Figure S1

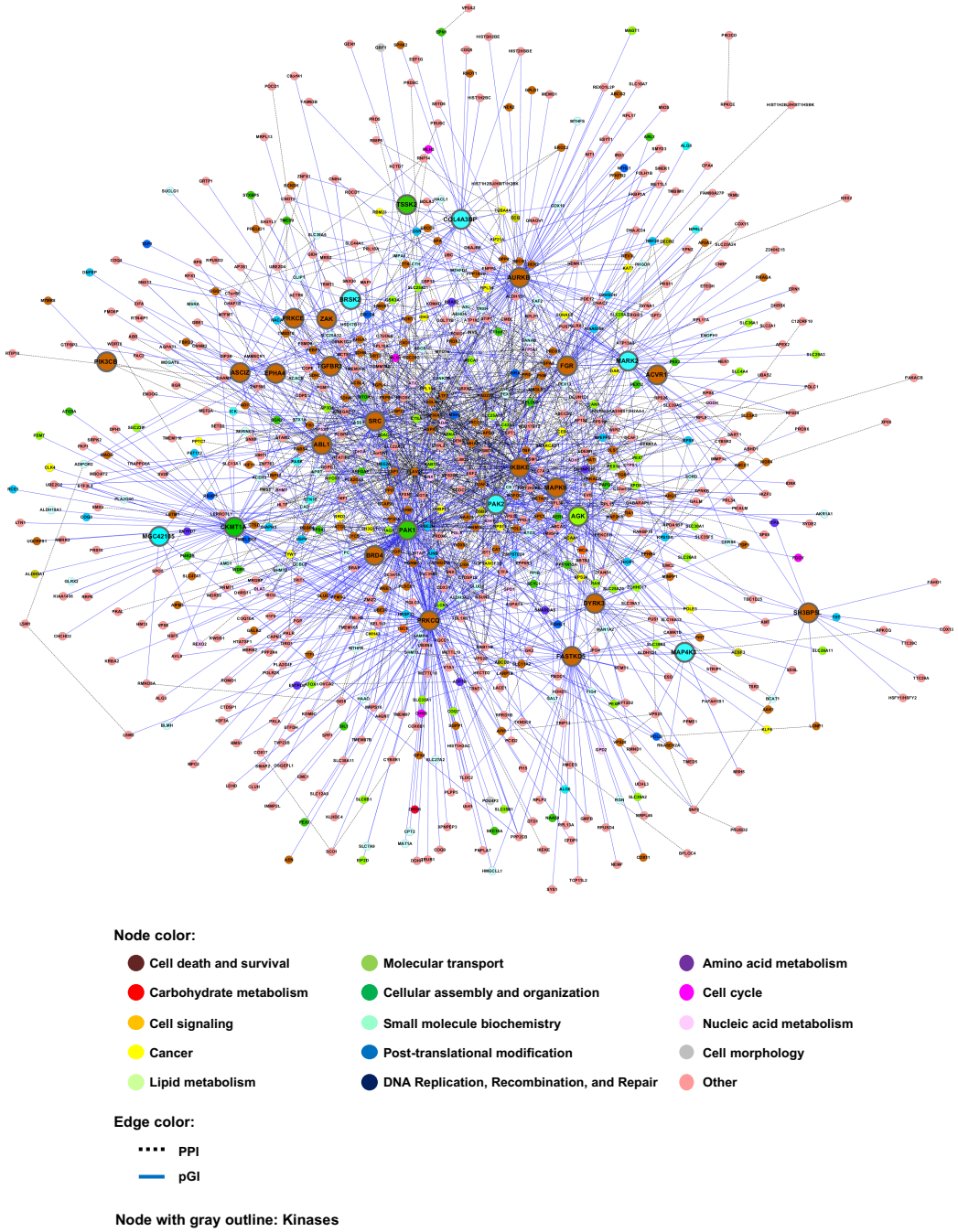
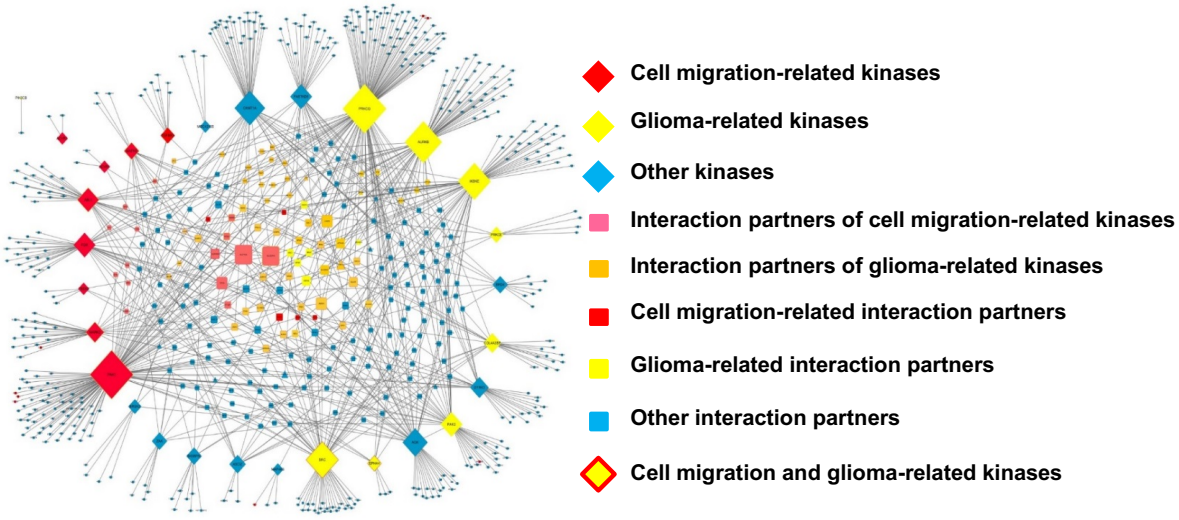


