

Article

Cell cycle stage and DNA repair pathway influence CRISPR/Cas9 gene editing efficiency in porcine embryos

Karina Gutierrez¹, Werner G. Glanzner¹, Mariana P. de Macedo¹, Vitor B. Rissi², Naomi Dicks¹, Rodrigo C. Bohrer¹, Hernan Baldassarre¹, Luis B. Agellon^{3,*} and Vilceu Bordignon^{1,*}

Supplementary material

Table S1. Primers used for sgRNA synthesis.

Name	Sequence of the forward primers
XBP1_sgRNA1	(T7) GCTTGGTGTAGACCATTCGT (px330)
XBP1_sgRNA2	(T7) CCCAGCTGATTAGTGTCTA (px330)
FABP3_sgRNA1	(T7) GCTGGGATTGAGGGACAGGA (px330)
FABP3_sgRNA2	(T7) GGAACTCATCCTGGTAAGA (px330)
FABP6_sgRNA1	(T7) ACTCTCGATCTCATACTTGC (px330)
FABP6_sgRNA2	(T7) CGATGAGTTCATGAAGCGCT (px330)

(T7) corresponds to TAATACGACTCACTATAGG. (px330) corresponds to GTTTAGAGCTAGAAATAGC. The sequence of the reverse primer used for all forward primers is: AAAAGCACCGACTCGGTGCC.

Table S2. Primers used for genomic DNA amplification.

Gene	Sense	Antisense	Amplicon
<i>XBP1</i>	GAGAGCCAAGCTAATGTGGT	TGTCCAGTGACCCTTACCCA	602 bp
<i>FABP3</i>	AGCTGGGCTGTCTGACTCTA	TCCACCCTCCACTATCCAG	472 bp
<i>FABP6</i>	AATGGGATTCCAGCCAGCAA	TCGCAGCAGTAACATTGGGT	521 bp

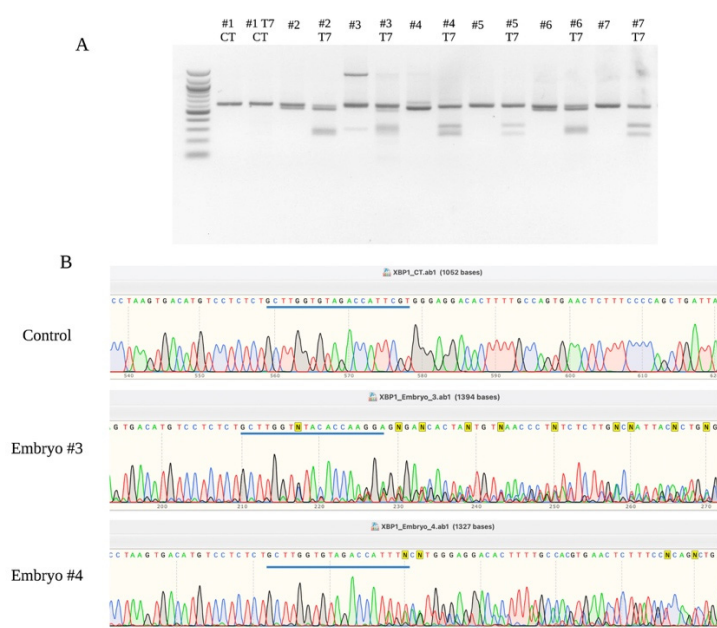


Figure S1. Genome editing analysis. **(A)** Agarose gel resolution before and after T7 Endonuclease I assay. Different pattern of bands is visible in the gel according to the induced mutations. **(B)** Direct Sanger Sequencing from three embryos: one control and two embryos where errors are visible in the chromatogram in the sgRNA position (blue line). This figure was assembled using BioRender.