

OncoTherapy Science, Inc.

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Announcement of additional sequencing services at our subsidiary company,
Cancer Precision Medicine, Inc. (CPM)

OncoTherapy Science, Inc. (OTS) hereby announces that CPM will start additional sequencing services, including the whole-genome sequencing.

According to recently increasing expectations for the cancer precision medicine and its applications in the early diagnosis and recurrence monitoring of cancers, CPM has conducted laboratory test services such as whole-exome sequencing (WES), RNA sequencing (RNA-seq), neoantigen analysis, liquid biopsy (like blood-based) for the early detection of cancer, T cell receptor (TCR) / B cell receptor (BCR) repertoire analysis, and several immune response analyses. In addition to current service categories, CPM will start new analysis services for whole-genome sequencing (WGS) (※1), single cell RNA sequencing (scRNA-seq) (※2), and meta-genome sequencing (※3).

Based on these updated sequencing analysis pipelines, CPM will be able to provide optimal genome analysis services for various purposes and can respond to laboratory test requests from medical institutions, research institutes, joint research partners, and business-related partners.

(※1) whole-genome sequencing (WGS)

WGS analysis examines DNA variations in the entire genome. The currently provided WES analysis focuses on protein encoding region of genes, which represents about 2% of the genome, hence can examine important DNA variations with high efficiency and low cost. However, it is difficult for WES to examine large-scale genetic replacements and deletions in cancer cell. In contrast, WGS can also detect these variations, which thus provides more comprehensive information about genetic alterations in cancer cell.

(※2) single cell RNA sequencing (scRNA-seq)

By use of scRNA-seq analysis, the gene expression level in each isolated cell is investigated individually. It is known that tumor is composed of various cancer cells which differentiate and proliferate into multiple cell populations harboring different mutations. Therefore, it may be difficult to accurately understand the characteristics of cancer if tumor tissue is analyzed in a mixed state of very diverse cancer cell populations. Characterization of individual cancer cells by scRNA-seq analysis is expected to be useful

for more accurate selection of treatment and prediction of prognosis.

(※3) meta-genome sequencing

Meta-genome sequencing analyzes the genome of each microorganism, and thereby can characterize a wide variety of microorganisms in the sample by clarification of their species and abundance ratios. As an example in the cancer research, it is applied in the analysis of intestinal bacterial flora (microbiome) to examine role of specific intestinal bacteria in the carcinogenesis of colorectal cancer, and to investigate its relationship with host immunity or drug metabolism.