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# Vulnerability versus resilience to prenatal stress in male and female rats; Implications from gene expression profiles in the hippocampus and frontal cortex



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# **KEYWORDS**

Prenatal stress; Depression; Anxiety; Microarray; Resilience; Epigenetics

### **Abstract**

Adverse life events during pregnancy may impact upon the developing fetus, predisposing prenatally stressed offspring to the development of psychopathology. In the present study, we examined the effects of prenatal restraint stress (PS) on anxiety- and depression-related behavior in both male and female adult Sprague-Dawley rats. In addition, gene expression profiles within the hippocampus and frontal cortex (FC) were examined in order to gain more insight into the molecular mechanisms that mediate the behavioral effects of PS exposure. PS significantly increased anxiety-related behavior in male, but not female offspring. Likewise, depression-related behavior was increased in male PS rats only. Further, male PS offspring showed increased basal plasma corticosterone levels in adulthood, whereas both PS males and

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females had lower stress-induced corticosterone levels when compared to controls. Microarray-based profiling of the hippocampus and FC showed distinct sex-dependent changes in gene expression after PS. Biological processes and/or signal transduction cascades affected by PS included glutamatergic and GABAergic neurotransmission, mitogen-activated protein kinase (MAPK) signaling, neurotrophic factor signaling, phosphodiesterase (PDE)/ cyclic nucleotide signaling, glycogen synthase kinase 3 (GSK3) signaling, and insulin signaling. Further, the data indicated that epigenetic regulation is affected differentially in male and female PS offspring. These sex-specific alterations may, at least in part, explain the behavioral differences observed between both sexes, i.e. relative vulnerability versus resilience to PS in male versus female rats, respectively. These data reveal novel potential targets for antidepressant and mood stabilizing drug treatments including PDE inhibitors and histone deacetylase (HDAC) inhibitors. © 2012 Elsevier B.V. and ECNP. All rights reserved.

# 1. Introduction

Environmental adversity, either physical or emotional, experienced by the mother during pregnancy, may impact upon the developing fetus, adversely affecting its physical and mental wellbeing in later life. In humans, prenatal stress (PS) has been associated with the development of various cognitive and affective disorders, such as depression and anxiety (Huizink et al., 2004; Van den Bergh et al., 2005; Weinstock, 2001). Likewise, PS in rats has been associated with altered stress responsivity and increased anxiety- and depression-related behavior, see review by Huizink et al. (2004). These behavioral effects of PS can be counteracted by treating prenatally stressed rat offspring with various kinds of antidepressants (Alonso et al., 1999; Morley-Fletcher et al., 2003a, 2004; Poltyrev et al., 2005; Poltyrev and Weinstock, 2004). Therefore, PS in rats is regarded as a valid 'etiological' animal model to obtain more insight into the pathophysiology of affective disorders.

Similar to the human situation, the effects of PS exposure in rats are highly sex-dependent. More specifically, PS in Sprague-Dawley rats has been shown to particularly affect male offspring, whereas females are relatively resilient at the behavioral level (Zuena et al., 2008). Along similar lines, e.g. the hippocampus - a brain structure that is subject to sex-dependent development and is well-known for its role in affective regulation - has been shown to be differentially affected by PS in male and female rat offspring, which is indicative of sex-specific vulnerability to disturbed glutamatergic and GABAergic neurotransmission and reduced hippocampal neuroplasticity (e.g. Zuena et al., 2008; Morley-Fletcher et al., 2011; Laloux et al., 2012).

In the present study, we examined the effects of PS in both male and female Sprague-Dawley rats. Adult anxiety-and depression-related behavior was studied using the elevated zero maze test, the home cage emergence test, the forced swim test, and the sucrose intake test. Further, basal and stress-induced activity of the hypothalamus-pituitary-adrenal (HPA) axis was studied. Finally, we examined the effects of PS on gene expression profiles within the hippocampus and frontal cortex (FC), two brain regions known to be critically involved in the pathophysiology of depressive disorders and the response to antidepressant treatment (Sheline et al., 2003; Taylor et al., 2008). For this purpose, as a hypothesis-generating approach, a whole genome microarray-based design was used in order to

identify the genes and related molecular pathways that mediate vulnerability versus resilience to the behavioral effects of developmental stress exposure in male and female PS offspring, respectively.

# 2. Experimental procedures

# 2.1. Animals and procedures

This study was approved by the Animal Ethics Board of the Maastricht University, The Netherlands. Acclimatized Sprague-Dawley rats (Charles River, The Netherlands) were used. The animals were housed individually within a temperature-controlled environment (21 $\pm$ 1 °C) with a 12 h light/12 h dark cycle (lights on from 7.00-19.00 h) and had access to standard rat chow and water ad libitum. Pregnancy was determined by observation of vaginal plugs (embryonic day 0-E0). Restraint stress was performed daily during the last week of pregnancy (E14-E21). Pregnant female rats (n=8) were individually restrained 3 times a day (at approximately 9.00, 13.00, and 17.00 h) for 45 min in transparent plastic cylinders, whilst being exposed to bright light (Van den Hove et al., 2005; Ward and Weisz, 1984). Control (C) pregnant females (n=8) were left undisturbed in their home cages. Only litters of 8 or more pups were included in this study. Litters were culled to 8 pups if necessary. A maximum of 2 male and female pups per litter were examined to prevent litter effects (Chapman and Stern, 1978).

At postnatal day 21 (P21), pups were weaned and group-housed for further examination (2 male or 2 female rats/cage; n=14 rats per experimental condition per sex). Rats were kept at a reversed day-night cycle from this point onwards (lights on from 17.00-5.00 h). Anxiety- and depression-related behavior of the rats was analyzed from P120 onwards (in the order as discussed below). Subsequently, at P143, plasma corticosterone secretion was assessed. One week later, at P150, the animals were killed by quick decapitation, after which the brains were removed. The hippocampus and FC were dissected, weighed and bilateral tissue samples were placed in a single tube and snapshot frozen in liquid nitrogen after which they were stored at -80 °C until further analysis.

# 2.2. Anxiety- and depression-related behavior

The elevated zero maze (EZM) introduced by Shepherd et al. (1994) consisted of a circular alley (diameter of 100 cm; path width 10 cm) made from black plastic material that was transparent for infrared light and elevated 20 cm above the floor. The maze was divided into four parts, i.e., two opposite open parts and two opposite closed parts with sidewalls 30 cm in height. The open parts had borders with a height of 5 mm to prevent the rat from stepping down from the apparatus. For the test, the rat was placed into one of the open

parts facing a closed part of the apparatus. After 5 min the rat was removed from the apparatus and the maze was cleaned with ethanol (70%) and water and dried thoroughly. The movements of the rat were scored automatically under dark conditions with a computerized system using an infrared video camera (Ethovision Pro, Noldus, The Netherlands). Percentage of time spent in the open part of the maze and total distance traveled were determined.

In the home cage emergence (HCE) test the rat's home cage (opened) was placed in the center of an open field (1 m<sup>2</sup>; under low light conditions) and the rat was allowed to leave its cage via a grid walkway. The latency to emerge from the home cage (i.e., four paws on the grid) was scored. If the rat did not emerge from its home cage within 300 s, the session was ended, the home cage was closed again and the rat was given a score of 300 s. The scores of 3 trials carried out on 3 consecutive days were averaged (Prickaerts et al. 1996)

In the forced swimming test (FST), originally designed by Porsolt et al. (1978), four cylindrical glass tanks (50 cm tall, 20 cm in diameter) were filled to a height of 30 cm with 25 °C water. The movements of the rat were scored automatically with a computerized system (Ethovision Pro, Noldus, The Netherlands) during a 5 min session under low light conditions. Scored were 'immobility', which reflects no movement at all and/or minor movements necessary to keep the nose above the water, and 'strong mobility', reflecting 'escape behavior' (e.g. climbing against the walls and diving). Settings within Ethovision were adjusted based on manually recorded sessions and were attuned for each sex separately (immobility/mobility threshold: 12 and 20; mobility/strong mobility threshold: 16.5 and 23.9 for males and females, respectively; Strackx et al., 2009).

The sucrose intake (SI) test was used to examine anhedonia (Willner et al., 1992; Dalla et al., 2005; Gronli et al., 2005). Rats were allowed to acclimatize to a 1% sucrose solution 2 days before the actual experiment. At 5.00 h on the test day, at the start of the dark phase, rats were deprived of food and water for 14 h. At 19.00 h, i.e., 2 h after the lights had turned on a 1% sucrose solution was offered. After 1 h sucrose consumption was measured and the intake was expressed in ml 1% sucrose/kg body weight consumed to control for intake differences due to possible differences in body weight (Dalla et al., 2005; Gronli et al., 2005).

# 2.3. Corticosterone response and radioimmuno-assay

To test the HPA axis responsivity, rats were individually placed in a type II (mouse) cage filled with 500 ml 25 °C water. Experiments were performed in an isolated room between 13.00 and 15.00 h. Immediately after taking the rat from its home cage, a first blood sample was collected via a saphenous vein puncture representing the basal corticosterone level. Immediately after this first sample was taken, the rat was put in the cage filled with water for 20 min after which a second blood sample was taken. Afterwards, the animal was returned to its home cage and left undisturbed for 40 min after which a final blood sample was taken. Blood samples were kept on ice and centrifuged at 5000 rpm for 10 min at 4 °C, after which the plasma was frozen down to -75 °C for subsequent determination of corticosterone levels (in duplicate). For this purpose, 50 µl of plasma was extracted with 3 ml dichloromethane and vortexed for 1 min. Corticosterone was subsequently measured directly on 1 ml dried dichloromethane and extracted for radioimmunoassay using corticosterone-125 l. The radioimmunological reaction was performed overnight at 4 °C, after which a second antibody system was used to separate bound and unbound steroid as previously described in detail (Sulon et al., 1978). The average intra- and inter-assay coefficients of variation for all assays were below 10%. The assay had a sensitivity of 7.7 ng/mL.

# 2.4. RNA preparation

Total RNA was extracted using RNeasy Mini kits (QIAGEN, Venlo, The Netherlands). Glass beads of 1 mm together with buffer RLT (provided by the RNeasy Mini kit) were added to the frozen tissues, and subsequently homogenized in a Minibead Beater (Biospec Products, OK, USA). After removal of cellular debris by centrifugation, extraction was continued according to instructions of the RNeasy Mini kit.

### 2.5. Microarray hybridization

Analysis of whole genome expression was performed at the facilities of ServiceXS (Leiden, The Netherlands). Quality of RNA samples was assessed by electrophoresis using the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). Of each experimental group four pools of three samples were prepared. Pools were subsequently hybridized on the RatRef-12 Expression BeadChip (Illumina, San Diego, CA, USA).

