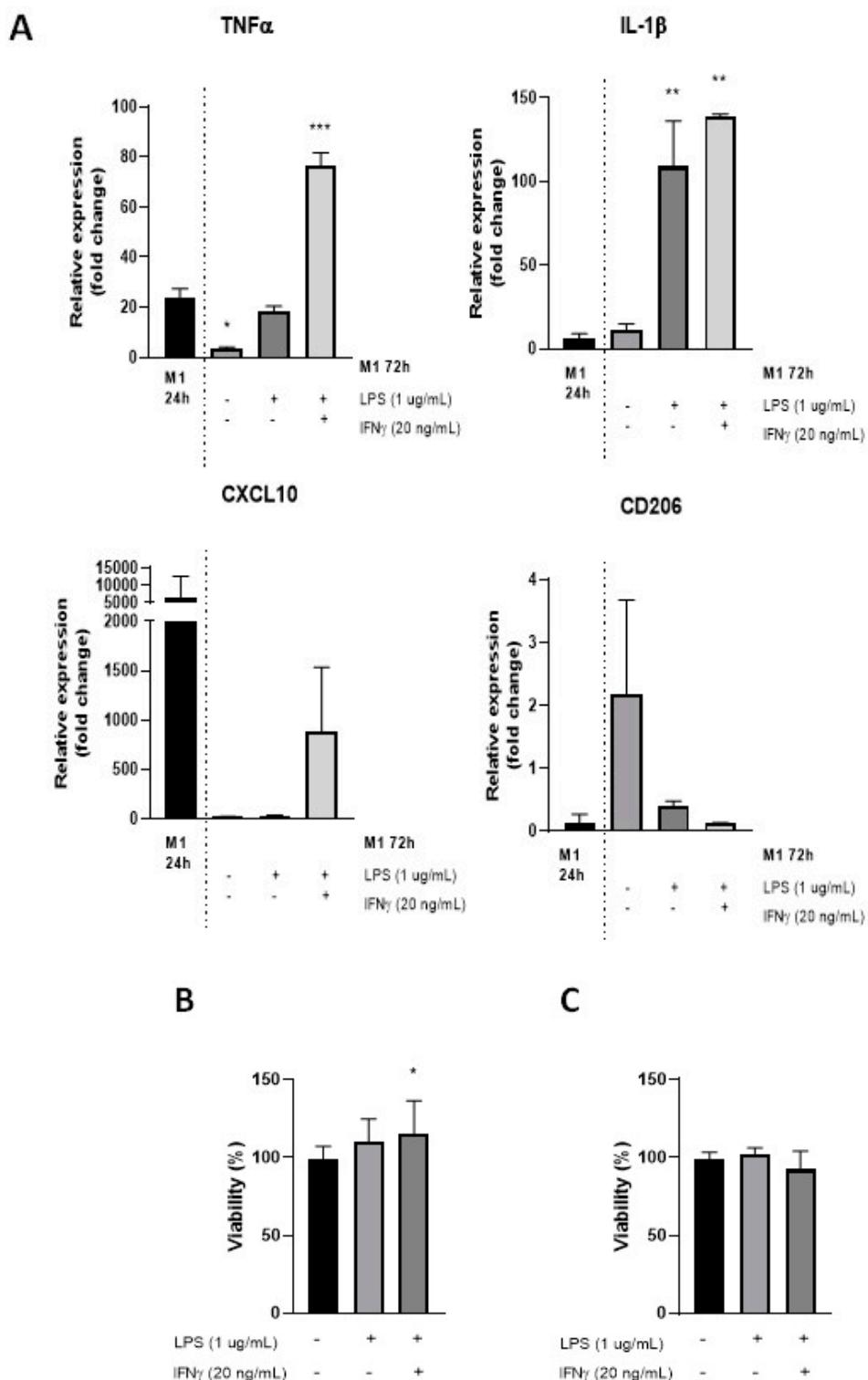
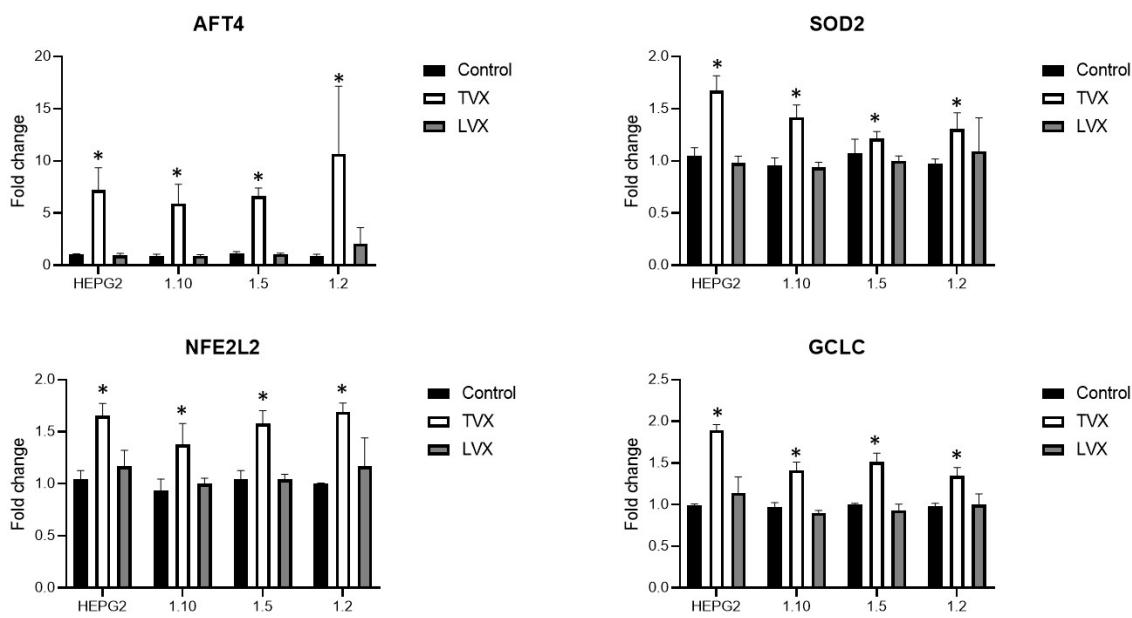


