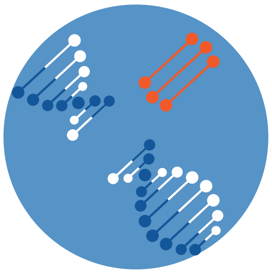
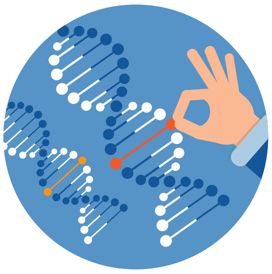
Precision Mutant Libraries

Control Built to Perfection

Expedite your downstream screening time with unbeatable control and complete coverage of your designed variants



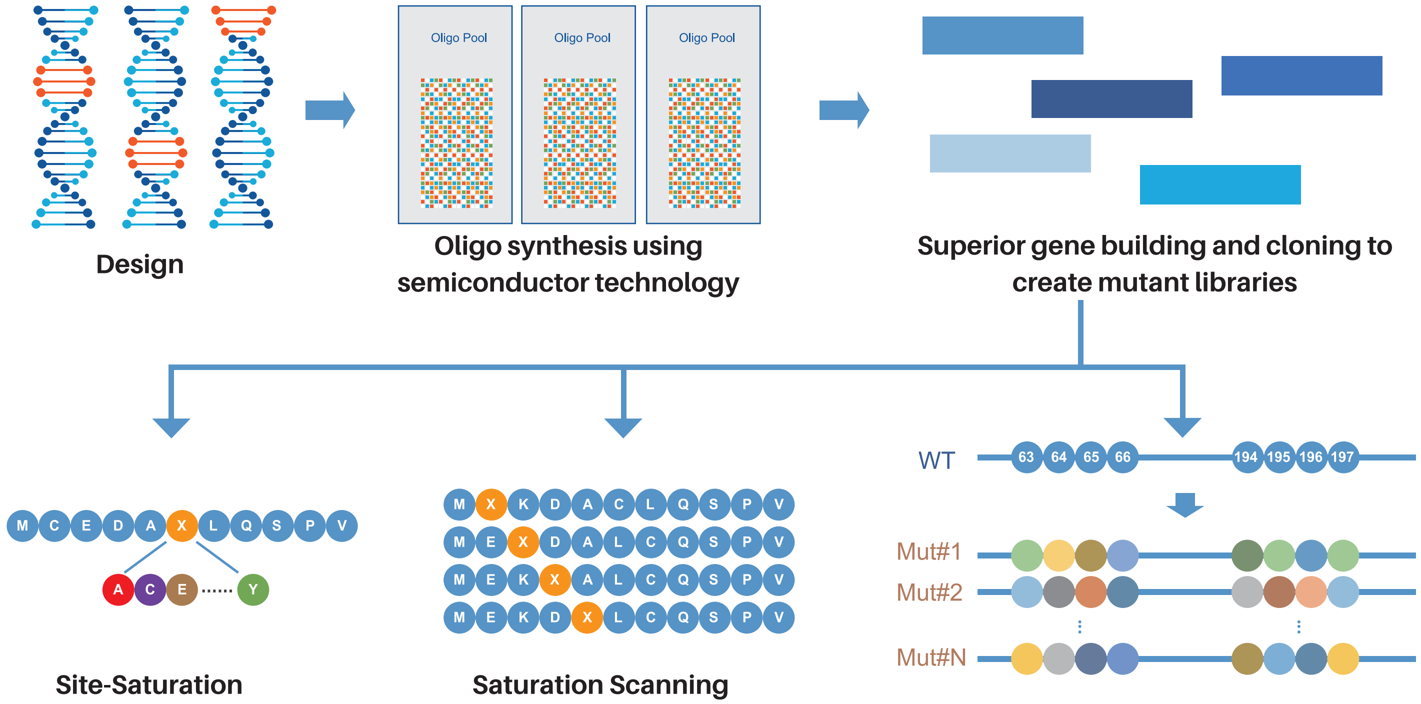
Precise control of codon usage



Superior library diversity

Minimize screening burden

Library assembly is powered by our expertise in de novo gene synthesis and advanced semiconductor technology.