### 2.6. Data normalization

Normalization of expression data was performed as previously described (Alttoa et al., 2010). In summary, the raw microarray data were processed using the Beadarray (Dunning et al., 2007) PreprocessCore (Bolstad et al., 2003) and PUMA (Sanguinetti et al., 2006) R packages of bioconductor (Bioconductor). In the Beadarray package the BackgroundCorrect method used was "minimum", whilst variables for the CreatebeadsummaryData method were as follows: log=TRUE, n=10. Data were normalized using the quantile normalization algorithm from the PreprocessCore package. An important outcome measure of the PUMA analysis is the Probability of Positive Log Ratio (pplr) statistic, a probability measure of differential expression that considers uncertainty of expression levels. Statistically significant differentially expressed genes were defined as genes with a minimum pplr value (the minimum of pplr or 1-pplr) less than 0.001. As such, separate sets of differentially expressed genes between control and PS animals for each gender and brain region (hippocampus and FC) were generated.

# 2.7. Microarray data analysis

To find significantly over-represented molecular pathways within the sets of genes differentially regulated by PS, we searched the pathway database of the Kyoto Encyclopedia of Genes and Genomes (KEGG) using the DAVID Functional Annotation Tool (http://david.abcc.ncifcrf.gov/, see also (Huang da et al., 2009)). The KEGG pathway database is a collection of manually drawn graphical diagrams that represent the current knowledge of molecular interactions involved in various cellular processes (http://www.genome.ad.jp/kegg/pathway.html). The DAVID tool produces a gene enrichment score (EASE score, which is a modified Fisher Exact p-value) for each KEGG pathway. For identifying significant enriched pathways the cut-off value was set at p<0.05. Additionally, the lists of differentially expressed genes were manually screened to identify genes encoding proteins, known to be implicated in signaling pathways in the pathophysiology and/or treatment of mood disorders.

# 2.8. Statistical analysis

EZM, FST and SI data were explored by using a two-way ANOVA (sex x condition). In addition, since all of these tests displayed either a significant sex x condition interaction effect and/or highly significant sex effects, a stratified analysis was performed for each sex separately. For the HCE test, the data were not normally distributed

since some rats remained in the home cage for the entire observation period. Therefore, these data were transformed to rank scores, after which average escape latencies were compared between groups. Plasma corticosterone values were ln-transformed to normality. HCE data and corticosterone levels were analyzed by a repeated measures ANOVA (sex x condition) and also independently at the different time points using a two-way ANOVA (sex x condition). Correlation analysis was performed using Pearson's correlation coefficient  $(r_p)$ . Statistical significance was assumed to exist at P < 0.05, except when studying the effects of PS on corticosterone levels at the individual time points, in order to correct for multiple testing (P < 0.017). All statistics were carried out using SPSS software version 12.0.1 (SPSS Inc, USA).

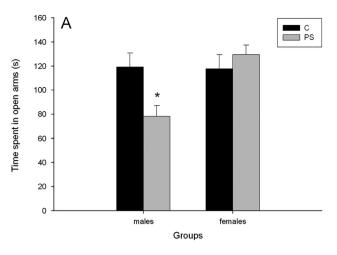
# 3. Results

# 3.1. Maternal weight gain, offspring birth weight, litter size and pre-weaning mortality

Maternal stress exposure in this cohort of animals was associated with reduced maternal weight gain over gestation, concomitant with impaired fetal growth in both sexes, as reported previously (Van den Hove et al., 2010). No differences were observed in litter size (13.6 $\pm$ 0.9 and 14.1 $\pm$ 0.5 pups per litter for C and PS, respectively) or pre-weaning mortality (no pups died in either group after litters had been culled to 8 pups).

# 3.2. Anxiety- and depression-related behavior

The percentage of time spent in the open arms of the EZM as well as the distance covered in the EZM are depicted in Figure 1. An overall sex x condition interaction was observed ( $F_{1,49}$ =6.662; P=0.013) as well as an overall sexeffect ( $F_{1.49}$ =5.983; P=0.018). The overall condition effect did not reach statistical significance ( $F_{1,49}$ =2.050; P=0.159). Stratified analyses showed that PS male rats spent less time in the open arms of the EZM as compared to C males (PS effect: -34.4%,  $F_{1,24}=7.557$ ; P=0.011). In addition, an overall sex-effect for the total distance moved in the EZM was found ( $F_{1,49}$ =18.369; P<0.001), whereas there was no overall condition-effect or sex x condition interaction  $(F_{1,49}=1.491; P=0.228 \text{ and } F_{1,49}=3.587; P=0.064, \text{ respec-}$ tively). Stratified analysis revealed that male PS rats covered less distance during the 5 min trial as compared to C males (PS effect: -25.3%,  $F_{1,24}=4.970$ ; P=0.035). No differences were observed between PS and C females in this respect ( $F_{1,25}$ =0.704; P=0.409 for time spent in the open arms, and  $F_{1,25}$ =0.222; P=0.642 for total distance moved). The average escape latencies in the HCE test are shown in Figure 2. Over time, a significant overall effect for PS was found ( $F_{1.48}$ =6.423; P=0.015) as well as a significant sex effect ( $F_{1.48}$ =49.482; P<0.001). The sex x condition interaction effect over time, however, failed to reach statistical significance ( $F_{1,48}$ =0.031; P=0.860). More specifically, over the three trials, male PS rats took more time to leave the home cage as compared to controls (PS effect: +25.3%,  $F_{1,25}$ =4.863; P=0.037). A similar trend was observed in female offspring, although this was not significance (PS effect: +33.7%,  $F_{1,23}=3.026$ ; P=0.095). Results from the FST are shown in Figure 3. The immobility time did not show overall PS effects, nor did it show a sex x condition



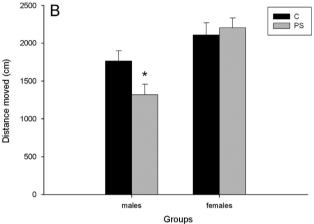
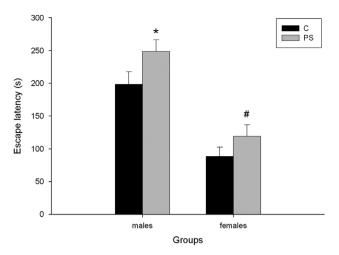


Figure 1 Percentage of time spent in the open arms of (A) and total distance moved in (B) the elevated zero maze (EZM). Values represent means+S.E.M. Male prenatally stressed (PS) rats spent less time in the open arms of the EZM as compared to control (C) males. Further, male PS rats covered less distance during the 5 min trial as compared to C males. No differences were observed between PS and C females.  $^*P < 0.05$  (One-way ANOVA).

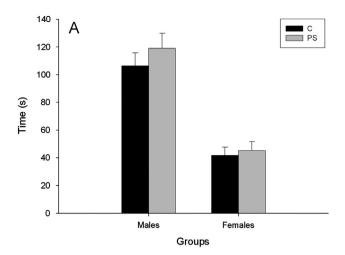
interaction ( $F_{1.52}$ =0.957; P=0.333 and  $F_{1.52}$ =0.309; P=0.581, respectively). However, a profound overall sex effect was observed ( $F_{1.52}$ =69.658; P<0.001), while stratified analysis per sex revealed no differences between PS and controls (males:  $F_{1,26}$ =0.807; P=0.377; females:  $F_{1,26}$ =0.164; P=0.688). Strong mobility in the FST showed an overall trend ( $F_{1,52}$ =3.239; P=0.078), a highly significant sex effect ( $F_{1,52}$ =16.952; P<0.001) and a trend for a sex x condition interaction ( $F_{1,52}$ =3.466; P=0.068). Stratified analysis indicated that PS in males resulted in less strong mobility as compared to controls (PS effect: -21.7%,  $F_{1.26}$ =4.241; P<0.05), whereas no differences in strong mobility were observed between female groups ( $F_{1.26}$ = 0.005; P=0.947). Overall, no differences in SI were observed between PS and C offspring ( $F_{1,24}$ =2.401; P=0134). While there was no sex x condition interaction ( $F_{1,24}$ =0.422; P=0.522), a significant overall sex effect was found  $(F_{1.24}=11.158; P=0.003)$ . Stratified analysis showed no differences between PS and control offspring in either sex (males:  $F_{1.12}$ =0.619; P=0.447; females:  $F_{1.12}$ =1.796; P=0.205) (Table 1).



**Figure 2** Average escape latencies in the home cage emergence (HCE) test. Values represent means (s)+S.E.M. Over the three trials, male prenatally stressed (PS) rats took more time to leave the home cage as compared to controls (C). A similar pattern was observed in female offspring, though this did not reach statistical significance. \*P<0.05, \*0.05<P<0.10 (ANOVA based on ranks).

# 3.3. Corticosterone response

Plasma corticosterone levels under basal conditions, immediately after 20 min of restraint stress, or 40 min after being placed back into the home cage, are depicted in Figure 4. Analysis with repeated-measures ANOVA revealed a highly significant change in corticosterone levels over time  $(F_{2.90}=128.375; P<0.001;$  sphericity assumptions met), as well as a significant overall PS effect ( $F_{1.45}$ =4.947; P=0.031) and a highly significant overall sex effect ( $F_{1.45}$ =33.591; P < 0.001), whereas the sex x condition interaction was not significant ( $F_{1.45}$ =0.353; P=0.555). Looking at the three measurements individually (two-way ANOVA) indicated overall PS effects for basal corticosterone levels ( $F_{1.45}$ =9.871; P=0.003) and stress levels ( $F_{1.45}=14.194$ ; P<0.001), both of which were accompanied by highly significant sex differences  $(F_{1,45}=40.632; P<0.001 \text{ for basal levels and } F_{1,45}=73.856;$ P<0.001 for stress levels). Overall condition effects for recovery after stress were, however, not significant  $(F_{1.45}=2.511; P=0.120)$  and showed no sex or sex x treatment interaction effects ( $F_{1.45}$ =0.016; P=0.900 and  $F_{1.45}$ =0.102; P=0.751, respectively). Stratified analysis revealed a significant within-subjects effect in males both for time ( $F_{2,50}$ =83.926; P<0.001) and experimental group x time  $(F_{2,50}=7.803; P=0.001)$ . In addition, over time, a significant effect of PS was observed ( $F_{1,25}$ =4.933; P=0.036). Male PS rats further showed higher basal plasma corticosterone levels as compared to controls (PS effect: +108.7%,  $F_{1.25}=11.568$ ; P=0.002), whereas stress-induced corticosterone levels were again lower in male PS rats (PS effect: -21.9%,  $F_{1.25}=10.183$ ; P=0.004). In females, a significant within-subjects effect was observed only for time ( $F_{2,40}$ =65.937; P<0.001). Further, only stress-induced plasma corticosterone levels differed between groups, with PS females showing lower corticosterone levels as compared to controls (PS effect: -21.6%,  $F_{1.20}=4.876$ ; P=0.039). No difference between groups was observed after



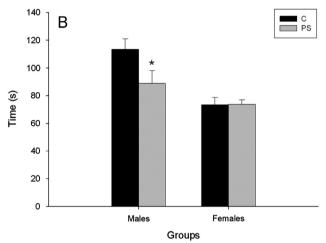


Figure 3 Immobility (A) and strong mobility (B) in the forced swim test (FST); Values represent means (s)+S.E.M. Whereas no differences between groups were observed in time spent immobile, prenatal stress (PS) in males resulted in less strong mobility as compared to controls (C). No differences in any parameter were observed between female groups.  $^*P$ <0.05 (One-way ANOVA).

