

## Method

# Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins

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RNA-guided engineered nucleases (RGENs) derived from the prokaryotic adaptive immune system known as CRISPR (clustered, regularly interspaced, short palindromic repeat)/Cas (CRISPR-associated) enable genome editing in human cell lines, animals, and plants, but are limited by off-target effects and unwanted integration of DNA segments derived from plasmids encoding Cas9 and guide RNA at both on-target and off-target sites in the genome. Here, we deliver purified recombinant Cas9 protein and guide RNA into cultured human cells including hard-to-transfect fibroblasts and pluripotent stem cells. RGEN ribonucleoproteins (RNPs) induce site-specific mutations at frequencies of up to 79%, while reducing off-target mutations associated with plasmid transfection at off-target sites that differ by one or two nucleotides from on-target sites. RGEN RNPs cleave chromosomal DNA almost immediately after delivery and are degraded rapidly in cells, reducing off-target effects. Furthermore, RNP delivery is less stressful to human embryonic stem cells, producing at least twofold more colonies than does plasmid transfection.

[Supplemental material is available for this article.]

The type II CRISPR (clustered, regularly interspaced, short palindromic repeat)/Cas (CRISPR-associated) system is an adaptive immune response in bacteria and archaea, which functions by recognizing and cleaving foreign DNA from phages and plasmids via Cas9 protein and guide RNAs, whose sequences are partially derived from the invaders (Horvath and Barrangou 2010; Wiedenheft et al. 2012). Recently, we and others exploited this system to develop RNA-guided endonucleases or engineered nucleases (RGENs) that enable targeted genome editing in cultured human cells (Cho et al. 2013a; Cong et al. 2013; Jinek et al. 2013; Mali et al. 2013b), zebrafish embryos (Hwang et al. 2013), and bacteria (Jiang et al. 2013). Since then, RGENs have been successfully used to modify genomes in various species including model organisms (Cho et al. 2013b; Dickinson et al. 2013; Friedland et al. 2013; Gratz et al. 2013; Li et al. 2013a,c; Wang et al. 2013; Sung et al. 2014) and plants (Li et al. 2013b; Nekrasov et al. 2013; Shan et al. 2013), rapidly catching up with their precursors, namely, zinc finger nucleases (ZFNs) (Bibikova et al. 2003; Porteus and Baltimore 2003) and transcription activator-like effector nucleases (TALENs) (Miller et al. 2011).

Thus, RGENs are now a new member in the growing family of engineered nucleases (Kim and Kim 2014). These enzymes cleave chromosomal DNA in cells, producing site-specific double-strand breaks (DSBs), the repair of which via endogenous homologous recombination (HR) or nonhomologous end joining (NHEJ) gives rise to targeted mutagenesis and chromosomal rearrangements. We have developed and improved all of these types of programmable nucleases over the last several years (Kim et al. 2009, 2010, 2011; Cho et al. 2013a; Kim et al. 2013a; Sung et al. 2013) and reported that the specificity and activity of RGENs are at least on par with those of their precursors. Unlike ZFNs and TALENs, whose DNA-targeting specificities are altered by protein engineering, new RGENs with desired specificities can be prepared

simply by replacing guide RNAs. Furthermore, use of in vitro transcribed guide RNAs rather than plasmids that encode them makes this system cloning-free (Cho et al. 2013a).

For efficient genome editing via RGENs, the successful delivery of guide RNA and Cas9 into cells is essential. In animal experiments, in vitro transcribed Cas9-encoding mRNA or recombinant Cas9 protein can be directly injected into one-cell stage embryos using glass needles to obtain genome-edited animals. To express Cas9 and guide RNA in cultured cells in vitro, typically, plasmids that encode them are transfected via lipofection or electroporation. Unfortunately, use of plasmids is often limited by random integration of all or part of the plasmid DNA into the host genome, a process known as stable transfection. Plasmid DNA can also be inserted at RGEN on-target and off-target sites (Gabriel et al. 2011). Indeed, we found that at least one out of three large insertions and six out of 26 (23%) small insertions at off-target sites, reported in two recent papers (Cradick et al. 2013; Fu et al. 2013), were derived from the Cas9- or sgRNA-encoding plasmid (Supplemental Table 1). Unwanted insertions of plasmid DNA sequences at off-target sites are difficult to detect and, therefore, more problematic than those at on-target sites. These foreign sequences can cause host immune responses (Hemmi et al. 2000; Wagner 2001), hampering the use of gene-edited primary or stem cells in cell therapy. In addition, DNA transfection is often stressful to cells. For example, plasmid DNA introduced into cells triggers cyclic GMP-AMP synthase activation (Sun et al. 2013). Furthermore, prolonged expression of RGENs from plasmid DNA, which can persist in cells for several days post-transfection, can aggravate off-target effects (Gaj et al. 2012). In line with these concerns, cells transfected with plasmids for biomedical applications or animals and plants derived from DNA-transfected cells are regarded as genetically modified by regulatory authorities (Podevin et al. 2013; Pauwels et al. 2014), requiring a costly and lengthy regulation procedure for approval in most developed countries.

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transfection. Thus, the delivery of the *CCR5*-specific RGEN RNP induced indels at frequencies of 19% and 23% in BJ fibroblasts and H9 ES cells, respectively, whereas plasmid transfection gave rise to indels at frequencies of 9% and 10%, respectively (Fig. 2A). We also tested three other RGEN RNPs in H9 cells and found that the four RGENs induced indels at a frequency of  $20 \pm 3\%$  on average (Fig. 2B). Notably, RNP delivery was less toxic to ES cells, producing at least twofold more colonies than did plasmid transfection (Fig. 2C). No apparent changes in the morphology of ES cell colonies were observed after RGEN RNP transfection (Fig. 2D). Furthermore, all of the colonies expressed alkaline phosphatase, a marker for pluripotency (Fig. 2D). These results suggest that use of RGEN RNPs rather than plasmids could facilitate isolation of genome-modified clones of ES cells or induced pluripotent stem cells.

