Applied Biosystems SOLiD[™] System

Technical Seminar <u>Next Generation Sequencer SOLiD™3 System</u>

| Date: | Wednesday, June 3, 2009 |
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| Time: | 16:00 – 17:30 |
| Place: | A7F Seminar Room, RIKEN Center for Developmental Biology |
| Speaker: | Hideki Hanaoka, Ph.D. |
| | Applied Biosystems Japan, Application Specialist |
| Title : | "Next Generation Sequencer SOLiD™3 System" |
| Topics: | SOLiD™ System Technology, Workflow, Chemistry SOLiD™ System Applications (collaboration data) |
| | Whole Transcriptome Analysis Genomic Structure Variation SNP detection |
| | •Methylation Analysis etc··· |

Abstract:

SOLiD[™]3 System is Applied Biosystems next generation sequencer which enables massive parallel sequencing. SOLiD[™]3 System can produce 20 billion bp (mappable), 400 millions reads (mappable) in a single run. Applying 2-base encoding system, SOLiD[™]3 can distinguish true SNPs and sequencing errors realizing high accuracy, 99.9%.

With such high throughput and accuracy of SOLiD system, various applications which were thought to be difficult have been demonstrated.

In gene expression analysis, data with much higher dynamic range compared to conventional method such as micro array was obtained. Besides, novel exon/intron structure was also able to be detected. In whole genome re-sequence, mate-pair analysis enabled detection of large insertion/deletion structure changes in the genome. Also, SNP detection in targeted region and genome-wide methylation analysis were reported. Recent collaboration data and future road map will also be presented.

Contact:

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