Gene expression profile and molecular pathway datasets resulting from benzo(a)pyrene exposure in the liver and testis of adult tilapia

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ABSTRACT

Benzo(a)pyrene (BaP), the prototype of polycyclic aromatic hydrocarbons, is known to exhibit genotoxic and carcinogenic effects promoting molecular impacts. The dataset presented here is associated with the research article paper entitled “Transcriptome Analysis Reveals Novel Insights Into the Response of Low-dose Benzo(a)pyrene Exposure in Male Tilapia”. In this article, we presented a transcriptomic characterization of male tilapia exposure to BaP in the short term. This data provides an extended analysis of changes in the gene expression and identification of pathways in the liver and testis of male tilapia exposure to BaP. We used gene set enrichment analysis (GSEA) and sub-network enrichment analysis (SNEA) to identify gene networks and pathways.
associated with molecular adverse effects of BaP exposure. The
data indicates that target pathways related to promoting carcino-
genesis such as DNA repair and DNA replication were affected as
well as other crucial biological processes. Moreover, to determine
whether some of the key reported genes of DNA damage are
affected by BaP exposure, Quantitative PCR (qPCR) was performed.
Gene set categories and sub-networks are provided and the cor-
responding signature differences from BaP exposure are listed. The
information in these datasets may contribute to understanding the
potential carcinogenesis mechanism of action from low BaP
exposure.

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| Specifications table |
|----------------------|
| Subject area         | Biology               |
| More specific subject area | Transcriptomics       |
| Type of data         | Table, text file.     |
| How data was acquired | mRNA data from RNA-Sequencing (RNA-Seq) technology and bioin-    |
|                      | foric analysis were used to identify a molecular signature and    |
|                      | pathways affected by BaP exposure.                                |
| Data format          | Filtered and analyzed.                                           |
| Experimental factors | Analysis of gene expression profile RNA-Seq data from a BaP   |
|                      | experiment                                                      |
| Experimental features| RNA-Seq reads were trimmed and the clean reads analyzed.         |
|                      | Gene read mapping, differential expression analysis (DE) and GSEA     |
|                      | and SNEA were performed from tilapia liver and testis tissue after     |
|                      | BaP-treatment.                                                   |
|                      | Quantitative PCR (qPCR) was used to evaluate the transcriptomic    |
|                      | changes observed in BaP-exposed male tilapia.                    |
| Data source location | Sample source and tissue harvest were located at Cinvestav-Merida,   |
|                      | Yucatan, Mexico. The BaP experiment was carried out at Cinvestav-    |
|                      | Merida. Sample analysis was performed at Cinvestav-Merida and the   |
|                      | University of Florida (Gainesville, FL, USA).                     |
| Data accessibility   | Transcriptomic data are presented in this article. All RNA-Seq data    |
|                      | were submitted to NCBI’s Gene Expression Omnibus (GEO) and can be    |
|                      | accessed via https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?      |
|                      | acc=GSE116687 (accession number GSE116687).                      |
| Related research article | [1] COLLI-DULA, R. C. et al. Transcriptome Analysis Reveals Novel   |
|                      | Insights Into the Response of Low-dose Benzo(a)pyrene Exposure in   |
|                      | Male Tilapia. Aquatic Toxicology, v. 201, n. 15, pp. 162–173, Aug 2018.
|                      | ISSN 0166-445 x .                                               |

Value of data

- The data explores the biological mechanism of action of BaP in the liver and testis of male tilapia by a high throughput transcriptomic approach (RNA-Sequencing).
- The data provides ample information of changes in gene expression, subnetworks and functional enrichment analysis associated with several biological processes after BaP treatment.
The molecular signature identified for BaP exposure is very useful to other researchers that may explore the mechanism of action of BaP in non-model organism such as tilapia.

- New gene sets associated with molecular adverse effects of BaP can be useful in understanding the role of BaP into the activation of apoptotic signals in tilapia.
- This data may contribute to understanding the BaP mechanisms associated with adverse effects in tilapia.

1. Data

These data sets provide information on the BaP molecular effects in tilapia testes and liver. Table 1 presents all the primer sets used for qPCR analysis. All primers used were previously validated as indicated in the $2^{-\Delta\Delta CT}$ method [2]. Of these genes evaluated, Cyp1b1, Ddit4, Gadd45b and Fasn showed significant changes in their levels of expression from BaP exposure ($p < 0.05$) (Table 5 in [1]). Table 2 presents a partial list of the characterization of gene expression profiling of RNA-data by BaP exposure. This data shows a larger number of altered genes in the liver related with adverse molecular effects on the cell cycle and with several other biological processes. Table 3 shows GO categories and Table 4 identifies gene networks altered by a low concentration of BaP in the liver and testis of male tilapia. All significantly altered genes are listed in Table SI as well as identified GO categories and subnetworks which are present.

