# Supplementary material

Table S1. Primer sequences for gene expression analysis

| Marker | Gene name | Gene symbol | Entrez Gene ID | Primer sequence (5´→3´) |
|---|---|---|---|---|
| **Oxidative Stress** | NAD(P)H: ehydrogenase, quinone 1 | *Nqo1* | 18104 | F: CAATCAGCGTTCGGAATTACGA |
| | | | | R:GCCAGTACAATCAGGGCTCTTC |
| | Superoxide dismutase 1 | *Sod1* | 20655 | F: GATTAACTGAAGGCCAGCATG |
| | | | | R: GTCATCTTGTTTCTCATGGACC |
| | Heme oxygenase 1 | *Hmox1* | 15368 | F: GGAGATAGAGCGCAACAAGC |
| | | | | R: CCATACCAGAAGGCCATGTC |
| **Xenobiotic metabolism** | Cytochrome P450, family 2, subfamily e, polypeptide 1 | *Cyp2e1* | 1571 | F: GGATGAATATGCCCTACATG |
| | | | | R: TGATGGGCAGCAGGTCTCAT |
| | Cytochrome P450, family 1, subfamily A, polypeptide 1 | *Cyp1a1* | 13076 | F: TCTCGTGGAGCCTCATGTACCT |
| | | | | R: TGCCGATCTCTGCCAATCA |
| | Aryl-hydrocarbon receptor (Ahr), transcript variant 2 | *Ahr* | 11622 | F: CGTCCCTGCATCCCACTACTT |
| | | | | R: GGACATGGCCCCAGCATAG |
| **Apoptosis** | Caspase 3 | *Casp 3* | 12367 | F: TCCTGGTCTTTGTACGCTACCA |
| | | | | R: CCTGATGTCGAAGTTGAGGTAGCT |
| | B cell leukemia/lymphoma 2 (Bcl2), transcript variant 1 | *Bcl2* | 12043 | F: GGTGGTGGAGGAACTCTTCA |
| | | | | R: ACGCTCTCCACACACATGAC |
| | Protein 53 (Trp53), transcript variant X4 | *Trp53* | 22059 | F: CACCACGCTGTGGCGAAAAGTCTG |
| | | | | R: CTCAAAAAACTTACCAGGGC |
| **Metabolismo de lípidos** | peroxisome proliferator activated receptor gamma, transcript variant X | *Ppar-γ* | 19016 | F: CTGCTCAAGTATGGTGTCCATGA |
| | | | | R: TGAGATGAGGACTCCATCTTTATTCA |
| **Inflammation** | Interleukin 1A | *IL1a* | 16175 | F: TGGCCAAAGTTCCTGACTTGTTTG |
| | | | | R:CAGGCTATTTAACCAAGTGGTGCT |
| **Housekeeping** | Glyceraldehyde-3-phosphate dehydrogenase | *Gapdh* | 14433 | F: CCTCGTCCCGTAGACAAAATG |
| | | | | R:TGAAGGGGTCGTTGATGGC |
| | Beta-actin | *Actb* | 11461 | F: CTTTGCAGCTCCTTCGTTGC |
| | | | | R: ACGATGGAGGGGAATACAGC |

F: Forward; R: Reverse

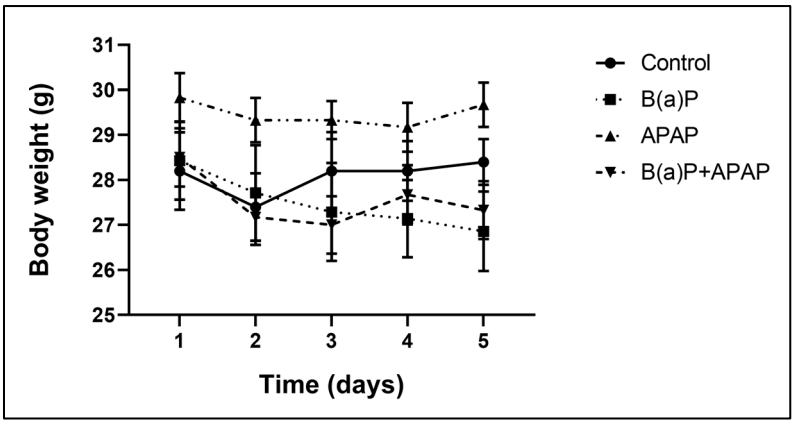


Figure S1. Body weight of the experimental groups.

