RNA-Seq Symposium

Centre for Genomic Regulation (CRG)
Wednesday, 22th of April 2015
10.30-13.00h

SMARTer
Solutions for Next Generation Sequencing

that's GOOD science!®

Abstract. Next-generation sequencing (NGS) has increased our understanding of biology by enabling highly sensitive RNA expression analysis across a wide dynamic range. As NGS applications continue to grow, so does the need for more powerful tools to work with less-than-ideal samples. As the core of the SMARTer kits for transcriptome analysis, Clontech's patented SMART® technology utilizes the template switching activity of reverse transcriptase to enable researchers to analyze their most challenging samples, such as single cells, low-input RNA, noncoding RNA, and RNA from degraded samples. In particular, single-cell RNA-seq is one of the more difficult, and fastest growing, applications of NGS. The high sensitivity and dT- primed protocol of the SMARTer Ultra™ Low family has made these kits the industry standard for single-cell analysis. Applications of SMART technology are constantly expanding and now include a novel, ligation-free method for generating ChIP (chromatin immunoprecipitation) sequencing libraries. The purpose of this symposium is to take a deeper look into the new technologies being developed for single-cell RNA-seq and other sensitive NGS applications.

10.30-11.00h: "**Novel methods for RNA and DNA-Seq analysis using SMART™ Technology**". Presented by Dr. Irit Paz. GLocal Sales Manager at Takara Clontech, France.

11.00-11.30h: "**Signatures of tumor evolution reveal cancer driving genes and networks**". Presented by Dr. Stephan Ossowski. Genomic and Epigenomic Variation in Disease, Group Leader at the Centre for Genomic Regulation (CRG), Barcelona.

11.30-12.00: **Coffee break**

Work SMARTer not harder! Learn by listening to the researchers who are already using the SMARTer kits.

12.00-12.30h: "**Gene expression analysis of the proepicardium during zebrafish heart development**". Presented by Dr. Alberto Benguria. Support Scientist at the Genomics Unit at National Centre for Cardiovascular Research (CNIC), Madrid.

12.30-13.00h: "**RNA-seq protocols for low input compromised samples and single-cell experiments**". Presented by Dr. María Méndez-Lago. Single-cell Genomics, Team Leader at National Center for Genome Analysis (CNAG), Barcelona.

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Venue

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