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Cell-intrinsic and -extrinsic functions of the ESCRT-III component Shrub in cytokinetic abscission of *Drosophila* Sensory Organ precursor

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Abstract

While the molecular mechanisms underlying the abscission of isolated cells are largely decrypted, those of fast-cycling, epithelial progenitors surrounded by epidermal cells (ECs) connected by junctions remain largely unexplored. Here, we investigated the remodeling of the permeability barrier ensured by septate junctions (SJs) during cytokinesis of *Drosophila* sensory organ precursor (SOP). We report that SOP cytokinesis involves the coordinated polarized assembly and remodeling of SJs in the dividing cell and its neighbors, which remained connected via membrane protrusions pointing toward the SOP midbody. SJs assembly and midbody basal displacement occur more rapidly in SOP than in ECs, leading to a faster disentanglement of the protrusions that precedes midbody release. As reported in isolated cells, the endosomal sorting complex required for transport-III component Shrub/CHMP4B is recruited at the midbody and cell-autonomously regulates abscission. In addition, we found that Shrub is recruited to membrane protrusions, is required for SJ integrity, and that alteration of SJ integrity leads to premature abscission. Our study uncovers cell- intrinsic and -extrinsic functions of Shrub in epithelial abscission to support the coordination of permeability barrier maintenance and abscission in SOPs.

1 **Introduction**

2 Cell junctions are essential for the chemical and mechanical functions of epithelia
3 (Higashi et al., 2016). Adherens junctions (AJs) and Tight junctions (TJ) in
4 vertebrates/ Septate Junctions (SJs) in invertebrate ensure the mechanical and
5 permeability barriers respectively (Banerjee et al., 2006; Harris and Tepass, 2010;
6 Shin et al., 2006; Tepass et al., 2001; Tsukita et al., 2001). *Drosophila* bicellular SJs
7 (bSJs) are composed of a highly stable core complex containing more than 20
8 proteins including–cytosolic proteins such as Coracle (Cora) and Disc-large (Dlg),
9 Claudin-like proteins including Kune Kune, cell adhesion molecules such as Fasciclin
10 III (Fas 3) transporters such as Na⁺/K⁺ ATPase alpha (ATP α) and beta (Nervana2
11 (Nrv2)) subunits (Faivre-Sarrailh, 2020; Genova and Fehon, 2003; Izumi and Furuse,
12 2014; Kaplan, 2002; Nelson et al., 2010; Snow et al., 1989; Ward et al., 1998). The
13 localization of SJ components are interdependent of each other (Oshima and Fehon,
14 2011).

15
16 While cells need to establish and maintain proper permeability barrier, SJs remain
17 highly plastic, especially during cell division, a fundamental process for the
18 development and function of all organs. Abscission is the final step of cytokinesis
19 that leads to the physical separation of the two daughter cells and has been
20 proposed to help regulate cell fate acquisition (Chaigne et al., 2020; Ettinger et al.,
21 2011). Cytokinesis is initiated at the onset of anaphase and begins with the formation
22 of an actomyosin ring that constricts to ultimately form the midbody (Fededa and
23 Gerlich, 2012; Glotzer, 2005; Green et al., 2012). The midbody present at the
24 intercellular bridge connects the two daughter cells, and recruits effectors of
25 abscission. In *Drosophila*, the centralspindlin protein complex recruits Alix to the
26 midbody which in turn recruits the endosomal sorting complex required for transport-
27 III (ESCRT III) component Shrub (the CHMP4B ortholog). Shrub/CHMP4B have the
28 property to form homopolymers that are proposed to drive abscission (Eikenes et al.,
29 2015; Guizetti et al., 2011; Lie-Jensen et al., 2019; Matias et al., 2015). In addition to
30 being required for multivesicular body formation and abscission, CHMP4B exerts
31 different functions including viral budding and, plasma and nuclear membrane
32 resealing (Agromayor and Martin-Serrano, 2013; Lie-Jensen et al., 2019; Vietri et al.,
33 2020). While there is a great deal of knowledge on the molecular mechanisms

34 underlying abscission of isolated cells, abscission in tightly packed polarized
35 epithelial cells possessing junctional complexes remains largely under-explored.

36

37 Several studies have described that the formation of the new AJs is coordinated with
38 the early steps of cytokinesis leading to the positioning of the midbody basal to the
39 newly formed adhesive interface (Firmino et al., 2016; Founounou et al., 2013;
40 Guillot and Lecuit, 2013; Herszterg et al., 2013; Higashi et al., 2016; Lau et al., 2015;
41 Morais-de-Sá and Sunkel, 2013). It has also been showed that the neighbor cells
42 maintain SJ contact with the dividing cell through SJ finger-like protrusions
43 connected to the midbody in the *Drosophila* pupal notum and wing imaginal disc
44 (Daniel et al., 2018; Wang et al., 2018). Novel SJ assembles below the AJs and
45 spread basally concomitantly with the basal displacement of the midbody. Once the
46 new SJ is formed, the midbody leaves the SJ about 1.5 hours after the onset of
47 anaphase and abscission is taking place more than 5 hours post anaphase (Daniel
48 et al., 2018; Wang et al., 2018). The sequence of events leading to abscission and
49 junction remodeling is proposed to ensure the maintenance of the epithelial barrier
50 functions in proliferative epithelia. This issue remains poorly characterized in
51 epithelia composed of cells with distinct identities.

52

53 *Drosophila* notum consists of a single-layer epithelium with two types of cells,
54 epidermal (EC) and sensory organs (SO) (Fig. 1A). Sensory organs precursor (SOP)
55 divides asymmetrically to generate pIIa and pIIb cells that undergo subsequent cell
56 divisions giving rise to the four cells composing the adult SO (Fig. 1A') (Fichelson
57 and Gho, 2003; Gho et al., 1999; Hartenstein and Posakony, 1989). At each cell
58 division, cell fate determinant Numb and Neuralized are unequally segregated to
59 control Notch-dependent binary fate acquisition (Langevin et al., 2005; Le Borgne
60 and Schweisguth, 2003; Rhyu et al., 1994). In contrast to EC, SO and daughters are
61 fast cycling cells (Audibert, 2005) (Fig. 1A') raising the question of how permeability
62 barrier and abscission occur during SOP cytokinesis to ensure the proper
63 progression of cell divisions while enabling cell fate determination. In this study, we
64 first characterized the coordination between the midbody basal displacement and the
65 SJ remodeling during SOP cytokinesis. We next investigated the functions of Shrub
66 and SJ components in abscission. We provided evidence that SJ components
67 negatively regulate the timing of abscission during SOP cytokinesis. We also report

68 that Shrub, by controlling the abscission and the remodeling of SJs, exerts two
69 complementary functions to orchestrate SO abscission.

70 **Results**

71

72 **Basal displacement of the midbody is faster in SOP than in epidermal cells**

73 To monitor SOP cell cytokinesis and compare it to that of epidermal cells (ECs), we
74 live-imaged non-muscle Myosin II light chain tagged with RFP (MyoIIIRFP) to label
75 the plane of AJs and the actomyosin contractile ring dynamics, ATP α tagged with
76 GFP (ATP α GFP) to monitor the SJs (Fig. 1B-B' and Fig. S1A-A'). SOP and its
77 pIIa/pIIb daughter cells were identified using Histone 2B::IRFP670 (H2BIR)
78 expressed under the minimal promoter of *neuralized* (Fig. 1B-1B'). In each movie,
79 time is expressed in min, with t0 corresponding to the onset of anaphase. In both EC
80 and SOP, the constriction of the actomyosin contractile ring gives rise to the midbody
81 located basal to the AJ, within the SJs (Fig. 1B-B', Fig.S1A-A' at t10 and (Daniel et
82 al., 2018; Founounou et al., 2013; Guillot and Lecuit, 2013; Herszterg et al., 2013;
83 Morais-de-Sá and Sunkel, 2013)). As described for dividing ECs (Fig. 1-Fig. S1A,
84 t10 ;(Daniel et al., 2018; Wang et al., 2018)), as a result of membrane ingression
85 induced by actomyosin ring pulling, neighboring cells remain tightly associated to
86 SOPs by finger-like protrusions, marked with the SJs components ATP α GFP and
87 Cora (Fig. 1B, t10; SJ plane, Fig. 1C-C', t10; SJ plane). While another commonality
88 of the SOPs and ECs is the displacement of the midbody towards the basal pole
89 (Fig. 1B', Fig. S 1A', arrows), we found that the basal displacement of the SOP
90 midbody is 1.75 times faster (2.8 ± 0.1 $\mu\text{m}/\text{h}$) than that of the EC (1.6 ± 0.1 $\mu\text{m}/\text{h}$) in the
91 80 min after anaphase onset (Fig. 1D-E). Then, we observed an inflection in the
92 curve, the SOP midbody being displaced with a faster kinetic towards the basal side
93 (6.9 ± 0.2 $\mu\text{m}/\text{h}$) (Fig. 1E), as it is progressively leaving the SJ domain (Fig. 1B',
94 between t90 and t115). As the newly assembled SJs acts as a conveyor belt that
95 triggers the basal displacement of the midbody in ECs (Daniel et al., 2018), the
96 difference in midbody basal displacement between EC and SOP predicts a faster SJ
97 remodeling in SOP that we next investigated.

98

99 **Remodeling of SJ coincides with SOP midbody basal displacement**

100 We then follow the SJs present in the finger-like protrusions, i.e. the junctions that
101 were present prior to entry into mitosis (Daniel et al., 2018), and discriminate the SJ
102 components of the dividing cell from those of the neighbors. For this purpose, we
103 generated clones of dividing EC or SOP cells expressing MyoIIIRFP and no

104 ATP α GFP, but expressing endogenous untagged ATP α , and imaged adjacent to
105 cells expressing ATP α GFP and MyoIIIRFP (Fig. 2A, Fig. 2-Fig. S 2A). At t10, the
106 presence of ATP α GFP signal in the finger-like protrusions pointing towards the
107 midbody is originating from the neighbor cell, confirming that the integrity of the SJ
108 barrier is preserved between the SOP and its neighboring EC, as we had previously
109 described between two ECs (Fig. 2A, Fig. 2-Fig. S 2A, SJ plane and (Daniel et al.,
110 2018)). In SOP, as the midbody underwent its basal displacement, at t70 \pm 7, the
111 finger-like protrusions thinned and both edges were no longer resolved by light
112 microscopy (t65, Fig. 2A; SJ plane, n=4). At t97 \pm 4.5, the finger-like protrusion was
113 barely detectable (t100, Fig. 2A, SJ plane, n=5). Then, the midbody was no longer
114 seen within the plane of the SJs (t110, Fig. 2A, and t115, Fig.1C), prior to be
115 displaced at distance, basal to pIIa nucleus that we interpret as the release of SOP
116 midbody (see below) (t120, Fig. 2A; see also Fig. 1C-C'). In contrast, in EC, the
117 finger-like protrusions connected to the midbody are persisting after t120 (Fig. 1, Fig.
118 S1A and (Daniel et al., 2018)), indicating that the disengagement of finger-like
119 protrusions and midbody release occurs faster in SOP daughters than in ECs.

