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1

2 **Title**

3 Early transcriptional similarities between two distinct neural lineages during ascidian embryogenesis

4

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15 **Abstract**

16 In chordates, the central nervous system arises from precursors that have distinct developmental and
17 transcriptional trajectories. Anterior nervous systems are ontogenically associated with ectodermal
18 lineages while posterior nervous systems are associated with mesoderm. Taking advantage of the well-
19 documented cell lineage of ascidian embryos, we asked how the transcriptional states of the different
20 neural lineages become similar during the course of progressive lineage restriction. We performed
21 single-cell RNA sequencing (scRNA-seq) analyses on hand-dissected neural precursor cells of the two
22 distinct lineages, together with those of their sister cell lineages, with a high temporal resolution
23 covering five successive cell cycles from the 16-cell to neural plate stages. A transcription factor binding
24 site enrichment analysis of neural specific genes at the neural plate stage revealed limited evidence for
25 shared transcriptional control between the two neural lineages, consistent with their different ontogenies.
26 Nevertheless, PCA analysis and hierarchical clustering showed that, by neural plate stages, the two
27 neural lineages cluster together. Consistent with this, we identified a set of genes enriched in both neural
28 lineages at the neural plate stage, including *miR-124*, *CELF3/5/6*, *Zic.r-b*, and *Ets1/2*.

29 **Introduction**

30 The dorsal neural tube of the central nervous system (CNS) is a synapomorphy of chordates (Sato et
31 al., 2014). In both vertebrate and invertebrate chordates, neural cells of anterior and posterior CNS have
32 followed distinct developmental and transcriptional trajectories (Gouti et al., 2015, 2014; Henrique et
33 al., 2015; Hudson and Yasuo, 2021). Using ascidian embryos, we wanted to address the extent that the
34 transcriptional states of two distinct neural lineages, arising from distinct embryonic origins, become
35 similar during early chordate embryogenesis. Ascidiates are invertebrate chordates that develop a well-
36 patterned dorsal CNS at larval stages. This consists of a sensory vesicle, or brain, followed by a trunk
37 ganglion and tail nerve cord (Fig 1A). The structure and underlying specification mechanisms of the
38 ascidian larval CNS are well documented (reviewed in (Hudson, 2016; Hudson and Yasuo, 2021; Liu
39 and Satou, 2020; Ryan and Meinertzhagen, 2019)). Uniquely among chordates, ascidian embryos
40 develop with an invariant cleavage pattern and their cell lineages are well described. At the 8-cell stage
41 of development, the four founder lineages arise with a- and b-line cells in the animal half, contributing
42 to predominantly ectodermal lineages, and A- and B-line cells in the vegetal half, contributing to
43 predominantly mesendodermal lineages (Nishida, 1987). The anterior part of the sensory vesicle
44 (=brain) originates from the a-line ectodermal lineage following a cell fate choice between neural and
45 epidermal lineages. The dorsal-most row of cells, from the posterior part of the sensory vesicle to the
46 tail nerve cord, derives from the b-line, following fate choices between neural and epidermal or neural
47 and muscle lineages. The remainder of the CNS, all lateral and ventral cells from the posterior part of
48 the sensory vesicle to the tail nerve cord, originates from the A-line mesendodermal lineage following
49 fate choices between neural and notochord or neural and muscle lineages. While the a- and A-line neural
50 lineages originate from the animal and vegetal hemispheres of the embryo respectively, they are found
51 juxtaposed at the “dorsal” marginal zone of early embryos and then collectively form the neural plate
52 (Fig 1B).