2. Experimental design, materials and methods

Liver and testis samples were collected as were controls. Analysis of gene expression profile RNA-Seq was performed as is mentioned in [1]. Briefly, Tilapia RNA-Seq reads were trimmed, clean reads aligned to reference genome using Tophat [3,4]. Differential expression analysis was conducted using exact test with R package EdgeR ($p < 0.05$; fold change $> \pm 1.5$ were considered as significant). Elsevier PathwayStudioTM V9 (Elsevier, Inc., Rockville, MD, USA) operating with the ResNet 10.0 database was used to identify the biological mechanism that underlie the BaP effects. The gene set enrichment analysis (GSEA) and subnetwork enrichment analysis (SNEA) algorithms (applying the Mann–Whitney test with an alpha level of $p < 0.05$) [5–7]. Quantitative PCR (qPCR) was used to evaluate the transcriptomic changes of key genes such as Ddit4, Gadd45b and Igf2, Tet3 and Fasn involved in important functions, i.e, DNA damage, growth and development. The rpl8 gene was used as the internal reference normalizer gene.

| Gene symbols | Description | Forward primer 5′ → 3′ | Reverse primer 5′ → 3′ | Amplicon size (bp) | Aligned temp (°C) |
|--------------|-------------|-------------------------|------------------------|--------------------|------------------|
| CYP1B1       | Cytochrome P450, family 1, subfamily B, polypeptide 1 | gggctacacgtaccacaaaga agcgctctgggtcaaagata | 104 | 56 |
| GADD45       | Growth arrest and DNA damage inducible beta | gggagcggggtgagtttcagctcgctctgggtcaaagata | 84 | 58 |
| DDIT4        | DNA-damage-inducible transcript 4 | ttcctgggacgtcctggttg | 99 | 58 |
| IGF2         | Insulin-like growth factor 2 | gccctctctgctctggttg | 92 | 58 |
| TET3         | Tet methylcytosine dioxygenase 3 | aagggccctctggttg | 80 | 58 |
| FASN         | Fatty acid synthase | gacgacgctggcctacagc | 79 | 58 |
| RPL8         | Ribosomal Protein L8 | ggtgctgagttgcaggtgcat | 125 | 56 |
**Table 2**
Partial list of the characterization of gene expression profiling of RNA-data. Identified transcripts are involved with electron transport/ATP synthesis, DNA methylation, growth and development, cell cycle machinery and apoptotic signals.

**Characterization of gene expression profiling of tilapia RNA-seq data**

| HGNC symbol | Description | Liver | Testis |
|-------------|-------------|-------|--------|
| **Electron transport/ATP synthesis** | | | |
| ACLY | ATP citrate lyase a [Source:ZFIN;Acc:ZDB-GENE-031113-1] | -5.5 | 1.0 |
| ATP6V1E1A | ATPase, H+ transporting, lysosomal, V1 subunit E1a [Source:ZFIN;Acc:ZDB-GENE-041212-51] | 3.8 | 3.8 |
| ATAD2 | ATPase family, AAA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:30123] | -4.1 | 0.7 |
| ATAD2 | ATPase family, AAA domain containing 2 [Source:ZFIN;Acc:ZDB-GENE-030131-7003] | -2.1 | 1.2 |
| PSMD1 | proteasome 26S subunit, non-ATPase 1 [Source:ZFIN;Acc:ZDB-GENE-040426-810] | -1.6 | 2.1 |
| ABCE1 | ATP-binding cassette, sub-family E (OABP), member 1 [Source:ZFIN;Acc:ZDB-GENE-040426-1995] | 1.8 | 2.5 |
| ABCA3 | ATP-binding cassette, sub-family A (ABC1), member 3b [Source:ZFIN;Acc:ZDB-GENE-050517-2] | -1.7 | 1.1 |
| CFTR | cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7) [Source:ZFIN;Acc:ZDB-GENE-050517-20] | 2.2 | 3.1 |
| LIG1 | ligase I, DNA, ATP-dependent [Source:ZFIN;Acc:ZDB-GENE-110404-2] | 2.0 | 3.7 |
| NKAIN1 | Na+/K+ transporting ATPase interacting 1 [Source:ZFIN;Acc:ZDB-GENE-040426-1472] | 2.1 | 4.1 |
| TAP2 | ATP-binding cassette, sub-family B (MDR/TAP), member 3 like 1 [Source:ZFIN;Acc:ZDB-GENE-030616-245] | -2.9 | 4.5 |
| AGTPBP1 | ATP/GTP binding protein 1 [Source:ZFIN;Acc:ZDB-GENE-081104-267] | -1.7 | 4.6 |
| OPLAH | 5-oxoprolinase (ATP-hydrolysing) [Source:ZFIN;Acc:ZDB-GENE-121214-293] | 1.6 | 4.6 |
| ATP6V1C1 | ATPase, H+ transporting, lysosomal, V1 subunit C1b [Source:ZFIN;Acc:ZDB-GENE-041010-104] | -1.6 | 3.1 |
| ATP5I | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit Ea [Source:ZFIN;Acc:ZDB-GENE-070928-12] | -2 | 1.6 |
| ATP7A | ATPase, Cu++ transporting, alpha polypeptide [Source:ZFIN;Acc:ZDB-GENE-060825-45] | -2.2 | 1.8 |
| **Solute carrier families** | | | |
| SLC22A7 | solute carrier family 22 member 7 [Source:HGNC Symbol;Acc:HGNC:10971] | 5.6 | 2.0 |
| SLC22A7 | solute carrier family 22 member 7 [Source:HGNC Symbol;Acc:HGNC:10971] | 5.6 | 2.2 |
| SLC34A2 | solute carrier organic anion transporter family, member 2A1 [Source:ZFIN;Acc:ZDB-GENE-060606-3] | 2.4 | 1.5 |
| **DNA methylation** | | | |
| METTL21A | methyltransferase like 21A [Source:ZFIN;Acc:ZDB-GENE-050320-145] | 4.4 | 2.0 |
| HNMT | histamine N-methyltransferase [Source:HGNC Symbol;Acc:HGNC:5028] | 3.1 | 2.4 |
### Table 2 (continued)
Characterization of gene expression profiling of tilapia RNA-seq data

