

1 **Cables2 Is a Novel Smad2-Regulatory Factor Essential for Early** 2 **Embryonic Development in Mice**

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45 **ABSTRACT**

46 CDK5 and Abl enzyme substrate 2 (Cables2), a member of the Cables family that has a C-
47 terminal cyclin box-like domain, is widely expressed in adult mouse tissues. However, the
48 physiological role of Cables2 *in vivo* is unknown. We show here that *Cables2*-deficiency
49 causes post-gastrulation embryonic lethality in mice. The mutant embryos progress to
50 gastrulation, but then arrest, and fail to grow. Analysis of gene expression patterns reveals
51 that formation of the anterior visceral endoderm and the primitive streak is impaired in
52 *Cables2*-deficient embryos. Tetraploid complementation analyses support the critical
53 requirement of Cables2 in both the epiblast and visceral endoderm for progression of
54 embryogenesis. In addition, we show that Cables2 physically interacts with a key mediator of
55 the canonical Nodal pathway, Smad2, and augments its transcriptional activity. These
56 findings provide novel insights into the essential role of Cables2 in the early embryonic
57 development in mice.

58 INTRODUCTION

59 The Nodal, bone morphogenetic protein (BMP) and Wnt signalling pathways are essential for
60 early mouse development. These pathways coordinately control formation of the proximal–
61 distal (P–D) axis during the egg cylinder stage and the subsequent conversion of this axis into
62 the anterior–posterior (A–P) axis early in gastrulation (reviewed in Arkell and Tam, 2012;
63 Robertson, 2014; Shen, 2007; ten Berge et al., 2008; Wang et al., 2012; Winnier et al., 1995).
64 Initially, ligands of these signalling pathways (including BMP4 and Nodal) and pathway
65 activators (Furin, Pace) are expressed in proximal portions of the embryo whereas antagonists
66 of each pathway (including Cer1, Lefty1, Dkk1) are expressed in the distal-most tissue of the
67 embryo (the distal visceral endoderm: DVE). Subsequently, the distal population of
68 antagonist expressing cells expands and relocates to the anterior of the embryo in a region
69 known as the anterior visceral endoderm (AVE) (Ben-Haim et al., 2006; Shen, 2007).
70 Concurrently, the expression domains of both the Nodal and Wnt3 ligands are confined to the
71 posterior side of the embryo (the primitive streak; PS and overlying visceral endoderm or
72 posterior visceral endoderm PVE). This realignment of the P–D signalling gradient into A–P
73 gradients signals the onset of gastrulation and the formation of the primitive streak, which is
74 the structure that will generate tissues that constitute and elaborate the embryonic A–P axis.
75 The Nodal pathway is crucial for many aspects of A–P axis formation. Mouse embryos that
76 lack any Nodal activity fail to establish molecular pattern in the pre-gastrula VE and lack
77 AVE function. Additionally, these embryos fail to establish posterior identity at the
78 beginning of gastrulation (Brennan et al., 2001; Conlon et al., 1994). Other experiments, in
79 which altered Nodal signalling enables gastrulation to initiate, reveal that Nodal signalling
80 also patterns the primitive streak and its derivatives. High levels of Nodal signalling early in
81 gastrulation ensure the production of the anterior mesendoderm that patterns the embryonic
82 anterior, whereas as gastrulation proceeds the level of Nodal signalling is reduced, ensuring

83 that more-posterior primitive streak derivatives are formed correctly (Vincent et al., 2003).
84 During early mouse development, the Nodal signal is propagated via binding to its receptors
85 activin A receptor, type 1B (Acvr1b, also known as ALK4) and activin A receptor, type 1C
86 (Acvr1c, also known as ALK7). The activated receptors phosphorylate the receptor-regulated
87 Smads (R-Smads; Smad2 and Smad3), which form homomeric complexes and heteromeric
88 complexes with the common Smad (SMAD4). These activated Smad complexes accumulate
89 within the nucleus, where they often complex with tissue specific transcription factors to
90 directly regulate transcription of target genes (Massagué, 2012).

91 Genetic evidence also implicates the canonical Wnt/ β -catenin pathway in multiple
92 aspects of A-P axis formation. Mutations that remove (Huelsen et al., 2000) or increase
93 (Chazaud and Rossant, 2006) Wnt activity prevent correct formation of the DVE.
94 Subsequently, in the 24 hours prior to gastrulation Wnt3 expression is initiated, first being
95 detected in the PVE and then in the posterior epiblast by 6.0 dpc (Rivera-Pérez and
96 Magnuson, 2005). Removal of this activity (Liu et al., 1999) prevents primitive streak
97 formation whereas reduction of this activity (Tortelote et al., 2013; Yoon et al., 2015a) allows
98 the streak to form but not elongate, resulting in impaired production of the tissues that
99 constitute the A-P axis. Generally, when canonical Wnt ligands bind and activate their
100 receptor, the intracellular molecule, β -catenin, is stabilised and translocates to the nucleus
101 where it complexes with the Tcf family of DNA binding proteins to regulate transcription of
102 Wnt target genes (Jamieson et al., 2012; Wang et al., 2012).

103 The precise level of Nodal and Wnt activity is dependent upon interactions between
104 these and the BMP pathway (Robertson, 2014; Tam and Loebel, 2007). For example, prior to
105 gastrulation, Nodal expression in the epiblast is activated in the overlying visceral endoderm
106 via a Smad2/Foxh1 dependent autoregulatory feedback loop (Norris et al., 2002). At the same
107 time, a slow acting feedback loop is established in which Nodal signals from the epiblast

108 maintain the extraembryonic expression of BMP4 (Ben-Haim et al., 2006; Brennan et al.,
109 2001). BMP4 activates Wnt3 expression in the posterior epiblast and Wnt3 amplifies Nodal
110 expression (Ben-Haim et al., 2006). Although much is known about the signalling events that
111 establish the murine A–P axis, it is clear that many molecules required for this process
112 remain to be discovered.

113 Cdk5 and Abl enzyme substrate 1 (Cables1, also known as ik3-1) is the founding
114 member of the Cables family, each member of which has a C-terminal cyclin box-like
115 domain. Cables1 has been shown to physically interact with cyclin-dependent kinase 2
116 (Cdk2), Cdk3, Cdk5, and c-Abl molecules, and to be phosphorylated by Cdk3, Cdk5, and c-
117 Abl (Matsuoka et al., 2000; Yamochi et al., 2001; Zukerberg et al., 2000). Furthermore, in
118 primary cortical neurons, c-abl phosphorylation of Cables1 augments tyrosine
119 phosphorylation of Cdk5 to promote neurite outgrowth (Zukerberg et al., 2000). It has also
120 been demonstrated that Cables1 functions as a bridging factor linking Robo-associated Abl
121 and the N-cadherin-associated β -catenin complex in chick neural retina cells (Rhee et al.,
122 2007). Of note, *Cables1*-deficient mice showed increased cellular proliferation resulting in
123 endometrial hyperplasia, colon cancer, and oocyte development (Kirley et al., 2005; Lee et
124 al., 2007; Zukerberg et al., 2004). Additionally, a dominantly acting, truncated version of
125 Cables1 revealed a requirement in the development of the corpus callosum in mice (Mizuno
126 et al., 2014). During zebrafish development, *Cables1* is required for early neural
127 differentiation and its loss subsequently causes apoptosis of brain tissue and behavioral
128 abnormalities (Groeneweg et al., 2011). Zebrafish have only one Cables gene (Cables1),
129 whereas the mouse and human genomes contain a paralogous gene, Cables2 (also known as
130 ik3-2), which has a C-terminal cyclin-box-like region with a high degree of identity to that of
131 Cables1. Similarly, Cables2 has been shown to physically associate with Cdk3, Cdk5, and c-
132 Abl (Sato et al., 2002). Moreover, forced expression of Cables2 induced apoptotic cell death

133 in both a p53-dependent manner and a p53-independent manner *in vitro* (Matsuoka et al.,
134 2003). The *Cables2* gene is known to be expressed in a variety of adult mouse tissues,
135 including the brain, but the *in vivo* role of this gene has yet to be explored.

136 To elucidate the role of *Cables2* *in vivo*, we generated *Cables2*-deficient mice and
137 found that *Cables2* deficiency caused post-gastrulation embryonic lethality. The mutant
138 embryos progress to gastrulation, but then arrest, and fail to grow. Analysis of gene
139 expression patterns revealed that AVE and PS formation is impaired in *Cables2*-deficient
140 embryos. The expression of both positive and negative components of the Nodal and Wnt
141 signalling pathways are altered at the onset of gastrulation in the mutant embryos. By
142 comparison with many other mouse mutant phenotypes, these defects may be anticipated to
143 give rise either to highly dysmorphic embryos or to embryos with patterning defects. Instead,
144 the *Cables2*-deficient embryos fail to thrive once gastrulation begins but retain the egg
145 cylinder morphology of the early gastrula. This suggests multiple roles for *Cables2* during
146 the immediate post-implantation period. This hypothesis is supported by the ubiquitous
147 expression of *Cables2* and by tetraploid complementation analyses which demonstrate that
148 *Cables2* functions in visceral endoderm (VE) for AVE and PS formation, whereas epiblast
149 expression of *Cables2* regulates embryo growth. We further demonstrated that *Cables2* can
150 physically interact with key mediators of the canonical Wnt and Nodal pathways (β -catenin
151 and Smad2 respectively) and augment transcriptional activity of these pathways in cell-based
152 reporter assays. These findings provide novel insights into the essential role of *Cables2* in the
153 early embryonic development in mice.

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155 RESULTS

156 Expression of *Cables2* during early mouse development

157 *Cables2* is widely expressed at equivalent levels in mouse tissues, including the brain, heart,
158 muscle, thymus, spleen, kidney, liver, stomach, testis, skin, and lung (Sato et al., 2002). We
159 first investigated the expression of *Cables2* in mouse embryonic stem cells (ESCs),
160 blastocysts, and embryos at E7.5 by reverse transcription polymerase chain reaction (RT-
161 PCR). The results indicated that *Cables2* was expressed in all three stages of early
162 development (**Figure 1A**). To confirm *Cables2* gene expression in mouse embryogenesis,
163 localization of *Cables2* mRNA expression was examined in embryos by WISH (**Figure**
164 **1B–F**). The data for the whole embryo and transverse sections showed that *Cables2* was
165 expressed ubiquitously at E6.5 (**Figure 1B and C**). *Cables2* was detected in both extra- and
166 embryonic parts at E7.5 (**Figure 1D**) and strongly expressed in the allantois and heart-field at
167 E8.5 (**Figure 1E**). At E9.5, the whole embryo and extraembryonic tissues, including the yolk
168 sac, expressed *Cables2* (**Figure 1F**). Overall, these data indicate that *Cables2* is expressed
169 ubiquitously during early development, including throughout gastrulation in mouse embryos.

170 Early embryonic lethality of *Cables2* deficiency

171 Next, we generated *Cables2*-deficient mice to investigate the physiological role of *Cables2* *in*
172 *vivo*. *Cables2* heterozygous mice on an inbred C57BL/6N genetic background were produced
173 using conventional aggregation with *Cables2*-targeted ES cell clones. While the
174 heterozygotes were viable and fertile, no homozygous *Cables2*-deficient mice were observed
175 following intercrossing heterozygous mice (**Table 1, Figure 1—figure supplement 1A**). To
176 identify the critical point in development at which *Cables2* is essential for survival, embryos
177 were collected and genotyped at various time points during embryonic development (**Table**
178 **1**). Homozygous *Cables2* mutant mice were detected in Mendelian ratios at E6.5–E9.5 but no

179 homozygous embryos were observed at or beyond E12.5, indicating that *Cables2*-deficient
180 mice die and are resorbed between E9.5 and 12.5 (**Table 1, Figure 1—figure supplement**
181 **1B**). All of the *Cables2*-deficient embryos collected at E7.5–9.5 were considerably smaller
182 than their wild-type littermates and did not progress beyond the cylindrical morphology of
183 the wild-type early-mid-gastrula (**Table 1, Figure 2A–D**). Considerably small *Cables2*^{-/-}
184 embryos had barely progressed beyond E8.5 (**Figure 2B**). In section, it was apparent that
185 E7.5 homozygous mutant embryos lacked pattern and instead resembled wild-type embryos
186 in which the primitive streak is just beginning to form (i.e. E6.5 embryos) in both
187 morphology and size (**Figure 2E and F**). In contrast, all embryos recovered at E6.5 were
188 morphologically indistinguishable from their wildtype littermates (**Table 1**). Histological
189 analyses confirmed that pre-streak stage (E6.0) *Cables2*^{-/-} embryos were structurally normal,
190 exhibiting a normal-sized epiblast, extraembryonic ectoderm, and primitive endoderm
191 (**Figure 2G–H**). These results suggest that *Cables2* lost-of-function causes growth and
192 patterning arrest early in gastrulation accompanied by post-gastrulation embryonic lethality.

193 **Normal cell proliferation and death status in *Cables2*-deficient embryos at E6.5**

194 Cell proliferation and apoptotic cell death are key events during development. To clarify the
195 cell growth status, we performed EdU assay and measured the percentage of EdU-positive
196 cells. There was no significant difference in the percentage of proliferation cells between
197 wild-type and *Cables2*^{-/-} embryos at E6.5 (**Figure 2—figure supplement 1A–C**).
198 Furthermore, a simultaneous TUNEL assay was performed to determine whether the reduced
199 size of *Cables2*-deficient embryos could be attributed to increased programmed cell death.
200 Although apoptotic cells were detected in both the epiblast and embryonic VE, the average
201 percentage of dead cells in *Cables2*^{-/-} embryos was not significantly different from that in
202 wild-type embryos (**Figure 2—figure supplement 1D–H**). These results suggest that cell
203 proliferation and apoptotic cell death are normal in *Cables2*-deficient embryos until E6.5.

204 **Impaired formation of PS and A–P axis in *Cables2* deficiency**

205 To characterize the phenotype of *Cables2*-deficient embryos, we first analysed the expression
206 of *Brachyury* (*T*). Prior to gastrulation, *T* transcripts are first detected in a ring at the
207 embryonic/extraembryonic junction, whereas once gastrulation is initiated they are found in
208 the PS and nascent mesoderm and subsequently in the axial mesendoderm (Wilkinson et al.,
209 1990). It therefore serves as a marker of the transition from the P-D to A-P axis. At E6.5,
210 *Cables2*^{-/-} embryos exhibited normal spatial *T* expression with decreased signal intensity
211 relative to wild-type embryos (**Figure 3A and B**). By E7.5, *T* transcripts were observed in
212 the PS of the *Cables2*^{-/-} embryos, but the transcripts did not extend to the distal point of the
213 embryo and there was no signal in the axial mesendoderm (**Figure 3I and J**). To confirm the
214 abnormal PS formation in *Cables2*^{-/-} embryos, we further investigated the expression of *Fgf8*,
215 a member of fibroblast growth factor family expressed in the PS (Crossley and Martin,
216 1995), and found that *Fgf8* was decreased in mutant embryos at E6.5 (**Figure 3E and F**).

217 PS formation and progression is dependent upon canonical Wnt signalling driven by
218 the expression of *Wnt3* in the proximal-posterior epiblast and PVE (Mohamed et al., 2004;
219 Yoon et al., 2015a) and *T* is a direct target of this Wnt activity (Arnold et al., 2000). WISH
220 showed that expression of *Wnt3* was also impaired in the proximal-posterior part of epiblast
221 and the PVE of E6.5 *Cables2*^{-/-} mutants although the expression remained in the proximal
222 epiblast adjacent to the extraembryonic ectoderm (ExE) (**Figure 3C and D**). To assess the
223 functional significance of altered *Wnt3* expression, *Cables2*-deficient animals were crossed
224 with the TOPGAL transgenic mice, which express the β -galactosidase under the control of
225 three copies of the Wnt-specific LEF/TCF binding sites (Moriyama et al., 2007). In wild-type
226 E7.5 embryos carrying TOPGAL, the β -galactosidase was detected in the fully elongated
227 primitive streak and in the adjacent posterior tissues as expected (**Figure 3G**). In contrast,
228 E7.5 *Cables2*^{-/-} embryos carrying TOPGAL showed the weak expression of β -galactosidase

229 only in proximal-posterior PS (**Figure 3H**). Meanwhile, *Bmp4* is known to be expressed in
230 the ExE of the post-implantation mouse embryo where it promotes *Wnt3* expression in the
231 proximal epiblast for PS formation. WISH analyses showed that *Bmp4* was similarly
232 expressed in the ExE of *Cables2*^{-/-} embryos compared with wild-type embryos at E6.5
233 (**Figure 3K and L**), suggesting that the ExE is normally developed in mutant embryos at
234 least until E6.5. These findings are consistent with *Cables2* promoting the formation of *Wnt3*-
235 expressing PVE to induce and maintain PS formation.

236 Given that apparent impairment of proximal/posterior development in the *Cables2*^{-/-}
237 embryos, we next examined markers of the distal/anterior components of the axis. *Lhx1*,
238 which is normally expressed in the AVE and nascent mesoderm of wild-type embryos, was
239 accumulated in the distal part of E6.5 *Cables2*-deficient embryos (**Figure 3M and N**),
240 whereas the normal formation of extraembryonic VE in mutant embryo was confirmed by the
241 expression of *Sox17* (**Figure 3O and P**). Our data also showed that *Cerberus 1* (*Cer1*) and
242 *Lefty1*, antagonists of Nodal signalling, were expressed at lower levels in *Cables2*^{-/-} embryos
243 compared to the wild-type at E6.5 (**Figure 3Q–T**). Furthermore, WISH analyses
244 demonstrated absent or decreased expression of *Lefty2* in the posterior epiblast of *Cables2*-
245 deficient embryos at E6.5 (**Figure 3S and T**). Taken together, the results of WISH analyses
246 suggest that *Cables2* depletion impairs the correct AVE formation at the gastrulation stage.

247 **Activation and interaction of Cables2 with β -catenin**

248 Accumulating evidences have suggested that Wnt/ β -catenin signalling is implicated in the
249 formation of AVE (Engert et al., 2013; Huelsken et al., 2000; Lickert et al., 2002) and it is
250 known that the Cables2 paralog (*Cables1*) can bind to β -catenin (Rhee et al., 2007). We
251 therefore examined whether Cables2 facilitates β -catenin activity at Wnt target sites and
252 physically interacts with β -catenin. The results indicated that Cables2 activated β -

253 catenin/TCF-mediated transcription *in vitro* with an almost two-fold increase in relative
254 TOP/FOP luciferase activity (**Figure 4A**). Moreover, co-IP using N-terminal FLAG-tagged
255 Cables2 (FLAG-Cables2)-transfected 293FT cell lysates with or without exogenous β -catenin
256 indicated that β -catenin was present in the precipitated complexes with Cables2 (**Figure 4B**
257 **and Figure 4–figure supplement 1**). These data suggest that Cables2 can physically
258 associated with β -catenin and increases its transcriptional activity at Wnt-responsive genes.

259 **Activation and interaction of Cables2 with Smad2**

260 Beside β -catenin, proper activation of the Nodal/Smad2 signalling in VE is required for the
261 AVE formation (Takaoka and Hamada, 2012). Thus, we conducted *in vivo* and *in vitro*
262 experiments to examine whether Cables2 impacts Nodal/Smad2 signalling. WISH analysis
263 revealed the normal expression of *Nodal* in *Cables2*^{-/-} embryos at E6.0 (**Figure 5A and B**).
264 Subsequently *Nodal* expression normally localizes to the nascent PS and the posterior
265 epiblast at E6.5, however, in E6.5 *Cables2*-deficient embryos *Nodal* expression remains
266 throughout the epiblast (**Figure 5C and D**). To determine whether this mislocalisation of
267 *Nodal* expression altered Anterior axis formation, we examined expression of *Foxa2*, a
268 downstream target of Nodal/Smad2 signalling (Brennan et al., 2001; Liu et al., 2004), which
269 is an early marker of Anterior axis formation and necessary for mesendodermal specification
270 (Dufort et al., 1998). As the result, *Foxa2* expression is downregulated in E7.5 *Cables2*^{-/-}
271 embryos (**Figure 5E and F**). In addition, we examined the expression of neuroectoderm
272 markers *Sox2* and *Otx2*. WISH revealed that the localized expression of *Sox2* to the anterior
273 embryonic part was decreased in *Cables2*^{-/-} embryos (**Figure 5G and H**), whereas *Otx2* was
274 ectopically expressed in the posterior region of *Cables2*^{-/-} embryos at E7.5 (**Figure 5I and J**).
275 These results, in conjunction with the AVE analyses, support our notion that loss of *Cables2*

276 also impairs distal/anterior axis formation and suggest that Cables2 is involved in
277 reinforcement of Nodal/Smad2 signalling in the AVE.

278 We next investigated whether Cables2 enhanced the transcriptional activity of Smad2 by
279 luciferase reporter assay with the ARE-luc vector, which expresses firefly luciferase in a
280 Smad2- and FAST1-dependent manner. We co-transfected 293FT cells with the ARE-luc,
281 FAST1 expression vectors and a constitutive-active mutant form of TGF- β receptor together
282 with an empty vector or FLAG-Cables2 expression vector. The data indicated that forced
283 expression of Cables2 facilitated Smad2 activity in 293FT cells (**Figure 5K**). Intriguingly,
284 Cables2 had no effect on luciferase activity of the Smad3/4-specific reporter vector
285 (CAGA)₉-luc (Dennler et al., 1998) (**Figure 5K**), suggesting that Cables2 does not function
286 as an activator for Smad3. Luciferase assays also revealed that Cables1 had no effect on the
287 transcriptional activities of both Smad2 and Smad3 (**Figure 5K**). These findings suggest that
288 the promoting activity on Smad2 function is a unique property of Cables2 rather than a
289 conserved function of the Cables family. We further conducted co-IP experiments of Cables2
290 with exogenous and endogenous Smad2 and found that Cables2 physically interacted with
291 Smad2 in 293FT cells (**Figure 5L–N and Figure 5—figure supplement 1**). Moreover, co-IP
292 experiments with fractionated extracts demonstrated that FLAG-Cables2 and HA-Smad2
293 were precipitated from both cytoplasmic and nuclear extracts (**Figure 5L–N**), suggesting that
294 Cables2 forms a complex with Smad2 in both cytoplasm and nucleus. These results suggest
295 that Cables 2 can act as a positive regulatory factor of Smad2.

