

Perspective

The sound of silence: Transgene silencing in mammalian cell engineering

Alan Cabrera,^{1,28} Hailey I. Edelstein,^{2,3,29} Fokion Glykofrydis,^{4,29} Kasey S. Love,^{5,29} Sebastian Palacios,^{5,29} Josh Tycko,^{6,29} Meng Zhang,^{7,29} Sarah Lensch,⁸ Cara E. Shields,⁹ Mark Livingston,¹⁰ Ron Weiss,^{5,11,12} Huimin Zhao,⁷ Karmella A. Haynes,⁹ Leonardo Morsut,⁴ Yvonne Y. Chen,^{13,14,15} Ahmad S. Khalil,^{16,17} Wilson W. Wong,¹⁶ James J. Collins,^{4,12,17,18,19,20} Susan J. Rosser,²¹ Karen Polizzi,^{22,23} Michael B. Elowitz,^{24,25} Martin Fussenegger,^{26,27} Isaac B. Hilton,¹ Joshua N. Leonard,^{2,3} Lacramioara Bintu,⁸ Kate E. Galloway,²⁸ and Tara L. Deans^{10,*}

¹Department of Bioengineering, Rice University, Houston, TX 77005, USA

²Center for Synthetic Biology, Northwestern University, Evanston, IL 60208, USA

³The Eli and Edythe Broad CIRM Center, Department of Chemical and Biological Engineering, Northwestern University, Evanston, IL 60208, USA

⁴Department of Stem Cell Biology and Regenerative Medicine, University of Southern California, Los Angeles, CA 90033-9080, USA

⁵Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

⁶Department of Genetics, Stanford University, Stanford, CA 94305, USA

⁷Department of Chemical and Biomolecular Engineering, University of Illinois at Urbana-Champaign, Champaign, Urbana, IL 61801, USA

⁸Department of Bioengineering, Stanford University, Stanford, CA 94305, USA

⁹Wallace H. Coulter Department of Biomedical Engineering, Emory University, Atlanta, GA 30322, USA

¹⁰Department of Biomedical Engineering, University of Utah, Salt Lake City, UT 84112, USA

¹¹Department of Electrical Engineering and Computer Science, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

¹²Synthetic Biology Center, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

¹³Department of Microbiology, Immunology, and Molecular Genetics, University of California, Los Angeles, Los Angeles, CA 90095, USA

¹⁴Department of Chemical and Biomolecular Engineering, University of California, Los Angeles, Los Angeles, CA 90095, USA

¹⁵Parker Institute for Cancer Immunotherapy Center at UCLA, Los Angeles, CA 90095, USA

¹⁶Biological Design Center and Department of Biomedical Engineering, Boston University, Boston, MA 02215, USA

¹⁷Wyss Institute for Biologically Inspired Engineering, Harvard University, Boston, MA, USA

¹⁸Institute for Medical Engineering and Science, Massachusetts Institute of Technology, Cambridge, MA, USA

¹⁹Harvard-MIT Program in Health Sciences and Technology, Cambridge, MA 02139, USA

²⁰Broad Institute of MIT and Harvard, Cambridge, MA 02139, USA

²¹School of Biological Sciences, University of Edinburgh, Edinburgh, UK

²²Department of Chemical Engineering, Imperial College London, South Kensington Campus, London, UK

²³Imperial College Centre for Synthetic Biology, South Kensington Campus, London, UK

²⁴Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, CA 91125, USA

²⁵Howard Hughes Medical Institute, California Institute of Technology, Pasadena, CA 91125, USA

²⁶Department of Biosystems Science and Engineering, ETH Zurich, Mattenstrasse 26, Basel 4058, Switzerland

²⁷Faculty of Science, University of Basel, Mattenstrasse 26, Basel 4058, Switzerland

²⁸Department of Chemical Engineering, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

²⁹These authors contributed equally

*Correspondence: tara.deans@utah.edu

<https://doi.org/10.1016/j.cels.2022.11.005>

SUMMARY

To elucidate principles operating in native biological systems and to develop novel biotechnologies, synthetic biology aims to build and integrate synthetic gene circuits within native transcriptional networks. The utility of synthetic gene circuits for cell engineering relies on the ability to control the expression of all constituent transgene components. Transgene silencing, defined as the loss of expression over time, persists as an obstacle for engineering primary cells and stem cells with transgenic cargos. In this review, we highlight the challenge that transgene silencing poses to the robust engineering of mammalian cells, outline potential molecular mechanisms of silencing, and present approaches for preventing transgene silencing. We conclude with a perspective identifying future research directions for improving the performance of synthetic gene circuits.

INTRODUCTION

Genome engineering within mammalian cells enables the stable expression of transgenes (Box 1) to support the design and implementation of custom genetic programs across a wide range of biotechnology applications.^{1–9} Engineered cells

must retain control over the expression of transgenes over many cell generations. However, stably integrated transgenes often experience silencing, or diminished expression over time, thus limiting the use of engineered cells for applications that require weeks or more of expression.¹⁰ In the context of synthetic gene circuits, silencing interferes with circuit



Box 1. Glossary

Transgene: a gene that is delivered and expressed in a cell to produce a desired phenotype. A transgene can refer to a native gene that is introduced artificially (for example, for high expression), a gene from another organism, or an entirely synthetic gene. A transgene is often implemented as a transcriptional unit with other components that regulate its expression such as a promoter, a Kozak consensus sequence, and poly-adenylation signal.

Transgene silencing: loss or downregulation of expression of a transgene in a cell despite its encoding DNA remaining present in the cell's nucleus.

Hysteresis: a property or phenomenon in a system, where the state of the system depends on its history or prior events.

Cassette: a single unit consisting of a transgene that has yet to be integrated into a genome.

Synthetic gene circuit or genetic program: an assembly of cassettes that encode RNA or protein molecules that interact with each other to perform one or more biological functions.

Transcriptional unit: the DNA sequence necessary to produce a single, unified RNA transcript. The transcriptional unit supports expression of one gene or unit of genes. A transcriptional unit often includes a promoter sequence, coding sequence and poly-adenylation sequence. Transcriptional units may include additional elements within the coding sequence such as a splice site or other regulatory elements within the untranslated regions (UTRs).

Safe-harbor site or safe-harbor locus: a locus in the genome with an open chromatin state that is amenable for stable transgene expression without adversely affecting normal cellular functions (e.g., the activation of nearby oncogenes).

Insulator: DNA elements that serve as barriers to transcriptional and epigenetic regulation of surrounding genes. Specifically, DNA insulators can exhibit barrier activity to block the spreading of heterochromatin or repressive epigenetic modifications. Alternatively, DNA insulators may function as enhancer blockers to prevent the acting of enhancers on the promoters of neighboring genes. Certain DNA insulators such as the prototypic cHS4 exhibit both functions.

Enhancer: DNA elements that interact with target promoters to amplify initiation of transcription.

Epigenetic effector: a protein that can modulate the addition or removal of epigenetic modifications on histones or DNA.

Poly-adenylation signal (pA): DNA sequence that signals the transcription complex to poly-adenylate the RNA being transcribed. This stabilizes RNA molecules by preventing their degradation to enable their export from the nucleus to the cytoplasm to be translated into protein by ribosomes.

Long terminal repeat (LTR): one of a pair of DNA sequences that form a retrotransposon, retrovirus or provirus. LTRs flank retroviral genomes and are common in lentiviral vectors and lentiviral integrations.

CpG islands (CGIs): large DNA segments with high content of CpGs, particularly as compared to other regions of DNA.

H3K9me3: a heterochromatin associated mark that is associated with the downregulation of nearby genes.

Viral vectors: engineered or modified viruses that serve as a vehicle for efficient delivery of nucleic acids to cells. Examples include lentiviral vectors and adeno-associated virus (AAV) vectors.

Topologically associating domains (TADs): TADs are self-interacting chromosomal domains identified by chromosome conformation capture technologies. DNA sequences located within the same TAD interact more frequently with each other than with DNA sequences outside the TAD. TADs are proposed as the fundamental regulatory units of the genome three-dimensional architecture.

Serine integrases: single protein systems, derived from mobile genetic elements, that can integrate a large DNA sequence into the genome by mediating recombination between attachment sites (DNA motifs of ~30 bp) on the genome and donor. Examples include the BxB1, PhiC31, and Pa01 large serine recombinases.

Transposon systems: systems for transgene integration in the genome that utilize transposition as a mechanism for genomic integration. Examples include the piggyBac system and the Sleeping Beauty system.

EF1 α and EFS promoters: EF1 α is the promoter sequence derived from the human *EEF1A1* gene that expresses the alpha subunit of eukaryotic elongation factor 1. EF1 α is known as one of the strong promoters in various mammalian cell lines. The EFS promoter is the short, intron-less form of the EF1 α promoter.

cHS4 and cHS4 core insulators: the cHS4 (chicken hypersensitive site 4) insulator is the prototypical chromatin insulator derived from the chicken β -like globin gene cluster. It possesses both the enhancer-blocking and barrier activities and has been adopted for transgene insulation in various mammalian cell lines. The cHS4 core usually refers to the 5' 250 bp of the full-length cHS4 insulator.

CUT&RUN: cleavage under targets and release using nuclease.

TALE: transcription activator-like effector.

ATAC-seq: assay for transposase-accessible chromatin with high-throughput sequencing.

regulation, limiting the translation of engineered gene circuits for therapeutic and other applications. In this perspective, we highlight the challenge that transgene silencing poses to the robust engineering of mammalian cells, along with opportunities to mitigate this phenomenon.

Transgene silencing appears conserved across diverse organisms.^{11–13} Host cell identity, sequence of the integrated transgene(s), its location of integration, and gene delivery methods all putatively contribute to the rate and degree of transgene silencing. Silencing can manifest as an all-or-nothing

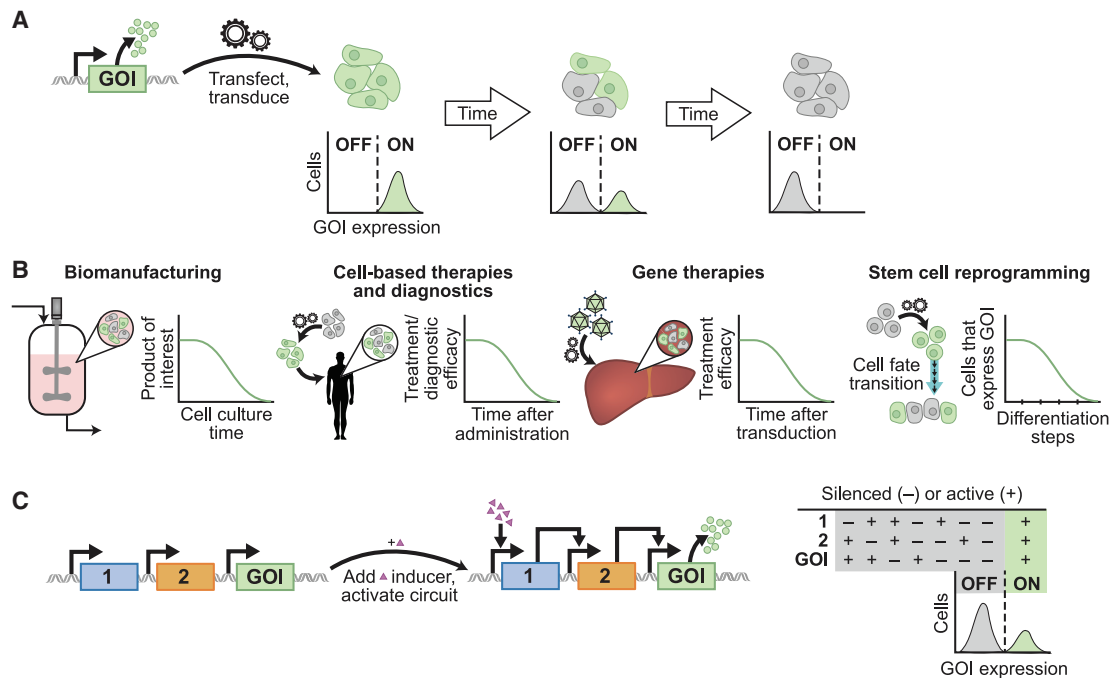


Figure 1. Definition and impact of transgene silencing in mammalian cells

(A) Mammalian cells engineered to express a transgene often undergo silencing. A variety of host cell mechanisms contribute to transgene silencing which correlates with changes in chromatin structure at the site of the integrated transgene. Over time, transgene silencing generates a proportion of the engineered cell population that does not express the gene of interest (GOI). Transgene silencing is often observed as a bimodal distribution of cells that express the transgene (are in the ON state) or do not express the transgene (are in the OFF state) as shown.^{14,15} Transgene silencing may also be observed as a decrease in the relative levels of transgene expression rather than a complete loss of expression.

(B) Diverse applications in biotechnology rely on stable expression of transgenes in engineered mammalian cells. In biomanufacturing, silencing of mammalian cells engineered to produce a product of interest results in a decrease in product produced over time.^{21,22} Similarly, silencing of theranostic circuits in mammalian cells engineered *ex vivo* or engineered *in vivo* via gene therapies leads to waning efficacy over time.²³ In cellular reprogramming and differentiation, cells engineered to express a gene or circuit of interest often undergo silencing as they change cell fates. In particular, differentiation of induced pluripotent stem cells into mature cell types often generates the desired cell type with a low proportion of cells that retain expression of the GOI.²⁴

(C) Gene circuits often require robust expression of multiple transgenes. Silencing of any individual transgene may limit the performance of stably integrated genetic circuits.²⁵ In the example shown, a cascade of inducible transgenes regulates expression of the GOI. Silencing of any of the transgenes will result in failure to express the GOI.

phenomenon in which a portion of cells do not express the transgene. Often the proportion of engineered cells that express the transgene decreases over time in culture^{14–17} (Figure 1A). In some cases, transgene silencing can be observed as a decrease in transgene expression levels in individual cells,^{18,19} and it often appears as a heritable change passed down through cell generations.^{14,15,20}

Transgene silencing represents a bottleneck for many mammalian-cell-based biotechnology applications (Figure 1B). For instance, in industrial cell lines such as Chinese hamster ovary (CHO) cells, or human embryonic kidney (HEK) 293 cells, the silencing of integrated transgenes reduces the long-term production yield for biopharmaceutical manufacturing.^{21,22} Similarly, silencing of sense-and-respond theranostic circuits lead to waning efficacy over time.^{23,25,26} Additionally, more complex synthetic gene circuits with multiple transgenes may be more susceptible to performance failure as silencing of any individual transgene renders the whole circuit nonfunctional (Figure 1C). Furthermore, silencing can spread to neighboring genes through direct and indirect effects, resulting in silencing compounding over time.^{25,27} Moreover, loss of expression of transgenes delivered via retroviruses has been well-documented

in reprogramming, which may inhibit cell-fate transitions and lead to partially reprogrammed cells.^{28–31} Thus, transgene silencing is a critical challenge to understand and overcome for effective cell-based technologies.

In this perspective, we provide an overview of known mechanisms for transgene silencing, provide practical guidelines on how to avoid transgene silencing, and offer a look into future efforts that can further expand our understanding and improve our ability to control transgene expression in synthetic gene circuits. In addition, we suggest that future publications include discussions of observed cases of transgene silencing to help move toward more predictable and reliable cell reprogramming (Box 2).

Mechanisms of transgene silencing

Cells rely on transcriptional regulation to tune gene expression, respond to environmental stressors, and generate phenotypic diversity in complex multicellular organisms. Epigenetic regulation complements dynamic transcriptional control. Through the deposition, recognition, and erasure of covalent modifications to DNA and histones, epigenetic regulation confers stable memory and hysteresis within biological systems. Epigenetic

Box 2. Publishing transgene silencing—making the invisible discoverable

A large swath of valuable information generated by routine cell engineering goes unreported due to the lack of a system to share findings that are typically not incentivized for publication. Customarily, only the best-performing transgenic lines or clones take center stage in the final manuscript. We encourage scientists to include in figures, supplemental data, or materials and methods the frequencies of transgene silencing (e.g., rates of expressing and non-expressing clones). For example, a succinct description of “transgene performance” accompanied by tabulation of sub-optimal and misbehaving clones will not only provide discoverable data for meta-analyses but also give authors an opportunity to highlight the magnitude of effort behind their work. For this reporting, we recommend inclusion of cell type, special culturing conditions (if applicable), promoter type, transfection/transduction vector, number of passages since delivery when the transgene exhibited undesirable behavior, a description of the misregulation, and whether attempts were made to alleviate the silencing with their outcomes. Collectively, this reporting will help move the field forward to predictably and successfully engineer cells.

regulation harmonizes with transcriptional control including the assembly of the preinitiation complex, double-stranded DNA melting at the promoter, initiation, or elongation.³² In all, these can be affected by DNA modifications and influence the structure of the local chromatin and the protein-DNA complexes surrounding the gene of interest (GOI). Synthetic gene circuits must contend with native epigenetic and transcriptional regulatory mechanisms, which may support or impede transgene expression. As silencing often correlates with specific chromatin modification profiles of transgenes, epigenetic regulation putatively supports and reinforces transgene silencing. Therefore, an understanding of the epigenetic mechanisms that silence transgenic cargos in mammalian cells may facilitate the design of more robust genetic circuits and engineered transcriptional programs.³³

Cells engineered with multi-component circuits rely on the tight regulation of multiple transcriptional units to control cellular behavior. For example, cell-based therapies might employ circuits composed of multiple transgenic cassettes encoding biosensing and signal processing functions. Hence, one malfunctioning unit, or cassette, could result in the breakdown of the entire circuit (Figure 1C). In one study, a genetic circuit consisting of four transcription cassettes in HEK293T cells was silenced at an estimated rate of ~2% of the population per week,²⁵ whereas a more rapid shutdown of an 8-kb circuit was observed after approximately 3 weeks of culture in mouse embryonic stem cells (mESCs).²⁶ Notably, in both examples the DNA circuits were integrated at genomic safe-harbor sites. While safe-harbor sites provide genomic regions that support transgene integration without adversely affecting normal cellular functions, cassettes integrated at these sites are still subject to silencing. These results highlight the need for a better understanding of how genomic context and composition of the synthetic gene circuit can influence transgene silencing.

How do cells identify transgenes for silencing?

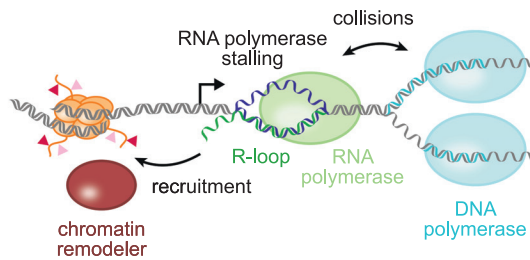
Over time, cells selectively silence integrated transgenes while maintaining endogenous genes at homeostatic levels.^{34,35} Given that silencing appears to selectively impact transgenic elements, how do cells distinguish transgenes from other genomic elements to generate specific profiles of silencing? As recruitment of chromatin-modifying enzymes likely serves an essential step in epigenetic silencing, cells may recruit these enzymes through mechanisms that are dependent and independent of the transgene sequence. In sequence-dependent

mechanisms, interactions at the exact site of transgene integration may prime transgenes for selective silencing. This may include protein recognition of specific DNA motifs, such as CpG islands (CGIs), and the subsequent formation of complexes with chromatin-modifying activity.³⁶ Additionally, sequence-dependent formation of DNA, RNA, or hybrid structures may recruit chromatin-modifying enzymes. For instance, GC-rich sequences can induce G-quadruplexes, R-loops, and other DNA structures that may contribute to RNA polymerase (RNAP) stalling and recruitment of chromatin modifiers through factors that directly recognize these structures.^{37,38} Furthermore, terminal repeat sequences that enable transposon-based insertion of transgenes into the genome can trigger RNAi-mediated silencing.³⁹ As the particular mechanism may vary based on the sequence of the transgene, we expect that interventions may show different efficacy across transgenic cargos.