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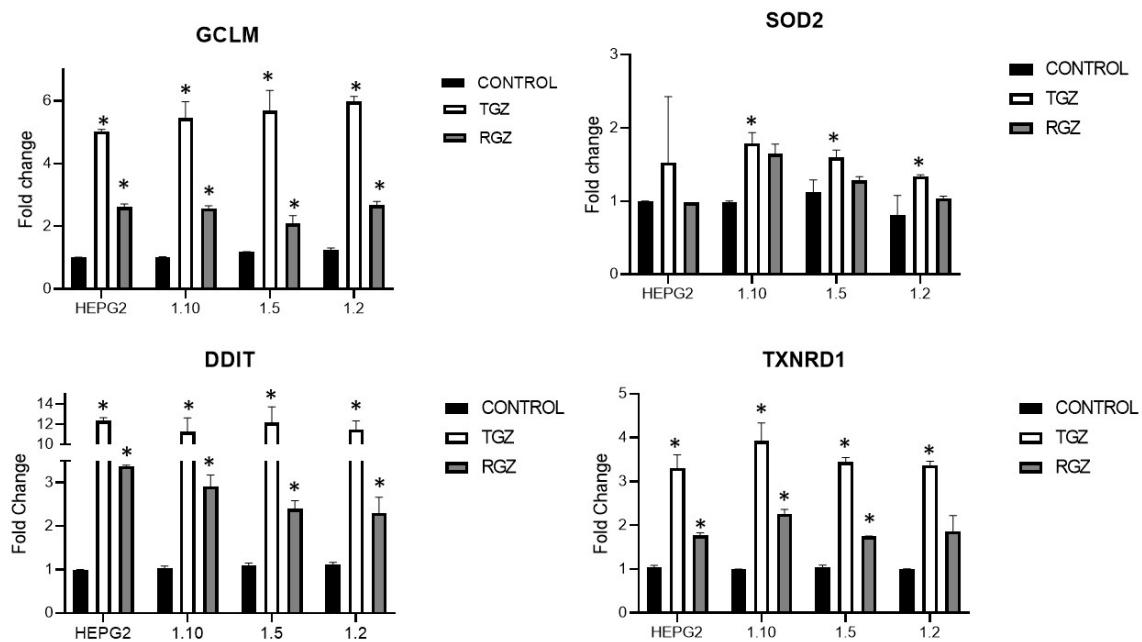
### SUPPLEMENTARY FIGURES