296 **Facilitation of *Nanog* expression and its promoter activity by *Cables2***

297 To further investigate a functional relationship between Cables2 and Smad2 in epiblast, we
298 established *Cables2*-deficient ESCs from homozygous embryos at E3.5 and induced their
299 differentiation into epiblast-like cells (EpiLCs). The morphology, proliferation, and
300 expression of pluripotency genes in *Cables2*-deficient ESCs were similar to those in wild-

301 type ESCs (**Figure 6—figure supplement 1A**). Both types of ESCs exhibited similar
302 morphological changes after EpiLC induction with activin and bFGF (**Figure 6—figure**
303 **supplement 1B**). *Nanog* plays a crucial role in early mouse embryonic development. The
304 expression of *Nanog* has been observed in the cells of the inner cell mass (ICM) of the E3.5
305 blastocyst and the epiblast in the egg cylinder at the PS stage (Chambers et al., 2003; Hatano
306 et al., 2005). The cytokine dependency of *Nanog* expression is known to switch from
307 LIF/Stat in the ICM to Nodal/Smad2 in the epiblast. It is noteworthy that *Nanog* expression is
308 highly dependent on Smad2 but not on Smad3 (Sakaki-Yumoto et al., 2013; Sun et al., 2014).
309 Since our luciferase assay revealed that *Cables2* functioned as an activator specific for Smad2
310 (**Figure 5K**), we focused on and analysed the expression level and promoter activity of
311 *Nanog* in EpiLCs lacking *Cables2*. Interestingly, quantitative RT-PCR showed that *Nanog*
312 mRNA level was decreased by approximately 40% in *Cables2*-deficient EpiLCs (**Figure**
313 **6A**). Moreover, luciferase assay demonstrated that *Cables2* deficit reduced *Nanog* promoter
314 activity in EpiLCs (**Figure 6B**). Intriguingly, *Cables2* physically interacted with Oct4 that is
315 a transcription factor activating *Nanog* and PS gene promoters synergistically with Smad2
316 (**Figure 6—figure supplement 2**). Together with the previous findings (**Figure 5K and L**)
317 (Funa et al., 2015; Sakaki-Yumoto et al., 2013; Sun et al., 2014), the results suggest that
318 *Cables2* positively regulates *Nanog* expression via the interaction with Smad2 and Oct4 in
319 EpiLCs.

320 To gain insight into changes in global gene expression in *Cables2*-deficient EpiLCs,
321 we performed RNA-seq and gene enrichment analyses for Gene ontology (GO) terms and
322 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways using the DAVID
323 Bioinformatics Resources (Huang et al., 2009a; Huang et al., 2009b). Notably, the analyses
324 showed GO term enrichments related to “nervous system development” and “negative
325 regulation of cell proliferation” and KEGG pathway enrichments related to several signalling

326 pathway including “p53 signalling pathway” among 122 out of 125 upregulated genes in
327 *Cables2*-deficient EpiLCs (**Figure 6—figure supplement 3A and B**). While, 52 out of 59
328 downregulated genes in *Cables2*-deficient EpiLCs represented GO terms related to
329 “proximal/distal pattern formation”, “positive regulation of cell proliferation”, and “male
330 gonad development” and KEGG pathway related to “signalling pathways regulating
331 pluripotency of stem cells” (**Figure 6—figure supplement 4A and B**).

332 Previous studies have addressed *Nanog* expression in mouse embryos at early
333 embryonic stages by immunostaining and WISH. The data indicated that *Nanog* is expressed
334 in the whole region of E5.5 epiblasts, but only in the posterior region of E6.5 and E7.5
335 epiblast (Hart et al., 2004; Hatano et al., 2005). Consistent with these previous reports, our
336 WISH data showed that *Nanog* was expressed in the posterior region of wild-type embryos at
337 E6.5 (**Figure 6C**). In contrast, *Cables2*-deficient embryos showed only a low level of *Nanog*
338 gene expression over the whole epiblast region at E6.5 (**Figure 6D**). On the other hand, the
339 pluripotency marker, *Oct4*, was expressed normally in *Cables2*^{-/-} mutants at E6.5 (**Figure 6E**
340 **and F**). To further confirm the expression pattern of *Nanog* in the E6.5 embryo, we utilized
341 *Nanog*-GFP transgenic mice (Okita et al., 2007). Mice carrying the *Nanog*-GFP reporter were
342 crossed with *Cables2*-deficient heterozygotes to obtain *Cables2*^{-/-} reporter embryos. At E6.5,
343 *Cables2*^{-/-} embryos showed no elevation of *Nanog*-GFP expression at the PS (**Figure 6G and**
344 **H**). Nevertheless, there was no difference in GFP expression between embryos of the same
345 litter at E5.5 (**Figure 6I and J**), suggesting no detectable phenotype of *Nanog* before PS
346 formation. Overall, loss of *Cables2* leads to downregulated *Nanog* expression at the start of
347 gastrulation.

348 **Requirement of *Cables2* in both epiblast and VE for the proper gastrulation in mice**

349 To determine whether *Cables2* is required in the VE, the epiblast, or both, chimera analysis
350 was performed using tetraploid wild-type embryos and *Cables2*^{-/-} ESCs. In tetraploid

351 complementation chimera has the advantage that the host tetraploid embryos can only
352 contribute to primitive endoderm derivatives and trophoblast compartment of the placenta,
353 whereas epiblast components are completely derived from ESCs (Tanaka et al., 2009).
354 Tetraploid wild-type morula was aggregated with *Cables2*^{-/-} ESCs to produce chimera in
355 which the *Cables2* was exclusively deleted in epiblast but not in the VE (*Cables2* VE rescue
356 chimera) (**Figure 7A**). *YFP* reporter gene was inserted into *ROSA26* locus of *Cables2*^{-/-} ESC
357 to construct *Cables2*^{-/-}; *ROSA26*^{YFP/+} ESC which gives the advantage for embryo visualisation
358 and imaging. We collected the *Cables2* chimeric embryos at the indicated embryonic days
359 and analysed the phenotype (**Table 2**). Like *Cables2*^{-/-} embryos, epiblast of *Cables2* VE
360 rescue embryos were smaller in size than that of control wild-type chimera littermates at E7.5
361 and E8.5 (**Figure 7B–E**). However, *T* and *Foxa2* were properly expressed in the posterior
362 epiblast and the anterior midline mesendoderm of E7.5 *Cables2* VE rescue embryos,
363 respectively (**Figure 7F and G**), suggesting that the embryos with *Cables2*^{-/-} epiblast and
364 wild-type VE can form the PS and A–P axis. Importantly, some *Cables2* VE rescue chimeras
365 developed up to E8.5 exhibited the clear structure of head-fold, node and tail bud although
366 embryo size was still extremely smaller compared with wild-type chimeras (**Figure 7H**).
367 These results suggest that *Cables2* in the VE plays an essential role in the formation of the PS
368 and AVE while *Cables2* in the epiblast is essential for epiblast growth.

369 To confirm the essential function of *Cables2* in epiblast, tetraploid wild-type morula
370 was aggregated with *Cables2*^{-/-}; *ROSA26*^{YFP/+}; *CAG-tdTomato-2A-Cables2* ESCs to produce
371 *Cables2* VE and epiblast rescue chimera (*Cables2* VE & Epi rescue) (**Figure 7I**). *CAG-*
372 *tdTomato* fused *2A-Cables2* was randomly integrated into the genome of *Cables2*^{-/-}
373 *ROSA26*^{YFP/+} ESC to ubiquitously overexpress *Cables2* in epiblast and its derivatives. Red
374 fluorescence was detected in *Cables2*^{-/-}; *ROSA26*^{YFP/+}; *CAG-tdTomato-2A-Cables2* ESCs,
375 suggesting that *tdTomato-2A-Cables2* was correctly translated in the cells (**Figure 7J–Q**). As

376 the result, *Cables2* VE & Epi rescue chimeras were indistinguishable from wild-type chimera
377 littermates at all time points examined (**Figure 7J–Q**). Of note, the lethal phenotype of
378 *Cables2*^{-/-} embryos during gastrulation was rescued by the exogenously expressed *Cables2*.
379 Altogether, the findings from chimera experiments indicate that *Cables2* in both epiblast and
380 VE is required for early embryonic development in mice.
381

382 DISCUSSION

383 In this study, we provided the first evidence regarding the physiological roles of *Cables2* in
384 mice. We demonstrated that *Cables2* is expressed ubiquitously during early embryonic
385 development and that disruption of the *Cables2* gene caused defective A–P axis formation,
386 growth retardation and post-gastrulation embryonic lethality. Many other mouse mutants with
387 impaired A–P axis formation either become highly dysmorphic, or complete gastrulation
388 without growth retardation and instead exhibit patterning defects. The divergent phenotype
389 that results from *Cables2* deficiency therefore suggests it may play multiple roles during
390 early mouse development. Tetraploid complementation experiments demonstrated that the
391 A–P axis and growth phenotypes can indeed be separated. The defective A–P axis formation
392 can be attributed to a requirement for *Cables2* expression in the VE of the mouse embryo,
393 whereas the growth retardation is caused by loss of *Cables2* function in the epiblast.
394 Similarly, at the molecular level *Cables2* may play multiple roles. We show here that *Cables2*
395 can interact with pivotal intracellular components of both the Nodal and Wnt pathways.

396 *Cables2*-deficient embryos show a defect in the establishment of the AVE as judged
397 by the downregulation of *Cer1* and *Lefty1* in this structure at E6.5 (**Figure 3Q–T**). The
398 expression of these genes, as well as other aspects of AVE formation, are Nodal/Smad2
399 dependent (Brennan et al., 2001; Conlon et al., 1994; Kumar et al., 2015; Nomura and Li,
400 1998; Waldrip et al., 1998; Weinstein et al., 1998). Notably, chimeric embryo experiments
401 have revealed that the Nodal pathway is required in the VE (but not epiblast) to ensure AVE
402 production (Brennan et al., 2001). Moreover, similar experiments have shown that, in the VE,
403 Smad2 alone transduces the Nodal signal required for AVE formation (Heyer et al., 1999;
404 Waldrip et al., 1998) consistent with the fact that Smad3 is not expressed in this tissue
405 (Tremblay et al., 2000). In contrast, Smad3 can compensate for the role of Smad2 in Nodal
406 signalling in the epiblast (Brennan et al., 2001; Dunn et al., 2005; Tremblay et al., 2000). The

407 chimeric experiments conducted here show that, like Nodal and Smad2, Cables2 is also
408 required in the VE to ensure correct AVE formation (**Figure 7A–H**). Furthermore, we
409 demonstrated that Cables2 can physically associated with Smad2 and enhanced the
410 Smad2/FAST1-mediated transcription when overexpressed in cells (**Figure 5K and L**).
411 During murine development, Nodal expression in the VE (but not epiblast) utilises an
412 intronic enhancer that is Smad2/FAST1 dependent (Norris et al., 2002). Overall, these data
413 are consistent with Cables2 interacting with the Nodal/Smad2 pathway in the VE to correctly
414 establish the AVE.

415 In embryos deficient for *Cables2*, Nodal expression does not become upregulated at
416 the prospective posterior of the embryo (**Figure 5C and D**). At this stage of normal
417 development, Nodal signals from the epiblast are required to promote the expression of
418 posterior genes such as *Wnt3* and *T*, both of which are downregulated in *Cables2*-deficient
419 embryos, as is TCF-mediated transcription measured by the TOPGAL reporter mouse
420 (**Figure 3A–D, G, H**). This posterior Wnt/ β -catenin activity is required for primitive streak
421 formation and elongation. The truncated primitive streak and derivatives seen in the *Cables2*
422 mutant embryos (**Figure 3I, J and 5E, F**) are therefore consistent with the decreased
423 posterior Wnt activity in these embryos. Both of these aspects of the phenotype are rescued
424 when *Cables2* is expressed in the VE alone, implying that in these embryos Wnt activity is
425 elevated to a level consistent with relatively normal streak formation and elongation. It is
426 possible that the VE source of *Cables2* elevates the posterior Wnt/ β -catenin activity directly
427 (via Cables2/ β -catenin interaction), or indirectly via the Nodal/Smad2 pathway and
428 associated upregulation of *Wnt3* expression.

429 Genetic experiments that ablate *Wnt3* activity in either the VE or epiblast alone (and
430 therefore reduce overall posterior Wnt signal) have shown that this activity regulates the
431 timing of primitive streak formation. Embryos in which VE *Wnt3* function is ablated have

432 delayed primitive streak formation but by E9.5 are indistinguishable from wild-type
433 littermates (Yoon et al., 2015a). When *Wnt3* function is removed from the epiblast, primitive
434 streak formation is delayed and by mid-gastrulation the embryos are highly dysmorphic with
435 the primitive streak bulging towards the amniotic cavity (Tortelote et al., 2013). In contrast,
436 *Cables2*-deficient embryos in which *Wnt3* expression and activity is reduced exhibit
437 primitive streak abnormalities but neither recover nor become highly dysmorphic. Instead,
438 they retain an egg-cylinder morphology and fail to grow. This suggests that the growth failure
439 of the *Cables2* is not caused by improper A–P axis specification and instead represents a
440 separate function of *Cables2*. This hypothesis is supported by the chimeric experiments that
441 demonstrate that *Cables2* expression in the VE is able to rescue the A–P axis, but not the
442 growth defects.

443 The underlying molecular cause of the growth defect in the *Cables2*-deficient
444 embryos remains unclear. We confirmed the requirement of *Cables2* in epiblast for proper
445 growth by tetraploid complementation analysis (**Figure 7I–Q**). Nodal signalling has shown
446 to be required for sustaining epiblast proliferation during egg cylinder stage in mice (Stuckey
447 et al., 2011; Yang et al., 1998). However, it is unlikely that the growth retardation of
448 *Cables2*-deficient embryos is associated with the Nodal/Smad2 signalling because epiblast
449 size is normal in *Smad2*-deficient mice due to functional compensation by Smad3 (Brennan
450 et al., 2001; Dunn et al., 2005; Tremblay et al., 2000). An alternative possibility is that
451 *Cables2* may function with other factors, e.g. BMP signalling-related proteins that is known
452 to be essential for epiblast proliferation (Mishina et al., 1995). However, proliferative defects
453 were apparent in the E6.5 embryos that lack the *Bmpr1* receptor (Mishina et al., 1995), unlike
454 in the *Cables2*-deficient embryos where no alterations in proliferation or cell death were
455 noted. On the other hand, analysis of global gene expression changes in *Cables2*-deficient
456 EpiLC showed enrichment of genes associated with “p53 signalling pathway” and “negative

457 regulation of cell proliferation” among upregulated genes in *Cables2*-deficient EpiLCs and
458 genes associated with “pluripotent of stem cells” and “positive regulation of cell
459 proliferation” among downregulated genes in *Cables2*-deficient EpiLCs. Moreover, the
460 marked downregulation of *Nanog* expression in EpiLCs was confirmed *in vivo* and reporter
461 assays in EpiLCs indicated *Nanog* expression is *Cables2*-dependent. Given that epiblast
462 expression of *Nanog* is known to be Nodal/Smad2-dependent (Sakaki-Yumoto et al., 2013;
463 Sun et al., 2014), it is possible that *Cables2* in the epiblast interacts with this pathway to
464 ensure *Nanog* expression. The possibility that loss of *Cables2* causes some dysregulation of
465 pluripotency and/or proliferation-related genes, including *Nanog* and *Cdkn1a/p21*, in epiblast
466 after E5.5 warrants further investigation.

467 To date, there is no report addressing the molecular function of *Cables2* *in vitro* and *in*
468 *vivo*. Analysis of the *Cables2* protein sequence using publicly available protein domain
469 prediction tools fails to predict any enzymatic, DNA-binding, nor transcription regulatory
470 domains. Thus, we speculate that *Cables2* functions as a bridging factor, or scaffold protein,
471 mediating interaction between transcription regulatory factors. A similar role for *Cables1* in
472 connecting CDKs and nonreceptor tyrosine kinases has been proposed. Indeed, our co-IP
473 experiments showed the interaction of *Cables2* with transcription regulatory factors, β -
474 catenin, Smad2 and Oct4, which are known to form a protein complex to activate the
475 promoter of common target genes (**Figure 4B, 5L and Figure 6—figure supplement 2**)
476 (Funa et al., 2015). We also demonstrated that *Cables2* interacted with Smad2 in nuclear and
477 cytoplasm (**Figure 5M and N**). These results suggest that *Cables2* functions as a nuclear
478 cofactor for Smad2 although the mechanism underlying enhancement of Smad2
479 transcriptional activity by *Cables2* remains to be elucidated. Interestingly, extracellular
480 signal-regulated kinase (ERK) promotes Smad2 transcriptional activity, but suppresses
481 Smad3 transcriptional activity by phosphorylation of their linker region in helper T cells

482 (Chang et al., 2011; Funaba et al., 2002; Yoon et al., 2015b). The linking function of *Cables2*
483 could promote complex formation between Smad2 and other transcription factors to form a
484 transcription complex or it could provide a platform for posttranslational modifiers such as
485 ERK.

486 In conclusion, *Cables2* plays an essential role in mouse embryogenesis and targeted
487 disruption of *Cables2* leads to post-gastrulation embryonic lethality. *Cables2* is required in
488 both the VE to promote axis formation and in the epiblast to promote continued growth of the
489 embryo. Our investigations support a role for *Cables2* in one or more of the signalling
490 pathways crucial for the development of the peri-implantation stage mouse embryo since it
491 can physically interact with both β -catenin and Smad2. *Cables2* may serve as a scaffold
492 protein that facilitates a variety of molecular interactions. Given the pleiotropic nature of the
493 *Cables2* null phenotype it is likely that further genetic and molecular analyses will uncover
494 additional roles for the protein.

495

496 **METHODS**

497 **Animals and husbandry**

498 ICR mice were purchased from CLEA Japan Co. Ltd. (Tokyo, Japan); C57BL/6N mice were
499 purchased from Charles River Laboratory Japan Co. Ltd (Yokohama, Japan). For production
500 of staged embryos, the day of fertilization as defined by the appearance of a vaginal plug was
501 considered to be embryonic day 0.5 (E0.5). Animals were kept in plastic cages (4 – 5 mice
502 per cage) under specific pathogen-free conditions in a room maintained at $23.5^{\circ}\text{C} \pm 2.5^{\circ}\text{C}$
503 and $52.5\% \pm 12.5\%$ relative humidity under a 14-h light:10-h dark cycle. Mice had free
504 access to commercial chow (MF; Oriental Yeast Co. Ltd., Tokyo, Japan) and filtered water
505 throughout the study. Animal experiments were carried out in a humane manner with
506 approval from the Institutional Animal Experiment Committee of the University of Tsukuba
507 in accordance with the Regulations for Animal Experiments of the University of Tsukuba and
508 Fundamental Guidelines for Proper Conduct of Animal Experiment and Related Activities in
509 Academic Research Institutions under the jurisdiction of the Ministry of Education, Culture,
510 Sports, Science, and Technology of Japan.

511 **Generation of *Cables2*-deficient mice**

512 The targeted ES cell clone *Cables2*^{tm1(KOMP)vlcg} was purchased from KOMP (project ID:
513 VG1608, clone number: 16085A-D3). To generate *Cables2*-deficient mice, ES cells were
514 aggregated with the wild-type morula and transferred to pseudopregnant female mice. Male
515 chimeras that transmitted the mutant allele to the germ line were mated with wild-type
516 females to produce *Cables2*-deficient mice with the C57BL/6N background. Adult mice were
517 genotyped using genomic DNA extracted from the tail. For whole-mount *in situ*
518 hybridization, embryos were genotyped using a fragment of yolk sac and Reichert membrane.
519 Samples were dispensed into lysis solution (50 mM Tris-HCl, pH 8.5, 1 mM EDTA, 0.5%

520 Tween 20) and digested with proteinase K (1 mg/mL) at 55°C for 2 hours, inactivated at 95
521 °C for 5 minutes, and then subjected to PCR. For paraffin slides, embryos were genotyped
522 using tissue picked from sections and digested directly with proteinase K (2 mg/mL) in PBS.
523 For others experiments, after collecting data, the whole embryos were used for genotyping.
524 Genotyping PCR was performed with AmpliTag Gold 360 Master Mix (Thermo Fisher
525 Scientific K.K., Tokyo, Japan) using the following primers: *Cables2* D3-1: 5'-
526 ACTGCAGAAGCTGGAGGAAA-3'; *Cables2* D3-2: 5'-TCAAGGTGTCTGCCCTATCC-3';
527 *Cables2* D3-3: 5'-AGGGGATCCGCTGTAAGTCT-3'.

528 ***Nanog*-GFP reporter mice**

529 *Nanog*-GFP transgenic mice (RBRC02290) were obtained from Riken BioResource Center
530 (BRC; Tsukuba, Japan). Animals were kept and maintained under the same conditions as
531 described above. To produce the *Nanog*-GFP reporter in the homozygous *Cables2*
532 background, *Cables2* heterozygotes were first crossed with *Nanog*^{GFP/+} to obtain
533 *Cables2*^{+/-}:*Nanog*^{GFP/+}. Subsequently, to obtain *Cables2*^{-/-}:*Nanog*^{GFP/+} embryos, *Cables2*
534 heterozygotes were mated with *Cables2*^{+/-}:*Nanog*^{GFP/+} mice and the embryos were collected
535 at E6.5 or E5.5. All embryos were then genotyped using both *Cables2* genotyping primers
536 and the GFP following primers: GFP F: 5'-ACGTAAACGGCCACAAGTTC-3'; GFP R: 5'-
537 TGCTCAGGTAGTGGTTGTCG-3'.

