# Supporting Information

# Modulation of Benzo[a]pyrene-induced Toxic Effects in Japanese Medaka (*Oryzias latipes*) by 2,2′,4,4′-Tetrabromodiphenyl Ether

Yanbin ZHAO, Kai LUO, Zhanlan FAN, Chong HUANG, and Jianying HU*

MOE Laboratory for Earth Surface Processes, College of Urban and Environmental Sciences, Peking University, Beijing 100871, China

**Address for Correspondence**

Prof. Dr. Jianying HU

College of Urban and Environmental Sciences

Peking University, Yi Fu Second Building

Beijing 100871 China

TEL & FAX: 86-10-62765520

Email: hujy@urban.pku.edu.cn

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**Chemicals and Reagents for Analysis.** BaP, BDE-47, and their surrogate standards, perylene-$d_{14}$ and PCB153 were obtained from AccuStandard (New haven, Connecticut, USA). BaP-3sulfate were obtained from Midwest Research Institute, NCI Chemical Carcinogen Repository (Kansas City, MO, USA). E2 and E2-$d_3$ were obtained from Wako Pure Chemical Industries, Ltd. (Tokyo, Japan). All solvents (dichloromethane, methanol, acetonitrile and hexane) were HPLC grade purchased from Fisher Scientific (New Jersey, USA). Sodium chloride, sodium sulfate and aluminum oxide were analytical grade and heated at 400°C for 4 hours before use.

**GC-MS Analysis of BaP and BDE47.** Identification and quantification of BDE47 and BaP were performed using a gas chromatography-electron capture negative ionization mass spectrometry (GC-ENCI-MS) (Shimadzu QP 2010 plus, Japan) and a gas chromatography-electron impact-mass spectrometry (GC-EI-MS) (Alilent 6890N GC; Alilent 5975C inert XL MSD), respectively. Chromatographic separation was achieved on a DB-5MS capillary column (30m × 0.25 mm × 0.1 μm film thickness; J&W Scientific, USA). A splitless injector was used and the injector was maintained at 250°C. For BaP analysis, the temperature program was from 110°C (1 min) to 180°C at the rate of 10°C/min, then increased to 220°C (5 min) at the rate of 5°C/min, and then to 310°C (5 min) at a rate of 20°C/min. For BDE47 analysis, the temperature program was from 110°C (1 min) to 180°C at the rate of 10°C/min, then increased to 220°C (5 min) at the rate of 5°C/min, and then to 310°C (5 min) at a rate of 20°C/min. The interface and ion temperatures were 320°C and 280°C, respectively. The carrier gas was helium at a constant flow rate of 2 ml/min. Data acquisition was conducted in selected ion monitoring mode.

**UPLC-MS/MS for BaP-3-Sulfate Analysis.** The concentrations of BaP-3-Sul in each exposure groups were determined every two weeks through the exposure period. Equal volumes (15 ml) of test water samples collected from both chambers of each exposure group were combined, and then extracted through the SPE C18 cartridges (500mg, 6cc, Waters Sep-Pek), which were preconditioned with 6 mL methanol and 6 mL distilled water. The cartridges were dried under nitrogen flow and then the target analytes were subsequently eluted with 6 mL methanol. The eluates were evaporated to dryness under a gentle stream of nitrogen and reconstituted with 0.2 ml of methanol for UPLC-MS/MS analysis. The recovery for spiked samples was 95.85±0.42%, and the MDL was 0.0007 ng/L.

