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Data Article

Integration of genome-wide mRNA and miRNA expression, and DNA methylation data of three cell lines exposed to ten carbon nanomaterials

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ARTICLE INFO

Article history:

Received 8 May 2018

Accepted 18 May 2018

Available online 25 May 2018

ABSTRACT

We present data derived from an exposure experiment in which three cell-lines representative of cell types of the respiratory tissue (epithelial type-I A549, epithelial type-II BEAS-2B, and macrophage THP-1) have been exposed to ten different carbon-based nanomaterials for 48 h.

In particular, we provide: genome-wide mRNA and miRNA expression, and DNA methylation; gene tables, containing information on the aberrations induced in these three genomic data layers at the gene level; mechanism of action (MOA) maps representing the comparative functional alteration induced in each cell line and each exposure.

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DOI of original article: <https://doi.org/10.1016/j.impact.2018.05.003>

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<https://doi.org/10.1016/j.dib.2018.05.107>

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Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Nanotoxicology</i>
Type of data	<i>Tables, figures, omics data matrices</i>
How data was acquired	<i>Microarray based assays</i>
Data format	<i>Raw, analyzed</i>
Experimental factors	<i>Cells were cultured with corresponding media and supplements. THP-1 cells were differentiated with 50 nM PMA for 48 h before treatments.</i>
Experimental features	<i>Cells were exposed to 10 µg/ml of 10 different carbon nanomaterials for 48 h. DNA, mRNA and miRNA were extracted, purified and quality checked for arrays.</i>
Data source location	<i>University of Tampere, Finland</i>
Data accessibility	<i>Figures and tables are in this article. Raw and processed microarray data are available through Array Express repository (Accession Numbers ArrayExpress: E-MTAB-6396, E-MTAB-6406, E-MTAB-6397)</i>

Value of the data

- Omics datasets can be used to integrate and compare molecular alterations consequent to nano-materials exposure studies.
- Gene (expression) tables can serve as a reference in future studies modelling the cell specific response of each gene at different molecular layers.
- MOA maps can be used as a starting point to draft adverse outcome pathways (AOP) that take into account cell type-specific responses.

1. Data

The data presented in this paper includes three sets of microarray data for 33 mRNA, miRNA and methylation samples available on ArrayExpress platform, 30 gene tables containing multi-omic differential information on these three layers for human genes, and 3 maps representing functional alteration of all exposures at the pathways level.

Microarray data samples summarized in [Table 1](#) are composed of 96 raw and preprocessed data matrices reporting mRNA expression values for refseq genes in control and exposed cell lines, 91 raw and preprocessed matrices reporting mirRNA expression values in control and exposed cell lines and 99 raw and preprocessed matrices reporting DNA methylation values at the CpGs level in control and exposed cell lines.

For each data layer and each exposure, we performed a differential analysis between the control and the exposed samples with limma linear models and annotated a list of 22,789 human gene symbols where we summarized DNA methylation change (p-value and log fold-change) in promoter and body regions; targeting miRNAs expression changes (p-value and log fold-change), symbolically linked to the gene body region; and mRNA expression changes (p-value and log fold-change). All these values were used to compute a cumulative score for the gene determining the overall impact of all molecular aberrations on any given particular gene. [Supplementary Table S1](#) is an excel file reporting the summary information shown in [Table 2](#) in the first sheet, as well as the above described annotation for each exposure in the remaining 30 sheets.

The functional alteration map data ([Fig. S1–S3](#)) report, for each exposure, the KEGG pathways significantly enriched from the high scoring genes. Each pathway is annotated with the leading direction (red for upregulation and green for downregulation) of expression change of its genes for the corresponding exposure. Pathways are grouped based on KEGG hierarchical structure in six categories: “Metabolism”, “Genetic Information Processing”, “Environmental Information Processing”,

Table 1
Summary of array data.

Accession	Type	# samples	Platform	RAW data	Preprocessed data
E-MTAB-6396	mRNA	96	Agilent SurePrint G3Human GE 8 × 60K	Yes	Yes
E-MTAB-6406	miRNA	91	Agilent SurePrint G3 Unrestricted Human miRNA_V21 8 × 60K	Yes	Yes
E-MTAB-6397	DNA methylation	99	Illumina HumanMethylation450 BeadChip	Yes	Yes

Table 2
Multi-omic gene annotation data.

