**Review Article**

*When Long Noncoding RNAs Meet Genome Editing in Pluripotent Stem Cells*

Fuquan Chen,1,2 Jiaojiao Ji,1,2 Jian Shen,1,2 and Xinyi Lu1,2

1State Key Laboratory of Medicinal Chemical Biology, Nankai University, Tianjin 300371, China
2College of Pharmacy, Nankai University, Tianjin 300350, China

Correspondence should be addressed to Xinyi Lu; luxy@nankai.edu.cn

Received 30 August 2017; Accepted 25 October 2017; Published 23 November 2017

Academic Editor: Qiang Wu

Copyright © 2017 Fuquan Chen et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Most of the human genome can be transcribed into RNAs, but only a minority of these regions produce protein-coding mRNAs whereas the remaining regions are transcribed into noncoding RNAs. Long noncoding RNAs (lncRNAs) were known for their influential regulatory roles in multiple biological processes such as imprinting, dosage compensation, transcriptional regulation, and splicing. The physiological functions of protein-coding genes have been extensively characterized through genome editing in pluripotent stem cells (PSCs) in the past 30 years; however, the study of lncRNAs with genome editing technologies only came into attentions in recent years. Here, we summarize recent advancements in dissecting the roles of lncRNAs with genome editing technologies in PSCs and highlight potential genome editing tools useful for examining the functions of lncRNAs in PSCs.

1. **Introduction: Discovery of lncRNAs Expressed in Pluripotent Stem Cells**

Pluripotent stem cells (PSCs) can unlimitedly self-renew and differentiate into specialized cell types of all three germ layers. Therefore, they have been used as an important *in vitro* model system for studying early development and generating an *in vivo* genome-edited animal model to analyze the physiological functions of a gene. Furthermore, they were used as a cell source for regenerative medicine to treat macular degeneration recently [1]. The two most frequently used types of PSCs are embryonic stem cells (ESCs), which are derived from inner cell mass of blastocyst, and induced pluripotent stem cells (iPSCs), which are established from somatic cells through reprogramming.

Long noncoding RNAs (lncRNAs) are >200 bp long RNA transcripts that lack coding capacity. Most of lncRNAs have evolved rapidly during evolution while a minority of lncRNAs are conserved through species [2]. The rapid evolution of lncRNAs could be partially explained by the presence of transposable elements in lncRNAs, since TEs are major contributors of lncRNA origination and diversification [3]. In the past two decades, expression arrays were first applied to identify novel lncRNAs [4–6]. Later, ENCODE Project Consortium and FANTOM Consortium used a high-throughput sequencing (HTS) method to identify novel transcripts from a genome [7, 8]. Currently, there are ~87,774 lncRNAs discovered in mouse cells and ~96,308 lncRNAs in human cells according to the NONCODE database [9]. Databases of lncRNAs have been established to catalogue novel lncRNAs and their functions (Table 1) [10, 11]. Given the importance of PSCs, further cataloguing of lncRNAs is essential for us to understand the complex regulatory network in PSCs. With the advancement of HTS technologies, ChIP-seq experiments revealed histone modifications as markers of gene transcription units. H3K4me3 was found to be a marker of promoter whereas H3K36me3 marked the gene body [12–14]. Therefore, H3K4me3 in combination with H3K36me3 could define the location of a transcribed gene [15]. With the application of histone marks to recognize discrete transcriptional units between protein-coding genes, the first genome-wide discovery of long intergenic noncoding RNAs (lincRNAs) was carried out in four cell types including embryonic stem cells (ESCs) [15]. The same study found that core pluripotency regulators Oct4, Sox2, and Nanog have driven the expression of lincRNAs, which in
| Name | Date | Species | Function | Website | Ref. |
|------|------|---------|----------|---------|------|
| Comprehensive annotations of IncRNAs | | | | | |
| NONCODE | 2005 | 17 species | Gene function annotation | http://www.noncode.org/ | [9] |
| IncRNAdb | 2011 | 68 species | Comprehensive annotations of functional IncRNAs | http://www.lncrnadb.org/ | [29] |
| IncRNNome | 2013 | Human | Integrating annotations on a wide variety of biologically significant information | http://genome.igib.res.in/IncRNNome/ | [30] |
| IncRNAnytor | 2014 | 6 species | Functional investigation of IncRNAs | http://lncrnator.ewha.ac.kr/ | [31] |
| LncRNAWiki | 2015 | Human | Comprehensive integration of information on human IncRNAs | http://lncrna.big.ac.cn | [32] |
| Annotation of IncRNA interactions | | | | | |
| LNCipedia | 2013 | Human | Annotation of IncRNA transcript sequences and structures | https://www.lncipedia.org | [33] |
| Linc2GO | 2013 | Human | IncRNA function annotation based on ceRNA hypothesis | – | [34] |
| Starbase | 2014 | Human, mouse, and *C. elegans* | Annotation of miRNA-IncRNA/mRNA interactions | – | [35] |
| NPIinter | 2014 | 18 species | Interactions between ncRNAs and biomolecules | http://www.bioinfo.org/NPIinter | [36] |
| LncACTdb | 2015 | Human | IncRNA-miRNA-gene interactions | – | [37] |
| Transcriptional regulatory networks of IncRNAs | | | | | |
| ChIPBase | 2013 | 6 species | Transcriptional regulatory networks of ncRNAs and PCGs | – | [38] |
| SNP@lncTFBS | 2014 | Human | Annotation of SNPs in potential TFRs of IncRNAs | http://bioinfo.hrbmu.edu.cn/SNP_lncTFBS | [39] |
| TF2lncRNA | 2014 | Human | Identifying common transcription factors of IncRNAs | – | [40] |
| IncRNA-associtated pathways | | | | | |
| LncReg | 2015 | Human and mouse | IncRNA-associated regulatory networks | http://bioinformatics.ustc.edu.cn/LncReg/ | [41] |
| Co-LncRNA | 2015 | Human | Investigating the IncRNA combinatorial effects in GO annotations and KEGG pathways | http://www.bio-bigdata.com/Co-LncRNA/ LncReg/ | [42] |
| IncRNA-disease associations | | | | | |
| C-It-Loci | 2015 | Human, mouse, and zebrafish | Tissue-specific IncRNAs | http://c-it-loci.uni-frankfurt.de | [43] |
| LncRNADisease | 2013 | Human | IncRNA-disease associations | – | [44] |
| lnCaNet | 2016 | Human | IncRNA-cancer gene coexpression network | http://lncanet.bioinfo-minzhao.org/ | [45] |
| Lnc2Cancer | 2016 | Human | Exploring IncRNA deregulation in various cancers | http://www.bio-bigdata.net/lnc2cancer | [46] |
Table 2: Classification of lncRNA functional mechanisms and the location of lncRNAs.

