Figure S1. Associations of total celiprolol AUC\textsubscript{0-\infty} with genotype scores calculated with SLCO1A2 c.516A>C and ABCB1 SNVs.

(a) The genotype score equation of the candidate gene linear regression model employing ABCB1 SNVs, where n is the number of variant alleles (0, 1, or 2) of SLCO1A2 c. 516A>C, ABCB1 c.3435T>C, or ABCB1 c.2677T/G>A. (b) The total celiprolol geometric mean AUC\textsubscript{0-\infty} ratios between groups below and above each genotype score limit (circles) and respective $P$ values (triangles). The arrow depicts the optimal cut-off value.

(c) Genotype scores (GS) for individuals with different genotype combinations. ABCB1 and SLCO1A2 reference genotypes are depicted with white, heterozygous with gray and homozygous variant genotypes with black rectangles. (d) The LBW-adjusted AUC\textsubscript{0-\infty} values of total celiprolol grouped by genotype scores. The black lines in the gray areas depict the geometric mean and dashed lines the ± geometric standard deviation AUC\textsubscript{0-\infty} values for genotype score groups below and above the cut-off limit. The c.2677K indicates either the T or the G allele. (e) Geometric mean (90% CI) LBW-adjusted plasma concentrations of celiprolol after a single 200 mg oral dose of celiprolol in 195 healthy volunteers with different combinations of SLCO1A2 and ABCB1 genotypes. The insets depict the same data on a semilogarithmic scale. The volunteers were grouped according to the genotype score (GS) limit 0.65: GS $\leq$ 0.65 ($n$ = 22) and GS $>$ 0.65 ($n$ = 173).