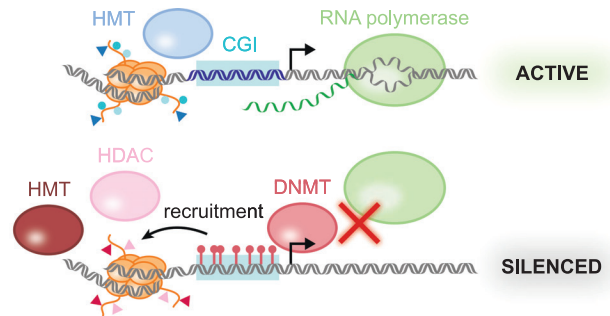
Alternatively, sequence-independent silencing may result from passive loss of transcriptional activity, which may be influenced by local genomic context effects. For instance, activity of chromatin modifiers near the locus of transgene integration may contribute to nonspecific silencing through spreading of heterochromatin. Additionally, chromatin-modifying enzymes may broadly survey the genome, actively silencing genes through reversible, transient modification.⁴⁰ Nascent chromatin remains inaccessible and transcriptionally inactive following DNA replication, and transcriptional reactivation is required to regain accessibility.⁴¹ Potentially, gene activity is reestablished for endogenous genes through selective transcriptional reactivation by combinations of endogenous transcription factors after DNA replication. Lacking such mechanisms, transgenes may remain nonspecifically silenced.

In principle, sequence-dependent and -independent mechanisms may combine to induce transgene silencing. Whether recruited in a sequence-dependent manner or not, chromatin-modifying enzymes may prevent expression of synthetic circuits through heterochromatin formation, DNA methylation, and post-translational modifications (PTMs) to histones. Processes that lead to silencing may be induced at the site of transgene integration via direct recruitment of chromatin regulators, encroachment of heterochromatin, activation of viral and transposon defense systems, or proliferation-mediated processes. Below, we discuss these mechanisms and their relation to transgene silencing.

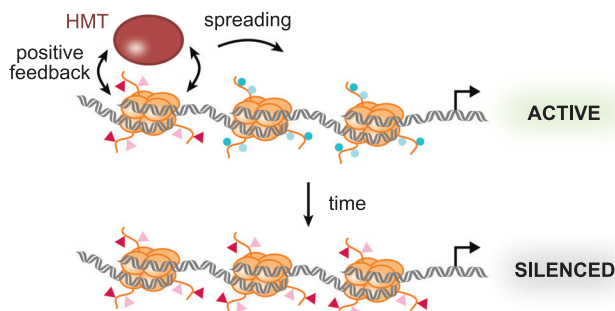
A Proliferation-Associated Silencing



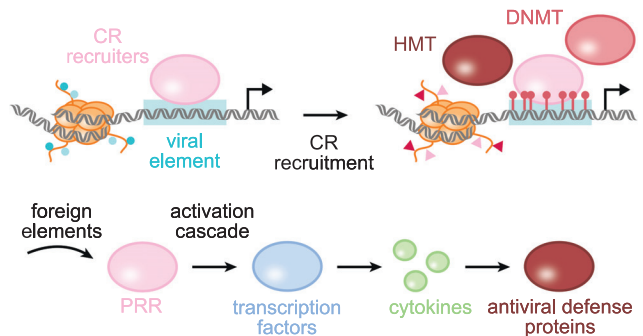
B DNA Methylation & Histone Modifications



C Encroachment of Nearby Heterochromatin



D Viral & Transposon Defense



LEGEND	
▲ H3K4me3	⬮ meCpG
● H3K9ac	▲ H3K9me3
● H3K27ac	▲ H3K27me3
	GC-rich sequences

CGI	CpG island	HDAC	histone deacetylase
CR	chromatin remodeler	HMT	histone methyltransferase
DNMT	DNA methyltransferase	PRR	pattern recognition receptor

Figure 2. Mechanisms of transgene silencing

(A) Proliferation may contribute to gene silencing via antagonism between transcription and replication machinery. Increased strain on the DNA and collisions between RNA polymerases and DNA polymerases can promote the formation of structures such as R-loops, which can alter binding of chromatin remodelers and thus reshape epigenetic states at the sites of transgene integration.

(B) DNA methylation and histone modifications are associated with gene silencing. Top: hypomethylated CGIs can recruit histone methyltransferases (HMTs) and accrue H3K4me3, associated with active transcription by RNA polymerases. High GC content at promoter CGIs is correlated with resistance to silencing. Bottom: hypermethylation of CpGs (meCpG) by DNA methyltransferases (DNMTs) can recruit histone deacetylases (HDACs) and subsequently HMTs, replacing active H3K9ac and H3K27ac marks with repressive H3K9me3 and H3K27me3 marks. Competition between transcriptional machinery and DNMTs may reinforce the association of DNA methylation and gene expression states (i.e., hypomethylation/active, hypermethylation/silenced).

(C) Heterochromatin spreading to neighboring regions may silence transgenes. H3K9me3 and meCpG can spread to neighboring genes via positive feedback supported by HMT recruitment to methylated sites, establishing a repressive chromatin state at nearby integrated synthetic circuits.

(D) Endogenous pathways that recognize viral and transposon elements may suppress transgene expression. Top: Proteins that recognize viral DNA sequences, such as LTRs, recruit chromatin remodelers (CRs), including HDACs, HMTs, and DNMTs. Bottom: Recognition of foreign elements, such as unmethylated CpGs, by pattern recognition receptors (PRRs) activates transcription factors involved in innate immunity (e.g., NF- κ B). These factors promote cytokine production and lead to upregulation of antiviral defense proteins, which may result in transgene silencing.

Proliferation-associated processes promote silencing

Transgene silencing increases over time in proliferating cells and correlates with the number of cell divisions. Both the fraction of cells that express the transgene and the mean expression level of marker-positive cells can decrease over time and with cell division.^{25,28,42} Putatively, processes linked to the cell cycle provide a mechanism that enhances transgene silencing.

Transgene silencing may be accelerated by the inherent antagonism between transcription and the DNA replication necessary for proliferation, each increasing torsional strain and steric interference on the DNA polymer.^{43,44} These processes can lead to the accumulation of positive and negative supercoiling (over- or under-wound DNA, respectively), which can in turn

promote the formation of structures such as R-loops, interactions between DNA and nascent RNA.^{45,46} R-loops have been shown to alter the binding of chromatin remodelers (CRs),³⁷ suggesting a potential mechanism by which persistent changes in gene expression could arise (Figure 2A). Indeed, overexpression of transcription factors in reprogramming induces markers of genomic stress including increased negative DNA supercoiling, R-loop formation, and DNA replication fork stalling.²⁸ Thus, collisions between the transcription and replication machinery in proliferating cells may contribute to transgene silencing.

Proliferation and silencing are intimately linked in the process of stem cell reprogramming and differentiation. For example, proliferation promotes cellular reprogramming to induced

pluripotent cells and induced neurons.^{28,47} The loss of transgene expression delivered via retroviruses is well documented in reprogramming, and this loss of expression may inhibit cell-fate transitions and lead to partially reprogrammed cells.^{28–31} On the other hand, proliferation can also drive transgene silencing while simultaneously increasing the probability that a cell will reprogram.^{28,47} A trade-off between transgene expression and proliferation emerges, leaving a narrow window of time for reprogramming. Notably, in a recent study, cells that sustain high transgene expression while undergoing rapid proliferation reprogrammed to neurons at high rates and display increased functional maturity.²⁸ While the loss of transgene expression may induce heterogeneity and reduce efficiency, the loss of reprogramming factors may improve differentiation of pluripotent stem cells to new cell fates.³¹ Silencing of transgenes has been observed after they have been placed in various safe-harbor loci during human pluripotent stem cell (hPSC) and mESC differentiation into various lineages.^{24,48–50} In some cases, transgene expression could be maintained by the introduction of a flanking chromatin insulator derived from the chicken β -globulin hypersensitivity site 4 (cHS4).²⁴ In fibroblast conversion to induced pluripotent stem cells, Velychko et al. found that retroviral silencing varied based on the reprogramming factors used and that silencing could occur early in the reprogramming process, even before the loss of fibroblast identity.²⁹ In particular, inclusion of cMyc, which drives proliferation, increased transgene silencing. In reprogramming to neurons, loss of expression of retroviral transgenes occurs at higher rates in hyperproliferative cells.²⁸ In addition to these proliferation-associated phenomena, silencing also occurs in post-mitotic or slowly dividing cells.^{23,51} Overall, silencing is often enhanced by proliferation but does not require proliferation.

DNA methylation contributes to stable silencing

Cytosine methylation at CpG motifs contributes to epigenetic silencing (Figure 2B). The distribution of CpG dinucleotides delineates DNA with different states of methylation and plays a key role in epigenetic regulation.⁵² When interspersed across genomic tracks including introns and exons, CpGs are canonically methylated and may contribute to transgene silencing. On the other hand, when CpGs cluster at promoters and enhancers to form CGIs, they are often hypomethylated.⁵³

Methyltransferases establish and maintain CGI methylation. During embryogenesis, DNA methyltransferase 3 Alpha, Beta, and like (DNMT3A, DNMT3B, and DNMT3L) establish CpG methylation that is maintained during DNA replication by DNA methyltransferase 1 (DNMT1).^{54–57} Understanding CGI methylation and transcriptional repression may guide strategies to mitigate CpG-mediated transgene silencing.^{58–61} In addition to a direct contribution to epigenetic silencing, DNA methylation can be involved in the recruitment of H3K9me3 to nucleosomes, which contributes to the formation of heterochromatin.⁶² Heterochromatin is associated with limited DNA accessibility, nuclear reorganization, and silenced transcription, as discussed further below.^{63,64}

CGIs associate with ubiquitously expressed genes, but not with tissue-specific genes.⁶⁵ The presence of CpGs on promoters significantly impacts the silencing of downstream genes.^{55,57,66–71} Furthermore, CGI hypomethylation and active transcription may reinforce one another through competition between transcription

and methylase complexes, causing active promoters to remain hypomethylated and inactive genes to accrue methylation.^{65,72}

Native and synthetic CGIs may confer specific patterns of DNA methylation. Endogenous promoters ectopically inserted into the β -globin locus of mESCs exhibited CGI methylation patterns that resemble their native counterparts.⁷³ Similarly, synthetic elements comprising CGIs and bacterial sequences recapitulate expected patterns of methylation.⁷³ However, CGIs do not effectively shield promoters from methylation if positioned beyond 100–200 bp from the transcription start site.^{61,68,74} Synthetic promoter-less CGIs may recruit histone methyltransferases (HMTs) and accrue H3K4me3, but the capacity to remain CpG-hypomethylated requires both high CpG density and high GC content, suggesting that AT-rich sequences act as DNMT docking sites.⁷¹ Overall, DNA CpG methylation is implicated in transcriptional silencing, whereas high GC-content CGIs associated with transcription sites remain hypomethylated.

Heterochromatin-associated histone modifications are found at silenced transgenes

Histone modifications play a central role in epigenetic gene silencing through constitutive heterochromatin formation.^{75,76} Heterochromatin is characterized by regions with relatively high nucleosomal density, which may impede transcription initiation. DNA methylation can initiate formation of heterochromatin through the recruitment of histone deacetylase enzymes (HDACs), which remove histone acetylation, a feature typically associated with transcriptionally active chromatin (Figure 2B). Importantly, treatment of cells with the HDAC inhibitor sodium butyrate can restore inducible gene activation in mouse embryonic stem and transformed mammalian breast cancer cells.^{26,77} To induce durable silencing, deacetylated histones are subsequently trimethylated by HMTs.^{78–80} Silencing is facilitated by nuclear proteins such as heterochromatin protein-1 (HP1) which promote heterochromatin maintenance.⁸¹ Targeted inhibitions of these processes at sites of transgene integration may prevent local heterochromatin formation without the global epigenetic perturbations induced by broad chemical inhibitors, potentially offering an approach to mitigate silencing due to heterochromatin formation.

Spreading of heterochromatin silences proximal regions at the locus of integration

Although heterochromatin formation may initiate focally, proximal regions may be silenced through spreading of heterochromatin (Figure 2C). Silencing of proximal regions was identified in *Drosophila* and termed position effect variegation in 1930 by Muller et al.^{82,83} Although this phenomenon was initially described with genomic rearrangement of endogenous genetic elements, integration of transgenic payloads mimics these phenomena.^{84–86} Encroachment of the surrounding heterochromatin can disrupt transcription. Spreading of H3K9me3 propagates via a feedback loop of chromatin regulators.^{75,87,88} Combined with DNA methylation, spreading of H3K9me3 leads to heterochromatinization and transcriptional repression. In the case of an integrated transgene heterochromatinization of a nearby gene can spread to, and silence, the transgene.²⁷ Furthermore, spreading of heterochromatin has been observed using multi-copy transcription arrays in hamster, mouse, and *Drosophila* cells showing that gene silencing correlates with appearance of repressive chromatin at transgene arrays.^{89–91}

Epigenetic silencing of transgenes depends on the specific locus and genomic context of integration.^{92,93} Integration within topological associated domains (TADs) may impact transgene activity through TAD-specific determinants of chromatin state.⁹⁴ For example, H3K9me3 often spreads throughout a TAD.⁹⁵ Notably, integration near centromeres may influence the epigenetic silencing of nearby transgenes. In cases when random integration methods are used to engineer synthetic genetic circuits in mammalian cells, wide variability in gene expression and epigenetic silencing may result.

Site-specific genome engineering methods can be utilized to integrate transgenes at so-called safe-harbor loci, yet there remain associated complexities that require further examination. For example, silencing of safe-harbor loci is well documented.^{24,26,48,96} Furthermore, transgene insertion can alter the local chromatin state in a locus-specific manner and affect transgene expression.³³ A key open challenge is understanding why transgene insertion into safe-harbor loci confers stable, consistent gene expression in some scenarios (e.g., cell types, transgene sequences, and insertion conditions) but not others. For a comprehensive review of silencing of transgenes in safe-harbor sites and discussions of criteria for identifying genomic safe harbors, we direct readers to the following perspective.⁹⁷

Viral and transposon defense systems contribute to transgene silencing

Viral vectors and transposon systems provide powerful tools to integrate transgenic cargo into mammalian cells with high efficiency, but they confer specific challenges in maintaining transgene activity. Key gene therapy delivery agents such as lentiviral and gammaretroviral vectors are subject to transcriptional silencing upon integration into the mammalian genome.^{98–100} Mechanistically, the silencing of lentiviral vectors is often associated with promoter methylation, especially during differentiation of stem cells.¹⁰¹ Viral promoters appear to be more prone to epigenetic silencing compared with endogenous promoters,¹⁰¹ highlighting the need to choose an appropriate promoter for clinical gene delivery when viral vectors are used for transgene delivery. For example, DNA methylation and silencing was observed in murine hematopoietic stem cells (HSCs) following Moloney murine leukemia virus (MoMuLV)-based retroviral transduction *in vivo* following serial transplantation.¹⁰² In these studies, both murine stem cell virus (MSCV) and human immunodeficiency virus type 1 (HIV-1) virus led to DNMT activity independent of silencing in transgenic mice, murine embryonic stem cells, and *Drosophila*.¹⁰³

As a defensive adaptation against pathogens and transposon-mediated genomic instability, mammalian cells use epigenetic regulatory mechanisms to specifically identify and repress virally integrated transgenes.¹⁰⁴ Mammalian hosts possess dedicated machinery that detects proviral sequences and recruits histone-modification complexes that mediate transcriptional repression (Figure 2D). One such proviral sequence is the primer-binding site, an 18-bp element residing near the 5' long terminal repeat (LTR) from which viral reverse transcription is initiated. The LTR sequence varies across viruses and is complementary to ribosomal tRNAs, allowing retroviruses to hijack tRNAs and prime reverse transcription of the minus strand.^{105,106} Reciprocally, the host cell can use this site as a target for transcriptional repression. For example, pluripotent cells strongly

repress gene expression from MoMuLV.^{107–109} Biochemical analyses have shown that ZFP809 and TRIM28 (KAP1) bind the primer-binding site and form a complex^{110,111} that recruits the H3K9 methyltransferase SETDB1^{112,113} and components of the nucleosome remodeling and deacetylase complex (NuRD) HDAC complex.¹¹⁴ Accordingly, ZFP809 and TRIM28 are enriched in an endogenous retrovirus sequence spanning the LTR, 5' untranslated region (UTR) and beginning of gag, and are essential for H3K9me3 deposition, histone deacetylation, and repression of proviral genomes.^{113,115,116} Additional native proteins have been implicated in reinforcing this epigenetic repression complex by acting as a scaffold for SETDB1 and NuRD components.¹¹⁷ In this way, endogenous proteins recognize viral DNA motifs and induce epigenetic changes in a sequence-dependent manner.

Viral LTRs serve as prominent targets for CpG methylation. The DNMT-binding scaffold protein Daxx mediates repression of invading viruses and contributes to maintenance of LTR methylation.¹¹⁸ Additionally, methylation of endogenous proviruses is facilitated by the ZFP809-TRIM28-SETDB1 complex.¹¹⁹ Combining TRIM28 knockout with 5-azacytidine-induced CpG demethylation increases provirus transcriptional reactivation stronger than either treatment alone.¹¹⁵ However, SETDB1 knockout reactivates endogenous retroviruses without affecting CpG methylation, and SETDB1-mediated H3K9me3 deposition is unaffected by co-deletion of *Dnmt3a/Dnmt3b/Dnmt1*.¹¹³ Hence, it appears that DNMT-Daxx-mediated CpG methylation and SETDB1-NuRD histone modifications act synergistically to robustly ensure retrovirus and transposon repression. It therefore seems plausible that engineering of viral vectors, e.g., modifying the ZFP809 recognition sequence in the LTR, could result in stealth variants that are less susceptible to epigenetic silencing.

Another defense mechanism involves the recognition of non-self-macromolecules carrying pathogen-associated molecular patterns (PAMPs). Recognition of PAMPs by host-expressed pattern recognition receptors (PRRs) triggers an innate immune signaling reaction.^{120,121} The Toll-like receptor (TLR) 9 recognizes bacterial and viral DNA lacking methylated CpGs, triggering activation of NF- κ B and resulting in the production of cytokines in dendritic cells and macrophages.^{122,123} An shRNA screen of baculovirus-infected A549 cells identified genes of the TLR, interferon, and interleukin families that silence transgene expression.^{124,125} In another example of immune-mediated transgene silencing, influenza and Sendai virus infections of macrophages trigger IFN- α -mediated upregulation of TLR1-3 and TLR7.¹²⁶ IFN- α reduces histone acetylation and transcription of hepatitis B viral mini chromosomes in HepG2 cells¹²⁷ and upregulates Daxx in HeLa cells.¹¹⁸ PAMP-PRR reactions thus convert infected cells into cytokine hubs that signal an upregulation of repressive barriers against invading transgenes (Figure 2D). To ensure transgene expression, these reactions should be avoided through careful consideration and engineering of delivery vectors.