The LC apparatus was an Acquity Ultra Performance LC (Waters, USA). Acquity UPLC® BEH C8 column (100 × 2.1 mm, 1.7 μm particle size) (Waters, USA) was used for separation. The column was maintained at 40°C at a flow rate of 0.3 mL/min, and the injection volume was 5 μL. Methanol and ultrapure water containing 0.1% $NH_4OH$ (v/v) were used as mobile phases. Methanol was initially increased linearly from 10% to 50% within 1.0 min, and then increased to 100% at 4 min and kept for 1.0 min, followed by a decrease to initial conditions of 10% and held for 2 min to allow for equilibration. Mass spectrometry was performed using a Premier XE tandem quadrupole mass spectrometer (Waters, USA) equipped with a Z-Spray ionization (ESI) source in the negative ion mode. The optimized parameters were as follows: source temperature, 110°C; desolvation temperature, 350°C; capillary voltage, 2.50 kV; desolvation gas flow, 800 L/h; cone gas flow, 50 L/h.

**UPLC-MS/MS for Estrogen Analysis.** The whole medaka fish (about 0.4 g wet weight) was freeze-dried and spiked with 10 ng E2-$d_3$ as surrogate standard. The sample was then

63 extracted with 8 mL of methanol/acetonitrile (1:1, v/v) three times by ultrasonication of 10
64 min. The homogenate was centrifuged at 6000 r/s for 10 min and the supernatants were
65 decanted into an eggplant-shaped flask to be combined. The collected extract was dried using
66 a rotary evaporator and redissolved with 6 mL of methanol/methyl tert-butyl ether (1:1, v/v).
67 The solution then was normally passed through a NH2-SPE cartridge preconditioned with 6
68 mL of methanol/methyl tert-butyl ether (1:1, v/v). The filtrate was collected, then dried and
69 redissolved in 0.2 mL of ethyl acetate and 1.8 mL of hexane. The mixed solution was applied
70 to silica cartridges (3 mL, 500 mg, Waters) which had been preconditioned with 4 mL
71 water-saturated ethyl acetate and 4 mL hexane/ethyl acetate (90:10, v/v). After the cartridges
72 were rinsed with 3 mL of hexane/ethyl acetate (90:10, v/v), the fraction containing 17β-E2
73 was eluted with 3 mL of hexane/ethyl acetate (38:62, v/v). The elution was dried and
74 redissolved with 1 mL hexane-methylene chloride (DCM) (1:1, v/v), and then passed through
75 the preconditioned Florisil cartridges (6 mL, 1 g, Waters). 10 mL of a mixture of
76 hexane-DCM (1:1, v/v) were discarded and the fraction containing all estrogens was eluted
77 with 6 mL of acetone-DCM (1:9, v/v). The solution was evaporated to dryness under a gentle
78 stream of nitrogen and reconstituted with 0.2 mL of methonal for LC-ESI-MS/MS analysis.
79 The recovery of E2-$d_3$ was 82%±6%, and the recovery of E2 for spiked samples was
80 88%±11%. The MDL of E2 were 0.2 ng/g dry weight (dw).

81 The LC apparatus was an Acquity Ultra Performance LC (Waters, USA). Acquity
82 UPLC® BEH C8 column (100 × 2.1 mm, 1.7 μm particle size) (Waters, USA) was used for
83 separation. The column was maintained at 40°C at a flow rate of 0.3 mL/min and the injection
84 volume was 5 μL. Methanol and ultrapure water were used as mobile phases. Methanol was

initially increased linearly from 10% to 50% in 0.5 min, to 80% in the next 5.5 min, to 100% in the following 1.0 min, and kept for 1.0 min. The column was then equilibrated for 3.0 min.

Mass spectrometry was performed using a Quattro Premier™ XE detector (Waters, USA) which was operated with ESI in the negative ion (NI) mode. The detection conditions of the mass spectrometer were as follows: capillary voltage, 3.0 kV; source temperature, 110°C; desolvation temperature, 400°C; desolvation gas flow, 800 L/h; and cone gas flow, 50 L/h. Finally, the data acquisition was performed under time-segmented conditions based on the chromatographic separation of the target compounds to maximize sensitivity of detection (Table S1).