53 Segregation of neural fate within the different lineages depends upon a distinct sequence of
54 signalling inputs. Neural induction in the a-line, mediated by FGF signals, begins at the 32-cell stage
55 with transcriptional induction of *Otx* in a6.5 cells, segregating the neural lineage (CNS and placode)
56 from ectoderm (Bertrand et al., 2003; Nishida, 1987). a-line neural precursors become CNS-specific at
57 the early gastrula stage when the CNS-neural precursors segregate from the precursors of a specialized
58 proto-placodal region of the anterior ectoderm (Abitua et al., 2015; Wagner and Levine, 2012). From
59 the 16-cell stage of development, the a-line neural cells are exposed to a series of signalling inputs (Fig
60 1B). At the 16-cell stage, they are found in a territory in which the canonical β -catenin signalling
61 pathway is inactive (β -catenin OFF) (Imai et al., 2000; Rothbacher et al., 2007). From the 32-cell to
62 early gastrula stage, the ERK-signalling pathway is active (ERK-ON) in the a-line neural precursors
63 (Hudson et al., 2003; Nishida, 2003; Wagner and Levine, 2012). The A-line neural lineages segregate
64 at the 64-cell stage from the sister mesodermal lineage and follow a distinct sequence of signalling
65 inputs compared to their a-line counterparts. At the 16-cell stage, A-line neural precursors are found in

66 the β -catenin-ON territory, followed by β -catenin-OFF and ERK-ON at the 32-cell stage and then ERK-
67 OFF from the 64-cell to early gastrula stage (Hudson et al., 2003; Imai et al., 2000; Minokawa et al.,
68 2001; Picco et al., 2007; Rothbacher et al., 2007). These distinct sequences of combinatorial signalling
69 inputs are required for the correct specification of neural precursors from the two neural lineages and
70 the ON-OFF status of these signal inputs dictates their binary cell fate decisions. Thus, a-line and A-
71 line neural precursors derive from different lineages and are specified by distinct molecular mechanisms.
72 Across the medial-lateral axis of the neural plate, both neural lineages are patterned by Nodal and Delta
73 signals (Esposito et al., 2016; Hudson et al., 2007). In this manuscript, we focused on the medial neural
74 precursors that do not depend on Nodal signals (Fig 1B).

75 Single-cell RNA sequencing (scRNA-seq) analyses have been used in ascidians to study the
76 transcriptome trajectories of differentiating embryonic cells and mostly recapitulate known
77 developmental lineage segregations (Cao et al., 2019; Sladitschek et al., 2020; Winkley et al., 2021;
78 Zhang et al., 2020). In particular, during development of the CNS lineages from the early gastrula to
79 larva stages, a progressive increase in cell type complexity was revealed, with 41 neural subtypes
80 identified at larval stages (Cao et al., 2019). A trajectory inference analysis was able to assign each of
81 these neural subtypes to a specific developmental lineage origin, indicating that differentiating neural
82 precursors retain transcriptional “identities” that can be connected, through a sequence of intermediates,
83 to their developmental origins (Cao et al., 2019). These previous scRNA-seq studies have highlighted
84 the diversification of cell types during ascidian embryogenesis with single cell transcriptome trajectories
85 following developmental lineage segregations.

86 In this study, by applying the scRNA-seq approach to early developmental stages of ascidian
87 embryogenesis, we addressed whether the transcriptional states of the a- and A-line neural lineages
88 become similar to each other while diverging from their sister lineages. Following the medial a- and A-
89 line cells with a high temporal resolution of each cell cycle from the 16-cell to the neural plate (mid-
90 gastrula) stages, using scRNA-seq of hand-dissected cells, we looked for evidence of a shared “pan-
91 neural” transcriptional state. While neural lineage cells cluster with their corresponding sister lineage
92 cells up to early gastrula stage, we found that, by mid-gastrula (neural plate stage), the a- and A-line
93 neural cells cluster together, indicating that these distinct neural lineages are converging in some aspects
94 of their transcriptional states. Consistent with this observation, we could identify a set of genes
95 significantly enriched in both neural lineages. Further, we could not detect lineage-based clustering
96 between the 41 larval neural cell type endpoints (Cao et al., 2019), supporting the notion that during
97 development of the CNS, the transcriptional state of the cells becomes dominated by the functional end
98 point rather than the lineage origin .