| HGNC symbol | Description | Liver | Testis |
|-------------|-------------|-------|--------|
|             | Fold change | p-value | Fold change | p-value |
| HMGCS1      | 3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) [Source:ZFIN;Acc:ZDB-GENE-040426-1042] | 2.8 | 1.0E–02 | 1.1 | NS |
| TRMT11      | tRNA methyltransferase 11 homolog (S. cerevisiae) [Source:ZFIN;Acc:ZDB-GENE-040426-953] | 2.6 | 2.8–02 | −1 | NS |
| METTL18     | methyltransferase like 18 [Source:HGNC Symbol;Acc:HGNC:28793] | 2.6 | 1.3E–02 | −1.2 | NS |
| TET3        | tetratetrahydrofolate reductase 3 [Source:ZFIN;Acc:ZDB-GENE-060526-109] | −2.1 | 1.6E–02 | −1.2 | NS |
| METTL5      | methyltransferase like 5 [Source:ZFIN;Acc:ZDB-GENE-041010-21] | −2.4 | 7.4E–03 | 1 | NS |
| DPY30       | dpy-30 histone methyltransferase complex regulatory subunit [Source:ZFIN;Acc:ZDB-GENE-040718-136] | −2.5 | 2.1E–03 | −1.1 | NS |
| TRMT44      | tRNA methyltransferase 44 homolog (S. cerevisiae) [Source:ZFIN;Acc:ZDB-GENE-041010-189] | −3 | 8.2E–03 | −1.2 | NS |

#### Growth and development

| HGNC symbol | Description | Liver | Testis |
|-------------|-------------|-------|--------|
| IGFBP3      | insulin-like growth factor binding protein 3 [Source:ZFIN;Acc:ZDB-GENE-040412-1] | 4.9 | 1.9E–02 | −1.4 | NS |
| RXFP4       | relaxin/insulin like family peptide receptor 4 [Source:HGNC Symbol;Acc:HGNC:14666] | 2.7 | 3.1E–02 | −1 | NS |
| IGF2        | insulin-like growth factor 2 [Source:RefSeq peptide;Acc:NP_001266572] | 2.5 | 1.8E–02 | 1.1 | NS |
| IGFBP7      | insulin-like growth factor binding protein 7 [Source:ZFIN;Acc:ZDB-GENE-040426-2423] | 1.8 | 3.0E–02 | 1 | NS |
| IGF2R       | insulin-like growth factor 2 receptor [Source:ZFIN;Acc:ZDB-GENE-041014-300] | −1.8 | 2.7E–02 | −1.1 | NS |
| THR6        | thyroid hormone receptor beta [Source:ZFIN;Acc:ZDB-GENE-990415-268] | −2 | 2.5E–03 | − | NS |
| THR5P       | thyroid hormone responsive [Source:ZFIN;Acc:ZDB-GENE-081022-19] | −4.8 | 1.3E–03 | − | NS |

