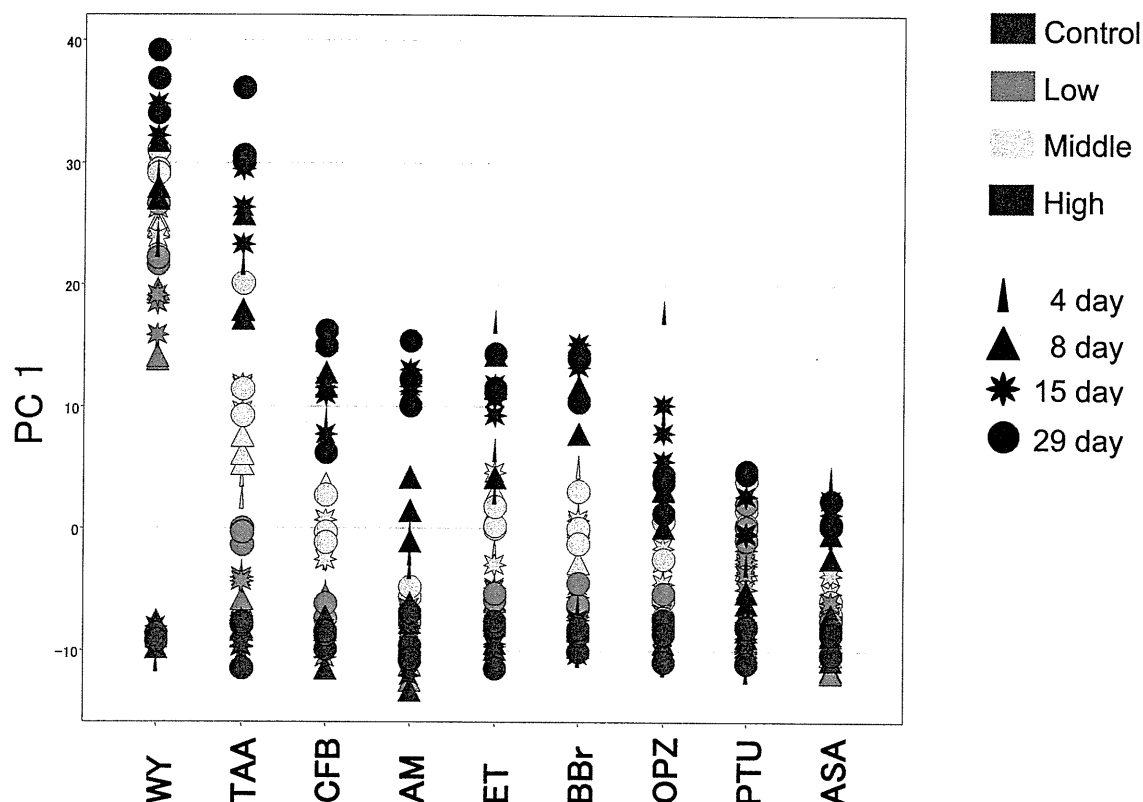


**Fig. 6.** Principal component analysis of gene expression profiles of 8 coagulopathic compounds with ASA. Results are expressed as a two dimensional graph for PC1 and 2. For simplicity, only dose and time are expressed by different symbols and each drug is not distinguished. In order to highlight the small separation of ASA, drugs other than ASA are eliminated from the graph and depicted in the lower panel.

## Gene expression profiling in rat liver inducing coagulopathy



**Fig. 7.** Principal component analysis of gene expression profiles of 8 coagulopathic compounds with ASA. Results are expressed as a one dimensional graph with PC1 (contribution rate: 38.5%). For each drug, each individual rat is depicted by a symbol with a different color and shape, as shown on the right panel. Note that ASA and PTU show low PC1 values.

anti-coagulation factors leads to prolongation. When the opposite phenomena were observed, they could be a feedback mechanism to maintain homeostasis. This might enable us to analyze the underlying toxicological mechanism of coagulopathy or hepatic dysfunction.

Vitamin K is an essential co-factor for biosynthesis of factors II, VII, IX and X, as well as proteins C, S and Z, as it catalyzes  $\gamma$ -carboxylation of glutamic acid in their amino-terminal region (Vacca, 2000). Blood coagulation time is prolonged in vitamin K deficiency or warfarin therapy. In the consequence of severe vitamin K deficiency, it was reported that decarboxylated precursors, named precursors induced by vitamin K absence (PIVKA), were produced causing coagulopathy because of their diminished activity (Amitrano *et al.*, 2002). It is possible that the reduction of coagulation factors in plasma observed in the present study was due to vitamin K-related events. *Vkorc1*, which synthesizes vitamin K from vitamin K epoxide, has been identified as a target of warfarin, and

its genetic variation explains the variability of the effective warfarin dose among individuals (Wadelius *et al.*, 2007). In the present study, typical coagulopathy-inducing drugs generally inhibit the expression of *Vkorc1*, and this was consistent with their reduced coagulation. Interestingly, however, its paralogous gene, *Vkorc111*, was up-regulated in most cases (Fig. 4). *Vkorc111* was proved not to be involved in the variability of warfarin dose requirement and its physiological function is totally unknown (Yin *et al.*, 2008). It is of interest that the directions of expression changes in these two paralogous genes were opposed. Further investigation is necessary to elucidate the role of their products in the pathogenesis of drug-induced coagulopathy.

$\alpha$ 1-Antitrypsin (AAT; SERPIN A1) is a serpin in plasma (Silverman *et al.*, 2001; Kalsheker *et al.*, 2002). AAT has a broad range of activities, including inhibition of the serine proteinases. Increase of serpins might also be related to prolongation of coagulation time, since

Kazal type serine protease inhibitors have been suggested as candidates for thrombin inhibition (van de Locht *et al.*, 1995; Gettins, 2002). In the present study, the expression of serpins were mostly reduced, namely, opposite to what is expected from coagulation. This could be interpreted as a feedback mechanism against prolonged coagulation. Some cytokines, such as interleukin-6 (IL-6), have the largest stimulatory effect on production of hepatocyte derived AAT. Interferon C and transforming growth factor  $\beta$  also modulate the hepatocyte response to IL-6 (Mackiewicz and Kushner, 1990; Magielska-Zero *et al.*, 1988). As IL-6 and TNF- $\alpha$  were also both markedly increased in acute liver injury (Kerr, 2003), the interpretation of the results of serpins are quite complex and difficult.

In the present study, fibrates, such as WY and CFB, and BBr, which has PPAR $\alpha$  agonistic activity (Tamura *et al.*, 2006), were separated from their controls by PCA. It is reported that PPAR $\alpha$  agonists down-regulated human fibrinogen- $\beta$  via negative interference with C/EBP $\beta$  as a result of titration of GRIP1/TIF2 (Gervois *et al.*, 2001). This explains the present observation that PPAR $\alpha$  agonists decreased plasma fibrinogen, whereas a question remains why BBr did not reduce the fibrinogen level.

Using PC1 as an indicator of coagulopathy, PTU and ASA were the lowest among the compounds. It is well known that ASA at its clinical dose elicits a selective anti-platelet activity without affecting blood coagulation by the route of inactivating cyclooxygenase-1 via irreversible acetylation and subsequent reduction of thromboxane A2 (Selwyn, 2003). In the overdose range, especially in animal toxicity studies, ASA may induce prolongation of PT, attributed not to ASA itself, but to its metabolite, salicylate (Cattaneo *et al.*, 1983). Sustained elevation of serum salicylate causes reduction of vitamin K-dependent coagulation factors II, VII and X, by inhibiting vitamin K quinone reductase (Yip, 2004). As for PTU, it is also known to inhibit the vitamin K dependent step in clotting factor synthesis (Lipsky and Gallego, 1988). In fact, blood coagulation-related genes among selected genes showed quite weak changes by both drugs. Albeit the same phenotype was observed, we could still distinguish ASA and PTU, which directly affected synthesis of coagulation factors, from other drugs that caused coagulation abnormality due to hepatic failure.

In conclusion, the genes extracted in the present study could be a useful source for developing biomarkers for hepatotoxicant-induced coagulation abnormality. Although further refinement and tuning of the present strategy is obviously needed, it is a good candidate for a starting point that could lead to mechanism-based diag-

nosis or prediction of coagulopathy in toxicity tests in the early stage of drug development.

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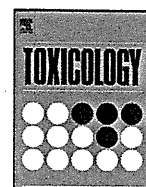
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## Identification of genomic biomarkers for concurrent diagnosis of drug-induced renal tubular injury using a large-scale toxicogenomics database

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### ABSTRACT

Drug-induced renal tubular injury is one of the major concerns in preclinical safety evaluations. Toxicogenomics is becoming a generally accepted approach for identifying chemicals with potential safety problems. In the present study, we analyzed 33 nephrotoxicants and 8 non-nephrotoxic hepatotoxicants to elucidate time- and dose-dependent global gene expression changes associated with proximal tubular toxicity. The compounds were administered orally or intravenously once daily to male Sprague-Dawley rats. The animals were exposed to four different doses of the compounds, and kidney tissues were collected on days 4, 8, 15, and 29. Gene expression profiles were generated from kidney RNA by using Affymetrix GeneChips and analyzed in conjunction with the histopathological changes. We used the filter-type gene selection algorithm based on *t*-statistics conjugated with the SVM classifier, and achieved a sensitivity of 90% with a selectivity of 90%. Then, 92 genes were extracted as the genomic biomarker candidates that were used to construct the classifier. The gene list contains well-known biomarkers, such as *Kidney injury molecule 1*, *Ceruloplasmin*, *Clusterin*, *Tissue inhibitor of metalloproteinase 1*, and also novel biomarker candidates. Most of the genes involved in tissue remodeling, the immune/inflammatory response, cell adhesion/proliferation/migration, and metabolism were predominantly up-regulated. Down-regulated genes participated in cell adhesion/proliferation/migration, membrane transport, and signal transduction. Our classifier has better prediction accuracy than any of the well-known biomarkers. Therefore, the toxicogenomics approach would be useful for concurrent diagnosis of renal tubular injury.

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### 1. Introduction

Toxicogenomics, which is the application of microarray technologies to toxicology, is becoming a generally accepted approach for identifying chemicals with potential safety problems. Identifying drug safety liabilities or predictive biomarkers for drug-induced organ damage at or before the preclinical stages of drug devel-

opment is of great importance to pharmaceutical companies. The ability to determine whether or not to pursue the development of a drug based on safety would greatly reduce the cost of drug development and improve the attrition rate of new chemical entities. Currently, preclinical drug safety evaluation relies mainly on complex histopathological or clinical pathological analysis. These traditional approaches have proven to be highly successful but may fail to detect prodromal and early stages of toxicity. Genomic data can be more sensitive and objective than traditional methods for the early prediction of compound-induced toxicity. Microarray expression profiling during preclinical drug development is expected to aid in uncovering unexpected or secondary pharmacology, predicting adverse effects, and understanding the mechanisms of drug action or toxicity (Battershill,

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2005; Heinloth et al., 2004; Irwin et al., 2004; Searfoss et al., 2005).

