NOVEMBER 2011

# InSight

*Latest news and innovations from NuGEN*

## Press Releases

**NuGEN Launches Library Preparation Solutions for the Ion PGM Sequencer**
NuGEN Technologies and Ion Torrent announced the release of three new products developed by NuGEN for the Ion Personal Genome Machine (PGM™). Ion PGM customers can now order the NuGEN Encore® NGS Library Systems for Ion Torrent from the Ion Torrent webstore; these products are also available for purchase directly from NuGEN.

## New Products

**Encore® Complete RNA-Seq System**
Provides an end-to-end solution for **strand-specific RNA-Seq** library construction using as little as 100 ng of total RNA…

**Ovation® Ultralow Library System**
Simple, fast and scalable solution for producing libraries used in next-generation sequencing starting with as little as **1.0 ng of DNA**…

**Mondrian™ SP**
**Plug and play automation** to significantly reduce hands on time for genomic sample preparation…

**Prelude® FFPE RNA Isolation Module**
Fast and easy method optimized for isolating **total RNA from formalin-fixed paraffin-embedded** (FFPE) tissue samples…

Coming soon!

**Encore® Rapid DNA Library System**
The Encore® Rapid DNA Library System will enable automated NGS library construction that eliminates the need for any amplifications steps. Using input of 100-500ng of genomic DNA or double stranded cDNA, the hands-free protocol will be completed within 2 hours.

## Join Us At These Events

February 15-18 **AGBT**
Marco Island, FL

March 5-8 **XGen Congress and Expo**
San Diego, CA

March 17-20 **ABRF**
Orlando, FL

April 18-19 **Innovative Sample Prep/Target Enrichment**
Newport, CA

**Distributor Events**

## Customer Feature

**KFB Regensburg validates Ovation PicoSL WTA Amplification System v2 on the Gene Titan Platform**
*Thomas Stempfl, Ph.D., Head of the Kompetenzzentrum Fluoreszente Bioanalytik (KFB), University of Regensburg, Germany*

*Pictured l to r: Thomas Stempfl, Ph.D. (Leader), Jutta Schipka (Technician), Susanne Schwab (Technician), Christoph Moehle, Ph.D. (Lab Mgr)*

More than 9 years ago, the KFB was founded as part of a joint technology platform initiative of the University of Regensburg, Germany. Since then, the team at the KFB has been offering a wide spectrum of genomics services for a constantly growing number of customers all across Europe. With a throughput of several thousand samples per year, the KFB today is one of the largest academic core facilities for microarray and deep sequencing applications in Germany. In order to stay at the forefront of current technologies, we actively monitor and invest into new analysis platforms as well as assay types. As a certified Affymetrix® Service Provider, we were one of the first to acquire a GeneTitan® Instrument in 2009.

With its most recent release of the Ovation® PicoSL WTA System V2 and the Encore® Biotin Module, NuGEN® offers a fast, easy to use and highly efficient sample preparation workflow that produces sufficient hybridization target i.e. for Affymetrix peg arrays. The assay is easily finished within a work day and results in a fragmented and labeled cDNA that is compatible with the appropriate Affymetrix HWS kit to formulate the hyb cocktail.

Encouraged by the streamlined workflow and by experiences we have made with NuGEN assays in the past, we tested the new assay formulation with MAQC-A and MAQC-B model RNA in order to assess the performance on Human Gene 1.1 ST peg arrays. Both sample types are ideal to test for technical performance as they have been used in the MAQC project back in 2006 and hence have been extensively described in the literature. Furthermore, qPCR data for a set of genes is publicly available that serves as a gold standard for differential gene expression in these samples. Aim of this proof of concept study was to test how robust the NuGEN assay would work in our hands and if it could easily be implemented in our routine laboratory workflow. Furthermore, we were interested to see the influence of different amounts of input RNA on the overall yield of cDNA and also the array data. Finally, we wanted to assess how well the genes found differentially

**TaKaRa**
November 17-18 - Korean Association of Immunologists

December 13-16 - Molecular Biology Society of Japan
Korean Society for Stem Cell Research

**SeouLin Bioscience Co**
Korean Society Biochemistry and Molecular Biology

**Millennium Science Pty Ltd**
February 9-11 Lorne Cancer
February 12-14 Lorne Genome

## Publication To Share?

If you have a publication or data from a project using our products that you would like to share, please contact us. We would welcome your submission for future newsletter issues!

## NuGEN's Newest Partner

**Ion Torrent**
As part of the Ion Torrent developer network, NuGEN has launched three Encore NGS Library kits to enable and expand the scope of applications available to customers on the PGM™. These novel products are available through the Ion Torrent webstore and directly from NuGEN to enable customers to purchase their Ion Torrent compatible products simply and with confidence.

ion torrent
by life technologies™

**Press release**

expressed in our experiment correlate with qPCR data.

For the experiment, we processed both samples at different dilutions between 500 pg and 40 ng total RNA with replicates. A total of 24 reactions was carried out and hybridized in parallel on a 24 array peg plate. The assay was done on two different days by two technicians and we found it user friendly and easy to finish within a day. In all cases, cDNA yield was above 2.5 µg and hence all samples could be hybridized. As expected, the overall yield did increase with an increasing amount of RNA, but this behavior is not linear and stabilizes at about 5 µg cDNA product with 20 ng input RNA. Agilent Bioanalyzer traces were obtained for basic QC and their shape looked as referenced in the assay's user guide. A PCA plot of the array data showed a clear separation of both sample types. At the very low end of total RNA input, a slight increase of noise could be observed, but at 2 – 5 ng RNA, we found the noise to be comparable with the higher concentrated samples. For differential expression analysis, we ran a t-test and compared the fold changes of regulated genes in log2 space to the available qPCR data. At a p-value threshold of 0.001, there were 165 genes that could be directly compared that way. The correlation coefficient was calculated as 0.943, demonstrating an excellent overlap between the two technologies. We did, however, observe a tendency for a fold change compression in the array data which is typical for arrays in general and hence expected. More importantly, we did not find any genes discordantly regulated at this level of stringency.

The excellent outcome of his study encourages us to offer the Ovation PicoSL WTA System v2 workflow as a standard assay for expression analysis on ST-type arrays to our customers. We are confident that we found a highly reliable and cost efficient solution not only for challenging sample types where limited amount of total RNA is available, but also for standard samples.

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