Thiazide diuretics, commonly used antihypertensives, may cause QT interval (QT) prolongation, a risk factor for highly fatal and difficult to predict ventricular arrhythmias. We examined whether common single-nucleotide polymorphisms (SNPs) modified the association between thiazide use and QT or its component parts (QRS interval, JT interval) by performing ancestry-specific, trans-ethnic and cross-phenotype genome-wide analyses of European (66%), African American (15%) and Hispanic (19%) populations (N = 78,199), leveraging longitudinal data, incorporating corrected standard errors to account for underestimation of interaction estimate variances and evaluating evidence for pathway enrichment. Although no loci achieved genome-wide significance (P < 5 × 10−8), we found suggestive evidence (P < 5 × 10−6) for SNPs modifying the thiazide-QT association at 22 loci, including ion transport loci (for example, NELL1, KCNQ3). The biologic plausibility of our suggestive results and simulations demonstrating modest power to detect interaction effects at genome-wide significant levels indicate that larger studies and innovative statistical methods are warranted in future efforts evaluating thiazide–SNP interactions.

The Pharmacogenomics Journal (2018) 18, 215–226; doi:10.1038/tpj.2017.10; published online 18 July 2017
INTRODUCTION

Over the past decade, the use of prescription drugs has skyrocketed, with nearly half of all Americans now taking at least one prescription drug. Accompanying the increased prevalence of drug use is a high burden of adverse drug reactions (ADRs), which account for approximately 100,000 deaths and 2.2 million serious health effects annually.\(^2\) QT interval (QT) prolongation, which can trigger fatal ventricular arrhythmias, is a long-recognized adverse effect of numerous common medications, such as antipsychotics, antibiotics, antiarhythmics and antihypertensives.\(^3\) Within the past ten years, QT prolongation has represented the most common cause for withdrawal of a drug from the market (or relabeling) after approval by the US Food and Drug Administration (FDA).\(^4\) However, drug-induced QT prolongation remains difficult to predict.\(^5\)

Genetic variants are known to mediate both pharmacokinetic and pharmacodynamic processes, thereby playing a major role in drug response.\(^6\) Pharmacogenomics, which evaluates the role of genetics in drug response, offers a promising avenue for understanding variation in drug response,\(^7\) illuminating novel pathways, informing drug development and selection,\(^8\)\(^–\)\(^10\) optimizing dosing regimens\(^11\)\(^–\)\(^13\) and avoiding ADRs.\(^14\)\(^–\)\(^20\) QT is highly heritable (35–40%).\(^21\)\(^–\)\(^27\) Previous pharmacogenomics studies of drugs associated with QT prolongation, including thiazide diuretics, a common anti-hypertensive therapy used by over a quarter of the United States hypertensive population,\(^28\) identified multiple loci associated with anti-hypertensive response and ADRs.\(^29\)\(^–\)\(^34\) Furthermore, thiazide diuretics are used unequally across race/ethnic groups in the United States, with approximately 10% of Hispanic/Latinos, 13% of European Americans, and 23% of African Americans taking a thiazide diuretic.\(^28\)\(^,\)\(^35\)\(^–\)\(^36\) Therefore, the pharmacogenomics of thiazide-induced QT prolongation represents an excellent but understudied candidate for pharmacogenomic inquiry.

We previously examined evidence for common single-nucleotide polymorphisms (SNPs) that modified the association between thiazide use and QT and failed to identify any genome-wide significant loci (\(P < 5 \times 10^{-8}\)).\(^37\) However, our previous study was limited to European descent populations and cross-sectional analyses, despite many of the contributing studies having longitudinal drug and electrocardiographic data.\(^37\) Here, we expand upon that work, applying recent statistical innovations to leverage longitudinal data and including an additional 44,418 participants of European, African American, and Hispanic/Latino descent to perform the first trans-ethnic genome-wide association study (GWAS) to examine genetic associations that modify the association between thiazides and QT, as well as the component parts of QT (JT interval (JT), QRS interval (QRS)).

MATERIALS AND METHODS

Study populations

Fourteen cohorts from in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE)\(^38\) Pharmacogenomics Working Group (PWG) participated in this analysis, contributing 78,199 participants: European descent (51,601), African American (11,482), and Hispanic/Latino (15,116) participants (Table 1; Supplementary Text). Among the fourteen cohorts, six (55% of the total population) had repeated measurements of medication use and electrocardiogram (ECG) assessments and contributed longitudinal data to the analysis: Age, Gene/Environment Susceptibility—Reykjavik Study (AGES), Atherosclerosis Risk in Communities (ARIC) Study, Cardiovascular Health Study (CHS), Rotterdam Study (RS), Multi-Ethnic Study of Atherosclerosis (MESA), and Women’s Health Initiative (WHI). The remaining eight cohorts contributed cross-sectional data to the analysis: Framingham Heart Study (FHS), Erasmus Rucphen Family (ERF) Study, Health 2000 (H2000), Health, Aging, and Body Composition (Health ABC), Prospective Study of Pravastatin in the Elderly at Risk (PROSPER), Jackson Heart Study (JHS), Netherlands Epidemiology of Obesity (NEO) Study, and Hispanic Community Health Study/Study of Latinos (HCHS/SOL).

Study design

Participants with ECG measurements, medication assessment, and genome-wide genotype data were eligible for inclusion. The following exclusion criteria were applied: poor ECG quality, atrial fibrillation detected by ECG, pacemaker implantation, second or third degree atrioventricular heart block, QRS greater than 120 ms, prevalent heart failure, pregnancy, missing ECG, missing medication assessment, missing genotype information, or race/ethnicity other than European descent, African American, or Hispanic/Latino. For studies with longitudinal data, exclusion criteria were applied on a visit-specific basis.

Medication assessment

Medication use was assessed through medication inventories conducted during clinic visits, home interviews, or through pharmacy databases (Supplementary Table 1). Six studies captured medication used on the day of the study visit. A further six of the 14 participating cohorts captured medications used 1–2 weeks preceding ECG assessment. HCHS/SOL ascertainment medications used within four weeks preceding ECG measurement, and the RS captured medication used within 30 days preceding ECG assessment. Participants were classified as thiazide diuretic users if they took a thiazide or thiazide-like diuretic in a single or combination preparation, with or without potassium (K)-sparing agents, and with or without K-supplements.

