

1 **PIK3C2B promotes epithelial to mesenchymal  
2 transition and EGFR inhibitors insensitivity in  
3 epidermal squamous cell carcinoma.**

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12 cells**

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15 traffic**

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## 24 Abstract

25 While the class I of PI3Ks has been deeply studied due to its clear implication in  
26 cancer development, little is known about the class II of PI3Ks. However, recent  
27 accumulation of data is now revealing that PI3KC2 $\beta$ , one isoform of this class of  
28 PI3Ks, may also play a role in cancer. Specifically, recent studies have suggested  
29 an implication of PI3KC2 $\beta$  in metastasis formation through the promotion of  
30 epithelial to mesenchymal transition (EMT). Here, we report that the  
31 overexpression of PI3KC2 $\beta$  in the epidermal squamous cell carcinoma (ESCC)  
32 cells A431 promotes apparent EMT transformation. We further confirm this EMT  
33 by showing modification in several biochemical markers (E-cadherin,  $\beta$ -catenin,  
34 Snail, Twist1 and Vimentin). Furthermore, an intracellular co-localization of E-  
35 cadherin,  $\beta$ -catenin and EGFR was observed. This transformation decreased  
36 EGFR signaling and the sensitivity to inhibitors targeting this receptor. To confirm  
37 our results, we have used the colon adenocarcinoma cells HT29 and induced  
38 overexpression of PI3KC2 $\beta$  in these cells. We could recapitulate in this model  
39 some of our major findings regarding EMT in the PI3KC2 $\beta$  overexpressing A431  
40 cells. Taken together, these data support a role of PI3KC2 $\beta$  in promoting EMT.

41

## 42 Introduction

43 Phosphoinositide-3-kinases (PI3Ks) are a family of lipid kinases that play a role  
44 in coordinating main intracellular signaling pathways following the activation by  
45 upstream agonists such as receptor tyrosine kinases (RTKs) or G protein coupled  
46 receptors (GPCR) (1). They phosphorylate the 3'-hydroxyl group of the inositol  
47 ring of three species of phosphatidylinositol (PI) lipid substrates. This triggers the  
48 formation of the second messengers PI(3)P (phosphatidylinositol 3-phosphate),  
49 PI(3,4)P<sub>2</sub> (phosphatidylinositol 3,4-bisphosphate) and PIP3 (phosphatidylinositol  
50 3,4,5-trisphosphate), specifically enriched in different cellular compartments (1).  
51 Subsequently, different effectors will be recruited and bind to these PI3K  
52 phospholipid products, changing their conformation and inducing the propagation  
53 of signals involved in cell cycle progression, cell growth, survival, migration, and  
54 intracellular vesicular transport (2).

55 In mammals, the PI3K family is formed by eight different catalytic PI3K  
56 isoforms, classified into three classes (I, II and III), based on sequence homology  
57 and *in vitro* substrate specificity (2). The different PI3K isoforms can be expressed  
58 in a tissue-specific manner and seem to have non-redundant roles. Among the  
59 PI3K classes, mutations in class I PI3K isoforms are especially linked with cancer  
60 development, being *PIK3CA* the second most frequently mutated oncogene (3).  
61 However, while class I PI3Ks have been well studied, little is known about the  
62 function of class II. This is mainly because they were first identified by PCR and  
63 homology cloning approaches, not based on their cellular function (4,5). Finally,  
64 the lack of specific inhibitors and mouse models hindered the discrimination  
65 between the biological functions of each isoform.

66 PI3KC2 $\beta$  is one of the three isoforms from class II PI3K. It is ubiquitously  
67 transcribed, showing the highest levels in placenta and thymus (6,7). This lipid  
68 kinase is a monomer mainly activated downstream of RTKs, like EGFR, and other  
69 GPCRs (8,9). It has a substrate specificity directed towards PI and PI(4)P,  
70 generating a pool of PI(3)P or PI(3,4)P<sub>2</sub> in the plasma membrane and endosomes  
71 (10,11). Through the recruitment of different secondary messengers and the  
72 subsequent activation of AKT/mTOR or RAC signaling pathways, PI3KC2 $\beta$   
73 regulates different cellular functions like cell migration, cell growth, cell survival,  
74 invasion, cell cycle progression and K<sup>+</sup> channel activation (12–15).

75 PI3KC2 $\beta$  is the isoform of the class II of PI3Ks that has the most  
76 documented implication in cancer development. Its overexpression at the protein  
77 and mRNA level in a variety of human tumors (12,13,16,17), and the promising  
78 effects of PI3KC2 $\beta$  inhibition observed in leukemia, brain and neuroendocrine  
79 tumors (18), are a few of the observations that support this hypothesis. Recent  
80 studies have observed a correlation between PI3KC2 $\beta$  expression and  
81 metastasis formation in breast, prostate cancer and esophageal squamous cell  
82 carcinoma (12,13,19).

83 Most of cancer-related death are due to metastases formation. To that  
84 end, primary tumors need to undergo the biological process known as epithelial-  
85 mesenchymal transition (EMT). This process allows immobile epithelial cells to  
86 acquire a mobile mesenchymal phenotype, losing cell-cell contact dependency.  
87 This transformation is promoted by the expression of several transcription factors  
88 like Snail, Slug, and Twist. Two important mechanisms are the replacement of  
89 keratin cytoskeleton by a more plastic Vimentin cytoskeleton and the decreased  
90 membranal expression of cell–cell adhesion proteins such as E-cadherin or  $\beta$ -

91 Catenin (20). Different studies have suggested an implication of PI3KC2 $\beta$  in EMT  
92 (12,13). However, the exact mechanism by which this kinase is participating in  
93 this process is still unknown.

94 In the epidermal squamous cell carcinoma (ESCC) cells A431, the  
95 overexpression of PI3KC2 $\beta$  has been reported to enhance membrane ruffling,  
96 migration speed of the cells, protection from anoikis and cell proliferation (14).  
97 We decided to assess if some of these previously reported effects could be  
98 consequence of a possible process of EMT induced in these cells after the  
99 overexpression of PI3KC2 $\beta$ . For this purpose, A431 cells stably expressing  
100 PI3KC2 $\beta$  were evaluated for different EMT markers expression. The cytoplasmic  
101 localization of different cell-cell adhesion proteins was also visualized. Moreover,  
102 the functional impact of PI3KC2 $\beta$  overexpression was assessed in relation to its  
103 effect in EGFR signaling and the sensitivity to inhibitors targeting this receptor.  
104 Finally, to further validate our results, PI3KC2 $\beta$  overexpression was induced in  
105 an additional cell line, HT29.

106

## 107 **Materials and methods**

### 108 **Cell Lines**

109 A431 human epidermoid carcinoma cells and HT29 cells were purchased from  
110 the American Type Culture Collection. A431 cells were grown in DMEM (Sigma  
111 Aldrich, cat. no. D5796) supplemented with 10% (v/v) fetal bovine serum (FBS)  
112 (Gibco, cat. no. 10082147), 2 mM L-glutamine (Gibco, cat. no. 25030081) and  
113 50.000 units of penicillin/streptomycin (Gibco, cat. no. 15140122). HT29 cells  
114 were grown in McCoy's 5A Medium (Gibco, cat. no. 26600-023) supplemented  
115 with 10% (v/v) fetal bovine serum (FBS) (Gibco, cat. no. 10082147), 2 mM L-

116 glutamine (Gibco, cat. no. 25030081) and 50.000 units of penicillin/streptomycin  
117 (Gibco, cat. no. 15140122). Cells were passaged every 3 to 4 days and were kept  
118 incubated in a humidified atmosphere of 5% CO<sub>2</sub> at 37 °C. Stably transfected  
119 HT29 and A431 clones were grown in the presence of 0.8 mg/ml G418 (Life  
120 Technologies).

121

122 **Stable transfection**

123 A431 cell lines stably expressing PI3KC2β were generated as previously  
124 described (8). HT29 cell lines stably expressing PI3KC2β were generated as  
125 follows. The cDNA of N-terminal myc-tagged (MEQKLISEEDL) PI3KC2β wild-  
126 type was cloned into pcDNA3 vector (Invitrogen) using EcoRI and Xhol sites as  
127 described in Arcaro et al. 1998. The transfection of the pcDNA3-PI3KC2β plasmid  
128 was performed using Lipofectamine 2000 (Invitrogen) according to  
129 manufacturer's instructions. 48 h post-transfection cells were split into selection  
130 medium containing 1 mg/ml G418. Cells were cultured in the selection medium  
131 for 2-3 following weeks. Medium was changed each 72 h. When the single G418  
132 resistant colonies appeared, they were further selected and expanded. After 2-3  
133 passages, expression of PI3KC2β was verified by qPCR and western blot.

134

135 **Western blotting**

136 Proteins were extracted in RIPA buffer (20 mM Tris-base pH=8, 150 mM NaCl,  
137 1% TritonX-100, 0.1% SDS, 0.5% sodium deoxycholate. Sigma, cat. no. D6750-  
138 10G) supplemented with Halt™ protease/phosphatase inhibitor cocktail (Pierce,  
139 cat. no. 78444). Protein concentration was assessed by Pierce BCA protein  
140 assay kit (Thermo Scientific, cat. no. 23225) and 20 µg of total proteins were

141 separated by SDS-PAGE. Protein gels were transferred into nitrocellulose  
142 membranes and blocked with Tris buffered saline (TBS 1x 130 mM, NaCl 30 mM,  
143 Tris-Cl pH=7.5) containing 5% Bovine Serum Albumin (BSA) for 2 h. Western  
144 blots were probed with rabbit anti-PI3KC2 $\beta$  polyclonal antibody (1/1000,  
145 described in (6), rabbit anti-pAKT S473 (1/1000, Cell signaling, cat. no. 4090),  
146 rabbit anti-pERK (1/2000, Cell signaling, cat. no. 4370), mouse anti-panAKT  
147 (1/1000, cat. no. 2920, Cell signaling), mouse anti-ERK (1/5000, Cell signaling,  
148 cat. no. 9107), mouse anti- $\beta$ -ACTIN antibody (1/15000, Sigma-Aldrich, cat. no.  
149 A5316), mouse anti-E-cadherin (1/1000, Abcam, cat. no. 76055), rabbit anti- $\beta$ -  
150 catenin (1/1000, Abcam, cat. no. 32572) and rabbit anti-EGFR (1/1000, Cell  
151 signaling, cat. no. 4267).

152 Primary antibodies were detected using goat anti-rabbit IR680 (1/10'000,  
153 Li-Cor Bioscience, cat. no. 926-68071) and goat anti-mouse IR800 (1/10'000, Li-  
154 Cor Bioscience, cat. no. 926-32210) and imaged by a LI-COR OdysseySa®  
155 scanner. Antibodies were diluted in TBS x1 containing 2% BSA, 0.1% Tween and  
156 0.1% sodium azide.

157

### 158 **Proliferation assays**

159 The EGFR kinase inhibitors, Gefitinib and Erlotinib, were purchased from  
160 ChemieTek (Indianapolis, IN, USA). Cells were seeded at a density of 3-5 x 10<sup>3</sup>  
161 cells/well (depending on the cell line) in a 96-well plate using the cell line-specific  
162 culture medium. Cells were allowed to adhere overnight and were then treated  
163 with the indicated concentration of drugs for 72 h. After the treatment, cells were  
164 fixed with 10% buffered formalin, stained with 0.2% crystal violet (Sigma-Aldrich,  
165 cat. no. C3886-25G) in 2% ethanol, washed 5 times in dH<sub>2</sub>O and lysed with 100

166  $\mu$ L 1% SDS to recover the dye. Optical density (OD) at 550 nm was measured  
167 with a microplate reader and normalized to the DMSO control. Dose-response  
168 curves were carried out by using the medium described previously.

