

# Circuit-level analysis identifies target genes of sex steroids in ewe seasonal breeding

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- 1 Circuit-level analysis identifies target genes of sex steroids in ewe seasonal breeding.
- 2
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- 9
- 10 Abstract
- 11

Thyroid hormone (TH) and estradiol (E2) direct seasonal switches in ovine reproductive 12 physiology. In sheep, as in other mammals and birds, control of thyrotropin (TSH) production 13 14 by the pars tuberalis (PT) links photoperiod responsiveness to seasonal breeding. PT-derived TSH governs opposite seasonal patterns of the TH deiodinases Dio2/Dio3 expression in 15 tanycytes of the neighboring medio-basal hypothalamus (MBH), which explain the key role of 16 17 TH. We recently used RNA-Seq to identify seasonal markers in the MBH and define the impact of TH. This impact was found to be quite limited, in terms of number of target genes, and very 18 restricted with regards to neuroanatomical location, as TH specifically impacts genes expressed 19 in tanycytes and hypothalamus, not in the PT. Here we address the impact of E2 on these 20 seasonal markers, which are specifically expressed in either PT, tanycytes or hypothalamus. 21 22 We also investigate if progesterone (P4) may be involved in timing the seasonal transition to anestrus. Our analysis provides circuit-level insights into the impact of sex steroids on the ewe 23 seasonal breeding cycle. First, seasonal gene expression in the PT is independent of the sex 24 steroid status. The fact that seasonal gene expression in the PT is also TH-independent 25 strengthens the view that the PT is a circannual timer. Second, select tanycytic markers display 26

some level of responsiveness to E2 and P4, which indicates another potential level of feedback
control by sex steroids. Third, *Kiss1* neurons of the arcuate nucleus are responsive to both TH
and E2, which places them at the crossroads of photoperiodic transduction pathway and sex
steroid feedback. This provides strong support to the concept that these *Kiss1* neurons are
pivotal to the long-recognized "seasonal switch in the ability of E2 to exert negative feedback",
which drives seasonal breeding.

# 34 Keywords

Biological rhythms, breeding, circannual clock, estradiol, GnRH, kisspeptin, Kiss1, melatonin,
 *pars tuberalis*, photoperiod, pituitary, progesterone, RFRP3, seasonality, sheep, tanycytes,
 thyrotropin.

#### **Declaration of interest**: none.

### 41 Abbreviations

DEG: differentially expressed genes; E2: estradiol; IdF: Ile-de-France breed; ISH: *in situ*hybridization; LH: luteinizing hormone; LP: long photoperiod; MBH: medio-basal hypothalamus;
OVX: ovariectomized; P4: progesterone; PGR: P4 receptor; PT: *pars tuberalis* of the pituitary;
RIA: radioimmunoassay; Rom: Romanov breed; SCN: suprachiasmatic nucleus of the
hypothalamus; SP: short photoperiod; TH: thyroid hormones; T3: triiodothyronine; TRH:
thyrotropin-releasing hormone; TSH: thyrotropin; ZT: zeitgeber time.

### 52 Introduction

The pars tuberalis (PT) of the pituitary is the key target tissue of melatonin for the control of 53 seasonal breeding (Dardente et al 2014; Dardente et al 2019a; Wood and Loudon 2018). In the PT, 54 a short duration of nightly melatonin production, typical of longer spring/summer days, triggers 55 the expression of *Tshb* through TEF/EYA3/SIX1, a triad of transcription factors and co-activators 56 (Dardente et al 2010). This specific PT-derived TSH acts on neighboring tanycytes, which line the 57 walls of the third ventricle, to induce the expression of deiodinase II (Dio2) and repress expression 58 of Dio3, leading to increased local T3 production (Nakao et al 2008; Hanon et al 2008; Ono et al 59 2008). This opposite photoperiodic control over *Dio2* and *Dio3* is responsible for the tight seasonal 60 control of T3 levels within the medio-basal hypothalamus (MBH), which governs physiological 61 switches in the annual breeding cycle of multiple species, including sheep (Karsch et al 1995; 62 Dardente 2012). 63

64

Our recent RNAseq analysis of the MBH in ovariectomized estradiol-implanted (OVX+E2) ewes revealed that ~10% of protein-coding genes display differential expression levels between May and November, which illustrates the potent transcriptome-wide impact of photoperiod (Lomet et al 2018; Dardente & Lomet 2018). We validated seasonal changes in the expression level for the top ~30 differentially expressed genes (DEG). Most DEG were found either in the PT (e.g. *Tshb*, *Fam150b*, *Vmo1*, *Ezh2*, *Suv39H2*, *Vcan*, *Aa-Nat* and *Chga*) or in tanycytes of the beta subtypes, located at the bottom of the third ventricle (e.g. *Dio2*, *Tmem252*, *Shh*, *SlcO1c1*, *Dct* and *NpSR1*).