Practical guidelines for avoiding transgene silencing

Loss of transgene expression compounds with the myriad other challenges of cell engineering. The field needs improved methodological guidelines and data sharing of successes and failures alike across diverse systems to identify common, useful tools

Table 1. Summary of published studies on the effect of promoter choice in transgene yields (“levels”) and sustained expression (“stability”) over culture time

Transgene delivery method	Host cell type	Transgene expression	Locus of integration	Clone information	Top three promoters		Reference
					Levels	Stability	
Lentiviral vector	various	stable	random	polyclonal	CAG hEF1 α CMV	–	Qin et al. ¹²⁸
Lipofectamine 2000	HEK293F	stable	random or episomal	polyclonal	CAG hEF1 α CMV	CAG hEF1 α CMV	Dou et al. ¹²⁹
Lipofectamine 2000	CHO-K1	stable	random or episomal	clonal lines	hEF1 α CMV CAG	only hEF1 α tested	Wang et al. ¹²⁴
Lentiviral vector	mESC (J1)	transient	random	polyclonal	hEF1 α CAG hPGK1	only hEF1 α tested	Hong et al. ¹³⁰
Lentiviral vector	mESC (JM8.N4)	stable	random	polyclonal	–	hPGK hEF1 α CMV	Herbst et al. ¹⁰¹
ϕ C31 integrase	mESC (IDG26.10-3)	stable	<i>rosa26</i>	clonal lines	CAG hUbC hEF1 α	–	Chen et al. ¹³¹
Electroporation	mESC (E14Ju09)	stable	random	clonal lines	CAG; mPGK1	–	Malaguti et al. ¹³²
Lentiviral vector	hESC (SA121; Hues-4)	stable	random	polyclonal	hEF1 α hACTB PGK	hACTB PGK EF1 α	Norrmann et al. ³⁴

For stability in stem cells, the list refers to robust transgene expression over prolonged stem cell maintenance (for differentiation, please see text). Abbreviations are as follows: CAG, CMV early enhancer/ β -actin synthetic hybrid promoter; CMV, cytomegalovirus promoter; EF1 α , elongation factor 1-alpha promoter; PGK1, phosphoglycerate kinase 1 promoter; and UbC, polyubiquitin-C promoter. *m* or *h* indicate mouse or human promoter origin and cells respectively; and –: not determined.

and frameworks. Here, we propose practical guidelines for stable engineering of mammalian cells.

Choice of promoter influences the probability of transgene silencing

Promoters vary in their transcriptional activities and sensitivity to epigenetic silencing. Transgene expression is dependent on multiple factors that vary across genetically engineered clones (e.g., loci of integration, copy number, and target cell), which can obscure the role of the promoter in silencing. Thus, it is important to test the effect of the promoter while controlling for genomic context, for instance, by comparing multiple clones with the transgene cassette integrated in the same location, differing only in the selected promoter. To our knowledge, there has not been a comprehensive comparison that systematically evaluated the long-term activity of all promoters commonly used in mammalian synthetic biology. Here, we surveyed the literature to assess promoter performance in terms of expression levels and stable activity over time in the context of their respective experimental details (Table 1).

Inducible systems provide extra safety by offering the ability to turn on and off expression of a transgene using external control, such as the addition of a small molecule, light, or other user-imposed or cell-sensed stimuli. Regulation by inducible promoters allows stably integrated transgenes to be left in the inactive or OFF state for periods of time before induction. These periods of inactivity correlate with an increase in the proportion

of cells that do not respond to induction. This phenomenon has been documented for tetracycline-inducible promoter systems, where continuous induction or higher basal activity of the promoter results in less silencing compared with versions with tightly regulated OFF states.^{77,133} More recently, inducible expression systems have been developed that resist silencing over longer time periods compared with a tetracycline-inducible promoter, employing constitutive transgene transcription with post-transcriptional regulation to mitigate silencing.¹³⁴

Viral promoters such as cytomegalovirus (CMV), spleen focus-forming virus (SFFV), and Rous sarcoma virus (RSV) undergo CpG methylation resulting in silencing of the transgene within a few cell divisions; however, this silencing can be alleviated with 5-azacytidine, a DNMT inhibitor, to partially restore the transgene expression.^{22,101,135,136} A gene driven by the RSV promoter has also been shown to be silenced by polycomb repression complex 2 (PRC2) in CHO cells.²⁷ However, silencing of the cassette containing RSV and a downstream transgene can be prevented by proximal chS4 insulators, perhaps due to increased local histone acetylation and protection of the promoter from DNA methylation.^{137,138} In mESCs, transgenes containing LTR and SV40 promoters can also be acutely silenced.^{139–141} However, unlike in pluripotent stem cells, 5-azacytidine may not rescue transgene expression, as has been observed in undifferentiated pluripotent stem cells.²⁶ Additionally, while episome disappearance and provirus methylation

Table 2. Summary of commonly used insulators in mammalian cells

Insulator	Size (bp)	Source	Chromosome coordinate	Reference
cHS4	1,200 (full) 250 (core)	chicken beta-globin locus	Chr1:197,298,879–197,300,081 (galGal6)	Chung et al. ¹⁴⁵
A2-UCOE	1,500	human HNRPA2B1-CBX3 locus	Chr7:26,239,804–26,241,504 (hg19)	Williams et al. ¹⁵⁹
CBX3-UCOE	700	human HNRPA2B1-CBX3 locus	Chr7:26,240,735–26,241,449 (hg19)	Müller-Kuller et al. ¹⁴⁹
MAR 1–68	3,630	human chromosome 1 intergenic between SPATA6 and AGBL4	Chr1:48,947,776–48,951,409 (hg19)	Girod et al. ¹⁴⁷
tDNA	1,200	human tRNA genes	Chr17: 7,963,112–7,964,183 (hg19)	Raab et al. ¹⁵⁰

Insulator elements are described in terms of their size and genomic source. cHS4, chicken hypersensitive site 4. UCOE, ubiquitous chromatin opening element. MAR, matrix attachment region. tDNA, tRNA gene.

occurred 7–10 days after infection, the viral cassette was silenced prior to that point, supporting a DNA methylation-independent mechanism of provirus silencing in pluripotent stem cells.^{108,109} This mechanism appears to be histone methylation (H3K9me3 and H4K20me3) catalyzed by SETDB1 in complex with TRIM28 and ZFP809. A mutation in the LTR-associated primer-binding site demonstrated improved long-term transgene expression in bone marrow cells transplanted into irradiated recipient mice.¹⁴² Together, these data show that viral promoters alone should be avoided for long-term transgene expression due to their propensity to be silenced, but engineered variants show promise.

Comparison of various promoters in their ability to drive GFP expression via lentiviral transduction of murine and human cell lines has shown that elongation factor 1-alpha (EF1 α) and CMV early enhancer/ β -actin (CAG) promoters consistently produce high fluorescence intensities; CAG exhibited the least variation between transductions, whereas the CMV promoter demonstrated fluorescent variability depending on the host cellular context (e.g., HEK293T and human MRC5 fibroblasts).¹²⁸ Similarly, high CMV activity in HEK293T cells is corroborated by transient transfections when transgenes are not permanently integrated into the genome.¹⁴³ Non-viral lipofectamine-mediated transgene delivery into HEK293F cells showed that the top three promoters driving highest yields were, in descending order, CAG, EF1 α and CMV, and the ranking remained consistent over time.¹²⁹ Therefore, the EF1 α and CAG promoters are commonly used in workhorse mammalian cells because they seem to be the most suitable for long-term expression of high transgene levels.

The choice of promoter in stem cells appears to be more complicated. For example, EF1 α , CAG and phosphoglycerate kinase (PGK) promoters all have been successfully used to drive long-term transgene expression in undifferentiated mESCs.^{101,130,132} However, their performance is influenced by context-specific factors such as viral elements or locus of integration.^{130,131} With respect to differentiation, EF1 α promoter activity has been observed to suffer the least silencing during early-stage embryoid body differentiation,^{101,130} however, during neuronal maturation, the CMV promoter outperformed EF1 α and CAG promoters in mESC-derived neurons, illustrating lineage-dependent promoter performance.¹³⁰ In hESCs transduced with lentiviral vectors, fluorescence intensity was highest when the EF1 α , β -actin, and PGK promoters were used to drive GFP expression.³⁴ Moreover, pro-

motors can exhibit different behaviors based on the type of silencing considered. For example, β -actin remained the most active during long-term hESC maintenance; however, during differentiation it drove the highest overall GFP intensity. In contrast, EF1 α retained the largest percentage of GFP-positive cells and overall activity across a number of lineage markers.³⁴ Overall, EF1 α , CAG, and β -actin promoters efficiently drive transgene expression in stem cells; however, it is important to consider the context of reprogramming stem cells and whether the goal is for long-term stem cell maintenance, differentiation, or both.

Additionally, beyond stability of the mean expression level, consideration of the expression dynamics may also be relevant for some applications. Future work to characterize these parameters of common promoters across contexts is therefore needed. Ultimately, promoter choice should be considered in concert with other factors including insulating elements, locus of integration, and cell type.

Insulators can block transgene silencing

One commonly adopted strategy to counteract transgene silencing is to include insulating DNA elements in the expression cassette. Two types of DNA insulator functions exist: barrier activity that blocks the spreading of heterochromatin from nearby repressive regions and enhancer-blocking activity that prevents enhancer-dependent gene activation.¹⁴⁴ In the context of mitigating transgene silencing, the prevention of heterochromatin spreading is important. Various insulating elements have been reported and tested in mammalian cells, including the prototypic insulator, cHS4,^{145,146} scaffold/matrix attachment regions (S/MARs),¹⁴⁷ ubiquitous chromatin opening elements (UCOEs),^{148,149} and human tRNA gene tDNA¹⁵⁰ (Table 2). Readers are directed to other reviews for more detailed discussions on this topic.^{151–153} Barrier elements typically function by recruiting proteins (e.g., histone-modifying enzymes and CRs) that prevent the spreading of repressive heterochromatin and thus establish a local transcriptionally permissive environment.¹⁵¹ More specifically, the core region of the cHS4 insulator has protein binding sites for VEZF1, CTCF, and USF1/2, which protect against DNA methylation, help form chromosomal loops, and recruit histone-modifying enzymes associated with active expression states, respectively.¹⁵⁴ Accumulating evidence has shown the significant role that chromatin insulators play in regulating the 3D genome architecture.¹⁵⁵ For instance, the binding of CTCF, the primary insulator protein in mammals, is essential to establish the boundaries of TADs.¹⁵⁶ The role of CTCF as an enhancer blocker has

been well characterized, leading to the discovery of highly potent enhancer-blocking insulators from the high affinity CTCF-binding sites in the human genome.¹⁵⁷ Interestingly, genome-wide analysis of CTCF-binding sites in chromatin barrier regions indicate that CTCF may also play an important role in the barrier activity of insulators.¹⁵⁸ Hence, future studies on chromatin boundary regions will likely contribute to the discovery of novel insulators beneficial for mammalian synthetic biology.

The insulating DNA elements identified so far face various challenges that limit their use in mammalian cell engineering. Incorporating the cHS4 sequence into the transgene cassette can significantly reduce the titer of packaged lentivirus carrying the transgene.^{160,161} In addition, the relatively large size of S/MAR elements (e.g., the S/MAR 1–68 element is ~3.6 kb) renders them unfavorable when using vectors with limited cargo capability. Although UCOEs have been shown to prevent silencing when used with numerous promoters in stem cells,¹⁴⁹ their potential bidirectional promoter activity may lead to transcriptional activation of nearby genes upon integration, which poses a safety concern in gene therapy.¹⁶² Interestingly, a recent study screened candidate UCOEs with various truncations, demonstrating their potential to function as barrier-type insulators without intrinsic promoter activity.¹⁶³ However, there is a lack of systematic comparison of the barrier activity of different insulating elements under the same conditions (e.g., cell line, chromosome context, and copy number). Therefore, both direct comparison of existing insulators within the same context and identification of other novel insulators with better features (e.g., compact size, broad tissue compatibility, and no intrinsic promoter activity) would be beneficial to the synthetic biology community. Overall, the choice of promoter and insulator combined with exclusion of transcriptional repression target elements is important to stabilize high levels of transgene expression (Figure 3A).

Genomic locus of integration affects stable transgene expression

One major driver of transgene silencing and the instability of expression over time is the local repressive environment of the integration site in the genome. Viral vectors (e.g., retroviruses or lentiviruses) or transposase/transposon systems (e.g., piggy-Bac or Sleeping Beauty transposase) can deliver synthetic DNA cargo into the mammalian genome with high efficiency in a semi-random manner, as different vectors and systems have their own integration biases.^{164,165} However, due to the uncontrolled integration, there is often minimal to no regulation over the integrant copy number or the integration site(s), which may result in concatemer-induced epigenetic silencing²¹ or silencing caused by the existence or spreading of local repressive chromatin at the integration site.¹⁶⁶ More importantly, because transgenes exhibit different levels of expression when integrated into different chromosomal sites, random insertion is often unfavorable when systematic comparison or characterization of multiple DNA elements (promoter, enhancer, insulator, etc.) is desired.

One strategy to avoid these drawbacks associated with uncontrolled integration is to insert transgenic DNA at a predefined, transcription-permissible locus in the genome. Often the empirically determined genomic safe-harbor regions were chosen for this purpose.¹⁶⁷ Currently, the popular choices of safe-harbor

loci include AAVS1, CCR5, and hRosa26 in the human genome, and Rosa26 and Hipp11 in the mouse genome. These commonly adopted safe-harbor loci have been validated in various models including human iPSCs and ESCs, human CD34⁺ T cells, HEK293T cells, CHO cells, as well as transgenic mice.^{168–172} Interestingly, a recent study by Aznauryan et al. identified two novel safe-harbor sites (Rogi1 and Rogi2) that are capable of stable and safe expression of transgenes.¹⁷³ These two sites were first tested in HEK293T and Jurkat cells for long-term transgene expression, and were further validated in primary T cells and dermal fibroblasts, thus offering more target choices in the human genome (Figure 3B). However, safe-harbor regions may remain vulnerable to epigenetic silencing for reasons discussed above. Potentially, a combination of strategies may most effectively reduce the probability of transgene silencing.

These loci can be targeted with programmable genome-editing tools such as the CRISPR-Cas9 system to achieve targeted insertion of relatively short DNA sequences (e.g., single gene cassettes) with high efficiency. However, considering that synthetic gene circuits typically consist of multiple transcription units, the inevitably large size (e.g., greater than 15 kb) of the circuit makes it challenging for CRISPR-based genomic insertion.^{26,174,175} A serine integrase, on the other hand, is capable of integrating large DNA cargos with high specificity in mammalian cells.^{26,174,175} Recently, the serine integrase-based landing-pad strategy has been widely adopted for various applications involving large DNA constructs, with examples including the rapid prototyping of synthetic DNA circuits,¹⁷⁶ the parallel assessment of large human gene variants library,¹⁷⁷ and the integration of up to nine copies (~100 kb) of a monoclonal antibody-expressing gene cassette to improve antibody production in mammalian cells.¹⁷⁸ Although serine integrases can be advantageous in their high specificity and large cargo capability, one caveat is that they require a landing pad (namely, an att recognition site) to be previously inserted at the chosen site to create a chassis cell line, which limits the ability to multiplex such a strategy. Therefore, recent development in novel genome-editing tools combining CRISPR and integrases for targeted insertion of large DNA sequences¹⁷⁹ as well as the discovery of novel integrases with better activities at both landing pads and directly targeting the human genome¹⁸⁰ could enable the synthetic biology community to more rapidly test locations in the genome to characterize synthetic gene circuits in mammalian cells.

Cell-type choice influences the stability of transgene expression

It is important not to assume that the transgene-silencing factors discussed here are present at the same levels in all cell types. Data downloaded from the Human Protein Atlas (HPA)¹⁸¹ show that one or more transgene-silencing-associated factors are expressed at high levels in cell lines that are often used as test beds for cell engineering, and levels vary across cell lines (Table 3). The wealth of available epigenomic data for these widely used cell lines (e.g., ENCODE¹⁸² and 4D Nucleome, <https://www.4dnucleome.org/cell-lines.html>) should be leveraged to investigate context-dependent transgene behavior. For instance, chromatin immunoprecipitation (ChIP) signals can be used to compare levels of transcriptional silencing or activating chromatin features at genomically mapped safe-harbor loci. Additionally, RNA-seq

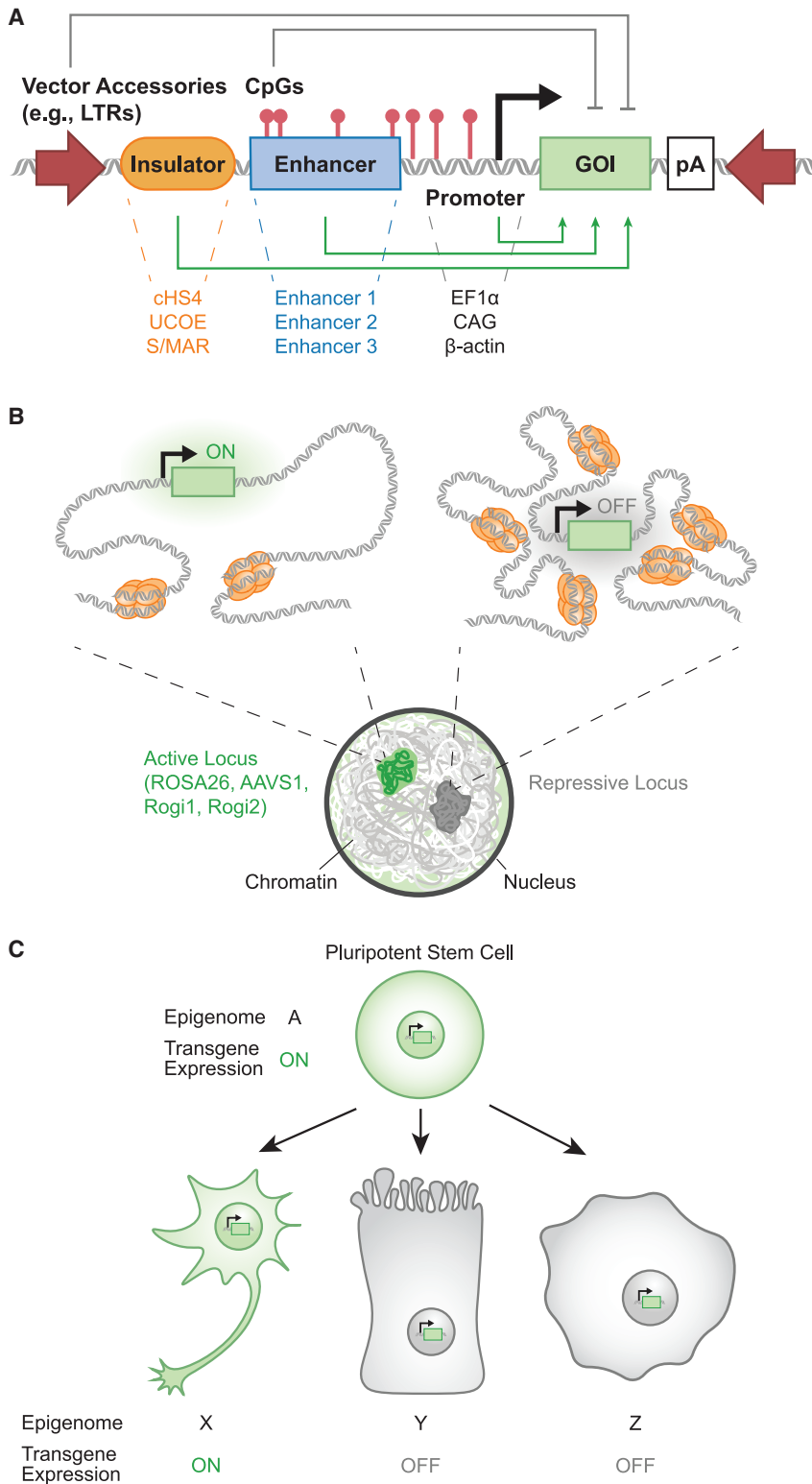


Figure 3. Design considerations for preventing transgene silencing via selection of genetic elements, locus, and cell type of interest

(A) Genetic elements including insulators, promoters, and the combination of activating and repressive elements regulate gene expression. Promoters, enhancers, insulators, and CGIs facilitate continuous gene expression. Elements such as low-density CpGs among GC-poor regions and viral sequences such as long terminal repeats act as targets for transcriptional repression. Stability of transgene expression can be improved through the inclusion of activating elements, exclusion of repressive elements, and sequence-specific parameter optimization.

(B) Transgene circuit integration into heterochromatic, repressive genomic loci increases the likelihood of silencing. Targeted integration of transgenes into genomic safe harbors that remain ubiquitously euchromatic may reduce silencing.

