SYNTAX SYSTEM

DNASCRIPT

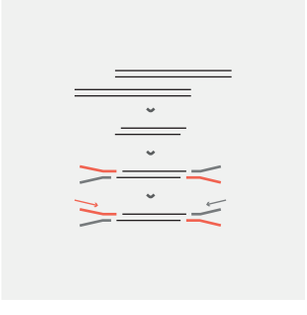
DON'T WAIT.

Print Custom Oligos for NGS and Sanger Sequencing in Your Lab.

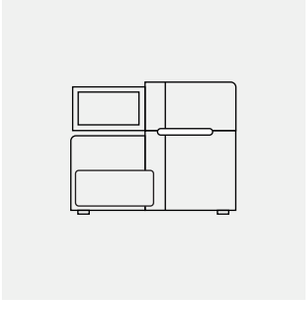
While others wait days, weeks, and sometimes months for commercial oligo providers to ship custom oligos for Sanger sequencing or NGS, the SYNTAX System enables on-demand printing of same-day custom oligos at your benchtop.

DAY 1
Design Primers & Probes

DAY 2
Print Oligos on the SYNTAX in your lab



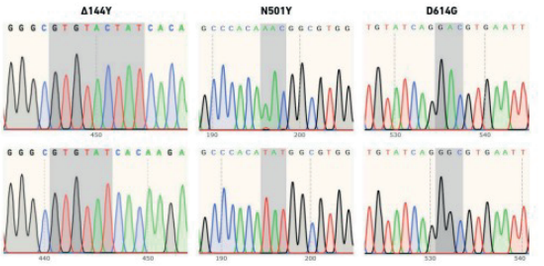
DAY 3
Library Prep



DAY 4
Sequencing

SANGER SEQUENCING

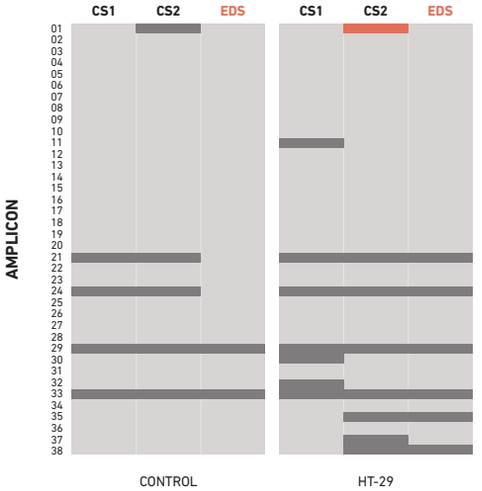
Save time using our SYNTAX Custom iDNA kits to print forward and reverse primers that include the M13 sequence.

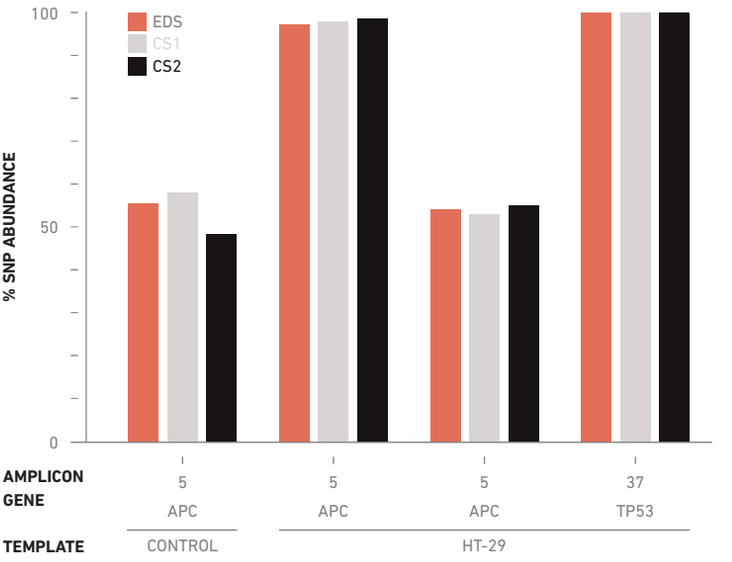


Multisite-directed mutagenesis was performed on the SARS-CoV-2 Wuhan Hu-1 S gene to produce an expression vector for the Alpha (B.1.1.7 lineage) spike protein. Sanger sequencing was used to confirm the successful mutations. All primers were synthesized using the SYNTAX System. Results for three modified sites are shown. Mutation N501Y required the use of mutagenesis primers that are challenging to synthesize, even with chemical synthesis (conventional phosphoramidite chemistry). This study confirmed that EDS primers support complex, multi-site mutagenesis as well as high-quality Sanger sequencing, thus allowing a fast and cost-effective workflow for variant gene production.

NGS TARGET ENRICHMENT

Same-day custom primers and probes with comparable performance to commercial oligos. Print primers containing p5 or p7 sequences and spike-in controls for amplicon sequencing or biotinlabeled probes for hybrid capture sequencing.





To compare the performance of the sequencing primers synthesized using the EDS on the SYNTAX System to those chemically synthesized (CS1 and CS2) and ordered from an oligo service provider, a cancer panel was sequenced using both type of primers and the data were demultiplexed, after which the percentage of sequences assigned to each of the 38 amplicons in the cancer panel was calculated. In all 38 amplicons, EDS primers had equivalent or superior performance to CS1 and CS2 primers (left). The results of amplicon sequencing data was used to calculate the percent abundance of specific SNPs associated with two tumor suppressor genes (APC and TP53). The %SNP abundance is comparable between EDS primers and those prepared by CS1 and CS2 (right).