*Kiss1* and *Npvf* (encoding the RF-amide peptides KISS1 and RFRP3), which are expressed by
discrete clusters of neurons within the MBH parenchyma (Smith 2009; Lomet et al 2018;
Angelopoulou et al 2019), were also identified as DEG. The MBH is key to the central control of
breeding and appears to host the long sought-after GnRH pulse generator. There is now strong

evidence that KNDy (KISS1/NeurokininB/Dynorphin) neurons located in the arcuate nucleus are 77 the GnRH pulse generator (Lehman et al 2010; Han et al 2015; Moore et al 2018; Herbison 2018). 78 We found that Kiss1 displays a marked (~10-fold) seasonal rhythm in expression in OVX+E2 79 ewes, leading to heightened expression during short winter days (Lomet et al 2018), consistent 80 with prior findings (Smith et al 2008; Wagner et al 2008; Urias-Castro et al 2019). In intact ewes, 81 this increase in KISS1 presumably leads to enhanced GnRH secretion, which triggers breeding 82 (Messager et al 2005; Caraty et al 2007; Caraty et al 2013). Furthermore, in sheep as in other 83 mammals a vast majority of KNDy neurons express receptors for E2 and P4 (ERa and PGR, 84 respectively; Goubillon et al 2000; Dufourny and Skinner 2002; Franceschini et al 2006; Smith 85 86 et al 2007; Foradori et al 2002; Campbell et al 2017; Chen et al 2017), which confers them direct responsiveness to sex steroid feedback. This is highly relevant since the current model for the 87 photoperiodic control of seasonal breeding, established in the early 80's (Legan et al 1977; Karsch 88 89 et al 1984; Goodman & Inskeep, 2015), emphasizes the role of "a seasonal switch in the ability of E2 to inhibit the GnRH pulse generator" as the key event responsible for timely onset and offset 90 91 of breeding. Indeed, OVX+E2 ewes display overt seasonal differences in the frequency and 92 amplitude of GnRH/LH pulses, which are lost in OVX ewes (Karsch et al 1993). The neural mechanism(s) driving the seasonal switch in the ability of E2 to exert negative feedback remain 93 unclear even though the MBH appears to be the key neural site (Blache et al 1991; Caraty et al 94 1998). Since OVX+E2 ewes undergo properly timed seasonal switches in LH/FSH, P4 appears 95 dispensable for these (Legan et al 1977). However, P4 exerts negative feed-back onto the MBH 96 during the luteal phase, which is mandatory for normal estrus cycles and fertility during the 97 breeding season (Dardente 2012; Goodman & Inskeep, 2015). 98

99

Even though KNDy neurons are strong contenders as a common conduit for photoperiod and sexsteroids towards GnRH seasonal control, we lack a comprehensive circuit-level analysis of the

cellular and molecular targets of E2 (and P4) responsible for the "seasonal switch". Indeed several
non-mutually exclusive hypotheses can be put forth: E2 may impair the photoperiodic read-out
mechanism in the PT, and/or modulate transduction of the signal towards tanycytes and/or
modulate signaling directly within the hypothalamic parenchyma. The latter possibility would
likely involve *Kiss1* neurons, but might also include an impact on *Npvf* neurons. Here, we used
our validated set of seasonal DEG to test these possibilities in ewes sampled at different times of
the year and under various sex steroid states (intact, OVX+E2 and OVX ewes).

109

## 110 Materials & Methods

#### 111 Ethics statement

All experimental procedures were performed in accordance with international (directive 112 2010/63/UE) and national legislation (décret n° 2013–118) governing the ethical use of animals in 113 research (authorization n° E37-175-2 and n°A38 801). All procedures used in this work were 114 evaluated by a local ethics committee (Comité d'Ethique en Expérimentation Animale Val de 115 Loire) and approved by the Ministry of Higher Education and Research (project n°00710.02). All 116 surgeries were performed after sodium thiopental anesthesia (Nesdonal®, 1g/80kg) under constant 117 isoflurane administration (Vetflurane®) and all efforts were made to minimize suffering. 118 Following surgery, animals received an injection of antibiotics (oxytetracycline, Terramycine 119 LA®, 1ml/10kg) and an injection of a non-steroidal anti-inflammatory drug (Finadyne®, flumixin 120 121 megumine, 2ml/50kgs). Animals were taken care of daily throughout the experiment and killed by decapitation under deep barbiturate anesthesia (Nesdonal®, 5mL). To minimize potential issues 122 linked to time-of-day fluctuation in gene expression (i.e. circadian rhythms) all animals were killed 123 in the early day (ZT1-6, with ZT0 being the time of lights on, or sunrise). 124

125

#### 127 Animals & Experimental procedures

128 Experiments were conducted on adult Ile-de-France (IdF) ewes (3–5 years old; weight 60–80 kg) and adult Romanov (Rom) ewes (3-5 years old; weight 60-80 kg) maintained under normal 129 husbandry at the research station of the Institut National de la Recherche Agronomique in Nouzilly 130 (PAO, INRA, 2018. Animal Physiology Experimental Facility, 131 DOI: 10.15454/1.5573896321728955E12). We used either intact, ovariectomized (OVX) or 132 ovariectomized, estradiol-implanted (OVX+E2; 1cm silastic implant) ewes. This OVX+E2 model 133 normalizes the level of circulating E2, which uncovers the well-documented central seasonal shift 134 in the negative feedback action of E2 on gonadotropin secretion (Legan et al 1977; Karsch et al 135 1984; Goodman & Inskeep, 2015). 136

137

For experiment 1, *in situ* hybridization (ISH) was performed on brain sections (see next section and Lomet et al 2018). For all other experiments RNA was extracted from a MBH block, which comprises the PT, the median eminence, the arcuate nucleus and the dorsomedial and ventromedial hypothalamic nuclei. The RNA samples were used to perform qRT-PCR; some of these samples have been used in prior studies (see below and Lomet al 2018, Dardente & Lomet 2018).