| Mechanism of function                        | Examples         | Ref. |
|----------------------------------------------|------------------|------|
| Nucleus                                      |                  |      |
| Regulating chromatin-modifying complexes     | ANRIL            | [47] |
|                                              | HOTAIR           | [48] |
|                                              | HERVH            | [17] |
| Recruiting transcription factors             | PWR1             | [49] |
|                                              | TUNA             | [50] |
|                                              | HOTTIP           | [51] |
| Chromatin remodeling                         | SRG1             | [52] |
|                                              | fbp1 ncRNA       | [53] |
| Influencing pre-mRNA splicing                |                  |      |
|                                              | MALAT1           | [18] |
| Cytoplasm                                    |                  |      |
|                                              | Linc-RoR         | [55] |
| Regulating mRNA stability                    | Gadd7            | [56] |
|                                              | MEG3             | [57] |
|                                              | lincRNA-p21      | [19] |
| Regulating mRNA translation                  | Antisense        | [58] |
|                                              | Uchl1            | [59] |
| Competing for microRNA binding               | HULC             | [60] |
| Translated in biologically active small peptides | LINC00961       | [61] |

2. Knockout IncRNAs in PSCs

The general strategy to study IncRNAs in PSCs is RNA interference (RNAi) mediated by short hairpin RNA (shRNA) or small interference RNA (siRNA). However, RNAi is unsuitable for a loss-of-function study of many IncRNAs. For instance, IncRNAs whose molecular functions are independent of the transcript, that is, the function of these IncRNAs, are from the transcription itself and not from the product of transcription. In addition, some IncRNAs, such as MALAT1, are highly abundant in the nucleus, so RNAi is inefficient in the depletion of these transcripts [62]. To study the physiological relevance of IncRNAs, their knockouts in ESCs or embryos are required to produce homozygous knockout animals. Therefore, it is critical to use genome editing for the loss-of-function study of IncRNAs in these cases to achieve the cleanest depletion of their expression.

2.1. Potential Challenges in the Generation of IncRNA Knockouts. Molecular scissors have been used to create point mutations in the critical domains of protein-coding genes and in turn induce an early termination of translation to knock out a gene. Different from protein-coding genes, the functional domains of transcripts are still unclear for most IncRNAs; therefore, it is impossible to study IncRNAs by loss-of-function point mutagenesis. Thus, to knock out an IncRNA, complete or partial deletion of the IncRNA gene is required. To avoid indirect influences from IncRNA knockout, we need to manipulate IncRNA genomic loci without affecting the genomic features of other genes. However, under some circumstances, this is difficult to achieve. For IncRNAs that are located at the promoter region of other genes or overlap with exons of protein-coding genes (Figures 1(a) and 1(b)), partial deletion of them by genome editing should only be applied under the circumstances that the expression of other genes remains unaffected. For IncRNAs within the intron of the protein-coding gene, the deletion of IncRNA genes without disturbing the splicing of the intron region is required (Figure 1(c)). The IncRNAs at the intergenic region (Figure 1(d)), which are distant from other genes, could be easily removed by genome editing technology in a similar manner with protein-coding genes. However, intergenic IncRNA loci which overlap with enhancers (Figure 1(e)), such as enhancer RNAs, are also difficult to study with genome editing, because the deletion of these loci may interfere with the functions of enhancers and affect the expression of distant genes [63]. Therefore, in this section, we will discuss the knockouts of intergenic IncRNAs that do not overlap with enhancers.

2.2. Deletion of the IncRNA Gene. Whole-gene ablation of IncRNAs is a classic way to learn their functions (Figure 2(a)). Initial work on IncRNA knockouts was done in mouse ESCs but not in human ESCs, because of its early establishment and ease to be manipulated by homologous recombination [64]. ESCs have been used as a model to study imprinting, which occurs during ESC differentiation [65]. One of the first IncRNAs that have been identified and knocked out in mouse ESCs is the IncRNA H19. The homologous recombination-mediated deletion of maternal H19 and its flanking sequences resulted in the expression activation of the imprinting gene Igf2, whereas the deletion of the paternal copy of H19 has no impact on Igf2 expression [66], suggesting H19 as a lncRNA regulating maternal Igf2...
imprinting. The lncRNA *Terc*, a 397 bp RNA component of the telomerase complex, is another primary example of lncRNA knockout [67–69]. Ablation of the *Terc* lncRNA gene resulted in telomere shortening, which subsequently affected chromosome stability and proliferation of mouse ESCs [70, 71]. To improve the gene targeting efficiency, molecular scissors were introduced to engineer lncRNAs in PSCs. ZFNs were used in combination with homologous recombination to delete the highly expressed lncRNA *MALAT1* in mouse ESCs. From *MALAT1*-knockout ESCs, homozygous *MALAT1*-deleted mice have been generated [62]. TALEN was also used to knock out lncRNAs in zebrafish [72]. With the emergence of the CRISPR/gRNA system, the efficiency of genome editing is higher than before. It was demonstrated that double gRNAs could be applied to efficiently knock out lncRNAs in human cell lines [73]. Using the CRISPR/gRNA system, a full-length lncRNA (*HPAT5*) was successfully knocked out in human ESCs for the first time [59]. Recently, it is possible to delete the whole *H19* transcription unit and imprinting control region (ICR) by the CRISPR/Cas9 system in ESCs [74, 75]. This successfully restored *Ig2* expression and faithfully improved the efficiency to generate viable mice from androgenetic zygote and haploid ESCs [74, 75]. These studies demonstrate the complete deletion of lncRNAs through genome editing as an efficient way to discover lncRNA function in ESCs and during differentiation.