169

170 **Quantitative Real-time PCR**

171 RNA was extracted using the RNeasy Mini Kit (Qiagen, cat. no. 74106) according  
172 to the manufacturer's protocol. Reverse-transcription was performed with  
173 Superscript II Reverse Transcriptase (Invitrogen, cat. no. 18064-014) following  
174 the manufacturer's protocol. The Sybr green® real-time primers used in this  
175 project were purchased from Applied Biosystems and are depicted in Table 1.  
176 PCR reactions were performed in a ViiA7 cycler (Applied Biosciences) using  
177 SybrSelect Mastermix (Applied Biosystems, cat. no. 4472908). Expression of  
178 mRNA was normalized to *ACTB* and *GAPDH* housekeeping genes using the  $2^{\Delta\Delta\text{act}}$   
179 method.

180

| qPCR primers   |                                   |                                    |
|----------------|-----------------------------------|------------------------------------|
| Gene name      | Forward                           | Reverse                            |
| <i>ACTB</i>    | CCT GGC ACC CAG CAC AAT           | GGA CAG CGA GGC CAG GAT            |
| <i>EGFR</i>    | GCA ATA TCA GCC TTA GGT GCG GCT C | CAT AGA AAG TGA ACA TTT AGG ATG TG |
| <i>GAPDH</i>   | CCA CCC ATG GCA AAT TCC ATG GCA   | TCT AGA CGG CAG GTC AGG TCC ACC    |
| <i>PIK3C2B</i> | CAG GCT TCA AGA GGC ACT CA        | TGG TCA TCA TTC ACC GTC CG         |
| <i>SNAIL</i>   | GGA AGC CCA ACT ATA GCG AGC       | CAG TTG AAG ATC TTC CGC GAC        |
| <i>TWIST</i>   | CAT CGA CTT CCT CTA CCA GGT C     | TCC ATT TTC TCC TTC TCT GGA A      |

181 **Table 1: list of primers used for qPCR quantifications.**

182

183 **Immunofluorescence staining**

184 Cells were grown for 24 h on glass coverslips in 24 well plates to around 60%  
185 confluence. After 10% formalin (Sigma Aldrich, cat. no. HT501128) fixation (10  
186 min), coverslips were washed 3x10 min in phosphate buffered saline (1x PBS:  
187 137 mM NaCl, 2.7 mM KCl, 18 mM KH<sub>2</sub>PO<sub>4</sub>, 10 mM Na<sub>2</sub>HPO<sub>4</sub>) and cells were  
188 subsequently permeabilized with a 1x PBS, 0.3% TritonX-100 solution. Following  
189 blocking with a 1% BSA, 0.2% gelatin, 0.05% saponin in 1x PBS solution and  
190 washing with a 0.1% BSA, 0.2% gelatin, 0.05% saponin in 1x PBS solution. Cells  
191 were incubated overnight at 4 °C with the primary antibodies, rabbit anti-Vimentin  
192 (1/300, Abcam, cat. no. 5741,), mouse anti-E-cadherin (1/200, Abcam, cat. no.  
193 76055), rabbit anti-β-catenin (1/200, Abcam, cat. no. 32572), rabbit anti-EGFR  
194 (1/300, Cell Signalling cat. no. 4267), rabbit anti-PI3KC2β polyclonal antibody  
195 (1/200, described in (6)), mouse anti-58K (5 µg/ml, cat. Abcam, no. 27043,),  
196 mouse anti-RAB 7 (1/300, cat. no. 376362, Santa Cruz Biotechnology) and  
197 mouse anti-RAB 11 (1/300, Cell Signalling, cat. no. 5589). The secondary  
198 antibodies, goat anti-rabbit Alexa-488 (1:400, Life Technologies, cat. no. A11034)  
199 and goat anti-mouse Alexa-633 (1:300, Life Technologies, cat. no. A21052,) were  
200 used to detect antigen-antibody complexes; slides were counter-stained with  
201 DAPI (500 ng/ml, Sigma Aldrich, cat. no. 32670-25MG) to visualize DNA.

202

203 **Slide Scanning**

204 Slides were scanned using a Panoramic Midi digital slide scanner (3DHISTECH)  
205 and analyzed with the Panoramic Viewer software (3DHISTECH). For the  
206 quantification of Vimentin/DAPI positive cells, an area of the slide was selected  
207 and analyzed with CellQuant software (3DHISTECH).

208 **Confocal images**

209 Cells were examined by confocal Leica SP8 X STED inverted microscope under 63 $\times$   
210 magnifications. Image files were collected as a matrix of 1024  $\times$  1024 pixels and  
211 analyzed using the Leica Application Suite X Microscope Software.

212

213 **Wound healing assay**

214 Cells were grown to confluence in 6-well tissue culture plates. The resulting cell  
215 monolayer was scratched with a 200  $\mu$ L pipette tip generating two parallel  
216 wounds and returned to a humidified incubator at 37 °C 5% CO<sub>2</sub>. Two replicates  
217 for each treatment and four phase-contrast images were acquired along the  
218 length of each wound every 2-4 h under 40x magnifications. Cell migration was  
219 also assessed in a 96-well format using ORIS cell migration assay from Platypus  
220 Technologies (cat. no. CMA1.101). Cells were seeded at a density of 7x10<sup>4</sup>  
221 cells/well in 100  $\mu$ l of medium around the stoppers and left to attach for 24 h.  
222 Next day, the stoppers were removed, and phase-contrast images were  
223 acquired from each well every 2-4 h. The wound area was determined from  
224 these images after delineating the edges digitally using Adobe Photoshop CS4  
225 software.

226

227 **Statistical analysis**

228 Data is presented as average  $\pm$  SD. All experiments were performed in triplicates.  
229 Statistical analyses were conducted using GraphPad Prism 7 (GraphPad  
230 Software). The statistical test used is indicated in the respective figure legend. P  
231 < 0.05 was considered as statistically significant.

232

233 **Results**

234 **The overexpression of PI3KC2 $\beta$  changes the migration front of A431**

235 To further study the implication of PI3KC2 $\beta$  in regulating cell migration (14,21),  
236 stably transfected A431 cells were used. First, *PIK3C2B* overexpression was  
237 validated at the protein level. Results of the conducted western blots indicated  
238 strong PI3KC2 $\beta$  overexpression in stably expressing clones, increasing the levels  
239 of this kinase to  $233.88 \pm 16.95\%$  of the parental cell line expression level (Fig  
240 1A). We then tested the effect of this overexpression in terms of cellular migration.  
241 The PI3KC2 $\beta$  overexpressing cells presented increase in wound healing closure  
242 speed compared to the parental cell line A431 (Fig 1B). During these migration  
243 assays, A431 cells appeared to have tighter cell-to-cell junctions, typical from  
244 epithelial cells, whereas A431C2 $\beta$  showed a more fibroblastic spindle-like  
245 morphology (Fig 1C).

246

247 **PI3KC2 $\beta$  overexpression increases EMT markers expression.**

248 Following the primary observation, the levels of EMT markers in A431 and  
249 A431C2 $\beta$  cells were evaluated. E-cadherin and  $\beta$ -catenin expression were  
250 reduced in A431C2 $\beta$  cells compared to A431 by 21% and 71% respectively (Fig  
251 2A). Snail and Twist, two transcription factors involved in EMT presented elevated  
252 transcription with almost 4 folds for *SNAI1* and more than 3 folds for *TWIST1* (Fig  
253 2B) of the parental transcription levels in the A431C2 $\beta$ . Finally, immunostaining  
254 of Vimentin (green) showed a higher positivity index (more than 7 folds higher) in  
255 A431C2 $\beta$  compared to A431 (fig 2C).

256

257 **Cytoplasmic co-localization of E-Cadherin,  $\beta$ -Catenin in A431C2 $\beta$**

258 To study further the effect of PI3KC2 $\beta$  overexpression, the cellular localizations  
259 of E-cadherin and  $\beta$ -catenin were visualized by confocal microscopy after  
260 immunofluorescence staining. While in A431 cells, E-cadherin and  $\beta$ -catenin  
261 showed staining mainly at the plasma membrane, A431C2 $\beta$  cells, showed  
262 staining at both the plasma membrane and in a cytoplasmic region close to the  
263 nucleus (Fig 3A).

264 To better define the cytosolic sub compartment of the cell where E-  
265 cadherin and  $\beta$ -catenin were localized, dual-color immunofluorescence stainings  
266 of  $\beta$ -catenin with either 58K (22) used as a marker of the Golgi apparatus (Fig  
267 3B) or Rab 7 (23) as a marker for late endosomes (Fig 3C) were performed.  $\beta$ -  
268 catenin co-localized with neither 58K nor Rab 7.

269

270 **Cytoplasmic co-localization of PI3KC2 $\beta$  and EGFR with E-cadherin/ $\beta$ -  
271 catenin aggregates**

272 In attempt to explain the effect of PI3KC2 $\beta$ -induced cytoplasmic localization of E-  
273 cadherin and  $\beta$ -catenin, we tested if PI3KC2 $\beta$  localization was overlapping with  
274 E-cadherin and  $\beta$ -catenin. Dual-colour immunofluorescence staining of PI3KC2 $\beta$   
275 with E-Cadherin was also performed revealed partial co-localization of these  
276 proteins in the cytoplasm (Fig 4A).

277 We performed here a dual-color immunofluorescence staining of EGFR  
278 with E-cadherin (Fig 4B). The overlap of the two signals in the cytoplasm showed

279 that the two proteins co-localize suggesting that PI3KC2 $\beta$  overexpression is  
280 leading to the internalization of E-cadherin,  $\beta$ -catenin and EGFR together in the  
281 same intracellular compartment.

282

283 **PI3KC2 $\beta$  overexpression reduces EGFR signaling**

284 The PI3KC2 $\beta$ -driven relocalization of EGFR has been further examined.  
285 Quantitative PCR analysis showed a significant reduction of *EGFR* transcription  
286 (-88.47  $\pm$ 18.87%) but also a significant reduction of EGFR expression (-81.38  
287  $\pm$ 7.42%) in the A431C2 $\beta$  cells (Fig 5A and 5B) compared to the parental cell line  
288 A431. Consequently, alterations in EGFR downstream signaling were analyzed.  
289 We could find that A431C2 $\beta$  cells showed decreased phosphorylation levels for  
290 AKT (29.81  $\pm$ 0.69%) and ERK (22.68  $\pm$ 4.72%) (Fig 5C) compared to their  
291 respective total expression. This reduction was less remarkable when compared  
292 to beta-Actin, since a strong increase of total-ERK was also found (Fig 5C).

293 PI3KC2 $\beta$  has also been suggested to participate in chemo-resistance to  
294 different drugs (6–8). We therefore tested if this PI3KC2 $\beta$ -driven relocalization of  
295 EGFR translates into modified response to EGFR kinase inhibitors. Cell  
296 proliferation of the two lines, A431 and A431C2 $\beta$ , was measured after 72 h of  
297 treatment with 0.1% DMSO or with increasing concentrations of EGFR kinase  
298 inhibitors, Erlotinib and Gefitinib. Results obtained from the crystal violet assay  
299 showed that PI3KC2 $\beta$  overexpression increases Erlotinib and Gefitinib resistance  
300 (Fig 5D). More specifically, the measured IC50 for Erlotinib shifted from 0.652  $\mu$ M  
301 to 4.434  $\mu$ M between A431 and A431C2 $\beta$ , and the measured IC50 for Gefitinib  
302 shifted from 0.084  $\mu$ M to 0.47  $\mu$ M.

