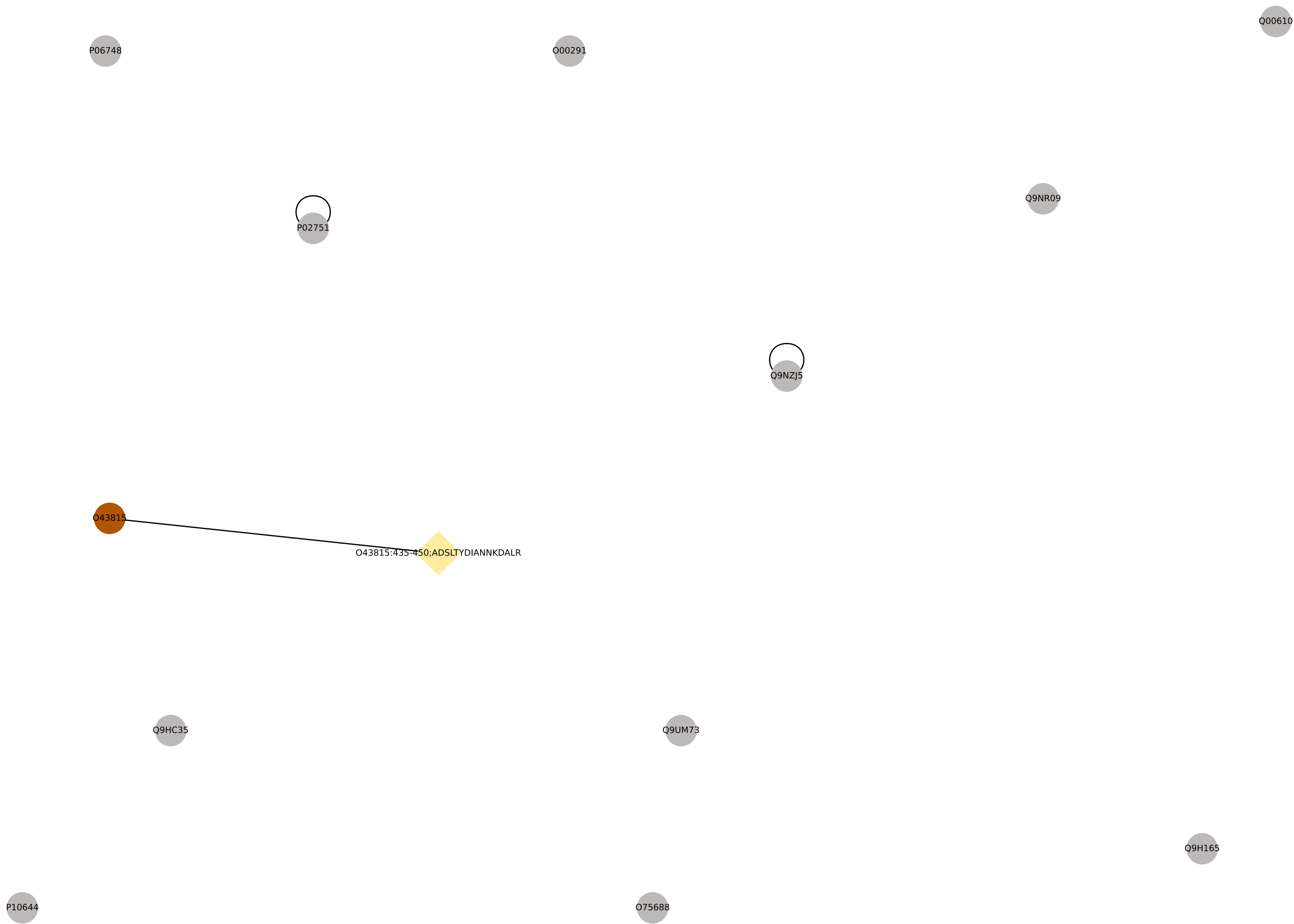


Protein Log2 fold change: gluc vs. control

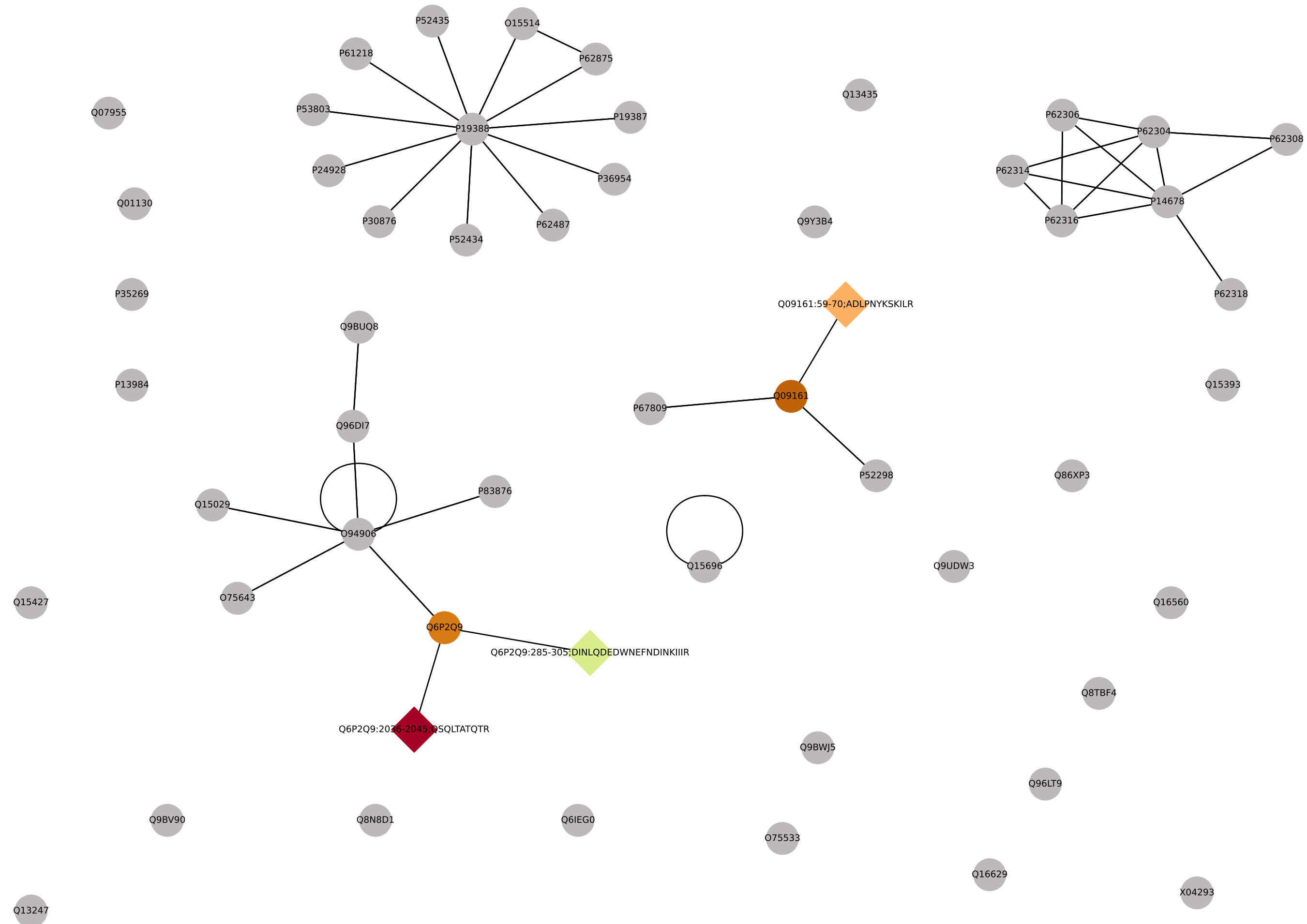


Peptide Log2 fold change: gluc vs. control

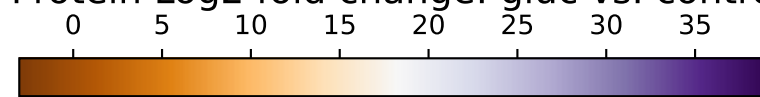
Log2 fold change: gluc vs. control
R-HSA-9700645: ALK mutants bind TKIs
p-value: 0.04468226372702311



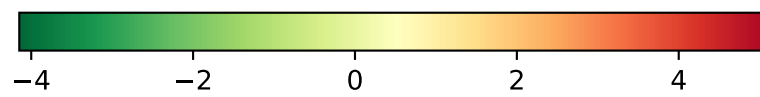
Log2 fold change: gluc vs. control
R-HSA-72165: mRNA Splicing - Minor Pathway
p-value: 0.018216773752471993



