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LETTER TO THE EDITOR

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Painting a specific chromosome with CRISPR/Cas9 for live-cell imaging

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Dear Editor,

Visualization of chromosome shapes and dynamics in a live cell is highly desirable and necessary in many areas of cell biology. For example, the copy number of a particular chromosome in cancer cells is often abnormal (e.g., more than two), and therefore probing chromosome copy numbers can aid cancer diagnosis. During interphase, each chromosome exists in its own territory in the nucleus, which can be imaged by fluorescence *in situ* hybridization (FISH) using sequence-specific probes of different colors [1, 2]. However, such chromosome painting has only been possible in fixed cells, and is not suitable for dynamic monitoring of live cells. Therefore, it would be valuable to visualize DNA replication of one chromosome during interphase, and follow chromosome dynamics in the M phase.

Recent development of clustered regularly interspaced short palindromic repeats/CRISPR-associated proteins (CRISPR/Cas) [3] has provided a powerful tool for live-cell imaging of genomic loci [4]. In particular, the nuclease defective Cas9 (dCas9) fused with enhanced green fluorescent protein (EGFP) is used to target a particular DNA sequence upstream of a protospacer adjacent motif (PAM) sequence. Such targeting is achieved through Watson-Crick base pairing of ~20-bp single-guide RNA (sgRNA) that is pre-complexed with the dCas9-EGFP protein. The targeted loci can thus be fluorescently labeled in live mammalian cells [5-8]. However, the labeling achieved by this method is usually restricted to the genomic loci that consist of repetitive sequences, and has not been attempted to track an entire chromosome in a live cell.

Here we report the specific labeling of a large number of loci in the genome, which makes it possible to paint an entire chromosome in a live cell. To do so, we designed a new strategy using a large number of sgRNAs targeting mainly the non-repetitive regions of the chromosome (Figure 1A and Supplementary information, Figure S1A). To design sgRNAs, we scanned the sequence of the entire chromosome 9 on human reference genome hg19. Each 19-23 bp genome sequence upstream of a PAM sequence NGG was taken as a candidate target region. Because the efficiency of sgRNA binding is dependent on its GC content [9, 10], sgRNAs with GC content of 45%-65% were selected (Supplementary information, Figure S1B). The sgRNAs that could also bind to other chromosomes were removed in order to assure labeling specificity and reduce fluorescent background. Additionally, when multiple targeting sequences overlapped in a chromosome region, only one of them was selected. Among all sgRNAs, only one protein-coding gene (*DNAJB5*) contains sgRNA-binding sites in the exon region (Supplementary information, Figure S1C), but its expression level was not affected by lentivirus infection or dCas9-EGFP/sgRNA targeting (Supplementary information, Figure S1D).

To obtain high densities of sgRNA that would give signals significantly above the intracellular fluorescent background, especially when the chromatin is in open state during G and S phases, we chose 15 clusters of target sites (c1-c15) on chromosome 9, each spanning 5 Kb and containing more than 30 targets. The clusters are placed at least 5 Mbp away from each other (Figure 1A). In total, we selected 1 124 sgRNAs that are distributed on chromosome 9 (Supplementary information, Table S1).

As shown in Supplementary information, Figure S1A, a cell line stably expressing dCas9-EGFP was constructed from one HeLa cell by lentiviral infection. In the meantime, the 1 124 sgRNAs were packaged into lentiviruses and used to infect HeLa cells expressing dCas9-EGFP for three times. After labeling the chromosome with the 1 124 sgRNAs, we imaged cells in the S phase using a Nikon structured illumination microscope (N-SIM) equipped with a 100× TIRF oil immersion objective (NA 1.49). Figure 1B shows that the projected z-stack EGFP images. We attribute the three bright EGFP signal regions in the nucleus to three copies of chromosome 9, which is consistent with the karyotype of the HeLa cells we used (Supplementary information, Figure S1E). We noted that the EGFP signal is stronger in the S phase, when DNA replication takes place, than in the G1 phase, indicating that dCas9-EGFP can bind rapidly to newly synthesized DNA. Taken together, the imaging results suggest the efficacy of our method in visualizing a desired chromo-