Field	Explanation
test_annotation.score_data.genes scores	Gene symbol SMITE score
methylation_promoter_effect	Combined methylation log fold-change for promoter region
methylation_body_effect	Combined methylation log fold-change for body region
mirna_body_effect	Combined log fold-change of targeting miRNAs
expression_effect	MRNA expression log fold-change
methylation_promoter_pvalue	Combined methylation p-value for promoter region
methylation_body_pvalue	Combined p-values of targeting miRNAs
mirna_body_pvalue	Combined methylation p-value for body region
expression_pvalue	MRNA expression p-value

“Cellular Processes”, “Organismal Systems” and “Human Diseases”. Fig. S1 reports the pathways enriched from all altered genes. Fig. S2 and Fig. S3 report pathways enriched in the two partitions of genes (concordant and discordant), based the adherence with a set of general rules of interaction linking the induced changes in DNA methylation levels and miRNA expression levels with observed changes in gene expression levels. In particular, we defined a gene alteration to be “concordant” if its expression upregulation was coupled with hypomethylation in the promoter region, hypermethylation in the gene body region, or with downregulation of a microRNA specifically predicted to potentially target that gene. Likewise, we defined a gene alteration to be “concordant” if its expression downregulation was coupled with hypermethylation in the promoter region, or with upregulation of a microRNA specifically predicted to potentially target that gene, regardless of the methylation status of the gene body. The genes not following these rules were classified to be “discordant”, and their alteration was hypothesized to be not under the control of DNA methylation or microRNA expression, but other unknown regulatory factors, such as histone modifications.

2. Experimental design, materials and methods

2.1. Cell cultivation

THP-1 cells (ATCC TIB-202) were cultivated in complete RPMI 1640 media (Gibco, Thermo Fisher Scientific, Life Technologies, USA) supplemented with 10% FBS (Gibco, USA) and 1% Ultraglutamine (Gibco, USA) and differentiated with 50 nM PMA (phorbol-12-myristate-13-acetate) for 48 h before exposures. BEAS-2B (American Type Culture Collection through LGC Promochem AB (Borås, Sweden))

were cultured in LHC-9 media (Gibco, USA) and A549 cells (ATCC CCL-185) were grown in DMEM media (including L-glutamine, Gibco, USA) supplemented with 10% FBS (Gibco, USA).

2.2. Exposure settings

Exposures were performed on 12-well plates, with 10 µg/ml nanomaterial concentration for 48 h.

THP-1: 800,000 cells per well for RNA and DNA and 900,000 cells/well to miRNA extractions; **BEAS-2B:** 100,000 cells/well to RNA, DNA and miRNA extractions; **A549:** 50,000 cells/well to RNA, DNA and miRNA extractions.

2.3. RNA and DNA extraction protocols

After 48 h exposure, cells were washed with PBS, and lysed (Qiagen lysing buffer). DNA, RNA and miRNA were extracted using Qiagen extraction kits: Qiagen AllPrep 96 DNA/RNA extraction kit for mRNA and DNA and Qiagen miRNeasy 96 extraction kit for miRNA (Qiagen, Germany). Quality of the RNA was confirmed by NanoDrop (ND-1000, Thermo Fisher Scientific Inc., Wilmington, NC, USA) and Bioanalyzer (Agilent Technologies, USA). RNA samples with high RNA integrity values (> 9) were used in microarray analyses.

2.4. Experimental settings

Low Input Quick Amp, two-color microarray-based gene expression protocol: 100 ng of total RNA labeled with Cy3 or Cy5 dyes were hybridized to Agilent SurePrint G3Human GE 8 × 60K DNA microarrays (Agilent, USA).

miRNA Microarray System with miRNA Complete Labeling and Hyb Kit protocol: 100 ng of miRNA labeled with Cyanine 3-pCp dye and hybridized to Agilent SurePrint G3 Unrestricted Human miRNA_V21 8 × 60K microarrays (Agilent, USA).

