1	A shared role for sonic hedgehog signalling in patterning				
2	chondrichthyan gill arch appendages and tetrapod limbs				
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4	Running title: Shh signalling patterns skate gill arches				
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7	1. Dependence of Zealany, University of Correlations, Develop Other at Correlation				
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14					
15	Key words: Sonic hedgehog, gill arch, evolution, skate, appendage patterning				
16					
17	Summary statement: Shh signalling polarizes skate gill arches, and maintains				
18	proliferative expansion of gill arch appendage endoskeletal progenitors, mirroring the				
19	function of Shh signalling in the tetrapod limb.				
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36 Chondrichthyans (sharks, skates, rays and holocephalans) possess paired 37 appendages that project laterally from their gill arches, known as "branchial 38 rays". This led Carl Gegenbaur to propose that paired fins (and hence tetrapod 39 limbs) originally evolved via transformation of gill arches. Tetrapod limbs are 40 patterned by a Sonic hedgehog (Shh)-expressing signalling centre known as 41 the zone of polarizing activity, which establishes the anteroposterior axis of 42 the limb bud, and maintains proliferative expansion of limb endoskeletal 43 progenitors. Here, we use loss of function, label-retention and fate-mapping 44 approaches in the little skate to demonstrate that Shh secretion from a 45 signalling centre in the developing gill arches establishes gill arch 46 anteroposterior polarity and maintains the proliferative expansion of branchial 47 ray endoskeletal progenitor cells. These findings highlight striking parallels in 48 the axial patterning mechanisms employed by chondrichthyan branchial rays 49 and paired fins/limbs, and provide mechanistic insight into the anatomical 50 foundation of Gegenbaur's gill arch hypothesis.

51

#### 52 Introduction

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54 Chondrichthyans are unique among extant jawed vertebrates in possessing 55 appendages, known as branchial rays, which project laterally from their gill arches 56 (Gillis et al., 2009a). This anatomy mirrors the configuration of paired fins (including 57 limbs) and their proximal girdle, and led the comparative anatomist Carl Gegenbaur 58 to propose that paired fins evolved by transformation of a gill arch, with the epi- and 59 ceratobranchial cartilages of the gill arch giving rise to the girdle, and branchial rays 60 giving rise to the fin proper (Gegenabur, 1878). This hypothesis of serial homology 61 (Fig. 1) would predict that the gill arches of chondrichthyans and the paired fins/limbs 62 of jawed vertebrates share axial patterning mechanisms. However, while a great deal 63 is known about the molecular basis of paired fin and limb patterning (Zeller et al., 64 2009), comparable data on axial patterning of chondrichthyan gill arches and 65 branchial rays are lacking. 66 67 Limbs are patterned, in part, by a signalling centre known as the zone of polarizing

68 activity (ZPA): a population of *sonic hedgehog* (*Shh*)-expressing cells in the posterior

69 limb bud mesenchyme that signals to adjacent mesenchymal cells and to the

verlying apical ectodermal ridge (Pearce et al., 2001), and that functions both in the

establishment of the anteroposterior axis of the limb bud, and in the proliferative

expansion of limb endoskeletal progenitors (Riddle et al., 1993; Towers et al., 2008;

73 Zhu et al., 2008). We previously demonstrated that the branchial rays of 74 chondrichthyans also develop under the influence of a Shh-expressing signalling 75 centre (Gillis et al., 2009b; Gillis et al., 2011), though the precise function of this 76 signalling centre remains unclear. To address this, we have used gene expression 77 analysis, fate mapping and loss-of-function experiments to investigate the function of 78 the gill arch Shh signalling in the little skate (Leucoraja erinacea). We demonstrate 79 that gill arch Shh signalling functions similarly to the limb bud ZPA, both in the 80 establishment of the skate gill arch anteroposterior axis, and in the proliferative 81 expansion of branchial ray endoskeletal progenitors.