303 **The overexpression of PI3KC2 $\beta$  induces also EMT markers expression in**  
304 **HT29 cells**

305 To confirm our observations, HT29 cells were stably transfected with the same  
306 Myc-tagged *PIK3C2B* expression vector used for the A431 cells. After  
307 transfection, the different generated clones were evaluated on a transcriptional  
308 level for *PIK3C2B* overexpression. The clone HT29C2 $\beta$  (1/14) was selected for  
309 its highest expression of *PIK3C2B* with a relative expression of  $751 \pm 81.96\%$  in  
310 comparisons to the parental HT29 cell line (Fig 7A) or the cells transfected with  
311 the empty pcDNA3 vector. The levels of different EMT markers were also  
312 evaluated by western blot. In HT29 cells *PIK3C2B* overexpression resulted in a  
313 decrease in the expression levels of E-cadherin ( $-40.05 \pm 8.62\%$ ) in relation to the  
314 parental HT29 cell line (Fig 6A). Furthermore, HT29C2 $\beta$  cells also showed  
315 increased mRNA levels for *SNAI1* (2.5 folds) (Fig 6B). Finally, the comparison of  
316 the morphology of the migration front between HT29 and HT29C2 $\beta$  cells showed  
317 in HT29 an apparent tighter cell-to-cell contacts than in HT29C2 $\beta$  (Fig 6C).

318

319 **Discussion**

320 In this study, we have confirmed that PI3KC2 $\beta$  overexpression in A431  
321 epidermoid carcinoma cells is promoting a more motile phenotype increasing  
322 wound healing closure (Fig 1B). Katso *et al.* previously reported that the  
323 increased expression of PI3KC2 $\beta$  stimulates Rac activity in these cancer cells,  
324 increasing membrane ruffling and migration speed of the cells (14). Moreover,  
325 the overexpression of this PI3KC2 $\beta$  also renders A431 cells resistant to anoikis  
326 (14). Additionally, in the present study we have observed a change in the

327 morphology of the cells from the migration front, that switch from apparently tight  
328 cell-to-cell contact to a more fibroblastic spindle-like morphology after PI3KC2 $\beta$   
329 overexpression (Fig 1C). This morphology change resembles the cytoskeleton  
330 reorganization typical of a EMT process (24,25).

331 We observed that the overexpression of PI3KC2 $\beta$  induced an increased  
332 expression of different EMT markers: mRNA levels of Snail and Twist, increase  
333 positivity index of Vimentin and decreased protein levels of E-cadherin and  $\beta$ -  
334 catenin (Fig 2). This is consistent with what has been already observed, in  
335 prostate cancer that PI3KC2 $\beta$  has been reported to control cell invasion by  
336 regulating SLUG expression, a transcription factor promoting EMT progression  
337 (13). Additionally, in breast cancer cell lines, PI3KC2 $\beta$  regulates cell invasion and  
338 activates the transcription factor STAT3, that controls the expression of master  
339 EMT transcription factors (12).

340 In A431, the induction of EMT can be elicited by a chronic EGF treatment  
341 that promotes the endocytosis of E-cadherin followed by the dissociation of the  
342 E-cadherin/ $\beta$ -catenin complex and the subsequent trans-activation of the  $\beta$ -  
343 catenin/lymphoid enhancer factor 1 (LEF-1) pathway (26,27). We are reporting  
344 here that PI3KC2 $\beta$  overexpression is promoting a perinuclear localization of E-  
345 cadherin,  $\beta$ -catenin and EGFR instead of mainly at the plasma membrane (Fig  
346 3A, 4A). However, we were not able to determinate their specific cytoplasmic  
347 localization as they do not co-localize with markers of Golgi apparatus or late  
348 endosomes (Fig 3B-C). Despite this, the proximity to late endosomes markers  
349 suggest that these molecules could be localized in another type of endosomes.  
350 A similar phenotype was observed in A431 after the treatment with  
351 lysophosphatidic acid (LPA) (28). In this study E-cadherin and  $\beta$ -catenin were co-

352 localized by immunostaining in a discrete region near the nucleus that was  
353 identical to the perinuclear endocytic recycling compartment (ERC). The authors  
354 proposed that the ERC may be a site of residence for  $\beta$ -catenin destined to enter  
355 the nucleus, and that this accumulation of  $\beta$ -catenin levels in the ERC could  
356 effectively affects  $\beta$ -catenin substrate levels available for downstream pathways  
357 and being critical for cancer progression (28).

358 In our study, the dual-colour immunofluorescence staining of PI3KC2 $\beta$   
359 with E-Cadherin revealed a partial co-localization of these proteins in a similar  
360 discrete perinuclear region (Fig 4A). This supports the hypothesis that PI3KC2 $\beta$   
361 could be promoting the internalization of E-cadherin,  $\beta$ -catenin and EGFR.  
362 PI3KC2 $\beta$  is one of the major producers of PI3P in endosomes (29). Moreover, an  
363 *in vivo* study performed by Alliouachene *et al.* reported that the reduction of PI3P  
364 upon PI3K-C2 $\beta$  inactivation has selectively impact on endosomal trafficking (11),  
365 specifically in the maturation of the APPL1-positive very early endosomes.  
366 Moreover, in this study they also observed that PI3K-C2 $\beta$  inactivation led to an  
367 accumulation of the insulin receptors in these early endosomal  
368 compartments. Therefore, we think that the overexpression of PI3KC2 $\beta$ , probably  
369 though an increase in PI3P production, is strongly increasing the level of  
370 internalization of E-cadherin,  $\beta$ -catenin and EGFR inducing their accumulation  
371 possibly in the ERC. This notably decreases the presence of these molecules in  
372 the plasma membrane and adherent junctions, consequently affecting the  
373 stabilization of cell-cell adhesion and probably leading to EMT (Fig 7) (28).

374 In addition to the observed effect in the cellular localization of EGFR, a  
375 decrease in EGFR expression was also reported after PI3KC2 $\beta$  overexpression  
376 (Fig 5B). This observation is in agreement with previous studies showing that in

377 A431 cells specific cellular context, EMT is also associated with a coordinated  
378 loss of EGFR (30). Consistency with the decrease of EGFR, the phosphorylation  
379 status of AKT and ERK, downstream targets of this receptor, was also decreased  
380 (Fig 5C). This reduction was less remarkable when compared to  $\beta$ -Actin levels,  
381 since a strong increase of total-ERK was also found (Fig 5C), suggesting in  
382 addition a possible compensatory mechanism.

383 Together with the decrease in EGFR expression, a reduced sensitivity to  
384 the Erlotinib and Gefitinib was also observed (Fig 5D). This is in agreement with  
385 the transition to a mesenchymal-like phenotype that is known to decrease the  
386 cellular dependence on EGFR signalling, as alternative growth pathways are  
387 activated (31) (Fig 7). This has been confirmed in different clinical trials where  
388 NSCLC with high expression of E-cadherin showed a beneficial response to  
389 Erlotinib treatment in comparison to E-cadherin-negative patients who have an  
390 overall deteriorated condition (32). Carcinoma cell lines expressing epithelial  
391 proteins, such as E-cadherin, are sensitive to growth inhibition by erlotinib,  
392 whereas those tumour cell lines that had undergone an EMT-like transition are  
393 less sensitive to EGFR inhibition (33). Similar patterns have been reported for  
394 pancreatic and colorectal tumour cell lines (34).

395 Additionally, PI3KC2 $\beta$  has also been suggested to participate in the  
396 resistance to different chemotherapeutic compounds like tamoxifen, cisplatin,  
397 Etoposide and Doxorubicin (18,19,35). Moreover, PI3KC2 $\beta$  expression has also  
398 been significantly correlated to resistance towards Erlotinib in glioblastoma  
399 pathogenesis which supports our results (36).

400 In HT29 cells the stable overexpression of PI3KC2 $\beta$  was able to reproduce  
401 the most notable changes observed in A431 cells. HT29C2 $\beta$  showed increased

402 mRNA levels of Snail and decreased protein levels of E-Cadherin (Fig 6A-B). A  
403 change in migration pattern decreasing cell-to-cell contact was also observed in  
404 this cancer cell line (Fig 6C). These results further validate our hypothesis where  
405 the overexpression of PI3KC2 $\beta$  is promoting EMT.

406

407 To conclude, our study shows a link between the overexpression of  
408 PI3KC2 $\beta$ , the regulation of intracellular vesicular trafficking and EMT. Further  
409 studies are needed to test PI3KC2 $\beta$  as a drug target to revert this malignant  
410 phenotype and prevent metastasis formation. Moreover, there is still a necessity  
411 to clarify the signalling pathways specifically regulated by PI3KC2 $\beta$  because the  
412 recompilation of previous studies suggest that it could be cell/tissue specific. For  
413 example, while in some cancers AKT has been proposed as a downstream  
414 target (18,19,37), in others this lipid kinase has been associated with MAPK  
415 signalling pathway (13), or an alternative miR-449a/ $\beta$ -catenin/cyclin B1 pathway  
416 (12). Therefore, the implication of PI3KC2 $\beta$  in EMT could variate depending on  
417 the cellular context, and this makes urgent further studies to understand the  
418 specific role of this lipid kinase in human biology and tumorigenesis.

419

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421

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430

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545

546

547 **Figure legends**

548

549 **Figure 1: The overexpression of PI3KC2 $\beta$  changes the migration front of**  
550 **A431. A** Western blot and Relative protein expression of PI3KC2 $\beta$  in A431 and  
551 A431C2 $\beta$  cells. **B** Wound healing closure in A431 and A431C2 $\beta$  cells after 18 h  
552 of generating a wound with a 200  $\mu$ L pipette tip. Images are representative of 4  
553 different experiments performed in a 6 well plate. **C** Comparison of the cell  
554 morphology during cell migration of A431 and A431C2 $\beta$  cells in 96 well plates.  
555 Representative images obtained through phase-contrast microscopy. Means  
556  $\pm$ SD; n = 4 independent experiments; unpaired two tailed t-test.

557

558 **Figure 2: The overexpression of PI3KC2 $\beta$  increases the expression of EMT**  
559 **markers in A431. A** Western blot and relative protein expression of E-cadherin  
560 and  $\beta$ -catenin in A431 and A431C2 $\beta$  cells. **B** Relative mRNA expression of SNAI1  
561 and TWIST1 in A431 and A431C2 $\beta$  cells. **C** Expression of Vimentin visualized by  
562 immunofluorescence in A431 and A431C2 $\beta$  cells. Nuclear staining with DAPI  
563 (blue) and anti-Vimentin antibody (green). The results of A431C2 $\beta$  were  
564 normalized to A431 samples. Means  $\pm$ SD; n  $\geq$  3 independent experiments;  
565 unpaired two tailed t-test. Size bar = 500 $\mu$ m.

566

567 **Figure 3: Cytoplasmic co-localization of E-cadherin,  $\beta$ -catenin in A431C2 $\beta$**   
568 Dual-color immunofluorescence co-localization was performed in A431 and  
569 A431C2 $\beta$  cells grown on glass coverslips. Images were obtained by confocal

570 microscopy. **A** Expression of E-cadherin (red) and  $\beta$ -catenin (green) visualized  
571 with immunofluorescence in A431 and A431C2 $\beta$  cells. **B** Expression of 58K, a  
572 golgi marker (red) and  $\beta$ -catenin (green) visualized with immunofluorescence in  
573 A431 and A431C2 $\beta$  cells. **C** Expression of Rab7, a late endosome marker (red)  
574 and  $\beta$ -catenin (green) visualized with immunofluorescence in A431 and A431C2 $\beta$   
575 cells. Nuclei counterstain with DAPI (blue). Size bar = 50 $\mu$ m.