120 We next analyzed the converse situation to monitor the *de novo* assembly of SJs at
121 the new SOP daughter interface by live-imaging SOP expressing ATP α GFP
122 surrounded by ECs expressing endogenous untagged ATP α . As the cell divides, we
123 observed the appearance of an ATP α GFP signal apical to the midbody (t20, Fig. 2B,
124 SJ plane) which then formed a continuous line, i.e. the novel SJ at t45 (t45, Fig. 2B,
125 SJ plane) compared to t80 in ECs (data not shown and (Daniel et al., 2018)). These
126 results suggest that SJ assembly is faster in SOP daughters than in EC daughters.
127 To confirm this, we performed fluorescence recovery of ATP α GFP signal after
128 photobleaching (FRAP) experiments (Fig. 2C). 40 min after photobleaching one of
129 the two finger-like protrusions of dividing ECs, ATP α GFP signal was barely
130 recovered, presenting mainly an immobile fraction (y_{max} = 17 % and a t1/2 = 7.4
131 min,—in agreement with previous observations (Fig. 2D, (Daniel et al., 2018)). In
132 contrast, following FRAP of the SOP daughter interface, identified with the plasma
133 membrane marker GAP43::IRFP670, about 50% of ATP α GFP signal was recovered
134 40 min at the new daughter interface above the midbody (y_{max} = 49 % and t1/2 =
135 10.2 min, Fig. 2C; SJ plane and Fig. 2D).

136 These data show that the formation of the new SJ, the disengagement of the SJ
137 finger-like protrusions and midbody release occur earlier in SOP daughters than in
138 EC daughters.

139

140 **Cytoplasmic isolation and midbody release following SOP division are**
141 **stereotyped and temporally decoupled**

142

143 In order to determine when the cytoplasm of the pIIa and pIIb cells are physically
144 separated, we used the photoconvertible probe KAEDE as previously described
145 (Daniel et al., 2018). When photoconverted in the pIIa (or pIIb) cell, photoconverted
146 KAEDE is expected to freely diffuse into the pIIb (or pIIa) cell prior to cytoplasmic
147 isolation, whereas it should be restricted to pIIa (or pIIb) cell after cytoplasmic
148 isolation (Fig. 3-Fig. S3A and data not shown). We used *pnr-Gal4* to express KAEDE
149 and to subsequently proceed to UAS-GAL4 driven gene silencing.

150 For each SOP, identified using GAP43IR, photoconversion of KAEDE was
151 conducted at a specific time point after the onset of anaphase. For example, when
152 photoconversion was performed in the pIIa 61 min after the onset of anaphase, the
153 photo-converted probe diffused into the pIIb cell (Fig. 3A-A'). By contrast, when
154 photoconversion was performed 63 min post anaphase onset, KAEDE remained
155 restricted in the pIIa cell indicating that cytoplasmic isolation had occurred (Fig. 3B-
156 B'). This experiment was repeated over several time points ranging from 46 to 71
157 min (Fig. 3-Fig. S3B), and the result of each individual experiment, i.e. KAEDE able
158 to diffuse or not, were modeled via logistic regression, using the generalized linear
159 model (GLM) (Fig. 3C, see method section). The proportion of cells exhibiting
160 cytoplasmic isolation increased as function of time (Fig. 3C). In our study, due to
161 lethality with the *pnr-Gal4* driver in one of our conditions, we had to use *scabrous*
162 (*sca-GAL4* (Mlodzik et al., 1990)). As in the control *pnr-GAL4* line, we noticed that
163 proportion of cells exhibiting cytoplasmic isolation increased as function of time, but
164 a delay was observed (Fig. 3-Fig. S3B-C and analysis of deviance Table S1A). We
165 estimated the time at which 50% of the pIIa/pIIb cell indicated cytoplasmic isolation
166 (herein termed $t_{1/2}$, see method section) and determined that $t_{1/2}$ are 58.9 ± 1.14 min
167 and 66.54 ± 1.36 min for *pnr-Gal4* and *sca-Gal4* respectively. The reason for the $t_{1/2}$
168 difference is unknown between the two conditions and is probably related to the
169 genetic background. For the sake of simplicity in the comparison of effect of gene

170 silencing (see below), since both Gal4 driver lines were used as control values, we
171 arbitrary set the t1/2 of control *pnr*-Gal4 and control *sca*-Gal4 to a relative time
172 centered to 0.

173

174 To determine if the cytoplasmic isolation is coupled to the physical cut and release of
175 the midbody, we next monitored the position of the midbody relative to the plasma
176 membrane of the SOP daughter cells, we imaged MyoII^{GFP} together with the
177 membrane marker GAP43IR (Fig. 3D). 10 min after anaphase onset, the midbody
178 colocalized with GAP43IR at the pIIa-pIIb daughter cells interface (t10, Fig. 3D, MB
179 level) and remained at the pIIa-pIIb interface until t100 (t100, Fig. 3A, MB level). At
180 t105, the midbody leaves the pIIa-pIIb daughter membrane interface (Fig. 3D, MB
181 level, 110.8 ± 12.9 min, n=12), just prior to or concomitant with the pIIb cell anaphase
182 onset (123.4 ± 6.9 min, n=13). After its departure from the pIIa-pIIb interface, the
183 midbody is mainly inherited by the pIIa cell (t105, t110, Fig. 3D, MB level, 91% of the
184 cases, n=11) where it remains attached to the plasma membrane (Fig. 3D') before
185 the MyoII^{GFP} signals becomes undetected in pIIa/pIIb cells at t115 (Fig. 3D,
186 121.5 ± 14 min, n=13). Based on the Fig. 3D, we illustrated the midbody displacement
187 at the pIIa membrane at each time point (Fig. 3D''). In isolated cells, midbodies can
188 be internalized/phagocytosed in acidic intracellular compartments following
189 abscission (Crowell et al., 2014). To test if the loss of MyoII^{GFP} signal reflects the
190 loss of GFP signal due to signal quenching by low endosomal pH (Couturier et al.,
191 2014) or the physical disappearance of the midbody, we co-imaged MyoII^{RFP} and
192 MyoII^{GFP} together with GAP43IR (Fig. 3-Fig. S3D). Both signals disappeared
193 simultaneously from the pIIa cell and are found outside of the daughter cells at t0
194 with some GAP43IR signal (Fig. 3-Fig. S3D-D'). We also live-imaged the kinesin-like
195 protein Pavarotti (Pav^{GFP}), a member of the centralsplindin complex, together with
196 MyoII^{RFP} and GAP43IR (Fig. 3-Fig. S3E) and observed that Pav^{GFP} and MyoII^{RFP}
197 signals disappeared simultaneously outside of the daughter cells at t0 with some
198 GAP43IR signal (Fig. 3-Fig. S3E-E'). These data argue that the midbody is not
199 internalized/phagocytosed in the pIIa cell. Instead, the midbody was found at
200 distance from the pIIa cell and was still marked by the GFP, RFP markers as well as
201 the plasma membrane marker GAP43IR indicating that it was in the extracellular
202 space, not in endocytic compartments of epidermal cells (Fig. 3-Fig. S3D', S3E').

203

204 The sequence of cytoplasmic isolation, the formation of the new bSJs, the
205 disengagement of the SJ finger-like protrusions, and the midbody release in SOP are
206 depicted on a chronological timeline (Fig. 3E). Having described the events and
207 established the timeline, we next investigated the molecular mechanisms underlying
208 epithelial cell abscission of SOP daughters.

209

210 **ESCRT III/Shrub localizes at the midbody and in the finger-like protrusions**

211 Based on the evolutionarily conserved function of ESCRT-III/CHMP4B in abscission
212 from archaia to vertebrates, we investigated Shrub function in SOP abscission. We
213 first monitored the localization of Shrub. Because available anti-Shrub antibodies
214 give no obvious membrane associated signal following chemical fixation (data not
215 shown; (Pannen et al., 2020)), we made use of a GFP tagged version of Shrub
216 engineered by CRISPR/Cas9 (ShrubGFP, (Mathieu et al., 2022)). We then live-
217 imaged MyoRFP and ShrubGFP (Fig. 4A). t30-60 after the onset of anaphase, a
218 faint signal of ShrubGFP is detected in the plane of the midbody and is slightly
219 enriched along the new daughter cell interface/finger-like protrusion (Fig. 4A', and
220 4A''). At t70±10, while the intensity of the ShrubGFP signal along the pIIa-pIIb
221 interface/finger-like protrusions decreased, ShrubGFP signal was detected in the
222 form of two punctae, one on each side of the midbody, a signal that was still present
223 at t120 (Fig. 4A', 4A''', n=16).

224

225 To determine if the ShrubGFP signal adjacent to the midbody was coming from the
226 SOP, the neighbors or both (Fig. 4A'), we imaged clones of SOP and EC dividing
227 cells expressing MyoIIIRFP devoid of ShrubGFP close to cells expressing ShrubGFP
228 under the *Ay-Gal4* system (Fig. 4B, Fig. 4-Fig. S4A). A ShrubGFP-positive punctum
229 emanating from the non-dividing neighboring cell was detected at the tip of the
230 finger-like protrusion pointing to the midbody of the SOP (from t18 to t72, Fig. 4B
231 and t36, Fig. 4B') or to the midbody of the EC (Fig. 4-Fig. S 4A and t36 Fig. 4-Fig.
232 S4A'). In the converse situation in which clones of SOP dividing cells expressing
233 ShrubGFP were close to cells devoid of ShrubGFP (Fig. 4C), at t26 a first punctum
234 of ShrubGFP was appearing at the midbody before the appearance of a second
235 punctum at t60 (Fig. 4C and Fig. 4C'). At t90, the punctae were still present on both
236 side of the midbody of the SOPs (Fig. 4C). In EC, a punctum is detected on one side
237 of the midbody from t28 to t90 (Fig. 4-Fig. S4B and t60 Fig. 4-Fig. S4B'). In contrast

238 to SOPs, we never observed punctae of ShrubGFP on each side of the midbody in
239 the EC. These data revealed the existence of two pools of Shrub, one in the finger-
240 like protrusion and one at the midbody of the SOP, calling for two distinct functions of
241 Shrub.

242

243 **Shrub regulates the timing of cytoplasmic isolation of SOP daughter cells**

244 Based on the localization of ShrubGFP at the midbody, we next investigated if Shrub
245 was involved in the abscission by interfering with Shrub function. However, Shrub is
246 required in several processes making difficult to analyze its function. Indeed, clones
247 of epithelial cells homozygous mutant for a null allele of *Shrub*^{G5} delaminate even
248 when apoptosis was suppressed by p35 expression (Hay et al., 1994), preventing us
249 from analyzing abscission in *Shrub* homozygote mutant cells. To circumvent this
250 problem, we opted for an UAS/Gal4-based tissue inducible-based RNAi approach
251 using *sca*-GAL4. We report that silencing of Shrub, in areas where shrub is highly
252 depleted, caused the enlargement of HRS-positive endosomes (Fig. 4- Fig. S4C),
253 the accumulation of Crumbs in endocytic compartments as reported in the
254 *Drosophila* trachea (Dong et al., 2014), and the accumulation of the Claudin-like
255 Kune Kune in intracellular compartments (Fig. 4D) as reported for other claudin-like
256 proteins (Pannen et al., 2020), NrXIV as well as sinuous (Fig. 4-Fig. S4D-E). These
257 three phenotypes are characteristic by the impact of loss of ESCRT-III on
258 intracellular trafficking (Dong et al., 2014; Vaccari et al., 2009), attesting to the
259 effectiveness of the silencing approach. We next determined the consequence of
260 Shrub depletion on the timing of cytoplasmic isolation using the KAEDE
261 photoconversion assay. We performed our experiments in areas in which KAEDE is
262 expressed only in SOP and daughters. In this part of the notum, this mild depletion of
263 shrub does not noticeably affect the distribution of SJ components (data not shown).
264 We found that SOP-specific silencing of Shrub caused a delay in cytoplasmic
265 isolation (Fig. 4E, with a t1/2 delayed of 5.9±1.4 min compared to the *sca* control and
266 Table S1B) indicating that Shrub regulates the timing of cytoplasmic isolation. This
267 data identifies a cell-autonomous function of Shrub in abscission.