Methylation protocol: 500 ng of DNA was bisulfite converted with the EZ-96 Methylation Kit Bisulfite-treated DNA was amplified, fragmented and hybridized to the HumanMethylation450 BeadChip (Illumina, USA).

3. Microarray data

Microarray data (Fig. 1, panel A), has been imported, preprocessed and analyzed using R as follows.

mRNA raw data has been imported using limma read.maimages, quality filtered based on negative probes distribution values, quantile normalized, log₂ transformed and median aggregated at RefSeq gene level using the corresponding Agilent annotation file. Batch effect removal of known technical batch effects been performed by using Combat method from the SVA package [1].

miRNA raw data has been quality filtered based on negative probes distribution values, quantile normalized, log₂ transformed and median aggregated at miRbase miRNA ids level. Batch effect removal of known technical batch effects been performed by using Combat method from the SVA package. [1] Differential expression analysis between each exposure and the corresponding controls has finally been performed using a limma model from limma package.

Methylation data has been preprocessed with minfi package. [2] Briefly, raw data has been imported from idat files, probes were filtered by keeping those having a detection p-value less than 0.01 in all samples. Data was then normalized using SWAN method [3], converted to M values and filtered for probes having a SNP in the interrogation or the extension site and probes known to be prone to as cross-hybridization problems [4].

Batch effect removal was performed by using sva function from SVA package [1] to detect the presence of surrogate variables, the obtained surrogate variables value has then been discretized into $n_samples(1/3)$ bins by using the discretize function from infotheo package [5] and finally corrected using ComBat method from the SVA package [1].

