**Supplementary information**

**Transcriptome changes of *Takifugu obscurus* liver after acute exposure to the oxygenated-PAHs 9,10-phenanthrenequione**

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**Fig. S1. Length distribution of genes.**

**Table S1. Primer sequences used for quantitative real-time PCR.**

|  |  |
| --- | --- |
| Gene name | Primer sequence |
| bnip3lb-F | 5'-AAGAGGAGGTGGTGGACAAGGAG-3' |
| bnip3lb-R | 5'-CTGAGCATCACAGAGCGACGAG-3' |
| gpx1a-F | 5'-GTGGCGTCACTCTGAGGAACAAC-3' |
| gpx1a-R | 5'-AACCACCTCCAGGACGGACATAC-3' |
| hk1-F | 5'-GTGCAGTGTATCAGCGACTTCCTC-3' |
| hk1-R | 5'-AGCAGTCCAACCACATCCTCTCC-3' |
| IGF1R-F | 5'-CGTTCGGTGTGGTGCTGTGG-3' |
| IGF1R-R | 5'-CAGGAAGGACGGACGCATCTTG-3' |
| nme2b.1-F | 5'-AGTCCAGACCAGGCAGCATCC-3' |
| nme2b.1-R | 5'-CTTGGCGTTCTCCAGCGTGTC-3' |
| pik3cd-F | 5'-CTCCACTGCCGCTGAAGAAGAAC-3' |
| pik3cd-R | 5'-ACCTCCGTGCTCGTCACCATC-3' |
| sik1-F | 5'-CTCCTCCACTGGCTGCTCCTC-3' |
| sik1-R | 5'-GGCGTCTGCTGGCTGATGTG-3' |
| smad7-F | 5'-GCTGAAGAGGCTGTCTTGCTGTG-3' |
| smad7-R | 5'-GTTCGCAGAGTCGGCTCATGTG-3' |
| β-actin-F | 5'-CATCACCATCGGCAACGAGAGG-3' |
| β-actin-R | 5'-CGTCGCACTTCATGATGCTGTTG-3' |

**Table S2. Statistics of clean sequencing data.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample name | Clean reads number (M) | Clean base Number (M) | Q20 ratio | GC content (%) |
| 9,10-PQ-R1 | 24.43 | 3,665.19 | 98.41% | 50.98 |
| 9,10-PQ-R2 | 23.88 | 3,581.94 | 98.51% | 52.16 |
| 9,10-PQR3 | 23.81 | 3,570.92 | 98.56% | 52.00 |
| Control-R1 | 24.51 | 3,676.76 | 98.47% | 50.62 |
| Control-R2 | 24.67 | 3,700.77 | 98.53% | 50.86 |
| Control-R3 | 23.86 | 3,579.71 | 98.53% | 50.51 |

**Table S3. Change folds of genes enriched in KEGG pathways.** Change folds represent the times of expression level in 9,10-PQ treatment compared with the control. \* indicates significant difference between 9,10-PQ treatment and the control by Student’s t-test (P < 0.05).