- 82
- 83 **Results and discussion**
- 84
- 85

5 Shh signalling in skate gill arch development

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87 In order to identify the source and targets of chondrichthyan gill arch Shh signaling, 88 we characterized the expression of Shh and Patched2 (Ptc2, a readout of Shh 89 signalling – Pearce et al., 2001) by mRNA in situ hybridisation in skate embryos. In 90 vertebrate embryos, pharyngeal arches are delineated by an iterative series of 91 endodermal pouches that outpocket from the foregut and contact overlying 92 pharyngeal ectoderm. In fishes, endodermal pouches fuse with overlying ectoderm, 93 giving rise to gill slits, and leaving, between presumptive gill slits, pharyngeal arches 94 filled with neural crest-derived mesenchyme and a central mesodermally-derived 95 core (Graham, 2001). In skate embryos at stage 22 (Ballard et al., 1993) (Fig. 2A), 96 Shh expression is observed in the region of the pharyngeal gill slits and pouches 97 (Fig. 2B). Expression analysis on paraffin sections reveals that Shh transcripts 98 localize to the posterior pharyngeal arch epithelium (Fig. 2C.D), consistent with 99 previous reports of Shh expression in the posterior hyoid arches of chick (Wall and 100 Hogan, 1995) and zebrafish (Richardson et al., 2012) embryos. Analysis of Ptc2 101 expression at stage 22 indicates that pharyngeal arch Shh signal is transduced 102 posteriorly within the developing gill arches, in pharyngeal arch epithelium, 103 mesenchyme and in the mesodermally-derived core (Fig. 2E). 104 105 By stage 27, all pharyngeal arches have formed, and the hyoid and gill arches are 106 expanding laterally (Fig. 2F). At this stage, Shh expression is restricted to the 107 epithelium along the leading edge of the expanding hyoid and gill arches (Fig. 2G-I),

108 with *Shh*-expressing cells having the appearance of a ridge (the gill arch epithelial

109 ridge, GAER). The GAER is reminiscent of the apical ectodermal ridge (AER) of the

110 developing fin and limb buds, and we have previously shown that, like the fin/limb 111 bud AER, the GAER also expresses the gene encoding the signaling molecule Fgf8 112 (Gillis et al., 2009b). Ptc2 expression reveals that GAER Shh signal is asymmetrically 113 transduced in posterior-distal arch mesenchyme, as well as in cells within the 114 mesodermally-derived core and distal arch epithelium (Fig. 2J). By stage 29, the 115 hyoid and gill arches continue to expand laterally, and have taken on a pronounced 116 posterior curvature (Fig. 2K). Shh expression persists in the GAER of the hyoid arch 117 and gill arches (Fig. 2L-N), and Ptc2 expression indicates transduction of GAER Shh 118 in posterior-distal arch mesenchyme, a few cells at the distal tip of the mesodermally-119 derived core, and in the GAER and adjacent epithelium (Fig. 20). At stages 27 and 120 29, cells of the GAER are distinguishable as a pseudostratified epithelial ridge, 121 approximately 5-6 cells in diameter (Fig. 2P). By stage 30, anlagen of pharyngeal 122 endoskeletal elements appear (Gillis et al., 2009a).

123

124 In summary, the GAER is a *Shh*-expressing signaling centre that spans the leading 125 edge of the expanding skate hyoid and gill arches. GAER Shh expression originates 126 within posterior pharyngeal arch epithelium, and persists through lateral expansion of 127 the hyoid and gill arches, resolving into a morphologically distinct pseudostratified 128 epithelial ridge, while signaling to posterior arch mesenchyme and epithelium. Thus, 129 while the GAER is distinct from the limb bud ZPA at the tissue level (the former is 130 epithelial, while the latter is mesenchymal), both provide a posteriorly localized 131 source of Shh signal that is transduced in adjacent mesenchymal and epithelial cell 132 populations.

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### 134 Shh-responsive mesenchyme gives rise to branchial rays

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136 The gill arch endoskeleton of chondrichthyans consists of proximal epi- and 137 ceratobranchial cartilages, and a series of branchial rays projecting laterally from 138 these (Fig. 3A,B). In the tetrapod limb, it has been demonstrated that ZPA Shh-139 responsive mesenchyme contributes extensively to the distal limb skeleton (Ahn and 140 Joyner, 2004), and these elements exhibit morphological defects following loss of 141 Shh signaling (Riddle et al., 1993; Chiang et al., 2001; Ros et al., 2003; Stopper and 142 Wagner, 2007; Towers et al., 2008; Zhu et al., 2008). To test the endoskeletal fate of 143 GAER Shh-responsive mesenchyme, we labeled this cell population by 144 microinjecting CM-Dil subjacent to the GAER of gill arches in skate embryos at 145 stages 27 and 29 (Fig. 3C,D - compare injection with Ptc2 expression in Fig. 2J). 146 Injected embryos were reared until stages 31-32 (~8-10 weeks of development,

when gill arches and branchial rays have differentiated,), and analyzed for the
presence and distribution of CM Dil-positive chondrocytes in histological sections of
the gill arch endoskeleton.

