



**Technical Manual**

**Screening**

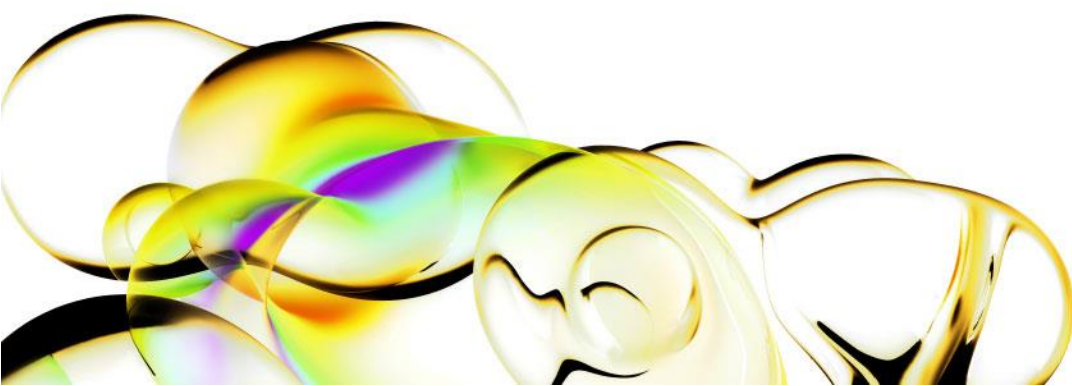
# Dharmacon™ Edit-R Lentiviral sgRNA Pooled Libraries

**Storage : -80°C**

**Version: 0001**

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For research only. Not for use in diagnostic procedures.



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# 1 Introduction

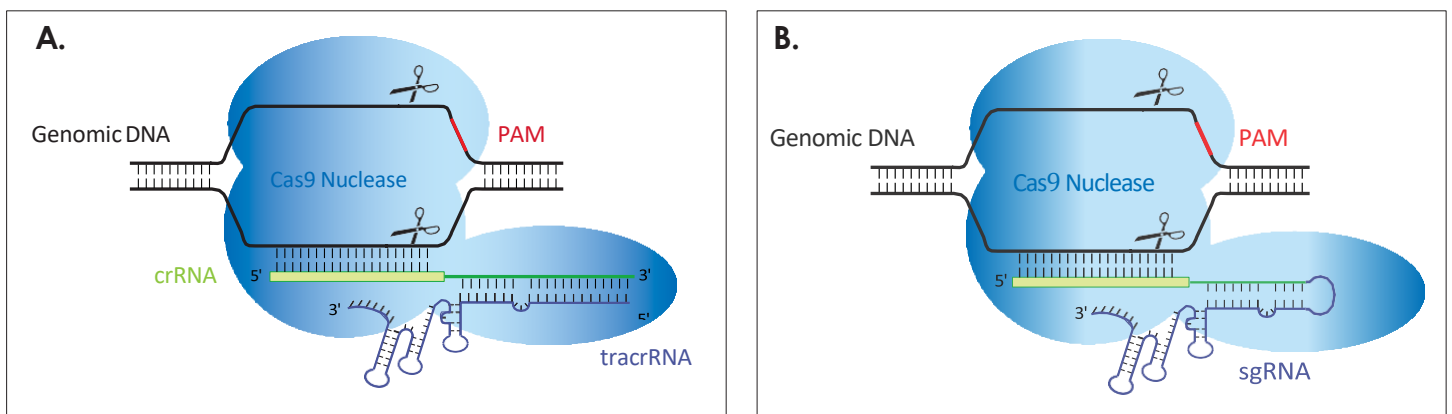
## A. CRISPR-Cas: An adaptive immunity defense mechanism in bacteria and archaea

The CRISPR (clustered regularly interspaced palindromic repeats)-Cas (CRISPR-associated protein) system is an adaptive bacterial and archaeal defense mechanism that serves to recognize and silence incoming foreign nucleic acids. Upon infection by bacteriophage or other foreign DNA elements, a host organism can incorporate short sequences from the invading genetic material, called protospacers, into a specific region of its genome (the CRISPR locus) between short palindromic DNA repeats of variable lengths. Multiple spacer-repeat units are clustered at the CRISPR locus to form the CRISPR array. The entire locus including the CRISPR array is transcribed by RNA polymerase into a primary transcript, the pre-CRISPR RNA (pre-crRNA), which is then processed into small, mature CRISPR RNAs (crRNAs) such that they include sequences complementary to the foreign, invading DNA. crRNAs guide a multifunctional protein or protein complex (the CRISPR-associated or Cas proteins) to cleave complementary target DNA that is adjacent to short sequences known as protospacer-adjacent motifs (PAMs). Thus, the organism acquires a way to protect itself from subsequent infection<sup>1</sup>.

## B. Engineering a CRISPR-Cas9 platform for mammalian genome editing

Many bacterial and archaeal CRISPR-Cas systems have been identified with diverse sets of mechanisms, Cas proteins and multi-subunit complexes. In particular, the processes and key components of the *Streptococcus pyogenes* CRISPR-Cas9 system have been well studied and adapted for genome engineering in mammalian cells. In *S. pyogenes*, only three components are required for targeted DNA cleavage at specific target sites adjacent to a PAM<sup>2</sup>: (1) The endonuclease Cas9, programmed by (2) a mature crRNA processed from transcription of the CRISPR locus/array which complexes with (3) another CRISPR locus-encoded RNA, the trans-activating CRISPR RNA (tracrRNA, Figure 1A)<sup>3</sup>. Alternatively, the crRNA can be fused to the tracrRNA creating a chimeric structure termed a single guide RNA (sgRNA, Figure 1B)<sup>2</sup>.

Upon site-specific double-strand DNA cleavage, a mammalian cell can repair such a break through either nonhomologous end joining (NHEJ) or homology directed repair (HDR). NHEJ is often imperfect, resulting in small insertions and deletions (indels) that can cause nonsense mutations resulting in gene disruptions to produce gene knockouts<sup>4,5</sup>. This endogenous DNA break repair process, coupled with the highly tractable *S. pyogenes* CRISPR-Cas9 system, allows for a readily engineered platform to permanently disrupt gene function.



**Figure 1.** Illustration of CRISPR-Cas9 system. Cas9 nuclease (light blue) programmed by the crRNA (green):tracrRNA (purple) complex (A) or the sgRNA (B) cutting both strands of genomic DNA 5' of the PAM (red).

## 2 Edit-R Lentiviral sgRNA Pooled Screening Platform

Edit-R Lentiviral sgRNA Pooled Libraries are pools of lentiviral constructs expressing sgRNAs targeting coding genes for knockout. Gene knockout pooled screening can be performed to identify the function of a coding gene in the regulation of cellular responses and signaling pathways without the need for costly automation and equipment required for arrayed screening. The Edit-R Lentiviral sgRNA Pooled Screening platform is a two-vector system that utilizes a lentiviral vector for Cas9 expression and a gene-specific vector for sgRNA expression designed to the target site of interest. Edit-R Lentiviral sgRNA Pooled Libraries are comprised of gene-specific sgRNAs and 50 or 100 non-targeting controls per pool for hit normalization. Table 1 lists the pre-defined pooled lentiviral libraries that are available. All libraries are delivered with a data file containing complete library information including gene annotations, sgRNA target sequences, complete list of

controls, and counts per millions of mapped reads obtained from high-throughput sequencing of library prior to lentiviral packaging.

**Table 1.** Available Edit-R Lentiviral sgRNA Pooled Libraries

Edit-R Lentiviral sgRNA Pooled Library <sup>1</sup>	HUMAN		MOUSE	
	Number of targeted genes <sup>2</sup>	Number of pools	Number of targeted genes	Number of pools x number of constructs per pool <sup>2,3</sup>
Whole Genome	18890	1 pool	19683	19 pools x 10 600 constructs
Druggable Genome	6411	1 pool	9827	10 pools x 10 170 constructs
GPCR	470	1 pool	498	1 pool x 5311 constructs
Ion Channel	581	1 pool	340	1 pool x 3818 constructs
Protein Kinase	1139	1 pool	708	1 pool x 7451 constructs
Phosphatase	282	1 pool	269	1 pool x 3089 constructs
Protease	689	1 pool	533	1 pool x 5712 constructs
Ubiquitin Conjugate	564	1 pool	517	1 pool x 5564 constructs

<sup>1</sup> Additional gene families are available by request ([technical@horizondiscovery.com](mailto:technical@horizondiscovery.com))

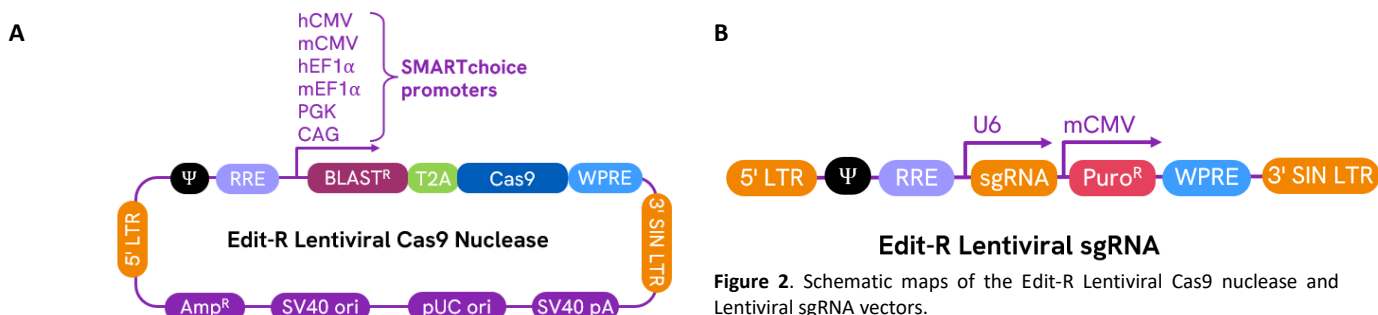
<sup>2</sup> The number of genes and constructs per pool are subject to change at any time without notice.

