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Supplementary information

CRISPR/nCas9-Based Genome Editing on GM2 Gangliosidoses Fibroblasts via Non-Viral Vectors

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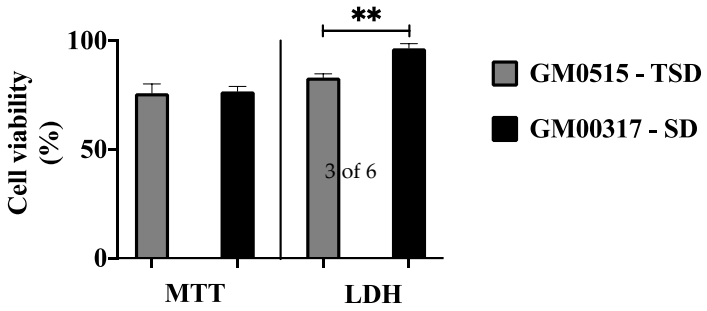
Content

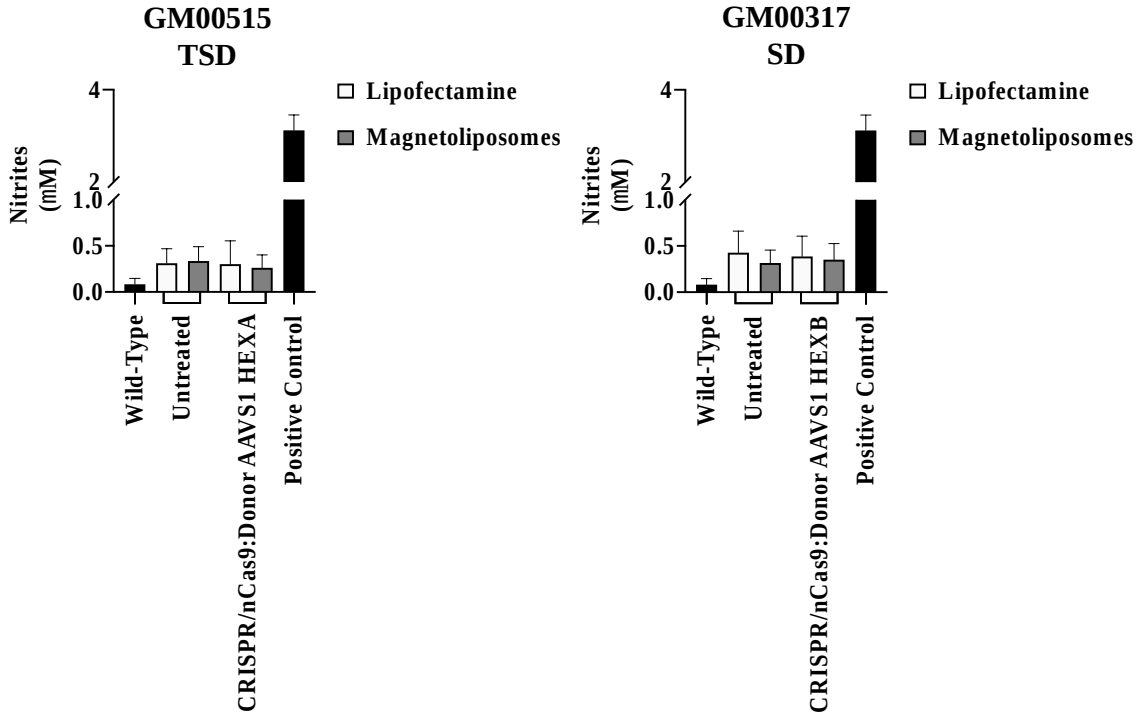
Supplementary Table S1. List of primers used in this study. The sequences for MfeI and MluI enzymes are highlighted in yellow and green, respectively. *Sequences correspond to Leal & Alméciga, 2022 [1].

Purpose	Target	Forward (5′ to 3′)	Reverse (5′ to 3′)
HEXA ORF amplification	*HEXA*	CGATCAATTGATGGCAAGCTCCAGGCTT	ATCGACGCGTGGTCTGTTCAAACTCCTG
HEXB ORF amplification	*HEXB*	CGATCAATTGATGGAGCTGTGCGGGCTG	ATCGACGCGTCATGTTCTCATGGTTACAA-TATCCAGC
*Homologous recombination assay	AAVS1-Out	TTCGATTGGAGTCGCTTTAACTG	-
	CMV	-	AGCTCTGCTTATATAGACCTCC

Supplementary Figure S1. MTT and LDH assays. The figure shows the % of cell viability of GM2 fibroblasts after their interaction with 25μg/mL/0.05mg/mL MNPs@Ag-pD/BUF-II:liposome for 48 hours. ** $p \leq 0.01$.



Supplementary Figure S2. Nitric oxide determination. The figure shows the effect of the long-term CRISPR/nCas9-based genome edition on GM2 fibroblasts. Positive control corresponds to the incubation of fibroblasts with 1μM lipopolysac-charide Escherichia coli O111:B4.



Supplementary Reference

1. Leal, A.F. and C.J. Alméciga-Díaz, *Efficient CRISPR/Cas9 nickase-mediated genome editing in an in vitro model of mucopolysaccharidosis IVA.* Gene Ther, 2022.