# Supplementary information

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**Supplementary Figure S1 – DNA methylation of the *Srebf2* promotor site per CpG position in fetal liver of preeclampsia-exposed offspring.** DNA methylation percentage was analysed using pyrosequencing for 7 CpG positions in the *Srebf2* promotor site. Control groups and sFlt1+LPS male n=9, sFtl1+ LPS female n=8. Analysed using repeated measure two-way ANOVA, data presented as mean ±SD. \* p<0.05 for treatment.



**Supplementary Figure S2 – DNA methylation per CpG position of Line1, *Bdnf* exon IV and *Auts2* in the fetal brain of preeclampsia-exposed offspring.** DNA methylation percentage was analysed with pyrosequencing on fetal whole brain. (a) Global DNA methylation was analysed with five CpG positions of repetitive element LINE1. (b) Six CpG positions were analysed for the *Bdnf* exon IV promotor site, positions are given relative to the transcription start site. Two of the significantly lower methylated CpG positions are located in a transcription factor binding motif. Transcription factor CaRF can bind to CaRE1 motif with CpG position -66 and CREB can bind to CRE with CpG position -35. (c) 20 CpG positions were analysed for the *Auts2* promotor site, positions are given relative to the transcription start site. DNA methylation of 12 of these CpG positions was significantly different between sFlt+LPS and control male offspring. Control groups and sFlt1+LPS male n=9, sFtl1+ LPS female n=8. Analysed using repeated measure two-way ANOVA, data presented as mean ±SD. \* p<0.05 for treatment; $ p<0.05 for treatment in the male subgroup.

CaRE1: Calcium-responsive elemet-1, CaRF: CaRE1 dependent transcription factor, CRE: cyclic adenosine monophosphate response element, CREB: CRE-binding protein, USF: upstream stimulatory factor.