### Oligonucleotide-directed genome editing via homology-directed repair

Next, we investigated whether RGEN RNPs can be co-transfected with homologous donor DNA to achieve genome editing via homology-directed repair. We used single-stranded oligodeoxynucleotides (ssODNs) (Chen et al. 2011) rather than gene-targeting vectors or PCR amplicons as donor DNA to avoid the possibility that vector- or amplicon-derived double-strand DNA segments could be inserted randomly in the genome or specifically at RGEN on- or off-target sites. Co-delivery of the *AAVS1*-specific RNP and an ssODN containing a diagnostic *XbaI* site gave rise to targeted genome modification in K562 cells at a frequency of 15% measured

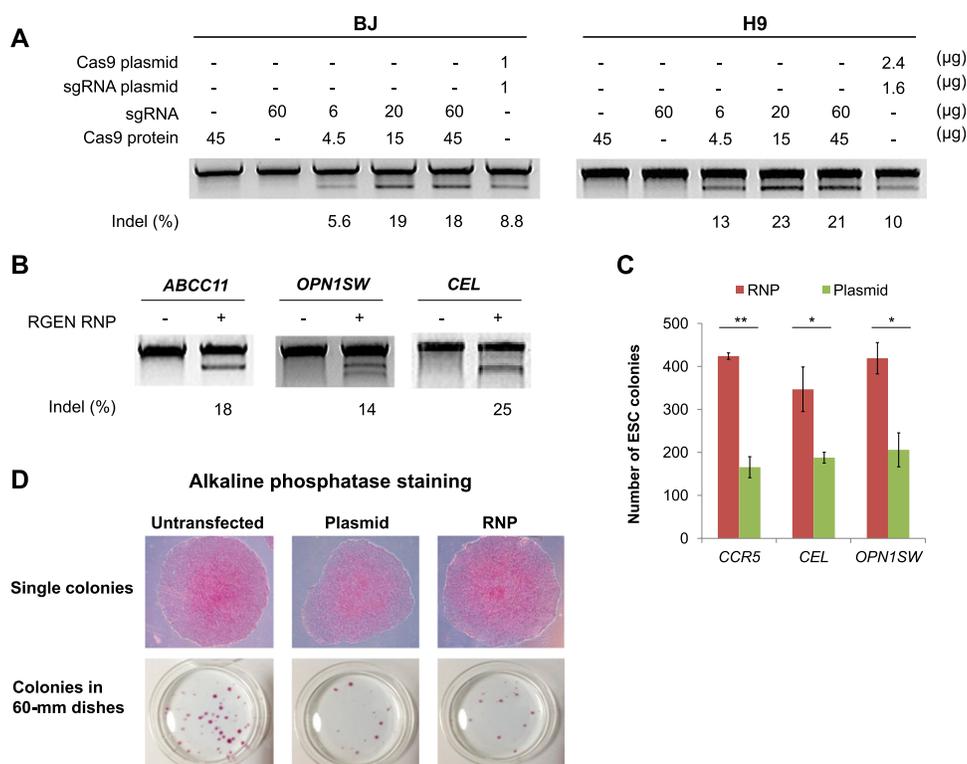
by *XbaI* digestion (Fig. 3). This method can be used to insert small DNA sequences such as *loxP* or those that encode affinity tags or antigens at pre-determined genomic sites.

### Large chromosomal deletions induced by RGEN RNPs

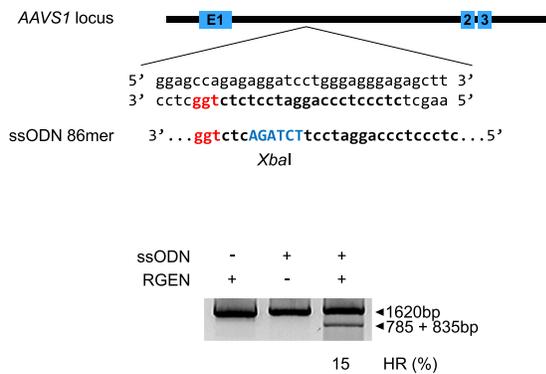
We and others have shown that the repair of two concurrent DSBs produced by ZFNs and TALENs gives rise to targeted chromosomal rearrangements such as deletions, inversions, and translocations (Brunet et al. 2009; Lee et al. 2010, 2012; Carlson et al. 2012; Kim et al. 2013a). Likewise, transfection of plasmids that encode Cas9 and sgRNA into human cells can cause chromosomal deletions and translocations in a targeted manner. We tested whether RGEN RNPs can induce large chromosomal deletions in K562 cells. As expected, use of two sgRNAs whose target sites are separated by 10- to 100-kb pairs caused targeted deletions of corresponding chromosomal segments (Fig. 4), demonstrating that RGEN RNP delivery enables multiplex genome engineering and targeted chromosomal rearrangements.

### Reducing off-target effects of RGENs via RNP delivery

RGENs can induce off-target mutations at sites that are highly homologous to on-target sites (Cradick et al. 2013; Fu et al. 2013; Hsu et al. 2013; Pattanayak et al. 2013; Cho et al. 2014). Off-target DNA cleavages by RGENs can cause unwanted chromosomal rearrangements such as translocations (Cho et al. 2014). We tested whether RNP delivery could reduce off-target effects of RGENs. To



**Figure 2.** Genome editing in BJ fibroblasts and H9 hES cell lines via direct delivery of RGEN RNPs. (A) *CCR5*-specific RGEN-driven mutations detected by the T7E1 assay in H9 and BJ cells. (B) RGEN-driven mutations in H9 ES cells detected by the T7E1 assay. A mixture of Cas9 protein (75  $\mu$ g) and sgRNA (100  $\mu$ g) was transfected into  $1 \times 10^6$  H9 cells. (C) Cytotoxicity of RGEN RNPs vs. RGEN plasmid in H9 ES cells. (\*\*)  $P < 0.01$ , (\*)  $P < 0.05$ . (D) No apparent changes in the physiology of ES cells after RGEN RNP treatment. Untransfected, RNP-, and plasmid-transfected ES cell colonies were subjected to AP staining.