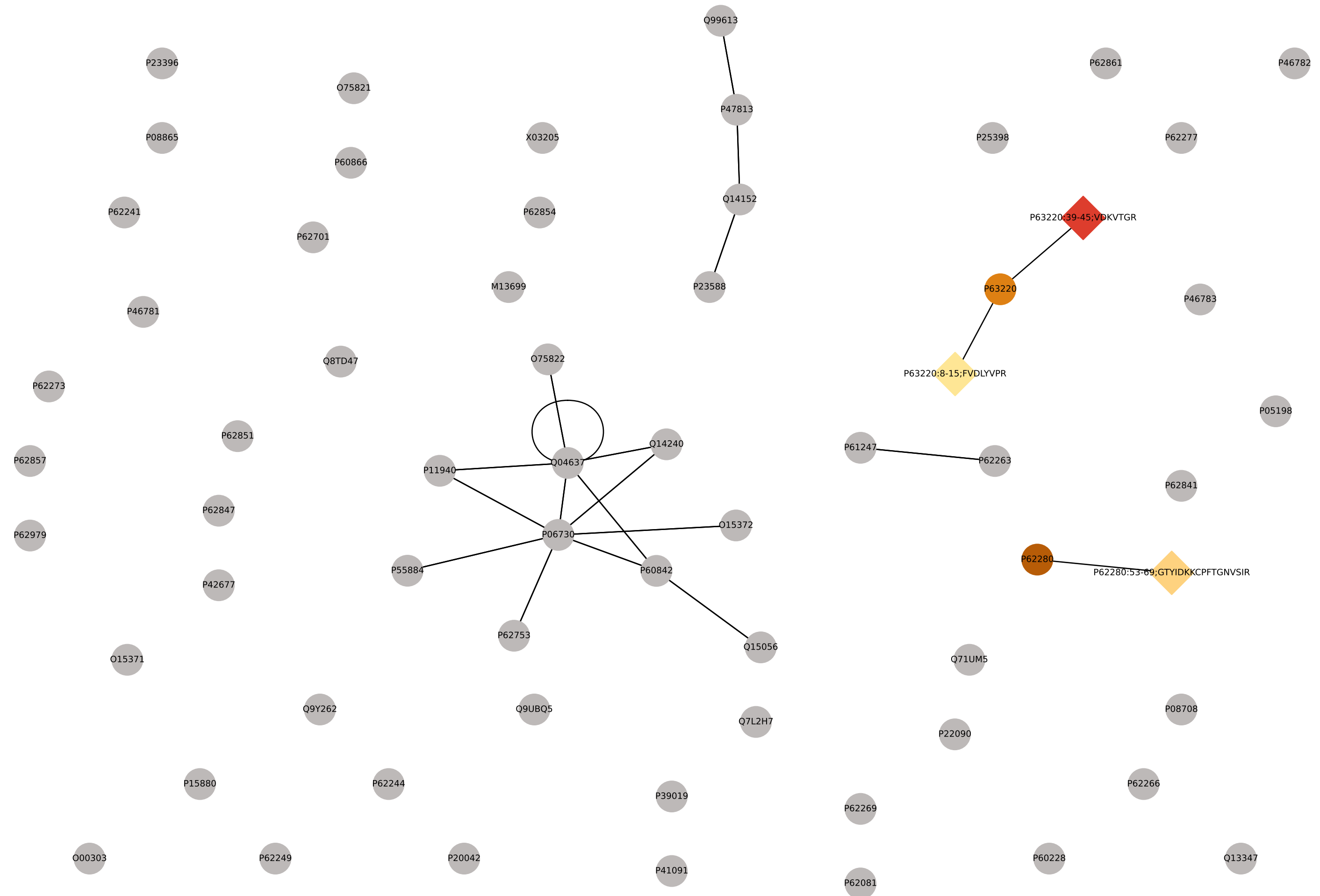
Protein Log2 fold change: gluc vs. control



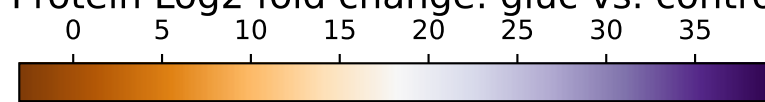
Peptide Log2 fold change: gluc vs. control



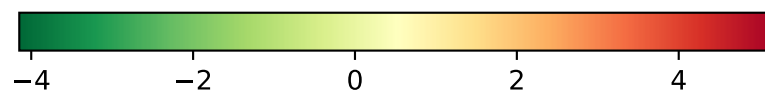
