PRCISR™ CRISPR:
PCR-free Libraries - Screening Services

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Vivlion's PRCISR™ CRISPR platform

PRCISR™ CRISPR is Vivlion's **full-service** CRISPR-enabled discovery platform that solves key challenges of CRISPR screening, thereby optimizing the target identification process.

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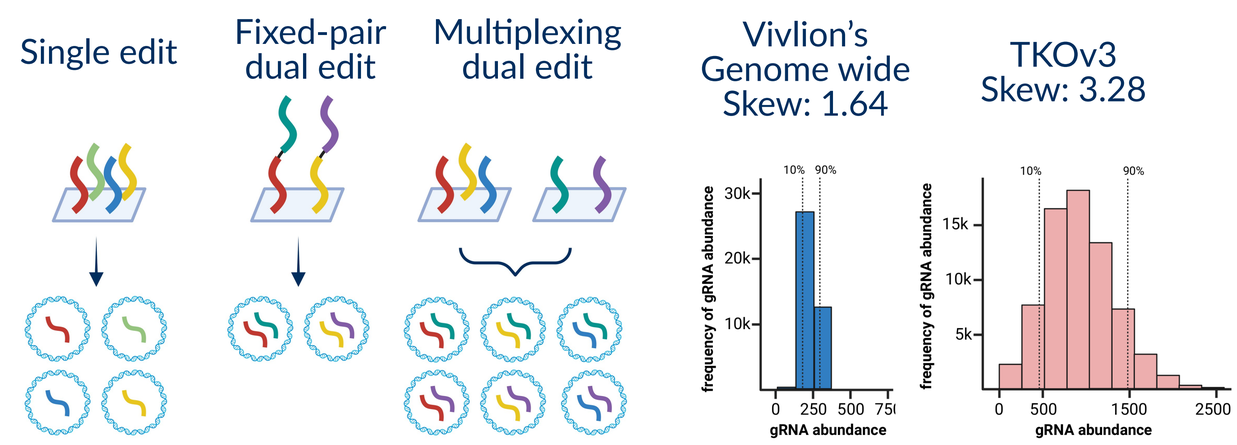
PRCISR™ CRISPR Libraries	**Consulting**	**HTP CRISPR Screening**	**Bioinformatics**
• PCR-free • Uniform • Validated gRNAs • Customized control concept	• Experimental setup • Controls • Orthogonal approaches • Barcoding and scRNA-seq	• Combinatorial setups • Downscaling • Parallelization • Drug synergy and landscapes	• Customizable for single and combinatorial edits • Established pipelines • Genetic interaction maps • Data integration

(1) Vivlion's PRCISR™ CRISPR libraries are **tailored** to customer requirements and in-house screening experiments. Drawing from validated gRNAs, PRCISR™ CRISPR libraries are designed to optimize editing efficiencies (up to 90%). The **PCR-free** generation process ensures **uniform** gRNA library distributions.
(2) Vivlion's **consulting expertise** enables customers to optimize the insights from screening experiments.
(3) Vivlion's uniform PRCISR™ CRISPR libraries enable experimental **downscaling and parallelization** to maximize the power of high-throughput single and combinatorial CRISPR screening.
(4) Vivlion's **customized bioinformatics** solutions enable hit discovery for optimum target identification.

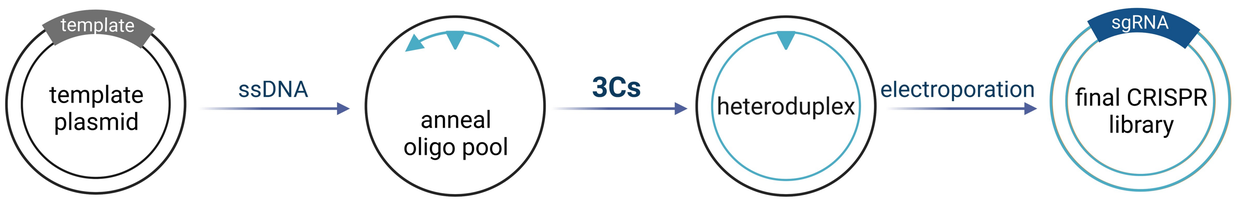
PCR-free and uniformly distributed CRISPR libraries



Vivlion's PRCISR™ CRISPR libraries are available in single-edit, fixed-pair dual-edit, and multiplexed formats. The library distribution skew quantifies the uniformity of a library and is measured by dividing the 90% percentile by the 10% percentile of the distribution of gRNA abundance.

PCR-free and uniformly distributed CRISPR libraries

The covalently-closed circular-synthesized (3Cs) technology is PCR-free and does not require any restriction- and ligation-based cloning steps.



