Identification of key genes using bioinformatics analysis in human small cell lung cancer (SCLC)

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Objective
Small cell lung cancer (SCLC) is a subtype of lung cancer with poor prognosis due to early dissemination and rapid growth. The aim of this study was to identify key genes and pathways in SCLC, in order to improve understanding of the mechanism of lung cancer.

Methods
The microarray expression dataset GSE43346 in the human small cell lung cancer (SCLC) and normal cells was downloaded from Affymetrix GPL570 platform (Affymetrix Human Genome U133 Plus 2.0 Array), which was submitted by Sato et al. [1]. This dataset has 65 samples, including 23 SCLC samples and 42 matched normal samples. The analysis of screening DEGs between SCLC and normal samples was carried out by GEO2R [2]. In order to analyze the functions of DEGs, GO enrichment and KEGG pathway analysis were conducted using the DAVID online tool; p<0.05 was set as the cutoff point [3].

Results
Enhancer of zeste homolog 2 (EZH2) was found to be highly expressed in SCLC samples compared to 42 normal tissues.

Conclusion
EZH2 was found to be highly expressed in SCLC samples.

References