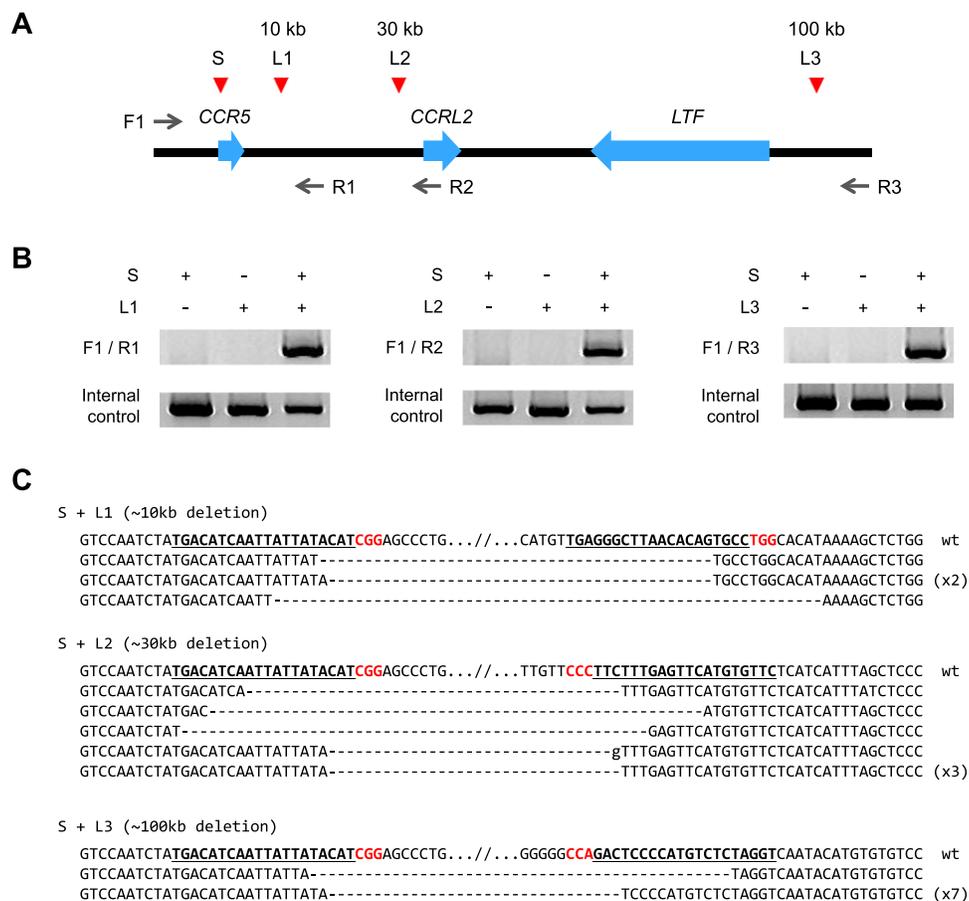


**Figure 3.** Homology-directed repair using ssODNs. The 86-mer ssODN includes an XbaI restriction enzyme site, which is absent at the target site, between two short homology arms. PCR amplicons were digested with XbaI in an RFLP assay to detect sequences that resulted from homology-directed repair.

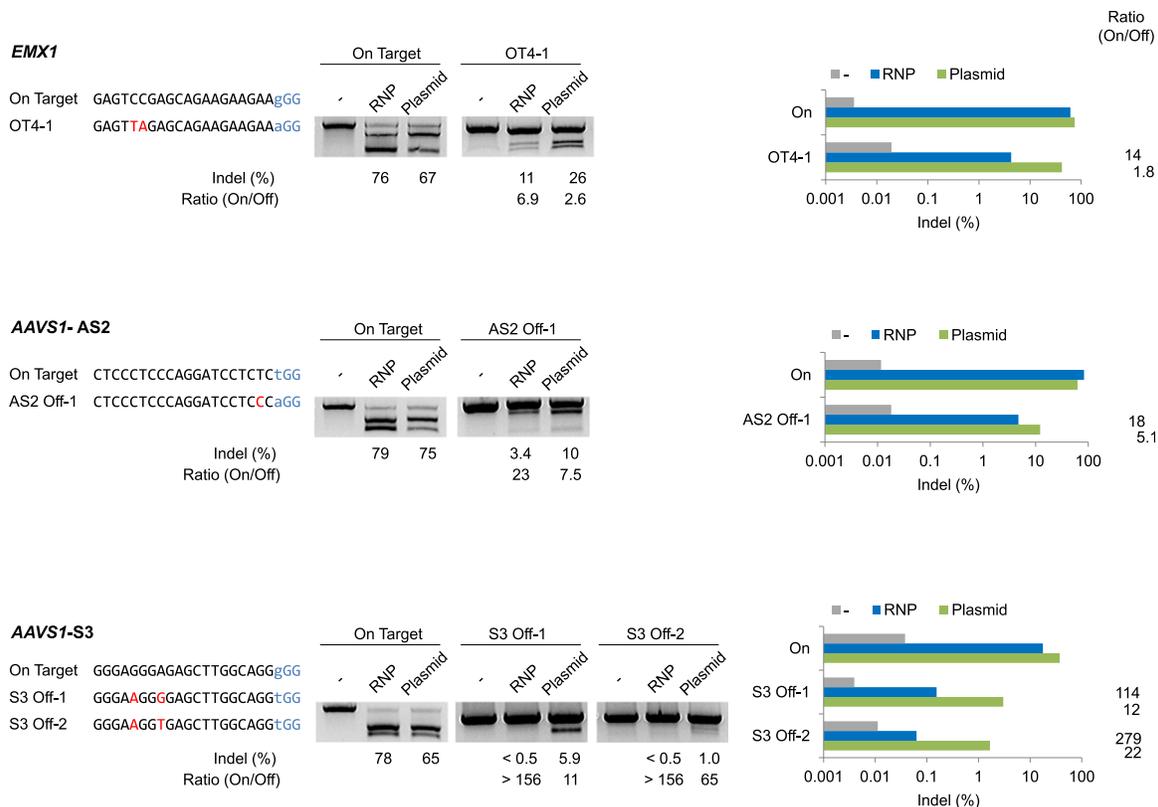
this end, we chose three RGENs that were previously shown to induce off-target mutations at high frequencies in human cells (Fu et al. 2013; Cho et al. 2014) and compared RNP delivery with