For cross-sectional studies, the number of exposed participants (\(N_{\text{exposed}}\)) was defined as the number of participants classified as thiazide users. For studies with longitudinal data, \(N_{\text{exposed}}\) was calculated as follows:

\[
N_{\text{exposed}} = \sum n_i \left(1 + \frac{n_i}{n_i - 1}\right) \frac{\#(E_i = 1)}{n_i}
\]

where \(n_i\) is the number of observations for participant \(i\), \(\rho\) is an estimate of the pairwise visit-to-visit correlation within participants from a Generalized Estimating Equation (GEE)-exchangeable model that does not contain genetic data, and \(\#(E_i = 1)\) is the number of observations for which participant \(i\) was exposed.\(^39\)

ECG interval measurement

QT and QRS were digitally recorded by each participating study using resting, supine or semi-recumbent, standard 12-lead ECGs (Supplementary Table 2). Comparable procedures were used for preparing participants, placing electrodes, recording, transmitting, processing, and controlling quality of ECGs. Studies used Marquette MAC 5000, MAC 12, MAC 1200 or MAC PC (GE Healthcare, Milwaukee, Wisconsin, USA), University of Glasgow (Cardiac Science, Manchester, UK), or ACTA (EASOTE, Florence, Italy) machines. Recordings were processed using one of the following programs (Marquette 125L, MEANS, University of Glasgow, Digital Calipers, or Health 2000 custom-made software). JT was calculated by the formula: JT = QT–QRS.

Genotyping and imputation

Each study conducted genome-wide genotyping independently using either Affymetrix (Santa Clara, CA, USA) or Illumina (San Diego, CA, USA) arrays (Supplementary Table 3). Sex mismatches, duplicate samples, and first-degree relatives (except in ERF, FHS, HCHS/SOL and JHS) were excluded. DNA samples with call rates less than 95–98% were excluded, as were SNPs with SNP call rates less than 90–98%, minor allele frequencies (MAF) less than 1%, or that failed Hardy-Weinberg equilibrium. To maximize genome coverage and comparisons across genotyping platforms, genotypes were imputed using HapMap2,\(^40\)\(^–\)\(^44\) 1000 Genomes Phase 1, or 1000 Genomes Phase 3 reference panels.\(^45\)\(^–\)\(^46\) Genotypes imputed using build 37 were lifted over to build 36,\(^45\)\(^–\)\(^46\) to enable comparisons between imputation platforms and results were restricted to SNPs present in HapMap2.

Statistical analyses

Genome-wide pharmacogenomic analyses were performed by each cohort independently across ~ 2.5 million SNPs for QT, QRS, and JT separately. Drug-SNP interactions were estimated assuming an additive genetic model, using mixed effect models, GEE, or linear regression with robust standard errors. The analytic model varied based on study design and the availability of longitudinal data (Supplementary Table 4). All analyses were adjusted for age (years), sex when applicable, study site or region, principal
components of genetic ancestry, visit-specific RR interval (ms), and visit-specific QT altering medications defined using the University of Arizona Center for Education and Research on Therapeutics (UAZ CERT) QT-prolonging drug classification.39 Furthermore, ERF, FHS, and HCHS/SOL incorporated estimates of relatedness into all analyses. Study-specific results were corrected for genomic inflation ($\lambda$). Previous simulations demonstrated that models using robust standard errors underestimate the variance of coefficient estimates for SNPs with low MAFs.39 To account for this underestimation, corrected standard errors were calculated using a (Student’s) $t$-reference distribution.39 The degrees of freedom (df) for the $t$-reference distribution were estimated using Satterthwaite’s method.39 When cohorts were unable to implement Satterthwaite’s method, an approximate df was calculated as twice the cohort- and SNP-specific product of the SNP imputation quality (range: 0.1), the MAF (range: 0.0,0.50), and $N_{\text{exposed}}$. Standard errors were then ‘corrected’ by assuming a normal reference distribution that yielded the $t$-distribution based $P$-values from the beta estimates.39 Furthermore, because simulations demonstrated that corrected standard errors were unstable when minor allele counts among the exposed were low, a cohort-specific df filter of 15 was applied across all SNPs.39

For each trait, race-stratified and trans-ethnic betas and corrected standard errors were combined with inverse-variance-weighted meta-analysis conducted in METAL.48 We used a genome-wide significance threshold of $P < 5 \times 10^{-8}$ and a suggestive threshold of $P < 5 \times 10^{-6}$. However, the assumptions of a fixed-effects meta-analysis do not always hold between race/ethnicities due to differences in patterns of linkage disequilibrium (LD) across ancestral populations, potential allelic heterogeneity, differences in gene-environment and gene-gene interactions, and differences in environmental and lifestyle factors.49,50 Therefore, trans-ethnic meta-analysis was also conducted using the Bayesian MANTRA approach and a genome-wide threshold of $\log_{10}(\text{Bayes Factor (BF)}) > 6$ and a suggestive threshold of $\log_{10}(\text{BF}) > 5$.51 Additionally, previous studies have demonstrated the potential to increase power and detect evidence of pleiotropy by conducting multi-trait analysis across correlated traits.52,53 To examine potential pleiotropy across ventricular depolarization and repolarization, we conducted cross-phenotype meta-analysis combining t-statistics across QRS and JT using an adaptive sum of powered score (aSPU) test, which tests both concordant and discordant associations across some or all of the included traits.54 The reference distribution for the aSPU test was calculated using $10^8$ simulations.

Genome-wide significant and suggestive meta-analysis results were examined for gene or pathway enrichment. Previous work has shown that it is beneficial to apply multiple methods of gene-set analysis (GSA) when the underlying etiology of the genetic mechanism is unclear.55–57 We therefore used two methods of GSA. We performed a multiple regression gene analysis approach followed by a self-contained GSA using gene-level regression as implemented in MAGMA.58 Post-meta-analysis $P$-values were used as input in the analysis and gene-sets were collected from Ingenuity,59 Panter,60 KEGG61 and ConsensusPathDB62,63 and restricted to biologically motivated pathways involved in the following: ion transport
and homeostasis, transcription and translation, renal and cardiac development and function, and pharmacokinetic/dynamic pathways. Additionally, we selected all SNPs with $P < 1 \times 10^{-5}$ for analysis with DEPICT, which searches for gene, gene-set and tissue enrichment among 14461 reconstituted gene-sets, eliminating the need to select candidate gene-sets. To account for multiple testing, we applied a false discovery rate (FDR) threshold of 5% for both GSA approaches.

