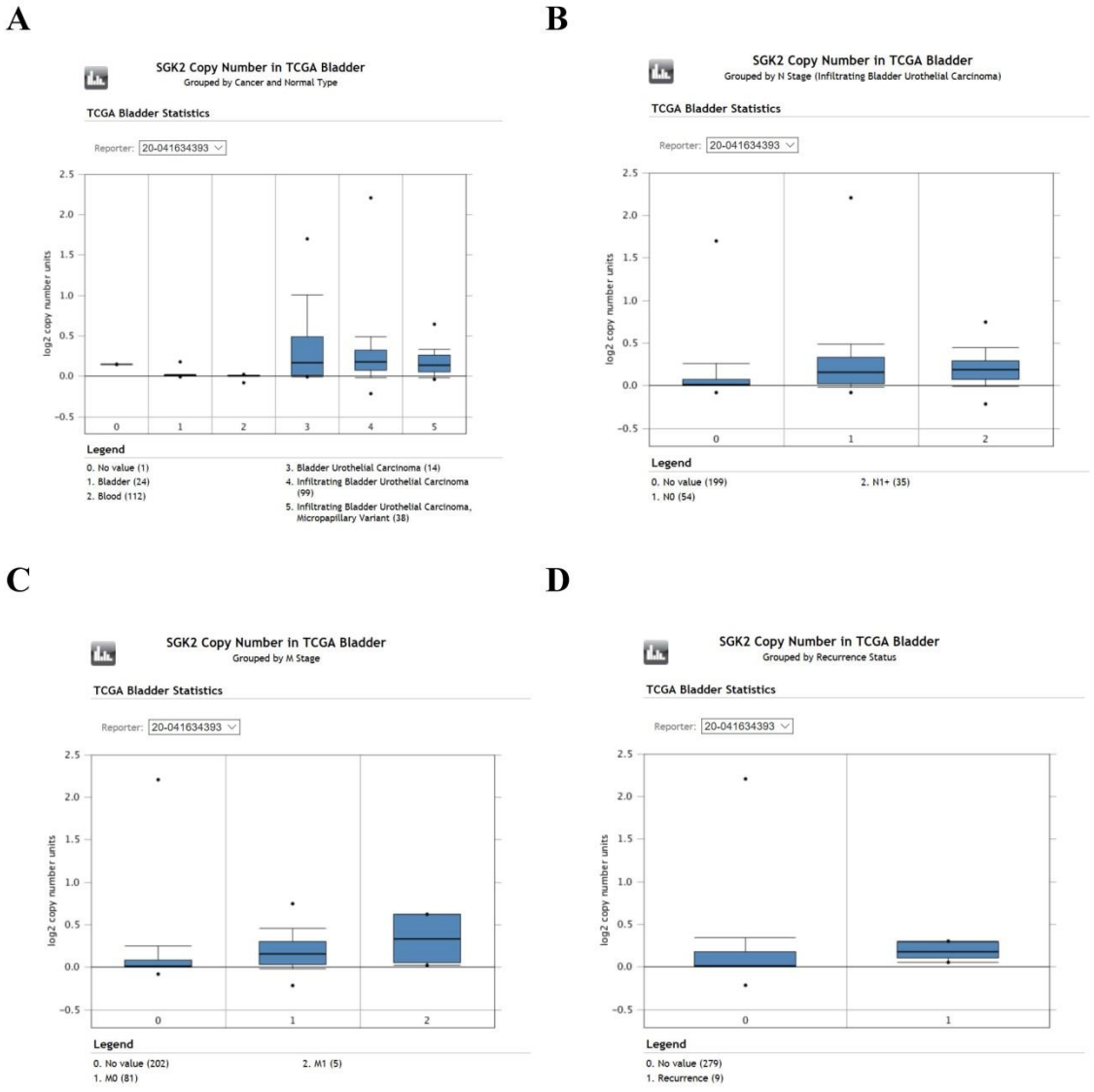

Figure S1: SGK2 copy number variations (CNVs) were positively related to high pathological and clinical stages, as well as the recurrence status in bladder cancer patients. (A). Copy number variation comparison between normal and cancer tissues; **(B).** Copy number variation comparison between different lymph node metastatic status; **(C).** Copy number variation comparison between different distant metastatic status; **(D).** Copy number variation comparison between different tumor recurrence status.