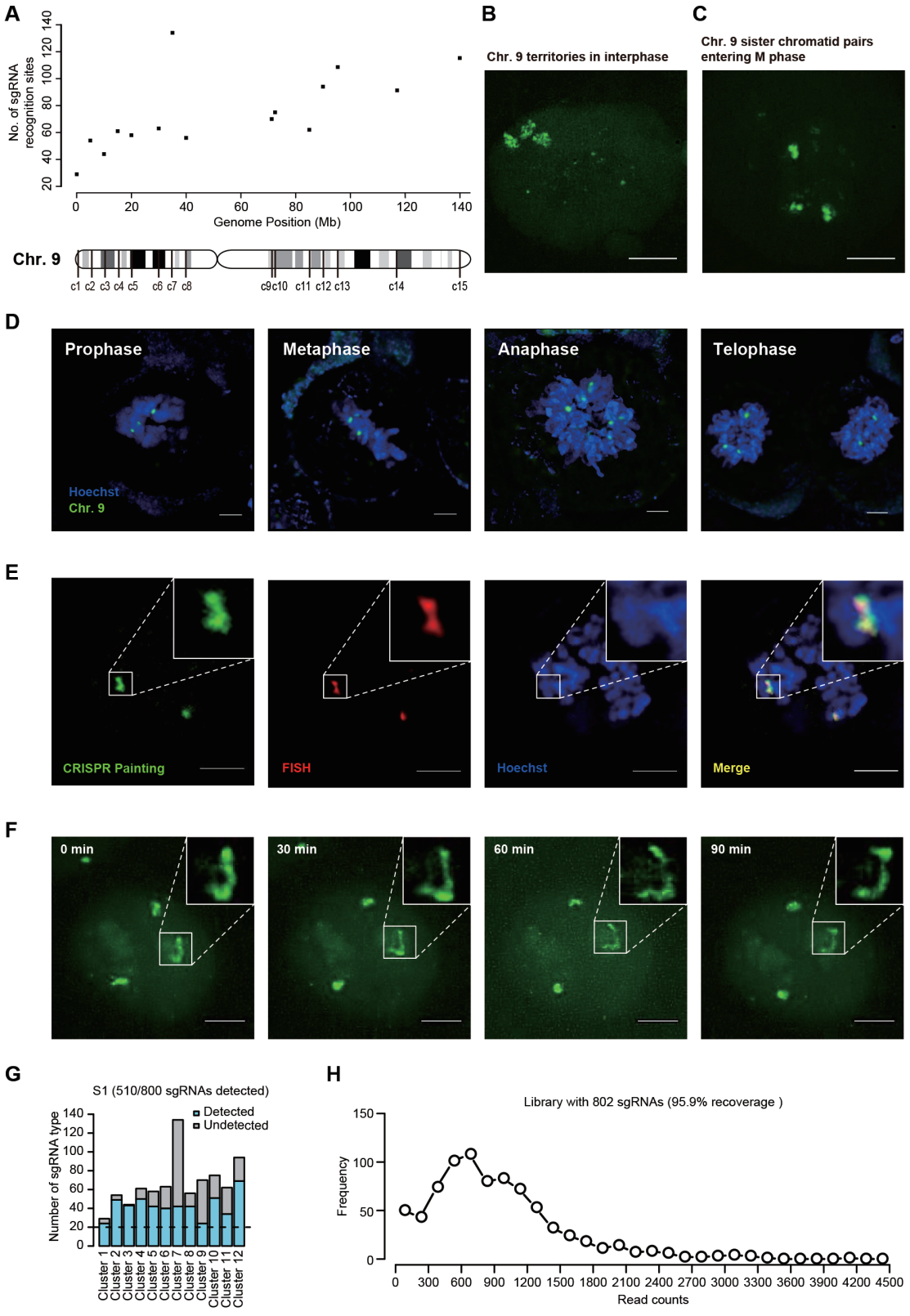
A
No. of sgRNA recognition sites
20 40 60 80 100 120 140
0 20 40 60 80 100 120 140
Genome Position (Mb)
Chr. 9
c1 c2 c3 c4 c5 c6 c7 c8 c9c10 c11 c12 c13 c14 c15
B
Chr. 9 territories in interphase
C
Chr. 9 sister chromatid pairs entering M phase
D
Prophase
Hoechst
Chr. 9
Metaphase
Anaphase
Telophase
E
CRISPR Painting
FISH
Hoechst
Merge
F
0 min
30 min
60 min
90 min
G
S1 (510/800 sgRNAs detected)
Detected
Undetected
Number of sgRNA type
0 20 40 60 80 100 120 140
Cluster 1 Cluster 2 Cluster 3 Cluster 4 Cluster 5 Cluster 6 Cluster 7 Cluster 8 Cluster 9 Cluster 10 Cluster 11 Cluster 12
H
Library with 802 sgRNAs (95.9% recoverage)
Frequency
0 50 100 150
0 300 600 900 1200 1500 1800 2100 2400 2700 3000 3300 3600 3900 4200 4500
Read counts