538 **TOPGAL reporter mice**

539 B6.Cg-Tg(TOPGAL) transgenic mice carrying LEF/TCF reporter of Wnt/ β -catenin
540 signalling were used for visualizing Wnt signalling pathway *in vivo*. TOPGAL mice were
541 obtained from Riken BRC (RBRC02228). Animals were kept and maintained under the same
542 conditions as described above. To produce the TOPGAL reporter in the homozygous *Cables2*
543 background, TOPGAL heterozygotes were crossed with *Cables2* heterozygotes subsequently

544 and finally, homozygous *Cables2* carrying TOPGAL transgene were collected at E7.5
545 together with littermates. All embryos were stained S-gal (Sundararajan et al., 2012) and then
546 genotyped using both *Cables2* genotyping primers and TOPGAL following primers:
547 TOPGAL-TK F: 5'-CGAGGTCCACTTCGCATATT-3'; LacZ R: 5'-
548 TATTGGCTTCATCCACCACA-3'.

549 **Cell culture**

550 NIH3T3, Cos-7, 293T cells were obtained from The American Type Culture Collection
551 (Manassas, Virginia) and 293FT cells were purchased from Thermo Fisher Scientific. These
552 cells were authenticated by the suppliers and no mycoplasma contamination was detected by
553 DAPI staining. Cells were cultured in Dulbecco's modified Eagle's medium (DMEM)
554 supplemented with 10% heat-inactivated fetal bovine serum. Mouse embryonic stem cells
555 (ESCs) were maintained on 0.1% gelatine-coated dishes in mouse ESC medium consisting of
556 DMEM containing 20% knockout serum replacement (KSR; Thermo Fisher Scientific), 1%
557 non-essential amino acids (Thermo Fisher Scientific), 1% GlutaMAX (Thermo Fisher
558 Scientific), 0.1 mM 2-mercaptoethanol (Thermo Fisher Scientific), and leukemia inhibitory
559 factor (LIF)-containing conditioned medium, supplemented with two chemical inhibitors (2i),
560 i.e., 3 μ M CHIR99021 (Stemgent inc., Cambridge, Massachusetts) and 1 μ M PD0325901
561 (Stemgent). The epiblast-like cells (EpiLCs) were induced by plating 2.0×10^5 ESCs on
562 human fibronectin (Corning inc., Corning, New York)-coated 6-well plates in N2B27-
563 containing NDiff 227 medium (Takara Bio Inc., Shiga, Japan) supplemented with 20 ng/mL
564 activin A, 12 ng/mL bFGF, and 1% KSR (Guo et al., 2009). All cells were cultured in an
565 atmosphere of 5% CO₂ at 37°C.

566 **RT-PCR, RT-qPCR and RNA-seq**

567 Cultured ES cells, about 130 blastocysts, and 21 embryos at E7.5 were collected. Total RNAs
568 from blastocysts and embryos were extracted using Isogen (Nippon Gene Co., Ltd., Tokyo,
569 Japan). RNA from ESCs was collected using an RNeasy Mini Kit (Qiagen K.K., Tokyo,
570 Japan). The cDNA was synthesized using Oligo-dT primer (Thermo Fisher Scientific) and
571 SuperScript III Reverse Transcriptase (Thermo Fisher Scientific) in a 20- μ L reaction mixture.
572 The primers were: *Cables2* F: 5'-CACCAGCTGGCACAGAACTA-3'; *Cables2* R: 5'-
573 GCTTGAGGATCAAGTGTGGTTCAAAGTC-3'; Glyceraldehyde-3-phosphate
574 dehydrogenase (*Gapdh*) F: 5'-ACCACAGTCGATGCCATCAC-3'; *Gapdh* R: 5'-
575 TCCACCACCCTGTTGCTGTA-3'.

576 RT-qPCR was performed using SYBR Premix Ex Taq II (Takara) and the Thermal
577 Cycler Dice Real Time System (Takara) according to the manufacturer's instructions. The
578 *Nanog* gene expression level was normalized to the endogenous *Gapdh* expression level. The
579 primers used were: *Nanog* F: 5'-CCTGAGCTATAAGCAGGTTAAG-3'; *Nanog* R: 5'-
580 GTGCTGAGCCCTTCTGAATC-3'; *Gapdh* qPCR F: 5'-TGGAGAAACCTGCCAAGTATG-
581 3'; *Gapdh* qPCR R: 5'-GGAGACAACCTGGTCCTCAG-3'.

582 RNA sequencing analysis was performed by Tsukuba i-Laboratory LLP as previously
583 described (Ohkuro et al., 2018). Briefly, total RNAs were extracted from wild-type and
584 *Cables2*-deficient EpiLCs at 2 days post-induction ($n = 3$) using RNeasy Plus Mini Kit
585 (Qiagen). RNA quality was evaluated using Agilent Bioanalyzer with RNA 6000 Pico kit
586 (Agilent Technologies Japan, Ltd., Tokyo, Japan). An amount of 500 ng total RNA was used
587 for RNA-seq library preparation with NEB NEBNext rRNA Depletion Kit and ENBNext
588 Ultra Directional RNA Library Prep Kit (New England Biolabs Japan Inc., Tokyo, Japan);
589 2×36 base paired-end sequencing was performed with NextSeq500 (Illumina K.K., Tokyo,
590 Japan) by Tsukuba i-Laboratory LLP (Tsukuba, Japan). The RNA-seq data have been
591 deposited in the NCBI GEO database (accession no. GSE120366). The DAVID

592 Bioinformatics Resources was used for GO terms and KEGG pathway enrichment analyses
593 of differentially expressed genes with at least 2-fold change and FDR < 0.05.

594 **Vector construction**

595 Part of *Cables2* cDNA containing exons 1 and 2 was cloned in-frame into pBlueScript KS+
596 at the *Bam*HI site, and the fragment containing exons 3 – 10 was cloned into the pcDNA3
597 vector at the *Bam*HI site. These fragments were obtained and amplified from a mouse embryo
598 E7.5 cDNA library and sequenced. The part covering *Cables2* exons 1 and 2 was cut at the
599 *Afe*I site and ligated into the pcDNA3 vector containing exons 3 – 10. The full-length
600 *Cables2*, FLAG-tagged *Cables1*, FLAG-tagged *Cables2*, and mouse Kpna (Importin α) NLS-
601 fused FLAG-tagged *Cables2* genes were cloned into the *Eco*RI site of pCAG vector. The
602 full-length *Smad2* and *Pou5f1* cDNA was amplified by PCR from mouse B6 ESC cDNA
603 library and cloned into the pCAG vector. A 1.5-kb *Cables2* riboprobe was prepared by
604 amplification from the full-length cDNA template with the pcDNA3 backbone, synthesized
605 with Sp6 polymerase, and labelled with digoxigenin as a riboprobe.

606 A ROSA26 knock-in vector was constructed by insertion of CAG-Venus-IRES Pac
607 gene expression cassette (Khoa et al., 2016) into the entry site of pROSA26-1 vector (kindly
608 gifted from Philippe Soriano, Addgene plasmid # 21714) (Soriano, 1999). The *Cables2*^{-/-};
609 *ROSA*^{YFP/+} was generated by electroporation of the ROSA26 knock-in vector (pROSA26-
610 CAG-Venus-IRES Pac) into *Cables2*^{-/-} ESCs. The CAG-tdTomato-2A and 3xFLAG
611 sequences were inserted in the upstream and downstream of *Cables2* cDNA, respectively, to
612 make CAG-tdTomato-2A-Cables2-3xFLAG vector. The expression of tdTomato and FLAG-
613 tagged *Cables2* in the CAG-tdTomato-2A-Cables2 vector-transfected 293FT cells were
614 evaluated by fluorescent microscopy and western blot analysis with anti-FLAG antibody,
615 respectively (data not shown).

616 **Production of *Cables2* rescue chimeras by Tetraploid complementation assay**

617 Tetraploid (4n) wild-type embryos were made by electrofusing diploid (2n) embryos at two-
618 cell-stage and cultured up to morula stage. The 4n wild-type morula were aggregated with
619 *Cables2*^{-/-}; *ROSA*^{YFP/+} or *Cables2*^{-/-}; *ROSA*^{YFP/+}; *CAG-tdTomato-2A-Cables2-3xFLAG* ESCs
620 to form blastocyst chimeras. B6N wild-type ESC was used as a control for tetraploid
621 complementation assay. To obtain comparable control embryos at each stage of development,
622 an equal number of control blastocyst chimeras were transferred together with *Cables2*^{-/-}
623 blastocyst chimeras to a pseudopregnant recipient mouse at E2.5. Embryos were recovered at
624 from E6.5 to E9.5 and the contribution of ESCs was evaluated by YFP or tdTomato
625 fluorescence signals.

626 **Whole-mount *in situ* hybridization (WISH)**

627 All embryos were dissected from the decidua in PBS with 10% fetal bovine serum and staged
628 using morphological criteria (Downs and Davies, 1993) or described as the number of days of
629 development. WISH was carried out following standard procedures, as described previously
630 (Rosen and Beddington, 1994). Briefly, embryos were fixed overnight at 4°C in 4%
631 paraformaldehyde in PBS, dehydrated, and rehydrated through a graded series of 25% – 50%
632 – 75% methanol/PBS. After proteinase K (10 µg/mL) treatment for 15 minutes, embryos
633 were fixed again in 0.1% glutaraldehyde/4% paraformaldehyde in PBS. Pre-hybridization at
634 70°C for at least 1 hour was conducted before hybridization with 1–2 µg/mL digoxigenin-
635 labelled riboprobes at 70°C overnight. Pre-hybridization solution included 50% formamide,
636 4×SSC, 1% Tween-20, heparin (50 µg/mL) (Sigma-Aldrich Japan K.K, Tokyo, Japan) and
637 hybridization was added more yeast RNA (100 µg/mL) and Salmon Sperm DNA (100
638 µg/mL) (Thermo Fisher Scientific). For post-hybridization, embryos were washed with hot
639 solutions at 70°C including 50% formamide, 4×SSC, 1% SDS, and treated with 100 µg/mL
640 RNase A at 37°C for 1 hour. After additional stringent hot washes at 65°C including 50%

641 formamide, 4×SSC, samples were washed with TBST, pre-absorbed with embryo powder,
642 and blocked in blocking solution (10% sheep serum in TBST) for 2–5 hours at room
643 temperature. The embryo samples were subsequently incubated with anti-digoxigenin
644 antibody conjugated with alkaline phosphatase anti-digoxigenin-AP, Fab fragments (Roche
645 Diagnostics K.K., Tokyo, Japan) overnight at 4°C. Extensive washing in TBST was followed
646 by washing in NTMT and incubation in NBT/BCIP (Roche) at room temperature (RT) until
647 colour development. After completion of in situ hybridization (ISH), embryos were de-
648 stained in PBST for 24 – 48 hours and post-fixed in 4% paraformaldehyde in PBS. Embryos
649 were processed for photography through a 50%, 80%, and 100% glycerol series. Before
650 embedding for cryosectioning, embryos were returned to PBS and again post-fixed in 4%
651 paraformaldehyde in PBS. The specimens were placed into OCT cryoembedding solution,
652 flash-frozen in liquid nitrogen, and cut into sections 14 µm thick using a cryostat (HM525
653 NX; Thermo Fisher Scientific). The following probes were used for WISH: *Bmp4* (Jones et
654 al., 1991), *Brachyury (T)* (Herrmann, 1991), *Cer1* (Belo et al., 1997), *Foxa2* (Sasaki and
655 Hogan, 1993), *Fgf8* (Bachler and Neubüser, 2001), *Lefty1/2* (Meno et al., 1996), *Lhx1*
656 (Shawlot and Behringer, 1995), *Nanog* (Chambers et al., 2003), *Nodal* (Conlon et al., 1994),
657 *Oct4* (Schöler et al., 1990), *Otx2* (Simeone et al., 1993), *Sox2* (Avilion et al., 2003), *Sox17*
658 (Kanai et al., 1996), and *Wnt3* (Roelink et al., 1990).

659 **Co-immunoprecipitation (Co-IP)**

660 At 1 day before transfection, aliquots of 5×10^4 293FT cells were seeded onto poly-L-lysine
661 (PLL)-coated 6-cm dishes and co-transfected with 2 µg of each pCAG-based expression
662 vector using Lipofectamine 3000 (Thermo Fisher Scientific). After 48 hours, the cells were
663 washed once with PBS, resuspended in RIPA buffer (50 mM Tris-HCl, pH 7.4, 150 mM
664 NaCl, 1 mM EDTA, 1% deoxycholic acid and 1% Nonidet P-40 [NP-40]) containing
665 protease inhibitor cocktail (Roche Diagnostics) and placed on ice for 30 minutes. The

666 supernatant was collected after centrifugation and incubated with Dynabeads Protein G
667 (Veritas Co., Tokyo, Japan) and mouse anti-DYKDDDDK (FLAG)-tag antibody (KO602-S;
668 TransGenic Inc., Fukuoka, Japan) overnight at 4°C. The beads were washed four times with
669 PBS, resuspended in Laemmli sample buffer, and boiled. The precipitated proteins were
670 analysed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) and western blotting
671 using the ECL Select Western Blotting Detection System (GE Healthcare Japan Co., Ltd.,
672 Tokyo, Japan) and a LAS-3000 imaging system (GE Healthcare). The FLAG antibody was
673 then washed out and the membrane was re-stained with anti- β -catenin antibody (#8480, Cell
674 Signalling Technology), anti-HA antibody (3F10, Roche), anti-Smad2 antibody (#5339, Cell
675 Signalling Technology) or anti-GAPDH antibody (sc-25778, Santa Cruz).

676 **Cell fractionation**

677 One day after seeding of 3×10^6 293FT cells on 10 cm dishes, the cells were co-transfected
678 with 2.5 μ g each of HA-Smad2 and FLAG-Cables2 expression vectors using Lipofectamine
679 3000 (Thermo Fisher Scientific). After 24 hours, the cells were washed once with PBS,
680 scraped from dishes and then collected using NE-PER Nuclear and Cytoplasmic Extraction
681 Reagents (Thermo Fisher Scientific). One-third of the cell suspension in 0.1% NP-40 was
682 used as whole cell lysate. The whole cell suspension and nuclear fraction were sonicated and
683 added the equal volume of RIPA buffer. Aliquots of each protein lysate were applied for co-
684 IP with Dynabeads Protein G and mouse anti-FLAG M2 antibody (F1804) or rat anti-HA
685 antibody (3F10) and the fractionation were confirmed by expression of α Tubulin (sc-5286,
686 Santa Cruz) and PARP-1 (sc-8007, Santa Cruz).

687 **Luciferase reporter assay**

688 A total of 50,000 cells were plated in PLL-coated 96-well tissue culture plates. After overnight
689 culture, the cells were transfected with a specific promoter-driven firefly reporter plasmid and

690 *Renilla* luciferase control plasmid, pRL-TK, using Lipofectamine 3000 (Thermo Fisher
691 Scientific) and opti-MEM (Thermo Fisher Scientific). Luciferase activity was analysed using
692 a luminometer and a Dual-Glo Luciferase assay kit according to the manufacturer's instructions
693 (Promega K.K., Tokyo, Japan). The firefly luciferase values were normalized to those of
694 *Renilla* luciferase. To evaluate β -catenin activity, cells were transiently transfected with
695 TOPflash (TOP) or FOPflash (FOP) reporter plasmids carrying multiple copies of a wild-type
696 or mutated TCF-binding site, respectively. Relative activity was calculated as normalized
697 relative light units of TOPflash divided by normalized relative light units of FOPflash. To
698 examine the SMAD2 activity, cells were transfected with ARE-luc reporter plasmid, which
699 expresses firefly luciferase driven by a SMAD2- and FAST1-dependent promoter, pRL-TK, a
700 FAST1 expression plasmid (Hayashi et al., 1997), and a constitutive-active mutant form of
701 ALK5 expression plasmid. The (CAGA)₉-luc reporter plasmid was used with pRL-TK and a
702 constitutive-active mutant form of ALK5 expression plasmid to evaluate the effect of Cables1
703 or 2 on the SMAD3 activity in 293FT cells (Dennler et al., 1998). *Nanog* promoter activity was
704 evaluated using the Nanog5p-luc reporter plasmid, which contains 2.5 kb of 5' promoter region
705 of the mouse *Nanog* gene. Nanog5p reporter was a gift from Austin Cooney (Addgene plasmid
706 #16337). The experiment was performed in triplicate and repeated at least three times.
707 Statistical analysis was performed using the Mann-Whitney U-test. Two-tailed *P*-values at less
708 than 0.05 were considered as statistically significant.

709 **Indirect immunofluorescence assay (IFA)**

710 After 24 or 48 hours transfection, cells were washed twice with PBS and then fixed with 4%
711 paraformaldehyde in PBS for 10 minutes. Permeabilization of cell membranes were done with
712 0.1% Triton X-100 in PBS for 20 minutes or methanol for 5 minutes. After blocking with 10%
713 goat serum or Superblock blocking buffer (Thermo Fisher Scientific) for 30 minutes, cells were
714 incubated overnight at 4°C with mouse anti-FLAG antibody. Then, the cells were washed with

715 PBS and incubated with Alexa Fluor-conjugated anti-mouse IgG antibody. Fluorescence signals
716 were detected using a BZ-X700 fluorescent microscope (Keyence Co., Ltd., Osaka, Japan).

717 **Histology, EdU, and TUNEL assay**

718 Mouse uteri including the decidua were collected and fixed in 4% paraformaldehyde in PBS.
719 Subsequently, paraffin blocks were made by dehydration in ethanol, clearing in xylene, and
720 embedding in paraffin. Embryo sections 5 µm thick were cut (Microm HM 335E; Thermo
721 Fisher Scientific) and placed on glass slides (Matsunami Glass Ind., Ltd., Osaka, Japan). For
722 haematoxylin-eosin (HE) staining, slides were deparaffinized and rehydrated through an
723 ethanol series, and then stained with HE.

724 To label the proliferating embryonic cells, pregnant mice at E6.5 were injected
725 intraperitoneally with 5-ethynyl-2'-deoxyuridine (EdU) at 200 µL/mouse and sacrificed 4
726 hours later. Embryos were embedded in paraffin blocks, and sections were refixed in 4%
727 paraformaldehyde and permeabilized in 0.5% Triton X-100/PBS. EdU assay was performed
728 with a Click-iT Plus EdU Imaging Kit (Thermo Fisher Scientific) and TUNEL assay was
729 performed with a Click-iT Plus TUNEL Assay for In situ Apoptosis Detection kit (Thermo
730 Fisher Scientific) according to the manufacturer's protocol. As the final step, embryo sections
731 were co-stained with Hoechst 33342, observed under a microscope (BZ-X700; Keyence), and
732 cell number was counted using ImageJ software.

733

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- 986
- 987

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992

993 **Competing interests**

994 The authors declare no competing or financial interests.

995

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1001 Technology, Japan.

1002

1003 **Table 1. Survival rate and Mendelian ratio of *Cables2*-mutant embryos**

Embryonic days (E)	Total number of embryos	Genotypes		
		+/+	+/-	-/-
E6.5	437	132 (30.2) ^a	221 (50.6)	80 (18.3)
E7.5	70	18 (25.7)	32 (45.7)	20 ^b (28.6)
E8.5	21	9 (42.9)	9 (42.9)	3 ^b (14.3)
E9.5	18	7 (38.9)	7 (38.9)	4 ^b (22.2)
E12.5	6	2 (33.3)	4 (66.7)	0 (0)
Adult	90	24 (26.7)	66 (73.3)	0 (0)

1004

1005 ^aNumber of embryos (percentage), ^bAbnormal phenotype.

1006 **Table 2. Phenotypes in *Cables2* VE rescue and *Cables2* VE & Epi rescue chimeras**

	Tetraploid embryo + <i>Cables2</i> ^{-/-} ; <i>ROSA26</i> ^{YFP/+} ESC (VE rescue chimera)			Wild-type chimera		
Embryonic days (E)	Total number of embryos	Phenotype		Total number of embryos	Phenotype	
		Normal	Abnormal		Normal	Abnormal
E6.5	2	1	1	4	3	1
E7.5	15	4	11	14	11	3
E8.5	13	0	13 ^a	7	6	1
	Tetraploid embryo + <i>Cables2</i> ^{-/-} ; <i>ROSA26</i> ^{YFP/+} ; <i>CAG-tdTomato-2A-Cables2-3xFLAG</i> ESC (VE & Epi rescue chimera)			Wild-type chimera		
Embryonic days (E)	Total number of embryos	Phenotype		Total number of embryos	Phenotype	
		Normal	Abnormal		Normal	Abnormal
E7.5	5	4	1	2	1	1
E8.5	4	3	1	5	4	1
E9.5	2	2	0	3	2	1

1007

1008 ^aAll embryos had A-P axis specification.

1009

1010 **Figure legends**

1011 **Figure 1.** *Cables2* expression during early mouse embryo development. (A) *Cables2* gene
1012 expression was examined by RT-PCR with ESC, blastocyst, and E7.5 embryo samples.
1013 *Gapdh* was used as an internal positive control. (B–F) Wild-type embryos from E6.5 to E9.5
1014 were examined by *in situ* hybridization with a *Cables2* probe. The whole embryo expressed
1015 *Cables2* at E6.5 (B). The black arrow indicates the position of the transverse section shown in
1016 (C). Scale bars, 20 μ m.

1017 The following figure supplement is available for figure 1:

1018 **Figure supplement 1.** Genotyping and expression of *Cables2*.

1019

1020 **Figure 2.** Morphological and histological analyses of *Cables2*-deficient embryos at early
1021 stages of development. Embryos were collected and genotyped at E8.5 (A, B) and E7.5 (C,
1022 D). Histological analysis was on HE-stained sections. Wild-type and *Cables2* mutant
1023 embryos were embedded in paraffin and stained at E7.5 (E, F) and E6.0 (G, H). Epc:
1024 ectoplacental cone, ps: primitive streak; pve: posterior visceral endoderm; ec: ectoderm; epi:
1025 epiblast. Scale bars, 100 μ m (A–D), 50 μ m (E–H).