plasmid transfection. The three RGENs delivered via RNPs were highly active, inducing site-specific mutations at frequencies that ranged from 76% to 79%, and discriminated on-target sites from off-target sites more efficiently than did those delivered via plasmid transfection (Fig. 5). Thus, no mutations were detected using the T7E1 assay at two off-target sites that differ by 2 nucleotides (nt) from the on-target site, when the RGEN specific to the AAVS1-S3 site was delivered via RNP electroporation. In contrast, the same RGEN delivered via plasmids induced off-target mutations at these sites at frequencies of 6% and 1%, respectively. Importantly, RNP delivery did not sacrifice genome-editing activities at on-target sites, while reducing off-target effects.

We then used deep sequencing to quantify off-target mutations induced by RGEN plasmids and RNPs more accurately. Again, the three RGEN RNPs discriminated on-target sites from off-target sites much more efficiently than did plasmid-driven RGENs. Thus, the RGEN RNP specific to the AAVS1-S3 site induced off-target indels at frequencies of 0.15% and 0.06%. As a result, the ratio of the indel frequency at the on-target site to that at the two off-target sites was 114 and 279, when RNPs were delivered, whereas the ratio was 12 and 22, respectively, when plasmids were transfected, demonstrating 9.5- (114/12) and 13-fold (279/22) differences, respectively, between the two methods.



**Figure 4.** Targeted chromosomal deletions via RGEN RNPs. (A) RGEN target sites in the region of the CCR5 locus. The distances between the CCR5 site and each of the other sites are shown. Arrows indicate PCR primers. Red arrowheads indicate sgRNA target sites. (B) PCR products corresponding to deletions in K562 cells treated with RGEN RNPs; 15  $\mu$ g of Cas9 protein premixed with 20  $\mu$ g each of two sgRNAs was transfected into  $2 \times 10^5$  K562 cells. (C) DNA sequences of deletion-specific PCR products. In cases in which a sequence was detected more than once, the number of occurrences is shown in parentheses.



**Figure 5.** Off-target mutations caused by RGEN RNPs vs. RGEN plasmids. RGEN RNPs or plasmids that encode Cas9 and sgRNA were electroporated into K562 cells. Mutations were detected using the T7E1 assay (left) and deep sequencing (right). The PAM sequence is shown in blue. Mismatched bases are shown in red.

### Kinetics of RGEN RNP-mediated genome editing

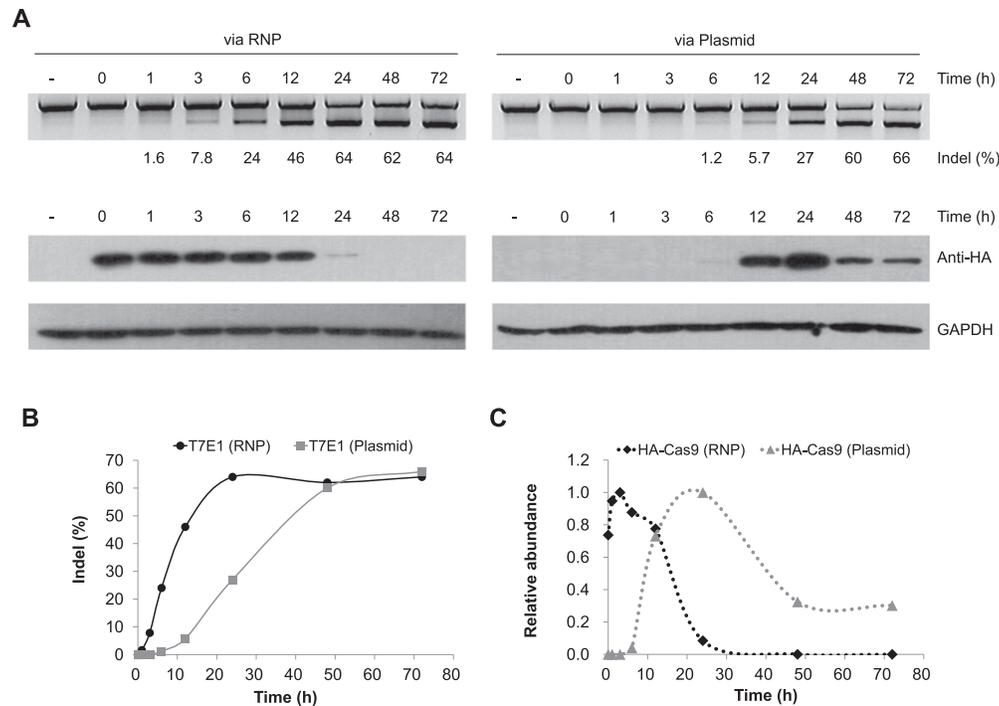
We performed a time-course T7E1 assay and Western blotting to understand the molecular basis of the discrepancy between RNP and plasmid delivery. The T7E1 assay showed that RGEN RNPs cleaved chromosomal DNA almost immediately after delivery and that the mutation frequency reached a plateau one day after electroporation (Fig. 6). In contrast, it took three days to reach an equivalent level of mutations when RGENs were expressed via plasmid transfection. Western blotting analysis showed that Cas9 protein was rapidly degraded in cells when delivered directly: At 24 h post-transfection, Cas9 was barely detected. In contrast, Cas9 protein was expressed from plasmid for several days. Apparently, continuous expression of Cas9 and sgRNA in cells gives rise to the accumulation of off-target mutations. These results are in line with those observed with the direct delivery of ZFNs, which reduces off-target effects (Gaj et al. 2012). Unlike ZFN production, however, preparation of new RGENs does not require time-consuming, fastidious, and labor-intensive steps to de novo engineer, express, and purify sequence-specific nucleases (Liu et al. 2014).