Certain lncRNAs are extremely long, so it is difficult to delete a full-length lncRNA gene. In these cases, partial deletion of the lncRNA gene through homologous recombination can be applied for the loss-of-function study (Figure 2(b)). The lncRNA *Xist*, discovered in the last century, was knocked out in this strategy. *Xist*, an ~18 kb lncRNA located on the X chromosome, functions as a central regulator of gene dosage compensation during ESC differentiation [76, 77]. Homologous recombination strategy was employed to delete part (~7 kb) of *Xist* in mouse ESCs [78], but the knockout efficiency is extremely low. More than 2500 clones were screened to identify a single homozygous knockout clone. Through this approach, *Xist* was found to be required for complete X chromosome inactivation during ESC differentiation [76, 77]. Heterogeneous knockout of *Xist* revealed a critical role of *Xist* for female embryo development [79]. Partial deletion of lncRNAs could also facilitate us to determine the function of RNA domains in lncRNAs. Through homologous recombination-mediated knockout in ESCs, an 890 bp region of the imprinting-related lncRNA *KCNQ1OT1* was found to be essential for *KCNQ1OT1* to recruit Dnmt1 protein to paternal differentially methylated regions [80, 81]. With the appearance of genome editing technology, megabase-scale genetic deletions with ZFN [82], TALEN [83, 84], or CRISPR [85] are achievable. The power of CRISPR technology in generating knockout of lncRNAs was demonstrated by the deletion of the lncRNA *Rian* in ESCs. A pair of sgRNAs in combination with CRISPR could delete 23 kb of the 57 kb *Rian* through zygote injection [86]. In addition, the knockout efficiency reached 33% if multiple sgRNAs were used [86].

![Figure 1: Location of lncRNAs on a human or mouse genome.](image)

(a) The lncRNA gene overlaps with the promoter of the protein-coding gene. (b) The lncRNA gene overlaps with exons of the protein-coding gene. (c) The lncRNA gene overlaps with the intron of the protein-coding gene. (d) The lncRNA gene is located between protein-coding genes. (e) lncRNAs, such as enhancer RNA, overlap with the enhancer region.
technology advancement may facilitate us to delete full-length extremely large lncRNAs in PSCs.

With the discovery of more lncRNAs and further understanding of lncRNAs’ functions, the homologous recombination-based knockout of lncRNAs has been more extensively applied to delete lncRNAs in PSCs. In one of the studies, 18 lncRNA genes were knocked out in mouse ESCs to produce lncRNA-knockout mice [87]. The replacement of the lncRNA locus with the \( \text{lacZ} \) reporter allowed the visualization of the temporal and spatial expression pattern of these lncRNAs in animal models. Another similar study created knockout ESC lines for 20 lncRNAs through gene targeting and used these ESCs to create knockout mice for studying the broad roles of lncRNAs in mice [88]. These lncRNA-knockout mice constitute valuable complements to the resource for studying the physiological roles of lncRNAs.

2.3. Knocking In Polyadenylation Signal. Another strategy to prevent lncRNA transcript production is the knockin of polyadenylation (polyA) signal at the transcription start site (TSS) (Figure 2(d)). Biallelic insertion of one copy or multiple copies of polyA signal at the beginning of lncRNA gene TSS will cause early termination of transcription and the subsequent failure of lncRNA production [89]. However, for lncRNAs with alternative promoters and transcription TSS, this strategy may not be applicable. This strategy was employed in ESCs to characterize the functions of the lncRNA \( \text{Fendrr} \) in embryo development [90, 91]. PolyA insertion-mediated \( \text{Fendrr} \) knockout led to malfunctioned heart and embryonic death by E13.75 in mice, while overexpression of \( \text{Fendrr} \) through BAC rescued the phenotype. Moreover, this method prevents lncRNA production without disturbing the transcription activity itself. Hence, this approach allows the distinguishing of the function of the

![Figure 2: Application of the lncRNA knockout in PSCs. The lncRNA gene knockout can be done through (a) knocking out the whole lncRNA gene from the genome, (b) knocking out part of the lncRNA gene, (c) knocking out the lncRNA promoter region, and (d) inserting poly(A) signal (pA) after the transcription start site. (e) Application of genome editing to study lncRNA functions in ESCs. (f) Application of genome editing in ESC to generate lncRNA-knockout mice.](image-url)
IncRNA itself from that of its genomic transcription activity. This is exemplified by the case of the imprinting IncRNA Airn. The Airn gene overlaps with Igf2r promoter regions and is transcribed in the opposite direction of Igf2r [92]. The Airn gene spans more than 100 kb of the mouse genome and encodes multiple spliced isoforms [92]. Expression of Airn on paternal allele represses the paternal expression of Igf2r, Slc22a3, and Scl22a2 during ESC differentiation [92, 93]. Surprisingly, truncation of Airn by insertion of polyA signals after TSS did not affect Igf2r gene expression [94]. In addition, the overlapped transcription at the Airn promoter region is sufficient to repress Igf2r after ESC differentiation [94]. Furthermore, the Airn gene is very large (>100 kb) and may be difficult to knock out. This study also demonstrates that polyA signal could be a more efficient way to prevent expression of macro IncRNA genes than whole-gene deletion.

2.4. Deletion of the IncRNA Promoter. Promoters of IncRNAs are critical to drive their expression. For intergenic IncRNAs, another strategy to disrupt their expression relied on the removal of the IncRNA promoter by genome editing (Figure 2(c)). With two gRNAs expressed simultaneously, the promoter of IncRNAs could be efficiently deleted to achieve silencing of IncRNA expression [95]. One example is from the classic IncRNA H19, whose knockout allows the derivation of bimaternal mice [96, 97]. Similar to H19 knock-out, deletion of DMRs of IncRNAs H19 and Gtl2 in haploid ESCs by CRISPR represses H19 and Gtl2 expression and allows the generation of semicolonized mice from haploid ESCs [16]. These suggest the deletion of the IncRNA promoter region as an efficient approach to silence IncRNA expression in PSCs.

2.5. Combination of Different IncRNA Knockout Methods. The above examples show that a single approach is insufficient to identify the all possible functions of IncRNAs. Multiple genome editing strategies need to be taken in order to discover the functions of IncRNAs and their transcription locus in PSCs. This is well demonstrated in the study of Haunt IncRNAs in ESCs. Yin et al. found that siRNA mediated Haunt IncRNA depletion and deleting a small fraction of the Haunt gene caused a consistent further increment in HOXA expression upon retinoic acid- (RA-) induced ESC differentiation [63]. However, large deletions of the Haunt gene ranging from 7.3 kb to 58 kb caused an opposite effect. Disruption of Haunt expression by CRISPR/ Cas9-mediated knockout of 2.3 kb of the Haunt promoter region or insertion of 4x polyA signal after transcription start sites also leads to enhanced activation of HOXa cluster genes after ESC differentiation. These observations demonstrate distinct roles of IncRNAs and their corresponding genomic loci in regulating RA-induced HOXA expression. Moreover, this study also implicates that the role of IncRNAs should be examined in different aspects and multiple approaches to reveal the functions of the IncRNA gene locus and its transcripts in PSCs (Figures 2(e) and 2(f)).