143

144 In experiment 1, intact IdF ewes were kept in an open barn and killed in May (non-breeding season, n=6) and November (breeding season, n=6). In experiment 2, intact IdF ewes were kept in an open 145 barn and killed in November (n=6), February (when breeding stops, n=5), May (n=6) and August 146 (when breeding resumes, n=6). For experiment 3 (IdF breed), a direct comparison of expression 147 levels between May and November was performed across three distinct conditions with respect to 148 sex steroid status: intact ewes (groups from Expt 2), OVX+E2 ewes (samples from Lomet et al 149 150 2018) and OVX ewes (n=5 for May and n=4 for November; see Fig S3A for details). In experiment 4, we used intact ewes of IdF (n=30) and Romanov (Rom; n=30) breeds. Ewes were 151

killed (n=10 per breed and time point) on February 13-16<sup>th</sup>, March 5-6<sup>th</sup> and March 15-16<sup>th</sup>, a
narrow seasonal time window during which anestrus develops in both breeds. The 1<sup>st</sup> two groups
(i.e. IdF and Rom breeds) were killed during a "natural" follicular phase (display of estrus behavior
when presented with a teaser ram). The remaining 40 ewes received a progestogen treatment
(vaginal sponge) on February 16-17<sup>th</sup>, which was removed on March 3-5<sup>th</sup> and followed by
pregnant mare serum gonadotropin (PMSG) injection. Ewes were killed 2 or 12 days later, when
displaying an "induced" follicular or luteal phase, respectively.

159

### 160 **RNA extraction and qRT-PCR analysis**

RNA extraction was performed on each MBH block using TriReagent (Sigma). Concentration and 161 purity of individual samples were determined with Nanodrop 2000 (ThermoScientific) and 162 integrity was checked by standard agarose gel electrophoresis. All procedures, including qPCR 163 assays for all target genes, have been thoroughly validated (Lomet et al 2018; Dardente and Lomet 164 2018). cDNA was synthesised from each individual RNA sample using Omniscript RT kit 165 166 (Qiagen) and Oligo-dT primers (synthesized by Eurofins, Germany). The optimal cDNA dilution and calibration curves for each PCR primer pair (Eurofins) were established using cDNA 167 synthesized from an equimolar mix of all individual RNA from each experiment. As a negative 168 control, the same mix with water instead of RT was prepared. Quantitative PCR (qPCR) was 169 performed using CFX-96 Real-Time PCR Detection System (Bio-Rad) and Sso Adv Universal 170 SYBR Green Supermix (Bio-Rad). All primer pairs had efficiencies ranging from 85% to 110%. 171 All samples (unknown, standard curves) were assessed in triplicate and Rplp0 (ribosomal subunit 172 P0, a.k.a 36B4) was used as a housekeeping gene. The quantification of mRNA level was obtained 173 by the 2<sup>-ΔCT</sup> method. Data are normalized and presented as fold-increase compared to the condition 174 with the lowest expression level. For Expt 4, all cDNA were re-synthesized in a single run to allow 175 direct comparison across conditions. The list of qPCR primers is provided in Table S1. 176

177

### 178 In situ hybridization

ISH was performed as described previously (Lomet et al 2018; Dardente et al 2019b). 179 180 Hypothalamic blocks for were cut into 20µm sections using a cryostat (CryoStar NX70, ThermoScientific) and thaw-mounted onto SuperFrost Plus slides (ThermoScientific). Specific 181 182 probes were generated and validated (cloning & sequencing) as described above, using a mix of 183 MBH cDNA as template. Details of the inserts used to generate radioactive probes are provided in 184 **Table S1.** Radioactive cRNA riboprobes were prepared by plasmid linearisation and *in vitro* 185 transcription (Riboprobe System, Promega) including <sup>35</sup>S-UTP (Perkin-Elmer). Probes were purified using Illustra Probe Quant G50 micro-columns (Fisher) and counted with a liquid 186 scintillation counter (Tri-Carb 2900TR, Packard). Slides were post-fixed at 4°C for 20 min in 4% 187 PFA, 0.1 M PB, rinsed with 0.1 M PB (2 X 5min), acetylated with 3.75% v/v of acetic anhydride 188 in 0.1 TEA, 0.05 N NaOH and finally rinsed with 0.1 M PB (2 X 5min). Slides were then 189 190 dehydrated through graded ethanol solutions (50%, 70%, 95% and 100%; 3min each) and dried under vacuum for 60 min. Sections were hybridized overnight at 58°C with 10<sup>6</sup> cpm of probe per 191 slide in hybridization buffer (50% deionized formamide, 10% dextran sulfate, 1 X Denhardt's 192 solution, 300 mM NaCl, 10 mM Tris, 10 mM DTT, 1 mM EDTA, 500 µg/mL tRNA). Sections 193 194 were then rinsed in 4 X SSC (3 X 5 min) and subjected to RNase-A digestion (20 µg/mL) in a buffer containing 500 mM NaCl, 1 mM Tris, 1 mM EDTA for 30 min at 37°C. Stringency washes 195 in SSC (with 1mM DTT) were performed to remove non-specific probe hybridisation: 2 X SSC (2 196 X 5 min), 1 X SSC (10 min), 0.5 X SSC (10 min), 0.1 X SSC (30 min at 60°C), 0.1 X SSC (5 min). 197 198 Slides were then dehydrated through graded ethanol solutions, dried under vacuum for 60 min and exposed to an autoradiographic film (BioMax MR, Kodak). Exposure duration was optimized for 199 each gene by repeated film exposures, depending on labeling intensity (from 3 days to 4 weeks). 200 Films were scanned on a transmittance image scanner (Amersham, UK) along with a calibrated 201

optical density (OD) transmission step wedge (Stouffer, USA). Calibrated Integrated OD (IOD)
 measurements of gene expression within the MBH were performed using ImageJ software.