### Discussion

RNA-guided genome editing with the repurposed type II CRISPR/Cas system has been transforming almost every discipline in the life sciences, biotechnology, and medicine (Kim and Kim 2014). Compared with ZFNs and TALENs, RGENs are easy to make, affordable, and scalable, lowering barriers to genome editing. However, these programmable nucleases are limited by off-target effects and unwanted integration of plasmid vectors in the genome, un-

less mRNA or proteins are used. Furthermore, plasmid transfection is often inefficient and stressful to cells. To sidestep these limitations, we delivered RGEN RNPs, rather than plasmids, directly into cells via electroporation and showed that RGEN RNPs enable efficient genome editing even in human primary and ES cells that are refractory to DNA transfection, while reducing off-target effects and avoiding unwanted integration of plasmid DNA in the host genome. In an accompanying paper published in this issue, Ramakrishna et al. (2014) report that a cell-penetrating peptide can be used to deliver both the Cas9 protein and sgRNA into human cells. In principle, Cas9 protein can be replaced with Cas9 mRNA. Unlike mRNA that must be translated in cells, Cas9 protein works immediately after transfection into cells. Furthermore, it is difficult to check the activity of Cas9 mRNA before transfection, whereas the activity of Cas9 protein can be tested easily in vitro before transfection. Cas9 protein can also be used for genotyping of mutations induced by the same RGENs (Kim et al. 2014).

Recently, several groups independently reported that RGENs can cause unwanted mutations at off-target sites that differ by up to 5 nt from on-target sites, raising concerns about their specificities (Cradick et al. 2013; Fu et al. 2013; Hsu et al. 2013; Pattanayak et al. 2013). Off-target effects may result in chromosomal translocations, inactivation of tumor suppressor or other essential genes, and activation of oncogenes. We and others have proposed several methods to reduce or avoid off-target effects of RGENs. First, the concentration of sgRNA and Cas9 can be titrated to improve the ratio of on-target to off-target mutation rates (Hsu et al. 2013). Unfortunately, titrating RGEN concentrations also reduces on-target mutation frequencies. Second, the use of guide RNA with



**Figure 6.** Time-course analyses of RGEN-mediated genome editing via RNP delivery or plasmid transfection. (A, top) Mutation frequencies were determined by the T7E1 assay. (Bottom) Western blot analysis of K562 cells transfected with the *CCR5*-specific RGEN via RNP or plasmid DNA delivery. (B,C) Line graphs showing the results of the T7E1 (B) and Western blot analysis (C). Note that only the relative abundance of Cas9 in each experiment is shown.

two additional guanine bases at the 5' end (that do not match with target DNA sequences), termed 5'-ggX<sub>20</sub> sgRNA or crRNA, can discriminate on-target sites from off-target sites that differ by 2 nt efficiently without sacrificing on-target activities both in animals (Cho et al. 2013b; Sung et al. 2014) and in cell lines (Cho et al. 2013a, 2014). Interestingly, truncated sgRNAs can also decrease undesired off-target mutations, improving the specificity of RGENs (Fu et al. 2014). Third, paired Cas9 nickases (or RGENickases) that generate two adjacent single-strand breaks on opposite DNA strands, producing composite DSBs, double the specificity of RNA-guided genome engineering (Mali et al. 2013a; Ran et al. 2013; Cho et al. 2014), a strategy adopted from paired zinc finger nickases (Kim et al. 2012). Fourth, as shown in this study, RGEN RNPs can be used to reduce off-target effects. Last but not least, one should choose unique target sites that do not have homologous sequences elsewhere in the genome, a strategy we had used to avoid off-target effects of TALENs (Kim et al. 2013a). A web-based computer program that can be used for the identification of such sites is available (Bae et al. 2014). It may even be possible to combine these approaches to avoid off-target effects completely. Thus, delivery of RGENickase RNPs with two ggX<sub>20</sub> sgRNAs to target a unique sequence in the genome may further reduce off-target effects that persist even with the use of monomeric RGEN RNPs.

In conclusion, RGEN RNPs enable efficient and precise genome editing in diverse human cells including recalcitrant primary and pluripotent stem cells, while avoiding unwanted integration of plasmids and reducing off-target effects. We propose that RGEN RNP delivery will broaden the utility of RNA-guided genome engineering not only in basic research but also in biomedical applications and biotechnology by circumventing regulatory requirements associated with DNA transfection.

## Methods

### Cell culture

K562 (ATCC, CCL-243) cells were grown in RPMI-1640 with 10% FBS and a penicillin/streptomycin mix. BJ (ATCC, CRL-2522) fibroblasts were maintained in alpha-MEM supplemented with 10% FBS, 0.1 mM nonessential amino acids, and a penicillin/streptomycin mix. H9 human ES cells were maintained in DMEM/F12 (Gibco) supplemented with 20% knockout serum replacement (Gibco), 0.1 mM 2-mercaptoethanol (Gibco), 1% nonessential amino acids (Invitrogen), 8 ng/mL fibroblast growth factor-2 (Invitrogen), 50 U/mL penicillin, and 50 µg/mL streptomycin on mitotically inactivated mouse stromal cells.