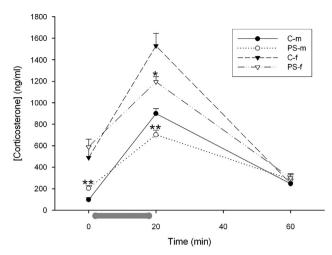
Table 1	able 1 Sucrose intake (ml/kg body weight).					
Sex	Group	Sucrose intake				
Males	C PS	39.5±4.7 45.1±5.4				
Females	C PS	56.6±6.8 70.1±7.6				

Values represent means ± S.E.M. Abbreviations: C: control and PS: prenatal stress. No significant differences between experimental groups were observed.

40 min of recovery (males:  $F_{1,25}$ =0.846; P=0.367; females:  $F_{1,20}$ =1.768; P=0.199).

# 3.4. Brain region weights

Weight data of the hippocampus and FC are listed in Table 2. Relative hippocampal weight was higher in PS females as



**Figure 4** Stress-induced corticosterone secretion. Values represent means (ng/ml)+S.E.M. Male prenatally stressed (PS) rats showed higher basal plasma corticosterone levels as compared to controls (C). Stress-induced corticosterone levels (the grey bar represents a 20 min period of stress) were lower in both male and female PS offspring. No difference between groups was observed 40 min after placing the animals back into their home cage. \*P < 0.05, \*\*P < 0.01 (One-way ANOVA).

Table 2 Brain region weights (mg/kg body weight).

Sex	Group	Hippocampus	FC
Males	C	$302.9 \pm 9.8$	79.2±4.7
	PS	$299.4 \pm 9.8$	95.4±6.4
Females	C	$485.9 \pm 14.5$	147.1 ± 5.6
	PS	$550.1 \pm 19.8^{a}$	164.6 ± 15.1

Values represent means  $\pm$  S.E.M. Abbreviations: C: control, PS: prenatal stress and FC: frontal cortex.

compared to C females (PS effect: 13.2%, P=0.015). No difference between groups was observed in any other case.

# 3.5. Gene expression profiles

# 3.5.1. Differential expression of genes related to stress and affective behavior

Within the hippocampus, PS affected the expression of 44 and 1084 genes in male and female offspring, respectively. Within the FC, 114 and 688 genes were expressed differentially by PS in male and female offspring, respectively. An overview of all genes regulated by PS exposure within the hippocampus and FC of male offspring is given in Tables 3 and 4, respectively. Individual genes regulated in the hippocampus and FC of female offspring is depicted in Supplemental Material S1 and S2.

# 3.5.2. Pathway analyses

DAVID-KEGG analysis showed that in male offspring no KEGG pathways were significantly enriched by PS within any of the brain regions, which was related to the limited number of

genes affected by PS in male offspring. Results from the KEGG pathway analyses on gene expression profiles within the female hippocampus and FC are depicted in Tables 5 and 6, respectively. Within the hippocampus, 'cell adhesion molecules (CAMs)', 'ErbB signaling pathway', 'focal adhesion', 'insulin signaling pathway', 'long term potentiation', 'mTOR signaling pathway', 'phosphatidylinositol (PI) signaling system', and 'tight junction' were significantly changed after PS. Within the FC, the KEGG pathways 'ribosome' and 'Wnt-signaling' were significantly affected by PS. In addition, manual browsing of the gene lists for candidate genes encoding proteins known to be involved in the pathophysiology and/or treatment of affective disorders revealed several differentially expressed genes involved in glutamate and gamma-aminobutyric acid (GABA) neurotransmission, cyclic adenosine monophosphate (cAMP)/ cyclic guanosine monophosphate (cGMP)/ phosphodiesterase (PDE) signaling, and epigenetic regulation, in both the hippocampus and FC of male and female PS offspring (see Table 7). An overview on relevant signaling cascades altered within the female hippocampus and FC, based on the expression profiles and subsequent functional clustering using DAVID is given in Figure 5.

# 4. Discussion

As a hypothesis-generating approach, in order to gain more insight into the molecular mechanisms that mediate the behavioral effects of developmental stress exposure, we examined the enduring effects of PS exposure on gene expression profiles within the hippocampus and FC of adult male and female Sprague-Dawley rats. While PS increased anxiety- and depression-related behavior particularly in male Sprague-Dawley rats, female offspring seemed to be relatively resilient to PS exposure. In addition, PS altered the expression of numerous genes in the hippocampus and FC in a sex-specific manner. These sex-specific alterations may, at least in part, explain the behavioral differences observed between both sexes, i.e. relative vulnerability versus resilience to PS in male versus female rats, respectively.

# 4.1. Sex differences in behavior and the response to stress

PS resulted in a significant increase in anxiety- and depression-related behavior in male offspring, while behavior in females was largely unaffected. In addition, only male PS offspring showed clearly increased basal plasma corticosterone levels, whereas PS offspring of both sexes failed to show an adequate response to stress. Among females, adult hippocampal weight was relatively increased after PS.

Although the overall prevalence of mood disorders is higher in female as compared to male humans (Blehar, 1995), a different pattern seems to be observed in PS-related psychopathology (Darnaudery and Maccari, 2007). Whereas only male PS Sprague-Dawley rats showed a clear increase in anxiety- and depression-related behavior, PS females seemed to remain relatively resilient to PS exposure in the present study. Studies by the group of

 $<sup>^{\</sup>rm a}P$ <0.05 (Student's t-test).

 Table 3
 Genes differentially regulated by PS exposure in the male hippocampus, sorted by fold change.

Entrez symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold change
Mrpl18_predicted	292244	mitochondrial ribosomal protein L18	ILMN_54513	ILMN_1359180	5.46
Sc5dl	114100	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. <i>cerevisiae</i> )-like	ILMN_263006	ILMN_1363277	2.59
Rbj	298859		ILMN_278305	ILMN_1355125	1.31
Kcnab2	29738	potassium voltage-gated channel, shaker-related subfamily, beta member 2	ILMN_267848	ILMN_1355212	1.28
mrpl11	293666	mitochondrial ribosomal protein L11	ILMN_291563	ILMN_1363330	1.28
Ttyh3_predicted	304315	tweety homolog 3 (Drosophila)	ILMN_272392	ILMN_1651087	1.27
Trrap_predicted	288471	transformation/transcription domain-associated protein	ILMN_267735	ILMN_1360742	1.25
Hdac4_predicted	363287	histone deacetylase 4	ILMN_266642	ILMN_1364573	1.24
LOC361990	361990	similar to DKFZP547E1010 protein; similar to Protein C1orf77 homolog	ILMN_66762	ILMN_1650076	1.21
Thg1l	303067	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	ILMN_286909	ILMN_1649860	1.20
RGD1307814_predicted	362559	zyg-11 homolog B (C. elegans)	ILMN_278965	ILMN_1375196	1.19
Rhcg	293048	Rh family, C glycoprotein	ILMN_281613	ILMN_1361451	1.19
RGD1565184_predicted			_	ILMN_1530385	
LOC501534	501534	NA	ILMN_66173	ILMN_1360820	1.16
RGD1566402_predicted	500127	homeo box A10	ILMN_285373	ILMN_1354843	1.16
Farsb	301544	phenylalanyl-tRNA synthetase, beta subunit	ILMN_265522	ILMN_1356564	1.15
lbrdc2_predicted	364681	ring finger protein 144B	ILMN_291094	ILMN_1366789	1.15
Lgals7	29518	lectin, galactoside-binding, soluble, 7	ILMN_297724	ILMN_1376402	1.15
Mrc2_predicted	295631	phospholipase A2 receptor 1	ILMN_277146	ILMN_1358009	1.15
Spn	24796	Sialophorin	ILMN_279075	ILMN_1361495	1.15
Dnajc11_predicted Sbk1	362666 113907	DnaJ (Hsp40) homolog, subfamily C, member 11 similar to SH3-binding kinase; SH3-binding domain		ILMN_1361685 ILMN_1353425	
		kinase 1			
LOC503147	503147	similar to FLJ45949 protein	ILMN_66420	ILMN_1361222	1.13
Wdr7	66031	WD repeat domain 7	ILMN_290962	ILMN_1351953	1.13
LOC500878	500878	similar to LRRGT00057	ILMN_48959	ILMN_1372001	1.11
Calr3_predicted	364529	calreticulin 3	ILMN_48314	ILMN_1375963	0.89
Dhh	84380	desert hedgehog homolog (Drosophila)	ILMN_53576	ILMN_1370554	0.89
Mif	81683	macrophage migration inhibitory factor (MIF)	ILMN_264813	ILMN_1356539	0.89
Olr1491_predicted	404969	olfactory receptor 1491	ILMN_277212	ILMN_1359277	0.89
Aspn	306805	asporin	ILMN_285309	ILMN_1369408	0.88
Pik3c2g	116720	phosphoinositide-3-kinase, class 2, gamma polypeptide	ILMN_273653	ILMN_1349959	0.88
Lhx6_predicted	311901	LIM homeobox 6	ILMN_60425	ILMN_1352539	0.87
Ufd1l	84478	ubiquitin fusion degradation 1 like (yeast)	ILMN_49407	ILMN_1372253	0.87
Sema6b	84609	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	ILMN_288957	ILMN_1650011	0.86
Limk1	65172	LIM domain kinase 1	ILMN_286066	ILMN_1372778	0.85
Traf3ip3	360900	TRAF3 interacting protein 3	ILMN_287167	ILMN_1365920	0.85
Olr556	405249	olfactory receptor 557; olfactory receptor 556	ILMN_269876	ILMN_1373130	0.84
Timm9	171139	translocase of inner mitochondrial membrane 9 homolog (yeast)	ILMN_271875	ILMN_2039665	0.83
Gnl3	290556	guanine nucleotide binding protein-like 3 (nucleolar); similar to guanine nucleotide binding protein-like 3 (nucleolar)	ILMN_263704	ILMN_1357924	0.80
Mrps2_predicted	362094	mitochondrial ribosomal protein S2	ILMN_50349	ILMN_1365807	0.80
Prim2	301323	primase, DNA, polypeptide 2	ILMN_270579	ILMN_1355020	
Arsb	25227	arylsulphatase B	ILMN_58825	ILMN_1366780	

