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Label-Free but Still Constrained: Assessment of Global Proteomic Strategies for the Quantification of Hepatic Enzymes and Transporters

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Abbreviations: HiN, high N ion intensity method; HLM, human liver microsomes; iBAQ, intensity-based absolute quantification; TPA, total protein approach.

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Abstract

Building and refining pharmacology models require 'system' data derived from tissues and *in vitro* systems analysed by quantitative proteomics. Label-free global proteomics offers a wide scope of analysis, allowing simultaneous quantification of thousands of proteins per sample. The data generated from such analysis offer comprehensive protein expression profiles that can address existing gaps in models. In this study, we assessed the performance of three widely used label-free proteomic methods, 'high N' ion intensity approach (HiN), intensity-based absolute quantification (iBAQ) and total protein approach (TPA), in relation to the quantification of enzymes and transporters in 27 human liver microsomal samples. Global correlations between the three methods were highly significant ($R^2 > 0.70$, $p < 0.001$, $n = 2232$ proteins). Absolute abundances of 57 pharmacokinetic targets measured by standard-based label-free methods (HiN and iBAQ) showed good agreement, while the TPA overestimated abundances by 2-3 fold. Relative abundance distribution of enzymes was similar for the three methods, while differences were observed with TPA in the case of transporters. Variability (CV) was similar across the methods, with consistent between-sample relative quantification regardless of methodology. The back-calculated amount of protein in the samples based on each method was compared with the nominal protein amount analysed in the proteomic workflow, revealing overall agreement with data from the HiN method with bovine serum albumin as standard. The findings herein present a critique of label-free proteomic data relevant to pharmacokinetics and evaluate the possibility of retrospective analysis of historic datasets.

Significance statement

This study provides useful insights for using label-free methods to generate abundance data applicable for populating pharmacokinetic models. The data demonstrated overall correlation between intensity-based label-free proteomic methods (HiN, iBAQ and TPA), while iBAQ and TPA overestimated the total amount of protein in the sample. The extent of overestimation can provide a means of normalization to support absolute quantification. Importantly, between-sample relative quantification was consistent (similar variability) across methods.

Introduction

Quantitative proteomics has become a standard method in molecular biology, with the central aim of measuring expression profiles at the protein level. Because of its broad scope of analysis (Wang *et al.*, 2019), label-free (global) proteomics allows measurement of a wide range of proteins that govern drug pharmacokinetics (principally drug-metabolizing enzymes and drug transporters) and their changes in response to pathological and environmental factors (El-Khateeb *et al.*, 2019; Prasad *et al.*, 2019). The methodology does not depend on the availability of isotopically-labelled standards, which are expensive (Al Feteisi *et al.*, 2015), and when used to quantify low abundance proteins, require additional care in data analysis (Achour *et al.*, 2018). Mass spectrometry is not, however, an inherently quantitative technique; the relationship between the concentration of the analyte and the intensity of the corresponding signal is complex (Couto *et al.*, 2011), and all label-free methods require assumptions that may not be fully justified (Arike *et al.*, 2012).

Label-free measurement relies on signal intensity either of all native peptides [e.g. the total protein approach (TPA) (Wiśniewski and Rakus, 2014) and intensity-based absolute quantification (iBAQ) (Schwanhäusser *et al.*, 2011)] or a set of unique/razor peptides [e.g. high N ion intensity approach (HiN) (Silva *et al.*, 2006)] assigned to a certain protein. Alternatively, relative quantification can be achieved based on spectral counts [e.g. the exponentially-modified protein abundance index (emPAI) (Ishihama *et al.*, 2005)], as a semi-quantitative approach to derive an estimate of protein expression.

During the past five years, the pharmacology community has produced approximately 20 publications quantifying human tissue proteomes by global proteomics, and this number is set to increase in the next few years. There are ongoing debates about whether samples should be fractionated and about sample preparation methods (Prasad *et al.*, 2019), although filter-aided methodology, FASP (Wiśniewski *et al.*, 2009), is widely adopted when sample is plentiful. More surprisingly, there is no consensus about methods for analysis of the (typically gigabyte) RAW files obtained from LC-MS/MS experiments. Different software packages for data analysis are available, which make data processing more streamlined, but these do not always produce completely

consistent results (Välikangas *et al.*, 2017). Processing can be done using different reference datasets and following different assumptions, and, above all, using different quantification methodologies (El-Khateeb *et al.*, 2021). These factors are particularly important when modelling the impact of different covariates, such as disease, is the focus of investigation, and therefore validating such data plays a major role in increasing trust in the outcome of predictive pharmacology models.

For the work described here, we used a well-characterized set of 27 human liver microsomal (HLM) samples. As previously described, sample preparation was done by standard FASP methodology and mass spectrometry was carried out on an Orbitrap HF QE instrument (Couto *et al.*, 2019). RAW files so generated have been uploaded to PRIDE and are freely available (Al-Majdoub *et al.*, 2020). The focus of this article is to evaluate the quality of label-free abundance data. In particular, we aimed to use these samples as controls for an investigation of experimentally demanding paediatric samples, analysed with no standards, and we therefore required that standard-free methods should be as reliable as possible.

Materials and Methods

Samples and proteomic methodology

The preparation of HLM samples (Supplemental Table 1) and analysis by mass spectrometry are fully described elsewhere (Couto *et al.*, 2019). Briefly, liver membrane fractions were prepared using differential centrifugation, first at low speed (10,000*g*) to separate cellular debris from the post-mitochondrial fraction, followed by high-speed centrifugation (100,000*g*) to isolate microsomes. Protein content was measured using the Bradford protein assay and sample preparation of 100 µg of each sample (n = 27) followed the FASP protocol with multi-enzyme digestion (lysyl endopeptidase and trypsin). Three exogenous protein standards were spiked in the samples: bovine serum albumin (BSA, 0.2 µg), bovine cytochrome *c* (0.15 µg) and equine myoglobin (0.3 µg). Peptides (1 µg) were analysed by LC-MS/MS using an UltiMate 3000 rapid separation liquid chromatography system (Dionex, Surrey, UK) coupled to a Q Exactive HF Hybrid Quadrupole-Orbitrap mass spectrometer (ThermoFisher Scientific, Bremen, Germany).

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RAW files were processed using Progenesis version 4.2 as a single batch, and the resulting mgf files were processed using Mascot version 2.7 for protein identification. The human database used was Uniprot 000005640, containing 77,027 protein entries. Files were processed four times with the settings: enzyme trypsin/P, MS tolerance 5 ppm, MS/MS tolerance 0.02 Da. In the initial run, up to one missed cleavage was allowed, carbamidomethyl (cysteine) was set as a fixed modification, and oxidation (methionine) was the only variable modification. In subsequent runs, a second missed cleavage, deamidation (of asparagine and glutamine) and phosphorylation (of serine, threonine and tyrosine) were (separately) permitted. Results were compiled using Progenesis, and exported as csv files.

Data analysis and label-free quantification

Peptides were assigned to proteins based on a bespoke razor as described previously (Al-Majdoub *et al.*, 2020) using Microsoft Excel 365. Assignment prioritized full length characterized sequences over truncated, uncharacterized and cDNA sequences. A best-fit analysis was then run to minimize the number of proteins assigned to account for all the peptides. Deamidated peptides with no corresponding native assignment and those that did not match any protein were deleted. The peptide MS intensities attributed to more than one protein were divided among those proteins based on the ratio of unique or razor (peptides with a single assignment within the current dataset) peptide intensities for each protein, as detailed previously (Al-Majdoub *et al.*, 2020).

Three potential standards (BSA, bovine cytochrome *c* and equine myoglobin) were assessed. The equations used in quantification by the HiN, iBAQ and TPA methods are detailed below (Equations 1-3). Rearrangement of these equations provide the means to compare the total sample estimated from the total intensity against the total sample analysed. These act as sanity checks on data analysis.

- ***High N (HiN) ion intensity method***

$$[Protein] = [Standard] \times \left(\sum_{i=1}^{n} \mathrm{I}_{rank\,(i)}/n\right) \Big/ \left(\sum_{j=1}^{m} \mathrm{I}_{rank\,(j)}/m\right) \quad (1)$$

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Where [*Protein*] is the abundance of a target protein, [*standard*] is the abundance of the standard protein, both expressed in units of pmol mg^{-1} total protein, and the fraction refers to the ratio of the average of the intensity of the *n/m* highest ion peaks of the target protein relative to the standard (in this case, *n* = *m* = 2 or 3). Peptides used for quantification are unique to the target proteins; other selection criteria were according to (Achour *et al.*, 2018).

- ***Intensity-based absolute quantification (iBAQ)***

$$[Protein] = [Standard] \times \left(\sum_{i=1}^{n} \mathrm{I}_{i,j}/T_j\right) \Big/ \left(\sum_{i=1}^{m} \mathrm{I}_{i,k}/T_k\right) \quad (2)$$

Where the summed intensity of all peptides *i* from the protein of interest *j* or the standard *k* is normalized to *T*, the number of theoretically observable peptides from digestion of protein *j* or standard *k*.

- ***The total protein approach (TPA)***

$$[Protein] = \sum_{i=1}^{n} \mathrm{I}_{i,j} \Big/ (MW \times \sum_{j=1}^{n} \mathrm{I}_j) \quad (3)$$

Where the ratio of the sum of intensity of all peptides *i* derived from a protein *j* of interest to the sum of intensity of all peptides (from all proteins) in a particular sample (expressed in parts per billion) is converted to an abundance value (pmol mg^{-1}) by normalizing to the molecular weight, MW, of the protein in daltons.

Statistical data analysis

Data were expressed as mean and standard deviation, and variability was assessed as coefficient of variation (CV) and fold difference (maximum-to-minimum ratio). Abundance and activity correlations were tested by linear regression (R^2). Relationships between abundance data and either age or BMI were tested using Pearson correlation (r) to show the direction of trends. Differences between abundance data generated using label-free and targeted methods and between male and female donors were assessed using a *t*-test. Differences across genotypes were assessed using either one-way ANOVA or a *t*-test. A probability cut-off of 0.05 was set for statistical significance.

Results

In this study, HLM samples were analysed using global proteomic methods. Percent identical peptides (PIP) reflected high integrity of analyses (86-99%) across replicates and across samples (Supplemental Tables 2 and 3). For the purpose of quantification, we chose to assess three MS intensity-based label-free methods on the basis that they provide more robust protein measurements than spectral counts (Arike *et al.*, 2012). Two methods (HiN and iBAQ) rely on exogenous protein standards at known concentrations, whereas the TPA is applied without the use of a standard. The methods allowed quantification of 2232 proteins, and data describing expression of 23 cytochrome P450 (CYP) enzymes, 11 glucuronosyltransferases (UGT), 17 ABC transporters and 6 solute carriers are shown in Supplemental Tables 4-6.

Choice of standard

For the iBAQ and HiN methods, three potential standards were included in the samples. The total amount of protein used in each experiment was 100 µg, and the amounts of standards were also known: BSA 0.2 µg (28.86 pmol mg^{-1} total protein), myoglobin 0.3 µg (175.61 pmol mg^{-1} total protein) and cytochrome *c* 0.15 µg (32.04 pmol mg^{-1} total protein). BSA was expected to give the best results because its molecular weight (69 kDa) is close to the average molecular weight of the detected proteins (60 kDa) and it yields a high number of unique peptides. Cytochrome *c* gave rise to a limited number of unique peptides and was therefore discarded. The HiN method was used to calculate the total analyte protein using BSA and myoglobin (Table 1, Figure 1A), with results of 53% for BSA and 207% for myoglobin compared with the nominal amount of protein analysed (assuming an average MW of 60 kDa for native proteins). In the HiN method, proteins represented by a single peptide as well as those falling below the limit of quantification are ignored, making 53% a reasonable value and 207% a substantial overestimate. Further calculations were therefore carried out using BSA as a standard.

Comparison between label-free quantification methods

While iBAQ and TPA clearly overestimate the total amount of protein (Figure 1A), both enable estimation of the abundance of proteins that give rise to a single detectable peptide, whereas the

HiN method does not. Our previous work (El-Khateeb *et al.*, 2021) indicated that all three methods perform quite well in assessing relative change from healthy baseline. We therefore investigated the correlation between absolute quantification values obtained using the three methods. An overall picture of correlations between quantifications (of 2232 proteins) using the different methods is presented in Figure 1B. The overall correlation between the three methods is strong ($R^2 > 0.70$, $p < 0.001$). The TPA overestimates by a factor of 2-3 fold relative to HiN. The iBAQ and HiN measurements are relatively comparable. Correlations between mean abundances of enzymes and transporters ($n = 57$) are presented in Figure 1C. Individual abundance data for these targets are presented in Supplemental Tables 4-6. Specific cases related to a number of proteins of interest to drug pharmacokinetics are shown in Figure 2. Figure 2 shows that in all cases a straight line can be drawn connecting iBAQ and HiN quantifications ($R^2 = 0.60$-0.97) and so is the case for TPA and HiN but with generally considerably more scatter ($R^2 = 0.25$-0.97). Generally, the TPA gives the highest estimation of the concentration of protein; for lower abundance proteins (e.g. low abundance transporters), TPA gives the lowest estimation. Relative abundances are presented in Supplemental Figure 1 for CYPs, UGTs and ABC transporters, reflecting overall agreement, except in the case of relative abundance of ABC transporters determined using the TPA method.

Correlation of label-free data with functional activity

Functional activity data were available for several CYP and UGT enzymes (Achour *et al.*, 2014, 2017). Correlations between abundance and activity of CYPs 3A4, 2D6, 1A2, 2B6 and 2C19 were moderate to strong across the three methods ($R^2 = 0.56$-0.88 with HiN, $R^2 = 0.57$-0.91 with iBAQ, and $R^2 = 0.63$-0.88 with TPA, Figure 3A). Correlation with CYP2C9 activity was the exception, with different levels of correlation across methods ($R^2 = 0.23$ with HiN, $R^2 = 0.43$ with iBAQ, and $R^2 = 0.71$ with TPA). Similarly, weak correlation was previously reported for CYP2C9 activity with targeted data for the set of samples (Achour *et al.*, 2014).