The kidney is a major organ for the filtration, secretion, re-absorption and ultimately the excretion of drugs or drug metabolites. Nephrotoxicity frequently occurs after administration of various drugs or xenobiotics. The tubular cells of the kidney are particularly vulnerable to drug-induced injury, and thus renal tubular toxicity is a major concern in preclinical safety evaluations. Drug-induced tubular damage has been well documented and extensively studied (Perazella, 2005). The prediction and diagnosis of preclinical renal tubular toxicity based on molecular methods that use microarray gene expression data have been attempted. Fielden et al. (2005) assessed predicative gene expression endpoints at early time points proceeding the onset of any signs of renal tubular pathology, and they achieved a prediction accuracy of 76%. In a separate study that assessed the expression profiling endpoints in parallel with the histopathological diagnosis of concurrent renal tubular toxicity, the performance was improved and a sensitivity of 82% was achieved with 100% of selectivity (Thukral et al., 2005). Furthermore, Jiang et al. (2007) achieved a sensitivity of 88% and a specificity of 91% using the expression profiling endpoints in parallel with the histopathological diagnosis of concurrent renal tubular toxicity. It is thought that concurrent diagnosis is easier than the prediction of future onset because the early stage toxic gene expression changes are heterogenic between different compounds, but the gene expression changes concurrent with the same toxic endpoints are comparatively homogenous among different compounds.

The Toxicogenomics Project (TGP) is a public–private collaborative project of the National Institute of Health Sciences, the National Institute of Biomedical Innovation, and 15 pharmaceutical companies in Japan that began in 2002 (Urushidani and Nagao, 2005). Its aim is to construct a large-scale toxicology database of transcriptomes that are useful to predict the toxicity of new chemical entities in the early stages of drug development. Until now, about 150 chemicals, primarily medicinal compounds, were selected and gene expression profiles of multiple doses and times in the rat liver and kidney, and rat and human hepatocytes were comprehensively analyzed by using the Affymetrix GeneChip® (over 27,000 profiles). These gene expression profiles, conjugated with the histopathological changes, the results of blood biochemical examinations, and the other phenotypic profiles, are stored in our database with a web-based tool for statistical analysis named TG-GATEs (Genomics Assisted Toxicity Evaluation System developed by Toxicogenomics Project in Japan). Thirteen of the 150 chemicals were typical nephrotoxicants or drugs showing clinical side effects (e.g., cisplatin, carboplatin, gentamicin, vancomycin, phenacetin, and bucetin), and 20 chemicals exhibited nephrotoxicity in addition to hepatotoxicity (e.g., phenylbutazone, ethionine, and indomethacin). We measured gene expression profiles in the kidney after exposure to the group of 33 nephrotoxicants and a negative control group of 8 hepatotoxicants; thus, data from 41 chemicals are presently available for the analysis of nephrotoxicity. The specific aim of the present study was to develop identifiers for concurrent diagnosis of drug-induced tubular injury based on gene expression profiles available from our toxicogenomics database.

The possibility that a genomics evaluation could lead to the elucidation of biomarkers that provide additional sensitivity and/or earlier detection of renal tubular damage is intriguing. A biomarker discovery effort requires experimental designs that encompass several compounds of diverse chemical natures that cause the same toxic endpoint. In addition, multiple time points and doses are necessary to tease out the gene expression changes that are early indicators of the severity and progression of lesions. Therefore, it is reasonable to at first elucidate genetic biomarkers for concur-

rent diagnosis at the same toxic endpoints, because these gene expression profiles are relatively homogenous compared to the profiles at the early stage of toxicity. Moreover, in the examination of sensitive toxicogenomics data, it is necessary to distinguish adverse changes from changes that are normal physiologic adaptive responses within a no observable adverse effect level (NOAEL). Also, when a biomarker is intended for broad research or regulatory use, the size and diversity of the training set must be considered, and validation of the biomarker on external data must be demonstrated (Somorjai et al., 2003; Ransohoff, 2004). A large-scale toxicogenomics database containing data from multiple time points and drug doses is useful to reliably assess hypotheses generated in other studies that have used comparatively small datasets.

In the present analysis, we extracted candidate biomarkers for the concurrent diagnosis of nephrotoxicity using the large-scale microarray dataset generated in our project. The microarray samples treated with nephrotoxicants and hepatotoxicants were divided into positives and negatives of the training set according to their histopathological findings, to perform supervised classification algorithms after selecting differentially expressed genes. We used three different types of algorithms for gene selection and classification to select the most appropriate method for our dataset and the development of statistically robust analysis. The external test sets were randomly generated 100 times by dividing the training set into subsets, and the prediction accuracy was calculated by summarizing the prediction results of the external test sets. As a result, we achieved a sensitivity of 90% with a selectivity of 90%. Then, 92 genes were extracted as the genomic biomarker candidates that were used to construct the classifier. The group of extracted genes contains well-known biomarkers, such as *Kidney injury molecule-1 (Kim1)*, *Ceruloplasmin (Cp)*, *Clusterin (Clu)*, *Tissue inhibitor of metalloproteinase 1 (Timp1)*, *Secreted phosphoprotein 1 (Spp1)*, and also novel biomarker candidates. Our multigene-based classifier had better classification accuracy than any of the single well-known biomarkers; therefore, toxicogenomics would be more useful for concurrent diagnosis of renal tubular injury than any of the previous criteria.

## 2. Materials and methods

### 2.1. Compounds

The chemical name, abbreviation, dosage, administration route and vehicle for each compound used in this study are summarized in Table 1.

### 2.2. Animal treatment

Five-week-old male Sprague-Dawley rats were obtained from Charles River Japan, Inc. (Kanagawa, Japan). After a 7-day quarantine and acclimatization period, 6-week-old animals were assigned to dosage groups (five rats per group) using a computerized stratified random grouping method based on individual body weight. The animals were individually housed in stainless-steel cages in an animal room that was lighted for 12 h (7:00–19:00) each day, ventilated with an air-exchange rate of 15 times per hour, and maintained at 21–25 °C with a relative humidity of 40–70%. Each animal was allowed free access to water and pellet diet (CRF-1, sterilized by radiation, Oriental Yeast Co., Ltd., Tokyo, Japan). Rats in each group received orally administered drugs that were suspended or dissolved in 0.5% methylcellulose solution (MC) or corn oil according to their dispersibility, with the exceptions of cisplatin, carboplatin, 2-bromoethylamine, cephalothin, puromycin aminonucleoside, gentamicin, vancomycin and doxorubicin, which were dissolved in saline and administered intravenously. The animals were treated for 3, 7, 14, or 28 days and sacrificed 24 h after the last dose. Blood samples from the abdominal aorta were collected in a heparinized tube after the rats were anesthetized with ether. After collecting the blood, the animals were euthanized by exsanguination from the abdominal aorta. For histopathological examination, kidney samples were fixed in 10% neutral-buffered formalin, dehydrated in alcohol and embedded in paraffin. Paraffin sections were prepared and stained using standard methods for hematoxylin and eosin staining (H&E). The experimental protocols were reviewed and approved by the Ethics Review Committee for Animal Experimentation of the National Institute of Health Sciences.

**Table 1**  
In vivo compound treatments used in training and testing.

Compound	Dose (mg/kg/day; repeated)	Vehicle	Route
Gentamicin sulphate	~100	Saline	iv
Vancomycin hydrochloride	~200	Saline	iv
2-Bromoethylamine hydrobromide	~20	Saline	iv
Phenylbutazone	~200	0.5% MC	po
Cyclosporine A	~100	Corn oil	po
Thioacetamide	~45	0.5% MC	po
K17	~600	0.5% MC	po
Triamterene	~150	0.5% MC	po
Allopurinol	~150	0.5% MC	po
Nitrofurantoin	~100	0.5% MC	po
Ethionine	~250	0.5% MC	po
N-Phenylanthranilic acid	~1000	0.5% MC	po
Cisplatin	~1	Saline	iv
Phenacetin	~1000	0.5% MC	po
Puromycin aminonucleoside	~40	Saline	iv
Lomustine	~6	0.5% MC	po
Cyclophosphamide	~15	0.5% MC	po
Carboplatin	~10	Saline	iv
Hexachlorobenzene	~300	Corn oil	po
Captopril	~1000	0.5% MC	po
Enalapril	~600	0.5% MC	po
Indomethacin	~5	0.5% MC	po
Doxorubicin hydrochloride	~1	Saline	iv
Ethinyl estradiol	~10	Corn oil	po
Monocrotaline	~30	0.5% MC	po
Acetaminophen	~1000	0.5% MC	po
Cephalothin sodium	~2000	Saline	iv
Bucetin	~1000	0.5% MC	po
Methyltestosterone	~300	0.5% MC	po
Rifampicin	~200	0.5% MC	po
Imipramine hydrochloride	~100	0.5% MC	po
Acetazolamide	~600	0.5% MC	po
Caffeine	~100	0.5% MC	po
Valproic acid	~450	0.5% MC	po
Clofibrate	~300	Corn oil	po
Allyl alcohol	~45	Corn oil	po
Omeprazole	~1000	0.5% MC	po
Bromobenzene	~300	Corn oil	po
Ketoconazole	~100	0.5% MC	po
Ciprofloxacin	~1000	0.5% MC	po
Erythromycin ethylsuccinate	~1000	0.5% MC	po

Male SD rats received oral or intravenous doses once daily (6 weeks of age,  $n=5$ ). Four, 8, 15, and 29 days after the start of repeated administrations, the kidney tissues were collected and used for gene expression analysis (Affymetrix GeneChip<sup>®</sup>,  $n=3/5$ ). Four doses were used for each compound including vehicle control (vehicle control, low, middle, high dose level). Different doses were used for single and repeated administration. po: peroral, iv: intravenous.

### 2.3. Microarray analysis

An aliquot of the tissue sample (whole slice; about 30 mg) for RNA analysis was obtained from the kidney in each animal immediately after sacrifice. Tissue samples were kept in RNAlater<sup>®</sup> (Ambion, Austin, TX, USA) overnight at 4 °C, and then frozen at -80 °C until use. Kidney samples were homogenized with buffer RLT that was supplied with the RNeasy mini kit (Qiagen, Valencia, CA, USA), and total RNA was isolated according to the manufacturer's instructions. Microarray analysis was conducted on 3 of 5 samples for each group by using GeneChip<sup>®</sup> Rat Genome 230 2.0 Arrays (Affymetrix, Santa Clara, CA, USA), which contain 31,042 probe sets. The procedure was conducted basically according to the manufacturer's instructions by using One-Cycle Target Labeling and Control Reagents (Affymetrix) for cDNA synthesis, purification, and the synthesis of biotin-labeled cRNA. Ten micrograms of fragmented cRNA was hybridized to a Rat Genome 230 2.0 Array for 18 h at 45 °C at 60 rpm, after which the array was washed and stained with streptavidin-phycoerythrin by using Fluidics Station 400 (Affymetrix) and then scanned with a Gene Array Scanner (Affymetrix). The digital image files were preprocessed by Affymetrix Microarray Suite version 5.0 (MAS5.0) and converted into base10 logarithmic values. Then, these values were normalized into Z-scores by using Tukey's biweight algorithm. The normalized datasets were reversed into non-logarithmic values by calculating their exponential numbers in decimal, and the log-ratio of base 2 to the means of the control groups were calculated.