<sup>3</sup> Number of constructs per pool includes gene specific and negative control sgRNA constructs for mouse genes and human libraries pre-2024. Gene specific positive controls: sgRNA constructs targeting up to 34 protein-coding genes including *Actb*, *Gapdh*, *Lamb1*, and *Ppib*; negative controls: 100 non-targeting sgRNA controls bioinformatically confirmed to not align with (target) any gene in the human, mouse and rat genomes.

## A. Edit-R Lentiviral Cas9 Nuclease and sgRNA vectors

The Edit-R Lentiviral Cas9 Nuclease expression vectors contain a human codon-optimized version of the *S. pyogenes cas9* (*csn1*) gene and the blasticidin resistance marker (Blast<sup>R</sup>). Blast<sup>R</sup> is placed upstream of the Cas9 coding region rather than on the 3' end so that no extra amino acids are added to the C-terminus, thus preserving the full Cas9 endonuclease activity. Both are expressed as a bicistronic transcript with a 2A peptide sequence linker under the control of a single promoter (Figure 2). Multiple promoter options are available (Figure 2A) so that the most active promoter driving Cas9 nuclease expression can be chosen for specific cells of interest. In the Edit-R Lentiviral sgRNA vector backbone (Figure 2B), the gene-specific sgRNA is expressed under the control of a human U6 promoter, while expression of the puromycin resistance marker (PuroR) is driven from the mouse CMV promoter and allows for rapid selection of cells with integrated sgRNA. The optimized sgRNA scaffold used in the Edit-R Lentiviral sgRNA can further improve gene knockout efficiency. The functional elements for both lentiviral vectors are listed and described in Table 2.

Each Edit-R Lentiviral sgRNA is specific to the gene or genomic site of choice. The crRNA region of the sgRNA is comprised of 19-20 nucleotides identical to the genomic DNA target site, followed by the non-variable sgRNA scaffold containing the tracrRNA sequence from *S. pyogenes*. The chosen genomic DNA target sequence must be immediately upstream of a PAM. The predominant *S. pyogenes* PAM nucleotide sequence is NGG.



**Figure 2.** Schematic maps of the Edit-R Lentiviral Cas9 nuclease and Lentiviral sgRNA vectors.

**Table 2.** Elements of the Edit-R Lentiviral Cas9 Nuclease Expression and sgRNA vectors.

Vector element	Utility
<b>Cas9</b>	Human codon-optimized <i>S. pyogenes</i> Cas9 nuclease for cleavage of targeted DNA when programmed with a sgRNA
<b>T2A</b>	Self-cleaving peptide allows for simultaneous expression of puromycin resistance and Cas9 protein from a single transcript
<b>Puro<sup>R</sup></b>	Puromycin resistance marker permits antibiotic selection of transduced mammalian cells
<b>Blast<sup>R</sup></b>	Blasticidin resistance marker permits antibiotic selection of transduced mammalian cells
<b>hCMV</b>	Human cytomegalovirus immediate early promoter
<b>mCMV</b>	Mouse cytomegalovirus immediate early promoter
<b>hEF1<math>\alpha</math></b>	Human elongation factor 1 alpha short promoter
<b>mEF1<math>\alpha</math></b>	Mouse elongation factor 1 alpha short promoter
<b>PGK</b>	Mouse phosphoglycerate kinase promoter
<b>CAG</b>	Human cytomegalovirus, chicken $\beta$ -actin hybrid promoter
<b>U6</b>	Human RNA polymerase III promoter U6
<b>sgRNA</b>	Optimized single guide RNA, a fusion of gene-specific crRNA with the tracrRNA scaffold
<b>5' LTR</b>	5' Long Terminal Repeat necessary for lentiviral particle production and integration of the construct into the host cell genome
<b><math>\Psi</math></b>	Psi packaging sequence allows lentiviral genome packaging using lentiviral packaging systems
<b>RRE</b>	Rev Response Element enhances titer by increasing packaging efficiency of full-length lentiviral genomes
<b>WPRE</b>	Woodchuck Hepatitis Post-transcriptional Regulatory Element enhances transgene expression in target cells
<b>3' SIN LTR</b>	3' Self-inactivating Long Terminal Repeat for generation of replication-incompetent lentiviral particles
<b>SV40 pA</b>	Simian virus 40 polyadenylation signal
<b>pUC ori</b>	pUC origin of replication
<b>SV40 ori</b>	Simian virus 40 origin of replication
<b>Amp<sup>R</sup></b>	Ampicillin resistance gene

## B. Overview of Edit-R Lentiviral sgRNA Pooled Library screening workflow

Once basic transduction and assay conditions have been optimized, Cas9-expressing cell lines can easily be generated with the Edit-R Lentiviral Cas9 Nuclease Expression particles. Cells are transduced at a low multiplicity of infection (MOI) with a lentiviral pooled library (see Figure 3 for a screening workflow diagram). Individual cells in the resulting transduced population will contain single constructs integrated into their genomes. Following transduction and puromycin enrichment for sgRNA-expressing cells, a selective pressure is applied such that those constructs involved in a specific biological response can be identified. As a result of the selective pressure, cells expressing the sgRNA construct are either enriched or depleted in the cell population.

To identify “hits,” gDNA is isolated from the initial transduced cell population (reference sample) and from the transduced cell population that remained following the application of selective pressure and/or phenotypic selection (experimental sample). sgRNA constructs within the isolated gDNA are amplified using vector-specific NGS Hit Identification Primers that have been designed and optimized to minimize amplification bias and introduce diversity into the high-throughput sequencing run. Illumina P5 and P7 adapters and TruSeq indexes can then be added to the amplified library through a second low amplification PCR step prior to high-throughput sequencing on an Illumina® platform. The differences in sgRNA construct abundance between reference and experimental cell populations can then be determined to identify hits from the primary screen. Each step of the Edit-R Lentiviral sgRNA Pooled Library workflow, from transduction to hit identification, has been empirically tested.

*For libraries targeting mouse genes and human libraries ordered prior to 2024, sgRNA constructs within the isolated gDNA are amplified using Edit-R Mouse Pooled sgRNA Forward and Reverse Index PCR primers that have been designed and*

optimized to minimize amplification bias. Following amplification, indexed reaction products can be directly loaded onto Illumina flow cells and sequenced using Edit-R Mouse Pooled sgRNA Read 1 and Index Read Sequencing primers. The differences in sgRNA construct abundance between reference and experimental cell populations can then be determined to identify hits from the primary screen. Protocols for multiplexing and Illumina platform sequencing can be found in Appendix A.

