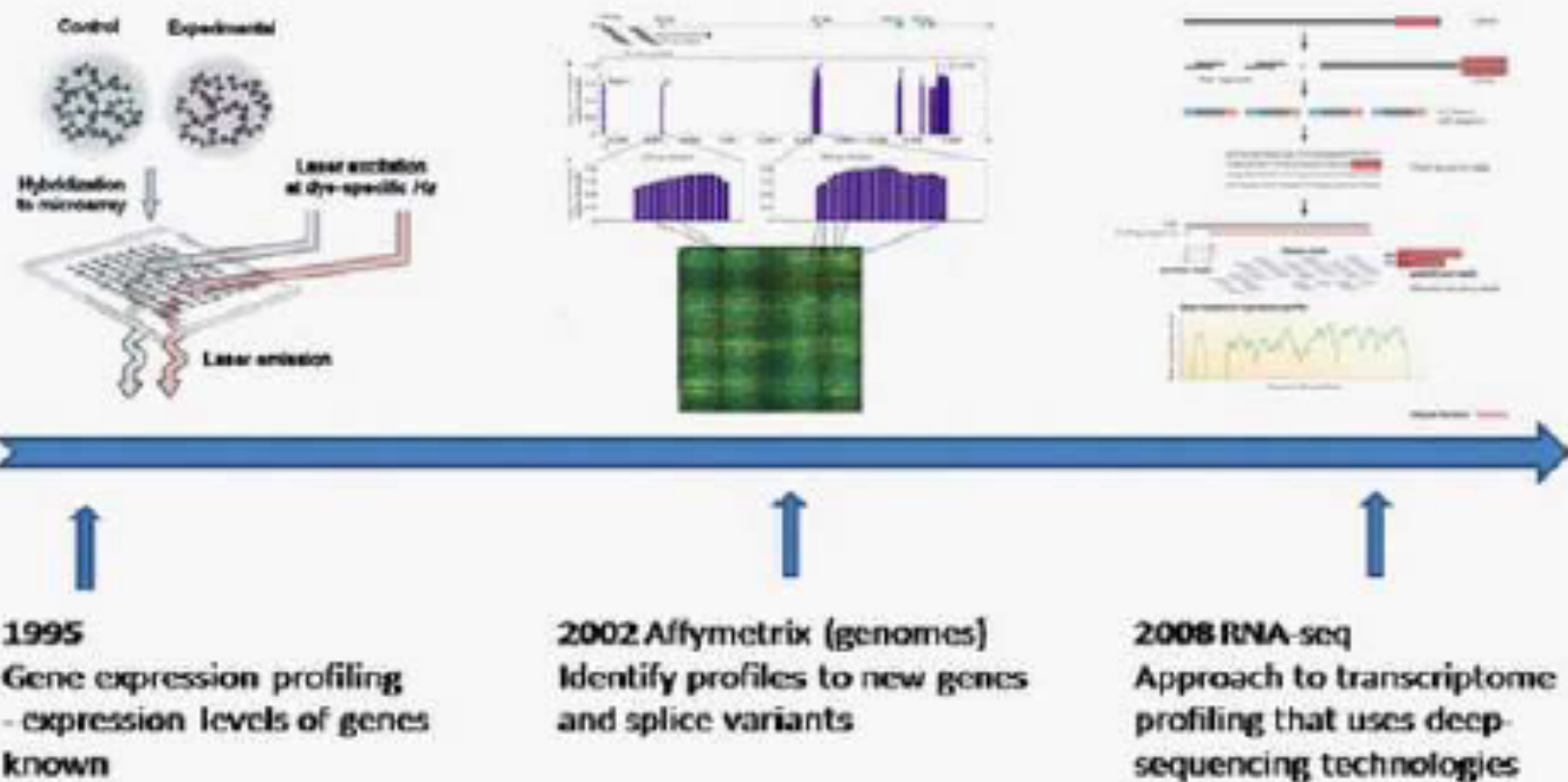




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Session 168: Transcriptomics: Definition and Applications of Transcriptomics, NGS in brief