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151 Histological analysis of gill arches of skates with labeled GAER Shh-responsive 152 mesenchyme revealed the presence of Dil-labeled chondrocytes in the branchial 153 rays (100% of examined individuals; n=5 for CM-Dil labeling at stage 27, and n=5 for 154 CM-Dil labeling at stage 29) (Fig. 3E). In individuals labeled at stage 27, Dil-positive 155 chondrocytes were distributed broadly throughout the branchial rays, whereas 156 individuals labeled at stage 29 possessed Dil-positive chondrocytes predominantly in 157 the distal tips of the rays. These data indicate that GAER Shh-responsive 158 mesenchymal cells contribute to branchial rays, which are the elements that

- 159 Gegenbaur serially homologized with the paired fin/limb endoskeleton (Fig. 1).
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Shh polarizes and maintains proliferative expansion of gill arch endoskeletalprogenitors

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164 In the tetrapod limb, Shh signaling from the ZPA functions both in the establishment 165 of the limb bud anteroposterior axis, and in the maintenance of proliferative 166 expansion of limb endoskeletal progenitors (Towers et al., 2008; Zhu et al., 2008). To 167 test the patterning function of Shh signalling during skate gill arch development, we 168 conducted a series of loss-of-function experiments by in ovo injection of the 169 hedgehog signalling antagonist cyclopamine (Chen et al., 2002). Skate eggs were 170 injected with cyclopamine to a final concentration of  $\sim 20 \mu$ M, at either stage 22, 27 171 and 29, and were then reared until endoskeletal differentiation (~8-12 weeks). As 172 with digit number in mice (Zhu et al., 2008) and salamanders (Wagner and Stopper, 173 2007), successively earlier loss of Shh signalling resulted in a progressively greater 174 reduction in the number of branchial rays on each arch. Specifically, cyclopamine 175 treatment at stages 22 and 27 resulted in significant reductions in branchial ray 176 number, relative to controls, but there was no significant reduction in branchial ray 177 number with cyclopamine treatment at stage 29 (Fig. 4A,B). We postulated that 178 reductions in branchial ray number were due to reduced proliferation of gill arch 179 mesenchyme in the absence of gill arch Shh signalling, and to test this, we 180 conducted a series of EdU (Salic and Mitchison, 2008) incorporation experiments. 181 Embryos at stage 27 were reared ex ovo in either 20µM cyclopamine or DMSO in 182 seawater for 24 hours, prior to intraperitoneal microinjection with EdU. Injected 183 embryos were left to develop for a further 24 hours, fixed and analyzed for EdU

- retention in gill arch mesenchyme. Embryos treated with cyclopamine showed a
- 185 significant reduction in the proportion of EdU-positive nuclei in gill arch mesenchyme,
- 186 relative to controls, indicative of reduced DNA replication (and hence, cell
- 187 proliferation) in the absence of Shh signalling (Fig. 4C). Together with our fate
- 188 mapping data, these findings indicate that gill arch Shh signalling functions, in part, to
- 189 maintain proliferative expansion of branchial ray progenitors during gill arch
- 190 development.
- 191

192 Finally, we noted a striking anteroposterior patterning defect in the gill arches of the 193 earliest cyclopamine-treated skate embryos. Chondrichthyan gill arches exhibit a 194 clear anteroposterior polarity, with branchial rays invariably articulating with the epi-195 and ceratobranchial cartilages along their posterior margins (Gillis et al., 2009a). In 196 skate embryos treated with cyclopamine at stage 22, the epi- and ceratobranchial 197 cartilages were severely misshapen, consistently lacking evidence of an 198 anteroposterior axis, with branchial rays articulating along their midlines (n=4/7) (Fig. 199 4D). Notably, this patterning defect was not observed in any embryos treated with 200 cyclopamine at stages 27 (n=0/7) or 29 (n=0/9). These findings suggest that, in 201 addition to its prolonged role in maintaining gill arch proliferative expansion, Shh 202 signalling also functions early in gill arch development, to establish gill arch 203 anteroposterior polarity.