Correlations between abundance and activity of UGTs 1A1, 1A3, 1A6 and 1A9 were moderate to strong ($R^2 = 0.34$-0.69 with HiN, $R^2 = 0.42$-0.85 with iBAQ, and $R^2 = 0.52$-0.77 with TPA, Figure 3B). The exception was UGT2B7, with different levels of correlation across methods ($R^2 = 0.24$ with HiN,

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R^2 = 0.44 with iBAQ, and R^2 = 0.59 with TPA), while correlations of UGT2B15 were generally weaker (R^2 = 0.15, 0.23 and 0.39 with HiN, iBAQ and TPA, respectively). Moderate correlations were previously reported for UGTs 2B7 and 2B15 activity with targeted data for the set of samples (Achour *et al.*, 2017).

Comparison of label-free quantification with targeted data

Label-free measurements were compared with previously reported targeted data for CYP and UGT enzymes in the same set of samples (Achour *et al.*, 2014, 2017). For CYP enzymes, overall agreement was observed with HiN and iBAQ data (Figure 4A), reflecting 74% of measurements within 2 fold of targeted data (Figure 4C). TPA however tended to overestimate measurements (only 53% of data within 2 fold). For UGT enzymes, TPA measurements were closer to targeted data (93% of measurements within 2 fold), while iBAQ and HiN tended to underestimate, with 77% and 60% of measurements within 2 fold, respectively.

Assessment of variability with label-free methods

Fold difference and coefficient of variation (CV), related to between sample variability, was very similar across the three methods for all measured proteins (Figure 5), indicating robustness of relative quantification regardless of methodology. The calculated CV combines technical and biological variability. Technical variability assessed using a pool of the same set of samples returned values < 30% for the targets across all methods. The calculated variability related to technical error, expressed as fold difference between the 5th and 95th percentiles $[(1 + 2 \times CV)/(1 - 2 \times CV)]$ was therefore within 4 fold, whereas total variability reflected up to 50 fold in abundance across the three methods.

Covariates of protein expression assessed by label-free methods

Donors' demographic and clinical information is summarized in Supplemental Table 1. In addition, CYP2B6, CYP2C9, CYP2C19, CYP2D6 and CYP3A5 genotype data were available for 25 (out of 27) samples. Abundance data were assessed against sex, age and body mass index (BMI) (Supplemental Table 7). The number of confirmed smokers and alcohol users at the time of donation was small (4 smokers and 3 drinkers), and therefore, the effect of these two factors was

not probed. No differences in protein expression levels between samples from male (*n* = 15) and female (*n* = 12) donors were observed with all three label-free methods (*t*-test, $p > 0.05$). Weak, negative correlations with age were revealed for CYP2C18, UGT2B4, UGT2B10 and ABCA1 with borderline significance across the label-free methods (r = -0.42 to -0.39, $p = 0.03$-0.05). The effect of BMI was moderate in the cases of UGT1A3, UGT1A4 and OATP1B3, with lower abundance in overweight and obese donors (r = -0.59 to -0.42, $p = 0.001$-0.03). The effect of genotype was significant in the cases of CYP2D6 (ANOVA, $p < 0.05$), CYP2C19 (*t*-test, $p = 0.01$) and CYP3A5 (*t*-test, $p < 0.05$).

Discussion

This study aimed to assess measurements of hepatic enzymes and transporters by widely used label-free proteomic methods (HiN, iBAQ and TPA). We have previously outlined the use of the Disease Perturbation Factor (DPF) (El-Khateeb *et al.*, 2021), which is essentially a factor connecting the amount of any given protein in a diseased tissue with the amount of the same protein in healthy control. The DPF has been shown to be independent of the quantification methodology (targeted *vs* global proteomics, HiN *vs* iBAQ *vs* TPA). Further, differences in absolute abundance are explored herein, and a key piece of information – the total analyte protein – which is usually discarded in proteomic data analysis, now allows us to adjudicate between the different methods of label-free quantification and even to estimate conversion factors from one method to another.

Absolute abundance correlated across the three methods, with targeted data and with functional activity. Correlation with targeted proteomics was previously reported (Vildhede *et al.*, 2018; Wiśniewski *et al.*, 2019; El-Khateeb *et al.*, 2021). While the HiN method (Silva *et al.*, 2006) generally produces data that seem biologically sensible, especially when BSA is used as a standard for human samples, it has two drawbacks. Firstly, the N in HiN is generally taken to mean 2, 3 or more, but not one. Thus, we are denied even an estimate of the abundances of proteins represented by a single peptide. Secondly, a high quality standard is required – one that should have similar properties to the proteins under study. The choice of a suitable standard in this study was, however, empirical as highlighted by the discrepancy between abundances against BSA and myoglobin, with

myoglobin clearly overestimating the total amount of protein. Prospectively, it is, of course, possible to include a protein standard at appropriate concentration in new samples; it is not, however, possible to do this retrospectively. Proteomic work in the drug metabolism and disposition arena involves the use of precious, small human samples. It is imperative, both scientifically and ethically, to derive maximum information from each sample, which means that historical samples, prepared by sub-optimal protocols, are still of value (Prasad *et al.*, 2019).

The TPA has proved an excellent method for dealing with such samples. No standards are necessary, and it provides broad coverage by allowing the quantification (albeit with low accuracy) of proteins represented by a single peptide. Non-unique peptides can be accommodated within the analysis. We have introduced small modifications to the data analysis so that these non-unique peptides are not over-represented (Al-Majdoub *et al.*, 2020), but the method is still inclined to overestimate protein concentration relative to other label-free methods. This is not surprising. The normalization in a TPA experiment is based on the total signal intensity, but we know that some signal (that due to proteins falling below the limit of quantification) is not measured. A 'proteomic ruler' incorporating MS signal of cellular histones was introduced to make TPA measurements more biologically sensible (Wiśniewski *et al.*, 2014). The DPF (El-Khateeb *et al.*, 2021), being a relative factor, allows for the use of the TPA without too much concern for the systematic overestimate.

Both the iBAQ and TPA methods overestimate the total amount of protein in the sample, and the extent of this overestimation can provide a means of normalization should absolute quantification be required. Robust quantification is biased toward higher abundance proteins, and therefore such normalization approach may only work with enzymes and highly abundant transporters. Relative quantification, both between sample and within sample, is often more pertinent than absolute estimates. Similar variability (CV) across individual measurements recovered by all methods indicates relative quantification is robust, regardless of the quantification approach provided consistent proteomic workflows are employed (El-Khateeb *et al.*, 2021; Neuhoff *et al.*, 2021). Relative data are particularly useful for assigning stoichiometry in protein expression (Fabre *et al.*, 2014). The current set reveals a particular example, stoichiometry of TAP1 (ABCB2) and TAP2

(ABCB3). The correlation between abundances generated by the methods for these two proteins was excellent (R^2 = 0.93-0.97), indicating strong agreement, and TAP2 to TAP1 ratio (average TAP2/TAP1 > 10) was within 3 fold across methods. TAP1 and TAP2 form a functional heterodimer that transports peptides for antigen presentation, and one would therefore expect 1:1 expression ratio. The clearly higher abundance of TAP2 may indicate divergence in regulatory mechanisms between TAP1 and TAP2, in support of previous observations (Bahram *et al.*, 1991; Zeidler *et al.*, 1997). Application of relative quantification can be useful to derive changes in abundance of enzymes in a disease population compared with healthy volunteers and assess the implications of such changes for drug-drug interactions.

In conclusion, historical samples without appropriate standards can be subject to relative quantification using the TPA method, with the expectation that similar results would be achieved by standard-based methods. Normalization, or simply adjustment by a factor of 2-3 leads to estimates of absolute quantification. Where standards are available, BSA is a good choice from readily available purified proteins. Importantly, relative quantification is robust across methods, which allows consistent assignment of between subject variability.

Data availability

The proteomic dataset has been deposited to the PRIDE repository under the identifier PXD020910.

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Authorship contributions

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Performed data analysis: Barber, Al-Majdoub, Couto, Achour

Wrote or contributed to the writing of the manuscript: Barber, Al-Majdoub, Couto, Vasilogianni, Tillmann, Alrubia, Rostami-Hodjegan, Achour

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Footnotes

- This work received no external funding.
- The authors declare that they have no actual or perceived conflicts of interest with the contents of this article.

Figure Legends

Figure 1. Comparison of liver proteome measurements using three label-free methods. (A) Percentage of the measured total protein content relative to the nominal content (dashed line) analysed by LC-MS/MS. The amount was determined using the TPA, HiN [based on either myoglobin (MYG) or BSA as standards] and iBAQ [based on BSA]. (B) Head-to-head comparison of average levels (of 2232 proteins) in 27 samples quantified by iBAQ (BSA) and TPA compared with HiN (BSA). (C) Correlation between mean abundance levels of 57 key pharmacokinetic targets measured by TPA or iBAQ and mean abundances measured by HiN. The data show that TPA overestimates protein amounts compared with the HiN method, while HiN and iBAQ methods produce comparable results in most cases. The data also indicate that it is possible to estimate absolute quantification by iBAQ or TPA using conversion factors. Abundance is expressed in units of pmol mg^{-1} total protein.

Figure 2. Correlation between protein levels of key pharmacokinetic targets measured by iBAQ (blue) or TPA (orange) relative to HiN method in 27 liver samples. The data show examples of drug-metabolizing enzymes and transporters. BSA was used as a standard for HiN and iBAQ, and abundance was measured in units of pmol mg^{-1} total protein.

Figure 3. Correlation of protein levels of (A) CYP and (B) UGT enzymes measured by HiN (red), iBAQ (blue), and TPA (orange) against functional activity in 27 liver samples. Activity was measured with metabolite formation assays against the substrates: phenacetin (CYP1A2), mephenytoin (CYP2B6), diclofenac (CYP2C9), mephenytoin (CYP2C19), bufuralol (CYP2D6), testosterone (CYP3A), β-estradiol (UGT1A1), chenodeoxycholic acid (UGT1A3), 5-hydroxytryptophol (UGT1A6), propofol (UGT1A9), zidovudine (UGT2B7) and S-oxazepam (UGT2B15). Abundance was measured in units of pmol mg^{-1} total protein; catalytic activity was measured in units of nmol metabolite min^{-1} mg^{-1} total protein.

Figure 4. Comparison of abundances of (A) CYP and (B) UGT enzymes measured using label-free methods (HiN, iBAQ and TPA) against targeted data. Ratios of label-free measurements relative to targeted data for (C) CYP and (D) UGT enzymes. In (A) and (B), the whiskers represent the

minimum-to-maximum range, the boxes represent the 25th and 75th percentiles, the lines represent the medians and + represent the means. Comparisons based on a *t*-test against targeted data are shown in black and against HiN measurements are shown in red; * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. In (C) and (D), the dashed lines denote the 2-fold range and the percentages are the proportion of label-free measurements within 2 fold of targeted data. Abundance was measured in units of pmol mg^{-1} total protein.

Figure 5. Comparison of between-sample variability across 27 liver samples in the abundance of enzymes and transporters measured by HiN, iBAQ and TPA, expressed as (A) fold difference [maximum/minimum ratio] and (B) % coefficient of variation (CV) [CV = SD × 100 / Mean]. BSA was used as a standard for HiN and iBAQ.

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Tables

Table 1. The total amount of protein in analyte estimated by the label-free quantification methods, averaged (± SD) over 27 samples.

Method	**Estimated total protein content**
Nominal protein content [a]	***16,667 pmol mg^{-1}***
HiN based on BSA	8,916 ± 1,775 pmol mg^{-1}
HiN based on myoglobin	34,580 ± 5,078 pmol mg^{-1}
iBAQ based on BSA	19,265 ± 2,937 pmol mg^{-1}
Total Protein Approach (TPA)	24,513 ± 4,620 pmol mg^{-1}

[a] Amount estimated assuming an average analyte protein MW of 60 kDa; units are pmol mg^{-1} total protein

