

**ADIÇÃO DE PROTEÍNA PLASMÁTICA A ASSOCIADA À PRENHEZ (PAPP-A)
DURANTE A MATURAÇÃO *IN VITRO* AUMENTA O IGF-1 BIODISPONÍVEL E
MODULA O PERFIL TRANSCRICIONAL DE COMPLEXOS CUMULUS-
OÓCITOS E EMBRIÕES BOVINOS**

ALAN BRUNHOLI GIROTO

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Dissertação apresentada a Pró-Reitoria de Pesquisa e Pós-Graduação, Universidade do Oeste Paulista, como parte dos requisitos para obtenção do título de Mestre em Ciência Animal - Área de Concentração: Fisiopatologia Animal.

Orientador: Prof. Dr. Anthony César de Souza Castilho

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Presidente Prudente, 25 de maio de 2018.

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DEDICATÓRIA

Primeiramente, dedico este trabalho à Deus, pois esta conquista foi apenas uma das vontades Dele.

Aos meus avôs Horácio Giroto e Antônio Brunholi.

Aos meus pais Terezinha e José, e ao meu irmão Alisson

Aos meus padrinhos Vera e Luis, exemplos de pessoas que sempre me apoiaram.

Dedico, também, a todos os meus amigos, aqueles que sempre estiveram ao meu lado.

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É muito melhor lançar-se em busca de conquistas grandiosas, mesmo expondo-se ao fracasso, do que alinhar-se com os pobres de espírito, que nem gozam muito nem sofrem muito, porque vivem numa penumbra cinzenta, onde não conhecem nem vitória, nem derrota.” (Theodore Roosevelt)

RESUMO

Adição de proteína plasmática A associada à prenhez (PAPP-A) durante a maturação *in vitro* aumenta o IGF-1 biodisponível e modula o perfil transcricional de complexos cumulus-oócitos e embriões bovinos

A proteína sérica associada à prenhez (PAPP-A) é capaz de modular a biodisponibilidade do IGF-1 (fator de crescimento semelhante à insulina tipo 1) pela quebra das ligação com as proteínas de ligação do IGF (IGFBPs). O objetivo foi avaliar como a adição da PAPP-A durante a maturação *in vitro* (MIV) afetou a biodisponibilidade de IGF-1, a abundância de transcritos nos oócitos e células do cumulus e blastocistos, a produção embrionária e a sobrevivência pós aquecimento. Foi realizada a MIV de 24 h em complexos cumulus oócitos (CCOs – 20/grupo) oriundos de abatedouro, em meio TCM199 livre de soro, com adição de PAPP-A (100 ng/mL; grupo PAPP-A) ou sem (controle). O IGF-1 foi quantificado no meio de maturação e os CCOs maturados foram utilizados na fertilização e cultivo *in vitro*. Oócitos e células do cúmulus foram separados; e blastocistos foram congelados para a realização da expressão gênica. Taxa de clivagem e produção de blastocistos foram calculados como porcentagem e transformados para arco seno. Dados de expressão gênica foram normalizados com a média do grupo de controle. Os resultados foram analisados por test t, porém a criopreservação embrionária foi testada por Qui-quadrado (JMP software, SAS). Diferenças foram consideradas significativas quando $p \leq 0,05$. O grupo PAPP-A apresentou 27% mais concentração de IGF-1 biodisponível. Na produção *in vitro* de embriões, não encontrou-se diferença na taxa de clivagem, produção e sobrevivência embrionária. Apenas o gene *TXNRD1* mostrou maior expressão nos oócitos do grupo PAPP-A. No entanto, nas células do cumulus PAPP-A, o *VNN1* e *HDAC2* apresentaram maior expressão, enquanto os genes *AGPAT1*, *AGPAT9*, *FASN*, *CASP3*, *EGFR*, *HAS2*, *IMPDH1* e *MTIF3* apresentaram menor expressão. Nos blastocistos PAPP-A, os genes *CPT2*, *CASP9*, *DNMT3A*, *TFAM* e *KRT8* apresentaram maior expressão, enquanto os genes *ATF4*, *CASP3* e *IFITM3* apresentaram menor expressão. Em conclusão, a adição de PAPP-A durante a MIV aumentou o IGF-1 biodisponível, mas não influenciou a produção e a sobrevivência embrionária após desvitrificação. No entanto, o aumento do IGF-1 biodisponível pode melhorar a competência embrionária através da modulação da expressão gênica em oócitos, células do cúmulus e blastocistos.

Palavras-chave: proteína de ligação do fator de crescimento semelhante à insulina, complexos cumulus-oócito, produção *in vitro* de embriões, criopreservação, bovinos.

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O presente manuscrito está redigido e submetido segundo as normas da revista *Molecular, Reproduction and Development*, exceto as imagens e tabelas dispostas ao longo do texto.

1 **Addition of pregnancy-associated plasma protein-A (PAPP-A) during *in vitro***
2 **maturation increases bioavailable IGF-1 and modulates transcriptional profile of bovine**
3 **cumulus-oocyte complexes and blastocysts**

4
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6 Santos², Eduardo Montanari Razza², Marcelo Fábio Gouveia Nogueira³, Marcos Antonio
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20
21 **ABSTRACT**

22 In this study we aimed to evaluate how PAPP-A addition during *in vitro* maturation affected
23 the IGF-1 quantification, transcript abundance related to cumulus oocyte complexes (COCs)
24 and blastocysts quality, embryonic yield, as well as post-warming survival. We matured
25 COCs through a 24 h treatment of TCM199 serum-free medium, either with PAPP-A

26 supplementation (100 ng/mL; PAPP-A group) or without (control). Maturation medium was
27 collected for IGF-1 quantification, and matured COCs were used for *in vitro* fertilization and
28 culturing. The PAPP-A group exhibited 1.27 times higher IGF-1 concentrations than control.
29 A comparison of *in vitro* embryo production across the groups found no difference in
30 cleavage rate, embryonic yield, and survival, 3 and 24 h post-cryopreservation. In PAPP-A
31 oocytes, only *TXNRD1* was up-regulated. However, in PAPP-A cumulus cells, *VNN1* and
32 *HDAC2* were up-regulated, while *AGPAT1*, *AGPAT9*, *FASN*, *CASP3*, *EGFR*, *HAS2*,
33 *IMPDH1*, and *MTIF3* were down-regulated. Finally, in PAPP-A blastocysts, *CPT2*, *CASP9*,
34 *DNMT3A*, *TFAM*, and *KRT8* were up-regulated, while *ATF4*, *CASP3*, and *IFITM3* were
35 down-regulated. We concluded that PAPP-A addition increased IGF-1 but did not influence
36 embryonic yield and survival. Nevertheless, elevated IGF-1 could improve embryo
37 competence through modulating expression of genes involved with lipid metabolism, oocyte
38 competence and apoptosis in COCs and blastocysts.

39 **Keywords:** insulin-like growth factor-binding protein, cumulus-oocyte complexes, *in vitro*
40 embryo production, cryopreservation, cattle.

41

42 1 INTRODUCTION

43 Insulin-like growth factor-1 (IGF-1) is one of several growth factors involved in
44 oocyte maturation, specifically in influencing gonadotrophin action during folliculogenesis
45 and meiosis progression (Mazerbourg & Monget, 2018; Sakaguchi et al., 2002). The IGF
46 system is composed of IGF-1 and IGF-2, along with their receptors IGF-1R and IGF-2R
47 (Kane, Morgan, & Coonan, 1997; Mazerbourg & Monget, 2018). In the bovine reproductive
48 system, IGF-1 functions have been confirmed by IGF-1R presence in the oocyte (Armstrong
49 et al., 2000; Satrapa, Castilho, et al., 2013; Satrapa, Razza, et al., 2013) and throughout stages
50 of early embryonic development, including the zygote, 2–4 cell embryo, 8–16 cell embryo,

51 morula, and blastocyst (Yaseen, Wrenzycki, Herrmann, Carnwath, & Niemann, 2001). This
52 system stimulates cell proliferation, differentiation, migration, survival, and metabolism
53 (Duan et al., 2005). In the reproductive system, these processes are important to oocyte
54 maturation (Sakaguchi et al., 2002; Sirotkin, Dukesová, Makarevich, Kubek, & Bulla, 2000;
55 Xia, Tekpetey, & Armstrong, 1994) and embryonic development (Velazquez, Zaraza,
56 Oropeza, Webb, & Niemann, 2009).

57 IGF binding proteins (IGFBPs) and pregnancy-associated plasma protein-A (PAPP-A)
58 both modulate IGF action during embryonic development. The former group modulates the
59 IGF action during cumulus-oocyte complexes (COCs) maturation and in subsequent growth
60 stages (Harvey, Kind, & Thompson, 2007; Heyner, Shi, Garside, & Smith, 1993; Kaye &
61 Harvey, 1995; Luciano, Modina, Gandolfi, Lauria, & Armstrong, 2000). Six IGFBP types (1–
62 6) (Mazerbourg & Monget, 2018) have been reported in oocytes and bovine embryos
63 (Lonergan, Rizos, Gutierrez-Adan, Fair, & Boland, 2003; Satrapa, Castilho, et al., 2013;
64 Satrapa, Razza, et al., 2013; Sawai et al., 2005).

65 The PAPP-A is a protein produced by the placenta (Petry et al., 2017) and isolated in
66 1974 from normal human pregnancy serum (Lin, Galbert, Kiefer, Spellacy, & Gall, 1974;
67 Petry et al., 2017). In women *PAPPA* knockout, incomplete fetal development and
68 deformities were observed (Lawrence et al., 1999), and in rodents, the *PAPPA* knockout
69 mouse subjected to ovarian stimulation ovulated fewer COCs (Nyegaard et al., 2010).

70 In cattle, PAPP-A has been found to increase IGF-1 through degrading IGFBPs,
71 including IGFBP2, 4, and 5 in cattle (Mazerbourg, Bondy, Zhou, & Monget, 2003; Rivera &
72 Fortune, 2003). A cross-breed comparison found higher *PAPPA* mRNA expression, but
73 decreased *IGF1*, *IGF1R*, *IGFBP2*, and *IGFBP4* expression in Nelore cows than in Holstein
74 cows (Satrapa, Castilho, et al., 2013). Corroborating with these previous findings, the

75 abundance of *PAPPA* mRNA was greater in oocytes and cumulus cells of Gir and Holstein ×
76 Gir hybrids than in Holstein cows (Lopes et al., 2017).

77 However, most studies only investigated the effects of direct exogenous IGF-1
78 addition during *in vitro* maturation (IVM) of bovine oocytes (Meiyu, Liu, & Roth, 2015;
79 Sakaguchi et al., 2002; Zhandi, Towhidi, Nasr-Esfahani, Eftekhari-Yazdi, & Zare-Shahneh,
80 2009). We therefore know very little regarding how PAPP-A modulates IGF-1 during IVM
81 and how this modulation affects *in vitro* embryo production in cattle and COCs or blastocyst
82 quality.

83 Here, we hypothesized that exogenous PAPP-A addition would release IGF-1 from
84 IGFBPs, thus increasing IGF-1 in the IVM medium. Therefore, our aim was to investigate
85 PAPP-A action on IGF-1, along with any subsequent impact on embryo production and
86 blastocyst viability post-cryopreservation. We were also interested in how PAPP-A influences
87 bovine COC and blastocyst transcriptional profiles.

88

89 **2 RESULTS**

90 **2.1 IGF-1 quantification in IVM medium and accompanying effects on *in vitro*** 91 **production and survival post warming**

92 After IVM, PAPP-A addition increased IGF-1 in IVM medium by 1.27-fold compared
93 with control ($p = 0.030$; Table 1). However, cleavage and blastocyst rates did not differ
94 between groups ($p = 0.694$ and $p = 0.539$, respectively; Table 1). After *in vitro* culture (IVC),
95 expanded blastocysts were vitrified and then warmed. Re-expansion rate after 3 and 24 h did
96 not differ between groups ($p > 0.05$; Table 1).

97

98

99 **Table 1.** IGF-1 quantification, blastocyst yield, and embryonic survival. In the IVM, IGF-1
 100 data are represented as fold change. To IVP, cleavage and blastocyst rates are represented as
 101 mean (%) \pm S.E.M and n = replicate; and blastocyst re-expansion is shown as percentages
 102 evaluated by chi-square test.

Groups	IVM	IVP		Blastocyst Re-expansion	
	IGF-1 [†]	Cleavage	Blastocysts	3 hours	24 hours
Control (n = 360 COCs)	1 \pm 0.0	83.7 \pm 1.66	38 \pm 1.79	56 (28/50)	54 (27/50)
PAPP-A (n = 360 COCs)	1.27 \pm 0.09*	84.6 \pm 1.61	38.2 \pm 2.71	56 (37/66)	43.9 (29/66)

103 * $p \leq 0.05$ in the same column

104 † insulin-like growth factor 1

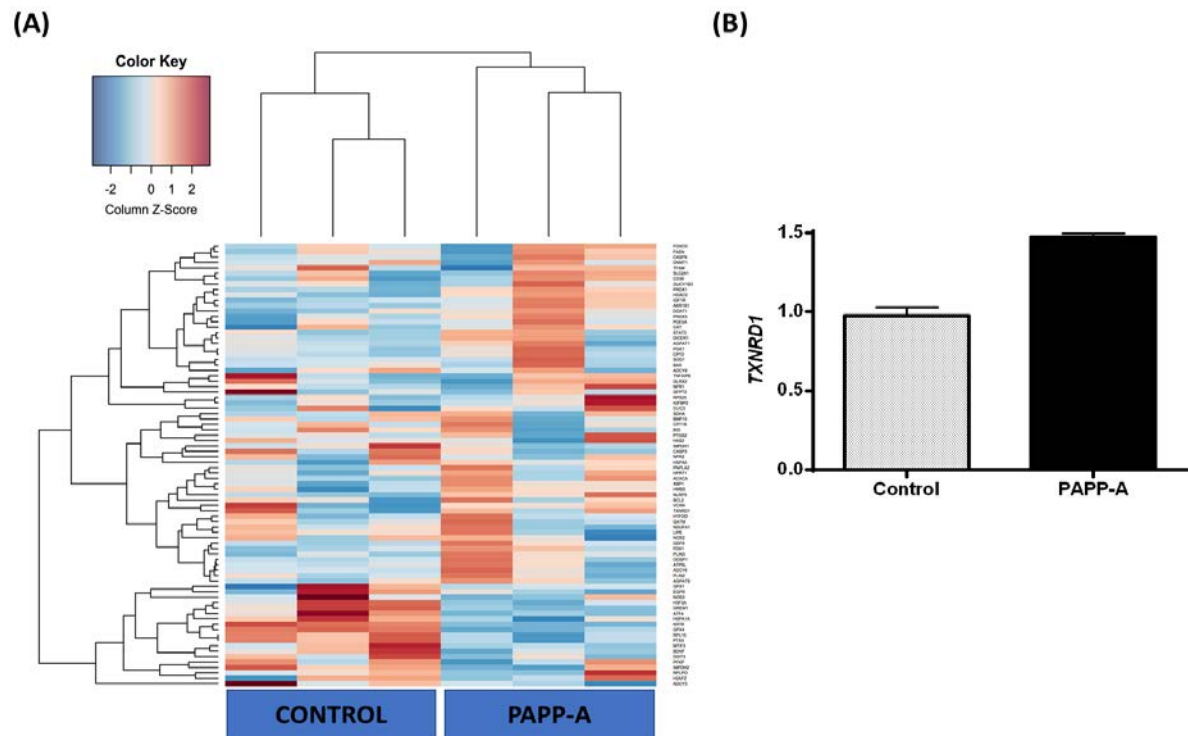
105 IVM, *in vitro* maturation; IVP, *in vitro*-embryo production; COCs, cumulus-oocyte complexes

106

107 2.2 Transcript profile in oocytes, cumulus cells, and blastocysts

108 We compared gene expression patterns between experimental and control groups
 109 using heat maps. In oocyte samples, only *TXNRD1* expression (based on mRNA abundance)
 110 differed significantly between treatments, being higher for PAPP-A-treated cells ($p \leq 0.05$;
 111 Figure 1).