268 We also observed that ShrubGFP is a mutant allele of Shrub, causing a delay in
269 abscission in the female germline stem cyst of *Drosophila* heterozygote for
270 ShrubGFP (67/ 181 GSC with delayed abscission, Fig. 5-Fig. S5A). Similarly in the
271 notum, we observe that the presence of one copy of ShrubGFP delayed the timing of

272 cytoplasmic isolation (Fig. 5, $t_{1/2} +10.3\pm 1.4$ min compared to *pnr* control, Table
273 S1C). This delay in abscission observed with *shrubGFP* is also likely to explain the
274 delay between the detection of two punctae of *ShrubGFP* at the midbody (Fig. 4A',
275 $t=70\pm 10$ min) and the timing of abscission measured in control cells devoid of
276 *ShrubGFP* (Fig. 3E, $t_{1/2}= 58.9\pm 1.1$ min). Although *ShrubGFP* is an allele of *Shrub*,
277 *ShrubGFP* signal observed on both sides of the midbody is specific as *CHMP2BGFP*
278 (charged multi vesicular body protein 2b tagged GFP), another ESCRT-III
279 component recruited in a *Shrub* dependent manner (Babst et al., 2002), exhibits a
280 similar localization pattern (Fig. 5-Fig. S5B). We conclude that *Shrub* is recruited in a
281 cell autonomous manner on both side of the SOP midbody to control cytoplasmic
282 isolation.

283

284 **Coordination between bSJs assembly and timing of abscission**

285 The fact that *Shrub* is recruited in the finger-like protrusion at a location where SJ
286 remodeling is taking place, and the fact that *Shrub* depletion has an impact on the
287 integrity of the SJs, prompted us to next investigate whether SJ components could
288 influence the timing of cytoplasmic isolation. We found that depletion of *Cora* in the
289 SOP and the ECS causes a premature cytoplasmic isolation (Fig. 6A, B; with a $t_{1/2} -$
290 5.8 ± 1.7 min compared to $t_{1/2}$ *pnr* reference control and Table S1C). We also
291 tracked the position of the midbody upon *Cora* depletion by live-imaging *MyoII*GFP
292 together with *GAP43IR* (Fig. 6C). 10 min after anaphase onset, the midbody co-
293 localized with *GAP43IR* at the interface between the two daughter cells (t_{10} , MB
294 level, Fig. 6C). Then, the midbody is released from the interface at t_{70} (Fig. 6C, MB
295 level, 88.7 ± 14.8 min, $n=8$) and is not detected within the *pIIa* cell at t_{85} (Fig. 6C,
296 94.3 ± 11.3 min, $n=7$). Thus, the midbody release and its disappearance from the *pIIa*
297 cell happen earlier than in the control (Fig. 6D and 6E respectively). This is not
298 caused by an acceleration of cell cycle in *Cora* depleted cells as the entry into
299 anaphase onset of *pIIb* and *pIIa* takes place later compared to the control (Fig. 6F).
300 Together, these data shows that abscission happens earlier upon *Cora* depletion
301 than in the control and indicates that the formation of SJs delays abscission timing of
302 the SOP.

303 Thus, *Shrub* and the SJ component *Cora* act as positive and negative regulators of
304 cytoplasmic isolation of SOP daughters, respectively. However, because depletion of
305 *Shrub* leads to altered localization of SJ components ((Pannen et al., 2020); Fig. 4D

306 and - Fig. S4D-E) the above results are counterintuitive at a first glance. Indeed, in a
307 simplistic model in which Shrub would only be required for SJ remodeling, depletion
308 of Shrub by causing a reduction in the amounts of SJ components should lead to
309 early cytoplasmic isolation. Nevertheless, as indicated above, Shrub also localizes at
310 the midbody level where it promotes abscission. These data on the dual function of
311 Shrub led us to further study the relationship between Shrub and Cora. Silencing of
312 Cora caused an increased recruitment of ShrubGFP within the finger-like protrusion
313 in one third of the cases, (n=6; Fig. 6G', t30-t70 and Fig. 6H) further suggesting a
314 function for Shrub at the site of local SJ remodeling (see discussion). Because,
315 ShrubGFP behaves like a mutant allele delaying abscission (Fig. 5E), we reasoned
316 that the presence of ShrubGFP could modify the timing of abscission measured
317 upon simple depletion of Cora. The timing of cytoplasmic isolation upon Cora
318 depletion in the presence of ShrubGFP mutant allele caused a premature isolation
319 compared to ShrubGFP allele alone (t_{1/2} difference of 12.1 min). Plotting results
320 also suggest a tendency for Cora depleted cells to exhibit greater proportions of a
321 premature cytoplasmic isolation than when shrubGFP allele is expressed in Cora
322 depleted cells (t_{1/2} difference of 4.09 min).

323 Overall, these data indicate that Shrub exerts two functions during SOP cytokinesis:
324 a first function, at the level of the SOP midbody to control the timing of cytoplasmic
325 isolation; and a second cell non-autonomous function in the finger-like protrusions for
326 the SJ-based remodeling (Fig. 6I).

327

328 **Discussion**

329 In this study, we further characterized the coordination of abscission and the
330 maintenance of epithelial permeability barrier functions during cytokinesis in dividing
331 SOPs and compared them to symmetrically dividing epidermal cells. In both types of
332 cells, the midbody assembles below the newly forming pIIa-pIIb adherens junctions.
333 In the plane of the midbody, the neighboring cells remains in contact with the divided
334 cell through finger-like protrusions. These finger-like protrusions are located within
335 the layer of SJs that were already connecting the neighbors and the SOP prior to
336 SOP mitosis. The disassembly of SJs appears to be the rate limiting step for the
337 disentangling of the finger-like protrusions. We reported that the basal displacement
338 of the midbody and the *de novo* assembly of SJs occurs faster in SOP than in EC,
339 resulting in a quicker disentanglement of the finger-like protrusions, an event that

340 precedes midbody release. We have described that cytoplasmic isolation is
341 temporally uncoupled to midbody release, suggesting that abscission is a two-step
342 process. At the molecular level, SJ components negatively regulate the timing of
343 cytoplasmic isolation implying a regulatory role of permeability barrier maintenance
344 on abscission. Finally, we reported that Shrub exerts two complementary functions in
345 SOP abscission. A first, cell autonomous control of the timing of cytoplasmic isolation
346 at the level of the SOP midbody. The second function of Shrub is at the finger-like
347 protrusions to remodel SJs and prevent premature abscission until the permeability
348 barrier is fully assembled.

349

350 **Dynamics of bSJs assembly and midbody release in SOP compared to EC**

351 FRAP analyses revealed that the percentage of mobile fraction of ATP α GFP is
352 increased in SOPs compared to ECs, suggesting that the assembly of SJs at the
353 new pIIa-pIIb interface occurs faster in SOPs. In addition, the disentanglement of the
354 finger-like protrusions, corresponding to the completion of disassembly of SJs
355 between SOP and neighbors also occurs faster in SOPs. This is associated with a
356 faster basal displacement of the midbody. These results add arguments in favor of
357 the concept that *de novo* assembly of SJs acts as a conveyor belt of midbody basal
358 displacement (Daniel et al., 2018). As the endosomal system actively contributes to
359 transport and turnover of SJ complexes (Nilton et al., 2010; Pannen et al., 2020;
360 Tempesta et al., 2017; Tiklová et al., 2010), our data suggest some differences in the
361 intracellular trafficking between SOP and EC. As SOP daughters enter into mitosis
362 about 90-120 min after the anaphase onset of SOP division, the dynamics of
363 membrane trafficking might be under cell cycle regulation. It is also possible that the
364 transcriptional program of SOPs includes specific membrane trafficking regulators or
365 SJ components that directly impact the kinetics of assembly of SJs. In addition, as
366 the disentanglement of the finger-like protrusions occurs faster in SOPs, our data
367 also implies that the dynamic of assembly and disassembly of SJs in the SOPs and
368 its daughters dictates the dynamics of SJ components in the neighboring ECs. Thus,
369 the dynamics of SJ between ECs and SOPs is different than between two ECs.

370

371 **Role of SJ components in regulating SOP cytoplasmic isolation**

372 We report that loss of SJ components results in premature cytoplasmic isolation,
373 raising the question of how can SJ components negatively regulate abscission? In

374 the finger-like protrusions formed as the result of cytokinetic ring constriction, the
375 nascent midbody is embedded in the SJs that were assembled between the SOP
376 and its EC neighbors prior to mitosis. This topology ensures that at the level of the
377 midbody within the finger-like protrusion, the permeability barrier function is
378 maintained. Above the midbody, the novel SJ between SOP daughters then
379 progressively assembles to build the permeability barrier between the daughters. We
380 envision the topology of the finger-like protrusions as a mean of maintaining the
381 mother-daughter permeability barrier throughout cytokinesis. The disentanglement of
382 finger-like protrusions corresponds to the dismantlement of the old SJ leading to the
383 release of the midbody. Thus, apical to basal displacement of the finger-like
384 protrusions involves intense membrane remodeling and probably membrane
385 trafficking which include Shrub-dependent trafficking. Upon Depletion of Cora, Shrub
386 is found at higher levels in the finger-like protrusions, and the process leading to
387 abscission and midbody release is accelerated. While the molecular trigger is yet to
388 be characterized, a simple possibility is that SJ components negatively regulate
389 Shrub recruitment at the level of the midbody and in the finger-like protrusions.

390

391 **Temporal uncoupling between cytoplasmic isolation and midbody release**

392 In isolated vertebrate cells, the cytoplasmic isolation is concomitant with abscission,
393 i.e. the physical separation of the divided cells (Guizetti et al., 2011; Steigemann et
394 al., 2009). We showed here, as demonstrated in the *C. elegans* one cell embryo
395 (Green et al., 2013), that cytoplasmic isolation and midbody release are temporally
396 separated events (Fig. 3F). A possible caveat in our study resides in the use of the
397 KAEDE probe, a 116kDa homotetramer (Ando et al., 2002). Indeed, we cannot
398 exclude that a probe of smaller size or a solute would still be able to equilibrate after
399 the time we have here determined as the timing of cytoplasmic isolation. However,
400 the fact that Shrub is recruited on both side of the midbody and regulates the time
401 when the KAEDE probe is no longer able to diffuse between the divided cells argues
402 that cytoplasmic isolation occurs several minutes prior to midbody release. As the
403 midbody release coincide with the disentanglement of the finger-like protrusions (Fig.
404 3F), we propose that the midbody is embedded within the SJ strands and released
405 only upon SJ disassembly. Following its release from the pIIa-pIIb interface, the
406 midbody is displaced on the surface of the pIIa cell until it detaches and found at
407 distance from the pIIa cell. There, the midbody is still labelled with

408 MyoIIIGFP/PavGFP, MyoIIRFP and GAP43IR markers suggesting that the midbody
409 is in the extracellular space rather than being internalized by adjacent epidermal
410 cells.

