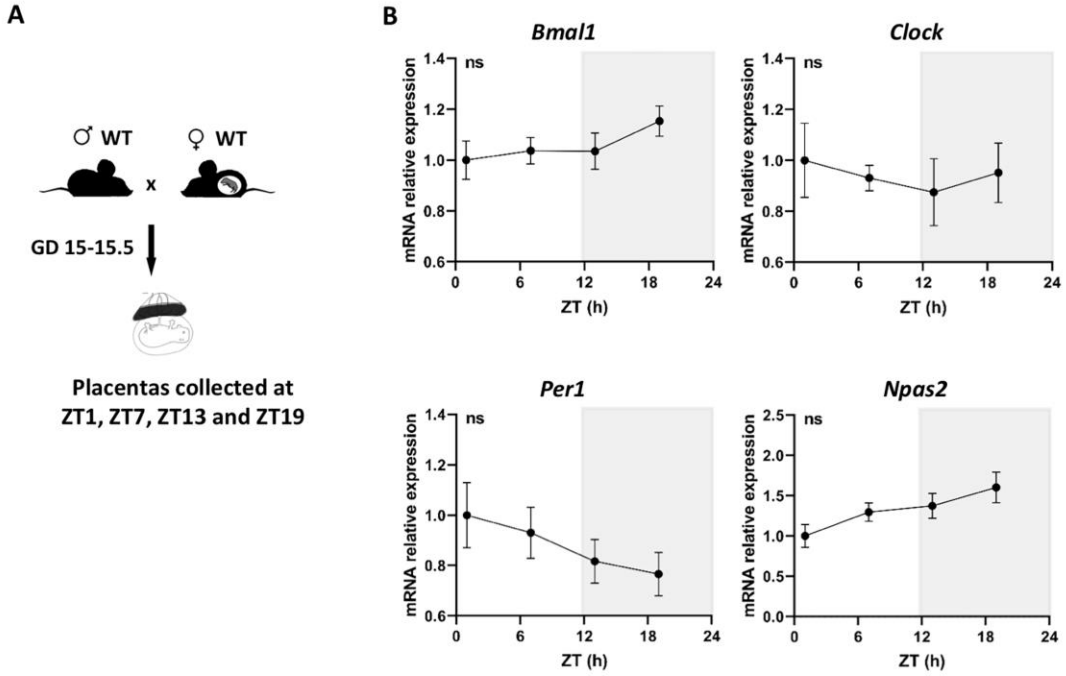

Fig. S1

A: Scheme of sample collection. B: mRNA relative expression of the clock genes *Bmal1, Clock, Per1* and *Npas2* in the LZ of the placenta from samples collected as described in (A). Data are shown as mean ± SEM (n=6). *CircWave* software was used to assess circadian rhythmicity by fitting the data to a cosine function and p value represent the statistical significance of that fit (ns: non-significant).

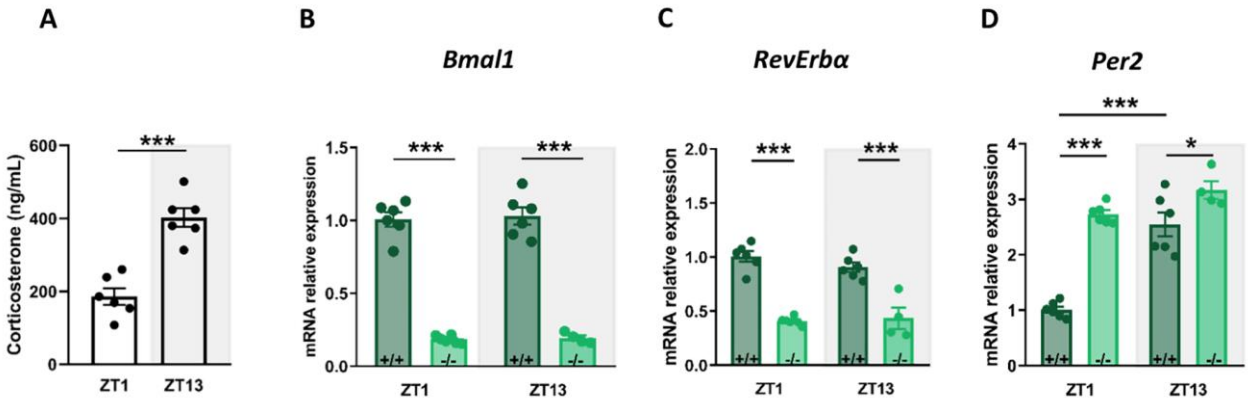

Fig. S2

A: Corticosterone levels in plasma of wild-type C57Bl/6 pregnant dams collected during GD 15-15.5, at ZT1 and ZT13. B-D: mRNA relative expression of *Bmal1, RevErbα and Per2* in the LZ of the placenta from samples collected from Bmal1 +/+ and -/- fetus collected at ZT1 and ZT13 and dissected under a magnifying lens. Dark grey area represents the dark phase (ZT13). Data are shown as mean ± SEM and analyzed in (A) by unpaired two-sided T-test (t=6.3, df=10, *** $p < 0.0001$ and in (B) by one-way ANOVA (in (B) $F(3,18)=118.7$, ***$p<0.0001$; (C) $F(3,18)=38.43$, ***$p<0.0001$ and (D) $F(3,18)=44.56$, ***$p<0.0001$).

Table S1

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