3. IncRNA Reporter Gene in PSCs

Creation of the IncRNA reporter gene in PSCs allows us to track IncRNA expression in vivo and study the regulation of IncRNAs. In order to create reporter genes of IncRNAs, the differences between IncRNAs and protein-coding genes have to be considered. Unlike protein-coding genes, IncRNAs do not encode proteins. For this reason, it is impossible to make fluorescent fusion proteins through addition of self-cleaving 2A peptide or introduction of internal ribosome entry sites (IRES) to create the IncRNA reporter gene. The addition of protein-coding gene sequences to IncRNAs may interfere the localization and function of IncRNAs, whereas the inclusion of IRES sequence may lead to the recruitment of ribosomes to IncRNAs and conversion of IncRNAs to mRNAs. Therefore, the creation of IncRNA promoter-driven reporters requires genome editing of IncRNAs by knocking in the IncRNA locus or introducing an independently expressed transgene to the genome (Figures 3(a) and 3(b)). However, knocking in the reporter gene to the IncRNA locus will destroy one copy of the IncRNA gene and affect the expression of neighboring genes if the IncRNA acts in cis. Introduction of the IncRNA promoter-driven transgenic reporter may not reflect the true expression pattern of IncRNAs because the usage of enhancers and silencers is different at distinct genomic loci. All these situations need to be considered prior to the establishment of the IncRNA reporter PSC cell line.

The earliest application of the IncRNA reporter in PSCs is to express foreign genes at the IncRNA transcription locus. A primary instance is the Rosa26 locus, which is used to constitutively overexpress genes for ~20 years. The Rosa26 locus was first discovered in 1991 during gene trapping in ESCs [98]. Later, it was found to encode two nuclear transcripts with no significant open reading frames (ORFs), suggesting them as IncRNAs [99]. Interrupting this locus with the proviral beta geo reporter gene led to ubiquitous expression of beta-galactosidase, suggesting that the Rosa26 locus encodes universally expressed IncRNAs in mice [99]. Since then, the Rosa26 locus has been used as a genetic safe harbor for gene knockin to achieve ubiquitous transgene expression [100, 101] (Figure 3(c)). Nowadays, the human Rosa26 locus was also discovered, and numerous genes have been knocked in the Rosa26 locus in ESCs to generate knockin mice and study the function of these genes [101, 102].

IncRNAs are involved in the essential gene regulatory processes during development. The reporter system of IncRNAs is also used to monitor the regulatory status of important biological processes in ESCs and during differentiation. One instance is using the paternal H19 reporter gene to monitor imprinting status during ESC differentiation. Since H19 expression is essential to maternal imprinting, to avoid the interruption of the H19 gene, the transgene carrying H19 promoter-driven lacZ and PLAP was used as the reporter to reflect the change of imprinting status [103] (Figure 3(d)). Using this reporter system, 1.1 kb control element was discovered to regulate maternal H19 imprinting [103]. A recent example of the application of the IncRNA reporter is to isolate naive human ESCs. Endogenous
retrovirus HERVH was discovered as ESC-specific lncRNAs that regulate pluripotency [17]. The HERVH promoter (LTR7Y) is active only in cells from inner cell mass of blastocyst. Thus, the transgenic LTR7Y-driven GFP reporter can be used for the isolation of naive-state human ESCs [104] (Figure 3(e)). It was also found that the reporter gene driven by the promoter of the HERVH-derived lncRNA ESRG marked naive human ESCs [105] (Figure 3(e)). All preceding examples demonstrate the power of lncRNA reporter genes in studying the regulation of lncRNAs and tracking their expression.

4. Activation and Repression of lncRNAs with Genome Editing Technologies

Since CRISPR/Cas9-based genome editing technology could efficiently delete large fragments of the genome [86], it has been utilized to perform genome-wide screening of lncRNA functions [106]. Multiple gRNAs were used against one single IncRNA to accomplish efficient ablation of the lncRNA gene expression; therefore, the paired gRNA library could only target a few hundreds of lncRNAs [106]. Using this approach, lncRNAs critical to cancer cell survival have been identified. An alternative approach to modulate lncRNAs with CRISPR-Cas9 is through CRISPR interference (CRISPRi) [107], which is constituted of deactivated Cas9 (dCas9) fused with transcription repressors, such as KRAB. Through the recruitment of dCas9-KRAB to the promoter regions of lncRNAs with multiple gRNAs, the expression of lncRNAs is hindered by the transcription repressors recruited by KRAB protein (Figure 4(a)). CRISPRi was applied to manipulate lncRNA (GAS5, H19, MALAT1, NEAT1, TERC, and XIST) expression in K562 cells [108]. In addition to these lncRNAs, CRISPRi was applied to probe the function of the cheRNA HIDALGO in K562 and H1 human ESCs [109]. This was adapted at a genome-wide scale to perform lncRNA repression screen in various cell types including human induced pluripotent stem cells (iPSCs) [110]. In this way, a number of lncRNAs were discovered as self-renewal regulators of human iPSCs [110]. The efficiency of genome editing is regulated by the epigenetic status of chromatin, such as chromatin conformation. The genome editing efficiency with TALEN and CRISPR is higher for genes at euchromatin than at heterochromatin [111]. This may introduce bias to genome-scale CRISPR-mediated screening of gene expression regulators.

Modified CRISPR is applicable not only for depleting gene expression but also for activating gene expression. CRISPR activation (CRISPRa), which utilizes dCas9 fused with multiple copies of strong viral transcription activators such as VP16, activates gene expression by bringing RNA polymerase II to TSS [107, 112]. This method can be adopted to activate IncRNA expression in ESCs (Figure 4(b)). Traditionally, in terms of the gain-of-function study of lncRNAs,
plasmid- or transgene-based overexpression of lncRNAs was used. However, different from protein-coding genes, some lncRNAs function during transcription, that is, the production of transcript [63, 94]. Therefore, exogenous expression of lncRNAs may not reflect the genuine function of lncRNAs. In addition, multiple isoforms are present for some lncRNAs [94]. It is difficult to overexpress all isoforms at the same time. What is more, for some lncRNAs that lack polyA tail or are derived from introns [113], it is important to clone the fraction longer than its expression region. Moreover, for the lncRNA acting in cis, introduction of the lncRNA transgene to other genomic locations for overexpression cannot reflect the true function of lncRNAs. Above difficulties in lncRNA overexpression could be conquered by the usage of CRISPRa to activate the lncRNA. Recently, Joung’s group applied CRISPRa in a genome-wide scale to identify lncRNAs that render melanoma cells’ drug resistance to vemurafenib [114]. CRISPRa directly activates the expression of endogenous genes from their genomic locus [107], and therefore, it keeps the function of the lncRNA transcriptional region and makes the simultaneous activation of multiple lncRNA isoforms possible. These methods could be applied to PSCs for the gain-of-function study of the lncRNA regulators of pluripotency maintenance.