Figure 1 Construction of the CRISPR/Cas9 imaging system for fluorescent labeling of a particular chromosome in live cells. **(A)** Scatter plot for numbers of sgRNA-binding sites in each cluster of 5 Kb width across human chromosome 9. In the model of sgRNA-binding sites on the entire chromosome 9, vertical lines labeled as c1-c15 indicate the locations of 15 sgRNA clusters' binding sites. **(B)** Maximum intensity projection of EGFP images recorded by N-SIM at the S phase of the cell cycle. Step size, 0.12 μm; Scale bar, 5 μm. Three copies of chromosome 9 in a HeLa cell are clearly visible. **(C)** Maximum intensity projection of EGFP images recorded by N-SIM in the prophase of mitosis. Step size, 0.12 μm; Scale bar, 5 μm. Two sister chromatids of each chromosome 9 are clearly resolved. **(D)** EGFP image (green) in live cells at different stages of the M phase, recorded by an Olympus inverted wide-field fluorescence microscope. Three pairs of the chromosome 9 in the prophase and metaphase, whose two sister chromatids are not clearly resolved due to the reduced resolution, separate in the anaphase and telophase. Cells are also stained with Hoechst (blue) for DNA. All step size, 0.2 μm; depth of maximum intensity projection for prophase, metaphase, anaphase and telophase, 4 μm, 7 μm, 8 μm and 6 μm, respectively; scale bar, 5 μm. **(E)** Co-localization of chromosome 9 labeled by dCas9-EGFP (green) and C9-1 and C9-2 loci labeled by Cy3-tagged FISH probes (red). Scale bar, 5 μm. **(F)** Dynamics of the three copies of chromosome 9 in S phase in a live HeLa cell. Z maximum intensity projection of 10.5 μm. Scale bar, 5 μm. See also Supplementary information, Movie S1. **(G)** Distribution of sgRNA sequences from a single clonal sample detected by DNA sequencing after PCR amplification using the common primers for the sgRNA sequences. Single clone 1 (S1) was selected from a cell pool that has been painted with 802 sgRNAs. Majority of the sgRNA sequences have been incorporated into a cell single clone. The horizontal dashed line indicates the level with 20 sgRNA sequences per cluster, which is necessary for effective chromosome painting. **(H)** Distribution of numbers of reads for different sgRNA sequences, showing efficient incorporation and even distribution of the pooled 802 sgRNA library in the cell population.

somal territory in a live cell.

Figure 1C shows a projected z-stack of N-SIM fluorescence images taken in the prophase during mitosis. The high resolution of structured illumination microscopy and the strong signal due to chromosome condensation, allowed for the visualization of the three pairs of sister chromatids (Figure 1C) after DNA replication.

We next aimed to verify the dCas9-EGFP signals with FISH using probes targeting repetitive sequences so that a single FISH probe could access many sites. We used another two sgRNA sequences, C9-1 and C9-2, which were previously described and named [7], to replace the three non-repetitive clusters c13-c15. C9-1 binds to a region with pericentromeric repeats on chromosome 9 and C9-2 targets 115 sites within a 5 Kb region.

We delivered 800 sgRNAs from c1-c12 clusters as well as C9-1 and C9-2 (802 sgRNAs in total) into the HeLa cells expressing dCas9-EGFP by lentivirus infection (Supplementary information, Figure S2A). Before painting the entire chromosome, we confirmed that each of the 12 clusters of sgRNAs could individually label the corresponding genomic locus efficiently (Supplementary information, Figure S2B). As expected, we observed the co-localization of dCas9-EGFP and FISH labeling of C9-1 and C9-2 (Supplementary information, Figure S2C).

After labeling the chromosome with the 802 sgRNAs, we found the imaging results for the chromosome territory and three pairs of sister chromatids are very similar to those labeled with c1-c15 containing 1 124 sgRNAs (Supplementary information, Figure S2D and E). The labeled chromosome 9 in the M phase can be easily seen even with a wide-field fluorescence microscopy. Figure 1D shows the cells in the prophase, metaphase, anaphase and telophase during mitosis. The cells were also stained with a DNA-specific dye Hoechst 33342, which allows co-localization of chromosome 9 with the rest of chromosomes. The three pairs of sister chromatids in the prophase and metaphase, though not clearly resolved with this reduced resolution, split to two sets of separate chromosomes in the anaphase and telophase. As a final control experiment, Figure 1E shows co-localization of labeled chromosome 9 of the EGFP signal with the Cy3-tagged C9-1 and C9-2 FISH probes. The fact that the EGFP areas were larger than the diffraction-limited FISH areas proves again the successful labeling of chromosome 9.