Statistical power simulations
Statistical power to detect drug–SNP interactions using cross-sectional and longitudinal modeling approaches was estimated via simulation studies. Assumptions, which were informed by European ancestry populations, included: (1) 50,000 participants; (2) a two-sided, per-SNP $\alpha = 5 \times 10^{-5}$; (3) a mean heart rate-corrected QT (standard deviation) = 400 (30) ms; (4) $N_{\text{exposed}} = 8100$; (5) a mean drug effect for those with zero copies of the minor allele = 5 ms; (6) a mean SNP effect for those not exposed to drug = 0 ms; (7) a MAF = 0.05 or 0.25; (8) an additive model of inheritance; (9) two study visits for longitudinal simulations; (10) within-person QT correlation = 0.80; (11) an attrition rate between visits for longitudinal simulations = 0.13; (12) random missingness rate across study visits = 0.09; and (13) an independent GEE correlation structure for longitudinal simulations. For longitudinal simulations, drug use was either temporally constant or variable. When variable, drug exposure was assumed to be completely random at both visits.

RESULTS
Study characteristics
A total of 78,199 participants were included in the analysis, of which 13,730 (18%) were exposed to thiazides (Table 1). Thiazide use was most common among African Americans (36%), compared with 16% and 9% among European descent and Hispanic/Latino populations, respectively. Mean age ranged from 40 (FHS) to 75 years (PROSPER) and the percentage of females ranged from 47% (NEO, PROSPER) to 100% (WHI). Average QT was between 389 ms (H2000) and 416 ms (HCHS/SOL).

Genome-wide analysis of thiazide–SNP interaction and QT interval
Q-Q plots for individual study results, as well as for meta-analyzed results, demonstrated adequate calibration of study-specific test statistics (Supplementary Figures 1–4). However, the family-based studies (ERF, FHS, HCHS/SOL) showed modest evidence of over-dispersion ($\lambda = 1.07–1.16$).

No genome-wide significant thiazide–SNP interaction effects were detected in any race/ethnic group (Figure 1). However, suggestive interaction effects ($P < 5 \times 10^{-5}$) were found for 22 loci in at least one race/ethnic group: European descent (seven loci), African American (six loci), Hispanic/Latino (six loci), or trans-ethnic (nine loci) (Figure 1; Table 2). Only the DNAH8/BTBD9 locus was suggestively significant in more than one race/ethnic group (rs862433 in African Americans, rs1950398 in Hispanic/Latinos). Only two of the suggestive SNPs were heterogeneous across populations with $P_{\text{het}} < 0.05$ (rs4890550 and rs13223427).

Additionally, examination of 35 loci previously associated with QT in a published main effects GWAS had no significant associations in European descent populations using a Bonferroni corrected threshold of $P < 0.001$ (0.001 = 0.05/35; Supplementary Table 5). The magnitude of the interaction effect was close to zero for all but six of the 35 SNP, which had interaction effects greater than 0.50 ms.

Similarly, while no locus showed genome-wide significance in our trans-ethnic MANTRA analysis (Supplementary Figure 5), one SNP (rs2765279) was above the suggestive threshold, with a $\log_{10}(BF)$ of 5.2. Rs2765279, located in RGSL1, a gene involved in G-protein signaling regulation, was also the most significant SNP in the fixed-effects trans-ethnic analysis ($P = 3 \times 10^{-5}$).

Genome-wide analysis of thiazide–SNP interaction and QRS interval or JT interval
Results for QRS showed a similar pattern to those for QT (Supplementary Figure 6 and Supplementary Table 6). Whereas no results achieved genome-wide significance, 28 loci showed suggestive evidence of modifying the thiazide-QRS association (four loci in European descent populations, 11 in African Americans, eight in Hispanic/Latinos, and seven in trans-ethnic populations) and only one SNP had a $P_{\text{het}} < 0.05$ (rs11591185). The most significant SNP, rs7638855 ($P = 2 \times 10^{-7}$), located upstream from GAP43, was also suggestively significant after trans-ethnic analysis in MANTRA ($\log_{10}(BF) = 5.4$; Supplementary Figure 5).

Similarly, no SNPs showed genome-wide significant interaction for JT, although 19 loci were suggestively associated (five loci in European descent populations, four in African Americans, five in Hispanic/Latino, and seven in trans-ethnic populations; Supplementary Figure 6 and Supplementary Table 7). No SNPs showed significant heterogeneity between populations. Moreover, MANTRA analysis identified two SNPs that achieved suggestive significance (Supplementary Figure 5). The rs1264878 variant near KCNIP4, a voltage-gated potassium channel interacting protein was the most significant SNP in our fixed-effects meta-analyses ($P = 3 \times 10^{-7}$) and had a $\log_{10}(BF) = 5.1$. However, most significant SNP in MANTRA meta-analyses was rs9303589, in CA10, with a $\log_{10}(BF) = 5.1$.

Cross-phenotype meta-analysis
Cross-phenotype meta-analysis found no genome-wide significant evidence of pleiotropy across QRS and JT (Figure 2 and Supplementary Figure 7). However, eight loci had a suggestive evidence of thiazide–SNP interaction after meta-analyzing QRS and JT results (Table 3). These included three loci that were nominally associated with QRS and JT ($P < 0.05$), but whose effects did not reach the suggestive association threshold in either univariate analysis (rs1295230 [PIK3R6], rs6931354 [ADGRB3] and rs8195157 [PREX1]).

Gene and pathway enrichment analysis
Although analysis with DEPICT found no enrichment in a single gene or tissue, gene-set enrichment analysis in European descent populations found enrichment in the ATXN3 subnetwork for the interactive effect of genotype and thiazide use on QT ($P = 1 \times 10^{-5}$). There was no enrichment found in QRS or JT analyses. MAGMA analyses found significant enrichment in six genes among African Americans in the interactive effect of genotype and thiazide use on QRS: CNTRL, CPN1, FAM65B, RAB14, ISY1, NELL1 (Supplementary Table 8). No other MAGMA analyses found gene enrichment. MAGMA GSA for QT and JT analyses found significant enrichment for transcription and translational pathways, although no gene-set enrichment was found in QRS analyses (Table 4).