5. Other Potential Applications of Genome Editing Tools in Studying lncRNAs in PSCs

CRISPR/Cas9 is a versatile tool for genome editing and expression regulation. Besides its applications in editing the genetic locus in ESCs, CRISPR/Cas9 can be adopted to investigate other aspects of lncRNA biology in ESCs. A number of nuclear lncRNAs may act by interacting with chromosomes to regulate gene expression [115, 116]. The inhibition of expression of these lncRNAs by CRISPR/Cas9-mediated truncation of their promoters will cause downregulation of neighboring genes’ expression [109, 117]. To study the role of these lncRNAs, a valuable tool, named CRISPR-Display, was developed to deliver an lncRNA-protein complex to DNA loci [118]. Functional RNA domains can be inserted into gRNAs, allowing the identification of the direct effect of ectopically targeting lncRNAs on chromatin (Figure 4(c)). In addition, this system can be multiplexed to investigate the influences of recruitment of lncRNAs on...
several genomic loci simultaneously. Moreover, it was recently discovered that the CRISPR system could be edited to interact with cellular RNAs. Cas9 directly binds or cuts RNAs in the assistance of DNA PAMmers [119]. This enables the cleavage of RNA or pulldown of mRNA through RNA-RNA hybridization by Cas9-gRNA [119]. It can be used to cleave IncRNAs with Cas9 or pull down IncRNAs with dCas9 in ESCs to analyze the potential interacting proteins of IncRNAs (Figures 4(d) and 4(e)). With this system, dCas9 fused with GFP is targeted to mRNAs to track their localization in live cells with the guidance of sgRNA [120]. This system can also be adopted to study IncRNA position in PSCs and track IncRNA localization in live PSCs (Figure 4(f)).

6. Conclusions and Perspectives

In the recent years, thousands of lncRNAs have been identified. Several of them were shown to play important roles in PSCs [116]. However, the advancements in genome editing technologies are just starting to be widely applied in PSCs [116]. The establishment of the lncRNA reporter of RNA or pulldown of mRNA through RNA-RNA hybridization by Cas9-gRNA [119]. It can be used to distinguish the functions of the lncRNA transcript(s), multiple genome editing approaches should be applied to distinguish the functions of the IncRNA transcript and its gene locus in PSCs. IncRNAs are important biomarkers in embryo development and disease progression. The establishment of the IncRNA reporter in vivo will enable the monitoring of these processes. The development of emerging CRISPR genome editing technologies opens new gates to IncRNA biology in PSCs. Future studies should adopt these novel strategies to probe the functions of lncRNAs in PSCs. These genome editing tools should also be exploited to explore physiological functions of lncRNAs in a systematic scope.

Conflicts of Interest

The authors declare that there is no conflict of interest present for this study.

Acknowledgments

This work is supported by grants from the Natural Science Foundation of Tianjin City (15JCZDJC65600) and National Science Foundation of China (31671352) and funding from the National Thousand Young Talents Program and Nankai University.

References

[1] M. Mandai, A. Watanabe, Y. Kurimoto et al., “Autologous induced stem-cell–derived retinal cells for macular degeneration,” The New England Journal of Medicine, vol. 376, no. 11, pp. 1038–1046, 2017.

[2] A. Necselea, M. Soumillon, M. Warnefors et al., “The evolution of IncRNA repertoires and expression patterns in tetrapods,” Nature, vol. 505, no. 7485, pp. 635–640, 2014.

[3] A. Kapusta, Z. Kronenberg, V. J. Lynch et al., “Transposable elements are major contributors to the origin, diversification, and regulation of vertebrate long noncoding RNAs,” PLoS Genetics, vol. 9, no. 4, article e1003470, 2013.

[4] P. Bertone, V. Stoc, T. E. Royce et al., “Global identification of human transcribed sequences with genome tiling arrays,” Science, vol. 306, no. 5705, pp. 2242–2246, 2004.

[5] P. Kapranov, S. E. Cawley, J. Drenkow et al., “Large-scale transcriptional activity in chromosomes 21 and 22,” Science, vol. 296, no. 5569, pp. 916–919, 2002.

[6] P. Kapranov, J. Cheng, S. Dike et al., “RNA maps reveal new RNA classes and a possible function for pervasive transcription,” Science, vol. 316, no. 5830, pp. 1484–1488, 2007.

[7] P. Carminci, T. Kasukawa, S. Katayama et al., “The transcriptional landscape of the mammalian genome,” Science, vol. 309, no. 5740, pp. 1559–1563, 2005.

[8] E. Birney, J. A. Stamatoyannopoulos, A. Dutta et al., “Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project,” Nature, vol. 447, no. 7146, pp. 799–816, 2007.

[9] C. Liu, B. Bai, G. Skogerbo et al., “NONCODE: an integrated knowledge database of non-coding RNAs,” Nucleic Acids Research, vol. 33, Database issue, pp. D112–D115, 2005.

[10] C. C. Hon, J. A. Ramlowski, J. Harshbarger et al., “An atlas of human long non-coding RNAs with accurate 5′ ends,” Nature, vol. 543, no. 7644, pp. 199–204, 2017.

[11] G. Bussotti, T. Leonardi, M. B. Clark et al., “Improved definition of the mouse transcriptome via targeted RNA sequenc- ing,” Genome Research, vol. 26, no. 5, pp. 705–716, 2016.

[12] G. Liang, J. C. Y. Lin, V. Wei et al., “Distinct localization of histone H3 acetylation and H3-K4 methylation to the transcription start sites in the human genome,” Proceedings of the National Academy of Sciences of the United States of America, vol. 101, no. 19, pp. 7357–7362, 2004.

