# Supplementary tables

Supplementary Table S1 – Primer and probe sequence of genes amplified with (a) SYBR Green PowerUp Mastermix and (b) Taqman Fast Advanced Master Mix.

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| **(*a*) SYBR Green PowerUp Mastermix** | | |
| **Gene** | **Forward primer** | **Reverse primer** |
| *Auts2* | GGTATACCCCCCATGATCCC | AGGGTTGGATGTCTTCGGC |
| *Axin2* | AAGCCCCATAGTGCCCAAA | CGGCTGACTCGTTCTCCTG |
| *Bdnf* | CTCTGGAGAGCGTGAATGGG | CGTGCTCAAAAGTGTCAGCC |
| *Mag* | AGGAACCTCTATGGCACCCA | GACCGATTTTGGCCCACA |
| *Mbp* | GCTCCCTGCCCCAGAAGT | CGAGGTGTCACAATGTTCTTGAA |
| *Mecp2* | GCCTGAAGGTTGGACACGAA | GGAGGTGTCTCCCACCTTTTC |
| *Nrxn1* | TTGACCCCTGTGAGCCGA | TGGTTCACGGCCACCTACTC |
| *Pparg* | CACAATGCCATCAGGTTTGG | GCTGGTCGATATCACTGGAGATC |
| *Pou4f1* | GGCACACTGGGGAGCTG | CTCCTGCCCCCAAATGAGAG |
| *Reln* | AGGACAACCTCGACCCGG | CAGCTATGCTTGACCGTTGC |
| *Vldlr* | CCACAGCAGTATCAGAAGTCAGTGT | CACCTACTGCTGCCATCACTAAGA |
| *Socs3* | GGACCAAGAACCTACGCATCCA | CACCAGCTTGAGTACACAGTCG |
| *Maff* | TGCGAAAATGGCTGTGGAT | GGCGTGTTCTCGCTCAACTC |
| *Id1* | CCCACTGGACCGATCCGCCA | TGCTCTCGGTTCCCCAGGGG |
| *Dusp1* | GGCCAGCTGCTGCAGTTTGAGT | AGGTGCCCCGGTCAAGGACA |
| *Nfkb1* | TGGCCGTGGAGTACGACAA | GTGGGCATCACCCTCCAG |
| *Hmox1* | GTGATGGAGCGTCCACAGC | TGGTGGCCTCCTTCAAGG |
| *Afp* | TCCAAAGCATTGCACGAAAA | GCTTCCGGAACAAACTGGGT |
| *Sirt1* | GGTTGCAGGAATCCAAAGGATC | CACGAACAGCTTCACAATCAACTT |
| *Srebf2* | CTGCAGCCTCAAGTGCAAAG | CAGTGTGCCATTGGCTGTCT |
| *36b4* | GCTCCAAGCAGATGCAGCA | CCGGATGTGAGGCAGCAG |
| *Gapdh* | TGGCAAAGTGGAGATTGTTGCC | AAGATGGTGATGGGCTTCCCG |

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| **(*b*) Taqman Fast Advanced Master Mix** | | | |
| **Gene** | **Forward primer** | **Reverse primer** | **Probe** |
| *36b4* | GCTTCATTGTGGGAGCAGACA | CATGGTGTTCTTGCCCATCAG | TCCAAGCAGATGCAGCAGATCCGC |
| *Bactin* | AGCCATGTACGTAGCCATCCA | TCTCCGGAGTCCATCACAATG | TGTCCCTGTATGCCTCTGGTCGTACCAC |
| *Tat* | CAGCCACGTGCTTCGAGTAC | AACTCCTGGATCCGGCTACAAG | CATCACAGTCCCCGAGGTGATGATGC |
| *Tnfa* | GTAGCCCACGTCGTAGCAAAC | AGTTGGTTGTCTTTGAGATCCATG | CGCTGGCTCAGCCACTCCAGC |
| *Srebf2* | CTGCAGCCTCAAGTGCAAAG | CAGTGTGCCATTGGCTGTCT | CCATCCAGCAGCAGGTGCAGACG |
| *Cebpa* | CCAAGAAGTCGGTGGACAAGAA | AGGCGGTCATTGTCACTGGT | CGCAACAACATCGCGGTGCG |
| *Pepck* | GTGTCATCCGCAAGCTGAAG | CTTTCGATCCTGGCCACATC | CAACTGTTGGCTGGCTCTCACTGACCC |
| *G6pc* | TTCCCTGTCACCTGTGAGACC | GGCGCAGCAGGTGTATACTATGT | CAGGAAGTCCCTCTGGCCATGCC |
| *Fasn* | GGCATCATTGGGCACTCCTT | GCTGCAAGC ACAGCCTCTCT | CCATCTGCATAGCCACAGGCAACCTC |

Supplementary Table S2 - Pyrosequencing assays. The Y in the sequence indicates CpG position.