Having demonstrated stable labeling of chromosome 9, we next applied our method to dynamic monitoring using a DeltaVision Imaging System (Applied Precision/GE) equipped with a 100×/1.4 NA oil immersion objective, which allows less photobleaching, longer time for data acquisition, and confocality based on deconvolution. Figure 1F and Supplementary information, Movie S1 show chromosome dynamics at a single chromosome level for a cell in the S phase. Supplementary information, Figure S2F and Movie S2 show the dynamics of chromosome 9 during a period of 2 h from the late S phase to M phase. In addition to the three chromosome 9 spots, the nucleoli exhibit unintended EGFP signal, likely due to nonspecific binding of dCas9-EGFP protein with small RNAs in the nucleoli [8]. During the data collection period, EGFP signal from the nucleoli faded away due to the disappearance of the nucleoli in the M phase, while chromosome 9 fluorescent signal became stronger due to chromosome condensation. Supplementary information, Movie S3 shows another cell in the M phase for a period of ~3 h. After cell division, the two daughter cells maintained strong fluorescence signals from the replicated chromosomes, indicating that chromosome labeling is kept in the daughter cells. In this movie, significant conformational fluctuation of the condensed chromosomes was observed.

Although hundreds of sgRNAs were delivered by lentivirus into the cells, no obvious effects on cell proliferation were observed (Supplementary information, Figure S2G).

To evaluate how many sgRNAs were actually introduced to each cell, we carried out DNA sequencing of clonally amplified cells after PCR amplification with the common primers for sgRNA sequences [11]. Figure 1G shows the distribution of the detected 510 non-repetitive sgRNA sequences in chromosome 9 in one clonally amplified population. Single clones with higher labeling efficiency (S1) had more sgRNAs sequences incorporated than single clones with weaker fluorescence (S34) (Supplementary information, Figure S2H). Figure 1H shows the distribution of read numbers for all sgRNA sequences in the population of cells, showing that majority of the sgRNAs has been sufficiently incorporated into the cell population.

To address the question of how many sgRNAs are sufficient for painting a chromosome, we reduced the number of non-repetitive sgRNAs to 485. We found no significant deterioration of the image quality when compared with the images produced with 802 sgRNAs (Supplementary information, Figure S2I), when we imaged chromosome 9 at different phases of the M phase. Based on this, we conclude that more than 20 sgRNAs in each cluster and at least 300 types of total sgRNAs are needed in one cell for effective chromosome 9 painting. As the required number of the sgRNAs should be dependent on the length of the chromosome, we anticipate that using our design strategy ~800 sgRNAs should be enough to label the longest human chromosome 1, which is about twice as long as chromosome 9, while ~100 sgRNAs could be enough for the shortest chromosome. Of course, for painting other chromosomes, additional optimization and validation may be required.

In summary, by introducing hundreds of specific and non-repetitive sgRNAs in a human cell, we are able to paint an entire chromosome in a live cell for fluorescent imaging. We have visualized the spatial arrangements of homologous chromosomes and sister chromatids and tracked the movement of a particular chromosome in dividing cells. Our method will facilitate studies of functional organization of chromosomes, interactions among different chromosome regions, and long-term chromosomal dynamics in live mammalian cells.

