are presented. The genes shown inside the red boxes clustered together according to an approximately unbiased (AU) probability set at ≥95% level, after bootstrap re-sampling.

Supplementary Figures Legends

Figure 1S. Pair-wise Pearson correlation coefficients and LOESS analysis assessing gene co-expression patterns in the hippocampus of wt and casp1$^{-/-}$ mice.

Correlation analysis between mRNA expression levels of tested genes (All correlations were significant).

Significant hippocampal correlation coefficient differences between genotypes are shown: * = $P<0.05$, and ** = $P<0.01$. *P*-values were corrected using the FDR procedure.

Figure 2S. Pairwise Pearson correlation coefficients and LOESS analysis assessing gene co-expression patterns in the spleen of wt and casp1$^{-/-}$ mice.

◦ = Correlation analysis between mRNA expression levels of tested genes that were not statistically significant within each genotype.

Significant splenic correlation coefficient differences between genotype are shown: * = $P<0.05$, ** = $P<0.01$, and *** = $P<0.001$. *P*-values were corrected using the FDR procedure.

Figure 3S. Pairwise Pearson correlation coefficients and LOESS analysis assessing gene co-expression patterns in adrenal tissue of wt and casp1$^{-/-}$ mice.

◦ = Correlation analysis between mRNA expression levels of the tested genes that were not statistically significant within each genotype.

Significant spleen correlation coefficient differences between genotype were not found.