Pathway map

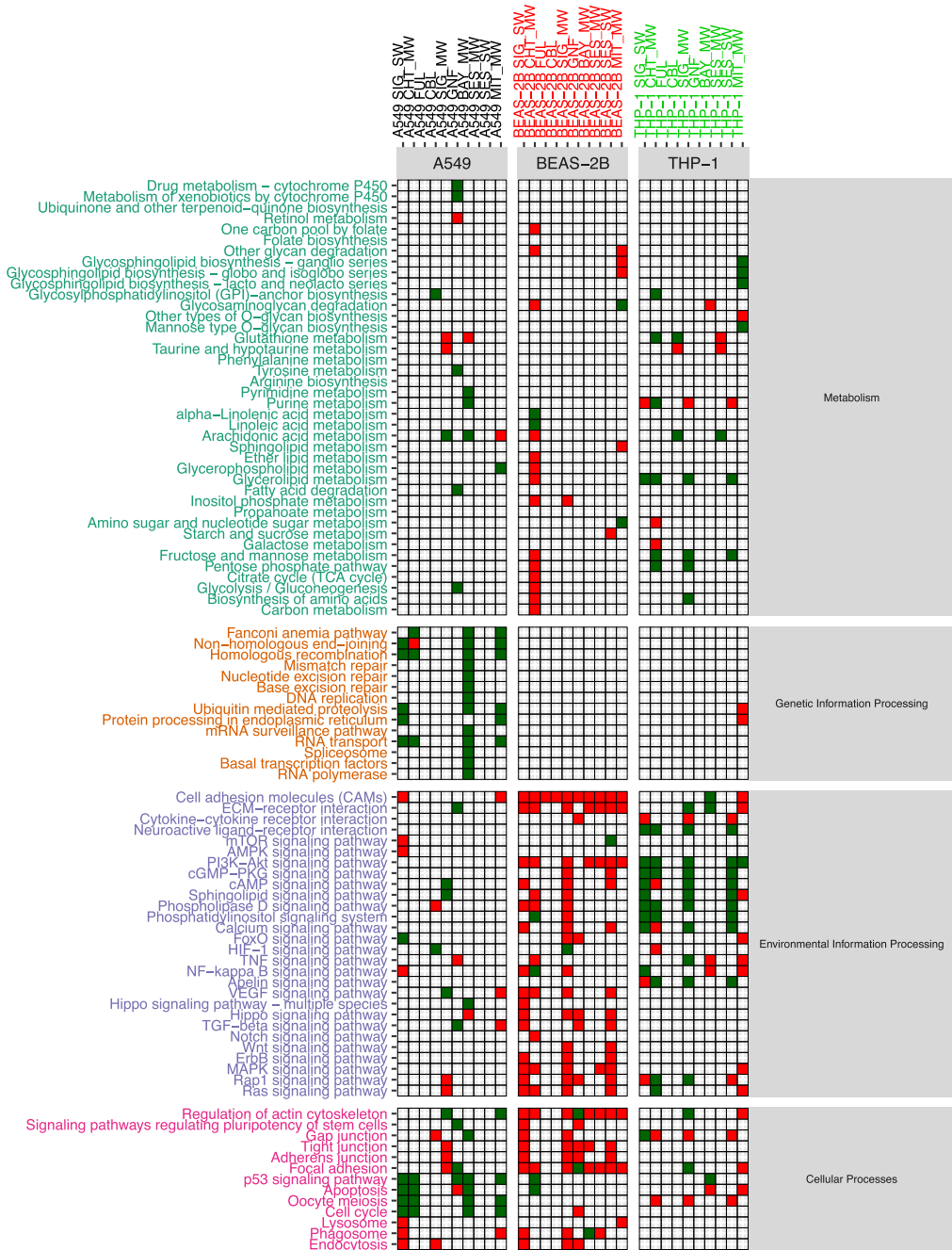


Fig. 1. Data generation scheme. Workflow of data generation: microarray preprocessing and analysis of single layers is reported in panel A; data integration and generation of scored gene tables is reported in panel B; gene module detection and functional profiling of each exposure is reported in panel C.