1026 The following figure supplement is available for figure 2:

1027 **Figure supplement 1.** Proliferating and apoptotic cells in E6.5 *Cables2* mutant embryos.

1028

1029 **Figure 3.** Expression of gastrulation markers in *Cables2*-deficient embryos. (A–F, K–T) All
1030 embryos were collected, genotyped, and used for WISH at E6.5. Several key gastrulation
1031 markers were examined using both wild-type and *Cables2*-deficient embryos: *T* ($n = 5$), *Wnt3*
1032 ($n = 3$), *Fgf8* ($n = 3$), *BMP4* ($n = 3$), *Lhx1* ($n = 3$), *Sox17* ($n = 3$), *Cer1* ($n = 3$) and *Lefty1/2* (n
1033 = 3). (G, H) β -galactosidase staining demonstrating the restricted activation of Wnt/ β -catenin

1034 signalling in *Cables2* homozygous embryo carrying the TOPGAL reporter ($n = 6$). (I, J)
1035 WISH analysis showing the expression of *T* in wild-type and *Cables2*-deficient embryos at
1036 E7.5 ($n = 5$). Scale bars, 100 μm .

1037

1038 **Figure 4.** Enhancement of β -catenin activity by *Cables2*. (A) Relative luciferase activities in
1039 293T cells transfected with an empty control or *Cables2* expression vectors together with an
1040 empty control or β -catenin expression vectors. Relative luciferase activity is expressed as the
1041 ratio of TOP/FOPflash reporter activity relative to the activity in cells transfected with an
1042 empty vector alone. Columns: Averages of at least three independent experiments performed
1043 in triplicate. Error bars, Standard deviation (SD). Statistical significance was determined
1044 using Student's *t* test (*, $P < 0.05$). (B) Co-IP was performed with FLAG-*Cables2* and β -
1045 catenin expression vectors. The results obtained using anti-FLAG and anti- β -catenin
1046 antibodies showed the appearance of β -catenin in the precipitated complexes with *Cables2*.

1047 The following figure supplement is available for figure 4:

1048 **Figure supplement 1.** Interaction of *Cables2* with endogenous β -catenin.

1049

1050 **Figure 5.** Enhancement of Smad2 activity by *Cables2*. (A–J) WISH analyses showing
1051 expression of *Nodal* (E6.0: $n = 3$; E6.5: $n = 4$), *Foxa2* ($n = 3$), and neuroectoderm markers
1052 *Sox2* ($n = 4$) and *Otx2* ($n = 5$). Scale bars, 100 μm . (K) Relative luciferase activities of ARE-
1053 luc or (CAGA)₉-luc reporter vectors in 293FT cells co-transfected with an empty control,
1054 FLAG-*Cables1*, or FLAG-*Cables2* expression vectors. Columns: Averages of at least three
1055 independent experiments performed in triplicate. Error bars: Standard deviation. Statistical
1056 significance was determined using Student's *t* test (*, $P < 0.05$). (L) Co-IP showing the
1057 physical interaction of FLAG-*Cables2* with HA-Smad2. (M, N) Co-IP/western blot analysis

1058 performed with whole cell lysates or fractionated lysates from 293FT cells transfected with
1059 HA-Smad2 and either FLAG-Cables2 or empty control vectors. PARP-1 and α Tubulin serve
1060 as a nuclear and cytoplasmic marker, respectively. W: whole cell lysate, C: cytoplasmic
1061 fraction, N: nuclear fraction.

1062 The following figure supplement is available for figure 5:

1063 **Figure supplement 1.** Interaction of Cables2 with endogenous Smad2.

1064

1065 **Figure 6.** Downregulated *Nanog* promoter activity and expression. EpiLCs were induced
1066 from homozygous *Cables2* mutant ESCs. RT-qPCR (A) and *Nanog*-luc assay (B)
1067 consistently showed decreased expression of *Nanog* in *Cables2*-deficient cells compared with
1068 wild-type EpiLCs. (C, D) *Nanog* expression in *Cables2* mutants was weaker and located
1069 evenly in the epiblast compare with wild-type on WISH analysis ($n = 4$). (E, F) *Oct4* was
1070 expressed normally in epiblast of mutant embryos ($n = 4$). (G, H) All embryos in the same
1071 litter were collected at E6.5, and those with GFP-positive cells were compared. *Cables2*^{-/-}
1072 embryos showed faint and ectopic expression of the *Nanog*-GFP signal. (I, J) There was no
1073 difference between wild-type and mutant embryos at E5.5. Columns: Averages of at least
1074 three independent experiments performed in triplicate. Y error bars: Standard deviation (SD).
1075 Statistical significance was determined using Student's *t* test (*, $P < 0.05$). Scale bars, 100
1076 μm (C–H); 50 μm (I, J).

1077 The following figure supplements are available for figure 6:

1078 **Figure supplement 1.** EpiLC induction from *Cables2*^{-/-} ESCs and expression of pluripotency
1079 genes.

1080 **Figure supplement 2.** Interaction of Cables2 with exogenous HA-Oct4.

1081 **Figure supplement 3.** Gene enrichment analyses of up-regulated genes by the loss of
1082 *Cables2*.

1083 **Figure supplement 4.** Gene enrichment analyses of down-regulated genes by the loss of
1084 *Cables2*.

1085

1086 **Figure 7.** A–P axis formation in *Cables2* VE rescue and normal phenotype of *Cables2* VE &
1087 Epi rescue chimeras. (A) Schematic diagram of tetraploid complementation experiment for
1088 *Cables2* VE rescue chimera. (B–E) Bright field (B, D) and YFP fluorescent (C, E) images of
1089 wild-type and *Cables2* VE rescue chimeric embryos at E7.5 or E8.5. *Cables2* VE rescue
1090 chimeras at E8.5 showed distinguishable phenotypes in compared with wild-type chimeras.
1091 (F, G) WISH analyses showing the expression of *T* (F) and *Foxa2* (G) in *Cables2* VE rescue
1092 chimeric embryos at E7.5. (H) Representative image of *Cables2* VE rescue chimeric embryo
1093 at E8.5 showing the head-fold and allantois bud formation. (I) Schematic diagram of
1094 tetraploid complementation experiment for *Cables2* VE and epiblast (*Cables2* VE and Epi)
1095 rescue chimeras. (J–Q) Bright field (J, L, N, P) and tdTomato fluorescent (K, M, O, Q)
1096 images of wild-type and *Cables2* VE and Epi rescue chimeric embryos at E7.5, E8.5, or E9.5.
1097 The *Cables2* VE and Epi rescue chimeric embryos developed normally until E9.5. Scale bars,
1098 100 μm (B, C, G, H); 500 μm (D, E).

1099

1100 **Figure supplements**

1101 **Figure 1—figure supplement 1.** Genotyping and expression of *Cables2*. (A) Genotyping by
1102 PCR analysis from 5 whole embryo samples using three primers. Bands at 985 bp and 599 bp
1103 represent mutant and 6 wild-type *Cables2* alleles, respectively. (B) At E6.5, *Cables2* was
1104 expressed ubiquitously in 7 both extra- and embryonic parts in wild-type (left), in comparison

1105 with homozygous mutants 8 (right). Antisense *Cables2* probe was used for WISH to confirm
1106 that *Cables2*-deficient 9 embryos lacked expression. Scale bar, 100 μm .

1107

1108 **Figure 2—figure supplement 1.** Proliferating and apoptotic cells in E6.5 *Cables2* mutant
1109 embryos. (A–C) The EdU-incorporating cells represented the proliferation of cells in both
1110 wild-type and *Cables*-deficient embryos ($n = 4$). The proliferated cells were counted in whole
1111 embryo (Total) or only in embryonic region. (D–F) Apoptotic cells were detected in both
1112 wild-type and *Cables2*-deficient embryos ($n = 3$), in whole embryo or in embryonic part. The
1113 average percentage was calculated by number of counted cells normalized to total number of
1114 cells within the embryo. At least 2 slides were counted per embryo. Y error bars: Standard of
1115 deviation (SD). Statistical significance was determined using Student's t test ($P < 0.05$).
1116 Scale bars, 50 μm .

1117

1118 **Figure 4—figure supplement 1.** Interaction of *Cables2* with endogenous β -catenin. Co-IP
1119 showing the physical interaction of FLAG-*Cables2* with endogenous β -catenin in 293FT
1120 cells. Anti-GAPDH antibody was used as a negative control for evaluating specific
1121 interaction. Experiment was repeated at least twice and reliably reproduced.

1122

1123 **Figure 5—figure supplement 1.** Interaction of *Cables2* with endogenous Smad2. Co-IP
1124 showing the physical interaction of FLAG-*Cables2* with endogenous Smad2 in 293FT cells.
1125 Anti-GAPDH antibody was used as a negative control for evaluating specific interaction.
1126 Experiment was repeated at least twice and reliably reproduced.

1127

1128 **Figure 6—figure supplement 1.** EpiLC induction from *Cables2*^{-/-} ESCs and expression of
1129 pluripotency genes. (A) RT-qPCR showing the expression levels of pluripotency genes in
1130 wild-type and *Cables2*^{-/-} ESCs. (B) Wild-type and *Cables2*^{-/-} ESCs were maintained with
1131 2i/LIF and induced to differentiate into EpiLCs within 3 days. No differences were observed
1132 between wild-type and *Cables2*^{-/-} EpiLCs in cell proliferation or cell morphology.

1133

1134 **Figure 6—figure supplement 2.** Interaction of *Cables2* with exogenous HA-Oct4. Co-IP
1135 showing the physical interaction of FLAG-*Cables2* with HA-Oct4 in 293FT cells. Anti-
1136 GAPDH antibody was used as a negative control for evaluating specific interaction.
1137 Experiment was repeated at least twice and reliably reproduced.

1138

1139 **Figure 6—figure supplement 3.** Gene enrichment analyses of up-regulated genes by the loss
1140 of *Cables2*. (A, B) GO term (A) and KEGG pathway (B) enrichment analyses of 122 up-
1141 regulated genes in *Cables2*-deficient EpiLCs compared with wild-type EpiLCs.

1142

1143 **Figure 6—figure supplement 4.** Gene enrichment analyses of down-regulated genes by the
1144 loss of *Cables2*. (A, B) GO term (A) and KEGG pathway (B) enrichment analyses of 52
1145 down-regulated genes in *Cables2*-deficient EpiLCs compared with wild-type EpiLCs.

