



第 7 回生命科学セミナー

演題 : Genomics and epigenomics analyses of primary tissue samples for personalized cancer medicine

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日時 : 2012 年 9 月 14 日 (金) 11:00-12:00

会場 : 生命科学動物資源センター 発生工学棟 2 階
リフレッシュコーナー

要旨 :

Biopsy tissue and FFPE archive are rich sources of molecular and genetic information for biomarker discovery and clinical diagnosis. This presentation will introduce micro-scale chromatin immunoprecipitation combined with massively parallel sequencing (ChIP-sequencing) workflow that allows analysis of limited amount of tissue samples for genome sequencing and prediction of gene expression status. One of the key components of the assay platform is amplification and processing of highly fragmented trace amount of DNA. This method links tissue-based micro-scale assays to second generation sequencing. Sequencing data sets are analyzed by customized computational algorithms for prediction of regulatory status of genomic loci, underlying somatic mutations and single nucleotide polymorphisms (SNPs). These genomics technologies are expected to be highly useful for system-level understanding of individual diseases and molecular diagnosis for personalized cancer medicine.

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