Fig. 1S. Hippocampus

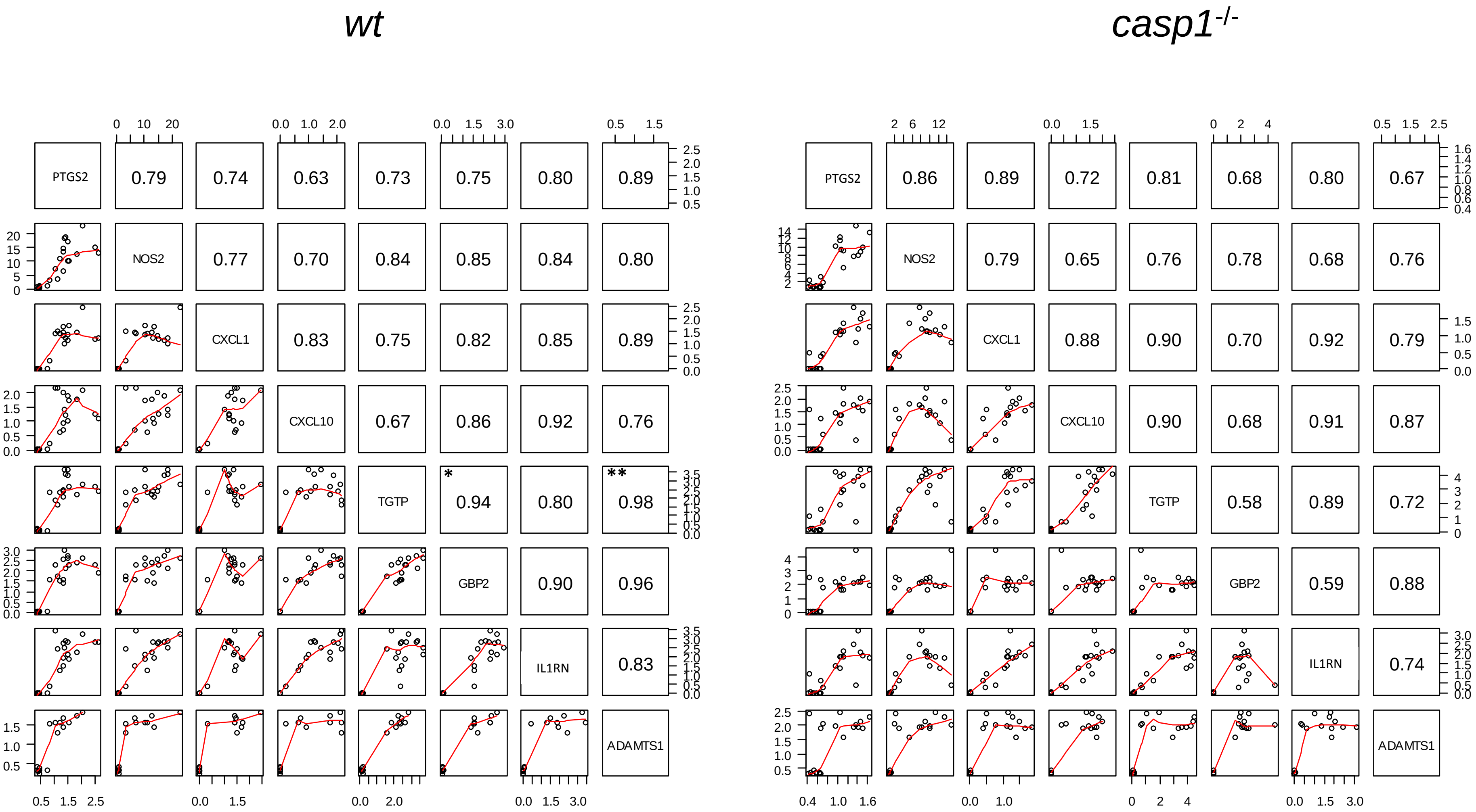


Fig. 2S. Spleen

