Supporting information

The position of single-base deletions in the VNTR sequence of the carboxyl ester lipase (CEL) gene determines proteotoxicity

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Figure S2. Predicted amino acid sequence of the VNTR region of the normal CEL protein (WT) and of the investigated DEL variants.
Figure S1. Potential O-glycosylation sites of the VNTR region of the normal CEL protein (WT) and of the investigated DEL variants. For each CEL variant, theoretical O-glycosylation sites were predicted by the NetOGlyc3.1 server at http://www.cbs.dtu.dk/services/NetOGlyc. These sites were all located in the VNTR region and are indicated as red bars above the black line, with the total number of predicted sites listed on the right. VNTR segment numbers and borders (blue lines) of each variant are shown below the black line. For all deletion variants, the reading frame terminates within repeat 13. As indicated, the truncated control variant of CEL (TRUNC) has only one predicted O-glycosylation site.
Figure S2. Predicted amino acid sequence of the VNTR region of the normal CEL protein (WT) and of the investigated DEL variants. One-letter amino acid nomenclature is used, with predicted glycosylated residues (serine, S; threonine, T) highlighted in red. Cysteine residues (C), which may potentially form intra- and intermolecular disulfide bridges, are highlighted in black/green. The truncated control variant of CEL (TRUNC) terminates after the three first amino acids in repeat 1.