**TABLE S1.** Parameters for Analyzing Estrogens by LC-ESI-MS/MS

| Compound | MRM transition | Cone voltage (V) | Collision energy (eV) |
|---|---|---|---|
| 17β-estradiol (E2) | 271 > 145 | 60 | 48 |
| | 271 > 183 | | 38 |
| 17β-estradiol-$d_3$ (E2-$d_3$) | 274 > 185 | 58 | 46 |

**TABLE S2.** Primers and their Amplicon Size (L) and Efficiency (E) for Quantitative Real-time PCR.

| Gene symble | Gene full name | Accession No. | Sequences (first row, forward primers; second row, reverse primers) | L (bp) | E (%) |
|---|---|---|---|---|---|
| RPL-7 | Ribosomal protein L7 | DQ118296 | 5'-CGCCAGATCTTCAACGGTGTAT-3'<br>5'-AGGCTCAGCAATCCTCAGCAT-3' | 72 | 99 |
| VTG-1 | Vitellogenin 1 | AB064320 | 5'-CTCCAGCTTTGAGGCCATTTAC-3'<br>5'-ACAGCACGGACAGTGACAACA-3' | 81 | 97 |
| P53 | tumor protein 53 | U57306.1 | 5'-TCTGGAAACCGAGGGTCTGG-3'<br>5'-TTTTTGGGCTGCGTTTTCTG-3' | 117 | 98 |
| CYP11 | cytochrome P450 cholesterol side-chain cleavage | EF537029 | 5'-TTGCCGTGAGTCTGCAAAGATA-3'<br>5'-AAAGTCCCAGCCGGGATGT-3' | 73 | 95 |
| CYP17 | P-450 17alpha- hydroxylase/ C17,20-lyase | D87121 | 5'-CCCCTGGTTACAGATTTTTCCC-3'<br>5'-TGCAGCAGCTGGTCTCTAACTG-3' | 78 | 96 |
| 17β-HSD 1 | 17-beta hydroxysteroid dehydrogenase type 1 | EF530597 | 5'-CTTGGCTGGAATGAAAGCACA-3'<br>5'-TGAAAGGAAGCCCATGGAGTC-3' | 80 | 96 |
| 17β-HSD 3 | 17-beta hydroxysteroid dehydrogenase type 3 | EF530598 | 5'-TCTTATACAGGCAGTGGCTCCA-3'<br>5'-GGTAAAAAGGTCACCCTGTTGG-3' | 81 | 91 |
| CYP19A | cytochrome P450, family 19, subfamily A | D82968 | 5'-GCGTAGAGCCCTTTTCGATGA-3'<br>5'-TGCGGCCCGTATTCAAGAT-3' | 80 | 93 |
| 20β-HSD | 20-beta-hydroxysteroid Dehydrogenase | EF537021 | 5'-GATGTGGACAGCATCAGCACTG-3'<br>5'-AGTCGTGTCTGCCACCTTGAAC-3' | 108 | 101 |
| CYP1A | cytochrome P450 1A | AY297923 | 5'-ATCGGCCTGAATCGAAATCC-3'<br>5'-TGTGTCCCTTGTTGTGCAGTGT-3' | 132 | 98 |
| CYP1B | cytochrome P450 1B | JF894387 | 5'-GCTGTTTCTCTTCGTGGCATTA-3'<br>5'-CGATGTCATAGGCGTGAGGTTT-3' | 119 | 93 |
| CYP2A | cytochrome P450 2A | EF546459 | 5'- ATATGGGATCGGGATCAGCAA-3'<br>5'- CCGCAGCGTCGTCAGAGTG-3' | 70 | 102 |
| CYP2C | cytochrome P450 2C | NP* | 5'-AGGAGAAAATGCAGGAGGAGATC-3'<br>5'-GTGAGGGAGGCTGAAAGGTGT-3' | 146 | 96 |
| CYP3A | cytochrome P450 3A | AF105018 | 5'-AGGAAACAGAGATCCCCTTCGA-3'<br>5'-AGGCACCAGCTTCAGAAAGATG-3' | 80 | 94 |
| EHPX1 | Epoxide hydrolase1 | NP | 5'-CCTTCTACGAGTTCTACGGGATTC-3'<br>5'-ATGTTGGTCGTGATGAGGGAG-3' | 232 | 95 |
| EHPX2 | Epoxide hydrolase2 | NP | 5'-GGTTTTCTGTCCAGCATTTACTCC-3'<br>5'-CTGGCCTGGCTTTCTTTTACAC-3' | 125 | 97 |
| GSTA | Microsomal glutathione S-transferase alpha | NP | 5'-TGAATTTGATGAGATGTATTTGAC-3'<br>5'-TTTTGCTTTACTCTGAATGTTGTCC-3' | 298 | 95 |
| GSTM | Microsomal glutathione S-transferase 1 | NP | 5'-CATCACCAGAGGGTCTTTTGTCA-3'<br>5'-AGCCAGGATGTAGGAAATCGTGT-3' | 256 | 104 |
| GSTP1 | Microsomal glutathione S-transferase P | NP | 5'-AATGGCAATGACTCTGGCTTACT-3'<br>5'-AGCTTCACCACAGACATAAAACTTG-3' | 115 | 94 |
| UGT1A | UDP glucuronosyltransferase 1 family, polypeptide A1 | EF546456 | 5'-TGACCTTTTAGCCCATCCCAA-3'<br>5'-GCAGATGCCCTCATAGATTCCA-3' | 76 | 101 |
| UGT2A | UDP-glucuronosyltransferase 2 family, polypeptide A | EF546458 | 5'-AGATCTGCCCGCTGACTTAGCT-3'<br>5'-CATTCTGTGGCAGCCAATCAA-3' | 140 | 90 |
| SULT1 | sulfotransferase 1 | EF546450 | 5'-AGAGAATCCTCGCCGTGAAGTT-3'<br>5'-CCACGATTTGGTTGATGACCTC-3' | 83 | 91 |