204

## 205 Hormonal profile in OVX ewes

Plasma levels of LH in OVX ewes (experiment 3) were assayed by RIA (Pelletier et al 1982). All
samples were included in a single assay and every sample was measured in duplicate. The assay
standard was 1051-CY-LH (equivalent to 0.31 NIH-LH-S1). Intra- and inter- assay coefficients of
variation averaged 9% and 15%, respectively with an assay sensitivity of 0.1 ng/mL.

210

### 211 Data analysis

Data were analysed using GraphPad Prism 6. ISH data were analysed by t-test (Mann-Whitney). Data for qRT-PCR were analysed by one-way ANOVA (followed by post-hoc Tukey test when applicable; Expts 2 and 4) or two-way ANOVA (Expt 3) using time (May and November) and treatment (intact, OVX+E2 and OVX) as variables. The Sidak's post-hoc test was used for multiple comparisons.

217

### 218 **Results**

We first used ISH to compare the seasonal expression pattern of candidate genes in the MBH of 219 220 intact ewes to the pattern we previously reported for OVX+E2 ewes (Lomet et al 2018; Dardente and Lomet 2018). The PT markers Tshb, Fam150b, Vmo1, Ezh2, Klkb1, Suv39H2, Vcan and Elovl6 221 were expressed at higher levels in May than in November, while Chga and Aa-Nat showed the 222 opposite seasonal pattern, with higher expression in November than in May (Fig 1A & Fig S1, see 223 Table S2 for stats). The markers of tanycytes Dio2, Tmem252, Shh and SlcO1c1 showed increased 224 225 seasonal expression in May, while NpSR1 was more expressed in November (Fig 1B). Therefore we conclude that seasonal molecular markers of PT and tanycytes showed similar expression 226

patterns in intact and OVX+E2 ewes (Lomet et al 2018; Dardente and Lomet 2018),
notwithstanding possible differences in amplitude, which are difficult to assess from comparing
independent experiments.

230

This situation in PT and tanycytes differed markedly for the hypothalamic markers *Kiss1* and *Npvf*, which did not display any difference in expression levels in intact ewes killed in May and November (**Fig 1C**). This result is in stark contrast with what we found in OVX+E2 ewes, which display *Kiss1* mRNA levels that are ~10-fold higher in November than in May, while *Npvf* displays the opposite pattern with mRNA levels ~10-fold higher in May than in November (Lomet et al 2018).

237

We then used qRT-PCR to track seasonal changes of DEG in intact ewes with a more quantitative 238 239 approach and a finer temporal resolution (every 3 months). Seasonal high-amplitude rhythms of expression were revealed for all PT markers (>50-fold for *Tshb*; Fig 2A & Fig S2, see Table S2 240 241 for stats) and for all tanycytic markers (>45-fold for *Tmem252*; Fig 2A, see Table S2 for stats), 242 whether peak expression level occurs in May, or in November as in the case of Chga and NpSR1. Dio2 and Dio3 displayed characteristic opposite patterns of seasonal expression, which predict 243 increasing and decreasing levels of T3 levels at the transition to anestrus and breeding, respectively 244 (deduced from the ratio *Dio2/Dio3*). Here again, expression levels for *Kiss1* and *Npvf* did not 245 246 display statistically significant seasonal rhythmicity (Fig 2C and Table S2).

247

To clarify the impact of E2 on molecular seasonal markers expressed in the three compartments of the photoperiod transduction cascade – PT, tanycytes and hypothalamus – we employed OVX ewes, and used qRT-PCR to allow a direct side-by-side comparison of relative expression levels in May and November between intact, OVX+E2 and OVX ewes. Efficacy of OVX was validated

252	by RIA for LH (Fig S3A). Following removal of the E2 implant in March, LH levels increased
253	rapidly, reaching a plateau after 3-4 weeks. For the November group, LH levels had already
254	increased to their near-maximal level when the E2 implant was removed in August.

255

E2 was found to have little, if any, impact on the expression of the 9 PT markers investigated (Fig
3A and Fig S3B): all DEG showed high-amplitude rhythms in intact, OVX+E2 and OVX ewes
(2-way ANOVA, Time effect p<0.0001 for all DEG; see Table S2).</li>

259

A slightly different conclusion emerged for the 7 tanycytic markers (**Fig 3B** and **Fig S3C**). All genes displayed statistically significant differences with time, even though the amplitude of the rhythms appeared differentially affected across genes (2-way ANOVA, Time effect p<0.005 for all DEG; see **Table S2**).. All May/Nov pairwise comparisons were statistically significant with two exceptions: *Dio3* and *Shh* both displayed an increase in expression in OVX+E2 ewes, but neither in intact nor in OVX ewes. Nevertheless, the *Dio2/Dio3* ratio remained higher in May for all 3 groups of animals: 4.6-fold for OVX+E2, 2.8- and 3.2-fold for intact and OVX, respectively.

Consistent with our earlier findings using these samples from OVX+E2 ewes (Lomet et al 2018), 268 we found a ~10-fold increase in expression for Kiss1 between May and November. Conversely, 269 *Npvf* expression decreased by ~10-fold between May and November. Most importantly, these large 270 271 opposite changes in *Kiss1* and *Npvf* expression were lost not only in intact ewes, but also in OVX ewes see Table S2 for stats). In intact ewes, Kiss1 and Npvf levels were clamped to low and 272 273 intermediate-high levels, respectively. Conversely, in OVX ewes Kiss1 and Npvf levels were clamped to intermediate-high and low levels, respectively. Therefore, across the distinctive 274 275 experimental conditions, *Kiss1* and *Npvf* display inverse patterns of expression.