### Recombinant Cas9 protein

Recombinant Cas9 protein was purchased from ToolGen, Inc. or purified from *E. coli*. The *Cas9* DNA sequence was subcloned into pET28-b(+). Recombinant Cas9 protein containing a nuclear localization signal, the HA epitope, and the His-tag at the N terminus was expressed in BL21(DE3) strain, purified using Ni-NTA agarose beads (Qiagen), and dialyzed against 20 mM HEPES pH 7.5, 150 mM KCl, 1 mM DTT, and 10% glycerol. The purified Cas9 protein was concentrated using Ultracel 100K cellulose column (Millipore). The purity and concentration of Cas9 protein were analyzed by SDS-PAGE.

### Guide RNA

RNA was in vitro transcribed through run-off reactions by T7 RNA polymerase using the MEGAshortscript T7 kit (Ambion) according to the manufacturer's manual. Templates for sgRNA or crRNA were

generated by annealing and extension of two complementary oligonucleotides (Supplemental Table 2). Transcribed RNA was purified by phenol:chloroform extraction, chloroform extraction, and ethanol precipitation. Purified RNA was quantified by spectrometry.

### Transfection

To introduce DSBs in mammalian cells using an RNP complex,  $2 \times 10^5$  cells were transfected with Cas9 protein (4.5–45  $\mu$ g) premixed with in vitro transcribed sgRNA (6–60  $\mu$ g). Cas9 protein in storage buffer (20 mM HEPES pH 7.5, 150 mM KCl, 1 mM DTT, and 10% glycerol) was mixed with sgRNA dissolved in nuclease-free water and incubated for 10 min at room temperature. No more than 4  $\mu$ L of the RNP mixture was added to 20  $\mu$ L of the Nucleofection solution. For plasmid-mediated expression of RGENs,  $2 \times 10^5$  cells were co-transfected with 1  $\mu$ g of Cas9-encoding plasmid and 1  $\mu$ g of sgRNA-expressing plasmid in K562 and BJ fibroblasts or 2.4  $\mu$ g of Cas9-encoding plasmid and 1.6  $\mu$ g of sgRNA-expressing plasmid in H9 hES cells. K562 cells were transfected with the Amaxa SF Cell Line 4D-Nucleofector Kit using Program FF-120 (Lonza), and H9 and BJ cells were transfected with the Amaxa P3 Primary Cell 4D-Nucleofector Kit using Program CB-150 and DT-130, respectively, according to the manufacturer's protocol. Cells were analyzed 2 d after transfection, unless indicated otherwise.

### Alkaline phosphatase (AP) staining

H9 human ES cells were fixed using 100% methanol for 10 min and then washed twice with Dulbecco's phosphate buffered saline (DPBS). AP staining was performed using the AP staining kit (Sigma) according to the manufacturer's instructions. Briefly, staining solution was prepared by mixing sodium nitrite solution, FRV-Alkaline solution, and AS-BI alkaline solution. Cells were incubated with the staining solution for 15 min and washed three times with DPBS.

### T7E1 assay

Genomic DNA was isolated using a genome isolation kit (Promega) according to the manufacturer's instructions. PCR amplicons including nuclease target sites were generated using the primers listed in Supplemental Table 2. The T7E1 assay was performed as previously described (Kim et al. 2009). Briefly, the PCR amplicons were denatured by heating and annealed to form heteroduplex DNA using a thermocycler and then digested with T7 endonuclease 1 (New England Biolabs) for 20 min at 37°C and then analyzed using agarose gel electrophoresis. For sequencing analysis, PCR products corresponding to genomic modifications were purified and cloned into the T-Blunt vector using the T-Blunt PCR Cloning Kit (SolGent). Cloned products were sequenced using the M13 primer.

### RFLP analysis for detection of ssODN-mediated homologous recombination

A total of  $2 \times 10^5$  K562 cells were co-transfected with 15  $\mu$ g of Cas9 protein mixed with 20  $\mu$ g of in vitro transcribed sgRNA and 500 pmol of ssODN (Supplemental Table 2). After 48 h, genomic DNA was isolated and subjected to PCR amplification with primers that flank the target site (Supplemental Table 2). PCR amplicons were digested with XbaI.

### Targeted deep sequencing

The on-target and off-target regions were amplified using Phusion polymerase (New England Biolabs) and used for library construc-

tion. Equal amounts of the PCR amplicons were subjected to paired-end read sequencing using Illumina MiSeq at Bio Medical Laboratories. Insertions or deletions located around the RGEN cleavage site (3 bp upstream of the PAM) were considered to be the mutations induced by RGENs.

### Data access

The deep sequencing data are available at the NCBI Sequence Read Archive (SRA) (<http://www.ncbi.nlm.nih.gov/sra>) under accession number SRX473144.

### Competing interest statement

The authors declare competing financial interests. S.K., S.W.C., and J.-S.K. have filed a patent application based on this work.