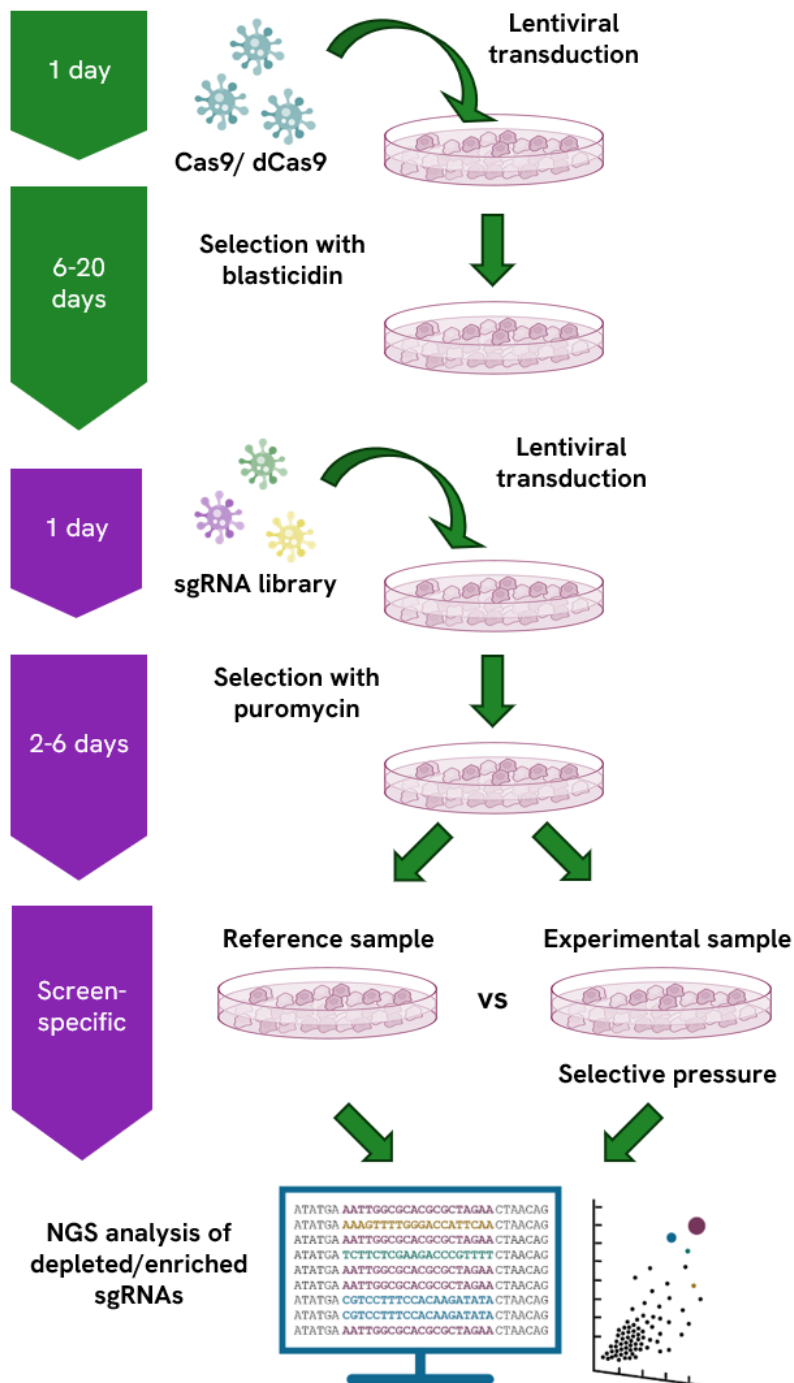


Figure 3. Gene knockout screening workflow using the Edit-R Lentiviral sgRNA Pooled Library platform.

### 3 Laboratory protocols and calculation tracking worksheet

The [Pooled-sgRNA-screening-protocol-tracking-worksheet](#) is a tool for the recording of key calculations and experimental parameters. Please review all the detailed protocols provided in this manual prior to using the worksheet. An electronic version of the worksheet can also be downloaded from the web page. The downloadable Excel worksheet allows users to incorporate specific input related to their screening and performs key calculations to simplify protocol planning. *For libraries targeting mouse genes and human libraries ordered prior to 2024, refer to the second tab of the worksheet.*

## 4 Required materials for lentiviral sgRNA pooled library screening

### A. Materials required

- Edit-R Lentiviral sgRNA Pooled Library
- **Human libraries:**
  - NGS Hit Identification Primers **mCMV**
- **Mouse libraries and pre-2024 human libraries:**
  - Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kit A for Illumina sequencing platform
  - Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kit B for additional reverse indexing PCR primers (if experimental design requires additional multiplexing capability)

### B. Additional materials required

The following additional materials are required but not supplied:

- Edit-R lentiviral positive and non-targeting sgRNA controls for gene editing validation and experimental optimization
- [SMARTvector Non-targeting Control Particles](#) with optimal promoter and fluorescent reporter (TurboGFP or TurboRFP) for determining relative transduction efficiency and optimizing transduction conditions in desired cells of interest.
- Transduction enhancer such as LentiBOOST® (<https://sirion-biotech.com/lentiboost>)
- Base Medium: antibiotic-free cell culture medium (without supplements or serum)
- Growth Medium: antibiotic-free cell culture medium (with serum and/or supplements) recommended for maintenance of the cells
- Transduction Medium: the base cell culture medium containing lentiviral particles (with transduction additives and serum (if necessary))
- Live/Dead indicator such as Zombie Dyes (BioLegend®, <https://www.biolegend.com/en-us/live-dead>)
- Blasticidin S (Fisher Scientific, Cat #BP2647-25; InvivoGen, Cat #ant-bl-1)
- HyClone™ Puromycin 2 HCl (Cytiva, Cat #SV30075.01 or similar)
- Phusion Hot Start II High-Fidelity DNA Polymerase and 5x Phusion HF Buffer (Thermo Scientific, Cat #F-549L; NEB, Cat #M0535L)
- Genomic DNA purification kit (Blood and Cell Culture DNA Purification Kit, Qiagen, Cat #13362 or similar)
- PCR purification kit (QIAquick™ PCR Purification Kit, Qiagen, Cat #28104 or similar)
- Nucleotide mix dNTP set, 100 mM each (NEB, Cat # N0446S or similar)

## 5 Assay development and optimization

Please use the [Pooled-sgRNA-screening-protocol-tracking-worksheet](#) as a guide.

### A. Selection of the optimal promoter for Cas9 expression

Expression levels of Cas9 nuclease can have a significant effect on gene knockout efficiency. Therefore, select the lentiviral Cas9 nuclease vector with the most active promoter in your cell line based on empirical testing or known promoter activity.

### B. Optimization of lentiviral transduction

While lentiviral particles exhibit broad cell tropism, the conditions for successful and efficient delivery can vary significantly. It is essential to determine the optimal transduction conditions in each cell line or type of interest. Please keep in mind that the conditions selected during these optimization steps must be compatible with primary screening protocols and conditions.

Edit-R Lentiviral Cas9 Nuclease Expression and sgRNA vectors do not contain a fluorescent reporter. Therefore, SMARTvector shRNA Non-targeting Control lentiviral particles (see Section 4.B. Additional materials required) containing either TurboGFP or TurboRFP reporter genes can be substituted for optimization of transduction conditions.

Detailed protocols for transduction optimization are described in the SMARTvector Lentiviral shRNA Technical Manual ([SMARTvector Lentiviral shRNA Technical Manual](#)).



Use conditions that produce the lowest or no loss of cell viability. Parameters that may influence the efficiency of lentiviral transduction include, but are not limited to:

**Transduction medium:** When possible, the transduction of cells with lentiviral particles should be performed in a small volume of low-serum (0.5-2%) or serum-free medium. For cells sensitive to low serum conditions, transduction optimization can be performed in complete medium.

**Transduction duration:** Incubation time can vary between 4 and 24 hours and will depend on the cells of interest.

**Transduction medium additives:** Cationic polymers such as hexadimethrine bromide (Polybrene) or transduction enhancers such as LentiBOOST® may be added to enhance lentiviral particle binding to the cell surface. We recommend testing a range of concentrations for identification of optimal transduction efficiency with minimal or no cell toxicity.

**Cell density at transduction:** The density at which cells are seeded may also influence transduction efficiency. We recommend seeding cells at a range of densities for optimization of transduction efficiency. Plate sizes for screening should be chosen accordingly.

### C. Determination of functional titer

The functional titers are found in the data file provided with all Dharmacon lentiviral pooled libraries. However, lentiviral transduction efficiency varies widely from one cell type to another. After determining optimal lentiviral transduction conditions, it is required to determine the functional titer in the experimental cell line of choice and calculate an MOI low enough such that the majority of cells will have single integrations.

To determine the relative titer in the experimental cell line, perform a functional titer protocol such as limiting dilution with cell viability assay by [crystal violet staining](#). Alternatively, SMARTvector Non-targeting Control lentiviral particles (see Section 4.B. Additional materials required) containing the optimal promoter and either TurboGFP or TurboRFP reporter genes can be substituted for determining relative transduction efficiency in your desired cells. Detailed protocols for determining functional titer in your cells are described in the [SMARTvector Lentiviral shRNA Technical Manual](#).

**Once the functional titer has been determined, use the formula below to calculate the relative transduction efficiency of your cell line of interest.**

$$\begin{array}{|c|} \hline \text{Functional titer of Edit-R GFP} \\ \text{Delivery Optimization Control in} \\ \text{your cell line (TU/mL)} \\ \hline \end{array} \div \begin{array}{|c|} \hline \text{Titer of Edit-R GFP Delivery} \\ \text{Optimization Control reported} \\ \text{on the C of A (TU/mL)} \\ \hline \end{array} = \begin{array}{|c|} \hline \text{Relative transduction} \\ \text{efficiency of your cell line} \\ \hline \end{array}$$

**Use the calculated relative transduction efficiency of your cell line to then calculate the relative functional titer for the Edit-R Lentiviral sgRNA pooled library using the following formula:**

$$\begin{array}{|c|} \hline \text{Relative transduction efficiency} \\ \text{of your cell line} \\ \hline \end{array} \div \begin{array}{|c|} \hline \text{Titer of the pooled library} \\ \text{reported in data file (TU/mL)} \\ \hline \end{array} = \begin{array}{|c|} \hline \text{Relative functional titer of} \\ \text{the pooled library in your} \\ \text{cell line (TU/mL)} \\ \hline \end{array}$$



### Calculation example

If the functional titer for the Edit-R Lentiviral sgRNA Non-targeting Control particles in your cells of interest is determined to be  $2.1 \times 10^7$  TU/mL and the titer on the C of A is listed as  $5.0 \times 10^7$  TU/mL, then the relative transduction efficiency of your cell type is calculated as follows:

$$2.1 \times 10^7 \text{ TU/mL (functional titer in your cell line)} \div 5.0 \times 10^7 \text{ TU/mL (titer reported on the C of A)} = 0.42 \text{ relative transduction efficiency}$$

If the relative transduction efficiency of your cell line is 0.42 and the titer of an Edit-R Lentiviral sgRNA Pooled Library, as indicated on the C of A, is  $5.6 \times 10^8$  TU/mL, the relative functional titer of the pool in your cell line would be determined as follows:

$$0.42 \text{ (relative transduction efficiency)} \times 5.6 \times 10^8 \text{ TU/mL (titer reported on the C of A)} = 2.35 \times 10^8 \text{ TU/mL relative functional titer in your cell line}$$

## D. Optimization blasticidin and puromycin selection

The Edit-R Lentiviral Cas9 Nuclease Expression vectors contain the blasticidin resistance marker while the Edit-R Lentiviral sgRNA vector contains the puromycin resistance marker for selection of cells after transduction. Prior to treating cells with blasticidin or puromycin, determine the optimal concentration of each antibiotic required to kill non-transduced cells. This concentration can be identified by generating an [antibiotic kill curve](#). The blasticidin concentration range for many mammalian cells is 2-20  $\mu\text{g/mL}$ ; for puromycin it is 0.5-10  $\mu\text{g/mL}$ .