Intact and OVX+E2 ewes display roughly similar basal levels of E2 throughout the year (Yuthasastrakosol et al 1975) but only intact ewes are further exposed to P4 during the breeding season (Goodman & Inskeep 2015). We therefore went on to consider the importance of P4 for the seasonal pattern of expression of *Kiss1* and *Npvf*, reasoning that the impact of cycling P4 might somehow superimpose to the tonic E2-dependent photoperiodic impact on their expression level.

282

We attempted to get circuit-level insights on the potential impact of P4 by probing expression of 283 photoperiod-driven DEG in intact ewes at different phases of the estrous cycle (follicular vs luteal) 284 and during anestrus. As shown before (Fig 2) most DEG in PT and tanycytes show heightened 285 286 expression with increasing daylengths from February/March onwards, concomittant with anestrus onset. We investigated a potential modulatory effect of P4 on DEG at this key transition, reasoning 287 that it might be easier to discern a modest impact in the course of photoperiodic induction. To do 288 289 so, we used a protocol in which expression of DEG was assessed on three occasions between mid-February and mid-March and in two different ovine breeds, IdF and Rom. These breeds enter 290 291 estrus at the same time of year but anestrus occurs slightly later in Rom than in IdF ewes (Ben said 292 et al 2007). For the first two sampling points, ewes were in follicular phase, characterized by high E2 levels and absence of P4, which allowed us to directly assess the impact of increasing 293 daylengths. The third group was killed 10 days after the second group, when ewes were in luteal 294 295 phase, characterized by high P4 and low E2. Results for the IdF and Rom breeds are shown in Fig. 296 4A-C and Fig 4D-F, respectively (also see Fig S4 and Table S2 for stats).

297

The expression level of PT-specific DEG (**Fig 4A & 4D**), steadily increased (or decreased, *Chga*) throughout the duration of the experiment, a trend which was more obvious in Rom compared to IdF ewes. For example, expression of *Tshb* or *Fam150b* increased by ~3-4 fold in IdF ewes and ~10-15 fold in Rom ewes. Therefore, P4 (Luteal, blue bars) does not appear to have any impact

upon photoperiodic induction or repression of PT-expressed DEG in either breed. As shown in 302 experiment 2 (see Fig 2B), PT and tanycyte DEG show almost synchronous and sustained increase 303 (or decrease) from February until May. In this paradigm, and contrasting with PT-expressed DEG, 304 305 the phase of the estrus cycle did appear to modulate the expression of DEG in tanycytes. Overall, photoperiodic induction (or repression for NpSR1) of tanycytic DEG in the Luteal group were 306 typically reduced compared to those in the 2<sup>nd</sup> Follicular group (green bars) for IdF ewes (**Fig 4B**). 307 However, this decrease reached statistical significance only for Tmem 252 and Shh. A very similar 308 309 trend was found for Rom ewes (Fig 4E), which displayed blunted induction (or decrease) of tanycytic DEG when compared to PT markers. However, none of these markers displayed any 310 statistically significant differences between the 2<sup>nd</sup> and 3<sup>rd</sup> group of ewes. *Dio3* did not display any 311 significant changes in expression in either breed (data not shown). Finally, concomittant Kiss1 312 repression and *Npvf* induction in response to increasing daylengths were observed in both breeds 313 314 (**Fig 4C & Fig 4F**).

315

#### 316 Discussion

Our analysis reveals the circuit-level logic of photoperiodic control of seasonal breeding (see 317 model, Fig 5). First, we show that seasonal rhythmicity of DEG in the PT is impervious to sex 318 steroids, which complements our earlier finding that these PT-expressed DEG are not impacted by 319 320 TH. These observations provide strong support for the hypothesis that the PT is a circannual timer. 321 Second, our analysis in IdF and Rom ewes at the transition towards anestrus point to a potential role for P4 in modulating photoperiodic output at the level of tanycytes. Third, we demonstrate 322 323 that seasonal expression of *Kiss1* and *Npvf* is strongly modulated by sex steroids, with an intriguing and consistent inverse relationship in their respective expression levels across experimental 324 conditions. Along with our prior finding that seasonal expression of Kiss1 and Npvf is impacted 325 by the TH status (Lomet et al 2018; see Fig S5), it places these two neuronal populations at the 326

327 crossroads between the photoperiodic input pathway and the sex steroid feedback. These findings
328 are most consistent with the notion that the "seasonal switch in the ability of E2 to inhibit the
329 GnRH pulse generator" occurs at the level of TH-responsive, *Kiss1*-expressing neurons of the
330 arcuate nucleus.

331

The possibility that the PT harbors the long sought-after circannual clock has now received strong 332 333 support from studies in sheep and hamsters (Lincoln et al 2006; Saenz de Miera et al 2013; Herwig et al 2013 ; Saenz de Miera et al 2014 ; Wood et al 2015 ; Lomet et al 2018 ; Dardente 334 335 2012; Wood and Loudon 2018). These studies demonstrated that expression of Tshb (and other markers) in the PT displays long-term endogenous switches under a constant photoperiod, a 336 hallmark of a circannual clock. Similar changes were seen at the level of Dio2/Dio3, which are 337 presumably triggered through circannual changes in PT-TSH, even though the possibility that 338 tanycytes themselves harbor circannual clocks can not be ruled out (Milesi et al 2017; Lomet et 339 al 2018). The circannual clock is predicted to be sheltered from cues other than melatonin in order 340 to consistently provide reliable timing information to downstream circuits. 341