#### Cell cycle machinery

| HGNC symbol | Description | Liver | Testis |
|-------------|-------------|-------|--------|
| CADM1       | cell adhesion molecule 1a [Source:ZFIN;Acc:ZDB-GENE-080505-2] | 8.2 | 1.3E–04 | −1.3 | NS |
| CEP152      | centrosomal protein 152 [Source:ZFIN;Acc:ZDB-GENE-111005-1] | 4.8 | 4.2E–04 | 1.2 | NS |
| CEP57       | centrosomal protein 57 [Source:HGNC Symbol;Acc:HGNC:30794] | 2.9 | 2.6E–03 | 1.1 | NS |
| CEP135      | centrosomal protein 135 [Source:ZFIN;Acc:ZDB-GENE-041210-325] | 2.3 | 3.4E–02 | −1.1 | NS |
| TACSTD2     | epithelial cell adhesion molecule [Source:ZFIN;Acc:ZDB-GENE-040426-2209] | 2.3 | 1.0E–03 | 1.2 | NS |
| NCAM1       | neural cell adhesion molecule 1a [Source:ZFIN;Acc:ZDB-GENE-990415-31] | −2.4 | 4.2E–02 | −1.5 | NS |
| CEBP4       | centromere protein W [Source:ZFIN;Acc:ZDB-GENE-100922-200] | −3.9 | 4.4E–02 | 1.1 | NS |
| CHL1        | cell adhesion molecule L1-like b [Source:ZFIN;Acc:ZDB-GENE-091105-1] | −4.3 | 1.4E–03 | 1.1 | NS |
| CENPF       | centromere protein F [Source:ZFIN;Acc:ZDB-GENE-041111-205] | −5.6 | 7.0E–04 | 1.3 | NS |
| NDC80       | NDC80 kinetochore complex component [Source:ZFIN;Acc:ZDB-GENE-030131-904] | −5.9 | 3.0E–03 | −1.0 | NS |
| GOS2        | G0/G1 Switch 2, Putative Lymphocyte G0/G1 Switch Gene | −8.2 | 7.5E–11 | −4.34 | 1.6E–14 |