lnerability versus re	nerability versus resilience to PS in male and female rats  123					
Table 4 Genes dif	ferentially re	egulated by PS exposure in the male FC, sorted by	fold change.			
Symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold change	
Mrpl18_predicted	292244	mitochondrial ribosomal protein L18	ILMN_54513	ILMN_1359180	6.40	
Sc5dl	114100	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	ILMN_263006	ILMN_1363277	2.00	
C4-2	406161	complement component 4, gene 2	ILMN_271471	ILMN_1361837	1.31	
Txnip	117514	thioredoxin interacting protein	ILMN_280023	ILMN_1359696	1.29	
Prim1	246327	DNA primase, p49 subunit	ILMN_271101	ILMN_1353345	1.28	
Gng11	64199	guanine nucleotide binding protein (G protein), gamma 11	ILMN_62822	ILMN_1354189	1.25	
Plac8_predicted	360914	placenta-specific 8	ILMN_292070	ILMN_1363160	1.24	
Tmem140	362334	transmembrane protein 140	ILMN_278563	ILMN_1372260	1.24	
Cyyr1	304138	cysteine/tyrosine-rich 1	ILMN_287228	ILMN_1374917	1.22	
Ifitm3	361673	interferon induced transmembrane protein 3	ILMN_265471	ILMN_1352762	1.22	
Heph	117240	Hephaestin	ILMN_269859	ILMN_1371544	1.21	
Lcp1	306071	lymphocyte cytosolic protein 1	ILMN_279425	ILMN_1376765	1.20	
Commd9	295956	COMM domain containing 9	ILMN_270917	ILMN_1370105	1.19	
LOC309349	309349	SLIT and NTRK-like family, member 2	_	ILMN_1357725		
Cyba	79129	cytochrome b-245, alpha polypeptide		ILMN_1366276		
Gpm6a	306439	glycoprotein m6a	_	ILMN_1367162		
Loxl1	315714	lysyl oxidase-like 1	_	ILMN_1376846		
Tnfrsf11b	25341	tumor necrosis factor receptor superfamily, member 11b	ILMN_285163	ILMN_1374220	1.18	
Slc37a1	294321	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	ILMN_297940	ILMN_1376690	1.15	
Sox17_predicted	312936	SRY (sex determining region Y)-box 17		ILMN_1359017		
Ssg1	64387	coiled-coil domain containing 80	ILMN_59129	ILMN_1362820	1.15	
Loxl2_predicted	290350	lysyl oxidase-like 2	ILMN_55682	ILMN_1351352	1.14	
Slpi	84386	secretory leukocyte peptidase inhibitor	ILMN 270427	ILMN 1360286	1.14	

Symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold chang
Mrpl18_predicted	292244	mitochondrial ribosomal protein L18	ILMN_54513	ILMN_1359180	6.40
Sc5dl	114100	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	ILMN_263006	ILMN_1363277	2.00
C4-2	406161	complement component 4, gene 2	ILMN_271471	ILMN_1361837	1.31
Txnip	117514	thioredoxin interacting protein	ILMN_280023	ILMN_1359696	1.29
Prim1	246327	DNA primase, p49 subunit	ILMN_271101	ILMN_1353345	1.28
Gng11	64199	guanine nucleotide binding protein (G protein), gamma 11	ILMN_62822	ILMN_1354189	1.25
Plac8_predicted	360914	placenta-specific 8	ILMN_292070	ILMN_1363160	1.24
Tmem140	362334	transmembrane protein 140	ILMN_278563	ILMN_1372260	1.24
Cyyr1	304138	cysteine/tyrosine-rich 1	ILMN_287228	ILMN_1374917	1.22
lfitm3	361673	interferon induced transmembrane protein 3	ILMN_265471	ILMN_1352762	1.22
Heph	117240	Hephaestin	ILMN_269859	ILMN_1371544	1.21
Lcp1	306071	lymphocyte cytosolic protein 1	ILMN_279425	ILMN_1376765	1.20
Commd9	295956	COMM domain containing 9	ILMN_270917	ILMN_1370105	1.19
LOC309349	309349	SLIT and NTRK-like family, member 2	ILMN_65982	ILMN_1357725	1.19
Cyba	79129	cytochrome b-245, alpha polypeptide	ILMN_279326	ILMN_1366276	1.18
Gpm6a	306439	glycoprotein m6a		ILMN_1367162	
Loxl1	315714	lysyl oxidase-like 1		ILMN_1376846	
Tnfrsf11b	25341	tumor necrosis factor receptor superfamily, member 11b	ILMN_285163	ILMN_1374220	1.18
Slc37a1	294321	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	ILMN_297940	ILMN_1376690	1.15
Sox17_predicted	312936	SRY (sex determining region Y)-box 17	ILMN_288748	ILMN_1359017	1.15
Ssg1	64387	coiled-coil domain containing 80	ILMN_59129	ILMN_1362820	1.15
_oxl2_predicted	290350	lysyl oxidase-like 2	ILMN_55682	ILMN_1351352	1.14
Slpi	84386	secretory leukocyte peptidase inhibitor	ILMN_270427	ILMN_1360286	1.14
Fxyd5	60338	FXYD domain-containing ion transport regulator 5	ILMN_274559	ILMN_1371590	1.13
Ms4a11_predicted	361735	membrane-spanning 4-domains, subfamily A, member 11	ILMN_295413	ILMN_1356010	1.13
LOC363259	363259	obscurin-like 1	ILMN_52302	ILMN_1351812	1.12
Ninj2	59115	ninjurin 2	ILMN_289402	ILMN_1370725	1.12
Rdm1_predicted	287726	RAD52 motif 1	ILMN_64467	ILMN_1363012	1.12
RGD1560542_predicted	499847	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	ILMN_277969	ILMN_1650382	1.12
RT1-S2	24994	RT1 class Ib, locus H2-TL-like (S2)	ILMN_264682	ILMN_1368215	1.12
Timeless	83508	timeless homolog (Drosophila)	ILMN_275078	ILMN_1370013	1.12
_OC497832	497832/ 89821	transient receptor potential cation channel, subfamily C, member 1	ILMN_64900	ILMN_1373735	1.11
RGD1561935_predicted		similar to hypothetical protein 4930474N05	ILMN_283847	ILMN_1367261	1.11
Arhgap21_predicted	307178	Rho GTPase activating protein 21	ILMN_280800	ILMN_1364451	1.10
Hhex	79237	hematopoietically expressed homeobox	ILMN_280416	ILMN_1353851	1.10
_OC498331	498331	protein tyrosine phosphatase, non-receptor type 13		ILMN_1365973	
Nr1h3	58852	nuclear receptor subfamily 1, group H, member 3		ILMN_1352599	
RGD1562979_predicted	305501	similar to DNA-binding protein Ikaros form 1 - mouse	ILMN_56783	ILMN_1367066	1.10
_OC364321	364321	similar to T-cell receptor alpha-chain precursor	ILMN_65095	ILMN_1649960	
RGD1310868_predicted		endo-beta-N-acetylglucosaminidase	ILMN_64738	ILMN_1368424	
Slc9a1	24782	solute carrier family 9 (sodium/hydrogen exchanger), member 1		1363067	
Hdgf	114499	hepatoma-derived growth factor	ILMN_299659	ILMN_1358138	1.07
RGD1560568_predicted	500914	basic transcription factor 3; similar to basic transcription factor 3	_	1359066	
Hp1bp3	313647	heterochromatin protein 1, binding protein 3	ILMN_297506	ILMN_1362886	0.94
Sf3b2_predicted	293671	splicing factor 3b, subunit 2	_	ILMN_1363457	
RGD1565310_predicted		similar to RIKEN cDNA 1110018J12	_	ILMN_1349900	
Trim27_predicted	291171	tripartite motif-containing 27		ILMN_1374685	

Symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold chang
RGD1305500_predicted	308004	similar to hypothetical protein FLJ13188	ILMN_69760	ILMN_1357698	0.92
40428	64551	septin 7	ILMN_277931	ILMN_1370494	0.91
Atp6v1b2	117596	ATPase, H transporting, lysosomal V1 subunit B2		ILMN_1360084	
lqcb1_predicted	303915	IQ motif-containing B1		ILMN_1367093	
Ntrk2	25054	neurotrophic tyrosine kinase, receptor, type 2		ILMN_1366426	
Oact2	313997	membrane bound O-acyltransferase domain containing 2		ILMN_1373404	
RGD1559475_predicted		similar to dynactin 3; dynactin 3	_	ILMN_1350986	
RGD1564628_predicted		ubiquitin specific peptidase 27, X-linked		ILMN_1350769	
Stap1	305269	signal transducing adapter family member 1		ILMN_1369894	
Tmem18	362722	transmembrane protein 18		ILMN_1367804	
Tsnax	64028	translin-associated factor X		ILMN_1352444	
Cd19_predicted	365367	CD19 molecule	_	ILMN_1367276	
Ddx47	297685	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47		ILMN_1350598	
Eif3d	362952	eukaryotic translation initiation factor 3, subunit D		ILMN_1650977	
Hars2_predicted	362227 296134	p-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)		ILMN_1364969	
Mrps5_predicted Npat_predicted	315666	mitochondrial ribosomal protein S5 nuclear protein, ataxia-telangiectasia locus		ILMN_1358174	
RGD1309216	361726	similar to hypothetical protein FLJ20487		ILMN_1366007 ILMN_1361771	
RGD1561681_predicted		similar to hypothetical protein 1220467 similar to Pyruvate kinase isozymes M1/M2 (Pyruvate kinase muscle isozyme)		ILMN_1374660	
Tmprss2	156435	transmembrane protease, serine 2	II MN 280888	ILMN_1353103	0.90
V1ra12	297439			ILMN_1368051	
Bbx_predicted	303970	bobby sox homolog (Drosophila)		ILMN_1368994	
Chchd4	312559	coiled-coil-helix-coiled-coil-helix domain containing 4; similar to coiled-coil-helix-coiled-coil-		ILMN_1350912	
		helix domain containing 4			
Foxp1_predicted	297480	forkhead box P1	_	ILMN_1351093	
lpo9_predicted	304817	importin 9		ILMN_1353713	
LOC500936	500936	RGD1560018		ILMN_1368595	
Ncor1	54299	nuclear receptor co-repressor 1	_	ILMN_1357958	
RGD1311456_predicted		family with sequence similarity 63, member B		ILMN_1354049	
RGD1311756_predicted		similar to hypothetical protein FLJ20950	_	ILMN_1356092	
Rp9h_predicted	363032	retinitis pigmentosa 9 (human)		ILMN_1650578	
Tcf15_predicted	296272	transcription factor 15		ILMN_1364142	
Tmem158		transmembrane protein 158		ILMN_1371878	
Ash2l_predicted Cdk105		ash2 (absent, small, or homeotic)-like (Drosophila) similar to TGF beta-inducible nuclear protein 1	_	ILMN_1361125 ILMN_2039008	
Ipmk	171458	(L-name related LNR42); CDK105 protein similar to inositol polyphosphate multikinase;	ILMN_267871	ILMN_1355219	0.88
LOC500483	500483	inositol polyphosphate multikinase RGD1559893	II MN 59110	ILMN_1650108	0.88
Mafb	54264	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	_	ILMN_1361027	
Pscd3	116693	cytohesin 3	ILMN_64245	ILMN_1355570	0.88
Bhlhb2	79431	basic helix-loop-helix family, member e40		ILMN_1374180	
Exosc9	294975	exosome component 9		ILMN_1362725	
Papola_predicted	314417	poly (A) polymerase alpha		ILMN_1367021	
Gsk3b	84027	glycogen synthase kinase 3 beta		ILMN_1349648	
LOC308976	308976	jumonji domain containing 5	_	ILMN_1370490	
Pftk1_predicted	362316	PFTAIRE protein kinase 1		ILMN_1355708	
Pou3f2	29588	POU class 3 homeobox 2		ILMN_1370881	
Gabra4	140675	gamma-aminobutyric acid (GABA) A receptor, alpha 4			
Galnt2_predicted	292090	UDP-N-acetyl-alpha-p-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)		 ILMN_1355124	
Grm5	24418	glutamate receptor, metabotropic 5	ILMN_292416	ILMN_1361607	0.85
Ktn1_predicted	361029	kinectin 1		ILMN_1354299	

Symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold change
LOC363410	363410	similar to Ras-related protein Rab-27B	ILMN_54002	ILMN_1370567	0.85
LOC500950	500950	zinc finger protein 317	ILMN_67762	ILMN_1351340	0.85
RGD1311340_predicted	309243	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ILMN_65042	ILMN_1372429	0.85
RGD1311723_predicted	363018	similar to KIAA1731 protein	ILMN_66607	ILMN_1360056	0.85
Tra1_predicted	362862	tumor rejection antigen gp96	ILMN_284286	ILMN_1376625	0.85
Cpsf2_predicted	299256	cleavage and polyadenylation specific factor 2	ILMN_49851	ILMN_1373200	0.84
Keap1	117519	Kelch-like ECH-associated protein 1	ILMN_289150	ILMN_1366907	0.83
Kpnb1	24917	karyopherin (importin) beta 1	ILMN_276390	ILMN_1373492	0.83
RGD1562526_predicted	499821	family with sequence similarity 171, member B	ILMN_54084	ILMN_1365584	0.82
Grin2a	24409	glutamate receptor, ionotropic, N-methyl p-aspartate 2A	ILMN_290907	ILMN_1376686	0.81
RGD1561386_predicted	500985	Cas-Br-M (murine) ecotropic retroviral transforming sequence	ILMN_291557	ILMN_1355687	0.79
Trak2	171086	trafficking protein, kinesin binding 2	ILMN_54675	ILMN_1352978	0.78
LOC497742	497742/	SWI/SNF related, matrix associated, actin dependent	ILMN_69842	ILMN_1349796	0.77
	361745	regulator of chromatin, subfamily a, member 2			
Arsb	25227	arylsulphatase B	ILMN_58825	ILMN_1366780	0.71
Hpcal4	50872	hippocalcin-like 4	ILMN_287235	ILMN_1373628	0.67

Morley-Fletcher et al. (2003a,b), which use the same PS model, i.e. repetitive restraint stress in Sprague-Dawley rats, illustrate a similar pattern with males showing a more vulnerable behavioral phenotype (Darnaudery and Maccari, 2007; Zuena et al., 2008). In addition to the increased vulnerability of males towards, for example, the development of an anxious phenotype, their latest study actually showed PS females to be less anxious as compared to control female offspring, i.e. two even more distinct behavioral phenotypes. The more distinct phenotype might be explained by the fact that Zuena and colleagues started restraining their pregnant dams from 11 days of gestation onwards. Furthermore, Zuena et al. (2008) studied the offspring at a younger age, i.e., 3 months. In line with these sex-specific behavioral phenotypes, prenatally stressed male Sprague-Dawley rats show impaired hippocampal plasticity, whereas female rats exposed to PS show signs of increased structural plasticity (Darnaudery and Maccari, 2007). Discrepancies between these findings and those from other groups may be explained by the use of other rat strains and/or maternal stress paradigms; an issue that has already been addressed recently (Zuena et al., 2008). Further, the age of the offspring studied may play an important role as well. The sex-dependent effects of PS are probably related to the sex-specific timing of relevant developmental processes over gestation (e.g., Owen and Matthews, 2003). The exact role of sex in relation to PS remains to be elucidated though.

# 4.2. Age-related differences in HPA axis (re-)activity

Similarly, the observed pattern of stress-induced corticosterone secretion in our study was substantially different from that of other investigations in Sprague-Dawley rats using the same PS model, but offspring of a different age. In a study by Morley-Fletcher et al. (2003a) using male Sprague-Dawley rats of 3 months of age, no effect of PS on either basal or stress-induced plasma corticosterone levels was found. In that study, however, recovery after 20 min of restraint stress was weaker after PS. In two other comparable studies by the same group using male Sprague-Dawley rats of 2 months of age, both stress-induced plasma corticosterone levels as well as levels after recovery were higher in PS animals (Dugovic et al., 1999; Morley-Fletcher et al., 2003b). An age-dependent relationship between adverse early-life experience (maternal deprivation) and HPA axis (re-)activity was already suggested by De Kloet and Oitzl (2003). Though different in nature, a comparable phenomenon seems to be involved in HPA axis (re-)activity after PS. We therefore hypothesize that alterations in HPA axis (re-)activity per se, rather than just HPA axis hyperactivity are of importance in relation to PS exposure.

# 4.3. Gene expression profiles

Microarray analysis revealed various region- and sex-specific effects of PS. Whereas the behavioral effects of PS were more pronounced in male offspring, gene expression was altered to a greater extent in female offspring. Relevant genes affected in male offspring that may explain, at least in part, the behavioral alterations induced by PS, include those encoding for Mrpl18 and Sc5dl (both of which were highly increased in both the hippocampus and FC), TrkB (decreased expression within the FC), hippocalcin (decreased expression within the FC) and HDAC4 (increased expression within the hippocampus). Concerning the female offspring, we hypothesize that the increased number of differentially expressed genes reflects an adaptive response to PS, involving mechanisms that contribute to resilience to the prodepressant effects of PS. Biological processes and/or signal transduction cascades affected by PS in female offspring

Table 5 KEGG pathways and associated genes regulated by PS exposure in the female hippocampus. Entrez symbol Entrez Gene name Transcript Probe ID Fold gene ID change Cell adhesion molecules (CAMs) **Alcam** 79559 activated leukocyte cell adhesion molecule ILMN\_298443 ILMN\_1370154 0.34 Cd226\_predicted 307199 cd226 antigen (predicted) ILMN\_58791 ILMN\_1350388 1.14 Cd276 315716 b7 homolog 3 ILMN\_61049 ILMN\_1360321 1.36 Cd80 25408 cd80 antigen ILMN\_300031 ILMN\_1353891 1.15 Cldn10\_predicted 290485 claudin 10 (predicted) ILMN\_272711 ILMN\_1358030 0.70 claudin 5 Cldn5 65131 ILMN 63515 ILMN 1352195 1.19 ILMN\_295743 ILMN\_1367489 1.35 Cntn2 25356 contactin 2 Itga6 114517 integrin; alpha 6 ILMN\_285522 ILMN\_1351793 0.78 neural cell adhesion molecule 1 24586 ILMN\_284523 ILMN\_1370085 0.48 Ncam1 59318 neuronal growth regulator 1 ILMN\_289426 ILMN\_1366196 0.39 Negr1 Nlgn1 116647 neuroligin 1 ILMN\_298217 ILMN\_1364761 1.27 Nrxn1 60391 neurexin 1 ILMN 263241 ILMN 1369278 0.53 Pdcd1\_predicted 301626 programmed cell death 1 (predicted) ILMN 269125 ILMN 1357025 1.16 RT1-Ba 309621 butyrophilin-like 2 (mhc class ii associated) ILMN\_302329 ILMN\_1376669 1.48 RT1-S3 294228 rt1 class ib; locus bm1 ILMN\_275620 ILMN\_1371428 1.47 Sdc4 24771 syndecan 4 ILMN\_284660 ILMN\_1352387 1.36 ErbB signaling Camk2b 24245 calcium/calmodulin-dependent protein kinase ii ILMN\_295816 ILMN\_1367246 0.37 beta subunit Cblb 171136 casitas b-lineage lymphoma b ILMN 290443 ILMN 1351226 0.50 Crk 54245 v-crk sarcoma virus ct10 oncogene homolog (avian) ILMN\_265349 ILMN\_1361978 0.68 25313 epidermal growth factor ILMN 284600 ILMN 1371224 1.15 Egf Egfr 24329 epidermal growth factor receptor ILMN 268935 ILMN 1362571 0.79 Elk1 314436 elk1; member of ets oncogene family ILMN\_56253 ILMN\_1651026 0.71 24525 kirsten rat sarcoma viral oncogene homolog 2 (active) ILMN\_284143 ILMN\_1373027 0.65 Kras 58960 mitogen activated protein kinase kinase 2 ILMN\_273342 ILMN\_1362844 1.32 Map2k2 Mapk1 116590 mitogen activated protein kinase 1 ILMN\_267006 ILMN\_1349290 0.66 Pak3 29433 p21 (cdkn1a)-activated kinase 3 ILMN\_283805 ILMN\_1373238 0.40 Pik3cb 85243 phosphatidylinositol 3-kinase; catalytic; beta ILMN\_296182 ILMN\_1368644 0.82 polypeptide Pik3r3 60664 phosphatidylinositol 3 kinase; regulatory subunit; ILMN\_268148 ILMN\_1358018 0.57 polypeptide 3 Rps6kb2 361696 ribosomal protein s6 kinase; polypeptide 2 ILMN\_275356 ILMN\_1370952 1.29 Focal adhesion Actg\_predicted 287876 ILMN\_55178 ILMN\_1362269 0.78 actin; gamma; cytoplasmic 25404 ILMN\_288688 ILMN\_1376388 0.63 Cav1 caveolin Crk 54245 v-crk sarcoma virus ct10 oncogene homolog (avian) ILMN\_265349 ILMN\_1361978 0.68 Egf 25313 epidermal growth factor ILMN\_284600 ILMN\_1371224 1.15 Egfr 24329 epidermal growth factor receptor ILMN 268935 ILMN 1362571 0.79 Elk1 314436 elk1; member of ets oncogene family ILMN\_56253 ILMN\_1651026 0.71 Flnb\_predicted 306204 filamin; beta (predicted) ILMN\_64302 ILMN\_1362723 0.83 Itga10\_predicted 310683 integrin; alpha 10 (predicted) ILMN\_274071 ILMN\_1373558 1.18 114517 integrin; alpha 6 ILMN\_285522 ILMN\_1351793 0.78 Itga6 Mapk1 116590 mitogen activated protein kinase 1 ILMN\_267006 ILMN\_1349290 0.66 Pak3 29433 p21 (cdkn1a)-activated kinase 3 ILMN 283805 ILMN 1373238 0.40 platelet-derived growth factor; d polypeptide Pdgfd 66018 ILMN\_299016 ILMN\_1352347 0.90 Pdpk1 81745 3-phosphoinositide dependent protein kinase-1 ILMN\_276807 ILMN\_1359177 0.28 Pik3cb 85243 ILMN\_296182 ILMN\_1368644 0.82 phosphatidylinositol 3-kinase; catalytic; beta polypeptide Pik3r3 60664 phosphatidylinositol 3 kinase; regulatory subunit; ILMN\_268148 ILMN\_1358018 0.57 polypeptide 3 Vtn 29169 vitronectin ILMN\_291791 ILMN\_1374141 1.29 Insulin signaling 60581 acetyl-coenzyme a carboxylase alpha ILMN\_264748 ILMN\_1374107 0.78 Acaca