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### References

- Bae S, Park J, Kim JS. 2014. Cas-OFFinder: a fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. *Bioinformatics* doi: 10.1093/bioinformatics/btu048.
- Bibikova M, Beumer K, Trautman JK, Carroll D. 2003. Enhancing gene targeting with designed zinc finger nucleases. *Science* **300**: 764.
- Brunet E, Simsek D, Tomishima M, DeKaveler R, Choi VM, Gregory P, Urnov F, Weinstock DM, Jasin M. 2009. Chromosomal translocations induced at specified loci in human stem cells. *Proc Natl Acad Sci* **106**: 10620–10625.
- Budman J, Chu G. 2005. Processing of DNA for nonhomologous end-joining by cell-free extract. *EMBO J* **24**: 849–860.
- Carlson DE, Tan W, Lillico SG, Stverakova D, Proudfoot C, Christian M, Voytas DF, Long CR, Whitelaw CB, Fahrenkrug SC. 2012. Efficient TALEN-mediated gene knockout in livestock. *Proc Natl Acad Sci* **109**: 17382–17387.
- Chen F, Pruett-Miller SM, Huang Y, Gjoka M, Duda K, Taunton J, Collingwood TN, Frodin M, Davis GD. 2011. High-frequency genome editing using ssDNA oligonucleotides with zinc-finger nucleases. *Nat Methods* **8**: 753–755.
- Cho SW, Kim S, Kim JM, Kim JS. 2013a. Targeted genome engineering in human cells with the Cas9 RNA-guided endonuclease. *Nat Biotechnol* **31**: 230–232.
- Cho SW, Lee J, Carroll D, Kim JS. 2013b. Heritable gene knockout in *Caenorhabditis elegans* by direct injection of Cas9-sgRNA ribonucleoproteins. *Genetics* **195**: 1177–1180.
- Cho SW, Kim S, Kim Y, Kweon J, Kim HS, Bae S, Kim JS. 2014. Analysis of off-target effects of CRISPR/Cas-derived RNA-guided endonucleases and nickases. *Genome Res* **24**: 132–141.
- Cong L, Ran FA, Cox D, Lin S, Barretto R, Habib N, Hsu PD, Wu X, Jiang W, Marraffini LA, et al. 2013. Multiplex genome engineering using CRISPR/Cas systems. *Science* **339**: 819–823.
- Cradick TJ, Fine EJ, Antico CJ, Bao G. 2013. CRISPR/Cas9 systems targeting  $\beta$ -globin and CCR5 genes have substantial off-target activity. *Nucleic Acids Res* **41**: 9584–9592.
- Dickinson DJ, Ward JD, Reiner DJ, Goldstein B. 2013. Engineering the *Caenorhabditis elegans* genome using Cas9-triggered homologous recombination. *Nat Methods* **10**: 1028–1034.
- Friedland AE, Tzur YB, Esvelt KM, Colaiacovo MP, Church GM, Calarco JA. 2013. Heritable genome editing in *C. elegans* via a CRISPR-Cas9 system. *Nat Methods* **10**: 741–743.
- Fu Y, Foden JA, Khayter C, Maeder ML, Reyon D, Joung JK, Sander JD. 2013. High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells. *Nat Biotechnol* **31**: 822–826.
- Fu Y, Sander JD, Reyon D, Cascio VM, Joung JK. 2014. Improving CRISPR-Cas nuclease specificity using truncated guide RNAs. *Nat Biotechnol* **32**: 279–284.
- Gabriel R, Lombardo A, Arens A, Miller JC, Genovese P, Kaepffel C, Nowrouzi A, Bartholomae CC, Wang J, Friedman G, et al. 2011. An unbiased