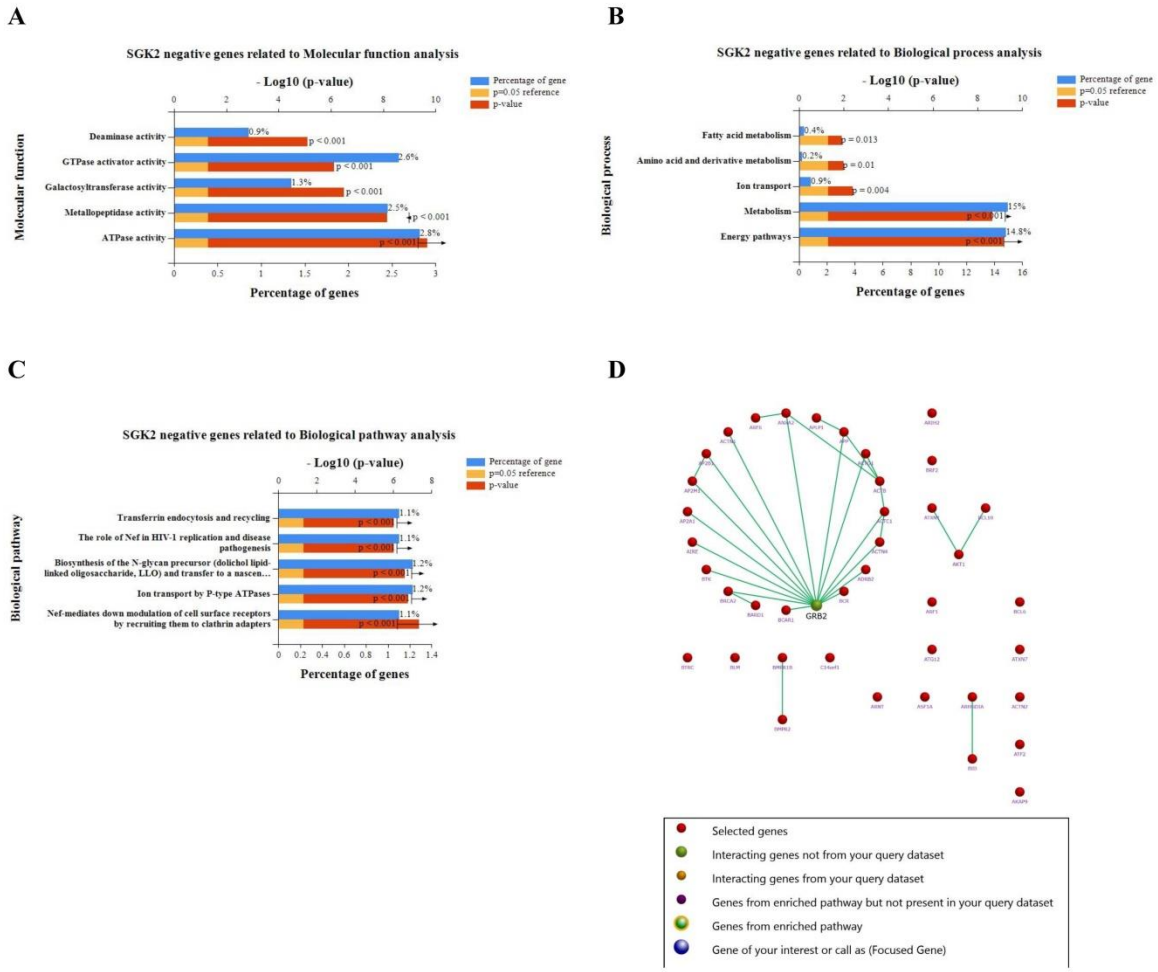

Figure S2: Negative molecular interaction and function analysis of SGK2. (A). Molecular function analysis suggested that negative genes of SGK2 were mainly enriched in ATPase activity, metallopeptidase activity, galactosyltransferase activity, GTPase activator activity and deaminase activity. **(B).** Biological process analysis indicated SGK2 negative related genes were mainly involved in energy, metabolism, ion transport, amino acid and derivative metabolism and fatty acid metabolism. **(C).** Biological pathway analysis indicated SGK2 negative related genes were enriched in Nef-mediates down modulation of cell surface receptors, Iron transporter by P-type ATPases, Biosythesis of the N-glycan precusor, Nef in HIV-1 replication and disease pathogenesis, transferrin endocytosis and recycling. **(D).** The protein network using FunRich software identified that GRB2 was the key enriched interactive protein in SGK2-negative gene network.