Log2 fold change: gluc vs. control
R-HSA-72649: Translation initiation complex formation
p-value: 0.023554931232115828



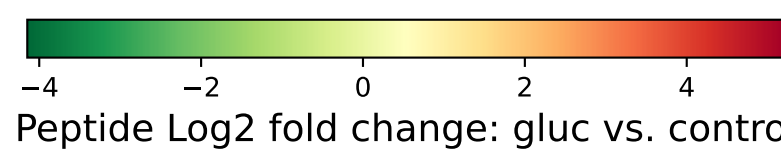
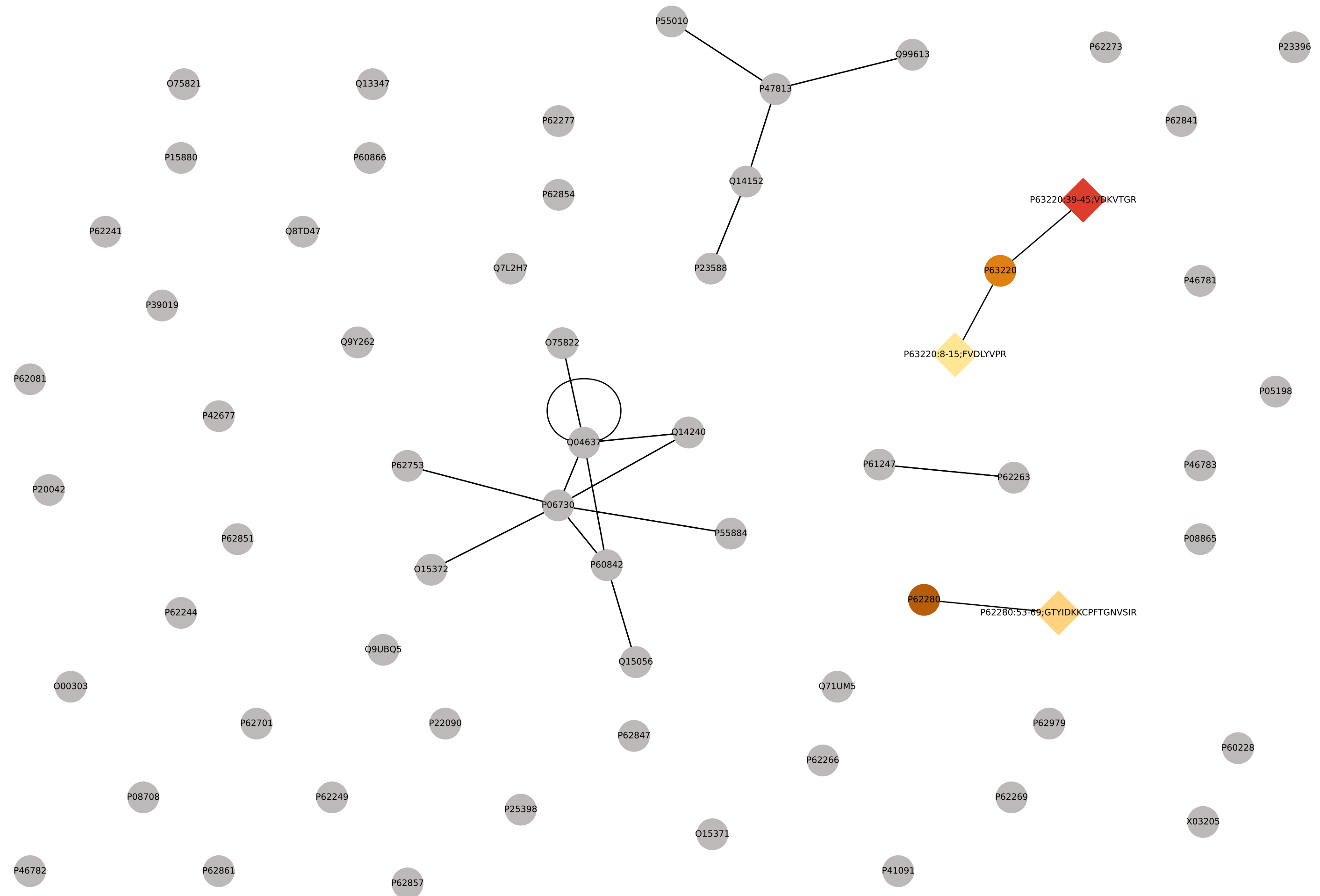
Protein Log2 fold change: gluc vs. control