342

We and others previously showed that gene expression in the PT is unresponsive to TRH and TH 343 (Bockman et al 1997; Dardente 2012; Lomet et al 2018). We now show that seasonal gene 344 expression in the PT is also unaffected by sex steroids. Therefore, neither TH nor E2, the two key 345 346 hormones in the progression of the seasonal breeding cycle, have any noticeable impact on photoperiod decoding in the PT. We believe this is a strong argument in favor of the view that 347 melatonin-responsive PT-specific thyrotropes (Klosen et al 2002; Dardente et al 2003) are indeed 348 349 circannual clocks. In this regard, a parallel between the PT and the SCN (master circadian clock) may be drawn. The SCN is entrained by the light-dark cycle, while being insensitive to multiple 350 resetting cues including glucocorticoids (Balsalobre et al 2000), temperature (Buhr et al 2010) or 351

feeding schedule (Yamzaki et al 2000; Damiola et al 2000), which are all able to phase-shift
peripheral clocks (Dibner et al 2010; Mohawk et al 2012).

354

355 We show that P4 has a modest and gene-specific impact in tanycytes. Considering that tanycytes receive photoperiodic information through PT-derived products (TSH and others; Lomet et al 356 2018 ; Dardente et al 2019a), it leaves open the possibility that P4 somehow modulates the impact 357 of these entraining signal(s). Similar trends in gene expression patterns were seen in two different 358 359 ovine breeds (IdF and Rom) and for multiple molecular markers, which are either induced (Dio2, Tmem252, Shh, SlcO1c1, Dct) or repressed (NpSR1) by lengthening photoperiods. We speculate 360 361 that functional relevance of this P4 feedback at the level of tanycytes, if any, may be more obvious when the strength of the photoperiodic input is comparatively weak, which would correspond to 362 physiological transitions to anestrus or breeding. In the latter case, since P4 can not increase unless 363 364 ovulation occurs, P4 is unlikely to play any role in timing breeding onset. However, P4 may modulate the timing of anestrus. However, we acknowledge that only Tmem252 ans Shh in IdF 365 366 ewes do show a statistically significant decrease upon P4 exposure. Once more, since OVX+E2 ewes undergo properly timed seasonal switches in LH/FSH, P4 is clearly dispensable for these 367 (Legan et al 1977). Therefore, great caution is required in the interpretation of the general trends 368 observed here, and the notion that P4 may exert a modulatory role will have to be tested further. 369

370

We notice that expression of *Shh* is affected by E2 (see **Fig 3B**) and P4 (in IdF ewes at least, see **Fig 4A**), which implies that E2 and P4 impact upon tanycytes in a gene-specific manner. The potential contribution of *Shh* to seasonal breeding through modulation of cell proliferation has been discussed before (Dardente et al 2019; Dardente and Lomet 2019); the current finding that E2 somehow modulates *Shh* suggests another layer of control. In sheep, the nuclear receptors ERa and PGR are expressed in cells lining the third ventricle (Lehman et al 1993; Scott et al 2000).

Whether these cells are tanycytes is unknown, and co-localization with tanycyte-specifc markers 377 378 would be required. In mouse, tanycytes appear to express ERa and PGR and display some responses to P4 (Parkash et al 2015). However, a recent scRNAseq study failed to detect ERa or 379 380 PGR in murine tanycytes (Campbell et al 2017). Further experiments are required to clarify expression of ERa and PGR in tanycytes and define whether they play any physiologically relevant 381 role. Considering the impact of tanycyte-derived T3 on the expression of *Kiss1* and *Npvf* in sheep 382 (Lomet et al 2018) and hamsters (Henson et al 2013; Klosen et al 2013), a potential role for sex 383 steroids in regulating DEG within tanycytes is of interest and warrants further investigation. 384

385

386 Amongst the DEG we characterized, *Kiss1* and *Npvf* are the only ones expressed by hypothalamic neurons. *Kiss1* and *Npvf* are also the only DEG for which seasonal expression is abolished in both 387 intact and OVX ewes, compared to OVX+E2 ewes (Fig 1, Fig 2 & Fig 3). Therefore, seasonal 388 389 expression of these two genes is governed by photoperiod and sex steroids. There is strong evidence that "final processes governing the onset of puberty in the lamb and the onset of the 390 annual season in the ewe share a common mechanism", based on a decrease in the ability of E2 to 391 392 inhibit the GnRH pulse generator (Legan et al 1977; Foster and Ryan 1979; Karsch et al 1984; Goodman & Inskeep, 2015). In this respect, Kiss1-expressing neurons of the arcuate nuclei are 393 prime candidate (Beltramo et al 2014; Pinilla et al 2012; Simonneaux 2018). 394

395

We show that *Kiss1* is expressed at basal low levels throughout the year in intact ewes, which contrasts with the large May/Nov difference seen in OVX+E2 ewes. While E2 is present at roughly similar levels throughout the year in intact ewes, not overlooking the functionally critical but modest 2-3 fold rise during the late follicular phase, P4 is produced exclusively during the breeding season (Yuthasastrakosol et al 1975; Goodman & Inskeep 2015). Therefore, sex steroid status during the anestrus season - presence of E2 and lack of P4 – can be considered similar in intact

