NEXT-GENERATION SEQUENCING SYSTEM

(mod. ILLUMINA NextSeq1000 Sequencing System)

SUPPLIER: ILLUMINA ITALY srl

YEAR OF ACQUISITION: 2024

SCIENTIFIC SUPERVISOR: Prof. Monica Gatti

Technical features:

- “Single-End” and “Paired-End” sequencing.
- Productivity:
  - minimum: 10 Gb;
  - maximim: 180 Gb;
  - number of “reads”: up to 400 million in “Single-End” (or 800 million in “Paired-End”).
- Sequencing speed: > 4 Gb in 1 hour.
- Integrated cartridges that include reagents, fluidics, and the waste holder.
- Instrument includes fully automated clonal amplification.
- High resolution integrated optical system.
- Accuracy:
  - ≥ 90% of bases with qualitative score higher than Q30 (2x50 bp).
  - ≥ 85% of bases with qualitative score higher than Q30 (2x150 bp).
  - ≥ 80% of bases with qualitative score higher than Q30 (2x300 bp).
- Integrated platform DRAGEN Bio-IT for an ultra-fast and accurate secondary analysis.
- Compatibility without conversion protocols with libraries from other suppliers.

Applications:

- Medical/pharmaceutical gene variants study applications.
- Transcriptomic analyses (gene expression sequencing of both single cells and populations).
- Amplicon sequencing: metataxonomic studies of microbial populations with target gene sequencing.
- Small whole-genome sequencing (bacteria, yeast, virus).
- Shotgun metagenomics: comprehensive study of all genomes in a sample.
- Study of small non-coding RNAs (e.g. siRNA, ncRNA, miRNA, etc.).

Acquired for the Department of Excellence MUR 2023-2027