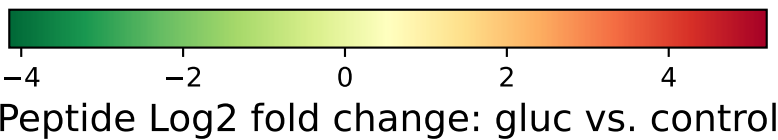
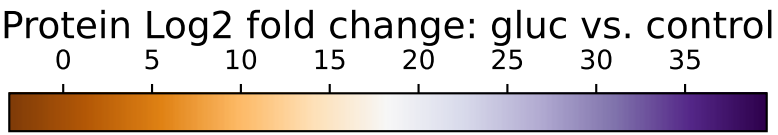
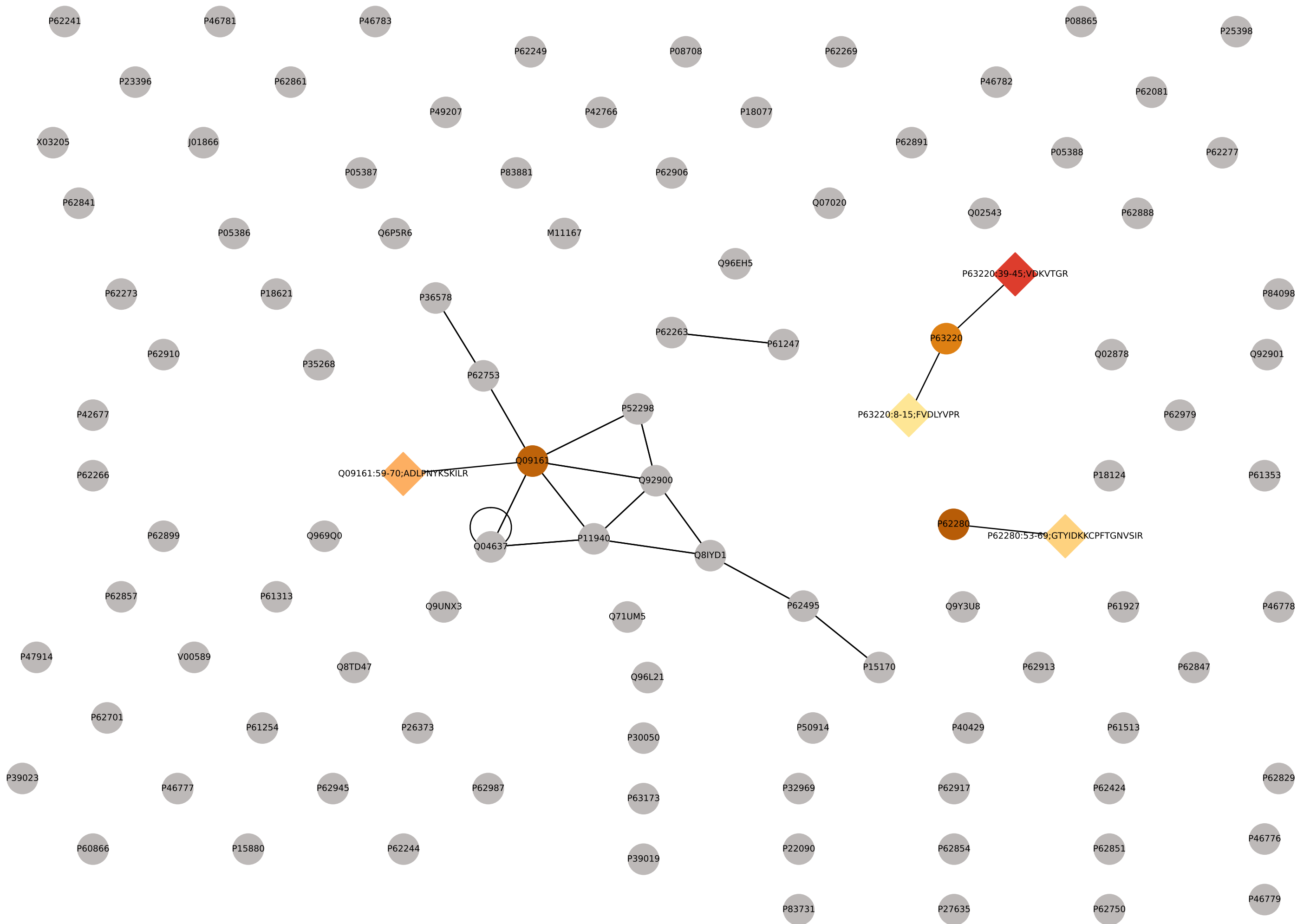
Peptide Log2 fold change: gluc vs. control