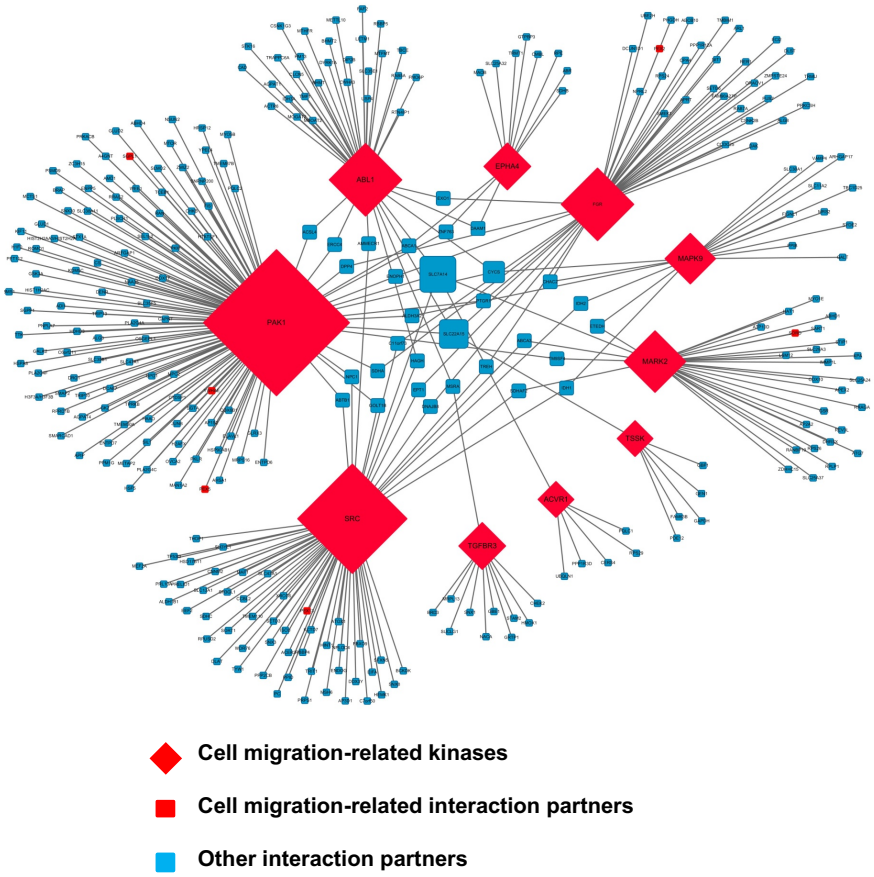
Figure S1. Human kinase-yeast interactome network. Human orthologs of yeast genes, the deletion of which suppressed the toxicity of the 28 kinase ORFs, were identified. A network view of these orthologs was generated using Cytoscape. The color of the node corresponds to the biological function category to which the gene belongs. The color of an edge indicates the type of interaction (PPI, protein-protein interaction, black dotted line; pGI, predicted genetic interaction, blue line).

