neochromosome

controlled mutagenesis library

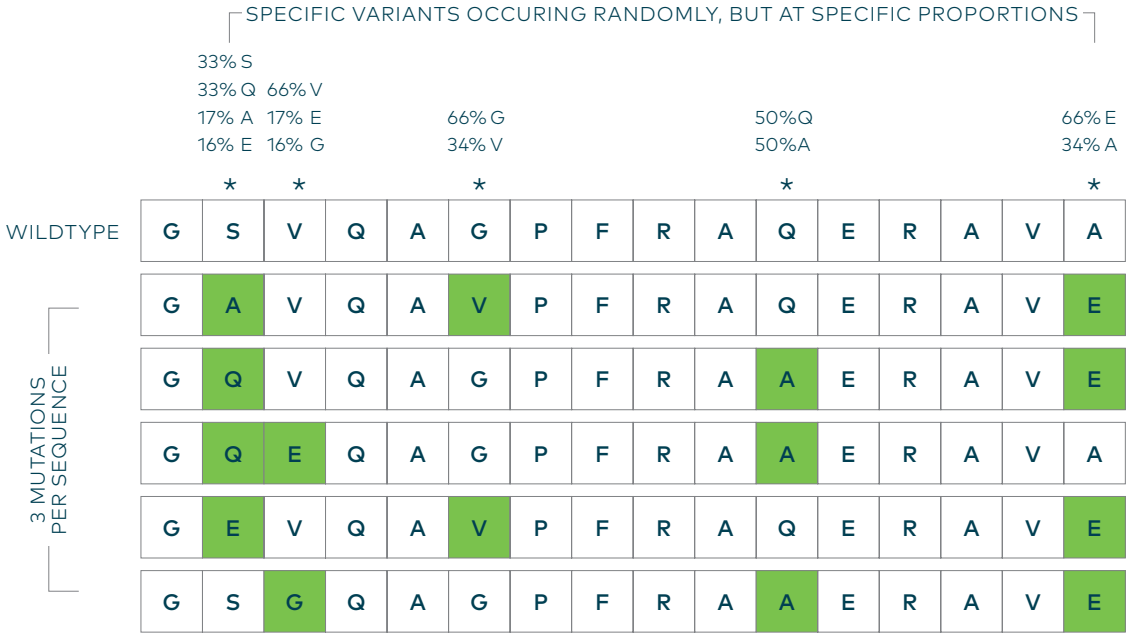
DNA libraries with precise control over mutational position and mutational frequencies.

While conventional gene synthesis providers treat each sequence as a separate synthesis event, Neochromosome takes a holistic approach, implementing part recycling to minimize costs and expedite library synthesis. Neochromosome offers precise, rapid, and budget-friendly DNA variant libraries. We build mutagenesis libraries with defined mutation ratios per location or a max number of deviations from a WT sequence to ensure that our partners are able to achieve their project goals. Neochromosome stores a replica of each library to enable rapid generation of sub libraries to generate additional diversity from top hits (Variant Mining). Expert consultation is available as the design and implementation of each project is led by PhD scientists. All in-process parts and final deliverables are archived in Neochromosome's NYC facility, allowing for fast iterative sequence builds and further cost savings.

Combine with other DNA services from Neo to create a **Flexible Workflow**

Customers have control over:

- Mutational position
- The percentages of sequences which contain a particular variant
- The max, min, or average number of mutations per sequence



Library Examples

EXAMPLE	CUSTOMER REQUIREMENTS
WT Distance Limited	"Variant libraries with a set of possible mutations, but no more than 4 mutations per sequence"
Controlled Percentages	"A library with 15% wildtype, 30% mutation A, 55% mutation B at one or multiple locations"
Randomization	"Random mutational diversity"

Product Features

DESCRIPTION	SYNTHESIS OF DEFINED SEQUENCE VARIANTS THAT SHARE HOMOLOGY
Turnaround Time	Starting at 2 weeks, project dependent
Sequence Verification	Sanger and/or NGS as requested
Pooled Linear DNA	>500 ng of Qubit-quantified linear DNA
Arrayed Linear DNA	>50 ng of Qubit-quantified linear DNA
Arrayed or Cloned Circular DNA	5 ug to 5 mg plasmid preps
Cost	Project dependent, economies of scale achieved with more sequences/homology
Cloning Options	Sequences may be cloned into any customer-provided vector
Customization	Neo's PhD scientists will partner with you to determine custom "Flexible Workflows" including scale-up and Variant Mining™
Deliverable	Delivered in pools or as individually arrayed variants 96/384 well plates or 1.5 ml tubes. Other delivery options available on request, but may increase turnaround time.

Parts Repository

STORAGE TYPE	DESCRIPTION
Short-Term	Store source oligos and purified DNA or glycerol stocks at Neo for short periods of time (e.g. 1–2 months) to enable rapid re-order and scale-up of assay winners.
Long-Term	Store source oligos and purified DNA or glycerol stocks at Neo for long periods of time (e.g. 1–2 years) for rapid re-order and scale-up of inventoried DNA products or for disaster recovery

Variant Mining™

After your initial sequences are assayed, you can then submit your top performing "hits" to have Neo perform Variant Mining™. Variant Mining™ will design all possible recombinants of your most promising leads using the source oligos on-hand, allowing for rapid turn around and greatly reduced cost for your evolution campaign. You can continue to assay and combine hits as the feedstock for Variant Mining™ until you have found the highest level of fitness for your process relevant conditions. We will keep your parts in our Parts Repository to enable iterative mining campaigns.

Check out our Variant Mining™ product sheet to learn more!

PLACING ORDERS AT NEO

To get started, please email a project description to **info@neochromosome.com**