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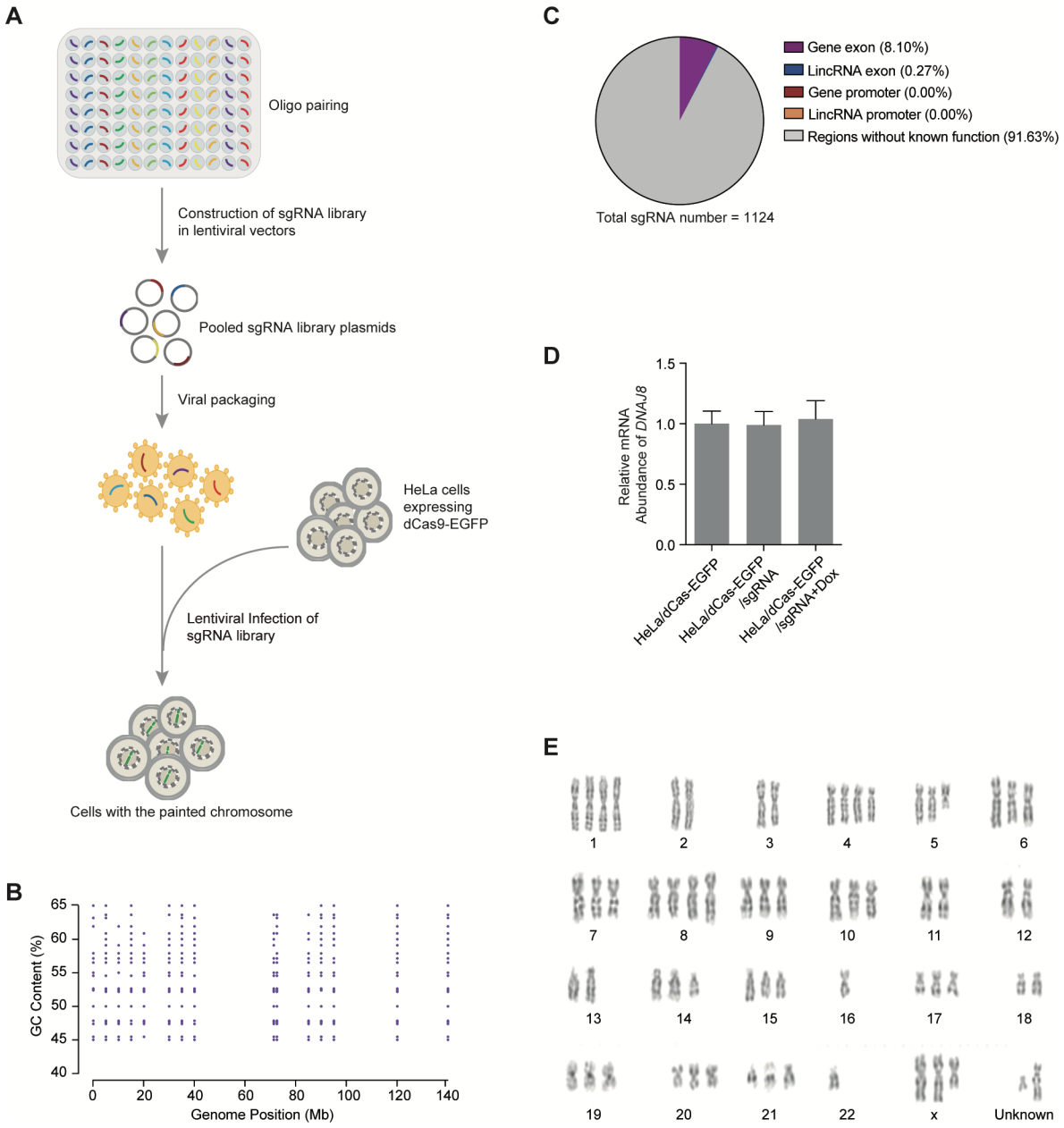
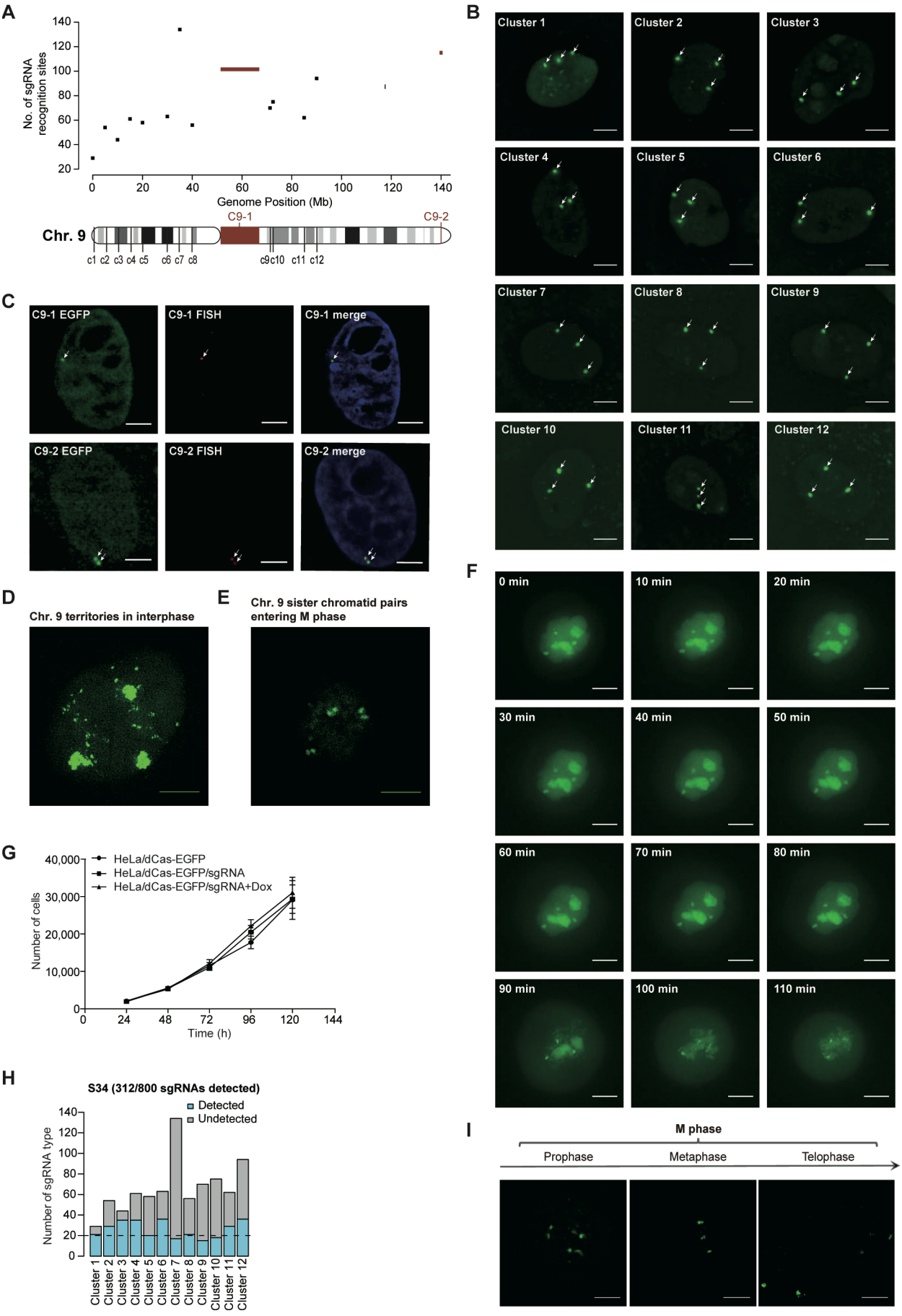
(**Supplementary information** is linked to the online version of the paper on the *Cell Research* website.)