**Supplementary Figure S1: Characterization of M1 macrophages under pro-inflammatory conditions during 72 h.** (A) mRNA expression of M1 (TNF- $\alpha$ , IL-1 and CXCL10) and M2 (CD206) markers after proinflammatory stimulation during 72 h. (B) HepG2 viability after proinflammatory stimulation during 72 h. (C) M1 viability after proinflammatory stimulation during 72 h. \*At least p≤0.05 (compared to M1 24 h or HepG2 24 h)



**Supplementary Figure S2. Expression of oxidative and apoptotic-related mRNA in cell culture models exposed to TVX or LVX.** mRNA expression of AFT4, SOD2, NFE2L2 and GCLC was analysed in monocultures of HepG2 or and co-cultures of HepG2 cells and M1-THP1 cells at different cell ratios exposed to 25 µM of TVX or LVX and compared to non-treated cultures (Control). \*At least p≤0.01 (compared to non-treated cultures, Student's t-test).



**Supplementary Figure S3. Expression of oxidative and apoptotic-related mRNA in cell culture models exposed to TGZ or RGZ.** mRNA expression of GCLM, SOD2, DDIT and TXNRD1 was analysed in monocultures of HepG2 or and co-cultures of HepG2 cells and M1-THP1 cells at different cell ratios exposed to 100 µM of TGZ or RGZ and compared to non-treated cultures (Control). \*At least p≤0.01 (compared to non-treated cultures, Student's t-test).

## SUPPLEMENTARY TABLES

**Supplementary Table S1. Antibodies used in the study.**

| Target  | Primary Antibody  | Secondary Antibody                                     |
|---------|---|--|
| Albumin | Goat Anti-Human Albumin<br>A80-229 <sup>a</sup> Bethyl                | Alexa Fluor 488 donkey anti-goat<br>A11055 invitrogen  |
| CD68    | Recombinant Anti-CD68<br>antibody [KP1]<br>ab233172 abcam             | Alexa Fluor 594 donkey anti-mouse<br>R37115 invitrogen |
| CD163   | Recombinant Alexa Fluor®<br>488 Anti-CD163 antibody<br>ab218293 abcam | Alexa Fluor 488 donkey anti-rabbit<br>A21202           |