112

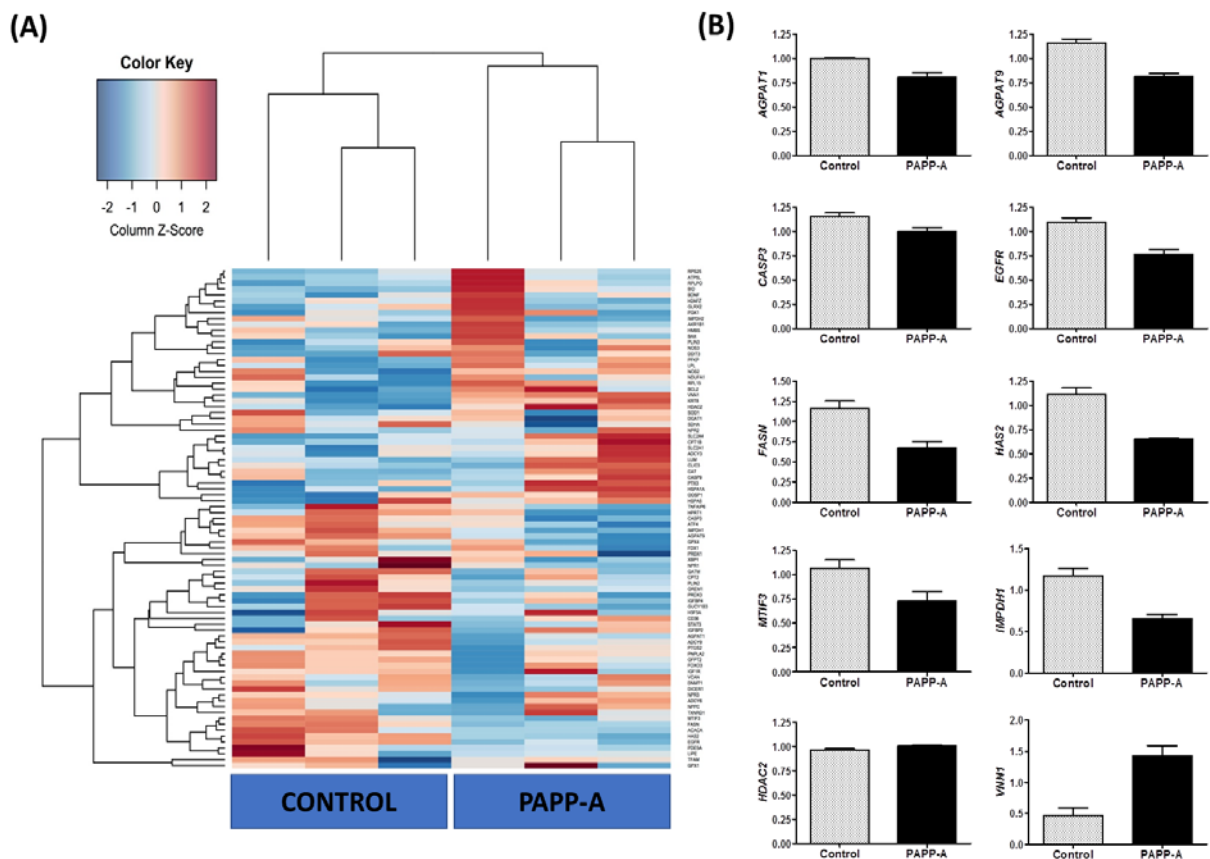


113

114 **Figure 1.** (A) Heat map showing gene expression differences between control and PAPP-A data in oocytes.
 115 Rows and columns are clustered by Euclidean distance and Ward-linkage hierarchical clustering. Color intensity
 116 represents the degree of between-group differences (based on Spearman's correlations). (B) Relative abundance
 117 of differentially expressed genes in oocytes ($p \leq 0.05$). Target genes were normalized with reference genes
 118 (*GAPDH*, *PPIA*, and *ACTB*), using the $2^{-\Delta Ct}$ method. Data are means \pm S.E.M. of three biological replicates
 119 tested by t test.

120

121 In cumulus cells, *VNN1* and *HDAC2* expression were higher in the PAPP-A group,
 122 whereas *AGPAT1*, *AGPAT9*, *EGFR*, *IMPDH1*, *FASN*, *HAS2*, *CASP3*, and *MTIF3* expression
 123 were lower ($p \leq 0.05$; Figure 2).



124

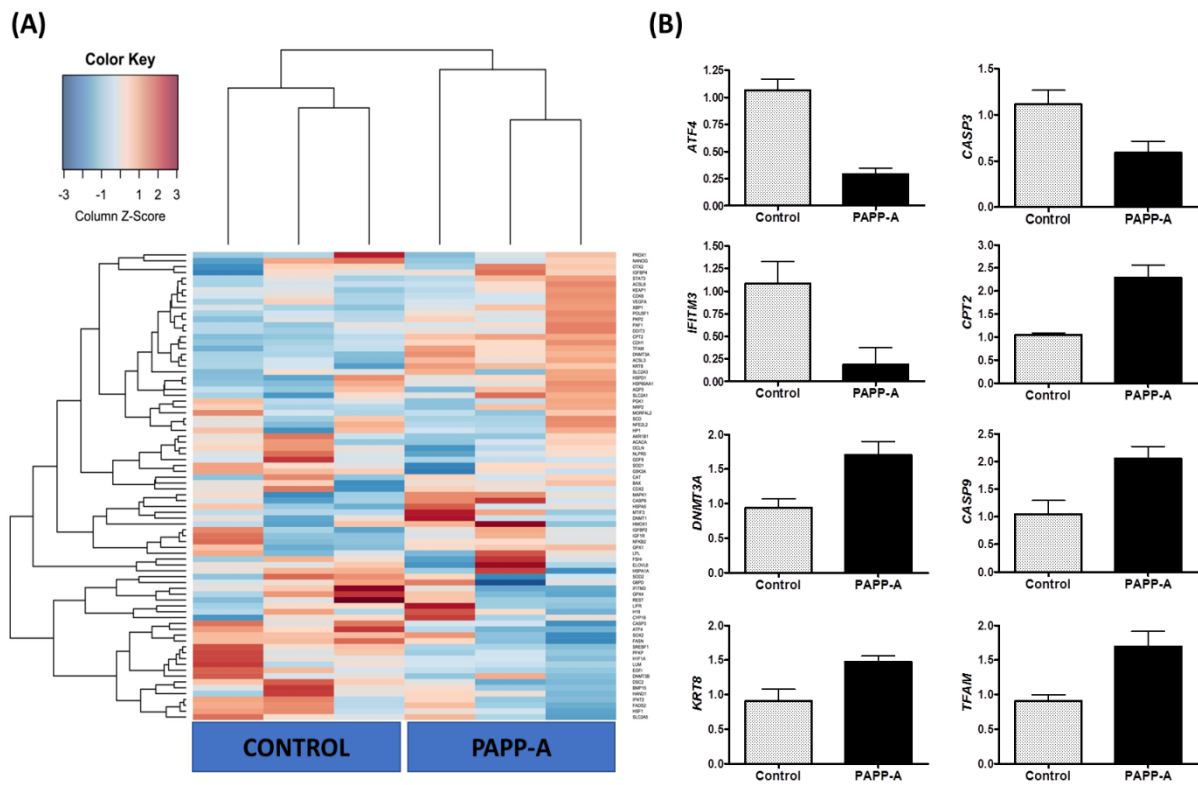
125 **Figure 2.** (A) Heat map showing gene expression differences between control and PAPP-A data in cumulus
 126 cells. Rows and columns are clustered by Euclidean distance and Ward-linkage hierarchical clustering. Color
 127 intensity represents the degree of between-group differences (based on Spearman's correlations). (B) Relative
 128 abundance of differentially expressed genes in cumulus cells ($p \leq 0.05$). Target genes were normalized with
 129 reference genes (*GAPDH*, *PPIA*, and *ACTB*), using the $2^{-\Delta C_t}$ method. Data are means \pm S.E.M. of three
 130 biological replicates tested by t test.

131

132 In blastocysts, the PAPP-A group showed higher *DNMT3A*, *CASP9*, *CPT2*, *TFAM*,
 133 and *KRT8* expression, but lower *ATF4*, *IFITM3*, and *CASP3* expression ($p \leq 0.05$; Figure 3).

134 To summary all data, a biological model was performed (Figure 4).

135



136

137 **Figure 3.** (A) Heat map showing gene expression differences between control and PAPP-A data in blastocysts.

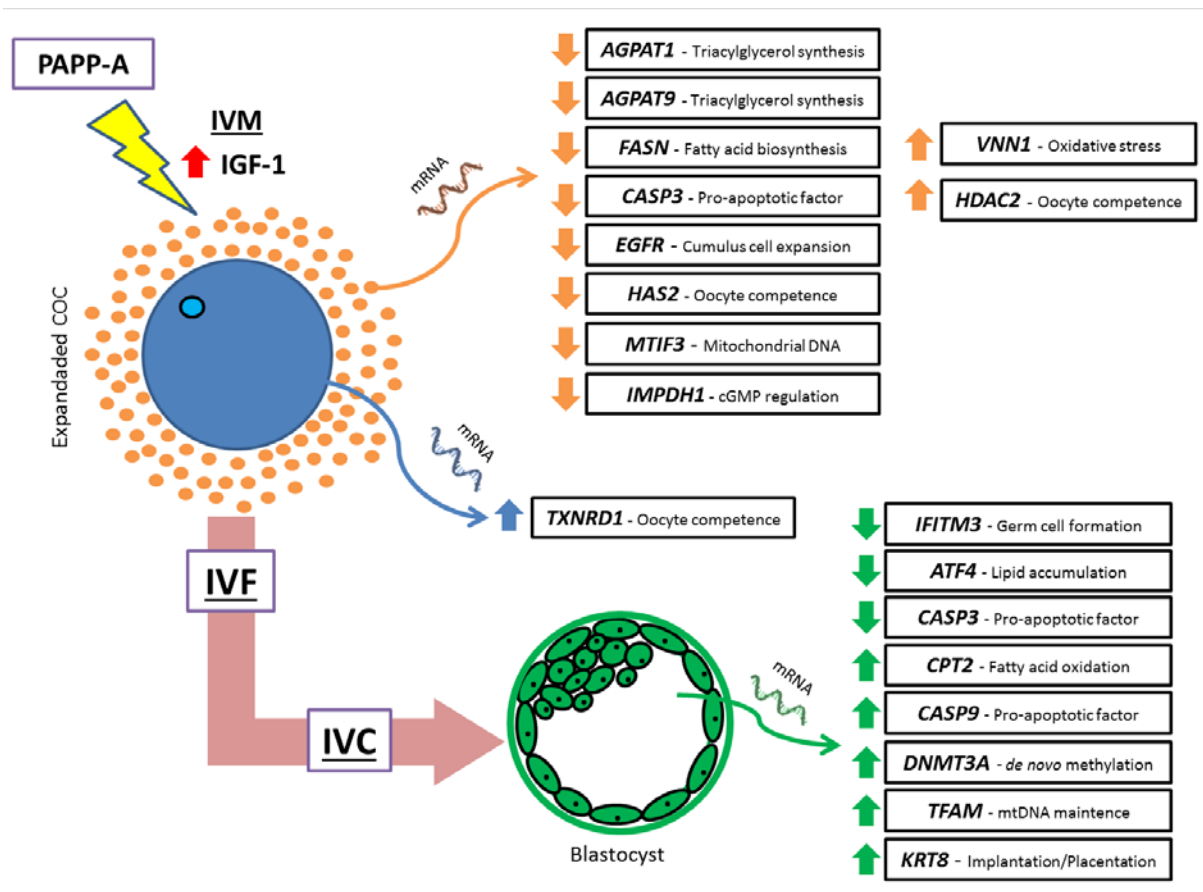
138 Rows and columns are clustered by Euclidean distance and Ward-linkage hierarchical clustering. Color intensity

139 represents the degree of between-group differences (based on Spearman's correlations). (B) Relative abundance

140 of differentially expressed genes in blastocysts ($p \leq 0.05$). Target genes were normalized with reference genes141 (*GAPDH*, *PPIA*, *ACTB* and *SDHA*), using the $2^{-\Delta C_t}$ method. Data are means \pm S.E.M. of three biological

142 replicates tested by t test.

143



144

145 **Figure 4.** Effects of PAPP-A addition during *in vitro* bovine embryo production. In summary, we propose that
 146 the greater amount of IGF-1 into maturation medium by the PAPP-A action was able to promote a down-
 147 regulation in cumulus cells and an up-regulation in blastocysts of transcripts related to the quality of COCs and
 148 blastocysts, particularly, cellular pathways involved in lipid metabolism, apoptosis, and embryonic development.
 149 The yellow ray indicates the PAPP-A action on IVM of bovine COC. The orange, blue and green arrows
 150 indicates mRNA abundance levels in PAPP-A group (cumulus cells, oocytes and blastocysts; respectively). The
 151 red arrow indicates the IGF-1 into the IVM medium. PAPP-A: pregnancy-associated plasma protein-A, IGF-1:
 152 insulin-like growth factor 1, COC: cumulus-oocyte complex, IVM: *in vitro* maturation, IVF: *in vitro* fertilization
 153 and IVC: *in vitro* culture. The genes are represented in the bold boxes.