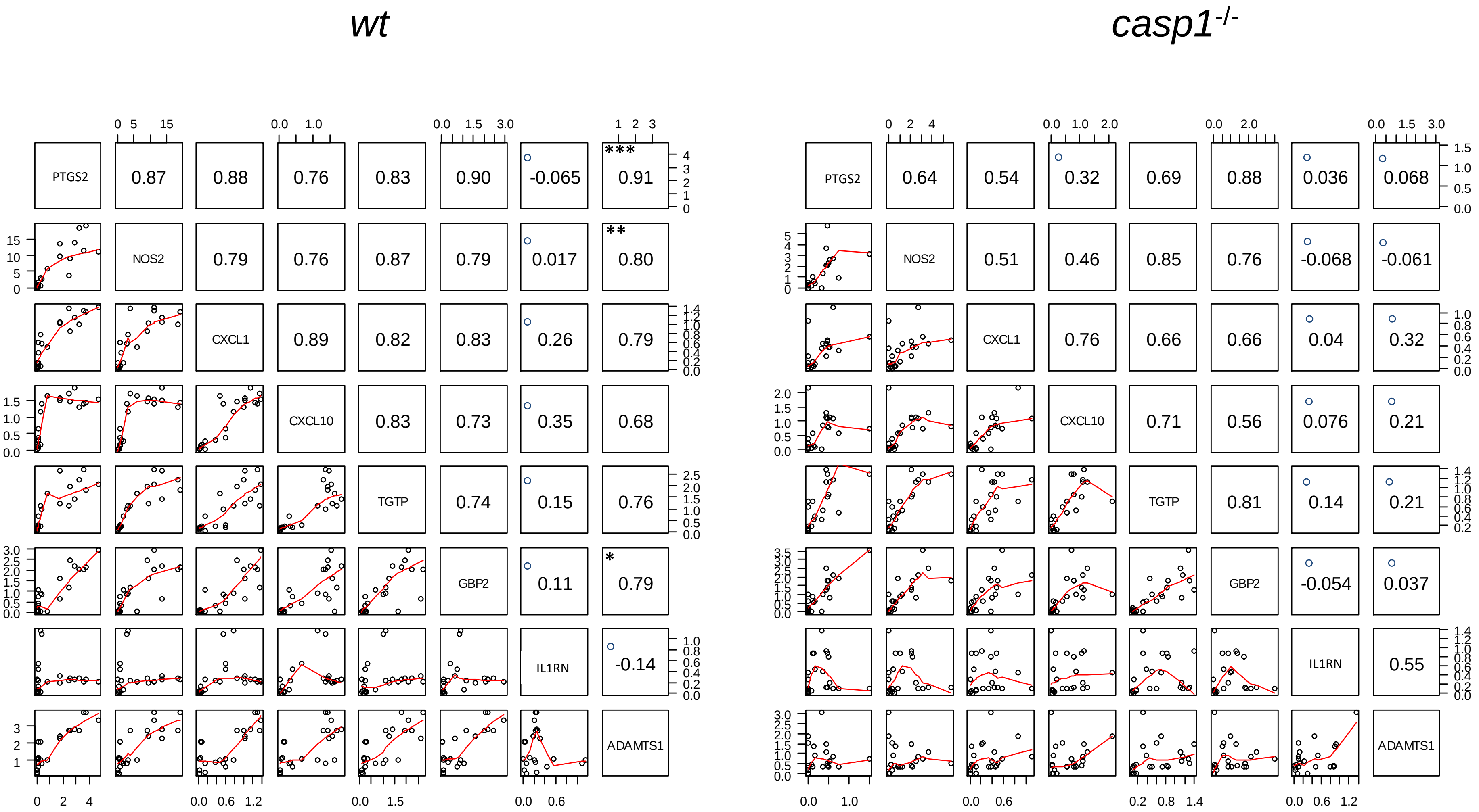
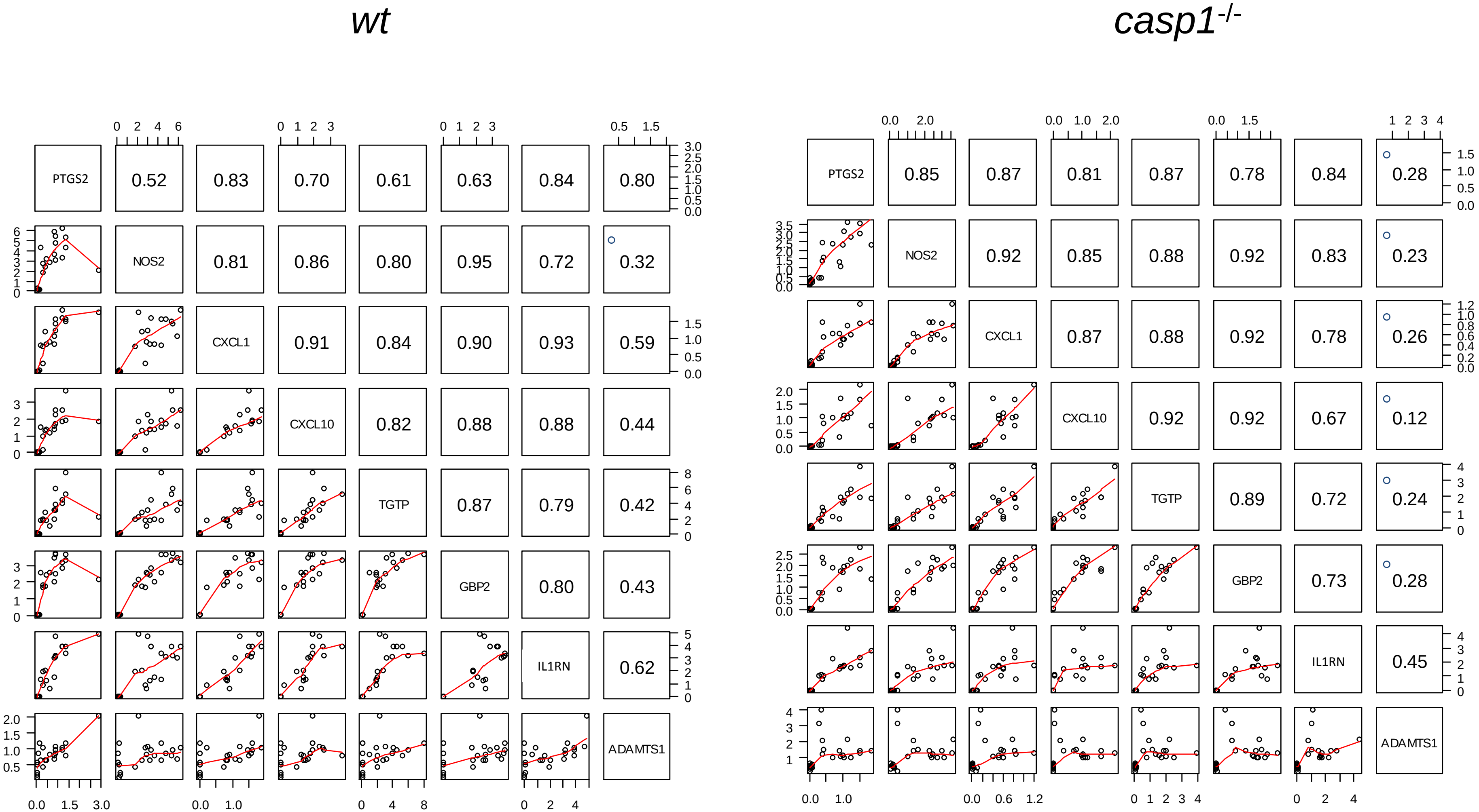


Fig. 3S. Adrenals



wt

$casp1^{-/-}$