SUPPLEMENTARY FIGURES



Supplementary information, Figure S1 Design and construction of CRISPR/Cas-mediated chromosome painting system. (**A**) Schematic of the CRISPR/Cas imaging system construction. Each complimentary pair of synthesized single-stranded sgRNA oligonucleotides were annealed separately. The double-stranded sgRNA oligos were ligated into the sgRNA expression plasmid. The library of plasmids of different sgRNAs were then mixed together to generate high titer lentivirus. A HeLa cell line stably expressing dCas9-EGFP was then infected three times by the sgRNA lentivirus to realize chromosome painting in live cells. (**B**) Scatter plot for the GC contents of sgRNA sequences. The x axis represents the position on human Chr. 9. (**C**) A pie chart for the distribution of sgRNA binding sites in gene context, including protein coding genes and long intergenic noncoding RNAs (lincRNAs). Most (91.63%) of the binding sites of sgRNAs were not overlapped with promoter or exon genes. (**D**) mRNA levels of *DNAJB5* (normalized to *GAPDH*) in lentivirus infected cells and Chr. 9 labeling cells, quantified by real-time PCR analysis. No obvious expression differences were observed. (**E**) Karyotype of dCas9-EGFP expressed HeLa cell line. Unknown indicates that the chromosome or segment doesn't have a typical G-bands, which is not caused by translocation of Chr. 9 with any other chromosomes.


A
No. of sgRNA recognition sites
Genome Position (Mb)
Chr. 9
C9-1
C9-2
c1 c2 c3 c4 c5 c6 c7 c8 c9c10 c11 c12
B
Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
Cluster 8
Cluster 9
Cluster 10
Cluster 11
Cluster 12
C
C9-1 EGFP
C9-1 FISH
C9-1 merge
C9-2 EGFP
C9-2 FISH
C9-2 merge
D
Chr. 9 territories in interphase
E
Chr. 9 sister chromatid pairs entering M phase
F
0 min
10 min
20 min
30 min
40 min
50 min
60 min
70 min
80 min
90 min
100 min
110 min
G
HeLa/dCas-EGFP
HeLa/dCas-EGFP/sgRNA
HeLa/dCas-EGFP/sgRNA+Dox
Number of cells
Time (h)
H
S34 (312/800 sgRNAs detected)
Detected
Undetected
Number of sgRNA type
I
M phase
Prophase
Metaphase
Telophase

