

**Supplemental Table 1.**  
**Gas chromatography (GC) /mass spectrometry (MS) parameters used for steroid identification and quantification in single ion monitoring mode**

<b>Steroids (MW)</b>	<b>Derivatized steroids (MW)</b>	<b>GC: retention time (min.)</b>	<b>MS: diagnostic ions (m/z)</b>
Progesterone (314)	Progesterone-3-HFB (510)	17.47	495 and <b>510</b>
5 $\alpha$ -DHP (316)	5 $\alpha$ -DHP-3,20-TMS <sub>2</sub> (460)	19.87	<b>445</b> and 460
Allopregnanolone (318)	Allopregnanolone-3-HFB (514)	16.47	496 and <b>514</b>
Corticosterone (346)	Corticosterone-3,21-HFB <sub>2</sub> - H <sub>2</sub> O (720)	19.68	<b>705</b> and 720
<b>Internal standards</b>			
19 norprogesterone (300)	19 nor-progesterone-3-HFB (496)	17.28	481 and <b>496</b>
<sup>2</sup> H <sub>6</sub> -5 $\alpha$ -DHP (322)	<sup>2</sup> H <sub>6</sub> -5 $\alpha$ -DHP-3,20-TMS <sub>2</sub> (466)	19.80	<b>448-451</b> and 466
<sup>2</sup> H <sub>8</sub> -corticosterone (354)	<sup>2</sup> H <sub>8</sub> -Corticosterone-3,21-HFB <sub>2</sub> - H <sub>2</sub> O (728)	19.58	<b>709-713</b> and 728

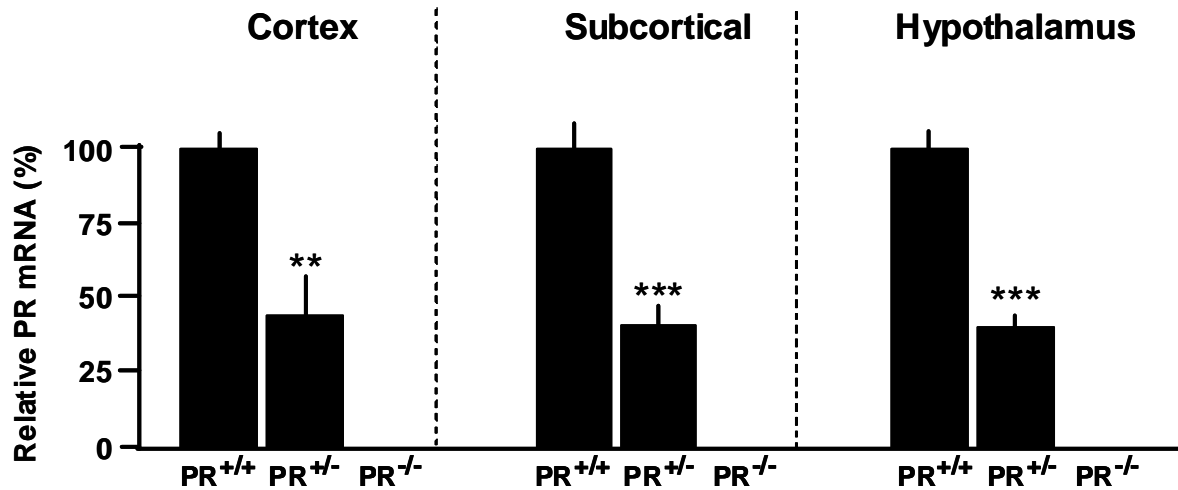
Two diagnostic ions were used for identification and the one in bold was used for quantification.

(MW: molecular weight, 5 $\alpha$ -DHP: 5 $\alpha$ -dihydroprogesterone, HFB: heptafluorobutyrate derivative, TMS: trimethylsilyl derivative).

**Supplemental Table 2. Quantitative polymerase chain reaction (qPCR).**

<b>mRNA</b>	<b>Primer sequences 5' to 3'</b>	<b>Ex</b>	<b>r</b>
<b>PR</b>	PR F: CCGGAGAAGGACAGCAGACT PR R: GGGCTGGCGTGACTCTGTT	<b>93.68 ± 1.73</b>	<b>0.997± 0.003</b>
<b>Cyc b</b>	Cyc F: GTGGCAAGATCGAAGTGGAGAAAC Cyc R: TAAAAATCAGGCCTGTGGAAT GTG	<b>92.08 ± 2.11</b>	<b>0.997 ± 0.01</b>

Correlation coefficients (r) confirm the linear relationship between the threshold cycle and the logarithm of the cDNA concentration. The PCR efficiency (Ex) was calculated using the equation  $Ex = (10^{-1/\text{slope}}) - 1 \times 100$ . Similar amplification efficiency rates between target and reference genes were obtained (Ex close to 1). The r and Ex values showed that PCR conditions have been properly optimized (PR = progesterone receptor; Cyc b = cyclophilin b; F = Forward; R = reverse).



**Supplemental Figure 1. Analysis of PR mRNA expression in brains of  $PR^{+/+}$ ,  $PR^{+/-}$  and  $PR^{-/-}$  mice by qPCR.** When compared to  $PR^{+/+}$  male mice (= 100%), PR mRNA expression is reduced by about 60% in cerebral cortex, subcortical regions and hypothalamus of  $PR^{+/-}$  mice, and is not detected in  $PR^{-/-}$  mice (means  $\pm$  s.e.m.,  $n=4$  per group). Comparisons between  $PR^{+/+}$  and  $PR^{+/-}$  were performed by unpaired Student's t-test for each brain region (\*\* $P < 0.01$ , \*\*\* $P < 0.001$ ).