Statistical power
Given the biologic plausibility of the suggestive results for all three traits, we examined statistical power for our analysis to assess our ability to detect interaction effects. Simulations demonstrated that all analyses were underpowered to detect thiazide–SNP interaction effects less than 3 ms (e.g. 15% power to detect an interactive effect of 2 ms; Figure 3). However, even with time-varying drug exposure (that is, observed QT measurement on and off drug within an individual), which demonstrated the greatest power, analyses for SNPs with MAF = 5% did not achieve 80% power until the thiazide–SNP interaction effect reached 6 ms.
In this study, we examined 78,199 participants of European, African American or Hispanic/Latino descent for evidence of thiazide–SNP interactions influencing QT. Although we used a comprehensive approach that considered multi-ethnic populations, leveraged pleiotropy, accommodated population...
Table 2. Loci with suggestive evidence of association with the thiazide–SNP interaction effect on QT interval

| Locus | SNP | Chr | Position | CA | CAF | Interaction effect in ms (s.e.) | P-value | P_{het} |
|-------|-----|-----|----------|----|-----|---------------------------------|---------|---------|
| European descent | KIAA2013 | rs17367934 | 1 | 11890791 | A | 0.89 | 2.4 (0.5) | 2 × 10^{-6} | 0.9 |
|     | SLC1A42 | rs4890550 | 18 | 41409189 | C | 0.44 | −1.4 (0.3) | 3 × 10^{-6} | 0.01 |
|     | RPS29 | rs10143493 | 14 | 47999650 | A | 0.01 | −10.6 (2.3) | 3 × 10^{-6} | 0.4 |
|     | NELL1 | rs12225793 | 11 | 21057283 | T | 0.12 | 2.3 (0.5) | 4 × 10^{-6} | 1.0 |
|     | STC2 | rs10079004 | 5 | 172704698 | A | 0.71 | −1.5 (0.3) | 4 × 10^{-6} | 0.4 |
|     | LCLAT1 | rs7608507 | 2 | 30447424 | A | 0.75 | 1.6 (0.3) | 4 × 10^{-6} | 0.7 |
|     | PPP1R3A | rs13223427 | 7 | 113199332 | T | 0.56 | 1.4 (0.3) | 4 × 10^{-6} | 0.02 |
| African American | ZBTB16 | rs10789991 | 11 | 113424299 | T | 0.03 | 12.3 (2.4) | 5 × 10^{-7} | 0.6 |
|     | DNAH8 | rs862433 | 6 | 38968057 | A | 0.25 | −2.6 (0.5) | 7 × 10^{-7} | 0.2 |
|     | Intergenic | rs9376483 | 6 | 140352934 | T | 0.94 | 7.2 (1.4) | 7 × 10^{-7} | 0.5 |
|     | CASP8AP2 | rs7753194 | 6 | 90597484 | A | 0.02 | −11.4 (2.4) | 3 × 10^{-6} | 0.2 |
|     | EBF1 | rs11135035 | 5 | 157833407 | A | 0.41 | 2.1 (0.5) | 4 × 10^{-6} | 0.9 |
|     | LAMA4 | rs6926485 | 6 | 112630302 | T | 0.64 | 2.4 (0.5) | 5 × 10^{-6} | 0.5 |
| Hispanic/Latino | SPDYA | rs12475612 | 2 | 28883510 | T | 0.48 | −3.5 (0.7) | 1 × 10^{-6} | 0.9 |
|     | BTBD9 | rs1950398 | 9 | 38666897 | T | 0.97 | 9.6 (2.0) | 2 × 10^{-6} | 0.05 |
|     | TDRP | rs6558894 | 8 | 480495 | C | 0.14 | −4.9 (1.0) | 2 × 10^{-6} | 0.3 |
|     | COLCA2 | rs10749974 | 11 | 116096967 | A | 0.09 | −6.0 (1.3) | 3 × 10^{-6} | 0.2 |
|     | CRYGGP | rs17868255 | 2 | 51884417 | A | 0.97 | 10.3 (2.2) | 3 × 10^{-6} | 0.5 |
|     | RYR3 | rs16968989 | 15 | 31376213 | A | 0.18 | 4.5 (1.0) | 3 × 10^{-6} | 1.0 |
| Trans-Ethnic | RGL1 | rs2765279 | 1 | 180693520 | T | 0.28 | 1.4 (0.3) | 3 × 10^{-7} | 0.4 |
|     | ZBTB16 | rs10789991 | 11 | 113424299 | T | 0.03 | 12.3 (2.4) | 5 × 10^{-7} | 0.6 |
|     | PPP1R3A | rs17619887 | 7 | 113142601 | A | 0.47 | 1.2 (0.3) | 2 × 10^{-6} | 0.07 |
|     | KIAA2013 | rs17367934 | 1 | 11890791 | A | 0.89 | 2.3 (0.5) | 2 × 10^{-6} | 1.0 |
|     | LCLAT1 | rs6756908 | 2 | 30446501 | A | 0.65 | 1.3 (0.3) | 2 × 10^{-6} | 0.5 |
|     | FAR1 | rs7130476 | 11 | 13711632 | C | 0.90 | 2.0 (0.4) | 3 × 10^{-6} | 0.5 |
|     | CASP8AP2 | rs7753194 | 6 | 90597484 | A | 0.02 | −11.4 (2.4) | 3 × 10^{-6} | 0.2 |
|     | SMARC2A | rs188626 | 9 | 2163590 | A | 0.75 | 1.5 (0.3) | 3 × 10^{-6} | 0.9 |
|     | ZKSCAN8 | rs1305911 | 6 | 28232093 | T | 0.09 | −2.5 (0.5) | 5 × 10^{-4} | 0.6 |

Abbreviations: CA, coded allele; CAF, coded allele frequency; Chr, chromosome; P_{het}, P-value of heterogeneity; SNP, single-nucleotide polymorphism. *Build 36 base-pair position.