(C) Stem cell differentiation induces genome-wide changes across CpG methylation, histone modification, and chromatin remodeling landscapes. Transgene expression depends on the epigenome of the differentiated lineage; expression might be safeguarded through CGIs, tissue-specific enhancers, and transgene integration into ubiquitously open genomic safe harbors. Abbreviations are as follows: GOI, gene of interest; pA, poly-adenylation signal; and LTR, long terminal repeat.

Table 3. Expression levels (normalized transcripts per million [TPM]) from public RNA-seq data from the Human Protein Atlas for key mediators of transgene silencing, [proteinatlas.org](https://www.proteinatlas.org)

	HKG	HDAC					HMT	DNMT				NuRD		Viral defense				%max row value
	TBP	HDAC1	HDAC2	HDAC4	SIN3A	SIN3B	SETDB1	DNMT1	DNMT3A	DNMT3B	DNMT3L	CHD3	RBBP4	DAXX	RIPK1	TLR9	TRIM28	
HeLa	16.6	105.7	102.1	5.1	46.2	35.6	27.3	39.5	12.8	3.3	0.4	148.5	112.0	29.9	4.5	0.0	407.6	
HEK293	23.2	176.8	185.0	1.8	42.1	36.8	43.3	100.9	4.3	14.0	0.0	67.2	88.3	39.6	9.4	0.1	2817.1	
HepG2	26.1	130.1	131.8	5.8	27.9	16.7	20.8	27.1	25.4	18.5	0.0	2.7	111.9	39.9	6.9	0.0	537.7	
HUVEC	15.9	106.1	199.6	2.4	30.0	29.1	31.2	39.9	19.5	6.6	0.0	76.9	77.2	15.5	20.6	0.0	301.3	
Jurkat	37.2	298.5	179.2	49.1	47.5	19.7	28.3	37.6	34.0	6.2	0.0	54.1	139.8	16.2	6.2	0.9	597.7	
K-562	49.7	215.2	326.4	3.7	51.5	22.1	43.4	75.0	18.0	98.6	0.0	41.5	138.0	39.1	19.4	0.0	507.1	
MCF7	19.3	115.7	105.5	4.7	36.2	33.7	44.1	37.6	20.6	15.7	0.0	42.6	48.0	23.2	17.8	0.0	705.0	
PC-3	11.0	229.6	116.3	2.8	26.3	46.6	20.6	76.6	4.2	3.2	0.0	40.3	67.8	9.1	12.7	0.0	637.5	
U-2 OS	19.1	106.2	122.9	0.4	54.5	18.5	15.7	42.2	4.7	12.3	0.0	68.8	61.6	29.1	12.1	0.1	273.2	

HKG, housekeeping gene (shown for comparison), HDAC, histone deacetylase, HMT, histone H3K9 methyltransferase, DNMT, DNA methyltransferase, NuRD, nucleosome remodeling and deacetylase complex.

data can be used to identify factors that are expressed at high levels, and their impact on transgene silencing can be tested by genetic knockdown or chemical inhibition. For example, high HDAC1 expression may contribute to transgene silencing in T cells, as indicated by the HPA data for Jurkat cells. In T cells that showed lentiviral and retroviral transgene silencing after 4 weeks of passaging, treatment with HDAC inhibitors was used to restore transgene expression.¹⁸³ Future work could similarly identify context-specific methods to mitigate transgene silencing.

For cancer-derived cell lines, components of the switch/sucrose non-fermentable (SWI/SNF) ATP-dependent chromatin remodeling complex frequently show loss-of-function mutations or low expression.^{184,185} This needs to be taken into consideration when attempting to modify histone marks via HDAC inhibition or epigenome editing to restore transgene expression because SWI/SNF is often required to act in concert with chromatin modifications such as histone acetylation to activate transcription.

Pluripotent stem cells allow for unlimited self-renewal and the ability to contribute to all germ layers that give rise to the adult body. The pluripotent state entails unique epigenetic properties as unveiled through MoMuLV infection experiments of mouse embryos and pluripotent cells.^{107–109} First, ESCs express Zfp809 that mediates Setdb1-catalyzed H3K9 and H4K20 methylation of retroviral sequences through the Zfp809-Trm28-Setb1 complex, allowing the cells to efficiently repress expression of transgenes delivered and integrated through viral vectors.^{110,111,113,186} Second, mouse preimplantation stem cells abundantly express tRNA-derived fragments that inhibit translation of retroviral transcripts by competing for the primer-binding site.¹⁸⁷ Third, mouse embryos carrying a human β -globin gene regulated by a Cre-excisable methylation-resistant CGI methylate and silence the transgene only if the island is excised before implantation.⁶¹ These findings illustrate that pluripotent cells

possess unique mechanisms that could silence transgene expression, and exit from pluripotency concomitant to implantation involves *de novo* methylation that is associated with transcriptional silencing.^{54,55}

During mouse development, high-density CpG promoters and CGIs are resistant to *de novo* methylation, most of which occurs during implantation at the E4.5-E5.5 transition catalyzed by DNMT3A and DNMT3B.⁵⁵ Given the comparability of naive pluripotent ESCs to preimplantation E4.5 epiblast cells,¹⁸⁸ it is conceivable that differentiation recapitulates passage through the developmental stage of implantation and the surge of *de novo* DNA methylation. Indeed, mESCs exiting naive pluripotency exhibited increased DNMT3A/DNMT3B expression and genome-wide CpG methylation after 24 h of differentiation triggered by PD0325901/CHIR99021 withdrawal from the media (with notable resistance of CGI promoters), although no correlation between promoter methylation and respective gene expression was determined.¹⁸⁹ Similarly, differentiating mESCs accrue DNMT3A and DNMT3B-dependent CpG methylation in the Oct4 promoter (curiously reduction of Oct4 mRNA preceded methylation,¹⁹⁰ which has been described as a non-CpG promoter).⁶⁸ High-density CpG and CGI promoters might provide candidates for safeguarding promoter activity during pluripotent stem cell differentiation.

Differentiation encompasses dynamic chromatin state changes, with different loci changing from an open to a closed chromatin state and vice versa. This can lead to silencing of randomly integrated transgenes in a promoter-independent and locus-dependent manner. Constitutively active loci allowing ubiquitous transgene expression have been identified to tackle this problem: the Rosa26 locus in the mouse genome,¹⁹¹ and AAVS1, CCR5, and Rosa26 in the human genome.^{97,168} It will be interesting to see how the two newly identified human

genomic safe harbors¹⁷³ fare in ensuring ubiquitous transgene expression during human stem cell differentiation. Altogether, global changes in DNA methylation and chromatin states are critical factors of transgene activity during stem cell differentiations and reprogramming (Figure 3C). CGIs and safe harbors may provide solutions to these barriers.

Avoiding nutrient limitations supports active transgene expression

Engineered cell lines may encounter signals from the microenvironment that induce dramatic shifts in metabolic states that could impact epigenetic regulation of transgenes. A pool of metabolites that become depleted or replenished in response to environmental cues also provides substrates for the chromatin modification machinery. For instance, the free pool of acetyl-CoA, the sole substrate for acetylation of histones in transcriptionally active chromatin, is heavily regulated by signals linked to nutrient availability and is primarily derived from extracellular glucose levels. Exposure to fatty acids or insulin can increase lipid storage and synthesis.^{192–194} In yeast, when glucose becomes unavailable and cells enter the stationary phase, lipid synthesis outcompetes histone acetyltransferases (HATs) for acetyl-CoA, and histone acetylation levels decrease,^{195,196} which favors the formation of closed chromatin. Human cancer cells show increased lipogenesis and broad reprogramming of gene expression in response to signals from adipocytes.^{197–199} Thus, low levels of glucose in cell culture media could lead to transgene silencing through decreased availability of acetyl-CoA, as well as high levels of fatty acids or insulin. Lactate can play a similar role to acetylation through lactylation of histones. Evidence thus far of this novel histone mark supports that lactylation promotes maintenance of active genes,^{200,201} so low levels of lactate could result in silencing. However, a delicate balance must be struck as high levels of lactate generally reduce cell growth and protein production.²⁰² Furthermore, inhibition of histone demethylases by D-2-hydroxyglutarate (D2HG), an “oncometabolite” produced by mutated IDH1/2, has been implicated in gene silencing in cancer cells and has been mechanistically linked to elevated H3K39me3 and gene silencing in yeast.²⁰³ Taken together, these observations suggest the importance of careful growth medium design and feeding strategies to reduce transgene silencing, focusing on providing sufficient glucose and reducing flux through the D2HG pathway.

Prospects for the future

Despite the identification of abundant potential mechanisms and diverse strategies for mitigating transgene silencing, silencing persists as a challenge for cellular engineering, highlighting the importance of new descriptive studies and novel strategies for stable transgene expression. Basic research into the biology of silencing could elucidate its molecular and physical basis, identify the responsible host genes and pathways, and inform new strategies to address this challenge. Here, we propose future research directions that could propel the field of mammalian synthetic biology past the current challenges of transgene silencing. This research includes the application of publicly available data to investigate silencing at the epigenetic level or identify silencing-resistant promoters, CRISPR-based screens to identify genes associated with silencing and massively parallel reporter assays (MPRAs) to evaluate new circuit components to

prevent silencing. Finally, alternative engineering solutions could be further developed to mitigate transgene silencing, including non-integrating methods of stable expression, post-transcriptional and translational regulation, and epigenetic modifying circuits.

Mapping chromatin modifications in the transgene and at the integration loci

Mapping chromatin modifications both at endogenous integration loci and in silenced transgenes will be useful for better understanding the characteristics of effective safe-harbor loci as well as the mechanisms by which transgenes are epigenetically silenced (Figure 4A). Investigating chromatin modifications at integration sites across different cell types of interest could help identify any differences that affect silencing of a transgene upon integration. Several databases including ENCODE,¹⁸² 4D Nucleome,²⁰⁴ and Human Cell Atlas²⁰⁵ contain data on chromatin modifications (ChIP-seq, CUT&RUN), chromatin accessibility (ATAC-seq), and gene expression (RNA-seq) in both human cell lines and primary cells. Using this epigenetic information to better characterize existing safe-harbor loci will also aid the discovery of new integration sites that are less prone to transgene silencing. Similar epigenetic profiling of silenced transgenes for different chromatin modifications such as DNA methylation, H3K27me3, H3K9me3, and H3K27ac will provide insights into how transgenes are silenced, including which chromatin complexes are involved and how transgenes are recognized or potentially targeted for silencing by the cell. Mapping these chromatin modifications will help inform larger screens to determine genes that are responsible for transgene silencing.

Identifying constitutive endogenous promoters by harnessing publicly available data

Identification of additional stable constitutive promoters could also be useful for maintaining transgene expression, as these elements may be silencing resistant. This could be accomplished by scanning the mammalian transcriptomes for ubiquitously expressed housekeeping genes (HKGs), mapping their respective promoters in the genome, and utilizing highly conserved candidates for stable transgene expression. The FANTOM5 database lists such HKG promoters for mouse and human cells, making it an attractive tool for identifying species-conserved stable promoter sequences.²⁰⁶ Indeed, the ubiquitous-uniform promoter category contains β -actin and EF-family genes (e.g., EF1 α), along with p53 and members of the ribonucleoprotein processing machinery. On the other hand, promoters of non-coding RNAs showed the least cross-species conservation, while non-TATA and CGI-based promoters demonstrated non-ubiquitous expression.²⁰⁶ CGIs are thought to confer resistance to DNA-methylation-dependent gene silencing, so the non-ubiquitous expression associated with CGI promoters possibly reflects differential methylation: most CGIs are ubiquitously unmethylated, about 25% are ubiquitously methylated, and a few thousand exhibit tissue-specific methylation.⁶⁸ Therefore, the subcategory of housekeeper-associated unmethylated CGIs might hold attractive candidates for safeguarding transgene expression. Alternatively, novel CGI-promoter hybrid combinations could create synthetic promoters with desired properties. In support of this notion, fusion of the CGI of the CHO-K1 β -actin promoter to the CMV promoter improved long-term transgene expression and antibody production yields in CHO-K1 cells, compared with

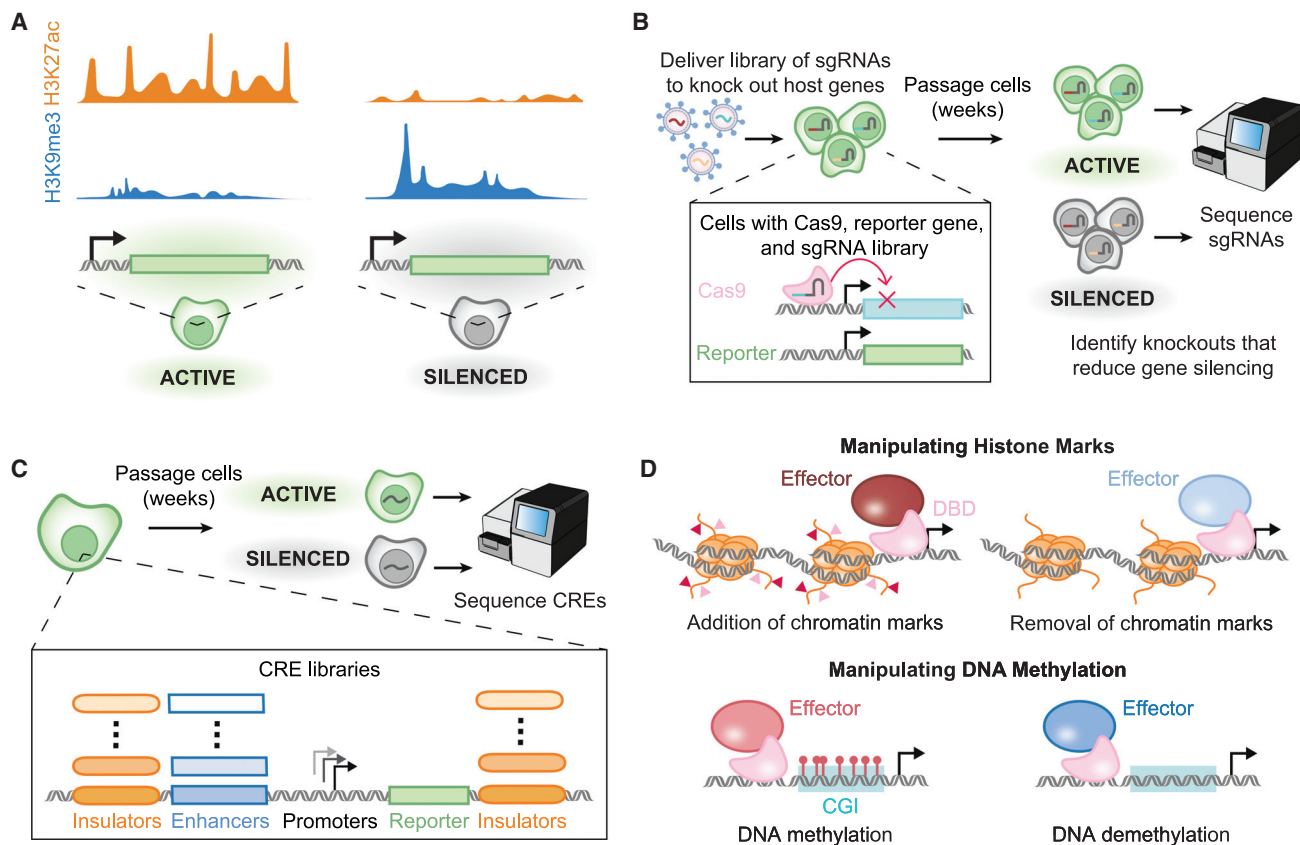


Figure 4. Technologies being applied to better understand or manipulate transgene silencing

(A) Measurement of chromatin marks and DNA methylation can inform the epigenetic state of a synthetic genetic element as well as the epigenetic modifications involved. The measurements can be performed using techniques such as ChIP-seq.

(B) CRISPR screens can identify genetic dependencies for transgene silencing. A reporter gene is engineered in cells that also express Cas9. A library for sgRNAs is delivered to the cells. A cell receives a unique sgRNA that targets and knocks out a unique endogenous gene. The cells are passaged, and time is allowed for gene silencing to occur. Sequencing of the gRNAs is performed to identify knockouts that reduce epigenetic silencing.

(C) Massively parallel reporter assays (MPPRAs) enable systematic identification of cis-regulatory elements (CREs), including promoters, enhancers, and insulators that can maintain transgene expression and prevent silencing. A library of CREs regulating a reporter gene is installed in a population of cells, the cells are passaged to allow time for gene silencing to occur, the cells are separated by reporter level, and the CREs are sequenced to identify library elements that are enriched in the population of cells with maintained gene expression.

(D) Synthetic chromatin regulators can be engineered by fusing DNA-binding domains (DBDs) to epigenetic modifying effectors, such as enzymes that catalyze specific additions or removal of methylation on histones or DNA. This and other technologies such as ChIP-qPCR, CUT&RUN, methylated DNA immunoprecipitation, and bisulfite conversion enable synthetic biologists to understand the effect of different epigenetic effectors and to manipulate epigenetic silencing.

the original CMV promoter.²⁰⁷ A high-throughput synthetic biology approach utilizing databases listing CGIs, transcription start sites⁶⁸ and mammalian promoters²⁰⁶ could facilitate the computational design and genetic engineering of novel CGI-promoter variants optimized to ensure stable transgene expression.

CRISPR screens to map genes responsible for transgene silencing

CRISPR screens can provide a better understanding of mechanisms that have evolved to avoid silencing and will inspire new synthetic biology strategies.^{208–210} Endogenous cellular pathways are responsible for the silencing of transgenic payloads. Therefore, an identification of such pathways could facilitate the prevention of these silencing mechanisms. In order to map the cellular pathways involved in transgene silencing, one could perform high-throughput loss-of-function screens, using gene-perturbation strategies to avoid unintended consequences associated with the use of small-molecule inhibitors, such as

effects on native gene expression and potential cellular toxicity.^{211,212} Pooled CRISPR screens are a promising strategy to identify the host genes required for silencing (Figure 4B). One could use a genome-wide or epigenetics-focused sgRNA library to knockout host genes and then measure sgRNA enrichments in cells where a synthetic gene circuit is silenced versus maintained. Identification of the required host genes could be immediately useful. CRISPR screens have been used to identify genes involved with drug resistance, influenza A virus infections, and cellular reprogramming.^{213–215} For example, one could generate stable knockout or knockdown cell lines that are silencing incompetent, or transiently inhibit the host silencing machinery with small molecules or siRNAs to prevent or reverse silencing.^{125,216–218}

Aside from the practical outcomes of stable transgene expression, a deeper investigation of these host silencing pathways could expand our understanding of how the host machinery

evolved to silence synthetic genes. Additionally, studies of the cGAS-STING pathway²¹⁹ and chromatinization of episomal transgenes indicate that DNA (e.g., linear DNA donor template for CRISPR editing and plasmid DNA used in Sleeping Beauty transposon system) can be sensed by the cell and modified prior to integration. Therefore, CRISPR screens prior to, and post, integration can provide insights into the pathways involved in silencing. One possible outcome is the identification of new mechanisms that have evolved to defend the cell against other foreign DNA including viruses and transposable elements.