99

100 **Results and Discussion**

101 *Isolation of neural and sister cell lineages from the 16-cell stage to neural plate stage of development*

102 We used *Ciona robusta* (*C. intestinalis* type A) since its genome is better annotated than that of *Ciona*
103 *intestinalis* (*C. intestinalis* type B) (Satou et al., 2021, 2019). In order to generate scRNA-seq datasets
104 for individual neural lineage cells of each cell cycle from the 16-cell to neural plate stages, we manually
105 dissected cells of interest. In parallel, we also isolated cells of the corresponding early segregating sister
106 lineages. All the isolated cells are shown in Figure 1B (Fig 1B). While hand-dissection has the
107 disadvantage that it is only feasible to isolate limited numbers of cells, a clear advantage of the approach
108 is that the precise identity of the cell is known and that cells can be frozen immediately following
109 isolation. Neural lineage precursors, a5.3 and A5.1, were dissected at the 16-cell stage. At the 32-cell
110 stage, we isolated neural a6.5 and epidermal a6.6 sister precursors from the a-line and neuromesodermal
111 A6.2 and endodermal A6.1 sister cells from the A-line (Fig 1B). At the 64-cell stage, the neural precursor
112 a6.5 has divided in a medio-lateral direction and we isolated the medial neural precursor a7.10 and the
113 epidermal precursor a7.11, a daughter cell of a6.6. In the A-line, the neuromesodermal cell has divided
114 asymmetrically, generating a notochord precursor A7.3 and a neural precursor A7.4. We isolated each
115 of these sister cells, together with the A7.2 endoderm precursor, a daughter cell of A6.1. At the early
116 gastrula stage corresponding to the 112-cell stage, the a7.10 neural precursor has divided into a CNS
117 precursor a8.19 and a placodal precursor a8.20. We isolated the a8.19 neural cell together with a8.22
118 epidermal precursor, which is a daughter cell of a7.11. In terms of the A-line of the early gastrula, both
119 neural and notochord precursors have divided medio-laterally by this stage and we isolated the medially
120 positioned neural precursor A8.7 and notochord precursor A8.5. At the 6-row neural plate stage, the
121 neural plate exhibits a grid-like structure with six rows of cells along the A-P axis (Fig 1B). This results
122 from all neural precursors of the early gastrula stage dividing along the anterior-posterior axis. At this
123 stage, differential ERK activation takes place between row I and row II cells of the A-line neural
124 precursors and between row III and row IV of the a-line neural precursors (Haupaix et al., 2014; Nishida,
125 2003). Since we wanted to compare the a-line and A-line neural lineages globally, and for technical
126 facility, we isolated medial neural plate cells as pairs, row I/row II (A-line) and row III/row IV (a-line),
127 which we called AN (neural, daughters of A8.7) and aN (neural, daughters of a8.19) , and their
128 counterpart sister lineage cells, AM (notochord, daughters of A8.5) and aE (epidermis, daughters of
129 a8.22) (Fig 1B). The total number of manually isolated cells (or cell pairs for aN, aE, AN, and AM)
130 resulted in a 6-9-fold coverage of each cell type (Fig 1B). Altogether, the sampled cells represent five
131 successive cell cycles of the a- and A-neural lineages and of their sister lineages, covering the 16-cell to
132 the neural plate stages.

133

134 ***Differential enrichment of transcriptomes between pairs of cells***

135 As a consequence of the hand dissection procedure, our cell transcriptomes were already labelled by
136 cell type of origin. All our downstream computational analyses were based on the KH2013 gene models
137 (Satou et al., 2008). We analysed cells for differential expression between neural and sister lineages
138 using DESeq2, treating each cell (n = 6 to 9) as a single replicate instance of its type (see supplementary

139 data link at end of manuscript). Inspection of principal component analysis (PCA) plots of rlog-
140 transformed gene expression levels for cells of a particular embryonic stage revealed a strong tendency
141 of cells isolated at the early stages (16- and 32-cell stages) to cluster by batch or embryo of origin, as
142 previously observed by others in *Ciona* (Ilsley et al., 2020; Winkley et al., 2021). Accordingly, for these
143 stages, we added the animal of origin to the DESeq2 design formula. Genes were ranked by adjusted P-
144 values and values < 0.01 regarded as significant (S1 Table: DESeq2). Our DESeq2 analysis successfully
145 recovered genes whose expressions were previously reported to be differentially expressed between the
146 pairs of cells analysed in the current study (Fig 1C), showing that manual dissections were conducted
147 with accurate cell identification.