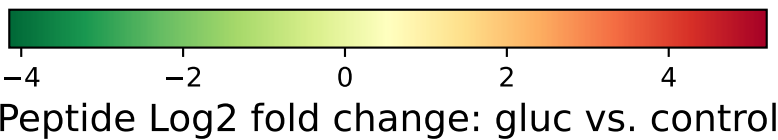
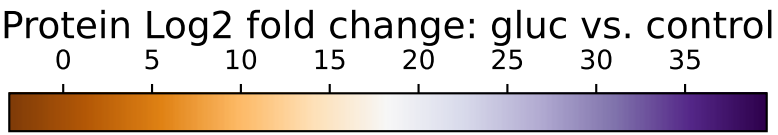
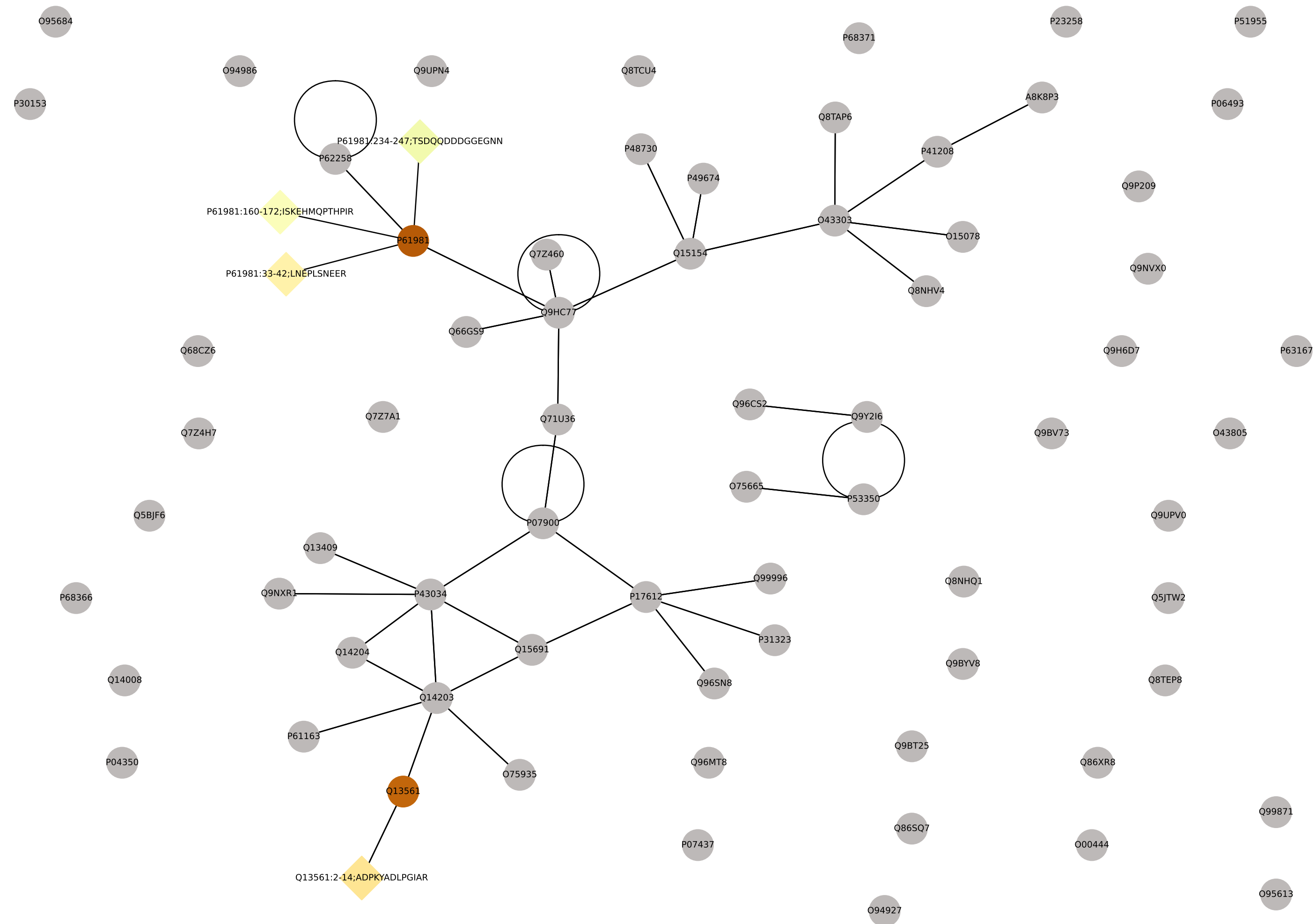
Log2 fold change: gluc vs. control
R-HSA-72702: Ribosomal scanning and start codon recognition
p-value: 0.024978417082091475