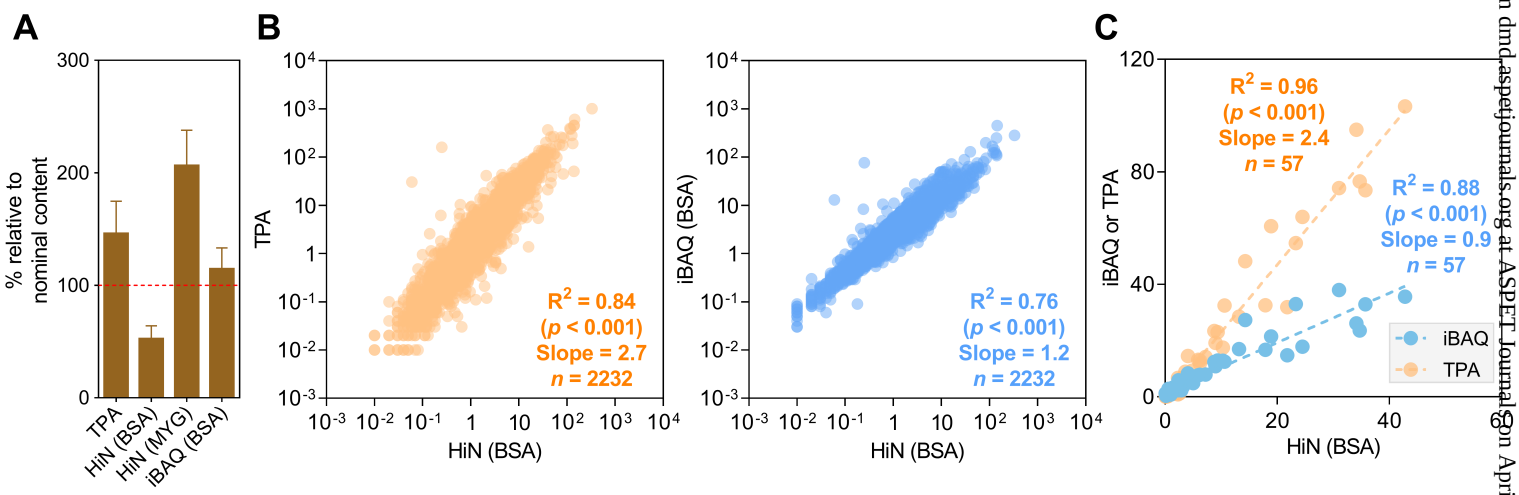


Figure 1

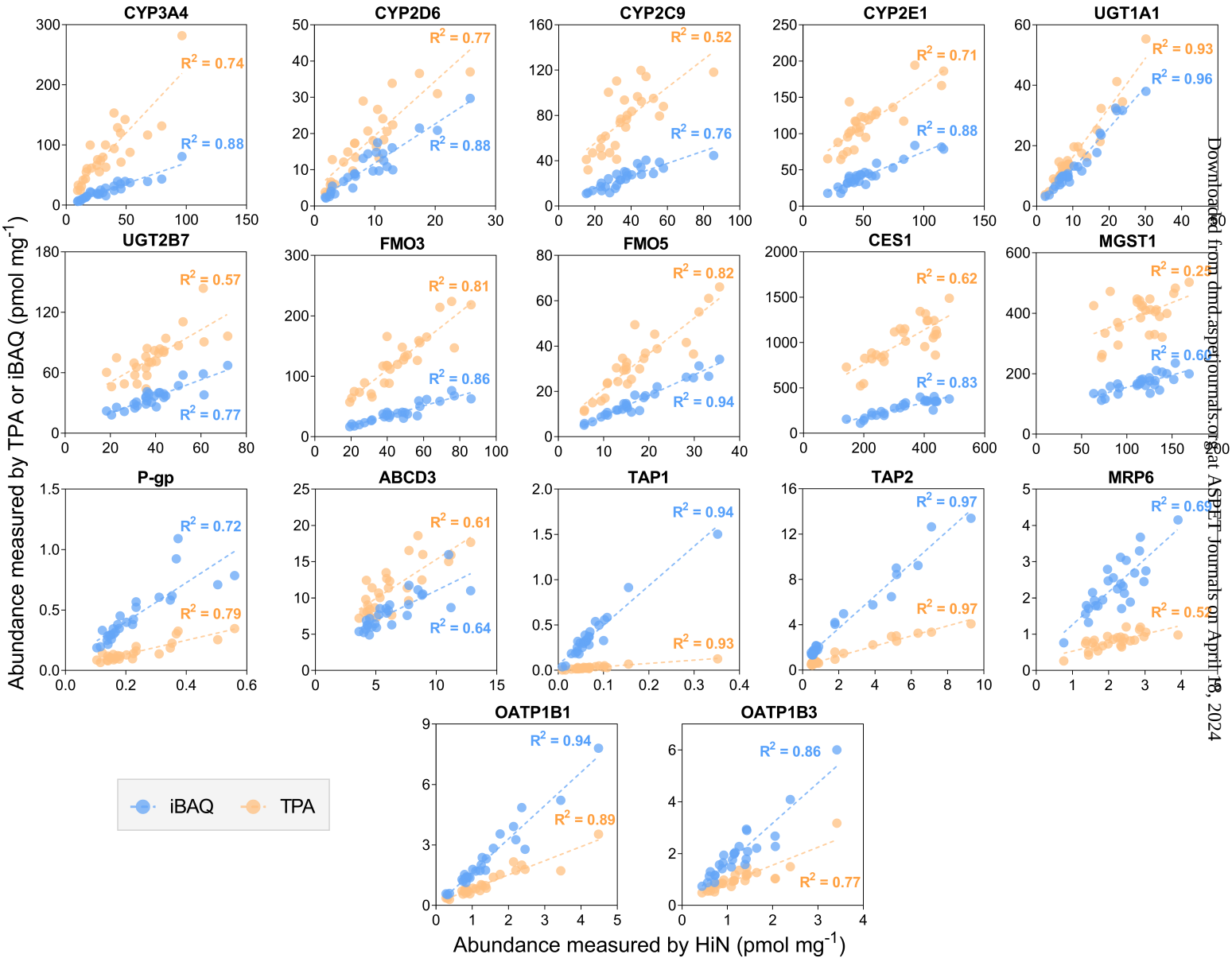


Figure 2

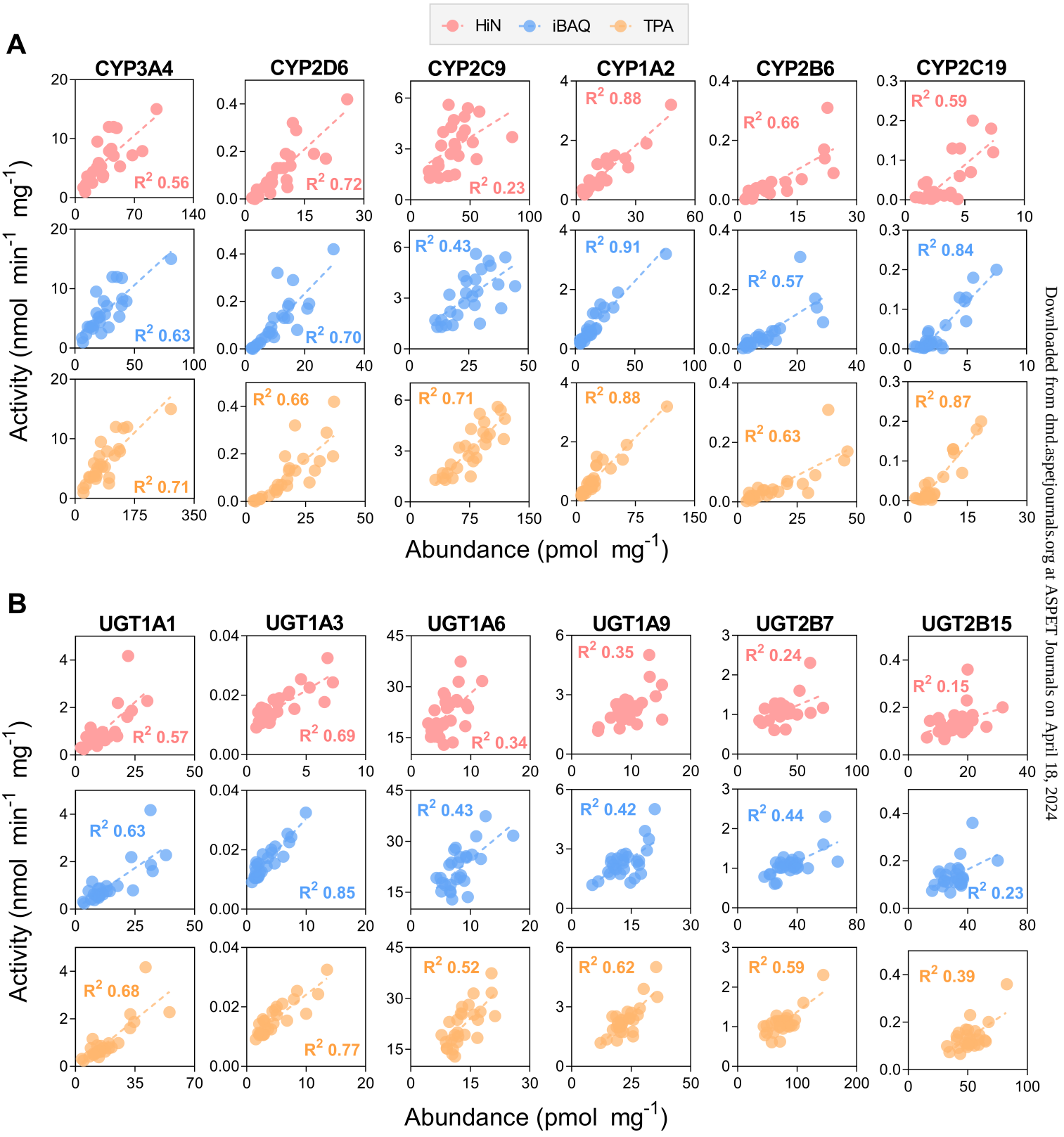


Figure 3

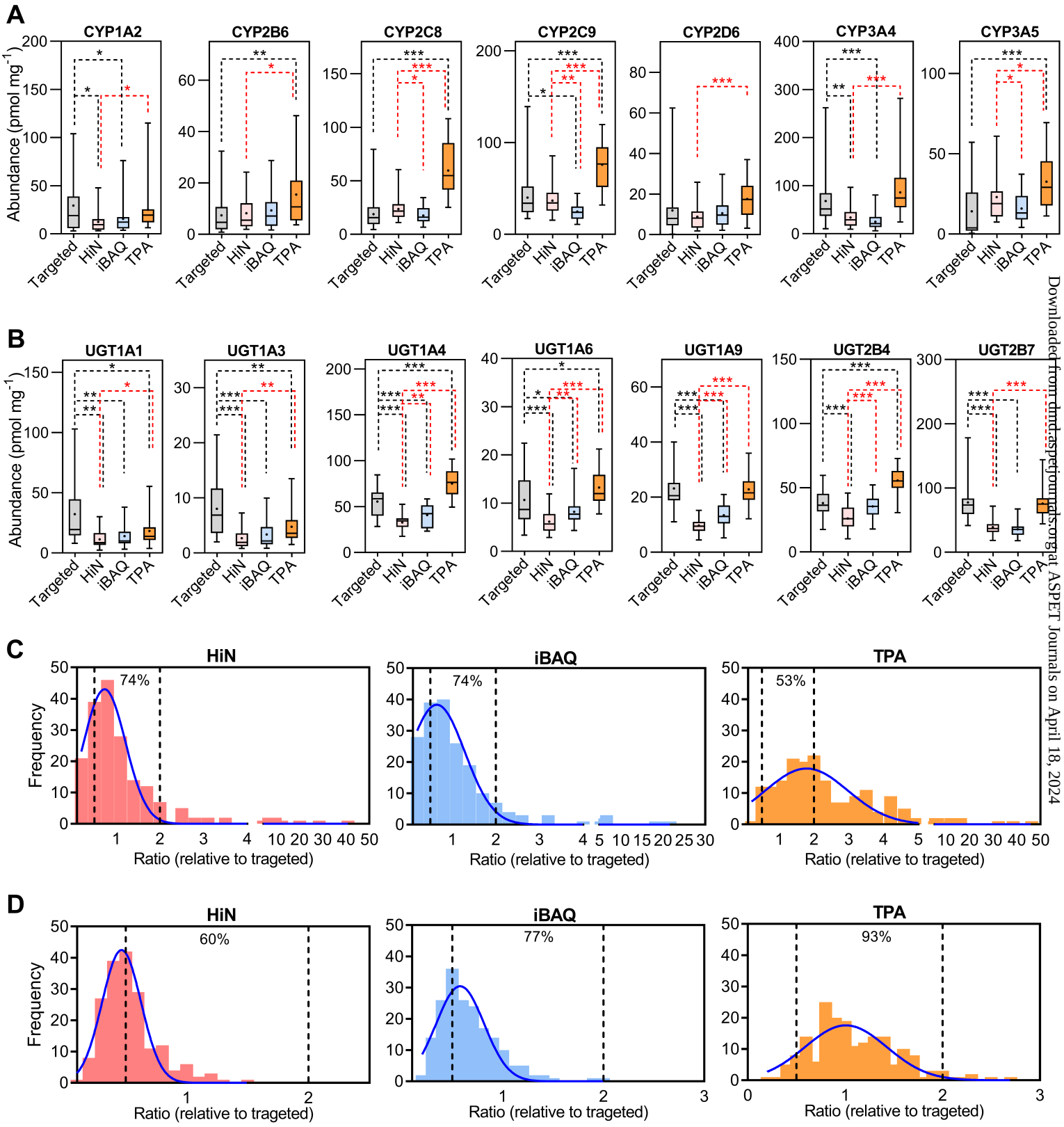


Figure 4

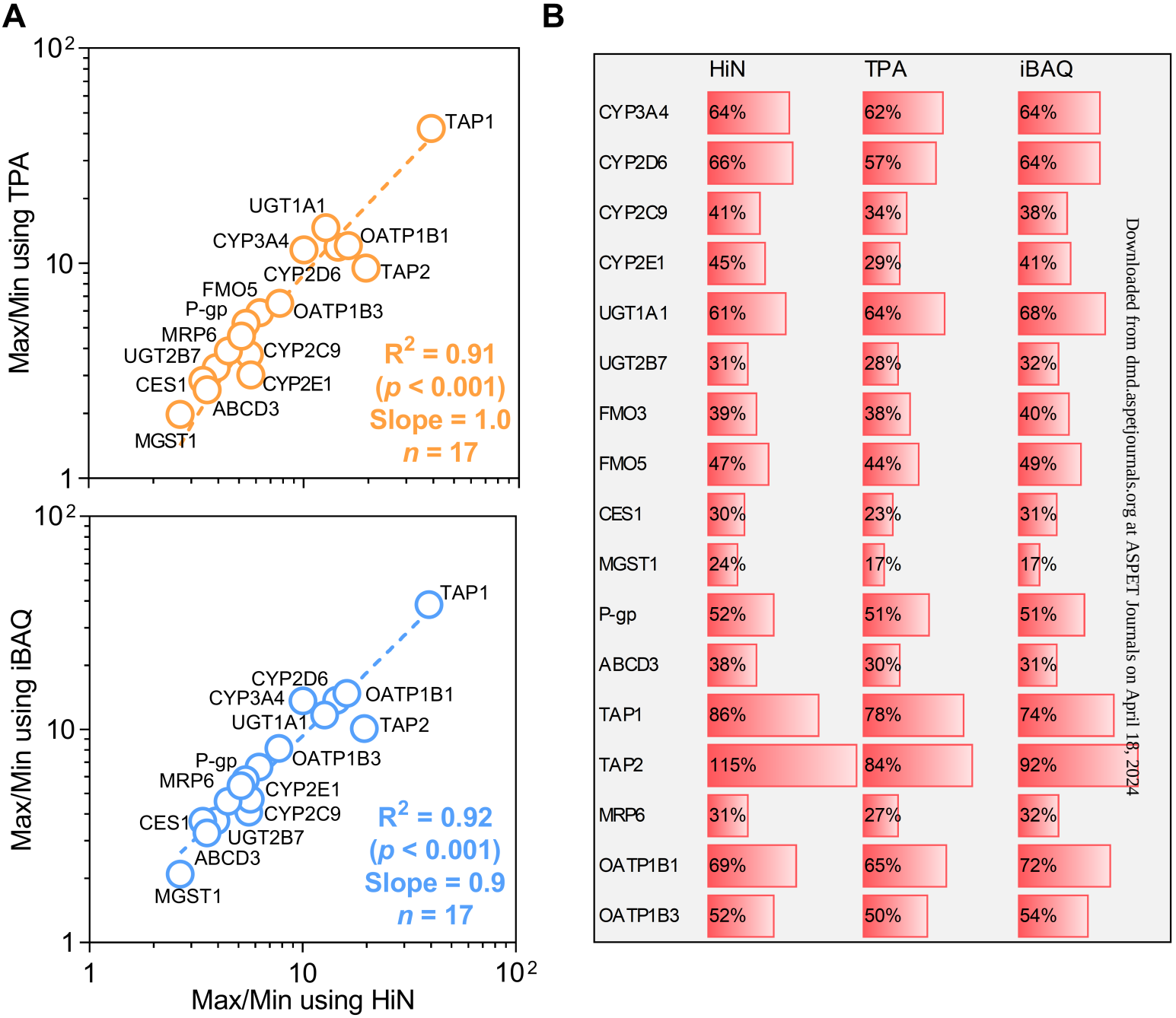


Figure 5

Supplemental Information

Drug Metabolism and Disposition

Label-Free but Still Constrained: Assessment of Global Proteomic Strategies for the Quantification of Hepatic Enzymes and Transporters

Jill Barber, Zubida M Al-Majdoub, Narciso Couto, Areti-Maria Vasilogianni, Annika Tillmann, Sarah Alrubia, Amin Rostami-Hodjegan, Brahim Achour

Supplemental Table 1. Demographic and clinical details of the donors of the 27 liver samples.