148

149 ***Trajectory of transcriptional states during the course of neural lineage segregation up to neural plate*** 150 ***stages***

151 A PCA of the variance stabilized (vst) expression data for all cells showed two dominant themes: 1) PC
152 1 reflecting embryonic stage or time and 2) PC 2 reflecting the different lineages (Fig 2A). Separation
153 between lineages becomes stronger through developmental time. At the neural plate stage, separation is
154 strongest between the aE and AM lineages, with the neural aN and AN lineages appearing relatively
155 closer to each other. To investigate this effect further, we performed a hierarchical clustering analysis
156 (see methods and Fig 2B). This showed a clustering of the aN and AN cells of the neural plate stage as
157 each other's closest neighbours, in contrast to neural precursors at earlier stages that clustered with their
158 sister lineage cells. These data suggest that, as lineage segregation proceeds, transcriptional similarity
159 attributable to shared lineage history is overwritten by similarity caused by the acquired developmental
160 identity of the cell. In order to further address this converging trend, we used the available scRNA-seq
161 dataset of larval neural cell types, which emerge following a maximum of four rounds of cell divisions
162 of neural plate cells (Cao et al., 2019), and clustered them based on the shared presence or absence of
163 marker genes. The hierarchical clustering showed no obvious segregation of these CNS neural cell types
164 by lineage of origin ('A' or 'a') (Fig 3).

165 Altogether, we observe that the transcriptional states of the two neural lineages become more
166 similar to each other than they are to their early diverging sister lineages by the neural plate stage of
167 development (Fig 2) followed by extensive mixing of differentiated neural cell types derived from these
168 distinct lineages at larval stages (Fig 3). In other words, the transcriptional signature of their lineage
169 identity becomes weaker as development proceeds.

170

171 ***Identification of neural genes whose transcripts are enriched in both neural lineages***

172 The above data suggest that neural cells from both lineages shared some aspects of their transcriptional
173 state at the neural plate stage (Fig 2). We therefore searched for transcripts enriched in both neural
174 lineages in our DESeq2 analysis (S1 and S2 Tables). We identified six genes whose transcripts are
175 enriched in both of the neural lineages at the early gastrula stage and 11 genes at the neural plate stages.

176 (S2 Table: shared neural genes) (Figs 4 and 5). This list contains many genes already known to be
177 expressed in developing neural tissue: *CELF3/5/6* (KH.C6.128, an ELAV family RNA-binding protein),
178 *Zic.r-b,c,d,e,f* (multicopy gene: KH.S816.1, KH.S816.2, KH.S816.4, KH.L59.1, and KH.L59.12, a
179 transcription factor), *Ets1/2* (KH.C10.113, a transcription factor), *Noggin* (KH.C12.562, a secreted
180 signalling molecule and antagonist of BMP), and *Pans/miR-124* (KH.C7.140, see later) (Alfano et al.,
181 2007; Brozovic et al., 2018; Chen et al., 2011; Fujiwara et al., 2002; Gainous et al., 2015; Hudson et al.,
182 2003; Hudson and Yasuo, 2005; Imai et al., 2004, 2002; Mita and Fujiwara, 2007). However, the list
183 also includes genes whose expression in neural lineages at the neural plate stage has not been reported.
184 We confirmed expression of some of these genes, with most of them detected in both a- and A-line
185 neural cells (Fig 5). *Noggin* was previously reported to be expressed broadly in the CNS at tailbud stages
186 (Imai et al., 2004). At neural plate stages, we found that *Noggin* is expressed at higher levels in the a-
187 line neural precursors compared to A-line neural plate precursors (Figs 4 and 5). *SLC35F* (KH.C4.90),
188 encoding a putative solute carrier family 35, and *ZCCHC24* (KH.C14.310), encoding a CCHC-type zinc
189 finger protein, were detected in neural plate cells of both a- and A-line lineages at the neural plate stage
190 (Fig 5). Expression of *FAM167* (KH.C14.33), encoding a protein of unknown function, and *PQLC2*
191 (KH.L18.113), encoding a lysosomal cationic amino acid transporter, were detected in both a- and A-
192 line neural precursors at the early gastrula and neural plate stages (Fig 5). *CELF3/5/6*, *Noggin* and
193 *ZCCHC24* are also reported to be expressed in developing central nervous system of vertebrates (Gallo
194 and Spickett, 2010; Kang et al., 2012; Knecht et al., 1995; McMahon et al., 1998).