204

## 205 Conclusion

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207 Gegenbaur's gill arch hypothesis of paired fin origins is often regarded as the flawed 208 alternative to the lateral fin fold hypothesis of Thacher (1877), Mivart (1879) and 209 Balfour (1881), which purports that paired fins evolved from a bilateral median fin-like 210 structure. While neither the gill arch nor lateral fin fold hypotheses are supported by 211 paleontological data (Coates, 2003), consensus has largely shifted toward the latter, 212 owing to the discovery of shared expression of developmental patterning genes 213 between paired and dorsal median fins (Freitas et al., 2006; Dahn et al., 2007). Our 214 demonstration of a dual role for Shh signaling in patterning the endoskeleton of 215 chondrichthyan gill arches points to a common molecular mechanism underlying the 216 axial patterning of branchial rays and paired fins/limbs, and highlights chondrichthyan 217 branchial rays as an important feature in the evolutionary story of gnathostome 218 paired appendages. Conserved developmental mechanisms are generally regarded 219 as the basis of serial homology (Roth, 1984; Wagner, 1989, 2007), though it remains 220 to be determined whether developmental mechanisms shared by branchial rays and

221	paired fins/limbs reflect conservation, parallel evolution (i.e. the independent co-					
222	option of deeply conserved developmental mechanisms, or "deep homology") or					
223	convergent evolution (Hall, 2003; Shubin et al., 2009). In the absence of					
224	paleontological data illustrating the step-wise acquisition of the paired fin					
225	endoskeleton, comparative studies of axial patterning mechanisms in diverse					
226	vertebrate appendages – e.g. fins/limbs, branchial rays, median fins and external					
227	genitalia (Cohn, 2011) – will allow us to formulate testable hypotheses of nested					
228	relationships among body plan features, in order to explain morphological similarity					
229	by extent of shared developmental information.					
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231	Materials and methods					
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233	Embryo collection and fate mapping					
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235	Skate (Leucoraja erinacea) eggs were obtained at the Marine Biological Laboratory					
236	(Woods Hole, MA, USA) and maintained in a flow-through seawater system at					
237	~17°C. CM-Dil fate mapping experiments were carried out as described (Gillis et al.,					
238	2012). All animal work complied with protocols approved by the Institutional Animal					
239	Care and Use Committee at the MBL. Embryos were fixed in 4% paraformaldehyde					
240	in phosphate-buffered saline (PBS) overnight at 4°C, rinsed three times in PBS,					
241	dehydrated into methanol and stored at -20°C.					
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243	Histology and mRNA in situ hybridization					
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245	Embryos were embedded in paraffin wax and sectioned as described (O'Neill et al.,					
246	2007). Sections of CM-DiI-labelled embryos were counterstained with DAPI. In situ					
247	hybridization experiments for L. erinacea Shh (GenBank Accession Number					
248	EF100667) and Ptc2 (GenBank Accession Number EF100663) were performed as					
249	described (Gillis et al., 2012).					
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251	In ovo cyclopamine treatment and skeletal preparations					
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253	To achieve a final <i>in ovo</i> cyclopamine concentration of $\sim$ 20µM, 25µL of a 9mM stock					
254	solution of cyclopamine in DMSO was injected into 25 skate egg cases each at					
255	stages 22, 27 and 29, using a syringe and 30 gauge needle. This volume was					
256	determined based on a mean egg volume of ~10mL. For controls, an equivalent					
257	volume of DMSO alone was injected. Embryos were reared for 8-12 weeks.					

Surviving embryos (n=7, 7 and 9 for cyclopamine treatment at stage 22, 27 and 29,
respectively) were analysed for skeletal defects by wholemount skeletal preparation
(Gillis et al., 2009a).