**Supplementary Table S2:** The oligonucleotides used for quantitative RT-PCR

| Symbol              | Gene   | Forward (5'->3')        | Reverse (5'->3')         | RefSeq        | nt position |
|---------------------|--|-------------------------|--------------------------|---------------|-------------|
| <b>HMBS</b>         | hydroxymethylbilane synthase                   | CGGAAGAAAACAGCCCAAAGA   | TGAAGCCAGGAGGAAGCACAGT   | NM_000190.4   | 185-478     |
| <b>TBP</b>          | TATA-box binding protein                       | AAAATGGTGTGCACAGGAGCC   | CACATCACAGCTCCCCACCAT    | NM_003194.5   | 895-1035    |
| <b>ACTB</b>         | Actin beta                                     | CGTACCACTGGCATCGTGTAT   | GTGTTGGCGTACAGGTCTTG     | NM_001101.5   | 523-974     |
| <b>RPLP0</b>        | Ribosomal Protein Lateral Stalk Subunit P0     | TGGTCATCCAGCAGGTGTTGAA  | ACAGACACTGGCAACATTGCGG   | NM_001002.4   | 637-755     |
| <b>ALB</b>          | Albumin  | CACAGAACCTTGGTGAACAGG   | TGCGAAATCATCCATAACAGC    | NM_000477.7   | 1544-1769   |
| <b>HNF4A</b>        | Hepatocyte nuclear factor 4 alpha              | GCCTACCTCAAAGCCATCAT    | GACCCCTCCCAGCAGCATCTC    | NM_000457.6   | 993-1267    |
| <b>AFP</b>          | Alpha-fetoprotein                              | GCTTGGTGGTGGATGAAACA    | TCCTCTGTTATTGTGGCTTTG    | NM_001134.3   | 1583-1739   |
| <b>IL1-<i>B</i></b> | Interleukin-1beta                              | GCAGAACAGTACCTGAGCTCGC  | TCCATGGCCACAACAACTGA     | NM_000576.3   | 91-302      |
| <b>TNF-<i>α</i></b> | Tumor necrosis factor alpha                    | GCAACAAGACCACCACTTCG    | GATCAAAGCTGTAGGCCCA      | NM_000594.4   | 1020-1143   |
| <b>CXCL10</b>       | C-X-C Motif Chemokine Ligand 10                | GCTTCCAAGGATGGACCACAA   | GCAGGGTCAGAACATCCACT     | NM_001565.4   | 392-644     |
| <b>MRC1</b>         | Mannose receptor C type 1                      | CGTTCCCTTGGACGGATGGA    | CCTCGTTACTGTCGCAGGT      | NM_002438.4   | 3174-3345   |
| <b>ABCC2</b>        | ATP binding cassette subfamily C member 2      | TCAGACGACCATCCAAAACGA   | GGGTCCAGGGATTGTAGCAG     | NM_000392.5   | 4630-4786   |
| <b>ABCC4</b>        | ATP binding cassette subfamily C member 4      | ATTATCGGAAGGCACCTCGT    | CAAGGGCAGGAGAATGATTAGA   | NM_00110551.3 | 657-887     |
| <b>CYP1A2</b>       | Cytochrome P450 family 1 subfamily A member 2  | CCTTCGCTACCTGCCTAACCC   | CTCTAGGCCCTTCTGCTG       | NM_000761.5   | 785-951     |
| <b>CYP3A5</b>       | Cytochrome P450 family 3 subfamily A member 5  | CTCCTCTATCTATATGGGACCCG | TGACCTTCATACGTTCCCCAC    | NM_000777.5   | 161-333     |
| <b>SULT1A1</b>      | Sulfotransferase family 1A member 1            | CTGGAGAACGTTCATGGTCGGA  | CCACGAAGTCCACGGTCTC      | NM_001055.4   | 593-770     |
| <b>SULT1B1</b>      | Sulfotransferase family cytosolic 1B member 1  | GCCTATGGTTCCTGGTTACTC   | AGTAATTCTCCAGTCACCAGC    | NM_014465.3   | 803-1082    |
| <b>UGT1A1</b>       | UDP-glucuronosyltransferase family 1 member A1 | TGCGACGTGGTTATTCCCC     | AGGCTCAAATTCTGGATAGTG    | NM_012683.2   | 682-869     |
| <b>UGT2B7</b>       | UDP-glucuronosyltransferase family 2 member b7 | AGGAGCTAACACCTTCGGG     | TGCTGGAATAACTGAAGTAGTCTC | NM_001074.4   | 1460-1699   |
| <b>GSTT1</b>        | Glutathione S-transferase theta 1              | ACGGGGACTTCACCTTGAC     | GTACTCATCCACACGGGCAC     | NM_000853.4   | 216-334     |