and OVX+E2 ewes. This suggests that it is the presence of P4 during the breeding season, which 402 actively down-regulates the photoperiodic drive upon Kiss1 expression. On the other hand, OVX 403 ewes display intermediate-to-high levels of Kiss1 in both May and November, consistent with 404 405 prior findings (Pompolo et al 2006; Smith et al 2007; Smith et al 2008; Smith et al 2009; Merkley et al 2012; Goodman & Inskeep, 2015). As assessed by c-Fos labeling, OVX is 406 accompanied by activation of KNDy neurons - but not of Kiss1 neurons of the preoptic area -407 which suggests that only Kiss1 neurons in the arcuate nucleus are important for the E2 negative 408 409 feedback (Merkley et al 2012). Collectively, seasonal expression of Kiss1 reflects E2-mediated inhibition during anestrus, while E2-independent increase during the breeding season would be 410 411 masked by P4 inhibition during the luteal phase, and unmasked during the follicular phase. There is prior evidence that both E2 and, to a lesser extent, P4 exert negative feedback on Kiss1 412 expression (Smith et al 2007; Smith et al 2008; Goodman et al 2011; Goodman & Inskeep, 2015). 413 414 We acknowledge that our experimental paradigm is not suitable to reveal a potential negative impact of P4 upon Kiss1 expression (Fig 4), which is decreasing at the transition towards anestrus 415 416 due to lengthening photoperiod.

417

Following a line of reasoning similar to the one developed above for Kiss1, we conclude that 418 seasonal expression of Npvf reflects E2-mediated activation during anestrus, while neither E2 nor 419 420 P4 impinge on Npvf expression during the breeding season. Consistent with our findings in intact 421 IdF ewes, we previously reported that photoperiod had little impact on Npvf expression in intact Soay ewes (Dardente et al 2008). Furthermore, *Npvf* expression is not impacted by the transition 422 to long days in either intact Soay ewes (Dardente et al 2008) or OVX+E2 IdF ewes (Lomet et al 423 2018). Since such acute photoperiodic transition almost immediately impacts the gonadotropic 424 425 axis, we conclude that changes in Npvf transcription are not necessary for this physiological response, a conclusion which holds true also for Kiss1 (Lomet et al 2018). Interestingly, the 426

number of RFRP3-ir cells is 40% higher during the non-breeding season in OVX+E2 ewes (Smith
et al 2008). However, the expression level of *Npvf* was similar across breeding and non-breeding
seasons, in both OVX and OVX+E2 ewes (Smith et al 2008), which is not congruent with our
current findings. The reasons for this are unclear but may relate to the methods used (nonradioactive ISH vs qRT-PCR).

432

Compared to KNDy neurons, the evidence for a direct control of Npvf-expressing neurons by sex 433 steroids is scarce (Goodman & Inskeep, 2015). In hamsters, about 40% of Npvf neurons express 434 ERa and E2 injection in OVX animals induces c-Fos in a subset of Npvf cells (Kriegsfeld et al 435 436 2006). In mouse, however, only 20-25% of Npvf neurons co-express ERa as assessed by ISH (Molnar et al 2011; Poling et al 2012), while scRNAseq provides no evidence for co-expression 437 (Chen et al 2017). In sheep, we also found no evidence for co-expression (our unpublished 438 439 observations) while others reported that ~20% of Npvf neurons may express ERa (unpublished observations, cited in Clarke & Arbabi 2016). These data are consistent with the overall distinct 440 441 distribution patterns of Npvf- (Dardente et al 2008) and ERa-expressing cells in the ovine MBH 442 (Lehman et al 1993; Blache et al 1994). Npvf neurons are most numerous at the level of the VMH/DMH, where they tend to cluster medially, close to the third ventricle, while ERa-ir cells 443 are few at this level and rather scattered in lateral regions, farther from the third ventricle. In sheep, 444 the distribution of PGR does not provide support for co-expression with Npvf, since labeled nuclei 445 are not found in the DMH/VMH (Goubillon et al 2000; Dufourny and Skinner 2002; Smith et al 446 2007; Foradori et al 2002). These neuroanatomical considerations suggest that *Npvf*-expressing 447 neurons are not primary targets of sex steroids, even though the possibility that ERa/PGR are 448 expressed at low levels (i.e. below the detection threshold) can not be excluded. 449

Overall, the opposite expression patterns for Kiss1 and Npvf in intact, OVX+E2 and OVX ewes 451 is striking. We suggest two non-mutually exclusive scenarios to explain this : sex steroids have 452 independent and opposite actions on both genes, or the two neuronal populations are somehow 453 454 connected such that the impact of sex steroids on one population leads to inhibition of expression in the other. In both scenarios, the interplay between T3 and E2 is required to govern 455 proper seasonal timing (Lincoln and Short 1980; Karsch et al 1984; Karsch et al 1995; 456 Dardente 2012 ; Dardente et al 2014). The idea that Npvf-expressing neurons might be the 457 primary target for photoperiodic control has already been put forth in hamsters (Henningsen et 458 al 2016; Angelopoulou et al 2019). However, we deem this unlikely for several reasons. As 459 460 discussed above, KNDy cells do directly respond to sex steroids (presence of ERa and PGR) and also contain the thyroid hormone receptor TRa (Dufourny et al 2016); they are therefore 461 well-placed to mediate the T3- and E2- dependent switches in seasonal breeding. Anatomically, 462 463 KNDy cells are also likely to receive contacts from beta-tanycytes processes, which traverse the arcuate nucleus and reach the median eminence (Rodriguez et al 2005; Prévot et al 2018; 464 465 Rodriguez et al 2019). Indeed, KNDy cells might also receive signals, including T3, directly 466 from PT cells through the peculiar micro-vasculature of the arcuate nucleus region (Clarke 2015). Finally, the evidence that KISS1 is the key activator of reproduction in mammals is 467 overwhelming (Beltramo et al 2014; Pinilla et al 2012; Simonneaux 2018), while evidence 468 implicating RFRP3 is weak (Leon and Tena-Sempere 2016; Angelopoulou et al 2019). 469

