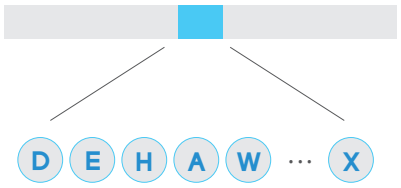
Advancing life science with Synbio innovation

Precision Variant Libraries

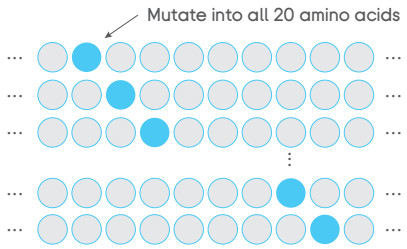
DNA Variant Libraries, both directed and random, are used to change the amino acid sequence of a protein. The use of variant libraries has become an important tool in developing antibody drugs, DNA/RNA vaccines, developing gene therapies, or engineering novel proteins, etc.

GCATbio's mMPS (microchip-based Massive in Parallel Synthesis) DNA synthesis platform is uniquely suited in the industry to produce high quality variant libraries with high yields at reasonable cost. Producing hundreds of thousands of oligonucleotides in parallel with high accuracy and with ease of producing degenerate bases with great flexibility, GCATbio can produce multiple types of libraries and customized with degeneracies, to address all of your library needs at a low price.

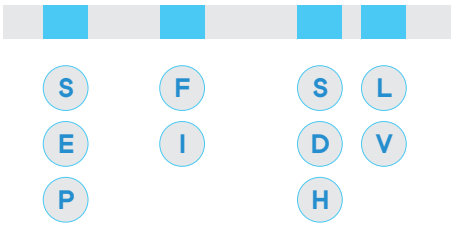
Precision site saturation variant library



Precision scanning saturation variant library



Precision combinatorial variant library



KEY BENEFITS

Precise synthesis

Enables precise control of codon ratio, avoiding unnecessary mutations and facilitating subsequent screening and characterization

Superior uniformity

Uniform distribution of amino acids and high library diversity prevent specific amino acid deficiencies or over expression, which avoid downstream screening biases

High library coverage

Every mutation site can be mutated to all other 19 non-wild-type amino acids, ensuring 100% coverage

High yield

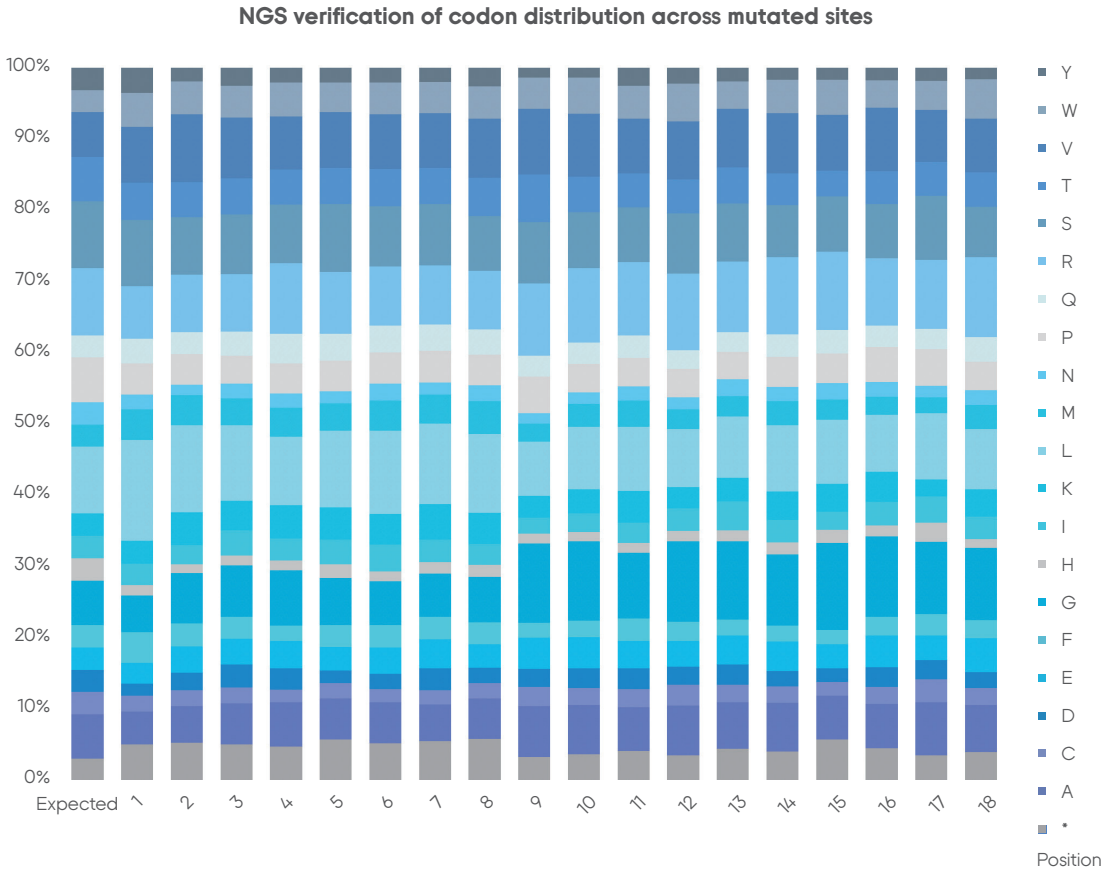
The yield per oligo reaches pmol level and libraries do not require amplification or enzyme treatment

CASE

01 Precision Scanning Saturation Variant Libraries Support Genotype-Phenotype Association Studies

- High-throughput screening of variant libraries provides the ultimate tool for protein directed-evolution and engineering, and has been widely used in genotype-phenotype association studies as well as therapeutic discoveries, etc.

- GCATbio provided tailored services to design and synthesize a NNK scanning saturation variant library for target gene regions (100-300 bp). Customer requirements include adjustable codon distribution and proportional distribution of degenerate bases. After library synthesis, high-throughput sequencing analysis confirmed the uniform distribution of introduced 32 codons, with results indicating no significant codon preference at each site and 100% library coverage.



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