Figure S2.

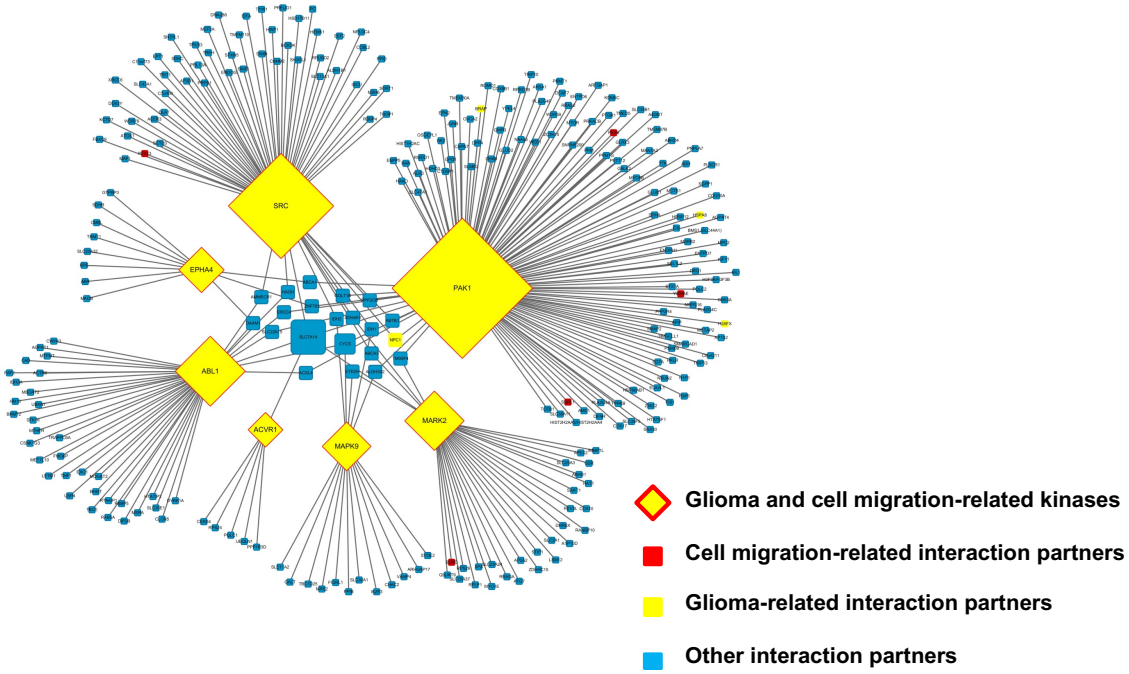
a **Kinase network**



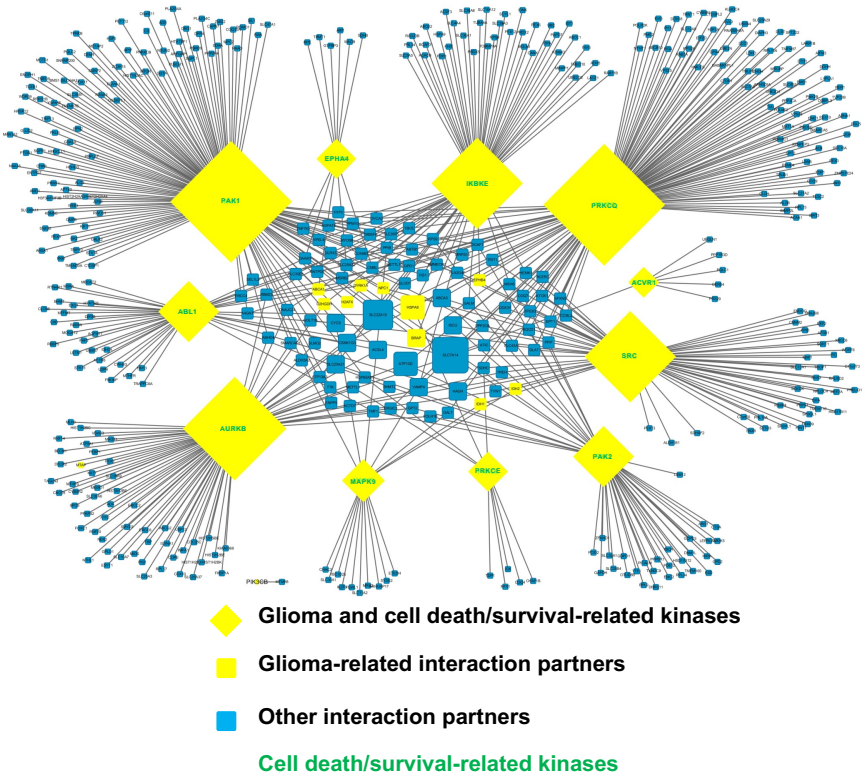
b **Subnetwork of cell migration-related kinases**