The evolution of transcriptomics



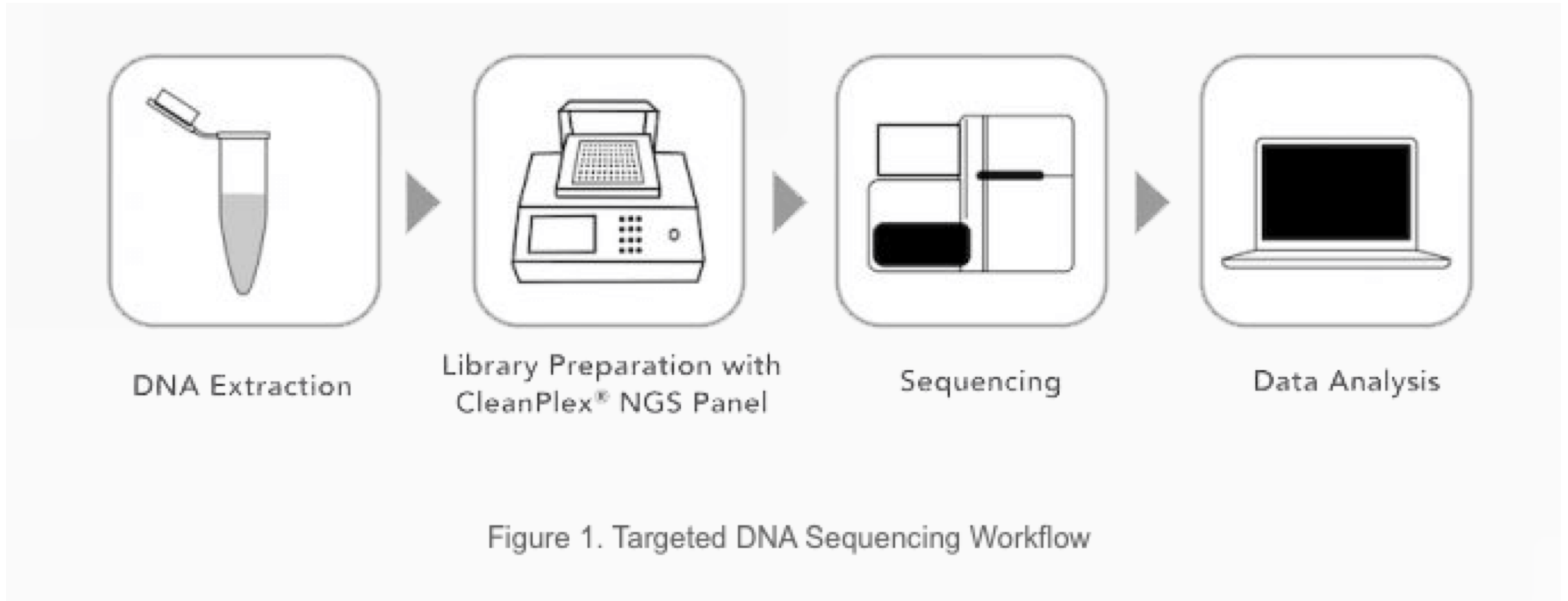
Transcriptomics:

The study of the RNA transcripts of a cell, tissue, or organism (i.e. the transcriptome). Transcriptomics is concerned with determining how the transcriptome, and hence pattern of gene expression, changes with respect to various factors, such as type of tissue, stage of development, hormones, drugs, or disease. It complements and overlaps with proteomics.

Transcriptome: The complete complement of mRNA molecules generated by an organism or cell type.

The most advanced NGS amplicon sequencing technology for targeted DNA and RNA seq

A high-level targeted sequencing workflow (Figure 1) starting from DNA extraction to sequencing data analysis.