Supplementary information, Figure S2 Labeling of genomic loci by 12 clusters of sgRNA and validation of Chr. 9 labeling in live cells. (**A**) Scatter plot for the number of sgRNA binding sites in each cluster of 5 kb width across the human Chr. 9. In the model of sgRNA binding sites on the entire Chr. 9, short horizontal lines labeled as c1-c12 indicated the locations of 12 sgRNA clusters binding locations. The red block indicated the binding sites of C9-1 and C9-2 sequences. The number of C9-1 binding sites is an approximate value. (**B**) Maximum intensity projection images of individual sgRNA clusters labeled genomic loci in live HeLa cells. dCas9-EGFP stable expressing HeLa cells were infected by individual sgRNA cluster through lentivirus infection. Images were taken by an Olympus wide field fluorescence microscope with a 0.3 μm step size. Scale bar, 5 μm. White arrows indicate the three cluster regions labeled by the sgRNAs in Chr.9. (**C**) Co-localization of dCas9-EGFP labeling (green) and FISH labeling (red) for C9-1 and C9-2 loci. Cells were stained with Hoechst 33342 (blue). Scale bars, 5 μm. (**D**) Maximum intensity projections for EGFP images recorded by a Nikon structured illumination microscope (N-SIM) at the S phase of interphase. Step size 0.12 μm, 8 μm depth. Scale bar, 5 μm. (**E**) Maximum intensity projections for EGFP images recorded by N-SIM in the prophase of M phase. Step size 0.24 μm, 11 μm depth. Scale bar, 5 μm. (**F**) Dynamics of the three copies of Chr. 9 from late S phase to prophase within 2 hr. During this time, the unintended strong EGFP signal within nucleoli decreased when nucleoli disappeared in M phase. Images were taken at 24 evenly separated time points, 12 of them were shown here, showing z maximum projection of 10.5 μm. Scale bar, 5 μm. See also **Supplementary information, Movie S2**. (**G**) Cell proliferation curve of dCas9-EGFP expressed HeLa cells, HeLa cells infected by lentivirus containing 802 different sgRNAs and Chr. 9 labeled HeLa cells. Values represent the mean ± S.E.M. of 9 independent experiments. No obvious effects on cell proliferation were observed. (**H**) Distribution of detected sgRNA sequences by DNA sequencing after PCR amplification with the common primers for the sgRNA sequences for a single clonal sample. Single clone S34 was selected from cell pool with 802 sgRNAs. The horizontal dashed lines indicate the level with 20 sgRNA sequences per cluster, which is necessary for effective chromosome painting. (**I**) Chr. 9 labeling with decreased number of sgRNAs at different stages of M phase imaged by N-SIM. Snapshots of Chr. 9 in X-Y plane were shown. The images were maximum intensity projection of 11 μm depth with 0.24 μm step size. Scale bars, 5 μm.

Supplementary information, Data S1 Materials and Methods

sgRNA design

Chromosome 9 sequence information were downloaded from UCSC genome browser. Sequences in the forms of $N_{19\text{-}23}$NGG and with the GC content ranging from 45% to 65% in non-PAM regions were selected as candidate sgRNA targeting sites. sgRNA sequences were then mapped to human genome using bowtie (v2.2.5) to discard the sgRNAs which could also target to the other chromosomes. Overlapped sgRNA sequences were removed so that each binding site was covered by only one sgRNA. We placed 15 clusters of target sites along chromosome 9 (Figure 1A), each cluster spans 5 kb and contains more than 30 targets and the clusters are placed at least 5 Mbp away. Because dCas9 protein binding may affect the expression of endogenous genes, we evaluate the distribution of sgRNA binding sites in the different gene context. No sgRNAs were mapped to the -50 ~ +300 bp of the gene TSS regions, which were reported to significantly affect the expression of target genes [9]. Only one protein coding gene (*DNAJB5*) and one long intergenic noncoding RNA (lincRNA) (RP11-274B18.4) contained sgRNA binding sites in the exon region (Supplementary information, Figure S1C). The expression level of DNAJB5 would not be affected by lentivirus infection or dCas9-EGFP/sgRNA targeting (Supplementary information, Figure S1D).

Cell culture and plasmid construction

HeLa cells and HEK293 cells were cultured in Dulbecco's modified Eagle medium (DMEM) (Gibco) with 10% FBS (Gibco) and 1% P/S (Life Technologies). All cells were cultured at 37°C and 5% CO_2 in a humidified incubator.

The lentiviral sgRNA vector was constructed by substituting EGFP gene in pLenti-sgRNA-Lib [11] for Puromycin resistant gene. The oligonucleotides for each sgRNA-coding sequence were individually synthesized (GENERAY, Inc.). Paired oligonucleotides were mixed in 96-well plates to the final concentration of 9 μM in 50 μl of 1×TransTaq HiFi Buffer II (Transgen) for annealing. Annealed oligonucleotide pairs belonging to the same labeling cluster were then mixed, phosphorylated and ligated into the lentiviral sgRNA vector using Golden Gate method. Different clusters of ligation mixtures were transformed separately into Trans1-T1 competent cells (Transgen) to obtain the sgRNA plasmids for each of the labeling clusters.

Lentivirus package and stable expression of dCas9-EGFP and sgRNAs

4×10^6 of HEK293 cells were seeded at 10 cm plate 24 hr before transfection. 0.4 μg pVSVG plasmid, 4 μg pR8.74 and 4 μg dCas9-EGFP expressed plasmid or Tet on 3G or mixed plasmids of sgRNAs were co-transfected into HEK293 cells by X-tremeGENE HP (Roche). Virus was harvested at 72 hr post-transfection then concentrated by Lenti-X Concentrator (Clontech) as the recommended protocol. For dCas9-EGFP expressed cell line construction, HeLa cells were infected by mixture of dCas9-EGFP and Tet on 3G virus. After induction of 200 ng/ml Doxycycline (Clontech), EGFP positive single clones were sorted by FACS. For chromosome labeling, HeLa cells were infected with sgRNA mixture virus for 3 times (For each time of infection, MOI = 60). The individual sgRNA cluster lentivirus was packaged in the same way as mentioned above.