195 For the gene encoding *Pans/miR-124* (KH.C7.140), *Pans* expression has been reported in the
196 neural lineages of *Ciona* from the 64-cell stage until tailbud stages (Alfano et al., 2007; Chen et al.,
197 2011; Fujiwara et al., 2002). The predicted *Pans* protein coding gene is very short (22 amino acids) and
198 a role in neural specification has not been reported (Alfano et al., 2007). Within the second intron of
199 this gene, are two tandem copies of the *miR-124* micro-RNA (Chen et al., 2011). The *miR-124* family
200 is highly conserved across metazoans with its expression enriched in nervous systems, in particular, in
201 neuronal lineages (Aboobaker et al., 2005; Clark et al., 2010; Konrad and Song, 2023; Lagos-Quintana
202 et al., 2002; Rajasethupathy et al., 2009; Vidyandand et al., 2017). In *Ciona* embryos, previously
203 published *in situ* hybridisation against the mature *miR-124* product revealed an expression pattern very
204 similar to *Pans* itself (Chen et al., 2011). We observed pan-neural expression of the mature *miR-124*
205 product at the neural plate stage (Fig 5). In vertebrates, *miR-124* expression coincides with neurogenesis,
206 being largely restricted to committed neuronal precursors and post-mitotic neurons, and may play a role
207 in accelerating neuronal differentiation (Visvanathan et al., 2007). In ascidians, *miR-124* appears to be
208 involved in the specification of peripheral epidermal sensory neurons (ESNs) in the epidermal midline:
209 misexpression of *miR-124* in epidermal lineages results in formation of extra ESNs (Chen et al., 2011).
210 It has also been suggested to play a role in downregulation of mesoderm genes, such as *macho-1* (*Zic-*
211 *r.a*) and notochord genes, to prevent expression of these genes in the CNS lineages (Chen et al., 2011).
212 To further investigate the potential role of *miR-124* in neural specification, we searched for *miR-124*

213 seed sites in the 3'UTRs of genes identified as differentially expressed at the neural plate stage (see
214 methods). In the a-line comparisons, we found an enrichment of *miR-124* binding sites in genes that
215 were upregulated in epidermal lineage cells (aE>aN, p=0.008; aN>aE, p≈1.0). In the A-line comparisons,
216 we found an enrichment of *miR-124* binding sites in genes that were upregulated in mesodermal cells
217 (AM>AN, p=0.0001; AN>AM, p=0.4). It is possible then that *miR-124* might be “fine-tuning” neural
218 lineage segregation by suppressing sister-lineage genes as has been observed for other *miRs*, though this
219 will require additional studies (Alberti and Cochella, 2017).

220 KH.C1.29 encodes a translation initiation factor EIF4EBP1/3. The predicted transcript of
221 KH.C7.59 is very small (312bp; 18 amino acids) and in close proximity to *miR-219* (Brozovic et al.,
222 2018; Hendrix et al., 2010) (S2 Table). *miR-219* has been implicated in some aspects of neural
223 development in vertebrates (Dugas et al., 2010; Hudish et al., 2013).

224 Among this list of genes enriched in both neural lineages, there are only two genes encoding
225 transcription factors, namely, *Ets1/2* and *Zic.r-b*. *Ets1/2* is known to be directly phosphorylated by MAP
226 kinase ERK1/2, leading to an increase in its transcriptional activity, and roles for ERK signalling and
227 *Ets1/2* have been described during ascidian nervous system development (Bertrand et al., 2003; Gainous
228 et al., 2015; Haupaix et al., 2014; Ikeda et al., 2013; Racioppi et al., 2014; Yang et al., 1996). *Zic.r-b*
229 has also previously been shown to play a critical role in neural specification (Imai et al., 2006, 2002).