[13] M. G. Guenther, S. S. Levine, L. A. Boyer, R. Jaenisch, and R. A. Young, “A chromatin landmark and transcription initiation at most promoters in human cells,” Cell, vol. 130, no. 1, pp. 77–88, 2007.

[14] T. S. Mikkelsen, M. Ku, D. B. Jaffe et al., “Genome-wide maps of chromatin state in pluripotent and lineage-committed cells,” Nature, vol. 448, no. 7153, pp. 553–560, 2007.

[15] M. Guttmann, I. Amit, M. Garber et al., “Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals,” Nature, vol. 458, no. 7235, pp. 223–227, 2009.

[16] C. Zhong, Q. Yin, Z. Xie et al., “CRISPR-Cas9-mediated genetic screening in mice with haploid embryonic stem cells carrying a guide RNA library,” Cell Stem Cell, vol. 17, no. 2, pp. 221–232, 2015.

[17] X. Lu, F. Sachs, L. A. Ramsay et al., “The retrovirus HERVH is a long noncoding RNA required for human embryonic stem cell identity,” Nature Structural & Molecular Biology, vol. 21, no. 4, pp. 423–425, 2014.

[18] V. Tripathi, J. D. Ellis, Z. Shen et al., “The nuclear-retained noncoding RNA MALAT1 regulates alternative splicing by modulating SR splicing factor phosphorylation,” Molecular Cell, vol. 39, no. 6, pp. 925–938, 2010.

[19] J. H. Yoon, K. Abdelmohsen, S. Srikantan et al., “LincRNA-pp21 suppresses target mRNA translation,” Molecular Cell, vol. 47, no. 4, pp. 648–655, 2012.

[20] T. P. Zwaka and J. A. Thomson, “Homologous recombination in human embryonic stem cells,” Nature Biotechnology, vol. 21, no. 3, pp. 319–321, 2003.
[21] A. Giudice and A. Trounson, “Genetic modification of human embryonic stem cells for derivation of target cells,” *Cell Stem Cell*, vol. 2, no. 5, pp. 422–433, 2008.
[22] D. Hockemeyer and R. Jaenisch, “Induced pluripotent stem cells meet genome editing,” *Cell Stem Cell*, vol. 18, no. 5, pp. 573–586, 2016.
[23] A. Hotta and S. Yamanaka, “From genomics to gene therapy: induced pluripotent stem cells meet genome editing,” *Annual Review of Genetics*, vol. 49, no. 1, pp. 47–70, 2015.
[24] S. Alwin, M. B. Gere, E. Guhl et al., “Custom zinc-finger nucleases for use in human cells,” *Molecular Therapy*, vol. 12, no. 4, pp. 610–617, 2005.
[25] J. C. Miller, S. Tan, G. Qiao et al., “A TALE nuclease architecture for efficient genome editing,” *Nature Biotechnology*, vol. 29, no. 2, pp. 143–148, 2011.
[26] F. Zhang, L. Cong, S. Lodato, S. Kosuri, G. M. Church, and M. Jinek, K. Chylinski, I. Fonfara, M. Hauer, J. A. Doudna, “A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity,” *Science*, vol. 337, no. 6096, pp. 816–821, 2012.
[27] L. Ma, A. Li, D. Zou et al., “TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChiP-Seq data,” *BioMed Research International*, vol. 2014, Article ID 317642, 5 pages, 2014.
[28] J. H. Yang, J. H. Li, S. Jiang, H. Zhou, and L. H. Qu, “ChIP-Base: a database for decoding the transcriptional regulation of long non-coding RNA and microRNA genes from ChiP-Seq data,” *Nucleic Acids Research*, vol. 41, no. D1, pp. D177–D187, 2013.
[29] S. Ning, Z. Zhao, J. Ye et al., “SNP@lincTFBS: an integrated database of polymorphisms in human LincRNA transcription factor binding sites,” *PLoS One*, vol. 9, no. 7, article e103851, 2014.
[30] Q. Jiang, J. Wang, Y. Wang, R. Ma, X. Wu, and Y. Li, “TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChiP-Seq data,” *BioMed Research International*, vol. 2014, Article ID 317642, 5 pages, 2014.
[31] Z. Zhou, Y. Shen, M. R. Khan, and A. Li, “lncReg: a reference resource for lncRNA-associated regulatory networks,” *Database*, vol. 2015, article ba083, 2015.
[32] Z. Zhao, J. Bai, A. Wu et al., “Co-LncRNA: investigating the lncRNA combinatorial effects in GO annotations and KEGG pathways based on human RNA-Seq data,” *Database*, vol. 2015, article ba082, 2015.
[33] T. Weirick, D. John, S. Dimmeler, and S. Uchida, “C-It-Loci: a knowledge database for tissue-enriched loci,” *Bioinformatics*, vol. 31, no. 21, pp. 3537–3543, 2015.
[34] G. Chen, Z. Wang, D. Wang et al., “LncRNA Disease: a database for long non-coding RNA-associated diseases,” *Nucleic Acids Research*, vol. 41, no. D1, pp. D983–D986, 2013.
[35] Y. Liu and M. Zhao, “InCaNet: pan-cancer co-expression network for human IncRNA and cancer genes,” *Bioinformatics*, vol. 32, no. 10, pp. 1595–1597, 2016.
[36] S. Ning, J. Zhang, P. Wang et al., “Lnc2Cancer: a manually curated database of experimentally supported lncRNAs associated with various human cancers,” *Nucleic Acids Research*, vol. 44, no. D1, pp. D980–D985, 2016.
[37] K. L. Yap, S. Li, A. M. Muñoz-Cabello et al., “Molecular interplay of the noncoding RNA ANRIL and methylated histone H3 lysine 27 by polycomb CBX7 in transcriptional silencing of INK4a,” *Molecular Cell*, vol. 38, no. 5, pp. 662–674, 2010.
[38] J. L. Rinn, M. Kertesz, J. K. Wang et al., “Functional demarcation of active and silent chromatin domains in human HOX loci by noncoding RNAs,” *Cell*, vol. 129, no. 7, pp. 1311–1323, 2007.
[39] S. L. Bumgarner, G. Neuert, B. F. Voight et al., “Single-cell analysis reveals that noncoding RNAs contribute to clonal heterogeneity by modulating transcription factor recruitment,” *Molecular Cell*, vol. 45, no. 4, pp. 470–482, 2012.
[40] N. Lin, K. Y. Chang, Z. Li et al., “An evolutionarily conserved long noncoding RNA TUNA controls pluripotency and neural lineage commitment,” *Molecular Cell*, vol. 53, no. 6, pp. 1005–1019, 2014.
[41] K. C. Wang, Y. W. Yang, B. Liu et al., “A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression,” *Nature*, vol. 472, no. 7341, pp. 120–124, 2011.
[42] S. J. Hainer, J. A. Prunescu, R. D. Mitchell, R. M. Monteverde, and J. A. Martens, “Intergenic transcription causes repression by directing nucleosome assembly,” *Genes & Development*, vol. 25, no. 1, pp. 29–40, 2011.
[43] K. Hirota, T. Miyoshi, K. Kugou, C. S. Hoffman, T. Shibata, and K. Ohta, “Stepwise chromatin remodelling by a cascade...
of transcription initiation of non-coding RNAs,” Nature, vol. 456, no. 7218, pp. 130–134, 2008.

