



## The IMBB-Genomics Facility: supporting scientists in their everyday research

Vasiliki Theodorou #\*<sup>1</sup>, Eirini Stratidaki #<sup>1</sup>, Niki Gounalaki <sup>1</sup>, Manolis Dialinas <sup>1</sup> and Ioannis Talianidis \*<sup>1</sup>

<sup>1</sup> Genomics Facility, Institute of Molecular Biology and Biotechnology (IMBB), Foundation for Research and Technology - Hellas (FORTH)

Nikolaou Plastira 100

GR-70013, Heraklion, Crete, Greece

# Presenting author: [v.theodorou@imbb.forth.gr](mailto:v.theodorou@imbb.forth.gr), [stratida@imbb.forth.gr](mailto:stratida@imbb.forth.gr),

\* Corresponding author: [v.theodorou@imbb.forth.gr](mailto:v.theodorou@imbb.forth.gr); [talianid@imbb.forth.gr](mailto:talianid@imbb.forth.gr),

### ABSTRACT

In the era of omics, genomics applications are widely used to elucidate scientific questions from a global, genome-wide perspective. Even though the cost of such experiments has dropped over the past decade, thus making these applications more accessible, it is still a major consideration for scientists. Apart from the costs, there are two additional considerations when it comes to genomic experiments: first, the generation of top-quality data able to successfully address the imposed scientific question and second, the storage of the generated data and the downstream bioinformatics analysis, which is often the bottleneck of genome-wide experiments.

The **IMBB Genomics Facility** (<https://www.imbb.forth.gr/imbb-people/en/genomics-facility-description>) provides services in high-throughput sequencing technologies to IMBB researchers and the broader academic community. Over the past two years, the Facility has been restructured aiming to advance its services and to make genomics more understood and accessible to scientists. We have improved existing applications (technically and economically), introduced novel cost-effective protocols and established on our dedicated server basic pipelines for archiving and bioinformatics analysis. Within these two years, we have processed a few hundreds of samples of various species.

We will present the workflow of designing and conducting a genomics experiment, starting from the newly established 'Experimental Design Meeting' between the scientists and the members of the Genomics team and ending in the delivery of the analyzed data. Moreover, we will present a data comparison of a Full RNA-seq that covers the full-length of RNA-transcripts, versus a more cost-effective 3' Quant RNA-seq experiment, which uses only the 3' UTR of transcripts for measuring mRNA levels. Lastly, we will present the specific requirements and adjustments that need to be taken into account for a successful genomics experiment depending on the project.