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262 EdU incorporation assay

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264 For 5-ethynyl-2-deoxyuridine (EdU) incorporation experiments, stage 27 embryos 265 were removed from their egg cases, and reared in 10cm diameter petri dishes in 266 either 20µM cyclopamine in seawater (n=5), or in seawater with an equivalent 267 volume of DMSO (n=5). After 24 hours, embryos received an intraperitoneal 268 microinjection of ~0.5µL of 5mM EdU (ThermoFisher Scientific, Waltham, MA, USA) 269 in 1X PBS, using a pulled glass capillary needle and a Picospritzer pressure injector. 270 Embryos were then returned to their cyclopamine/DMSO baths for a further 24 hours. 271 EdU-injected embryos were fixed and processed for histology as described above. 272 EdU was detected in sections using the Click-iT EdU Alexa Fluor 488 Imaging Kit 273 (ThermoFisher Scientific, Waltham, MA, USA), and sections were counterstained 274 with DAPI. Counts of EdU-positive nuclei were carried out manually, using the Cell 275 Counter plugin for ImageJ. Mean proportion of EdU-positive nuclei in gill arch 276 mesenchyme was calculated for three individuals per treatment or control (with cell 277 counts from three consecutive sections per individual), and statistical significance 278 was determined by unpaired T test.

279

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- 284 Center.
- 285

# 286 Competing interests

287 No competing interests declared.

288

## 289 Author contributions

JAG conceived the study. JAG designed and conducted all experiments, analyzed alldata and wrote the manuscript (with input from BKH).

292

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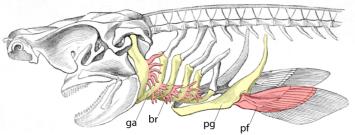
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421						
422	Figure legends					
423						
424	Figure 1: Hypothesis of gill arch-paired fin serial homology. A shark head					
425						
	skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.					
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426 427	skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.					
	skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton. Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br)					
427	skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton. Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br)					
427 428 429 430	<ul> <li>skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.</li> <li>Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br) and the pectoral fin (pf) are coloured red (modified from Owen, 1866).</li> <li>Figure 2: Shh signaling during skate gill arch development. A. At stage 22, BD. Shh is expressed in the developing gill arches, with transcripts localizing to posterior</li> </ul>					
427 428 429 430 431	<ul> <li>skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.</li> <li>Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br) and the pectoral fin (pf) are coloured red (modified from Owen, 1866).</li> <li>Figure 2: Shh signaling during skate gill arch development. A. At stage 22, BD. <i>Shh</i> is expressed in the developing gill arches, with transcripts localizing to posterior arch epithelium. E. <i>Ptc2</i> expression indicates that this signal is transduced in</li> </ul>					
427 428 429 430 431 432	<ul> <li>skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.</li> <li>Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br) and the pectoral fin (pf) are coloured red (modified from Owen, 1866).</li> <li>Figure 2: Shh signaling during skate gill arch development. A. At stage 22, BD. <i>Shh</i> is expressed in the developing gill arches, with transcripts localizing to posterior arch epithelium. E. <i>Ptc2</i> expression indicates that this signal is transduced in posterior gill arch mesenchyme, epithelium, and core mesoderm. F. By stage 27, G</li> </ul>					
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427 428 429 430 431 432 433	<ul> <li>skeleton illustrating putative serial homology of the gill arch and pectoral fin skeleton.</li> <li>Gill arches (ga) and the pectoral girdle (pg) are coloured yellow; branchial rays (br) and the pectoral fin (pf) are coloured red (modified from Owen, 1866).</li> <li>Figure 2: Shh signaling during skate gill arch development. A. At stage 22, BD. <i>Shh</i> is expressed in the developing gill arches, with transcripts localizing to posterior arch epithelium. E. <i>Ptc2</i> expression indicates that this signal is transduced in posterior gill arch mesenchyme, epithelium, and core mesoderm. F. By stage 27, GI. <i>Shh</i> expression has resolved into a ridge of epithelial cells (the gill arch epithelial</li> </ul>					

- 437 expression of *Shh* is maintained in the GAER, and **O**. *Ptc2* expression indicates
- 438 sustained posterior-distal transduction of this signal in posterior-distal arch
- 439 mesenchyme, epithelium and core mesoderm. **P.** The GAER is recognizable as a
- 440 pseudostratified ridge of *Shh*-expressing epithelial cells. *m*, mandibular arch; *h*, hyoid
- 441 arch; 1-5, gill arch 1-5. Dashed lines in **B.**, **G.**, and **L.** indicate plane of section in **C.**-
- 442 E., H.-J. and M.-O., respectively. Scale bars: A, F, K =  $500\mu m$ ; C, H, M =  $30\mu m$ ; P
- 443 =  $5\mu m$ .
- 444