### 2.4. Gene selection and supervised classification

High-dose groups of 23 compounds that caused necrosis, degeneration, or regeneration in the renal tubules during chronic exposure were defined as the positive set. Low-dose groups of all of 41 compounds and high-dose groups of the eight hepatotoxicants, which had no histopathological findings, were defined as the neg-

ative set. Other high-dose groups of 10 compounds and middle-dose groups were treated as the external test set. Both filter-type and wrapper-type gene selection algorithms and Support Vector Machine (SVM; Vapkin, 1995) and Prediction Analysis of Microarrays (PAM; Tibshirani et al., 2002) supervised classification algorithms were used to extract the biomarker candidates and construct classifiers using the selected genes. Recursive feature elimination (SVM-RFE; multivariate type; Guyon et al., 2002) and nearest shrunken centroid (PAM; univariate type) were used as wrapper-type gene selection algorithms, and Intensity-Based Moderated *T*-statistics (IBMT; Sartor et al., 2006) was used as a filter-type gene selection algorithm (SVM was used as the classifier, in this case).

Five-fold cross-validation (CV) was executed for optimization of the classifiers and to calculate their prediction accuracies. At first, the whole positive and negative training datasets were randomly divided into five subsets of roughly equal size. The SVM and PAM were trained with a selection of optimal genes on eight subsets (four positive subsets and four negative subsets) and then applied to the remaining subset as the test dataset. The negative samples of the test subset were randomly excluded to adjust the number to the positive samples before prediction. Before training of the SVM, optimal genes were selected from the training set by using "Recursive Feature Elimination" (SVM-RFE) or "Intensity-Based Moderated *T*-statistics" (SVM+IBMT). One to 99 of the top-ranked genes of each selection strategy were used to construct the classifiers. Also, in the case of the PAM classifier, 3 to 10 were used as the threshold of the centroid shrinkage to select top-ranked genes. The feature genes used in each training set were filtered by MAS5.0 P/A-call (excluded the probes that were judged as absent in all samples of the training set) and fold change (excluded the probes whose absolute log<sub>2</sub> ratio values were less than 1 between the positives and the negatives) during the 5-fold CV, before being selected and ranked by the feature selection algorithms.

The classifiers were also tested by making the external test datasets by randomly dividing 23 compounds containing positive samples and 18 compounds containing

only negative samples into 5 subsets. An arbitrary subset (combining a positive subset and a negative subset) and the remaining subsets were respectively treated as the external test set and the training set. Compounds of the test subset containing only negative samples were randomly excluded to adjust the number of negative samples to the positive samples before prediction. The feature genes were selected from the training set and used to construct the classifier, which was used to predict the external test set. This process was repeated 100 times, and the prediction accuracy was calculated as the sum of all of the prediction results calculated. Then, the whole positive and negative datasets were used to construct the classifier and to predict the external test set (high-dose groups of 10 compounds and middle-dose groups of all of 41 compounds).

### 3. Results

#### 3.1. Histopathological examination

The results of the histopathological examinations for all compounds are summarized in Table 2. The high-dose groups of 23 tubular toxicants (gentamicin sulphate, vancomycin hydrochloride, 2-bromoethylamine hydrobromide, phenylbutazone, cyclosporine A, thioacetamide, K17, triamterene, allopurinol, nitrofurantoin, ethionine, *N*-phenylanthranilic acid, cisplatin, phenacetin, puromycin aminonucleoside, lomustine, cyclophosphamide, carboplatin, hexachlorobenzene, captopril, enalapril, indomethacin, and doxorubicin hydrochloride) exhibited necrosis, degeneration, and/or regeneration of the renal tubules at one or more sacrifice time during chronic exposure (days 4, 8, 15, and 29). Among them, 10 compounds (gentamicin sulphate, vancomycin hydrochloride, phenylbutazone, cyclosporine A, thioacetamide, K17, triamterene, allopurinol, *N*-phenylanthranilic acid, and cisplatin) exhibited the histopathological findings at all sacrifice time points. Tubular damage caused by nitrofurantoin or ethionine was repaired by day 15 or 29. The other 11 compounds caused nephrotoxicities only after a long period of chronic exposure (2-bromoethylamine hydrobromide, phenacetin, puromycin aminonucleoside after day 8, lomustine after day 15, and cyclophosphamide, carboplatin, hexachlorobenzene, captopril, enalapril, indomethacin, and doxorubicin hydrochloride after day 29). Although 10 of the potential tubular toxicants did not cause necrosis, degeneration, or regeneration, 6 of these 10 compounds caused other histopathological findings, such as vacuolation, anisonucleosis, hyaline droplet, swelling, hypertrophy, eosinophilic body, and cytoplasmic granule.

The middle-dose groups of 14 of the 23 tubular toxicants (gentamicin sulphate, cyclosporine A, thioacetamide, K17, triamterene, allopurinol, nitrofurantoin, ethionine, *N*-phenylanthranilic acid, cisplatin, puromycin aminonucleoside, hexachlorobenzene, captopril, and enalapril) had histopathological findings. Triamterene and allopurinol had histopathological findings at all of the sacrifice time points. The tubular damage in the middle-dose groups of nitrofurantoin and ethionine was repaired after long-time chronic exposure, which is consistent with their high-dose groups. The other 10 compounds yielded histopathological findings only after long-time chronic exposure. Thioacetamide only had histopathological findings at day 15. Although low-dose groups of 19 of the 23 tubular toxicants had no histopathological findings, the low-dose groups of gentamicin sulphate, triamterene, puromycin aminonucleoside, and hexachlorobenzene had degeneration or regeneration in renal tubules and/or cortex. In the case of gentamicin sulphate, triamterene, and hexachlorobenzene, only one or two animals in a group of five animals had minimal/slight degeneration/regeneration in the renal tubules. The animal that had the histopathological findings was not used for the microarray experiment (in the case of triamterene). The low-dose group of puromycin aminonucleoside had slight degeneration ( $n=4/5$ ) and regeneration ( $n=2/5$ ) in the renal tubules on day 29. But, the animals did not have apparent necrosis findings or significant changes

in BUN/CRE. Therefore, we considered these findings to be negative.

#### 3.2. Microarray data analysis

##### 3.2.1. Gene selection and supervised classification

For statistical reliability and regulatory perspective to determine the most appropriate analytical methods for the large-scale toxicogenomics database, we examined three different types of classification strategies, SVM-RFE, SVM+IBMT, and PAM. As the result of 5-fold cross-validation (randomly divided samples), we achieved the sensitivity of each classifier of 94% (SVM-RFE; 99 probes), 93.8% (SVM+IBMT; 99 probes), and 90% (PAM; threshold=5.4), when we allowed 10% of false positives (Supplementary figures). Although the SVM-RFE was expected to have the highest classification accuracy, the correspondence rate of the feature gene list selected by recursive feature elimination between the sub-training sets was smaller than for the other two algorithms. The SVM-RFE classifier appeared to be over-fitted to the training set, so that the selected genes were not robust and were inadequate to be used as the biomarkers. In contrast, the feature genes selected by SVM+IBMT and PAM were similar between different training datasets generated during 5-fold CV. The prediction accuracy of the SVM+IBMT classifier was better than the PAM classifier. Therefore, we selected SVM+IBMT as the gene selection and classification algorithm.

We also tested prediction accuracy using the external test set. The group of 23 compounds containing positive samples and the group of 18 compounds containing only negative samples were randomly divided into 5 subsets 100 times. An arbitrary subset was used as the external test set, and the remaining subsets were used as the training set. We summarized the prediction results and achieved a sensitivity of 94.7% (SVM-RFE; 62 probes), 90% (SVM+IBMT; 98 probes), and 85.7% (PAM; threshold=10) with a selectivity of 90% (Supplementary figures). In all three algorithms, the prediction accuracies calculated by using the external test sets were decreased compared to the accuracies calculated by 5-fold CV randomly divided samples. In the latter case, the training set and the test set possibly shared samples of the same compounds, times, and doses, such that the estimated accuracy was inappropriately high. It is always desirable to calculate the prediction accuracy using an external test set.

We used the top 98 probes (92 genes) to construct the SVM+IBMT classifier, considering the prediction accuracy and to avoid over-fitting (Table 3). The prediction accuracy was almost saturated and not significantly decreased compared to the max value, the number of support vectors was adequately lowered, and the number of feature genes was substantially smaller than the number of samples to avoid over-fitting (Supplementary figures). Also, the feature gene list is long enough to interpret their biological relevance. The probes ranked below the top 98 were also induced in renal tubular injury and biologically relevant. But around the top 600 genes, the number of support vectors was gradually increased, which means that these genes provided no more or little information for classification and tended to be over-fitting. The whole feature genes ranking is provided in the Supplementary Table. In addition, we tested the classifiers constructed from well-established single-genetic biomarkers and found that the classifier constructed from the multiple feature genes had much better prediction accuracy (Supplementary figures).