Design

Oligo synthesis using semiconductor technology

Superior gene building and cloning to create mutant libraries

Site-Saturation Mutagenesis

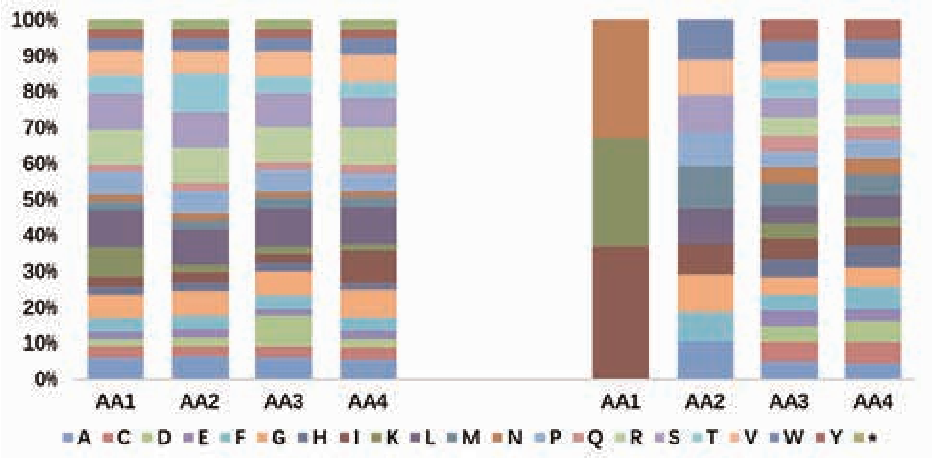
Saturation Scanning Mutagenesis

Combinatorial Mutagenesis

GenScript
Make Research Easy

Next generation semiconductor technology versus conventional degenerate method for library construction

A combinatorial mutagenesis library for 4 sequential amino acid positions was created. Designed distribution required only 3 amino acids in the first position, 10 amino acids in the second position, and all 20 amino acids in the final two positions in all combinations. NGS verification of variant frequency was performed.



Library constructed with NNK degenerate oligo

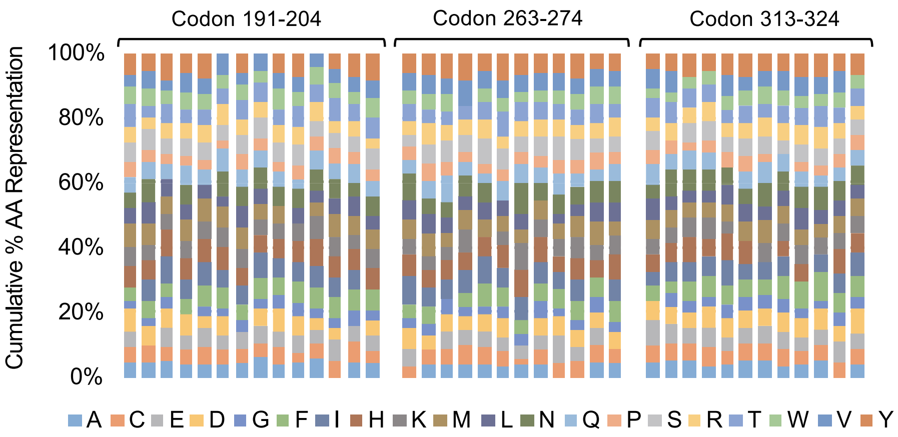
Library constructed with semiconductor-based oligos

- Codon distribution was significantly biased for libraries constructed with NNK degenerate oligos.
- Semiconductor-based oligos achieves user-defined distribution at each position.
- Equal representation of variants containing the desired amino acids at each position.

Using semiconductor-based oligos eliminates codon bias and poor representation of desired amino acids, thereby increasing screening efficiency.

Equal representation of variants per position

Saturation scanning mutagenesis library of 38 codon positions within three separate regions of a protein. NGS verification of variant frequency was performed.



Each bar represents a mutated position and each color represents the frequency of variants with a particular amino acid.

- Near 100% coverage of all mutated variants at each position.
- Equal representation of amino acids per position indicating there is no over- or underrepresentation of variants.

GenScript
Make Research Easy