#### Cyclin

| HGNC symbol | Description | Liver | Testis |
|-------------|-------------|-------|--------|
| CDK5        | cyclin dependent kinase like 5 [Source:HGNC Symbol;Acc:HGNC:11411] | 2.6 | 8.0E–03 | 1.20 | NS |
| CCNG1       | cyclin G1 [Source:ZFIN;Acc:ZDB-GENE-020322-1] | 2.2 | 3.8E–03 | −1.00 | NS |
| NUCKS1      | nuclear casein kinase and cyclin-dependent kinase substrate 1a [Source:ZFIN;Acc:ZDB-GENE-040912-175] | 2.0 | 9.9E–03 | 1.16 | NS |
| MRRF        | mitochondrial ribosome recycling factor [Source:ZFIN;Acc:ZDB-GENE-040704-12] | 2.0 | 2.4E–02 | −1.25 | NS |
| Gene Name                   | Description                                                                 | Abundance | p-value   | Fold Change | p-value   | Significance |
|----------------------------|------------------------------------------------------------------------------|-----------|-----------|-------------|-----------|--------------|
| **CDK6**                   | cyclin-dependent kinase 6 [Source:ZFIN;Acc:ZDB-GENE-060503-786]             | 1.9       | 2.0E-02   | 1.17        | NS        |              |
| **CCNI**                   | cyclin I [Source:ZFIN;Acc:ZDB-GENE-040426-2898]                              | 1.7       | 3.0E-02   | -1.15       | NS        |              |
| **CCNT2**                  | cyclin T2b [Source:ZFIN;Acc:ZDB-GENE-030131-183]                             | 1.6       | 4.1E-02   | 1.01        | NS        |              |
| **CCNG2**                  | cyclin G2 [Source:ZFIN;Acc:ZDB-GENE-021016-1]                                | -2.1      | 1.6E-02   | -1.28       | NS        |              |
| **CCNB2**                  | cyclin B2 [Source:ZFIN;Acc:ZDB-GENE-030426-12]                               | -2.1      | 1.3E-02   | -1.07       | NS        |              |
| **CNNM1**                  | cyclin and CBS domain divalent metal cation transport mediator 1             | -2.2      | 9.8E-03   | 1.05        | NS        |              |
| **CDK1**                   | cyclin-dependent kinase 1 [Source:ZFIN;Acc:ZDB-GENE-010320-1]               | 3.2       | 9.3E-03   | 1.16        | NS        |              |
| **CCNB3**                  | cyclin B3 [Source:ZFIN;Acc:ZDB-GENE-060929-684]                              | 1.29      | 4.5E-04   | -1.04       | NS        |              |
| **Mitotic spindle dynamics**|                                                                              |           |           |             |           |              |
| **MZT2B**                  | mitotic spindle organizing protein 2B [Source:ZFIN;Acc:ZDB-GENE-040801-87]   | 2.3       | 3.4E-02   | -1.2        | NS        |              |
| **CDK2**                   | cyclin-dependent kinase 2 [Source:ZFIN;Acc:ZDB-GENE-040426-2741]             | -2.4      | 4.8E-02   | 1.11        | NS        |              |
| **NUSAP1**                 | nucleolar and spindle associated protein 1 [Source:ZFIN;Acc:ZDB-GENE-030827-5] | -3.5      | 3.4E-03   | -1.1        | NS        |              |
| **BUB1**                   | BUB1 mitotic checkpoint serine/threonine kinase [Source:ZFIN;Acc:ZDB-GENE-081104-75] | -4.5      | 6.1E-03   | -1.0        | NS        |              |
| **PLK1**                   | polo-like kinase 1 [Drosophila] [Source:ZFIN;Acc:ZDB-GENE-021115-7]         | -8.1      | 3.8E-04   | -1.0        | NS        |              |
| **Apoptotic signals**      |                                                                              |           |           |             |           |              |
| **VWA11**                  | von Willebrand factor A domain containing 11 [Source:ZFIN;Acc:ZDB-GENE-141211-58] | 44.3      | 1.0E-08   | 5           | 1.4E-02  |              |
| **ID4**                    | inhibitor of DNA binding 4 [Source:ZFIN;Acc:ZDB-GENE-051113-208]            | 2.2       | 1.2E-03   | -2.2        | NS        |              |
| **TBRG4**                  | transforming growth factor beta regulator 4 [Source:ZFIN;Acc:ZDB-GENE-091020-8] | 1.9       | 4.4E-02   | 1.2         | NS        |              |