Donor	Age	Ethnicity	Sex	BMI (kg m^{-2})	Smoking	Alcohol	Cause of death	Medical history	Medication history
HH01	31	C	F	29.8	Yes	No	Vehicle accident	-	-
HH02	54	C	M	30.5	Yes	Yes	Ascending aorta aneurysm	-	-
HH06	62	C	F	38.5	No	No	Cerebral vascular aneurysm	Hypertension, congestistive heart failure	Insulin, hypertension and heart meds
HH08	62	C	F	29.0	No	No	Head trauma	Hypertension	Hypertension meds
HH09	51	C	M	25.8	No	Yes	Intracranial bleeding	Hypertension, CVA	-
HH11	51	C	F	39.5	Yes	No	Intracranial haemorrhage	Asthma, benign breast cyst, arthritis	Inhalers
HH25	66	C	F	39.6	No	No	Intracranial haemorrhage	Hypertension, RA	Unknown
HH35	42	C	F	28.1	No	No	Anoxia	Asthma	Accolate, claritin, paxil, pirbuterol
HH38	41	H	F	32.1	No	Occasional	Cerebral vascular aneurysm	Hypertension, mild stroke	Atenolol
HH41	58	C	F	35.3	No	No	Pulmonary Hypertension	CHF, emphysema	Coumadin, digoxin lasix, k-dur, flovent, convent, flomax, cordizem
HH48	62	C	M	34.7	No	No	Intracranial bleeding	Diabetes, COPD	Insulin
HH71	58	C	M	27.4	No	No	Intracranial bleeding	Healthy	-
HH72	54	C	M	18.0	No	No	Intracranial bleeding	Healthy	-
HH73	48	C	M	32.8	No	No	Head trauma	Healthy	-
HH74	55	C	M	24.5	No	No	Intracranial bleeding	Hypertension	Prozac and cozaar
HH75	55	C	M	36.7	Yes	No	Anoxia	Asthma, hypertension, diabetes, heart disease	-
HH76	50	C	M	25.8	No	No	Cerebral vascular aneurysm	Healthy	-
HH77	44	C	F	36.0	No	Social	Cerebral vascular aneurysm	Healthy	-
HH78	28	C	F	25.8	No	Social	Head trauma	Asthma	-
HH79	60	C	M	36.3	No	No	Intracranial bleeding	Asthma	Albuterol
HH80	28	C	M	24.8	No	No	Vehicle accident	Diabetes	Insulin
HH89	33	C	M	22.1	No	No	Stroke	Diabetes	Insulin
HH90	56	C	M	25.1	No	Social	Head trauma	Hypertension	-
HH91	55	C	F	26.6	No	No	Cerebral vascular aneurysm	Healthy	-
HH100	38	AA	M	28.7	No	Social	Head trauma	Healthy	-
HH108	27	C	F	22.1	No	Social	Closed head injury	Healthy	-
HH117	47	C	M	26.6	No	Yes	Intracranial bleeding	Hypertension	Pseudogest

AA, African-American; C, Caucasian; H, Hispanic; BMI, Body mass index; CHF, Congestive heart failure; COPD, Chronic obstructive pulmonary disease; CVA, Cerebral vascular aneurysm; F, Female; M, Male; RA, Rheumatoid arthritis. BMI, Body mass index.

Supplemental Table 2. Agreement in identification between technical replicates. Percent identical peptide (PIP) was in the range 86-99%.

Donor	PIP (%)
HH01	94
HH02	97
HH06	96
HH08	99
HH09	86
HH11	99
HH25	97
HH35	97
HH38	95
HH41	99
HH48	99
HH71	94
HH72	98
HH73	99
HH74	96
HH75	94
HH76	96
HH77	99
HH78	96
HH79	96
HH80	93
HH89	99
HH90	99
HH91	94
HH100	95
HH108	98
HH117	97

Supplemental Table 3. Similarity matrix between biological samples based on percent identical peptide (PIP). The range of PIP was 96-99%.

	HH117	HH108	HH100	HH91	HH90	HH89	HH80	HH79	HH78	HH77	HH76	HH75	HH74	HH73	HH72	HH71	HH48	HH41	HH38	HH35	HH25	HH11	HH09	HH08	HH06	HH02
HH01	96	96	96	96	96	96	96	97	96	96	96	97	96	96	96	97	96	96	96	96	96	96	96	96	97	96
HH02	98	98	97	97	98	98	97	99	99	98	99	97	99	98	98	97	98	98	97	99	99	98	98	98	96	
HH06	98	98	97	97	98	98	97	99	99	98	99	97	99	98	98	97	98	98	97	99	99	98	98	98		
HH08	99	99	97	96	99	99	97	98	98	99	99	97	99	98	99	96	99	99	97	99	99	99	98			
HH09	98	98	97	96	98	98	97	98	98	98	98	97	98	98	98	96	98	98	97	98	98	98				
HH11	99	99	97	96	99	99	97	98	98	99	99	96	99	98	99	96	99	99	97	99	99					
HH25	99	98	97	97	99	99	97	99	99	98	99	97	99	98	98	97	99	99	97	99						
HH35	99	98	97	97	99	99	97	99	99	99	99	97	99	98	98	96	99	99	97							
HH38	97	96	97	97	96	96	97	97	97	96	97	97	97	96	96	97	97	97								
HH41	99	99	97	96	99	99	97	98	98	99	98	97	99	99	99	96	99									
HH48	99	99	96	96	99	99	96	98	98	99	98	96	99	98	99	96										
HH71	96	96	97	97	96	96	97	97	97	96	97	97	97	96	96											
HH72	98	98	96	96	98	98	96	98	98	98	98	96	98	98												
HH73	98	98	96	96	98	99	96	98	98	98	98	96	98													
HH74	99	98	97	97	98	99	97	99	99	98	99	97														
HH75	97	96	97	97	96	96	97	97	97	96	97															
HH76	99	98	97	97	98	98	97	99	99	98																
HH77	98	98	96	96	99	99	96	98	98																	
HH78	99	98	97	97	98	98	97	99																		
HH79	98	98	97	97	98	98	97																			
HH80	97	96	97	97	96	96																				
HH89	99	99	96	96	99																					
HH90	99	99	96	96																						
HH91	96	96	97																							
HH100	97	96																								
HH108	99																									

Supplemental Table 4. Abundance (in pmol mg^{-1}) of cytochrome P450 enzymes, UGT enzymes, ABC transporters, and solute carriers using HiN with BSA as a standard.