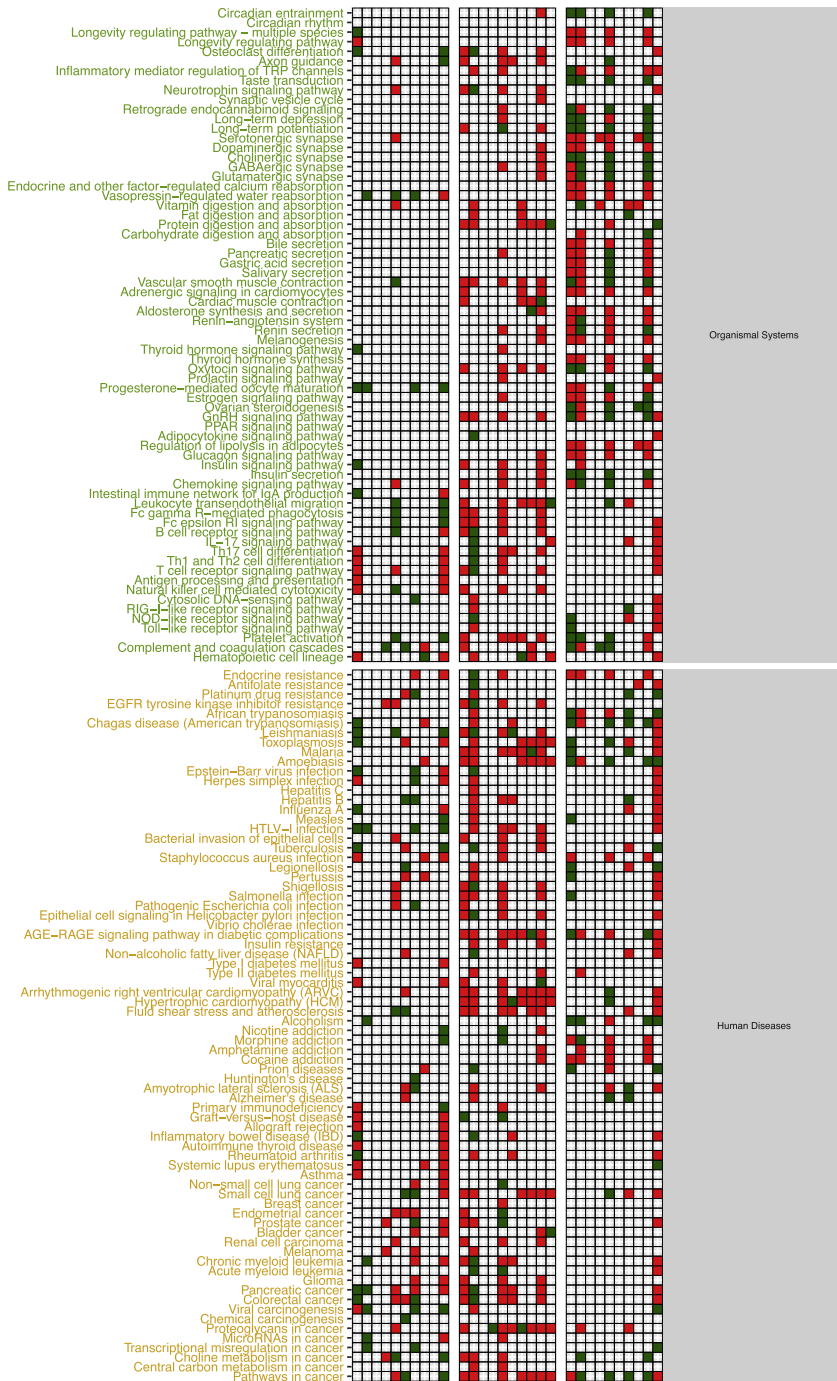


Fig. 1. (continued)



Fig. 1. (continued)