*Nucleotide sequence which was identified in our lab and not published

**TABLE S3.** Mean Numbers of Spawned Eggs per Female per Day, Prevalence of Skeletal Deformation, Protein Content of Egg, VTG-1 Transcription Level and E2 Concentration.

| **Single BaP exposure groups** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Measured BaP Concentration (μg/L) | ND[a] | 0.033 | 0.034 | 0.235 | 1.602 | 11.356 | | |
| Egg number /female /day | 18.11±1.57 | 16.60±1.41 | 12.76±1.14 | 13.46±1.51 | 10.84±0.88 | 7.96±0.92 | | |
| Prevalence of skeletal deformation (%) | 0.02±0.01 | 0.04±0.01 | 0.10±0.02 | 0.08±0.02 | 0.12±0.03 | 0.22±0.03 | | |
| Protein content per/egg (μg) | 89.19±3.10 | 84.79±2.54 | 78.82±4.43 | 80.39±2.15 | 68.76±2.09 | 60.91±3.32 | | |
| **BaP and BDE47 coexposure groups** | | | | | | | | |
| Measured BaP Concentration (μg/L) | ND | ND | ND | ND | 1.206 | 0.950 | 0.564 | 0.464 |
| Measured BDE47 Concentration (μg/L) | ND | 0.039 | 0.771 | 5.377 | ND | 0.053 | 0.439 | 2.584 |
| Egg number /female /day | 14.86±1.16 | 13.62±1.72 | 14.47±1.99 | 15.18±1.23 | 8.23±0.88 | 8.01±1.15 | 12.29±0.60 | 13.80±1.19 |
| Prevalence of skeletal deformation (%) | 0.01±0.01 | 0.01±0.01 | 0.02±0.01 | 0.02±0.01 | 0.10±0.02 | 0.09±0.01 | 0.19±0.02 | 0.16±0.02 |
| Protein content per/egg (μg) | 89.91±3.61 | 87.33±2.44 | 90.82±3.71 | 85.44±3.87 | 63.11±3.15 | 59.72±3.32 | 90.98±3.69 | 97.12±3.50 |
| mRNA expression of VTG1 | 1.000±0.134 | 1.413±0.115 | 1.708±0.133 | 1.562±0.156 | 0.597±0.131 | 1.052±0.166 | 1.159±0.208 | 1.655±0.157 |
| Concentration of 17β-$E_2$ (ng/g d.w.) | 3.22±0.30 | 3.31±0.34 | 2.61±0.30 | 2.93±0.26 | 0.83±0.16 | 0.68±0.35 | 2.25±0.57 | 3.07±0.65 |

