



Supplementary Figure S4. Integrated functional annotation and interaction network analysis of differentially expressed genes in response to AKT inhibition. (a–d) Enrichment analyses of consensus DEGs in LNCaP and BxPC-3 cells based on UniProt Annotated Keywords and TISSUES database categories. Results are presented as dot plots grouped by semantic similarity (threshold = 0.4). Dot size represents the number of genes associated with each term, and color intensity reflects statistical significance (FDR). Panels (a–b) correspond to BxPC-3 cells, and panels (c–d) to LNCaP cells. (e–f) Protein–protein interaction networks constructed from consensus DEGs in LNCaP (e) and BxPC-3 (f) cells using STRING and visualized in Cytoscape. (g–h) Community detection analyses highlighting modular organization of lineage-specific functional clusters. Supporting enrichment statistics are provided in Supplementary Tables S6 and S7.