Supplementary information

Efficient CRISPR-Cas9-based knockdown of RUNX2 to induce chondrogenic differentiation of stem cells

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Materials and Methods

T7E1 assay

Genomic DNA was extracted from control hMSCs and hMSCs transfected with CRISPR-Cas9 vectors #1 and #2. Mismatched duplex DNA was obtained by denaturation/renaturation of 25 μ l of the genomic PCR samples using the following conditions: 95°C for 10 min, 95°C to 85°C (-2.0°C/s), 85°C for 1 min, 85°C to 75°C (-0.3°C/s), 75°C for 1 min, 75°C to 65°C (-0.3°C/s), 65°C for 1 min, 65°C to 55°C (-0.3°C/s), 55°C for 1 min, 55°C to 45°C (-0.3°C/s), 45°C for 1 min, 45°C to 35°C (-0.3°C/s), 35°C for 1 min, 35°C to 25°C (-0.3°C/s), 25°C for 1 min, and hold at 4°C. Each sample was supplemented with 3 μ l of 10× NEB buffer 2, 0.3 μ l of T7E1, and distilled water up to 30 μ l. Digestion reactions were incubated for 1 h at 37°C. T7E1-digested PCR products were analyzed by electrophoresis. The undigested PCR product migrated at 616 bp and the digestion products of CRISPR-Cas9 vectors #1 and #2 migrated at approximately 292/392 bp and 224/324 bp, respectively.

Gel retardation assay

After complexation of DNPs, LPEI, and vectors, various amounts of each sample were loaded into a 1.5% agarose gel and stained with MG04 (Midori Green Advance; Nippon Genetics). Electrophoresis was performed in 0.5× TAE buffer at 100 V for 13 min. DNA bands were detected by a gel documentation imaging system (BR170-8265, Bio-Rad Laboratories).



Figure S1. Schematic diagram of the complexation of CRISPR-Cas9 (A) and shRNA (B) vectors with NPs.



Figure S2. T7E1 assay of CRISPR-Cas9 plasmids for knockdown of RUNX2



(a) Control
(b) One shRNA vector
(c) Two shRNA vectors
(d) CRISPR-Cas9 vector
(e) DNP + empty vector
(f) DNP + One shRNA vector
(g)DNP + Two shRNA vectors
(h) DNP + CRISPR-Cas9 vector

Figure S3. Gel electrophoresis analysis of shP-NPs and CASP-NPs.

Confirmation of complexation between DNPs and shRNA and CRISPR-Cas9 vectors.



Figure S4. DLS analysis of DNPs complexed with various vectors.

DLS analysis of the sizes and zeta-potentials of DNPs complexed with various vectors.



Figure S5. FACS analysis of MG63 cells treated with shP-NPs and CASP-NPs.

FACS analysis of the transfection efficiency of shP-NPs and CASP-NPs in MG63 cells.

The percentage of cells positive for GFP was determined.



Figure S6. Investigation of the cytotoxic effects of shPNP, shPNPs, and CasPNP on MG63 cells after 72 h by the LIVE/DEAD assay.



Figure S7. Analysis of mRNA and protein expression of RUNX2 over time in MG63 cells treated with control NPs (CPNP) and CasPNP by RT-PCR (a) and Western blotting (b).



Figure S8. Effects of shPNP, shPNPs, and CasPNP on mRNA expression of RUNX2 in hMSCs.

RT-PCR analysis of the mRNA levels of RUNX2 in hMSCs treated with shP-NP, shP-NPs, and CASP-NP for 24, 48, and 72 h.



Figure S9. Assessment of inorganic mineralization in hMSCs treated with shP-NP, shP-NPs, and CASP-NP by Alizarin Red staining.