Massively parallel reporter assays as a method to find novel elements and understand their optimal deployment

Advances in technologies for genetic screening, epigenomics, and synthetic gene circuit design are creating new opportunities to characterize and prevent transcriptional silencing in mammalian cells. Furthermore, high-throughput screening of endogenous genetic elements could facilitate the rational design of new construct components and aid in the understanding of epigenetic regulation with the ability to rapidly screen synthetic gene circuit stability after integration into the genome. MPRAs including CapSTARR-seq, a high-throughput method to quantify enhancer activity^{220,221} and functional identification of regulatory elements within accessible chromatin (FIREWACH)²²² for mammalian cells have primarily been used to measure enhancer and promoter activity; however, most studies probe enhancers with the same minimal promoter that is decoupled from genomic locus as most reporters are not integrated into the genome.^{223,224} Chromosomal domains have long been shown to affect transgene expression,²²⁵ and lentivirus-based MPRA has shown that genomically integrated reporters have different expression than their episomal counterparts.²²⁶ A method termed thousands of reporters integrated in parallel (TRIP), allows high-throughput investigation of the influence of genomic integration loci on transgene expression.¹⁶⁶ Analysis of two promoters, mPGK and tet-Off, at 27,000 loci in mESCs showed 1,000-fold variation in expression levels, where chromatin state is related to expression level and lamina-associated domains attenuated transcription, while nearby enhancers increased expression.¹⁶⁶ Additionally, MPRA of enhancers have also shown cell-type specificity.²²⁷ While there are numerous screens on the effect of enhancer-promoter interactions, promoters and insulators have been less well characterized. Screening human promoters at AAVS1 safe-harbor locus in K562 cells found that core promoters drive unidirectional transcription.²²⁸ Screening more broadly across loci, promoter activity scales across regions of integration suggesting that integration context provides a factor over the promoter-intrinsic properties.²²⁹ However, there remain many human promoters to characterize for their variance in expression levels in different cell types and for their propensity of transgene silencing (Table 3). Using MPRAs to better characterize promoters in different genomic contexts and cell types would help identify which loci and promoter combinations in specific cell types reduce transgene silencing, as well as help further understand the mechanisms that drive silencing (Figure 4C). In addition to testing different cell types, promoters should also be tested in different cell states such as under various metabolic conditions or in the presence of immune stimulation. High-throughput screening may facilitate identification of novel insulator elements that resist transgene silencing. When encoded proximal to transgenes, existing in-

ulators such as UCOE and cHS4 promote stable transgene expression. Candidate UCOE elements vary in their ability to limit transgene silencing and depend upon the choice of the promoter.¹⁶³ Further efforts to screen and characterize diverse insulators will help add more reliable insulators to the synthetic biology toolbox.

New genetic elements should be benchmarked against current gold-standard regulatory elements to define their effectiveness. As noted above, genetic elements function differently between cell types and lines, so the performance of these elements will likely require a systematic comparison within the relevant cellular context. MPRAs have immense potential to discover new parts and optimize circuit configuration, but researchers ought to begin standardizing currently available genetic elements. For instance, alternate sequences of related genetic elements such as EF1 α and EFS promoters can have drastically different performance and properties.²³⁰ Therefore, a systematic comparison of currently available elements is a necessary step toward standardization of best practices to inform optimal construction, enhance circuit robustness, and minimize systemic inefficiencies.

Inspiration from evolved solutions to transgene silencing

Viruses have evolved many mechanisms to avoid identification and silencing of viral elements. Therefore, there is significant potential in repurposing evolved viral defense mechanisms to design novel stable transgene expression strategies. For instance, incorporation of the S/MAR element was shown to enhance nuclear transport of transfected episomal DNA.²³¹ Engineering of this phenomenon may eventually yield robust expression of transgenes and synthetic circuits. As another example, viral covalently closed circular DNA (cccDNA) persistence is a hallmark of hepatitis B virus (HBV) infection and there are non-integrated HBV elements that are believed to interact with host chromatin related proteins to regulate viral gene transcription. Additionally, the persistence of these foreign elements is believed to be the cause of relapse after viral infection clearance.²³² The production of recombinant cccDNA has been employed in the search for drugs to treat and remove these persistent HBV elements.²³³ Although these tools will need to be further explored and engineered, recombinant cccDNA may be leveraged for stable transgene expression. Another viral defense mechanism involves the suppressors of RNA silencing (VSRs), a mechanism used by viruses to interfere with host RNA interference following infection of plant, insect, and mammalian cells.²³⁴ Engineering elements inspired by these and newly discovered viral defense mechanisms have the potential to result in the design of robust genetic circuits.

Managing silencing in extrachromosomal vectors

Our understanding of the challenges associated with silencing in extrachromosomal vectors is informed in part by substantial experience with adeno-associated virus (AAV) vectors, which exist as episomal DNA. AAVs have attracted a significant amount of attention for use as a gene therapy vector to deliver DNA *in vivo* because they can have low immunogenicity and low rates of insertional mutagenesis.²³⁵ Nevertheless, two early-phase clinical trials of gene therapy for inherited vision loss reported only short-term vision improvement following the treatment of patients with recombinant AAV.^{236,237} Although the underlying

mechanism of the decline in improved vision in the long-term remains unclear, transgene silencing was proposed as a potential cause in one of the studies.²³⁶ The hypothesis that transgene silencing was the major cause of the poor robustness of AAV gene therapy approaches has yet to be proven, especially since cellular turnover and immune responses could also play a significant role. Determining the mechanism(s) involved in the durability of AAV gene therapy *in vivo* presents a challenge, and this challenge becomes increasingly complicated as studies focus on more complex and therapeutically relevant systems. For example, a preclinical study of liver-targeted AAV found a strong correlation between liver vector DNA copy number and transgene protein expression level in mice, but that there was very little protein expression from non-human primate liver despite DNA levels of approximately 1–100 vector copies per cell. The authors proposed vector silencing as one possible culprit.²³⁸ A recent preprint describes a study on the loss of AAV transgene expression in the primate liver that used *in situ* hybridization and found a disproportionate loss of transgene RNA relative to DNA over time.²³ At day 14, there was high transgene expression and AAV DNA was found dispersed throughout the nucleus, whereas by day 77, the expression was largely lost and AAV DNA was found in a few distinct foci, which may be transcriptionally inactive. Since AAV rarely integrates into the genome and is not rapidly diluted in non-dividing cells, the use of AAV is viewed as one of the safest and most practical approaches for gene therapies.²³⁵ However, with a positional bias toward transcriptionally active regions,^{239–241} it has been proposed that the few integration events may drive what is left of transgene expression after the virus wanes through cell divisions. Further, SETDB1, the H3K9 methyltransferase, has been identified by several groups as a host factor that can reduce both the percentage of transgene-expressing cells and the level of expression among those transduced cells when using AAV, lentivirus, and adenovirus delivery methods.^{242–244} These findings further implicate chromatin-mediated transgene silencing as a mechanism with significant influence over long-term AAV expression. In summary, the loss of AAV expression is an important area of active investigation, and transgene silencing of gene therapy vectors may be a major barrier to achieving long-term high treatment efficacy.

Introducing artificial chromosomes may avoid silencing mechanisms inherent to integration in endogenous loci. Human artificial chromosomes (HACs) are a potential solution to limitations regarding transgene size limits, positional regulation effects and silencing associated with viral elements.^{245,246} So far, the complexity of assembling HACs has limited their construction as well as their benchmarking with other transgene delivery methods.²⁴⁷ Ongoing efforts have resulted in more streamlined assembly and delivery of HACs into human T cells and iPSCs.²⁴⁸ However, transcriptional silencing does occur on current-generation HACs. Thus, while bottom-up engineering may provide silencing-resistant HACs in the future, further characterization is required for HACs to become a viable method for preventing transgene silencing.

Post-transcriptional and post-translational mechanisms as alternative regulatory strategies

Genetic circuit designs that robustly resist epigenetic silencing may not be compatible with common methods of transcriptional

control, meaning alternative regulatory strategies are needed. For instance, synthetic circuits that are exclusively composed of active promoters may silence less than transcriptionally regulated circuits. In order to achieve the regulatory function of the genetic circuit, post-transcriptional or post-translational mechanisms could be employed instead. Post-transcriptional control can be achieved by including regulatory elements in UTRs of mRNA. These parts include microRNA and microRNA-binding sites, RNA-binding protein motifs, and ribozyme switches. For a more detailed review on this topic, see Pardi et al.²⁴⁹ Recently, CRISPR-Cas-binding motifs^{134,250} and toehold switches²⁵¹ have also been used to engineer post-transcriptional or translational control. Alternatively, regulation can be implemented at the post-translational level using protein domains responsive to external inputs (such as small-molecule- or light-inducible degrons) or by engineering protein-protein interactions. Complex logic has been achieved entirely post-translationally using proteases.^{252–254} Because these circuits act independently from transcription, they are compatible with an array of promoters and expression methods. Thus, post-transcriptional and post-translational regulatory strategies could facilitate the decoupling of functional modules from transcriptional components that resist epigenetic silencing, allowing each to be optimized separately.

Engineered epigenetic modulation to counteract silencing

Synthetic biology tools for epigenetic modulation can be potentially used in genetic circuits to directly counteract epigenetic silencing. Previously developed tools include engineered synthetic chromatin regulators, which typically consist of a DNA-binding domain (DBD) fused to an epigenetic effector domain.²⁵⁵ The DBD can be programmable, including zinc-finger proteins, TALEs, and CRISPR proteins.^{256,257} This enables epigenetic modifications to be targeted to synthetic genetic circuits, such as removal of silencing modifications (e.g., demethylases) or addition of activating modifications (e.g., acetyltransferases)^{258,259} (Figure 4D). Besides using these approaches to study and modulate epigenetic silencing,¹⁴ engineered synthetic chromatin regulators can be used as part of synthetic gene circuits to counteract transgene silencing. A potential approach involves the use of feedback, which is already employed in synthetic gene circuits and natural epigenetic regulatory pathways. For instance, in a positive autoregulatory synthetic gene circuit, synthetic chromatin regulators could be used to constitutively remove repressive epigenetic marks and maintain an open chromatin structure or maintain epigenetic marks associated with active transcription. This approach can be complemented with control theoretic systems biology strategies that mathematically model and study the role of feedback in epigenetics.^{260,261} In another approach, a circuit could employ mechanisms to detect epigenetic silencing and subsequently activate an effector to remove the repressive marks. In this case, VP64-based transcriptional activators have been engineered to specifically bind repression-associated histone marks such as H3K27me3,²⁶² and ChIP data from the epithelial cell line, U2OS, suggests a change in chromatin state from silenced to active perhaps through Mediator recruitment (MED25 and MED17).²⁶³ To use this approach for transgenes, a DNA sequence recognition module would need to be incorporated to achieve transgene-specific regulation and avoid off-target activation elsewhere in the genome. Finally, synthetic chromatin

regulators can be used to engineer efficient transitions between closed and open chromatin states. Linking the establishment of an epigenetic state to an input of interest would enable the use of epigenetic memory as a form of information storage.

Conclusions

In conclusion, although transgene silencing poses significant challenges for mammalian cell engineering, efforts are underway to elucidate the molecular mechanisms responsible for this phenomenon and develop solutions to mitigate it. The field of mammalian synthetic biology can overcome the challenge of transgene silencing by sharing silencing data with current elements, discovering new regulatory elements and delivery approaches, identifying and intervening with problematic pathways, and employing additional layers of transcriptional and post-transcriptional regulation. The design of more robust tools for mammalian cell engineering will undoubtedly accelerate the fields of cell and gene therapy, biomanufacturing, and basic biology research.

ACKNOWLEDGMENTS

Funding for this work was supported in part by the National Institutes of Health grants 1DP2CA250006-01 (T.L.D.), 1R01GM129011 (W.W.W.), R01EB029483 (W.W.W.), 1R01EB026510 (J.N.L.), R21EB030772 (I.B.H.), R35GM143532 (I.B.H.), R35GM143033 (K.E.G.), R35GM138256 (L.M.), 4K00DK126120-03 (J.T.), R01EB029483 (A.S.K.), R35GM128947 (L.B.), R01EB030946 (R.W.), R01EB025256 (R.W.), 1UM1HG009402 (H.Z.), U54DK107965 (H.Z.), R21CA232244 (K.A.H.), 1RC2DK120535-01A1 (J.J.C.), and 1U01 DK 127420-01 (M.B.E.), the National Science Foundation grants CBET-2034495 (L.M.), CBET-2145528 (L.M.), 2141064 (K.S.L.), EF-1921677 (A.S.K.), and EF-2021552 under subaward UWSC10142 (M.B.E.). Further support was also provided by the Biotechnology and Biological Sciences Research Council (BBSRC) BB/S006206/1 (K.P.) and BB/M018040/1 (S.J.R.), ElectroGene 785800 (M.F.), the SNF (M.F.), the Paul Allen Foundation (W.W.W.), AOFSR FA9550-22-1-0316 (K.E.G.), the Wellcome Sanger Institute LEAP 21-275 (L.M.), the Parker Institute for Cancer Immunotherapy (Y.Y.C.), the W.H. Coulter Department of Biomedical Engineering at Emory University (C.E.S.), and the DoD Vannevar Bush Faculty Fellowship N00014-20-1-2825 (A.S.K.). M.B.E. is a Howard Hughes Medical Institute investigator. The authors listed with equal contribution are listed in the author list in alphabetical order.

DECLARATION OF INTERESTS

J.T. and L.B. acknowledge outside interest in Stylus Medicine.

REFERENCES

- Xie, M., and Fussenegger, M. (2018). Designing cell function: assembly of synthetic gene circuits for cell biology applications. *Nat. Rev. Mol. Cell Biol.* *19*, 507–525.
- Kitada, T., DiAndreth, B., Teague, B., and Weiss, R. (2018). Programming gene and engineered-cell therapies with synthetic biology. *Science* *359*, eaad1067. <https://doi.org/10.1126/science.aad1067>.
- Kis, Z., Pereira, H.S., Homma, T., Pedrigi, R.M., and Krams, R. (2015). Mammalian synthetic biology: emerging medical applications. *J. R. Soc. Interface* *12*, 20141000. <https://doi.org/10.1098/rsif.2014.1000>.
- Lienert, F., Lohmueller, J.J., Garg, A., and Silver, P.A. (2014). Synthetic biology in mammalian cells: next generation research tools and therapeutics. *Nat. Rev. Mol. Cell Biol.* *15*, 95–107.
- Johnson, M.B., March, A.R., and Morsut, L. (2017). Engineering multicellular systems: using synthetic biology to control tissue self-organization. *Curr. Opin. Biomed Eng.* *4*, 163–173.

- Wang, N.B., Beitz, A.M., and Galloway, K.E. (2020). Engineering cell fate: applying synthetic biology to cellular reprogramming. *Curr. Opin. Syst. Biol.* *24*, 18–31.
- MacDonald, I.C., and Deans, T.L. (2016). Tools and applications in synthetic biology. *Adv. Drug Deliv. Rev.* *105*, 20–34.
- Deans, T.L., Cantor, C.R., and Collins, J.J. (2007). A tunable genetic switch based on RNAi and repressor proteins for regulating gene expression in mammalian cells. *Cell* *130*, 363–372.
- Keung, A.J., Joung, J.K., Khalil, A.S., and Collins, J.J. (2015). Chromatin regulation at the frontier of synthetic biology. *Nat. Rev. Genet.* *16*, 159–171.
- E., Subkhankulova, O., T., and Tolmachev, T. (2013). Silencing of transgene expression: A gene therapy perspective. In *Gene Therapy – Tools and Potential Applications (InTech)*.
- Brachmann, C.B., Sherman, J.M., Devine, S.E., Cameron, E.E., Pillus, L., and Boeke, J.D. (1995). The SIR2 gene family, conserved from bacteria to humans, functions in silencing, cell cycle progression, and chromosome stability. *Genes Dev.* *9*, 2888–2902.
- Duan, B., Ding, P., Navarre, W.W., Liu, J., and Xia, B. (2021). Xenogeneic silencing and bacterial genome evolution: mechanisms for DNA recognition imply multifaceted roles of xenogeneic silencers. *Mol. Biol. Evol.* *38*, 4135–4148.
- Gartenberg, M.R., and Smith, J.S. (2016). The nuts and bolts of transcriptionally silent chromatin in *Saccharomyces cerevisiae*. *Genetics* *203*, 1563–1599.
- Bintu, L., Yong, J., Antebi, Y.E., McCue, K., Kazuki, Y., Uno, N., Oshimura, M., and Elowitz, M.B. (2016). Dynamics of epigenetic regulation at the single-cell level. *Science* *351*, 720–724.
- Hathaway, N.A., Bell, O., Hodges, C., Miller, E.L., Neel, D.S., and Crabtree, G.R. (2012). Dynamics and memory of heterochromatin in living cells. *Cell* *149*, 1447–1460.
- Felsenfeld, G. (1992). Chromatin as an essential part of the transcriptional mechanism. *Nature* *355*, 219–224.
- Behe, M., and Felsenfeld, G. (1981). Effects of methylation on a synthetic polynucleotide: the B–Z transition in poly(dG–m5dC).poly(dG–m5dC). *Proc. Natl. Acad. Sci. USA* *78*, 1619–1623.
- Uckelmann, M., and Davidovich, C. (2022). An added layer of repression for human genes. *Nature* *604*, 41–42.
- Tchavonnikarova, I.A., Timms, R.T., Matheson, N.J., Wals, K., Antrobus, R., Göttgens, B., Dougan, G., Dawson, M.A., and Lehner, P.J. (2015). Gene silencing. Epigenetic silencing by the HUSH complex mediates position-effect variegation in human cells. *Science* *348*, 1481–1485.
- Sutherland, H.G., Kearns, M., Morgan, H.D., Headley, A.P., Morris, C., Martin, D.I., and Whitelaw, E. (2000). Reactivation of heritably silenced gene expression in mice. *Mamm. Genome* *11*, 347–355.
- Chusainow, J., Yang, Y.S., Yeo, J.H.M., Toh, P.C., Asvadi, P., Wong, N.S.C., and Yap, M.G.S. (2009). A study of monoclonal antibody-producing CHO cell lines: what makes a stable high producer? *Biotechnol. Bioeng.* *102*, 1182–1196.
- Yang, Y., Mariati, Chusainow, J., and Yap, M.G. (2010). DNA methylation contributes to loss in productivity of monoclonal antibody-producing CHO cell lines. *J. Biotechnol.* *147*, 180–185.
- Greig, J.A., Breton, C., Martins, K.M., Zhu, Y., He, Z., White, J., Bell, P., Wang, L., and Wilson, J.M. (2022). Loss of transgene expression limits liver gene therapy in primates. Preprint at bioRxiv. <https://doi.org/10.1101/2022.03.24.485675>.
- Ordovás, L., Boon, R., Pistoni, M., Chen, Y., Wolfs, E., Guo, W., Sambathkumar, R., Bobis-Wozowicz, S., Helsen, N., Vanhove, J., et al. (2015). Efficient recombinase-mediated cassette exchange in hPSCs to study the hepatocyte lineage reveals AAVS1 locus-mediated transgene inhibition. *Stem Cell Rep.* *5*, 918–931.
- Zimak, J., Wagoner, Z.W., Nelson, N., Waechter, B., Schlosser, H., Kopecky, M., Wu, J., and Zhao, W. (2021). Epigenetic silencing directs