411

412 **Cell autonomous and cell non-autonomous functions of Shrub**

413 We report that Shrub positively and cell autonomously regulates abscission in SOP
414 as also observed in mammalian cultured cells and *Drosophila* germline stem cell
415 (Eikenes et al., 2015; Matias et al., 2015). ShrubGFP appears in the form of
416 punctiform signal in a stereotyped manner on both sides of the SOP midbody. These
417 two puncta of ShrubGFP are recruited at the midbody long before the midbody
418 release. This is also observed in female *Drosophila* germline stem cells where Shrub
419 is recruited to the ring canal from G1/S prior to abscission in G2 phase of the
420 following cell cycle (Eikenes et al., 2015; Matias et al., 2015). Interestingly,
421 recruitment of Shrub occurs around the S to G2 transition of the daughter cells and
422 about one hour after the entry of SOP into mitosis (Audibert, 2005). Then, the
423 midbody release takes place just before the G2/M transition of the pIIb cell. Thus, the
424 temporal regulation of abscission in SOP appears to follow a similar cell-cycle
425 dependent regulation as the *Drosophila* germline stem cells. Whether this cell-cycle
426 dependence is specific to stem cells and progenitors or also applies to epidermal
427 cells await further investigation.

428 Another pool of Shrub is acting in a cell non-autonomous manner. As in SOPs,
429 ShrubGFP is also recruited at the midbody of the dividing epidermal cell and is
430 recruited in the finger-like protrusions. What could be the function of the pool of
431 ShrubGFP in the finger-like protrusions? Based on the fact that Shrub regulates SJs
432 steady state distribution and dynamics (Pannen et al., 2020), and is also known to
433 regulate endosomal sorting, Shrub could locally participate in SJ remodeling.
434 Alternatively, based on the geometry of the tip of the finger-like protrusions and
435 possible local constraints linked to basal displacement of the SOP midbody, Shrub
436 could be recruited there to promote membrane repair (Jimenez et al., 2014; Scheffer
437 et al., 2014) and/or locally compensate for leakage in permeability barrier function.
438 Consistent with this model, when the permeability barrier function is challenged, as
439 for example during Cora depletion, ShrubGFP is prone to accumulate in the finger-
440 like protrusions.

441

442 **Abscission timing, midbody inheritance and cell fate decision**

443 A link between the regulation of cell division and fate decision is reported and
444 abscission is thought to regulate fate acquisition (Chaigne et al., 2020; Ettinger et al.,
445 2011). Here, we found that the abscission is asymmetric with the midbody remnant
446 inherited by the pIIa cell in most cases. By analogy with the *C. elegans* single-cell
447 embryo, the midbody could be inherited by default by the cell that will divide later
448 than its daughter (Green et al., 2013). Can SOP midbody remnant signal and impact
449 on proliferation, differentiation and/or cell fate as in mammalian cells (Ettinger et al.,
450 2011; Kuo et al., 2011; Peterman et al., 2019; Pohl and Jentsch, 2009) ? Whether
451 SOP midbody exerts a function on proliferation awaits further monitoring of its
452 behavior (uptake?) after its release from the pIIa cell.

453

454 The fact that abscission occurs rather late after the anaphase onset while Notch-
455 dependent fate acquisition is initiated about 15 min after the onset of anaphase
456 raises an intriguing question (Bellec et al., 2018; Couturier et al., 2012). Indeed, our
457 photo-activation experiment shows that pIIa and pIIb share their cytoplasm until t60
458 after anaphase, which contrasts with the fact that the Notch intracellular domain
459 (NICD) is translocated exclusively in the nucleus of pIIa . The cell fate determinants
460 Numb and Neuralized, two cytosolic proteins, are also unequally inherited by the pIIb
461 cell before cytoplasmic isolation. An interesting question is how NICD, and Numb,
462 Neuralized remain confined to pIIa and pIIb cells respectively, while at the same time
463 the KAEDE probe freely diffuses bidirectionally. This situation is reminiscent to that
464 of phospho-Mad that remains restricted to the most anterior of *Drosophila* germline
465 stem cells in stem cysts (Eikenes et al., 2015; Mathieu et al., 2013; Matias et al.,
466 2015). Unless, Notch signaling components are assembled in very large protein
467 complexes or with cytoskeletal components that prevent them from diffusing through
468 the opened intercellular bridge, these data imply that selective passage must be
469 regulated at the intercellular bridge (Mullins and Biesele, 1977; Norden et al., 2006;
470 Steigemann et al., 2009), as reported for proteins and organelles in yeast (Lengefeld
471 and Barral, 2018).

472

473 Overall, our study sheds light on a complex coordination of abscission, maintenance
474 of epithelial permeability barrier functions and fate acquisition in SOPs. Based on the
475 apico-basal topology of mechanical and permeability barriers, apical positioning of

476 the midbody within the tight junctions in vertebrates (Dubreuil et al., 2007; Higashi et
477 al., 2016; Jinguji and Ishikawa, 1992) and the role of ESCRT components in tight
478 junction protein trafficking (Dukes et al., 2011; Raiborg and Stenmark, 2009), it is
479 tempting to speculate that the cell autonomous and non-autonomous effects we
480 described in this study may also be at play during epithelial abscission of progenitors
481 in vertebrates.

482

483

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495

496 **Competing interests**

497 The authors declare no competing or financial interests.

498

499 **Author contributions**

500

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505

506

507 **Materials and Methods**

508 **Key resources table**

REAGENT OR RESOURCES	SOURCE	IDENTIFIER
Antibodies		
Mouse anti-Coracle (1:200)	DSHB	C615.16
Rabbit anti- Kune Kune (1:1500)	Kind gift from Mikio Furuse (Nelson et al., 2010)	N/A
Rabbit anti-NrxIV (1:1000)	(Stork et al., 2009)	N/A
Rabbit anti Sinuous (1:1000)	Kind gift from Dr. Greg Beitel (Wu et al., 2004)	N/A
mouse-anti- α -spectrin (1:500)	DSHB	Clone 1A9
Rat anti-Crumbs (1:1000)	Kind gift from Elisabeth Knust (Richard et al., 2006)	N/A
Rat anti-DE-cad (1:250)	DSHB	DCAD2
Mouse anti-HRS (1:200)	DSHB	Clone 27-4
Cy2, Cy3 or Cy5-coupled secondary antibodies (1:300)	The Jackson laboratory	N/A
Chemicals		
Hoechst	Thermofischer	62249
CityFluor	Agar scientific	AGR1320
DABCO	Sigma	S8032
N-Propyl-Gallate	Sigma	200-289-5
Paraformaldéhyde	EMS	19340-72
Phosphate Buffer Saline	Lonza	BE17-515F
Triton X-100	Euromedex	2000 B
Voltalef 10S	VWR	24627.188

REAGENT OR RESOURCES	SOURCE	IDENTIFIER
Experimental models: Organisms/ Strain		
<i>D. melanogaster</i> : w ¹¹¹⁸	BDSC	BL3605
<i>D. melanogaster</i> . MyoII::RFP ^{crispr}	(Daniel et al., 2018)	N/A
<i>D. melanogaster</i> . MyoII::GFP ^{crispr}	(Esmangart de Bournonville and Le Borgne, 2020)	N/A
<i>D. melanogaster</i> . Shrub::GFP ^{crispr} /CyO	(Mathieu et al., 2022)	N/A
<i>D. melanogaster</i> . CHMP2B::GFP ^{crispr} /CyO	(Mathieu et al., 2022)	N/A
<i>D. melanogaster</i> . Pavarotti::GFP	inDroso	N/A
<i>D. melanogaster</i> . ATPα::GFP/TM6, Sb, Tb	BDSC	BL59297
<i>D. melanogaster</i> . FRT82B ATPα::GFP/TM6, Tb	(Daniel et al., 2018)	N/A
<i>D. melanogaster</i> . <i>hs-FLP</i> ;; FRT82B nls::RFP	BDSC	BL30555
<i>D. melanogaster</i> . ;;MyoII-MyoII::mcherry	(Martin et al., 2009)	N/A
<i>D. melanogaster</i> . UAS-Shrub RNAi	BDSC	BL38305
<i>D. melanogaster</i> . UAS-KAEDE	BDSC	BL26161
<i>D. melanogaster</i> . UAS-KAEDE	BDSC	BL38622
<i>D. melanogaster</i> . UAS-Shrub::GFP	(Sweeney et al., 2006)	N/A
<i>D. melanogaster</i> . UAS-Cora RNAi	VDRC	9788
<i>D. melanogaster</i> . <i>neur</i> -H2B::IR	(Houssin et al., 2021)	N/A
<i>D. melanogaster</i> . <i>neur</i> -GAP43::IR	(Houssin et al., 2021)	N/A
<i>D. melanogaster</i> . <i>pnr</i> -Gal4/ TM6, Tb	(Calleja et al., 1996)	N/A
<i>D. melanogaster</i> . <i>neur</i> -GAP43::IR, <i>pnr</i> -Gal4/TM6, Tb	(Houssin et al., 2021)	N/A

REAGENT OR RESOURCES	SOURCE	IDENTIFIER
<i>D. melanogaster</i> : Ay-Gal4/Cyo	BDSC	BL3953
<i>D. melanogaster</i> : sca-Gal4	(Mlodzik et al., 1990)	N/A
Software and Algorithms		
Photoshop CS4		N/A
EasyFRAP-web	Open Source Program	N/A
Image J / FIJI	Open Source Java	N/A
Prism 8	GraphPad Version 8	N/A
R version 4.2.1	(R Core Team, 2022)	https://www.r-project.org/
Others		
Microscopes confocaux	Leica LSM TCS	SP8, SP5 and SPE

509
510
511
512
513
514
515

516 ***Drosophila* stocks and genetics**

517 *Drosophila melanogaster* stocks were maintained and crossed at 25°C.

518 Somatic clones were induced using the *hs-FLP* with two heat shocks (60 min at
519 37°C) at second and third instar larvae. *pnr-Gal4* was used to drive the expression of
520 UAS-Cora RNAi and the photoconvertible probe UAS-KAEDE. *Ay-Gal4* was used to
521 drive the expression of UAS-ShrubGFP. *sca-Gal4* was used to drive the expression
522 of UAS-ShrubRNAi and UAS-KAEDE.

523 Declaration of contained use of genetically modified organisms (GMOs) of
524 containment class n°2898 from the French Ministère de l'Enseignement Supérieur,
525 de la Recherche et de l'Innovation.