Entrez symbol	Entrez gene ID			Probe ID	Fold chang	
Cblb	171136	casitas b-lineage lymphoma b	ILMN_290443	ILMN_1351226	0.50	
Crk	54245	v-crk sarcoma virus ct10 oncogene homolog (avian)	ILMN_265349	ILMN_1361978	0.68	
Elk1	314436	elk1; member of ets oncogene family	ILMN 56253			
Ins1	24505	insulin 1	ILMN_66664	_		
Kras	24525	kirsten rat sarcoma viral oncogene homolog 2 (active)		ILMN_1373027		
Map2k2	58960	mitogen activated protein kinase kinase 2		ILMN_1362844		
•			_	_		
Mapk1	116590	mitogen activated protein kinase 1		ILMN_1349290		
Pdpk1	81745	3-phosphoinositide dependent protein kinase-1		ILMN_1359177		
Pik3cb	85243	phosphatidylinositol 3-kinase; catalytic; beta polypeptide		ILMN_1368644		
Pik3r3	60664	phosphatidylinositol 3 kinase; regulatory subunit; polypeptide 3	ILMN_268148	ILMN_1358018	0.57	
Rps6kb2	361696	ribosomal protein s6 kinase; polypeptide 2	ILMN_275356	ILMN_1370952	1.29	
Long-term potent	iation (LTF					
Camk2b	24245	calcium/calmodulin-dependent protein kinase ii beta subunit	ILMN_295816	ILMN_1367246	0.37	
Gnaq	81666	guanine nucleotide binding protein; alpha q polypeptide	ILMN_280496	ILMN_1355584	0.48	
Grm5	24418	glutamate receptor; metabotropic 5	ILMN_292416	ILMN_1361607	0.71	
Kras	24525	kirsten rat sarcoma viral oncogene homolog 2 (active)				
LOC317203	317203	similar to ribosomal protein s6 kinase polypeptide 6		ILMN_1374028		
Map2k2	58960	mitogen activated protein kinase kinase 2	_	ILMN_1362844		
Mapk1	116590	mitogen activated protein kinase 1		ILMN_1349290		
Ppp3ca	24674	protein phosphatase 3; catalytic subunit; alpha isoform	ILMN_2/1084	ILMN_13/2414	0.45	
mTOR signaling Ins1	24505	insulin 1	ILMN_66664	ILMN_1370839	1 12	
LOC317203			_			
	317203	similar to ribosomal protein s6 kinase polypeptide 6	ILMN_68494	ILMN_1374028		
Mapk1	116590	mitogen activated protein kinase 1		ILMN_1349290		
Pdpk1	81745	3-phosphoinositide dependent protein kinase-1		ILMN_1359177		
Pik3cb	85243	phosphatidylinositol 3-kinase; catalytic; beta polypeptide	ILMN_296182	ILMN_1368644	0.82	
Pik3r3	60664	phosphatidylinositol 3 kinase; regulatory subunit; polypeptide 3	ILMN_268148	ILMN_1358018	0.57	
Rps6kb2	361696	ribosomal protein s6 kinase; polypeptide 2	ILMN_275356	ILMN_1370952	1.29	
Phosphatidylinosit	tol (PI) sign	naling				
Impa1	83523	inositol (myo)-1(or 4)-monophosphatase 1	ILMN_302173	ILMN_1364531	0.85	
LOC497681	25666/	diacylglycerol kinase, gamma	_			
	497681	, , ,				
Pik3c2a_predicted	361632	phosphatidylinositol 3-kinase; c2 domain containing; alpha polypeptide (predicted)	ILMN_264548	ILMN_1361702	0.57	
Pik3c2g	116720	phosphatidylinositol 3-kinase; c2 domain containing; gamma polypeptide	ILMN_273653	ILMN_1349959	1.14	
Pik3cb	85243	phosphatidylinositol 3-kinase; catalytic; beta polypeptide	ILMN_296182	ILMN_1368644	0.82	
Pik3r3	60664	phosphatidylinositol 3 kinase; regulatory subunit; polypeptide 3	ILMN_268148	ILMN_1358018	0.57	
Pip4k2b	89812	phosphatidylinositol-4-phosphate 5-kinase; type ii; beta	ILMN_291864	ILMN_1349115	0.63	
Synj1	85238	synaptojanin 1	ILMN_59553	ILMN_1355054	0.50	
Tight junction fur						
Actg_predicted	287876	actin; gamma; cytoplasmic	_	ILMN_1362269		
Cldn10_predicted	290485	claudin 10 (predicted)	ILMN_272711	ILMN_1358030	0.70	
Cldn5	65131	claudin 5	ILMN_63515	ILMN_1352195	1.19	
Epb4.1l1	59317	erythrocyte protein band 4.1-like 1		ILMN_1376582		

Entrez symbol Entrez gene ID				Probe ID	Fold change	
Hcls1	288077	hematopoietic cell specific lyn substrate 1	ILMN_272174	ILMN_1376482	1.18	
Kras	24525	kirsten rat sarcoma viral oncogene homolog 2 (active)	ILMN_284143	ILMN_1373027	0.65	
Magi2	113970	activin receptor interacting protein 1	ILMN_276385	ILMN_1369780	0.61	
Myh13	29605	myosin; heavy polypeptide 13; skeletal muscle	ILMN_301178	ILMN_1360194	1.13	
Myh3	24583	myosin; heavy polypeptide 3; skeletal muscle; embryonic	ILMN_302443	ILMN_1360458	1.44	
Pard6g_predicted	307237	par-6 partitioning defective 6 homolog gamma (C. elegans) (predicted)	ILMN_53782	ILMN_1650781	0.85	
Prkce	29340	protein kinase c; epsilon	ILMN_294755	ILMN_1373193	0.32	

include glutamatergic and GABAergic neurotransmission, MAPK/CREB signaling, cAMP/cGMP/PDE signaling, GSK3B signaling, IP signaling, and central insulin signaling. Further, epigenetic regulation seemed to be affected to a different degree in both male and female offspring exposed to PS. These findings may indicate new potential therapeutic targets in the treatment of affective disorders. Below we will discuss the role of several biological processes in more detail.

### 4.3.1. Glutamate and GABA

The observed gene expression profiles suggest a significant role for glutamatergic neurotransmission in mediating the effects of PS. For example, female offspring exposed to PS showed a decrease in the expression of the ionotropic N-methyl D-aspartate (NMDA) receptors 1 and 2A within the FC, as well as a decreased metabotropic glutamate receptor 5 (mGluR5) expression in both the hippocampus and FC. Recent evidence has suggested that altered glutamatergic neurotransmission, which may have its origin in early development, plays an important role in the pathophysiology of mood disorders (Hashimoto, 2009a, 2009b). Both the NMDA and mGlu receptors have been proposed as potential therapeutic targets in this respect (Pilc et al., 2008; Pittenger et al., 2007). Pilc et al. (2008) suggested a model in which mGlu5 antagonists may possess antidepressant activity through NMDA receptor blockade. Likewise, the observed decrease in mGlu5 receptor expression within both the hippocampus and FC, together with the observed decrease in the expression of the NMDA1 and 2A receptors within the FC of female offspring exposed to PS, may relate to the resilience towards PS in this sex. Whether these changes represent a compensatory response to the decreased expression of glutamic acid decarboxylase (GAD; decreased in both the hippocampus and FC of PS females), the enzyme that catalyzes the decarboxylation of glutamate to GABA, remains to be elucidated. In a recent investigation by Zuena et al. (2008), PS was shown to result in a reduction in mGlu5 receptor protein levels within the hippocampus of male offspring only. These rats further showed increased anxietyrelated behavior. In contrast, female PS rats in that same study displayed reduced anxiety and no change in mGlu5 receptor levels in the hippocampus. The authors suggested that the decrease in mGlu receptor function observed in PS male rats represents "an unsuccessful homeostatic mechanism aimed at restoring the physiological levels of the anxiety response" (Zuena et al., 2008). Though mRNA expression is markedly different from protein expression, the discrepancy between their study and ours may further be explained by the fact that the rats used in our study are older as compared to those in the study by Zuena et al. (2008).

Closely related to glutamate function is the role of the inhibitory neurotransmitter GABA and its receptors. Dysfunction of the GABAergic neurotransmitter system has recently been associated with the development of both mood and anxiety disorders (Kalueff and Nutt. 2007; Price et al., 2009). Moreover, in both human and animal studies, positive modulators of GABAergic neurotransmission generally exert anxiolytic and antidepressant effects, while negative modulators possess anxiogenic- or depressive-like activity (Kalueff and Nutt, 2007). It is known that stress as well as many GABAergic psychotropic drugs is both capable of affecting GABA receptor subunit composition, which in turn may dramatically affect its functions (Zhang et al., 1998). Similarly, the expression of multiple GABAergic receptor subunits was affected after PS in the present study. For example, within the FC of male offspring, the expression of the alpha 4 subunit was decreased in PS as compared to control animals. Within females, the expression of various GABA receptor subunits was affected by PS in both brain regions. Further, as mentioned above, the expression of GAD was decreased in both the hippocampus and FC of PS females.

Altogether, these data suggest that changes in glutamatergic and GABAergic neurotransmission may play a prominent role in the regulation of affective state and reiterate the need for further research on their possible therapeutic value in disorders like anxiety and depression.

