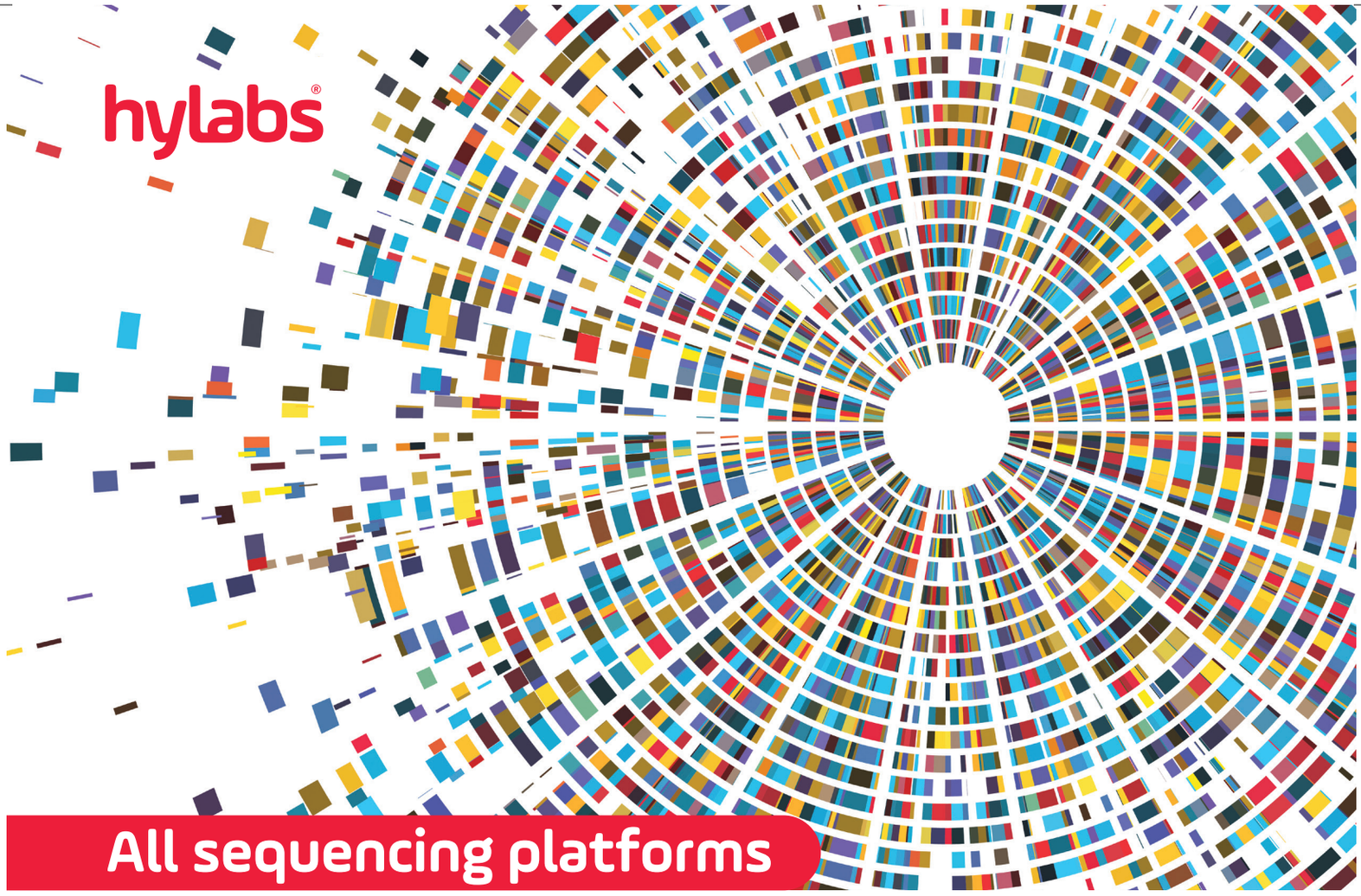

All sequencing platforms

■ **MiSeq:** Access focused applications such as targeted resequencing, metagenomics, small genome sequencing, targeted gene expression profiling, and more.
MiSeq reagents enable up to 15 Gb of output with 25 million sequencing reads and 2 × 300 bp read lengths.

■ **NextSeq 1000:** Multiple Flow Cell Configurations

- Enables sequencing output of 10-360 Gb per run, providing adjustable output based on project needs
- Increased flexibility to support new and emerging applications

Maximum Output: 120 Gb (with P2 reagents)
Maximum Reads per Run: Up to 400M single reads (with P2 reagents)

■ **NovaSeq 6000:** System performs whole-genome sequencing efficiently and cost-effectively. Its tunable output generates up to 6 Tb and 20B single reads in dual flow cell mode with streamlined workflows.

■ **NovaSeq X:** 16 Tb output per run on the dual flow cell NovaSeq X Plus System or up to 8 Tb on the single flow cell NovaSeq X System.

■ **PacBio:** long-read sequencing average read length 15–20 kb.

For more information please contact:
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PHL-MB-167-01-NGS-Services

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Our NGS Services

your specific needs and objectives

Extraction → Automated Processes

Library prep → Wide range of Libraries offered

Sequencing → Latest platforms/ Technology

Bioinformatics → Customizable Offerings

- **Microbiome (16s, ITS, 18s):** Microbiome analysis, allows one to identify and quantify (relatively) the microbial community in a given set of samples. This is done by sequencing of amplicon libraries for 16s (bacteria/Archaea), ITS (Fungi) or 18s (Eukaryotes). Services included are DNA extraction, library preparation, sequencing, and bioinformatic analysis of the data

- **Metagenomics:** Whole genome sequencing of DNA extracted from environmental samples, allows for the identification of the microbial community of a sample as well as the de novo assembly of genomes. Services included are DNA extraction, library preparation, sequencing, and bioinformatic analysis of the data.

- **Whole genome sequencing:** Sequencing of small genomes (phage, bacteria) and large (human) are done by making libraries from the sample, and then sequencing. Services include: DNA extraction, library preparation, sequencing and Bioinformatic analysis

- **Amplicon sequencing:** For amplicon sequencing we utilize a two-step PCR protocol, to amplify your region of interest and add the adaptor and index sequences required for Illumina sequencing. Service includes primer design, first and second step PCR, QC of second PCR, sequencing, and analysis.

- **RNA sequencing/transcriptome:** RNAseq studies are done to compare gene expression levels between different samples, or to study splicing patterns or post-transcriptional modifications. Services include RNA extraction, poly-A selection, rRNA depletion, directional RNA library prep, sequencing, and analysis. We can sequence RNA from FFPE samples and RNA with low quantities and of poor quality.

- **Small RNA sequencing:** Small RNA sequencing includes sequencing of microRNAs (miRNA), piwi-interacting RNA, small nucleolar RNA (snoRNA), small nuclear RNA (snRNA), or any other non-protein-coding RNA short in length (<200 nt). Services include: RNA extraction, small RNA library prep, sequencing, and analysis.

- **Bioinformatics:** in addition to the analysis of the services that we offer above, we also provide high-quality data analysis and interpretation. Whether you need to perform statistical tests, visualize results, apply machine learning algorithms, or integrate different types of data, we can help you find the best solutions for your research questions. We can also design and implement bioinformatics pipelines and workflows that are tailored to your specific needs and objectives.