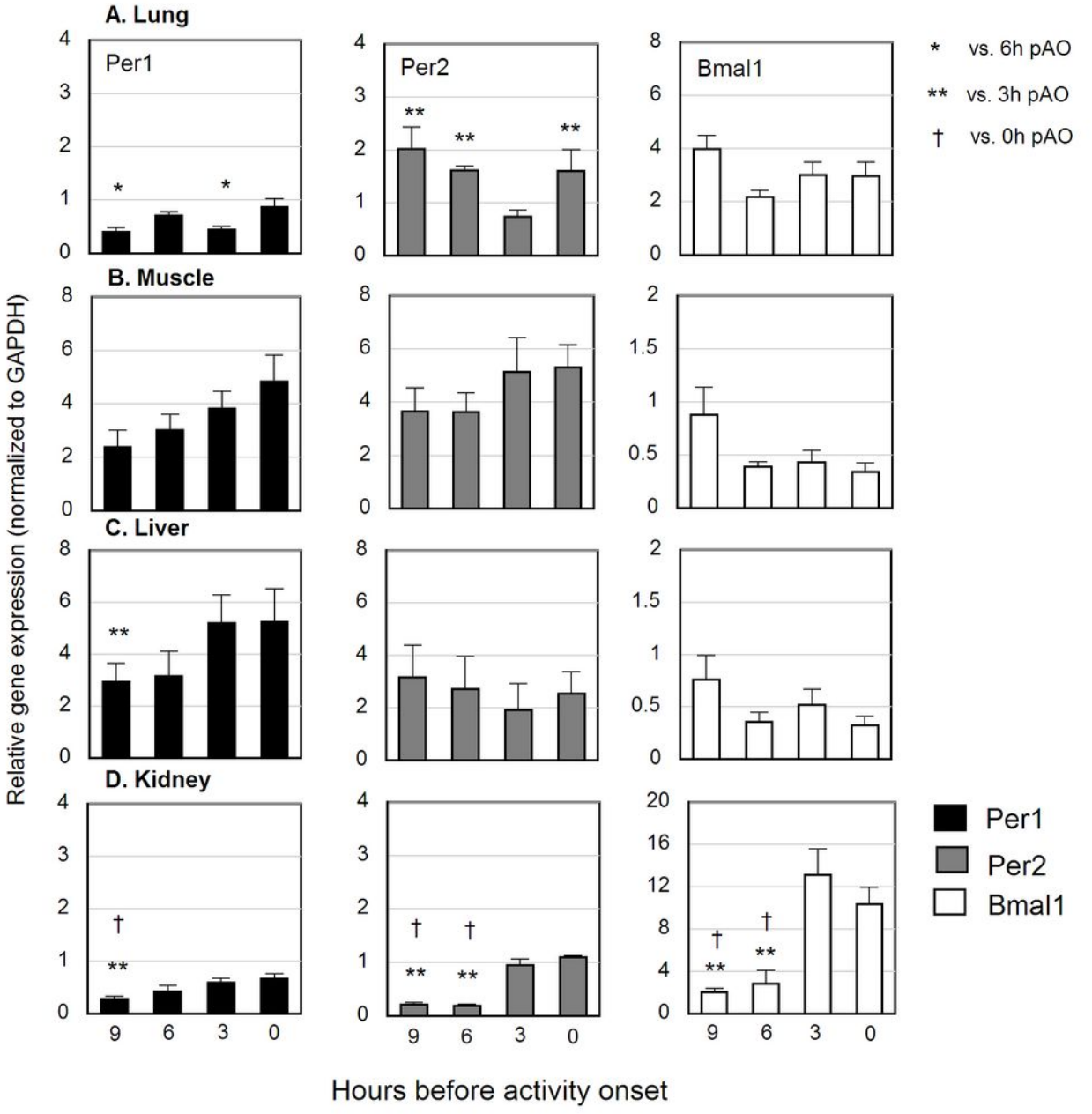
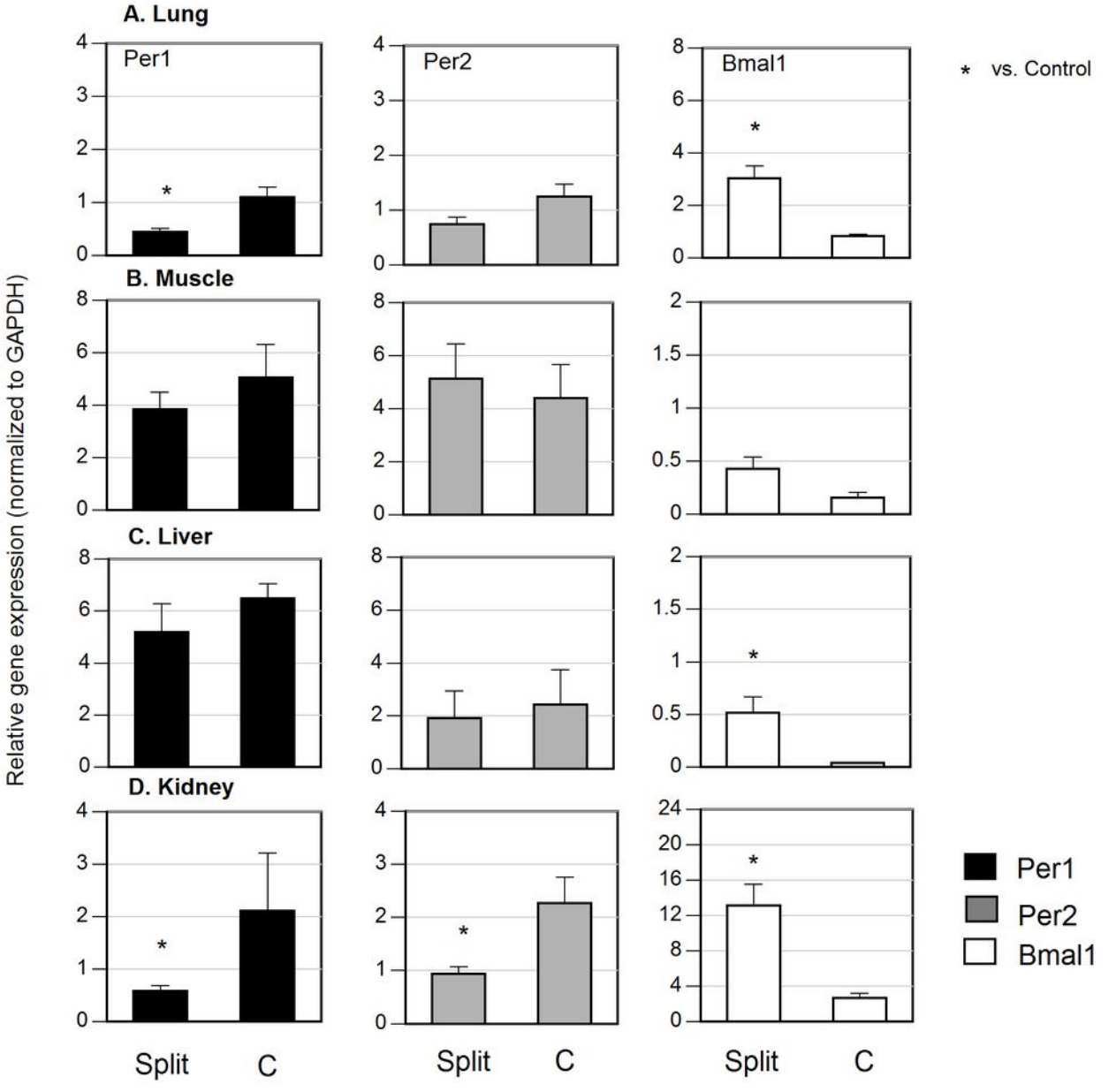
