

Supplementary data for the manuscript named:

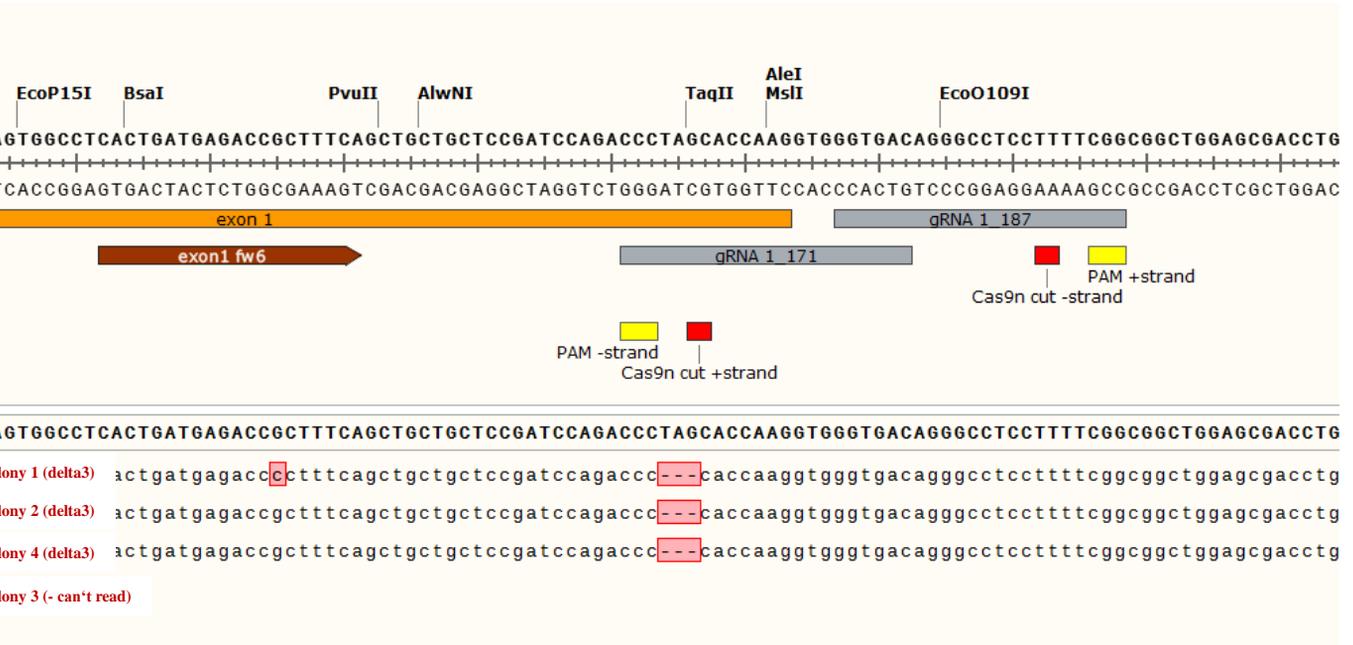
**Loss of Glyoxalase 1 Induces Compensatory Mechanism to Achieve
Dicarbonyl Detoxification in Mammalian Schwann Cells**