Data are presented as means±standard errors. [a]ND: not detected.

**TABLE S4.** Relative mRNA Expressions of Steroidogenesis Enzyme Genes and *p*53 Gene in Gonad and Phase I and Phase II Metabolism Enzyme Genes in Liver of Medaka Fish [α].

| | DMSO | 0.039μg/L BDE47 | 0.771 μg/L BDE47 | 5.377 μg/L BDE47 | - | 0.053 μg/L BDE47 | 0.439 μg/L BDE47 | 2.584 μg/L BDE47 |
|---|---|---|---|---|---|---|---|---|
| | | | | | 1.206 μg/L BaP | 0.950 μg/L BaP | 0.564 μg/L BaP | 0.464 μg/L BaP |
| **Steroidogenesis Enzyme Genes** | | | | | | | | |
| **Female** | | | | | | | | |
| CYP11 | 1.00±0.14 | 1.06±0.08 | 1.36±0.18 | 1.15±0.23 | 1.29±0.39 | 1.03±0.53 | 1.15±0.18 | 0.82±0.33 |
| CYP17 | 1.00±0.44 | 0.87±0.12 | 0.85±0.05 | 0.73±0.17 | 0.92±0.23 | 0.63±0.30 | **0.43±0.15*** [#] | 0.57±0.21 |
| 17β-HSD1 | 1.00±0.23 | 1.18±0.16 | 1.57±0.31 | 1.65±0.42 | **0.49±0.35*** | 0.56±0.39 | 0.92±0.18 | **1.51±0.16**[#] |
| 17β-HSD3 | 1.00±0.18 | 1.42±0.41 | 0.78±0.18 | 0.72±0.51 | 0.96±0.20 | 0.69±0.30 | 0.67±0.56 | **0.38±0.31*** [#] |
| CYP19A | 1.00±0.58 | 1.67±0.27 | 1.09±0.27 | 0.90±0.11 | 1.16±0.42 | 0.72±0.56 | 0.54±0.20 | 0.62±0.35 |
| 20β-HSD | 1.00±0.31 | 1.02±0.77 | 0.77±0.76 | 0.73±0.88 | 0.62±0.83 | 1.41±0.20 | 0.96±0.30 | 0.80±0.69 |
| **Male** | | | | | | | | |
| CYP11 | 1.00±0.21 | 1.13±0.13 | 0.96±0.10 | 0.81±0.25 | 1.01±0.32 | 0.77±0.20 | 1.14±0.14 | 1.32±0.20 |
| CYP17 | 1.00±0.38 | 1.68±0.22 | 1.10±0.14 | 0.94±0.13 | 1.09 ±0.39 | 0.80±0.05 | 0.97±0.37 | 0.75±0.25 |
| 17β-HSD1 | 1.00±0.42 | 0.72±0.38 | 1.41±0.22 | 1.60±0.50 | **0.58±0.24*** | 0.73±0.65 | 1.37±0.38 | **1.80±0.47**[#] |
| 17β-HSD3 | 1.00±0.19 | 1.91±0.45 | 1.64±0.33 | 0.89±0.20 | 1.70±0.47 | 1.30±0.21 | 0.78±0.35 | 0.97±0.13 |
| CYP19A | 1.00±0.23 | 0.63±0.28 | 0.83±0.04 | **0.32±0.09*** | 0.83±0.41 | 0.95±0.45 | 0.94±0.23 | 0.88±0.41 |
| 20β-HSD | 1.00±0.32 | 0.59±0.68 | 0.85±0.21 | 0.65±0.13 | 0.88±0.21 | 0.88±0.22 | 0.88±0.40 | 0.74±0.44 |
| **Phase I Metabolism Enzyme Genes** | | | | | | | | |
| **Female** | | | | | | | | |