576

577 **Figure 4: Cytoplasmic co-localization of PI3KC2 $\beta$  and EGFR with E-**  
578 **cadherin/ $\beta$ -catenin aggregates.** Dual-color immunofluorescence co-  
579 localization was performed in A431 and A431C2 $\beta$  cells grown on glass  
580 coverslips. Images were obtained by confocal microscopy. **A** Expression of E-  
581 cadherin (red) and PI3KC2 $\beta$  (green) visualized with immunofluorescence in  
582 A431C2 $\beta$  cells. **B** Expression of E-cadherin (red) and EGFR (green) visualized  
583 with immunofluorescence in A431C2 $\beta$  cells. Nuclei counterstain with DAPI (blue).  
584 Size bar = 50 $\mu$ m.

585

586 **Figure 5: The effect of PI3KC2 $\beta$  overexpression in EGFR signalling**

587 **EGFR transcription (A)** and EGFR expression (B) compared by qPCR and  
588 western blots in A431C2 $\beta$  cell line compared to parental cell line. **C** Western blot  
589 picture and analyses for EGFR, AKT phosphorylation and ERK phosphorylation  
590 in A431 and in A431C2 $\beta$ . **D** A431 and A431C2 $\beta$ , dose response to EGFR TKIs,  
591 Erlotinib and Gefitinib. Cell viability was measured via Crystal violet assay. Means  
592  $\pm$ SD; n = 3 independent experiments; unpaired two tailed t-test.

593

594 **Figure 6: The overexpression of PI3KC2 $\beta$  induces the expression of some**  
595 **EMT markers in HT29. A** Relative protein expression of E-cadherin in HT29  
596 cells, HT29 cells transfected with pcDNA3 plasmid, and HT29C2 $\beta$  (clone 1/14)  
597 cells transfected with a pcDNA3-PI3KC2 $\beta$  plasmid (evaluated by Western blot).  
598 **B** Relative mRNA transcription of SNA/1 in HT29 and HT29C2 $\beta$  cells (evaluated  
599 by qPCR). The results were normalized to HT29 samples. Means  $\pm$  SD; n  $\geq$  3  
600 independent experiments; unpaired two tailed t-test. **C** Comparison of the cell  
601 morphology during cell migration of HT29 and HT29C2 $\beta$ . Representative images  
602 obtained through phase-contrast microscopy.

603

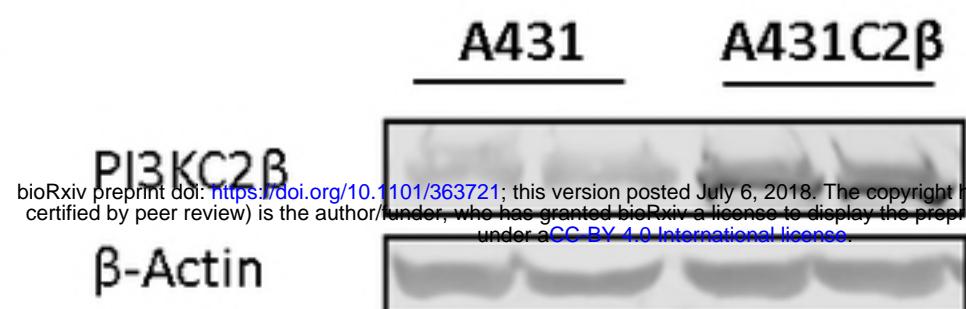
604 **Figure 7: Proposed model of how the overexpression of PI3KC2 $\beta$  affects**  
605 **intracellular vesicular trafficking of E-cadherin,  $\beta$ -catenin and EGFR and**  
606 **promotes EMT.**

607 Left: Early phase of EMT: PI3KC2 $\beta$  induces the endocytic internalization of  
608 EGFR, E-cadherin and  $\beta$ -catenin removing these adherent components and the  
609 receptor from cell surface. Additionally, the overexpression of PI3KC2 $\beta$  contribute  
610 to the activation of the expression of different transcription factors like Twist and  
611 Snail. This constitutes the transcriptional machinery that will lead to EMT.

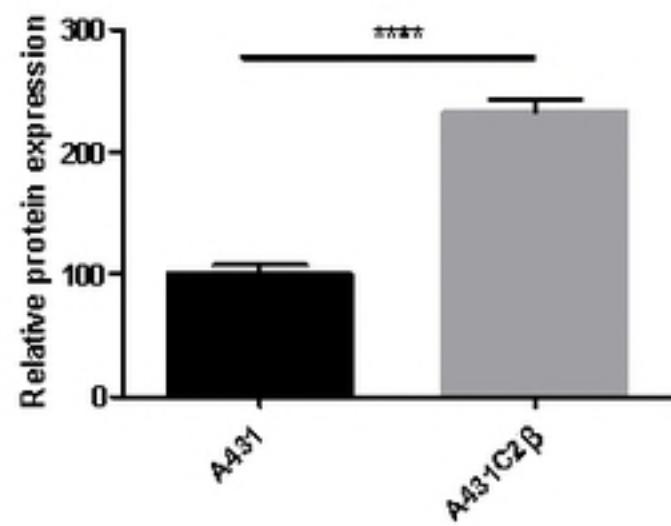
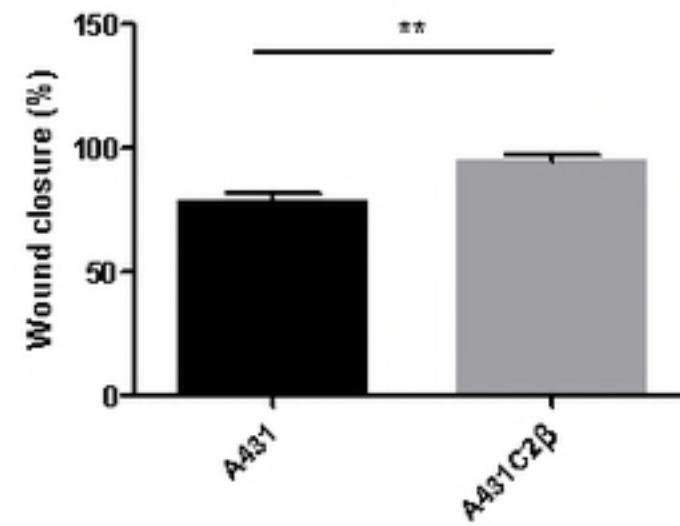
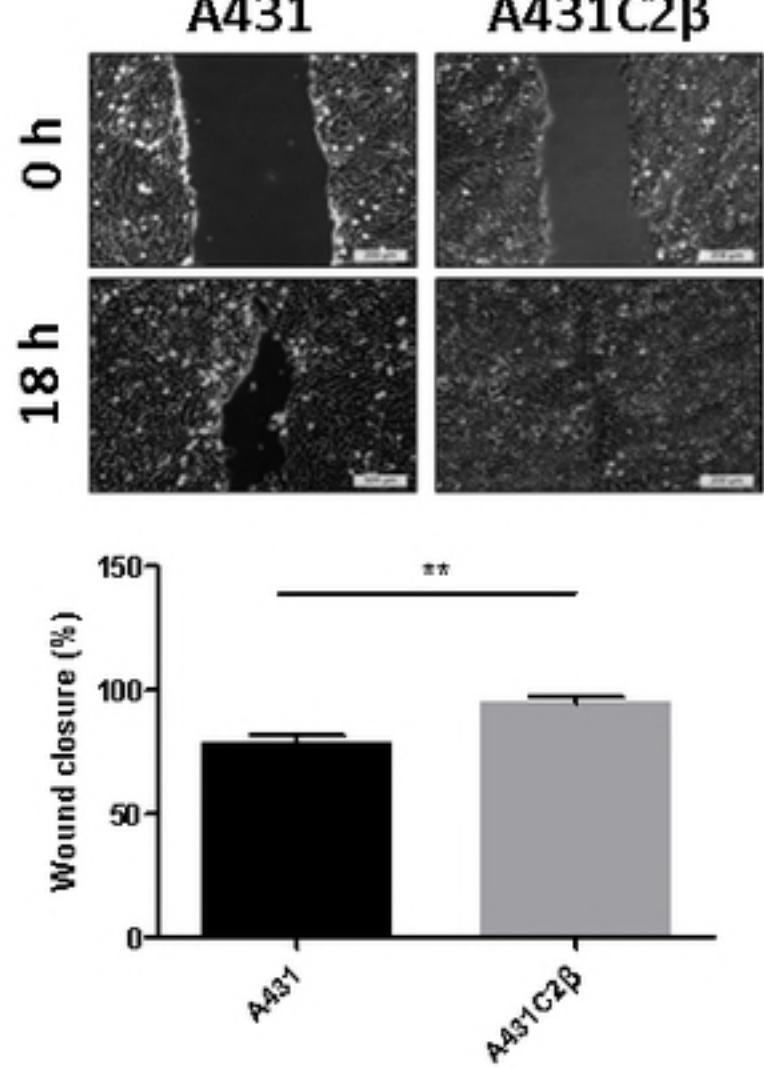
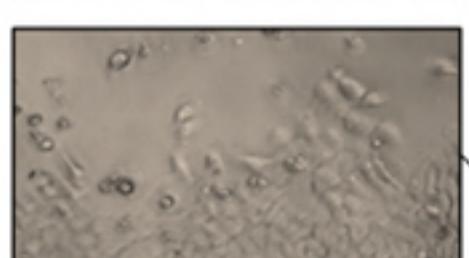
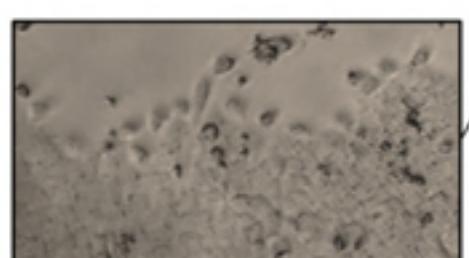
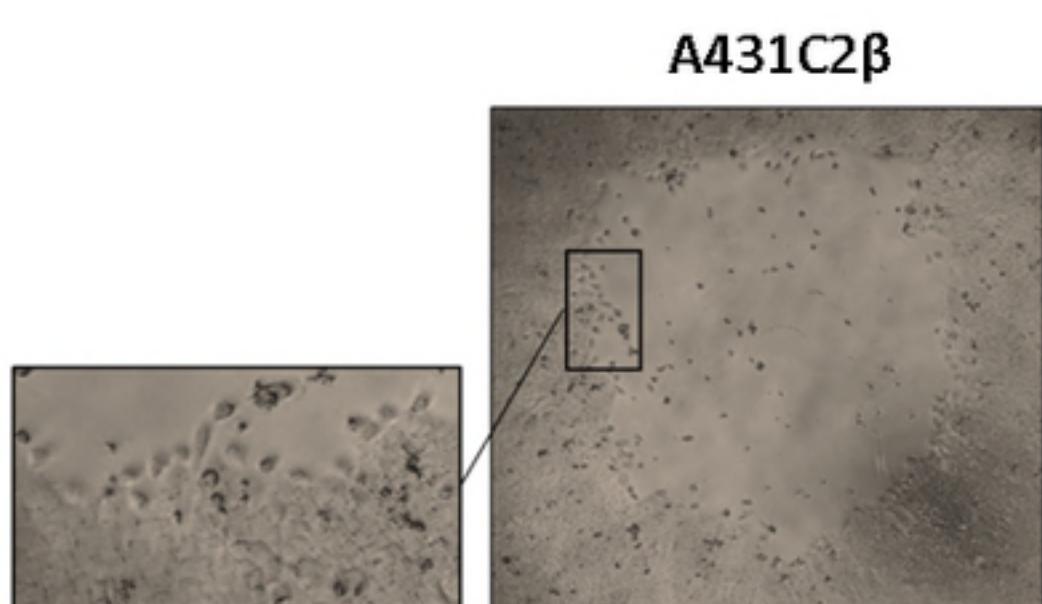
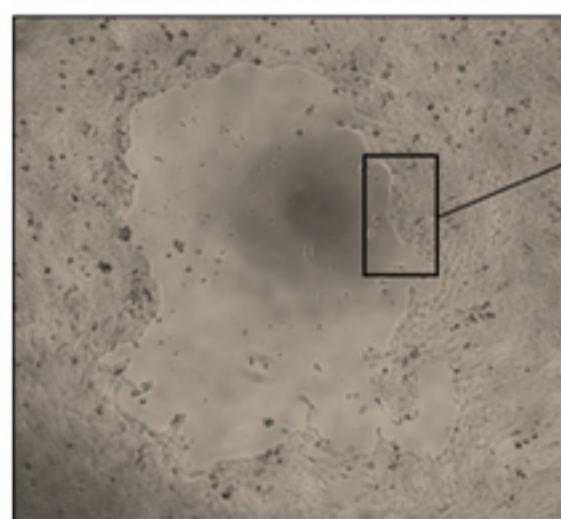
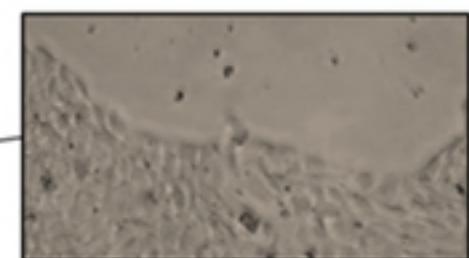
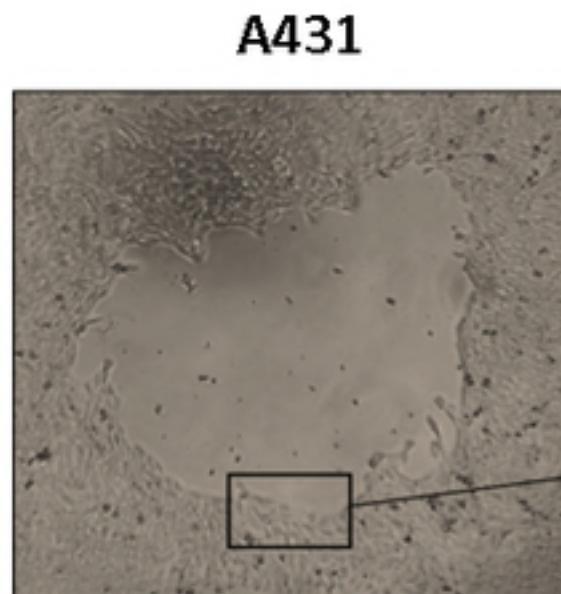
612 Right: Late phase of EMT: Twist and Snail will repress the expression of E-  
613 cadherin and EGFR. The reduced expression of E-cadherin destabilizes cell-cell  
614 adhesions promoting a change in the morphology of the cell.