### Day 1:

1. Plate cells in Growth Medium at a density appropriate for your cell type. Incubate overnight.

### Day 2:

2. Change the medium to Selection Medium (Growth Medium supplemented with the antibiotic being tested) at a range of concentrations.

### Days 4-15:

3. Approximately every 2-3 days replace medium with freshly prepared Selection Medium.

4. Monitor the cells daily and visually observe the percentage of surviving cells. Optimum effectiveness should be reached in 2-6 days under puromycin selection or 5-15 days under blasticidin selection.

5. The minimum antibiotic concentration to use is the lowest concentration that kills 100% of the cells in 2-15 days from the start of antibiotic selection.

## E. Determination of assay-specific screening conditions

The pooled screening workflow described here facilitates identification of genetic regulators of a range of biological processes. Variables to consider when planning screening conditions include, but are not limited to, assay duration, conditions of selective pressure (for example, concentration or duration), and method of phenotypic selection (for example, measuring viability, proliferation, surface marker expression or migration). We recommend that you optimize all assay conditions prior to beginning a lentiviral sgRNA pooled library screen using, if possible, an Edit-R lentiviral sgRNA construct targeting a gene known to be involved in the phenotype(s) of interest.

## F. Selection of average fold representation and number of biological replicates

A critical consideration of lentiviral pooled screening is the extent to which any given construct in a pooled library will be represented in the screen; in other words, the number of cells that contain an independent genomic integration of any given sgRNA or the number of biological replicates of each sgRNA integration event and subsequent phenotypic selection. High sgRNA fold representation results in improved reproducibility between biological replicates and ensures that there is a sufficient window for detection of changes in sgRNA abundance<sup>6</sup>.

## Recommendations:

- At least 200 independent integrations per sgRNA (*i.e.*, at least 200-fold representation)
- At least two biological replicates

**We have observed that fold representation has a greater impact on the ability to identify hits than the number of biological replicates. Therefore, we recommend performing at least two biological replicates, while maintaining an average sgRNA fold representation as high as is practical or technically feasible for your screen.**

## G. Calculation of number of cells needed for transduction

Once transduction optimization experiments have been performed and the assay-specific screening parameters determined, cells need to be prepared for transduction. The calculations below outline how to determine the number of cells required at the time of transduction.

Multiplicity of infection (MOI) is defined as the ratio of transducing units of lentiviral particles to target cells. At high MOIs, each cell will likely be transduced by more than one lentiviral particle. Conversely, at low MOIs, the probability that any cell is transduced with more than one lentiviral particle is lower (Table 3). For lentiviral pooled screens, each cell will ideally express a single sgRNA. This ensures that the knockout of a single gene in a particular cell is responsible for the resulting phenotype. Therefore, we recommend performing lentiviral transductions at an  $MOI \leq 0.3$ .

**Table 3.** Poisson distribution showing the distribution of cells with the indicated number of lentiviral integrations at various MOIs.

MOI	Number of lentiviral integrants per cell				
	0	1	2	3	4
0.1	0.90	0.09	0.00	0.00	0.00
0.2	0.82	0.16	0.02	0.00	0.00
0.3	0.74	0.22	0.03	0.00	0.00
0.4	0.67	0.27	0.05	0.01	0.00
0.5	0.61	0.30	0.08	0.01	0.00
0.6	0.55	0.33	0.10	0.02	0.00
0.7	0.50	0.35	0.12	0.03	0.00
0.8	0.45	0.36	0.14	0.04	0.01
0.9	0.41	0.37	0.16	0.05	0.01
1.0	0.37	0.37	0.18	0.06	0.02

At each MOI, the portion of cells having 0, 1, 2, 3, or 4 lentiviral integrants is indicated. For example, at an MOI of 0.3, only 3% of cells are predicted to contain more than one lentiviral integrant.

**To calculate the number of lentiviral integration events required to achieve a given sgRNA fold representation, use the following formula:**

$$\begin{array}{c} \text{Number of lentiviral} \\ \text{sgRNAs in the pool} \end{array} \times \begin{array}{c} \text{Desired fold} \\ \text{representation} \end{array} = \begin{array}{c} \text{Desired number of cells with} \\ \text{lentiviral sgRNA integrations} \end{array}$$

**Use the following formula to calculate the number of cells you will need per sample at the time of transduction:**

$$\begin{array}{c} \text{Desired number of cells with} \\ \text{lentiviral sgRNA integrations} \end{array} \div \begin{array}{c} \text{MOI} \end{array} = \begin{array}{c} \text{Number of cells required} \\ \text{at the time of transduction} \end{array}$$

### Calculation example

If you have a pool of 76000 sgRNAs and you wish to achieve a 200-fold average representation, the desired number of lentiviral integration events would be calculated as follows:

$$76000 \text{ (number of sgRNA)} \times 200 \text{ (average representation)} = 1.52 \times 10^7 \text{ lentiviral integration events}$$

Then calculate the number of cells needed at the time of transduction as follows:

$$1.52 \times 10^7 \text{ (lentiviral integration events required)} \div 0.3 \text{ (maximum recommended MOI)} = 5.1 \times 10^7 \text{ cells needed at the time of transduction}$$

Plate sizes should be chosen such that the required number of cells can reach the optimum density for transduction, as determined above, at the time of transduction. Prepare additional plates of cells for each pool and biological replicate that you wish to transduce. The calculations below outline how to determine cell plating requirements.

**To determine the number of plates required for each biological replicate, use the following formula:**

$$\text{Number of cells required at the time of transduction} \div \text{Cell density at transduction} \div \text{Size of plate (mm}^2\text{)} = \text{Number of plates required per sample}$$

**To determine the total number of plates to seed, use the following formula:**

$$\text{Number of plates required per sample} \times \text{Number of biological replicates} = \text{Number of plates required}$$

Table 4 provides examples of cell and plate numbers and plate sizes for various targeted sgRNA fold representations, assuming a pool size of 76000 sgRNAs and a cell line with optimal transduction density of 250 cells/mm<sup>2</sup>.

**Table 4.** Number of cells required at the time of transduction and cell plating recommendations for indicated average fold representation assuming a whole genome pool of 76000 sgRNAs, MOI of 0.3, optimal transduction density of 250 cells/mm<sup>2</sup> and an effective surface area on 100 mm plates of 7800 mm<sup>2</sup>.

Fold representation	Number of lentiviral integrations required	Number of cells required at transduction	Recommended cell plating
200	$1.52 \times 10^7$	$5.1 \times 10^7$	26 plates × 100 mm
400	$3.04 \times 10^7$	$1.02 \times 10^8$	52 plates × 100 mm

## H. Calculation of volume of lentiviral particles needed for transduction

Before proceeding with the Edit-R Lentiviral sgRNA pooled library screen, confirm that you have sufficient lentiviral particles to perform the screen at the desired fold coverage, given the relative transduction efficiency of your cell line and the number of biological replicates you wish to perform. Follow the steps below to calculate the volume of lentiviral particles required for each pool. Additional lentiviral particles can be ordered separately.

**First, identify the number of lentiviral particles (or transducing units, TU) necessary for each biological replicate based on the required number of cells at the time of transduction by applying the following formula:**

$$\text{MOI} \times \text{Number of cells required at the time of transduction} = \text{Required number of lentiviral particles (TU)}$$

Next, determine the volume of lentiviral particles required based on the following formula:

$$\text{Required number of lentiviral particles (TU)} \div \text{Functional titer in your cell line (TU/mL)} = \text{Volume of lentiviral particles per biological replicate (mL)}$$

To determine the total volume of lentiviral particles required for the screen, use the following formula:

$$\text{Volume of lentiviral particles per biological replicate (mL)} \times \text{Number of biological replicates} = \text{Total volume of lentiviral particles (mL)}$$

### Calculation example

For example, at an MOI of 0.3 and a 200-fold average sgRNA representation at transduction, you will have prepared  $5.1 \times 10^7$  cells at the time of transduction. Based on the above formula, calculate the number of lentiviral particles needed:

$$0.3 \text{ (MOI)} \times 5.1 \times 10^7 \text{ cells} = 1.52 \times 10^7 \text{ TU of lentiviral particles are required for transduction}$$

If you have determined that you need  $1.52 \times 10^7$  TU and you have a functional titer of  $2.35 \times 10^8$  TU/mL in your cell line, you can calculate the volume of lentiviral particles needed as follows:

$$1.52 \times 10^7 \text{ TU} \div 2.35 \times 10^8 \text{ TU/mL} = 0.065 \text{ mL of lentiviral particles}$$

If you are performing two biological replicates, you can determine the total volume of lentiviral particles required as follows:

$$0.065 \text{ mL of lentiviral particles} \times 2 \text{ biological replicates} = 0.13 \text{ mL of lentiviral particles}$$

## 6 Primary screen

The following sections describe the primary screening workflow (Figure 3). Please use the [Pooled-sgRNA-screening-protocol-tracking-worksheet](#) as a guide.