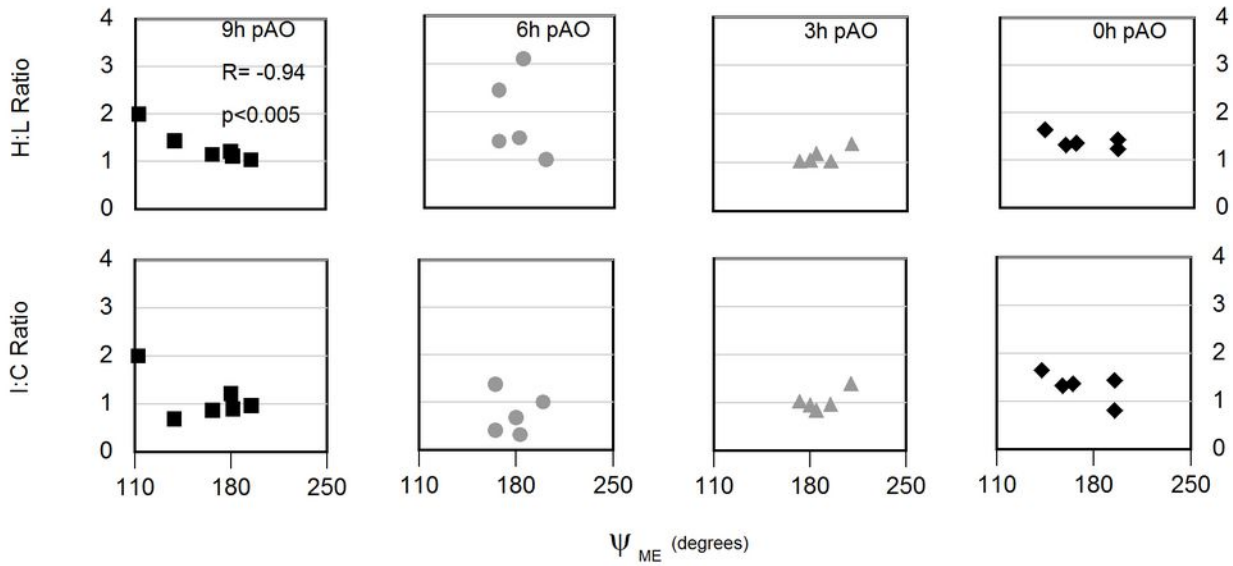
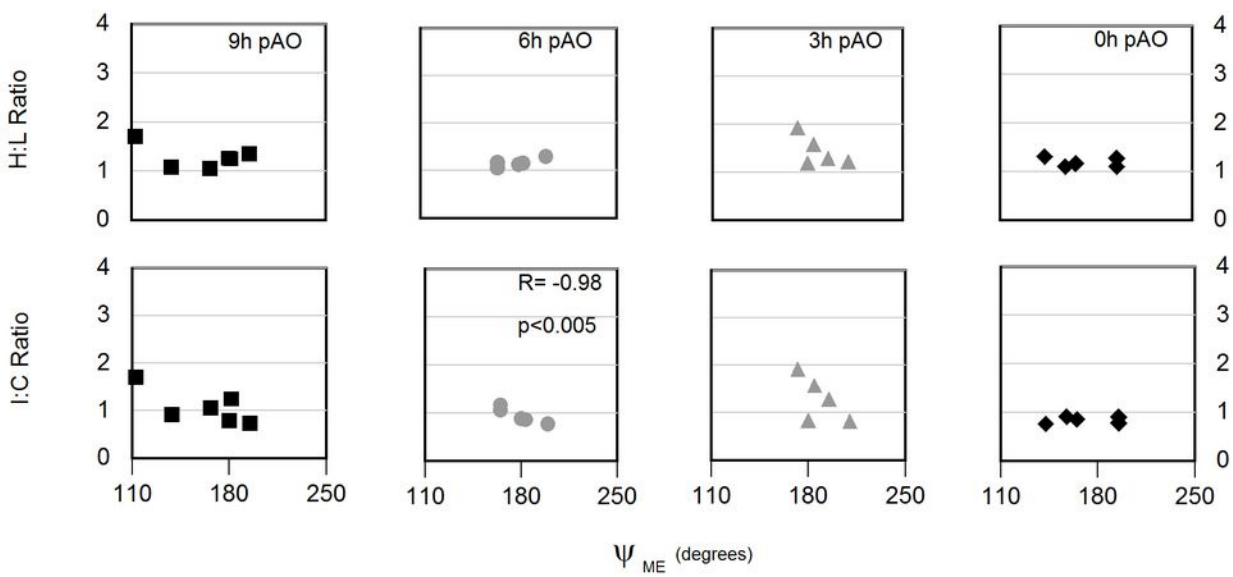