	HH01	HH02	HH06	HH08	HH09	HH11	HH25	HH35	HH38	HH41	HH48	HH71	HH72	HH73	HH74	HH75	HH76	HH77	HH78	HH79	HH80	HH89	HH90	HH91	HH100	HH108	HH117	Mean	SD
CYP2E1	42.3	46.5	60.1	51.1	36.7	36.9	44.2	44.1	31.2	38.4	43.1	57.0	47.5	20.5	48.0	33.2	54.2	39.7	74.4	92.5	114.7	38.0	28.9	116.4	51.9	60.9	83.4	**53.2**	**24.0**
CYP3A4	79.5	11.8	14.1	45.3	27.7	16.7	96.4	32.8	10.1	20.1	9.6	30.7	42.8	39.9	49.1	40.0	16.2	17.4	25.6	21.1	45.7	12.8	26.2	67.8	33.1	28.6	53.2	**33.9**	**21.6**
CYP2C9	85.5	45.7	34.2	23.1	16.2	18.8	40.4	36.3	28.2	32.0	25.8	23.8	48.3	27.5	33.9	52.3	37.8	45.4	37.0	43.5	32.0	23.6	15.3	57.8	31.3	37.4	55.6	**36.6**	**15.0**
CYP2A6	30.7	8.0	12.2	13.1	13.0	14.2	38.8	9.6	7.2	16.4	10.9	21.5	31.5	37.1	10.7	43.4	17.3	15.0	10.5	19.0	22.7	28.1	20.8	19.8	10.2	17.5	51.6	**20.4**	**11.7**
CYP2C8	60.4	18.4	14.5	16.9	21.8	14.4	36.6	29.0	21.1	22.3	11.0	23.1	28.3	26.0	31.2	28.2	15.5	20.8	22.0	20.4	33.1	14.0	20.7	25.9	15.2	16.3	33.6	**23.7**	**10.0**
CYP3A5	60.9	14.2	8.5	33.4	26.1	9.5	50.0	15.6	7.5	10.7	10.9	18.6	19.0	20.2	26.6	20.1	8.5	9.0	14.5	11.0	41.3	13.6	24.3	52.0	25.5	25.3	45.4	**23.0**	**15.0**
CYP4F2	9.3	12.2	9.1	12.7	12.2	8.1	8.4	6.9	18.5	7.1	14.4	8.6	10.9	9.4	8.0	11.7	12.3	15.1	10.0	14.4	12.7	12.1	6.3	15.3	14.8	4.6	19.3	**11.3**	**3.6**
CYP1A2	10.0	11.2	3.8	6.7	16.1	24.8	7.3	4.2	3.9	3.3	4.2	35.5	47.9	6.6	10.7	12.9	9.6	7.4	4.2	15.3	19.3	5.5	3.3	15.3	26.3	7.6	13.6	**12.5**	**10.6**
CYP4A11	8.1	6.4	9.7	6.9	5.8	10.5	8.7	10.4	5.2	8.5	8.2	11.0	17.4	6.5	6.8	9.6	18.7	11.4	11.3	19.1	6.8	11.1	4.4	11.1	12.2	8.0	17.7	**10.1**	**4.1**
CYP2D6	20.4	2.6	9.7	11.3	11.5	6.7	17.4	2.5	13.0	8.1	6.7	3.4	10.5	3.0	4.8	12.0	2.8	5.5	6.8	1.9	25.8	1.8	12.9	10.7	6.4	8.9	10.3	**8.8**	**5.8**
CYP2B6	16.2	3.7	2.6	3.0	2.8	2.9	22.0	4.7	2.2	8.5	2.0	12.1	5.5	12.5	21.8	22.7	3.7	3.2	3.5	7.0	6.3	3.9	6.9	8.1	3.1	7.6	24.2	**8.2**	**7.0**
CYP8B1	6.9	10.6	8.6	6.0	3.4	4.0	4.6	8.0	6.7	3.6	3.4	8.4	5.9	7.0	4.6	3.9	6.4	5.1	6.5	6.5	7.5	3.3	5.2	7.2	7.9	9.4	11.8	**6.4**	**2.2**
CYP27A1	4.6	6.9	4.5	4.6	4.0	3.1	3.8	7.0	10.1	2.6	4.0	4.5	4.1	4.0	3.8	5.0	4.3	3.2	3.9	4.2	10.5	4.0	3.4	5.3	5.9	4.2	8.4	**5.0**	**2.0**
CYP4A22	2.3	4.0	6.5	4.3	3.5	5.7	5.2	6.4	2.0	5.5	5.1	4.2	10.5	4.5	4.2	2.8	11.0	7.0	6.8	10.6	2.4	7.8	2.5	7.6	10.9	6.8	10.0	**5.9**	**2.8**
CYP4F11	7.9	4.9	3.6	3.6	2.5	3.0	2.8	2.4	4.3	2.5	3.2	4.3	4.0	2.0	2.7	3.4	4.5	2.3	2.9	3.7	4.2	2.9	1.8	3.9	3.8	3.2	7.3	**3.6**	**1.4**
CYP4F3	3.6	4.1	2.6	2.7	4.1	2.4	2.8	2.3	3.8	2.8	3.4	3.7	3.3	2.7	4.3	4.1	6.0	3.4	4.8	5.3	2.5	1.6	2.2	4.8	5.3	3.1	6.7	**3.6**	**1.2**
CYP2C19	7.4	2.4	1.2	1.6	2.2	1.8	5.5	3.8	1.3	2.5	0.9	2.5	5.7	2.3	4.6	2.8	2.0	2.4	4.6	4.0	4.4	1.5	2.2	3.3	7.2	2.1	3.9	**3.2**	**1.8**
CYP20A1	2.5	2.8	2.7	1.6	3.3	1.1	2.0	1.9	7.8	1.0	2.7	2.9	1.6	1.8	2.2	3.9	2.5	2.3	2.6	2.2	3.2	1.9	1.8	4.3	5.0	1.4	3.4	**2.7**	**1.4**
CYP3A7	7.8	0.4	0.3	1.5	0.5	0.7	7.1	0.2	0.4	10.1	0.6	0.3	1.3	0.6	0.4	0.8	0.3	1.6	0.2	0.5	0.9	0.2	3.8	0.7	0.4	0.5	0.7	**1.6**	**2.6**
CYP4V2	0.9	2.0	1.7	1.5	1.1	1.1	1.8	2.1	0.7	1.1	1.3	1.6	2.3	0.9	1.4	0.6	2.0	2.2	3.0	2.5	1.5	1.6	1.1	1.1	1.9	1.6	5.2	**1.7**	**0.9**
CYP7B1	1.5	2.2	1.3	1.4	1.2	1.3	1.6	1.6	1.5	0.7	1.5	1.3	1.7	1.2	1.2	1.5	1.7	1.1	1.6	2.1	1.7	1.2	0.9	1.8	1.2	1.7	1.9	**1.5**	**0.3**
CYP2C18	1.1	1.4	0.7	1.0	0.7	1.4	0.7	1.0	1.6	0.7	0.8	0.7	1.1	0.9	0.7	0.5	1.0	1.0	1.0	1.0	1.1	1.1	0.8	0.6	1.5	0.9	1.5	**1.0**	**0.3**
CYP2J2	0.8	1.0	0.9	0.8	0.2	0.4	0.6	0.5	0.7	0.3	0.3	0.9	0.8	0.2	0.4	0.6	0.7	0.4	0.4	0.6	1.0	0.4	0.3	1.1	1.3	0.7	1.1	**0.6**	**0.3**
UGT2B7	31.8	30.8	26.2	41.9	50.0	30.4	31.5	35.7	40.3	18.3	44.4	43.6	52.1	22.7	39.5	38.2	43.6	61.0	41.3	35.7	35.8	36.2	20.5	36.1	61.4	37.0	71.8	**39.2**	**12.3**
UGT1A4	47.2	27.8	26.8	39.7	36.8	18.1	36.7	29.0	34.1	17.7	20.1	39.6	42.6	18.0	34.4	33.9	35.9	30.1	36.0	28.3	37.1	36.0	21.3	52.6	27.9	36.9	38.2	**32.7**	**8.8**
UGT2B4	37.8	21.3	14.7	26.8	28.9	19.7	27.3	20.0	35.3	10.3	19.9	25.9	23.6	15.0	28.2	35.5	22.8	26.2	26.4	20.7	45.9	19.7	15.6	34.6	40.3	21.1	37.8	**26.0**	**8.8**
UGT2B15	21.6	12.8	10.3	17.2	19.7	12.6	19.1	13.0	19.9	6.3	12.7	15.5	12.2	7.3	18.2	21.6	18.1	20.0	18.0	15.0	18.3	10.6	10.2	18.4	26.3	14.9	31.7	**16.4**	**5.6**
UGT2B10	42.1	22.7	24.5	16.7	11.9	13.9	13.3	18.2	12.1	8.6	18.9	18.2	19.2	10.4	17.9	13.7	12.2	16.4	19.6	30.3	52.3	14.9	31.1	17.3	18.9	31.4	24.7	**20.4**	**9.9**
UGT1A9	7.5	15.2	7.7	9.6	14.1	7.9	13.0	9.0	8.5	4.5	8.5	10.8	11.0	4.5	7.7	6.6	9.8	9.5	11.0	8.0	8.1	13.1	7.8	15.2	11.8	11.0	10.9	**9.7**	**2.8**
UGT1A1	23.7	16.6	6.4	8.6	2.4	10.3	22.1	7.8	9.1	6.2	8.5	8.8	7.2	7.0	17.8	30.2	3.5	11.4	8.4	6.7	21.8	5.1	4.6	13.9	12.5	7.0	17.5	**11.3**	**6.9**
UGT1A6	7.8	7.7	5.7	4.8	8.0	3.3	8.3	5.5	9.6	3.4	4.3	6.0	4.0	4.3	6.7	9.3	5.5	2.9	5.4	4.0	11.9	5.8	5.5	6.7	9.1	4.4	7.0	**6.2**	**2.2**
UGT2B17	9.6	2.7	0.9	0.9	6.6	1.8	0.9	0.5	2.8	4.3	4.7	5.8	15.5	0.5	0.7	6.9	0.6	6.5	5.9	0.5	1.2	9.2	0.5	2.0	1.0	1.7	1.2	**3.5**	**3.7**
UGT1A3	3.5	1.1	2.3	2.0	3.6	1.0	1.0	1.5	1.9	1.5	0.8	7.2	6.8	1.2	1.3	1.6	4.0	1.2	2.6	2.7	5.3	2.6	1.2	1.9	6.5	4.6	1.4	**2.7**	**1.9**
UGT2A3	3.1	3.7	1.7	2.3	1.2	2.2	1.3	1.9	2.8	1.0	1.5	1.9	1.7	0.8	1.4	4.8	1.3	3.0	1.7	2.5	1.9	1.2	1.7	4.5	2.5	1.9	3.6	**2.2**	**1.0**
ABCB1	0.2	0.4	0.1	0.4	0.4	0.2	0.1	0.1	0.6	0.1	0.2	0.1	0.2	0.1	0.2	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.1	0.2	0.5	0.2	0.3	**0.2**	**0.1**
ABCB2	0.1	0.4	0.0	0.2	0.1	0.1	0.0	0.1	0.1	0.0	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.0	0.1	0.1	**0.1**	**0.1**
ABCB4	0.7	0.9	0.4	0.5	0.4	0.4	0.5	0.4	0.6	0.4	0.3	0.3	0.5	0.3	0.4	0.4	0.3	0.5	0.3	0.5	0.4	0.3	0.3	0.3	0.4	0.4	1.0	**0.4**	**0.2**
ABCD3	6.3	8.9	4.0	6.1	5.1	5.9	5.2	7.7	11.2	4.2	8.5	4.5	4.3	4.7	4.3	7.6	6.0	5.9	4.9	5.3	7.7	3.6	4.2	8.8	12.8	4.5	11.0	**6.4**	**2.5**
ABCB3	9.3	1.8	0.8	0.7	0.5	0.6	0.7	0.7	4.9	0.5	0.5	5.2	0.5	0.6	0.7	3.9	0.6	0.6	0.6	2.3	7.1	0.6	0.6	5.2	6.4	0.9	1.8	**2.2**	**2.5**
ABCA6	2.5	2.6	2.9	2.5	2.8	1.9	2.9	2.2	2.8	1.8	1.7	3.0	2.9	4.2	3.2	2.6	2.8	1.7	2.7	3.0	3.1	3.8	1.8	3.6	3.4	2.0	3.6	**2.7**	**0.7**
ABCC6	2.3	3.0	3.0	2.8	2.7	2.5	1.8	1.6	2.6	1.4	2.4	1.4	2.9	1.4	1.6	0.8	2.4	2.2	2.1	2.3	1.4	2.0	1.6	1.7	2.4	2.0	3.9	**2.2**	**0.7**
ABCB7	0.7	0.6	0.7	0.6	0.7	0.4	0.4	0.8	1.5	0.3	0.7	0.6	0.4	0.5	0.4	0.9	0.9	0.5	0.7	0.7	1.2	0.6	0.4	1.0	0.9	0.2	0.9	**0.7**	**0.3**
ABCB8	0.01	0.06	0.08	0.05	0.01	0.03	0.03	0.09	0.22	0.02	0.05	0.03	0.03	0.07	0.03	0.05	0.07	0.02	0.09	0.02	0.10	0.03	0.03	0.06	0.03	0.03	0.14	**0.05**	**0.04**
ABCD1	0.1	0.2	0.1	0.1	0.0	0.1	0.0	0.2	0.1	0.0	0.1	0.0	0.1	0.1	0.0	0.1	0.1	0.1	0.0	0.1	0.0	0.1	0.1	0.1	0.0	0.1	0.2	**0.1**	**0.1**
ABCA1	0.5	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.3	0.0	0.1	0.3	0.1	0.1	0.1	0.2	0.2	0.1	0.2	0.1	0.1	0.2	0.1	0.1	0.3	0.1	0.2	**0.2**	**0.1**
ABCD4	0.11	0.13	0.06	0.10	0.03	0.09	0.11	0.06	0.07	0.08	0.10	0.03	0.08	0.09	0.07	0.06	0.06	0.06	0.09	0.06	0.07	0.12	0.06	0.12	0.07	0.12	0.24	**0.09**	**0.04**
ABCB11	0.15	0.26	0.21	0.17	0.10	0.18	0.10	0.15	0.23	0.11	0.09	0.17	0.17	0.06	0.08	0.15	0.22	0.14	0.11	0.20	0.13	0.14	0.08	0.11	0.21	0.17	0.23	**0.15**	**0.05**
ABCB10	0.3	0.4	0.5	0.3	0.3	0.2	0.3	0.4	0.9	0.1	0.4	0.3	0.3	0.2	0.2	0.3	0.5	0.2	0.5	0.4	0.6	0.3	0.2	0.4	0.5	0.2	0.6	**0.4**	**0.2**
ABCB6	0.6	0.6	0.3	0.3	0.3	0.2	0.3	0.2	0.7	0.1	0.2	0.7	0.2	0.2	0.3	0.6	0.2	0.1	0.1	0.2	1.0	0.3	0.2	0.6	0.5	0.2	0.3	**0.4**	**0.2**
ABCC3	0.9	1.1	0.4	0.5	0.2	0.4	0.4	0.4	0.6	0.4	0.4	0.4	0.4	0.4	0.6	0.8	0.5	0.4	0.4	0.5	0.8	0.5	0.4	1.0	0.6	0.4	0.7	**0.5**	**0.2**
ABCC2	0.2	0.4	0.1	0.2	0.1	0.2	0.1	0.2	0.4	0.1	0.1	0.1	0.3	0.1	0.2	0.3	0.2	0.2	0.1	0.2	0.3	0.2	0.2	0.2	0.1	0.2	0.3	**0.2**	**0.1**
SLCO1B1	1.2	2.2	0.8	1.0	1.8	2.1	0.9	1.6	2.5	0.3	0.8	0.8	4.5	0.3	1.2	0.4	1.1	0.7	0.7	2.4	1.4	0.8	0.8	0.9	1.4	1.3	3.4	**1.4**	**1.0**
SLCO1B3	2.1	1.6	0.8	0.9	0.6	1.3	1.1	1.2	1.4	0.6	0.6	1.4	3.4	0.4	1.4	0.7	1.1	0.9	0.7	1.4	2.4	0.9	0.7	1.1	1.4	1.2	2.1	**1.2**	**0.7**
SLCO2B1	0.4	1.4	0.9	0.3	0.2	0.4	0.4	0.4	0.5	0.5	0.3	0.6	0.8	0.4	0.3	0.6	0.3	0.3	0.3	0.6	1.1	0.5	0.6	0.7	0.4	0.1	0.8	**0.5**	**0.3**
SLC22A1	2.3	2.7	2.3	2.2	2.5	2.3	2.5	2.2	2.8	1.1	1.9	2.5	2.5	1.6	2.4	2.9	2.5	1.8	2.0	2.6	2.8	3.2	1.7	4.3	2.9	1.7	2.8	**2.4**	**0.6**
SLC22A7	0.6	0.4	0.1	0.2	0.3	0.3	0.2	0.2	0.5	0.1	0.2	0.3	0.2	0.2	0.2	0.1	0.1	0.2	0.1	0.3	0.2	0.1	0.2	0.3	0.1	0.1	0.5	**0.2**	**0.1**
SLC22A9	0.5	0.6	0.7	0.7	0.3	1.1	0.4	0.6	1.9	0.2	0.5	0.5	0.8	0.3	0.6	0.4	0.6	0.6	0.4	0.8	1.3	0.5	0.4	0.9	0.6	0.3	1.1	**0.7**	**0.4**

Supplemental Table 5. Abundance (in pmol mg^{-1}) of cytochrome P450 enzymes, UGT enzymes, ABC transporters, and solute carriers using iBAQ with BSA as a standard.