| **TIGAR**                  | tp53-induced glycolysis and apoptosis regulator a [Source:ZFIN;Acc:ZDB-GENE-060312-25] | 1.6       | 3.2E-02   | -1.4        | NS        |              |
| **RABGAP1**                | RAB GTase activating protein 1 [Source:HGNC Symbol;Acc:HGNC:17155]          | -1.7      | 2.9E-02   | -1.1        | NS        |              |
| **RAB6C**                  | RAB6A, member RAS oncogene family [Source:ZFIN;Acc:ZDB-GENE-040426-2849]     | -1.8      | 1.7E-02   | 1.1         | NS        |              |
| **RAB4B-EGLN2**            | RAB4B, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9782]         | -2.4      | 4.2E-02   | 1.4         | NS        |              |
| **DDIT3**                  | DNA-damage-inducible transcript 3 [Source:ZFIN;Acc:ZDB-GENE-070410-90]      | -2.4      | 9.7E-03   | -1.1        | NS        |              |
| **RASGEF1B**               | RasGEF domain family member 1B [Source:HGNC Symbol;Acc:HGNC:24881]          | -3.2      | 1.9E-03   | -2.2        | NS        |              |
| **RASLI1A**                | RAS-like, family 11, member A [Source:ZFIN;Acc:ZDB-GENE-050417-384]         | -4.5      | 2.0E-04   | -1.5        | NS        |              |
| **RAB29**                  | RAB29, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9798]         | -5.1      | 5.0E-03   | -1.1        | NS        |              |
| **DDIT4L**                 | DNA damage inducible transcript 4 like [Source:HGNC Symbol;Acc:HGNC:30555]   | -9.3      | 2.0E-04   | -1.2        | NS        |              |
| **Others**                 |                                                                              |           |           |             |           |              |
| **KRT4**                   | keratin 4 [Source:ZFIN;Acc:ZDB-GENE-000607-83]                               | 7.1       | 2.1E-02   | 6           | 1.79E-02 |              |
| **ASTL**                   | six-cysteine containing astatin protease 1 [Source:ZFIN;Acc:ZDB-GENE-070621-1] | 6.1       | 8.3E-08   | 4.7         | 3.61E-04 |              |
| **RNY5K2P275**             | RNY5K2P275 (RNA, 75K Small Nuclear Pseudogene 275) is a Pseudogene            | 6.1       | 1.3E-02   | -2.3        | 2.78E-02 |              |
| **BPIFC**                  | BPI Fold Containing Family C                                                 | 4.6       | 1.0E-02   | 3.5         | 4.06E-02 |              |
| **ITI1H**                  | inter-alpha-trypsin inhibitor heavy chain 1 [Source:ZFIN;Acc:ZDB-GENE-130530-650] | 4         | 7.2E-06   | 2           | 3.16E-02 |              |
| **PENK**                   | proenkephalin a [Source:ZFIN;Acc:ZDB-GENE-030729-31]                        | 3.1       | 2.2E-02   | -4.4        | 2.81E-02 |              |
| **PGLYRP2**                | peptidoglycan recognition protein 2 [Source:HGNC Symbol;Acc:HGNC:30013]     | 2.8       | 1.6E-03   | 4.6         | 1.74E-02 |              |
| **DIO2**                   | Iodothyronine Deiodinase 2                                                   | 2.8       | 0.003     | 1.2         | NS        |              |
| **LECT2**                  | leukocyte cell derived chemotaxin 2 [Source:HGNC Symbol;Acc:HGNC:6550]       | 2.5       | 7.00E-04  | 16.6        | 2.20E-06 |              |
| **APOA1**                  | apolipoprotein A-la [Source:ZFIN;Acc:ZDB-GENE-990415-14]                    | 1.7       | 3.40E-02  | 4.7         | 4.18E-03 |              |
| **APOAI**                  | apolipoprotein A [Source:HGNC Symbol;Acc:HGNC:616]                          | 1.7       | 2.80E-02  | 3.7         | 1.53E-02 |              |
| **NCOA7**                  | Nuclear Receptor Coactivator 7                                               | -10.2     | 4.60E-15  | -2.7        | 4.00E-02 |              |
Table 3
Representative list of GO terms significantly affected in the liver and testis of male tilapia exposed to BaP. Determined by Gene Set Enrichment Analysis (GSEA; \( p < 0.05 \), fold change \( \geq 10\% \)).