### A. Cell transductions and selection screen

The experimental conditions described here serve as a guide for performing lentiviral transductions. However, the precise cell number and volume of lentiviral particles necessary to achieve the desired MOI and average sgRNA fold representation should be determined specifically for each cell line of interest and each intended screening experiment, as outlined in **Section 5**. Similarly, conditions should be clearly defined prior to starting the screen for application of selective pressure and/or sorting of cells exhibiting the phenotype of interest.

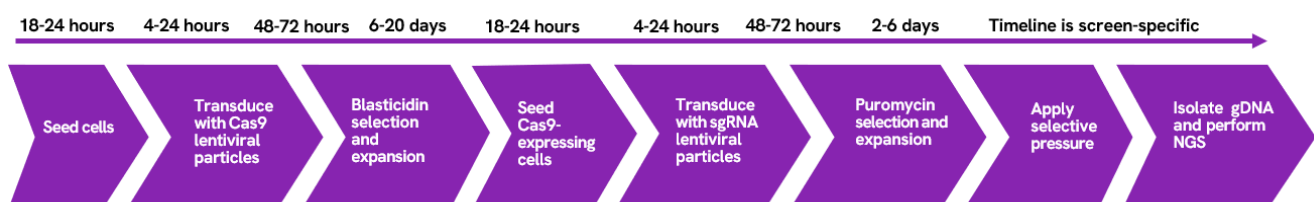


Figure 4. Timeline of primary screen.

## i. Transduction of cells with Edit-R Lentiviral Cas9 Nuclease particles

Prior to performing the screen, a population of stable Cas9-expressing cells is first generated using Edit-R Lentiviral Cas9 particles (with the most active cellular promoter). If a clonal Cas9-expressing cell line is preferred, isolate and characterize clonal cell lines using protocols appropriate for your cells of interest.

### Day 1:

1. Seed cells in Growth Medium. The number of cells seeded should be determined by extrapolating from the number of cells desired at the time of transduction and the doubling time of your cell type. Incubate overnight.

### Day 2:

1. The next day, remove the medium and add optimized Transduction Medium (see **Section 5.B.**) with the appropriate amount of Edit-R Lentiviral Cas9 Nuclease particles so that the cells are just covered.

2. After the appropriate transduction time (see **Section 5.B.**), add additional Growth Medium to your cells such that the cells can be incubated for 48-72 hours.

### Days 4-15:

1. At 48-72 hours post-transduction begin **blasticidin** selection to remove non-transduced cells.

2. Every 48-72 hours, replace with fresh Selection Medium containing **blasticidin** and passage cells as needed.

**Use the appropriate concentration of puromycin and the minimum number of days required to kill non-transduced cells as determined by a puromycin kill curve (see Section 5.D.).**

Once a pure population of transduced cells has been obtained (7-15 days), expand the cell population to have enough cells for your screen with the pooled lentiviral sgRNA library as determined in Section 5.G. Calculation of number of cells needed for transduction.

**We recommend evaluating the generated Cas9-expressing cell line by estimating gene editing events with sgRNA positive control lentiviral particles (see Section 4.B.) before performing the screen.**

## ii. Transduction of cells with Edit-R Lentiviral sgRNA Pooled Library

### Day 1:

1. Seed the Cas9-expressing cells in Growth Medium in the number of plates determined in **Section 5.G.** The number of cells seeded should be determined by extrapolating from the number of cells needed at the time of transduction and the doubling time of your cell type. Incubate overnight.

### Day 2:

1. The next day, remove the medium and add optimized Transduction Medium (see **Section 5.B.**) with the appropriate volume of lentiviral particles (**Section 5.H.**) so that the cells are just covered. If a single lentiviral pool will be added to multiple plates, as determined in Section 5, divide the volume of lentiviral particles evenly among plates.

2. After the appropriate transduction time (see **Section 5.B.**), add additional Growth Medium to your cells such that the cells can be incubated for 48-72 hours.

### Days 4-18:

1. At 48-72 hours post-transduction, begin **puromycin** selection to remove non-transduced cells.

2. Every 48-72 hours, replace with fresh Selection Medium containing **puromycin** and passage cells as needed.

**Use the appropriate concentration of puromycin and the minimum number of days required to kill non-transduced cells as determined by a puromycin kill curve (see Section 5.D.).**

Once a pure population of puromycin-resistant cells has been obtained (2-6 days), begin screening. Split cells into at least two populations: one as a reference and another (experimental) for application of selective pressure and/or sorting of cells exhibiting the phenotype of interest. To maintain your desired sgRNA fold representation at each cell passage, always retain at least the number of cells that corresponds to the desired number of lentiviral integrants.

## B. Genomic DNA isolation

Following selection, gDNA should be isolated from control and experimental cell populations. Isolation of gDNA from cells transduced with lentiviral pooled libraries has been optimized in the protocol below using a **Qiagen Blood and Cell Culture DNA Maxi Kit**; however, kits from other manufacturers may also be suitable.

1. Collect cells by trypsinization for counting and gDNA isolation. To maintain your desired sgRNA fold representation during gDNA isolation, use at least the number of cells that corresponds to the desired number of lentiviral integrants. The most accurate results can be obtained by counting cell number prior to gDNA isolation. Follow the manufacturer's protocol for purification of gDNA from cell cultures.

**It is important that you elute gDNA samples in EDTA-free buffer to prevent inhibition of subsequent PCR reactions.**

2. Quantify the isolated gDNA using a spectrophotometer and assess the DNA purity by measuring the ratio of the absorbance at 260 and 280 nm ( $A_{260/280}$ ) and at 230 nm ( $A_{260/230}$ ). High-quality gDNA samples should have an  $A_{260/280}$  ratio of 1.8 to 2.0, indicating the absence of contaminating proteins, and an  $A_{260/230}$  ratio of  $> 2.0$ , indicating the absence of other organic contaminants.

## C. PCR amplification of constructs from genomic DNA

The PCR amplification step described here has been designed to amplify sgRNA constructs from gDNA without bias, such that differences in sgRNA representation after sequencing are due to enrichment or depletion that occurs during the primary screen. It is important to use adequate template copies per construct in the PCR amplification step such that the desired fold representation at transduction is maintained. This ensures assay reproducibility and facilitates hit identification<sup>6</sup>. Note that the NGS Hit Identification Primers have been designed to add partial TruSeq<sup>®</sup> adapters designed for use with Illumina<sup>®</sup> sequencing platforms. They are not compatible with other high-throughput sequencing systems. *Libraries targeting mouse genes and human libraries ordered prior to 2024 must be amplified with Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kits.*

### i. Number of PCR reactions

Calculate the minimum amount of gDNA required to maintain sgRNA fold representation, assuming a single lentiviral integration event per cell (genome), using the following formula:

Number of cells with  
lentiviral integrations

×

$6.6 \times 10^{-3}$  ng/ genome (see  
note below)

=

Mass of gDNA required to  
maintain representation of  
each sgRNA (ng)

**The calculation above assumes a diploid human genome. For cells that are not diploid, calculations should be adjusted accordingly.**

We have optimized the PCR conditions to remain in the linear phase of log amplification using Phusion Hot Start II DNA Polymerase. We recommend a maximum of 825 ng of gDNA per PCR; using more gDNA per PCR will inhibit the efficiency of the reaction and will result in either failure of the PCR or biased amplification.

Calculate the number of PCRs required for each sample using the following formula:

$$\begin{array}{|c|} \hline \text{Mass of gDNA required to} \\ \text{maintain representation of} \\ \text{each sgRNA (ng)} \\ \hline \end{array} \div \begin{array}{|c|} \hline 825 \text{ ng per reaction} \\ \hline \end{array} = \begin{array}{|c|} \hline \text{Number of PCR reactions required} \\ \text{to maintain representation of} \\ \text{each sgRNA (ng)}^* \\ \hline \end{array}$$

\* Round up the value obtained to the next whole number

The calculations above are used to determine the number of PCR reactions required per sample. To determine the total number of PCR reactions required for your screen use the following formula:

$$\begin{array}{|c|} \hline \text{Number of PCR reactions per} \\ \text{sample} \\ \hline \end{array} \times \begin{array}{|c|} \hline \text{Number of samples} \\ \hline \end{array} = \begin{array}{|c|} \hline \text{Total number of PCR reactions} \\ \hline \end{array}$$

#### Calculation example

If you anticipate  $1.52 \times 10^7$  cells with lentiviral integrations, the mass of gDNA required would be calculated as follows:

$$1.52 \times 10^7 \text{ lentiviral integrations} \times 6.6 \times 10^{-3} \text{ ng/genome} = 1 \times 10^5 \text{ ng}$$

The maximum amount of gDNA per PCR is 825 ng, therefore the number of PCR reactions necessary can be calculated as follows:

$$1 \times 10^5 \text{ ng gDNA} \div 825 \text{ ng/PCR} = 122 \text{ PCR reactions}$$

If you have four samples (reference and experimental samples in biological duplicates), then you need the following total number of PCR reactions:

$$122 \text{ PCR reactions} \times 4 \text{ samples} = 488 \text{ PCR reactions}$$

## ii. PCR from genomic DNA

Once you have determined the number of PCR reactions you need per sample, you can proceed with the PCR amplification of the gDNA samples. Sequence amplification from gDNA has been optimized using Phusion Hot Start II DNA Polymerase. The amplification conditions recommended below have been determined to provide maximum yields of PCR product while staying within the linear phase of log amplification.

