



Supporting Information

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Exosome–Liposome Hybrid Nanoparticles Deliver CRISPR/
Cas9 System in MSCs

*Yao Lin, Jiahua Wu, Weihuai Gu, Yulei Huang, Zhongchun
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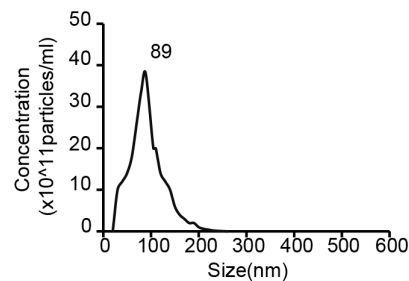


Figure S1. Size distribution of HEK293FT cell derived exosomes determined by Nanoparticle Tracking Analysis.

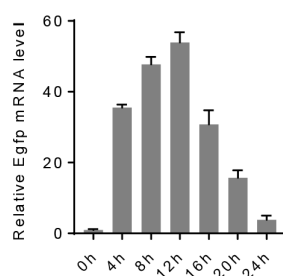


Figure S2. qRT-PCR analysis of EGFP mRNA level in the MSCs treated with hybrid exosomes encapsulating pEGFP-C1 plasmid manipulated by incubation for 0h, 4h, 8h, 12h, 16h, 20h and 24h.

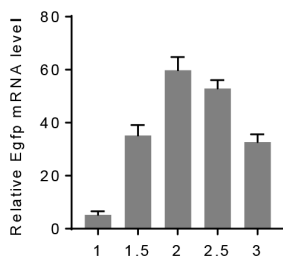


Figure S3. qRT-PCR analysis of EGFP mRNA level in the MSCs treated with the hybrid exosomes manipulated by incubating indicated ratio of exosomes (10^9 in $100 \mu\text{L}$) to liposomes.

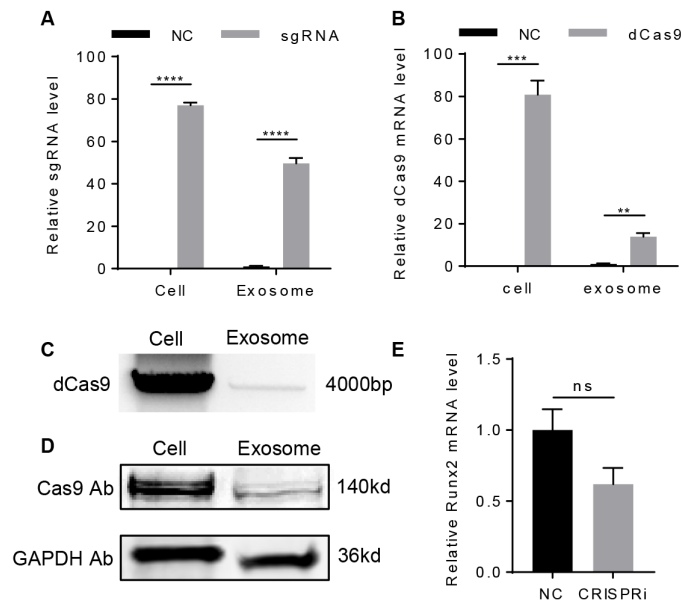


Figure S4. Transfection in cells fails to encapsulate CRISPR/dCas9 into exosomes. (A) qRT-PCR analysis of cellular and exosomal sgRNA levels in HEK293FT cells and the derivative exosomes. Cells were transfected with control or sgRNA expressing lentiviral vector. Data were expressed as mean \pm SEM of three different experiments. * p <0.05. (B) qRT-PCR analysis of cellular and exosomal dCas9 mRNA levels in HEK293FT cells and the derivative exosomes. Cells were transfected with control or dCas9 expressing lentiviral vector. Data were expressed as mean \pm SEM of three different experiments. * p <0.05. (C) Semi-quantitative PCR analysis of the expression of full length of dCas9 mRNA in HEK293FT cells and the derivative exosomes. Cells were transfected with dCas9 expressing lentiviral vector. Representative image of three different experiments. (D) The protein levels of Cas9 and GAPDH in HEK293FT cells and the derivative exosomes. Cells were transfected with dCas9 expressing lentiviral vector. GAPDH served as internal control. Representative image of three different experiments. (E) Runx2 mRNA level in mesenchymal stem cells with the exosomes derived from HEK293FT cells transfected with control or Runx2 sgRNA plus dCas9

expressing plasmids. Data were expressed as mean \pm SEM of three different experiments.

*p<0.05.

Table S1. Sequences of the primers used in the study.

| Primer | Sequence |
|---------------------|-----------------------------------|
| mRunx2 sgRNA F | CACCGTCACAGTACTCAAAGTAAAG |
| mRunx2 sgRNA R | AAACCTTTACTTTGAGTACTGTGAC |
| hCTNNB1 sgRNA F | CACCGGACAAAAGTCTAAATGACG |
| hCTNNB1 sgRNA R | AAACCGTCATTTAGCAGTTTTGTCC |
| dCas9 PCR F | GGAAGCTTCCATGGACAAGAAGTACAGCATCGG |
| dCas9 PCR R | CCGGATCCTTAAGCGGCCGCCACCTTCCTCTT |
| hCTNNB1 PCR F | CTGAAAGTCAGAATGCAGTTTTGAG |
| hCTNNB1 PCR R | TGGTATTGGGTAGACATTCTGAAAC |
| eGFP qPCR F | CTCGTGACCACCCTGACCTAC |
| eGFP qPCR R | GTTACCTTGATGCCGTTCTT |
| mRunx2 qPCR F | GGAGTGGACGAGGCAAGAGTTT |
| mRunx2 qPCR R | AGCTTCTGTCTGTGCCTTCTGG |
| dCas9 qPCR F | GTGGACGCTATCGTGCCT |
| dCas9 qPCR R | GCCGCCAGTAGTTCTTCAT |
| mRunx2 sgRNA qPCR F | AAAGATTGAGAAAGAGGGAGT |
| mRunx2 sgRNA qPCR R | GCCAAGTTGATAACGGACTA |
| mGAPDH qPCR F | GTGAAGGTCGGTGTGAAC |
| mGAPDH qPCR R | TGAGTGGAGTCATACTGGAA |