

1 **Anti-Müllerian hormone is expressed and secreted by bovine oviductal and**
2 **endometrial epithelial cells**

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13 Running head

14 AMH in bovine oviduct and uterus

15

16 **Abstract**

17 In this study, we investigated whether bovine oviducts and endometria produce AMH (for
18 paracrine and autocrine signaling). Reverse transcription-polymerase chain reaction and
19 western blotting detected AMH expression in oviductal and endometrial specimens.
20 Immunohistochemistry revealed robust AMH expression in the ampulla and isthmus
21 epithelia, and the glandular and luminal endometrial epithelia (caruncular endometria). *AMH*
22 mRNA (measured by real-time PCR) and protein expression in these layers did not
23 significantly differ among estrous phases in adult Japanese Black (JB) heifers ($P > 0.1$).
24 Furthermore, the expression in these layers also did not differ among Holsteins cows ($93.8 \pm$
25 5.8 months old), JB heifers (25.5 ± 0.4 months old), and JB cows (97.9 ± 7.9 months old).
26 We also compared AMH concentrations in the oviduct and uterine horn fluids among the
27 three groups (measured by immunoassays). Interestingly, the AMH concentration in the
28 oviduct fluid, but not in the uterine horn fluid, of Holsteins cows, were lower than those in
29 JB heifers and cows ($P < 0.05$). Therefore, bovine oviducts and endometria express AMH
30 and likely secrete it into the oviduct and uterine fluids.

31

32 **KEY WORDS**

33 age, AMH receptor type 2, Holstein dairy cow, Müllerian-inhibiting substance, ruminant

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36 1 INTRODUCTION

37 Anti-Müllerian hormone (AMH) is a member of the transforming growth factor
38 (TGF)- β family. Preantral and small antral follicles secrete AMH in female animals (Bhide
39 & Homburg, 2016). AMH expression is well-characterized in ovaries and plays important
40 roles in regulating follicular development (Hernandez-Medrano et al., 2012) and inhibiting
41 follicular atresia (Sefrioui et al., 2019). Concentrations of circulating AMH can help to
42 predict the number of high-quality embryos produced by various mammals, including cows
43 and humans (Arouche et al., 2015; Sefrioui et al., 2019). High-quality embryos result from
44 synchronous regulation by the sperm, ovum, oviduct, and endometrium. Further, plasma
45 AMH concentrations are positively correlated with pregnancy rates in various animals,
46 including humans and cows (Ribeiro et al., 2014; Josso, 2019).

47 Accordingly, women with low blood AMH concentrations have an increased risk of
48 miscarriage (Tarasconi et al., 2017; Lyttle et al., 2018). Moreover, mares with delayed uterine
49 clearance have significantly lower blood AMH concentrations than those without delayed
50 uterine clearance (Gharagozlou et al., 2013). Therefore, AMH might play vital roles in the
51 oviduct and endometrium. Anti-Müllerian hormone can act at the extragonadal level by
52 activating its primary receptor, AMH receptor type 2 (AMHR2), in the gonadotrophs of
53 anterior pituitaries of rats and bovines (Garrel et al., 2016; Kereilwe & Kadokawa, 2019).
54 We have previously shown that bovine gonadotrophs express AMH, which likely acts in
55 paracrine and autocrine manner (Kereilwe et al., 2018). Endometrial tissues of healthy
56 women also express AMHR2 (Kim et al., 2019). We recently discovered that AMHR2 is
57 expressed in parts of the bovine oviducts and uterus that are important for fertility and

58 embryogenesis, namely, the epithelium of the tunica mucosa of the ampulla and isthmus, the
59 epithelium of uterine glands, and the luminal epithelium of the endometrium (Ferdousy et al.,
60 2020). Therefore, these tissues might express AMH for different paracrine and autocrine
61 roles.

62 Old age is associated with decreased fertility in cows and humans (Osoro & Wright,
63 1992; Scheffer et al., 2018); however, the exact mechanisms underlying this association
64 remains unclear. Several studies in humans have linked aging to plasma AMH concentrations.
65 Blood AMH concentrations are highest in pubertal girls and gradually decrease starting at
66 age 25 until they are undetectable after menopause (Dewailly et al., 2014), suggesting that
67 low AMH is a marker of ovarian aging (Bhide & Homburg, 2016). Studies on the relationship
68 between age and plasma AMH concentrations in adult female ruminants are not common,
69 but one study showed that Japanese Black cows have higher blood AMH concentrations than
70 post-pubertal heifers (Koizumi & Kadokawa, 2017). Therefore, age might be a determinant
71 of AMH expression levels in the oviducts and endometria, although there could be species-
72 specific differences as well.

73 Therefore, in this study, we evaluated the association between oviductal and
74 endometrial AMH expression and various physiological factors, such as the stage of the
75 estrous cycle, age, and breed. We also compared AMH concentrations in the oviduct and
76 uterine horn fluids collected from Holsteins cows and Japanese Black heifers and cows.

77

78

79 **2 MATERIALS AND METHODS**

80 All experiments were performed according to the Guiding Principles for the Care and
81 Use of Experimental Animals in the Field of Physiological Sciences (Physiological Society
82 of Japan) and approved by the Committee on Animal Experiments of Yamaguchi University
83 (approval no. 301).

84

85 **2.1 Sample collection**

86 We obtained oviductal and endometrial samples from cattle managed by contract
87 farmers in western Japan. All cattle born in Japan since 2003 are registered at birth with an
88 individual identification number in a database of National Livestock Breeding Center of
89 Japan. We utilized both individual identification numbers to search the database and
90 information given by the contract farmers for the cattle in this study.

91

92 **2.2 Experiment 1**

93 Experiment 1 was conducted to evaluate whether AMH was expressed in the oviduct
94 and endometrium in heifers utilizing reverse transcription-polymerase chain reaction (RT-
95 PCR), western blotting, and immunofluorescence staining. We obtained the ipsilateral side
96 of the ampulla, isthmus, caruncular, and intercaruncular area of endometria from four post-
97 pubertal (26 months of age) Japanese Black heifers at a local abattoir. The four heifers were
98 at days 2 to 3, 8 to 12, 15 to 17, and 19 to 21 (day 0 = day of estrus), as determined via
99 macroscopic examination of the ovaries and uterus (Miyamoto et al., 2000). The ampulla,
100 isthmus, caruncle, and intercaruncle samples collected were from the side ipsilateral to
101 ovulation in the three heifers from days 2 to 3, 8 to 12, or 15 to 17 but were from the side
102 ipsilateral to the dominant follicle in the remaining heifer at day 19 to 21. We collected

103 ampullar samples from areas at least 3 cm from the fimbriated infundibulum, from the
104 ampullary–isthmic junction, and the isthmus samples from areas also at least 3 cm from the
105 ampullary–isthmic junction, and the utero-tubal junction. Half of the ampulla and half of the
106 isthmus were frozen in liquid nitrogen and preserved at -80°C until RNA or protein
107 extraction. The remaining halves of the ampulla and isthmus were stored in 4%
108 paraformaldehyde at 4°C for 16 hr for immunohistochemistry. The middle area of the uterine
109 horn was opened longitudinally using scissors, and caruncle tissues were carefully dissected
110 so as not to include the intercaruncle; then, intercaruncle areas were excised. The collected
111 caruncle and intercaruncle samples were frozen in liquid nitrogen and preserved at -80°C
112 until RNA or protein extraction or stored in 4% paraformaldehyde at 4°C for 16 hr for
113 immunohistochemistry. Granulosa cells in preantral and small antral follicles express AMH
114 (Campbell et al., 2012; Kereilwe et al., 2018). Therefore, we also collected ovarian tissue
115 samples from the same heifers to use as a positive control of AMH expression for RT-PCR
116 and western blotting assays.

117

118 **2.3 Experiment 2**

119 Experiment 2 was conducted to compare AMH expression in oviductal and
120 endometrial samples among different stages of the estrous cycle utilizing quantitative RT-
121 PCR and western blotting described subsequently. The ampulla, isthmus, caruncle, and
122 intercaruncle tissues were harvested from adult (26-month-old) non-pregnant Japanese Black
123 heifers in the pre-ovulatory phase (day 19 to 21; $n = 5$), day 1 to 3 ($n = 5$), day 8 to 12 ($n =$
124 5), or day 15 to 17 ($n = 5$), as determined via macroscopic examination of the ovaries and

125 uterus (Miyamoto et al., 2000). Samples were obtained at the local abattoir and immediately
126 frozen in liquid nitrogen and preserved at -80°C until RNA or protein extraction.
127

128

129 **2.4 Experiment 3**

130 Experiment 3 was conducted to compare AMH expression in oviductal and
131 endometrial samples based on age or breed utilizing the quantitative RT-PCR and western
132 blotting described subsequently. The ampulla, isthmus, caruncle, and intercaruncle tissues
133 were harvested during the luteal phase (day 8 to 12) from post-pubertal Japanese Blacks
134 heifers (25.5 ± 0.4 months of age; $n = 6$), Japanese Black cows (97.9 ± 7.9 months of age; n
135 $= 6$), and Holstein cows (93.8 ± 5.8 months of age; $n = 6$) from the local abattoir. We
136 compared these three groups due to the following reasons. First, it was impossible to obtain
137 samples from post-pubertal Holstein heifers since they were kept in dairy farms for milking
138 purposes. Second, in our previous study (Kereilwe et al., 2018), we compared expression
139 levels of AMH in gonadotrophs between Holsteins cows (approximately 80 months of age),
140 and Japanese Black heifers (approximately 26 months of age) and cows (approximately 90
141 months of age), finding significant differences in *AMH* mRNA and AMH protein among
142 them. Third, we previously observed a significant difference in blood AMH concentrations
143 between Japanese Black cows (approximately 81 months of age) and Japanese Black heifers
144 (approximately 22 months of age) (Koizumi & Kadokawa, 2017). The collected samples
145 were frozen in liquid nitrogen and preserved at -80°C until RNA or protein extraction. All
146 heifers and cows in the three groups were non-lactating and non-pregnant, with no follicular
147 cysts, luteal cysts, or other ovarian or uterine disorders upon macroscopic ovarian

148 examination (Kamomae, 2012). The Holstein cows were slaughtered because they had not
149 become pregnant after at least five artificial insemination attempts.