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| **Assay** |  |  |
| **LINE1** | Forward primer | 5'-TTTGGGGTTAGGATTTGGGGTATAAG-3' |
| Reverse primer | 5'-biotin-CCACTCACCAAAAATCTTAAAATC-3' |
| Sequence primer | 5'-GATTTGGGGTATAAGTTTTT-3' |
| Sequence to analyse | TTYGTTYGATTYGWGATTYGAGTTTYGGYTA |
| ***Bdnf exon IV*** | Forward primer | 5'- AGGATTGGAAGTGAAAATATTTATAAAGT -3' |
| Reverse primer | 5'-biotin- ACAACCAAAACAATCCTCTCCT -3' |
| Sequence primer | 5'- AATAAAAGATGTATTATTTTAAATG -3' |
| Sequence to analyse | YGYGGAATTTTGATTTTGGTAATTYGTGTATTAGAGTGTT TATTTYGAGGTAGAGGAGGTATTATATGATAGTTTAYGTT AAGGTAGYGTGGAGTTTTTTYGTGGATTTTTATTTATTTT  TTTATTTATYGAGGAGAGGATTGTTTT |
| ***Auts2*** | Forward primer | 5'- AGGAGTGGAGGAGATAAGG -3' |
| Reverse primer | 5'-biotin- CCCCCCTCCCCTAATTATAAAATA -3' |
| Sequence primer 1 | 5’- GGAGAAAGGTGTTTGTT-3' |
| Sequence to analyse 1 | AYGYGTGYGYGYGYGAGTTTTTYGTGYGTTTGGYGGGATG TTGGGGTAGTTTTTAAGTTTTYGAATTTTAATTTTATATY GGTTTGTGATYGATTTTTTTAATATATTTT |
| Sequence primer 2 | 5’- TTTTTATAGTTTTTGGAGATTTTT-3' |
| Sequence to analyse 2 | TTYGTTTTTAAGTGYGTAGGTTYGGTYGTTTTAGYGYGTA TGTTTTGGGTTYGTGGAGYGGTGGTTAGTTTTTTAGTTTTTTTG |
| ***Srebf2*** | Forward primer | 5’-GGTTAATGTAGGTTTGGTTTTATTGAT-3’ |
| Reverse primer | 5’-biotin-ATAACACCCCACAACCCCCACCTAATA-3’ |
| Sequence primer | 5’-GTAGGTTTGGTTTTATTGATAATA-3 |
| Sequence to analyse | AATTTGGGGGTGYGGAGGTTYGGGGYGGGGTTGTAGTGGGYGYGGTTYGGGGYGGGGGAA |

Supplementary Table S3 – Expression of inflammation and oxidative stress, maturation marker and metabolic markers genes in fetal liver of preeclampsia-exposed offspring. Relative gene expression was calculated using the 2-ΔCt method, normalized against housekeeping genes *36b4* and *bactin* and analysed using two-way ANOVA. Data presented as median (interquartile range). Control groups and sFlt1+LPS male n=9, sFtl1+ LPS female n=8. Significantly altered genes are shown in the main text (Fig. 1).