##### 3.2.2. The gene expression profile of the feature genes

Fig. 1 shows the expression profile of the top 98 probes (92 genes) described above. Each color represents the Z-score of the log-ratio to the mean expression value of the corresponding control samples. The Z-scores were calculated by dividing the log-ratio



**Table 2**  
Summary of histopathological findings.

Compound	Toxicity class	Findings (renal tubule)	Low				Middle				High			
			4D	8D	15D	29D	4D	8D	15D	29D	4D	8D	15D	29D
Gentamicin sulphate		Necrosis; degeneration; regeneration	0	0	0	1	0	0	0	1	1	1	1	1
Vancomycin hydrochloride		Degeneration; regeneration	0	0	0	0	0	0	0	2	1	1	1	1
2-Bromoethylamine hydrobromide		Regeneration	0	0	0	0	0	0	2	2	2	1	1	1
Phenylbutazone		Regeneration	0	0	0	0	0	0	0	0	1	1	1	1
Cyclosporine A		Degeneration; regeneration	0	0	0	0	0	1	1	1	1	1	1	1
Thioacetamide		Regeneration	0	0	0	0	0	0	1	0	1	1	1	1
K17		Necrosis; degeneration; regeneration	0	0	0	0	0	0	1	1	1	1	1	1
Triamterene		Regeneration	0	0	0	1	1	1	1	1	1	1	1	1
Allopurinol		Regeneration	0	0	0	0	1	1	1	1	1	1	1	1
Nitrofurantoin	Tubular toxicant (direct/indirect)	Regeneration	0	0	0	0	1	1	0	0	1	1	1	0
Ethionine		Degeneration; regeneration	0	0	0	0	1	0	0	0	1	1	0	0
N-Phenylanthranilic acid		Regeneration	0	0	0	0	0	2	0	1	1	1	1	1
Cisplatin		Necrosis; degeneration; regeneration	0	0	0	0	0	0	1	1	1	1	1	1
Phenacetin		Regeneration	0	0	0	0	0	0	0	0	0	1	1	1
Puromycin aminonucleoside		Degeneration; regeneration	0	0	1	1	0	2	1	2	2	1	1	1
Lomustine		Degeneration; regeneration	0	0	0	0	0	0	0	2	0	0	1	1
Cyclophosphamide		Regeneration	0	0	0	0	0	0	0	0	0	0	0	1
Carboplatin		Degeneration	0	0	0	0	0	0	0	0	0	0	0	1
Hexachlorobenzene		Regeneration	0	0	2	1	0	0	2	1	0	2	2	1
Captopril		Regeneration	0	0	0	0	0	0	0	1	0	0	0	1
Enalapril		Necrosis; regeneration	0	0	0	0	0	0	0	1	0	0	0	1
Indomethacin		Regeneration	0	0	0	0	0	0	0	0	0	2	1	1
Doxorubicin hydrochloride		Necrosis; degeneration	0	0	0	0	0	0	0	0	0	0	0	1
Ethinyl estradiol		Vacuolization	0	0	0	2	0	0	2	2	0	0	0	2
Monocrotaline		Anisonucleosis; vacuolization	0	0	0	0	0	0	0	2	0	2	2	2
Acetaminophen		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Cephalothin sodium		Cytoplasmic granule	0	0	0	2	0	0	2	2	0	2	2	2
Bucetin		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Methyltestosterone	Potential tubular toxicant	Hypertrophy	0	0	0	0	0	0	0	2	0	0	2	2
Rifampicin		Hyaline droplet; eosinophilic body	0	2	2	2	0	2	2	2	0	2	2	2
Imipramine hydrochloride		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Acetazolamide		No-findings	0	0	0	0	0	0	0	2	0	0	2	2
Caffeine		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Valproic acid		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Clofibrate		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Allyl alcohol		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Omeprazole		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Bromobenzene	Hepatotoxicant (non-nephrotoxicant)	No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Ketoconazole		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Ciprofloxacin		No-findings	0	0	0	0	0	0	0	0	0	0	0	0
Erythromycin ethylsuccinate		No-findings	0	0	0	0	0	0	0	0	0	0	0	0

The absence or presence of renal tubular toxicity is indicated as 0 or 1 according to the following findings: necrosis, degeneration, and regeneration. Other histopathological findings, such as tubular vacuolation, hypertrophy, or intracytoplasmic hyaline droplet, are indicated as 2.

**Table 3**  
Top 98 probes (92 genes) ranked by Intensity-Based Modified T-statistics.

Function	Rank	IBMT-value	Probe ID	Gene symbol	Gene title
Tissue remodeling	67	16.58035006	1368419.at	Cp	Ceruloplasmin
	53	17.38025275	1367655.at	Tmsb10	Thymosin, beta 10
	42	18.32495826	1368418.a.at	Cp	Ceruloplasmin
	35	18.71625959	1370511.at	Fgb	Fibrinogen, B beta polypeptide
	34	18.75582061	1370992.a.at	Fga	Fibrinogen, alpha polypeptide
	25	19.4777112	1368160.at	Igf1	Insulin-like growth factor binding protein 1
	23	20.04881639	1387011.at	Lcn2	Lipocalin 2
	5	23.34760498	1367581.a.at	Spp1	Secreted phosphoprotein 1
	4	24.99287138	1367784.a.at	Clu	Clusterin
	3	25.55598409	1368420.at	Cp	Ceruloplasmin
Immune response/inflammatory response	2	27.31956855	1367712.at	Timp1	Tissue inhibitor of metalloproteinase 1
	1	32.37802533	1387965.at	Havcr1	Kidney injury molecule 1
	95	15.48262595	1367850.at	Fcgr3	Fc receptor, IgG, low affinity III
	85	15.87707814	1367786.at	Psm8	Proteasome (prosome, macropain) subunit, beta type 8
	82	15.95556487	1370892.at	C4-2	Complement component 4a
	57	17.08681361	1368490.at	Cd14	CD14 antigen
	49	17.46443444	1379889.at	Lamc2	Laminin, gamma 2
	36	18.6392526	1367794.at	A2m	Alpha-2-macroglobulin
	31	19.03400005	1374033.at	Psm10	Proteasome (prosome, macropain) subunit, beta type 10
	26	19.3233011	1374119.at	Elf3	E74-like factor 3
Cell adhesion/proliferation/migration	21	20.17343592	1368921.a.at	Cd44	CD44 antigen
	12	20.92295884	1367614.at	Anxa1	Annexin A1
	10	21.33883134	1379340.at	Lamc2	Laminin, gamma 2
	7	22.90158183	1387952.a.at	Cd44	CD44 antigen
	68	-16.55652999	1368131.at	Capn6	Calpain 6
	89	-15.74490892	1372869.at	Gtpbp4	GTP-binding protein 4
	98	-15.44895153	1370144.at	Gtpbp4	GTP-binding protein 4
	59	16.9871558	1367574.at	Vim	Vimentin
	56	17.09543212	1388587.at	Ier3	Immediate early response 3
	50	17.46375719	1367914.at	Emp3	Epithelial membrane protein 3
Membrane transport	47	17.49603392	1370177.at	PVR	Poliovirus receptor
	45	17.78791131	1388802.at	Bex1	Brain expressed X-linked 1
	40	18.45920696	1368612.at	Itgb4	Integrin beta 4
	32	18.86869018	1375170.at	S100a11	S100 calcium binding protein A11 (calizzarin)
	20	20.20478694	1373421.at	Tgif	TG interacting factor
	19	20.41704079	1386879.at	Lgals3	Lectin, galactose binding, soluble 3
	18	20.63006692	1371785.at	Tnfrsf12a	Tumor necrosis factor receptor superfamily, member 12a
	16	20.67075085	1386890.at	S100a10	S100 calcium binding protein A10 (calpactin)
	14	20.72852871	1368187.at	Gpnmb	Glycoprotein (transmembrane) nmb
	70	-16.51359077	1388097.at	Cacng5	Calcium channel, voltage-dependent, gamma subunit 5
Metabolism	94	15.49715091	1380909.at	-	Transcribed locus
	73	16.25219965	1368497.at	Abcc2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
	9	22.17460015	1368168.at	Slc34a2	Solute carrier family 34 (sodium phosphate), member 2
	93	15.55951107	1370813.at	Gstm5	Glutathione S-transferase, mu 5
	87	15.78307408	1372691.at	Upp1	Uridine phosphorylase 1
	65	16.68114127	1374070.at	Gpx2	Glutathione peroxidase 2
	61	16.95386475	1374784.at	Prtfcd1_predicted	Phosphoribosyl transferase domain containing 1 (predicted)
	44	17.95904453	1370561.at	A3galt2	Alpha-1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase)
	39	18.4925478	1370445.at	Pspla1	Phosphatidylserine-specific phospholipase A1
	33	18.84407902	1387925.at	Asns	Asparagine synthetase
Apoptosis	84	15.89635722	1370113.at	Birc3	Baculoviral IAP repeat-containing 3
	75	16.23159672	1368308.at	Myc	Myelocytomatosis viral oncogene homolog (avian)
Signal transduction	38	-18.53296844	1370522.at	Gcgr	Glucagon receptor
	69	16.51817598	1390510.at	Ms4a6b	Membrane-spanning 4-domains, subfamily A, member 6B
Angiogenesis/fibrinolysis	30	19.03449106	1367584.at	Anxa2	Annexin A2
Blood coagulation	52	17.3941316	1368052.at	Tspan8	Tetraspanin 8
Cell-cell communication	81	16.08958043	1388547.at	Cldn4	Claudin 4

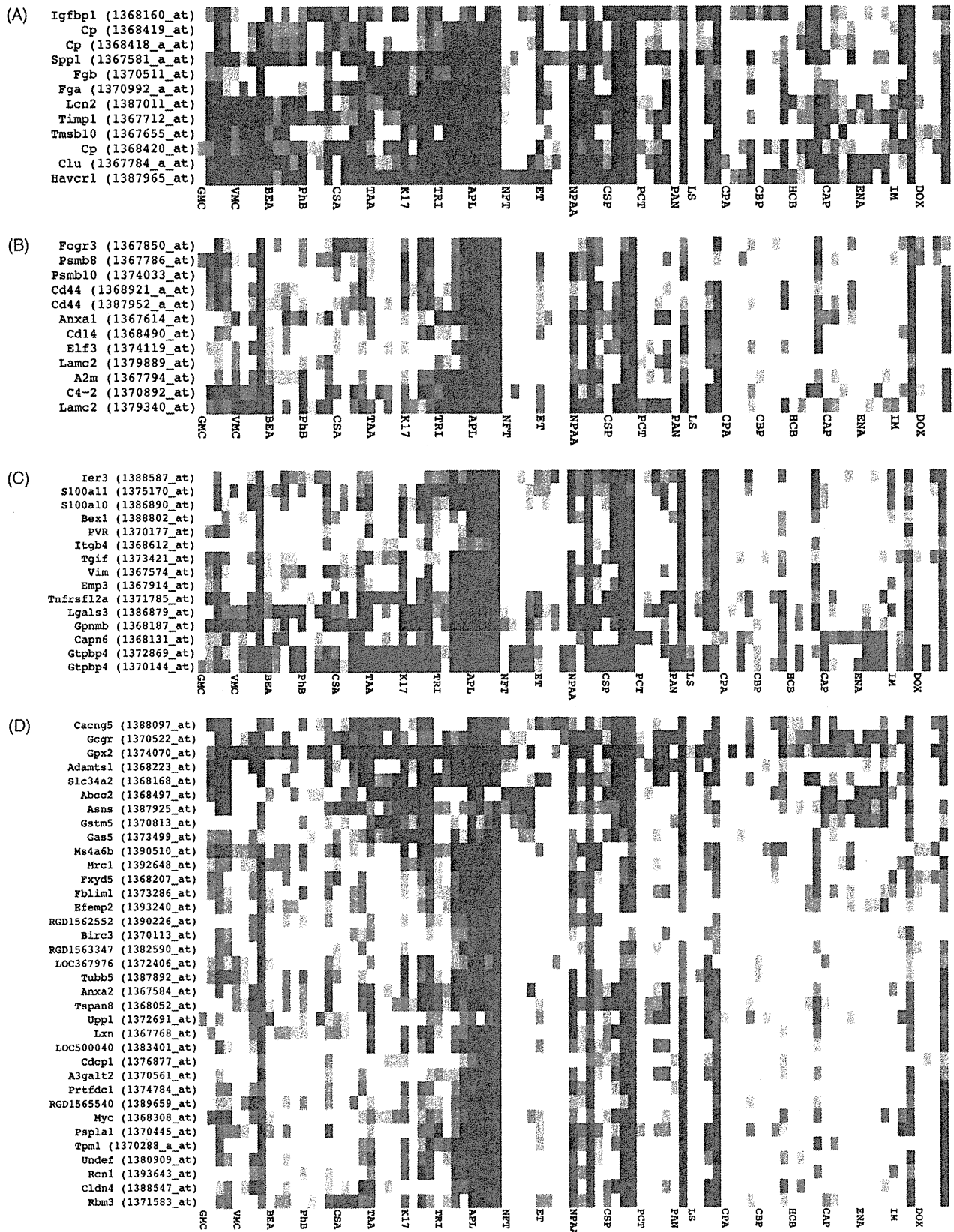
Table 3 (Continued)

