Research Skills Training Program					
Module	**Content**	**Event**	**Days**	**Leader**	**Contributors**
Technologies I	Functional genomics in transcriptional regulation studies: *Introduction to genomic approaches used to investigate transcriptional regulation and enhancer function (e.g. RNA-seq, ChIP-seq, whole-genome bisulfite sequencing (WGBS).*	2	0.5d	Rada-Iglesias (UNICAN)	HUNIMED
Technologies II	Topological control of gene expression and enhancer function: *Introduction to 3C-related technologies (e.g. 4C-seq, Hi-C, ChIA-PET, HiChIP, C-HiC, MC-4C); Confirmed Guest Speaker: Yijun Ruan (The Jackson Laboratory, USA) "The 4D Nucleome Consortium".*	3	0.5d	de Laat (KNAW)	KTH
Technologies III	Functional genomics using single-cell and microfluidic technologies: *Overview of recent genomic approaches using single-cell and microfluidic technologies (e.g. single-cell RNA-seq, low-cell ChIP-seq, etc).*	4	0.5d	Deplancke (EPFL)	Elvesys
Technologies IV	CRISPR applications to investigate enhancer function: *Overview of different CRISPR-based technologies: genetic deletions, knock-ins, structural rearrangements, CRISPR-activation, CRISPR-interference, screens, etc.*	4	0.5d	Mandrup (SDU)	CRG
Technologies V	Massive parallel reporter assays: *Overview of different reporter assays to investigate enhancer activity*	5	0.5d	Arensbergen (Gen-X)	Inserm
Technologies VI	Model systems to study enhancer function: *Overview of different in vitro and in vivo biological systems to study enhancer function. Confirmed Guest speakers: Hans Clevers (Hubrecht Institute, The Netherlands) "Disease modelling using 3D organoids"; Stefanie Schindler (AnimalFreeResearch Foundation, Switzerland) "Models to replace animal experimentation".*	5	0.5d	Alberich-Jorda (IMG)	HUNIMED SDU
Genomic Medicine I	Genomics and Precision Medicine. Mendelian diseases, complex diseases, GWAS, whole-genome sequencing, statistical genetics, accessing and exploitation oflarge public genetic resources (UKBiobank, GE, etc). Prediction of pathogenic variants. Guest speakers: Charles Lee (The Jackson Laboratory, USA) "The 1000 Genomes Project Consortium", Anna Need (Genomics England) "100,000 Genomes: genomics in a national health care setting". Tim Frayling (Exeter) "UK biobank", James Meigs (TOPMed Initiative, Harvard)	2	1.5d	Ferrer (CRG) Meigs (TOPMed)	Genomics England
Genomic Medicine II	From GWAS and whole-genome sequencing to causal genetic variants: *Overview of experimental and computational tools available to identify non-coding disease-causative genetic variants; Calling SNVs and structural variants in whole genome sequence data; Machine learning approaches to prioritise pathogenic mutations in enhancers; Statistical genetic analysis of common regulatory variants, eQTLS.*	3	1.5d	Ferrer (CRG)	UNICAN EPFL TOPMed
Genomic Medicine III	Pharmacogenomics and gene-environmental interactions	3	0.25 d	Terranova (Novartis/NIBR)	ABD
Genomic Medicine IV	Vector targeting and gene therapy	4	0.25 d	Thirion (Sirion)	
Bioinformatics I	Analysis and visualization of transcriptomic and epigenomic data: *Computational tools to process, analyse and visualize RNA-seq and ChIP-seq data. Theoretical overview and practical exercises.*	2	2 d	Andersson (UCPH)	CNRS-IFB UoW
Bioinformatics II	Computational tools for 3C-related data: *processing, statistical analysing modelling and visualization of 4C-seq, Hi-C, ChIA-PET, HiChIP, Capture-HiC. Theoretical overview and practical exercises.*	3	1.5d	Plewczynski (UoW)	KTH, KNAW CNRS-IFB
Bioinformatics III	Computational tools for single-cell genomics: *Computational tools to process, analyse and visualize single-cell RNA-seq, single-cell ChIP-seq and single-cell Hi-C data. Theoretical overview and practical exercises.*	4	1.5d	Deplancke (EPFL)	EMBL, UoW CNRS-IFB
Bioinformatics IV	Mining and depositing genomic data: *Overview of public repositories to mine and deposit genomic data.*	4	0.5d	Ordonez (Dreamgenics	UoW, UCPH EMBL
Bioinformatics V	Computational prediction of non-coding disease causative variants: *Computational pipelines to link enhancers to genes and to prioritize potential disease-causative genetic variants. Supervised and unsupervised learning methods, multidimensional tensor representation of underlying data. Theoretical overview and practical exercises*	5	2d	Zaugg (EMBL)	UCPH Gen-X Dreamgenics CNRS-IFB