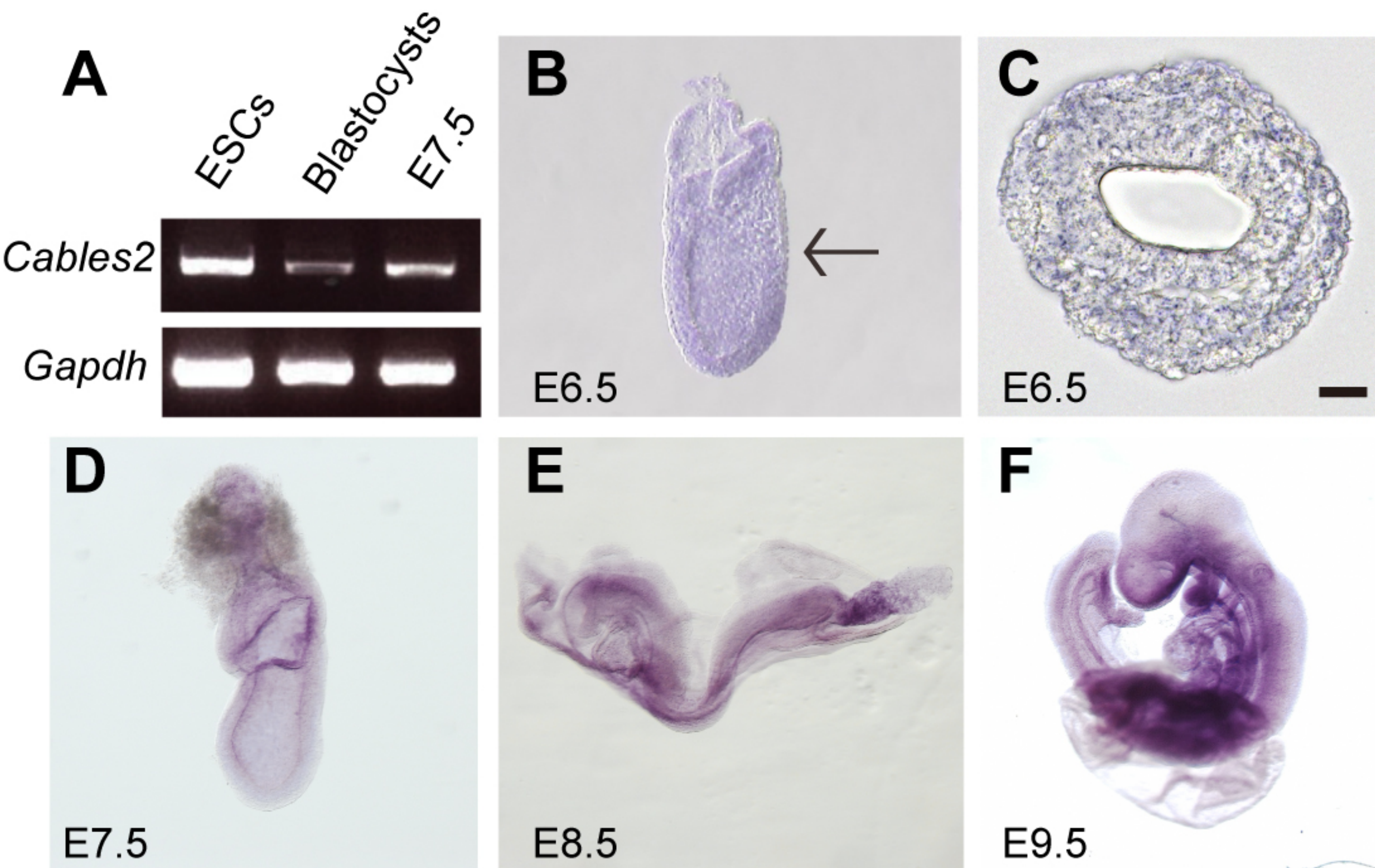


Figure 1

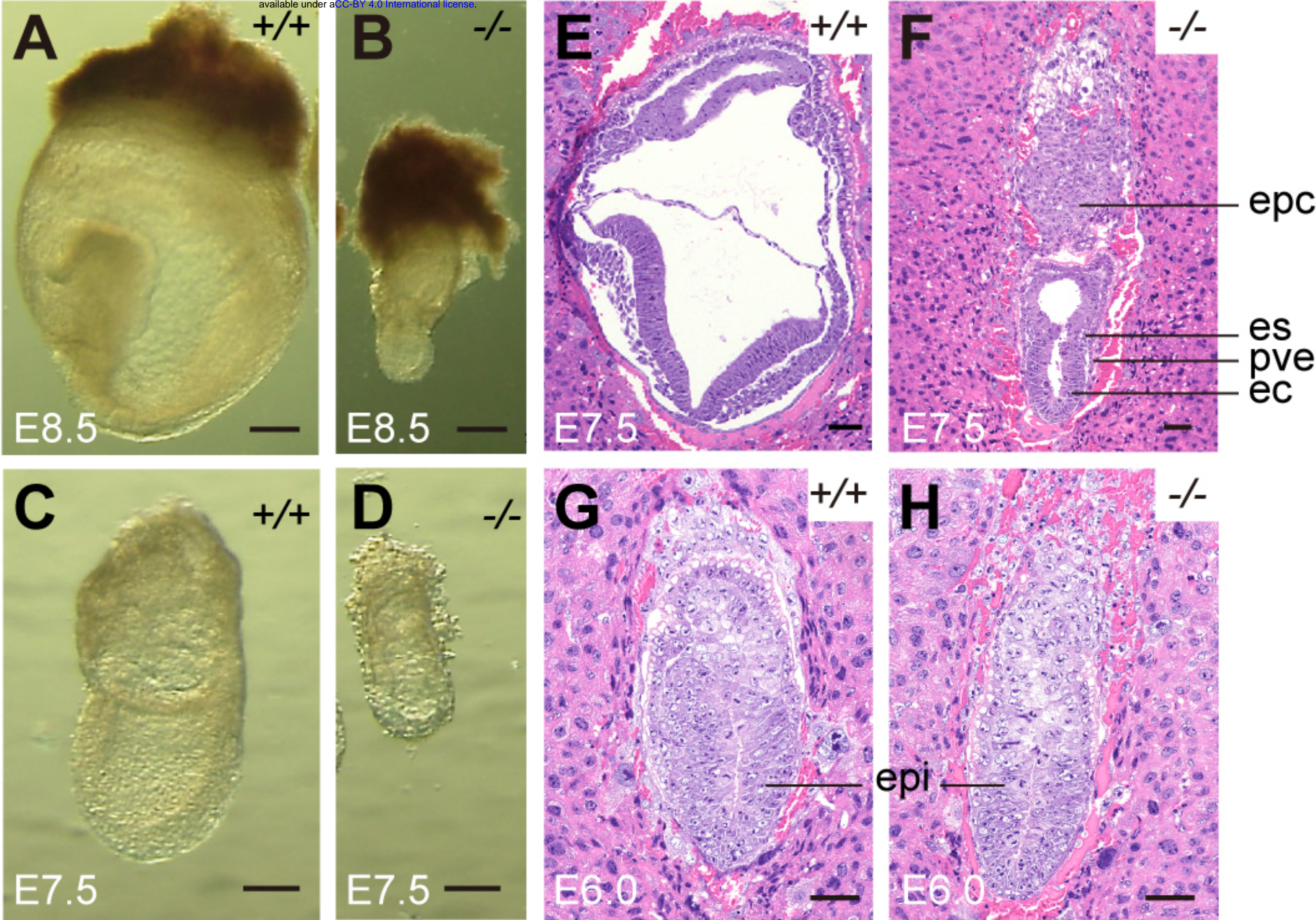


Figure 2

E6.5

E7.5

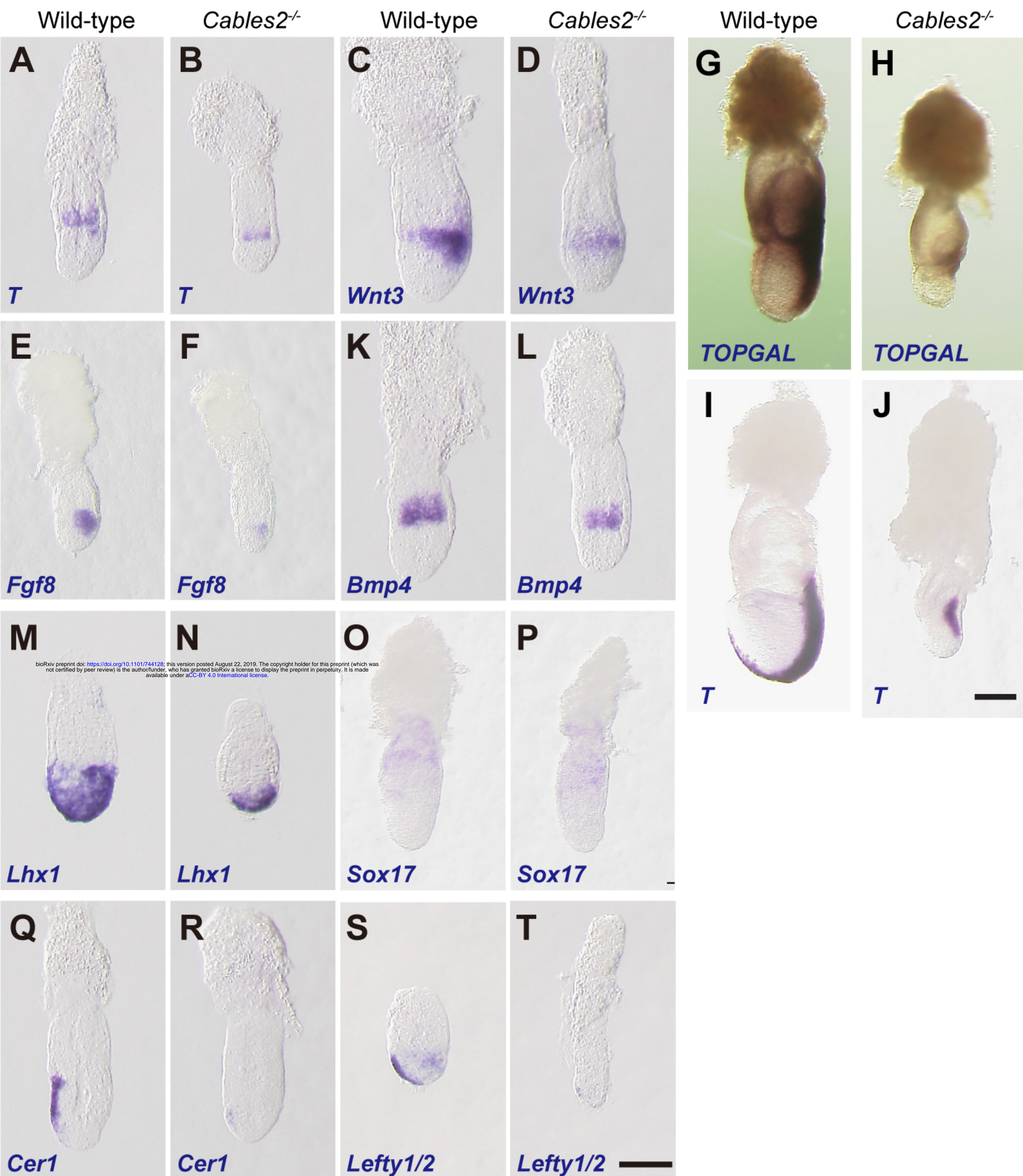
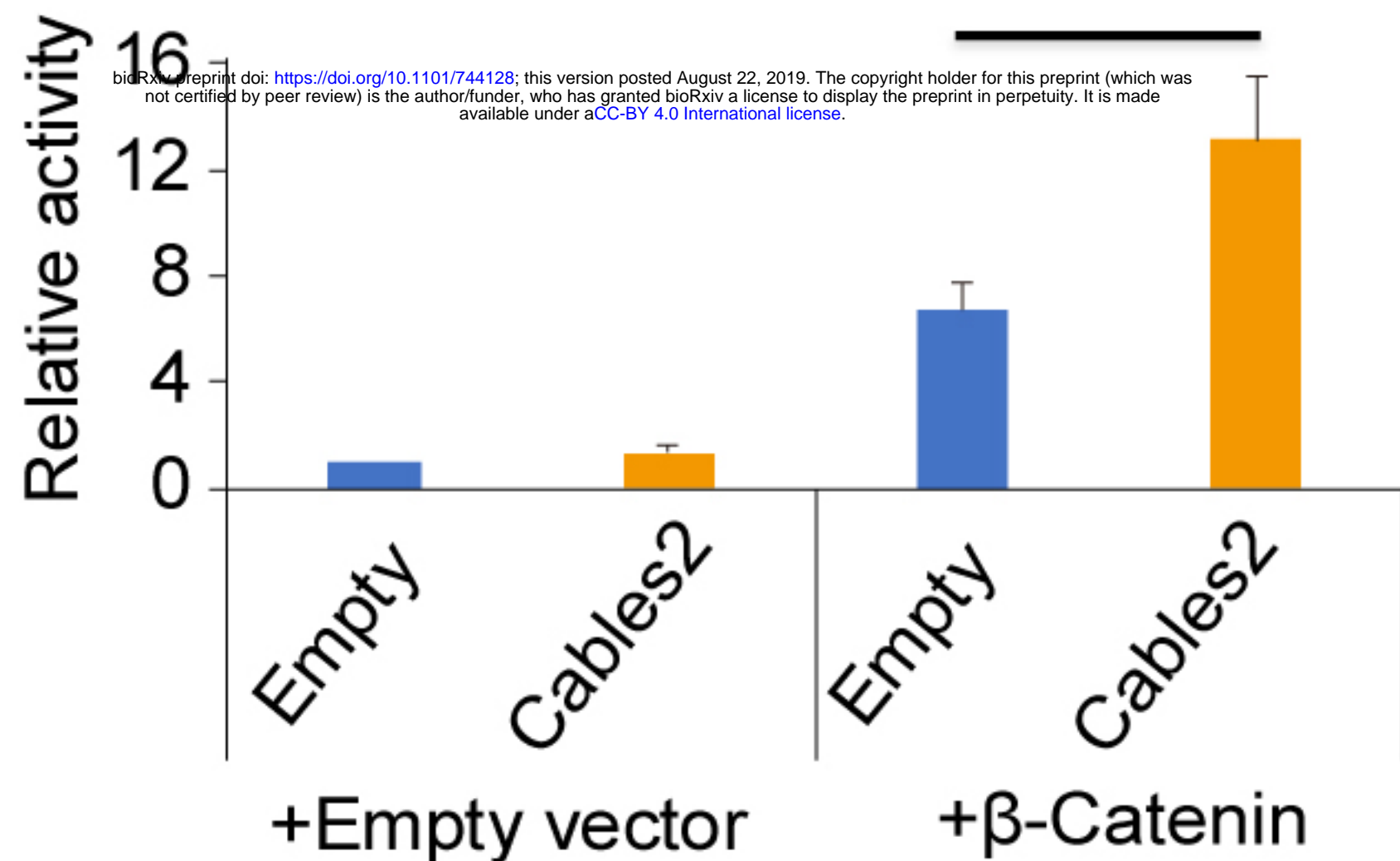
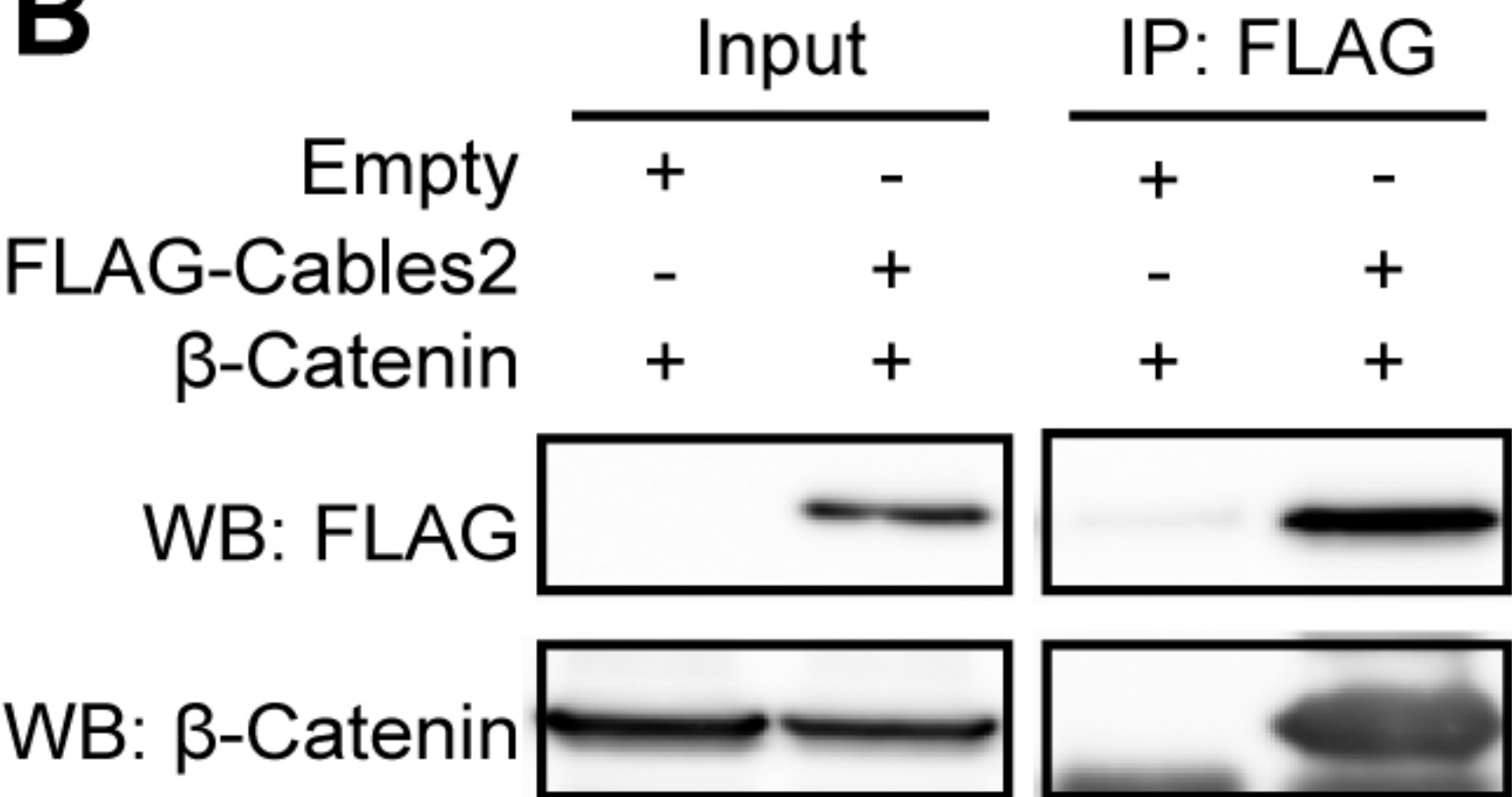