150

151 **2.5 Experiment 4**

152 Experiment 4 was conducted to analyze AMH concentrations in the oviduct and
153 uterine horn fluids using an AMH enzyme immunoassay. We collected oviduct fluids on day
154 1 to 3, i.e. when oocytes are in oviduct (El-Banna & Hafez, 1970), and uterine horn fluids on
155 day 8 to 14 in order to compare AMH concentrations among groups of Japanese Black heifers
156 (26.2 ± 0.7 months of age; $n = 6$), Japanese Black cows (111.0 ± 12.2 months of age; $n = 6$),
157 and Holstein cows (91.9 ± 6.4 months of age; $n = 6$). The females were killed at the
158 slaughterhouse; the ipsilateral sides of oviducts to ovulation were closed at the uterine end
159 and then cut to separate the uterine end from the utero-tubal junction. The oviducts were then
160 separated from the surrounding connective tissue. A blunt 20-gauge needle was inserted from
161 the infundibulum side of the oviducts and used to gently flush the oviducts with 0.01 M
162 phosphate-buffered 0.14 M saline (pH 7.3) (PBS; 2 mL/oviduct). The resultant oviductal
163 fluids were collected from the opposite sides of the oviducts and pooled into 2-mL
164 microtubes. For the collection of uterine fluids, a blunt 20-gauge needle was inserted into the
165 tip of a cut uterine horn in which the uterine-body side had been closed by artery forceps.
166 After gently flushing with PBS (10 mL/horn), the resultant fluids were collected from the tip
167 of the cut uterine horn and pooled into 50-mL tubes. Tubes were centrifuged at $800 \times g$ for
168 20 min at 4°C , and the supernatants were stored at -35°C until analyzed for AMH.

169

170 **2.6 RT-PCR, sequencing of amplified products, and homology search in gene databases**

171 We utilized the same RT-PCR and sequencing methods as reported previously
172 (Kereilwe et al., 2018) to determine the expression of AMH mRNA in the ovary, ampulla,
173 isthmus, caruncle, or intercaruncle from the four heifers for experiment 1. Briefly, total RNA
174 was extracted from the samples using RNAzol RT Reagent (Molecular Research Center Inc.,
175 Cincinnati, OH, USA) according to the manufacturer's protocol. The extracted RNA samples
176 were treated with ribonuclease-free deoxyribonuclease (Thermo Fisher Scientific, Waltham,
177 MA, USA) to eliminate possible genomic DNA contamination. The concentration and purity
178 of each RNA sample were evaluated to ensure that the A260/A280 nm ratios were in the
179 acceptable range of 1.8–2.1. The mRNA quality of all samples was verified by
180 electrophoresis of total RNA followed by staining with ethidium bromide, and confirming
181 that the 28S:18S ratios were 2:1. The cDNA was synthesized from 1 µg of the total RNA per
182 sample using SuperScript IV VILO Master Mix (Thermo Fisher Scientific) according to the
183 manufacturer's protocol. No reverse transcription controls (NRCs) were prepared for RT-
184 PCR; they were generated by treating the extracted RNA with the same deoxyribonuclease
185 but not with cDNA synthetase. PCR was conducted using the previously reported primers
186 (Kereilwe et al., 2018): nucleotides 1486 - 1813, forward primer: 5' -
187 GCTCATCCCCGAGACATACC- 3' ; reverse primer: 5' -
188 TTCCCGTGTTTAATGGGGCA-3'). Primers were designed by the Primer3 algorithm
189 (<https://www.ncbi.nlm.nih.gov/tools/primer-blast/>) based on a reference sequence of bovine
190 AMH [the National Center for Biotechnology Information (NCBI) reference sequence of
191 bovine AMH is NM_173890]. The expected PCR-product size of AMH using the primer pair
192 is 328 bp. Using a Veriti 96-Well Thermal Cycler (Thermo Fisher Scientific), PCR was

193 performed using 20 ng of cDNA, 20 ng RNA as the NRC or water as the no template control
194 (NTC), and polymerase (Tks Gflex DNA Polymerase, Takara Bio Inc., Shiga, Japan) under
195 the following thermocycling conditions: 94 °C for 1 min for pre-denaturation followed by 35
196 cycles of 94 °C for 60 sec, 60 °C for 15 sec, and 68 °C for 30 sec. PCR products were
197 separated on 1.5% agarose gels by electrophoresis along with a molecular marker [Gene
198 Ladder 100 (0.1–2 kbp), Nippon Gene, Tokyo, Japan], stained with fluorescent stain (Gelstar,
199 Lonza, Allendale, NJ, USA), and observed using a charge-coupled device (CCD) imaging
200 system (GelDoc; Bio-Rad, Hercules, CA, USA). The PCR products were purified with the
201 NucleoSpin Extract II kit (Takara Bio Inc.) and subsequently, sequenced with a sequencer
202 (ABI3130, Thermo Fisher Scientific) using one of the PCR primers and the Dye Terminator
203 v3.1 Cycle Sequencing Kit (Thermo Fisher Scientific). The sequences obtained were used as
204 query terms to search the homology sequence in the DNA Data Bank of NCBI using the basic
205 nucleotide local alignment search tool (BLAST) optimized for highly similar sequences
206 (available on the NCBI website).

207

208 **2.7 Anti-AMH antibody used in this study**

209 We utilized the same anti-human AMH rabbit polyclonal antibody (ARP54312;
210 Aviva Systems Biology, CA, USA) that we previously verified with bovine ovaries
211 (Kereilwe et al., 2018) to determine the expression of AMH in the bovine samples by western
212 blotting and immunohistochemistry. Human AMH is secreted as a homodimeric precursor
213 consisting of two identical monomers (560 amino acids; NCBI accession number
214 AAA98805.1) (Mamsen et al., 2015). Each monomer consists of two domains, specifically
215 (i) a mature C-terminal region, which becomes bioactive after proteolytic cleavage and binds

216 AMHR2, and (ii) a pro-region, which is important for AMH synthesis and extracellular
217 transport. The human AMH precursor is cleaved at amino acid 451 (arginine) between the
218 two domains. The pro-region has another cleavage site at amino acid 229 (arginine), causing
219 three potential cleavage products, namely pro-mid-mature, mid-mature, and mature (Mamsen
220 et al., 2015). The bovine AMH precursor monomer (575 amino acids; NCBI accession
221 number NP_776315.1) has a 91% sequence homology to the human protein. The bovine
222 AMH precursor contains an arginine cleavage site between the two domains at amino acid
223 466 but not at the residue corresponding to amino acid 229. The rabbit polyclonal anti-AMH
224 antibody recognizes the mature C-terminal form of human AMH (corresponding to amino
225 acids 468–517;
226 SVDLRAERSVLIPETYQANNCQGVCGWPQSDRNPRYGNHVVLLLKMQARG). This
227 sequence has 98% homology to amino acids 483–532 of the mature C-terminal form of
228 bovine AMH but no homology to other bovine proteins, as determined based on protein
229 BLAST.