Function	Rank	IBMT-value	Probe ID	Gene symbol	Gene title
Detection of temperature stimuli	15	20.67755397	1367768.at	Lxn	Latexin
DNA replication initiation	97	15.47163164	1372406.at	LOC367976	Minichromosomemaintenancedeficient3 (S.cerevisiae)(predicted)
Endocytosis	80	16.0961982	1392648.at	Mrc1_predicted	Mannose receptor, C type 1 (predicted)
Kidney development	78	16.13533388	1368223.at	Adamts1	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
Microtubule-based process	71	16.33428851	1387892.at	Tubb5	Tubulin, beta 5
miRNA-mediated gene silencing	88	15.75295308	1371583.at	Rbm3	RNA binding motif protein 3
rRNA processing	24	19.83460167	1373499.at	Gas5	Growth arrest specific 5
Stress fiber formation	58	17.05771651	1373286.at	Fblim1	Filamin binding LIM protein 1
Structural constituent of cytoskeleton	86	15.805369	1370288.a.at	Tpm1	Tropomyosin 1, alpha
	92	15.57704782	1382590.at	RGD1563347_predicted	Similar to RIKEN cDNA 2310015N21 (predicted)
	79	16.12099714	1376877.at	Cdcp1_predicted	CUB domain containing protein 1 (predicted)
	77	16.15247506	1368207.at	Fxyd5	FXD domain-containing ion transport regulator 5
	62	16.9053337	1390226.at	RGD1562552_predicted	Similar to hypothetical protein LOC340061 (predicted)
	55	17.14203525	1389659.at	RGD1565540_predicted	Similar to ctla-2-beta protein (141 AA) (predicted)
	51	17.42187372	1393240.at	Efemp2	EGF-containing fibulin-like extracellular matrix protein 2
	29	19.0788577	1393643.at	Rcn1_predicted	Reticulocalbin 1 (predicted)
	28	19.09794144	1383401.at	LOC500040	Similar to Testis derived transcript
	13	-20.76507248	1390847.at	Tmem86a_predicted	Transmembrane protein 86A (predicted)
ESTs	17	-20.6670163	1373309.at	Tmem86a_predicted	Transmembrane protein 86A (predicted)
	96	-15.4719928	1374167.at	LOC361399	Similar to autoantigen
	90	15.72117787	1388340.at	Ns5atp9	NS5A (hepatitis C virus) transactivated protein 9
	83	15.92546837	1375224.at	Phlda3	Pleckstrin homology-like domain, family A, member 3
	72	16.3017568	1373035.at	-	-
	66	16.62012551	1390109.at	-	-
	64	16.80319643	1373908.at	-	-
	60	16.96481687	1371782.at	Nipsnap3a	Nipsnap homolog 3A (C. elegans)
	54	17.20576139	1373504.at	Gilpr1	GLI pathogenesis-related 1 (glioma)
	43	17.9919912	1379957.at	Slfn8	Schlafen 8
	27	19.2586905	1388900.at	RGD1566118_predicted	RGD1566118 (predicted)
	22	20.17177219	1390839.at	Pqlc3	PQ loop repeat containing 3
	41	-18.40682675	1372911.at	-	Transcribed locus
	46	-17.76332084	1376913.at	-	Transcribed locus
	91	-15.59722933	1378292.at	-	Transcribed locus
	76	16.20156037	1385190.at	-	Transcribed locus
	74	16.23557955	1377994.at	-	Transcribed locus
	63	16.82551948	1397769.at	-	Transcribed locus
	48	17.48169748	1393252.at	-	Transcribed locus
	37	18.59863244	1376109.at	-	Transcribed locus
	11	20.9365083	1377092.at	-	Transcribed locus
	8	22.29041324	1391106.at	-	Transcribed locus
	6	23.16631514	1390659.at	-	Transcribed locus

values by the variance of the log-ratio value of the control samples calculated for each arbitrary range of the expression values. Then, the expression values of the control samples were pooled for each compound and time point ( $n=3$ ). Among the 92 genes, 83 genes were significantly up-regulated, and 9 genes were down-regulated in most of the positive samples (Fig. 1, Table 3). Most of the genes involved in tissue remodeling, the immune/inflammatory response, cell adhesion/proliferation/migration, and metabolism were up-regulated. Several up-regulated genes were also involved in membrane transport, signal transduction, apoptosis, and some of the other genes that were probably related to reconstruction of the kidney tissues (e.g., structural constituent of cytoskeleton). In particular, genes involved in tissue remodeling and the

immune/inflammatory response had many well-known biomarker candidates for renal tubular injury, as described by Wang et al. (2008) (8/10 and 2/10, respectively). Down-regulated genes participated in cell adhesion/proliferation/migration, membrane transport, and signal transduction.

Most of the 10 genes that participated in tissue remodeling were strongly up-regulated ( $Z$ -score > 2.5) in most of the positive samples (Fig. 1a). On day 4, a lot of genes already had been up-regulated after treatment with vancomycin hydrochloride, 2-bromoethylamine hydrobromide, phenylbutazone, cyclosporine A, thioacetamide, K17, triamterene, allopurinol, ethionine, *N*-phenylanthranilic acid, cisplatin, phenacetin, captopril, enalapril, and indomethacin. With the exceptions of 2-bromoethylamine



**Fig. 1.** The gene expression profile of the feature genes. Rows – genes, columns – sample groups. Each color represents the Z-score of the log-ratio to the mean expression value of the corresponding control samples (same compound and time point). Up-regulated genes (Z-score  $\geq 2.5$ ) are represented by red colors, and down-regulated genes (Z-score  $\leq -2.5$ ) are represented by blue colors. Each sample group is labeled with the compound abbreviation on day 4. The columns of each compound are ordered in time (from day 4 to day 29). (a) Tissue remodeling, (b) immune/inflammatory response, (c) cell adhesion/proliferation/migration, and (d) the others (membrane transport, metabolism, signal transduction, apoptosis). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

hydrobromide, phenacetin, captopril, enalapril, and indomethacin, histopathological findings had been observed in the animals treated with the above 10 compounds on day 4 (Table 2). In the case of 2-bromoethylamine hydrobromide, phenacetin, captopril, enalapril, and indomethacin, the histopathological findings were observed after day 8; therefore, these feature genes had been up-regulated before histopathological changes (in 2-bromoethylamine hydrobromide, slight dilatation of the cortex was observed in 1 of 5 animals). The animals treated with gentamicin sulphate and nitrofurantoin had histopathological findings on day 4, but predominant up-regulation of tissue remodeling-related genes was not observed. Puromycin aminonucleoside-, lomustine-, cyclophosphamide-, carboplatin-, hexachlorobenzene-, and doxorubicin hydrochloride-treated samples had neither histopathological findings nor induction of tissue remodeling-related genes on day 4 (in puromycin aminonucleoside, a slight hyaline droplet in the cortex was observed in 1 of 5 animals). Although, except for puromycin aminonucleoside, predominant up-regulation of the feature genes related to tissue remodeling was observed before the histopathological changes. On the other hand, nitrofurantoin-treated animals did not exhibit predominant induction of the genes at any of the time points examined. Ethionine-treated animals had histopathological findings on day 4, but recovered from pathological status on day 15, which is the same as nitrofurantoin-treated animals. In contrast to nitrofurantoin, predominant up-regulation was found in the animals treated with ethionine on days 4, 8, and 15, but the up-regulated genes gradually decreased in a time-dependent manner. While some of the feature genes were also up-regulated in some of the negative samples, the extent of up-regulation of these genes was weak compared to those in the high-dose groups of the positive compounds.

Although the immune/inflammatory response-related genes were not universally induced in the positive samples as compared to tissue-remodeling related genes, predominant up-regulation was observed in most of the positive compounds (Fig. 1b). The animals treated with 2-bromoethylamine hydrobromide exhibited predominant up-regulation on day 4, and some of the genes were up-regulated in phenacetin, captopril, and indomethacin before histopathological changes in a similar manner seen in tissue remodeling. Nitrofurantoin- and enalapril-treated animals did not exhibit predominant up-regulation of the genes at any of the time points. In the case of thioacetamide and ethionine, predominant up-regulation was only found on day 4, despite the histopathological findings observed after day 4.

Among the 14 cell adhesion/proliferation/migration-related genes, 2 genes were predominantly down-regulated, and 12 genes were predominantly up-regulated in most of the positive compounds (Fig. 1c). In 2-bromoethylamine hydrobromide, cyclophosphamide, hexachlorobenzene, captopril, enalapril, indomethacin, and doxorubicin hydrochloride, some of the feature genes were induced before histopathological changes. In nitrofurantoin and ethionine, some of the feature genes were induced after histopathological findings disappeared. *Gtbbp4* (*GTP-binding protein 4*) was down-regulated in most of the positive compounds and up-regulated in a lot of negative compounds.

Genes in other functional categories were also induced (Fig. 1d). Seven genes related to metabolism were up-regulated. Among them, *Gpx2* (*glutathione peroxidase 2*) was not only up-regulated in most of the positive compounds, but also in some of the negative compounds. The other xenobiotic metabolic enzyme, *Gstm5* (*glutathione S-transferase, mu 5*), was not induced in some of the positive compounds. Most of the genes related to metabolism (probably involved in secondary compensatory mechanism of cell toxicity) were strongly up-regulated in the positive compounds that exhibited histopathological findings throughout chronic administration. On the other hand, *Asns* (*asparagines*

*synthetase*) was also induced in nitrofurantoin, thioacetamide, captopril, and enalapril, which exhibited histopathological findings only at the beginning or after long-term administration. *Abcc2* (*ATP-binding cassette, sub-family C, member 2*), which act as a multi-drug transporter, was also up-regulated in nitrofurantoin, thioacetamide, captopril, and enalapril. But, these two genes were also predominantly induced in the negative compounds (clofibrate or omeprazole). In summary, the same as for the other functional categories, the late-onset compounds (e.g., cyclophosphamide, captopril, enalapril) did not tend to predominantly induce the genes of the above functional categories at the early stage of administration, and the recovered compounds (e.g., 2-bromoethylamine hydrobromide, nitrofurantoin, and ethionine) did not induce these genes at the late stage. It seems that the expression profiles of the feature genes were not necessarily correlated to the severity of the histopathological findings at the time point; rather, they were correlated to the time-dependent profile of histopathological changes.