Figure 3

A**B****Figure 4**

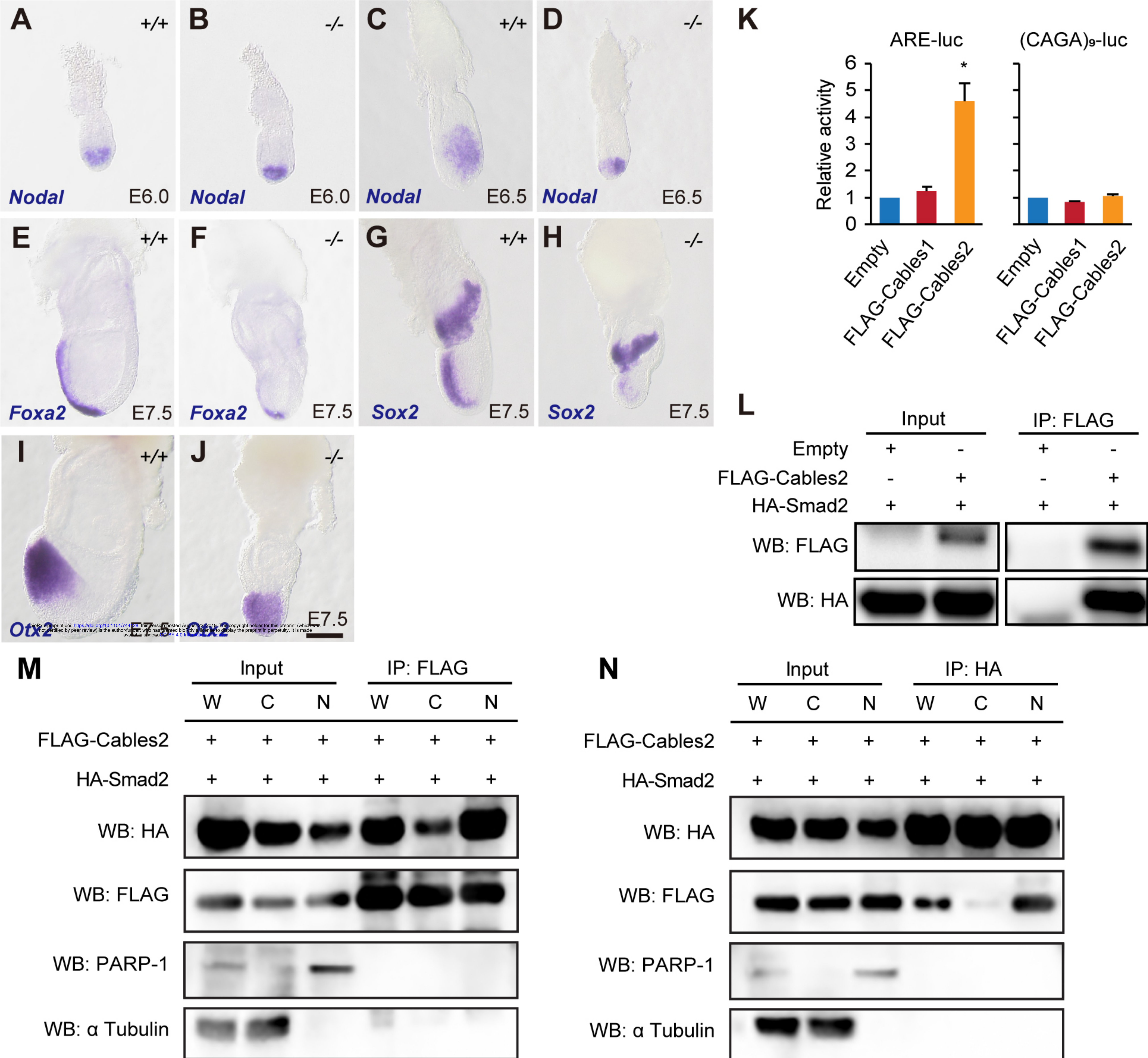


Figure 5

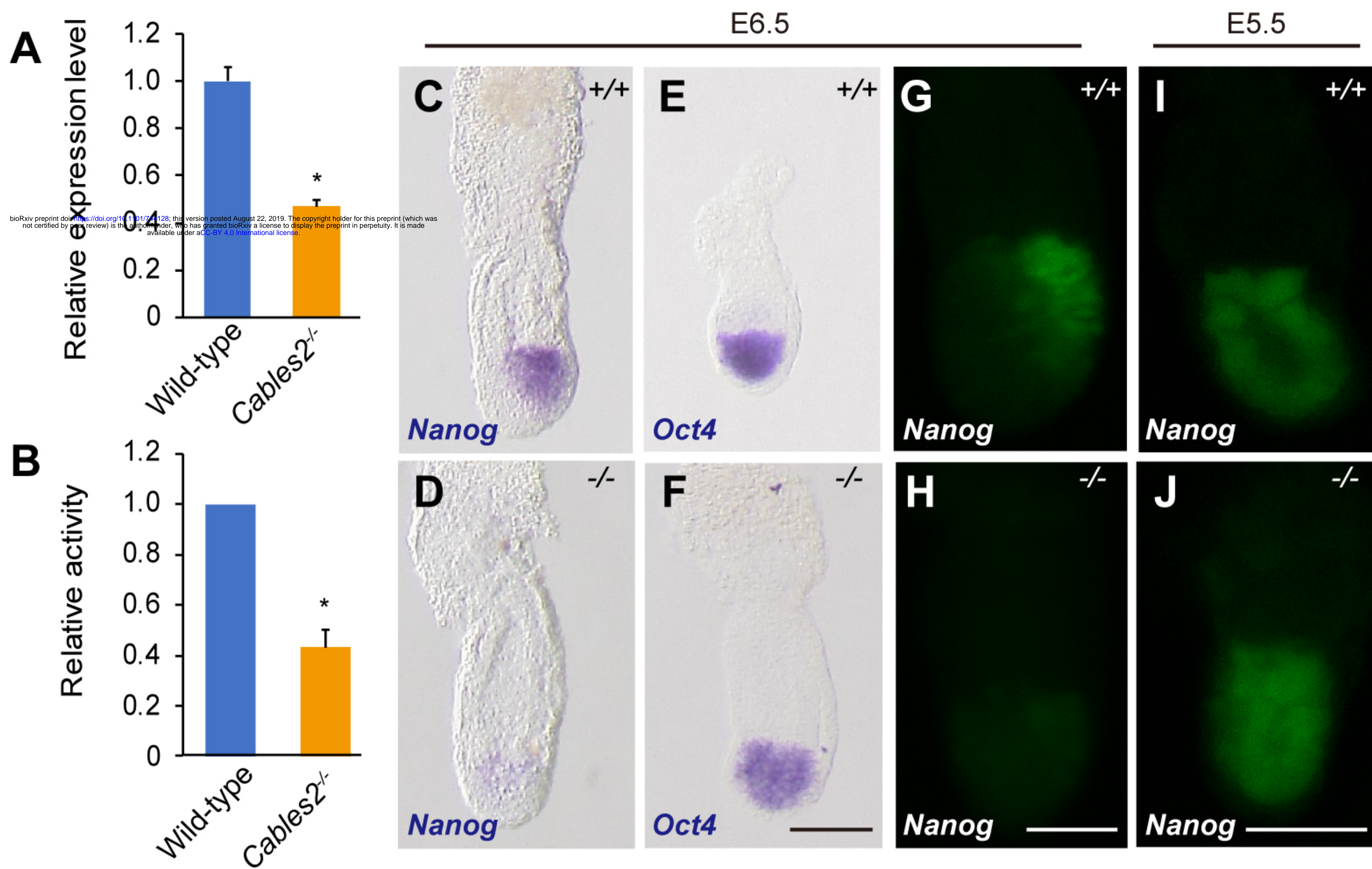


Figure 6

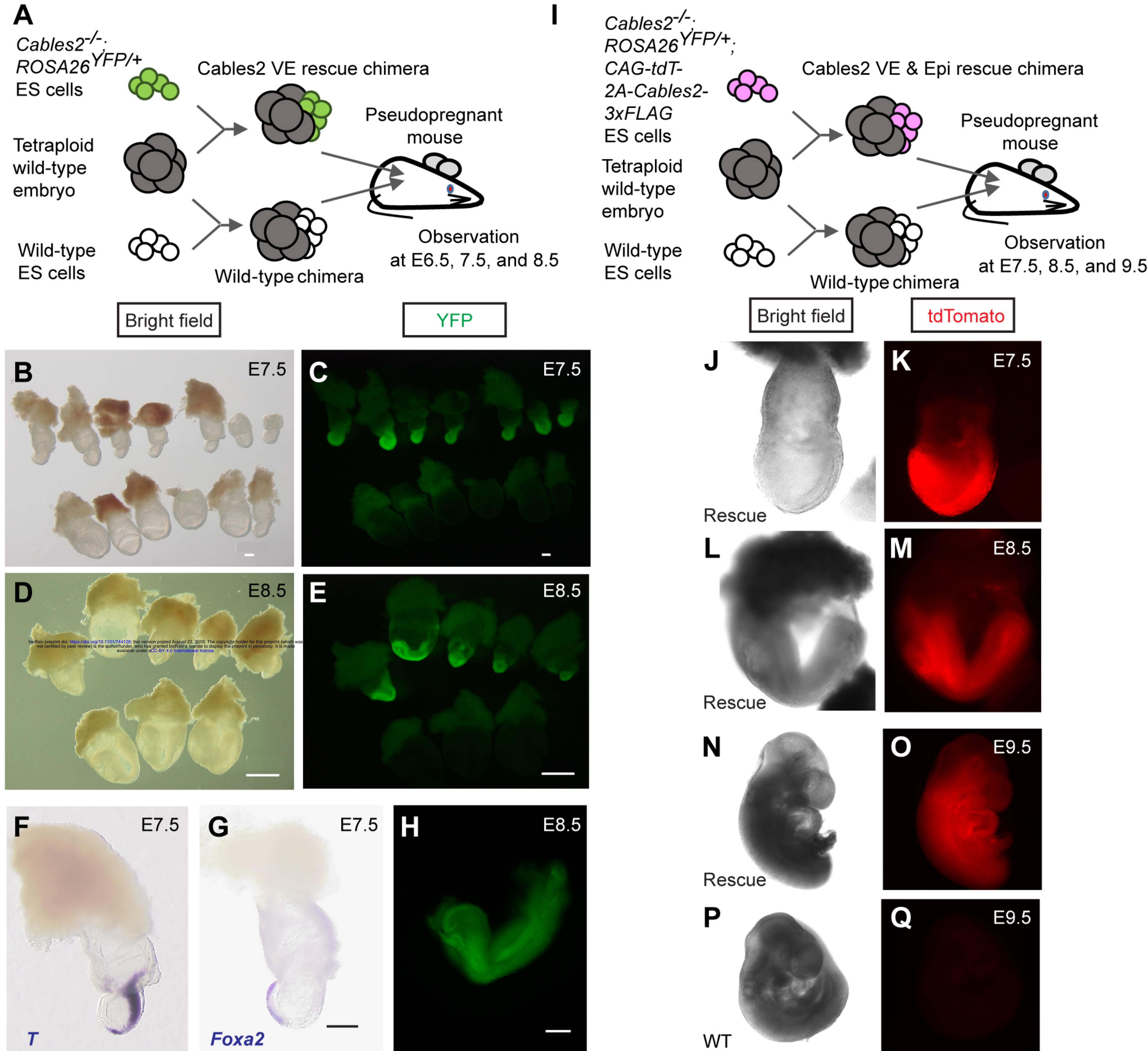


Figure 7

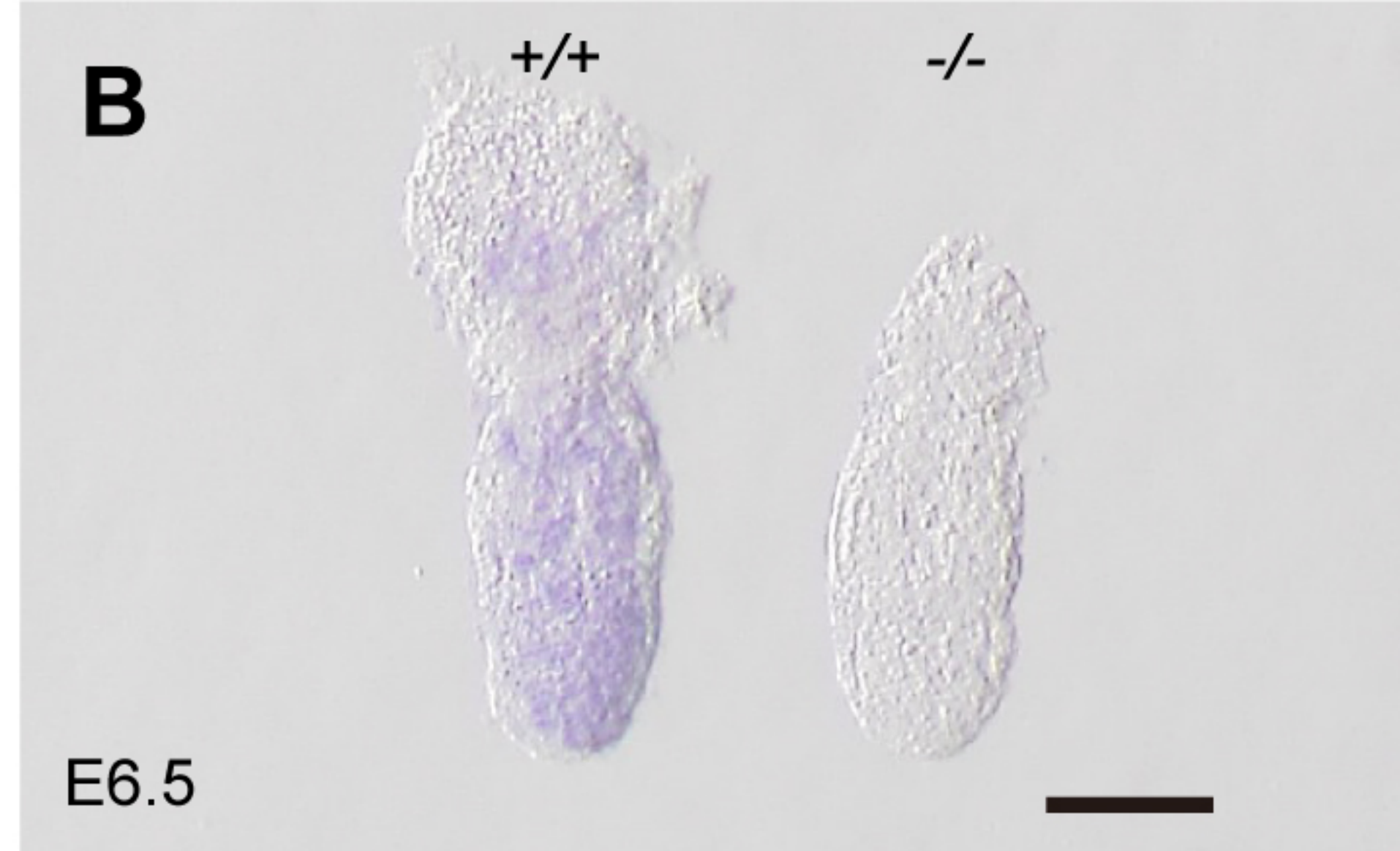
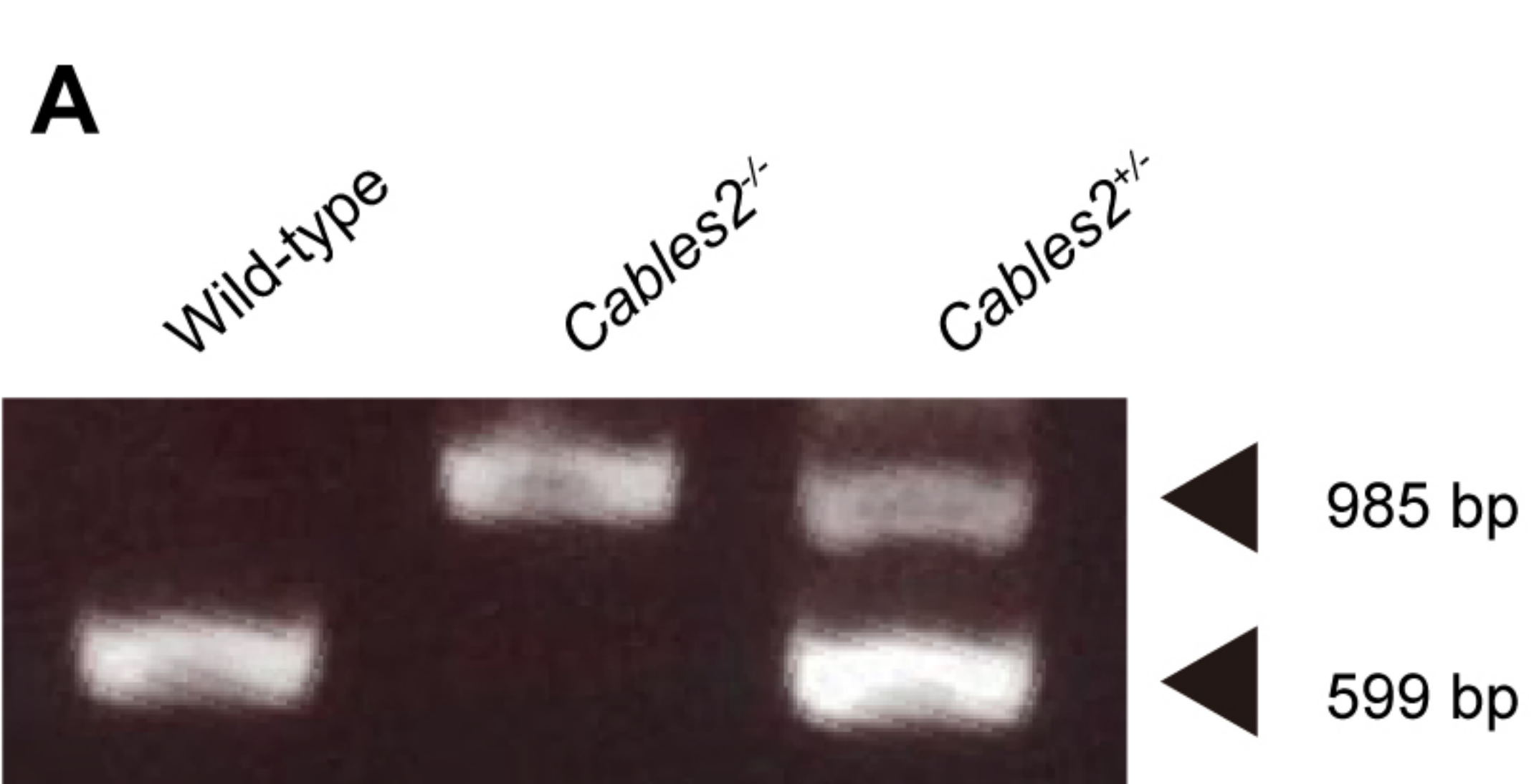


Figure 1—figure supplement 1

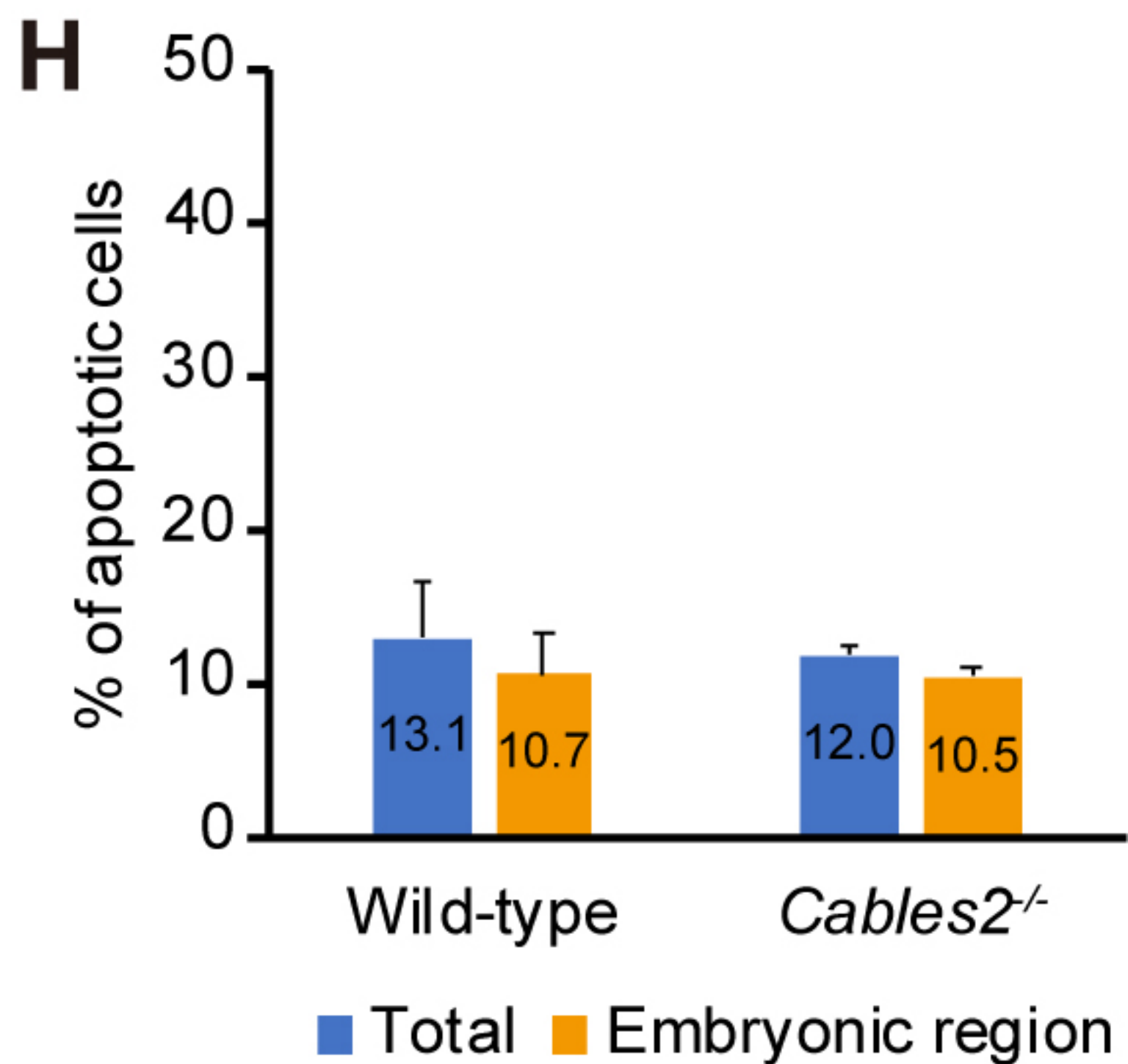
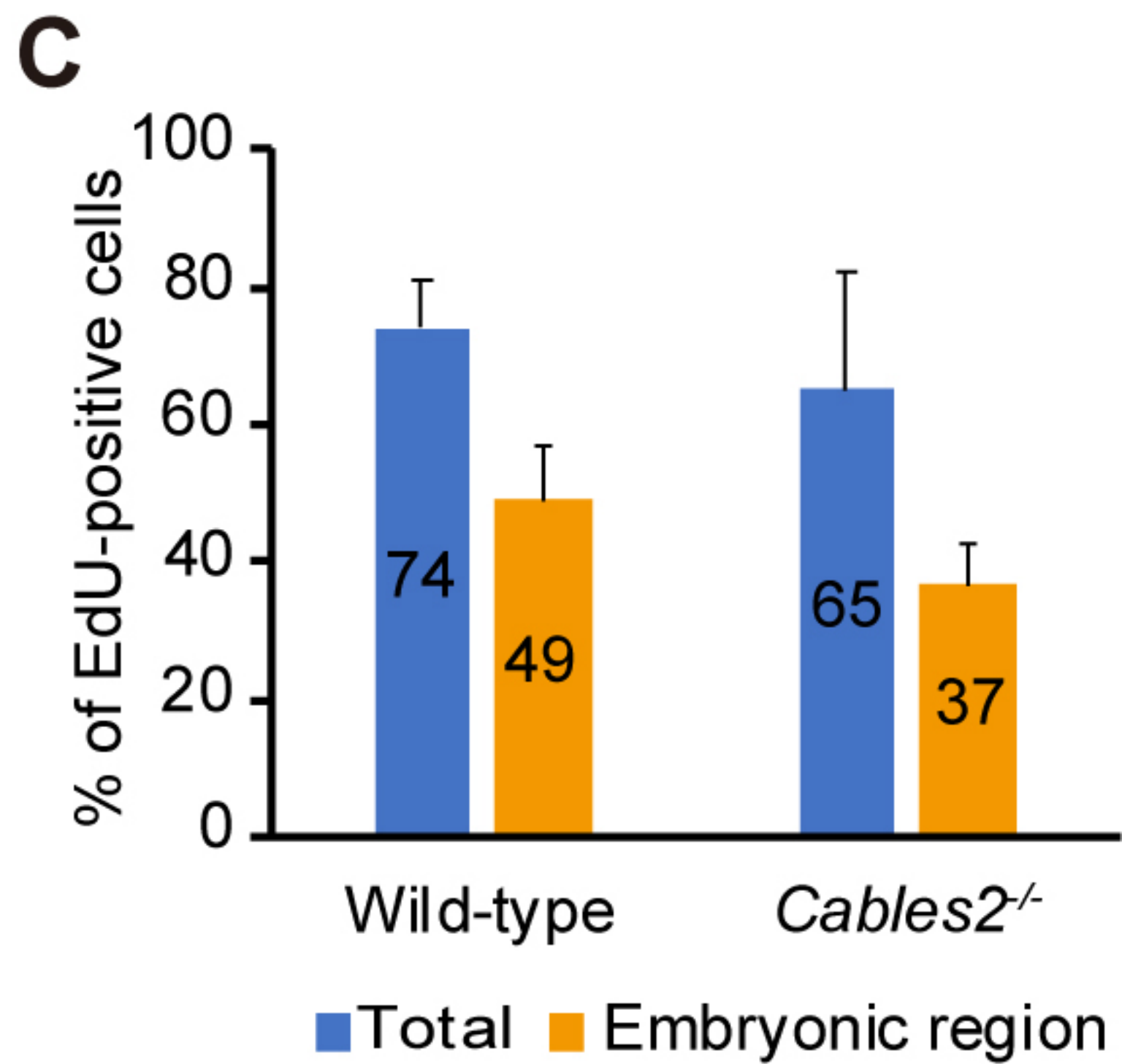
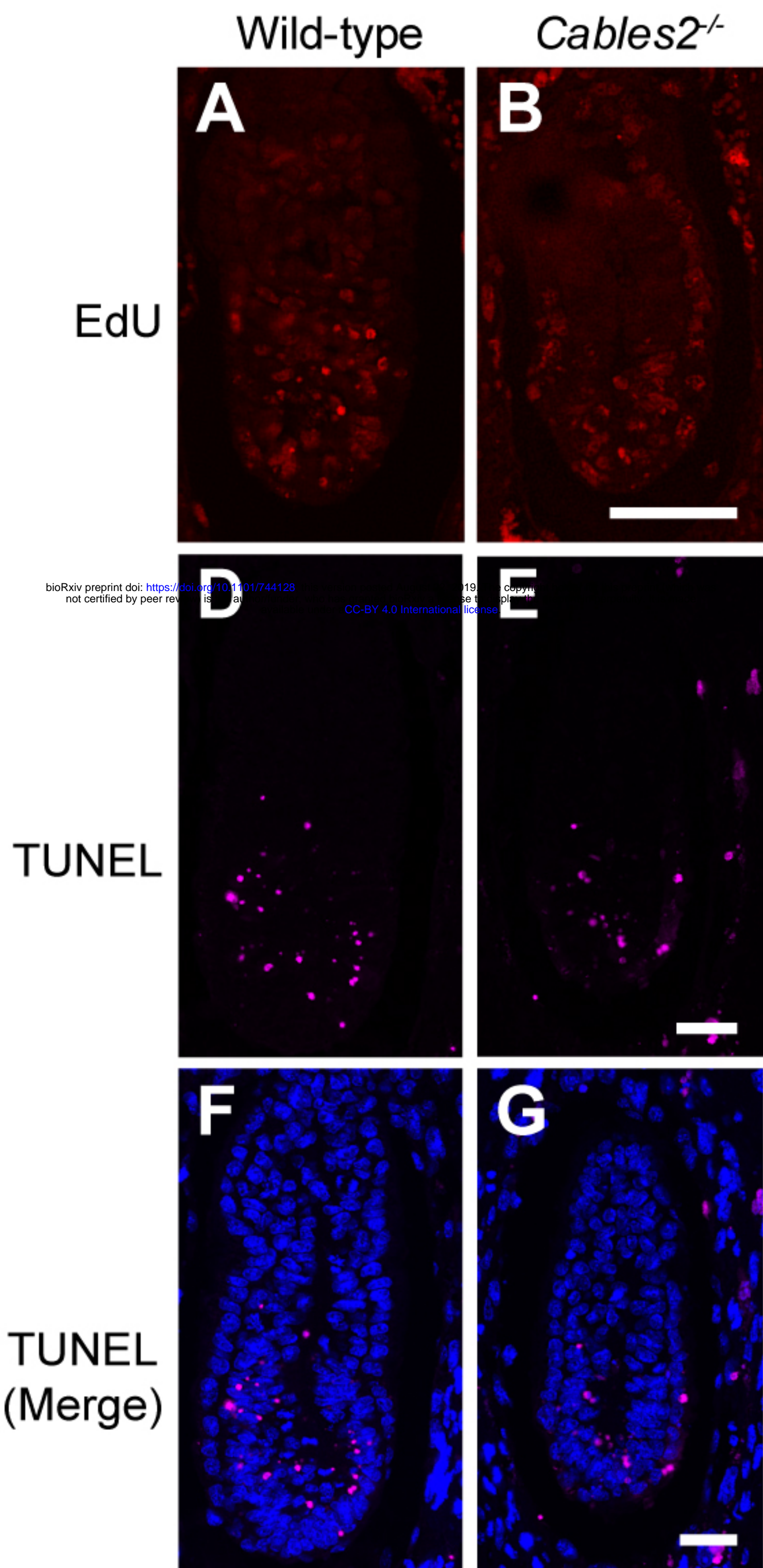