heterogeneity, and examined QT as well as its component parts (QRS, JT), we did not identify any genome-wide significant SNPs modifying the association between thiazides and these ECG intervals. However, we identified 74 loci with suggestive evidence of association through either univariate or cross-phenotype analyses as well as evidence of enrichment in pathways involved in transcription and translation. Interestingly, our suggestive results included multiple loci involved in ion transport and handling, the disruption of which is believed to be an underlying mechanism in drug-induced QT prolongation, supporting the hypothesis that common SNPs modify the thiazide-QT relationship. For example, the NELL1 locus was previously associated with changes in fasting plasma triglyceride levels in response to hydrochlorothiazide use. Other interesting suggestive results include the PITX2 and RYR3 QRS loci identified in Hispanic/Latinos, which may directly regulate ion channel genes and genes involved in calcium handling. Moreover, we found suggestive evidence of thiazide–SNP interactions on QT, QRS, or JT in other genes involved in ion transport and handling, including STC2, EDN1, TRPC7, PKP2 and DISC1, as well as a voltage-gated potassium channel gene (KCNQ3). Despite these intriguing results, our power simulations suggested there was limited power to detect interaction effects of 2 ms, sizes consistent with QT main effects analyses. The low power suggests that larger sample sizes and/or innovative statistical methods may be required to study gene-environment interactions given the stringent genome-wide significance threshold. Furthermore, our power simulations demonstrated insufficient power to detect interaction effects of 5 ms or less for less common SNPs (MAF = 5%). Therefore, future work should utilize larger sample sizes, particularly studies with longitudinal data, if available. Another limitation of our work was that medication use data were collected infrequently, e.g. years apart. Particularly, medication assessments covered only one to two weeks of medication use in most participating cohorts and variables such as medication dosage and duration of use were not available universally across studies. Previous work has demonstrated a dose-dependent relationship between thiazide use and cardiac arrest, a potential outcome of QT prolongation. However, we were unable to identify participants using high dose thiazides because medication dosage data was unavailable in all cohorts. Furthermore, K+ measurements and information on K+ supplements was not obtained across all cohorts so we were unable to adjust for K+ levels in our analyses, despite the known role of thiazide diuretics in inducing hypokalemia and the role of hypokalemia in causing QT prolongation.

Furthermore, ECG intervals are known to vary in the presence of cardiovascular disease (CVD). While we did exclude participants with certain types of CVD including prevalent heart failure and atrial fibrillation, we were not able to further characterize the role...
of CVD in the pharmacogenomics of thiazide use and QT duration. Given that we saw larger mean QT and JT intervals in Hispanic/Latino populations than in European descent or African American populations in our study sample, as well a substantial difference in mean exposure to thiazides, ranging from just 9% in Hispanic/Latinos to 37% in African Americans, our analyses are limited by the heterogeneity of exposure and outcome in our population. The large difference in thiazide exposure between race/ethnic groups could also indicate an underlying difference in CVD prevalence among our populations. Considering that pharmacogenomic studies such as this one are already limited in their power to detect effects, the addition of unmeasured heterogeneity such as CVD status could further reduce our power to detect genetic effects modifying the relationship between thiazides and QT. Therefore, future work should consider alternate study designs, such as clinical trials or specially collected cohorts, as settings for pharmacogenomics work. In clinical trials or specialty cohorts, populations can be more closely controlled and therefore more homogeneous in traits that may confound the relationship between thiazides and QT.

Additionally, observational cohort studies are known to be susceptible to selection biases, such as prevalent user bias, whereby long-term medication users are least likely to suffer from ADRs and users with ADRs often stop therapy and therefore have a lower chance of being seen while on therapy.\textsuperscript{81,82} Unfortunately, without information on duration of use, it is difficult to evaluate the effect of prevalent user bias on study results. Indeed, it is unclear if these biases are of concern in pharmacogenomic studies.\textsuperscript{83,84} Additional work is needed to assess whether selection bias requires more consideration in pharmacogenomic research and to assess possible advantages of alternative designs, such as active comparator designs (whereby the control group contains participants using a different class of medications with similar indications to the medication of interest) or new user

Figure 2. Manhattan plots of \(P\)-values thiazide–SNP interaction estimates after cross-phenotype meta-analysis (QRS interval, JT interval) using aSPU among European descent populations (\(N = 47,836\)), African American populations (\(N = 11,482\)), and Hispanic/Latino populations (15,116). For each trait separately, each study was analyzed using linear regression, mixed-effects models, or generalized estimating equations and SNPs with a study-specific degree of freedom measure (df = twice the cohort- and SNP-specific product of the SNP imputation quality (range: 0,1), the MAF (range: 0.0,0.50), and the number of individuals exposed to thiazide (\(N_{\text{exposed}}\) < 15 were excluded from cross-phenotype meta-analysis. The \(x\)-axis represents the chromosomal position and the \(y\)-axis represents the \(-\log_{10}(P\text{-value})\). On each plot, genome-wide significance (\(P < 5 \times 10^{-8}\)) and suggestive significance (\(P < 5 \times 10^{-6}\)) are denoted with dashed lines.
Table 3. Loci with suggestive evidence modifying the effect of Thiazide on QRS and JT intervals after cross-phenotype meta-analysis

| Locus       | SNP     | Chr | Position (bp) | CA  | CAF   | P-value   | Univariate P-value |
|-------------|---------|-----|---------------|-----|-------|-----------|--------------------|
| European descent |
| PIK3R6      | rs1295230 | 17  | 8682305       | T   | 0.02  | 3 × 10^{-6} | 0.008              |
| African American
| ADGRB3      | rs6931354 | 6   | 69527128      | A   | 0.21  | 1 × 10^{-7} | 0.005              |
| ADGRB3      | rs10108730| 8   | 131767803     | T   | 0.79  | 2 × 10^{-6} | 1 × 10^{-5}        |
| PREX1       | rs8119517 | 20  | 46464282      | A   | 0.94  | 3 × 10^{-6} | 0.0005             |
| CDH13       | rs11649358| 16  | 81415652      | A   | 0.75  | 5 × 10^{-6} | 9 × 10^{-6}        |
| Hispanic/Latino
| AK2         | rs11591185| 1   | 33274771      | A   | 0.07  | 2 × 10^{-6} | 7 × 10^{-7}        |
| ASS1P14     | rs12578228| 12  | 33030528      | T   | 0.10  | 2 × 10^{-6} | 2 × 10^{-6}        |
| GALNT13     | rs17553946| 2   | 155055407     | A   | 0.23  | 4 × 10^{-6} | 9 × 10^{-7}        |

Abbreviations: CA, coded allele; CAF, coded allele frequency; Chr, chromosome; JT, JT interval; QRS, QRS interval; SNP, single-nucleotide polymorphism. *Build 36 base-pair position.