| <b>GSTT2</b>  | Glutathione S-transferase theta 2           | CGACGCTCAAGGATGGTGA    | CTCCTCCAGGCCATGAGAT    | NM_000854.5    | 228-580   |
|---------------|---|------------------------|------------------------|----------------|-----------|
| <b>GSTA1</b>  | Glutathione S-transferase alpha 1           | CCTGAGGAAAAAGATGCCAA   | GAUTGGAGTCAAGCTCCTCG   | NM_145740.5    | 402-582   |
| <b>GSTA2</b>  | Glutathione S-transferase alpha 2           | TCCCTCTCTGCCCTTAGTC    | GCTGAAATAAGGCTAGAGTCAA | NM_000846.5    | 379-593   |
| <b>GSTA4</b>  | Glutathione S-transferase alpha 4           | GTTGGTACAGACCCGAAGCA   | GCTTGTCGTGACCCCTTA     | NM_001512.4    | 246-492   |
| <b>GSR</b>    | Glutathione-disulfide reductase             | GGCCGAAAATTGCCCATC     | ATCGGGTAAAGCTCGTTGA    | NM_000637.5    | 1179-1360 |
| <b>GPX1</b>   | Glutathione Peroxidase 1                    | GTCGGTGTATGCCTTCGG     | TCTGGCGTTCTCGATGC      | NM_000581.4    | 117-340   |
| <b>GPX2</b>   | Glutathione peroxidase 2                    | TGAGAATGTGGCTCGCTCTG   | ACCCCCAGGACGGACATAC    | NM_002083.4    | 118-298   |
| <b>GPX4</b>   | Glutathione peroxidase 4                    | CGCTGTGGAAGTGGATGAAG   | AGAAATAGTGGGCAGGTCC    | NM_002085.5    | 475-642   |
| <b>CASP3</b>  | Caspase 3                                   | TGCATACTCCACAGCACCTG   | TCTGTTGCCACCTTCGGTT    | NM_004346.4    | 820-972   |
| <b>CASP7</b>  | Caspase 7                                   | AGCCTGGTTTGACGTGAT     | CCCCTAAAGTGGCTGTCAA    | NM_001227.5    | 374-570   |
| <b>DDIT</b>   | DNA damage inducible transcript 3           | ATGAACGGCTAACGAGCAGGAA | GGGAAAGGTGGGTAGTGTGG   | NM_001195053.1 | 750-897   |
| <b>ATF4</b>   | Activating Transcription Factor 4           | GAAGCGATTAAACGAGCGCC   | ATCTTGGTCCTGCCACGTT    | NM_001675.4    | 293-489   |
| <b>ATF6</b>   | Activating Transcription Factor 6           | GTATCAGGAACTCAGGGAGTG  | GCAGGTGATCCCTCGAAAT    | NM_001410890.1 | 1639-1767 |
| <b>CAT</b>    | Catalase                                    | TCAGGTGGGGCATTCTATG    | TGATGAGCGGGTTACACGGA   | NM_001752.4    | 1403-1724 |
| <b>SOD1</b>   | Superoxide dismutase 1                      | ACAAAGATGGTGTGGCCGAT   | CGACTTCCAGCGTTCCGT     | NM_000454.5    | 349-508   |
| <b>SOD2</b>   | Superoxide Dismutase 2                      | CTCAGGTTGGGTTGGCTTG    | TGCTCCCACACATCAATCCC   | NM_000636.4    | 506-634   |
| <b>NFE2L2</b> | NFE2 like bZIP transcription factor 2       | GCGACGAAAGAGTATGAGC    | TACAAACGGGAATGTCTGCG   | NM_006164.5    | 274-541   |
| <b>GCLC</b>   | Glutamate-Cysteine Ligase Catalytic Subunit | TCAATGGGAAGGAAGGTGT    | TGGTTGCGATAAACTCCCTCA  | NM_001498.4    | 2027-2227 |
| <b>GCLM</b>   | Glutamate-Cysteine Ligase Modifier Subunit  | AATCTGCCCTCTGCTGTGT    | ACTCGTGCCTGAATGTCAG    | NM_002061.4    | 832-991   |
| <b>TXNRD1</b> | Thioredoxin Reductase 1                     | GGTGCTTGCCCTTCTGA      | GGACCCAGTACGTGAAAGCC   | NM_182729.3    | 1365-1552 |
| <b>HMOX1</b>  | Heme oxygenase 1                            | GAUTGCCTCGCTAACAT      | GGCTCTGGCCTTGGTGTCA    | NM_002133.3    | 690-766   |
| <b>NQO1</b>   | NAD(P)H Quinone Dehydrogenase 1             | TCCAGAAAGGACATCACAGGT  | ATGAACACTCGCTCAAACCA   | NM_000903.3    | 275-486   |

**Table S3. IC50 values ( $\mu$ M) for test compounds in different in vitro models.**

|     | <b>HepG2</b> | <b>Co-culture 1.10</b> | <b>Co-culture 1.5</b> | <b>Co-culture 1.2</b> |
|-----|--------------|------------------------|-----------------------|-----------------------|
| TVX | 675          | 531                    | 529                   | 74                    |
| LVX | >800         | >800                   | >800                  | >800                  |
| TGZ | 223          | 208                    | 203                   | 188                   |
| RGZ | >250         | >250                   | >250                  | >250                  |