230

231 **2.8 Western blotting for AMH detection**

232 Western blotting was performed as described previously (Kereilwe et al., 2018). Briefly,
233 proteins were extracted from the ampulla, isthmus, caruncle, intercaruncle, or ovary samples
234 (used as positive controls) from the four heifers used in experiment 1. The extracted protein
235 sample (33.4 µg of total protein in 37.5 µl) was mixed in 12.5 µl of 4× Laemmli sample
236 buffer (Bio-rad) containing 10% (v/v) β-mercaptoethanol, and then boiled for 3 min at 100 °C.
237 The boiled protein samples were quickly cooled on ice. Then, 12 µl of boiled protein samples

238 (8 μ g of total protein) was loaded onto a sodium dodecyl sulfate-polyacrylamide
239 polyacrylamide gel (Any KD Criterion TGX precast gel; 567-1125; Bio-Rad) along with a
240 molecular weight marker (Precision Plus Protein All Blue Standards; Bio-Rad) and resolved
241 by electrophoresis at 100 V for 90 min. Proteins were then transferred to polyvinylidene
242 fluoride (PVDF) membranes. Blocking was performed with 5% non-fat dry milk containing
243 0.1% tween 20 for 1 hr at 25 °C; subsequently, immunoblotting was performed with the anti-
244 AMH rabbit antibody (1:25,000 dilution) overnight at 4 °C. After washing the membrane
245 with 10 mM tris-HCl (pH 7.6) containing 150 mM NaCl and 0.1% tween 20, the PVDF
246 membrane was incubated with horseradish peroxidase (HRP)-conjugated anti-rabbit IgG
247 goat antibody (Bethyl Laboratories, Inc., Montgomery, TX, US; 1:50,000 dilution) for 1 hr
248 at 25 °C. Protein bands were visualized using an ECL-Prime chemiluminescence kit (GE
249 Healthcare, Amersham, UK) and CCD imaging system (Fujifilm, Tokyo, Japan). We defined
250 bovine AMH bands based on band size as the AMH precursor or the mature form (four sizes)
251 according to previous studies (Mamsen et al., 2015; Kereilwe et al., 2018). Antibodies were
252 removed from the PVDF membrane with a stripping solution (Nacalai Tesque Inc., Kyoto,
253 Japan); then, the membrane was used for immunoblotting with the anti- β -actin mouse
254 monoclonal antibody (A2228, 1:50,000 dilution; Sigma-Aldrich, St. Louis, MO, USA).

255 Western blotting was also conducted to compare AMH protein expression levels in the
256 ampulla, isthmus, caruncle, and intercaruncle among different estrous phases or the groups
257 of Japanese Black heifers, Japanese Black cows, and Holstein cows from experiment 2 or 3.
258 Briefly, boiled samples (8 μ g total protein of each sample) were loaded on a polyacrylamide
259 gel along with the molecular weight marker and four standard samples (2, 4, 8, and 16 μ g

260 total protein for each of five randomly selected samples diluted with protein extraction
261 reagent). MultiGauge v.3.0 software (Fujifilm) was used to quantify the signal intensity of
262 the protein bands. The intensities of bands representing AMH (as the mature C-terminal
263 form) for 16, 8, 4, and 2 μg protein samples were set as 100%, 50%, 25%, and 12.5%,
264 respectively, and the intensity of other samples was calculated as a percentage of these
265 standards using MultiGauge software. After antibodies were removed from the PVDF
266 membrane with a stripping solution, the membrane was used for immunoblotting with the
267 anti- β -actin mouse monoclonal antibody. The intensities of the β -actin band for 16, 8, 4, and
268 2 μg protein samples were set as 100%, 50%, 25%, and 12.5%, respectively, and the intensity
269 of other samples was calculated as a percentage of these standards using MultiGauge
270 software. The AMH expression level was normalized to that of β -actin in each sample.

271

272

273 **2.9 Fluorescent immunohistochemistry and confocal microscopy**

274 We utilized the same method of immunohistochemistry to detect ovarian AMH and
275 AMHR2 as reported previously (Kereilwe et al., 2018; Kereilwe & Kadokawa, 2019) for
276 experiment 1. Briefly, the fixed tissue blocks were placed in 30% sucrose PBS until the
277 blocks were infiltrated with sucrose. The blocks were then frozen in an embedding medium
278 (Tissue-Tek OCT compound; Sakura Finetechnical Co. Ltd, Tokyo, Japan) and maintained at
279 -80°C . Next, the blocks were sectioned into 15- μm -thick cross-sections using a cryostat
280 (Leica Microsystems Pty Ltd, Wetzlar, Germany) and mounted on microscope slides (MAS
281 coat Superfrost; Matsunami-Glass, Osaka, Japan). The sections were treated with 0.3 %

282 triton X-100-PBS for 15 min and blocked by incubating them with 0.5 mL of PBS containing
283 10% normal goat serum (Wako Pure Chemicals, Osaka, Japan) for 1 hr at room temperature.
284 The slides were incubated with a cocktail of primary antibodies containing the anti-AMH
285 (Kereilwe et al., 2018), anti-AMHR2 (Kereilwe & Kadokawa, 2019), anti-cytokeratin
286 antibodies (Sigma-Aldrich) (all diluted as 1:1,000) for 12 hr at 4 °C. After the primary
287 antibody incubation, the sections were washed twice with PBS and then incubated with a
288 cocktail of fluorochrome-conjugated secondary antibodies (Alexa Fluor 488 goat anti-
289 chicken IgG, Alexa Fluor 546 goat anti-mouse IgG, and Alexa Fluor 647 goat anti-rabbit IgG
290 [all from Thermo Fisher Scientific and diluted to 1 µg/mL]) and 1 µg/mL of 4', 6'-diamino-
291 2-phenylindole (DAPI; Wako Pure Chemicals, Osaka, Japan) for 4 hr at room temperature.

292 The stained sections on slides were observed by confocal microscopy (LSM710; Carl
293 Zeiss, Göttingen, Germany) equipped with a diode laser 405 nm, argon laser 488 nm, and
294 HeNe laser 533 nm. Images obtained by fluorescence microscopy were scanned with a 20×,
295 40×, 63× or 100× objective and recorded with a CCD camera system controlled by ZEN2012
296 black edition software (Carl Zeiss). The DAPI is shown in blue, and AMH is shown in green
297 in the confocal images. To verify the specificity of the signals, we included several negative
298 controls in which the primary antiserum had been omitted, or in which normal rabbit IgG,
299 normal mouse IgG, and normal chicken IgG (all from Wako Pure Chemicals) were used
300 instead of the primary antibody.

301

302 2.10 Quantitative RT-PCR

303 Quantitative RT-PCR was performed to compare *AMH* expression among estrous phases
304 or the groups of Japanese Black heifers, Japanese Black cows, and Holstein cows in
305 experiment 2 or 3. The preparation of high-quality total RNA and cDNA synthesis were
306 performed as described herein. We utilized the same method of quantitative RT-PCR and the
307 same primers to measure *AMH* mRNA or two housekeeping genes, *C2orf29* (NCBI accession
308 number XM_002691150.2) and *SUZ12* (NCBI accession number NM_001205587.1), as
309 reported previously (Nahar & Kadokawa 2017; Kereilwe et al., 2018). Table 1 lists the primer
310 sequences for *AMH* and the two housekeeping genes. The two housekeeping genes were
311 selected since they are the most stable and reliable housekeeping genes in the bovine oviducts
312 and endometria (Walker et al., 2009; Nahar & Kadokawa 2017) based on both geNorm and
313 Normfinder programs (Vandesompele, 2002; Nahar & Kadokawa 2017).

314 Levels of gene expression were measured in duplicate by quantitative RT-PCR
315 analyses with 20 ng cDNA, using the CFX96 Real Time PCR System (Bio-Rad) and Power
316 SYBR Green PCR Master Mix (Thermo Fisher Scientific), with a six-point relative standard
317 curve, the NTC, and the NRC. Standard 10-fold dilutions of purified and amplified cDNA
318 fragments were prepared. The cycle conditions for all genes were: 95 °C for 10 min for pre-
319 denaturation; five cycles each of 95 °C for 15 sec and 66 °C for 30 sec; 40 cycles each of
320 95 °C for 15 sec, and 60 °C for 60 sec. Melting curve analyses were performed at 95 °C for
321 each amplicon and each annealing temperature to ensure the absence of smaller non-specific
322 products, such as dimers. To optimize the quantitative RT-PCR assay, serial dilutions of a
323 cDNA template were used to generate a standard curve by plotting the log of the starting
324 quantity of the dilution factor against the C_q value obtained during amplification of each

325 dilution. Reactions with a coefficient of determination (R^2) > 0.98 and efficiency between 95
326 and 105% were optimized. The coefficients of variation of quantitative RT-PCRs were less
327 than 6%. The concentration of PCR products was calculated by comparing the C_q values of
328 unknown samples with the standard curve using software (CFXmanagerV3.1, Bio-Rad). The
329 gene expression levels of *AMH* genes were normalized to the geometric mean of the
330 expression levels of two housekeeping genes; thus, the *AMH* amount was divided by the
331 geometric mean of *C2orf29* and *SUZ12* in each sample.

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335 **2.11 AMH immunoassay**

336 AMH concentrations in samples of the oviduct and uterine fluids were assessed by using
337 a bovine AMH ELISA kit (Ansh Labs, TX, USA) using a protocol described previously
338 (Akbarinejad et al., 2019). The pair of mouse monoclonal antibodies used has epitopes in the
339 N-terminal or C-terminal of the mature C-terminal form of bovine AMH. The ELISA has no
340 cross-reactivity with bovine LH, FSH, inhibins, and activins (personal communication with
341 Dr. Ajay Kumar of Ansh Labs). The detection limit was 0.011 ng/mL, and the intra- and
342 inter-assay coefficient of variation were 4.3% and 8.6%, respectively.