Figure 2—figure supplement 1

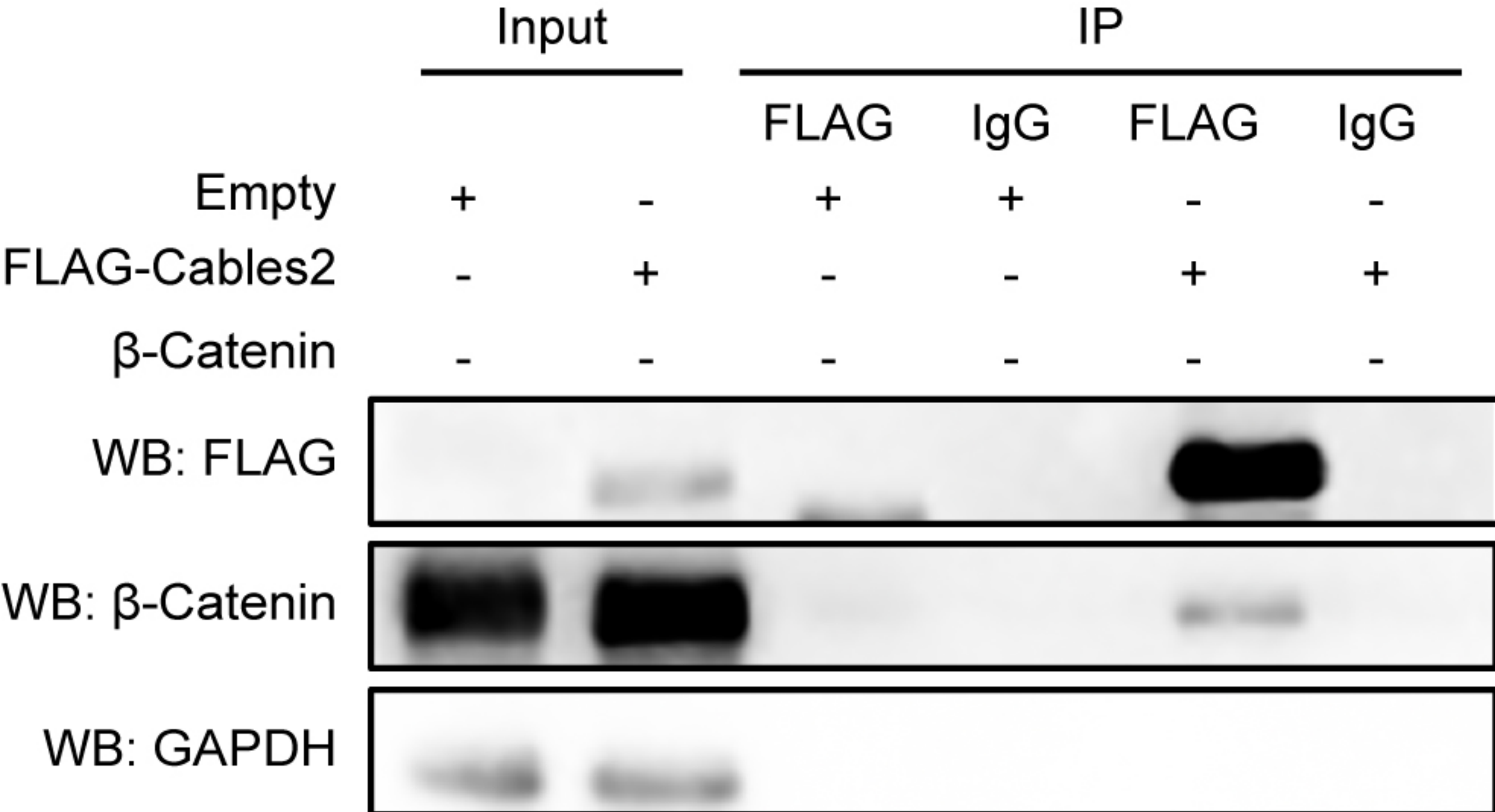


Figure 4—figure supplement 1

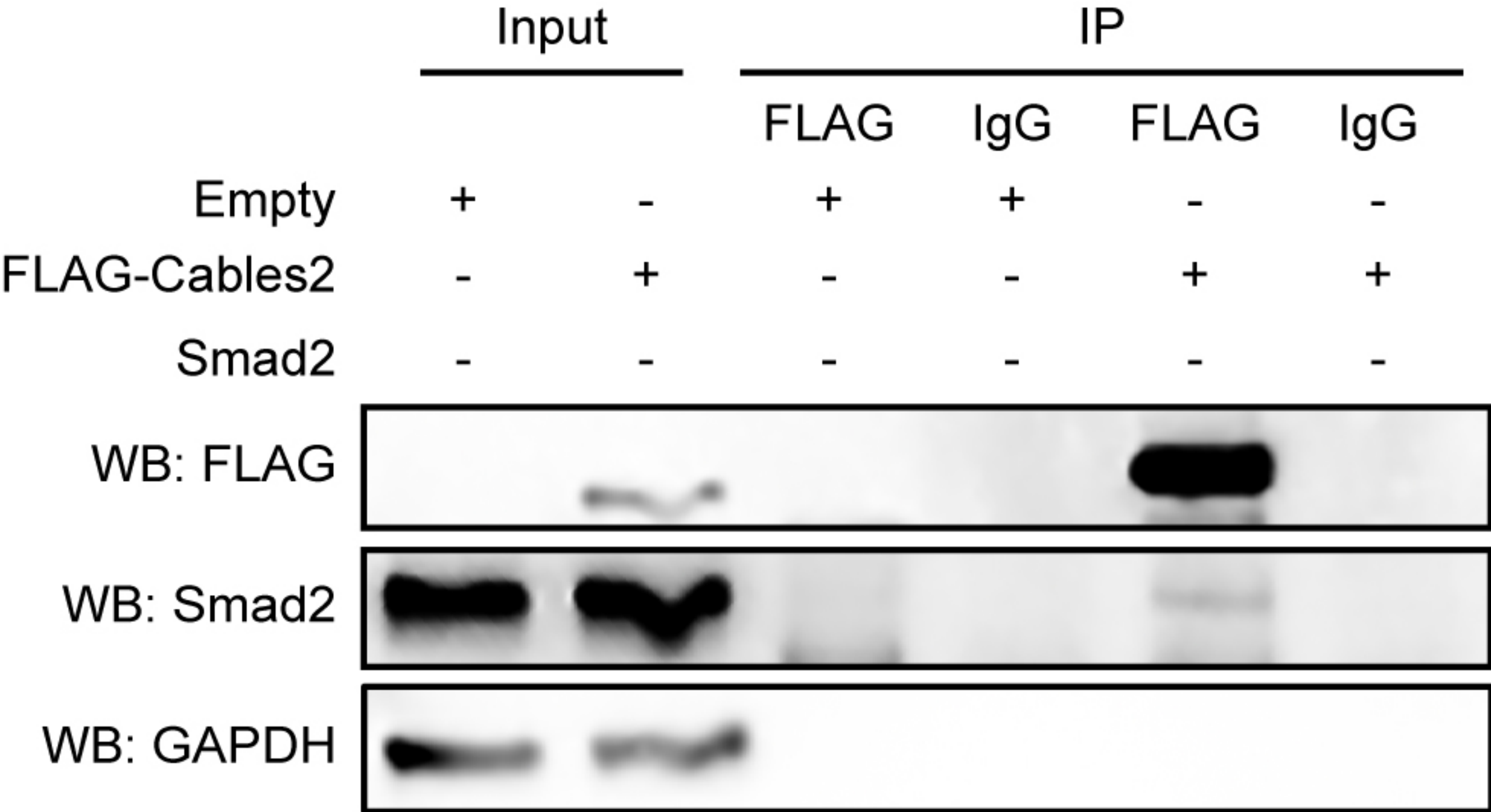
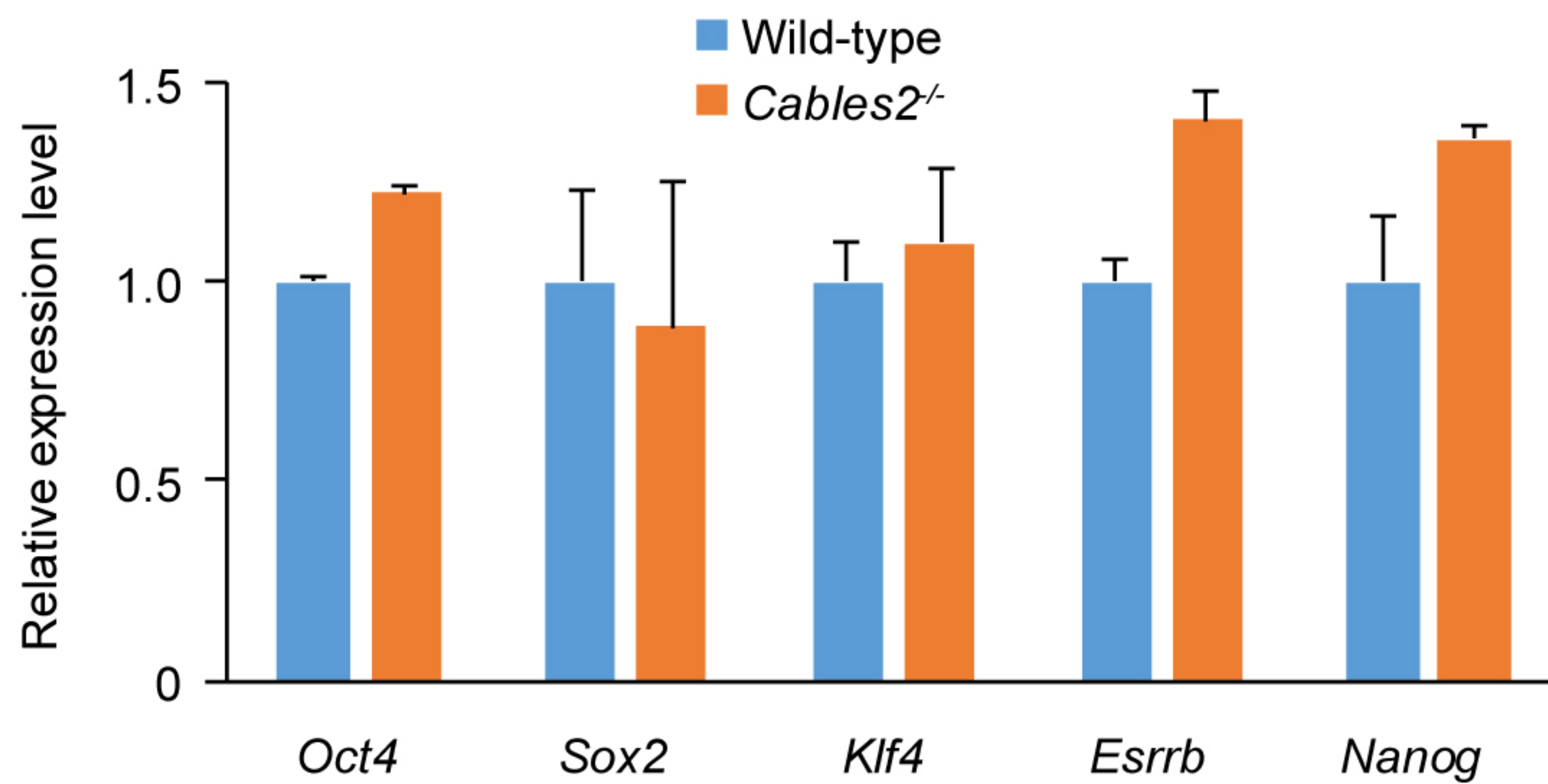


Figure 5—figure supplement 1

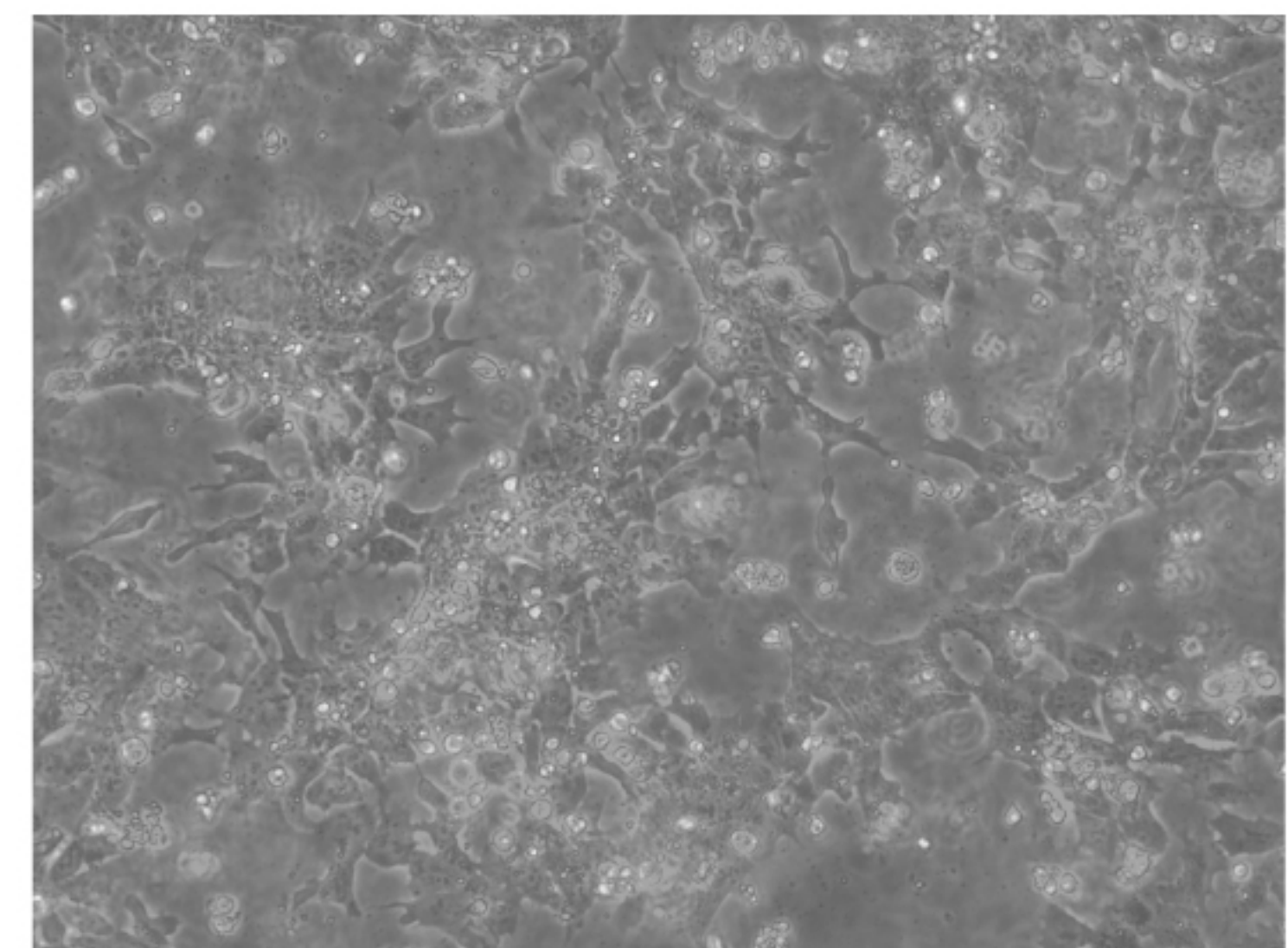
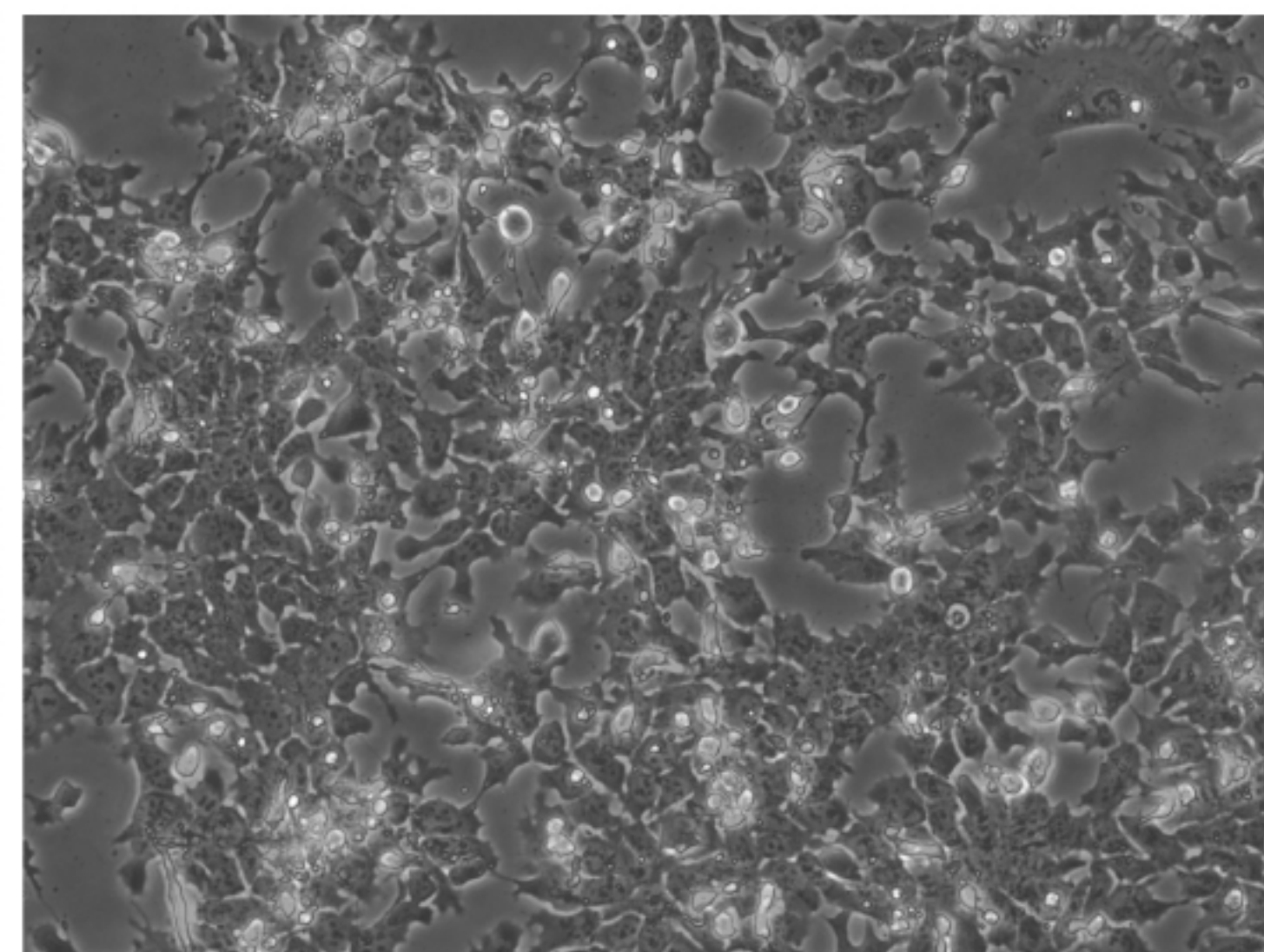
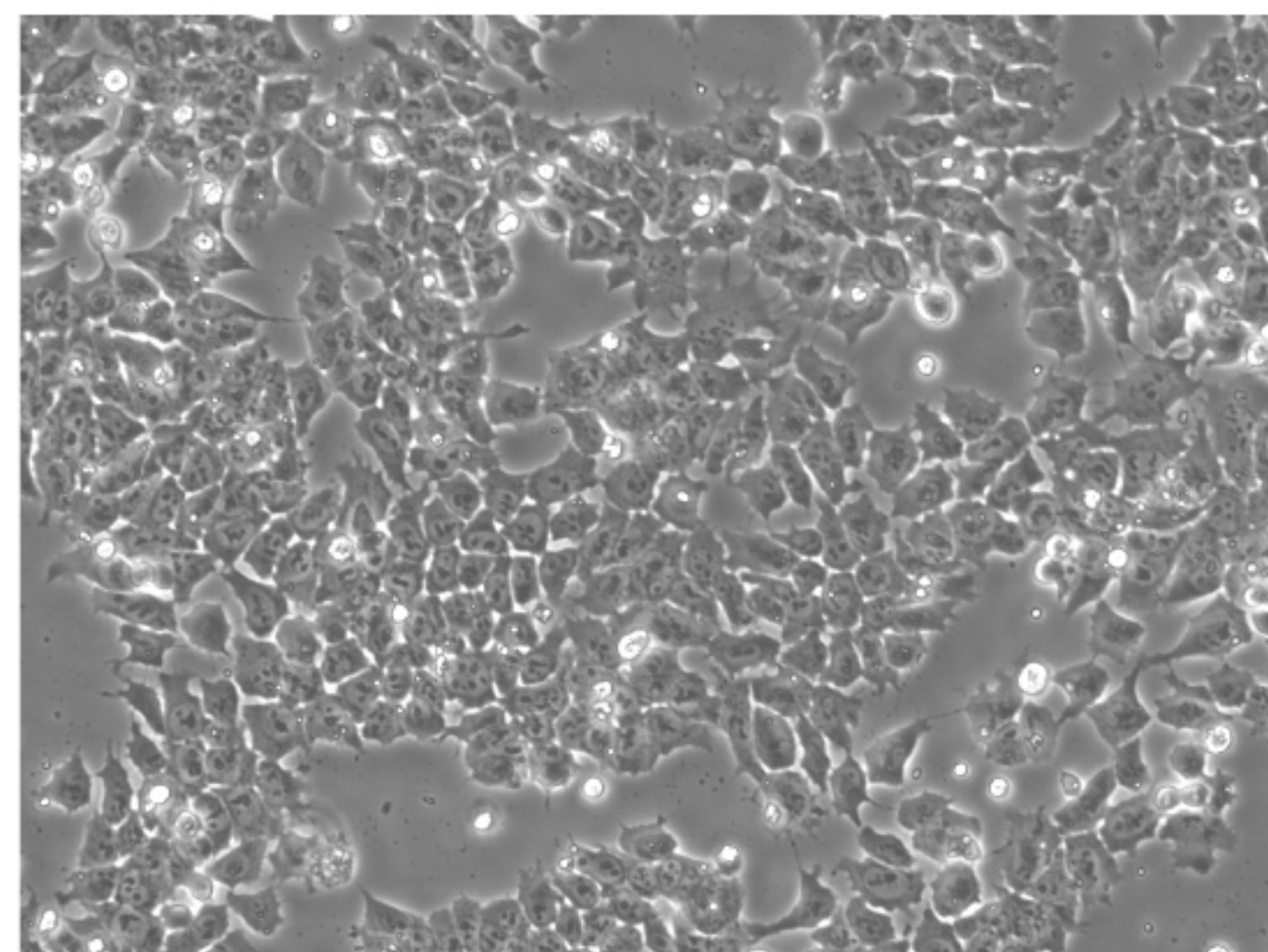
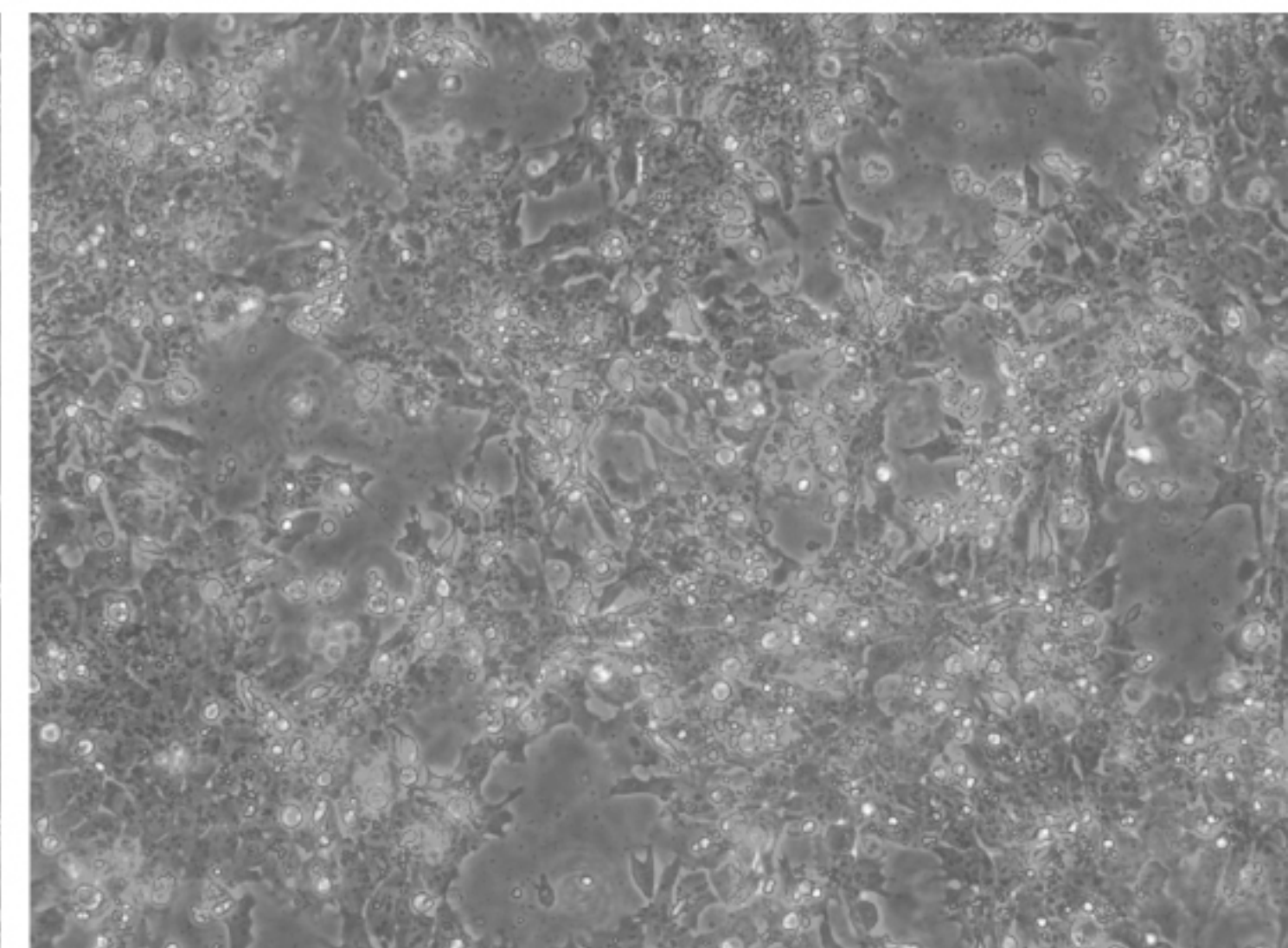
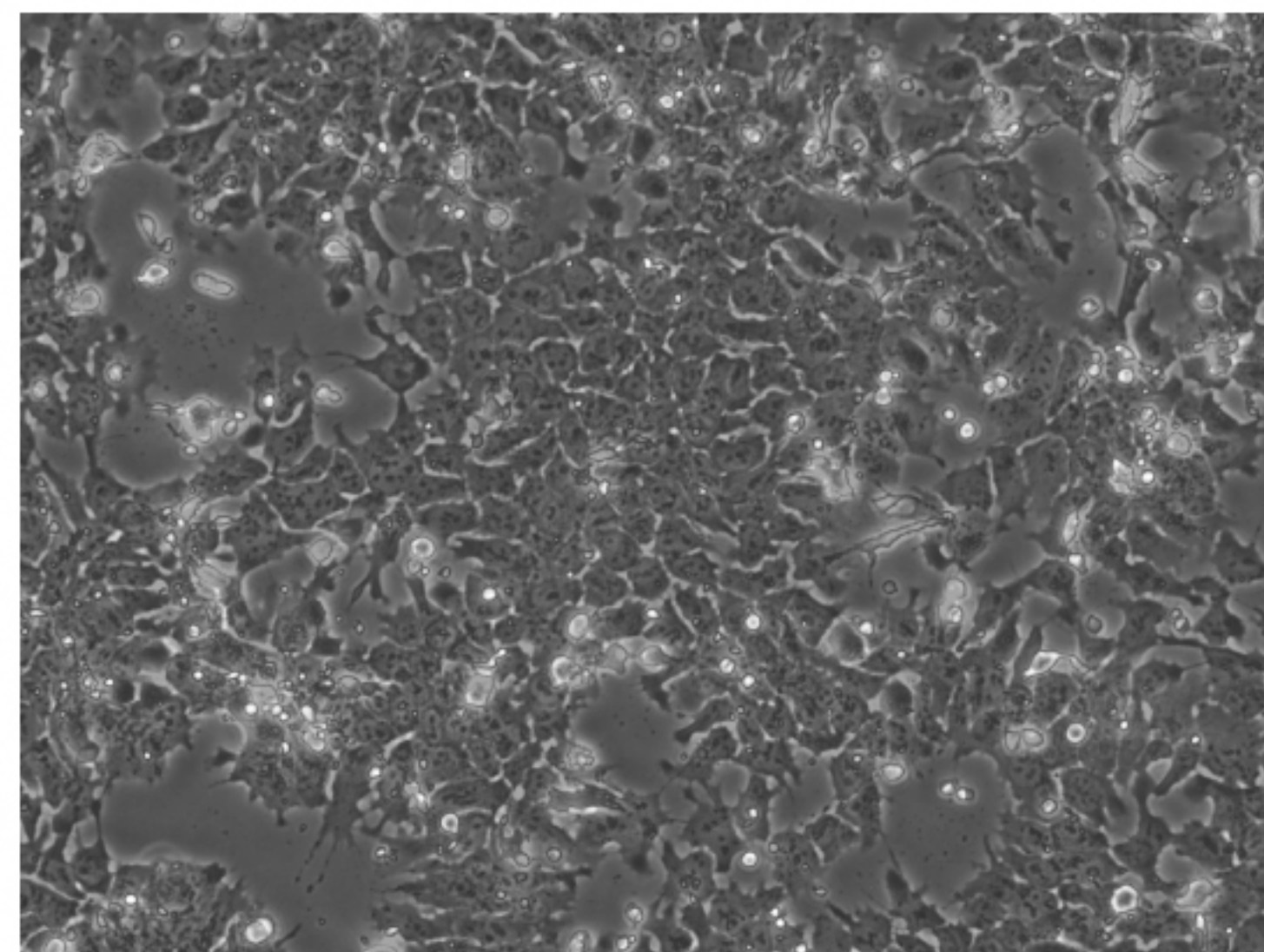
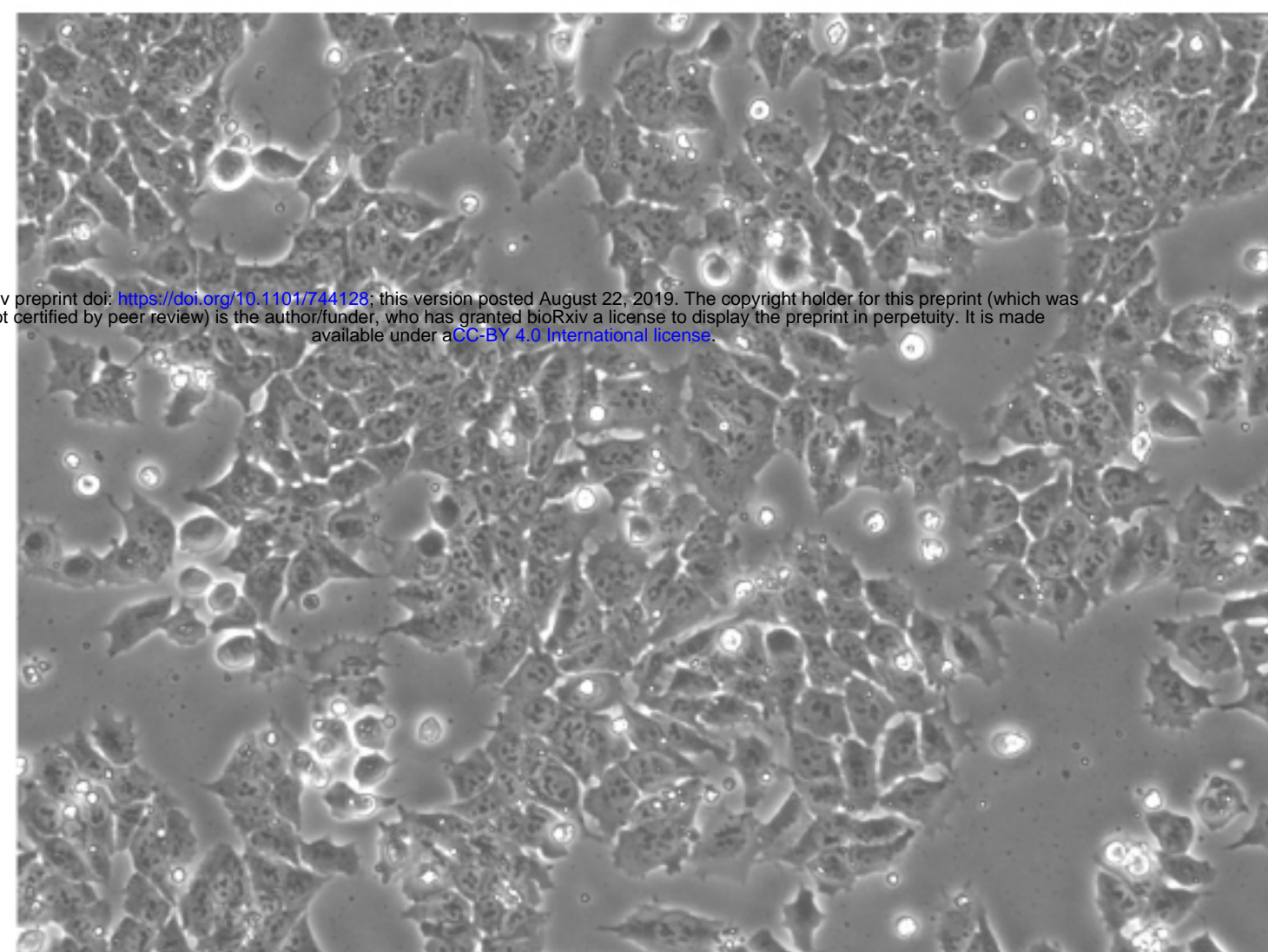
A**B**