1. Perform PCR in 50  $\mu$ L reactions using 96-well PCR plates. PCR conditions have been optimized to amplify 825 ng of gDNA per 50  $\mu$ L reaction. As described above, calculate the number of reactions needed for the amplification of total gDNA necessary to maintain the fold representation used at transduction. Table 5 provides the components and volumes needed for one 50  $\mu$ L PCR amplification reaction. *Libraries targeting mouse genes and human libraries ordered prior to 2024 must be amplified with Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kits.*



**Table 5.** PCR components for amplification of genomic DNA.

Component	Volume per reaction (μL)	Final concentration
5x Phusion HF Buffer	10	1x
10 mM dNTPs	1	200 μM
NGS Hit Identification Primers <b>mCMV*</b> (50 μM)	1	1 μM
gDNA (825 ng) + PCR grade H <sub>2</sub> O	36	16.5 ng/μL
Phusion Hot Start II DNA Polymerase (2 U/μL)	2	0.08 U/μL
<b>TOTAL</b>	<b>50 μL</b>	

\*For libraries targeting mouse genes and human libraries ordered prior to 2024, use the **Edit-R Mouse Pooled sgRNA Forward PCR Primer** and **Edit-R Mouse Pooled sgRNA Reverse Index PCR Primers** included with the **Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kit** in place of NGS Hit Identification Primers with Forward and Reverse primers each at a final concentration of 0.5 μM.

2. To PCR amplify the Edit-R sgRNA constructs, use the cycling conditions outlined in Table 6. The conditions indicated in this protocol ensure that amplification is in the exponential phase when using Phusion Hot Start II DNA Polymerase; if using another polymerase, the optimal cycle conditions should be determined empirically.

**Table 6.** PCR cycle parameters

Temperature	Time	
98 °C	3 minutes	
98 °C	10 seconds	23 Cycles
60 °C	15 seconds	
72 °C	15 seconds	
72 °C	5 minutes	

3. Confirm that amplicons of the appropriate size are obtained from each sample by running 10 μL of PCR product on a 2% agarose gel. The amplicons will be 330-339 bp. *For libraries targeting mouse genes and human libraries ordered prior to 2024, gDNA amplification with Edit-R Mouse Pooled sgRNA Reverse Index PCR Primers will result in a 357 bp amplicon.*

**Due to the low number of PCR cycles, the product will be a faint band on a gel before purification. Note too that the NGS Hit Identification FWD primers are staggered to introduce diversity and will generate ten roughly equimolar amplicons varying by 1 bp in length.**

4. Combine reactions amplifying the same gDNA sample into a single 1.5 mL tube. Purify the combined PCR amplicons for each gDNA sample using a PCR purification kit.

**Please be aware that gDNA often co-purifies with the PCR products. Although, contaminating gDNA does not interfere with the next-generation sequencing, it does affect the quantification of the amount of PCR amplicons by spectrophotometric or fluorometric methods. Therefore, it is recommended to evaluate the concentration of each amplicon using quantitative PCR or chromatographic methods such as analysis on a Revvity LabChip Nucleic Acid Analyzer. Alternatively, the amplicons can be purified and quantified by a fluorometric DNA quantification method, such as QuBit (Thermo Fisher).**

## 7 Library prep and Illumina platform sequencing

Illumina P5 and P7 adapters and TruSeq indexes can be added to the amplified library generated in **Section 6.C.ii** through a second low amplification PCR step prior to sequencing. Please follow the manufacturer's instructions for Illumina platform sequencing.

*Libraries targeting mouse genes and human libraries ordered prior to 2024 must be amplified with Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kits. Following gDNA amplification, please refer to **Appendix A** for information regarding multiplexing and sequencing.*

For accurate hit identification, we recommend obtaining a minimum of 1000 1 × 150 bp reads per sgRNA. If the output of your sequencing platform is higher than the number of reads required per sample, it may be possible to multiplex samples in the same run. To calculate the maximum number of samples that can be loaded per lane, it is advisable to assume a lower number of sequence reads than the maximum obtained on an optimum sequencing run. We suggest estimating the number of reads by adjusting the manufacturer's specifications by a factor of 0.7.

## 8 Hit identification and follow up

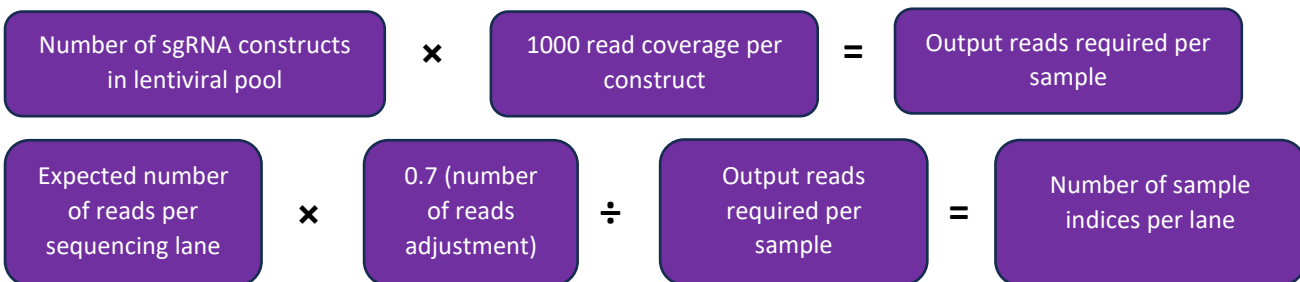
Alignment of sequence files and hit identification can be performed using open-source programs that require some bioinformatics knowledge. We recommend that you consult with a bioinformatician with proficiency in using command line tools for data analysis and hit identification. A detailed protocol utilizing freely available software can be downloaded from the Edit-R Lentiviral sgRNA Pooled Library webpage under the Resources tab. Samples should be de-multiplexed on the sequencer to bin each index tag with the appropriate sample. Sequences should be trimmed so that the first 19 bases of each read correspond to the sgRNA target sequence. The remaining bases in the read include the sgRNA vector backbone and can be ignored in the subsequent analysis. Using an alignment tool, such as Bowtie 2<sup>7</sup>, align the first 19 bases of each read to the reference file provided with your lentiviral pooled library. Bowtie 2 has an option to ignore bases on the 3' end of the read; use this option to align only the first 19 bases of the sgRNA strand. Using the output of the aligner, count the number of alignments for each construct. Next, use a differential expression tool built for discrete count data, such as DESeq2<sup>8</sup>, to determine primary hits. Hits can be confirmed and studied further using individual Edit-R Lentiviral sgRNAs.

## 9 Appendix

### A. Multiplexing and Illumina platform sequencing of gDNA amplified with Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kits (for mouse and pre-2024 libraries)

The workflow described here (Figure 5) has been designed to amplify and sequence sgRNA constructs from gDNA without bias, such that differences in sgRNA representation after sequencing are due to enrichment or depletion that occurs during the primary screen. For accurate hit identification, we recommend obtaining a minimum of 1000 reads per sgRNA. Most high-throughput sequencing platforms provide a sufficiently high number of sequence reads to allow multiplexing of samples in sequencing runs (running multiple samples in one lane). If the output of your sequencing platform is higher than the number of reads required per sample, it may be possible to multiplex samples in the same run. To calculate the maximum number of samples that can be loaded per lane, it is advisable to assume a lower number of sequence reads than the maximum obtained on an optimum sequencing run. We suggest estimating the number of reads by adjusting the manufacturer's specifications by a factor of 0.7.