| Tissue    | Gene set category | Name                                                   | Median fold change | \( p\)-value |
|-----------|-------------------|--------------------------------------------------------|--------------------|-------------|
| Liver     | Biological process| mitosis                                                | -2.8               | 1.9E – 04   |
|           |                   | cell cycle                                             | -2.5               | 2.7E – 04   |
|           |                   | triglyceride biosynthetic process                      | -3.0               | 7.9E – 04   |
|           |                   | long-chain fatty-acyl-CoA biosynthetic process         | -3.2               | 8.2E – 04   |
|           |                   | mitotic cytokinesis                                    | -6.6               | 1.1E – 03   |
|           |                   | cell-cell signaling                                    | 2.9                | 1.1E – 03   |
|           |                   | G2-M transition of mitotic cell cycle                  | -2.4               | 1.3E – 03   |
|           |                   | cytokinesis                                            | -5.8               | 1.7E – 03   |
|           |                   | cellular response to calcium ion                       | -3.3               | 2.5E – 03   |
|           |                   | cellular response to organic substance                 | -3.9               | 3.3E – 03   |
|           |                   | synaptic transmission                                  | -2.0               | 4.5E – 03   |
|           |                   | peptidyl-serine phosphorylation                       | -2.6               | 4.7E – 03   |
|           |                   | mitotic cell cycle                                     | -2.4               | 7.3E – 03   |
|           |                   | activation of MAPK activity                            | -2.1               | 7.7E – 03   |
|           |                   | cell division                                          | -2.4               | 1.1E – 02   |
|           |                   | lipid homeostasis                                      | -5.0               | 1.3E – 02   |
|           |                   | exocytosis                                             | -3.4               | 1.4E – 02   |
|           |                   | mitotic spindle assembly checkpoint                    | -4.5               | 1.5E – 02   |
|           |                   | response to ethanol                                    | -2.3               | 1.8E – 02   |
|           |                   | cellular response to glucose stimulus                 | -2.0               | 2.0E – 02   |
|           |                   | negative regulation of signal transduction            | 2.1                | 2.0E – 02   |
|           |                   | DNA metabolic process                                  | -4.2               | 2.0E – 02   |
|           |                   | fatty acid biosynthetic process                       | -2.7               | 2.1E – 02   |
|           |                   | microtubule-based movement                            | -3.2               | 2.4E – 02   |
|           |                   | cytokine-mediated signaling pathway                   | -2.2               | 2.4E – 02   |
|           |                   | epidermis development                                  | 2.1                | 2.4E – 02   |
|           |                   | positive regulation of MAPK cascade                   | 2.5                | 2.5E – 02   |
|           |                   | sterol biosynthetic process                           | 3.1                | 2.5E – 02   |
|           |                   | cellular lipid metabolic process                      | -2.5               | 2.7E – 02   |
|           |                   | positive regulation of JUN kinase activity            | -3.9               | 3.0E – 02   |
|           |                   | apoptotic process                                      | -2.1               | 3.1E – 02   |
|           |                   | cell surface receptor signaling pathway               | 1.8                | 3.2E – 02   |
|           |                   | response to testosterone                             | -2.5               | 3.2E – 02   |
|           |                   | lipid catabolic process                               | -3.2               | 3.2E – 02   |
|           |                   | actin cytoskeleton reorganization                     | -2.2               | 3.3E – 02   |
|           |                   | meiotic nuclear division                              | -3.4               | 3.9E – 02   |
|           |                   | positive regulation of gene expression               | -2.1               | 3.9E – 02   |
|           |                   | immune system process                                 | -1.7               | 4.4E – 02   |
|           |                   | biosynthetic process                                  | 2.9                | 4.6E – 02   |
|           | Cellular component| spindle pole                                           | -5.2               | 4.4E – 05   |
|           |                   | chromosome, centromeric region                        | -3.5               | 1.8E – 04   |
|           |                   | kinetochore                                            | -4.5               | 3.5E – 04   |
|           |                   | proteinaceous extracellular matrix                    | -2.1               | 1.8E – 03   |
|           |                   | condensed chromosome kinetochore                      | -4.5               | 2.1E – 03   |
|           |                   | spindle                                               | -2.8               | 2.8E – 03   |
|           |                   | chromosome                                            | -2.4               | 3.3E – 03   |
|           |                   | spindle microtubule                                    | -3.5               | 4.3E – 03   |
|           |                   | external side of plasma membrane                      | -1.9               | 4.5E – 03   |
|           |                   | extracellular region                                  | -1.6               | 9.1E – 03   |
|           |                   | anchored component of membrane                        | -2.6               | 1.8E – 02   |
|           |                   | axon                                                  | -2.4               | 2.6E – 02   |
|           |                   | cell-cell junction                                     | -1.7               | 2.7E – 02   |
|           |                   | cytoskeleton                                          | -2.1               | 2.8E – 02   |
|           |                   | kinesin complex                                       | -4.6               | 2.9E – 02   |
|           |                   | microtubule                                           | -2.4               | 2.9E – 02   |
|           |                   | cell                                                  | -2.2               | 3.3E – 02   |
|           |                   | microtubule organizing center                         | -2.0               | 4.0E – 02   |
|           | Molecular function| iron ion binding                                      | -2.3               | 1.1E – 03   |
|           |                   | protein C-terminus binding                            | -2.7               | 1.1E – 03   |
| Tissue | Gene set category | Name | Median fold change | p-value |
|--------|-------------------|------|--------------------|---------|
|        | microtubule binding | -2.7 | 3.2E–03            |
|        | heme binding      | -1.9 | 4.2E–03            |
|        | protein heterodimerization activity | -2.4 | 5.8E–03            |
|        | protein serine-threonine kinase activity | -2.1 | 7.7E–03            |
|        | hormone activity  | 2.5  | 9.0E–03            |
|        | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 2.5  | 9.6E–03            |
|        | growth factor activity | 2.5  | 1.2E–02            |
|        | drug binding      | -3.3 | 1.2E–02            |
|        | metallopeptidase activity | -1.9 | 1.6E–02            |
|        | microtubule motor activity | -3.2 | 1.8E–02            |
|        | protein homodimerization activity | -2.2 | 2.8E–02            |
|        | calmodulin binding | -2.4 | 4.3E–02            |
|        | structural constituent of cytoskeleton | -2.7 | 4.7E–02            |
|        | carbohydrate binding | -2.0 | 4.8E–02            |
|        | sequence-specific DNA binding RNA polymerase II transcription factor activity | -2.4 | 4.9E–02            |
| Testis | Biological process | regulation of proteolysis | 9.3  | 9.4E–06            |
|        | proteolysis       | 10.0 | 7.1E–05            |
|        | leukotriene biosynthetic process | 15.5 | 5.1E–04            |
|        | negative regulation of endopeptidase activity | 9.3  | 9.6E–04            |
|        | hemostasis        | 10.3 | 2.3E–03            |
|        | oxygen transport  | -7.5 | 5.9E–03            |
|        | protein heterooligomerization | -7.5 | 5.9E–03            |
|        | wound healing     | 7.5  | 7.3E–03            |
|        | fibrinolysis      | 6.0  | 1.6E–02            |
|        | cobalamin metabolic process | 11.1 | 1.8E–02            |
|        | cellular protein metabolic process | 8.6  | 3.0E–02            |
|        | response to calcium ion | 5.5  | 3.7E–02            |
|        | inflammatory response | 3.6  | 4.1E–02            |
|        | response to peptide hormone | 9.3  | 4.4E–02            |
|        | response to cytokine | 9.3  | 4.8E–02            |
|        | Cellular component | extracellular space | 5.0  | 2.7E–06            |
|        | extracellular region | 3.3  | 6.7E–05            |
|        | keratin filament  | 6.0  | 1.8E–04            |
|        | intermediate filament | 6.0  | 3.7E–04            |
|        | hemoglobin complex | -7.5 | 4.1E–04            |
|        | Golgi lumen       | -4.2 | 1.5E–03            |
|        | anchored component of external side of plasma membrane | 15.5 | 5.6E–03            |
|        | secretory granule | 8.6  | 2.7E–02            |
|        | platelet alpha granule | 9.3  | 3.1E–02            |