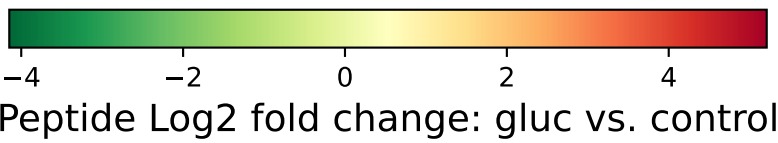
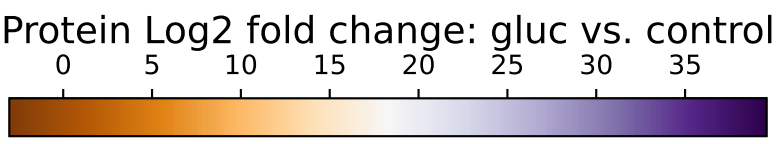
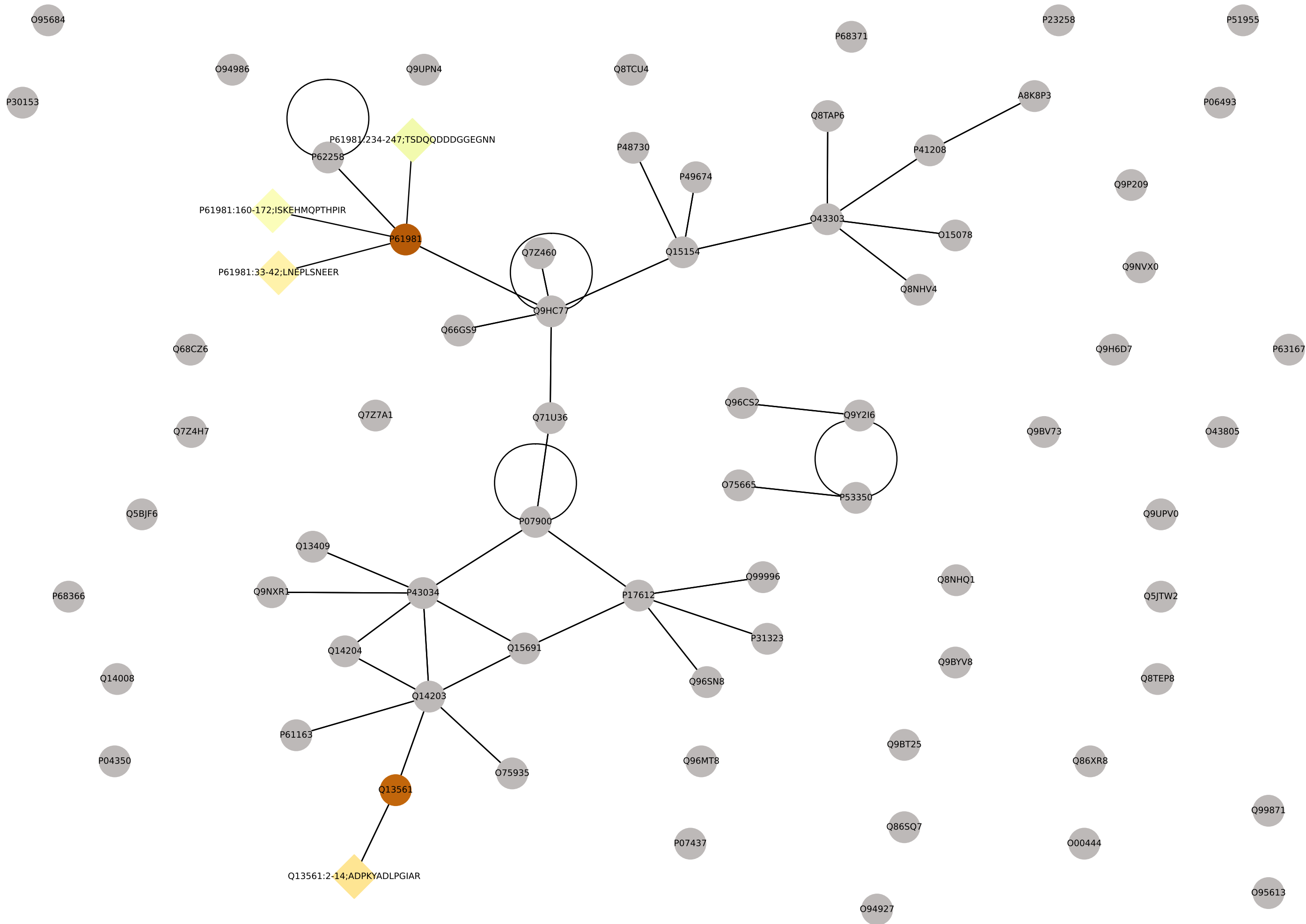
Log2 fold change: gluc vs. control
R-HSA-975956: Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
p-value: 0.006855569728165922