**From this information the number of samples you can run per lane can be determined using the following calculations:**



### Calculation example

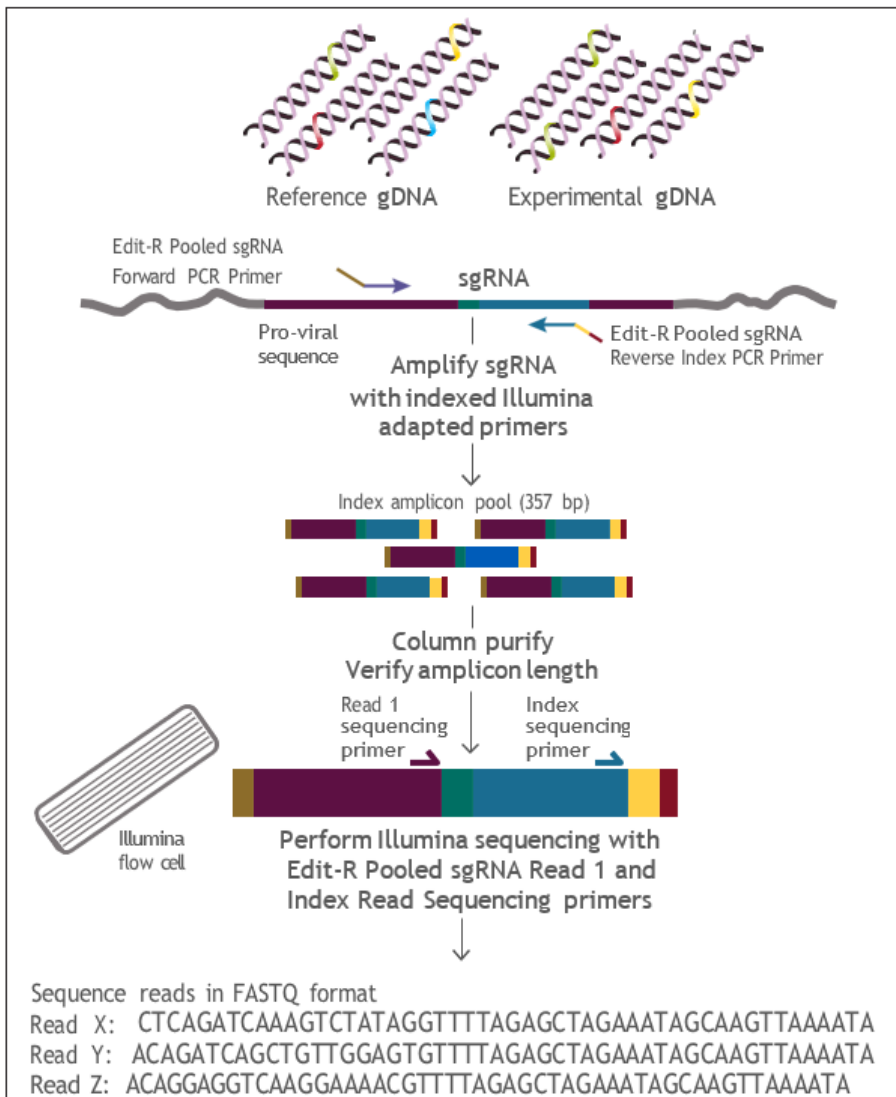
If your pool contains 1000 sgRNAs, then the number of output reads required per sample can be calculated as follows:

$$1000 \text{ sgRNAs} \times 1000 \text{ reads/sgRNA} = 1 \text{ million output reads required per sample}$$

If you are using a sequencing platform with a projected output of 15 million reads per lane then the number of samples per lane can be calculated as:

$$1.5 \times 10^7 \text{ reads per lane} \times 0.7 \text{ (number of reads adjustment)} \div 1 \times 10^6 \text{ output reads required per sample} = 10 \text{ samples per lane}$$

Edit-R Mouse Pooled sgRNA Indexing PCR primers are provided as 50  $\mu$ M forward and reverse indexed primers. The index tags are shown in Table 7.



**Figure 5.** PCR amplification and Illumina high-throughput sequencing workflow with Edit-R Mouse Pooled sgRNA Indexing PCR and Sequencing Primer Kits.

**Table 7.** The index tags on Edit-R Mouse Pooled sgRNA Indexing PCR primers are compatible with Illumina TruSeq LT indices.

<b>Kit A</b>		
<b>Item</b>	<b>Index</b>	<b>Index Sequence</b>
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 2	2	CGATGT
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 4	4	TGACCA
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 5	5	ACAGTG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 6	6	GCCAAT
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 7	7	CAGATC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 12	12	CTTGTA
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 13	13	AGTCAA
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 14	14	AGTTCC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 15	15	ATGTCA
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 16	16	CCGTCC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 18	18	GTCCGC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 19	19	GTGAAA

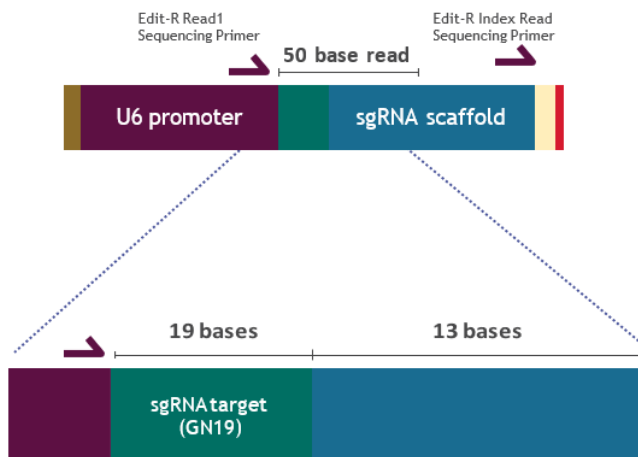
<b>Kit B</b>		
<b>Item</b>	<b>Index</b>	<b>Index Sequence</b>
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 1	1	ATCACG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 3	3	TTAGGC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 8	8	ACTTGA
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 9	9	GATCAG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 10	10	TAGCTT
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 11	11	GGCTAC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 20	20	GTGGCC
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 21	21	GTTTCG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 22	22	CGTACG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 23	23	GAGTGG
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 25	25	ACTGAT
Edit-R Mouse Pooled sgRNA Reverse Index PCR Primer 27	27	ATTCCT

Please follow the manufacturer's instructions for Illumina platform sequencing. Quantify the library using the quality standards that are recommended for your Illumina sequencing platform and then follow Illumina's instructions for dilution and denaturation of the library.

For the Illumina MiSeq Desktop Sequencer, we recommend spiking the library with 10% PhiX Control to serve as an internal control and loading the library onto the flow cell at 7 to 10 pM using standard loading volumes. After loading your sample into the Illumina MiSeq Reagent Cartridge, add 5  $\mu$ L of the 100  $\mu$ M Edit-R Mouse Pooled sgRNA Read 1 Sequencing Primer stock to the "Read 1 Primer mix" reservoir and 5  $\mu$ L of the 100  $\mu$ M Edit-R Mouse Pooled sgRNA Index Read Sequencing Primer stock to the "Index Primer Mix" reservoir on the Illumina MiSeq reagent cartridge (please check the MiSeq System User Guide to confirm the inlet positions).

For the Illumina HiSeq 2500 system, we recommend spiking the library with 10% PhiX Control to serve as an internal control and loading the library onto the flow cell at 6 pM for Rapid Run with onboard clustering or 7.5 pM for High Output Run with c-bot clustering using standard loading volumes. Dilute the Edit-R Mouse Pooled sgRNA Read 1 Sequencing Primer and Edit-R Mouse Pooled sgRNA Index Read Sequencing Primer into the respective Illumina primer reagents to a final concentration of 0.5  $\mu$ M.

At minimum, 19 base single-end reads are required to identify the sgRNA target sequence, as outlined in Figure 6.



**Figure 6.** Position of Edit-R Mouse Pooled sgRNA Read 1 and Index Read Sequencing primers and contents of 50 base sequencing read, including the sgRNA target sequence.

## B. Stability and storage

Edit-R Lentiviral sgRNA Pooled Libraries are shipped on dry ice and must be stored at  $-80^{\circ}\text{C}$ . Under these conditions, lentiviral particles are stable for at least 3 years. Repeated freeze-thaw cycles should be avoided, as this is expected to negatively affect titer. When setting up a pooled lentiviral screening experiment, lentiviral particles should be thawed on ice, divided into smaller aliquots (if necessary) and immediately returned to  $-80^{\circ}\text{C}$ .

## C. Quality assurance and control

Edit-R Pooled Lentiviral sgRNA Screening Libraries are subject to stringent quality control at multiple steps during the manufacturing process, including:

1. Evaluation of sgRNA representation by high-throughput sequencing on Illumina sequencing platform:

Lentiviral pooled libraries are sequenced using  $2 \times 250$  base reads, filtered by PHRED score  $> 30$ , and  $> 1000$ -fold read coverage. Pools have greater than 95% of the constituent constructs recovered. The library has high standards for uniform construct distribution with 70% and 90% of the population within 10-fold and 25-fold of each other, respectively. A data file with gene annotation, sgRNA target sequences information and counts per million mapped reads is provided with each screening library.

2. Lentiviral titering using quantitative PCR (qPCR) after transduction in HEK293T cells for functional titers.
3. Examination of each batch to ensure preparations are free from mold and bacterial contamination.
4. Specified lentiviral titers are included in data file with each shipment.

## 10 Frequently asked questions

### How many lentiviral particles do I need for my screen?

The number of lentiviral particles (reported as transducing units (TU)) required for a screen will depend on:

- 1) The relative transduction efficiency of your specific cell line/cell type
- 2) The fold representation you choose to maintain throughout the screen
- 3) The number of biological replicates you intend to include

Once these parameters have been determined, the [Pooled-sgRNA-screening-protocol-tracking-worksheet](#) can be used to calculate the number of TU needed for your screen.

### **How do I choose between the various Edit-R Lentiviral Cas9 Nuclease promoter options?**

Choose the promoter option that has been demonstrated by your own experimental observations or shown to actively express a transgene in your cells of choice through references in the published literature. For optimal experimental confidence or if such information is not available, consider testing multiple lentiviral promoter-Cas9 constructs.

### **I am using human cell lines in my research; should I always choose a human promoter for optimal Cas9 activity?**

In some instances, promoter activity correlates with the species from which it is derived. However, promoter activity does not always follow a species-specific expression pattern. For example, we have observed mouse promoters to be the most active in some human cell lines, whereas both human and mouse promoters were most active in some rat cells. Choosing the most effective promoter in a particular cell line is not always predictable, and therefore should be determined empirically.

### **Do the Edit-R Lentiviral sgRNA pooled libraries target lncRNAs or regulatory regions?**

No. The libraries only contain sgRNAs targeting protein-coding genes.