470

In sheep, KISS1 and analogues consistently trigger GnRH/LH release and ovulation, even during the anestrus season (Messager et al 2005; Caraty et al 2007; Beltramo et al 2015; Decourt et al 2016b; Beltramo & Decourt 2018). In comparison, we could not find any evidence for a role of RFRP3 in GnRH/LH secretion (Decourt et al 2016a), which contrasts with earlier findings (Clarke et al 2008). Genetic ablation of the RFRP3 receptor (NPFFR1) in mouse has

negligible impact upon reproduction (Leon et al 2014), while absence of KISS1R (a.k.a. 476 GPR54) leads to infertility (Messager et al 2005; Pinilla et al 2012; Beltramo et al 2014). 477 Finally, there are only minimal projections from RFRP3 cells towards the arcuate nucleus, 478 479 which makes it unlikely that RFRP3 neurons make synaptic input onto KISS1 neurons in sheep (Qi et al 2009). However, some evidence for such a unidirectional control has been found in 480 mouse (Poling et al 2013). Therefore, we can not exclude a primary role for *Npvf*-expressing 481 neurons in the seasonal response, but current evidence in sheep rather favor a model in which 482 these neurons are located downstream of KNDy neurons. 483

484

In conclusion our findings reveal the circuit-level logic of the impact of sex steroid of seasonal 485 breeding (Fig 5). The PT behaves as would be expected for a true circannual oscillator, sheltered 486 from the impact of sex steroids and TH, but acutely sensitive to photoperiod through melatonin. 487 488 Tanycytes display gene-specific regulation by both TH, E2 and P4, which we believe might help fine-tune the timing for the onset and offset of the breeding season. Finally, neurons expressing 489 490 Kissl emerge as a key node for the integration of environmental (photoperiod, through T3 responsiveness) and internal (feedback to sex steroid) cues, which together drive seasonal 491 breeding. Our analysis strongly suggests that Kiss1 neurons of the arcuate nuclei are the cellular 492 493 substrate for the "seasonal switch in the ability of E2 to inhibit the GnRH pulse generator". Finally the opposite transcriptional control of Kiss1 and Npvf expression over distinct states of sex steroid 494 495 feedback suggest some level of interconnection between these neuronal populations, the nature of which remains to be identified. 496

497

# 498 Figure legends

Figure 1 : Representative autoradiograms of *in situ* hybridization for a set of seasonal genes
expressed in the MBH of intact ewes in May and November : PT-expressed markers (black box),

tanycyte-specific markers (green box) and hypothalamic markers (red box). Note that all PT and
tanycyte markers display large seasonal variation in expression while *Kiss1* and *Npvf* show similar
expression levels in May and November (also see Fig S1).

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Figure 2 : qRT-PCR for a set of seasonal genes expressed in the MBH of intact ewes in November,
February, May and August : PT-expressed markers (black box), tanycyte-specific markers (green
box) and hypothalamic markers *Kiss1* and *Npvf* (red box). Note that all PT and tanycyte markers
display large seasonal variation in expression while *Kiss1* and *Npvf* show similar expression levels
in May and November (also see Fig S2).

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**Figure 3** : Direct comparison of expression levels (as assessed by qRT-PCR) for a set of seasonal genes expressed in the MBH of intact, OVX+E2 and OVX ewes in May and November. Note that PT markers (black box) appear to be unaffected by the sex steroid status while some tanycyte markers (green box) do show a moderate impact on amplitude (also see **Fig S3**). Also note that the opposite May-Nov differences in expression seen for *Kiss1* and *Npvf* (red box) in OVX+E2 ewes are lost in intact and OVX ewes. However, a consistent feature is the opposite pattern of expression of both markers across the various sex steroid states.

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**Figure 4** : qRT-PCR for a set of seasonal genes expressed in the MBH of intact ewes of the Ilede-France (panels A to C) and Romanov (panels D to F) breeds at the transition towards anestrus (from mid February to mid March) : impact of P4. The length of the photoperiod at the 3 sampling times is superimposed to the *Tshb* data in panels A and D (red dots). Ewes were in follicular phase for the first two sampling times and in luteal phase for the third sampling time. Molecular markers in the PT (black box) and hypothalamus (red box) do show the expected photoperiod-driven changes in expression in both breeds, with little (if any) overt impact of P4. In 526 contrast, photoperiod-driven changes in expression for tanycyte markers (green box) do seem to
527 be counterbalanced by P4 for both breeds (also see Fig S4).

528

Figure 5 : A revised circuit-level model for the photoperiodic control of seasonal breeding (see 529 Lomet et al 2018). Here we show that sex steroids do not impact seasonal gene expression in the 530 PT. Together with prior findings that T3 does not have any effect either we conclude that the PT 531 is solely responsive to melatonin, which strengthens its role as a circannual clock. E2 and P4 may 532 533 have a modest and gene-specific impact upon seasonal gene expression in tanycyte, which could play a modulatory role in timing the transition to anestrus. Finally, *Kiss1* and *Npvf* do show striking 534 opposite changes in expression under various sex steroid conditions, which suggest some form of 535 communication between these neuronal populations. Taking into account differential expression 536 of sex steroid receptors and neuroanatomical considerations, we favor a model in which Kiss1 is 537 538 the target neuronal population of T3 and E2/P4 signaling in the control of seasonal breeding.

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#### 541 Supplemental Materials

542 Figures S1-S5

543 Table S1 : Word document

544 Table S2 : Excel file

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Fig.3 Intact VS OVX+E2 VS OVX





Fig.4 Pg VS Long PP