526

527 ***Drosophila* genotypes**

528

529 **Fig. 1**

530 (B) MyoII::RFP ; *neur-H2B::IR/+* ; ATP α ::GFP/+

531 (C-C') *neur-H2B::IR*

532 (E) MyoII::RFP ; *neur-H2B::IR/+* (EC and SOP) and MyoII::RFP ; *neur-H2B::IR/+* ;

533 ATP α ::GFP/+ (EC and SOP)

534

535 **Fig. 2**

536 (A-B) *hs-FLP/MyoII::RFP* ; *neur-H2B::IR/+* ; FRT82B ATP α ::GFP/FRT82B nls::RFP

537 (C-D) MyoII::RFP ; ATP α ::GFP/*neur-GAP43::IR*

538

539 **Fig. 3**

540 (A-C) UAS::KAEDE; *neur-GAP43::IR*, *pnr-Gal4/+*

541 (D-D') MyoII::GFP, *neur-H2B*; *neur-GAP43::IR*, *pnr-Gal4/+*

542

543 **Fig. 4**

544 (A-A') MyoII::RFP ; Shrub::GFP/+; *neur-GAP43*, *pnr-Gal4::IR/+*

545 (B-C) *hs-FLP*; UAS-Shrub::GFP/*Ay-Gal4*; *MyoII-MyoII::mcherry*

546 (D) *sca-Gal4/UAS-Shrub-RNAi*; UAS-KAEDE/+

547 (E) *sca-Gal4/UAS-Shrub-RNAi*; UAS-KAEDE/+, *sca-Gal4/UAS-Shrub-RNAi*; UAS-

548 KAEDE/*neur-GAP43::IR* and *sca-Gal4/+*; UAS-KAEDE/+

549

550 **Fig. 5**

551 UAS::KAEDE; *neur-GAP43::IR*, *pnr-Gal4/+* and UAS::KAEDE/ShrubGFP; *neur-*

552 *GAP43::IR*, *pnr-Gal4/+*

553

554 **Fig. 6**

555 (A) UAS-KAEDE/+; *neur-GAP43::IR*, *pnr-Gal4/UAS-Cora RNAi*

556 (B) UAS-KAEDE/+; *neur-GAP43::IR*, *pnr-Gal4/+* and UAS-KAEDE/+; *neur-*

557 *GAP43::IR*, *pnr-Gal4/UAS-Cora RNAi* and UAS-KAEDE/Shrub::GFP; *neur-*

558 *GAP43::IR*, *pnr-Gal4/+* and UAS-KAEDE/Shrub::GFP; *neur-GAP43::IR*, *pnr-*

559 *Gal4/UAS-CoraRNAi*

560 (C) MyoII::GFP, *neur-H2B*; *neur-GAP43::IR*, *pnr-Gal4/ UAS::Cora RNAi*

561 (D-F) Myoll::GFP, *neur*-H2B;; *neur*-GAP43::IR, *pnr*-Gal4/+ and Myoll::GFP, *neur*-
562 H2B;; *neur*-GAP43::IR, *pnr*-Gal4/ UAS::Cora RNAi

563 (G-G') Myoll::RFP; *shrub*GFP/+; *neur*-GAP43::IR, *pnr*-Gal4/ UAS::Cora RNAi

564

565 **Fig. S 1**

566 (A) Myoll::RFP ; *neur*-H2B::IR/+ ; ATP α ::GFP/+

567

568 **Fig. S 2**

569 (A) *hs*-FLP/Myoll::RFP ; *neur*-H2B::IR/+ ; FRT82B ATP α ::GFP/FRT82B *nls*::RFP

570

571 **Fig. S 3**

572 (B) UAS::KAEDE; *neur*-GAP43::IR, *pnr*-Gal4/+ and *sca*-Gal4/+; UAS-KAEDE/+

573 (C) UAS::KAEDE; *neur*-GAP43::IR, *pnr*-Gal4/+ and *sca*-Gal4/+; UAS-KAEDE/+

574 (E) Myoll::RFP/Myoll::GFP;; GAP43::IR/+

575 (F) Myoll::RFP;; GAP43::IR/ Pav::GFP

576

577 **Fig. S 4**

578 (A,B) *hs*-FLP; UAS-Shrub::GFP/*Ay*-Gal4; *MyoII*-*MyoII*::mcherry

579 (C-E) *sca*-Gal4/UAS-Shrub-RNAi; UAS-KAEDE/+

580

581 **Fig. S 5**

582 (A) *w*¹¹¹⁸ and Shrb::GFP/+

583 (B) Myoll::RFP ; CHMP2BGFP/+ ; *neur*-GAP43/+

584

585

586 **Methods**

587

588 **Immunofluorescence**

589 Pupae aged from 16 to 24h after puparium formation (APF) were dissected using
590 Cannas microscissors in 1X Phosphate-Buffered Saline (1X PBS, pH 7.4) and fixed
591 15 min in 4% paraformaldehyde solution at room temperature (RT) (Gho et al.,
592 1996). Following fixation, dissected nota were permeabilized using 0.1% Triton X-
593 100 in 1X PBS (PBT) and incubated with primary antibodies diluted in PBT for 2
594 hours at RT. After 3 washes of 5 minutes in PBT, nota were incubated with

595 secondary antibodies diluted in PBT for 1 hour at RT. Following incubation, nota
596 were washed 3 times in PBT, and once in PBS prior mounting in 0,5% N-
597 propylgallate with DABCO dissolved in 1X PBS/90% glycerol.

598 For *Drosophila* germline stem cell identification, antibody staining and Hoechst
599 staining were performed according to standard protocols. Briefly, ovaries or testis
600 were dissected in PBS, fixed in 4% PFA, rinsed and permeabilized in PBT (PBS-
601 0,2%Triton) for 30 min, left overnight with primary antibodies in PBT at 4°C, washed
602 2 h in PBT, left with secondary antibodies in PBT for 2 hrs at room temperature,
603 washed 1 h in PBT and mounted in Citifluor (Eikenes et al., 2015; Matias et al.,
604 2015).

605 GSC were identified with the fusome staining (round or linking the CB) and counted.
606 Stem-cysts (more than 2 cells anchored to the niche and linked by a fusome) and
607 polyploid GSC (higher DNA and larger fusome than control) were counted. Stacks
608 were acquired every 0.7 µm.

609

610 **Live imaging and image analysis**

611 Live imaging was performed on pupae aged for 16 to 22h APF at 20-25°C (Gho et
612 al., 1999). Pupae were stucked on a glass slide with a double-sided tape, and the
613 brown pupal case was removed over the head and dorsal thorax using
614 microdissection forceps. Pillars made of 4 to 5 glass coverslips were positioned at
615 the anterior and posterior side of the pupae, respectively. A glass coverslip covered
616 with a thin film of Voltalef 10S oil is then placed on top of the pillars such that a
617 meniscus is formed between the dorsal thorax of the pupae and the glass coverslip.
618 Images were acquired with a confocal microscope Leica SP5, SP8 or SPE equipped
619 with a 63X N.A. 1.4. and controlled by LAS AF software. Confocal sections were
620 taken every 0.5 µm unless otherwise specified. All images were processed and
621 assembled using ImageJ/FIJI software and Photoshop CS4.

622

623 **Fluorescence recovery after photobleaching**

624 FRAP experiments were performed in pupae expressing MyoIIIRFP with ATPαGFP
625 and neur-GAP43IR. Regions of interest corresponding to one of the two ATPα::GFP
626 finger-like protrusions pointing to the midbody were bleached (488 nm at 100% laser,
627 1 iteration of 100 ms) using a LSM Leica SP8 equipped with a 63X N.A. 1.4 PlanApo
628 objective. Confocal stacks were acquired every 2 min and 30s after photobleaching.

629

630 **KAEDE photoconversion**

631 Photoconversion assays were performed in pupae expressing the green to red
632 photoconvertible probe KAEDE. KAEDE was photoconverted (405 nm laser at 0,5 to
633 2% power, point bleach, 1 to 2 iterations of 300 ms each) using a LSM Leica SP8
634 equipped with a 63X N.A. 1.4 PlanApo objective. Confocal stacks were acquired
635 every 2 min after photoconversion and imaged at 22-25°C.

636

637 **Quantification and statistical analysis**

638 **Midbody tracking**

639 The apico-basal position of the midbody was calculated measuring the distance
640 between the middle of the new Adherens junction and the midbody (both labeled
641 with MyoII::RFP) at each time. The x, y, z coordinates of AJ and the midbody were
642 manually tracked to record positions at each time, and then were used to calculate
643 the distance using the Pythagorean Theorem. The midbody apico-basal tracking
644 movement was calculated using the equation $y = -ax + b$, where a corresponds to the
645 midbody velocity toward the basal pole.

646

647 **Signal recovery upon photobleaching**

648 For each FRAP experiment, three measures were performed, the photobleached
649 junction, the control junction (the finger-like protrusion opposite to the FRAPed
650 finger-like protrusion) and the background.

651 Data were normalized using EasyFRAP-web software with the "Full scale" method.
652 Signal recoveries were approximated with the equation $y = y_{max} (1 - e^{-kx})$ with the
653 half-life $t_{1/2} = \ln(2) / k$.

654

655 **Statistical tests**

656 All information concerning the statistical tests are provided in the main text and in the
657 figure legends, including the number of samples analyzed in each experiment.
658 Prism 8 software or R 4.2.1 were used to perform the analyses.
659 Line plots use the following standards: thick lines indicate the means. Bar plots
660 represent mean and errors bars represent the SD.

661 Shapiro-Wilk normality test was used to confirm the normality of the data and the F-
662 test to verify the equality of SD. The statistical differences of Gaussian data sets
663 were analyzed using the Student unpaired two-tailed t test.

664 For the analysis of the midbody displacement, we performed an ANCOVA to test the
665 effect of the interaction between time (between 5 and 120 min) and the « condition »
666 parameter (SOP vs EC). For the midbody displacement and FRAP, the colored
667 areas show standard deviation (SD).

668 Time to cytoplasmic isolation was modeled via logistic regression, using the GLM
669 function in R, with a binomial error distribution and a logistic link function. We began
670 with a fully parameterized model in which cytoplasmic isolation varied as a function
671 of time, condition and the interaction between time and condition (i.e. both the slopes
672 and intercepts of the model describing temporal effects differed among condition
673 groups). Statistical significance of each model term was evaluated via analysis of
674 deviance, with forward model selection of terms and goodness-of-fit assessed
675 against a Chi-squared distribution. Additionally, we ran two additional nested
676 models: one excluding the interaction term (i.e. a common model slope with
677 differences amongst condition groups in their intercept terms; equivalent to
678 differences in the means amongst groups), and a second in which cytoplasmic
679 isolation state varied only as a function of time (i.e. no effective differences amongst
680 condition groups). We compared overall fit for each model using Akaike's
681 information criterion (AIC), selecting the parsimony model as the one with the lowest
682 AIC score. Results of analysis of deviance and model comparisons corroborated
683 each other, and so the parsimony model was used to predict the mean percentage of
684 cells demonstrating cytoplasmic isolation, as well as standard errors (SE) of the
685 estimates, and to visualize differences among groups. In some lines, the interaction
686 between time and treatment was not significant, however the interaction between
687 `sca>` and `pnr>` was slightly significant (Table S1). These results were corroborated
688 by model comparison via AIC, with the selection process favoring models including
689 only time and treatment effects, i.e. although proportions of cells in cytoplasmic
690 isolation differed among conditions at a given time point, the rate of relative increase
691 over time did not differ among groups. This lack of significant time-treatment
692 interaction facilitated the comparison of treatment effect size. To do so, we used
693 model results to estimate the time at which 50% of the pIIa/pIIb cell indicated
694 cytoplasmic isolation (herein termed $t_{1/2}$). Each $t_{1/2}$ were estimated using the two

695 models (sca> and sca>shrubRNAi) and (pnr>, pnr>+ ShrubGFP/+, pnr>+ Cora
696 RNAi, pnr>Cora RNAi+ ShrubGFP/+). Statistical significance were represented as
697 follow: p-value>0.05 ns (not significant); p-value≤0.05*; p-value≤0.01** and p-
698 value≤0.001***

699

700

701 **Figure Legends**

702

703 **Fig. 1. Midbody assembly and basal displacement throughout epithelial cell**
704 **cytokinesis**

705 (A) Schematic representation of the *Drosophila* pupal notum composed of epidermal
706 cells (white) and sensory organ precursors (SOP, grey). Adherens junctions (AJ) and
707 septate junctions (SJ) were represented in magenta and green respectively. (A') EC
708 daughter cells cytoplasmic isolation happens after 5 hours after anaphase onset of
709 their mother. In the meantime, SOP undergo four rounds of asymmetric cell division.
710 2h and 2h20 refers to the approximative time at which the respective daughter cells
711 start to divide. At each division, fate identity relies on differential activation of Notch
712 (Notch is activated in the cells depicted in blue).