445 Figure 3: Shh-responsive gill arch mesenchyme gives rise to branchial rays. A. 446 Lateral view of the skate pharyngeal endoskeleton, showing branchial rays (\*) 447 projecting laterally from the hyoid and gill arches. **B.** Frontal view of a gill arch, 448 showing branchial rays (br) articulating with the epibranchial (eb) and ceratobranchial 449 (cb) cartilages. C.-D. CM-Dil was microinjected subjacent to the GAER, from stages 450 27-29. E. After 8-10 weeks of development, CM-Dil-positive chondrocytes were 451 recovered in branchial rays. In E., the epibranchial cartilage is false coloured red, 452 and the branchial ray is false coloured yellow. ey, eye; ot, otic vesicle. Scale bars: A 453 = 1.5mm; B = 1.25mm; C =  $500\mu$ m; D-F =  $30\mu$ m.

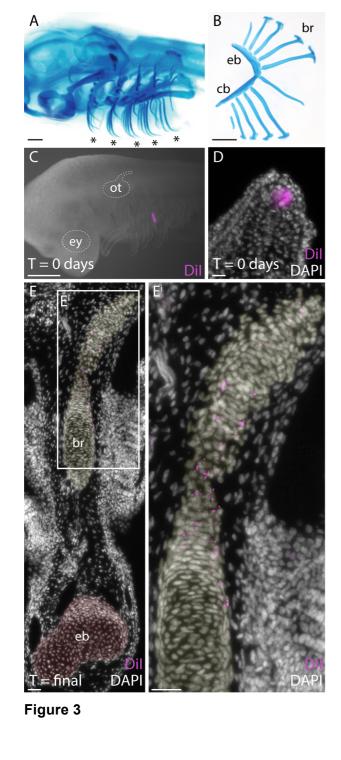
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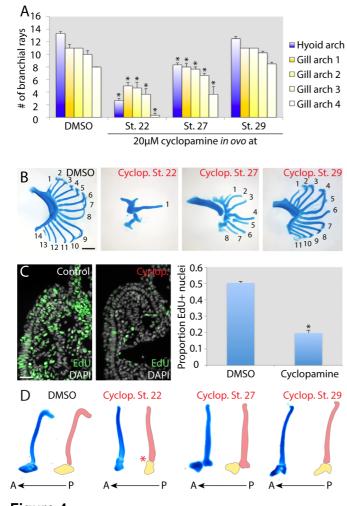
455 Figure 4: A dual role for Shh signaling in gill arch anteroposterior patterning 456 and proliferative expansion. A. Successively earlier treatment with cyclopamine 457 results in a progressively greater reduction in branchial ray number, with significantly 458 fewer branchial rays following cylopamine treatment at stages 22 and 27 (mean 459 number of branchial rays per arch +/- SEM; n=3 embryos per control or treatment; \* 460 indicates statistical significance at p<0.05). **B.** Example of a control (DMSO) arch, 461 and arches from embryos treated with cyclopamine at stages 22, 27 and 29. C. EdU 462 retention assays at stage 27 reveal reduced mesenchymal cell proliferation upon 463 treatment with cyclopamine (mean proportion of EdU+ cells +/- SEM; n=3 embryos 464 per control or treatment; \* indicates statistical significance at p<0.0001). **D.** Embryos 465 treated with cyclopamine at stage 22 also exhibit anteroposterior patterning defects. 466 In dorsal view, branchial rays can be seen to articulate with the posterior margin of 467 the epibranchial cartilage. Cyclopamine treatment at stage 22 results in a loss of 468 anteroposterior polarity within the gill arches, with branchial rays articulating down 469 the midline of the epibranchial (\*). This defect is not observed following cyclopamine 470 treatment at stage 27 or 29. In schematics in **D**., the epibranchial is yellow, and 471 branchial rays are red. Scale bars: B = 1.25mm;  $C = 30\mu m$ .



# Figure 1

A <u>St. 22</u> DAPI	B Shh	c C	0	h E Ptc2	
F <u>St.</u> 27 m <sup>612345</sup> DAPI				h J Ptc2	ALL
K St. 2 m <sup>t</sup> J 2 3 4 DAPI Figure 2	L Shh	M	N Sh	h O Ptc2	P <sup>ii</sup> GAER





**Figure 4**