



Figure S1. Associations of total celiprolol $AUC_{0-\infty}$ 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 $AUC_{0-\infty}$ 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 $AUC_{0-\infty}$ values of total celiprolol grouped by genotype scores. The black lines in the gray areas depict the geometric mean and dashed lines the \pm geometric standard deviation $AUC_{0-\infty}$ 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 $GS > 0.65$ ($n = 173$).