154

155 For a list of target genes that were not differentially expressed ($p > 0.05$) in tested
 156 cells, please see supplementary information (Table S1, S2, and S3).

157

158

159 3 DISCUSSION

160 To our knowledge, this study is the first to quantify IGF-1 after PAPP-A addition
161 during IVM and examine the resultant effects on *in vitro* embryo production. Previous studies
162 examining how exogenous IGF-1 addition influences cleavage rates and embryonic
163 production have yielded inconsistent results. For instance, cleavage rates have been reported
164 to increase (Palma, Müller, & Brem, 1997) or remain unaffected (Block, Wrenzycki,
165 Niemann, Herrmann, & Hansen, 2008; Green & Day, 2013; Matsui, Takahashi, Hishinuma, &
166 Kanagawa, 1995). Similarly, IGF-1 addition has both increased blastocyst rate (Green & Day,
167 2013; Matsui et al., 1995; Palma et al., 1997) and exerted no effect (Block et al., 2008).
168 However, although we found that PAPP-A addition did not improve blastocyst production and
169 cleavage rate, this result does not imply that embryonic quality would remain unaffected
170 (Block et al., 2008).

171 *In vitro* embryos are more sensitive to cryopreservation because of lipid accumulation
172 in their structure (Accorsi, Leão, Rocha-Frigoni, Perri, & Mingoti, 2016; Block et al., 2003;
173 Meneghel et al., 2017) but the mechanism of this accumulation is unclear (Leão et al., 2015).
174 Here, we found that PAPP-A treatment did not alter re-expansion rates of warmed blastocysts
175 after 3 and 24 h. Although embryonic survival rate did not improve after warming, PAPP-A
176 treatment increases IGF-1 (27% over) and modulates the expression of genes related to
177 apoptotic effects, oocyte competence, and lipid metabolism in oocytes, cumulus cells and
178 blastocysts.

179 The most interesting results were related to the regulation of genes associated with
180 COC and blastocyst quality. Among oocytes, only one gene experienced altered expression
181 (elevated transcript abundance) under PAPP-A treatment: *TXNRDI*, associated with oocyte
182 competence and highly expressed in cells with strong proliferative activity (Jakupoglu et al.,
183 2005). *TXNRDI* knockout mice showed embryonic lethality (Bondareva et al., 2007). On the

184 other hand, differences of gene expression were more apparent in cumulus cells, especially in
185 genes related to lipid metabolism, apoptosis, oocyte competence, oxidative stress, meiosis
186 resumption, and mitochondrial DNA transcription. In the PAPP-A group, *AGPAT1*, *AGPAT9*,
187 *FASN*, *CASP3*, *EGFR*, *HAS2*, *MTIF3*, and *IMPDH1* were down-regulated, while *HDAC2* and
188 *VNN1* were up-regulated. Additionally, lipid metabolism genes *AGPAT1*, *AGPAT9*, and
189 *FASN* differed in transcript profiles under PAPP-A treatment. The first two genes participate
190 in triacylglycerol synthesis and membrane-lipid biosynthesis (Körbes, Kulcheski, Margis,
191 Margis-Pinheiro, & Turchetto-Zolet, 2016; Zeng et al., 2017). The third gene acts on long
192 fatty acid biosynthesis (Ji et al., 2014; Z. Yang, Cappello, & Wang, 2015).

193 We also observed the modulation of three genes related to competence in cumulus
194 cells, specifically the down-regulation of *EGFR* and *HAS2*, as well as the up-regulation of
195 *HDAC2*. The first gene is involved in oocyte maturation and stimulates cumulus expansion
196 through regulating hyaluronic acid synthesis (Bhardwaj, Ansari, Parmar, Chandra, & Sharma,
197 2016; Nagyova, 2012). Next, *HAS2* expression is correlated with oocyte developmental
198 competence (Dunning et al., 2007), and down-regulation dampens hyaluronic acid synthesis
199 (Thompson, Lane, & Gilchrist, 2007). Finally, *HDAC2* is expressed in the oocyte MII stage,
200 suggesting its involvement in regulatory pathways affecting oocyte developmental
201 competence (S. Wang et al., 2010; Xu, Chen, Zhang, Wei, & Cao, 2015). In addition, IGF
202 components present in COCs accelerate nuclear maturation and promote oocyte competence
203 (Satrapa, Castilho, et al., 2013). Even down-regulation of the first two genes, which would
204 lead to the impairment of oocyte competition, there was no difference in the rates of cleavage
205 and blastocyst production indicating, indirectly, high meiotic resumption.

206 Still in cumulus cells, *VNN1* and *CASP3* are respectively up and down-regulated.
207 *VNN1* is a regulator of oxidative stress response, as well as a potential marker for follicular
208 growth and differentiation (Nivet, Vigneault, Blondin, & Sirard, 2013). Its activation may be

209 the result of decreased oocyte competence from oxidative stress (Nivet et al., 2013). The
210 second gene is a pro-apoptotic factor activated only during apoptotic processes; IGF-1 is
211 thought to increase *CASP3* levels (Raile et al., 2003). The increase of an oxidative stress
212 controller and the decrease of a pro-apoptotic factor could suggest a positive effect of IGF-1,
213 mediated by PAPP-A. In the same way, *IMPDH1* was down regulated in cumulus cells. The
214 *IMPDH1* is specifically associated with cGMP regulation, which influences meiosis
215 resumption (Wigglesworth et al., 2013). The *MTIF3* gene is involved in mitochondrial DNA
216 transcription, and its expression decreases during the germinal vesicle (GV) to oocyte MII
217 stages (Mtango, Harvey, Latham, & Brenner, 2008). Taken together, the modulations of both
218 genes were related to normal oocyte maturation and reflect the further *in vitro* embryo
219 development during PAPP-A treatment.

220 Similar to cumulus cells, differential gene expression in blastocysts was related
221 to apoptosis, DNA methylation, gastrulation, energetic metabolism, implantation/placentation,
222 and lipid metabolism. The latter function is unsurprising given the known role of IGFs as
223 regulators of lipogenesis (Ruan & Lai, 2010). Lipid-metabolism genes *ATF4* and *CPT2* were
224 respectively down and up-regulated in PAPP-A blastocysts. Elevated *ATF4* expression is
225 related to high lipid exposure to oocytes and embryos that causes embryonic stress (Wu et al.,
226 2010; X. Yang et al., 2012). Thus, PAPP-A down-regulation of *ATF4* reduced lipid
227 availability to the embryo. Similarly, *CPT2* is associated with ATP production and lipid
228 reduction from fatty acid oxidation (Gentile et al., 2004; Guo et al., 2017). As described
229 above, we observed that post immediate re-expansion and 24 h re-expansion are similar and
230 although the IGF-1 had not been improved on embryo survival after cryopreservation, the
231 PAPP-A treatment increased the expression of genes related to lipid metabolism in both
232 cumulus cells (*AGPAT1*, *AGPAT9*, and *FASN*) and blastocysts (*ATF4* and *CPT2*) and maybe
233 this regulation could impact the lipids accumulation during *in vitro* embryo production,

234 probably decreasing lipids accumulation. However, future studies should further examine the
235 link between PAPP-A and lipid metabolism in COCs and blastocysts.

236 Caspases are the regulators of apoptosis both extrinsic and intrinsic pathways, having
237 CASP9 as CASP3 activator, and CASP3 cell death performer (Deb, Dey, Bang, Lee, & Kong,
238 2012). PAPP-A treatment also affected apoptosis genes in blastocysts, specifically up-
239 regulating *CASP9* and down-regulating *CASP3*.

240 Other genes up-regulated under PAPP-A treatment were *DNMT3A*, *TFAM*, and *KRT8*
241 in blastocysts. The first gene is directly involved in *de novo* methylation of hemi-methylated
242 and unmethylated DNA as required for the *de novo* methylation, maintaining this process.
243 DNA methylation acts on the repression or activation of genes related to embryonic
244 development, including mechanisms of cell differentiation, tumorigenesis, and aging (Uysal,
245 Akkoyunlu, & Ozturk, 2015). A similar *de novo* methylation gene (*IMPDH1*) was also
246 present in cumulus cells, but was down-regulated.

247 Next, high *TFAM* expression is necessary for mtDNA maintenance (Rantanen,
248 Jansson, Oldfors, & Larsson, 2001; Silva & Larsson, 2002), as demonstrated in *TFAM*
249 knockout experiments that abolished mtDNA in the respiratory chain (J. Wang, Silva,
250 Gustafsson, Rustin, & Larsson, 2001). The third gene is associated with placenta development
251 and subsequent implantation (Bunel et al., 2015; Machado et al., 2012); *KRT8* appears to be
252 essential for bovine embryonic development, as low transcript levels have been linked to
253 embryonic lethality (Machado et al., 2012). Finally, we also observed down-regulation of
254 *IFITM3* in PAPP-A blastocysts. This gene is a germ cell formation marker (Hu et al., 2015),
255 but its exact role remains poorly understood (Shoubridge & Wai, 2007). In summary, the
256 higher expression of *DNMT3A*, *TFAM*, and *KRT8*, together with down-regulation of *IFITM3*
257 could reflect on blastocyst with remarkable characteristics to increases the possibility of
258 pregnancy probably improving a better oxidative metabolism, coordinating adequately

259 embryonic DNA methylation to reach a correct implantation and later the maintenance of
 260 gestation.

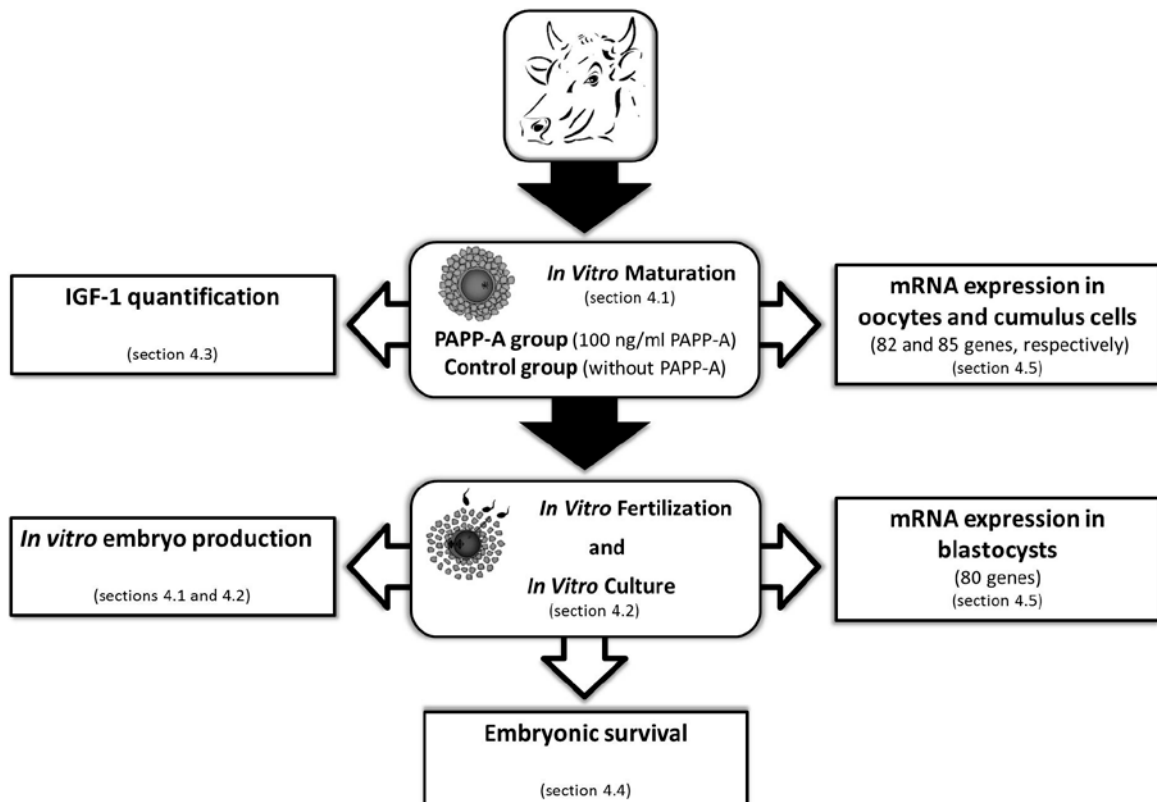
261 We concluded that PAPP-A addition during IVM elevated IGF-1 without affecting
 262 cleavage rate, embryo yield, and post-devitrification embryonic survival. The treatment also
 263 positively modulated genes related to COC and blastocyst quality. Specifically, these genes
 264 are involved in lipid metabolism, apoptosis, and the development of blastocyst competence
 265 (e.g., regulation of implantation and initial embryo differentiation).

266

267 4 MATERIAL AND METHODS

268 Unless otherwise noted, all products were purchased from Sigma-Aldrich Co. (St. Louis, MO,
 269 USA). The experimental design is shown in Fig. 5.

270



271

272

273 **Figure 5.** Experimental design to investigate the effects of the PAPP-A addition to the IVM medium of bovine
274 COCs (20 per group). We investigated the effects of the PAPP-A on IGF-1 into IVM medium, gene expression
275 in COCs, *in vitro* embryo production, gene expression in blastocysts and embryonic cryosurvival. PAPP-A:
276 pregnancy-associated plasma protein-A, COC: cumulus-oocyte complex and IGF-1: insulin-like growth factor 1.
277

278 **4.1 *In vitro* maturation of COCs**

279 Ovaries of predominantly *Bos taurus indicus* were obtained from a local abattoir
280 (Lençóis Paulista, São Paulo, Brazil; 22°35'41.8"S, 48°47'19.4"W) and transported to the
281 laboratory in a thermal container (36°C) containing saline solution (0.9% w/v). Ovarian
282 follicles (diameter 3–8 mm) were aspirated with a syringe and needle (18G). A
283 stereomicroscope was used to select COCs with homogeneous cytoplasm and surrounded by
284 three cumulus-cell layers for the experiment. The time between ovary collection and COC
285 selection did not exceed 3 hours.

286 Selected COCs (n = 600) were incubated in IVM medium, comprising TCM199 with
287 bicarbonate, bovine serum albumin (BSA, 5 mg/mL), pyruvate (0.22 mg/mL; 100 mM
288 solution), amikacin (75 mg/mL), and follicular stimulating hormone (FSH, 0.1 UI/mL
289 solution; Gonalf, Merck Serono, Bari, Italy).

