A potential role for human UDP-glucuronosyltransferase (UGT) 1A4 promoter SNPs in the pharmacogenomics of Tamoxifen and its derivatives

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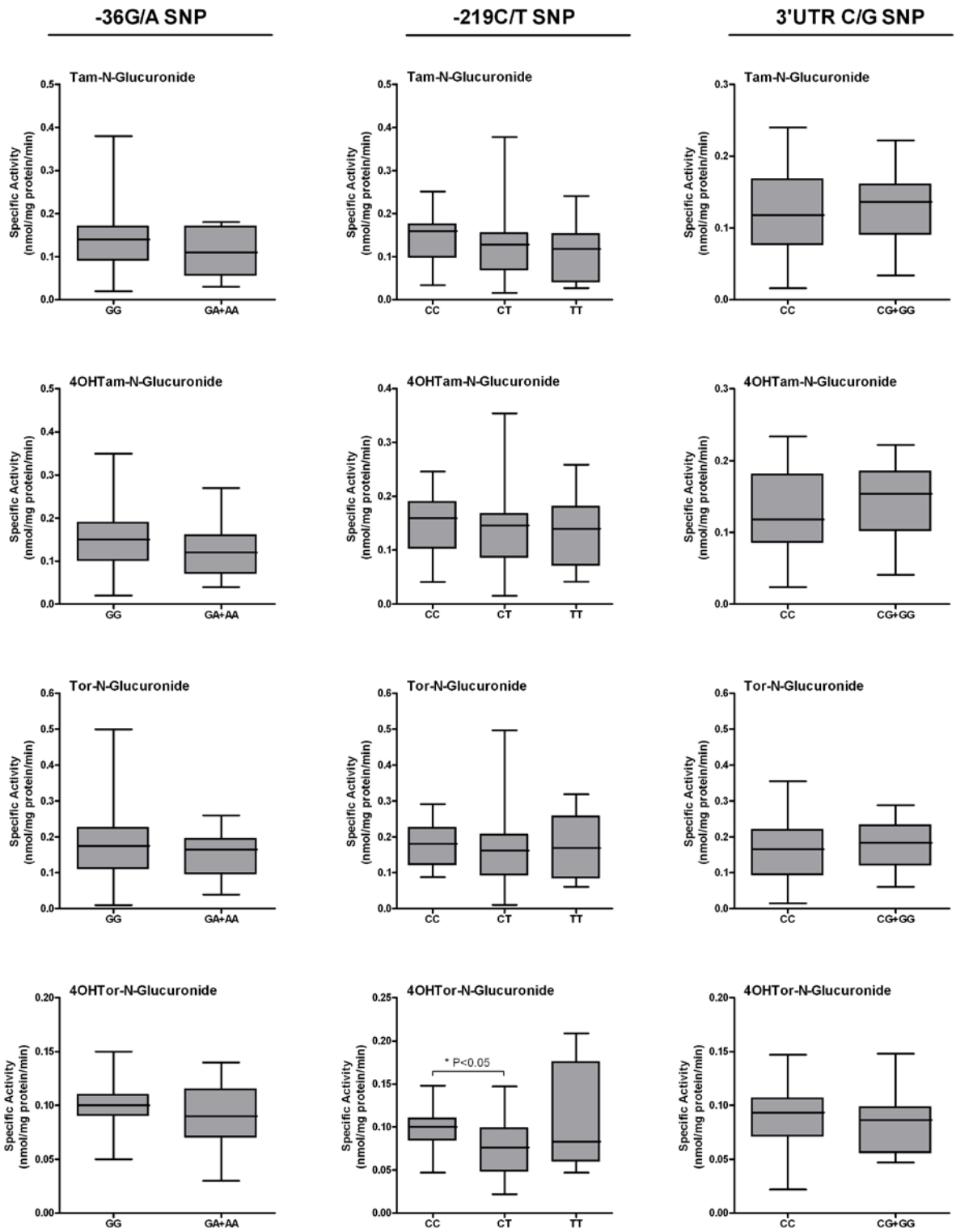
Supplemental Figure Legends

Supplemental Figure 1. Correlation between -36G/A and -219C/T Promoter and 3'UTR SNP genotypes and N-Glucuronidation. Activity toward Tam, 4OHTam, Tor, and 4OHTor among human liver microsomes with was compared among livers of known genotype at the -36G/A, -219C/T, and 3'UTR C/G positions. Because of the limited number of samples with the genotype AA at the -36 and 3'UTR SNPs, data were grouped as common allele vs. variant alleles. Data are displayed as box and whisker plots and were analyzed using either non-parametric ANOVA (Krustal-Wallis test) or to determine overall significance of the effect of this SNP with a Dunn's Multiple Comparison Post Test to determine the significance of the activity difference between each genotype (-219C/T) or a non-parametric t-test (Wilcoxon Rank Sums test; -36G/A & 3'UTR). No significant differences were seen unless indicated.

Supplemental Figure 2. Correlation between -36G/A, -136G/A, -217T/G and -219C/T Promoter SNP genotypes and O-Glucuronidation. Activity toward 4OHTam and 4OHTor among human liver microsomes with was compared among livers of known genotype at the -36G/A, -136G/A, -217T/G and -219C/T positions. Because of the limited number of samples with the genotype AA or GG at the -36 and 217 position, respectively, data were grouped as common allele vs. variant alleles. Data are displayed as box and whisker plots and were analyzed using either non-parametric ANOVA (Krustal-Wallis test) or to determine overall significance of the effect of this SNP with a Dunn's Multiple Comparison Post Test to determine the significance of the activity difference between each genotype (-136G/A & -219C/T) or a non-parametric t-test (Wilcoxon Rank Sums test; -36G/A & -217T/G). No significant differences were seen unless indicated. Because UGT1A4 only catalyzes N-glucuronidation, any changes to O-glucuronidation

activity are most likely due to alterations in another UGT1A subfamily enzyme.

Supplemenatal Figure 1.



Supplemental Figure 2.