	HH01	HH02	HH06	HH08	HH09	HH11	HH25	HH35	HH38	HH41	HH48	HH71	HH72	HH73	HH74	HH75	HH76	HH77	HH78	HH79	HH80	HH89	HH90	HH91	HH100	HH108	HH117	Mean	SD
CYP2E1	32.4	34.1	41.9	46.5	31.5	32	39.1	41.9	17.8	41.5	36.4	41.5	43.7	17.8	42.8	23.2	44.9	33.5	52.9	83.7	81.7	38.9	26.5	78.6	30	59.1	64.7	**42.9**	**17.5**
CYP3A4	43.3	6.7	10.9	35.2	18.2	13.9	80.8	28.3	7.4	22.1	5.9	20.8	39.8	31.6	39.5	24.2	12.6	15.1	19.8	20.9	27	9.4	17.9	39.3	15.6	25.2	37.3	**24.8**	**15.8**
CYP2C9	44.5	27.8	22.9	17.2	11.8	13.6	27.5	30.3	11.7	28	16.9	13.5	40.4	24.1	23	28.6	26.6	34.1	23.8	37.5	18.2	20.2	10.9	33.4	15.5	29.7	38.6	**24.8**	**9.4**
CYP2A6	30.9	5.1	12.6	15.4	13.6	16.3	44.4	12.2	5.6	23.5	11.2	22.2	43.8	43.9	10	40.4	18.3	18.6	11.2	24.8	21	38.8	24.5	20.3	8.5	24	56.9	**22.9**	**13.6**
CYP2C8	34.4	13.5	9.8	13	13.8	11.4	31.8	27.1	6.6	21.6	6.8	12.8	28.8	18.3	25.8	16	11.2	17.1	16.8	19.8	24.6	12.1	16.2	15.7	6.6	15.4	27.9	**17.6**	**7.8**
CYP3A5	37.2	13.9	6	27.1	22.4	6.7	26.5	10	4.1	7.7	9.9	10.4	13.1	11.5	14.4	9.5	6.3	6.5	9.2	9.1	28	14.1	20.7	29.7	15	23.8	37	**15.9**	**9.7**
CYP4F2	9.6	12.6	9.3	17.6	16.3	10.4	12	6.8	10.7	12.2	18.7	10	16.6	11.9	11	11.4	14.4	20.2	12.4	22	13.1	17.7	8.8	18.9	13.4	7.7	31	**14.0**	**5.2**
CYP1A2	10.1	13.3	4.1	9.7	17.5	32	11	5.8	3.9	5.7	4.4	35.9	76.3	8.5	15	12.2	13.2	10.4	4.3	24.4	21.1	7.6	4	17.1	24.2	12.2	17.6	**15.6**	**14.8**
CYP4A11	9.7	7.5	11.3	9.6	6.7	13.5	10.8	16.1	4.8	16.2	10.8	14.1	31.9	10.2	7.9	10	22.6	18.8	12.1	28.8	9.6	18.6	6.4	14.6	11	11.7	20.3	**13.5**	**6.5**
CYP2D6	20.9	3.3	9.7	14.5	12.5	9	21.5	2.6	10	13.2	8.8	3.3	17.5	5.5	6.8	10.9	4.1	7.9	8.2	2.2	29.7	2.4	16.1	9.7	4.9	14.4	14.8	**10.5**	**6.7**
CYP2B6	14.3	3.3	2.6	3.3	3.2	2.8	26.6	6.3	1.7	12.6	1.9	11.6	7.1	12.8	26.1	21.1	4.3	3.3	4.4	9.9	7.2	5.5	8.2	8.8	2.5	10.4	28.7	**9.3**	**7.9**
CYP8B1	7.8	11.9	9.3	8.2	4.2	5.9	6.3	11.4	5.6	6.4	4.5	9.1	9.1	8.7	6.8	3.8	8.6	6.9	8.2	10.7	8.6	6	6.8	6.9	6.3	14.6	16.6	**8.1**	**3.0**
CYP27A1	5.6	8.7	6.8	8.1	6.5	4.8	6.9	13.4	9.9	5.5	6.2	5.2	7.3	6.2	5.9	5.9	5.9	4.4	6	7.2	14.9	7.4	6	6.4	5.4	6.2	13.8	**7.3**	**2.7**
CYP4A22	1.8	2.8	5.3	4.8	3.1	5.1	5.1	6.4	1.4	7.9	5.1	3.8	10.3	5.4	4	2.1	8.7	6.5	5.8	10.3	2.7	9.3	2.7	7.1	6	7.6	9	**5.6**	**2.6**
CYP4F11	9.8	6.9	5	5.9	5.1	4.6	4.9	4	4.1	5	4.8	5.9	7.3	3.1	4.9	4.3	7.1	3.5	5.1	6.9	6.2	5.3	2.9	6.1	4.6	6.8	12.4	**5.6**	**2.0**
CYP4F3	3.4	3.9	2.6	3.5	5.4	2.9	3.7	2.7	2.5	4.5	3.9	3.8	4.5	3.3	5.5	4.1	6.7	3.9	5.8	6.8	2.7	2.1	2.8	5.6	4.2	5.2	8.3	**4.2**	**1.5**
CYP2C19	4.8	1.6	0.8	1.1	1.4	1.8	4.9	2.4	0.7	1.9	0.6	1.7	7.5	1.6	3.2	1.5	2	1.6	4.4	4.9	3	1.7	1.4	1.9	5.5	2.1	2.8	**2.5**	**1.7**
CYP20A1	2.6	2.9	3.1	2.7	3.7	1.6	2.7	2.7	5.4	2	3.1	2.8	2.8	2.3	2.7	3.6	3	2.8	3.1	3.5	3.7	3	2.2	4.1	4	2.1	4.3	**3.1**	**0.8**
CYP3A7	4.8	0.3	0.3	1.6	0.5	0.6	7.6	0.5	0.4	13.4	0.5	0.3	1.2	0.6	0.5	0.8	0.4	1.9	0.4	0.7	0.7	0.2	3.6	0.6	0.3	0.7	0.9	**1.6**	**2.9**
CYP4V2	1.6	3.2	2.9	2.9	1.5	1.8	3.7	4.1	1.2	2.8	2.4	2.4	4.8	1.8	2.1	1.6	3.3	4.9	5.3	5.7	3.2	3.1	1.5	2.1	2.6	3.5	9	**3.1**	**1.7**
CYP7B1	2.9	4.6	2.9	3.7	2.8	3	3.8	4.1	2.4	2.3	3.3	2.7	4.8	3	2.9	3	4	2.6	3.8	5.7	4.1	3.5	2.3	4.1	2.2	5	4.6	**3.5**	**0.9**
CYP2C18	0.8	1	0.6	0.9	0.6	1.1	0.7	1	0.9	0.7	0.7	0.5	1.2	0.9	0.6	0.3	0.8	0.8	0.9	1.1	0.9	1.3	0.7	0.5	0.9	0.9	1.3	**0.8**	**0.2**
CYP2J2	1.2	1.6	1.7	1.7	0.4	0.7	1.2	1.1	1	0.7	0.6	1.7	1.7	0.5	0.8	0.8	1.2	0.7	0.8	1.6	2.7	0.7	0.6	1.8	1.6	1.5	1.9	**1.2**	**0.6**
UGT2B7	27.1	24.9	21.6	40.3	47.2	29	30.9	35.4	26.2	22	37	35.4	57.7	25.8	36.8	30.6	39	58.9	40.1	36.1	28.9	41.2	18.1	32.1	38	39.3	67.3	**35.8**	**11.6**
UGT1A4	51.5	30.3	31.9	50.3	49.6	23.4	54.6	38.5	26.3	26.3	23.2	43.2	58.3	24.1	47.4	37.5	41.4	36.8	46	42.3	52.5	49.4	26.2	57	26.3	52.4	53.8	**40.8**	**11.8**
UGT2B4	44.7	29.1	17.8	44.1	38.8	31.6	41.6	33.4	27.6	19.4	26.1	31.8	50	25.4	41.1	40.7	32.4	36.1	36.7	37.5	49.2	35.4	22.1	44.2	34.9	35.4	52.1	**35.5**	**9.0**
UGT2B15	33.4	23.2	17.8	36.1	35.1	26.5	35.6	31.5	24.4	16.1	24	28.3	28.3	21.7	36.9	32.3	34.1	43.2	34.8	36.7	32.3	25.4	20.6	35.6	33.9	35.9	60.1	**31.3**	**8.8**
UGT2B10	29.7	19	17.1	16.9	11.6	17	14.4	21.6	9.1	10.6	17.6	18.4	20.7	10.2	18.7	12.5	14.6	19.1	23.7	31.7	35.3	17.4	20.9	21	13.2	31.5	27.9	**19.3**	**6.9**
UGT1A9	11.6	19.5	10.1	13	19	10.9	20.9	13.7	9.7	6.7	10.4	12.9	16.5	5.3	11.2	9.2	12.2	12.8	15.9	13.2	14.8	18.5	9.9	17.5	14.2	17	17	**13.5**	**3.9**
UGT1A1	31.6	17.7	7.1	10.8	3.3	13.2	31.6	10	8	8.7	9.6	9.7	10	7.8	23.5	38	3.7	13.1	10.2	9.4	32.4	6.6	5.6	14.4	11.6	9.8	24.2	**14.1**	**9.6**
UGT1A6	9.3	10.3	7.3	6.7	11	5.2	12.6	8.3	7.9	5.8	5.3	6.9	6.5	5	9.4	11.8	7	4.3	7.7	6.6	17.2	8.3	7.6	8.4	9	6.7	9.6	**8.2**	**2.7**
UGT2B17	14.5	5.3	1.9	2.3	13	3.9	2.1	1.5	3.7	10.3	9.4	10.4	37.1	1.3	1.7	11	1.3	13.9	11.4	1.4	2.7	21.5	1.1	4.2	1.7	4.2	2.4	**7.2**	**8.1**
UGT1A3	4.1	1.3	2.7	2.5	4.8	1.4	1.4	2.1	1.6	2.2	0.9	7.5	10	1.6	1.8	1.8	4.7	1.6	3.3	4.2	7.2	3.6	1.5	1.9	6.2	6.9	2	**3.4**	**2.4**
UGT2A3	4.9	6	2.9	4.7	2.2	4.2	2.7	4.3	2.7	2.2	2.8	2.3	3.8	1.2	2.7	5.4	2.2	5.5	3.4	5.5	2.6	2.5	3	6.4	3	4	7.2	**3.7**	**1.5**
ABCB1	0.3	0.6	0.2	0.9	1.1	0.5	0.2	0.2	0.8	0.3	0.3	0.3	0.3	0.2	0.3	0.6	0.4	0.3	0.4	0.5	0.4	0.4	0.3	0.3	0.7	0.6	0.6	**0.4**	**0.2**
ABCB2	0.3	1.5	0.2	0.9	0.3	0.4	0.3	0.4	0.3	0.3	0.3	0	0.2	0.3	0.3	0.2	0.2	0.6	0.3	0.3	0.4	0.5	0.5	0.3	0	0.4	0.6	**0.4**	**0.3**
ABCB4	0.9	1.3	0.6	1	1	0.8	0.8	0.7	0.9	0.9	0.5	0.6	1	0.6	0.6	0.6	0.6	0.9	0.6	1.2	0.6	0.7	0.6	0.6	0.6	0.9	1.7	**0.8**	**0.3**
ABCD3	6.3	10.5	5.2	9	5.9	8.5	7.7	11.7	8.7	6.9	11.1	4.9	6.3	6	6.2	7.6	8.2	7.9	6.5	8.5	9.1	5.4	5.7	10.4	11	7.2	16	**8.1**	**2.5**
ABCB3	13.4	4.2	1.8	2.2	1.5	1.4	1.7	2.1	6.5	1.4	1.4	9	1.3	1.5	1.6	5.8	1.6	1.4	1.7	5	12.6	1.8	1.5	8.4	9.2	2.1	4	**3.9**	**3.6**
ABCA6	2.3	2.2	3.3	3.2	3	2.1	3.4	2.6	2.2	2.8	1.5	3	4.9	3.9	3.1	2.1	2.8	1.8	3.2	3.7	2.8	4.5	2.3	3.4	2.3	2.6	3.8	**2.9**	**0.8**
ABCC6	2.4	2.4	2.7	3.3	2.7	3	1.9	2.2	1.9	1.8	2.1	1.3	3.7	1.6	1.8	0.8	2.3	2.2	2.6	3.1	1.7	2.8	1.9	1.8	1.7	2.5	4.2	**2.3**	**0.7**
ABCB7	0.9	1	1.5	1.1	1.4	0.8	1	1.8	1.7	0.8	1.3	0.8	1	1	0.8	1.2	1.6	0.9	1.6	1.4	2.1	1.3	0.8	1.6	1.1	0.7	1.9	**1.2**	**0.4**
ABCB8	0.04	0.15	0.19	0.14	0.04	0.09	0.12	0.27	0.40	0.06	0.13	0.06	0.11	0.19	0.09	0.13	0.21	0.05	0.24	0.07	0.28	0.09	0.10	0.14	0.08	0.11	0.39	**0.15**	**0.10**
ABCD1	0.3	0.9	0.2	0.4	0.1	0.3	0.2	0.8	0.3	0.2	0.2	0.1	0.4	0.3	0.1	0.4	0.3	0.5	0.2	0.3	0.1	0.3	0.3	0.3	0.2	0.3	0.9	**0.3**	**0.2**
ABCA1	0.7	0.5	0.2	0.3	0.3	0.3	0.2	0.2	0.4	0.1	0.2	0.4	0.2	0.2	0.2	0.3	0.3	0.2	0.3	0.3	0.3	0.5	0.2	0.2	0.4	0.2	0.4	**0.3**	**0.1**
ABCD4	0.45	0.54	0.29	0.58	0.14	0.50	0.65	0.36	0.22	0.57	0.51	0.13	0.52	0.51	0.39	0.23	0.31	0.35	0.49	0.38	0.40	0.76	0.35	0.56	0.21	0.80	1.28	**0.46**	**0.24**
ABCB11	0.24	0.58	0.46	0.52	0.28	0.59	0.23	0.33	0.33	0.43	0.21	0.37	0.52	0.19	0.19	0.25	0.57	0.39	0.32	0.58	0.25	0.51	0.24	0.21	0.29	0.59	0.54	**0.38**	**0.14**
ABCB10	0.7	0.8	1	0.8	0.8	0.6	0.8	1.2	1.5	0.3	0.9	0.5	0.7	0.6	0.5	0.7	1.1	0.4	1.2	1	1.4	1	0.5	1	1.1	0.4	1.4	**0.8**	**0.3**
ABCB6	1.6	2.3	1.3	1.4	1	0.7	1.3	0.7	1.7	0.4	0.7	2.2	0.9	0.9	1.0	1.8	0.8	0.3	0.5	0.9	3.3	1.3	0.9	1.8	1.2	0.8	1.3	**1.2**	**0.7**
ABCC3	1.5	2.1	0.7	1	0.5	0.9	0.9	1.1	0.8	1.0	0.8	0.8	0.9	0.8	1.1	1.1	0.8	0.9	0.8	1.1	1.5	1.2	0.9	1.6	0.8	0.9	1.4	**1.0**	**0.3**
ABCC2	0.3	0.7	0.3	0.6	0.4	0.5	0.3	0.5	0.6	0.4	0.2	0.3	0.7	0.4	0.3	0.5	0.3	0.4	0.2	0.5	0.9	0.4	0.5	0.3	0.2	0.7	0.8	**0.5**	**0.2**
SLCO1B1	1.7	3.3	1.4	1.8	3.5	3.9	1.4	2.8	2.8	0.6	1.4	1.1	7.8	0.5	2.0	0.6	1.7	1.3	1.2	4.9	2.3	1.5	1.3	1.4	1.7	2.4	5.2	**2.3**	**1.6**
SLCO1B3	2.3	2.2	1.6	1.6	1.3	2.3	1.8	2.0	1.8	1.1	0.9	2.1	6.0	0.7	2.9	0.9	2.0	1.4	1.2	2.9	4.1	1.9	1.2	1.5	1.6	2.0	2.7	**2.0**	**1.1**
SLCO2B1	0.8	3.2	2.2	0.8	0.4	1.1	1.1	1.3	1.0	1.8	0.8	1.5	2.4	1.1	0.9	1.2	0.8	0.9	0.8	1.7	2.5	1.4	1.7	1.6	0.6	0.4	2.0	**1.3**	**0.7**
SLC22A1	4.5	5.9	5.5	5.5	6.5	5.9	7.5	5.5	4.6	3.5	4.4	6.4	6.8	3.7	6.3	5.5	5.5	4.3	4.9	7.5	6.7	9.2	4.3	11.4	4.8	4.7	7.2	**5.9**	**1.7**
SLC22A7	2.6	1.7	0.6	1.1	1.6	1.8	1.2	1.2	1.5	1.1	0.9	1.4	1.5	1.2	1.0	0.4	0.5	1.0	0.5	2.1	1.2	0.6	1.2	1.3	0.3	0.8	2.8	**1.2**	**0.6**
SLC22A9	2.0	2.2	2.7	3.2	1.3	4.8	2.0	3.1	5.7	1.2	2.3	2.0	4.0	1.2	2.6	1.4	2.4	2.5	1.7	3.9	6.0	2.8	2.1	3.6	2.0	1.7	4.8	**2.8**	**1.3**

Supplemental Table 6. Abundance (in pmol mg^{-1}) of cytochrome P450 enzymes, UGT enzymes, ABC transporters, and solute carriers using the TPA method.