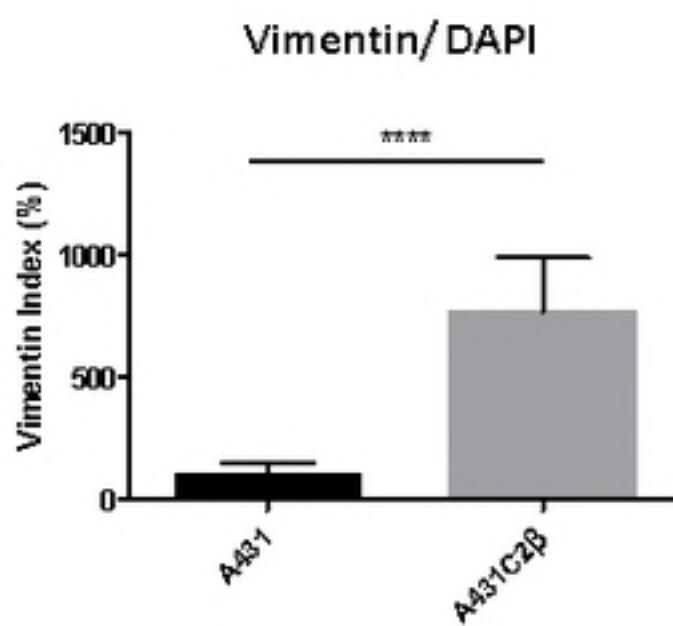
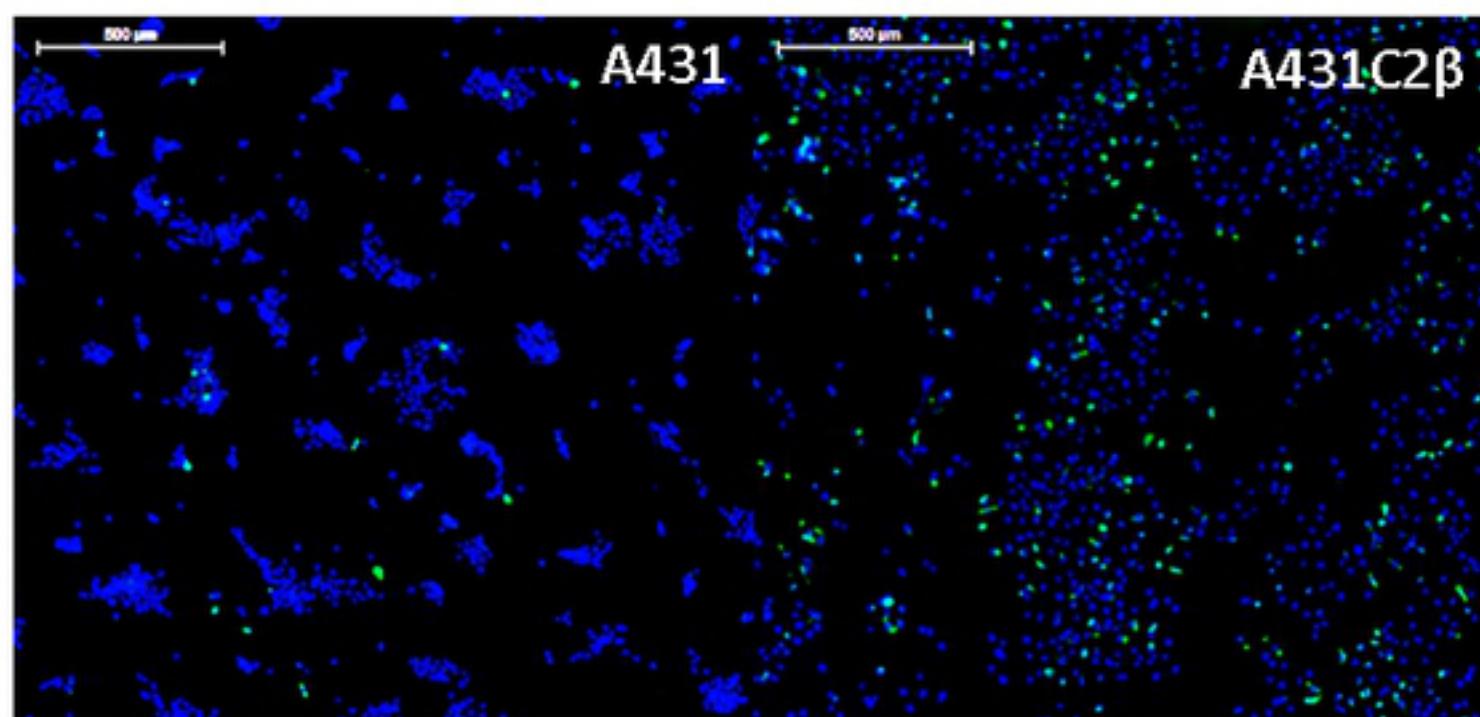
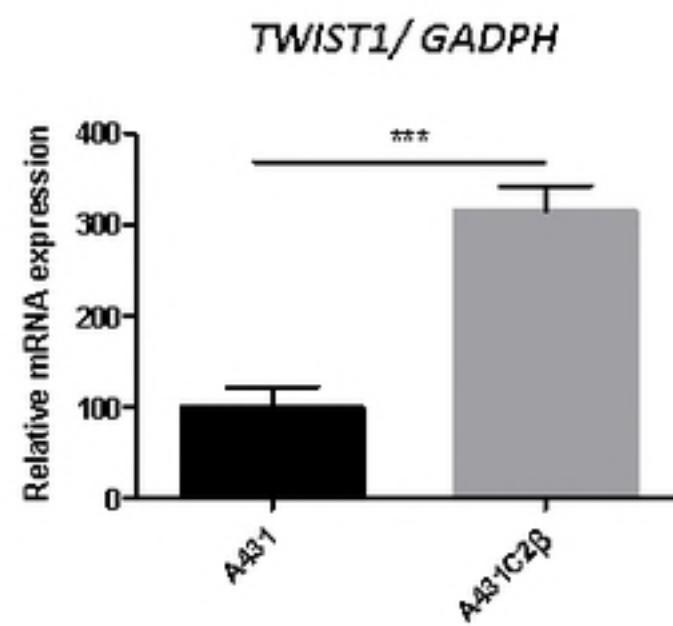
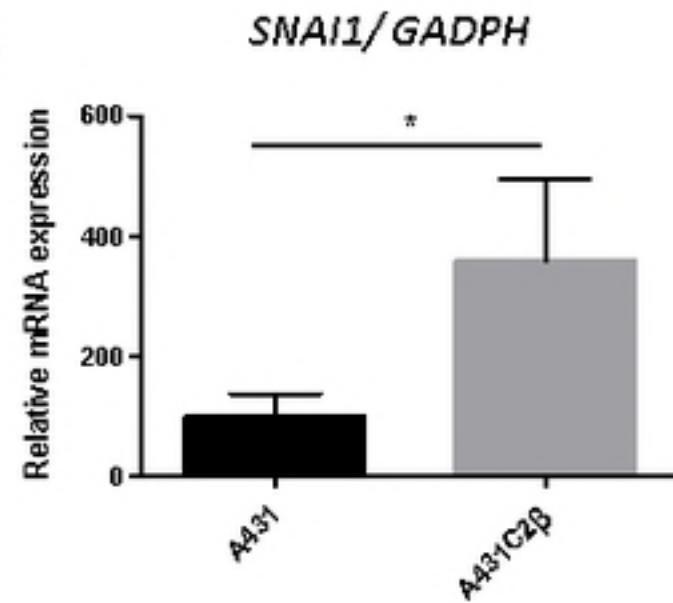
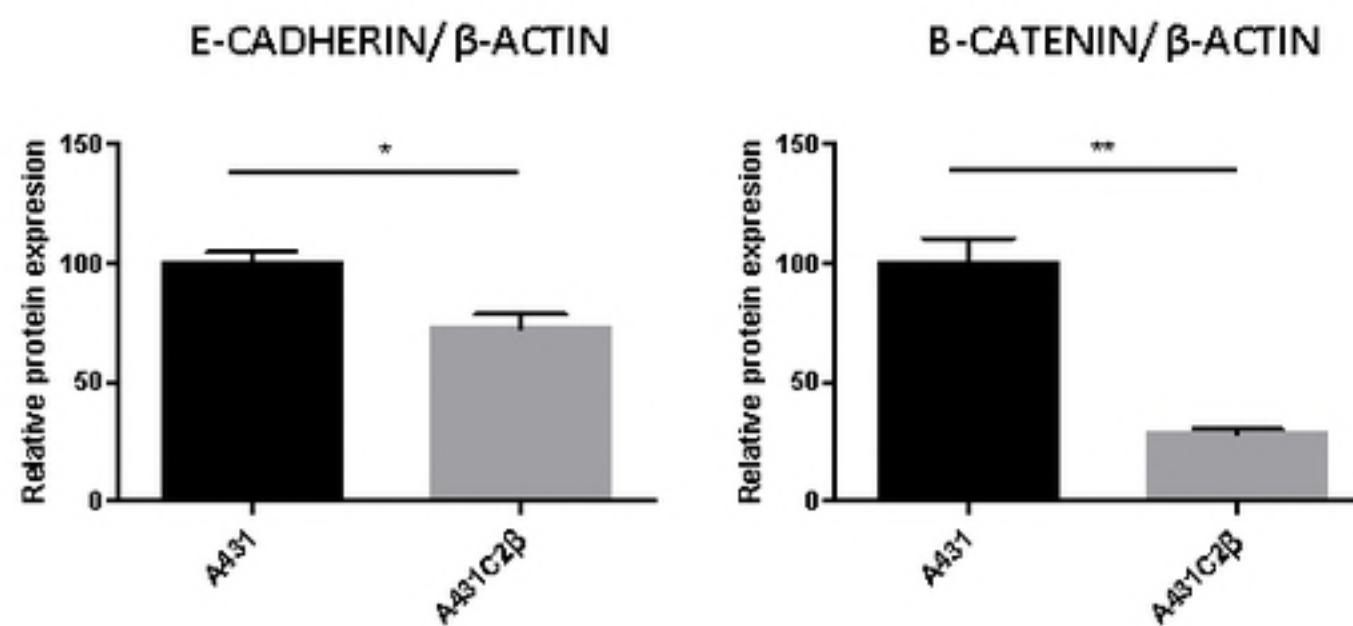
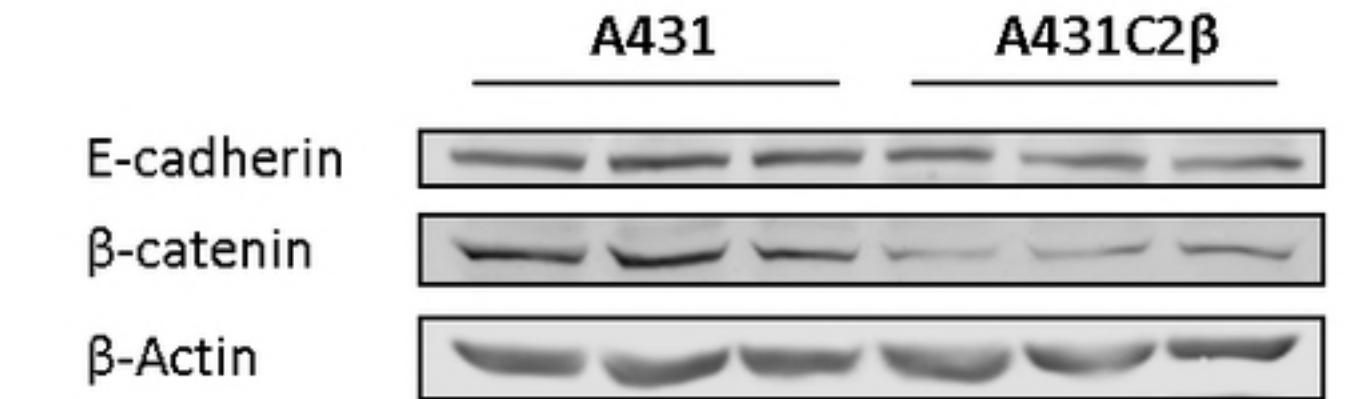