713 (B) Time-lapse of SOP cells (n=12) expressing MyoIIIRFP (magenta), ATP α GFP
714 (green) and Histone 2B IR (H2BIR) to identify the SOP (blue). B' correspond to the
715 orthogonal views along the white dashed lines depicted at t=10 min on panel B.
716 White arrows point to the midbody. AJ, adherens junction; SJ, septate junction; Ap:
717 Apical; Ba: Basal.

718 (C) Localization of E-Cad (cyan) and Cora (green) at the pIIa-pIIb cell stage
719 identified using H2BIR (white). Higher magnifications in (C') correspond to the ROI in
720 the white dotted line square depicted in (C) and white arrows show the finger-like
721 protrusions. (n>3, 3 nota per condition). Right: Schematic representation of the SOP
722 with the finger like protrusions in green as in (C').

723 (D) Schematic representation of the midbody basal displacement in EC and SOP
724 corresponding to t115 (1A' and 1B'). MB: Midbody

725 (E) Plot of the quantification of the apical to basal midbody displacement over time
726 relative to AJs in EC (black, n=40) and SOP (blue, n=30) dividing cells. ANCOVA, p-
727 value < 2.2.10⁻¹⁶***. Solid lines represent simple linear fit.

728 Time is in minute with t= 0 corresponding to anaphase onset (B-B', E). Scale bars
729 represent 5 μ m (B-C) and 1 μ m (C'). Red and blue dots mark the pIIb and pIIa
730 respectively (B-C).

731

732 **Fig. S1: Midbody assembly and basal displacement throughout EC**
733 **cytokinesis**

734 (A) Time-lapse of EC dividing cells (n=20) expressing MyoIIIRFP (magenta),
735 ATP α GFP (green). A' correspond to the orthogonal views along the white dashed
736 lines depicted at t=10 min on panels A. White arrows point to the midbody. AJ,
737 adherens junction; SJ, septate junction; Ap: Apical; Ba: Basal. Time is in minutes
738 with t=0 corresponding to anaphase onset and scale bars represents 5 μ m.

739

740

741 **Fig. 2. Kinetics of SJ assembly in SOP and EC**

742 (A) Time lapse of SOP (n=5) dividing cells expressing MyoIIIRFP and nlsRFP
743 (magenta) and H2BIR (white) adjacent to cells expressing MyoIIIRFP (magenta) and
744 ATP α GFP (green and grey on upper and bottom panels, respectively). Distances in
745 μ m represent the position relative to the AJ plane determined by apical MyoII signal.
746 White dashed line delineates the clone border at t0. White arrows point to the
747 midbody. Dashed white ring encircles the midbody at t110 and t120. The white
748 square at t120 represents a higher magnification of the midbody located below a
749 nucleus expressing nlsRFP (scale bar represents 1 μ m).

750 (B) Time lapse of dividing SOP (n=2) expressing MyoIIIRFP (magenta), H2BIR
751 (white) and ATP α GFP (green) close to cells expressing MyoIIIRFP (magenta) and
752 nlsRFP (magenta). Dashed white ring encircles the midbody at t120. Distances in
753 μ m represent the position relative to the AJ plane determined by apical MyoII signal.

754 (C) Time lapse of SOP dividing cell expressing MyoIIIRFP (magenta), ATP α GFP
755 (green and grey on upper and second panels, respectively) and the plasma
756 membrane marker GAP43IR (blue), and FRAP of ATP α GFP. Yellow dotted line
757 square inset indicates the photobleached region of interest. The white dotted line
758 rectangle at t=0 delineate the ROI shown in the right panels (t=10-40 min) at the
759 level of SJ and MB to monitor the recovery of ATP α GFP signal over time.
760 Photobleaching was done 20 min after the anaphase onset with t=0 corresponding to
761 the time of photobleaching.

762 (D) Plot of the quantification of fluorescence recovery of ATP α GFP signal after
763 photobleaching over time in EC (n=20, black) and SOP (n=13, blue) in the SJ plane
764 located 1 μ m below AJ. Solid white lines represent a simple exponential fit.

765 AJ: Adherens junctions, SJ: Septate junctions, MB: Midbody. In A, B, and C, SOPs
766 and daughters were identified using H2BIR in A and B (grey) or GAP43IR in C
767 (blue). Red and blue dots mark the pIIb and pIIa respectively (A-C). Time is in

768 minutes with t0 corresponding to the onset of SOP anaphase, except in (C, D) where
769 t0 corresponds to the time of photobleaching. Scale bars represent 5 μm (A-B) and 3
770 μm (C).

771

772

773 **Fig. S2: Evolution of SJ-positive finger-like protrusions and midbody contacts**
774 **throughout EC cytokinesis**

775 (A) Time lapse of EC (A, n=13) dividing cells expressing MyoII-RFP (magenta),
776 nlsRFP (magenta) close to cells expressing MyoII-RFP (magenta) and ATP α GFP
777 (green, grey bottom panels). White dashed lines delineate the clone border at t0.
778 White arrows point to the midbody. AJ, adherens junction; SJ, septate junction. Time
779 is in minutes with t0 corresponding to the onset of anaphase. Scale bar represents 5
780 μm .

781

782 **Fig. 3. cytoplasmic isolation of pll α -pll β and midbody release are temporally**
783 **controlled**

784 (A-B) Time lapse of SOP dividing cell expressing KAEDE under *pannier* driver.
785 Green to Red (magenta) photoconversion was performed (yellow lightning at t=0) in
786 the pll β cell at 61 min (A) or 63 min (B) after the onset of anaphase. A' and B'
787 correspond to the orthogonal views along the white dashed lines depicted at t=-1 min
788 on panels A and B, respectively. Ap: Apical, Ba: Basal. Time is in min where t=0
789 corresponds to the time of photoconversion.

790 (C) Plot representing the proportion of pll α -pll β cells to have cytoplasmic isolation
791 over time after anaphase onset in control (*pnr*>). Cytoplasmic isolation was
792 assessed based on the ability of photo-converted KAEDE in pll α /pll β cell to diffuse in
793 the pll β /pll α cell at different time point after the onset of anaphase. The dashed line
794 represents mean values, predicted from a generalized linear model (GLM). SE of the
795 estimates are represented in grey shading. n=62, 24 pupae.

796 (D) Time lapse of SOP dividing cell expressing MyoII-GFP (Green) and GAP43-IR
797 (Magenta). White arrows point to the midbody. Distances in μm represent the
798 position relative to the AJ plane determined by apical MyoII signal. (D') corresponds
799 to the orthogonal view depicted in (D, t110). (D'') scheme representing the
800 displacement of the midbody over the pll α membrane at the indicated time as in (D)

801 and adapted from (Houssin et al., 2021). The red and blue cells correspond to the
802 pIIb and pIIb respectively. Ap: Apical; Ba: Basal.

803 (E) Timeline of events during SOP cytokinesis

804 AJ: Adherens junctions, MB: Midbody. Red and blue dots mark the pIIb and pIIa
805 respectively (A, B, D). Time is in minutes with t₀ corresponding to the onset of
806 anaphase (D) except in A and B where t₀ corresponds to the time of
807 photoconversion. Scale bars represent 5 μm (A-B,D-D').

808

809 **Fig. S3: Maturation of the midbody and timing of cytoplasmic isolation**

810 (A) Schematic representation of KAEDE photoconversion in SOP cells. The two
811 daughter cells (pIIa and pIIb) are both expressing KAEDE (Green). After
812 photoconversion in pIIa cell, Green KAEDE is photoconverted into Red KAEDE
813 (Magenta). 2 min to until its equilibrium at 8 min after photoconversion, Red KAEDE
814 diffuses in the pIIb cell (No cytoplasmic isolation) or do not diffuse into pIIb
815 (Cytoplasmic isolation). adapted from (Houssin et al., 2021)

816 (B) Frequency of pIIa-pIIb control cells *pnr*> (black) and *sca*> (grey) photo-converted
817 at different time after anaphase onset.

818 (C) Plot representing the proportion of pIIa-pIIb cells to have cytoplasmic isolation
819 over time after anaphase onset in control *pnr*> (*pnr*>, dashed line, n=62, 24 pupae)
820 and control *sca*> (*sca*>, solid line, n=30, 11 pupae). Cytoplasmic isolation was
821 assessed based on the ability of photo-converted KAEDE in pIIa/pIIb cell to diffuse in
822 the pIIb/pIIa cell at different time point after the onset of anaphase. Lines represent
823 mean values, predicted from a GLM with the interaction between time and
824 conditions; SE of the estimates are represented in grey shading.

825 (D) Frequency of pIIa-pIIb control cells (*sca*>) photo-converted at different time after
826 anaphase onset.

827 (E) Time lapse of SOP dividing cells expressing MyoIIIRFP (magenta), MyoIIGFP
828 (green) and GAP43IR (grey). White arrows point to the midbody. (E') Higher
829 magnification of the white dashed square depicted at t₀ in (E) shows the midbody.

830 (F) Time lapse of SOP dividing cells expressing MyoIIIRFP (magenta), PavGFP
831 (green) and GAP43IR (grey). White arrows point to the midbody. (F') Higher
832 magnification of the white dashed square depicted at t₀ in (F) shows the midbody.

833 Time is in minutes. Blue dots mark the pIIa (E, F). Scale bars represent 5 μm (E-F')
834 and 1 μm (E', F').

835

836

837 **Fig. 4. Recruitment and function of Shrub in SOP daughter cells**

838 (A-A') Time lapse of SOP dividing cells expressing MyoIIIRFP (magenta), ShrubGFP
839 (green) and GAP43IR (grey). (A') Higher magnification of the white dashed line inset
840 depicted in (A) at t10 showing the recruitment of ShrubGFP (green) at the midbody
841 (magenta) over time. (A'') Schematic representation depicting ShrubGFP recruitment
842 at the presumptive finger like protrusions (between 40 and 60 min) and (A''') at the
843 midbody (magenta square) (between 70 and 120 min) corresponding to (A').

844 (B) Time lapse of SOP dividing cell expressing MyoIIImcherry (magenta) adjacent to
845 epidermal cell expressing MyoIIImCherry (magenta) together with ShrubGFP
846 expressed under *Ay Gal4* driver (green). White line delineates the border of clones of
847 cells expressing ShrubGFP at t0. The higher magnifications at the bottom right (MB
848 level, t10-72) correspond to the ROI in the white dotted line square of the
849 corresponding panel (scale bar represents 1 μ m). (B') Representation of the SOP at
850 t36 (B) surrounded by one EC positive for ShrubGFP (light green) and showing the
851 ShrubGFP puncta (dark green) at the tip of the finger-like protrusion pointing toward
852 the midbody (magenta square).