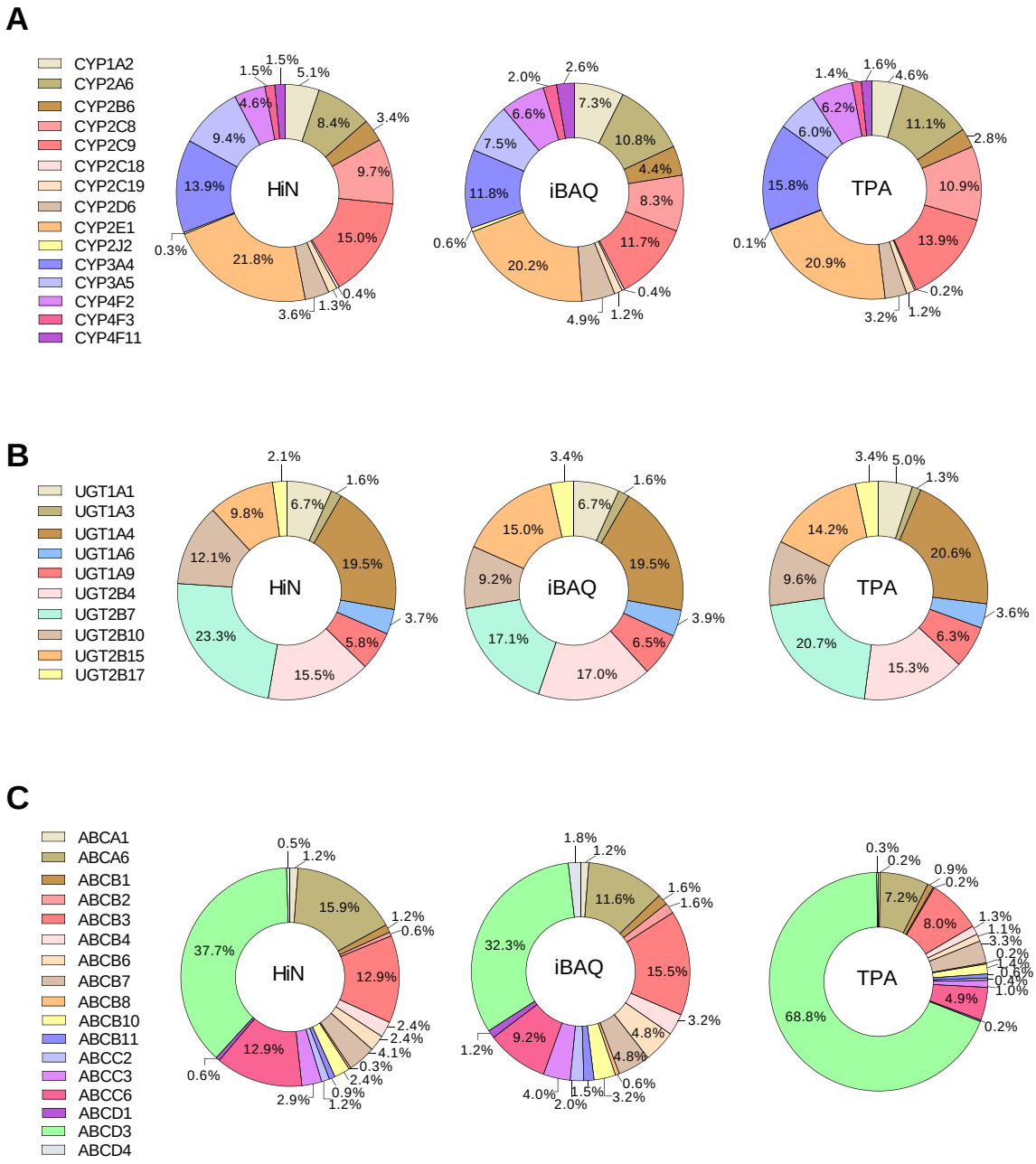
	HH01	HH02	HH06	HH08	HH09	HH11	HH25	HH35	HH38	HH41	HH48	HH71	HH72	HH73	HH74	HH75	HH76	HH77	HH78	HH79	HH80	HH89	HH90	HH91	HH100	HH108	HH117	Mean	SD
CYP2E1	77.5	101.9	126.2	122.0	75.2	95.3	107.3	116.4	64.3	143.8	117.3	125.2	109.0	65.4	123.2	70.8	119.2	103.4	136.2	194.3	166.3	100.6	87.9	186.3	94.9	131.2	117.3	**114.0**	**32.8**
CYP3A4	131.6	25.0	41.6	120.0	55.4	55.1	281.6	100.1	33.2	99.7	24.4	79.8	128.8	153.2	142.4	93.9	43.7	60.7	66.2	61.6	71.4	31.5	75.7	116.6	62.9	74.2	87.8	**85.9**	**53.3**
CYP2C9	118.2	92.4	76.7	51.4	31.8	46.9	83.6	93.5	47.0	110.4	61.7	44.4	114.4	100.4	73.7	95.1	80.1	119.7	69.6	96.6	41.3	59.3	41.0	87.9	53.5	76.5	79.5	**75.8**	**25.7**
CYP2A6	69.5	14.0	35.7	39.9	31.3	48.9	117.1	32.7	18.5	78.3	34.8	62.8	107.5	158.6	27.8	115.9	47.8	56.5	28.5	54.3	42.1	98.5	78.1	46.3	25.3	52.3	101.3	**60.2**	**35.9**
CYP2C8	101.9	50.0	36.7	43.1	41.8	43.8	107.9	93.5	29.6	95.1	27.6	47.8	91.1	85.4	92.2	58.5	37.8	67.0	54.8	57.0	61.1	39.5	68.3	45.2	25.3	44.4	64.1	**59.6**	**24.4**
CYP3A5	69.4	32.4	14.0	56.6	42.5	15.8	56.5	21.1	11.3	21.4	25.5	23.7	25.3	31.7	32.3	22.7	12.5	15.5	17.7	15.9	45.5	29.1	54.9	54.8	37.0	43.0	53.3	**32.6**	**16.6**
CYP4F2	20.4	32.7	24.2	41.8	34.5	28.2	28.5	16.4	34.4	37.4	53.5	26.3	36.7	39.6	27.5	30.2	34.0	55.3	29.0	44.3	24.2	40.5	25.3	39.8	37.7	15.5	49.8	**33.6**	**10.2**
CYP1A2	13.7	23.6	6.7	15.5	25.2	58.9	17.8	9.5	8.3	11.9	8.7	64.2	115.0	19.5	25.5	22.1	21.2	19.5	6.4	33.5	26.1	11.9	7.4	24.0	43.7	16.8	19.3	**25.0**	**23.0**
CYP4A11	15.0	14.4	22.0	16.0	10.6	27.9	19.7	29.7	10.8	35.9	22.2	26.5	54.0	23.1	14.7	19.8	40.8	37.1	21.3	44.5	12.4	31.7	13.6	21.6	22.5	18.0	23.4	**24.0**	**10.8**
CYP2D6	31.0	5.9	18.1	24.1	18.3	17.3	36.6	4.0	22.4	28.9	17.3	6.0	26.7	12.8	12.1	20.6	6.6	14.9	13.4	3.1	37.0	3.8	33.9	13.3	9.7	20.7	16.4	**17.6**	**10.0**
CYP2B6	21.0	6.1	4.9	5.4	4.8	5.4	44.8	10.7	3.6	27.4	3.8	20.7	11.2	29.6	46.1	38.1	7.1	6.4	7.1	14.1	8.6	8.9	17.1	12.3	4.6	14.8	32.7	**15.5**	**12.8**
CYP8B1	10.4	20.5	15.6	12.2	5.6	10.2	9.9	17.6	11.7	12.5	8.3	14.6	12.8	18.1	10.8	6.6	13.5	12.1	12.4	13.7	9.9	9.1	12.7	9.4	11.4	18.7	17.0	**12.5**	**3.6**
CYP27A1	5.8	11.2	8.8	9.4	6.8	6.4	8.2	16.1	15.4	8.4	8.8	6.8	8.0	10.0	7.4	7.7	7.0	6.1	6.8	6.8	13.4	8.4	8.8	6.6	7.0	6.2	11.0	**8.6**	**2.7**
CYP4A22	1.7	3.5	6.6	5.1	3.2	7.0	6.1	7.8	2.1	11.2	6.7	4.5	11.5	7.6	4.8	2.6	10.4	8.2	6.6	10.5	2.2	10.2	3.6	6.7	7.9	7.7	6.6	**6.4**	**2.9**
CYP4F11	13.0	11.5	8.4	8.7	7.2	8.3	7.4	6.2	8.5	9.9	8.8	10.2	10.4	6.5	7.8	7.6	10.7	6.2	7.7	9.2	7.4	7.7	5.5	8.0	8.4	8.8	12.8	**8.6**	**1.9**
CYP4F3	5.0	7.5	5.0	6.0	8.4	5.9	6.4	4.7	5.7	10.3	8.2	7.4	7.4	8.0	10.1	8.0	11.6	7.8	9.8	10.1	3.6	3.6	6.1	8.2	8.5	7.7	9.9	**7.4**	**2.1**
CYP2C19	11.7	4.6	2.2	2.9	3.4	5.3	13.7	6.7	2.5	6.6	1.9	5.2	18.5	6.0	9.0	4.5	5.4	5.0	11.5	11.4	6.0	4.4	4.4	4.5	17.4	4.7	5.0	**6.8**	**4.4**
CYP20A1	1.9	2.8	3.1	2.4	3.0	1.6	2.4	2.5	6.5	2.4	3.4	2.8	2.2	2.8	2.6	3.6	2.7	2.9	2.7	2.7	2.6	2.4	2.5	3.2	4.2	1.6	2.6	**2.8**	**0.9**
CYP3A7	10.7	0.9	0.9	4.0	1.2	1.8	19.6	1.1	1.2	45.1	1.6	0.9	2.7	2.1	1.2	2.1	1.0	5.7	0.9	1.4	1.4	0.4	11.5	1.2	0.9	1.3	1.4	**4.6**	**9.2**
CYP4V2	0.9	2.3	2.1	1.9	0.9	1.3	2.5	2.8	1.0	2.5	1.9	1.7	3.0	1.7	1.5	1.2	2.2	3.8	3.4	3.2	1.6	2.0	1.2	1.2	2.0	2.0	4.1	**2.1**	**0.9**
CYP7B1	0.9	1.7	1.1	1.2	0.9	1.2	1.3	1.5	1.1	1.0	1.4	1.0	1.5	1.4	1.1	1.2	1.4	1.1	1.3	1.7	1.1	1.2	1.0	1.2	0.9	1.5	1.1	**1.2**	**0.2**
CYP2C18	1.1	1.6	0.9	1.3	0.8	1.9	1.1	1.4	1.7	1.4	1.2	0.9	1.7	1.8	0.9	0.6	1.3	1.5	1.3	1.5	1.0	1.8	1.3	0.7	1.5	1.2	1.3	**1.3**	**0.4**
CYP2J2	0.5	0.9	1.0	0.9	0.2	0.4	0.6	0.6	0.7	0.5	0.4	1.0	0.9	0.3	0.4	0.5	0.6	0.4	0.4	0.7	0.8	0.4	0.4	0.8	1.0	0.7	0.7	**0.6**	**0.2**
UGT2B7	48.9	57.6	48.9	83.7	86.8	69.7	65.4	76.0	71.2	60.4	94.2	80.4	110.6	74.9	82.0	70.4	82.0	143.9	79.5	64.9	44.0	84.2	46.2	57.3	90.6	70.5	96.4	**75.6**	**21.3**
UGT1A4	83.7	61.5	65.3	91.6	82.3	49.4	101.7	72.7	64.6	63.3	52.0	88.5	100.9	61.6	92.8	77.7	76.4	79.0	79.9	64.6	74.2	88.6	60.5	91.8	56.6	82.5	65.6	**75.2**	**14.5**
UGT2B4	61.1	49.8	30.7	67.7	54.1	56.3	65.1	53.1	57.0	39.4	49.2	54.8	72.7	54.5	67.7	70.9	50.3	65.2	55.2	49.8	58.6	53.5	42.9	59.9	63.1	47.0	55.2	**55.7**	**9.6**
UGT2B15	48.6	42.2	32.6	58.9	52.1	50.0	59.3	53.2	51.7	34.7	48.0	50.2	43.7	49.4	64.5	59.8	56.3	82.8	55.7	51.7	40.9	40.7	42.5	49.6	65.1	50.5	67.6	**51.9**	**10.6**
UGT2B10	47.6	38.1	34.6	30.4	19.0	35.5	26.6	40.2	22.1	25.3	38.9	37.2	35.4	25.8	36.2	24.8	26.5	40.5	41.8	49.3	47.8	30.9	47.6	32.3	28.1	49.1	34.6	**35.0**	**8.7**
UGT1A9	17.1	36.0	18.8	21.6	28.6	20.9	35.5	23.5	21.7	14.8	21.3	24.1	26.0	12.2	20.0	17.4	20.5	25.1	25.8	18.9	19.1	30.2	20.8	25.6	27.8	24.3	19.4	**22.8**	**5.6**
UGT1A1	34.5	25.3	10.1	13.8	3.8	19.6	41.2	13.2	13.8	14.7	15.0	13.9	12.1	13.3	32.3	55.3	4.8	19.7	12.8	10.4	32.2	8.3	9.0	16.3	17.5	10.8	21.3	**18.3**	**11.7**
UGT1A6	12.7	17.5	13.0	10.6	15.8	9.1	20.3	13.6	16.9	11.7	10.3	11.8	9.7	11.1	15.9	21.2	11.2	7.8	12.0	9.1	20.4	13.0	14.6	11.8	16.8	8.9	10.5	**13.2**	**3.7**
UGT2B17	21.8	9.9	3.4	3.5	19.2	7.5	3.5	2.4	7.8	23.0	18.8	19.7	59.2	2.9	2.8	20.4	2.1	27.5	18.9	1.8	3.3	35.6	2.3	6.3	3.3	5.9	2.6	**12.4**	**13.4**
UGT1A3	5.1	2.1	4.3	3.6	6.0	2.2	2.1	3.0	2.9	4.1	1.5	12.0	13.5	3.1	2.7	2.9	6.8	2.7	4.5	4.8	8.0	5.0	2.8	2.4	10.0	8.5	1.9	**4.8**	**3.1**
UGT2A3	4.3	6.6	3.2	4.6	1.9	4.8	2.8	4.4	3.7	2.9	3.4	2.6	3.5	1.7	2.8	6.1	2.2	6.5	3.3	4.7	2.0	2.4	3.7	5.6	3.5	3.4	4.9	**3.8**	**1.4**
ABCB1	0.10	0.23	0.08	0.30	0.33	0.20	0.07	0.09	0.35	0.14	0.10	0.11	0.10	0.09	0.10	0.19	0.14	0.13	0.13	0.12	0.10	0.12	0.12	0.09	0.26	0.16	0.14	**0.15**	**0.08**
ABCB2	0.02	0.13	0.02	0.07	0.02	0.03	0.02	0.03	0.03	0.03	0.03	0.00	0.01	0.03	0.02	0.02	0.02	0.05	0.02	0.02	0.02	0.04	0.05	0.02	0.00	0.03	0.03	**0.03**	**0.02**
ABCB4	0.20	0.36	0.18	0.26	0.25	0.25	0.21	0.19	0.31	0.31	0.17	0.17	0.24	0.23	0.17	0.16	0.15	0.28	0.16	0.27	0.12	0.17	0.20	0.13	0.17	0.19	0.31	**0.21**	**0.06**
ABCD3	7.63	16.00	8.00	12.31	7.33	13.49	10.67	16.54	15.92	12.43	18.58	7.49	8.09	11.40	9.02	11.39	11.37	12.68	8.65	10.04	9.62	7.20	9.80	12.49	17.68	8.43	15.02	**11.45**	**3.38**
ABCB3	4.08	1.60	0.68	0.74	0.48	0.54	0.60	0.76	2.98	0.64	0.58	3.02	0.43	0.74	0.59	2.24	0.56	0.55	0.59	1.47	3.35	0.59	0.63	2.54	3.25	0.61	0.95	**1.33**	**1.12**
ABCA6	0.80	0.98	1.48	1.26	1.09	0.98	1.38	1.08	1.15	1.48	0.74	1.34	1.85	2.16	1.33	0.92	1.13	0.86	1.26	1.28	0.86	1.76	1.14	1.03	1.09	0.91	1.04	**1.20**	**0.33**
ABCC6	0.69	0.93	1.05	1.13	0.84	1.20	0.68	0.76	0.82	0.81	0.89	0.51	1.19	0.75	0.66	0.26	0.80	0.90	0.86	0.92	0.43	0.94	0.84	0.54	0.65	0.73	0.98	**0.81**	**0.22**
ABCB7	0.34	0.50	0.68	0.48	0.56	0.42	0.40	0.83	1.01	0.47	0.70	0.42	0.37	0.64	0.39	0.60	0.69	0.44	0.64	0.54	0.73	0.55	0.42	0.62	0.59	0.24	0.54	**0.55**	**0.16**
ABCB8	0.01	0.04	0.05	0.03	0.01	0.02	0.02	0.06	0.11	0.02	0.03	0.01	0.02	0.06	0.02	0.03	0.04	0.01	0.05	0.01	0.05	0.02	0.02	0.03	0.02	0.02	0.06	**0.03**	**0.02**
ABCD1	0.03	0.12	0.03	0.05	0.01	0.04	0.02	0.10	0.04	0.04	0.03	0.01	0.05	0.05	0.01	0.05	0.04	0.06	0.03	0.03	0.01	0.04	0.04	0.03	0.02	0.03	0.07	**0.04**	**0.03**
ABCA1	0.07	0.08	0.03	0.04	0.04	0.04	0.02	0.02	0.05	0.02	0.03	0.06	0.03	0.03	0.02	0.03	0.04	0.02	0.04	0.03	0.03	0.06	0.03	0.02	0.05	0.02	0.04	**0.04**	**0.02**
ABCD4	0.04	0.06	0.03	0.06	0.01	0.06	0.06	0.04	0.03	0.07	0.06	0.01	0.05	0.07	0.04	0.03	0.03	0.04	0.05	0.03	0.03	0.07	0.04	0.05	0.02	0.07	0.09	**0.05**	**0.02**
ABCB11	0.05	0.16	0.13	0.13	0.06	0.17	0.06	0.09	0.10	0.14	0.07	0.10	0.12	0.07	0.05	0.07	0.14	0.11	0.08	0.13	0.05	0.13	0.08	0.05	0.09	0.13	0.09	**0.10**	**0.04**
ABCB10	0.13	0.27	0.34	0.22	0.20	0.19	0.24	0.36	0.52	0.11	0.33	0.15	0.19	0.25	0.17	0.18	0.34	0.15	0.34	0.25	0.27	0.29	0.17	0.22	0.26	0.11	0.29	**0.24**	**0.09**
ABCB6	0.20	0.36	0.20	0.19	0.13	0.11	0.19	0.10	0.32	0.08	0.11	0.35	0.12	0.18	0.16	0.29	0.11	0.05	0.07	0.11	0.36	0.18	0.16	0.23	0.21	0.10	0.12	**0.18**	**0.09**
ABCC3	0.19	0.36	0.13	0.15	0.08	0.16	0.15	0.19	0.15	0.21	0.15	0.13	0.13	0.18	0.19	0.20	0.13	0.16	0.13	0.15	0.18	0.18	0.18	0.22	0.14	0.12	0.16	**0.17**	**0.05**
ABCC2	0.03	0.11	0.05	0.08	0.04	0.08	0.04	0.07	0.12	0.07	0.03	0.04	0.09	0.07	0.05	0.08	0.05	0.06	0.03	0.05	0.08	0.06	0.08	0.04	0.03	0.08	0.07	**0.06**	**0.02**
SLCO1B1	0.7	1.7	0.8	0.9	1.5	2.2	0.7	1.4	1.8	0.4	0.8	0.6	3.5	0.4	1.0	0.3	0.8	0.7	0.6	2.0	0.9	0.7	0.8	0.6	1.0	1.0	1.7	**1.1**	**0.7**
SLCO1B3	1.0	1.3	0.8	0.8	0.6	1.4	0.9	1.2	1.1	0.7	0.6	1.2	3.2	0.5	1.5	0.5	1.0	0.9	0.6	1.2	1.5	1.0	0.8	0.7	1.0	1.0	1.0	**1.0**	**0.5**
SLCO2B1	0.2	0.9	0.6	0.2	0.1	0.3	0.3	0.3	0.3	0.6	0.3	0.4	0.6	0.4	0.3	0.3	0.2	0.3	0.2	0.4	0.5	0.4	0.6	0.4	0.2	0.1	0.4	**0.4**	**0.2**
SLC22A1	1.3	2.1	2.0	1.8	1.9	2.2	2.5	1.9	2.0	1.5	1.7	1.9	2.1	1.7	2.2	2.0	1.8	1.7	1.6	2.1	1.7	3.0	1.8	2.7	1.9	1.3	1.6	**1.9**	**0.4**
SLC22A7	0.3	0.2	0.1	0.1	0.2	0.2	0.1	0.1	0.2	0.2	0.1	0.2	0.2	0.2	0.1	0.0	0.1	0.1	0.1	0.2	0.1	0.1	0.2	0.1	0.0	0.1	0.2	**0.1**	**0.1**
SLC22A9	0.3	0.4	0.5	0.5	0.2	0.9	0.3	0.5	1.2	0.3	0.5	0.4	0.6	0.3	0.5	0.3	0.4	0.5	0.3	0.5	0.7	0.4	0.4	0.5	0.4	0.2	0.5	**0.5**	**0.2**