Fluorescence in situ hybridization

Cells were fixed by 4% paraformaldehyde (Coolaber) for 15 min, permeabilize the cells with 0.5% NP-40 (Sigma) in 1× PBS (Gibco) for 10 min, wash samples with PBS for 5 min, then incubate cells with 2 ng/μl Cy3 labeled oligo-DNA FISH probe (GENERAY, Inc.) for 12 hr in a dark and humidified box at room temperature. Wash cells with 2×SSC (Invitrogen) three times and stain with Hoechst 33342 (Life Technologies).

FISH probe sequence (5'-3'):

C9-1: TTCCATTCCATTCCATTCCA

C9-2: GGGGAGCTTCCTCACAGACA

Cell cycle arrest

For imaging chromosome of cells in M phase, cells were seeded into a 35 mm glass bottom dish (In Vitro Scientific) and treated by 1×Thymidine (Sigma) for 23 hr, wash cells with PBS (Gibco) for three times. Cultured cells with fresh DMEM for 4-6 hr, then cultured cells with 1× Nocodazole (Sigma) for another 12 hr. For imaging interphase chromosome territories, cells were seeded into a 35 mm glass bottom dish one day in advance, and then treated by 1×Thymidine for 20 hours and released for 7 hr before imaging.

Quantitative real-time PCR (qRT-PCR)

RNA of different cells was extracted by RNAprep Pure Micro kit (TIANGEN), and the cDNA was synthesized separately by QuantScript RT kit (TIANGEN). SYBR Premix Ex Taq II

(TaKaRa) were used to perform Real-time PCR on LightCycler96 qPCR system (Roche). Expression levels of GAPDH were measured as normalized controls.
Specific primers for *DNAJB5* (5'-ACACCACAGACAAGACAGATCC-3'/5'-ATTGAGTGGAGTGAGTGTTGGG-3') were used for qRT-PCR.

Cell proliferation assay

For cell proliferation assay, cells were seeded in 96-well cell culture dishes in 9 repeats at a density of 2000 cells per well. Cell numbers at the indicated time points was determined by MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay.

sgRNA distribution analysis

sgRNA distributions in pool and clonal populations were identified by high-throughput deep-sequencing analysis as described before [11]. Briefly, the genomic DNA of two cell pools and different cell clones were isolated from 10^6 cells using the DNeasy Blood and Tissue kit (Qiagen). sgRNA-coding regions integrated into the chromosomes were PCR-amplified with 28 cycles of reaction using primers annealed to the flanking sequences of the sgRNAs (Primers sequences: 5'-TATCTTGTGGAAAGGACGAAACACC-3'/5'-AATACGGTTATCCACGCGGC-3'). Then the PCR products of each samples were purified and subjected to high-throughput sequencing analysis with Illumina HiSeq 2500.

Microscopy setup

Three different microscopes were used in our experiment. For the non-repetitive sequence single point labeling, z-scanning and C9-1, C9-2 FISH verification, images were acquired on an inverted wide-field fluorescence microscope (Olympus IX83) which equipped with a CCD camera (CoolSnap HQ2, Photometrics), a 100× UPlanSApo oil immersion objective lens (NA 1.40) and a LED light source (Spectra X Light Engine, Lumencor). EGFP was excited at 470/24 nm (wavelength/bandwidth), Hoechst was excited at 395/25 nm and Cy3 was excited at 550/15 nm.

Super resolution images were acquired on a Nikon Structured Illumination Microscope (N-SIM) with a SR Apo TIRF 100× oil immersion lens (NA 1.49), a Tokai Hit incubation chamber (at 37 °C) and an EMCCD (ANDOR iXon3). EGFP was excited at 488 nm. At the S phase of interphase, images were taken at step size 0.12 μm. At the prophase

of M phase, images were taken at a step size 0.12 μm for the 15 clusters and 0.24 μm for the 12 clusters.

For the long term time-lapse acquisition of cell division process, images were taken on a DeltaVision microscopy system with a UPlanSApo 100× oil immersion objective (NA 1.40), a CCD camera (CoolSnap HQ2) and a 37 °C stage incubator. EGFP was excited at 475/28 nm. 3D fluorescence images (2 μm step size) were collected every 3 min for about 3 hr to acquire 56 time points. For movies in interphase, 3D fluorescence images (1.5 μm step size) were collected every 5 min for about 2 hr.

Data analysis

All the wide-field fluorescence imaging data were analyzed by ImageJ. The N-SIM results were processed with NIS Element AR (Nikon). Images were projected in maximum intensity. All movies taken by DeltaVision microscopy system were deconvoluted and analyzed by SoftWoRx.