# 4.3.2. Ribosome function

The Mrpl18 gene encodes a 39S subunit protein that belongs to the L18P ribosomal protein family, the exact function of which remains largely unknown. Recently though, Mrpl18 has been shown to play a key role in mediating import of the nuclear DNA-encoded 5S rRNA into mitochondria, by which 5S rRNA molecules can be specifically withdrawn from the cytosolic pool and redirected to mitochondria, bypassing the classic nucleolar reimport pathway (Smirnov et al., 2011). The profound increase in Mrpl18 mRNA expression in

Entrez symbol	Entrez gene ID	Gene name	Transcript	Probe ID	Fold change
Ribosome function					
LOC501605	501605	ribosomal protein s2	ILMN_68333	ILMN_1364624	1.60
LOC684988	684988	ribosomal protein s13	ILMN_263434	ILMN_1351503	1.24
LOC690364	690364	ribosomal protein l21	ILMN_274137	ILMN_1363975	1.23
RGD1563431_predicted	501876	large subunit ribosomal protein 136a	ILMN_296283	ILMN_2040666	1.25
RGD1564290_predicted	498837	ribosomal protein s27a	ILMN_68667	ILMN_1362582	1.16
Rpl18a	290641	similar to 60s ribosomal protein l18a	ILMN_285160	ILMN_1370927	1.25
Rpl24	64307	ribosomal protein l24	ILMN_283110	ILMN_1353774	1.18
Rpl37	81770	ribosomal protein l37	ILMN_284909	ILMN_1354107	1.33
Rpl7	297755	ribosomal protein l7	ILMN_281851	ILMN_1370118	1.29
Rps11	81774	ribosomal protein s11	ILMN_288262	ILMN_1373412	1.25
Rps23	124323	ribosomal protein s23	ILMN_263631	ILMN_1369998	1.61
Rps7	29258	ribosomal protein s7	ILMN_62060	ILMN_1650594	1.26
Rps8	65136	ribosomal protein s8	ILMN_266152	ILMN_1362384	1.11
Wnt signaling					
Camk2b	24245	calcium/calmodulin-dependent protein kinase ii beta subunit	ILMN_295816	ILMN_1367246	0.81
Camk2g	171140	calcium/calmodulin-dependent protein kinase ii gamma	ILMN_290091	ILMN_1364240	0.88
Chd8	65027	beta-catenin binding protein	ILMN_53502	ILMN_1363589	0.80
Ctnnb1	84353	catenin (cadherin associated protein); beta 1; 88 kda	ILMN_297571	ILMN_1352752	1.31
Cxxc4	83824	cxxc finger 4	ILMN_273940	ILMN_1350191	0.85
Gsk3b	84027	glycogen synthase kinase 3 beta	_ ILMN_283436	_ ILMN_1349648	0.81
Lrp6_predicted	312781	low density lipoprotein receptor- related protein 6 (predicted)	ILMN_278789	ILMN_1349678	0.86
Map3k7_predicted	313121	mitogen activated protein kinase kinase kinase kinase 7 (predicted)	ILMN_265678	ILMN_1371190	1.16
Ppard	25682	peroxisome proliferator activated receptor delta	ILMN_272514	ILMN_1357865	0.88
Ppp3cb	24675	protein phosphatase 3; catalytic subunit; beta isoform	ILMN_263806	ILMN_1351926	1.22

both the hippocampus and FC of PS male offspring, in addition to the altered expression of related genes, e.g. Mrpl11 and Mrps2 (both in FC), as well as Mrps5 and

Ms4a11 (both in hippocampus) suggests a dysregulated

transport of 5s rRNA and associated ribosomal function.

Interestingly, PS increased the expression of numerous genes encoding ribosomal proteins in the FC of female offspring (13 differentially expressed, all of which increased by PS exposure). This suggests that the brain is increasing its capacity for protein synthesis, which could be interpreted as an attempt to compensate for impaired cytosolic translation (Bonow et al., 2009).

# 4.3.3. MAPK/CREB/neurotrophic factor signaling and hippocalcin

DAVID analysis showed a substantial overall negative effect of PS on MAPK signaling within the female hippocampus. Examples of genes downregulated by PS within this brain region were genes for the rat sarcoma viral oncogene homolog 2 (RAS), calcineurin (CaN), MAPK 1 (or ERK2), MAPK kinase kinase 1 (MAP3K1 or MEKK1), and ribosomal s6 kinase (RSK). Furthermore, the expression of the gene encoding for MAPK phosphatase-4 (MKP4), also known as dual specificity phosphatase 9 (DUSP9), which is known to deactivate MAPK, was increased in PS females.

A major substrate for the ERK/MAPK signaling pathway is the transcription factor CREB, which regulates the expression of, e.g. BDNF and is known to play an important role in mediating the antidepressant effects of neurotrophic factors and growth factors (Schmidt and Duman, 2011; Tanis et al., 2007). Interestingly, impaired function of BDNF and its receptor, the tyrosine kinase B (TrkB) receptor, have been linked to the development of major depression as well as a diminished response to antidepressant drugs (Dong et al., 2009; Duman and Monteggia, 2006; Tanis and Duman, 2007; Tanis et al., 2007). In the present study, Ntrk2 gene expression (which encodes the TrkB receptor) was decreased by PS in the FC of male offspring. CREB signaling can also be induced by Ca<sup>2+</sup>-calmodulin-regulated kinases

**Table 7** Overview of differentially expressed genes related to glutamatergic and GABAergic neurotransmission, cAMP/cGMP/PDE signaling, and epigenetic regulation, in the hippocampus and FC of male and female PS offspring.

Entrez symbol	Area	Sex	Entrez gene ID	Gene name	Transcript	Probe ID	Fold change
Glutamatergic/ (	GABAer	gic r	neurotransr	nission			
Gabra1	HIP	f	29705	gamma-aminobutyric acid (GABA) A receptor, alpha 1	ILMN_53178	ILMN_1348806	0.60
Gabrb1	HIP	f	25450	gamma-aminobutyric acid (GABA) A receptor, beta 1	ILMN_274145	ILMN_1357628	0.53
Gabbr1	HIP	f	81657	gamma-aminobutyric acid (GABA) B receptor 1	ILMN_60885	ILMN_1354454	0.64
Gad2	HIP	f	24380	glutamate decarboxylase 2	ILMN 296357	ILMN 1371012	0.67
Grm5	HIP	f	24418	glutamate receptor, metabotropic 5	_	ILMN_1361607	
LOC289606	HIP	f	289606	gamma-aminobutyric acid (GABA) A receptor, alpha 2		ILMN_1352358	
Grin2a	FC	m	24409	glutamate receptor, ionotropic, N-methyl p-aspartate 2A	ILMN_290907	ILMN_1376686	0.81
Grm5	FC	m	24418	glutamate receptor, metabotropic 5	ILMN_292416	ILMN_1361607	0.85
Gabrb1	FC	f	25450	gamma-aminobutyric acid (GABA) A receptor, beta 1	ILMN_274145	ILMN_1357628	0.89
Gad2	FC	f	24380	glutamate decarboxylase 2	ILMN_296357	ILMN_1371012	0.63
Grin1	FC	f	24408	glutamate receptor, ionotropic, N-methyl p-aspartate 1	ILMN_283876	ILMN_1365529	0.91
Grin2a	FC	f	24409	glutamate receptor, ionotropic, N-methyl p-aspartate 2A	ILMN_290907	ILMN_1376686	0.67
Grm5	FC	f	24418	glutamate receptor, metabotropic 5	ILMN_292416	ILMN_1361607	0.75
cAMP/cGMP/PDE	signali	ing					
Pde4b	_	f	24626	phosphodiesterase 4B	ILMN_295710	ILMN_1353078	0.54
Pde7a	HIP	f	81744	phosphodiesterase 7A	ILMN_60421	ILMN_1353897	0.84
Pde8b	HIP	f	309962	phosphodiesterase 8B		 ILMN_1348973	
Pde10a	HIP	f	63885	phosphodiesterase 10A	_	ILMN_1361915	
Pde2a	FC	f	81743	phosphodiesterase 2A		ILMN_1372916	
Pde4b	FC	f	24626	phosphodiesterase 4B			
Epigenetic regul	ation						
Hdac4_predicted		m	363287	histone deacetylase 4	ILMN_266642	ILMN_1364573	1.24
Mbd1_predicted		f	291439	methyl-CpG binding domain protein 1		_ ILMN_1375594	
Mettl2_predicted		f	363687	methyltransferase-like 2	_	ILMN_1370775	
Hdac4_predicted		f	363287	histone deacetylase 4	_	ILMN_1364573	
Sirt2	FC	f	361532	sirtuin 2 (S. <i>cerevisiae</i> )			

(CAMKs), e.g., after stimulation of glutamatergic alphaamino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) receptors (Tanis and Duman, 2007). Interestingly, the expression of CAMKII was decreased both within the hippocampus and FC of PS female as compared to control offspring. Further, the expression of *Gria 3*, encoding for the AMPA3 receptor, was decreased within the FC of PS females.

Hippocalcin, a member of the neuronal calcium sensor (NCS) protein family, is another protein involved in CREB signaling. Hippocalcin-deficient mice display a defect in CREB activation, associated with impaired spatial and associative memory (Kobayashi et al., 2005; Noguchi et al., 2007). In the present study, the expression of hippocalcin was decreased in the FC of male offspring exposed to PS, which may reflect impaired CREB-signaling in the FC of these animals.

# 4.3.4. GSK3B signaling

GSK-3B is implicated in the signaling pathways of various neurotransmitters and growth factors and has a repressing effect on transcription factors including CREB and B-catenin (Grimes and Jope, 2001; Salas et al., 2003). GSK-3B has been implicated in the etiology of various psychiatric disorders, such as major depression, schizophrenia, and bipolar disorder (Emamian et al., 2004; Gould et al., 2004b; Hur and Zhou, 2010; Li and Jope, 2010; Wada, 2009). The mood stabilizer lithium is a selective inhibitor of GSK-3 (Gould et al., 2004b). Data of rodent studies suggest that pharmacological inhibition of GSK-3 has antidepressant-like effects (Gould et al., 2004a; Kaidanovich-Beilin et al., 2004). In the present study, we observed a decrease in GSK-3B mRNA expression in the FC of both male and female PS offspring. In PS females though, GSK-3B mRNA expression was reduced to a greater extent as

compared to PS male offspring. In addition, the expression of B-catenin, one of the major downstream targets of GSK3B and the function of which is inhibited by GSK-3B activity, was increased substantially within the FC of PS females. Furthermore, the expression of *Chd8*, the gene encoding for B-catenin binding protein, which normally binds to B-catenin thereby inhibiting its function, was decreased, indicating an even more impaired GSK signaling in PS females. As such, impaired GSK-3B signaling may represent another interesting mechanism of action mediating resilience to PS in female offspring.

# 4.3.5. cAMP/cGMP/PDE signaling

Phosphodiesterases (PDEs) are enzymes that degrade the phosphodiester bond in the second messenger molecules cyclic adenosine monophosphate (cAMP) and/or cyclic guanosine monophosphate (cGMP) (Bender and Beavo, 2006). Within the hippocampus of PS female offspring, the expression of PDE4b, PDE7a, PDE8b and PDE10a was decreased. In addition, within the FC of PS females, the expression of PDE2a and PDE4b was reduced.