290 The COCs were randomly divided in two groups (20 per group): untreated control and
291 PAPP-A treatment (100 ng/mL rhPappalysin-1; R&D Systems, Minneapolis, MN, USA).
292 Both groups were deposited in 90 µL drops of IVM medium and covered with silicone oil
293 (Quimesp Química, Guarulhos, SP, Brazil) for 24 h in a controlled environment (5.5% CO₂,
294 humidified air, 38.5°C). The final concentration of 100 ng/mL PAPP-A was selected for the
295 main experiment based on a pilot study testing 1, 10, and 100 ng/mL; only the highest
296 concentration caused observable gene expression differences in oocytes, cumulus cells, and
297 blastocysts.

298 At the end of each IVM, the medium was recovered for quantification of IGF-1 (six
299 replicates; section 4.2). Fifteen replicates were performed: six for *in vitro* embryo production
300 (section 4.3), three for embryonic cryosurvival (section 4.4), three for gene expression in
301 oocytes and cumulus cells (section 4.5), and three for gene expression in blastocysts (section
302 4.5).

303

304 **4.2 *In vitro* fertilization and culture**

305 Mature COCs were transferred to TALP drops (Tyrode's medium base) containing BSA (6
306 mg/mL), pyruvate (0.22 mg/mL; 100 mM), amikacin (75 µg/mL), heparin (2 mg/mL), and
307 PHE solution (44 µL/mL; 0.2 nM penicillamine; 0.1 mM hypotaurine; and 1 mM
308 epinephrine). Frozen-thawed semen from a Nelore bull (CRV Lagoa, Sertãozinho, SP, Brazil)
309 was separated with a Percoll gradient (90% and 45%), diluted to 1×10^6 sperm/mL, and
310 added into each drop (6 µL of semen/drop). After *in vitro* fertilization (18–20 h, 5.5% CO₂,
311 humidified air, and 38.5°C), probable zygotes were denuded via vortexing and transferred to
312 culture medium (SOFaaci [Synthetic Oviduct Fluid] with 5 mg/mL BSA, 2.5% fetal calf
313 serum (FCS), and 13 mM pyruvate). Embryos were cultured for 7 d in a humid atmosphere
314 with controlled gases (5% CO₂, 5% O₂, and 90% N₂) at 38.5°C.

315 Fifty microliters of medium was renewed on day 3 and 5 of culture. Cleavage rate of
316 total fertilized COCs was evaluated (n = 6 replicates) on day 3. On day 7, blastocyst
317 formation rate was determined (n = 6 replicates) before they were collected and stored in
318 RNA-free microtubes at -80°C, until RT-qPCR.

319 Three replicates of *in vitro* embryo production were also performed to obtain
320 expanded blastocysts for vitrification.

321

322

323 **4.3 Quantification of IGF-1 with ELISA**

324 To measure IGF-1 in IVM medium, in-house ELISA tests were performed. Medium
325 from both treated and control groups were collected (n = 6) after 24 h of maturation, stored in
326 1.5 mL microtubes, and kept at -80°C until quantification.

327 Each well of a 96-well microplate (Thermo Fisher Scientific, Waltham, MA, USA)
328 was coated with 100 µL of 0.0522 M carbonate buffer (pH = 9.6), containing 0.25 µg of goat
329 anti-rabbit IgG. After overnight incubation at 4°C, a microplate washer (Thermo Fisher
330 Scientific, Waltham) was used to wash the plate twice with 300 µL/well of 0.05% Tween 80
331 solution. Next, 300 µL of 1% PBS-BSA (pH = 7.2) was added per well as a blocking agent.

332 Because PAPP-A was assumed to have disrupted the bond between IGF-1 and
333 IGFBPs, extraction of bound IGF-1 was not performed. Total IGF-1 was quantified with
334 ELISA using the biotin-streptavidin-peroxidase amplification system in a competitive assay.
335 Each well contained 60 µL of control or experimental medium, 100 µL of 1:250.000 diluted
336 anti-IGF-1 antibody (Harbor-UCLA Medical Center, Carson, CA, USA), and 100 µL of
337 biotinylated IGF-1 (0.06 ng/well). After 24 h of incubation at 4°C, two washes were
338 performed. Next, 2.5 mU peroxidase/100 µL was added per well (streptavidin-POD conjugate
339 500 U/mL; Roche, São Paulo, SP, Brazil).

340 Microplates were covered to block light, incubated for 30 min at 4°C, and then washed
341 twice before the addition of 100 µL substrate per well, comprising 2 mM 3,3',5,5'-
342 tetramethylbenzidine (TMB), 100 mM citric acid, 10.63 mM urea peroxide, 126.8 mM
343 Na₂HPO₄, and 4% DMSO.

344 Covered microplates were incubated again for 40 min at 37°C, followed by the
345 addition of 2 M sulfuric acid (30 µL/well) to stop substrate oxidation. Optical density
346 determination at 450 nm was immediately performed with a Tecan microplate reader.

347 For dosage calculation, concentrations of standards were first log-transformed. Next,
348 optical densities were converted to percentage of maximum binding (% B/B₀) and then
349 transformed with the logit function. Transformations were performed through interpolation
350 after linear regression.

351

352 **4.4 Vitrification/warming and subsequent culture**

353 On day 7 of *in vitro* culturing, expanded control (n = 50) and PAPP-A (n = 66)
354 blastocysts were vitrified and warmed (three replicates/group) to evaluate post-warming
355 embryonic survival.

356 Procedures followed protocol from Vitri-Ingá[®] (Ingámed, Maringá, PR, Brazil). High-
357 quality expanded blastocysts were selected for vitrification following previous methods (Leão
358 et al., 2015), removed from culture medium, and transferred to a plate containing 20 µL of
359 maintenance solution. They were next transferred to equilibrium solution for 5 min and then
360 to three 20 µL droplets of vitrification solution for 60 s. During the final 20 s, all embryos
361 were removed, along with the last vitrification-solution droplet, and deposited on the end of a
362 0.7 mm thick polypropylene rod (up to eight embryos/rod), then dipped directly into liquid
363 nitrogen (-196°C). Rods containing vitrified embryos were stored in a cryogenic cylinder at -
364 196°C until warming.

365 Rods were removed from the cryogenic cylinder and immediately immersed for 1 min
366 in 100 µL of warming solution 1 at 37°C. Subsequently, they were transferred to 50 µL of
367 warming solution 2 for 3 min, and to 50 µL of warming solution 3 for 5 min. *In vitro* survival
368 (i.e., embryonic re-expansion rates) were determined at 3 and 24 h post-reheating, upon
369 placing embryos in four-well plates each containing 500 µL of SOF culture medium (20%
370 FCS). Embryos were considerable survivors when presented blastocoel re-expansion without

371 presence of vacuoles. The embryonic re-expansion rate was calculated by the number of
372 surviving embryos divided by the total of heated embryos.

373

374 **4.5 Determining gene expression in cumulus cells, oocytes, and blastocysts through RT-** 375 **qPCR**

376 After 24 h of IVM, oocyte and cumulus cells (20 each/pool; three pools/experimental
377 or control group) were separated through successive pipetting and vortexing. The oocyte
378 (cumulus free) was stored at -80°C until RNA extraction. The cumulus cells resulting from the
379 separation (vortexing) was stored at -80°C until RNA extraction.

380 Total RNA extraction was performed using Microkit RNeasy[®] (Qiagen, Valencia,
381 CA, USA), following manufacturer's protocol. Total RNA concentration was measured in a
382 Nanodrop 2000[®] Spectrophotometer. The 2100 Bioanalyzer[®] system (Agilent, Santa Clara,
383 CA, USA) was used to analyze RNA quality. Only samples with an RNA Integrity Number
384 (RIN) above seven (scale of 0-10) were used.

385 After IVC, blastocysts were frozen (-80°C) as samples for RNA extraction (one
386 replicate = three blastocysts; five pools/group). Total RNA was extracted using the PicoPure[®]
387 RNA Isolation Kit (Thermo Fisher Scientific, Foster City, CA, USA) following
388 manufacturer's protocol. Concentrations of total blastocyst RNA concentration and quality
389 were determined following the same methods as for oocyte/cumulus cell RNA.

390 Reverse transcription of RNA was performed following manufacturer protocol in the
391 High Capacity Kit (Applied Biosystem[®], Foster City, CA, USA). 100 and 50 ng of RNA per
392 sample was used for cumulus cells and blastocysts, respectively. All oocyte samples (10 µL)
393 were used for reverse transcription.

394 Gene expression analysis was performed using Applied Biosystems[™] TaqMan[®]
395 Assays, specific for *Bos taurus*. Target genes numbered 82 in oocyte samples (Table S4), 85

396 in cumulus cell (Table S5), and 80 in blastocysts (Table S6). Prior to RT-qPCR, sequence-
397 specific pre-amplification was performed as follows: 1.25 μ L assay mix (Taqman[®] Assay
398 pooled to a final concentration of 0.2 \times per assay), 2.5 μ L TaqMan PreAmp Master Mix
399 (Thermo Fisher Scientific, Foster City), and 1.25 μ L cDNA (5 ng/ μ L). The pre-amplification
400 thermocycling schedule was 95°C for 10 min (reactivation), 95°C for 15 s (denaturing), and
401 14 cycles of 60°C for 4 min (annealing and amplification). Amplicons were then diluted six-
402 fold.

403 The RT-qPCR reaction solution consisted of 2.25 μ L cDNA (pre-amplified products),
404 2.5 μ L of TaqMan Universal PCR 2 \times Master Mix (Thermo Fisher Scientific, Foster City), and
405 0.25 μ L of 20 \times GE Sample Loading Reagent (Fluidigm, San Francisco, CA, USA). The assay
406 solution contained 2.5 μ L of 20 \times TaqMan Gene Expression Assay (Thermo Fisher Scientific,
407 Foster City) and 2.5 μ L of 2 \times Assay Loading Reagent (Fluidigm). Data collection involved
408 the 96.96 Dynamic Array[™] Integrated Fluidic Circuits (Fluidigm) chip. After priming, the
409 chip was loaded with 5 μ L each of assay and sample solutions. The Biomark HD System
410 (Fluidigm) and TaqMan GE 96 \times 96 Standard was used for RT-qPCR. Thermocycling
411 conditions comprised one Thermal Mix stage (50°C for 2 min, 70°C for 20 min, 25°C for 10
412 min), one Hot Start stage (50°C for 2 min and 95°C for 10 min), followed by 40 cycles of
413 denaturation (95°C for 15 s), annealing, and extension (60°C for 60 s).

414 Relative expression was calculated using Δ Ct (Livak & Schmittgen, 2001) and
415 transformed into fold change ($2^{-\Delta$ Ct}). To normalize oocyte and cumulus cell data, geometric
416 means of housekeeping genes *GAPDH*, peptidyl isomerase A (*PPIA*), and β -actin (*ACTB*)
417 genes were used. Blastocyst data normalization involved the additional inclusion of succinate
418 dehydrogenase complex flavoprotein subunit A (*SDHA*).

419

420

421 **4.6 Statistical analysis**

422 Cleavage, blastocyst development, and embryonic survival rates were calculated as
423 percentages and arcsine-transformed. The IGF-1 concentration was expressed as fold change.
424 The IGF-1, cleavage, and blastocysts rate were subjected to t-test. To embryonic survival, chi-
425 square test was applied. For gene expression profile the bioinformatics analysis was
426 performed using R version 3.0.1 (<http://www.r-project.org>) and Bioconductor
427 (<http://www.bioconductor.org/>). Gene expression heat maps were generated using the
428 averaged control group data for normalization. Target genes were sorted with hierarchical
429 clustering using the *heatplot* function from the *made4* R package (Culhane, Thioulouse,
430 Perrière, & Higgins, 2005). The analyses were performed using JMP software (SAS Institute,
431 Cary, NC, USA). Differences were considered significant when $p \leq 0.05$.

432

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440

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444

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691 **SUPPLEMENTARY MATERIAL**692 **Table S1.** Relative abundance of target genes with similar expression ($p > 0.05$) in oocytes.693 Data represent the group mean \pm S.E.M. from three biological replicates. Gene expressions

694 were generated using the averaged control group data for normalization. Housekeeping genes

695 *GAPDH*, peptidyl isomerase A (*PPIA*), and β -actin (*ACTB*) were used for data normalization.

Gene Symbol	Control	PAPP-A	P-value
<i>ACACA</i>	1.032 \pm 0.084	1.540 \pm 0.354	0.124
<i>ADCY3</i>	1.000 \pm 0.247	1.087 \pm 0.461	0.793
<i>ADCY6</i>	0.643 \pm 0.139	0.755 \pm 0.407	0.689
<i>ADCY9</i>	1.015 \pm 0.163	0.751 \pm 0.122	0.093
<i>AGPAT1</i>	1.002 \pm 0.256	0.944 \pm 0.168	0.761
<i>AGPAT9</i>	1.021 \pm 0.174	1.045 \pm 0.212	0.886
<i>AKR1B1</i>	1.067 \pm 0.269	1.038 \pm 0.137	0.881
<i>ATF4</i>	1.154 \pm 0.552	0.536 \pm 0.150	0.186
<i>ATP5L</i>	1.044 \pm 0.156	1.089 \pm 0.318	0.839
<i>BAX</i>	0.986 \pm 0.272	0.785 \pm 0.020	0.329
<i>BCL2</i>	1.000 \pm 0.188	1.768 \pm 0.494	0.101
<i>BDNF</i>	0.985 \pm 0.187	0.760 \pm 0.066	0.163
<i>BID</i>	0.901 \pm 0.320	0.994 \pm 0.351	0.753
<i>BMP15</i>	1.066 \pm 0.221	1.267 \pm 0.175	0.287
<i>CASP3</i>	1.099 \pm 0.402	1.238 \pm 0.215	0.634
<i>CASP9</i>	0.852 \pm 0.300	0.661 \pm 0.215	0.426
<i>CAT</i>	1.072 \pm 0.277	0.902 \pm 0.282	0.498
<i>CD36</i>	1.000 \pm 0.504	0.845 \pm 0.333	0.683
<i>CLIC3</i>	1.000 \pm 0.913	1.754 \pm 1.228	0.445
<i>CPT1B</i>	0.401 \pm 0.089	0.517 \pm 0.138	0.298
<i>CPT2</i>	1.128 \pm 0.367	1.069 \pm 0.113	0.812
<i>DDIT3</i>	1.167 \pm 0.121	1.076 \pm 0.048	0.324
<i>DGAT1</i>	1.192 \pm 0.281	1.107 \pm 0.177	0.684
<i>DICER1</i>	0.853 \pm 0.184	0.864 \pm 0.154	0.945
<i>DNMT1</i>	0.819 \pm 0.068	0.739 \pm 0.036	0.172
<i>EGFR</i>	1.000 \pm 0.219	0.761 \pm 0.173	0.216
<i>FASN</i>	1.045 \pm 0.209	0.755 \pm 0.245	0.195
<i>FDX1</i>	0.950 \pm 0.145	0.964 \pm 0.194	0.924
<i>FOXO3</i>	0.800 \pm 0.117	0.693 \pm 0.147	0.381
<i>GATM</i>	1.000 \pm 0.951	2.686 \pm 1.804	0.247
<i>GDF9</i>	1.046 \pm 0.184	1.188 \pm 0.292	0.523
<i>GFPT2</i>	0.796 \pm 0.104	0.816 \pm 0.119	0.843
<i>GLRX2</i>	1.000 \pm 0.364	1.036 \pm 0.395	0.913
<i>GPX1</i>	1.188 \pm 0.105	0.980 \pm 0.130	0.100
<i>GPX4</i>	0.887 \pm 0.384	0.712 \pm 0.245	0.549
<i>GREM1</i>	0.999 \pm 0.735	0.486 \pm 0.117	0.350

