16th CRG Symposium: Seventh International Workshop on Genomic Epidemiology

Wednesday, Sept 20th	
14:00 – 14:15	Welcome
	Session 1 – Technology
14:15 - 14:45	**Ivo Gut**, CNAG-CRG, ES Recent advances in nucleic acid sequencing technologies
14:45 - 15:15	**Holger Heyn**, CNAG-CRG, ES Single-Cell RNA Sequencing of Complex Tissues
15:15 – 15:30	Selected Abstract talk **Jessica Nordlund** - SPlinted Ligation Adapter Tagging (SPLAT), a novel library preparation method for whole genome bisulfite sequencing
15:30 - 15:45	Selected Abstract talk **Nina Görner** - Metabolomics: The Missing Link in Precision Medicine
15:45 - 16:15	Coffee break
16:15 – 16:45	**Marc Marti-Renom,** CNAG-CRG, ES Rational design of non-resistant targeted cancer therapies
16:45 - 17:00	Selected Abstract talk **Masato Akiyama** - Genetic study of body mass index in Japanese population links cell-types to body weight regulation
17:00 - 17:30	**Manolis Kogevinas**, ISGlobal, ES The exposome complements the genome: a new era in epidemiology
17:30 - 19:30	Welcome Reception + Poster Session (Terrasse)

Thursday, Sept 21st	
	Session 2 - Epigenetics
09:00 - 09:30	**Peter Jones**, Van Andel Institute, USA Targeting Human Endogenous Retroviruses for Epigenetic Therapy
09:30 - 10:00	**Caroline Relton**, University of Bristol, UK Causal inference in epigenetic epidemiology
10:00 - 10:30	**Iñaki Martin-Subero**, IDIBAPS, Spain Epigenetic insights into chronic lymphocytic leukemia biology and clinical behavior: from DNA methylomes to reference epigenomes
	Session 3 – Resources / Big Initiatives
10:30 - 11:00	**Hanns Lochmüller**, Newcastle University, UK RD-Connect – linking, analysing and sharing multi-source omics data for Rare Disease Research
11:00 - 11:30	Coffee break
11:30 – 12:00	**Sergi Beltran**, CNAG-CRG, ES The BBMRI-LPC call to sequence 900 Rare Disease exomes: a successful transnational collaborative initiative with EuroBioBank and RD-Connect
12:00 - 12:15	Selected Abstract talk **Maria Alvarellos** - PharmGKB: The Pharmacogenomics Knowledgebase
12:15 - 12:45	**Roderic Guigó**, CRG, ES The human transcriptome across tissues and individuals
12:45 – 14:00	Lunch
	Session 4 – Diseases - Cancer
14:00 - 14:30	**Nuria Malats**, CNIO, ES Towards the integration of Omics data in epidemiological studies: A Pancreatic Cancer Journey

14:30 – 14:45	Selected Abstract talk **Evangelina López de Maturana** - Genome-scale data integration for deciphering pancreatic cancer aetiology
14:45 – 15:00	Selected Abstract talk **Juan R. González** - Transcriptomic and epigenomic mechanism of mosaic loss of chromosome Y (LOY) in cancer
15:00 - 15:30	**Richard Houlston**, Institute Cancer Research, UK Polygenic susceptibility to colorectal cancer: mechanisms and impact
15:30 – 15:45	Selected Abstract talk **Izaskun Mallona** - DNA co-methylation networks for colon cancer patient stratification
15:45 – 16:00	**Sven Bocklandt**, Sr. Application Specialist, Bionano Genomics Beyond NGS: Genome Mapping Reveals Structural Variation in Cancer and Genetic Disease
16:00 – 16:30	Coffee break
16:30 – 16:45	Selected Abstract talk **Miranda Stobbe** - Recurrent somatic mutations reveal new insights into mutational processes in cancer
16:45 – 17:00	Selected Abstract talk **Solip Park** - Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits
17:00 – 17:30	**Ben Lehner**, CRG, ES Mutations and their interactions in individuals

Friday, Sept 22nd	
09:00 - 09:30	**Nuria López-Bigas**, IRB, ES Coding and non-coding cancer mutations
	Session 4 – Diseases – Common Diseases
09:30 – 10:00	**Florence Demenais**, Inserm, FR TBA
10:00 – 10:30	**Momoko Horikoshi**, RIKEN, JP Genomic loci associated with birth weight identify genetic links between intrauterine growth and adult metabolic disease
10:30 – 11:00	**Patricia Munroe**, Queen Mary University of London, UK New insights into blood pressure regulation from large-scale genetic studies
11:00 - 11:30	Coffee break
11:30 - 12:00	**George Thanassoulis**, McGill, CA A Genomewide association study of aortic stenosis
12:00 – 12:15	Selected Abstract talk **Jon Sánchez** - A Transcriptomic Investigation on Patient–Specific Comorbidities
12:15 - 12:30	Selected Abstract talk **Oscar Lao** - Identification of polygenic adaptation in attention deficit hyperactivity disorder using GWAS data
12:30 - 13:00	**Stephanie Debette**, University Bordeaux, FR Genomics of complex cerebrovascular disease
13:00 - 14:00	Lunch
	Session 5 – Analytical methods and resources
14:00 - 14:30	**George Davey-Smith**, University of Bristol, UK Mendelian randomization: what does the future hold?
14:30 - 15:00	**Dorret Boomsma,** Vrije Universiteit Amsterdam, The Netherlands Contributions from twin studies to gene discovery

15:00 - 15:30	**Gonçalo Abecasis**, University of Michigan, USA Sequencing and Analysis of 10,000s of Human Genomes: Challenges and Opportunities
15:30 - 16:00	**Mark Caulfield**, Genomics England, UK The 100,000 Genomes Project transforming healthcare
16:00 – 16:30	**Closing Remarks**