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



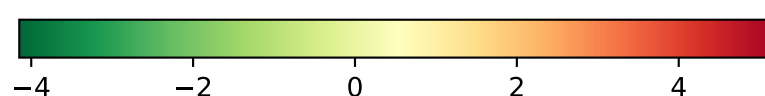
Log2 fold change: gluc vs. control
R-HSA-380259: Loss of Nlp from mitotic centrosomes
p-value: 0.030227589686308676



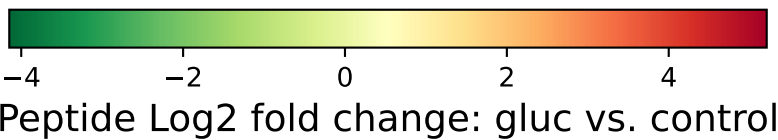
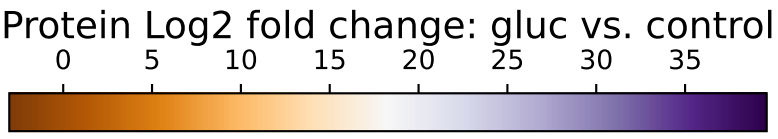
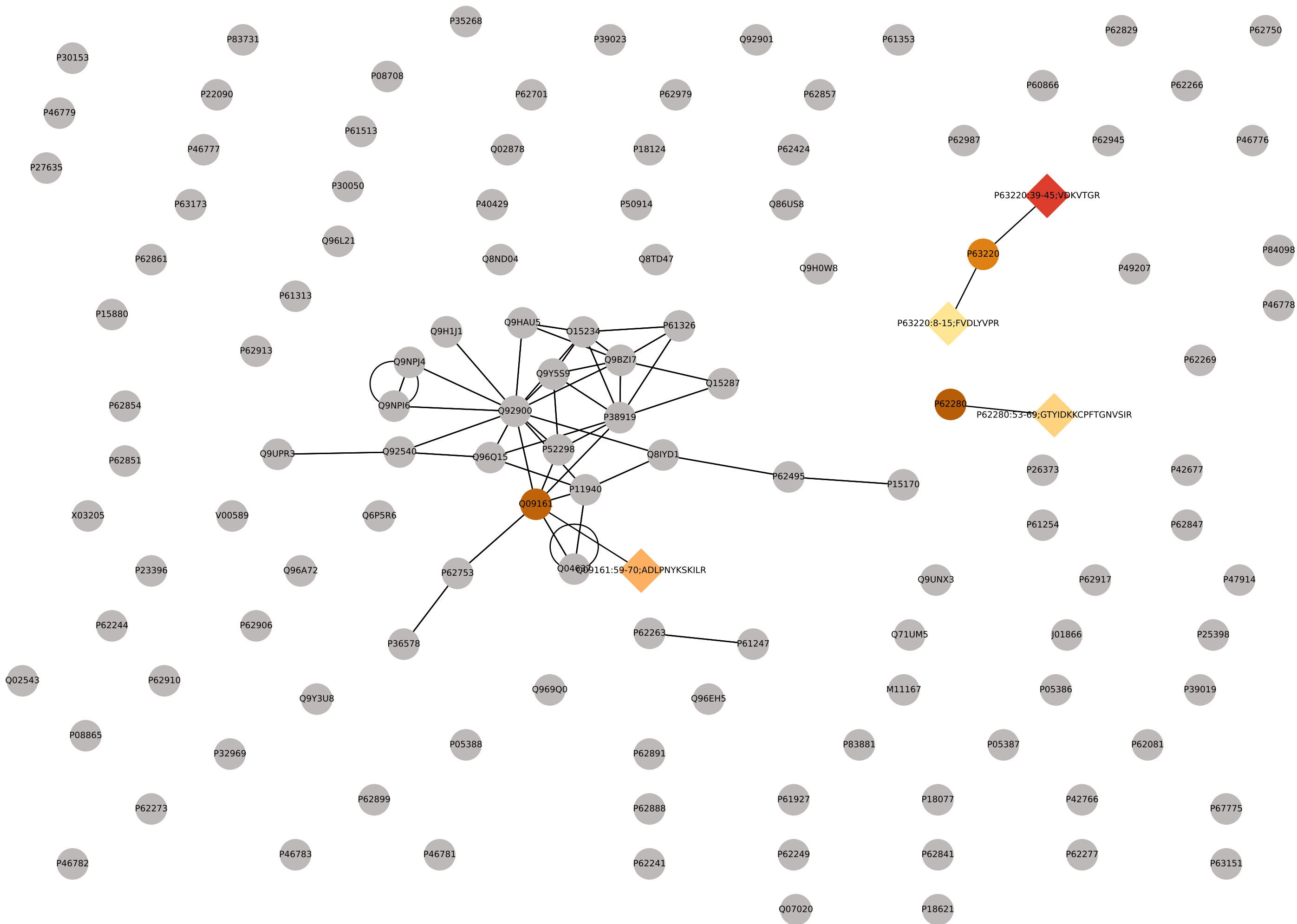


The diagram illustrates a network of protein interactions. Key features include:

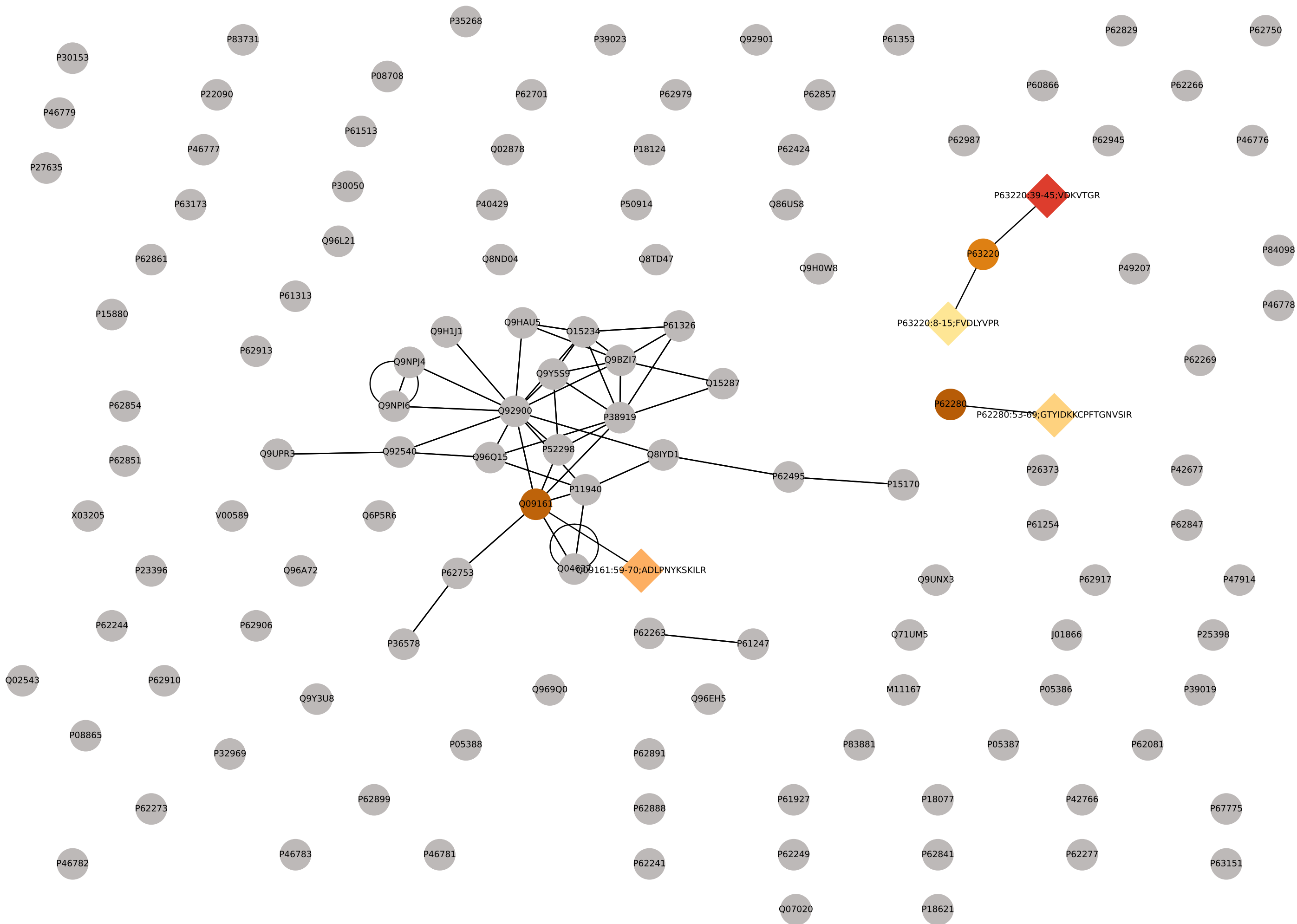
- Nodes:** Represented by grey circles. Notable nodes include P61981 (orange), P13561 (orange), and several yellow-highlighted nodes representing specific protein domains or regions.
- Edges:** Lines connecting nodes, representing interactions. Some nodes have self-loops, indicating self-interactions.
- Clusters:** Groups of nodes that are highly interconnected, suggesting functional modules or complexes.
- Labels:** Node labels are provided in a standard font, often followed by a description of the protein or domain in a smaller font.



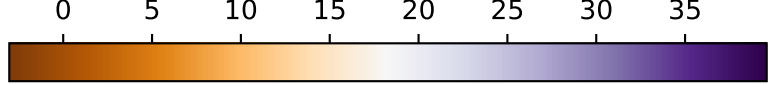
Log2 fold change: gluc vs. control
R-HSA-927802: Nonsense-Mediated Decay (NMD)
p-value: 0.011931898374331729



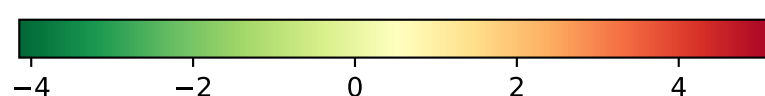
Log2 fold change: gluc vs. control
R-HSA-975957: Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
p-value: 0.011931898374331729



Protein Log2 fold change: gluc vs. control



Peptide Log2 fold change: gluc vs. control

[illegible]

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