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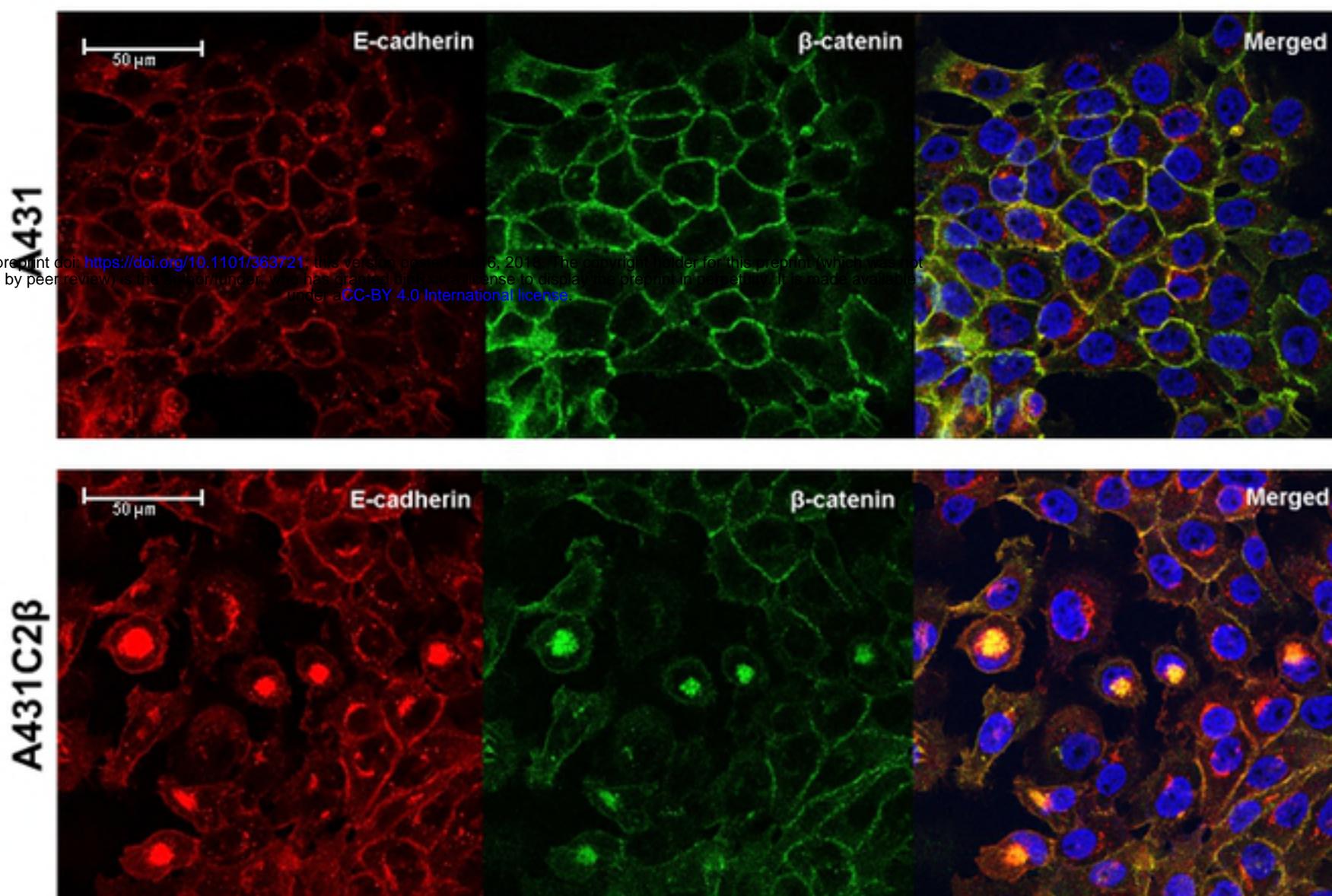
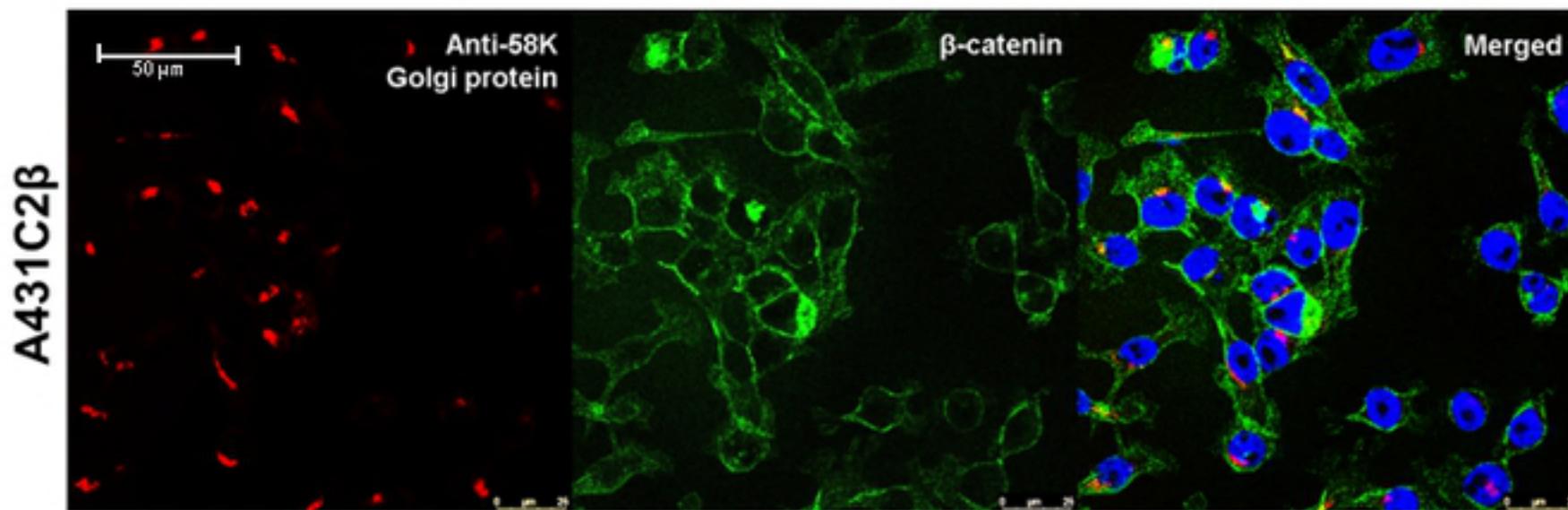
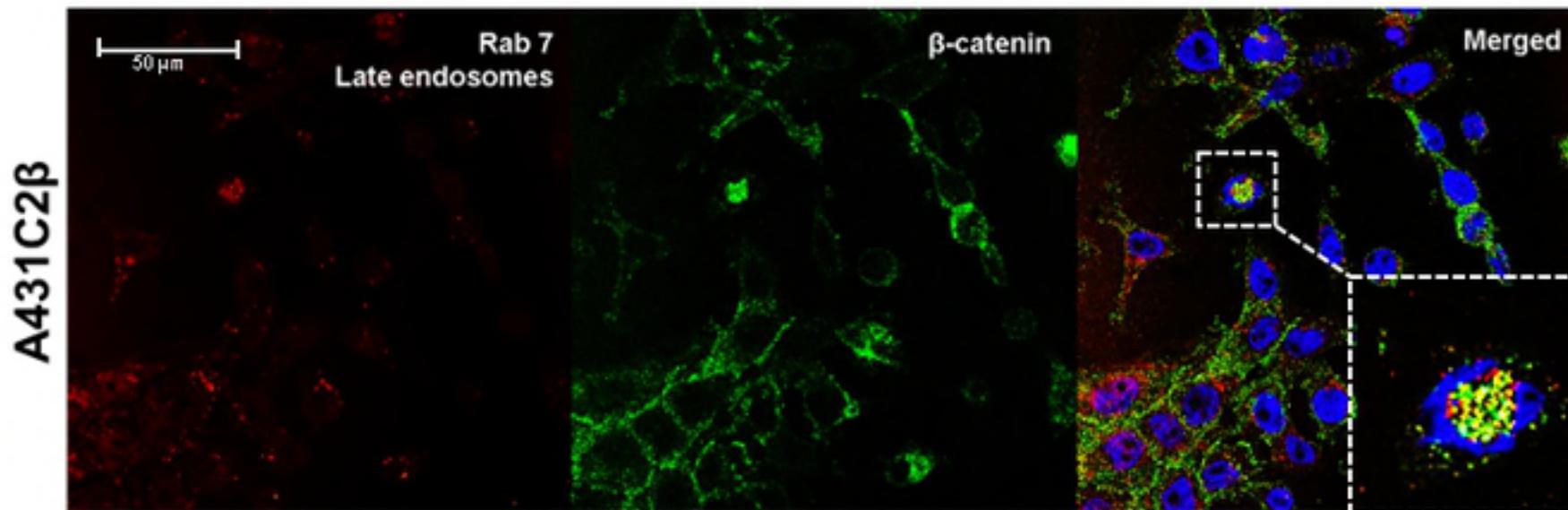
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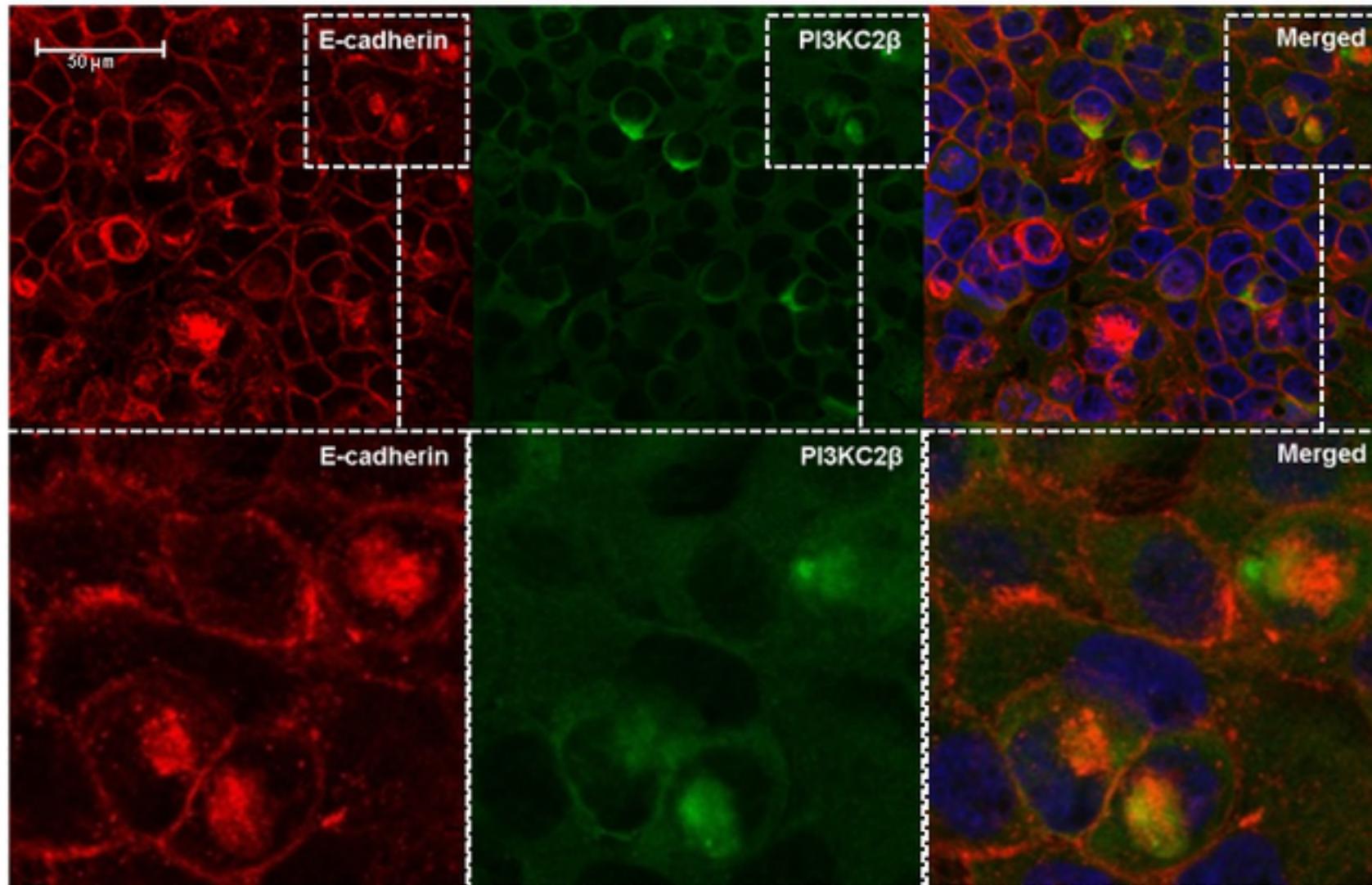
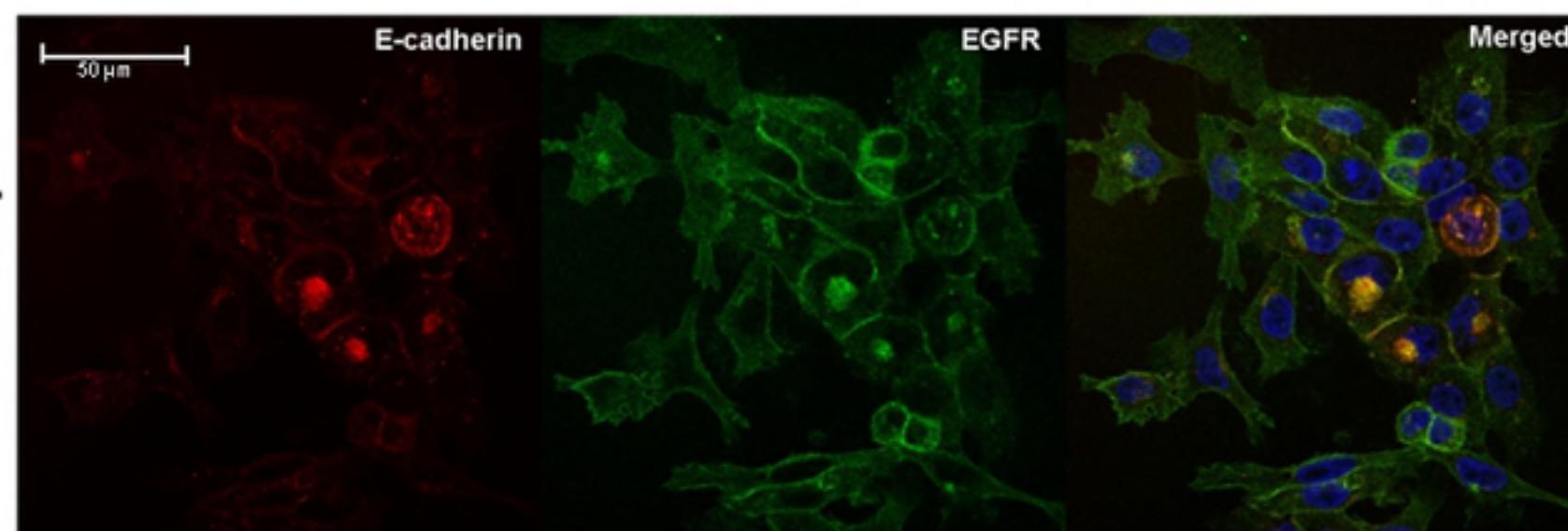
**A**