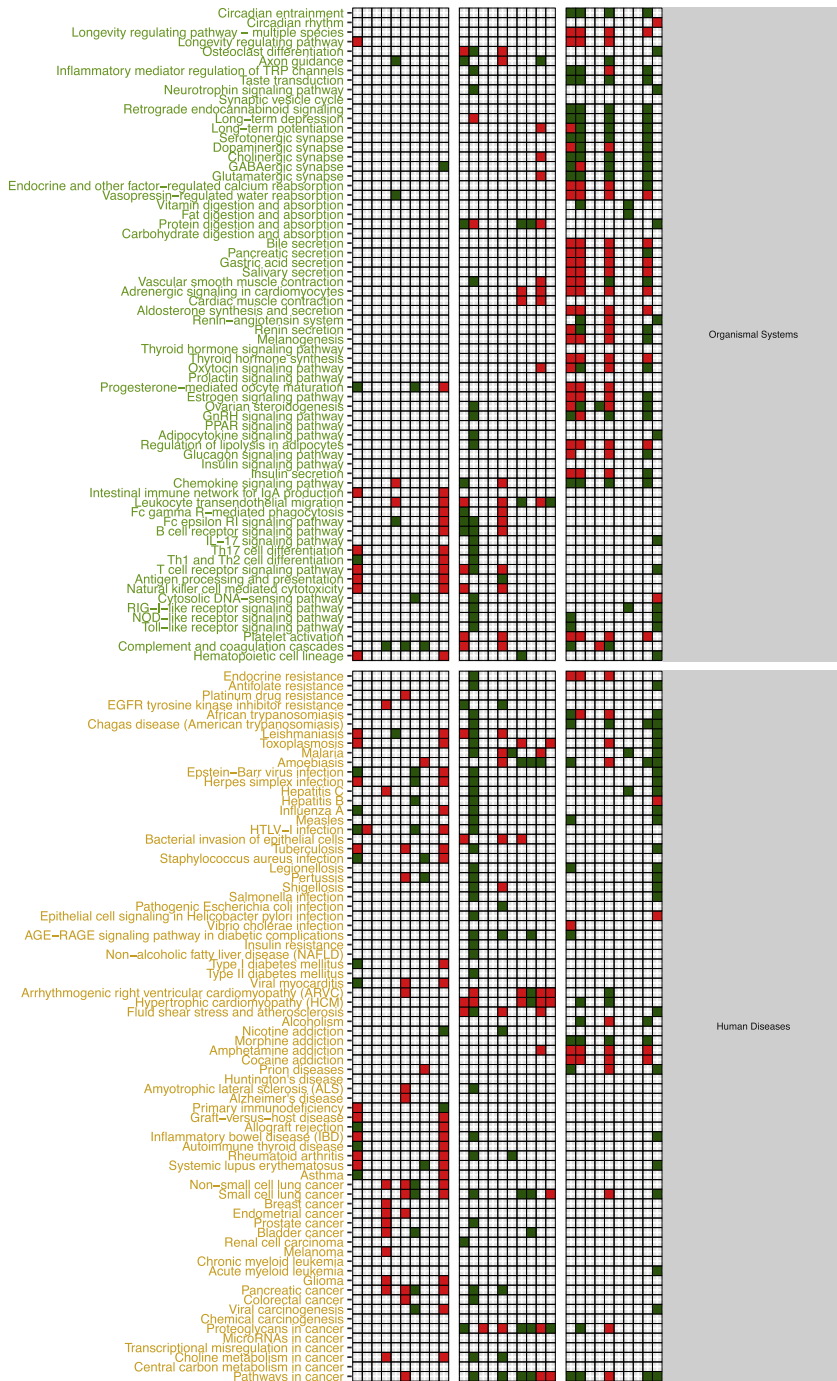


Fig. 1. (continued)