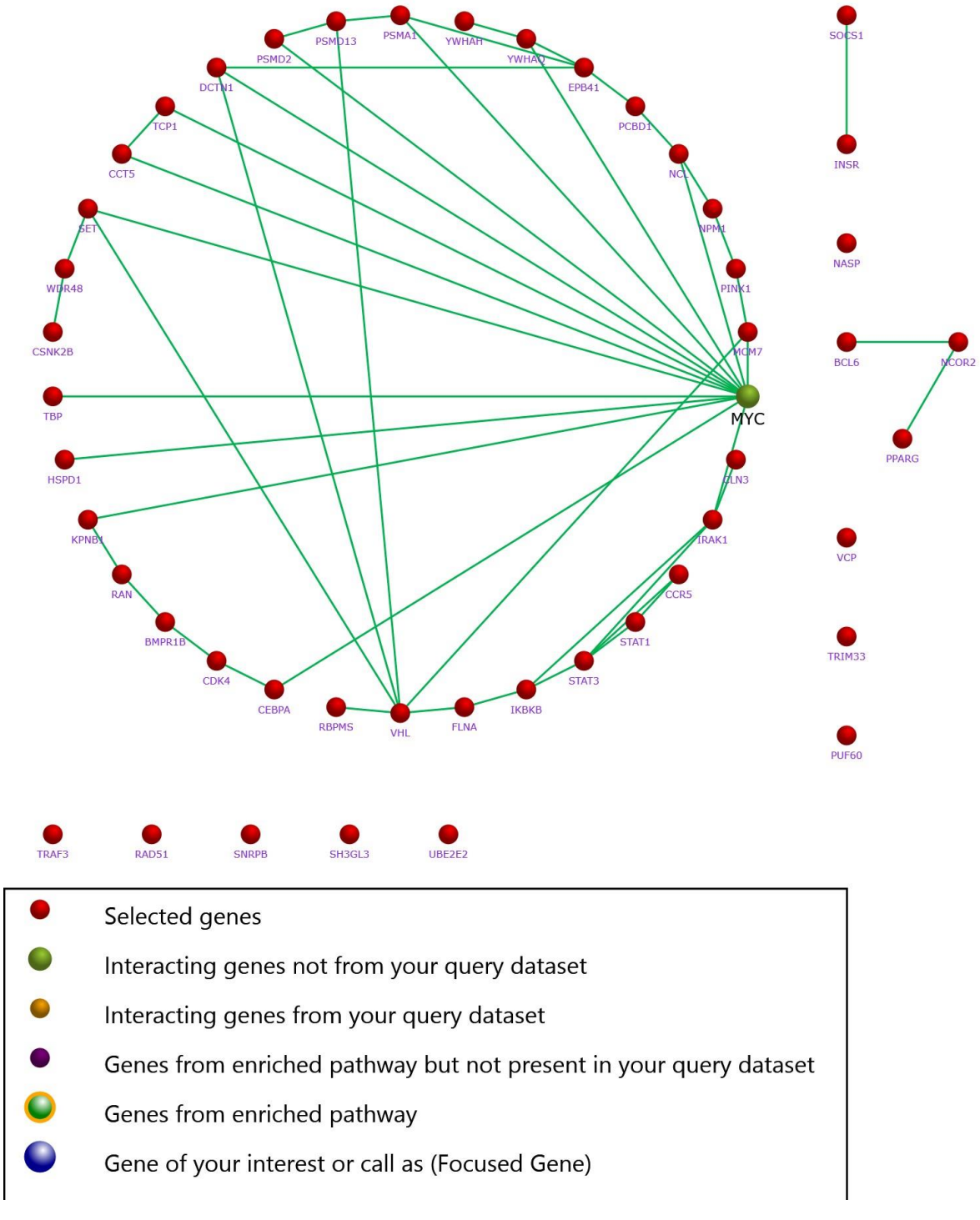

Figure S3: The protein network using FunRich software identified that c-Myc was the key enriched interactive protein in SGK2-positive gene network.