

## SEMINARIO : “Explore the World of RNA”

Day: **7 de Noviembre 2017**

Location: **Auditorio del PARQUE CIENTIFICO DE MADRID – CANTOBLANCO**

**1. 10h-10:10h : Welcome and presentation**

Ricardo Ramos- Responsable de la Unidad de Genomica del PCM

**2. 10:10-10:20h How to improve RNA and miRNA isolation and RNA stability with King Fisher platforms and Mag Max technology**

**3. 10:20 – 11:15 qPCR workflows**

- Overview of RNA Applications by RT-qPCR
- cDNA synthesis kits for RT-qPCR: a solution for improved processivity
- 1-step RT-qPCR or 2-step RT-qPCR
- Gene Expression RNA Workflow
- microRNA analysis: Taqman Advanced miRNA technology.
- Medium and High Throughput: TaqMan Array Card and Open Array
- Overview of Gene Expression/microRNA analysis with the Relative Analysis
- Software in the Cloud and Introducing the QuantStudio 3 and 5 systems: the first cloud-enabled real-time PCR systems

Maria Jesús Garcia TFS

**11:15- 11:30 Pausa café**

**4. 11:30- 11:50 Take the best of the transcriptome with Microarrays technology: miRNA, mRNA, alternative splicing and lncRNA**

**5. 11:50- 12:15 Data integration and analysis with Transcriptome Analysis Console: hands on demo**

Elena Aller, TFS

**6. 12:15- 13:00 ION Torrent Module: RNA sequencing using Ion Torrent™ Technology**

- RNA sequencing applications on Ion Torrent
  - Non-targeted RNAseq methods on Ion Torrent platforms :
    - o Whole transcriptome
    - o Small RNAseq
- Ion AmpliSeq Technology and Ion AmpliSeq RNA solutions

Marcos Morey , TFS

**13:00h-13:30h How to identify CNV at the Whole genome, even in paraffin samples and cfDNA?**

Elena Aller, TFS

**CONFIRMAR ASISTENCIA**

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