Concordant Pathways Map

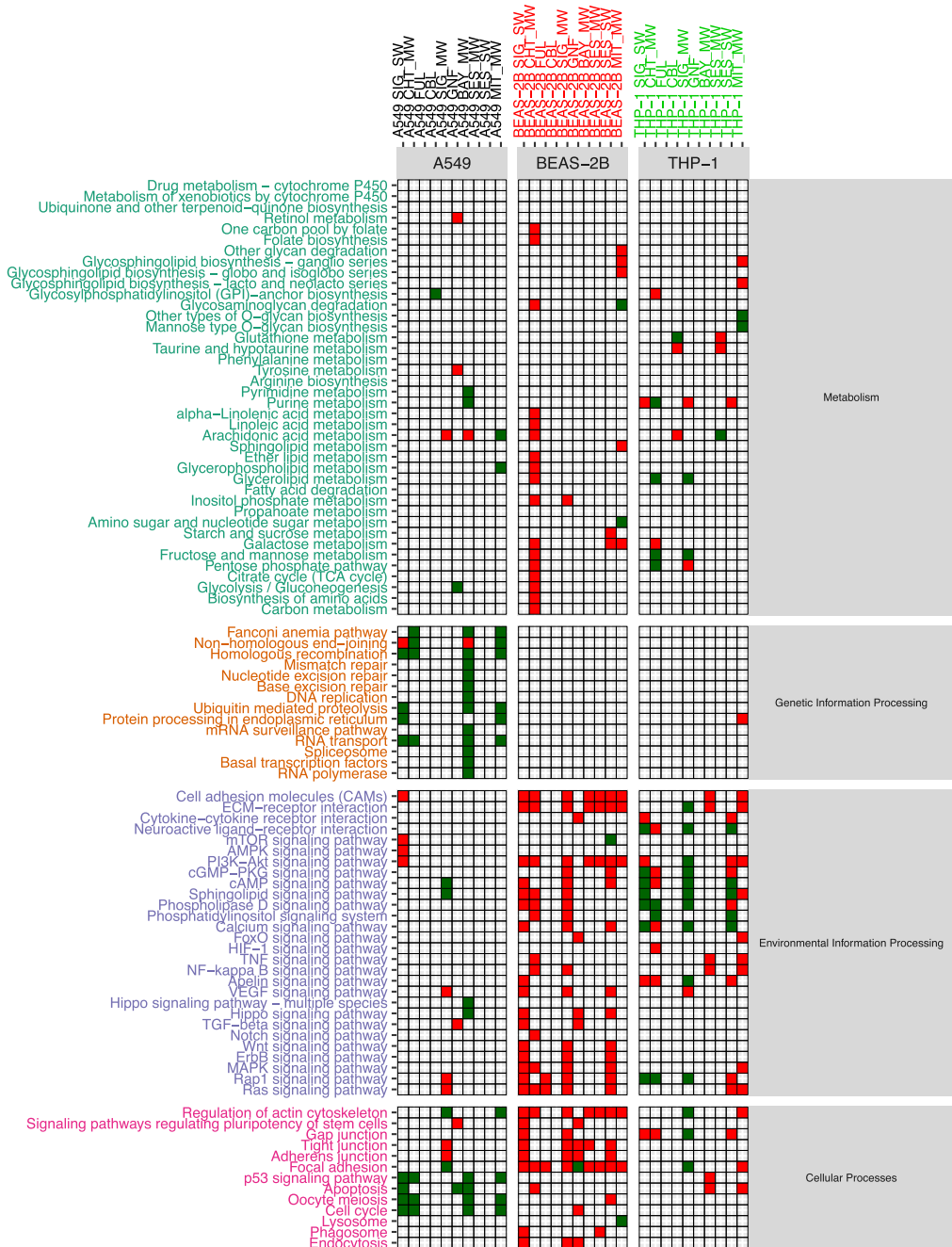


Fig. 1. (continued)