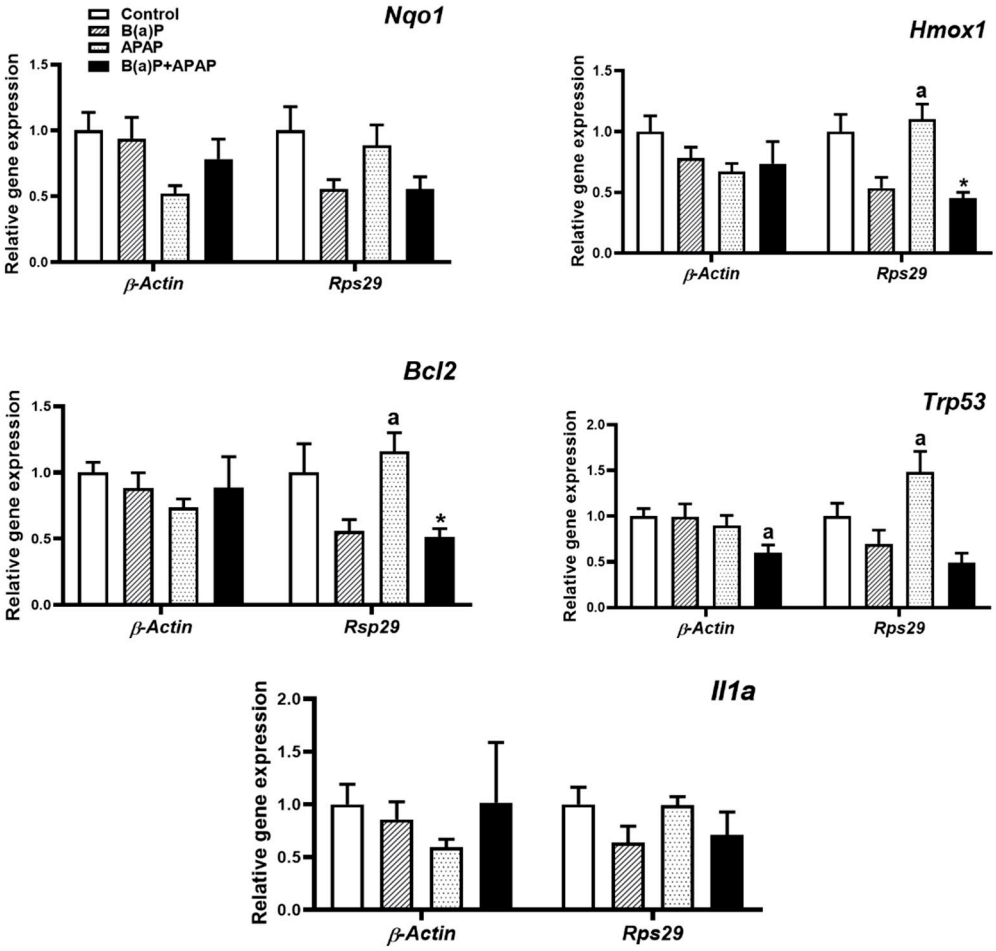


Figure S2. Relative gene expression in liver of ICR mice exposed to different treatment. Expression was normalized against β-Actin and Rps29 (Housekeeping genes). Data are expressed as mean ± SEM. Significant difference when compared to control (*), and B[a]P (a). The level of significance was set at $p<0.05$.