343

344 **2.12 Statistical analysis**

345 The statistical analyses were performed using StatView version 5.0 for Windows
346 (SAS Institute, Inc., Cary, NC, USA). The Grubb's test was used to verify the absence of

347 outliers. The Shapiro-Wilk test or the Lilliefors test were used to evaluate the normality or
348 log-normality of each variable, respectively—all variables were normally distributed. The F-
349 test was used to verify the homogeneity of variance of all variables between estrous stages
350 and ages. Using Grubb's test, we verified that there were no outliers for the variables.
351 Analysis of variance (ANOVA) and Fisher's protected least significant difference (PLSD)
352 test were used to evaluate differences in *AMH* mRNA or protein expression in either the
353 ampulla, isthmus, caruncle, or intercaruncle collected from bovines at different estrous stages
354 or different groups. ANOVA and Fisher's PLSD tests were also used to evaluate differences
355 in the logarithm of AMH concentrations in the oviduct or uterine fluids collected from
356 females at different estrous stages or different groups. The level of significance was set at P
357 < 0.05 . Data are expressed as mean \pm standard error of the mean (SEM).

358

359 **3 RESULTS**

360 **3.1 Experiment 1**

361 An amplicon of 328 bp, indicating AMH, was obtained from samples of the ovary,
362 ampulla, isthmus, caruncle, and intercaruncle and confirmed using agarose gel
363 electrophoresis (Fig. 1). Neither the NTC nor NRC yielded any PCR-amplified products. A
364 homology search against the gene databases for the sequenced amplified products revealed
365 bovine AMH (NM_173890.1) as the best match, with a query coverage of 100%, e-value of
366 0.0, and maximum alignment identity of 99%. No other bovine gene displayed homology
367 with the PCR-product described, indicating that the amplified product was bovine AMH.

368 AMH expression in the ampulla, isthmus, caruncle, and intercaruncle, and in ovarian
369 specimens used as positive controls was analyzed via western blotting (Fig. 2). Similar

370 protein bands for AMH were observed among all the tissue samples (Fig. 2A). The ovary,
371 isthmus, caruncle, and intercaruncle, however, showed multiple bands for full-length AMH,
372 whereas the ampulla showed a single band for full-length AMH. The mature C-terminal form
373 was found only in the ovary and intercaruncle but not in the ampulla, isthmus, and caruncle.
374 No protein bands were observed on the blotting membranes used as negative controls, on
375 which the primary antiserum had been pre-absorbed with an antigen peptide. β -actin was the
376 loading control, as shown in Figure 2b.

377 Fig. 3 and Fig. 4 show the results of immunofluorescence staining for cytokeratin,
378 AMHR2, and AMH in the ampulla or isthmus samples. Immunohistochemistry revealed
379 robust AMH expression in the epithelium of the tunica mucosa, shown as a cytokeratin-
380 positive layer, of the ampulla (Fig. 3A, 3C) and isthmus (Fig. 4A, 4C), where AMH receptor
381 type 2 was also expressed. Further, fibroblasts, which were cytokeratin-negative, too
382 expressed AMH. Fig. 5 and Fig. 6 show the results of immunofluorescence staining for
383 cytokeratin, AMHR2, and AMH in the caruncle or intercaruncle samples. The strong AMH
384 signals were localized to the luminal epithelium (Fig. 5A, 5C), the vasculature in the stroma
385 (Fig. 5A), and the epithelium of endometrial glands (Fig. 6A, 6C). Negative control staining
386 using the normal IgGs showed no immunostaining signal in these layers or cells (Fig. 3B, 4B,
387 5B, 6B).

388 Fig. 3 and Fig. 4 show the results of immunofluorescence staining for cytokeratin,
389 AMHR2, and AMH. Immunohistochemistry revealed robust AMH expression in the
390 epithelium of the tunica mucosa, shown as a cytokeratin-positive layer, of the ampulla (Fig.
391 3A) and isthmus (Fig. 3C), where AMH receptor type 2 was also expressed. Further,
392 fibroblasts, which were cytokeratin-negative, too expressed AMH. The strong AMH signals

393 were localized to the luminal epithelium (Fig. 4A), the vasculature in the stroma (Fig. 4A),
394 and the epithelium of endometrial glands (Fig. 4C). Negative control staining using the
395 normal IgGs showed no immunostaining signal in these layers or cells (Fig. 3B, 3D, 4B, 4D).

396

397 **3.2 Experiment 2**

398 Quantitative RT-PCR and western blotting revealed no significant differences in *AMH*
399 mRNA and protein expression among various estrous phases in the ampulla (Fig. 7A, 7E),
400 isthmus (Fig. 7B, 7F), caruncle (Fig. 7C, 7G), and intercaruncle (Fig. 7D, 7H).

401

402 **3.3 Experiment 3**

403 There were no significant differences in AMH mRNA and protein expression levels
404 in the ampulla (Fig. 8A, 8E), isthmus (Fig. 8B, 8F), caruncle (Fig. 8C, 8G), and intercaruncle
405 (Fig. 8D, 8H) among the Holsteins cows and the Japanese Black heifers and cows.

406

407

408 **3.4 Experiment 4**

409 AMH concentrations in the oviduct fluids on day 1 to 3 of Holsteins cows were
410 lower than those in the oviduct fluids of Japanese Black heifers and cows ($P < 0.05$; Fig.
411 9A). Anti-Müllerian hormone concentrations in uterine horn fluid on day 8 to 14, did not
412 differ among these three groups (Fig. 9B).

413

414 **4 DISCUSSION**

415 The results revealed robust high-intensity AMH signals in the tunica mucosa of the
416 ampulla and isthmus, and in the glandular and luminal epithelium of endometria, where
417 AMHR2 is constitutively expressed (Ferdousy et al., 2020). Little is known about AMH
418 expression in the oviduct and endometrium in all species. However, a previous study utilizing
419 immunohistochemistry detected AMH expression in the human endometrium (Wang et al.,
420 2009) and human endometrial cancer tissue (Gowkielewicz et al., 2019). Recently, AMHR2
421 expression was discovered in healthy human endometrial tissues (Kim et al., 2019). We
422 recently discovered that AMHR2 is expressed in the tunica mucosa of the ampulla and
423 isthmus and the glandular and luminal epithelium of bovine endometria (Ferdousy et al.,
424 2020), and this study validates previous findings. These data led to the speculation of
425 potential roles of AMH and AMHR2 in these layers; however, little is known regarding AMH
426 functions in the oviduct and endometrium. The roles of AMH in these layers might depend
427 on the observed constitutive expression, the downstream cytoplasmic pathway of AMHR2,
428 and other tissue-specific TGF- β family members.

429 Of note, we need to have in mind that the contribution of extragonadal AMH secretion
430 to the blood AMH concentration is unknown. However, no significant difference was
431 observed in the AMH expression levels among the estrous phases in the ampulla, isthmus,
432 caruncle, and intercaruncle tissues. Previous *in vivo* studies have not reported considerable
433 changes in circulating AMH concentrations during the estrous cycle in ruminants (El-Sheikh
434 et al., 2013; Pfeiffer et al., 2014; Koizumi & Kadokawa, 2017). Concurrent with the present
435 findings, the 5' -flanking region upstream of the bovine AMH gene lacks the consensus
436 response element sequences for estrogen and progesterone (Kereilwe et al., 2018). Therefore,

437 AMH expression might not change during the estrous cycle in the tunica mucosa of the
438 ampulla and isthmus, and in the glandular and luminal endometrial epithelia. The
439 constitutively expressed AMH in the layers of the oviduct and uterine horns might not play
440 a temporal role, such as that during sperm capacitation and fertilization.

441 AMH shares an intracellular pathway with another TGF- β family member, bone
442 morphogenetic protein (BMP) (McLennan & Pankhurst 2015). Bovine oviduct epithelial
443 cells express both BMP and BMP receptors, and BMPs might play autocrine roles at the
444 epithelial lining of the oviduct (Valdecantos et al., 2017). Smas and mothers against
445 decapentaplegic (Smads) are the cytoplasmic pathway for BMP receptors in murine oviduct
446 and uterus (Rodriguez et al., 2016). AMH induce Smad1/5/8 phosphorylation via AMHR2
447 in human granulosa cells (Merhi 2019). AMH signaling regulates expression of BMP
448 receptor type 2, supports Smad signaling, and influences BMP-dependent signaling in non-
449 small cell lung cancer (Beck et al., 2016). Furthermore, uteri from Smad1/5/4-AMHR2-
450 conditional knockout females exhibit multiple defects in the stroma, epithelium, and smooth
451 muscle layers, and fail to assemble a closed uterine lumen upon embryo implantation, with
452 defective uterine decidualization that lead to pregnancy loss at early to mid-gestation
453 (Rodriguez et al., 2016). Mossa & Ireland (2019) suggested that dairy cows with a low antral
454 follicle count (follicles ≥ 3 mm in diameter) have lower blood concentrations of AMH and
455 their endometrium is thinner than those with high antral follicle counts. Therefore, further
456 studies must clarify whether AMH in bovine oviduct and uterus have important autocrine
457 and/or paracrine roles in uterine function.