| CYP1A | 1.00±0.54 | 1.19±0.41 | 0.62±0.35 | 0.71±0.55 | **3.06±0.37*** | **3.70±0.91*** | **2.33±0.63*** | **1.63±0.31**[#] |
| CYP1B | 1.00±0.44 | 1.43±0.19 | 1.14±0.36 | 0.70±0.25 | 1.54±0.26 | 1.73±0.52 | 0.88±0.21 | 1.07±0.24 |
| CYP2A | 1.00±0.24 | 0.77±0.72 | 0.89±0.51 | 0.69±0.13 | 1.66±0.54 | 1.64±0.94 | 1.25±0.62 | 0.76±0.21 |
| CYP2C | 1.00±0.37 | 1.18±0.55 | 1.02±0.50 | 0.72±0.31 | 1.55±0.39 | 1.36±0.15 | 0.76±0.32 | **0.50±0.17**[#] |
| CYP3A | 1.00±0.27 | 1.62±0.49 | **2.01±0.37*** | **2.29±0.46*** | 0.80±0.37 | 0.64±0.17 | **2.75±0.59*** [#] | **3.10±1.06*** [#] |
| EHPX1 | 1.00±0.19 | 1.64±0.32 | **1.80±0.29*** | 1.34±0.20 | 1.73±0.15 | 1.53±0.52 | 1.17±0.24 | 1.30±0.13 |
| EHPX2 | 1.00±0.22 | 1.32±0.07 | 1.39±0.30 | 1.17±0.13 | 1.62±0.11 | **2.65±0.33*** | 1.64±0.67 | 0.96±0.02 |
| **Male** | | | | | | | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| CYP1A | 1.00±0.77 | 1.20±0.14 | 1.46±0.48 | 1.80±0.31 | 1.66±0.37 | 1.39±0.63 | **3.55±0.81*** # | **5.28±1.13*** # |
| CYP1B | 1.00±0.33 | 0.88±0.20 | 1.04±0.12 | 1.42±0.33 | 0.76±0.40 | 0.81±0.16 | 1.45±0.68 | **1.93±0.25*** # |
| CYP2A | 1.00±0.42 | 0.60±0.47 | 0.93±0.11 | 1.33±0.11 | 0.82±0.22 | 0.78±0.68 | 0.93±0.81 | 0.74±0.26 |
| CYP2C | 1.00±0.47 | 0.72±0.13 | 0.84±0.04 | 0.99±0.18 | 0.69±0.18 | **0.43±0.18*** | 1.07±0.45 | 0.77±0.09 |
| CYP3A | 1.00±0.56 | 1.24±0.37 | **1.83±0.19*** | **2.05±0.24*** | 0.75±0.20 | 0.90±0.49 | 1.70±0.26 | **1.86±0.17**# |
| EHPX1 | 1.00±0.11 | 0.88±0.20 | 1.08±0.23 | 0.88±0.15 | 1.20±0.20 | **0.24±0.33*** # | 1.06±0.07 | 0.83±0.41 |
| EHPX2 | 1.00±0.16 | 0.96±0.06 | 1.20±0.27 | 0.88±0.09 | 0.61±0.24 | 0.49±0.34 | 1.12±0.11 | 1.05±0.40 |
| **Phase II Metabolism Enzyme Genes** | | | | | | | | |
| **Female** | | | | | | | | |
| GSTA | 1.00±0.37 | 1.39±0.40 | 1.91±0.45 | **2.11±0.30*** | **0.48±0.22*** | **0.34±0.43*** | **2.27±0.45*** # | **1.71±0.18**# |
| GSTM | 1.00±0.73 | 1.15±0.48 | 1.44±0.62 | 1.29±0.55 | 1.42±0.15 | 1.35±0.85 | 0.62±0.08 | 1.21±0.31 |