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene name** | **Change fold** |
| **ko00010 Glycolysis/Gluconeogenesis** | | |
| ENSTRUG00000008209 | phosphoenolpyruvate carboxykinase (PCK) | 0.36 |
| ENSTRUG00000015558 | alcohol dehydrogenase class-3 (ADH) | 0.40\* |
| ENSTRUG00000015762 | FBPase 2.5 | 0.41 |
| ENSTRUG00000002288 | phosphoglucomutase 2 (PGM2) | 0.48 |
| ENSTRUG00000008984 | triosephosphate isomerase (TIM/TPI) | 2.65\* |
| ENSTRUG00000017358 | glyceraldehyde-3-phosphate dehydrogenase 2 (GAPDH) | 2.68 |
| ENSTRUG00000009070 | enolase 1 (ENO1) | 3.06 |
| ENSTRUG00000002415 | hexokinase 1 (HK1) | 3.21 |
| ENSTRUG00000011575 | ATP-dependent 6-phosphofructokinase, liver type (ATP-PFK) | 3.25 |
| ENSTRUG00000017142 | fructose-bisphosphate aldolase C-B (FBA) | 3.68 |
| ENSTRUG00000007592 | phosphoglycerate mutase 1 (PGAM1) | 9.78 |
| ENSTRUG00000004795 | ATP-dependent 6-phosphofructokinase, platelet type (ATP-PFK) | 12.68\* |
| ENSTRUG00000010800 | L-lactate dehydrogenase A chain (LDHA) | 23.44 |
| ENSTRUG00000016548 | glucokinase (GK) | 33.97 |
| **ko00100** **Steroid biosynthesis** | | |
| ENSTRUG00000009132 | squalene epoxidase (SQLE) | 0.07\* |
| ENSTRUG00000018507 | 25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial (CYP27B1) | 0.10 |
| ENSTRUG00000013093 | lanosterol synthase (LSS) | 0.31 |
| ENSTRUG00000017301 | vitamin D 25-hydroxylase (CYP2R1) | 0.33 |
| ENSTRUG00000018343 | 1,25-dihydroxyvitamin D (3) 24-hydroxylase, mitochondrial (CYP24A1) | 0.30 |
| ENSTRUG00000015761 | methylsterol monooxygenase 1 (MSMO1) | 0.35\* |
| ENSTRUG00000006606 | sterol O-acyltransferase 1 (SOAT1) | 0.38 |
| ENSTRUG00000013309 | lanosterol 14-alpha demethylase (CYP51A1) | 0.38\* |
| ENSTRUG00000016297 | 24-dehydrocholesterol reductase (DHCR24) | 0.43\* |
| **ko04068 FoxO signaling pathway** | | |
| ENSTRUG00000008209 | phosphoenolpyruvate carboxykinase (PEPCK) | 0.36 |
| ENSTRUG00000010851 | growth arrest and DNA damage-inducible protein GADD45 beta (GADD45b) | 2.77 |
| ENSTRUG00000007584 | phosphatidylinositol 3-kinase regulatory subunit alpha (PI3Ka) | 2.65 |
| ENSTRUG00000009972 | insulin receptor substrate 2 (IRS2) | 2.58 |
| ENSTRUG00000002784 | serum/glucocorticoid regulated kinase 1 (SGK1) | 2.66 |
| ENSTRUG00000001816 | G1/S-specific cyclin-D2 (CCND2) | 3.42\* |
| ENSTRUG00000004751 | TGF-beta receptor type-1 (TGF-β) | 3.26 |
| ENSTRUG00000001458 | forkhead box O3 (FOXO3) | 4.00\* |
| ENSTRUG00000013228 | polo like kinase 2 (PLK2) | 4.13\* |
| ENSTRUG00000012281 | insulin receptor (INSR) | 4.12 |
| ENSTRUG00000005173 | insulin-like growth factor 1 receptor (IGF-1R) | 4.21\* |
| ENSTRUG00000010895 | G1/S-specific cyclin-D2 (CCND2) | 4.74\* |
| ENSTRUG00000010193 | phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta (PIK3CD) | 5.59\* |
| ENSTRUG00000014802 | SMAD family member 3 (SMAD3) | 6.86 |
| **ko04145 Phagosome** | | |
| ENSTRUG00000009578 | calreticulin (CALR3) | 0.33 |
| ENSTRUG00000004597 | calreticulin (CALR) | 0.36 |
| ENSTRUG00000008876 | SEC61 translocon alpha 1 subunit (SEC61a1) | 0.39 |
| ENSTRUG00000002296 | major histocompatibility complex class I-related gene protein (MHC-I) | 2.54\* |
| ENSTRUG00000002063 | transferrin receptor (TFRC) | 2.56 |
| ENSTRUG00000000566 | cathepsin S | 2.58 |
| ENSTRUG00000000441 | toll-like receptor 2 (TLRs) | 3.09\* |
| ENSTRUG00000018123 | thrombospondin-1 (TSP-1) | 4.22\* |
| ENSTRUG00000002062 | H-2 class II histocompatibility antigen, E-S beta chain (HLA) | 10.36\* |

**Table S4. Top 20 of up-regulated DEGs in 9,10-PQ treatment.** Change folds represent the times of expression level in 9,10-PQ treatment compared with the control.