853 (C) Time lapse of dividing SOP expressing MyoIIImcherry (magenta) together with
854 ShrubGFP expressed under *Ay Gal4* driver (Green) close to cells expressing
855 MyoIIImcherry (magenta) but not ShrubGFP. White dashed line delineates the clone
856 border at t=0. The higher magnifications at the bottom right (MB level, t10-90)
857 correspond to the ROI in the white dotted line square of the corresponding panel
858 (scale bar represents 1 μ m). (C') Representation of the ShrubGFP positive SOP
859 (light green) at t60 (C) surrounded by ECs negative for ShrubGFP and showing the
860 ShrubGFP punctae (dark green) recruitment at the midbody (magenta square).

861 (D) Localization of KAEDE (green), Kune Kune (magenta) and Crumbs (grey) in nota
862 expressing Shrub RNAi and KAEDE. The white dashed lines separate control from
863 Shrub RNAI (KAEDE expressing cells). Ap: apical, Ba: basal.

864 (E) Plot representing the proportion of pIIa-pIIb cells to have cytoplasmic isolation
865 over time after anaphase onset. Cytoplasmic isolation was assessed based on the
866 ability of photo-converted KAEDE in pIIa/pIIb cell to diffuse in the pIIb/pIIa cell at
867 different time point after the onset of anaphase in control (*sca*>, solid line, n=30, 11
868 pupae) and ShrubRNAi (*sca*> ShrubRNAi, dashed line, n=30, 14 pupae). Lines

869 represent mean values, predicted from a GLM of t1/2 values for *sca>* centered to 0;
870 SE of the estimates are represented in grey shading. p-value=0,003, **)

871

872 **Fig. S4: Recruitment of Shrub at the midbody and function of Shrub in**
873 **cytoplasmic isolation**

874 (A) Time lapse of EC dividing cell expressing MyoIImcherry adjacent to cells
875 expressing MyoIImcherry (magenta) together with ShrubGFP expressed under *Ay*
876 *Gal4* driver (green). White line delineates the border of clones of cells expressing
877 ShrubGFP at t0. The higher magnifications at the bottom right (MB level, t10-36)
878 correspond to the ROI in the white dotted line square of the corresponding panel
879 (scale bar represents 1 μ m). (A') Representation of the EC at t36 (A) surrounded by
880 EC positive for ShrubGFP (light green) and showing the ShrubGFP punctae (dark
881 green) recruitment at the tip of the finger-like protrusion pointing toward the midbody
882 (magenta square).

883 (B) Time lapse of dividing EC expressing MyoIImcherry (magenta) together with
884 ShrubGFP under the *Ay Gal4* driver (Green) close to cells expressing MyoIIIRFP
885 (magenta) but not ShrubGFP. White dashed line delineates the clone border at t=0.
886 The higher magnifications at the bottom right (MB level, t12-90) correspond to the
887 ROI in the white dotted line square of the corresponding panel (scale bar represents
888 1 μ m). (B') Representation of the ShrubGFP positive EC (light green) at t60 (B)
889 surrounded by ECs negative for ShrubGFP and showing the ShrubGFP puncta (dark
890 green) recruitment at the midbody (magenta square).

891 (C) Localization of KAEDE (green) and HRS (magenta) in nota expressing Shrub
892 RNAi and KAEDE. The white dashed lines separate control from Shrub RNAi
893 (KAEDE expressing cells).

894 (D) Localization of KAEDE (green) and NrXIV (magenta) in nota expressing Shrub
895 RNAi and KAEDE. The white dashed lines separate control from Shrub RNAi
896 (KAEDE expressing cells).

897 (E) Localization of KAEDE (green) and Sinus (magenta) in nota expressing Shrub
898 RNAi and KAEDE. The white dashed lines separate control from Shrub RNAi
899 (KAEDE expressing cells).

900 (F) Higher magnification of a SOP midbody (magenta) showing CHMP2BGFP
901 recruitment (green).

902 AJ, adherens junction; MB, Midbody. Time is in minutes with t0 corresponding to
903 anaphase onset (A-B'). Scale bars represent 5 μm (A, B, C-E) and 1 μm (F).

904

905 **Fig. 5. ShrubGFP is a mutant allele that impacts the timing of cytoplasmic**
906 **isolation**

907 (A) Plot representing the proportion of pIIa-pIIb cells to have cytoplasmic isolation
908 over time after anaphase onset. Cytoplasmic isolation was assessed based on the
909 ability of photo-converted KAEDE in pIIa/pIIb cell to diffuse in the pIIb/pIIa cell at
910 different time point after the onset of anaphase in control (*pnr* >, dashed line, n=62,
911 24 pupae) and ShrubGFP/+ (*pnr* >+ ShrubGFP/+ ,dotted line, n=52, 12 pupae).

912 Lines represent mean values, predicted from a GLM of t1/2 values for *pnr*> centered
913 to 0; SE of the estimates are represented in grey shading (p-value=1,68.10⁻⁶, ***).

914 Time is in minutes.

915

916 **Fig. S5:**

917 (A) Z-projection of confocal images obtained on control (left) or ShrubGFP/+ ovaries
918 (green, middle and right) stained for α -Spectrin (magenta) to visualize the fusome
919 linking the germline stem cell (GSC) to its progeny. In control, the GSC is only linked
920 to its daughter cystoblast (CB). In ShrubGFP/+ ovaries, GSC are either as in control
921 (middle) or linked to several progeny and form stem cysts (right). Scale bars
922 represent 5 μm .

923 (B) Higher magnification of a SOP midbody (magenta) showing CHMP2BGFP
924 recruitment (green). Scale bars represent 1 μm .

925

926

927 **Fig. 6. Interplay between Shrub and SJ components in the control of**
928 **cytoplasmic isolation**

929 (A) Localization of Cora (magenta) upon silencing of Cora (A). The white dashed
930 lines separate wild type from KAEDE expressing cells, which correspond to the area
931 of Cora depletion.

932 (B) Plot representing the proportion of pIIa-pIIb cells to have cytoplasmic isolation
933 over time after anaphase onset. Cytoplasmic isolation was assessed based on the
934 ability of photo-converted KAEDE in pIIa/pIIb cell to diffuse in the pIIb/pIIa cell at

935 different time point after the onset of anaphase in control (*pnr*>, dashed line, n=62,
936 24 pupae), Cora RNAi (*pnr*>CoraRNAi, dotdashed line, n=32, 16 pupae),
937 ShrubGFP/+ (*pnr*>+ ShrubGFP/+, dotted line, n=52, 12 pupae) and Cora RNAi +
938 ShrubGFP/+ (*pnr*>CoraRNAi+ShrubGFP/+ solid line, n=30, 6 pupae). Lines
939 represent mean values, predicted from a GLM of t1/2 values for *pnr*> centered to 0;
940 SE of the estimates are represented in grey shading. (*pnr*> vs *pnr*>CoraRNAi, p-
941 value=0,029,*; *pnr*> vs Cora RNAi + ShrubGFP/+, p-value=0.425, ns; Cora RNAi +
942 ShrubGFP/+ vs *pnr*>+ ShrubGFP/+, p-value=4,52.10⁻⁷,***; *pnr*>CoraRNAi vs Cora
943 RNAi + ShrubGFP/+, p-value=0.075,ns).

944 (C) Time lapse of SOP dividing cell depleted of Cora expressing MyoII GFP (Green)
945 and GAP43IR (Magenta). White arrows point to the midbody. Distances in μm
946 represent the position relative to the AJ plane determined by apical MyoII signal.

947 (D) Plot representing the time after anaphase onset (min) when the midbody is
948 released from the new interface between pll_b and pll_a in control (white, n=12) and
949 Cora depleted cells (light grey, n=8). Time is in min. (unpaired t-tests; p-value=0,002,
950 **)

951 (E) Plot representing the time after anaphase onset (min) when the midbody is
952 disappearing from the SOP in control (white, n=13) and Cora depleted cells (light
953 grey, n=7). Time is in min. (unpaired t-tests; p-value=0.0004, ***)

954 (F) Plot of the time of the onset of pll_a and pll_b anaphase after the onset of SOP
955 anaphase in control (black, n=13) and Cora depleted (grey, n=8) cells. Time is in
956 min. (unpaired t-tests; p-value=0.000045 and p-value=0,00081,*** for pll_b and pll_a
957 respectively)

958 (G) Time lapse of SOPs expressing MyoII RFP (magenta) and ShrubGFP (green)
959 depleted from Cora. (G') Higher magnifications of the white dotted square inset
960 depicted in (C) at t10 showing ShrubGFP (green) recruitment to the midbody
961 (magenta) (n= 2/6).

962 (H) Scheme depicting Shrub recruitment (Green) in the finger-like protrusions and at
963 the level of the midbody (magenta rectangle) during cytokinesis in SOP control and
964 depleted with Cora RNAi.

965 (I) Scheme proposing a model representing Shrub functions during epithelial
966 cytokinesis. Shrub exerts a cell autonomous function in the control of the separation
967 of the pll_a-pll_b cytoplasm. Shrub (green spiral) is recruited at the level of the
968 midbody (magenta rectangle). Shrub exerts a cell non-autonomous function in the

969 remodeling of the SJs within the finger-like protrusions. This activity is linked to SJ
970 trafficking via endosomes.

971 Time is in minutes with t0 corresponding to the onset of anaphase (C-E, G-G'). Red
972 and blue dots mark the p11b and p11a respectively (C, G). Scale bars represent 5 μ m
973 (A, C, G) and 1 μ m (G').