Table 4. Gene-sets with enrichment for genotype-thiazide interaction effects

| Trait | Population | Gene-set                                                                 | P-value   | FDR   |
|-------|------------|---------------------------------------------------------------------------|-----------|-------|
| QT    | Hispanic/Latino | Nucleotide Binding                                                         | 5 × 10^{-6} | 0.004 |
|       |            | Metal Ion Binding                                                          | 6 × 10^{-6} | 0.004 |
|       |            | tRNA Adenine-N1 Methyltransferase Activity                                 | 6 × 10^{-5} | 0.03  |
|       |            | Transcription Coactivator Activity                                         | 8 × 10^{-5} | 0.03  |
|       |            | Transcriptional Activity of SMAD2, SMAD3, SMAD4, Heterotrimer              | 0.0001    | 0.03  |
|       |            | Zinc Ion Binding                                                           | 0.0002    | 0.04  |
|       |            | Other RNA Binding Protein                                                  | 0.0002    | 0.04  |
|       |            | Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPS/IMPS/VICKZS)   | 0.0003    | 0.05  |
|       |            | Trans-Ethnic General RNA Polymerase II Transcription                       | 4 × 10^{-6} | 0.006 |
|       |            | Transcription                                                             | 4 × 10^{-5} | 0.03  |
| JT    | African American | Transcription Factor TFIIA Complex                                         | 7 × 10^{-5} | 0.05  |
|       |            | Aminoacyl-tRNA Synthetase Multienzyme Complex                              | 0.0001    | 0.05  |
|       |            | tRNA Aminoacylation for Protein Translation                                | 0.0001    | 0.05  |
|       |            | Transcription Factor TFIIA Complex                                         | 3 × 10^{-5} | 0.03  |
|       |            | Transcription Factor TFCI Complex                                          | 4 × 10^{-5} | 0.03  |
|       |            | General RNA Polymerase II Transcription Factor Activity                    | 4 × 10^{-5} | 0.03  |

Abbreviations: FDR, false discovery rate; JT, JT interval; QT, QT interval.

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designs (whereby prevalent users are excluded). Moreover, medication inventories may be associated with non-negligible measurement error. For example, while Smith et al. reported good agreement between thiazide use measured using medication inventories and serum thiazide measurements, specificity remained moderate.85

Given the challenges associated with assembling an adequately powered pharmacogenomics study, electronic medical records (EMRs) represent a potential untapped resource that may merit evaluation. Strengths of EMRs include the potential to provide a more complete medication history, which could enable sensitivity analyses examining variables such as medication dose and duration of use. Furthermore, consortia such as eMERGE have demonstrated the feasibility of linking EMRs to genetic data for use in genetic research, and have successfully identified genetic variants modifying drug response.87 However, EMRs have limitations. Investigators using EMR data cannot control participant recruitment, timing and accuracy of data collection, or population representativeness.88 Considering ECG research specifically, cohort studies administer ECGs to all participants at study visits, whereas EMRs may capture ECGs for patients with medical indications, providing an inherently different population. EMRs therefore have the potential to greatly advance pharmacogenomic research but warrant further evaluation.

In conclusion, our findings suggest that additional work is needed to fully elucidate potential pharmacogenomic effects influencing the thiazide-QT relationship. Our suggestive results support a possible role of genetics in modifying the association between thiazides and QT. However, these findings can inform the biology of thiazide-induced QT prolongation and do not preclude the possibility of common variants with small effects or rare variants with larger effects. Future work that leverages larger sample sizes, such as those available in EMRs, and innovative statistical methods to validate these suggestive findings is needed. The FDA considers further regulation of drugs that prolong QT by as little as 5 ms, a small increment easily achieved by the combination of genetic and pharmaceutical effects, making it critical that we unravel the complex etiology of drug-induced QT prolongation. Pharmacogenomics remain a promising avenue for understanding variability in drug
response and for utilizing genetics to improve public health but innovative solutions are needed to overcome inherent challenges.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGMENTS

Age, Gene/Environment Susceptibility—Reykjavik Study (AGES): This study has been funded by NIH contracts N01-AU-22196 and 2712020002CC, the NIA Intramural Research Program, Hjartavélab (the Icelandic Heart Association), and the Althingi (the Icelandic Parliament). The study is approved by the Icelandic National Bioethics Committee, VSN: 00-063. The researchers are indebted to the participants for their willingness to participate in the study.

Atherosclerosis Risk in Communities (ARIC): The Atherosclerosis Risk in Communities Study is carried out as a collaborative study supported by National Heart, Lung and Blood Institute Contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C and HHSN268201100012C), R01HL078641, R01HL93967 and R01HL86694; National Human Genome Research Institute Contract U01HG004402; and National Institutes of Health Contract HHSN268200625226C. We thank the staff and participants of the ARIC study for their important contributions. Infrastructure was partly supported by Grant no. UL1TR000124, a component of the National Institutes of Health and NIH Roadmap for Medical Research (FIC). AAS was supported by the Southern California Diabetes Endocrinology Research Center (grant DK063491 to the Southern California Diabetes Endocrinology Research Center). NS was supported by the National Institutes of Health and NIH Roadmap for Basic Research (NWD-RFBR 047.017.043). Exome sequencing in ER was supported by the ZonMW grant (project 91111025). We are grateful to all study participants and their relatives, general practitioners and neurologists for their contributions to the ER study and to P. Verhaar for her help in genealogy. J. Vergeer for the supervision of the laboratory work and P. Snijders for his help in data collection.