Table S2. Relative gene expression for experimental groups

| GENE | RELATIVE GENE EXPRESSION | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | HK1 | | | | HK2 | | | |
| | Control | B[a]P | APAP | B[a]P+ APAP | Control | B[a]P | APAP | B[a]P+ APAP |
| ***Ahr*** | 1 ±0.09 | 0.62±0.09 | 0.76±0.07 | 0.44±0.09$^{ab}$ | 1±0.11 | 0.43±0.07$^{b}$ | 1.29±0.18 | 0.35±0.08$^{ab}$ |
| ***Cyp1a1*** | 1±0.18 | 106.40±27.69$^{b}$ | 0.59±0.05 | 1325±1084$^{ab}$ | 1±0.28 | 63.11±15.24$^{ab}$ | 0.93±0.13 | 705.8±472.70$^{ab}$ |
| ***Cyp2e1*** | 1±0.11 | 0.73±0.18 | 0.80±0.06 | 0.47±0.15 | 1±0.06 | 0.55±0.15$^{b}$ | 1.38±0.15 | 0.39±0.10$^{ab}$ |
| ***Sod1*** | 1±0.12 | 0.97±0.34 | 0.60±0.05 | 0.27±0.08$^{abc}$ | 1±0.04 | 0.57±0.12 | 1.02±0.08 | 0.20±0.04$^{ab}$ |
| ***Ppar-γ*** | 1±0.09 | 0.77±0.10 | 0.62±0.03 | 0.56±0.14$^{a}$ | 1±0.12 | 0.52±0.08$^{ab}$ | 1.05±0.11 | 0.38±0.07$^{ab}$ |
| ***Casp3*** | 1±0.15 | 0.52±0.06 | 0.45±0.04 | 0.42±0.11$^{a}$ | 1±0.13 | 0.35±0.04$^{ab}$ | 0.77±0.10 | 0.29±0.04$^{ab}$ |
| ***Nqo1*** | 1±0.14 | 0.94±0.16 | 0.52±0.06 | 0.78±0.15 | 1±0.18 | 0.56±0.07 | 0.89±0.15 | 0.56±0.09 |
| ***Hmox1*** | 1±0.13 | 0.78±0.09 | 0.67±0.07 | 0.74±0.18 | 1±0.14 | 0.54±0.09$^{ab}$ | 1.10±0.12 | 0.45±0.05$^{ab}$ |
| ***Bcl2*** | 1±0.08 | 0.88±0.12 | 0.73±0.07 | 0.89±0.23 | 1±0.22 | 0.56±0.08$^{b}$ | 1.16±0.14 | 0.51±0.07$^{ab}$ |
| ***Trp53*** | 1±0.08 | 0.99±0.14 | 0.90±0.11 | 0.60±0.09 | 1±0.14 | 0.70±0.15 | 1.48±0.23 | 0.49±0.11$^{ab}$ |
| ***Il1a*** | 1±0.19 | 0.86±0.17 | 0.59±0.08 | 1.02±0.57 | 1±0.16 | 0.64±0.15 | 0.99±0.08 | 0.71±0.22 |

HK1. Houskeeping 1: β-Actin, HK2. Houskeeping 2: Rps29.
Data are expressed as mean ± SEM. Significant difference ($p$<0.05) when compared to control (a), APAP (b), or B[a]P (c).

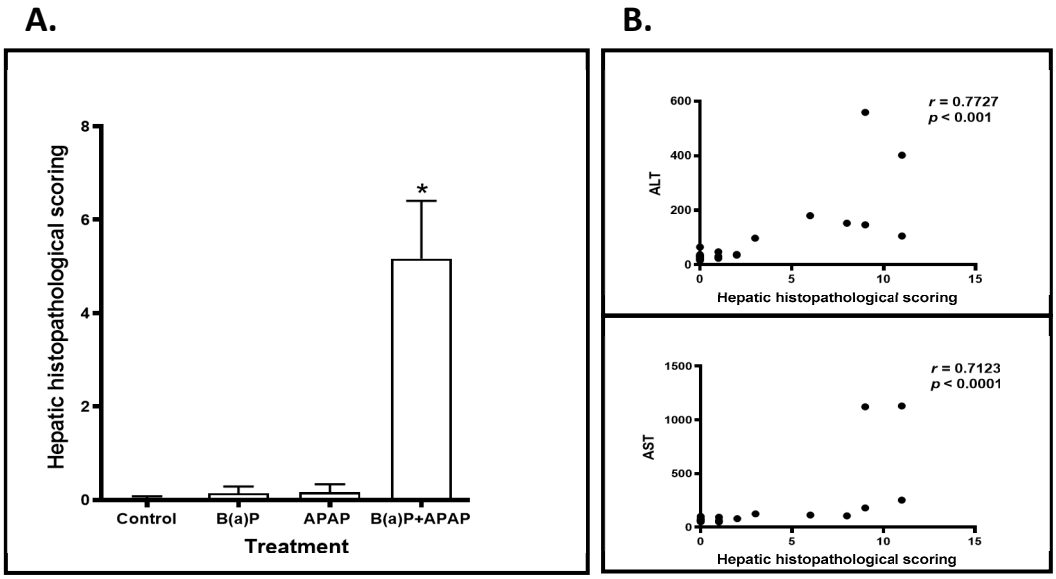


Figure S3. Effects of B[a]P/APAP on hepatic morphology and transaminase levels on ICR mice. A. Hepatic histopathological scoring calculated as the sum of scores for each parameter based on the scoring system described in ‘‘Materials and Methods’’. B. Spearman correlations between hepatic histopathological scores and serum transaminase activities. Data are expressed as mean ± SEM. Asterisks indicate statistical differences between means ($p$<0.05).