458 Our results on the effects of breed and age on such measurements should be interpreted
459 with caution since we could not obtain specimens from Holsteins heifers. However, despite
460 no differences in the AMH expression levels were observed in the ampulla and isthmus
461 among Holsteins cows and the Japanese Black heifers and cows, the AMH concentration in
462 the oviduct fluids of Holsteins cows were lower than those in oviduct fluids from Japanese
463 Black heifers and cows. The comparable results between Japanese Black heifers and cows
464 were unexpected since Japanese Black cows were reported to have higher blood AMH levels
465 than post-pubertal heifers (Koizumi & Kadokawa, 2017). One possible explanation of our
466 results relates to the relevant AMH source. While the AMH in the oviduct fluids may be a
467 direct result of AMH secretion by the oviductal epithelial cells (and not from the blood
468 circulating levels), the blood AMH concentration is not greatly affected by AMH secreted
469 by the oviductal epithelia. However, Japanese Black cattle were fed for meat production, and
470 Holstein cows were infertile. Therefore, since these animals were raised under varied
471 conditions not only different breed and age, it is difficult to interpret the results. Hence,
472 further studies are needed to clarify age- or breed-related differences in the AMH
473 concentration in fluid samples.

474 Western blotting showed differences in band strength or size between the oviducts and
475 ovaries. The oviduct samples exhibited weaker bands for the mature C-terminal form of
476 AMH than those of the ovary samples, suggesting that the oviducts store less mature C-
477 terminal protein than the ovaries. The oviduct samples also exhibited weaker bands for the
478 AMH precursor than those of the ovary samples. One possible reason for this difference is
479 that the oviducts express lower levels of AMH precursor compared to the ovaries. Another

480 possible explanation is that the oviducts secrete the C-terminal form soon after maturation
481 without storing it subcellularly.

482 Western blotting showed differences in the number of full-length AMH bands among
483 the ovary, ampulla, isthmus, caruncle, and intercaruncle. Since, different organs show
484 different patterns of AMH O-glycosylation (Meczekalski et al. 2016; Skaar et al., 2011),
485 therefore, differential glycosylation may explain the differences observed in the full-length
486 form in our study.

487 Collectively, these results show that bovine oviducts and endometria express AMH
488 and likely secrete AMH into the oviduct and uterine fluids. AMH expression might be useful
489 to assess fertility status in bovines. Further studies must examine the roles of AMH in
490 oviducts and the uterus.

491 In conclusion, these results show that bovine oviducts and endometria express AMH
492 and likely secrete AMH into the oviduct and uterine fluids.

493

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500

501

502

503 **CONFLICT OF INTERES**

504 The authors declare that they have no competing interests.

505

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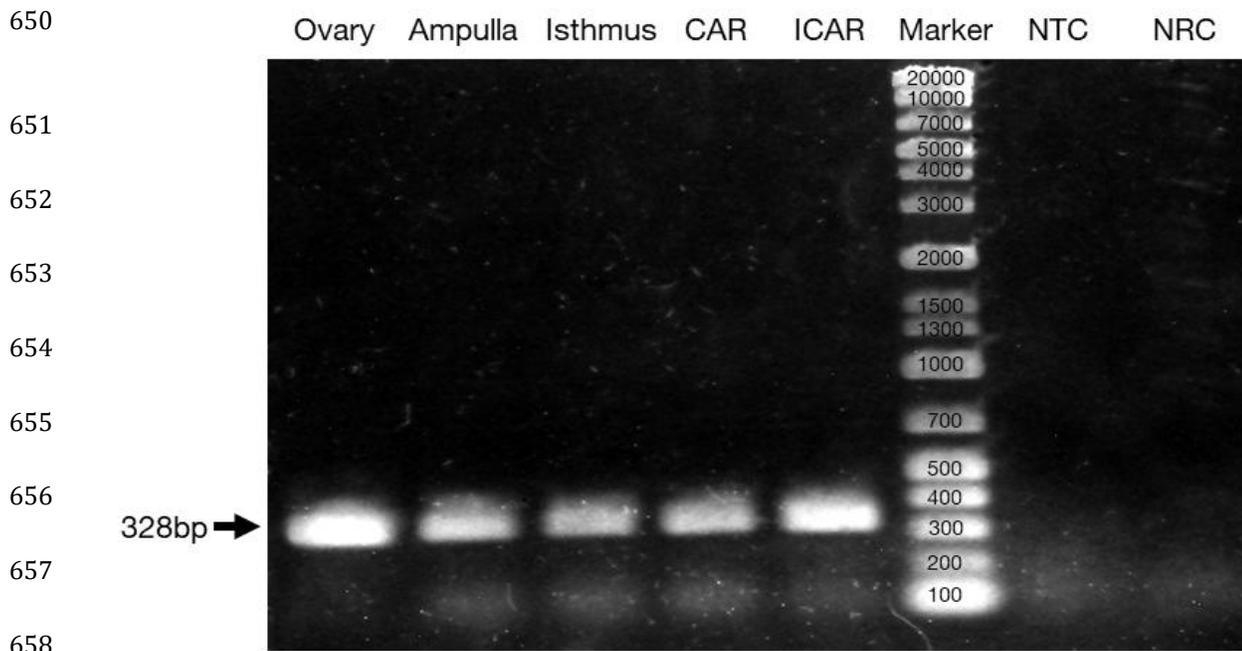
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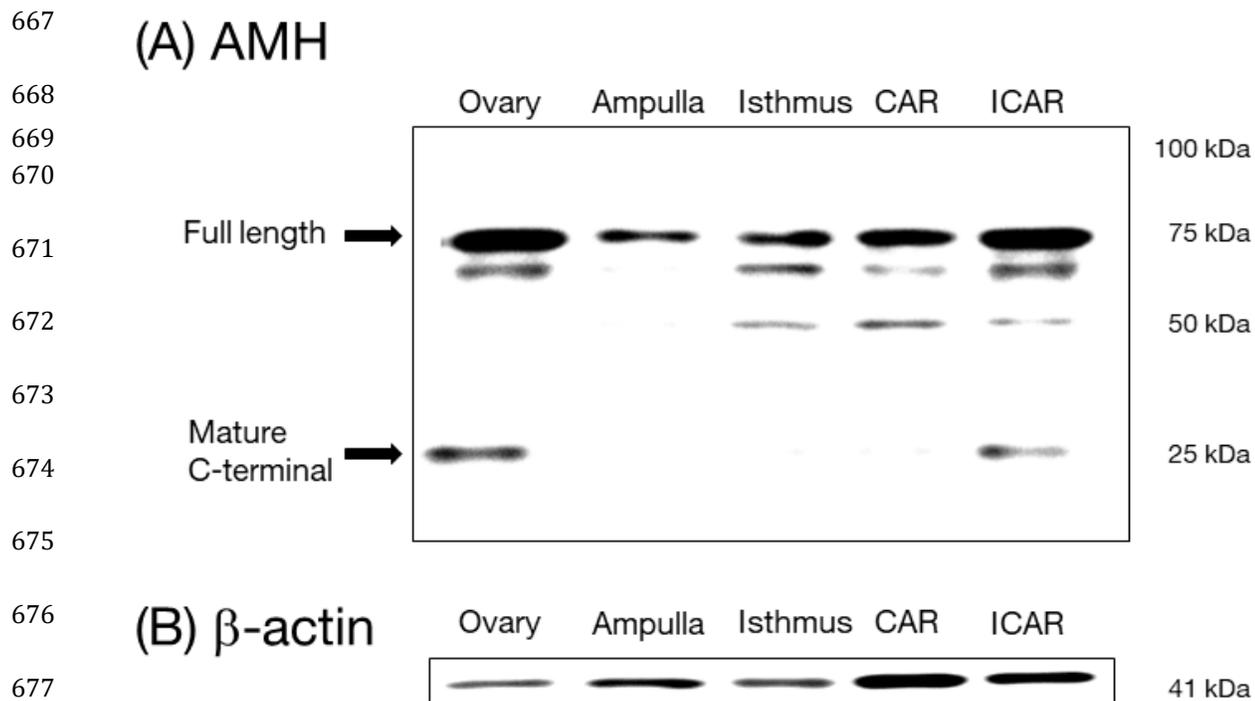
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649 **Figure legends**