Table 4
Partial list of subnetworks significantly affected in the liver and testis of male tilapia exposed to BaP (p < 0.05, fold change \( \geq 10\% \)).

| Tissue       | Gene set seed                        | Median fold change | p-value |
|--------------|--------------------------------------|--------------------|---------|
| Liver        | kinetochore assembly                 | -3.2               | 2.5E–04 |
|              | telophase                            | -3.8               | 5.4E–04 |
|              | microtubule cytoskeleton assembly    | -2.2               | 8.3E–04 |
|              | anaphase                             | -3.1               | 9.7E–04 |
|              | mitotic spindle positioning          | -3.2               | 1.4E–03 |
|              | meiosis                              | -2.2               | 2.1E–03 |
|              | mitotic nuclear membrane assembly/ disassembly | -3.2 | 2.3E–03 |
| Tissue | Gene set seed | Median fold change | p-value |
|--------|---------------|-------------------|---------|
| microtubule/kinetochore interaction | −5.6 | 2.6E−03 |
| mitotic checkpoint | −3.2 | 3.0E−03 |
| mitotic spindle checkpoint | −3.2 | 3.2E−03 |
| nuclear division | −3.2 | 4.7E−03 |
| mitotic spindle assembly | −4.2 | 8.3E−03 |
| meiosis II | −4.5 | 8.8E−03 |
| fatty acid oxidation | −2.3 | 9.1E−03 |
| nuclear fragmentation | −2.3 | 9.7E−03 |
| sister chromatid cohesion | −3.2 | 1.0E−02 |
| chromosome condensation | −2.4 | 1.1E−02 |
| mitotic spindle orientation | 2.4 | 1.1E−02 |
| spindle assembly | −2.7 | 1.4E−02 |
| Schwann cell migration | −3.2 | 1.5E−02 |
| DNA replication during S phase | −3.9 | 1.7E−02 |
| mitotic prometaphase | −3.2 | 1.7E−02 |
| mesenchymal stem cell differentiation | −1.9 | 1.8E−02 |
| synapase maturation | −2.4 | 2.0E−02 |
| monocyte differentiation | −2.5 | 2.0E−02 |
| mitotic sister chromatid segregation | −3.2 | 2.6E−02 |
| mitotic metaphase plate congression | −3.2 | 2.7E−02 |
| chromosome segregation | −2.8 | 2.8E−02 |
| regulation of action potential | 1.7 | 2.9E−02 |
| adipogenesis | −2.2 | 3.0E−02 |
| nerve sprouting | −2.4 | 3.0E−02 |
| interphase | −2.4 | 3.0E−02 |
| microtubule bundling | −2.8 | 3.1E−02 |
| cellular extravasation | −3.1 | 3.1E−02 |
| lipid oxidation | −3.0 | 3.5E−02 |
| blood-retinal barrier | −2.0 | 3.7E−02 |
| Glycogen degradation | −2.2 | 3.8E−02 |
| Testis | blood clotting | 5.5 | 5.2E−04 |
| neutrophil chemotaxis | 5.5 | 7.3E−04 |
| fibrinolysis | 5.6 | 9.1E−04 |
| blood vessel permeability | 3.7 | 1.2E−03 |
| myoblast proliferation | 7.5 | 1.4E−03 |
| muscle fiber development | 5.8 | 4.4E−03 |
| blood clot lysis | 5.8 | 5.6E−03 |
| T-cell homeostasis | −2.3 | 5.7E−03 |
| neutrophil recruitment | 3.6 | 7.6E−03 |
| degranulation | 3.9 | 7.9E−03 |
| fibroblast proliferation | 3.3 | 8.2E−03 |
| neutrophil adhesion | 3.1 | 8.7E−03 |
| autolysis | 7.5 | 1.1E−02 |
| zymogen activation | 5.6 | 1.1E−02 |
| complement activation | 5.0 | 1.2E−02 |
| hemolysis | 3.0 | 1.5E−02 |
| chondrocyte proliferation | 2.9 | 1.6E−02 |
| neutrophil extravasation | 5.6 | 1.9E−02 |
| skin changes | 7.5 | 1.9E−02 |
| blood coagulation, intrinsic pathway | 5.8 | 2.0E−02 |
| cellular extravasation | 3.6 | 2.1E−02 |
| hepatic regeneration | 3.7 | 2.3E−02 |
| myoblast fusion | 3.2 | 2.3E−02 |
| neutrophil migration | 3.3 | 2.7E−02 |
| bacterial load | 4.7 | 2.8E−02 |
| antigen expression | 4.5 | 3.1E−02 |
| positive chemotaxis | 3.6 | 3.2E−02 |
| superoxide anion generation | 3.3 | 3.3E−02 |
| neutrophil activation | 3.6 | 3.4E−02 |
| immune cell chemotaxis | 3.6 | 3.5E−02 |
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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.2018.08.206.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2018.08.206.

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Table 4 (continued)

| Tissue                        | Gene set seed | Median fold change | p-value |
|-------------------------------|---------------|--------------------|---------|
| hepatocyte apoptosis          | 5.8           | 3.7E−02            |
| dendritic cell differentiation | 3.3           | 3.8E−02            |
| tissue invasion               | 5.0           | 3.8E−02            |
| muscle fiber contraction      | 3.0           | 3.9E−02            |
| myoblast differentiation      | 5.8           | 4.3E−02            |
| epidermal cell differentiation| 6.0           | 4.4E−02            |
| innate immune response        | 3.3           | 4.4E−02            |
| leukocyte recruitment         | 3.1           | 4.7E−02            |