Supplemental Table 7. Effect of age, body mass index (BMI) and genotype on the abundance of enzymes and transporters measured using HiN, iBAQ and TPA label-free methods.

	Age [a]			BMI [a]			Genotype [b]		
	HiN	**iBAQ**	**TPA**	**HiN**	**iBAQ**	**TPA**	**HiN**	**iBAQ**	**TPA**
CYP2E1	-	-	-	-	-	-			
CYP3A4	-	-	-	-	-	-			
CYP2C9	-	-	-	-	-	-	-	-	-
CYP2A6	-	-	-	-	-	-			
CYP2C8	-	-	-	-	-	-			
CYP3A5	-	-	-	-	-	-	***p* = 0.02**	***p* < 0.001**	***p* < 0.001**
CYP4F2	-	-	-	-	-	-			
CYP1A2	-	-	-	-	-	-			
CYP4A11	-	-	-	-	-	-			
CYP2D6	-	-	-	-	-	-	***p = 0.04***	-	***p* = 0.02**
CYP2B6	-	-	-	-	-	-	-	-	-
CYP8B1	-	-	-	-	-	-			
CYP27A1	-	-	-	-	-	-			
CYP4A22	-	-	-	-	-	-			
CYP4F11	-	-	-	-	-	-			
CYP4F3	-	-	-	-	-	-			
CYP2C19	-	-	-	-	-	-	-	***p* = 0.01**	***p* = 0.01**
CYP20A1	-	-	-	-	-	-			
CYP3A7	-	-	-	-	-	-			
CYP4V2	-			-	-	-			
CYP7B1	-	-	-	-	-	-			
CYP2C18	**r - = 0.42, *p* = 0.03**	-	-	-	-	-			
CYP2J2	-	-	-	-	-	-			
UGT2B7	-	-	-	-	-	-			
UGT1A4	-	-	-	**r - = 0.50, *p* = 0.01**	**r = -0.53, *p* = 0.005**	**r = -0.43, *p* = 0.03**			
UGT2B4	**r = -0.39, *p* = 0.05**	-	-	**-**	**r = -0.41, *p* = 0.04**	-			
UGT2B15	-	-	-	-	-	-			
UGT2B10	**r = -0.42, *p* = 0.03**	**r = -0.42, *p* = 0.03**	-	-	-	-			
UGT1A9	-	-	-	-	**r = -0.38, *p* = 0.05**	-			
UGT1A1	-	-	-	-	-	-			
UGT1A6	-	-	-	-	-	-			
UGT2B17	-	-	-	-	-	-			
UGT1A3	-	-	-	**r = -0.53, *p* = 0.004**	**r = -0.59, *p* = 0.001**	**r = -0.54, *p* = 0.004**			
UGT2A3	-	-	-	-	-	-			
ABCB1	-	-	-	-	-	-			
ABCB2	-	-	-	-	-	-			
ABCB4	-	-	-	-	-	-			
ABCD3	-	-	-	-	-	-			
ABCB3	-	-	-	-	-	-			
ABCA6	-	-	-	-	**r = -0.41, *p* = 0.03**	-			
ABCC6	-	-	-	-	-	-			
ABCB7	-	-	-	-	-	-			
ABCB8	-	-	-	-	-	-			
ABCD1	-	-	-	-	-	-			
ABCA1	-	**r = -0.40, *p* = 0.04**	-	-	-	-			
ABCD4	-	-	-	-	-	-			
ABCB11	-	-	-	-	-	-			
ABCB10	-	-	-	-	-	-			
ABCB6	-	-	-	-	-	-			
ABCC3	-	-	-	-	-	-			
ABCC2	-	-	-	-	-	-			
SLCO1B1	-	-	-	-	-	-			
SLCO1B3	-	-	-	**r = -0.42, *p* = 0.03**	**r = -0.46, *p* = 0.02**	**r = -0.42, *p* = 0.03**			
SLCO2B1	-	-	-	-	-	-			
SLC22A1	-	-	-	-	-	-			
SLC22A7	-	-	-	-	-	-			
SLC22A9	-	-	-	-	-	-			

[a] Effect of age and BMI on protein abundance were assessed using Pearson correlation (r); [b] effect of genotype was assessed using one-way ANOVA and *t*-test. Genotype data were available only for CYPs 2B6 (*1/*1, *1/*4, *1/*5, *1/*6, *1/*7, *4/*5, *4/*6, *6/*6), 2C9 (*1/*1, *1/*2, *1/*3, *2/*2), 2C19 (*1/*1, *1/*2, *2/*2), 2D6 (*1/*1, *1/*2, *1/*4, *2/*2, *2/*3, *2/*4, *2/*15, *2/*15 x 2, *4/*6) and 3A5 (*1/*3, *3/*3).

- denotes no effect ($p > 0.05$).



Supplemental Figure 1. Relative abundance of (A) CYPs, (B) UGTs and (C) ABC transporters in human liver determined using either HiN, iBAQ or TPA.