- genome-wide analysis of zinc-finger nuclease specificity. *Nat Biotechnol* **29**: 816–823.
- Gaj T, Guo J, Kato Y, Sirk SJ, Barbas CF III. 2012. Targeted gene knockout by direct delivery of zinc-finger nuclease proteins. *Nat Methods* **9**: 805–807.
- Gratz SJ, Cummings AM, Nguyen JN, Hamm DC, Donohue LK, Harrison MM, Wildonger J, O'Connor-Giles KM. 2013. Genome engineering of *Drosophila* with the CRISPR RNA-guided Cas9 nuclease. *Genetics* **194**: 1029–1035.
- 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.
- Horvath P, Barrangou R. 2010. CRISPR/Cas, the immune system of bacteria and archaea. *Science* **327**: 167–170.
- Hsu PD, Scott DA, Weinstein JA, Ran FA, Konermann S, Agarwala V, Li Y, Fine EJ, Wu X, Shalem O, et al. 2013. DNA targeting specificity of RNA-guided Cas9 nucleases. *Nat Biotechnol* **31**: 827–832.
- Hwang WY, Fu Y, Reyon D, Maeder ML, Tsai SQ, Sander JD, Peterson RT, Yeh JR, Joung JK. 2013. Efficient genome editing in zebrafish using a CRISPR-Cas system. *Nat Biotechnol* **31**: 227–229.
- Jiang W, Bikard D, Cox D, Zhang F, Marraffini LA. 2013. RNA-guided editing of bacterial genomes using CRISPR-Cas systems. *Nat Biotechnol* **31**: 233–239.
- Jinek M, East A, Cheng A, Lin S, Ma E, Doudna J. 2013. RNA-programmed genome editing in human cells. *eLife* **2**: e00471.
- Kim H, Kim JS. 2014. A guide to genome engineering with programmable nucleases. *Nat Rev Genet* **15**: 321–334.
- Kim HJ, Lee HJ, Kim H, Cho SW, Kim JS. 2009. Targeted genome editing in human cells with zinc finger nucleases constructed via modular assembly. *Genome Res* **19**: 1279–1288.
- Kim JS, Lee HJ, Carroll D. 2010. Genome editing with modularly assembled zinc-finger nucleases. *Nat Methods* **7**: 91 (author reply 91–92).
- Kim S, Lee MJ, Kim H, Kang M, Kim JS. 2011. Preassembled zinc-finger arrays for rapid construction of ZFNs. *Nat Methods* **8**: 7.
- Kim E, Kim S, Kim DH, Choi BS, Choi IY, Kim JS. 2012. Precision genome engineering with programmable DNA-nicking enzymes. *Genome Res* **22**: 1327–1333.
- Kim Y, Kweon J, Kim A, Chon JK, Yoo JY, Kim HJ, Kim S, Lee C, Jeong E, Chung E, et al. 2013a. A library of TAL effector nucleases spanning the human genome. *Nat Biotechnol* **31**: 251–258.
- Kim Y, Kweon J, Kim JS. 2013b. TALENs and ZFNs are associated with different mutation signatures. *Nat Methods* **10**: 185.
- Kim JM, Kim D, Kim S, Kim JS. 2014. Genotyping with CRISPR-Cas-derived RNA-guided endonucleases. *Nat Commun* **5**: 3157.
- Lee HJ, Kim E, Kim JS. 2010. Targeted chromosomal deletions in human cells using zinc finger nucleases. *Genome Res* **20**: 81–89.
- Lee HJ, Kweon J, Kim E, Kim S, Kim JS. 2012. Targeted chromosomal duplications and inversions in the human genome using zinc finger nucleases. *Genome Res* **22**: 539–548.
- Li D, Qiu Z, Shao Y, Chen Y, Guan Y, Liu M, Li Y, Gao N, Wang L, Lu X, et al. 2013a. Heritable gene targeting in the mouse and rat using a CRISPR-Cas system. *Nat Biotechnol* **31**: 681–683.
- Li JF, Norville JE, Aach J, McCormack M, Zhang D, Bush J, Church GM, Sheen J. 2013b. Multiplex and homologous recombination-mediated genome editing in *Arabidopsis* and *Nicotiana benthamiana* using guide RNA and Cas9. *Nat Biotechnol* **31**: 688–691.
- Li W, Teng F, Li T, Zhou Q. 2013c. Simultaneous generation and germline transmission of multiple gene mutations in rat using CRISPR-Cas systems. *Nat Biotechnol* **31**: 684–686.
- Liu J, Gaj T, Patterson JT, Sirk SJ, Barbas CF III. 2014. Cell-penetrating peptide-mediated delivery of TALEN proteins via bioconjugation for genome engineering. *PLoS ONE* **9**: e85755.
- Mali P, Aach J, Stranges PB, Esvelt KM, Moosburner M, Kosuri S, Yang L, Church GM. 2013a. CAS9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering. *Nat Biotechnol* **31**: 833–838.
- Mali P, Yang L, Esvelt KM, Aach J, Guell M, DiCarlo JE, Norville JE, Church GM. 2013b. RNA-guided human genome engineering via Cas9. *Science* **339**: 823–826.
- Miller JC, Tan S, Qiao G, Barlow KA, Wang J, Xia DF, Meng X, Paschon DE, Leung E, Hinkley SJ, et al. 2011. A TALE nuclease architecture for efficient genome editing. *Nat Biotechnol* **29**: 143–148.
- Nekrasov V, Staskawicz B, Weigel D, Jones JD, Kamoun S. 2013. Targeted mutagenesis in the model plant *Nicotiana benthamiana* using Cas9 RNA-guided endonuclease. *Nat Biotechnol* **31**: 691–693.
- Pattanayak V, Lin S, Guilinger JP, Ma E, Doudna JA, Liu DR. 2013. High-throughput profiling of off-target DNA cleavage reveals RNA-programmed Cas9 nuclease specificity. *Nat Biotechnol* **31**: 839–843.
- Pauwels K, Podevin N, Breyer D, Carroll D, Herman P. 2014. Engineering nucleases for gene targeting: safety and regulatory considerations. *New Biotechnol* **31**: 18–27.
- Podevin N, Davies HV, Hartung F, Nogue F, Casacuberta JM. 2013. Site-directed nucleases: a paradigm shift in predictable, knowledge-based plant breeding. *Trends Biotechnol* **31**: 375–383.
- Porteus MH, Baltimore D. 2003. Chimeric nucleases stimulate gene targeting in human cells. *Science* **300**: 763.
- Ramakrishna S, Kwaku Dad AB, Beloor J, Gopalappa R, Lee SK, Kim H. 2014. Gene disruption by cell-penetrating peptide-mediated delivery of Cas9 protein and guide RNA. *Genome Res* (this issue). doi: 10.1101/gr.171264.113.
- Ran FA, Hsu PD, Lin CY, Gootenberg JS, Konermann S, Trevino AE, Scott DA, Inoue A, Matoba S, Zhang Y, et al. 2013. Double nicking by RNA-guided CRISPR Cas9 for enhanced genome editing specificity. *Cell* **154**: 1380–1389.
- Shan Q, Wang Y, Li J, Zhang Y, Chen K, Liang Z, Zhang K, Liu J, Xi JJ, Qiu JL, et al. 2013. Targeted genome modification of crop plants using a CRISPR-Cas system. *Nat Biotechnol* **31**: 686–688.
- Sun L, Wu J, Du F, Chen X, Chen ZJ. 2013. Cyclic GMP-AMP synthase is a cytosolic DNA sensor that activates the type I interferon pathway. *Science* **339**: 786–791.
- Sung YH, Baek IJ, Kim DH, Jeon J, Lee J, Lee K, Jeong D, Kim JS, Lee HW. 2013. Knockout mice created by TALEN-mediated gene targeting. *Nat Biotechnol* **31**: 23–24.
- Sung YH, Kim JM, Kim HT, Lee J, Jeon J, Jin Y, Choi JH, Ban YH, Ha SJ, Kim CH, et al. 2014. Highly efficient gene knockout in mice and zebrafish with RNA-guided endonucleases. *Genome Res* **24**: 125–131.
- Wagner H. 2001. Toll meets bacterial CpG-DNA. *Immunity* **14**: 499–502.
- Wang H, Yang H, Shivalila CS, Dawlaty MM, Cheng AW, Zhang F, Jaenisch R. 2013. One-step generation of mice carrying mutations in multiple genes by CRISPR/Cas-mediated genome engineering. *Cell* **153**: 910–918.
- Wiedenheft B, Sternberg SH, Doudna JA. 2012. RNA-guided genetic silencing systems in bacteria and archaea. *Nature* **482**: 331–338.

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