Discordant Pathways Map

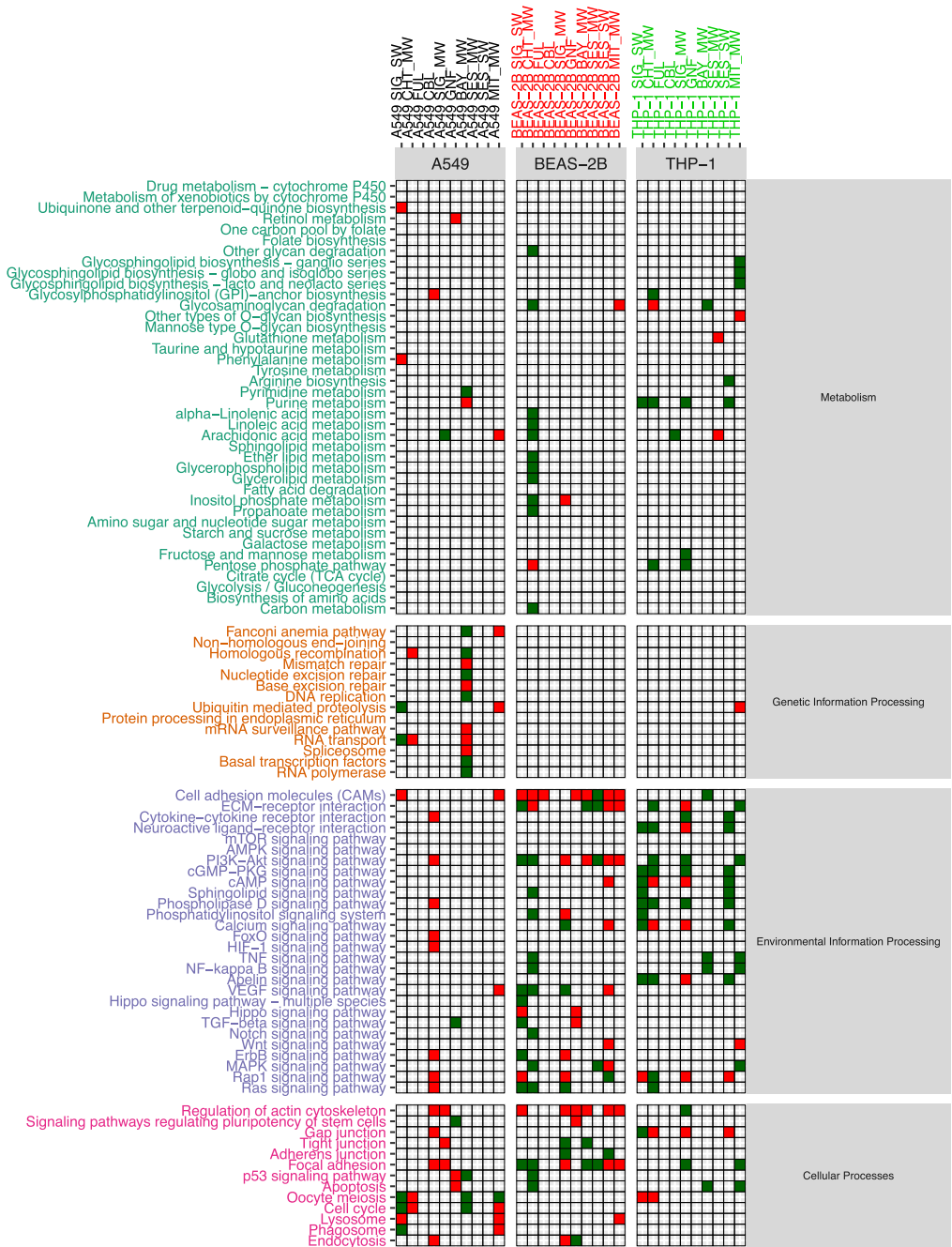


Fig. 1. (continued)

4. Multi-omic gene annotation data

For each of the three analyzed layers, differential expression (DNA methylation) analysis between each exposure and the corresponding controls has been performed using a limma model from limma package. [4].

Data in [Supplementary Table S1](#) (Fig. 1, panel B) has been obtained by integrating differential expression and methylation results using custom scripts and SMITE package. [6] In particular, differential expression and methylation data (in the form of p-values and log fold changes) has been annotated to each UCSC gene transcription start site [TSS – 1 kb, TSS + 1 kb] and gene body region [TSS + 1 kb, TES] as follows.

CpG methylation has been associated in SMITE to TSS and body regions of genes by using their genomic location, while miRNAs have been symbolically associated with the gene bodies of their top 10% target genes using t-scores from TargetScan database [7].

A score has finally been assigned to each gene by integrating the expression p-value and fold-change with the same values from the two modification layers using in SMITE the weights shown in [Table 3](#).

5. MOA maps data

Data presented in [Figs. S1–S3](#) (Fig. 1, panel C) has been obtained by using scored gene lists from [Supplementary Table S1](#). In particular given a scored list of gene for a particular exposure comparison, we used SMITE to detect modules of high scoring genes using a SpinGlass algorithm with 1000 randomizations on the Reactome52 interaction network [8]. We then derived, for each exposure, the KEGG pathways enriched for the all the genes detected from the obtained set of modules. Given an exposure, each enriched pathway was classified as up- or down-regulated if the sign of the median mRNA expression change of the genes in the pathway was respectively positive or negative.

[Fig. S1](#) report the map of all enriched pathways, divided by exposure and cell line, obtained by taking in consideration the whole set of genes from the corresponding table when computing the modules.

[Figs. S2 and S3](#) were generated by only using the modules computed from a subset of the genes from each exposure, respectively the concordant and the discordant genes.

Given an exposure and its associated table in [Supplementary Table S1](#), concordant genes were defined as up-regulated genes with hypo-methylated promoter or targeted by down-regulated miRNAs or down-regulated genes with hyper-methylated promoter or up-regulated targeting miRNAs. Discordant genes are defined as the complement of the concordant gene set with respect to the starting table.

All the data and associated statistics presented in this manuscript has been produced using R software environment. [9] The R code used to generate these datasets is provided in [Supplementary file S2](#).

Table 3
SMITE weights.

Feature/relationship	mRNA Expression	Gene promoter methylation	Gene body methylation	Targeting miRNA expression
Relationship with mRNA level	Direct correlation	Inverse correlation	Direct correlation	Inverse correlation
Weight	0.70	0.15	0.05	0.10

Acknowledgements

This study was supported by the Academy of Finland (Grant agreements 275151 and 292307), EU H2020 caLIBRatE Project (Grant agreement 686239), EU H2020 LIFEPAATH (Grant agreement 633666), and EU FP7 NANOSOLUTIONS Project (Grant agreement FP7-309329).

The authors would also wish to thank Hannu Norppa (FIOH) for providing the cell lines used in these study, Sirpa Hyttinen (FIOH) for her technical assistance, and Silvia Polidoro (HUGEf) for her valuable help with performing the genome-wide DNA methylation assays.

Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2018.05.107>.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2018.05.107>.

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