### 3.2.3. Prediction of the external test compounds

Middle-dose groups of all 41 compounds and high-dose groups of 10 compounds (and also high-dose groups of the remaining 31 compounds at the time points without histopathological findings), which had not been used as the training set, were used as the test set for further external validation of the classifier. As a result, 11 of 14 (78.5%) compounds of the middle-dose groups with histological lesions were correctly classified into the positive group of renal tubular injury, when we used SVM positive probability of 0.5 as the threshold (Table 4). Among them, captopril and enalapril exhibited predominant induction of tissue remodeling-related genes and some of the other genes (e.g., *Gtbbp4*, *Gpx2*, *Abcc2*) and were predicted as positive before any signs of tubular damage had occurred. The middle-dose group of LS on day 29 was classified into the positive group without the presence of tubular damage (the high-dose groups of the compound exhibited tubular damage). On the other hand, allopurinol, nitrofurantoin, and *N*-phenylanthranilic acid, which had histopathological findings at the middle-dose groups, were classified into the negative group. Although, in the case of allopurinol and *N*-phenylanthranilic acid, many feature genes were induced and had comparatively higher SVM probabilities.

Among 23 tubular toxicants, the high-dose groups of 11 compounds exhibited late onset of the histopathological findings. Seven of these 11 compounds (63.6%) were predicted as positive before histopathological changes (2-bromoethylamine hydrobromide, phenacetin, carboplatin, hexachlorobenzene, captopril, enalapril, and indomethacin). We also calculated SVM probabilities for the high- and middle-dose groups of 10 potential tubular toxicants and predicted 5 of the 10 compounds as positive (ethinyl estradiol, monocrotaline, acetaminophen, imipramine hydrochloride, and acetazolamide). In most of the compounds predicted as positive without histopathological findings at the early stage of drug-administration or at the lower dosage, a lot of feature genes of most of the functional categories had been already induced (especially tissue remodeling).

## 4. Discussion

In the present study, we identified 98 genomic biomarker candidates (92 genes) and successfully constructed a highly accurate classifier for the concurrent diagnosis of renal tubular injury using diverse groups of nephrotoxicants and hepatotoxicants. We first compared different types of gene selection and classification algorithms to select the best analytical methods (SVM+IBMT; Supplementary figures). Then, the external test sets were randomly generated 100 times to validate the classifiers. Most of the previous reports that executed a toxicogenomics analysis of renal tubular

**Table 4**  
Histopathological findings and the result of the prediction of the further external test set.

Compound	Toxicity class	SVM positive probability											
		Low				Middle				High			
		4D	8D	15D	29D	4D	8D	15D	29D	4D	8D	15D	29D
Gentamicin sulphate		0.007	0.017	0.144	0.088	0.012	0.067	0.391	1.000	0.121	1.000	1.000	1.000
Vancomycin hydrochloride		0.002	0.003	0.006	0.008	0.004	0.003	0.006	0.036	0.929	0.901	1.000	1.000
2-Bromoethylamine hydrobromide		0.024	0.015	0.020	0.010	0.039	0.103	0.024	0.023	0.996	0.853	0.996	0.879
Phenylbutazone		0.054	0.029	0.066	0.015	0.064	0.062	0.115	0.020	0.996	0.524	0.872	1.000
Cyclosporine A		0.015	0.045	0.053	0.035	0.129	0.887	0.857	0.990	0.992	1.000	1.000	1.000
Thioacetamide		0.057	0.030	0.014	0.027	0.348	0.176	0.680	0.848	1.000	0.992	1.000	1.000
K17		0.006	0.308	0.148	0.035	0.320	0.107	0.996	0.992	1.000	1.000	1.000	1.000
Triamterene		0.044	0.016	0.006	0.013	0.581	0.046	0.947	0.721	1.000	0.991	1.000	1.000
Allopurinol		0.005	0.003	0.018	0.050	0.068	0.417	0.025	0.244	1.000	1.000	1.000	1.000
Nitrofurantoin		0.040	0.003	0.013	0.018	0.018	0.005	0.021	0.064	0.328	0.179	0.192	0.906
Ethionine		0.095	0.040	0.038	0.018	0.819	0.030	0.046	0.028	0.983	0.460	0.164	0.040
N-Phenylanthranilic acid	Tubular toxicant (direct/indirect)	0.076	0.030	0.040	0.035	0.032	0.164	0.128	0.400	1.000	1.000	1.000	1.000
Cisplatin		0.013	0.097	0.010	0.109	0.044	0.433	0.910	0.996	0.966	1.000	1.000	1.000
Phenacetin		0.005	0.006	0.027	0.004	0.008	0.011	0.034	0.012	0.688	0.931	1.000	1.000
Puromycin aminonucleoside		0.007	0.028	0.028	0.098	0.015	0.024	1.000	1.000	0.418	1.000	NA	NA
Lomustine		0.012	0.048	0.101	0.011	0.015	0.022	0.287	0.721	0.007	0.155	1.000	1.000
Cyclophosphamide		0.009	0.061	0.032	0.008	0.044	0.024	0.009	0.014	0.044	0.132	0.152	0.919
Carboplatin		0.006	0.014	0.020	0.009	0.007	0.046	0.116	0.277	0.046	0.331	0.600	1.000
Hexachlorobenzene		0.010	0.011	0.098	0.536	0.058	0.174	0.121	1.000	0.027	0.300	0.743	1.000
Captopril		0.004	0.015	0.063	0.031	0.028	0.552	0.639	0.953	0.970	0.967	0.910	0.959
Enalapril		0.039	0.343	0.066	0.064	0.058	0.423	0.920	0.674	0.307	0.958	0.574	0.972
Indomethacin		0.069	0.004	0.004	0.011	0.053	0.013	0.029	0.061	0.661	0.910	1.000	NA
Doxorubicin hydrochloride		0.008	0.015	0.013	0.025	0.010	0.022	0.009	0.018	0.004	0.021	0.025	1.000
Ethinyl estradiol		0.048	0.069	0.108	0.138	0.252	0.079	0.612	0.605	0.640	0.191	0.642	0.668
Monocrotaline		0.004	0.018	0.019	0.051	0.011	0.116	0.218	0.864	0.044	0.986	1.000	NA
Acetaminophen		0.026	0.039	0.011	0.042	0.021	0.185	0.019	0.365	0.458	0.143	0.932	0.981
Cephalothin sodium		0.011	0.013	0.009	0.008	0.109	0.008	0.006	0.042	0.143	0.047	0.060	0.120
Bucetin		0.005	0.007	0.024	0.023	0.019	0.016	0.003	0.035	0.007	0.030	0.119	0.038
Methyltestosterone	Potential tubular toxicant	0.024	0.011	0.001	0.005	0.003	0.004	0.006	0.011	0.005	0.030	0.081	0.170
Rifampicin		0.014	0.017	0.004	0.008	0.007	0.024	0.010	0.090	0.224	0.052	0.060	0.317
Imipramine Hydrochloride		0.016	0.009	0.027	0.018	0.022	0.012	0.068	0.002	0.022	0.104	0.547	0.118
Acetazolamide		0.049	0.034	0.017	0.011	0.049	0.586	0.098	0.035	0.039	0.209	0.192	0.159
Caffeine		0.007	0.008	0.011	0.005	0.003	0.011	0.006	0.014	0.047	0.019	0.016	0.021
Valproic acid		0.002	0.003	0.026	0.006	0.007	0.011	0.029	0.008	0.020	0.041	0.056	0.016
Clofibrate		0.034	0.032	0.007	0.006	0.026	0.017	0.007	0.024	0.158	0.022	0.077	0.072
Allyl alcohol		0.004	0.010	0.015	0.008	0.004	0.017	0.006	0.004	0.003	0.031	0.006	0.013
Omeprazole		0.007	0.015	0.036	0.032	0.032	0.244	0.079	0.008	0.011	0.036	0.136	0.052
Bromobenzene	Hepatotoxicant	0.006	0.004	0.005	0.007	0.019	0.007	0.039	0.009	0.005	0.007	0.039	0.026
Ketoconazole		0.004	0.004	0.012	0.003	0.007	0.004	0.011	0.007	0.022	0.009	0.015	0.010
Ciprofloxacin		0.008	0.009	0.007	0.026	0.007	0.015	0.009	0.012	0.010	0.003	0.007	0.020
Erythromycin ethylsuccinate		0.006	0.013	0.025	0.020	0.009	0.018	0.045	0.083	0.054	0.025	0.073	0.113

injury did not use an external test set or used only one external test set. These approaches were not statistically robust or biologically appropriate, because the prediction accuracy was possibly differentiated and deviated depending on how the whole dataset was split into the external test set and the training set. Because we used a variety of compounds, it was especially important to randomize the external test set for our analysis to avoid statistical deviations. Furthermore, we validated their prediction accuracies using middle-dose groups of all 41 compounds and the high-dose groups of 23 compounds that were not used in the training of the classifier. The classifier constructed by the genomic signatures exhibited a higher sensitivity than the histopathological findings in detecting renal tubular damage at lower doses and at earlier time points (Table 4). Our large-scale, high-quality toxicogenomics database and algorithms for gene selection and classification have higher statistical power than any of the previous studies and are very useful for robust biomarker selection and the prediction of drug-induced toxicities.

The feature genes that could be biomarker candidates for drug-induced renal tubular injury include several well-known biomarker candidate genes, such as *Kim1*, *Cp*, *Clu*, *Timp1*, and *Spp1*. We also identified several genes that were not frequently reported in previous studies but are included in functional categories thought to be mechanistically related to tubular toxicity, and the expression levels of these genes were correlated to the severity of the histopathological findings (Fig. 1). Wang et al. (2008) recently conducted a literature survey to collect tubular injury biomarkers that were described in multiple published studies, and they validated these biomarkers by using RT-PCR. Our gene list contains 11 of 24 validated genes (Table 3). Among the 11 genes, 8 genes are involved in tissue remodeling, and 2 genes are involved in the immune/inflammatory response. All of tissue remodeling and immune/inflammatory response-related genes were up-regulated, as described in the previous studies. These genes are thought to be related to secondary compensatory mechanisms of renal tubular injury (Huang et al., 2001). Eight of 10 tissue remodeling-related genes were consistent with the genes reported by Wang et al., and most of these genes were strongly up-regulated in most of the positive samples. The genes that participated in these two functional categories were strongly suggested as genomic biomarker candidates for drug-induced renal tubular injury.

