Springer Link

Deep Transcriptome Profiling of Ovarian Cancer Cells Using Next-Generation Sequencing Approach

Ovarian Cancer pp 139-169 | Cite as

Protocol
First Online: 24 June 2013

Part of the Methods in Molecular Biology book series (MIMB, volume 1049)

Abstract

The next-generation sequencing technology allows identification and cataloging of almost all mRNAs, even those with only one or a few transcripts per cell. To understand the chemotherapy response program in ovarian cancer cells at deep transcript sequencing levels, we applied two next-generation sequencing technologies to study two ovarian chemotherapy response models: the in vitro acquired cisplatin-resistant cell line model (IGROV-1-CP and IGROV1) and the in vivo ovarian cancer tissue resistant model. We identified 3,422 signatures (2,957 genes) that are significantly differentially expressed between IGROV1 and IGROV-1-CP cells ($P < .001$). Our database offers the first comprehensive view of the digital transcriptomes of ovarian cancer cell lines and tissues with different chemotherapy response phenotypes.

Key words

Ovarian cancer Gene expression Next-generation sequencing RNA-seq Cufflinks SAMtools

References

1. Lin B et al (2005) Evidence for the presence of disease-perturbed networks in prostate cancer cells by genomic and proteomic analyses: a systems approach to disease. Cancer Res 65(8):3081–3091
PubMed (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Abstract&list_uids=15833837)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Evidence%20for%20the%20presence%20of%20disease-