[54] D. S. W. Tan, F. T. Chong, H. S. Leong et al., “Long noncoding RNA EGFR-AS1 mediates epidermal growth factor receptor addiction and modulates treatment response in squamous cell carcinoma,” Nature Medicine, vol. 23, no. 10, pp. 1167–1175, 2017.

[55] S. Loewer, M. N. Cabili, M. Guttman et al., “Large intergenic non-coding RNA-Ro modulates reprogramming of human induced pluripotent stem cells,” Nature Genetics, vol. 42, no. 12, pp. 1113–1117, 2010.

[56] X. Liu, D. Li, W. Zhang, M. Guo, and Q. Zhan, “Long noncoding RNA gadd2 interacts with TDP-43 and regulates Cdk6 mRNA decay,” The EMBO Journal, vol. 31, no. 23, pp. 4415–4427, 2012.

[57] L. Zhang, Z. Yang, J. Trottrick, O. Barbier, and L. Wang, “Long noncoding RNA MEG3 induces cholestatic liver injury by interaction with PTBP1 to facilitate shp mRNA decay,” Hepatology, vol. 65, no. 2, pp. 604–615, 2017.

[58] C. Carrieri, L. Cimatti, M. Biagioli et al., “Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat,” Nature, vol. 491, no. 7424, pp. 454–457, 2012.

[59] J. Durruthy-Durruthy, V. Sebastiani, M. Wossidlo et al., “The primate-specific noncoding RNA HPAAT5 regulates pluripotency during human preimplantation development and nuclear reprogramming,” Nature Genetics, vol. 48, no. 1, pp. 44–52, 2016.

[60] Y. Wang, F. Chen, M. Zhao et al., “The long noncoding RNA HULC promotes liver cancer by increasing the expression of the HMGA2 oncogene via sequestration of the microRNA-186,” The Journal of Biological Chemistry, vol. 292, no. 37, pp. 15395–15407, 2017.

[61] A. Matsumoto, A. Pasut, M. Matsumoto et al., “mTORC1 and muscle regeneration are regulated by the LINC00961-encoded SPAR polypeptide,” Nature, vol. 541, no. 7636, pp. 228–232, 2017.

[62] M. Eissmann, T. Gutschner, M. Hämmerle et al., “Loss of the abundant nuclear non-coding RNA MALAT1 is compatible with life and development,” RNA Biology, vol. 9, no. 8, pp. 1076–1087, 2012.

[63] Y. Yin, P. Yan, J. Lu et al., “Opposing roles for the lncRNA Haunt and its genomic locus in regulating HOXA gene activation during embryonic stem cell differentiation,” Cell Stem Cell, vol. 16, no. 5, pp. 504–516, 2015.

[64] M. R. Capecchi, “Gene targeting in mice: functional analysis of the mammalian genome for the twenty-first century,” Nature Reviews Genetics, vol. 6, no. 6, pp. 507–512, 2005.

[65] P. A. Latos, S. H. Stricker, L. Steenpass et al., “An in vitro ES cell imprinting model shows that imprint expression of the Igf2r gene arises from an allele-specific expression bias,” Development, vol. 136, no. 3, pp. 437–448, 2009.

[66] P. A. Leighton, R. S. Ingram, J. Eegenschwiler, A. Efstratiadis, and S. M. Tilghman, “Disruption of imprinting caused by deletion of the H19 gene region in mice,” Nature, vol. 375, no. 6526, pp. 34–39, 1995.

[67] M. Blasco, W. Funk, B. Villepontneau, and C. Greider, “Functional characterization and developmental regulation of mouse telomerase RNA,” Science, vol. 269, no. 5228, pp. 1267–1270, 1995.
human cell line,” *Genome Research*, vol. 24, no. 12, pp. 2059–2065, 2014.

[86] J. Han, J. Zhang, L. Chen et al., “Efficient in vivo depletion of a large imprinted lncRNA by CRISPR/Cas9,” *RNA Biology*, vol. 11, no. 7, pp. 829–835, 2014.

[87] M. Sauvageau, L. A. Goff, S. Lodato et al., “Multiple knockout mouse models reveal lincRNAs are required for life and brain development,” *eLife*, vol. 2, article e01749, 2013.

[88] K. M. V. Lai, G. Gong, A. Atanasiu et al., “Diverse phenotypes and specific transcription patterns in twenty mouse lines with ablated lincRNAs,” *PLoS One*, vol. 10, no. 4, article e0125522, 2015.

[89] T. Gutschner, M. Baas, and S. Diederichs, “Noncoding RNA gene silencing through genomic integration of RNA destabilizing elements using zinc finger nucleases,” *Genome Research*, vol. 21, no. 11, pp. 1944–1954, 2011.

[90] P. Grote and B. G. Herrmann, “The long non-coding RNA *Fendrr* links epigenetic control mechanisms to gene regulatory networks in mammalian embryogenesis,” *RNA Biology*, vol. 10, no. 10, pp. 1579–1585, 2013.

[91] P. Grote, L. Wittler, D. Hendrix et al., “The tissue-specific lncRNA *Fendrr* is an essential regulator of heart and body wall development in the mouse,” *Developmental Cell*, vol. 24, no. 2, pp. 206–214, 2013.

[92] F. Sleutels, R. Zwart, and D. P. Barlow, “The non-coding Air RNA is required for silencing autosomal imprinted genes,” *Nature*, vol. 415, no. 6873, pp. 810–813, 2002.

[93] F. Santoro, D. Mayer, R. M. Klement et al., “Imprinted Igf2r silencing depends on continuous *Air* lncRNA expression and is not restricted to a developmental window,” *Development*, vol. 140, no. 6, pp. 1184–1195, 2013.

