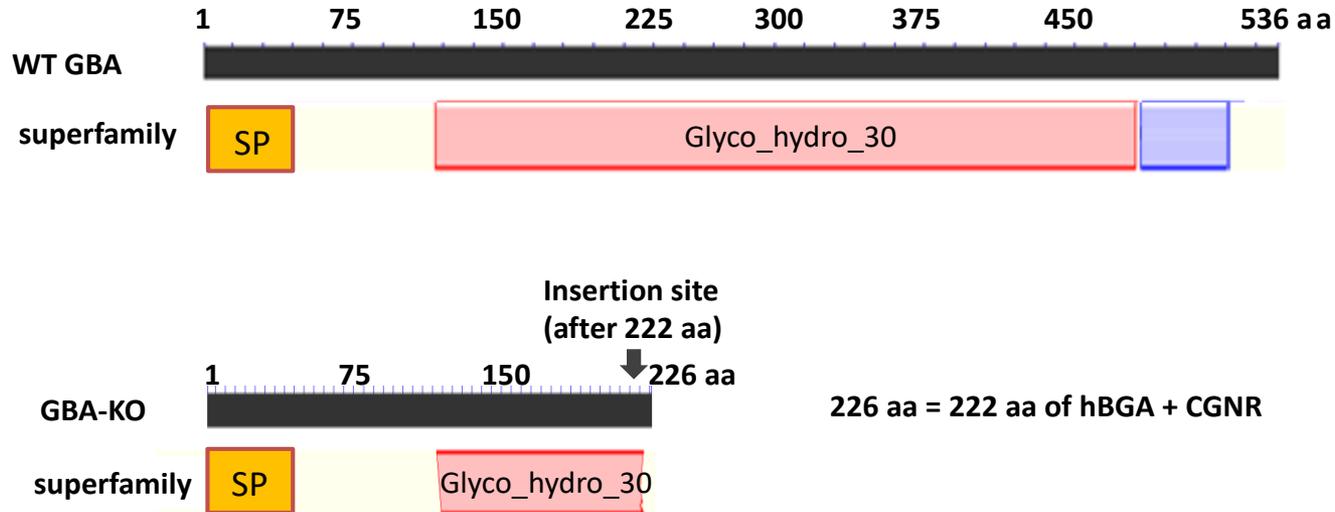


## A Conserved domain analysis of GBA in WT and KO line



## B Sequences of the 479 bp insertion

TGTGGCAACCGCTGAATATCGCCACCACCAGCGTGCTGCTGACGCTGGCCGATAACGACACGCCGGTGTGGCTTTCTACCC  
 CATTAAATAACGATATCGTCAACCAGAGCCTGCGTTTTTCATACCAACGCGCCGCTGGTCAGCCAGCCGGAACAGGCGACCT  
 TCGCGGTGACGGATGAGGCGATTTCCAGCGAACAGCTCAACGCCCTTTCCACCGGCACCGCCGTTGCGCCGGAAGCGGG  
 TGCGACGCTGATTTTACAGGTCGCCAGCCTGAGCGGCGGACGCATGTTGCGCCTTACTGGTGCGGGTATTGCCGAAGAAC  
 GAATGATCGCTCCGAGCTGCCGAAGTGCATTCTGCACGAACTCACCGAGCGCCCGCATCCGTTCCCCTCGGCATCGACC  
 TGATCCTGACCTGTGGCGAGCGCCTGCTGGCTATTCCGCGAACCACTCATGTGGAGGTGTGCTGATGTACGTTGCCG

**Supplementary Figure S1. (A)** Conserved domain analysis of WT and KO. Insertion in Exon 6 causes a premature termination of hBGA, resulting a truncation of the conserved catalytic domain of GBA. The deduced coding sequences for both WT-GBA and GBA-KO were used to search the conserved domain database (Marchler-Bauer A et al. CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. *Nucleic Acids Res.* 2017. 45(D)200-3). The conserved catalytic domain (glycol\_hydro\_30) is preserved in the WT (upper panels), but is mostly truncated in the GBA-KO line (lower panels). SP indicates the signal peptides (yellow box). The SP is predicted by SignalP-5.0 Server (Nielsen, H et al. A Brief History of Protein Sorting Prediction. *Protein J.* 2019. 38, 200–216). **(B)** Sequences of the 479 bp insertion after codon 222. The in-frame sequences of the insertion were underlined, which code CGNR before the stop codon of TGA.