**EDITORIAL**

# Editor's Introduction to This Issue (G&I 15:1, 2017)

Yeun-Jun Chung*

IRCGP, College of Medicine, The Catholic University of Korea, Seoul 06591, Korea

Clinical sequencing has become a part of medical practice. It is widely accepted that clinical sequencing is the main tool of precision medicine and can facilitate the selection of the right drug at right dose to the right patient at the right time. To reflect the importance of clinical sequencing, in this issue, Genomics & Informatics opens a new section, termed 'Clinical Genomics'. Genomics & Informatics would like to encourage medical scientists to submit any type of clinical sequencing data if they have potential implications in medical practice or provide biological insights. The first paper in the Clinical Genomics section is on the successful detection of somatic mutations from circulating plasma DNA of a breast cancer patient. Dr. Seung-Hyun Jung's group (The Catholic University of Korea, College of Medicine, Korea) examined the mutation profile of primary tumor tissue from a breast cancer patient using a cancer panel that they developed and identified several somatic point mutations and copy number alterations. They examined whether the alterations identified from tumor tissue were consistently detected in plasma DNA isolated from the same patient and confirmed that both point mutations and copy number alterations were consistently identified in two sources.

There are five original articles in this issue. Dr. Jong-Keuk Lee's group (Ulsan University, Korea) evaluated digital PCR as a system for monitoring graft status using SNP-based detection of donor DNA in plasma or urine. They found that donor DNA was almost undetectable in plasma DNA samples, whereas a high percentage of donor DNA was detected in urine DNA samples. Therefore, they suggested that urine is a good source of cfDNA for monitoring acute rejection in patients after kidney transplantation. Dr. Seon-Young Kim's group (KRIBB, Korea) developed a new ChIP-seq data analysis pipeline, based on Bioconductor packages. They also developed a graph-based database and reported its feasibility. In the application note section, Dr. Ju Han Kim's group (Seoul National University, Korea) proposed an R-based RNA-seq analysis pipeline called TRAPR, which is an integrated tool that facilitates the statistical analysis and visualization of RNA-seq expression data.

For further details, please visit the G&I homepage (http://www.kogo.or.kr/webapp/kogo_publish/genomics_and_informatics/).

*Corresponding author: Tel: +82-2-2258-7343, Fax: +82-2-537-0572, E-mail: yejun@catholic.ac.kr