EpiLC induction (Activin A + bFGF + KSR (1%) + N2B27)

Day 1

Day 2

Day 3



Wild-type

Cables2^{-/-}

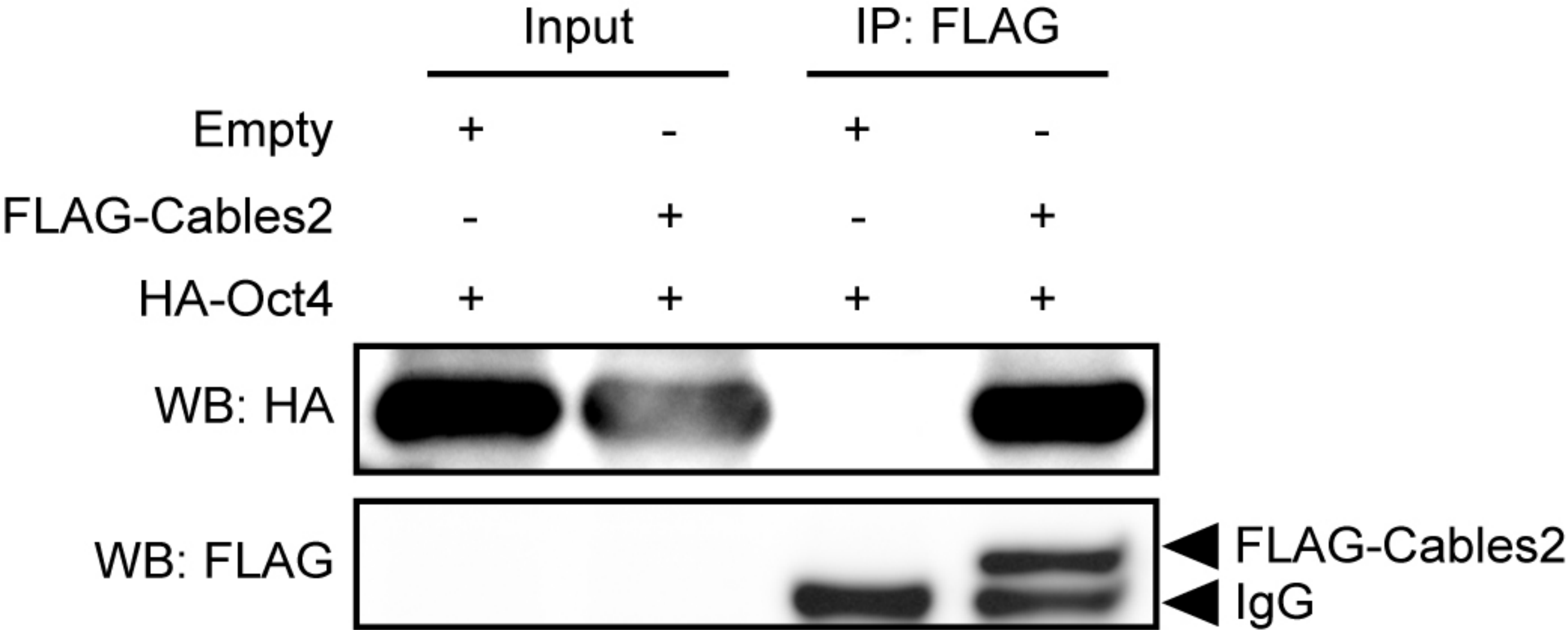


Figure 6—figure supplement 2

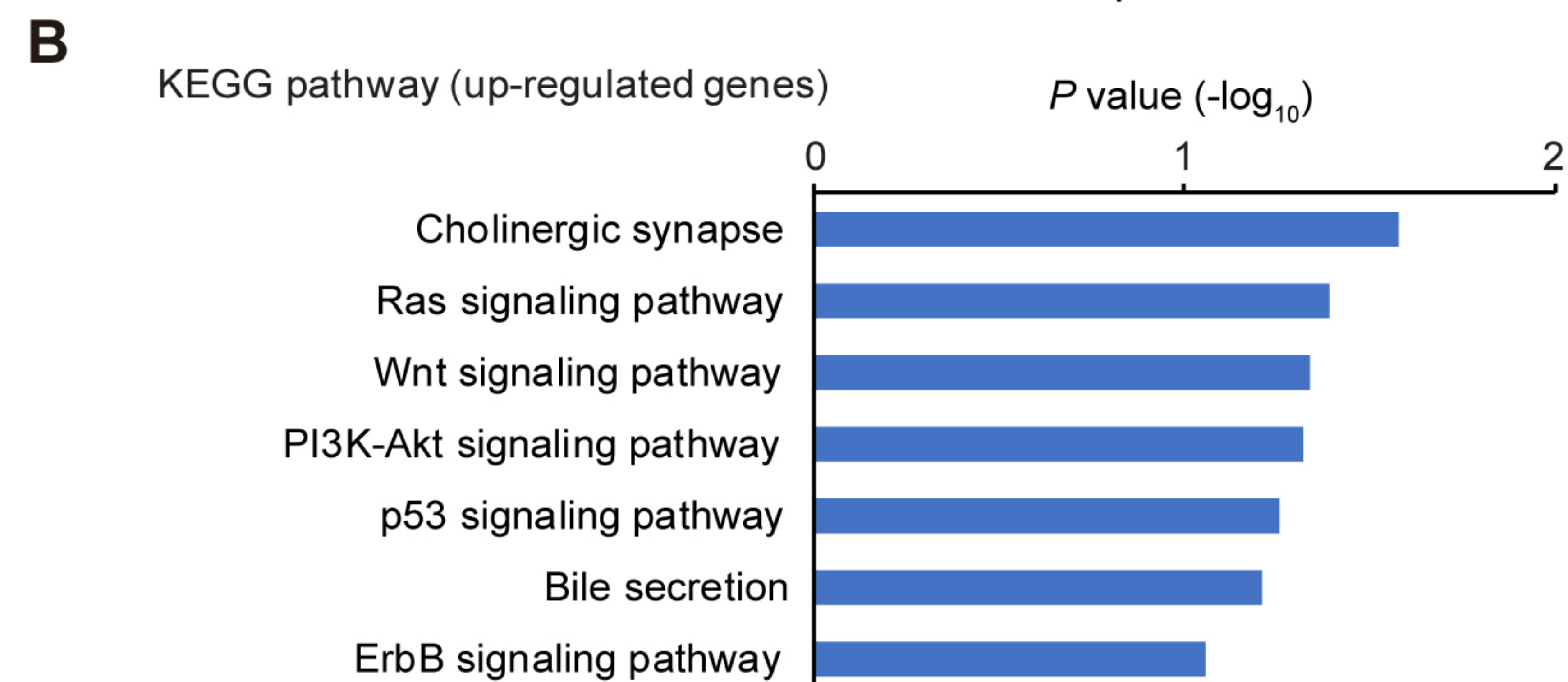
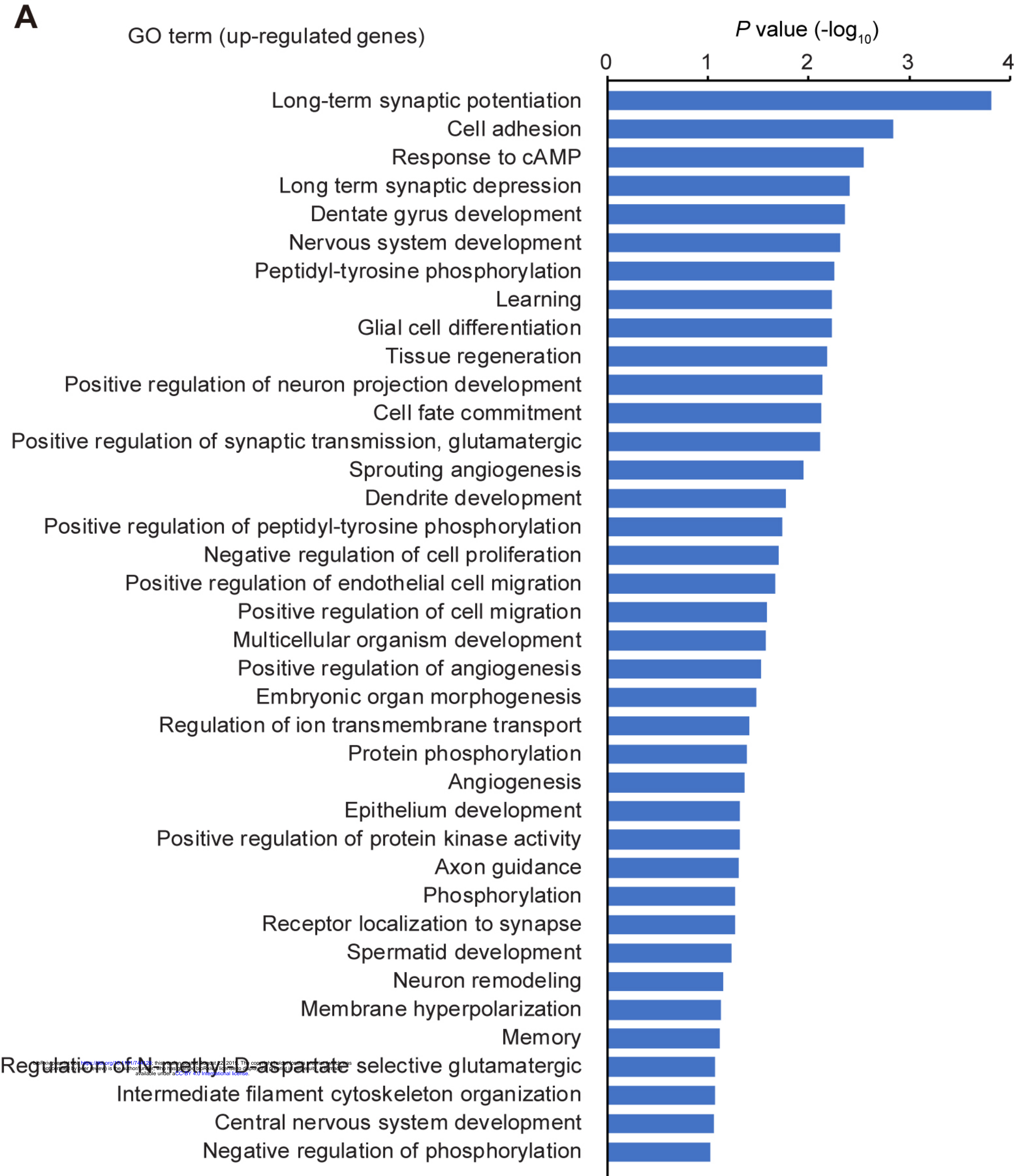


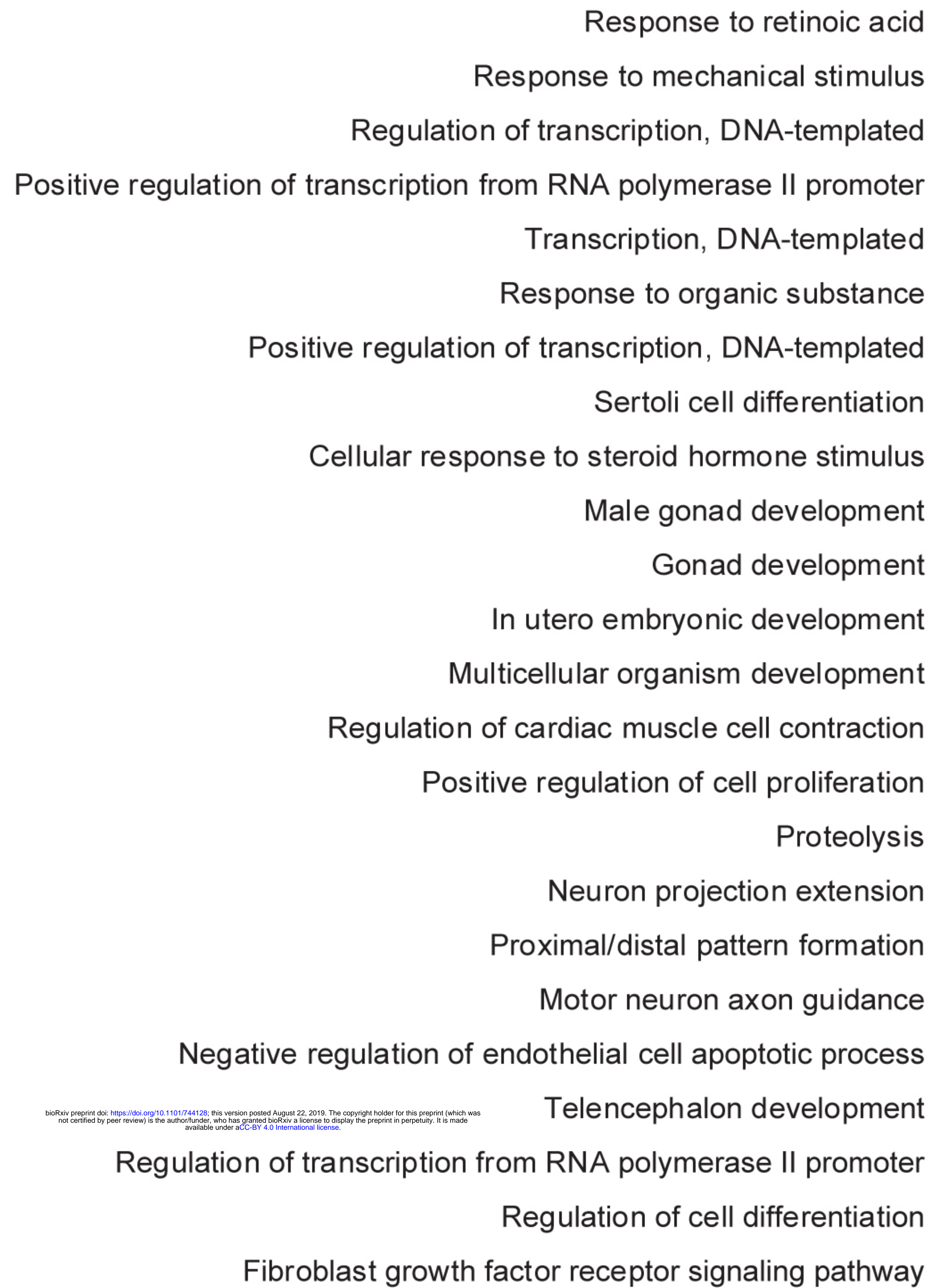
Figure 6—figure supplement 3

A

GO term (down-regulated genes)

 P value ($-\log_{10}$)

0 1 2 3 4



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B

KEGG pathway (down-regulated genes)

 P value ($-\log_{10}$)

0 1 2

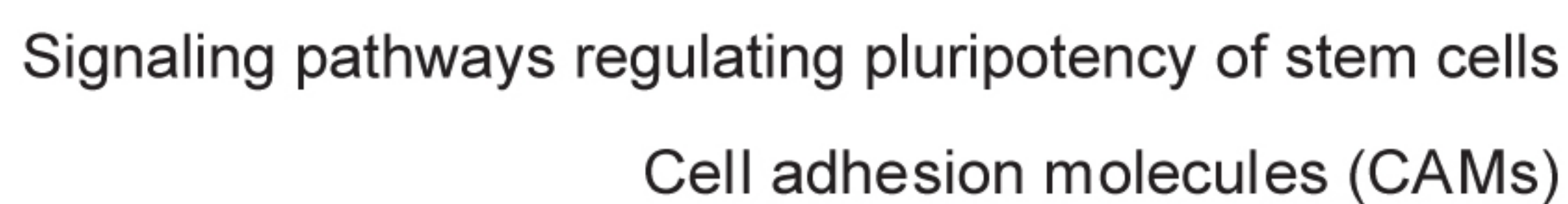


Figure 6—figure supplement 4