Sequencing results

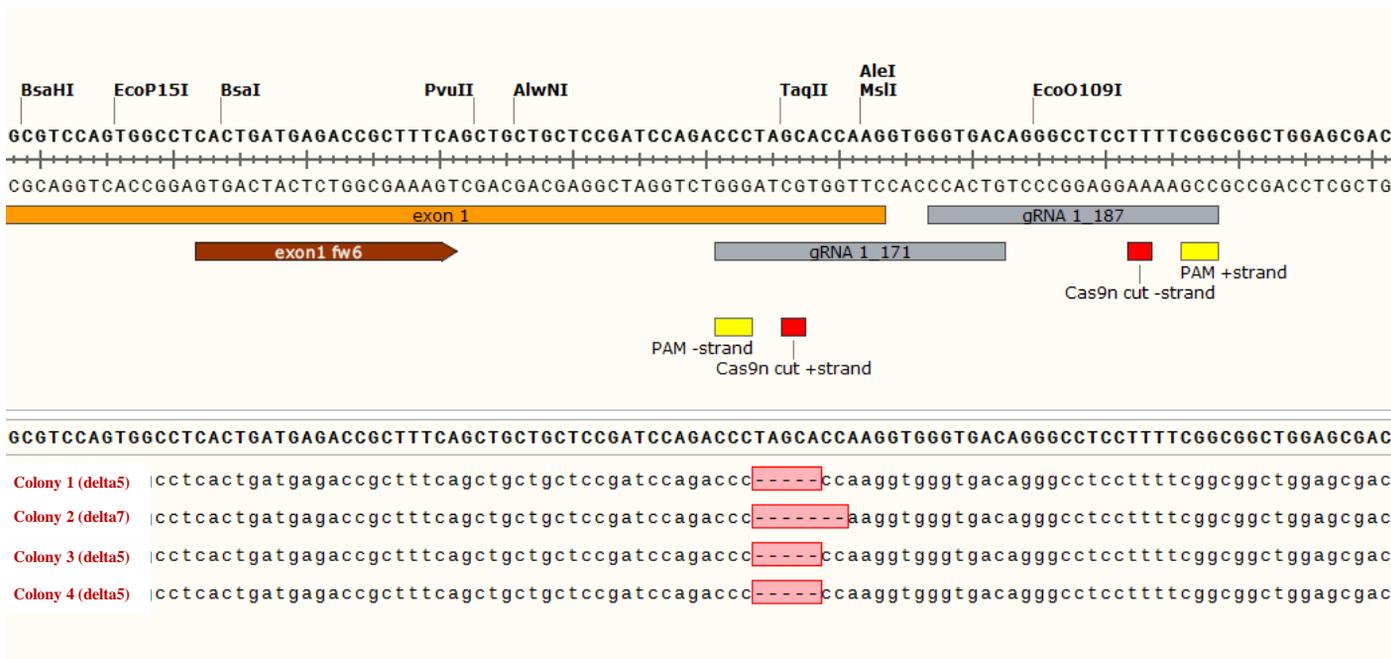
Clone #1 corresponds to #1 GLO^{-/-} in the manuscript



Clone #3 corresponds to #2 GLO^{-/-} in the manuscript



Clone #4 corresponds to #3 GLO^{-/-} in the manuscript



Materials & Methods for Sequencing:

CRISPR genotyping via subcloning & sequencing of PCR product DNA was extracted from one well of 6-well plate for each clone with the Qiagen DNeasy blood & tissue kit (catalog #69506) according to manufacturer's recommendations for cells. A PCR product with primers covering 421 bp around the Cas9 cleavage site of sgRNA_171 (forward: 5'-GCTGGCCTGTTTGCTACTAG-3'; reverse: 5'-AGACACGGAATCTGACCCTG-3') was generated with the following PCR conditions: The PCR product was run on a 2% agarose gel, the band was cut and extracted with the Qiagen QIAquick gel extraction kit (catalog #28706) according to manufacturer's recommendations. 20 ng DNA of the eluate from the gel extraction was subcloned into the pJET1.2/blunt vector with the Thermo Fisher Scientific CloneJET PCR Cloning Kit (catalog #K1231) according to the blunting protocol of the manufacturer. 2.5 μ L of the ligation reaction per clone was transformed into chemocompetent *E. coli* (DH5 α) and plated on ampicillin-containing agar plates. At least four colonies per clone were picked, grown overnight in ampicillin-containing LB medium and DNA was extracted with the Qiagen QIAprep spin miniprep kit (catalog #27106) according to manufacturer's recommendations. 15 μ L of the recovered DNA at a concentration of 75 ng/ μ L and 2 μ L of a nested sequencing primer (pJET1.2 forward sequencing primer: 5'-CGACTCACTATAGGGAGAGCGGC-3') at a concentration of 10 μ M were mixed and sent for Sanger sequencing to Eurofins MWG Operon. The sequences obtained from Eurofins were analyzed with SnapGene software.