- expression heterogeneity of stably integrated multi-transcript unit genetic circuits. *Sci. Rep.* 11, 2424.
26. Fitzgerald, M., Livingston, M., Gibbs, C., and Deans, T.L. (2020). Rosa26 docking sites for investigating genetic circuit silencing in stem cells. *Synth. Biol. (Oxf)* 5, ysaa014. <https://doi.org/10.1093/synbio/ysaa014>.
 27. Lensch, S., Herschl, M.H., Ludwig, C.H., Sinha, J., Hinks, M.M., Mukund, A., Fujimori, T., and Bintu, L. (2021). Dynamic spreading of chromatin-mediated gene silencing and reactivation between neighboring genes in single cells. Preprint at bioRxiv. <https://doi.org/10.1101/2021.11.04.467237>.
 28. Babos, K.N., Galloway, K.E., Kisler, K., Zitting, M., Li, Y., Shi, Y., Quintino, B., Chow, R.H., Zlokovic, B.V., and Ichida, J.K. (2019). Mitigating antagonism between transcription and proliferation allows near-deterministic cellular reprogramming. *Cell Stem Cell* 25, 486–500.e9.
 29. Velychko, S., Adachi, K., Kim, K.P., Hou, Y., MacCarthy, C.M., Wu, G., and Schöler, H.R. (2019). Excluding Oct4 from Yamanaka cocktail unleashes the developmental potential of iPSCs. *Cell Stem Cell* 25, 737–753.e4.
 30. Okada, M., and Yoneda, Y. (2011). The timing of retroviral silencing correlates with the quality of induced pluripotent stem cell lines. *Biochim. Biophys. Acta* 1810, 226–235.
 31. Hu, X., Wu, Q., Zhang, J., Kim, J., Chen, X., Hartman, A.A., Eastman, A.E., Park, I.H., and Guo, S. (2021). Reprogramming progressive cells display low CAG promoter activity. *Stem Cells* 39, 43–54.
 32. Fernández-Tornero, C. (2018). RNA polymerase I activation and hibernation: unique mechanisms for unique genes. *Transcription* 9, 248–254.
 33. Lombardo, A., Cesana, D., Genovese, P., Di Stefano, B., Provasi, E., Colombo, D.F., Neri, M., Magnani, Z., Cantore, A., Lo Riso, P., et al. (2011). Site-specific integration and tailoring of cassette design for sustainable gene transfer. *Nat. Methods* 8, 861–869.
 34. Norrman, K., Fischer, Y., Bonnamy, B., Wolfhagen Sand, F., Ravassard, P., and Semb, H. (2010). Quantitative comparison of constitutive promoters in human ES cells. *PLOS One* 5, e12413.
 35. Pfaff, N., Lachmann, N., Ackermann, M., Kohlscheen, S., Brendel, C., Maetzig, T., Niemann, H., Antoniou, M.N., Grez, M., Schambach, A., et al. (2013). A ubiquitous chromatin opening element prevents transgene silencing in pluripotent stem cells and their differentiated progeny. *Stem Cells* 31, 488–499.
 36. Smith, E., and Shilatfard, A. (2010). The chromatin signaling pathway: diverse mechanisms of recruitment of histone-modifying enzymes and varied biological outcomes. *Mol. Cell* 40, 689–701.
 37. Urci, S., Lo, C.S.Y., Wheeler, D., and Taneja, N. (2021). R-loops and its chro-mates: the strange case of Dr. Jekyll and Mr. Hyde. *Int. J. Mol. Sci.* 22, 8850. <https://doi.org/10.3390/ijms22168850>.
 38. Reina, C., and Cavalieri, V. (2020). Epigenetic modulation of chromatin states and gene expression by G-quadruplex structures. *Int. J. Mol. Sci.* 21, 4172. <https://doi.org/10.3390/ijms21114172>.
 39. Rauschhuber, C., and Ehrhardt, A. (2012). RNA interference is responsible for reduction of transgene expression after Sleeping Beauty transposase mediated somatic integration. *PLOS One* 7, e35389.
 40. Davidovich, C., Zheng, L., Goodrich, K.J., and Cech, T.R. (2013). Promiscuous RNA binding by Polycomb repressive complex 2. *Nat. Struct. Mol. Biol.* 20, 1250–1257.
 41. Stewart-Morgan, K.R., Reverón-Gómez, N., and Groth, A. (2019). Transcription restart establishes chromatin accessibility after DNA replication. *Mol. Cell* 75, 408–414.
 42. Zopf, C.J., Quinn, K., Zeidman, J., and Maheshri, N. (2013). Cell-cycle dependence of transcription dominates noise in gene expression. *PLoS Comput. Biol.* 9, e1003161.
 43. Kotsantis, P., Silva, L.M., Irmischer, S., Jones, R.M., Folkes, L., Gromak, N., and Petermann, E. (2016). Increased global transcription activity as a mechanism of replication stress in cancer. *Nat. Commun.* 7, 13087.
 44. Keszthelyi, A., Minchell, N.E., and Baxter, J. (2016). The causes and consequences of topological stress during DNA replication. *Genes* 7, 134. <https://doi.org/10.3390/genes7120134>.
 45. Gan, W., Guan, Z., Liu, J., Gui, T., Shen, K., Manley, J.L., and Li, X. (2011). R-loop-mediated genomic instability is caused by impairment of replication fork progression. *Genes Dev.* 25, 2041–2056.
 46. Manzo, S.G., Hartono, S.R., Sanz, L.A., Marinello, J., De Biasi, S., Cos-sarizza, A., Capranico, G., and Chedin, F. (2018). DNA topoisomerase I differentially modulates R-loops across the human genome. *Genome Biol.* 19, 100.
 47. Guo, S., Zi, X., Schulz, V.P., Cheng, J., Zhong, M., Koochaki, S.H.J., Megyola, C.M., Pan, X., Heydari, K., Weissman, S.M., et al. (2014). Nonstochastic reprogramming from a privileged somatic cell state. *Cell* 156, 649–662.
 48. Bhagwan, J.R., Collins, E., Mosqueira, D., Bakar, M., Johnson, B.B., Thompson, A., Smith, J.G.W., and Denning, C. (2019). Variable expression and silencing of CRISPR-Cas9 targeted transgenes identifies the AAVS1 locus as not an entirely safe harbour. *F1000Res* 8, 1911.
 49. Beard, C., Hochedlinger, K., Plath, K., Wutz, A., and Jaenisch, R. (2006). Efficient method to generate single-copy transgenic mice by site-specific integration in embryonic stem cells. *Genesis* 44, 23–28.
 50. Haenebalcke, L., Goossens, S., Naessens, M., Kruse, N., Farhang Ghahremani, M., Bartunkova, S., Haigh, K., Pieters, T., Dierckx, P., Drogat, B., et al. (2013). Efficient ROSA26-based conditional and/or inducible transgenesis using RMCE-compatible F1 hybrid mouse embryonic stem cells. *Stem Cell Rev. Rep.* 9, 774–785.
 51. Pelascini, L.P.L., Janssen, J.M., and Gonçalves, M.A.F.V. (2013). Histone deacetylase inhibition activates transgene expression from integration-defective lentiviral vectors in dividing and non-dividing cells. *Hum. Gene Ther.* 24, 78–96.
 52. Lyko, F. (2018). The DNA methyltransferase family: a versatile toolkit for epigenetic regulation. *Nat. Rev. Genet.* 19, 81–92.
 53. Hughes, A.L., Kelley, J.R., and Klose, R.J. (2020). Understanding the interplay between CpG island-associated gene promoters and H3K4 methylation. *Biochim. Biophys. Acta Gene Regul. Mech.* 1863, 194567.
 54. Reik, W., Dean, W., and Walter, J. (2001). Epigenetic reprogramming in mammalian development. *Science* 293, 1089–1093.
 55. Auclair, G., Guibert, S., Bender, A., and Weber, M. (2014). Ontogeny of CpG island methylation and specificity of DNMT3 methyltransferases during embryonic development in the mouse. *Genome Biol.* 15, 545.
 56. Veland, N., Lu, Y., Hardikar, S., Gaddis, S., Zeng, Y., Liu, B., Estecio, M.R., Takata, Y., Lin, K., Tomida, M.W., et al. (2019). DNMT3L facilitates DNA methylation partly by maintaining DNMT3A stability in mouse embryonic stem cells. *Nucleic Acids Res.* 47, 152–167.
 57. Ooi, S.K.T., Qiu, C., Bernstein, E., Li, K., Jia, D., Yang, Z., Erdjument-Bromage, H., Tempst, P., Lin, S.-P., Allis, C.D., et al. (2007). DNMT3L connects unmethylated lysine 4 of histone H3 to de novo methylation of DNA. *Nature* 448, 714–717.
 58. Busslinger, M., Hurst, J., and Flavell, R.A. (1983). DNA methylation and the regulation of globin gene expression. *Cell* 34, 197–206.
 59. Kruczek, I., and Doerfler, W. (1983). Expression of the chloramphenicol acetyltransferase gene in mammalian cells under the control of adenovirus type 12 promoters: effect of promoter methylation on gene expression. *Proc. Natl. Acad. Sci. USA* 80, 7586–7590.
 60. Keshet, I., Yisraeli, J., and Cedar, H. (1985). Effect of regional DNA methylation on gene expression. *Proc. Natl. Acad. Sci. USA* 82, 2560–2564.
 61. Siegfried, Z., Eden, S., Mendelsohn, M., Feng, X., Tsuberi, B.Z., and Cedar, H. (1999). DNA methylation represses transcription in vivo. *Nat. Genet.* 22, 203–206.
 62. Rose, N.R., and Klose, R.J. (2014). Understanding the relationship between DNA methylation and histone lysine methylation. *Biochim. Biophys. Acta* 1839, 1362–1372.

63. Elgin, S.C.R., and Reuter, G. (2013). Position-effect variegation, heterochromatin formation, and gene silencing in *Drosophila*. *Cold Spring Harb. Perspect. Biol.* 5, a017780.
64. Richards, E.J., and Elgin, S.C.R. (2002). Epigenetic codes for heterochromatin formation and silencing: rounding up the usual suspects. *Cell* 108, 489–500.
65. Bird, A.P. (1986). CpG-rich islands and the function of DNA methylation. *Nature* 321, 209–213.
66. Weber, M., Hellmann, I., Stadler, M.B., Ramos, L., Pääbo, S., Rebhan, M., and Schübeler, D. (2007). Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. *Nat. Genet.* 39, 457–466.
67. Illingworth, R.S., Gruenewald-Schneider, U., Webb, S., Kerr, A.R.W., James, K.D., Turner, D.J., Smith, C., Harrison, D.J., Andrews, R., and Bird, A.P. (2010). Orphan CpG islands identify numerous conserved promoters in the mammalian genome. *PLoS Genet.* 6, e1001134.
68. Straussman, R., Nejman, D., Roberts, D., Steinfeld, I., Blum, B., Benvenisty, N., Simon, I., Yakhini, Z., and Cedar, H. (2009). Developmental programming of CpG island methylation profiles in the human genome. *Nat. Struct. Mol. Biol.* 16, 564–571.
69. Clouaire, T., Webb, S., Skene, P., Illingworth, R., Kerr, A., Andrews, R., Lee, J.-H., Skalnik, D., and Bird, A. (2012). Cfp1 integrates both CpG content and gene activity for accurate H3K4me3 deposition in embryonic stem cells. *Genes Dev.* 26, 1714–1728.
70. Thomson, J.P., Skene, P.J., Selfridge, J., Clouaire, T., Guy, J., Webb, S., Kerr, A.R.W., Deaton, A., Andrews, R., James, K.D., et al. (2010). CpG islands influence chromatin structure via the CpG-binding protein Cfp1. *Nature* 464, 1082–1086.
71. Wachter, E., Quante, T., Merusi, C., Arczewska, A., Stewart, F., Webb, S., and Bird, A. (2014). Synthetic CpG islands reveal DNA sequence determinants of chromatin structure. *eLife* 3, e03397.
72. Turker, M.S. (2002). Gene silencing in mammalian cells and the spread of DNA methylation. *Oncogene* 21, 5388–5393.
73. Lienert, F., Wirbelauer, C., Som, I., Dean, A., Mohn, F., and Schübeler, D. (2011). Identification of genetic elements that autonomously determine DNA methylation states. *Nat. Genet.* 43, 1091–1097.
74. Brandeis, M., Frank, D., Keshet, I., Siegfried, Z., Mendelsohn, M., Nemes, A., Temper, V., Razin, A., and Cedar, H. (1994). Sp1 elements protect a CpG island from de novo methylation. *Nature* 371, 435–438.
75. Saksouk, N., Simboeck, E., and Déjardin, J. (2015). Constitutive heterochromatin formation and transcription in mammals. *Epigenetics Chromatin* 8, 3.
76. Kouzarides, T. (2007). Chromatin modifications and their function. *Cell* 128, 693–705.
77. Yu, Y., Lowy, M.M., and Elble, R.C. (2016). Tet-On lentiviral transductants lose inducibility when silenced for extended intervals in mammary epithelial cells. *Metab. Eng. Commun.* 3, 64–67.
78. Cedar, H., and Bergman, Y. (2009). Linking DNA methylation and histone modification: patterns and paradigms. *Nat. Rev. Genet.* 10, 295–304.
79. Müller, M.M., Fierz, B., Bittova, L., Liszczak, G., and Muir, T.W. (2016). A two-state activation mechanism controls the histone methyltransferase Suv39h1. *Nat. Chem. Biol.* 12, 188–193.
80. Maison, C., Bailly, D., Quivy, J.-P., and Almouzni, G. (2016). The methyltransferase Suv39h1 links the SUMO pathway to HP1 α marking at pericentric heterochromatin. *Nat. Commun.* 7, 12224.
81. Maison, C., and Almouzni, G. (2004). HP1 and the dynamics of heterochromatin maintenance. *Nat. Rev. Mol. Cell Biol.* 5, 296–304.
82. Muller, H.J. (1930). Types of visible variations induced by X-rays in *Drosophila*. *J. Genet.* 22, 299–334.
83. Henikoff, S., and Dreesen, T.D. (1989). Trans-inactivation of the *Drosophila* brown gene: evidence for transcriptional repression and somatic pairing dependence. *Proc. Natl. Acad. Sci. USA* 86, 6704–6708.
84. Sun, F.-L., Haynes, K., Simpson, C.L., Lee, S.D., Collins, L., Wuller, J., Eissenberg, J.C., and Elgin, S.C.R. (2004). Cis-acting determinants of heterochromatin formation on *Drosophila melanogaster* chromosome four. *Mol. Cell. Biol.* 24, 8210–8220.
85. Haynes, K.A., Caudy, A.A., Collins, L., and Elgin, S.C.R. (2006). Element 1360 and RNAi components contribute to HP1-dependent silencing of a pericentric reporter. *Curr. Biol.* 16, 2222–2227.
86. Riddle, N.C., Leung, W., Haynes, K.A., Granok, H., Wuller, J., and Elgin, S.C.R. (2008). An investigation of heterochromatin domains on the fourth chromosome of *Drosophila melanogaster*. *Genetics* 178, 1177–1191.
87. Villaseñor, R., and Baubec, T. (2021). Regulatory mechanisms governing chromatin organization and function. *Curr. Opin. Cell Biol.* 70, 10–17.
88. Becker, J.S., Nicetto, D., and Zaret, K.S. (2016). H3K9me3-dependent heterochromatin: barrier to cell fate changes. *Trends Genet.* 32, 29–41.
89. Wang, F., Koyama, N., Nishida, H., Haraguchi, T., Reith, W., and Tsukamoto, T. (2006). The assembly and maintenance of heterochromatin initiated by transgene repeats are independent of the RNA interference pathway in mammalian cells. *Mol. Cell. Biol.* 26, 4028–4040.
90. Calero-Nieto, F.J., Bert, A.G., and Cockerill, P.N. (2010). Transcription-dependent silencing of inducible convergent transgenes in transgenic mice. *Epigenetics Chromatin* 3, 3.
91. Sabl, J.F., and Henikoff, S. (1996). Copy number and orientation determine the susceptibility of a gene to silencing by nearby heterochromatin in *Drosophila*. *Genetics* 142, 447–458.
92. Barrett, C.M., McCracken, R., Elmer, J., and Haynes, K.A. (2020). Components from the Human c-myc Transcriptional Regulation System Reactivate Epigenetically Repressed transgenes. *Int. J. Mol. Sci.* 21, 530. <https://doi.org/10.3390/ijms21020530>.
93. Tsai, S.Q., Zheng, Z., Nguyen, N.T., Liebers, M., Topkar, V.V., Thapar, V., Wyvekens, N., Khayter, C., Iafrate, A.J., Le, L.P., et al. (2015). GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. *Nat. Biotechnol.* 33, 187–197.
94. Szabo, Q., Bantignies, F., and Cavalli, G. (2019). Principles of genome folding into topologically associating domains. *Sci. Adv.* 5, eaaw1668.
95. Penagos-Puig, A., and Furlan-Magaril, M. (2020). Heterochromatin as an important driver of genome organization. *Front. Cell Dev. Biol.* 8, 579137.
96. Klatt, D., Cheng, E., Hoffmann, D., Santilli, G., Thrasher, A.J., Brendel, C., and Schambach, A. (2020). Differential transgene silencing of myeloid-specific promoters in the AAVS1 safe harbor locus of induced pluripotent stem cell-derived myeloid cells. *Hum. Gene Ther.* 31, 199–210.
97. Sadelain, M., Papapetrou, E.P., and Bushman, F.D. (2011). Safe harbours for the integration of new DNA in the human genome. *Nat. Rev. Cancer* 12, 51–58.
98. Ellis, J. (2005). Silencing and variegation of Gammaretrovirus and Lentivirus vectors. *Hum. Gene Ther.* 16, 1241–1246.
99. Chang, A.H., Stephan, M.T., and Sadelain, M. (2006). Stem cell-derived erythroid cells mediate long-term systemic protein delivery. *Nat. Biotechnol.* 24, 1017–1021.
100. Mok, H.P., Javed, S., and Lever, A. (2007). Stable gene expression occurs from a minority of integrated HIV-1-based vectors: transcriptional silencing is present in the majority. *Gene Ther.* 14, 741–751.
101. Herbst, F., Ball, C.R., Tuorto, F., Nowrouzi, A., Wang, W., Zavidij, O., Dieter, S.M., Fessler, S., van der Hoeven, F., Kloz, U., et al. (2012). Extensive methylation of promoter sequences silences lentiviral transgene expression during stem cell differentiation in vivo. *Mol. Ther.* 20, 1014–1021.
102. Challita, P.M., and Kohn, D.B. (1994). Lack of expression from a retroviral vector after transduction of murine hematopoietic stem cells is associated with methylation in vivo. *Proc. Natl. Acad. Sci. USA* 91, 2567–2571.
103. Pannell, D., Osborne, C.S., Yao, S., Sukonnik, T., Pasceri, P., Karaiskakis, A., Okano, M., Li, E., Lipshitz, H.D., and Ellis, J. (2000). Retrovirus vector silencing is de novo methylase independent and marked by a repressive histone code. *EMBO J.* 19, 5884–5894.