<i>GUCY1B3</i>	0.890 ± 0.951	0.568 ± 0.199	0.619
<i>HIFOO</i>	0.972 ± 0.144	1.266 ± 0.235	0.153
<i>H2AFZ</i>	1.000 ± 0.312	0.736 ± 0.646	0.571
<i>H3F3A</i>	0.914 ± 0.317	0.740 ± 0.056	0.442
<i>HAS2</i>	1.150 ± 0.165	1.376 ± 0.125	0.136
<i>HDAC2</i>	1.056 ± 0.287	1.159 ± 0.118	0.610
<i>HMBS</i>	0.941 ± 0.329	1.223 ± 0.202	0.287
<i>HPRT1</i>	1.062 ± 0.118	1.216 ± 0.117	0.183
<i>HSPA1A</i>	1.002 ± 0.551	0.960 ± 0.105	0.907
<i>HSPA5</i>	1.054 ± 0.232	1.105 ± 0.139	0.762
<i>IGF1R</i>	1.178 ± 0.319	1.091 ± 0.198	0.713
<i>IGFBP2</i>	1.134 ± 0.102	1.218 ± 0.295	0.679
<i>IMPDH1</i>	0.489 ± 0.224	0.430 ± 0.078	0.702
<i>IMPDH2</i>	1.046 ± 0.337	1.149 ± 0.283	0.708
<i>KRT8</i>	0.876 ± 0.366	0.736 ± 0.278	0.627
<i>LIPE</i>	0.879 ± 0.112	0.971 ± 0.332	0.686
<i>MTIF3</i>	1.157 ± 0.217	0.966 ± 0.013	0.267
<i>NDUFA1</i>	1.064 ± 0.314	1.418 ± 0.599	0.431
<i>NLRP5</i>	0.973 ± 0.224	1.227 ± 0.267	0.277
<i>NOS2</i>	0.766 ± 0.145	0.774 ± 0.182	0.952
<i>NOS3</i>	1.152 ± 0.488	0.940 ± 0.320	0.570
<i>NPR1</i>	1.000 ± 0.358	1.085 ± 0.510	0.827
<i>NPR2</i>	0.799 ± 0.389	0.940 ± 0.076	0.596
<i>OOSP1</i>	1.001 ± 0.251	1.128 ± 0.465	0.706
<i>PDE5A</i>	1.214 ± 0.301	0.980 ± 0.193	0.331
<i>PFKP</i>	0.902 ± 0.197	0.920 ± 0.226	0.923
<i>PGK1</i>	1.240 ± 0.468	1.135 ± 0.133	0.739
<i>PLIN2</i>	0.927 ± 0.121	1.008 ± 0.227	0.626
<i>PLIN3</i>	1.194 ± 0.127	1.292 ± 0.303	0.647
<i>PNPLA2</i>	0.833 ± 0.075	0.995 ± 0.138	0.170
<i>PRDX1</i>	0.902 ± 0.318	0.946 ± 0.188	0.851
<i>PRDX3</i>	0.993 ± 0.240	0.907 ± 0.192	0.651
<i>PTGS2</i>	1.008 ± 0.072	1.181 ± 0.132	0.137
<i>PTX3</i>	1.043 ± 0.788	1.028 ± 0.234	0.978
<i>RPL15</i>	1.043 ± 0.788	1.028 ± 0.234	0.978
<i>RPLP0</i>	1.013 ± 0.126	1.057 ± 0.188	0.752
<i>RPS25</i>	0.933 ± 0.268	1.213 ± 0.779	0.605
<i>SDHA</i>	1.004 ± 0.178	1.131 ± 0.173	0.427
<i>SLC2A1</i>	1.000 ± 0.556	0.828 ± 0.374	0.683
<i>SOD1</i>	1.069 ± 0.242	0.929 ± 0.041	0.424
<i>STAT3</i>	0.942 ± 0.323	1.003 ± 0.221	0.803
<i>TFAM</i>	1.000 ± 0.224	0.681 ± 0.414	0.323
<i>TNFAIP6</i>	1.000 ± 1.434	1.805 ± 1.609	0.553
<i>VCAN</i>	1.009 ± 0.221	1.332 ± 0.042	0.122
<i>XBPI</i>	0.984 ± 0.241	1.218 ± 0.244	0.303

697 **Table S2.** Relative abundance of target genes with similar expression ($p > 0.05$) in cumulus
698 cells. Data represent the group mean \pm S.E.M from three biological replicates. Gene
699 expressions were generated using the averaged control group data for normalization.
700 Housekeeping genes *GAPDH*, peptidyl isomerase A (*PPIA*), and β -actin (*ACTB*) were used
701 for data normalization.

Gene Symbol	Control	PAPP-A	P-value
<i>ACACA</i>	1.118 \pm 0.268	0.670 \pm 0.063	0.095
<i>ADCY3</i>	0.791 \pm 0.277	1.028 \pm 0.470	0.504
<i>ADCY6</i>	0.940 \pm 0.079	0.873 \pm 0.183	0.599
<i>ADCY9</i>	1.041 \pm 0.061	0.740 \pm 0.199	0.109
<i>AKR1B1</i>	1.039 \pm 0.112	1.074 \pm 0.217	0.820
<i>ATF4</i>	1.162 \pm 0.097	0.959 \pm 0.096	0.063
<i>ATP5L</i>	1.030 \pm 0.033	1.243 \pm 0.456	0.504
<i>BAX</i>	1.022 \pm 0.121	1.121 \pm 0.176	0.471
<i>BCL2</i>	0.943 \pm 0.226	1.219 \pm 0.146	0.163
<i>BDNF</i>	0.837 \pm 0.781	0.956 \pm 0.166	0.350
<i>BID</i>	0.916 \pm 0.133	1.390 \pm 0.509	0.245
<i>CASP9</i>	0.943 \pm 0.137	1.019 \pm 0.211	0.636
<i>CAT</i>	0.847 \pm 0.161	0.962 \pm 0.226	0.520
<i>CD36</i>	0.870 \pm 0.302	0.810 \pm 0.298	0.816
<i>CLIC3</i>	0.707 \pm 0.298	0.916 \pm 0.824	0.714
<i>CPT1B</i>	0.685 \pm 0.039	0.985 \pm 0.522	0.424
<i>CPT2</i>	1.050 \pm 0.102	0.888 \pm 0.133	0.173
<i>DDIT3</i>	0.965 \pm 0.278	1.051 \pm 0.344	0.755
<i>DGAT1</i>	0.988 \pm 0.099	0.894 \pm 0.255	0.599
<i>DICER1</i>	0.984 \pm 0.130	0.733 \pm 0.148	0.093
<i>DNMT1</i>	0.976 \pm 0.113	0.865 \pm 0.193	0.448
<i>FDX1</i>	1.079 \pm 0.172	0.942 \pm 0.201	0.422
<i>FOXO3</i>	1.015 \pm 0.102	0.680 \pm 0.314	0.198
<i>GATM</i>	0.962 \pm 0.133	0.702 \pm 0.134	0.076
<i>GFPT2</i>	1.096 \pm 0.061	0.804 \pm 0.227	0.147
<i>GLRX2</i>	1.122 \pm 0.146	1.205 \pm 0.526	0.815
<i>GPX1</i>	1.037 \pm 0.072	1.046 \pm 0.069	0.890
<i>GPX4</i>	1.180 \pm 0.145	0.944 \pm 0.194	0.171
<i>GREM1</i>	1.138 \pm 0.367	0.522 \pm 0.257	0.084
<i>GUCY1B3</i>	1.128 \pm 0.291	0.583 \pm 0.070	0.068
<i>H2AFZ</i>	1.057 \pm 0.108	1.102 \pm 0.591	0.907
<i>H3F3A</i>	1.139 \pm 0.522	1.072 \pm 0.318	0.860
<i>HMBS</i>	1.045 \pm 0.123	1.129 \pm 0.180	0.544
<i>HPRT1</i>	1.029 \pm 0.075	0.873 \pm 0.113	0.128
<i>HSPA1A</i>	0.668 \pm 0.154	1.082 \pm 0.431	0.232
<i>HSPA5</i>	0.827 \pm 0.159	0.898 \pm 0.099	0.554

<i>IGF1R</i>	1.003 ± 0.008	0.862 ± 0.211	0.368
<i>IGFBP2</i>	0.949 ± 0.384	0.880 ± 0.419	0.843
<i>IGFBP4</i>	1.236 ± 0.459	0.795 ± 0.220	0.235
<i>IMPDH2</i>	1.085 ± 0.108	1.014 ± 0.252	0.685
<i>KRT8</i>	0.556 ± 0.444	1.253 ± 0.439	0.129
<i>LIPE</i>	1.033 ± 0.602	0.685 ± 0.163	0.425
<i>LPL</i>	0.702 ± 0.233	1.169 ± 0.390	0.165
<i>LUM</i>	0.771 ± 0.136	0.976 ± 0.389	0.464
<i>NDUFA1</i>	0.992 ± 0.402	1.057 ± 0.330	0.841
<i>NOS2</i>	0.834 ± 0.406	1.100 ± 0.154	0.378
<i>NOS3</i>	1.104 ± 0.228	1.331 ± 0.607	0.593
<i>NPPC</i>	0.858 ± 0.489	0.792 ± 0.690	0.901
<i>NPR1</i>	1.089 ± 0.428	0.692 ± 0.147	0.245
<i>NPR2</i>	1.069 ± 0.389	1.013 ± 0.568	0.896
<i>NPR3</i>	0.972 ± 0.182	0.742 ± 0.649	0.606
<i>OOSP1</i>	0.741 ± 0.313	1.200 ± 0.322	0.151
<i>PDE5A</i>	1.150 ± 0.391	0.771 ± 0.059	0.233
<i>PFKP</i>	0.929 ± 0.156	1.061 ± 0.165	0.369
<i>PGK1</i>	1.029 ± 0.093	1.181 ± 0.272	0.441
<i>PLIN2</i>	1.074 ± 0.097	0.975 ± 0.040	0.215
<i>PLIN3</i>	1.081 ± 0.078	1.170 ± 0.259	0.622
<i>PNPLA2</i>	1.139 ± 0.140	0.764 ± 0.386	0.229
<i>PRDX1</i>	1.061 ± 0.048	0.988 ± 0.087	0.290
<i>PRDX3</i>	1.106 ± 0.252	0.816 ± 0.105	0.174
<i>PTGS2</i>	0.969 ± 0.089	0.712 ± 0.235	0.190
<i>PTX3</i>	0.844 ± 0.237	1.186 ± 0.5517	0.379
<i>RPL15</i>	0.924 ± 0.475	1.484 ± 0.363	0.184
<i>RPLPO</i>	1.025 ± 0.019	1.493 ± 0.605	0.312
<i>RPS25</i>	1.094 ± 0.120	1.481 ± 0.686	0.433
<i>SDHA</i>	1.101 ± 0.098	0.890 ± 0.186	0.180
<i>SLC2A1</i>	0.809 ± 0.155	0.960 ± 0.237	0.414
<i>SLC2A4</i>	0.738 ± 0.090	1.017 ± 0.264	0.200
<i>SOD1</i>	1.063 ± 0.146	1.035 ± 0.145	0.829
<i>STAT3</i>	1.001 ± 0.238	0.783 ± 0.247	0.334
<i>TFAM</i>	0.971 ± 0.196	0.964 ± 0.032	0.955
<i>TNFAIP6</i>	1.249 ± 0.509	0.686 ± 0.205	0.186
<i>TXNRD1</i>	0.926 ± 0.230	0.807 ± 0.273	0.596
<i>VCAN</i>	0.955 ± 0.088	0.806 ± 0.290	0.472
<i>XBPI</i>	1.086 ± 0.301	0.842 ± 0.230	0.331

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705 **Table S3.** Relative abundance of target genes with similar expression ($p > 0.05$) in
 706 blastocysts. Data represent the group mean \pm S.E.M from three biological replicates. Gene
 707 expressions were generated using the averaged control group data for normalization.
 708 Housekeeping genes *GAPDH*, peptidyl isomerase A (*PPIA*), β -actin (*ACTB*), and Succinate
 709 Dehydrogenase Complex Flavoprotein Subunit A (*SDHA*), were used for data normalization.