We found that the up-regulation of tissue remodeling and immune/inflammatory-related genes was most prominently induced and roughly consistent with or induced earlier than the histopathological findings (Fig. 1a and b). Up-regulated genes also participated in metabolism, cell adhesion/proliferation/migration, apoptosis, membrane transport, and signal transduction (Fig. 1c and d). Two xenobiotics metabolism-related genes (*Gpx2*, *Gstm5*) were up-regulated, probably in response to oxidative stress (Rokushima et al., 2008). *Asns* (*Asparagine synthetase*) is crucial for asparagine synthesis and may be important for progression through the G1 phase of the cell cycle (Hutson and Kilberg, 1994). *A3galt2* (*alpha-1,3-galactosyltransferase 2*) is involved in the synthesis of the isoglyco-series of glycosphingolipids, which are suggested to be involved in apoptosis. *Pspl1* (*phosphatidylserine-specific phospholipase A1*) stimulates histamine release and, therefore, may be involved in the inflammatory response (Hosono et al., 2001). Some membrane transporters including the multi-drug transporter were up-regulated and probably are commonly induced by the toxicities of the diverse class of nephrotoxicants. Up-regulated genes related to cell adhesion/proliferation/migration and apoptosis also would be related to secondary compensatory mechanisms, the same as for genes related to tissue remodeling and the immune/inflammatory response. Several of these genes have been reported as genomic biomarkers of renal tubular injury.

Down-regulated genes participated in cell adhesion/proliferation/migration, membrane transport, and signal transduction (Fig. 1c and d). The down-regulation may be a response to drug-induced toxicity or an adverse effect and may serve to maintain a low cellular energy status to minimize further damage (Safirstein et al., 1990). Down-regulation occurs during the acute phase of tubular damage induced by nephrotoxicants and acute ischemic renal injury (Amin et al., 2004; Hu et al., 2000; Huang et al., 2001). Representative down-regulated genes observed in our analysis were *Cacng5* (*calcium channel, voltage-dependent, gamma subunit 5*) and *Gcgr* (*glucagons receptor*). Calcium channels transport calcium ions in cell cytoplasm to the outside and maintain their gradient of concentration. Down-regulation of *Cacng5* may be a consequence of lower energy status or the perturbation of calcium homeostasis. Glucagons are peptide hormones that suppress glycolysis and accelerate gluconeogenesis. Therefore, down-regulation of *Gcgr* probably suppresses gluconeogenesis. Our results show that the down-regulation of energy-consuming processes is also observed in chronic renal tubular injury.

In summary, our results support previous studies that described correlations between well-known biomarker candidate genes or their functional categories and renal tubular injury. We used not only typical compounds that cause renal tubular injury but also a lot of compounds that have diverse effects and different patterns of histopathological changes with multiple time points and dosages. Our results suggest that well-known biomarkers and their functional categories for renal tubular injury are also induced by a wide variety of nephrotoxicants. On the other hand, we also found inconsistent and novel analytical results and heterogeneities between compounds that have different patterns of histopathological changes. It is thought that our gene list preferentially contains genes concerning secondary compensatory mechanisms rather than drug toxicity because of the diversity of the compounds used in our analysis. The feature genes were highly and commonly induced in the compounds, thus, the feature genes are highly statistically reliable and useful as genomic biomarkers during the drug-development process. On the other hand, it is also important to investigate the differences in gene expression profiles corresponding to the toxicity between diverse classes of compounds.

We used middle-dose groups and high-dose groups, which had not been used in the training set, as a further external test set for our classifier constructed from 98 top-ranked genomic biomarkers. Eleven of 14 compounds (78.5%) with histopathological findings at middle-dose groups were correctly classified as positive (Table 4). Also, some of these compounds were predicted as positive at the time points before the emergence of the tubular injury. These results indicate that genomic biomarkers are more sensitive than histopathological findings. On the other hand, although the middle-dose groups of allopurinol, nitrofurantoin, and *N*-phenylanthranilic acid exhibited histopathological findings, these compounds were predicted as negative. In the case of high- and middle-dose nitrofurantoin, renal tubular necrosis had been already observed within 24 h after administration (data not shown) and recovered after day 15. We found that most of our 98 genomic biomarker candidates were not significantly induced at the middle-dose groups of nitrofurantoin (Supplementary figure). Instead, the high-dose groups of nitrofurantoin exhibited gene expression changes in some of the 92 genes, and were predicted as positive (day 29). Therefore, it is thought that the gene expression profiles of middle-dose nitrofurantoin may reflect the recovery from tubular injury, even though the histopathological findings were still observed. In the case of *N*-phenylanthranilic acid, 3 of 5 animals sacrificed on day 29 did not exhibit any histopathological changes. In the case of allopurinol and *N*-phenylanthranilic

acid, many feature genes were induced and had comparatively higher SVM probabilities. These samples should be included in the training set to construct better classifiers, or heterogeneity may exist.

We also used the high-dose groups of 10 potential tubular toxicants as the test set. These compounds exhibited no histopathological findings of renal tubules (necrosis, degeneration, and regeneration), but the induction of renal tubular injury and/or other nephrotoxicities have been described in previous reports. Five of the 10 compounds (ethinyl estradiol, monocrotaline, acetaminophen, imipramine hydrochloride, and acetazolamide) were predicted as renal tubular injury positive. Monocrotaline- and ethinyl estradiol-treated animals had no tubular injury, and these compounds have not been reported as tubular toxicants. But, these compounds had anisonucleosis and/or vacuolization at cortex/proximal tubules. Acetaminophen was reported as a tubular toxicant. Therefore, it is reasonable that these three compounds were predicted as renal tubular toxicants. Imipramine hydrochloride- and acetazolamide-treated animals had no tubular injury, and these compounds have not been reported as tubular toxicants; thus, these may be false positives. However, in the high-dose group of imipramine hydrochloride on day 15, many of the feature genes, such as *Cp*, *Igfbp1*, *Fcgr3*, and *Cd14*, were induced. In the middle-dose group of acetazolamide on day 8, most of the genes related to tissue remodeling were strongly up-regulated, including *Kim1*, *Clu*, *Timp1*, *Cp*, and *Spp1*. Although these changes may reflect the early onset of nephrotoxicity, the possibility of false positives cannot be completely excluded.

The classifier constructed from multiple feature genes had much better prediction accuracy than classifiers constructed from any of the single or multiple well-known genomic biomarkers described above, histopathological findings, and any previous study (Fig. 3, Supplementary figure). Toxicogenomics and the large-scale database would be very useful in drug discovery and also helpful in risk estimation of nephrotoxicity. But, our analytical results suggest that there still exists unknown heterogeneity of gene expression between compounds that have different patterns of histopathological changes (times, severity, type of histopathological findings, etc.), even though the gene expression changes are concurrent with the histopathological findings. Also, further work is needed to adapt these genes into a toxicity screen by validating their reversibility and developing robust and convenient assays. We are now preparing experimental validation of our genomic biomarkers for concurrent diagnosis and gene expression analysis of further compounds. Accumulation of knowledge about various types of toxicities is very useful and important not only to identify specific biomarkers for an arbitrary toxicity, but also to understand mechanisms of drug-inducible toxicities.

#### Conflict of interest statement

The authors declare that there are no conflicts of interest.

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#### Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.tox.2009.09.003.

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## キーワード解説

## Toxicogenomics

## トキシコゲノミクス

漆谷 徹郎

## 1. トキシコゲノミクスとは

最近生命科学の分野に大きなインパクトを与えた技術に、オミクステクノロジー omics technology がある。Omics とは、「全体」を表すラテン語 ome に「学問」を表す接尾語 ics をつけた造語で、「すべて」を扱う学問であり、遺伝子全体 genome を扱うゲノミクス genomics に始まる。遺伝子を扱う学問であるジェネティクス genetics がゲノミクスと呼ぶものに進化したのは、ヒトゲノムプロジェクト、および全遺伝子の発現量を一枚のチップで一挙に測定することを可能としたマイクロアレイの開発による。

生体成分の分離・検出・定量法の発達は、タンパク質全体 proteome や代謝物全体 metabolome を取り扱うことを可能にし、プロテオミクス proteomics, メタボロミクス metabolomics (metabonomics) という領域をも生み出した。タンパク質の網羅的解析には、2次元電気泳動法、代謝物の網羅的解析には HPLC や NMR の飛躍的な改良が寄与した。また、分離された各成分を同定するに当たって、質量分析装置の改良がブレークスルーとなったことから、島津の田中耕一研究員のノーベル賞は記憶に新しい。なお、オミクステクノロジーの測定原理に関しては別稿を参照されたい(1)。

ゲノミクステクノロジーを毒性学 toxicology や薬理学 pharmacology に応用すれば、トキシコゲノミクス toxicogenomics, ファーマコゲノミクス pharmacogenomics となる。ただしこれらの用語は上記の定義よりも限定的に使用される場合が多い。ファーマコゲノミクスは通常、特定疾患群の患者に共通な遺伝的特徴を把握して最適な薬剤の開発を目指す「ゲノム創薬」、および患者個々の遺伝的特徴に最適な薬剤を投与する「テーラーメイド医療」への応用を意味し、トキシコゲノミクスは、非臨床毒性試験において網羅的遺伝子発現解析によって毒性予測を行おうとする戦略を指す場合が多い。それは、実際の応用例がその分野に集中

しているからである。

旧来の薬理学では病態モデル動物で薬効評価を行っていたが、ヒトの疾患関連遺伝子を同定することが可能となった今、「ゲノム創薬」の効率が良いのは明らかである。また、臨床における薬効の個体差の多くが、薬物代謝酵素やトランスポーターの一塩基多型で説明できるようになり、実質的な成果が得られているため、ファーマコゲノミクス = SNPs 解析、という印象が強い。毒性が薬効の延長である場合には、そのままトキシコゲノミクスにつながるはずであるが、現在トキシコゲノミクスに期待されているのは「新薬が臨床展開して初めて明らかになるような予想外の有害作用を前臨床の段階で予測すること」である。例えば糖尿病治療薬 troglitazone が市販後重篤な肝障害の発生により回収されたことは記憶に新しいが、現在の技術ではこれを前臨床の段階で予測することは原理的に不可能である。これを可能とするものとしてトキシコゲノミクスに期待が集まっている。この場合には、動物実験で、薬物に対する応答をすべての遺伝子の発現変化として観察する、という戦略をとる。転写産物 transcript の全体を扱うという意味でトランスクリプトミクス transcriptomics と呼ぶべきであるが、これも通常ゲノミクスと称される。