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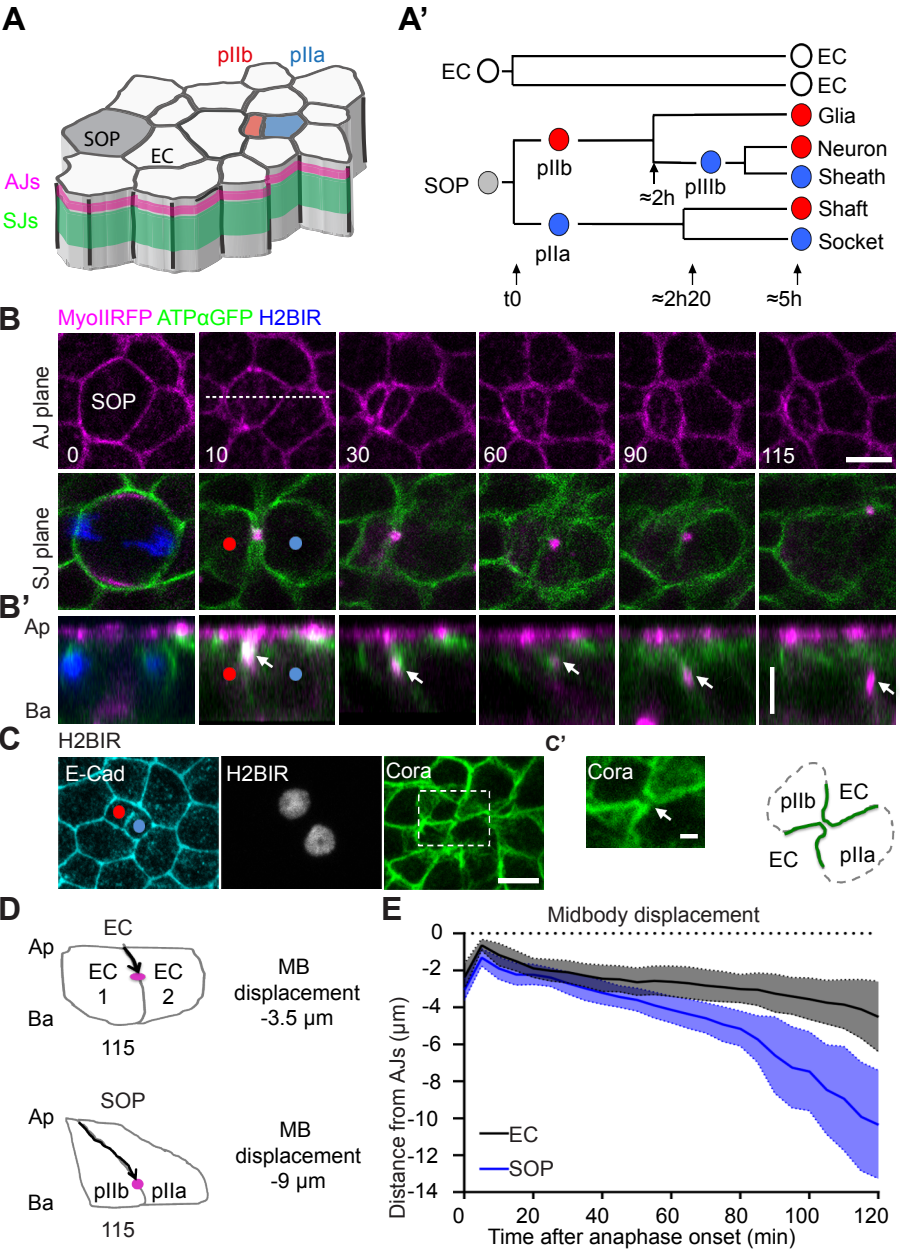
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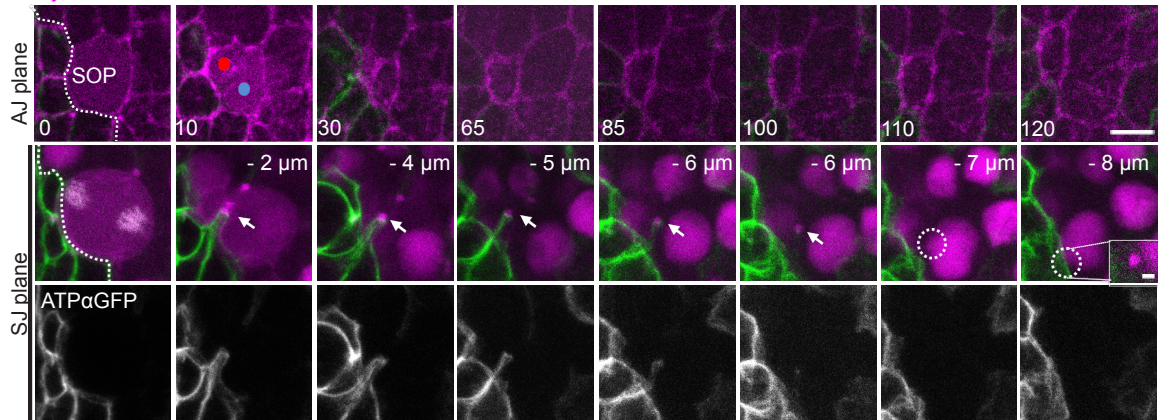
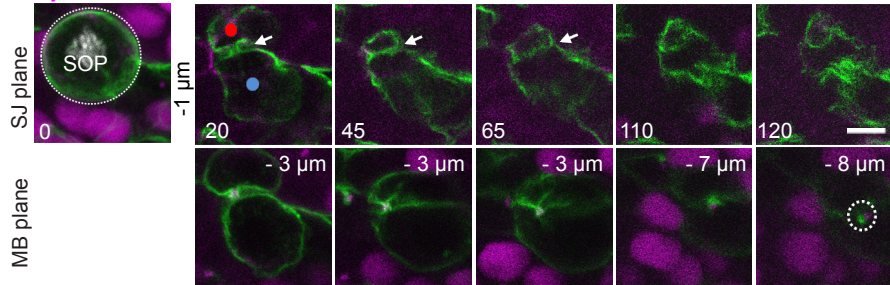
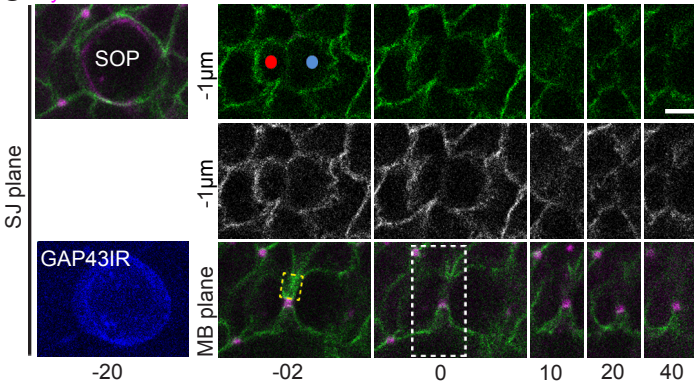
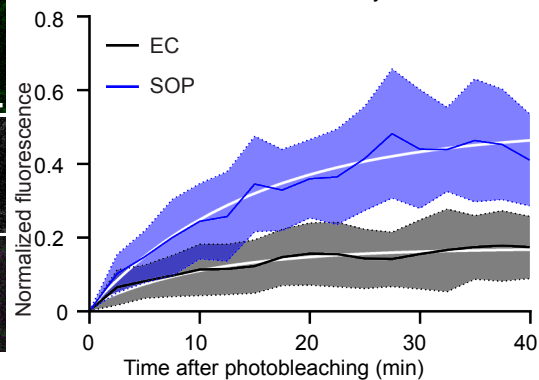
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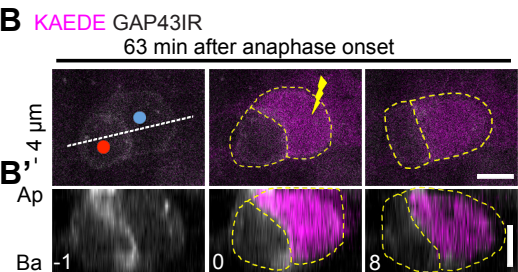
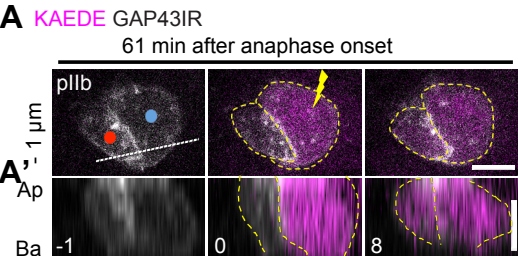
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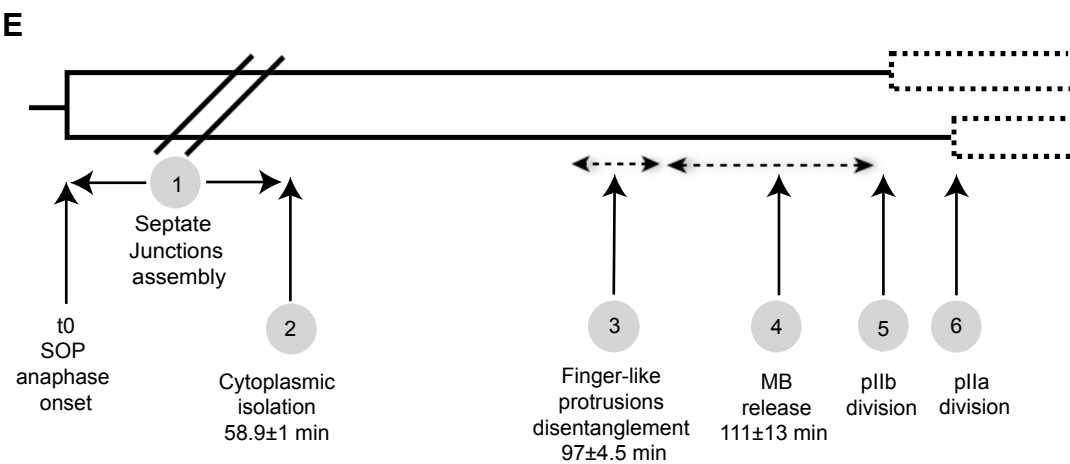
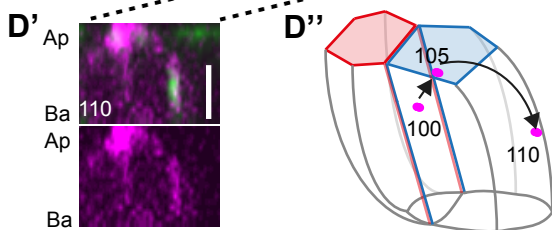
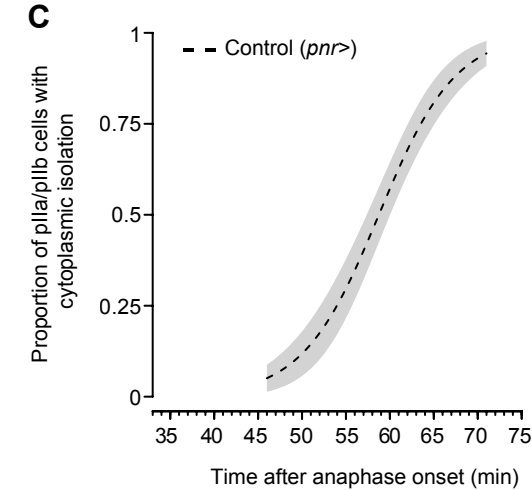
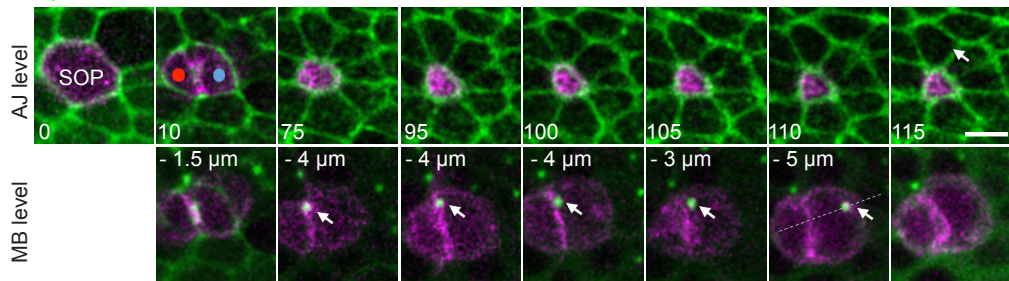
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A MyoIIIRFP nlsRFP ATP α GFP H2BIR**B** MyoIIIRFP nlsRFP ATP α GFP H2BIR**C** MyoIIIRFP ATP α GFP GAP43IR**D** ATP α ::GFP recovery



D **MyoII**GFP **GAP43IR**



A