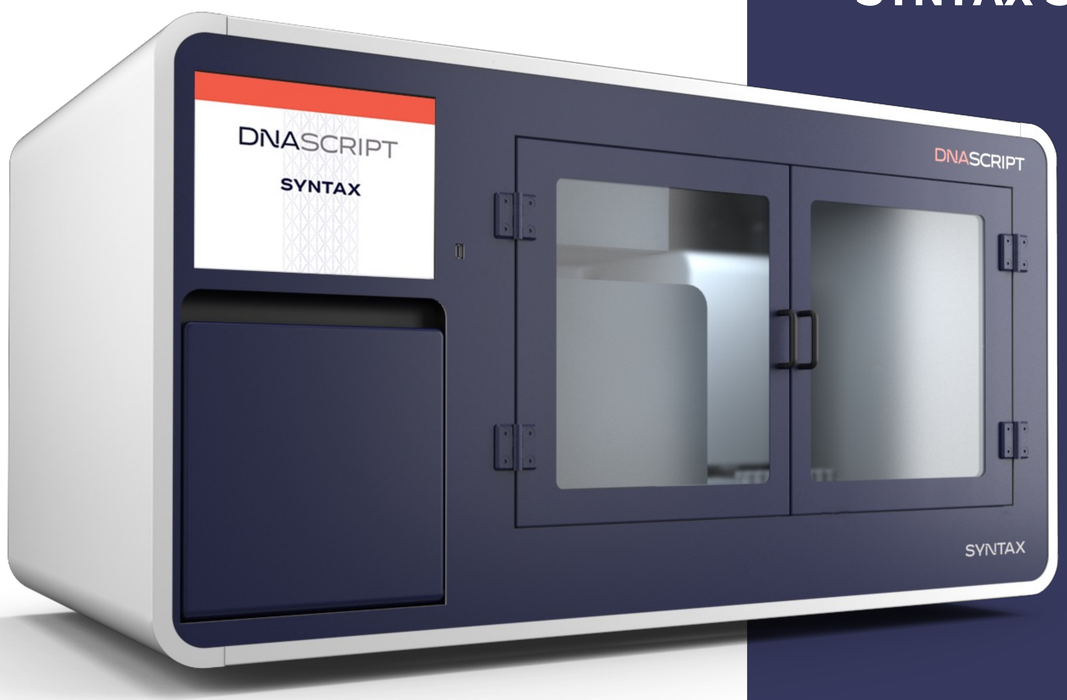
INTRODUCTION

- Precision health and individual genetic profile characterization require synthetic oligos. Typically, these primers and/or probes (for Next-Generation sequencing (NGS), Sanger sequencing, qPCR, or FISH assays) are supplied by an external distributor.
- When problems surface at the manufacturing and distribution level, effects can be felt downstream in the laboratory resulting in lag time and/or unpredictable assay performance.
- The DNA Script SYNTAX System, an in-house benchtop instrument that uses Enzymatic DNA Synthesis (EDS) to print the precise oligos required for a variety of applications, can provide labs with complete control over their workflows.

SYNTAX SYSTEM: THE FIRST BENCHTOP DNA PRINTER POWERED BY EDS

- Produces normalized, desalted, ready to use oligos at micromolar scale.
- Enables full privacy and control over sequence information.
- Offers predictable oligo supply resulting in rapid iteration of assays, higher productivity, and shorter time-to-results.



A benchtop instrument for oligo synthesis results in faster genetic test development.

Take a photo to download full poster.

SYNTAX SYSTEM SPECS

- Default 5'-phosphate
- Custom iDNA: 1 – 45 nt

Labels/modifications:
- 5 fluorophores (green to deep red emission)
- 3 quenchers
- 5'-, 3'- or internal biotin

Final oligo concentration:
- ≥7 µM (no labels)
- ≥5 µM (with labels)

- Up to 600 pmol per well
- Fully automated, walk-away synthesis
- Up to 96 oligos per run
- 15-minute setup time per run
- Same-day synthesis of 15 – 30 nt oligos
- 15 – 80 nt *de novo* oligo synthesis (A, C, G, T)

BENCHTOP EDS OLIGOS FOR A VARIETY OF NUCLEIC ACID-BASED TECHNIQUES

- Amplicon sequencing
  - targeted cancer genes (Fig. 1)
  - SARS-CoV-2 variant analysis
- End-point PCR
- Probe-based quantitative real-time PCR
- Sanger sequencing for variant confirmation
- smFISH detecting viruses in drosophila gut

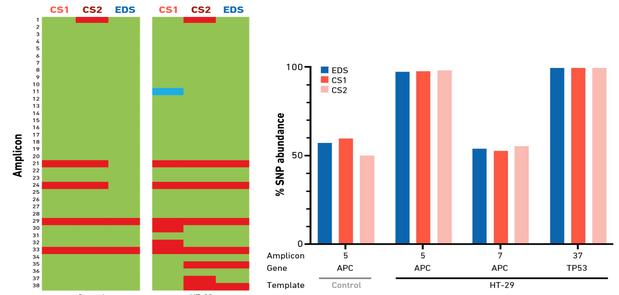


Fig 1. **Comparison of amplicon coverage uniformity and identification of genetic variants (right) in amplicon libraries prepared using EDS or chemically synthesized (CS1 and CS2) sequencing primers.** A cancer panel was sequenced. Amplicons were considered to be adequately represented if they were covered between 0.2X - 5X of the average coverage (green), while coverage <0.2X (red) or >5X (blue) were considered to be under- and over-represented, respectively. Besides, amplicons 29 and 33, which were under-represented in all libraries, suggesting suboptimal primer design or amplification efficiency, in all 38 amplicons, EDS primers had equivalent or superior performance to CS1 and CS2 primers (left). The percent abundance of specific SNPs associated with two tumor suppressor genes (*APC* and *TP53*) were identified by EDS and CS primers. The %SNP abundance is comparable between EDS primers and those prepared by CS1 and CS2 (right).

Lesnick, J.[1], Quistad, S.[1], Nigg, J.[2], Saleh, M.[2], Ngan C.[3], Maurya, R.[3], Tardieu, N.[1], Lachaize, H.[1], Martinez-Fierro, M.[4], Garza-Veloz, I.[4], Centeno-Ramirez, A.[5], Derrien B.[1], Romero S.[1], Lourenco N.[1], Kevin M.[1], Lachaize H.[1], Appel M.[1], Blumenfeld M.[1], Peponnet C.[1] and Wei C.[3], Godron X.[1]

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