Gene Symbol	Control	PAPP-A	P-value
<i>ACACA</i>	0.991 \pm 0.251	0.957 \pm 0.223	0.871
<i>ACSL3</i>	1.041 \pm 0.174	1.426 \pm 0.245	0.098
<i>ACSL6</i>	0.938 \pm 0.233	1.538 \pm 0.775	0.311
<i>AKR1B1</i>	0.913 \pm 0.516	0.663 \pm 0.496	0.577
<i>AQP3</i>	0.964 \pm 0.171	1.287 \pm 0.700	0.512
<i>BAX</i>	0.895 \pm 0.272	1.053 \pm 0.161	0.447
<i>BMP15</i>	1.193 \pm 1.075	0.326 \pm 0.394	0.296
<i>CAT</i>	0.953 \pm 0.403	1.116 \pm 0.203	0.576
<i>CDH1</i>	1.003 \pm 0.059	1.647 \pm 0.453	0.131
<i>CDK6</i>	1.044 \pm 0.514	1.564 \pm 1.095	0.514
<i>CDX2</i>	0.957 \pm 0.237	0.983 \pm 0.024	0.866
<i>CYP19</i>	1.228 \pm 0.660	1.955 \pm 0.840	0.307
<i>DDIT3</i>	0.950 \pm 0.158	2.257 \pm 1.484	0.266
<i>DNMT1</i>	0.939 \pm 0.170	1.192 \pm 0.334	0.328
<i>DNMT3B</i>	1.101 \pm 0.244	0.933 \pm 0.162	0.383
<i>DSC2</i>	0.929 \pm 0.223	0.549 \pm 0.112	0.079
<i>EGFR</i>	1.033 \pm 0.379	0.669 \pm 0.010	0.238
<i>ELOVL6</i>	1.058 \pm 0.025	1.032 \pm 0.283	0.890
<i>FADS2</i>	0.955 \pm 0.520	0.578 \pm 0.342	0.362
<i>FASN</i>	0.976 \pm 0.011	0.742 \pm 0.135	0.095
<i>FSHR</i>	1.058 \pm 0.654	1.154 \pm 1.078	0.902
<i>G5K3A</i>	1.052 \pm 0.063	0.933 \pm 0.108	0.189
<i>G6PD</i>	1.028 \pm 0.025	0.986 \pm 0.199	0.749
<i>GDF9</i>	1.087 \pm 1.290	0.359 \pm 0.400	0.436
<i>GPX1</i>	1.011 \pm 0.370	1.371 \pm 0.220	0.236
<i>GPX4</i>	0.936 \pm 0.235	0.649 \pm 0.205	0.188
<i>H19</i>	0.807 \pm 0.985	1.038 \pm 1.094	0.799
<i>HIF1A</i>	0.923 \pm 0.606	0.407 \pm 0.114	0.277
<i>HAND1</i>	1.166 \pm 0.874	0.843 \pm 0.362	0.601
<i>HMOX1</i>	1.182 \pm 0.295	1.695 \pm 0.597	0.276
<i>HPI1</i>	1.025 \pm 0.203	1.095 \pm 0.221	0.707
<i>HSF1</i>	0.990 \pm 0.409	0.624 \pm 0.201	0.261
<i>HSP90AA1</i>	1.002 \pm 0.337	1.554 \pm 0.674	0.295
<i>HSPA1A</i>	0.976 \pm 0.197	0.619 \pm 0.660	0.452
<i>HSPA5</i>	0.901 \pm 0.175	1.052 \pm 0.127	0.297
<i>HSPD1</i>	1.010 \pm 0.244	1.322 \pm 0.291	0.231

<i>IFNT2</i>	0.655 ± 0.384	0.363 ± 0.177	0.323
<i>IGF1R</i>	1.020 ± 0.602	1.155 ± 0.172	0.741
<i>IGFBP2</i>	0.993 ± 0.189	1.055 ± 0.047	0.633
<i>IGFBP4</i>	1.024 ± 0.326	1.409 ± 0.181	0.168
<i>KEAP1</i>	0.996 ± 0.293	1.325 ± 0.523	0.409
<i>LIFR</i>	0.540 ± 0.301	0.746 ± 0.939	0.747
<i>LPL</i>	1.000 ± 1.069	1.343 ± 1.192	0.729
<i>LUM</i>	1.124 ± 1.864	0.025 ± 0.029	0.415
<i>MAPK1</i>	1.021 ± 0.237	1.391 ± 0.042	0.110
<i>MORF4L2</i>	1.016 ± 0.484	0.948 ± 0.420	0.863
<i>MTIF3</i>	0.800 ± 0.182	1.454 ± 0.672	0.230
<i>NANOG</i>	1.156 ± 0.549	1.057 ± 0.461	0.823
<i>NFE2L2</i>	0.995 ± 0.217	1.139 ± 0.543	0.702
<i>NFKB2</i>	0.932 ± 0.317	0.998 ± 0.033	0.756
<i>NLPR5</i>	1.000 ± 0.643	0.651 ± 0.656	0.547
<i>NRP2</i>	0.920 ± 0.566	1.327 ± 0.908	0.552
<i>OCLN</i>	1.022 ± 0.158	0.862 ± 0.231	0.385
<i>OTX2</i>	1.112 ± 0.228	1.277 ± 0.234	0.430
<i>PAF1</i>	0.992 ± 0.091	1.640 ± 0.769	0.281
<i>PFKP</i>	0.941 ± 0.742	0.144 ± 0.145	0.200
<i>PGK1</i>	1.000 ± 0.372	1.043 ± 0.710	0.932
<i>PKP2</i>	1.042 ± 0.201	1.477 ± 0.412	0.202
<i>POU5F1</i>	0.979 ± 0.230	1.651 ± 0.697	0.232
<i>PRDX1</i>	1.056 ± 0.320	1.045 ± 0.348	0.969
<i>REST</i>	1.107 ± 0.448	0.898 ± 0.197	0.517
<i>SCD</i>	1.052 ± 0.232	1.247 ± 0.912	0.751
<i>SLC2A1</i>	1.052 ± 0.093	1.308 ± 0.161	0.091
<i>SLC2A3</i>	0.913 ± 0.255	1.275 ± 0.525	0.364
<i>SLC2A5</i>	1.008 ± 0.274	0.783 ± 0.226	0.338
<i>SOD1</i>	1.028 ± 0.238	0.857 ± 0.353	0.529
<i>SOD2</i>	1.075 ± 0.681	0.648 ± 0.503	0.435
<i>SOX2</i>	1.067 ± 0.089	0.841 ± 0.256	0.263
<i>SREBF1</i>	1.185 ± 0.657	0.247 ± 0.055	0.131
<i>STAT3</i>	1.121 ± 0.167	1.392 ± 0.333	0.298
<i>VEGFA</i>	0.927 ± 0.486	1.356 ± 0.750	0.459
<i>XBPI</i>	0.981 ± 0.359	1.655 ± 0.594	0.183

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716 **Table S4.** Housekeeping and target genes analyzed in oocytes samples by RT-qPCR.

Gene Symbol	Assys ID[†]	Gene Name
<i>ACACA</i>	Bt03213389_m1	Acetyl CoA Carboxylase
<i>ACTB</i>	Bt03279174_g1	Actin, Beta (Housekeeping)
<i>ADCY3</i>	Bt04289077_m1	Adenylate Cyclase 3
<i>ADCY6</i>	Bt03816767_m1	Adenylate Cyclase 6
<i>ADCY9</i>	Bt04287024_m1	Adenylate Cyclase 9
<i>AGPAT1</i>	Bt03224587_g1	1-Acylglycerol-3-Phosphate O-Acyltransferase 1
<i>AGPAT9</i>	Bt04292093_m1	1-Acylglycerol-3-Phosphate O-Acyltransferase 9
<i>AKR1B1</i>	Bt03218049_g1	Aldo-Keto Reductase Family 1, Member B1
<i>ATF4</i>	Bt03221057_m1	Activating Transcription Factor 4
<i>ATP5L</i>	Bt03210836_g1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex subunit E
<i>BAX</i>	Bt03211777_g1	BCL2-Associated X Protein
<i>BCL2</i>	Bt04298952_m1	B-cell CLL/Lymphoma 2
<i>BDNF</i>	Bt03287437_s1	Brain-Derived Neurotrophic Factor
<i>BID</i>	Bt03241255_m1	BH3 Interacting Domain Death Agonist
<i>BMP15</i>	Bt03286494_u1	Bone Morphogenetic Protein 15
<i>CASP3</i>	Bt03250954_g1	Caspase 3, Apoptosis-Related Cysteine Peptidase
<i>CASP9</i>	Bt04282453_m1	Caspase 9, Apoptosis-Related Cysteine Peptidase
<i>CAT</i>	Bt03228713_m1	Catalase
<i>CD36</i>	Bt03212335_mH	CD36 molecule (thrombospondin receptor)
<i>CLIC3</i>	Bt03263038_m1	Chloride Intracellular Channel 3
<i>CPT1B</i>	Bt03244645_m1	Carnitine Palmitoyltransferase 1B
<i>CPT2</i>	Bt03233823_m1	Carnitine Palmitoyltransferase 2
<i>DDIT3</i>	Bt03251320_g1	DNA-Damage-Inducible Transcript 3
<i>DGAT1</i>	Bt03251719_g1	Diacylglycerol O-Acyltransferase 1
<i>DICER1</i>	Bt03217754_m1	Dicer 1, Ribonuclease III
<i>DNMT1</i>	Bt03224737_m1	DNA (Cytosine-5-)-Methyltransferase 1
<i>EGFR</i>	AJT96D7	Epidermal Growth Factor - Receptor
<i>FASN</i>	Bt03210485_m1	Fatty Acid Synthase
<i>FDX1</i>	Bt03217449_m1	Ferredoxin 1
<i>FOXO3</i>	Bt03649334_s1	Forkhead Box O3
<i>GAPDH</i>	Bt03210912_g1	Glyceraldehyde-3-Phosphate Dehydrogenase (Housekeeping)
<i>GATM</i>	Bt03237896_m1	Glycine Amidinotransferase
<i>GDF9</i>	Bt03223996_m1	Growth Differentiation Factor 9
<i>GFPT2</i>	Bt03250351_m1	Glutamine-Fructose-6-Phosphate Transaminase 2
<i>GLRX2</i>	Bt03229700_m1	Glutaredoxin 2
<i>GPX1</i>	Bt03259217_g1	Glutathione Peroxidase 1
<i>GPX4</i>	Bt03259611_m1	Glutathione peroxidase 4
<i>GREM1</i>	Bt03255355_m1	Gremlin 1
<i>GUCY1B3</i>	Bt03215602_m1	Guanylate Cyclase 1, Soluble, Beta 3
<i>H1FOO</i>	Bt03228652_g1	H1 Histone Family, Member O, Oocyte-Specific
<i>H2AFZ</i>	Bt03216346_g1	H2A Histone Family, Member Z
<i>H3F3A</i>	Bt03278804_g1	H3 Histone, Family 3 ^a
<i>HAS2</i>	Bt03212695_g1	Hyaluronan Synthase 2

<i>HDAC2</i>	Bt03244871_m1	Histone Deacetylase 2
<i>HMBS</i>	Bt03234763_m1	Hydroxymethylbilane Synthase
<i>HPRT1</i>	Bt03225311_g1	Hypoxanthine Phosphoribosyltransferase 1
<i>HSPA1A</i>	Bt03292670_g1	Heat Shock 70kDa Protein 1A
<i>HSPA5</i>	Bt03244880_m1	Glucose-Regulated Protein, 78kDa
<i>IGF1R</i>	Bt03649217_m1	Insulin-Like Growth Factor 1 Receptor
<i>IGFBP2</i>	Bt01040719_m1	Insulin-Like Growth Factor Binding Protein 2
<i>IMPDH1</i>	Bt00995384_m1	IMP (inosine 5'-monophosphate) Dehydrogenase 1
<i>IMPDH2</i>	Bt03226238_g1	IMP (inosine 5'-monophosphate) Dehydrogenase 2
<i>KRT8</i>	Bt03225178_g1	Keratin 8
<i>LIPE</i>	Bt03253691_m1	Lipase, Hormone-Sensitive (HSL)
<i>MTIF3</i>	Bt03231844_m1	Mitochondrial Translational Initiation Factor 3
<i>NDUFA1</i>	Bt03216720_g1	NADH: Ubiquinone Oxidoreductase Subunit A1
<i>NLRP5</i>	Bt03218031_m1	NLR Family, Pyrin Domain Containing 5
<i>NOS2</i>	Bt03249597_m1	Nitric Oxide Synthase 2, Inducible
<i>NOS3</i>	Bt03217679_m1	Nitric Oxide Synthase 3
<i>NPR1</i>	Bt04297034_g1	Natriuretic Peptide Receptor 1
<i>NPR2</i>	Bt04316732_m1	Natriuretic Peptide Receptor 2
<i>OOSP1</i>	Bt03233533_g1	Oocyte-Secreted Protein 1
<i>PDE5A</i>	Bt03214261_m1	Phosphodiesterase 5A, cGMP-Specific
<i>PFKP</i>	Bt04316551_m1	Phosphofructokinase
<i>PGK1</i>	Bt03225854_mH	Phosphoglycerate Kinase 1
<i>PLIN2</i>	Bt03212182_m1	Perilipin 2
<i>PLIN3</i>	Bt03230537_m1	Perilipin 3
<i>PNPLA2</i>	Bt03234129_g1	Patatin-Like Phospholipase Domain Containing 2
<i>PPIA</i>	Bt03224617_g1	Peptidylprolyl Isomerase A (Housekeeping)
<i>PRDX1</i>	Bt03223684_m1	Peroxiredoxin-1
<i>PRDX3</i>	Bt03214402_m1	peroxiredoxin 3
<i>PTGS2</i>	Bt03214489_m1	Prostaglandin-Endoperoxide Synthase 2
<i>PTX3</i>	Bt03249011_m1	Pentraxin 3, Long
<i>RPL15</i>	Bt03288449_g1	Ribosomal Protein L15
<i>RPLP0</i>	Bt03218086_m1	Ribosomal Protein, Large, P0
<i>RPS25</i>	Bt03220440_g1	Ribosomal Protein S25
<i>SDHA</i>	Bt04307509_m1	Succinate Dehydrogenase Complex Flavoprotein Subunit A
<i>SLC2A1</i>	Bt03215314_m1	Solute carrier family 2 (facilitated glucose transporter), member 1
<i>SOD1</i>	Bt03215423_g1	Superoxide dismutase 1, soluble
<i>STAT3</i>	Bt03259871_g1	Signal Transducer and Activator of Transcription 3
<i>TFAM</i>	Bt03260078_m1	Transcription Factor A, Mitochondrial
<i>TNFAIP6</i>	Bt03210223_m1	Tumor necrosis factor, alpha-induced protein 6
<i>TXNRD1</i>	Bt03215471_m1	Thioredoxin reductase 1
<i>VCAN</i>	Bt03217633_m1	Versican
<i>XBPI</i>	Bt03227621_g1	X-Box Binding Protein 1

717 † Thermo Fisher Scientific (Wilmington, DE, USA)

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720 **Table S5.** Housekeeping and target genes analyzed in cumulus cells samples by RT-qPCR.