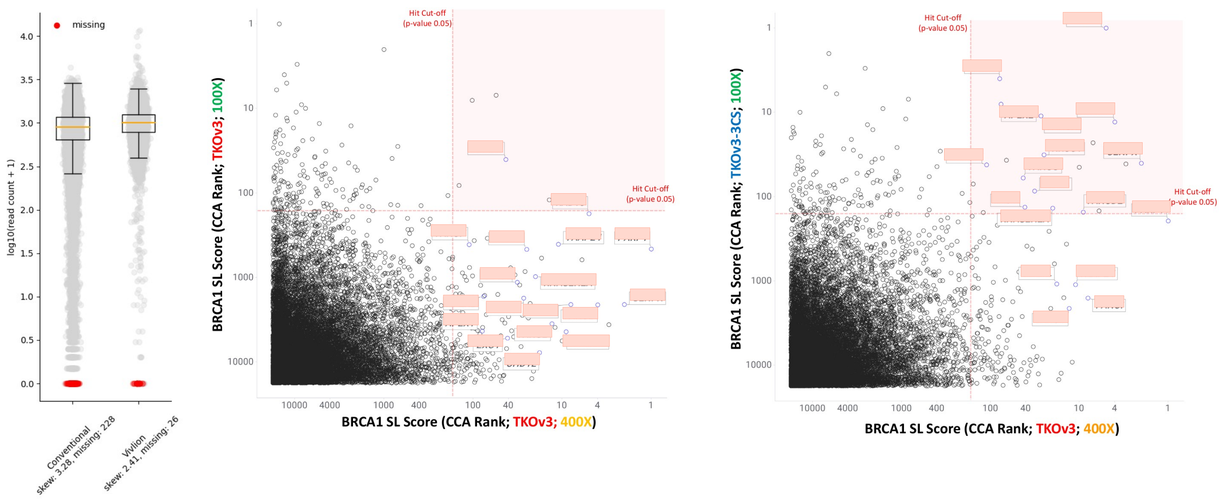
Any template plasmid can be adapted and transformed into single-stranded DNA to hybridize with gRNA-encoding oligonucleotide pools. The heteroduplex is generated with a polymerase and a ligase. The final library is obtained by bacterial amplification. The distribution of the input oligo pool determines the distribution of the final CRISPR library.

All libraries undergo extensive QC including HTP sequencing to ensure their completeness and uniform distribution.

Vivlion proudly works with: REPARE THERAPEUTICS

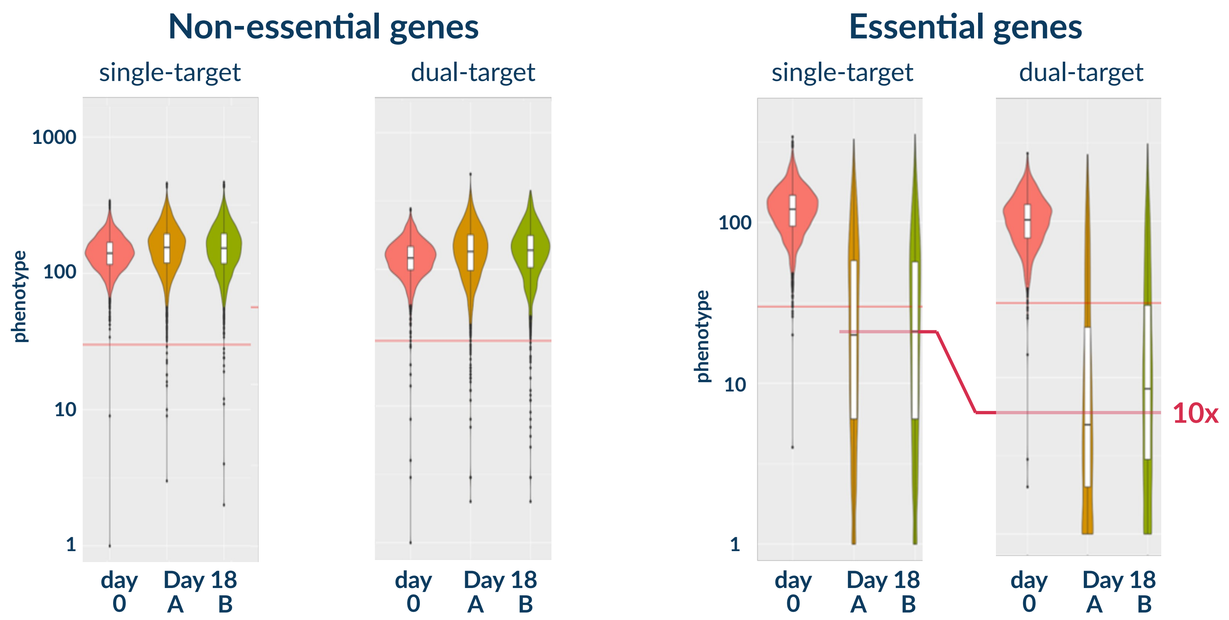
Low Skews facilitate downscaling and parallelization

Conventionally cloned CRISPR libraries have high skews that lead to low confidence in potential hits as shown by Vivlion's partner Repare Therapeutics. The conventional library had a higher skew and showed significant less hits when screened at 100x as compared to 400x. The TKOv3-3Cs maintained a high hit retention rate even at a 100x as compared to the conventional library at 400x.



Dual-targeting increases editing efficiency up to 10x

Targeting the same gene with two gRNAs increases the probability of efficient gene knock out by a factor of 10x as shown by Vivlion's partner Repare Therapeutics.



Figures courtesy of Repare Therapeutics.

Vivlion enables parallelization and combinatorics at scale

Gene editing capacity per screen	Conventional	vivlion
Very high >1 mio	Prohibitive zone	Enable combinatorics and new target discoveries
High 0.2 - 1 mio	Challenging zone	Drive parallelization
Low <0.2 mio	Status quo	Expand cellular systems

Screening a high number of gene edits is challenging to prohibitive with conventional libraries. Vivlion's PRCISR™ CRISPR libraries enable downscaling and parallelization and unlock the combinatorial space for new target discoveries.

References: Wegner et al., eLife 2019
Wegner et al., Bio-Protocol., 2020
Diehl et al., Nucleic Acids Research, 2021
Figures created with BioRender.com