Framingham Heart Study (FHS): FHS work was supported by the National Heart Lung and Blood Institute of the National Institutes of Health and Boston University School of Medicine (Contract No. N01-HC-2519S and Contract No. HHSN268201500001I), its contract with Affymetrix for genotyping services (Contract No. N02-HL-6-4278), based on analyses by FHS investigators participating in the SNP Health Association Resource (SHARE) project. A portion of this research was conducted using the Linux Cluster for Genetic Analysis (LiGA-II), funded by the Robert Dawson Evans Endowment of the Department of Medicine at Boston University School of Medicine and Boston Medical Center. Measurement of the Gen 3 ECGs was supported by grants from the Doris Duke Charitable Foundation and the Burroughs Wellcome Fund (Newton-Cheh) and the NIH (HL080025, Newton-Cheh).

Health 2000: Supported by the Orison-Farmos Research Foundation (KK and KP), the Finnish Foundation for Cardiovascular Research (KK, KP) and the Academy of Finland (Grant Nos. 129494 and 139635 to VJ).

Health, Aging, and Body Composition (Health ABC): This research was supported by NIA Contracts N01AG262101, N01AG262103 and N01AG262106. The genome-wide association study was funded by NIA Grant 1R01AG032098-01A1 to Wake Forest University Health Sciences and genotyping services were provided by the Center for Inherited Disease Research (CIDR). CIDR is fully funded through a federal contract from the National Institutes of Health to The Johns Hopkins University, Contract No. HHSN27520072896C. This research was supported in part by the Intramural Research Program of the NIH, National Institute on Aging.

Hispanic Community Health Study/Study of Latinos (HCHS/SOL): We thank the participants and staff of the HCHS/SOL study for their contributions to this study. The baseline examination of HCHS/SOL was carried out as a collaborative study supported by contracts from the National Heart, Lung, and Blood Institute (NHBLI) to the University of North Carolina (N01-HC65233), University of Miami (N01-HC65234), Albert Einstein College of Medicine (N01-HC65235), Northwestern University (N01-HC65236), and San Diego State University (N01-HC65237). The following Institutes/Centers/Offices contributed to the first phase of HCHS/SOL through a transfer of funds to the NHBLI: National Institute on Minority Health and Health Disparities, National Institute on Deafness and Other Communication Disorders, National Institute of Dental and Craniofacial Research (NIDCR), National Institute of Diabetes and Digestive and Kidney Diseases, National Institute of Neurological Disorders and Stroke, NIH Institute-Office of Dietary Supplements. The Genetic Analysis Center at University of Washington was supported by NHBLI and NIDCR contracts (HHSN268201300005C, AM03 and MOD03). Genotyping efforts were supported by NHLBI HSN 26220/20054C, NCATS CTSA grant UL1TR000124, and NIDDK Diabetes Research Center (DRC) grant DK063491.

Jackson Heart Study (JHS): We thank the American Heart Association, VSN: 00-063 and the Jackson Heart Study (JHS) participants and staff for their contributions to this work. The JHS is supported by contracts HHSN2682013000046C, HHSN2682013000047C, HSN2682013000048C, HHSN268201300049C, HHSN268201300050C from the National Heart, Lung, and Blood Institute and the National Institute on Minority Health and Health Disparities.

Multi-Ethnic Study of Atherosclerosis (MESA): MESA and MESA SNP Health Association Resource (SHARE) are supported and supported by the National Heart, Lung and Blood Institute (NHBLI) in collaboration with MESA investigators. Support is provided by grants and contracts N01-HC-95159, N01-HC-95160, N01-HC-95161, N01-HC-95162, N01-HC-95163, N01-HC-95164, N01-HC-95165, N01-HC-95166, N01-HC-95167, N01-HC-95168, N01-HC-95169 and RR-024156. Additional funding was provided by NHLBI Training grants T32HL7055 and T32HL07797.

Cardiovascular Health Study (CHS): This CHS research was supported by NHLBI contracts HHSN268201200036C, HHSN268200800007C, N01HC55222, N01HC56079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086; and NHLBI grants U01HL080295, R01HL078652, R01HL105756, R01HL103612, R01HL120939, HL130114, and R01HL085251 with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through R01AG026329 from the National Institute on Aging (NIA). A full list of principal CHS investigators and institutions can be found at CHS-NHLBI.org. The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, and the National Institutes of Health, CTSA grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Diseases and National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided by R01AG14716 from the National Institute on Aging (NIA). The National Heart, Lung, and Blood Institute Contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C and HHSN268201100012C), R01HL078641, R01HL93967 and R01HL86694; National Human Genome Research Institute Contract U01HG004402; and National Institutes of Health Contract HHSN268200625226C. We thank the staff and participants of the ARC study for their important contributions. Infrastructure was partly supported by Grant no. UL1TR002505, a component of the National Institutes of Health and NIH Roadmap for Medical Research. AAS was supported by NHLBI Training grants T32HL7055 and T32HL07797.