104. Suzuki, M.M., and Bird, A. (2008). DNA methylation landscapes: provocative insights from epigenomics. *Nat. Rev. Genet.* **9**, 465–476.
105. Berkhout, B. (1997). The primer binding site on the RNA genome of human and simian immunodeficiency viruses is flanked by an upstream hairpin structure. *Nucleic Acids Res.* **25**, 4013–4017.
106. Li, X., Mak, J., Arts, E.J., Gu, Z., Kleiman, L., Wainberg, M.A., and Paraniak, M.A. (1994). Effects of alterations of primer-binding site sequences on human immunodeficiency virus type 1 replication. *J. Virol.* **68**, 6198–6206.
107. Jähner, D., Stuhlmann, H., Stewart, C.L., Harbers, K., Löhler, J., Simon, I., and Jaenisch, R. (1982). De novo methylation and expression of retroviral genomes during mouse embryogenesis. *Nature* **298**, 623–628.
108. Gautsch, J.W., and Wilson, M.C. (1983). Delayed de novo methylation in teratocarcinoma suggests additional tissue-specific mechanisms for controlling gene expression. *Nature* **307**, 32–37.
109. Niwa, O., Yokota, Y., Ishida, H., and Sugahara, T. (1983). Independent mechanisms involved in suppression of the Moloney leukemia virus genome during differentiation of murine teratocarcinoma cells. *Cell* **32**, 1105–1113.
110. Wolf, D., and Goff, S.P. (2009). Embryonic stem cells use ZFP809 to silence retroviral DNAs. *Nature* **458**, 1201–1204.
111. Wolf, D., and Goff, S.P. (2007). TRIM28 mediates primer binding site-targeted silencing of murine leukemia virus in embryonic cells. *Cell* **131**, 46–57.
112. Schultz, D.C., Ayyanathan, K., Negorev, D., Maul, G.G., and Rauscher, F.J., 3rd (2002). SETDB1: a novel KAP-1-associated histone H3, lysine 9-specific methyltransferase that contributes to HP1-mediated silencing of euchromatic genes by KRAB zinc-finger proteins. *Genes Dev.* **16**, 919–932.
113. Matsui, T., Leung, D., Miyashita, H., Maksakova, I.A., Miyachi, H., Kimura, H., Tachibana, M., Lorincz, M.C., and Shinkai, Y. (2010). Proviral silencing in embryonic stem cells requires the histone methyltransferase ESET. *Nature* **464**, 927–931.
114. Schultz, D.C., Friedman, J.R., and Rauscher, F.J., 3rd (2001). Targeting histone deacetylase complexes via KRAB-zinc finger proteins: the PhD and bromodomains of KAP-1 form a cooperative unit that recruits a novel isoform of the Mi-2alpha subunit of NuRD. *Genes Dev.* **15**, 428–443.
115. Rowe, H.M., Jakobsson, J., Mesnard, D., Rougemont, J., Reynard, S., Aktas, T., Maillard, P.V., Layard-Liesching, H., Verp, S., Marquis, J., et al. (2010). KAP1 controls endogenous retroviruses in embryonic stem cells. *Nature* **463**, 237–240.
116. Wolf, G., Yang, P., Füchtbauer, A.C., Füchtbauer, E.-M., Silva, A.M., Park, C., Wu, W., Nielsen, A.L., Pedersen, F.S., and Macfarlan, T.S. (2015). The KRAB zinc finger protein ZFP809 is required to initiate epigenetic silencing of endogenous retroviruses. *Genes Dev.* **29**, 538–554.
117. Yang, B.X., El Farran, C.A., Guo, H.C., Yu, T., Fang, H.T., Wang, H.F., Schlesinger, S., Seah, Y.F.S., Goh, G.Y.L., Neo, S.P., et al. (2015). Systematic identification of factors for provirus silencing in embryonic stem cells. *Cell* **163**, 230–245.
118. Shalginskikh, N., Poleshko, A., Skalka, A.M., and Katz, R.A. (2013). Retroviral DNA methylation and epigenetic repression are mediated by the antiviral host protein Daxx. *J. Virol.* **87**, 2137–2150.
119. Rowe, H.M., Friedli, M., Offner, S., Verp, S., Mesnard, D., Marquis, J., Aktas, T., and Trono, D. (2013). De novo DNA methylation of endogenous retroviruses is shaped by KRAB-ZFPs/KAP1 and ESET. *Development* **140**, 519–529.
120. Akira, S., Uematsu, S., and Takeuchi, O. (2006). Pathogen recognition and innate immunity. *Cell* **124**, 783–801.
121. Chan, Y.K., and Gack, M.U. (2016). Viral evasion of intracellular DNA and RNA sensing. *Nat. Rev. Microbiol.* **14**, 360–373.
122. Hemmi, H., Takeuchi, O., Kawai, T., Kaisho, T., Sato, S., Sanjo, H., Matsumoto, M., Hoshino, K., Wagner, H., Takeda, K., et al. (2000). A toll-like receptor recognizes bacterial DNA. *Nature* **408**, 740–745.
123. Bauer, S., Kirschning, C.J., Häcker, H., Redecke, V., Hausmann, S., Akira, S., Wagner, H., and Lipford, G.B. (2001). Human TLR9 confers responsiveness to bacterial DNA via species-specific CpG motif recognition. *Proc. Natl. Acad. Sci. USA* **98**, 9237–9242.
124. Wang, C.-H., Naik, N.G., Liao, L.-L., Wei, S.-C., and Chao, Y.-C. (2017). Global screening of antiviral genes that suppress baculovirus transgene expression in mammalian cells. *Mol. Ther. Methods Clin. Dev.* **6**, 194–206.
125. Herold, M.J., van den Brandt, J., Seibler, J., and Reichardt, H.M. (2008). Inducible and reversible gene silencing by stable integration of an shRNA-encoding lentivirus in transgenic rats. *Proc. Natl. Acad. Sci. USA* **105**, 18507–18512.
126. Miettinen, M., Sareneva, T., Julkunen, I., and Matikainen, S. (2001). IFNs activate toll-like receptor gene expression in viral infections. *Genes Immun.* **2**, 349–355.
127. Belloni, L., Allweiss, L., Guerrieri, F., Pediconi, N., Volz, T., Pollicino, T., Petersen, J., Raimondo, G., Dandri, M., and Levrero, M. (2012). IFN- α inhibits HBV transcription and replication in cell culture and in humanized mice by targeting the epigenetic regulation of the nuclear cccDNA minichromosome. *J. Clin. Invest.* **122**, 529–537.
128. Qin, J.Y., Zhang, L., Clift, K.L., Huler, I., Xiang, A.P., Ren, B.-Z., and Lahn, B.T. (2010). Systematic comparison of constitutive promoters and the doxycycline-inducible promoter. *PLoS One* **5**, e10611.
129. Dou, Y., Lin, Y., Wang, T.-Y., Wang, X.-Y., Jia, Y.-L., and Zhao, C.-P. (2021). The CAG promoter maintains high-level transgene expression in HEK293 cells. *FEBS Open Bio* **11**, 95–104.
130. Hong, S., Hwang, D.-Y., Yoon, S., Isacson, O., Ramezani, A., Hawley, R.G., and Kim, K.-S. (2007). Functional analysis of various promoters in lentiviral vectors at different stages of in vitro differentiation of mouse embryonic stem cells. *Mol. Ther.* **15**, 1630–1639.
131. Chen, C.-M., Krohn, J., Bhattacharya, S., and Davies, B. (2011). A comparison of exogenous promoter activity at the ROSA26 locus using a Φ C31 integrase mediated cassette exchange approach in mouse ES cells. *PLoS One* **6**, e23376.
132. Malaguti, M., Portero Migueles, R., Annon, J., Sadurska, D., Blin, G., and Lowell, S. (2022). SynNPL: synthetic Notch pluripotent cell lines to monitor and manipulate cell interactions in vitro and in vivo. *Development* **149**, dev200226. <https://doi.org/10.1242/dev.200226>.
133. Zhu, P., Aller, M.I., Baron, U., Cambridge, S., Bausen, M., Herb, J., Sawinski, J., Cetin, A., Osten, P., Nelson, M.L., et al. (2007). Silencing and un-silencing of tetracycline-controlled genes in neurons. *PLoS One* **2**, e533.
134. DiAndrèth, B., Wauford, N., Hu, E., Palacios, S., and Weiss, R. (2022). PERSIST platform provides programmable RNA regulation using CRISPR endoRNases. *Nat. Commun.* **13**, 2582.
135. Bednarik, D.P., Cook, J.A., and Pitha, P.M. (1990). Inactivation of the HIV LTR by DNA CpG methylation: evidence for a role in latency. *EMBO J.* **9**, 1157–1164.
136. Garrison, B.S., Yant, S.R., Mikkelsen, J.G., and Kay, M.A. (2007). Postintegrative gene silencing within the Sleeping Beauty transposition system. *Mol. Cell. Biol.* **27**, 8824–8833.
137. Mutskov, V.J., Farrell, C.M., Wade, P.A., Wolffe, A.P., and Felsenfeld, G. (2002). The barrier function of an insulator couples high histone acetylation levels with specific protection of promoter DNA from methylation. *Genes Dev.* **16**, 1540–1554.
138. Zhao, H., and Dean, A. (2004). An insulator blocks spreading of histone acetylation and interferes with RNA polymerase II transfer between an enhancer and gene. *Nucleic Acids Res.* **32**, 4903–4919.
139. Stewart, C.L., Vanek, M., and Wagner, E.F. (1985). Expression of foreign genes into embryonic carcinoma cells by retrovirus infection: efficient expression from an internal promoter. *EMBO J.* **4**, 3701–3709.
140. Wagner, E.F., Vanek, M., and Vennström, B. (1985). Transfer of genes into embryonic carcinoma cells by retrovirus infection: efficient expression from an internal promoter. *EMBO J.* **4**, 663–666.

141. Stewart, C.L., Schuetz, S., Vanek, M., and Wagner, E.F. (1987). Expression of retroviral vectors in transgenic mice obtained by embryo infection. *EMBO J.* **6**, 383–388.
142. Rivière, I., Brose, K., and Mulligan, R.C. (1995). Effects of retroviral vector design on expression of human adenosine deaminase in murine bone marrow transplant recipients engrafted with genetically modified cells. *Proc. Natl. Acad. Sci. USA* **92**, 6733–6737.
143. Ede, C., Chen, X., Lin, M.-Y., and Chen, Y.Y. (2016). Quantitative analyses of core promoters enable precise engineering of regulated gene expression in mammalian cells. *ACS Synth. Biol.* **5**, 395–404.
144. Emery, D.W. (2011). The use of chromatin insulators to improve the expression and safety of integrating gene transfer vectors. *Hum. Gene Ther.* **22**, 761–774.
145. Chung, J.H., Whiteley, M., and Felsenfeld, G. (1993). A 5' element of the chicken beta-globin domain serves as an insulator in human erythroid cells and protects against position effect in *Drosophila*. *Cell* **74**, 505–514.
146. Rincón-Arano, H., Furlan-Magaril, M., and Recillas-Targa, F. (2007). Protection against telomeric position effects by the chicken *CHS4* beta-globin insulator. *Proc. Natl. Acad. Sci. USA* **104**, 14044–14049.
147. Girod, P.-A., Nguyen, D.-Q., Calabrese, D., Puttini, S., Grandjean, M., Martinet, D., Regamey, A., Saugy, D., Beckmann, J.S., Bucher, P., et al. (2007). Genome-wide prediction of matrix attachment regions that increase gene expression in mammalian cells. *Nat. Methods* **4**, 747–753.
148. Antoniou, M., Harland, L., Mustoe, T., Williams, S., Holdstock, J., Yague, E., Mulcahy, T., Griffiths, M., Edwards, S., Ioannou, P.A., et al. (2003). Transgenes encompassing dual-promoter CpG islands from the human TBP and HNRPA2B1 loci are resistant to heterochromatin-mediated silencing. *Genomics* **82**, 269–279.
149. Müller-Kuller, U., Ackermann, M., Kolodziej, S., Brendel, C., Fritsch, J., Lachmann, N., Kunkel, H., Lausen, J., Schambach, A., Moritz, T., et al. (2015). A minimal ubiquitous chromatin opening element (UCOE) effectively prevents silencing of juxtaposed heterologous promoters by epigenetic remodeling in multipotent and pluripotent stem cells. *Nucleic Acids Res.* **43**, 1577–1592.
150. Raab, J.R., Chiu, J., Zhu, J., Katzman, S., Kurukuti, S., Wade, P.A., Haussler, D., and Kamakaka, R.T. (2012). Human tRNA genes function as chromatin insulators. *EMBO J.* **31**, 330–350.
151. Barkess, G., and West, A.G. (2012). Chromatin insulator elements: establishing barriers to set heterochromatin boundaries. *Epigenomics* **4**, 67–80.
152. Guo, X., Wang, C., and Wang, T.-Y. (2020). Chromatin-modifying elements for recombinant protein production in mammalian cell systems. *Crit. Rev. Biotechnol.* **40**, 1035–1043.
153. Gaszner, M., and Felsenfeld, G. (2006). Insulators: exploiting transcriptional and epigenetic mechanisms. *Nat. Rev. Genet.* **7**, 703–713.
154. Raab, J.R., and Kamakaka, R.T. (2010). Insulators and promoters: closer than we think. *Nat. Rev. Genet.* **11**, 439–446.
155. Phillips-Cremins, J.E., and Corces, V.G. (2013). Chromatin insulators: linking genome organization to cellular function. *Mol. Cell* **50**, 461–474.
156. Kentepozidou, E., Aitken, S.J., Feig, C., Stefflova, K., Ibarra-Soria, X., Odom, D.T., Roller, M., and Flicek, P. (2020). Clustered CTCF binding is an evolutionary mechanism to maintain topologically associating domains. *Genome Biol.* **21**, 5.
157. Liu, M., Maurano, M.T., Wang, H., Qi, H., Song, C.-Z., Navas, P.A., Emery, D.W., Stamatoyannopoulos, J.A., and Stamatoyannopoulos, G. (2015). Genomic discovery of potent chromatin insulators for human gene therapy. *Nat. Biotechnol.* **33**, 198–203.
158. Cuddapah, S., Jothi, R., Schones, D.E., Roh, T.-Y., Cui, K., and Zhao, K. (2009). Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. *Genome Res.* **19**, 24–32.
159. Williams, S., Mustoe, T., Mulcahy, T., Griffiths, M., Simpson, D., Antoniou, M., Irvine, A., Mountain, A., and Crombie, R. (2005). CpG-island fragments from the HNRPA2B1/CBX3 genomic locus reduce silencing and enhance transgene expression from the hCMV promoter/enhancer in mammalian cells. *BMC Biotechnol.* **5**, 17.
160. Nielsen, T.T., Jakobsson, J., Rosenqvist, N., and Lundberg, C. (2009). Incorporating double copies of a chromatin insulator into lentiviral vectors results in less viral integrants. *BMC Biotechnol.* **9**, 13.
161. Urbinati, F., Arumugam, P., Higashimoto, T., Perumbeti, A., Mitts, K., Xia, P., and Malik, P. (2009). Mechanism of reduction in titers from lentivirus vectors carrying large inserts in the 3'LTR. *Mol. Ther.* **17**, 1527–1536.
162. Yi, Y., Noh, M.J., and Lee, K.H. (2011). Current advances in retroviral gene therapy. *Curr. Gene Ther.* **11**, 218–228.
163. Rudina, S.S., and Smolke, C.D. (2019). A novel chromatin-opening element for stable long-term transgene expression. Preprint at bioRxiv. <https://doi.org/10.1101/626713>.
164. Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H., Berry, C.C., Ecker, J.R., and Bushman, F.D. (2004). Retroviral DNA integration: ASLV, HIV, and MLV show distinct target site preferences. *PLoS Biol.* **2**, E234.
165. Liang, Q., Kong, J., Stalker, J., and Bradley, A. (2009). Chromosomal mobilization and reintegration of Sleeping Beauty and PiggyBac transposons. *Genesis* **47**, 404–408.
166. Akhtar, W., de Jong, J., Pindyurin, A.V., Pagie, L., Meuleman, W., de Ridder, J., Berns, A., Wessels, L.F.A., van Lohuizen, M., and van Steensel, B. (2013). Chromatin position effects assayed by thousands of reporters integrated in parallel. *Cell* **154**, 914–927.
167. Papapetrou, E.P., and Schambach, A. (2016). Gene insertion into genomic safe harbors for human gene therapy. *Mol. Ther.* **24**, 678–684.
168. Irion, S., Luche, H., Gadue, P., Fehling, H.J., Kennedy, M., and Keller, G. (2007). Identification and targeting of the ROSA26 locus in human embryonic stem cells. *Nat. Biotechnol.* **25**, 1477–1482.
169. Hong, S.G., Yada, R.C., Choi, K., Carpentier, A., Liang, T.J., Merling, R.K., Sweeney, C.L., Malech, H.L., Jung, M., Corat, M.A.F., et al. (2017). Rhesus iPSC safe harbor gene-editing platform for stable expression of transgenes in differentiated cells of all germ layers. *Mol. Ther.* **25**, 44–53.
170. Perez, E.E., Wang, J., Miller, J.C., Jouvenot, Y., Kim, K.A., Liu, O., Wang, N., Lee, G., Bartsevich, V.V., Lee, Y.-L., et al. (2008). Establishment of HIV-1 resistance in CD4+ T cells by genome editing using zinc-finger nucleases. *Nat. Biotechnol.* **26**, 808–816.
171. Chi, X., Zheng, Q., Jiang, R., Chen-Tsai, R.Y., and Kong, L.-J. (2019). A system for site-specific integration of transgenes in mammalian cells. *PLoS One* **14**, e0219842.
172. Tasic, B., Hippenmeyer, S., Wang, C., Gamboa, M., Zong, H., Chen-Tsai, Y., and Luo, L. (2011). Site-specific integrase-mediated transgenesis in mice via pronuclear injection. *Proc. Natl. Acad. Sci. USA* **108**, 7902–7907.
173. Aznauryan, E., Yermanos, A., Kinzina, E., Devaux, A., Kapetanovic, E., Milanova, D., Church, G.M., and Reddy, S.T. (2022). Discovery and validation of human genomic safe harbor sites for gene and cell therapies. *Cell Rep. Methods* **2**, 100154.
174. Zhang, M., Yang, C., Tasan, I., and Zhao, H. (2021). Expanding the potential of mammalian genome engineering via targeted DNA integration. *ACS Synth. Biol.* **10**, 429–446.
175. Jusiak, B., Jagtap, K., Gaidukov, L., Duportet, X., Bandara, K., Chu, J., Zhang, L., Weiss, R., and Lu, T.K. (2019). Comparison of integrases identifies Bxb1-GA mutant as the most efficient site-specific integrase system in mammalian cells. *ACS Synth. Biol.* **8**, 16–24.
176. Duportet, X., Wroblewska, L., Guye, P., Li, Y., Eyquem, J., Rieders, J., Rimchala, T., Batt, G., and Weiss, R. (2014). A platform for rapid prototyping of synthetic gene networks in mammalian cells. *Nucleic Acids Res.* **42**, 13440–13451.
177. Matreyek, K.A., Stephany, J.J., and Fowler, D.M. (2017). A platform for functional assessment of large variant libraries in mammalian cells. *Nucleic Acids Res.* **45**, e102.