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|  | **Male Control** | **Male sFlt+LPS** | **Female Control** | **Female sFlt+LPS** |
| ***Inflammation and oxidative stress*** | | | | |
| *Id1* | 0,012 (0,0081 - 0,016) | 0,0086 (0,0079 - 0,011) | 0,0078 (0,0073 – 0,018) | 0,0073 (0,0063 – 0,0084) |
| *Maff* | 0,011 (0,0060 - 0,016) | 0,0074 (0,0069- 0,0096) | 0,011 (0,0074 – 0,018) | 0,0074 (0,0059 – 0,0093) |
| *Nfkb1* | 0,014 (0,012 – 0,017) | 0,014 (0,010 – 0,016) | 0,012 (0,011 – 0,014) | 0,012 (0,011 – 0,014) |
| ***Maturation markers*** | | | | |
| *Afp* | 4,73 (4,07 – 6,46) | 4,63 (3,87 – 5,12) | 4,77 (3,97 – 5,46) | 5,27 (3,62 – 5,90) |
| *Cebpa* | 0,0429 (0,0405 – 0,0452) | 0,0414 (0,0364 – 0,0455) | 0,040 (0,038 – 0,043) | 0,041 (0,038 – 0,045) |
| *Tat* | 0,0057 (0,0035 – 0,0081) | 0,0046 (0,0032 – 0,0055) | 0,004 (0,0024 – 0,0065) | 0,0034 (0,0022 – 0,004) |
| ***Metabolic markers - gluconeogenesis*** | | | | |
| *Pgc1a* | 0,039 (0,034 – 0,048) | 0,053 (0,033 – 0,055) | 0,0511 (0,0428 – 0,0635) | 0,045 (0,033 – 0,031) |
| *Ppara* | 0,013 (0,012 – 0,014) | 0,013 (0,011 – 0,015) | 0,012 (0,011 – 0,014) | 0,012 (0,012 – 0,014) |
| ***Metabolic markers – lipid & cholesterol biosynthesis*** | | | | |
| *Fasn* | 0,51 (0,36 – 0,66) | 0,43 (0,31 – 0,46) | 0,42 (0,30 – 0,54) | 0,44 (0,33 – 0,52) |

Supplementary Table S4 - Expression of neurodevelopment-associated and inflammation and oxidative stress genes in fetal whole brain of preeclampsia-exposed offspring Relative gene expression was calculated using the 2-ΔCt method, normalized against housekeeping genes *Gapdh* and *36b4* and analysed using two-way ANOVA. Data presented as median (interquartile range). Control groups and sFlt1+LPS male n=9, sFtl1+ LPS female n=8. Significantly altered genes are shown in the main text (Fig. 2).

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| --- | --- | --- | --- | --- |
|  | **Male Control** | **Male sFlt+LPS** | **Female Control** | **Female sFlt+LPS** |
| ***Neurodevelopmental associated*** | | | | |
| *Mbp* | 0,11 (0,11 - 0,14) | 0,14 (0,095 - 0,15) | 0,12 (0,086 – 0,16) | 0,13 (0,069 – 0,20) |
| *Mecp2* | 0,78 (0,71 - 0,93) | 0,86 (0,83 - 0,87) | 0,80 (0,73 – 0,81) | 0,78 (0,70 – 0,93) |
| *Nrxn1* | 2,70 (2,42 - 3,15) | 3,27 (2,70 - 3,42) | 2,77 (2,57 - 3,17) | 2,96 (2,65 - 3,11) |
| *Pou4f1* | 0,073 (0,065 - 0,15) | 0,11 (0,10 - 0,17) | 0,10 (0,098 - 0,11) | 0,10 (0,078 - 0,14) |
| *Pparg* | 0,0076 (0,0064 - 0,011) | 0,0070 (0,0066 - 0,0076) | 0,0080 (0,0069 - 0,0088) | 0,0070 (0,0063 – 0,0076) |
| *Reln* | 2,63 (2,62 - 3,56) | 3,64 (2,88 - 4,41) | 2,94 (2,51 - 3,23) | 3,16 (2,89 - 3,76) |
| *Vldlr* | 0,38 (0,30 - 0,40) | 0,38 (0,36 - 0,42) | 0,35 (0,35 - 0,42) | 0,36 (0,32 - 0,39) |
| ***Inflammation and oxidative stress*** | | | | |
| *Dusp1* | 0,22 (0,22 - 0,27) | 0,28 (0,22 - 0,29) | 0,27 (0,24 - 0,28) | 0,26 (0,23 - 0,31) |
| *Id1* | 0,13 (0,13 - 0,14) | 0,13 (0,12 - 0,14) | 0,12 (0,11 -0,14) | 0,14 (0,12 - 0,15) |
| *Maff* | 0,014 (0,013 - 0,020) | 0,014 (0,013 - 0,018) | 0,026 (0,020 - 0,033) | 0,016 (0,014 - 0,022) |