



Analysis of the data from next generation sequencers



There are many next-generation sequencers (NGS) in Japanese research institutions; however the number and the quality of the papers using them are insufficient. That is because of the lack of the abilities to analyze the data and to interpret the results based on statistical genetics. Recently, simple analysis of the data has become easy because of the availability of pipelines. However the bottle necks are the analysis based on statistical genetics and interpretation of the results. StaGen Co. Ltd has a lot of experiences of the analyses of the data from various next-generation sequencers sold by Illumina Inc. and Life Technologies Inc. Based on such experiences, we provide consultations concerning the selection of the machines, important points for the preparation of the samples, installation of the computer systems, installation of necessary pipelines and data analysis from the beginning. In addition, we install the system for analyzing the data, send technicians for the bioinformatics analysis and analyze the data in our company. Recently, merely the analysis of the data from next-generation sequencers does not lead to the publication. The researchers have to analyze the data based on the knowledge of statistical genetics and complete the reports after adding high-quality discussion. StaGen Co. Ltd provides the consultations for the analysis of the data based on statistical genetics and for making manuscripts. Although the main focus is on humans, we can also analyze the data from animals and plants.

Examples of our service

Identify responsible mutations in genetic disease families using whole exome or whole genome data from members of the families.

We make a list of somatic mutations using whole exome or whole genome data from cancers and perform various analyses based on statistical genetics and bioinformatics.

We identify de novo mutations from the whole genome data from families.

We analyze RNA-seq and ChIP-seq data.

We analyze the whole genome data from animals or plants.

Papers to which employees of StaGen contributed

Miyagawa M et al. PLoS One. 2013;8(8):e71381.

Kohno T et al. Nat Med. 2012;18(3):375-7.

Fujimoto A et al. Nat Genet. 2012;44(7):760-4.

Furukawa T et al. Sci Rep. 2011;1:161.

Okumura A et al. Neuropathology. 2013;33(5):553-60.

and many others