[94] P. A. Latos, F. M. Pauler, M. V. Koerner et al., “*Airn* transcriptional overlap, but not its lncRNA products, induces imprinted *Igf2r* silencing,” *Science*, vol. 338, no. 6113, pp. 1469–1472, 2012.

[95] E. Aparicio-Prat, C. Arnan, I. Sala, N. Bosch, R. Guigó, and R. Johnson, “DECKO: single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs,” *BMC Genomics*, vol. 16, no. 1, p. 846, 2015.

[96] T. Kono, Y. Obata, Q. Wu et al., “Birth of parthenogenetic mice that can develop to adulthood,” *Nature*, vol. 428, no. 6985, pp. 860–864, 2004.

[97] M. Kawahara, Q. Wu, N. Takahashi et al., “High-frequency generation of viable mice from engineered bi-maternal embryos,” *Nature Biotechnology*, vol. 25, no. 9, pp. 1045–1050, 2007.

[98] G. Friedrich and P. Soriano, “Promoter traps in embryonic stem cells: a genetic screen to identify and mutate developmental genes in mice,” *Genes & Development*, vol. 5, no. 9, pp. 1513–1523, 1991.

[99] B. P. Zambrowicz, A. Imamoto, S. Fiering, L. A. Herzenberg, W. G. Kerr, and P. Soriano, “Disruption of overlapping transcripts in the *ROSA βgeo* 26 gene trap strain leads to widespread expression of β-galactosidase in mouse embryos and hematopoietic cells,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 94, no. 8, pp. 3789–3794, 1997.

[100] P. Soriano, “Generalized lacZ expression with the ROSA26 Cre reporter strain,” *Nature Genetics*, vol. 21, no. 1, pp. 70–1, 1999.

[101] M. Sadelain, E. P. Papapetrou, and F. D. Bushman, “Safe harbours for the integration of new DNA in the human genome,” *Nature Reviews Cancer*, vol. 12, no. 1, pp. 51–58, 2011.

[102] S. Irion, H. Luche, P. Gadue, H. J. Fehling, M. Kennedy, and G. Keller, “Identification and targeting of the ROSA26 locus in human embryonic stem cells,” *Nature Biotechnology*, vol. 25, no. 12, pp. 1477–1482, 2007.

[103] J. D. Brenton, R. A. Drewell, S. Viville et al., “A silencer element identified in *Drosophila* is required for imprinting of *H19* reporter transgenes in mice,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 96, no. 16, pp. 9242–9247, 1999.

[104] J. Goke, X. Lu, Y. S. Chan et al., “Dynamic transcription of distinct classes of endogenous retroviral elements marks specific populations of early human embryonic cells,” *Cell Stem Cell*, vol. 16, no. 2, pp. 135–141, 2015.

[105] J. Wang, G. Xie, M. Singh et al., “Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells,” *Nature*, vol. 516, no. 7531, pp. 405–409, 2014.

[106] S. Zhu, W. Li, J. Liu et al., “Genome-scale deletion screening of human long non-coding RNAs using a paired-guide RNA CRISPR–Cas9 library,” *Nature Biotechnology*, vol. 34, no. 12, pp. 1279–1286, 2016.

[107] L. S. Qi, M. H. Larson, L. A. Gilbert et al., “Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression,” *Cell*, vol. 152, no. 5, pp. 1173–1183, 2013.

[108] L. A. Gilbert, M. A. Horlbeck, B. Adamson et al., “Genome-scale CRISPR-mediated control of gene repression and activation,” *Cell*, vol. 159, no. 3, pp. 647–661, 2014.

[109] M. S. Werner, M. A. Sullivan, R. N. Shah et al., “Chromatin-enriched lncRNAs can act as cell-type specific activators of proximal gene transcription,” *Nature Structural & Molecular Biology*, vol. 24, no. 7, pp. 596–603, 2017.

[110] S. J. Liu, M. A. Horlbeck, S. W. Cho et al., “CRISPRi-based genome-scale identification of functional long noncoding RNA loci in human cells,” *Science*, vol. 355, no. 6320, article eaab7111, 2017.

[111] X. Chen, M. Rinsma, J. M. Janssen, J. Liu, I. Maggio, and M. A. F. V. Gonçalves, “Probing the impact of chromatin conformation on genome editing tools,” *Nucleic Acids Research*, vol. 44, no. 13, pp. 6482–6492, 2016.

[112] J. Hu, Y. Lei, W. K. Wong et al., “Direct activation of human and mouse *Oct4* genes using engineered TALE and Cas9 transcription factors,” *Nucleic Acids Research*, vol. 42, no. 7, pp. 4375–4390, 2014.

[113] H. Wu, L. Yang, and L. L. Chen, “The diversity of long non-coding RNAs and their generation,” *Trends in Genetics*, vol. 33, no. 8, pp. 540–552, 2017.

[114] J. Joung, J. M. Engreitz, S. Konermann et al., “Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood,” *Nature*, vol. 548, no. 7667, pp. 343–346, 2017.

[115] A. M. Khalil, M. Guttman, M. Huarte et al., “Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression,” *Proceedings of the National Academy of Sciences of the United States of America*, vol. 106, no. 28, pp. 11667–11672, 2009.

[116] M. Guttman, J. Donaghey, B. W. Carey et al., “lincRNAs act in the circuitry controlling pluripotency and differentiation,” *Nature*, vol. 477, no. 7364, pp. 295–300, 2011.
[117] J. M. Engreitz, J. E. Haines, E. M. Perez et al., “Local regulation of gene expression by lncRNA promoters, transcription and splicing,” Nature, vol. 539, no. 7629, pp. 452–455, 2016.

[118] D. M. Shechner, E. Hacisuleyman, S. T. Younger, and J. L. Rinn, “Multiplexable, locus-specific targeting of long RNAs with CRISPR-Display,” Nature Methods, vol. 12, no. 7, pp. 664–670, 2015.

[119] M. R. O’Connell, B. L. Oakes, S. H. Sternberg, A. East-Seletsky, M. Kaplan, and J. A. Doudna, “Programmable RNA recognition and cleavage by CRISPR/Cas9,” Nature, vol. 516, no. 7530, pp. 263–266, 2014.

[120] D. A. Nelles, M. Y. Fang, M. R. O’Connell et al., “Programmable RNA tracking in live cells with CRISPR/Cas9,” Cell, vol. 165, no. 2, pp. 488–496, 2016.