The target enrichment and library preparation workflow (Step 2) is critical and often times determines the quality of the sequencing data.

Below is a typical CleanPlex workflow (**Figure 2**) of DNA amplicon sequencing library prep. The workflow involves 3 simple steps, each consisting of a thermal cycling or incubation reaction followed by a library purification using magnetic beads. The streamlined protocol can be completed in just 3 hours.

In step 1: targets of interest are amplified in a multiplex PCR reaction.

In step 2: primer-dimers, non-specific PCR products, and complex molecular-debris are biochemically removed in a digestion reaction featuring the innovative and proprietary CleanPlex Background Cleaning chemistry.

In step 3: libraries are barcoded with sample indexes via a PCR indexing reaction. The input materials could be genomic DNA and DNA extracted from FFPE, fresh/frozen tissues or blood liquid biopsies. By adding a reverse transcription step in the front, the input material could be RNA too. (**Figure 3**)



Figure 2. CleanPlex DNA Target Enrichment and Library Preparation Workflow

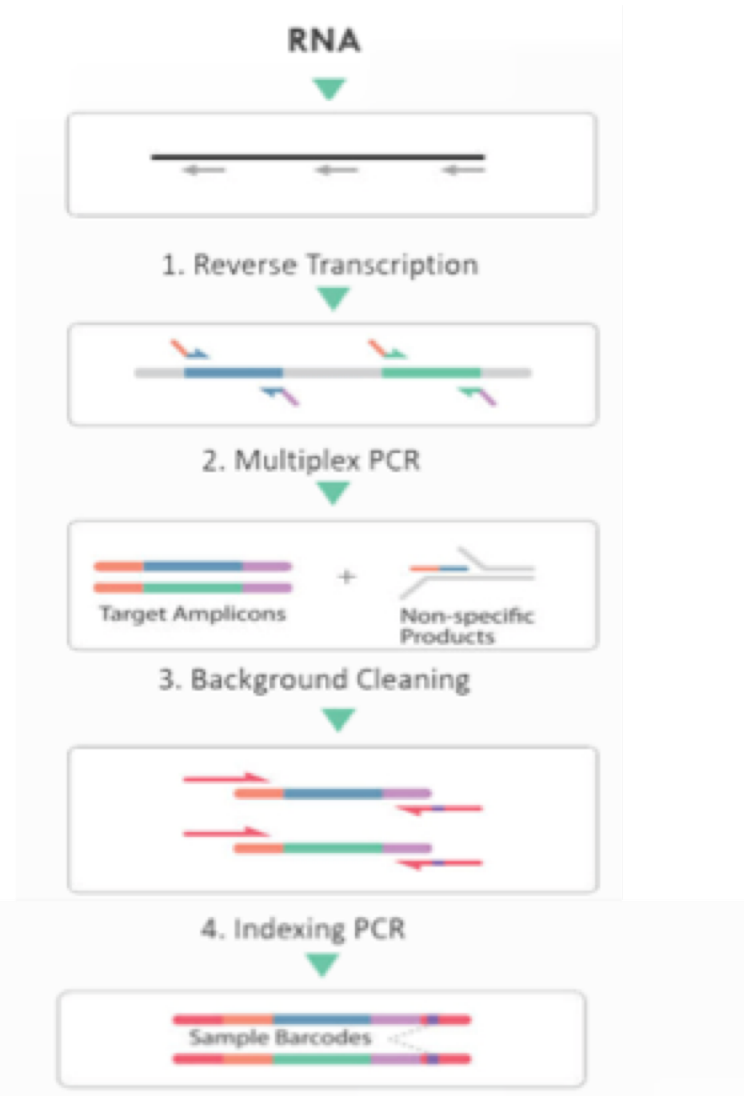


Figure 3. CleanPlex RNA Target Enrichment and Library Preparation Workflow

Reference:

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