Figure 3. Statistical power of a simulated pharmacogenomics study of QT. The x-axis represents the range of tested drug-SNP interaction effects in milliseconds (ms). The y-axis represents the power to detect the tested drug-SNP interaction effect. The following assumptions were used for the calculations: 2 serial visits measuring electrocardiograms (ECGs) and drug exposure, N = 50 000 participants, a single-nucleotide polymorphism (SNP) minor allele frequency (MAF) of 5% or 25%, and the Nsex = 2 8100. Simulation analyses were run using only the baseline visit (cross-sectional) and a longitudinal model. Under the longitudinal model, simulations were run with all participants having constant drug exposure across visits or having varied drug exposure across visits. Cross-sectional models were run using linear regression and longitudinal models were run using a generalized estimating equation with an independence working correlation.
pressure response to hydrochlorothiazide]. Zhonghua yi xue yi chuan xue za zhi 2012; 29: 68–71.
31 Li Y, Zhou Y, Yang P, Niu JQ, Wu Y, Zhao DD et al. Interaction of ACE and CYP11B2 genes on blood pressure response to hydrochlorothiazide in Han Chinese hypertensive patients. Clin Exp Hypertens 2011; 33: 141–146.
32 McDonough CW, Burbage SE, Duarte JD, Gong Y, Langela TV, Turner ST et al. Association of variants in NED4 with blood pressure response and adverse cardiovascular outcomes in hypertensive patients treated with thiazide diuretics. J Hypertens 2013; 31: 698–704.
33 Turner ST, Bailey KR, Friddle BL, Chapman AB, Schwartz GL, Chai HS et al. Gene-environment interactions and the search for missing heritability: a cross-sectional pharmaco-genomics study of the QT interval. Pharmacogenomics J 2014; 14: 6–13.
34 Psaty BM, D’OroNell CI, Gudnason V, Lunetta KL, Folsom AR, Rotter JI et al. Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: design of perspective meta-analyses of genome-wide association studies from 5 cohorts. Circ Cardiovasc Genet 2009; 2: 73–80.
35 Sittlani CM, Rice KM, Lummley T, McKnight B, Cupples LA, Avery CL et al. Generalized estimating equations for genome-wide association studies using longitudinal phenotype data. Stat Med 2014; 33: 118–130.
36 Go AS, Mozaffarian D, Roger VL, Benjamin EJ, Berry JD, Borden WB et al. Heart disease and stroke statistics–2013 update: a report from the American Heart Association Circulation 2013; 127: e6–e245.
37 Avery CL, Sittlani CM, Arking DE, Arnett DK, Bis JC, Boerwinkle E et al. Drug–gene interactions and the search for missing heritability: a cross-sectional pharmaco-genomics study of the QT interval. Pharmacogenomics J 2014; 14: 6–13.
38 Psaty BM, D’OroNell CI, Gudnason V, Lunetta KL, Folsom AR, Rotter JI et al. Cohort for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: design of perspective meta-analyses of genome-wide association studies from 5 cohorts. Circ Cardiovasc Genet 2009; 2: 73–80.
39 Sittlani CM, Rice KM, Lummley T, McKnight B, Cupples LA, Avery CL et al. Generalized estimating equations for genome-wide association studies using longitudinal phenotype data. Stat Med 2014; 33: 118–130.
40 International HapMap Consortium. The International HapMap Project. Nature 2003; 426: 789–796.
41 International HapMap Consortium. A haplotype map of the human genome. Nature 2005; 437: 1299–1320.
42 International HapMap Consortium, Altshuler DM, Gibbs RA, Peiltenon L, Altshuler DM, Gibbs RA et al. Integrating common and rare genetic variation in humans in genome-wide association studies. Nature 2010; 467: 52–58.
43 The 1000 Genomes Project Consortium. A map of human genome variation from population-scale sequencing. Nature 2010; 467: 1061–1073.
44 The 1000 Genomes Project Consortium. An integrated map of genetic variation from 1,092 human genomes. Nature 2012; 491: 56–65.
45 Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM et al. The Human Genome Browser at UCSC. Genome Res 2002; 12: 996–1006.
46 UCSC Human Genome Browser Lift Genome Annotations. Available at http://genome.ucsc.edu/cgi-bin/hgلوOver.
47 Satterthwaite FE. An approximate distribution of estimates of variance components. Biometrics 1946; 2: 110–114.
48 Miller CJ, Li Y, Abecasis GR. METAL: fast and efficient meta-analysis of genome–wide association scans. Bioinformatics 2010; 26: 2190–2191.
49 Ramos E, Doumatey A, Elkahlon AG, Shiner D, Huang H, Chen G et al. Pharmacogenomics, ancestry and clinical decision making for global populations. Pharmacogenom J 2013; 14: 217–222.
50 Thomas D. Gene–environment–wide association studies: emerging approaches. Nat Rev Genet 2010; 11: 259–272.
51 Morris AP. Transethnic meta-analysis of genomewide association studies. Genet Epidemiol 2011; 35: 809–822.
52 Bolormaa S, Pryce JL, Revetra A, Zhang Y, Barendse W, Kemper K et al. A multi-trait, meta-analysis for detecting pleiotropic polymorphisms for stature, fatness and reproduction in beef cattle. PLoS Genet 2014; 10: e1004198.
53 Chung D, Yang C, Li C, Gelernter J, Zhao H. GPA: a statistical approach to prioritizing GWAS results by integrating pleiotropy and annotation. PLoS Genet 2014; 10: e1004778.
54 Kim J, Bai Y, Fan W. An adaptive association test for multiple phenotypes with GWAS summary statistics. Genet Epidemiol 2011; 35: 651–663.
55 Gui H, Li M, Sham PC, Chen SS. Comparisons of seven algorithms for pathway analysis using the WTCCEC Cohr’s disease dataset. BMC Res Notes 2011; 4: 386.
56 The Network Pathway Analysis Subgroup of the Psychiatric Genomics Consortium. Psychiatric genome-wide association studies implicate neuronal, immune and histone pathways. Nat Neurosci 2015; 18: 199–209.
57 Varemo-Lindelof B, Nielsen J, Nookaew I. Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. Nucleic Acids Res 2013; 41: 4378–4391.
58 de Leeuw CA, Mooij JM, Heskes T, Posthuma D. MAGMA: generalized gene-set analysis of GWAS data. PLoS Comput Biol 2015; 11: e1004219.
85 Smith NL, Psaty BM, Heckbert SR, Tracy RP, Cornell ES. The reliability of medication inventory methods compared to serum levels of cardiovascular drugs in the elderly. *J Clin Epidemiol* 1999; 52: 143–146.

86 Kho AN, Pacheco JA, Peissig PL, Rasmussen L, Newton KM, Weston N et al. Electronic medical records for genetic research: results of the eMERGE consortium. *Sci Transl Med* 2011; 3: 79re1.

87 Birdwell KA, Grady B, Choi L, Xu H, Bian A, Denny JC et al. The use of a DNA biobank linked to electronic medical records to characterize pharmacogenomic predictors of tacrolimus dose requirement in kidney transplant recipients. *Pharmacogenet Genomics* 2012; 22: 32–42.

88 Schneeweiss S, Avorn J. A review of uses of health care utilization databases for epidemiologic research on therapeutics. *J Clin Epidemiol* 2005; 58: 323–337.

89 Iribarren C, Round AD, Peng JA, Lu M, Zaroff JG, Holve TJ et al. Validation of a population-based method to assess drug-induced alterations in the QT interval: a self-controlled crossover study. *Pharmacoepidemiol Drug Safety* 2013; 22: 1222–1232.

90 FDA. Guidance for Industry: E14 Clinical Evaluation of QT/QTc Interval Prolongation and Proarrhythmic Potential for Non-Antiarrhythmic Drugs. In: Services DoHaH, editor. 2005.

Supplementary Information accompanies the paper on the The Pharmacogenomics Journal website (http://www.nature.com/tpj)