In a study, dataset GSE50161 was used to construct a co-expression network for weighted gene co-expression network analysis. Two modules (dubbed brown and turquoise) were found to have the strongest correlation with glioblastoma (Glioblastoma). Functional enrichment analysis indicated that the brown module was involved in the cell cycle, DNA replication, and pyrimidine metabolism. The turquoise module was primarily related to circadian rhythm entrainment, glutamatergic synapses, and axon guidance. Hub genes were screened by survival analysis using The Cancer Genome Atlas and Human Protein Atlas databases and further tested using the GSE4290 and Gene Expression Profiling Interactive Analysis databases. The eight hub genes (NUSAP1, SHCBP1, KNL1, SULT4A1, SLC12A5, NUF2, NAPB, and GARNL3) were verified at both the transcriptional and translational levels, and these gene expression levels were significant based on the World Health Organization classification system. These hub genes may be potential biomarkers and therapeutic targets for the accurate diagnosis and management of Glioblastoma [1)].

1)
Li C, Pu B, Gu L, Zhang M, Shen H, Yuan Y, Liao L. Identification of key modules and hub genes in glioblastoma multiforme based on co-expression network analysis. FEBS Open Bio. 2021 Jan 10. doi: 10.1002/2211-5463.13078. Epub ahead of print. PMID: 33423377.