The inhibition of specific PDEs, which results in an increase in cAMP and/or cGMP dependent on the PDE type being inhibited, offers unique receptor-independent opportunities to modify cellular processes including apoptosis, differentiation, lipogenesis, glycogenolysis, gluconeogenesis and muscle contraction (Halene and Siegel, 2007). Thus, recently, PDE inhibitors have been identified as new potential therapeutics in areas such as dementia, depression, and schizophrenia (Halene and Siegel, 2007; Reneerkens et al., 2009; Tanis and Duman, 2007). The majority of the PDEs affected by PS degrade cAMP only, whereas PDE2 and PDE10 degrade both cAMP and cGMP. The cAMP system mediates the effect of monoamine neurotransmitters and is known to be downregulated in the brains of depressed patients (see review by Tanis and Duman, 2007). The depressive effect of impaired cAMP signaling is most likely related to the fact that cAMP activates protein kinase A (PKA), which, in turn, activates CREB. This notion is supported by the finding that chronic blockade of PDE4 with rolipram activates CREB and increases the expression of BDNF in the hippocampus, and that rolipram has antidepressant efficacy in both preclinical and clinical trials (Tanis and Duman, 2007). Along similar lines, it has been found that PDE4b-/- mice exhibited decreased immobility in the forced swimming test indicating an antidepressant-like effect (Zhang et al., 2008). PS male rat offspring in the present study showed increased depression-related behavior in the forced swimming test, whereas the behavior of PS female offspring was not affected as compared to control offspring. Thus, reduced levels of, e.g., PDE4b, as observed in PS female offspring in the present study, may explain the lack of depressive-like behavior in the forced swimming test in this sex after PS exposure. In this way, a decrease in PDE signaling may lead to increased cAMP/CREB signaling and related neurotrophic support. Expression levels of hippocampal PDE10a and FC PDE2a were reduced in PS females and, therefore, cGMP might also be of interest in mediating possible protective effects in PS females in the present study as it has recently been demonstrated that single nucleotide polymorphisms (SNPs) located in the genes encoding PDE2a, PDE10a, and the cGMP-specific PDE9a gene are associated with major depression (Wong et al., 2006).

Altogether, these data support the notion that specific PDE inhibitors might represent interesting candidates for possible treatment strategies for disorders such as major depression.

# 4.3.6. Central insulin signaling

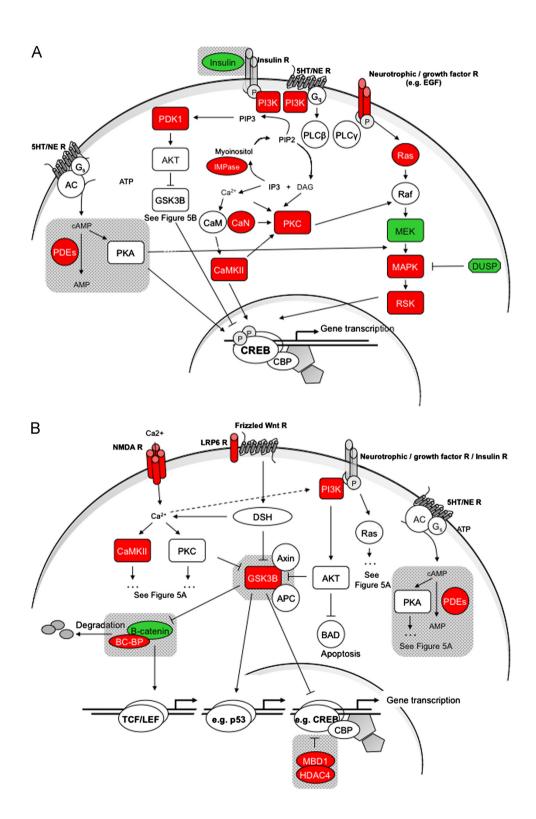
In addition to its well-known role in peripheral glucose regulation, the hormone insulin has an important role in regulating central nervous system (CNS) function, the significance of which is underscored by the increased vulnerability to co-morbidities such as dementia and depression seen with insulin resistance and diabetes (Brown et al., 2004; Lustman and Clouse, 2005; McEwen et al., 2002; Ott et al., 1999). Interestingly, insulin and the insulin receptor (IR) have been shown to be produced in neurons throughout the brain (Devaskar et al., 1994; Zhao and Alkon, 2001), whilst particularly the hippocampus seems to be vulnerable to chronic hyperglycemia and insulin resistance (Reagan, 2007). The pathophysiological similarities between diabetes and mood disorders suggest that common mechanistic pathways may be involved in the etiology and progression of the neurological aspects of these disorders. For more information on the link between insulin signaling, memory and mood, (see Reagan, 2007; Robertson et al., 2010). Notably, our microarray data now also suggest a pivotal role for central insulin signaling in mediating the effects of PS. Within the female hippocampus, several genes linked to insulin and related PI signaling (Yang et al., 2008; Daimon et al., 2008; Aberg et al., 2006) were differentially expressed in PS offspring when compared to controls. Among others, the expression of Ins1, encoding for insulin itself, was upregulated. In addition, the hippocampal expression of Slc2a3, the gene encoding glucose transporter-3, which is responsible for the influx of glucose into neurons, was decreased in the same offspring. We therefore hypothesize that enhanced hippocampal insulin signaling in PS female offspring might represent a compensatory effect explaining why behavior in females was largely unaffected.

# 4.3.7. Epigenetic regulation

Recently, it has been suggested that epigenetic mechanisms may account for the symptoms of mental illness and their (partial) reversal during treatment (Krishnan and Nestler, 2008; McClung and Nestler, 2008; Mill and Petronis, 2007; Renthal and Nestler, 2009; Tsankova et al., 2007). Evidently, the use of PS as a developmental rat model for affective disorders is of particular interest in relation to epigenetic programming. Specifically, the endogenously programmed massive loss and subsequent re-establishment of DNA methylation in the embryo and fetus comprises diverse critical periods, during which environmental stimuli can affect epigenetic regulation (Waterland and Jirtle, 2004). In this respect, the expression patterns of various genes involved in epigenetic regulation are remarkable. For example, the expression of HDAC4 was upregulated within the hippocampus of PS male offspring, whereas it was downregulated within the FC of PS females. Other proteins involved in epigenetic regulation that are affected by PS are methyltransferase-like 2 and MBD1 (both downregulated

within the FC of PS females). Thus, it is likely that changes in epigenetic regulation in reaction to fetal distress may contribute to the various physiological and behavioral changes observed in prenatally stressed subjects. Recent studies in rodents already provided evidence for epigenetic programming by early prenatal maternal stress (Bale, 2011; Darnaudery and Maccari, 2007; Matrisciano et al., 2012;

Morley-Fletche et al., 2011; Mueller and Bale, 2008; Zuena et al., 2008). Interestingly, recently, several studies have highlighted the antidepressant potential of HDAC inhibitors, although numerous challenges need to be addressed before being able to guarantee sufficient specificity, potency, and a benign side effect profile of this class of drugs (Covington et al., 2011; Grayson et al., 2010).



# 4.4. Limitations of the study

A major limitation of the present study is that the observed gene expression patterns may not be directly related to the behavioral measures assessed in the present study. For example, the observed changes in gene expression may just as well be associated with cognitive changes seen with PS (Zuena et al., 2008). In fact, many of the affected biological processes are known to be related to various types of affective and cognitive behavior and may therefore explain a general increased susceptibility to psychopathology observed in PS subjects. Furthermore, it is likely that the behavioral testing paradigms exerted an independent effect on central gene expression profiles. Although behavioral task exposure was identical for all groups, one cannot exclude that the animals' response to it was different among groups. Thus, behavioral testing may have left a permanent imprint on hippocampal and frontal gene expression patterns in a sex- and/or condition-dependent manner. Obviously, examining behavior and its underlying biological mechanisms in the same set of animals enables the possibility of linking both features in a more direct way. Moreover, evidently, the use of homogenates does not allow us to discriminate which specific anatomical subregions and/or populations of cells are affected.

# 4.5. Concluding remarks

In conclusion, the present study shows that prenatal maternal stress in Sprague-Dawley rats is associated with clearly increased anxiety- and depression-related behavior in adult male, but not female offspring. Male PS offspring further showed increased basal plasma corticosterone levels, whereas both PS males and females failed to show an adequate response to stress with lower stress-induced corticosterone levels as compared to controls. While the behavioral effects of PS were more pronounced in male offspring, gene expression was altered to a considerably greater extent in females. Thus, we hypothesize that part of the observed alterations in gene expression patterns in female offspring may indicate molecular mechanisms

inducing resilience to PS. As such, microarray analysis within the hippocampus and FC highlighted various signaling pathways which may be critically involved in the development of mood disorders and/or the actions of antidepressants. Examples include glutamatergic and GABAergic signaling, the cAMP/cGMP/PDE system, the MAPK pathway, insulin signaling, and the GSK-3 signaling pathway. Altogether, the current study suggests that resilience to developmental stress exposure may be mediated, at least in part, via these intracellular signaling cascades. Furthermore, these signaling pathways may provide potential targets for novel antidepressant and mood stabilizing drug treatments, including e.g. HDAC inhibitors and PDE inhibitors.

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Figure 5 Schematic overview of signaling cascades affected by prenatal maternal stress within the female hippocampus (A) and frontal cortex (B). Genes upregulated by prenatal stress are highlighted in green (or light grey). Genes downregulated after prenatal stress are shown in red (or dark grey). Arrows represent positive interactions; T-shaped arrows indicate negative interactions. For more information, see text. Abbreviations: 5-HT/NE: Serotonin (5-HT)/ norepinephrine (NE); AC: Adenylate cyclase; AMP: Adenosine monophosphate; APC: Adenomatous polyposis coli; ATP: Adenosine triphosphate; BAD: BCL2-associated agonist of cell death; BC-BP: B-catenin binding protein; Ca<sup>2+</sup>: Calcium <sup>2+</sup>; CaM: Calmoduline; CaMKII: Ca<sup>2+</sup>/calmodulin-dependent protein kinase; cAMP: Cyclic AMP; CaN: Calcineurin; CBP: CREB-binding protein; CREB: cAMP response element binding protein; DAG: Diacyl glycerol; DSH: Disheveled; DUSP: dual specificity phosphatase; EGF: Epidermal growth factor;  $G_q$ : Guanine-nucleotide binding protein, q; Gs: Guanine-nucleotide binding protein, stimulatory; GSK3B: Glycogen synthase kinase 3B; HDAC4: histone deacetylase 4; IMPase: Inositol monophosphatase; IP3: Inositol 1,4,5-triphosphate; MAPK: Mitogen-activated protein kinase; LRP6: Low-density lipoprotein receptor-related protein 6; MBD1: methyl-CpG-binding domain protein 1; MEK: MAPK kinase 1; NMDA: N-Methyl-D-aspartic acid; P: Phosphate/phospho-; p53: Protein 53; PDEs: Phosphodiesterases; PDK1: Phosphoinositide-dependent kinase 1; PI3K: Phosphoinositol 3-kinase; PIP2: Phosphatidylinositol (4,5)-bisphosphate; PIP3: Phosphatidylinositol (3,4,5)-trisphosphate; PKA: Protein kinase A; PKC: Protein kinase C; PLC: Phospholipase-C; R: Receptor; Raf: v-raf-1 murine leukemia viral oncogene; Ras: Rat sarcoma; RSK: Ribosomal protein S6 kinase; TCF/LEF: T-cell factor/lymphoid enhancer factor; Wnt: Wingless/Int. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

# Conflict of interest

We hereby declare that there is no conflict of interest for any of the contributing authors of the present manuscript. Dr. G. Kenis has received financial compensation as an independent symposium speaker from Eli Lilly. Dr J. Prickaerts has received research funds from Johnson & Johnson PRD, Abbott, Intracellular Therapeutics and Envivo, which, however, were not related to the present work.

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# Appendix A. Supporting information

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