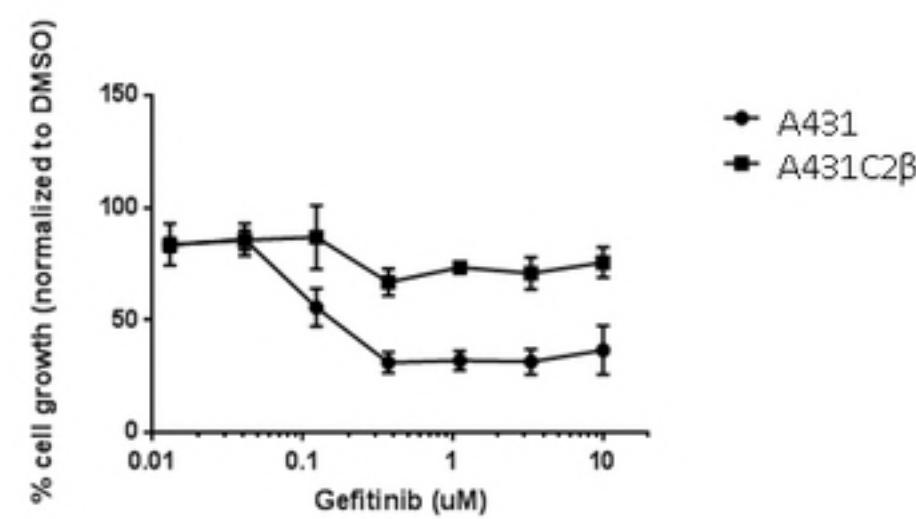
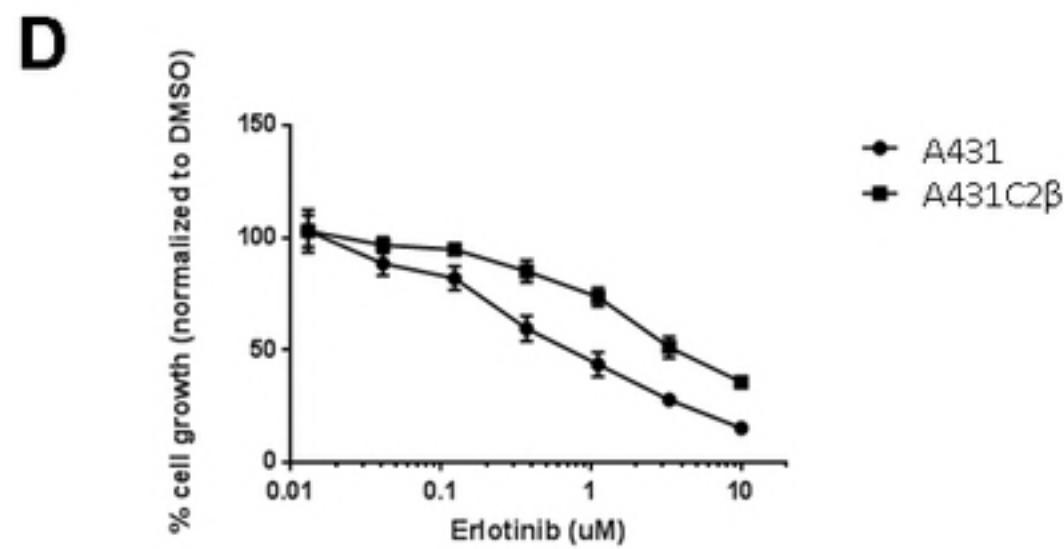
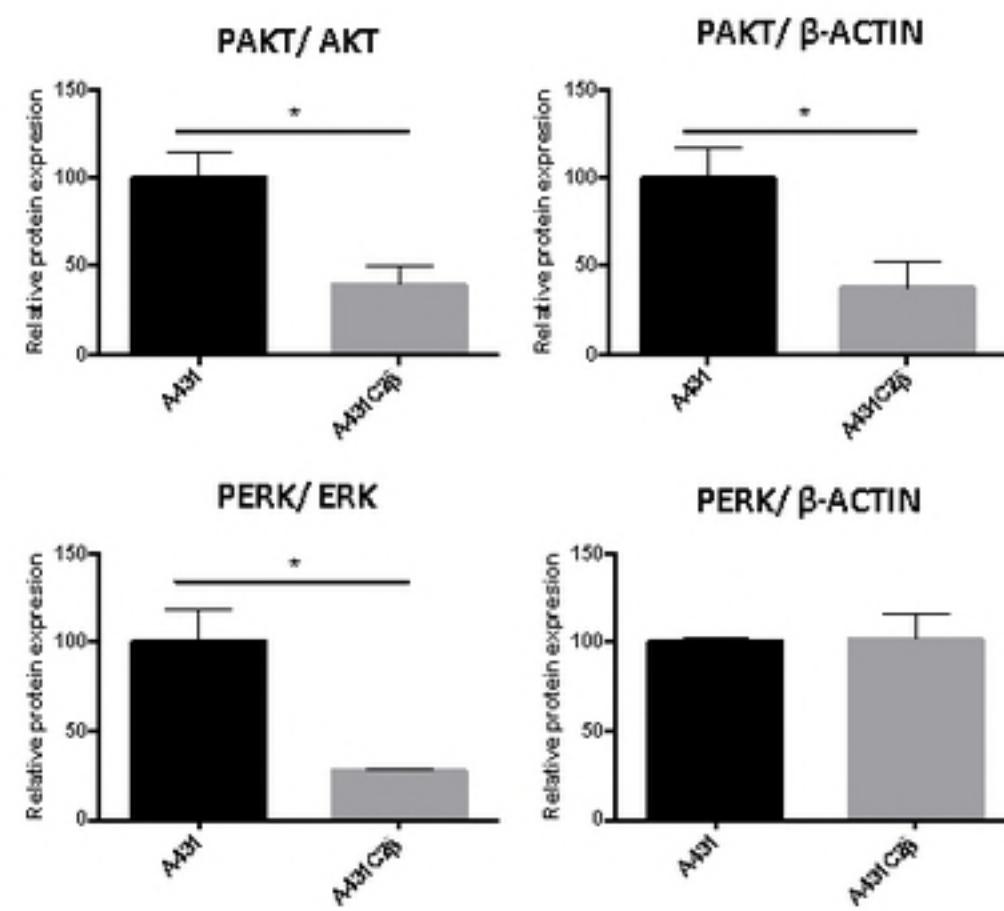
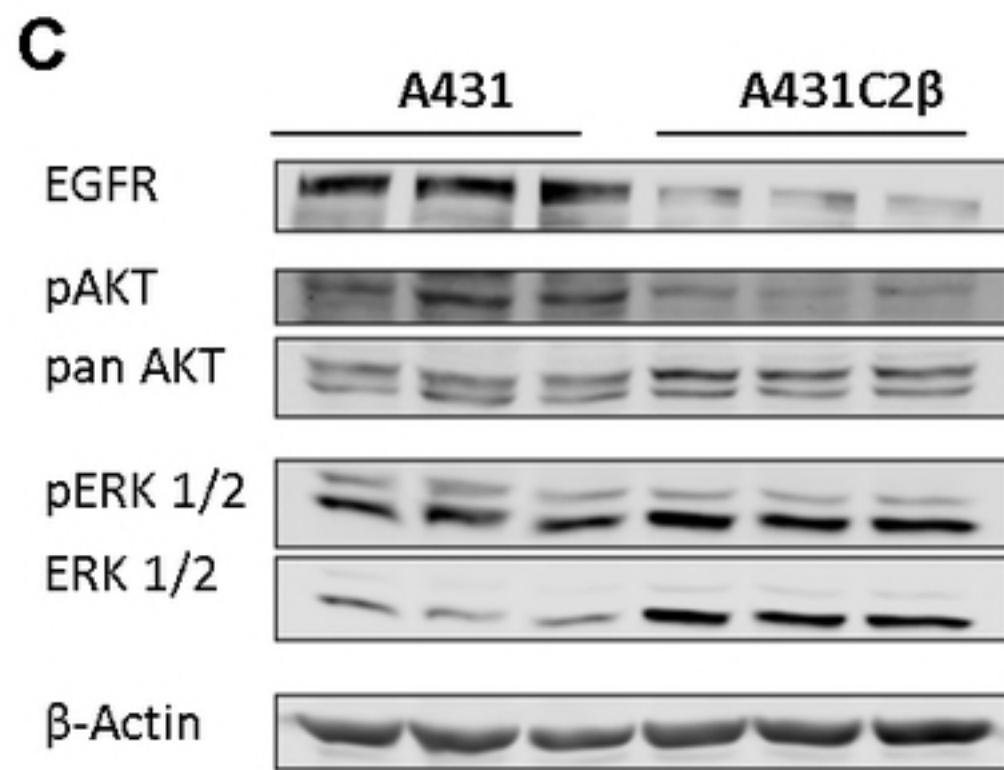
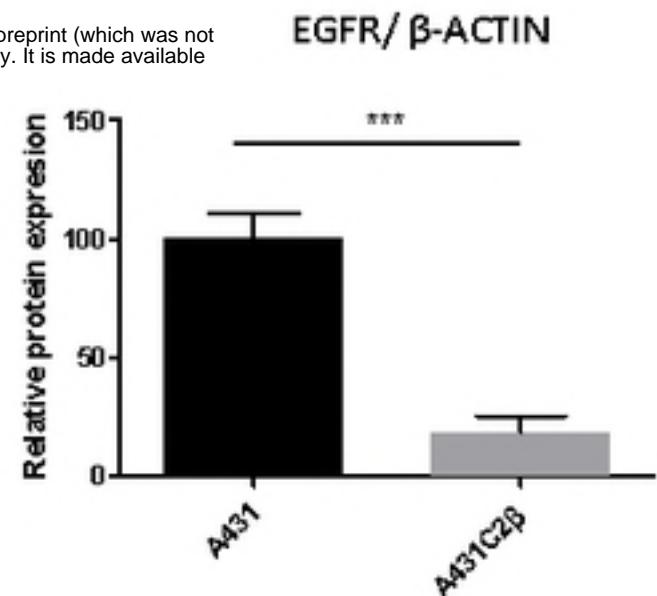
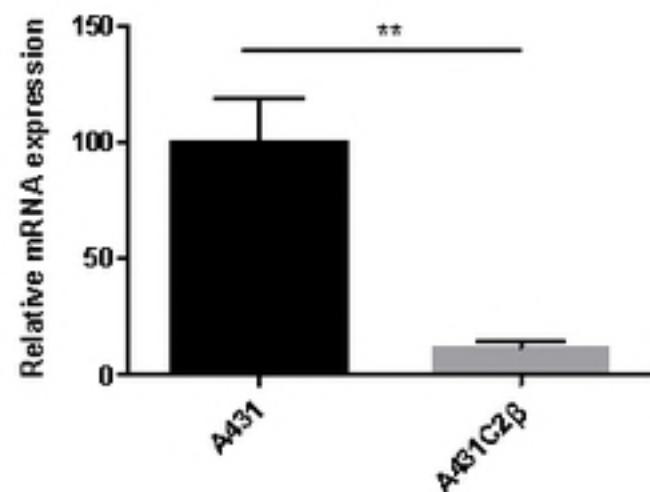
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**PI3KC2 $\beta$ /β-ACTIN****B****C**