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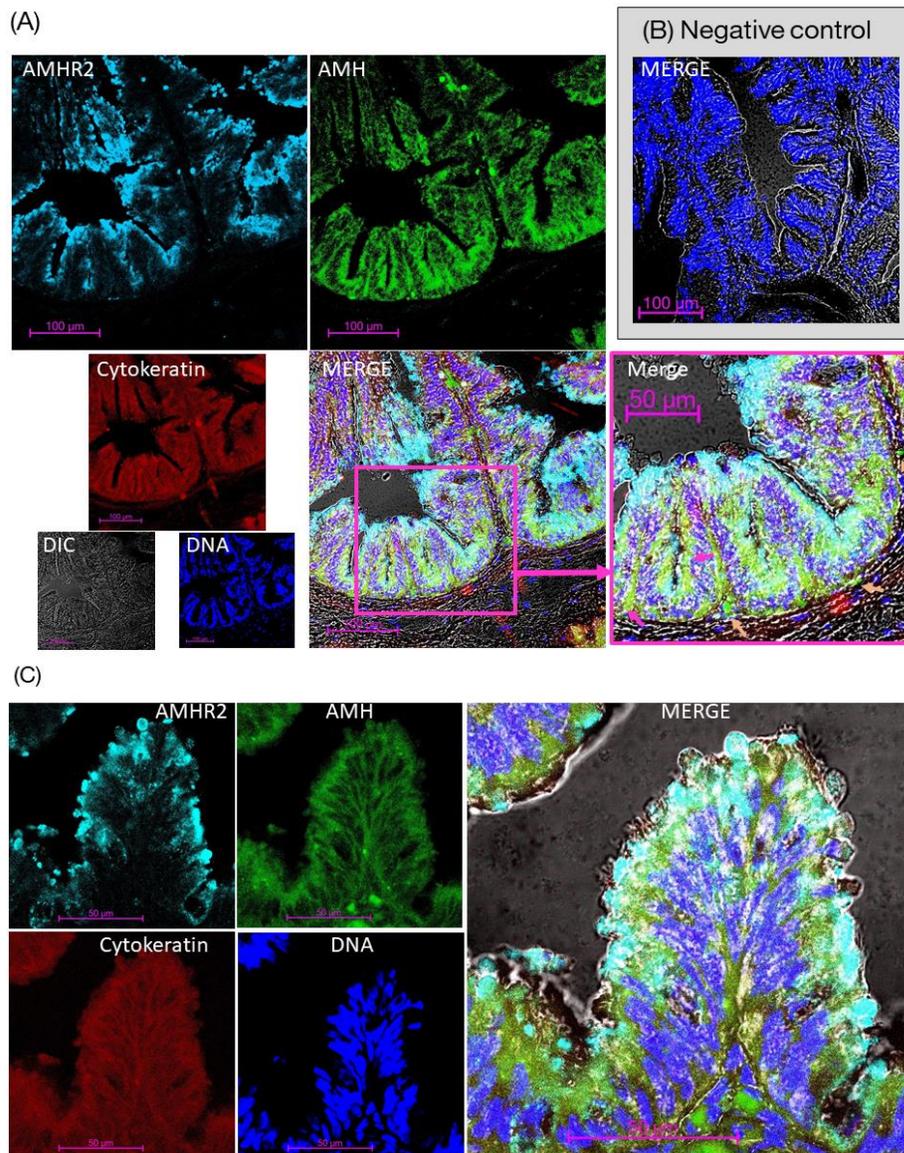
660

661 **Figure 1.** Expression of anti-Müllerian hormone (*AMH*) mRNA, detected by RT-PCR
 662 analysis. The electropherogram shows the expected size (328 bp) of PCR products of
 663 bovine *AMH* in the ovary, ampulla, isthmus, and caruncular (CAR) and intercaruncular
 664 (ICAR) areas of the endometrium in post-pubertal heifers; no amplicons were observed in
 665 the no template control (NTC) and no reverse transcription control (NRC) conditions.
 666



679 **Figure 2.** Western blotting using an anti-AMH rabbit antibody on protein extracts of ovaries,
 680 ampulla, isthmus, and caruncular (CAR) and intercaruncular (ICAR) areas collected from
 681 post-pubertal heifers (a); β -actin was used as a loading control (b).

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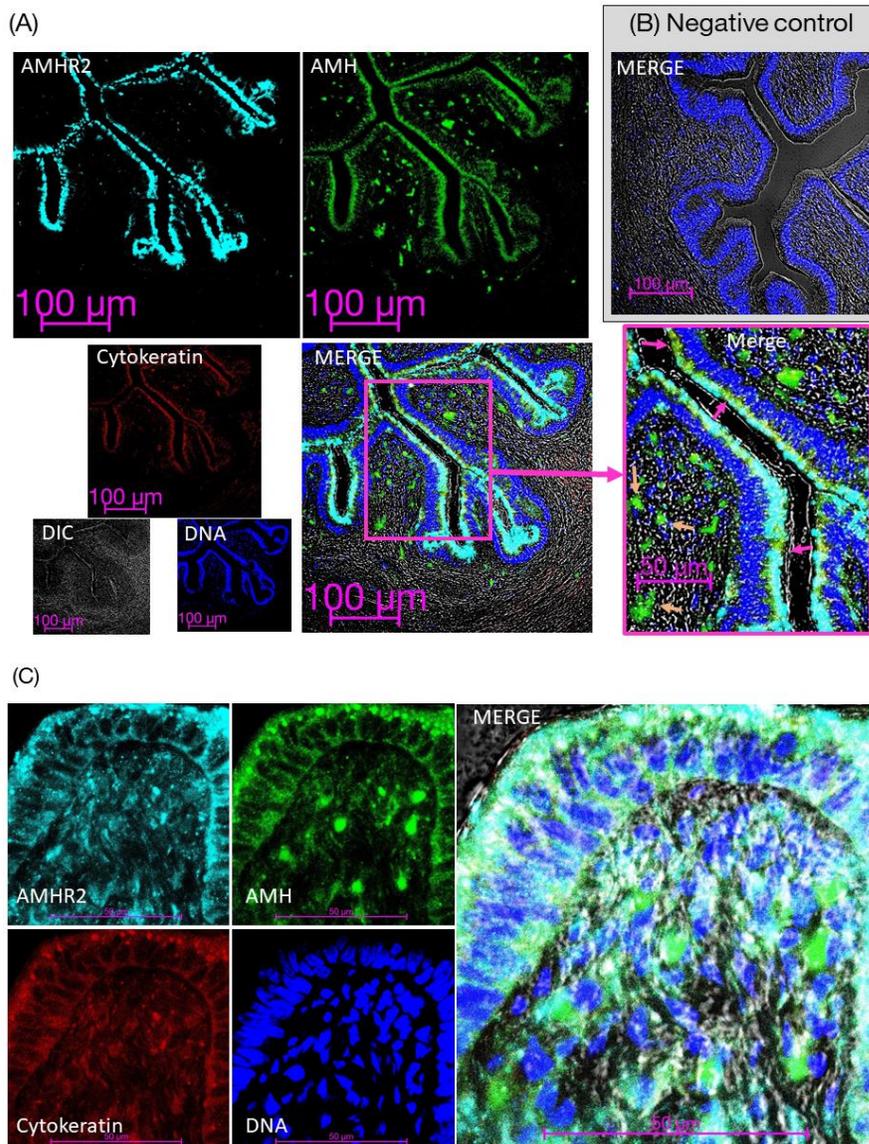
683

684 **Figure 3.** Immunofluorescence staining of AMH in the ampulla samples of post-pubertal
 685 heifers. Specimens were collected on day 3 (day 0 = day of estrus). Images were captured via
 686 laser-scanning confocal microscopy and show AMHR2 (light blue), AMH (green),
 687 cytokeratin (red), and counter-staining with DAPI nuclear stain (dark blue), and differential
 688 interference contrast (DIC) microscopy (grayscale). The pink rectangle within the low
 689 magnification image indicates the position of the high magnification. In the merged photos,

690 the pink arrows indicate the AMH signals in the luminal epithelium of mucosa. The brown
691 arrows indicate signals in fibroblasts. Right panel (B) show negative controls staining using
692 the normal animal IgGs. Scale bars represent 100 μm in the low magnification. Scale bars
693 represent 50 μm in the enlarged merge of (A) and (C), and 100 μm in other panels, which
694 shown as pink rectangular.

695

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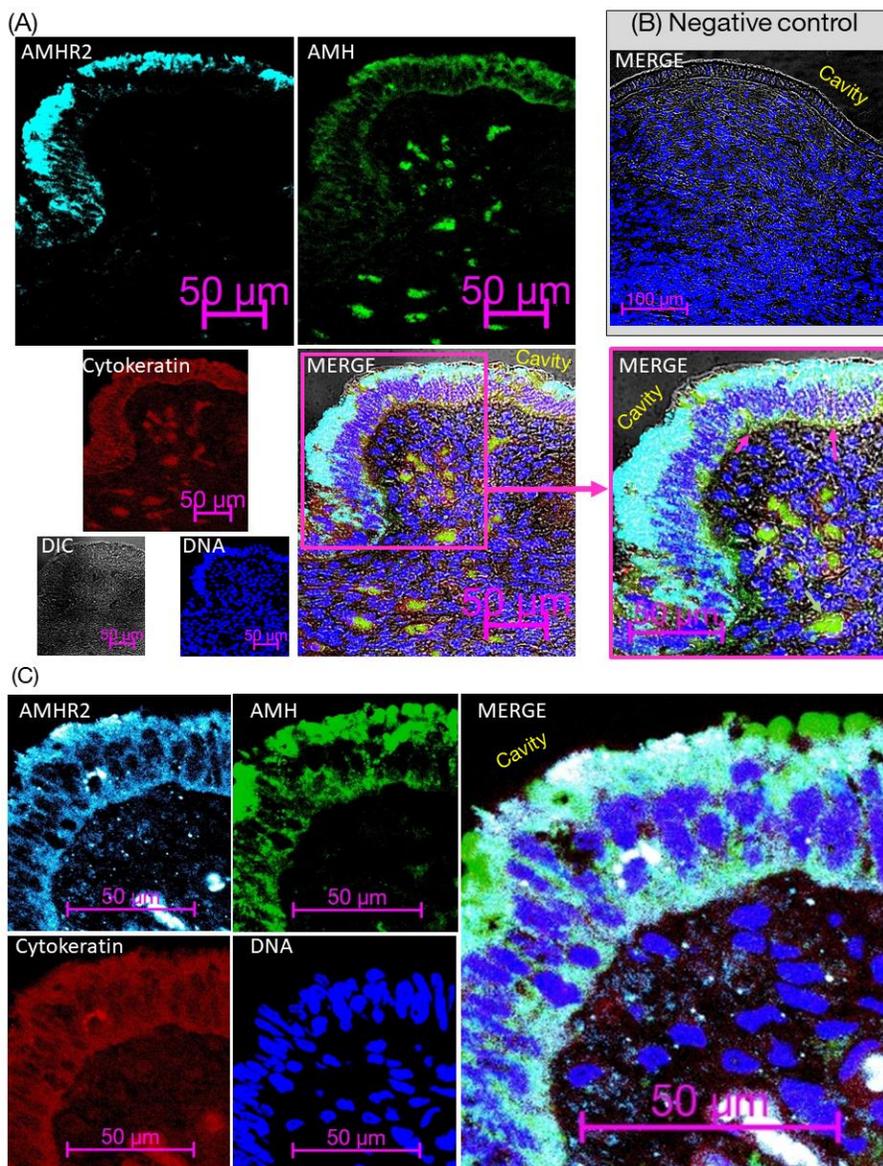