178. Gaidukov, L., Wroblewska, L., Teague, B., Nelson, T., Zhang, X., Liu, Y., Jagtap, K., Mamo, S., Tseng, W.A., Lowe, A., et al. (2018). A multi-landing pad DNA integration platform for mammalian cell engineering. *Nucleic Acids Res.* 46, 4072–4086.
179. Ioannidi, E.I., Yarnall, M.T.N., Schmitt-Ulms, C., Krajeski, R.N., Lim, J., Villiger, L., Zhou, W., Jiang, K., Roberts, N., Zhang, L., et al. (2021). Drag-and-drop genome insertion without DNA cleavage with CRISPR-directed integrases. Preprint at bioRxiv. <https://doi.org/10.1101/2021.11.01.466786>.
180. Durrant, M.G., Fanton, A., Tycko, J., Hinks, M., Chandrasekaran, S.S., Perry, N.T., Schaepe, J., Du, P.P., Lotfy, P., Bassik, M.C., et al. (2021). Large-scale discovery of recombinases for integrating DNA into the human genome. Preprint at bioRxiv. <https://doi.org/10.1101/2021.11.05.467528>.
181. Karlsson, M., Zhang, C., Méar, L., Zhong, W., Digre, A., Katona, B., Sjöstedt, E., Butler, L., Odeberg, J., Dusart, P., et al. (2021). A single-cell type transcriptomics map of human tissues. *Sci. Adv.* 7, eabh2169. <https://doi.org/10.1126/sciadv.abh2169>.
182. ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. *Nature* 489, 57–74.
183. Moore, T.V., Scurti, G.M., DeJong, M., Wang, S.-Y., Dalheim, A.V., Wagner, C.R., Hutchens, K.A., Speiser, J.J., Godellas, C.V., Fountain, C., et al. (2021). HDAC inhibition prevents transgene expression downregulation and loss-of-function in T-cell-receptor-transduced T cells. *Mol. Ther. Oncolytics* 20, 352–363.
184. Peinado, P., Andrades, A., Cuadros, M., Rodriguez, M.I., Coira, I.F., Garcia, D.J., Álvarez-Perez, J.C., Baliñas-Gavira, C., Arenas, A.M., Patiño-Mercau, J.R., et al. (2020). Comprehensive analysis of SWI/SNF inactivation in lung adenocarcinoma cell models. *Cancers* 12, 3712. <https://doi.org/10.3390/cancers12123712>.
185. Decristofaro, M.F., Betz, B.L., Rorie, C.J., Reisman, D.N., Wang, W., and Weissman, B.E. (2001). Characterization of SWI/SNF protein expression in human breast cancer cell lines and other malignancies. *J. Cell. Physiol.* 186, 136–145.
186. Karimi, M.M., Goyal, P., Maksakova, I.A., Bilenky, M., Leung, D., Tang, J.X., Shinkai, Y., Mager, D.L., Jones, S., Hirst, M., et al. (2011). DNA methylation and SETDB1/H3K9me3 regulate predominantly distinct sets of genes, retroelements, and chimeric transcripts in mESCs. *Cell Stem Cell* 8, 676–687.
187. Schorn, A.J., Gutbrod, M.J., LeBlanc, C., and Martienssen, R. (2017). LTR-retrotransposon control by tRNA-derived small RNAs. *Cell* 170, 61–71.e11.
188. Boroviak, T., Loos, R., Bertone, P., Smith, A., and Nichols, J. (2014). The ability of inner-cell-mass cells to self-renew as embryonic stem cells is acquired following epiblast specification. *Nat. Cell Biol.* 16, 516–528.
189. Kalkan, T., Olova, N., Roode, M., Mulas, C., Lee, H.J., Nett, I., Marks, H., Walker, R., Stunnenberg, H.G., Lilley, K.S., et al. (2017). Tracking the embryonic stem cell transition from ground state pluripotency. *Development* 144, 1221–1234.
190. Athanasiadou, R., de Sousa, D., Myant, K., Merusi, C., Stancheva, I., and Bird, A. (2010). Targeting of de novo DNA methylation throughout the Oct-4 gene regulatory region in differentiating embryonic stem cells. *PLoS One* 5, e9937.
191. Soriano, P. (1999). Generalized lacZ expression with the ROSA26 Cre reporter strain. *Nat. Genet.* 21, 70–71.
192. Hao, J.-W., Wang, J., Guo, H., Zhao, Y.-Y., Sun, H.-H., Li, Y.-F., Lai, X.-Y., Zhao, N., Wang, X., Xie, C., et al. (2020). CD36 facilitates fatty acid uptake by dynamic palmitoylation-regulated endocytosis. *Nat. Commun.* 11, 4765.
193. Manning, B.D., and Cantley, L.C. (2007). AKT/PKB signaling: navigating downstream. *Cell* 129, 1261–1274.
194. DeBose-Boyd, R.A., and Ye, J. (2018). SREBPs in lipid metabolism, insulin signaling, and beyond. *Trends Biochem. Sci.* 43, 358–368.
195. Zhang, M., Galdieri, L., and Vancura, A. (2013). The yeast AMPK homolog SNF1 regulates acetyl coenzyme A homeostasis and histone acetylation. *Mol. Cell. Biol.* 33, 4701–4717.
196. Galdieri, L., and Vancura, A. (2012). Acetyl-CoA carboxylase regulates global histone acetylation. *J. Biol. Chem.* 287, 23865–23876.
197. Koundouros, N., and Pouligiannis, G. (2020). Reprogramming of fatty acid metabolism in cancer. *Br. J. Cancer* 122, 4–22.
198. Micallef, P., Wu, Y., Bauzá-Thorbrügge, M., Chanclón, B., Vujčić, M., Peris, E., Ek, C.J., and Wernstedt Asterholm, I. (2021). Adipose tissue-breast cancer crosstalk leads to increased tumor lipogenesis associated with enhanced tumor growth. *Int. J. Mol. Sci.* 22, 11881. <https://doi.org/10.3390/ijms222111881>.
199. Nickel, A., Blücher, C., Kadri, O.A., Schwagarus, N., Müller, S., Schaab, M., Thiery, J., Burkhardt, R., and Stadler, S.C. (2018). Adipocytes induce distinct gene expression profiles in mammary tumor cells and enhance inflammatory signaling in invasive breast cancer cells. *Sci. Rep.* 8, 9482.
200. Zhang, D., Tang, Z., Huang, H., Zhou, G., Cui, C., Weng, Y., Liu, W., Kim, S., Lee, S., Perez-Neut, M., et al. (2019). Metabolic regulation of gene expression by histone lactylation. *Nature* 574, 575–580.
201. Yu, J., Chai, P., Xie, M., Ge, S., Ruan, J., Fan, X., and Jia, R. (2021). Histone lactylation drives oncogenesis by facilitating m6A reader protein YTHDF2 expression in ocular melanoma. *Genome Biol.* 22, 85.
202. Torres, M., Altamirano, C., and Dickson, A.J. (2018). Process and metabolic engineering perspectives of lactate production in mammalian cell cultures. *Curr. Opin. Chem. Eng.* 22, 184–190.
203. Janke, R., Iavarone, A.T., and Rine, J. (2017). Oncometabolite D-2-hydroxyglutarate enhances gene silencing through inhibition of specific H3K36 histone demethylases. *eLife* 6, e22451. <https://doi.org/10.7554/eLife.22451>.
204. Dekker, J., Belmont, A.S., Guttman, M., Leshyk, V.O., Lis, J.T., Lomvardas, S., Mirny, L.A., O’Shea, C.C., Park, P.J., Ren, B., et al. (2017). The 4D nucleome project. *Nature* 549, 219–226.
205. Regev, A., Teichmann, S.A., Lander, E.S., Amit, I., Benoist, C., Birney, E., Bodenmiller, B., Campbell, P., Carninci, P., Clatworthy, M., et al. (2017). Science forum: the human cell atlas. *Elife* 6, e27041.
206. FANTOM Consortium and the RIKEN PMI and CLST (DGT), Forrest, A.R.R., Kawaji, H., Rehli, M., Baillie, J.K., de Hoon, M.J.L., Haberle, V., Lassmann, T., Kulakovskiy, I.V., Lizio, M., et al. (2014). A promoter-level mammalian expression atlas. *Nature* 507, 462–470.
207. Zúñiga, R.A., Gutiérrez-González, M., Collazo, N., Sotelo, P.H., Ribeiro, C.H., Altamirano, C., Lorenzo, C., Aguillón, J.C., and Molina, M.C. (2019). Development of a new promoter to avoid the silencing of genes in the production of recombinant antibodies in Chinese hamster ovary cells. *J. Biol. Eng.* 13, 59.
208. Dull, T., Zufferey, R., Kelly, M., Mandel, R.J., Nguyen, M., Trono, D., and Naldini, L. (1998). A third-generation lentivirus vector with a conditional packaging system. *J. Virol.* 72, 8463–8471.
209. Wang, D., Tai, P.W.L., and Gao, G. (2019). Adeno-associated virus vector as a platform for gene therapy delivery. *Nat. Rev. Drug Discov.* 18, 358–378.
210. Wolf, G., Greenberg, D., and Macfarlan, T.S. (2015). Spotting the enemy within: targeted silencing of foreign DNA in mammalian genomes by the Krüppel-associated box zinc finger protein family. *Mobile DNA* 6, 17.
211. Liu, H., Wang, J., He, T., Becker, S., Zhang, G., Li, D., and Ma, X. (2018). Butyrate: A double-edged sword for health? *Adv. Nutr.* 9, 21–29.
212. Prasad, K.N., and Sinha, P.K. (1976). Effect of sodium butyrate on mammalian cells in culture: a review. *In Vitro* 12, 125–132.
213. Shalem, O., Sanjana, N.E., Hartenian, E., Shi, X., Scott, D.A., Mikkelsen, T., Heckl, D., Ebert, B.L., Root, D.E., Doench, J.G., et al. (2014). Genome-scale CRISPR-Cas9 knockout screening in human cells. *Science* 343, 84–87.

214. Li, B., Clohisey, S.M., Chia, B.S., Wang, B., Cui, A., Eisenhaure, T., Schweitzer, L.D., Hoover, P., Parkinson, N.J., Nachshon, A., et al. (2020). Genome-wide CRISPR screen identifies host dependency factors for influenza A virus infection. *Nat. Commun.* **11**, 164.
215. Yang, J., Rajan, S.S., Friedrich, M.J., Lan, G., Zou, X., Ponstingl, H., Garayfallo, D.A., Liu, P., Bradley, A., and Metzakopian, E. (2019). Genome-scale CRISPRa screen identifies novel factors for cellular reprogramming. *Stem Cell Rep.* **12**, 757–771.
216. Chung, S., Quarmby, V., Gao, X., Ying, Y., Lin, L., Reed, C., Fong, C., Lau, W., Qiu, Z.J., Shen, A., et al. (2012). Quantitative evaluation of fucose reducing effects in a humanized antibody on Fc γ receptor binding and antibody-dependent cell-mediated cytotoxicity activities. *mAbs* **4**, 326–340.
217. Grav, L.M., la Cour Karottki, K.J., Lee, J.S., and Kildegaard, H.F. (2017). Application of CRISPR/Cas9 genome editing to improve recombinant protein production in CHO cells. *Methods Mol. Biol.* **1603**, 101–118.
218. Martínez, M.A. (2009). Progress in the therapeutic applications of siRNAs against HIV-1. *Methods Mol. Biol.* **487**, 343–368.
219. Decout, A., Katz, J.D., Venkatraman, S., and Ablasser, A. (2021). The cGAS-STING pathway as a therapeutic target in inflammatory diseases. *Nat. Rev. Immunol.* **21**, 548–569.
220. Vanhille, L., Griffon, A., Maqbool, M.A., Zacarias-Cabeza, J., Dao, L.T.M., Fernandez, N., Ballester, B., Andrau, J.C., and Spicuglia, S. (2015). High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. *Nat. Commun.* **6**, 6905.
221. Sheng, T., Ho, S.W.T., Ooi, W.F., Xu, C., Xing, M., Padmanabhan, N., Huang, K.K., Ma, L., Ray, M., Guo, Y.A., et al. (2021). Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. *Genome Med.* **13**, 158.
222. Murtha, M., Tokcaer-Keskin, Z., Tang, Z., Strino, F., Chen, X., Wang, Y., Xi, X., Basilico, C., Brown, S., Bonneau, R., et al. (2014). FIREWACH: high-throughput functional detection of transcriptional regulatory modules in mammalian cells. *Nat. Methods* **11**, 559–565.
223. Babbitt, C.C., Markstein, M., and Gray, J.M. (2015). Recent advances in functional assays of transcriptional enhancers. *Genomics* **106**, 137–139.
224. Andersson, R., and Sandelin, A. (2020). Determinants of enhancer and promoter activities of regulatory elements. *Nat. Rev. Genet.* **21**, 71–87.
225. Gierman, H.J., Indemans, M.H.G., Koster, J., Goetze, S., Seppen, J., Geerts, D., van Driel, R., and Versteeg, R. (2007). Domain-wide regulation of gene expression in the human genome. *Genome Res.* **17**, 1286–1295.
226. Inoue, F., Kircher, M., Martin, B., Cooper, G.M., Witten, D.M., McManus, M.T., Ahituv, N., and Shendure, J. (2017). A systematic comparison reveals substantial differences in chromosomal versus episomal encoding of enhancer activity. *Genome Res.* **27**, 38–52.
227. Kheradpour, P., Ernst, J., Melnikov, A., Rogov, P., Wang, L., Zhang, X., Alston, J., Mikkelsen, T.S., and Kellis, M. (2013). Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. *Genome Res.* **23**, 800–811.
228. Weingarten-Gabbay, S., Nir, R., Lubliner, S., Sharon, E., Kalma, Y., Weinberger, A., and Segal, E. (2019). Systematic interrogation of human promoters. *Genome Res.* **29**, 171–183.
229. Hong, C.K.Y., and Cohen, B.A. (2022). Genomic environments scale the activities of diverse core promoters. *Genome Res.* **32**, 85–96.
230. Yaguchi, M., Ohashi, Y., Tsubota, T., Sato, A., Koyano, K.W., Wang, N., and Miyashita, Y. (2013). Characterization of the properties of seven promoters in the motor cortex of rats and monkeys after lentiviral vector-mediated gene transfer. *Hum. Gene Ther. Methods* **24**, 333–344.
231. Hagedorn, C., Antoniou, M.N., and Lipps, H.J. (2013). Genomic cis-acting Sequences Improve Expression and Establishment of a Nonviral Vector. *Mol. Ther. Nucleic Acids* **2**, e118.
232. Allweiss, L., and Dandri, M. (2017). The role of cccDNA in HBV maintenance. *Viruses* **9**, 156. <https://doi.org/10.3390/v9060156>.
233. Guo, X., Chen, P., Hou, X., Xu, W., Wang, D., Wang, T.Y., Zhang, L., Zheng, G., Gao, Z.-L., He, C.-Y., et al. (2016). The recombinant cccDNA produced using minicircle technology mimicked HBV genome in structure and function closely. *Sci. Rep.* **6**, 25552.
234. Li, F., and Ding, S.-W. (2006). Virus counterdefense: diverse strategies for evading the RNA-silencing immunity. *Annu. Rev. Microbiol.* **60**, 503–531.
235. Naso, M.F., Tomkowicz, B., Perry, W.L., 3rd, and Strohl, W.R. (2017). Adeno-associated virus (AAV) as a vector for gene therapy. *BioDrugs* **31**, 317–334.
236. Jacobson, S.G., Cideciyan, A.V., Roman, A.J., Sumaroka, A., Schwartz, S.B., Heon, E., and Hauswirth, W.W. (2015). Improvement and decline in vision with gene therapy in childhood blindness. *N. Engl. J. Med.* **372**, 1920–1926.
237. Bainbridge, J.W.B., Mehat, M.S., Sundaram, V., Robbie, S.J., Barker, S.E., Ripamonti, C., Georgiadis, A., Mowat, F.M., Beattie, S.G., Gardner, P.J., et al. (2015). Long-term effect of gene therapy on Leber’s congenital amaurosis. *N. Engl. J. Med.* **372**, 1887–1897.
238. Hurlbut, G.D., Ziegler, R.J., Nietupski, J.B., Foley, J.W., Woodworth, L.A., Meyers, E., Bercury, S.D., Pande, N.N., Souza, D.W., Bree, M.P., et al. (2010). Preexisting immunity and low expression in primates highlight translational challenges for liver-directed AAV8-mediated gene therapy. *Mol. Ther.* **18**, 1983–1994.
239. Nakai, H., Iwaki, Y., Kay, M.A., and Couto, L.B. (1999). Isolation of recombinant adeno-associated virus vector-cellular DNA junctions from mouse liver. *J. Virol.* **73**, 5438–5447.
240. Nakai, H., Montini, E., Fuess, S., Storm, T.A., Grompe, M., and Kay, M.A. (2003). AAV serotype 2 vectors preferentially integrate into active genes in mice. *Nat. Genet.* **34**, 297–302.
241. Miller, D.G., Trobridge, G.D., Petek, L.M., Jacobs, M.A., Kaul, R., and Russell, D.W. (2005). Large-scale analysis of adeno-associated virus vector integration sites in normal human cells. *J. Virol.* **79**, 11434–11442.
242. Ngo, A.M., and Puschnik, A.S. (2022). Genome-scale analysis of cellular restriction factors that inhibit transgene expression from adeno-associated virus vectors. Preprint at bioRxiv. <https://doi.org/10.1101/2022.07.13.499963>.
243. Smith-Moore, S., Neil, S.J.D., Fraefel, C., Linden, R.M., Bollen, M., Rowe, H.M., and Henckaerts, E. (2018). Adeno-associated virus Rep proteins antagonize phosphatase PP1 to counteract KAP1 repression of the latent viral genome. *Proc. Natl. Acad. Sci. USA* **115**, E3529–E3538.
244. Das, A., Vijayan, M., Walton, E.M., Stafford, V.G., Fiflis, D.N., and Asokan, A. (2022). Epigenetic silencing of recombinant adeno-associated virus genomes by NP220 and the HUSH complex. *J. Virol.* **96**, e0203921.
245. Kazuki, Y., and Oshimura, M. (2011). Human artificial chromosomes for gene delivery and the development of animal models. *Mol. Ther.* **19**, 1591–1601.
246. Harrington, J.J., Van Bokkelen, G., Mays, R.W., Gustashaw, K., and Willard, H.F. (1997). Formation of de novo centromeres and construction of first-generation human artificial microchromosomes. *Nat. Genet.* **15**, 345–355.
247. Kouprina, N., Earnshaw, W.C., Masumoto, H., and Larionov, V. (2013). A new generation of human artificial chromosomes for functional genomics and gene therapy. *Cell. Mol. Life Sci.* **70**, 1135–1148.
248. Kazuki, Y., Uno, N., Abe, S., Kajitani, N., Kazuki, K., Yakura, Y., Sawada, C., Takata, S., Sugawara, M., Nagashima, Y., et al. (2021). Engineering of human induced pluripotent stem cells via human artificial chromosome vectors for cell therapy and disease modeling. *Mol. Ther. Nucleic Acids* **23**, 629–639.
249. Pardi, M.L., Wu, J., Kawasaki, S., and Saito, H. (2022). Synthetic RNA-based post-transcriptional expression control methods and genetic circuits. *Adv. Drug Deliv. Rev.* **184**, 114196.
250. Kawasaki, S., Ono, H., Hirokawa, M., Kuwabara, T., and Saito, H. (2021). Programmable mammalian translational modulators by CRISPR-associated proteins. <https://doi.org/10.1101/2021.09.17.460758>.

251. Zhao, E.M., Mao, A.S., de Puig, H., Zhang, K., Tippens, N.D., Tan, X., Ran, F.A., Han, I., Nguyen, P.Q., Chory, E.J., et al. (2022). RNA-responsive elements for eukaryotic translational control. *Nat. Biotechnol.* **40**, 539–545.
252. Gao, X.J., Chong, L.S., Kim, M.S., and Elowitz, M.B. (2018). Programmable protein circuits in living cells. *Science* **361**, 1252–1258.
253. Chen, Z., Linton, J.M., Zhu, R., and Elowitz, M.B. (2022). A synthetic protein-level neural network in mammalian cells. Preprint at bioRxiv. <https://doi.org/10.1101/2022.07.10.499405>.
254. Fink, T., Lonžarić, J., Praznik, A., Plaper, T., Merljak, E., Leben, K., Jerala, N., Lebar, T., Strmšek, Ž., Lapenta, F., et al. (2019). Design of fast proteolysis-based signaling and logic circuits in mammalian cells. *Nat. Chem. Biol.* **15**, 115–122.
255. Thakore, P.I., Black, J.B., Hilton, I.B., and Gersbach, C.A. (2016). Editing the epigenome: technologies for programmable transcription and epigenetic modulation. *Nat. Methods* **13**, 127–137.
256. Brocken, D.J.W., Tark-Dame, M., and Dame, R.T. (2018). dCas9: a Versatile Tool for Epigenome Editing. *Curr. Issues Mol. Biol.* **26**, 15–32.
257. Waryah, C.B., Moses, C., Arooj, M., and Blancafort, P. (2018). Zinc fingers, TALEs, and CRISPR systems: A comparison of tools for epigenome editing. *Methods Mol. Biol.* **1767**, 19–63.
258. Kearns, N.A., Pham, H., Tabak, B., Genga, R.M., Silverstein, N.J., Garber, M., and Maehr, R. (2015). Functional annotation of native enhancers with a Cas9-histone demethylase fusion. *Nat. Methods* **12**, 401–403.
259. Hilton, I.B., D'Ippolito, A.M., Vockley, C.M., Thakore, P.I., Crawford, G.E., Reddy, T.E., and Gersbach, C.A. (2015). Epigenome editing by a CRISPR-Cas9-based acetyltransferase activates genes from promoters and enhancers. *Nat. Biotechnol.* **33**, 510–517.
260. Bruno, S., Williams, R.J., and Del Vecchio, D. (2022). Epigenetic cell memory: the gene's inner chromatin modification circuit. *PLoS Comput. Biol.* **18**, e1009961. <https://doi.org/10.1101/2022.02.02.476953>.
261. Bruno, S., Williams, R.J., and Del Vecchio, D. (2022). Epigenetic cell memory: the gene's inner chromatin modification circuit. *PLoS Comput. Biol.* **18**, e1009961.
262. Tekel, S.J., Vargas, D.A., Song, L., LaBaer, J., Caplan, M.R., and Haynes, K.A. (2018). Tandem histone-binding domains enhance the activity of a synthetic chromatin effector. *ACS Synth. Biol.* **7**, 842–852.
263. Nyer, D.B., Daer, R.M., Vargas, D., Hom, C., and Haynes, K.A. (2017). Regulation of cancer epigenomes with a histone-binding synthetic transcription factor. *NPJ Genom. Med.* **2**, 1. <https://doi.org/10.1038/s41525-016-0002-3>.