c **Subnetwork of glioma and cell migration-related kinases**



d **Subnetwork of glioma and cell death/survival-related kinases**



e **Subnetwork of glioma, cell migration and cell death/survival-related kinases**

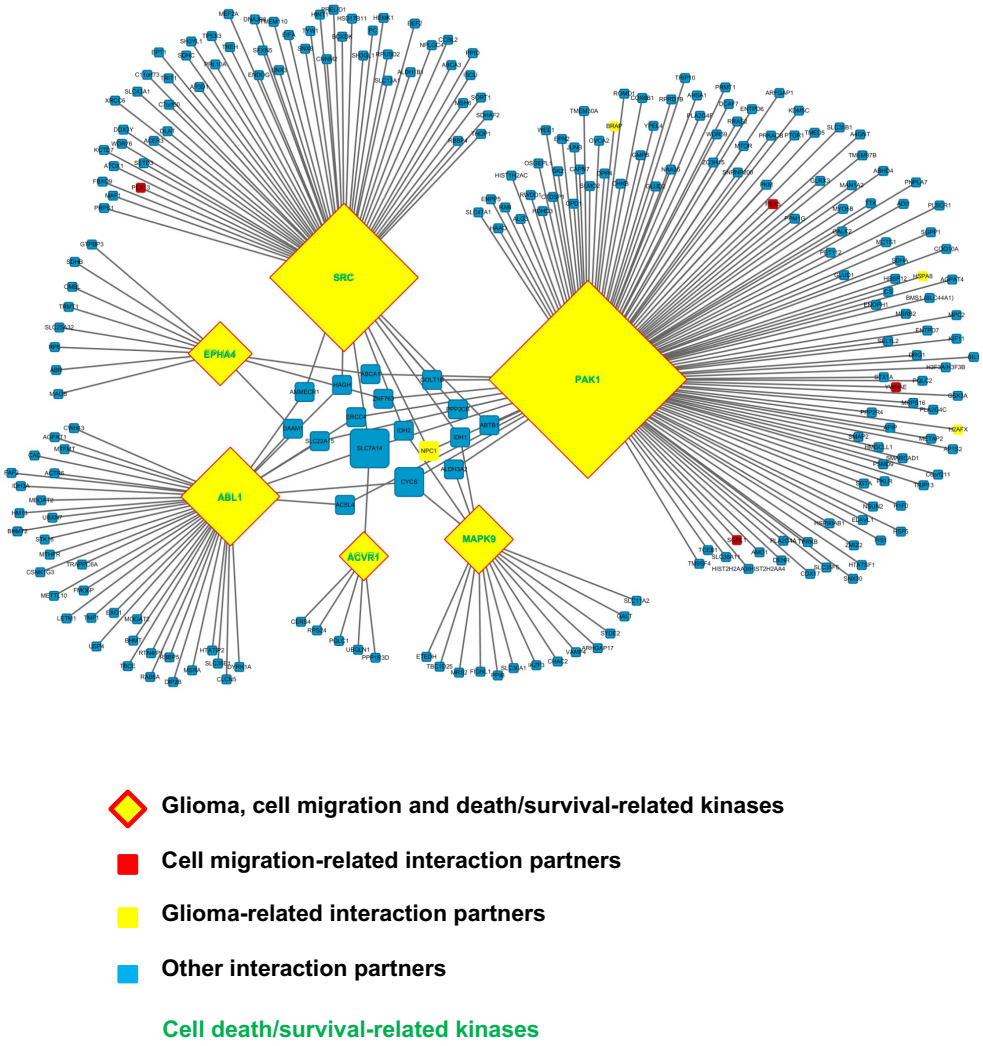


Figure S2. Subnetwork of human kinase-yeast genetic interactions. (a) Network of 28 kinases and their genetic interactions showing the relationships with cell migration and glioma. Subnetworks were also constructed with a focus on cell migration (b), glioma and cell migration (c), glioma and cell death/survival (d), and glioma, cell migration, and cell death/survival (e).