| GSTP1 | 1.00±0.32 | **2.70±0.26*** | **5.55±0.32*** | **2.88±0.17*** | 1.38±0.33 | **2.31±0.33*** # | **3.44±0.23*** # | **2.85±0.23*** # |
| UGT1A | 1.00±0.23 | 1.10±034 | 1.12±0.08 | 0.97±0.33 | 1.43±0.22 | **1.86±0.12*** | 1.24±0.15 | 0.98±0.15 |
| UGT2A | 1.00±0.26 | **0.52±0.38*** | **0.55±0.48*** | **0.25±0.38*** | 0.93±0.58 | **1.95±0.02*** | **0.44±0.32*** | 0.66±0.42 |
| SULT1 | 1.00±0.33 | 1.60±0.41 | 1.30±0.48 | 1.09±0.56 | 1.38±0.21 | 1.71±0.40 | 0.92±0.18 | 0.85±0.24 |
| **Male** | | | | | | | | |
| GSTA | 1.00±0.24 | 0.99±0.27 | 1.39±0.35 | 1.37±0.27 | **0.44±0.29*** | **0.33±0.51*** | **1.40±0.25**# | 1.13±0.39 |
| GSTM | 1.00±0.62 | 1.90±1.02 | 1.15±0.19 | 1.57±0.27 | 0.58±0.45 | 0.43±0.36 | 1.55±0.20 | 1.78±0.98 |
| GSTP1 | 1.00±0.25 | 0.96±0.32 | 1.67±0.21 | 1.63±0.29 | 0.56±0.42 | **0.38±0.26*** | **2.99±0.13*** # | **2.15±0.21*** # |
| UGT1A | 1.00±0.41 | 0.81±0.46 | 1.18±0.06 | 1.49±0.29 | 0.76±0.38 | 0.56±0.91 | 2.01±1.14 | 1.12±0.38 |
| UGT2A | 1.00±0.32 | **0.28±0.37*** | **0.31±0.12*** | **0.38±0.40*** | 0.70±0.80 | **0.18±0.64*** # | 0.67±0.58 | 0.62±0.83 |
| SULT1 | 1.00±0.21 | 0.80±0.25 | 0.89±0.33 | 0.74±0.26 | 0.61±0.43 | 0.44±0.71 | 1.25±0.60 | 0.98±0.62 |
| **Gene Involved in DNA Damage** | | | | | | | | |
| **Female** | | | | | | | | |
| P53 | 1.00±0.46 | 1.30±0.12 | 1.24±0.18 | 1.27±0.23 | 1.10±0.24 | 1.34±0.27 | 0.99±0.46 | 0.95±0.20 |
| **Male** | | | | | | | | |
| P53 | 1.00±0.23 | 1.01±0.07 | 0.99±0.37 | 1.22±0.57 | 0.96±0.31 | 1.07±0.22 | **1.64±0.26*** | **2.36±0.49*** # |

[α] Relative mRNA expression was calculated using RPL-7 as the internal control. The fold-change values are relative to expression in controls. Data are presented as means ± standard deviation (n=6). *: statistically significant differences between results of exposure group and results of the DMSO control. #: statistically significant differences between results in co-exposure of BaP and BDE47 and results of the 25 μg/L single BaP exposure group. -: The BaP control.