697

698 **Figure 4.** Immunofluorescence staining of AMH in the isthmus samples of post-pubertal
 699 heifers. Specimens were collected on day 5 (day 0 = day of estrus). Images were captured via
 700 laser-scanning confocal microscopy and show AMHR2 (light blue), AMH (green),
 701 cytokeratin (red), and counter-staining with DAPI nuclear stain (dark blue), and differential
 702 interference contrast (DIC) microscopy (grayscale). The pink rectangle within the low

703 magnification image indicates the position of the high magnification. In the merged photos,
704 the pink arrows indicate the AMH signals in the luminal epithelium of mucosa. The brown
705 arrows indicate signals in fibroblasts. Right panel (B) show negative controls staining using
706 the normal animal IgGs. Scale bars represent 100 μm in the low magnification. Scale bars
707 represent 50 μm in the enlarged merge of (A) and (C), and 100 μm in other panels.

708



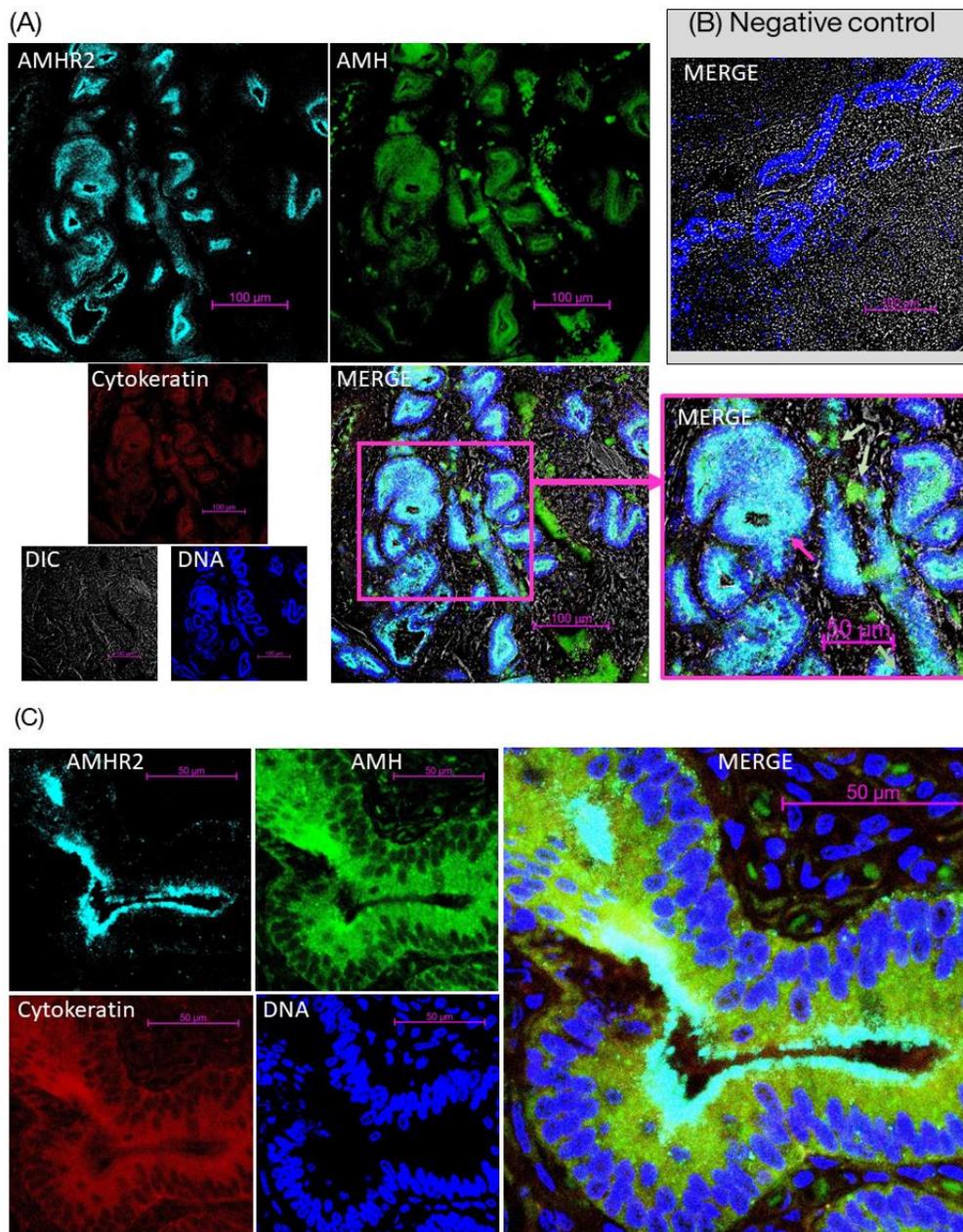
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710

711 **Figure 5.** Immunofluorescence staining of AMH in the caruncle samples of post-pubertal
 712 heifers. Specimens were collected on day 13. Images were captured via laser-scanning
 713 confocal microscopy and show AMHR2 (light blue), AMH (green), cytokeratin (red), and
 714 counter-staining with DAPI nuclear stain (dark blue), and DIC microscopy (grayscale). In
 715 the merge photos of (A), cavity indicates the uterine cavity. The pink arrows indicate the

716 AMH signals in the luminal epithelium of caruncle. The green arrows indicate AMH signals
717 in the vasculature. Right panel (B) show negative controls staining using the normal animal
718 IgGs1. Scale bars represent 100 μm in (B), and 50 μm in other panels.
719

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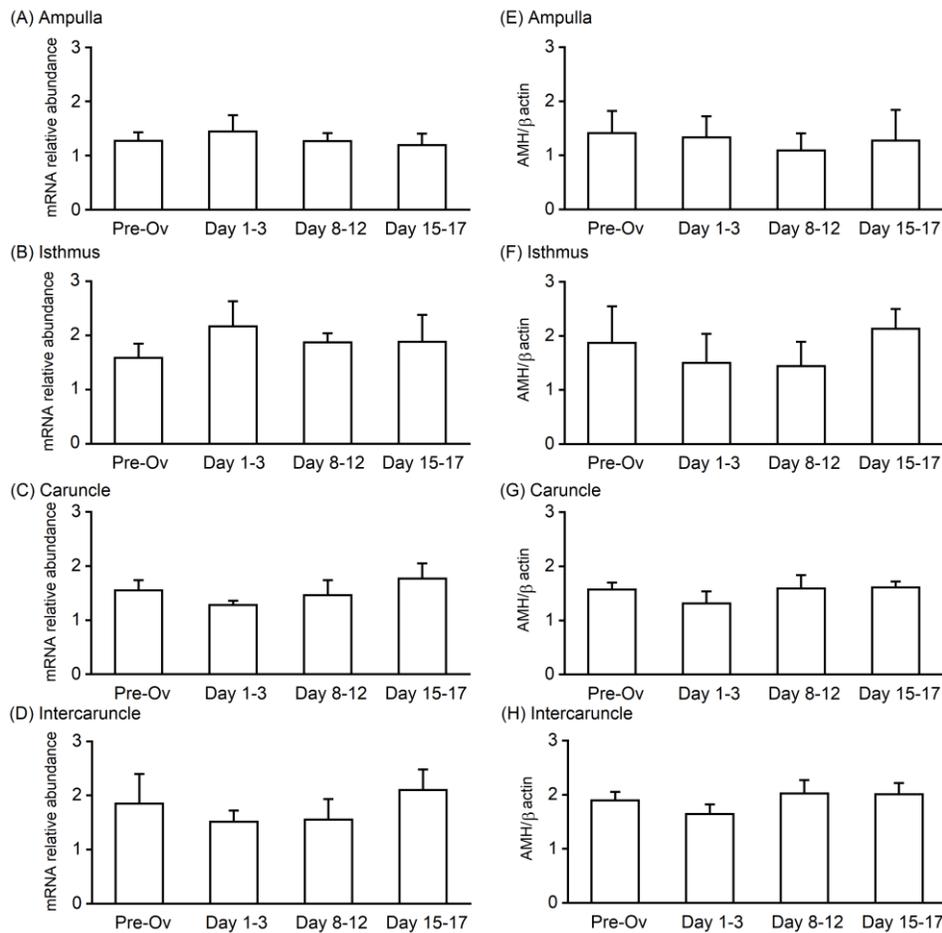


721

722 **Figure 6.** Immunofluorescence staining of AMH in the intercaruncle samples of post-
 723 pubertal heifers. Specimens were collected on day 13. Images were captured via laser-
 724 scanning confocal microscopy and show AMHR2 (light blue), AMH (green), cytokeratin

725 (red), and counter-staining with DAPI nuclear stain (dark blue), and DIC microscopy
726 (grayscale). The pink arrows indicate the AMH signals in the epithelium of endometrial
727 glands in intercaruncle. The green arrows indicate AMH signals in the vasculature. Right
728 panel (B) show negative controls staining using the normal animal IgGs. Scale bars represent
729 50 μm in the enlarged merge of (A) and (C), and 100 μm in other panels.

