

Supplementary data

Materials and Methods

TCGA RNA-Seq (IlluminaHiSeq_RNASeqV2) and corresponding clinical data were downloaded from TCGA website (<https://tcga-data.nci.nih.gov/tcga/>)^[1]. RNA-Seq analysis used data from 472 lung adenocarcinoma and 59 adjacent normal tissues. The data were analyzed with GraphPad Prism 5 software version 5.03 (GraphPad Software Inc., La Jolla, CA, USA), and statistical analyses were performed using SPSS software (version 16.0, SPSS Inc., Chicago, IL, USA). Results were analyzed by the Mann-Whitney U-test. A P-value of <0.05 was considered statistically significant.

Results

To identify the expression of NHERF1 in the tissues of patients with lung cancer, we analyzed the gene expression in the TCGA database. Results showed NHERF1 expression was significantly increased in lung adenocarcinoma tissues when compared with the normal tissues of patients in TCGA dataset.

References

1. E. Cerami, J. Gao, U. Dogrusoz, B. E. Gross, S. O. Sumer, B. A. Aksoy, A. Jacobsen, C. J. Byrne, M. L. Heuer, E. Larsson, Y. Antipin, B. Reva, A. P. Goldberg, C. Sander and N. Schultz, *CANCER DISCOV*, 2012, **2**, 401-404.

Supplementary Fig. 1: Analysis of NHERF1 expression in lung adenocarcinoma and adjacent normal tissues in TCGA dataset. Results showed NHERF1 expression was significantly increased in lung adenocarcinoma tissues when compared with the normal tissues of patients.

Suppl Fig. 1

