GENOMICS CORE UNIT

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Technicians
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Plan de Empleo Joven (Youth Employment Plan)

OVERVIEW

The Genomics Unit provides centralised research services as well as expert consultation in the fields of genomics and genetics. Contributing to uncover biological mechanisms, therapeutic targets, or prognostic biomarkers, these services encompass a broad range of applications, from traditional to cutting-edge technologies. These technologies, with their capacity to interrogate whole genomes and their activities, can reveal the entire package of structural features (mutation landscapes, chromosomal protein location, or chromatin structure) and molecular programmes (transcriptomic RNA profiles), even at the single-cell level. So-called next-generation sequencing (NGS) is a staple among them. More traditional methodologies, like Sanger capillary DNA sequencing, are also provided. As a side activity, we manage a genetically engineered mouse genotyping service.

"Our service portfolio is shaped by the requirements of CNIO's scientists in genomics and genetic technologies. It represents a flexible response to both generic and boutique services, from basic housekeeping activities to advanced explorations of biological complexity."

RESEARCH HIGHLIGHTS

Every cancerous tumour, even those of the same type and with a similar outcome, is different at the chromosomal level, has distinct molecular origins, and will likely differ in its most suitable therapeutic intervention. This variability can be comprehended through the use of powerful genomic technologies. These tools, with their capacity to analyse even whole genomes in a single assay, permit decoding structural changes and functional molecular programmes.

The Genomics Unit, with its array of molecular services, contributes to the dissection of molecular processes of biological complexity in research projects conducted by CNIO Research Groups. The genomic-wide level is addressed by NGS-based technologies. NGS constitutes the final readout for a variety of different applications at either the structural or functional levels: on the one hand, genome or exome tumour characterisations, mutation repertoires, location of relevant DNA-bound protein factors, variations in chromatin folding, or on/off functional states; on the other hand, transcriptional profiles reflecting functional choreographies, useful to decipher tumour compositions, uncover therapeutic targets, or predict disease course. Tissue composition, heterogeneity, and fate can be further explored with single cell resolution, by capturing individual cells in microdroplet emulsions and studying them by the tens of thousands through analysis in the NGS platform.

At the single locus level other services are provided. A traditional DNA capillary sequencing service is being used to find and confirm mutations in candidate genes, or to verify cloned genes or inserts. A cell authentication service, based on individual STR marker profiles, provides confidence in the identity of the samples used for experimentation. The Unit also manages a transgenic mouse genotyping service with custom allele-specific, real-time PCR test assays for a quick and efficient turnaround time. ■

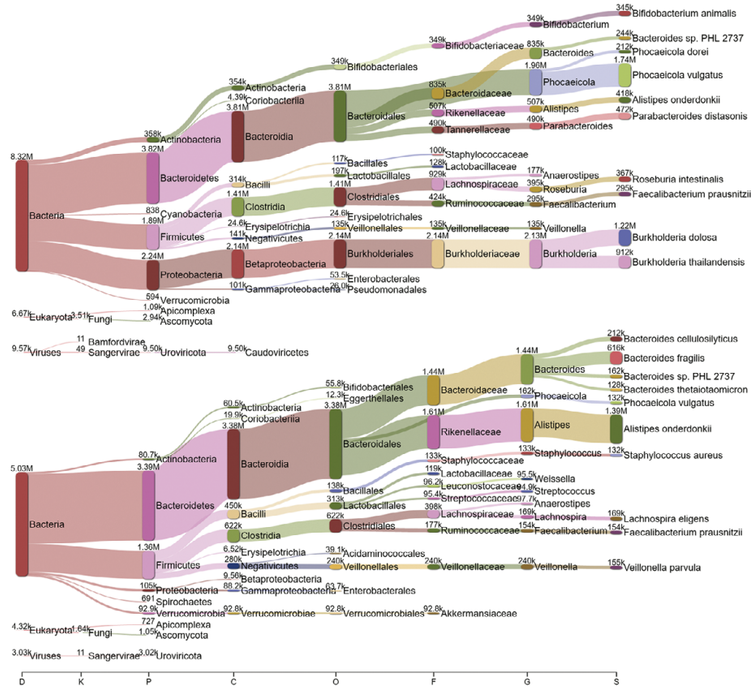

FIGURE 1 In order to ascertain variability factors that might influence each person's oncological process, gut microbiota diversity was explored. The Figure shows metagenomics classifications for 2 samples obtained at different time points from the same patient. Faecal DNA was sequenced (NGS), analysed with Kraken taxonomic classification software, and diagrams obtained from the Pavian web tool. Data kindly shared by M.A. Quintela and M.J. Bueno, from the CNIO Breast Cancer Clinical Research Unit.