A. Lung
Per1
Per2
Bmal1
B. Muscle
C. Liver
D. Kidney
* vs. 6h pAO
** vs. 3h pAO
† vs. 0h pAO
Relative gene expression (normalized to GAPDH)
Per1
Per2
Bmal1
9 6 3 0
Hours before activity onset


A. Lung
Per1
Per2
Bmal1
* vs. Control
B. Muscle
C. Liver
D. Kidney
Relative gene expression (normalized to GAPDH)
Split
C
Per1
Per2
Bmal1

A. Relationship between Per1 asymmetry in lung and ψ_{ME} in experimental data



B. Relationship between Per2 asymmetry in kidney and ψ_{ME} in experimental data



Supplement Figure 1. Relative expression (mean±SEM) of *haPer1* (*black bars*), *haPer2* (*grey bars*) and *haBmal1* (*white bars*) in the lung (A), muscle (B), liver (C) and kidney (D). In hamsters that split in LL, messenger RNA values from the left and right side of each peripheral organ were averaged for each individual before group means were calculated for each phase (pAO). Gene expression was assessed by qrtPCR and normalized to GAPDH (*see methods*). Statistical significance: * $p<0.05$ vs. unsplit control, ** $p<0.05$ vs. 3h pAO, † $p<0.05$ vs. 0h pAO.

Supplement Figure 2. Relative gene expression (mean±SEM) averaged for the left and right organs from split and unsplit animals killed at 3h pAO. Levels of *haPer1* (*black bars*), *haPer2* (*grey bars*) and *haBmal1* (*white bars*) mRNA in the lung (A), muscle (B), liver (C) and kidney (D) are illustrated. * $p<0.05$ vs. unsplit control.

Supplement Figure 3. H:L (*top row*) and I:C (*bottom row*) ratios of (A) relative *haPer1* expression in lung and (B) relative *haPer2* expression in kidney plotted as a function of ψ_{ME} Spearmann's correlation (R) and p values are indicated where statistical significance was observed.