Materials and Methods

Myc expression and survival analysis in sarcoma patients from TCGA data.

The Cancer Genome Atlas (TCGA) is a cancer genomics program that molecularly characterized over 20,000 primary cancer and matched normal samples spanning 33 cancer types. OncoLnc is a website tool for interactively exploring survival correlations, and for downloading clinical data coupled to expression data for mRNAs, miRNAs, or long noncoding RNAs (lncRNAs). It contains survival data for 8,647 patients from 21 cancer studies performed by TCGA. The analysis of Myc expression and survival in sarcoma patients from TCGA was performed by OncoLnc (http://www.oncolnc.org/)[1].

1.   Anaya J. 2016. OncoLnc: linking TCGA survival data to mRNAs, miRNAs, and lncRNAs. PeerJ Computer Science 2:e67 https://doi.org/10.7717/peerj-cs.67.