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene name** | **Change fold** |
| ENSTRUG00000007386 | Unknown | 310.04 |
| ENSTRUG00000004002 | Unknown | 206.81 |
| ENSTRUG00000000779 | nucleoside diphosphate kinase B (NDPK-B) | 148.03 |
| ENSTRUG00000001124 | Unknown | 137.76 |
| ENSTRUG00000014982 | SKI family transcriptional corepressor 1b (SKOR1B) | 106.07 |
| ENSTRUG00000006175 | Unknown | 71.52 |
| ENSTRUG00000008365 | Unknown | 55.94 |
| ENSTRUG00000005187 | male germ cell-associated kinase (MAK) | 55.62 |
| ENSTRUG00000002095 | Unknown | 36.70 |
| ENSTRUG00000017967 | Unknown | 36.33 |
| ENSTRUG00000007914 | DNA damage-inducible transcript 4 protein (DDIT4) | 35.76 |
| ENSTRUG00000011143 | Unknown | 33.64 |
| ENSTRUG00000016548 | glucokinase (GK) | 33.15 |
| ENSTRUG00000012715 | ATP-binding cassette, sub-family G (WHITE), member 2b (ABCG2B) | 27.30 |
| ENSTRUG00000012406 | heat shock protein 90, alpha (cytosolic), class A member 1, tandem duplicate 1 (HSP90AA1.1) | 27.14 |
| ENSTRUG00000007710 | solute carrier family 2 member 3b (SLC2A3B) | 26.37 |
| ENSTRUG00000006334 | Unknown | 26.24 |
| ENSTRUG00000010800 | L-lactate dehydrogenase A chain (LDHA) | 24.69 |
| ENSTRUG00000003712 | Unknown | 19.53 |
| ENSTRUG00000014418 | Unknown | 18.96 |

**Table S5.** **Top 20 of down-regulated DEGs up 9,10-PQ treatment.** Change folds represent the times of expression level in 9,10-PQ treatment compared with the control.

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene name** | **Change fold** |
| ENSTRUG00000009847 | unknown | 0.1263 |
| ENSTRUG00000018670 | lectin, mannose-binding 2a (LMAN2LA) | 0.1236 |
| ENSTRUG00000000138 | unknown | 0.1117 |
| ENSTRUG00000000962 | unknown | 0.1024 |
| ENSTRUG00000003410 | DnaJ (Hsp40) homolog, subfamily C, member 3a (DNAJC3A) | 0.1005 |
| ENSTRUG00000016254 | aquaporin 12 (AQP12) | 0.1000 |
| ENSTRUG00000004316 | unknown | 0.0979 |
| ENSTRUG00000003123 | cytosolic sulfotransferase 3 (SULT) | 0.0973 |
| ENSTRUG00000004087 | hypoxia up-regulated 1 (HYOU1) | 0.0962 |
| ENSTRUG00000018507 | 25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial (CYP27B1) | 0.0934 |
| ENSTRUG00000019060 | unknown | 0.0921 |
| ENSTRUG00000018680 | unknown | 0.0719 |
| ENSTRUG00000009132 | squalene epoxidase (SQLE) | 0.0652 |
| ENSTRUG00000018678 | unknown | 0.0610 |
| ENSTRUG00000001907 | NLR family CARD domain-containing protein 3 (NLRC3) | 0.0572 |
| ENSTRUG00000011939 | zona pellucida sperm-binding protein 3 (ZP3) | 0.0571 |
| ENSTRUG00000012416 | ADP-ribosylation factor-like 13A (ARL13A) | 0.0215 |
| ENSTRUG00000000701 | extracellular serine/threonine protein kinase Fam20C (FAM20C3) | 0.0209 |
| ENSTRUG00000018336 | hydroperoxide isomerase ALOXE3 (ALOXE3) | 0.0071 |
| ENSTRUG00000014523 | unknown | 0.0030 |