Gene Symbol	Assys ID[†]	Gene Name
<i>ACACA</i>	Bt03213389_m1	Acetyl CoA Carboxylase
<i>ACTB</i>	Bt03279174_g1	Actin, Beta (Housekeeping)
<i>ADCY3</i>	Bt04289077_m1	Adenylate Cyclase 3
<i>ADCY6</i>	Bt03816767_m1	Adenylate Cyclase 6
<i>ADCY9</i>	Bt04287024_m1	Adenylate Cyclase 9
<i>AGPAT1</i>	Bt03224587_g1	1-Acylglycerol-3-Phosphate O-Acyltransferase 1
<i>AGPAT9</i>	Bt04292093_m1	1-Acylglycerol-3-Phosphate O-Acyltransferase 9
<i>AKR1B1</i>	Bt03218049_g1	Aldo-Keto Reductase Family 1, Member B1
<i>ATF4</i>	Bt03221057_m1	Activating Transcription Factor 4
<i>ATP5L</i>	Bt03210836_g1	ATP Synthase, H ⁺ Transporting, Mitochondrial Fo Complex Subunit E
<i>BAX</i>	Bt03211777_g1	BCL2-Associated X Protein
<i>BCL2</i>	Bt04298952_m1	B-cell CLL/Lymphoma 2
<i>BDNF</i>	Bt03287437_s1	Brain-Derived Neurotrophic Factor
<i>BID</i>	Bt03241255_m1	BH3 Interacting Domain Death Agonist
<i>CASP3</i>	Bt03250954_g1	Caspase 3, Apoptosis-Related Cysteine Peptidase
<i>CASP9</i>	Bt04282453_m1	Caspase 9, Apoptosis-Related Cysteine Peptidase
<i>CAT</i>	Bt03228713_m1	Catalase
<i>CD36</i>	Bt03212335_mH	CD36 molecule (thrombospondin receptor)
<i>CLIC3</i>	Bt03263038_m1	Chloride Intracellular Channel 3
<i>CPT1B</i>	Bt03244645_m1	Carnitine Palmitoyltransferase 1B
<i>CPT2</i>	Bt03233823_m1	Carnitine Palmitoyltransferase 2
<i>DDIT3</i>	Bt03251320_g1	DNA-Damage-Inducible Transcript 3
<i>DGATI</i>	Bt03251719_g1	Diacylglycerol O-Acyltransferase 1
<i>DICER1</i>	Bt03217754_m1	Dicer 1, Ribonuclease III
<i>DNMT1</i>	Bt03224737_m1	DNA (Cytosine-5-)-Methyltransferase 1
<i>EGFR</i>	AJT96D7	Epidermal Growth Factor - Receptor
<i>FASN</i>	Bt03210485_m1	Fatty Acid Synthase
<i>FDX1</i>	Bt03217449_m1	Ferredoxin 1
<i>FOXO3</i>	Bt03649334_s1	Forkhead Box O3
<i>GAPDH</i>	Bt03210912_g1	Glyceraldehyde-3-Phosphate Dehydrogenase (Housekeeping)
<i>GATM</i>	Bt03237896_m1	Glycine Amidinotransferase
<i>GFPT2</i>	Bt03250351_m1	Glutamine-Fructose-6-Phosphate Transaminase 2
<i>GLRX2</i>	Bt03229700_m1	Glutaredoxin 2
<i>GPX1</i>	Bt03259217_g1	Glutathione Peroxidase 1
<i>GPX4</i>	Bt03259611_m1	Glutathione Peroxidase 4
<i>GREM1</i>	Bt03255355_m1	Gremlin 1
<i>GUCY1B3</i>	Bt03215602_m1	Guanylate Cyclase 1, Soluble, Beta 3
<i>H2AFZ</i>	Bt03216346_g1	H2A Histone Family, Member Z
<i>H3F3A</i>	Bt03278804_g1	H3 Histone, Family 3 ^a
<i>HAS2</i>	Bt03212695_g1	Hyaluronan Synthase 2
<i>HDAC2</i>	Bt03244871_m1	Histone Deacetylase 2
<i>HMBS</i>	Bt03234763_m1	Hydroxymethylbilane Synthase
<i>HPRT1</i>	Bt03225311_g1	Hypoxanthine Phosphoribosyl Transferase 1

<i>HSPA1A</i>	Bt03292670_g1	Heat Shock 70kDa Protein 1A
<i>HSPA5</i>	Bt03244880_m1	Glucose-Regulated Protein, 78kDa
<i>IGF1R</i>	Bt03649217_m1	Insulin-Like Growth Factor 1 Receptor
<i>IGFBP2</i>	Bt01040719_m1	Insulin-Like Growth Factor Binding Protein 2
<i>IGFBP4</i>	Bt03259500_m1	Insulin-Like Growth Factor Binding Protein 4
<i>IMPDH1</i>	Bt00995384_m1	IMP (inosine 5'-monophosphate) Dehydrogenase 1
<i>IMPDH2</i>	Bt03226238_g1	IMP (inosine 5'-monophosphate) Dehydrogenase 2
<i>KRT8</i>	Bt03225178_g1	Keratin 8
<i>LIPE</i>	Bt03253691_m1	Lipase, Hormone-Sensitive (HSL)
<i>LPL</i>	Bt03240493_m1	Lipoprotein Lipase
<i>LUM</i>	Bt03211920_m1	Lumican
<i>MTIF3</i>	Bt03231844_m1	Mitochondrial Translational Initiation Factor 3
<i>NDUFA1</i>	Bt03216720_g1	NADH: Ubiquinone Oxidoreductase Subunit A1
<i>NOS2</i>	Bt03249597_m1	Nitric Oxide Synthase 2, Inducible
<i>NOS3</i>	Bt03217679_m1	Nitric Oxide Synthase 3
<i>NPPC</i>	Bt03212844_m1	Natriuretic Peptide C (CNP)
<i>NPR1</i>	Bt04297034_g1	Natriuretic Peptide Receptor 1
<i>NPR2</i>	Bt04316732_m1	Natriuretic Peptide Receptor 2
<i>NPR3</i>	Bt03212867_m1	Natriuretic Peptide Receptor 3
<i>OOSP1</i>	Bt03233533_g1	Oocyte-Secreted Protein 1
<i>PDE5A</i>	Bt03214261_m1	Phosphodiesterase 5A, cGMP-Specific
<i>PFKP</i>	Bt04316551_m1	Phosphofructokinase
<i>PGK1</i>	Bt03225854_mH	Phosphoglycerate Kinase 1
<i>PLIN2</i>	Bt03212182_m1	Perilipin 2
<i>PLIN3</i>	Bt03230537_m1	Perilipin 3
<i>PNPLA2</i>	Bt03234129_g1	Patatin-Like Phospholipase Domain Containing 2
<i>PPIA</i>	Bt03224617_g1	Peptidylprolyl Isomerase A (Housekeeping)
<i>PRDX1</i>	Bt03223684_m1	Peroxiredoxin-1
<i>PRDX3</i>	Bt03214402_m1	Peroxiredoxin 3
<i>PTGS2</i>	Bt03214489_m1	Prostaglandin-Endoperoxide Synthase 2
<i>PTX3</i>	Bt03249011_m1	Pentraxin 3, Long
<i>RPL15</i>	Bt03288449_g1	Ribosomal Protein L15
<i>RPLP0</i>	Bt03218086_m1	Ribosomal Rrotein, Large, P0
<i>RPS25</i>	Bt03220440_g1	Ribosomal Protein S25
<i>SDHA</i>	Bt04307509_m1	Succinate Dehydrogenase Complex Flavoprotein Subunit A
<i>SLC2A1</i>	Bt03215314_m1	Solute Carrier Family 2 (facilitated glucose transporter), Member 1
<i>SLC2A4</i>	Bt03215316_m1	Solute Carrier Family 2 (facilitated glucose transporter), Member 4
<i>SOD1</i>	Bt03215423_g1	Superoxide Dismutase 1, Soluble
<i>STAT3</i>	Bt03259871_g1	Signal Transducer and Activator of Transcription 3
<i>TFAM</i>	Bt03260078_m1	Transcription Factor A, Mitochondrial
<i>TNFAIP6</i>	Bt03210223_m1	Tumor Necrosis Factor, Alpha-Induced Protein 6
<i>TXNRD1</i>	Bt03215471_m1	Thioredoxin Reductase 1
<i>VCAN</i>	Bt03217633_m1	Versican
<i>VNN1</i>	Bt03220248_m1	Vanin 1
<i>XBPI</i>	Bt03227621_g1	X-Box Binding Protein 1

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723 **Table S6.** Housekeeping and target genes analyzed in blastocysts samples by RT-qPCR.

Gene Symbol	Assys ID[†]	Gene Name
<i>ACACA</i>	Bt03213389_m1	Acetyl CoA Carboxylase
<i>ACSL3</i>	Bt04282138_m1	Acyl-CoA Synthetase 3
<i>ACSL6</i>	Bt03231692_m1	Acyl-CoA Synthetase 6
<i>ACTB</i>	Bt03279174_g1	Actin, Beta (Housekeeping)
<i>AKR1B1</i>	Bt03218049_g1	Aldo-Keto Reductase Family 1, Member B1
<i>AQP3</i>	Bt03253663_m1	Aquaporin 3
<i>ATF4</i>	Bt03221057_m1	Activating Transcription Factor 4
<i>BAX</i>	Bt03211777_g1	BCL2-Associated X Protein
<i>BMP15</i>	Bt03286494_u1	Bone Morphogenetic Protein 15
<i>CASP3</i>	Bt03250954_g1	Caspase 3, Apoptosis-Related Cysteine Peptidase
<i>CASP9</i>	Bt04282453_m1	Caspase 9, Apoptosis-Related Cysteine Peptidase
<i>CAT</i>	Bt03228713_m1	Catalase
<i>CDH1</i>	Bt03210093_g1	Cadherin 1
<i>CDK6</i>	Bt04311264_m1	Cyclin-Dependent Kinase 6
<i>CDX2</i>	Bt03649157_m1	Homeobox Protein CDX-2
<i>CPT2</i>	Bt03233823_m1	Carnitine Palmitoyltransferase 2
<i>CYP19A1</i>	Bt03213774_m1	Cytochrome P450 Family 19 Subfamily A Member 1
<i>DDIT3</i>	Bt03251320_g1	DNA-Damage-Inducible Transcript 3
<i>DNMT1</i>	Bt03224737_m1	DNA (Cytosine-5-)-Methyltransferase 1
<i>DNMT3A</i>	Bt01027164_m1	DNA (Cytosine-5-)-Methyltransferase 3A
<i>DNMT3B</i>	Bt03259810_m1	DNA (Cytosine-5-)-Methyltransferase 3B
<i>DSC2</i>	Bt03649202_m1	Desmocollin-II
<i>EGFR</i>	AJT96D7	Epidermal Growth Factor - Receptor
<i>ELOVL6</i>	Bt00907566_m1	ELOVL Fatty Acid Elongase 6
<i>FADS2</i>	Bt03256255_g1	Fatty Acid Desaturase 2
<i>FASN</i>	Bt03210485_m1	Fatty Acid Synthase
<i>FSHR</i>	Bt03212674_m1	Follicle-Stimulating Hormone Receptor
<i>GSK3A</i>	Bt03273695_m1	Glycogen Synthase Kinase 3 Alpha
<i>G6PD</i>	Bt03649181_m1	Glucose 6 Phosphate Deshydrogenase
<i>GAPDH</i>	Bt03210912_g1	Glyceraldehyde-3-Phosphate Dehydrogenase (Housekeeping)
<i>GDF9</i>	Bt03223996_m1	Growth Differentiation Factor 9
<i>GPX1</i>	Bt03259217_g1	Glutathione Peroxidase 1
<i>GPX4</i>	Bt03259611_m1	Glutathione Peroxidase 4
<i>H19</i>	<i>Custom TaqMan</i>	Imprinted Maternally Expressed Transcript
<i>HIF1A</i>	Bt03259341_m1	Hypoxia Inducible Factor 1 (transcription factor)
<i>HAND1</i>	Bt04318733_g1	Heart and Neural Crest Cell Derivative 1
<i>HMOX1</i>	Bt03218632_m1	Heme Oxygenase (decycling) 1
<i>HP1</i>	Bt03246076_m1	Heterochromatin Protein 1
<i>HSF1</i>	Bt03249686_m1	Heat Shock Transcription Factor 1
<i>HSP90AA1</i>	Bt03218068_g1	Heat Shock Protein 90kDa Alpha
<i>HSPA1A</i>	Bt03292670_g1	Heat Shock 70kDa Protein 1A

HSPA5	Bt03244880_m1	Glucose-Regulated Protein, 78kDa
HSPD1	Bt04301470_g1	Heat Shock 60kDa Protein 1A
IFITM3	Bt03292973_g1	Interferon Induced Transmembrane Protein 3
IFNT2	Bt03210589_g1	Interferon Tau-2
IGF1R	Bt03649217_m1	Insulin-Like Growth Factor 1 Receptor
IGFBP2	Bt01040719_m1	Insulin-Like Growth Factor Binding Protein 2
IGFBP4	Bt03259500_m1	Insulin-Like Growth Factor Binding Protein 4
KEAP1	Bt03817661_m1	Kelch-Like ECH-Associated Protein 1
KRT8	Bt03225178_g1	Keratin 8
LIFR	Bt04310863_m1	Leukaemia Inhibitory Factor Receptor
LPL	Bt03240493_m1	Lipoprotein Lipase
LUM	Bt03211920_m1	Lumican
MAPK1	Bt03216718_g1	Mitogen-Activated Protein Kinase
MORF4L2	Bt03270996_m1	Mortality Factor 4 Like 2
MTIF3	Bt03231844_m1	Mitochondrial Translational Initiation Factor 3
NANOG	Bt03220541_m1	Nanog Homeobox
NFE2L2	Bt03251880_m1	Nuclear Factor (erythroid-derived 2)-Like 2
NFKB2	Bt03272789_g1	Nuclear Factor of Kappa Light Polypeptide Gene Enhancer in B-Cells 2
NLPR5	Bt03218031_m1	NLR Family, Pyrin Domain Containing 5
NRP2	Bt04316732_m1	Natriuretic Peptide Receptor 2
OCLN	Bt03255219_m1	Occludin
OTX2	Bt04316301_g1	Orthodenticle Homeobox 2
PAF1	Bt03239371_g1	RNA Polymerase II Associated Factor
PFKP	Bt04316551_m1	Phosphofructokinase
PGK1	Bt03225854_mH	Phosphoglycerate Kinase 1
PKP2	Bt03257632_m1	Plakophilin
POU5F1	Bt03223846_g1	POU Class 5 homeobox 1 (OCT4)
PPIA	Bt03224617_g1	Peptidylprolyl Isomerase A (Housekeeping)
PRDX1	Bt03223684_m1	Peroxiredoxin-1
REST	Bt03278318_s1	RE1-Silencing Transcription Factor
SCD	Bt04307476_m1	Stearoyl-CoA Desaturase
SDHA	Bt04307509_m1	Succinate Dehydrogenase Complex Flavoprotein Subunit A (Housekeeping)
SLC2A1	Bt03215314_m1	Solute Carrier Family 2 (facilitated glucose transporter), Member 1
SLC2A3	Bt03259514_g1	Solute Carrier Family 2 (facilitated glucose transporter), Member 3
SLC2A5	Bt03258296_m1	Solute Carrier Family 2 (facilitated glucose/fructose transporter), Member 5
SOD1	Bt03215423_g1	Superoxide Dismutase 1, Soluble
SOD2	Bt03244551_m1	Superoxide Dismutase 2, Mitochondrial
SOX2	Bt03278318_s1	SRY (sex determining region Y)-Box 2
SREBF1	Bt03276370_m1	Sterol Regulatory Element Binding Transcription F1
STAT3	Bt03259871_g1	Signal Transducer and Activator of Transcription 3
TFAM	Bt03260078_m1	Transcription Factor A, Mitochondrial
VEGFA	Bt03213282_m1	Vascular Endothelial Growth Factor A
XBPI	Bt03227621_g1	X-Box Binding Protein 1

ANEXO

Molecular Reproduction & Development

1. SUBMISSION

Authors should kindly note that submission implies that the content has not been published or submitted for publication elsewhere except as a brief abstract in the proceedings of a scientific meeting or symposium.