## 2. 網羅的遺伝子発現解析による毒性予測とトキシコゲノミクスプロジェクト

オミクステクノロジーが目新しかった頃、きっかけとなるデータをマイクロアレイから得た場合、研究者としての主体性がない、と軽蔑される傾向にあった。現在でも「何が重要か良く分からないから、とりあえず全部測定してみよう」などという学生が研究室に溢れたら、教授の血圧は上がりっぱなしであろう。教育的効果はさておき、毒性学領域では、「全部測定してみよう」という姿勢は必須である。troglitazone の例で言えば、PPAR $\gamma$ 刺激作用を詳しく調べてもその肝

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障害の発生は予測できず、だからといって、毒性研究者が自分の思い入れのある毒性パスウェイを検討して問題なかったとしても、何の保証にもならない。何が起るかわからない毒性の場合は、起こりうるすべての可能性を検討しておかねばならない。オミクスの中でも、トランスクリプトミクスは圧倒的に有利である。それは、遺伝子が容易に増幅できるために感度が非常に高いこと、測定対象の同定が容易である（対象を配列既知のプロープで検出するため、測定値すべて同定と定量がセットになっている）ことによる。

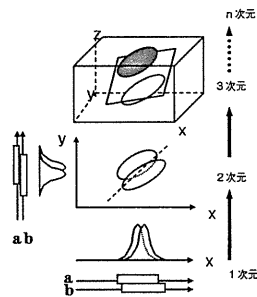
毒性学的機序が未知である新規開発薬物の有害作用を予測するためには、できるだけ多くの既存薬物のデータを蓄積しておき、これらと比較する方法がとられる。2000年以降、欧米の巨大製薬会社やベンチャー企業は、種々の薬物を投与した動物の各組織における遺伝子発現をデータベース化し始めた(2)。我が国では、製薬会社の規模が小さく、個別では対抗できないため、製薬17社が協同し、科研費の補助をうけて、官民共同のトキシゲノミクスプロジェクトが2002年に発足した(3)。5年間で50億円を費やしたこのプロジェクトでは、150種の医薬品を投与したラット24,000匹について、肝臓（一部は腎臓も）の遺伝子発現データ約8億件を各種毒性学的データとともに取得し、統合データベースを構築した。現在、第2期のトキシゲノミクス・インフォマティクスプロジェクトが進行中である。

蓄積されたデータを用いて、いかにして毒性予測が可能となるのであろうか。直接データを扱うと、最初に直面するのは例数に比して圧倒的に多い測定データ数の問題である。通常の科学実験では、一つの項目について5~10例をあて、統計解析で変化の有意性を検討する。しかしトランスクリプトミクスの場合、コストを考えると3~5例がせいぜいであるが、1例につき3~5万の測定値が得られてしまう。このような測定値の有意差検定は無意味に近く、第1種と第2種の過誤のどちらかが必ず極端に大きくなる。

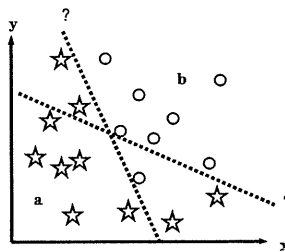
膨大なデータからどうやって意味のあるものを抽出するか、これが現在の最大の課題である。腫瘍マーカーの場合は単一の特異的な遺伝子産物から診断可能なものもあるが、薬剤性肝障害のような場合は、薬物に対する複雑な応答の結果であり、単独の変数で判定できるとは考えられない。むしろ、この複雑な過程を解析することにより、安全性を多角的に評価することが期待されている。これは多変量解析の領域である。

図Aに、多変量解析のイメージを示す。a, b2つの毒性学的フェノタイプがあるとし、遺伝子xの発現量で判別したいが、その発現には差があるものの、分布は大部分が重なっていて、少数例の測定では分別が困難である。ここで遺伝子yに注目する。これも分布が重なっているが、xとyの間に一定の関係性があれば、x-y平面上で大部分が分離される。ここでわずかに重なっている部分も、第3の遺伝子zの発現量を加味し

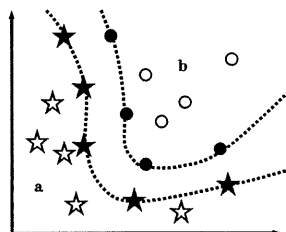
A. 多変量解析のイメージ



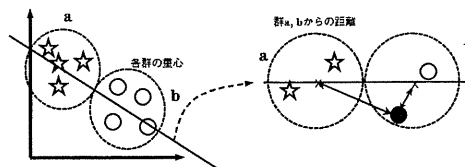
B. 2要素による線形分離



C. SVMによる分離のイメージ



D. PAMによる分離のイメージ



た3次元空間では完全に分離されている。これをn次元の空間まで拡張すれば、理想的なマーカー遺伝子が得られるが、実際はこれら遺伝子の選別が難しい。

薬物によってある毒性学的フェノタイプの有無がはっきりしている場合は、「教師付分類法」である判別分析が有効であり、マイクロアレイデータには、学習機械であるSupport Vector Machine (SVM) や Prediction Analysis of Microarrays (PAM) が適しているようである。図Bには、星印が毒性なし、丸印が毒性ありの個体で、簡単のためにx, yの2種類の遺伝子発現値をもつ場合を模式的に示す。SVMは、線形分離ができない場合(図Bの点線)でも、これを非線形写像によって高次元特徴空間に写像することによって線形分離するというもので、最適化された図Cでは、サポートベクターと呼ばれるマージン上の点(塗りつぶされている)で分類されている。SVMの場合は、サポートベクターだけが分離超平面に寄与しているが、PAMにおいては、多次元空間上の各点を、それぞれのnearest centroid(重心)からの距離でクラス確率を評価するという工夫がされている(図D)。実際、PAMを用いて、非遺伝子傷害性肝発癌のリスクを定量的に評価する試みに成功している(4)。

実際は、薬物誘起性臓器障害を単純に「ある・なし」に分けることは困難である。ある毒性が発現する用量より低い用量から遺伝子発現変化が生じることは十分考えられ、当該用量で「毒性なし」として学習させた場合には誤った結果を導く。そこで、「教師なし分類法」も重要になってくる。主成分分析Principal Component Analysis (PCA)は、なるべく少ない合成変数から多くの情報を把握するための情報の集約を達成するもので、うまく分離できたときは、毒性予測とともに、寄与率の大きい遺伝子の内容を精査することによって、毒性メカニズムにも迫ることができる。PCAによってリン脂質症の診断・予測の可能性を拓いた例を最近報告した(5)。

### 3. 問題点と将来展望

毒性学的・病理学的フェノタイプを個体の遺伝子型と関連づける場合には、統計学的に厳密な結論を導くことが可能である。ある疾患や薬物の有害作用に関して、患者の遺伝子型をデータベース化し、一定数以上の例数が蓄積されれば、ロジスティック回帰分析などにより、ある集団でそのフェノタイプが発生する確率を正確に評価できる。これは、特定の遺伝子型の集団における発病リスクや、治療の有効性、費用対効果が

精確に評価可能となることを意味する。問題はバイオサイエンスの部分にはなく、個人情報の取り扱いや、「ヒトの健康をすべて確率的に予言してしまう社会」を容認するか否か、などが直面する課題である。

一方、トランスクリプトームとしてのトキシコゲノミクスでは状況が異なる。ある個体の遺伝子の塩基配列は確定した事実であるが、「ある個体にある薬物を投与すると遺伝子Xの発現量が1.5倍になった」という現象が確定的でないことは、研究者であれば自明であろう。データのばらつきには生物学・技術的な原因の両者があるため、施設間で再現性の保証される遺伝子リストとそれを得るための標準プロトコルの策定が重要である。理想的には、信頼性の高い少数の遺伝子をバイオマーカーとして選定したいが、それが困難な場合は、ある程度の数の遺伝子を用いて、個々の発現値には多少のぶれがあっても、最終判定にぶれの少ないアルゴリズムを採用することになる。

この再現性・信頼性の問題は、創薬における安全性の確保がレギュラトリーサイエンスと密接に関係しているため、特に重要になる。2004年に米国FDAが新薬の承認申請に当たってゲノミクスデータの任意提出を受けるとを決定して以来、ゲノミクスデータを審査資料として使用するという流れとなっている(6)。わが国もそれに備えておく必要があり、現在のプロジェクトにおいても、施設間バリデーションを組み込んでいる。

オミクステクノロジーは確かに強力な手法である。将来的には、すべてのオミクステクノロジーを統合したトキシコパノミクス toxicopanomics も可能であるといわれ、医薬品の有害作用の検出感度はますます上昇していくであろう。しかしここで、注意すべきことがある。副作用のない薬などない。新しい技術がいたずらに薬の有害作用の部分を強調し、新薬の芽をつみ取るようなことはあってはならない。医薬品の安全性評価は、リスクとベネフィットの両者を精確に提示したうえでの客観的な判断基準を示すものであるべきだろう。

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## Collaborative work on evaluation of ovarian toxicity by repeated-dose and fertility studies in female rats

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**ABSTRACT** — The National Institute of Health Sciences (NIHS) and 18 pharmaceutical companies of the Japan Pharmaceutical Manufacturers Association (JPMA) have conducted a validation study intended to evaluate whether a 2-week repeated general toxicity period with histopathological examination is sufficient to detect ovarian toxicity or not. The current repeated dose general toxicity study is considered to be insufficient in terms of evaluating female reproductive function due to a lack of evidence indicating that it is adequate. Evaluation of ovarian toxicity by comprehensive histopathological examination of the female reproductive organs based on the underlying morphology of a normal cycle of the reproductive tract including the ovary and additional immunohistochemical staining with proliferative cell nuclear antigen (PCNA) to identify small follicles may be a good tool to assess female reproductive function. In the collaborative study, 2- or 4-week repeated dose toxicity studies with ovarian histopathological examinations were conducted. A female fertility study was also conducted to compare the results with those of the ovarian histopathological findings. A total of 17 test substances were evaluated and categorized into hormone analogues, primordial follicle damaging agents, metabolite imbalance inducers, and endocrine imbalance inducers. Based on the results, ovarian toxicity could be detected by a careful histopathological examination. A 2-week dosing period may be sufficient for the evaluation of ovarian toxicity, except for cytotoxic compounds such as alkylating agents. The pathological findings of ovarian toxicity (decreases in follicles, increases in atretic follicles, increases in currently formed corpora lutea, etc) reflected the female fertility parameters (irregular estrous cycle, pre-implantation loss).

**Key words:** Ovary toxicity validation pathology, Fertility study

### INTRODUCTION

At the International Conference on Harmonization (ICH) of Technical Requirements for Registration of Pharmaceuticals for Human Use, the Harmonized Tripartite Guideline, "Timing of Non-clinical Safety Studies for

the Conduct of Human Clinical Trials for Pharmaceuticals (M3(R1))" reached Step 4 in July 1997 and was amended in November 2000. However, regional differences in the timing of the reproduction toxicity studies to support the inclusion of women of childbearing potential (WOCBP) in clinical trials remain (ICH, 2008). In Japan, the assess-

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