

Abstract and Introduction

Endometrial carcinoma is a serious disease as it ranks first in gynecological diseases and second in uterine cancer, so it threatens the life of women.

The earlier it is detected, the better it is to avoid the development and complications of cancer, and to prevent it from spreading to malignant cancer.

Long noncoding RNA (lncRNA) is a noncoding RNA that its length is more than 200pb. lncRNA plays a major role in regulating transcription and translation and is found in physiological and pathological processes and we also explored that it plays a pivotal role in development of malignant tumors.

In this study, we investigated lncRNAs in endometrial carcinoma based on the Cancer Genome Atlas (TCGA) database and identified two lncRNA RP11-89K21.1 and RP11-357H14.17 and connect their role in developing, prognostic value and functional regulatory network of EC. We also found the upstream transcriptional regulatory factors, co-expression genes and binding proteins of lncRNAs and their relationship with immune infiltration. Furthermore, we found their potential roles and molecular mechanisms in EC utilizing competing endogenous RNA (ceRNA) (lncRNA-miRNA-mRNA) hypothesis, which is extremely useful to provide a new strategy for early diagnosis and treatment of EC.