Once the submission materials have been prepared in accordance with the Author Guidelines, manuscripts should be submitted via the journal's ScholarOne site: <https://mc.manuscriptcentral.com/mrd>. For more details on how to use ScholarOne, visit www.wileyauthors.com/scholarone. Note, this journal uses iThenticate's CrossCheck software to detect instances of overlapping and similar text in submitted manuscripts.

The submission system will prompt the author to use an ORCID ID (a unique author identifier) to help distinguish their work from that of other researchers. [Click here to find out more.](#)

For help with submissions, please contact the Editorial Office: mrreditorial@wiley.com. When necessary, the Editorial Office staff may refer questions to the Editor-in-Chief.

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2. AIMS AND SCOPE

Molecular Reproduction and Development takes an integrated, systems-biology approach to understand the dynamic continuum of cellular, reproductive, and developmental processes. This journal fosters dialogue among diverse disciplines through primary research communications and educational forums, with the philosophy that fundamental findings within the life sciences result from a convergence of disciplines.

Increasingly, readers of the Journal need to be informed of diverse, yet integrated, topics impinging on their areas of interest. This requires an expansion in thinking towards non-traditional, interdisciplinary experimental design and data analysis. For example, biologists need to know how nanodevices might be used, while bioengineers need to know how post-translational protein modifications affect developmental mechanisms. The Journal will provide a means for readers to integrate divergent scientific disciplines into their current and future research. Readers will turn to *Molecular Reproduction and Development* not only to learn the latest in research progress, but to become educated in frontier topics of the field of reproductive and developmental biology; students in particular will turn to the Journal to learn about current progress in the diversifying approaches that will become the foundation for the next generation of research.

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3. MANUSCRIPT CATEGORIES AND REQUIREMENTS

DESCRIPTION OF SUBMISSION TYPES:

VISIONS highlight the visual impact inherent in the field of reproduction and development. Researchers are encouraged to submit individual figures of visual scientific interest that convey important concepts or lessons without requiring significant text for this section of the journal. Each image should be submitted through the [ScholarOne Manuscripts website](#). Figure formatting must be at least 22 x 28 cm at a resolution of 600 dpi, and must include a title and a legend of less than 250 words that describes the image sufficiently to be understood by a broad audience of researchers. The Editorial Board will evaluate these submissions for their visual impact and scientific content. There are no color figure in-print charges.

CORRESPONDENCE

CORRESPONDENCE is a section of short, ~one journal page (500 words or less, or about one column length total) communications for the research field. This section is devoted to brief research results, announcements of interest to the community, new databases or software program availability, or other research results not appropriate for full-length Research Articles. A single figure may be included when essential, but these figures will be published at no larger than

one column width squared (9 x 9 cm), inclusive of the figure legend text. CORRESPONDENCES should start with a 1-2 sentence introduction or integration into the major point of the communication, and end with the major conclusion obtained. Up to three references may be included (not part of the 500 word limit), with formatting as below for Manuscripts. These submissions are evaluated by the Editorial Board and by external reviewers. At the Editors discretion, CORRESPONDENCE can be published with expanded size (in two journal pages): 1000 words, two figures, and six references.

REVIEWS and ESSAYS

Submissions of REVIEWS and ESSAYS are encouraged. The topics of the manuscript are flexible, but they are intended to reach a broad audience of readers in molecular reproduction and development—from investigators in the field, to students learning the material for the first time. Therefore, it is important that the reviews start generally or with a historical perspective to integrate the topic into a larger context. The bulk of the review should be a critical analysis of the current field and should end with important yet-unresolved questions, speculations, and directions for the field in the future. All other formats for the review are as listed below for manuscripts. ESSAYS follow a similar guideline, but the topics may be more speculative, of historical emphasis, or may integrate more than scientific content. There are no color figure in-print charges.

RESEARCH ARTICLES

Molecular Reproduction and Development is an international journal devoted to an integrated approach towards understanding the dynamic continuum of reproductive and developmental processes. As such, the journal is interested in RESEARCH ARTICLES that advance the field by mechanistic discoveries, and by functional understanding. Manuscripts reporting purely descriptive science must be of particular interest to be considered for the journal. MRD particularly encourages manuscripts with a convergence of disciplines, including systems biology, computational modeling, nanoscience, organic chemistry, bioengineering, evolutionary and synthetic biology - all within the framework that describes or reveals a mechanistic aspect of reproduction and development. These submissions are evaluated by the Editorial Board and by external reviewers in accordance with the Peer Review Policy of MRD (see <http://mc.manuscriptcentral.com/mrd>).

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Parts of the Manuscript

The manuscript should be submitted in separate files: main text file; figures.

Main Text File

The text file should be presented in the following order:

- i. The title;
- ii. The full names of the authors (do not include academic degrees);
- iii. The author's institutional affiliations where the work was conducted, with a footnote for the author's present address if different from where the work was conducted;
- iv. Grant numbers (as applicable-to ensure proper identification of funders with publication requirements-see note under Author Licensing; below);
- v. Abstract and keywords;
- vi. Main text;
- vii. Acknowledgments;
- viii. References;
- ix. Tables (each table complete with title and footnotes);
- x. Figure legends;
- xi. Appendices (if relevant)

Figures and supplementary/supporting information should be supplied as separate files (see below under "Additional Files"). Figures must be clearly labeled.

Authorship

Please refer to the journal's Authorship policy in the Editorial Policies and Ethical Considerations section for details on author listing eligibility.

Acknowledgements

Contributions from anyone who does not meet the criteria for authorship should be listed, with permission from the contributor, in an Acknowledgments section. Financial and material support should also be mentioned. Thanks to anonymous reviewers are not appropriate.

Conflict of Interest Statement

Authors will be asked to provide a conflict of interest statement during the submission process. For details on what to include in this section, see the Conflict of Interest section in the Editorial Policies and Ethical Considerations section below. Submitting authors should ensure they liaise with all co-authors to confirm agreement with the final statement.

Abstract

Please provide an abstract of 200 words (Brief Reports only: max 150 words) containing the major keywords summarizing the article.

Keywords

Please provide three to five keywords.

Main Text

The journal uses US spelling; however, authors may submit using either option, as spelling of accepted papers is converted during the production process.

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The accuracy of references is the responsibility of the authors. Only published papers and those in press may be included in the reference list. Unpublished data and submitted manuscripts must be cited parenthetically within the text. Personal communications should also be cited within the text; permission in writing from the communicator is required.

References should be prepared according to the *Publication Manual of the American Psychological Association* (6th edition). The APA website includes a range of resources for authors learning to write in APA style, including an overview of the manual, free tutorials on APA Style basics, and an APA Style Blog. For more information about APA referencing style, please also refer to the APA FAQ.

EndNote users can download the style here.

According to APA style, in text citations should follow the author-date method whereby the author's last name and the year of publication for the source should appear in the text, for example, (Jones, 1998). The complete reference list should appear alphabetically by name at the end of the paper.

Authors should note that the APA referencing style requires that a Digital Object Identifier (DOI) be provided for all references where available. Also, for journal articles, issue numbers are not included unless each issue in the volume begins with page one.

Reference examples follow:

Journal article

Beers, S. R., & De Bellis, M. D. (2002). Neuropsychological function in children with maltreatment-related posttraumatic stress disorder. *The American Journal of Psychiatry*, 159, 483–486. doi:10.1176/appi.ajp.159.3.483

Book

Bradley-Johnson, S. (1994). *Psychoeducational assessment of students who are visually impaired or blind: Infancy through high school* (2nd ed.). Austin, TX: Pro-ed.

Internet Document

Norton, R. (2006, November 4). How to train a cat to operate a light switch [Video file]. Retrieved from <http://www.youtube.com/watch?v=Vja83KLQXZs>

Footnotes

Footnotes should be placed as a list at the end of the paper only, not at the foot of each page. They should be kept to a minimum. Keep footnotes brief; they should contain only short comments tangential to the main argument of the paper and should not include references. They should be numbered in the list and referred to in the text with consecutive, superscript Arabic numerals.

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Tables should be self-contained and complement, not duplicate, information contained in the text. They should be supplied as editable files, not pasted as images. Legends should be concise but comprehensive – the table, legend, and footnotes must be understandable without reference to the text. All abbreviations must be defined in footnotes. Footnote symbols: †, ‡, §, ¶, should be used (in that order) and *, **, *** should be reserved for P-values. Statistical measures such as SD or SEM should be identified in the headings.

Figure Legends

Legends should be concise but comprehensive – the figure and its legend must be understandable without reference to the text. Include definitions of any symbols used and define/explain all abbreviations and units of measurement.

Figures

Although authors are encouraged to send the highest quality figures possible, for peer-review purposes, a wide variety of formats, sizes, and resolutions are accepted. Click [here](#) for the basic figure requirements for figures submitted with manuscripts for initial peer review, as well as the more detailed post-acceptance figure requirements.

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The following points provide general advice on formatting and style.

- **Abbreviations:** In general, terms should not be abbreviated unless they are used repeatedly and the abbreviation is helpful to the reader. Initially, use the word in full, followed by the abbreviation in parentheses. Thereafter use the abbreviation only.
- **Units of measurement:** Measurements should be given in SI or SI-derived units. Visit the Bureau International des Poids et Mesures (BIPM) website for more information about SI units.
- **Numbers:** numbers under 10 should be spelt out, except for: measurements with a unit (8 mmol/L); age (6 weeks old), or lists with other numbers (11 dogs, 9 cats, 4 gerbils).
- **Trade Names:** Chemical substances should be referred to by the generic name only. Trade names should not be used. Drugs should be referred to by their generic names. If proprietary drugs have been used in the study, refer to these by their generic name,

mentioning the proprietary name and the name and location of the manufacturer in parentheses.

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The acceptance criteria for all papers are the quality and originality of the research and its significance to journal readership. Papers will only be sent to review if the Editors determine that the paper meets the appropriate quality and relevance requirements.

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The journal encourages authors to share the data and other artefacts supporting the results in the paper by archiving it in an appropriate public repository. Authors should include a data accessibility statement, including a link to the repository they have used, in order that this statement can be published alongside their paper.

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For manuscripts reporting medical studies that involve human participants, a statement identifying the ethics committee that approved the study and confirmation that the study conforms to recognized standards is required, for example: Declaration of Helsinki; US Federal Policy for the Protection of Human Subjects; or European Medicines Agency Guidelines for Good Clinical Practice US Federal Policy for the Protection of Human Subjects;. It should also state clearly in the text that all persons gave their informed consent prior to their inclusion in the study.

Patient anonymity should be preserved. Photographs need to be cropped sufficiently to prevent human subjects being recognized (an eye bar must not be used because of insufficient de-identification). Images and information from individual participants will only be published where the authors have obtained the individual's free prior informed consent. Authors do not need to provide a copy of the consent form to the publisher; however, in signing the author license to publish, authors are required to confirm that consent has been obtained. Wiley has a standard patient consent form available for use.

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- US authors should cite compliance with the US National Research Council's Guide for the Care and Use of Laboratory Animals, the US Public Health Service's Policy on Humane Care and Use of Laboratory Animals, and Guide for the Care and Use of Laboratory Animals.
- UK authors should conform to UK legislation under the Animals (Scientific Procedures) Act 1986 Amendment Regulations (SI 2012/3039).
- European authors outside the UK should conform to Directive 2010/63/EU.

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The journal requires that clinical trials are prospectively registered in a publicly accessible database and clinical trial registration numbers are included in all papers that report their results. Authors are asked to include the name of the trial register and the clinical trial registration number at the end of the Abstract. If the trial is not registered, or was registered retrospectively, the reasons for this should be explained.

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- Randomized trials: CONSORT
- Observational studies: STROBE
- Systematic reviews: PRISMA
- Case reports: CARE
- Qualitative research: SRQR
- Diagnostic / prognostic studies: STARD
- Quality improvement studies: SQUIRE
- Animal pre-clinical studies: ARRIVE
- Study protocols: SPIRIT
- Clinical practice guidelines: AGREE

We also encourage authors to refer to and follow guidelines from:

- Future of Research Communications and e-Scholarship (FORCE11)
- National Research Council's Institute for Laboratory Animal Research guidelines
- The Gold Standard Publication Checklist from Hooijmans and colleagues
- Minimum Information Guidelines from Diverse Bioscience Communities (MIBBI) website
- FAIRsharing website

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Upon its first use in the title, abstract, and text, the common name of a species should be followed by the scientific name (genus, species, and authority) in parentheses. For well-known species, however, scientific names may be omitted from article titles. If no common name exists in English, only the scientific name should be used.

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Standard nomenclature format must be used according to the organisms discussed. Reference sites by organism include:

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- <http://www.informatics.jax.org/mgihome//nomen/strains.shtml> (mice, rats)
- <http://www.xenbase.org> (*Xenopus*)
- <http://zfin.org> (zebrafish)
- <http://www.echinobase.org> (echinoderms)
- <http://flybase.org/> (fruitflies)
- <http://www.wormbase.org/>

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Nucleotide sequence data can be submitted in electronic form to any of the three major collaborative databases: DDBJ, EMBL, or GenBank. It is only necessary to submit to one database as data are exchanged between DDBJ, EMBL, and GenBank on a daily basis. The suggested wording for referring to accession-number information is: 'These sequence data have been submitted to the DDBJ/EMBL/GenBank databases under accession number U12345'. Addresses are as follows:

- DNA Data Bank of Japan (DDBJ): www.ddbj.nig.ac.jp
- EMBL Nucleotide Archive: ebi.ac.uk/ena
- GenBank: www.ncbi.nlm.nih.gov/genbank

Protein sequence data should be submitted to either of the following repositories:

- Protein Information Resource (PIR): pir.georgetown.edu.
- SWISS-PROT: expasy.ch/sprot/sprot-top

Structural Data

For papers describing structural data, atomic coordinates and the associated experimental data should be deposited in the appropriate databank (see below). **Please note that the data in databanks must be released, at the latest, upon publication of the article.** We trust in the cooperation of our authors to ensure that atomic coordinates and experimental data are released on time.

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- Inorganic compounds: *Fachinformationszentrum Karlsruhe* (FIZ; fiz-karlsruhe.de).
- Proteins and nucleic acids: *Protein Data Bank* (rcsb.org/pdb).
- NMR spectroscopy data: *BioMagResBank* (bmr.b.wisc.edu).

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