**A****B****C**

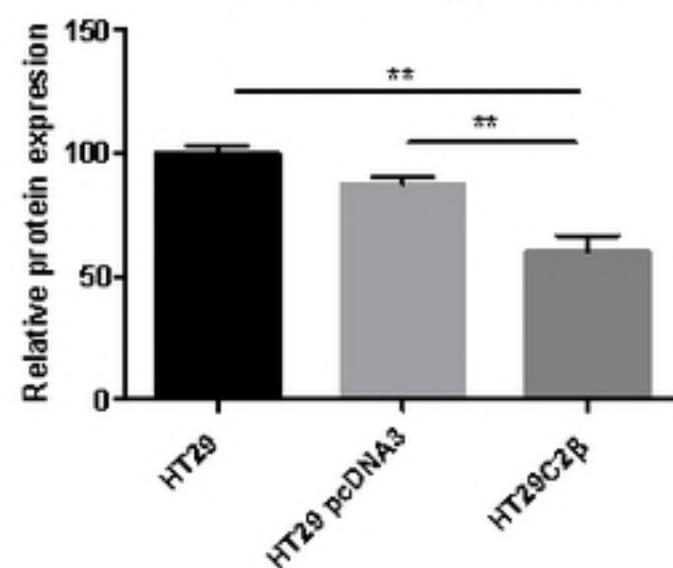
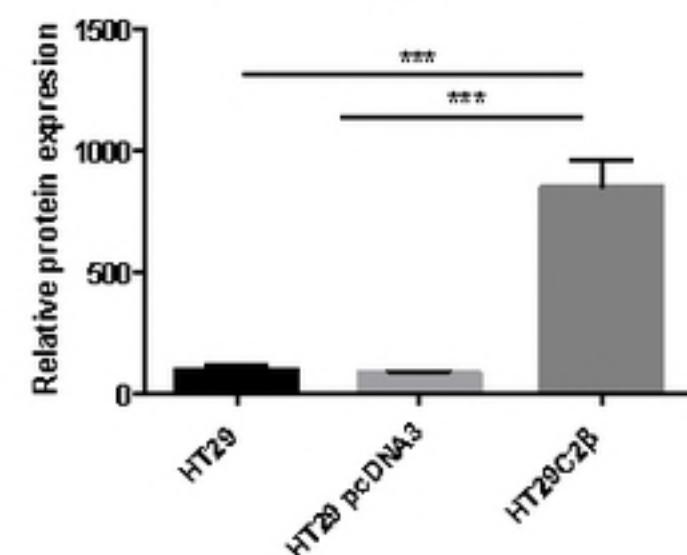
**A**A431C2 $\beta$ **B**A431C2 $\beta$ 



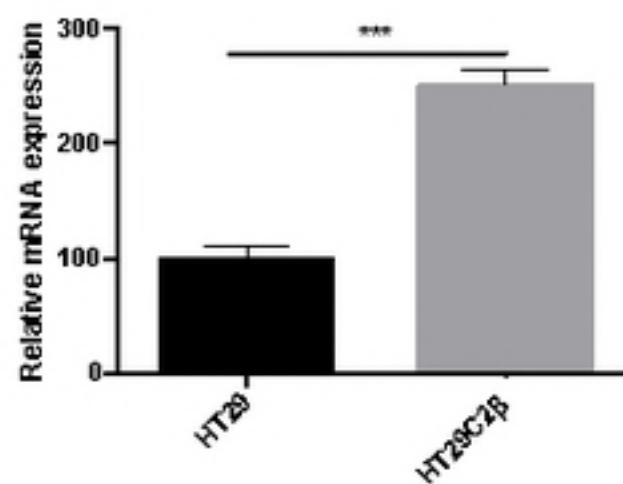
**A**HT29      HT29 pcDNA3      HT29C2 $\beta$  (1/14)PI3KC2 $\beta$ 

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E-cadherin

 $\beta$ -ActinPI3KC2 $\beta$  /  $\beta$ -ACTINE-CADHERIN /  $\beta$ -ACTIN**B**

SNAI1 / GADPH

**C**