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732

733 **Figure 7.** No significant differences in the relative expression levels of *AMH* mRNA

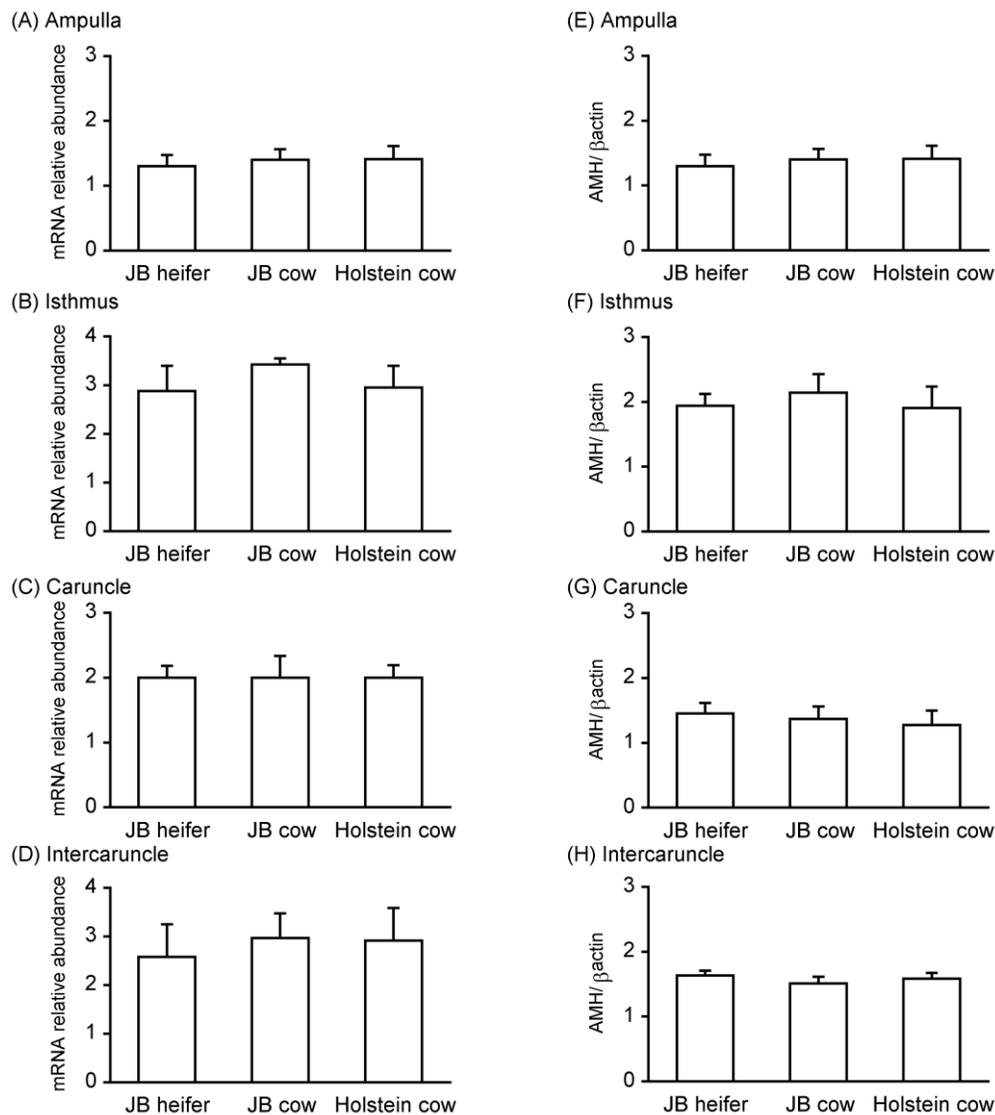
734 (determined by the quantitative RT-PCR) or protein (determined by western blotting) (all

735 data are shown as the mean \pm SEM) in the ampulla (A, E), isthmus (B, F), caruncle (C, G),

736 or intercaruncle (D, H) samples of post-pubertal heifers during pre-ovulatory phase (Pre-Ov;

737 day 19 to 21), day 1 to 3, day 8 to 12, or day 15 to 17. Relative *AMH* mRNA levels were738 determined by quantitative RT-PCR and normalized to the geometric means of *C2orf29* and739 *SUZ12* levels. Relative AMH protein expression levels were determined by western blotting740 and normalized to those of β -actin.

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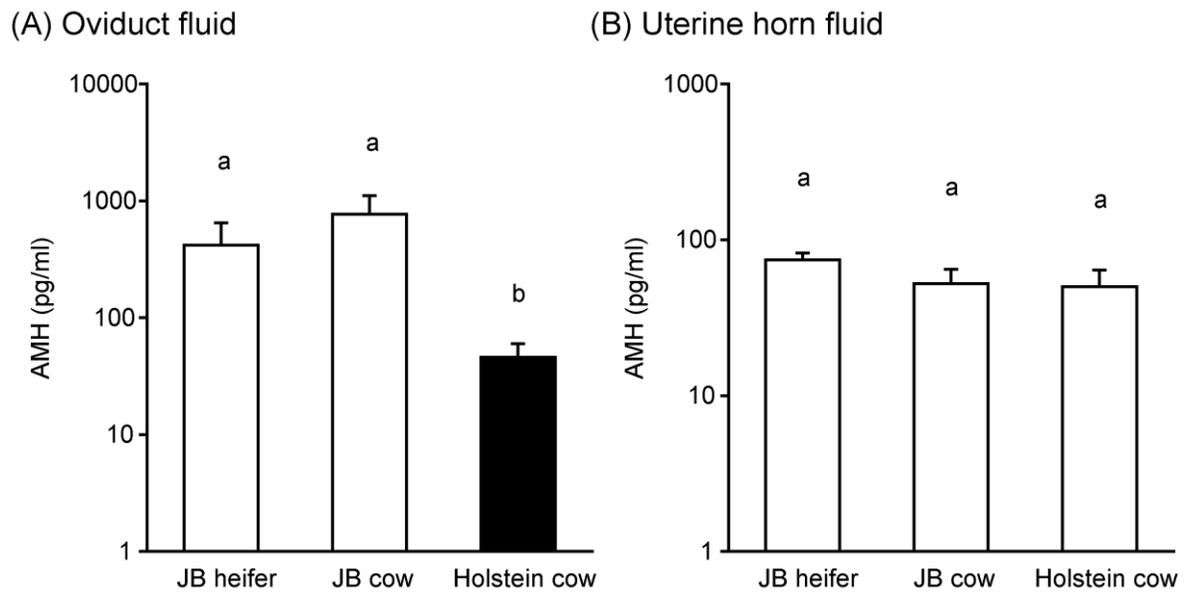
743

744 **Figure 8.** No significant differences in the relative expression levels (shown as the mean ±745 SEM) of *AMH* mRNA (determined by the quantitative RT-PCR) or protein (determined by

746 western blotting) in the ampulla (A, E), isthmus (B, F), caruncle (C, G), or intercaruncle (D,

747 H) samples among post-pubertal Japanese Black (JB) heifers, JB cows, and Holsteins cows.

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750

751 **Figure 9.** AMH concentrations, as measured by enzyme immunoassays in the oviduct fluid
 752 on day 1 to 3 (a) or uterine fluid on day 8 to 14 (b), collected from post-pubertal JB heifers,
 753 JB cows, and Holsteins cows. Different letters indicate significant differences ($P < 0.05$)
 754 among groups.

755

756 Table 1. Details of the primers used for quantitative RT-PCRs

757

Gene name		Primer sequence 5'-3'	Position		Size (bp)
			Nucleotide	Exon	
<i>AMH</i>	forward	GGGTTAGCCCTTACCCTGC	683–701	3	121
	reverse	GTAACAGGGCTGGGGTCTTT	784–803	4	
<i>C2orf29</i>	forward	TCAGTGGACCAAAGCCACCTA	928–948	3	170
	reverse	CTCCACACCGGTGCTGTTCT	1077–1097	4	
<i>SUZ12</i>	forward	CATCCAAAAGGTGCTAGGATAGA	1441–1465	13	160
	reverse	TTGGCCTGCACACAAGAATG	1581–1600	14	

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