### **Are Dharmacon™ lentiviral particle products safe to use in the laboratory? What precautions should be taken when handling lentiviral particles?**

Lentiviral delivery systems have been employed in many research laboratories worldwide without incident. Handling of lentiviral products requires extensive experience with cell culture techniques. It is vital that the protocols provided by Revvity and the safety guidelines described for appropriate handling and storage are fully understood and followed precisely (see Section 12, Lentiviral particle product safety level information).

### **Can Dharmacon™ lentiviral particles be further propagated in the lab?**

No. Edit-R lentiviral products are engineered for biosafety and are provided as replication-incompetent lentiviral particles.

### **Can I order the Edit-R Lentiviral sgRNA Pooled libraries as plasmid DNA or glycerol stocks?**

No. Our Edit-R Lentiviral sgRNA Pooled Libraries are sold exclusively as lentiviral particles.

### **How should lentiviral particle products be stored?**

All lentiviral particle products must be stored at -80 °C. If necessary, the particles can be aliquoted upon the first thaw to convenient volumes and the aliquots stored at -80 °C to minimize the number of future freeze-thaws. However, we recommend avoiding multiple freeze-thaw cycles as much as possible.

### **Can lentiviral particle products be kept at 4 °C?**

No. Once thawed, lentiviral particle preparations begin to decrease in titer. We advise against storing any lentiviral particles at 4 °C. All lentiviral particle products must be kept frozen and stored at -80 °C until transductions are performed.

### **How are lentiviral particle products shipped?**

Lentiviral particle products are shipped on dry ice for overnight domestic delivery or priority international for delivery outside of the U.S.

### **Where can I find titer information for my pooled library?**

The titer of your lentiviral pools will be indicated in the data file sent with your library shipment and can also be requested from [Scientific Support](#).

### **Where can I find the targeting sequences for sgRNAs included in my pooled library?**

The sgRNA target sequences are in the data files sent with your library shipment. Please contact Scientific Support with your Sales Order number (SO-XXXXXXG) if you did not receive the data files in your shipment.

### **How is gDNA input calculated to maintain desired construct fold representation?**

The quantity of gDNA required for maintaining a desired fold representation can be calculated using the formulas and values (Table 8) below.

**Table 8.** Constants needed for calculating gDNA input.

Constants	Value
Mass of a base pair	660 g/mol/bp
Base pairs per diploid human genome	$6 \times 10^9$ bp
Avogadro constant	$6.02 \times 10^{23}$ mol <sup>-1</sup>

**Example:**

Calculate the mass of human genome:

$$(6 \times 10^9 \text{ bp/genome}) \times (660 \text{ g/mol/bp}) = 4 \times 10^{12} \text{ g/mol/genome}$$

$$(4 \times 10^{12} \text{ g/mol/genome}) \div (6.02 \times 10^{23} \text{ mol}^{-1}) = 6.6 \times 10^{-12} \text{ g/genome}$$

**The calculation above assumes a diploid human genome. For cells that are not diploid, calculations should be adjusted accordingly.**

### How can I index and sequence the gDNA from my screen?

gDNA can be amplified, indexed, and prepared for NGS sequencing with a two-step PCR protocol. We provide vector-specific NGS hit identification primers for the first round of amplification of your gDNA. The forward and reverse primers contain the following Illumina® compatible TruSeq® partial adapters:

Forward primer extension: 5' ACACTCTTCCCTACACGACGCTCTTCCGATCT 3'

Reverse primer extension: 5' GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT 3'

Illumina P5 and P7 adapters and TruSeq indexes can then be added to the amplified library through a second low amplification PCR step prior to sequencing. Note that the forward primers contain a stagger site between the 5' Illumina extension and the priming site to introduce nucleotide diversity during sequencing, which will need to be adjusted for when the sequences are trimmed. For more information, please see our Bioinformatic Analysis of Dharmacon™ Lentiviral sgRNA Pooled Library Screens Protocol.

## 11 References

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## 12 Lentiviral particle product safety level information

This Lentiviral Particle Product Safety Level Information constitutes Product Documentation according to clause 1 of the Product Terms and Conditions. It is applicable to all Dharmacon lentiviral particle products.

Any investigator who purchases Dharmacon lentiviral particle products is responsible for consulting with their institution's health and biosafety personnel for specific guidelines on the handling of lentiviral vector particles. Furthermore, each investigator is fully responsible for obtaining the required permissions for research use and the acceptance of replication-incompetent SIN lentiviral vectors and replication-defective lentiviral particles into their local jurisdiction and institution.

The Products are solely for internal research use (as set forth in the Product Terms and Conditions) in laboratories where the containment measures stated below and in applicable laws and regulations are met. Products may not be used for diagnostic, therapeutic or other commercial purposes and may not be administered to humans for any purpose or to animals for therapeutic purposes. The Products are replication-incompetent, self-inactivating (SIN) and non-pathogenic (do not cause infectious human disease).



For questions concerning the design or production of the products, please contact our Scientific Support team.

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### In the US:

For US guidance on containment for lentiviral vectors, please refer to:

1. The Recombinant DNA Advisory Committee (RAC) guidelines for research with lentiviral vectors ([https://osp.od.nih.gov/wp-content/uploads/Lenti\\_Containment\\_Guidance.pdf](https://osp.od.nih.gov/wp-content/uploads/Lenti_Containment_Guidance.pdf));
2. The U.S. Department of Health and Human Services Centers for Disease Control and Prevention and National Institutes of Health, Biosafety in Microbiological and Biomedical Laboratories (BMBL);
3. The NIH Guidelines For Research Involving Recombinant DNA Molecules (NIH Guidelines) ([https://osp.od.nih.gov/wp-content/uploads/NIH\\_Guidelines.pdf](https://osp.od.nih.gov/wp-content/uploads/NIH_Guidelines.pdf))

### In the EU:

For the EU directives, please consult the following:

1. Council Directive 2009/41/EC of the European Parliament and of the Council of 6 May 2009 on the contained use of genetically modified micro-organisms. (revised version of Directive 90/219/EEC of the European Parliament and of the Council of 23 April 1990 on the contained use of genetically modified micro-organisms, amended by Council Directive 98/81/EC of 26 October 1998); and
2. Council Directive 2001/18/EC of the European Parliament and of the Council of 12 March on the deliberate release into the environment of genetically modified organisms and repealing Council Directive 90/220/EEC.

### In Germany:

Required Containment Measures: The containment requirements as stated in the German Genetic Safety Ordinance (Gentechnik-Sicherheitsverordnung) of Safety Level 2\* or higher have been assigned to the handling of the above- mentioned lentiviral vector particles. Please note a higher Security Level might be required if the lentiviral vector particles are used for genetic engineering operations with other products which require a higher Security Level.

\*Safety Level 2: activities of low risk for human health and the environment by the state of scientific knowledge (Stand der Wissenschaft).

For the German regulations, please consult the following:

1. German Genetic Engineering Act (Gentechnikgesetz - GenTG); and
2. Genetic Engineering Safety Ordinance (Gentechnik-Sicherheitsverordnung - GenTSV).

## 13 Limited use licenses

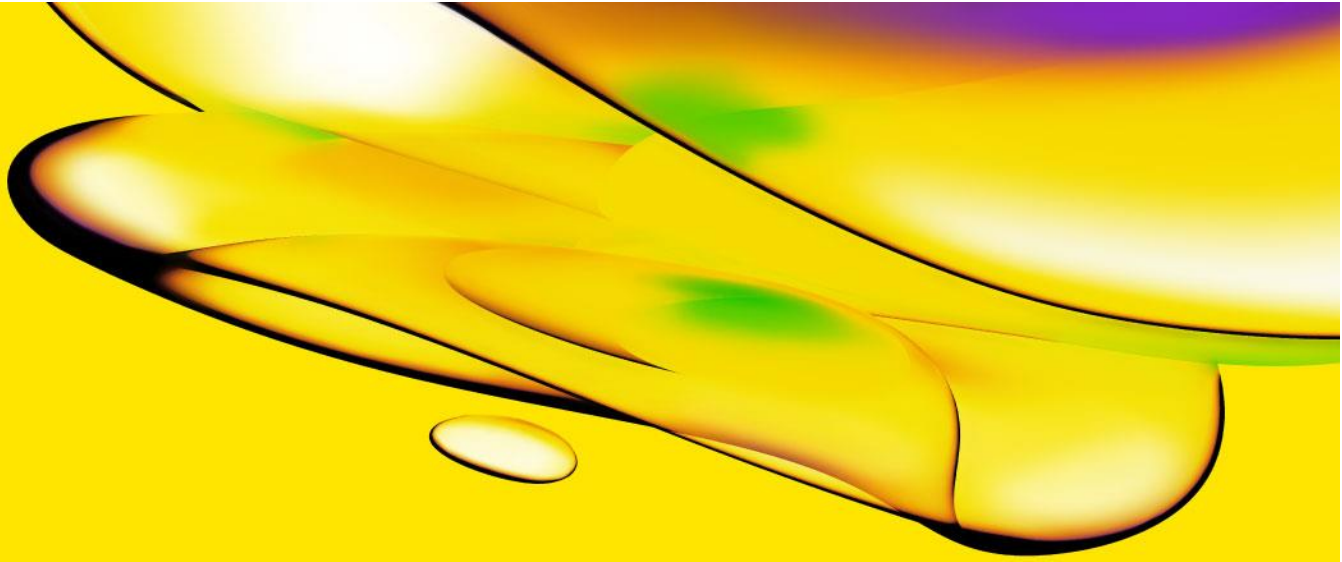
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