230

231 ***Transcription factor binding site enrichment in neural lineages at the neural plate stage***

232 The distinct mechanisms of neural lineage segregation in the a- and A-line suggests that neural gene
233 programs would be induced under the influence of different gene regulatory networks. However, the
234 enrichment of expression of two transcription factors, *Zic.r-b* and *Ets1/2* in both neural lineages,
235 described above, suggests that there may also be some common mechanisms by the neural plate stage.
236 In order to investigate this further, we looked for enrichment of transcription factor binding site motifs
237 in the 1kb upstream sequences of differentially expressed genes at neural plate stages (Fig 6 and S3
238 Table). Each of the four pairwise comparisons, that is, aN>aE, aE>aN, AN>AM, and AM>AN, revealed
239 a unique signature of enriched motifs. Notably, a significant enrichment of Otx-binding sites was found
240 in the genes of both neural lineage comparisons (aN>aE and AN>AM but not aE>aN and AM>AN).
241 Our DESeq2 analyses support differential expression of the *Otx* gene (KH.C4.84) in AN>AM
242 comparison but not in aN>aE comparison (S1 Table: DESeq2). Inspection of the underlying read counts
243 for *Otx* suggests that it is expressed at higher levels in aN>aE but these counts show higher variance,
244 such that the aN>aE comparison is not significant under the DESeq2 statistical model (S1 Fig). *In situ*
245 hybridisation with *Otx* probes shows strong expression in a-line neural lineages from the 32-cell stage,
246 and in both neural lineages from neurula stage (Hudson and Lemaire, 2001; Hudson et al, 2003). In
247 contrast to the neural lineage specific enrichment of Otx-binding sites, the epidermal lineage (aE)
248 showed very strong enrichment for AP2-binding sites. Consistent with this, *Tfap2-r.b* (KH.C7.43), one
249 of the two *Ciona* AP2-like genes, has been shown to play a key role in epidermal differentiation in

250 ascidian embryos (Imai et al., 2016, 2004) and its transcripts are enriched in epidermal lineages (aE>aN)
251 (S1 Table: DESeq2 and by *in situ* hybridisation (Oda-Ishii et al., 2016)). An enrichment of an Achaete-
252 scute like binding sites was specifically observed for A-line neural genes (AN>AM). The CAG half-site
253 is recognised as a DNA binding target by a subfamily of the class ‘A’ bHLH transcription factors (De
254 Martin et al., 2021). The genome-wide survey of the *Ciona* bHLH transcription factors has revealed a
255 handful of genes, whose human orthologues exhibit a preferential binding to the CAG half site. These
256 include *Ascl.a* (KH.L9.13), *Ascl.b* (KH.C2.880), *Ascl.c* (KH.C2.560), *Atoh* (KH.C8.175), *Atoh8*
257 (KH.C9.872), *Hand* (KH.C14.604), *Hand-r* (KH.C1.1116), *Mrf* (KH.C14.307), *Ptfla* (KH.C3.967),
258 *Ptfla-r* (KH.L116.39), and *Tcf3* (KH.C3.348) (De Martin et al., 2021; Satou et al., 2003). Inspection of
259 our scRNA-seq dataset revealed appreciable read counts only for *Tcf3*, which are observed in all the cell
260 types analysed (see supplementary link), indicating its ubiquitous expression. Its functional involvement
261 in segregation of the neural lineages remains to be addressed. *Zic-r.b* (*ZicL*)-like motifs were enriched
262 in gene sets from all comparisons. *Zic-r.b* is present as multi-copy genes in the *Ciona* genome (Satou
263 and Imai, 2018). Enrichment of *ZicL*-binding sites in neural lineages is consistent with the observation
264 that *Zic-r.b* transcripts are detected in our DESeq2 analyses in both neural lineages at the neural plate
265 stage (aN>aE and AN>AM) (S1 Table: DESeq2; Fig 4) and that *Zic-r.b* is necessary for the expression
266 of *CELF3/5/6* (KH.C6.128) (Imai et al., 2002). *Zic-r.b* also plays a critical role in the acquisition of
267 notochord fates (Imai et al., 2002), which is consistent with the enrichment of its binding site in AM-
268 specific genes and its high read counts (KH.S816.1, KH.S816.2, KH.S816.4, KH.L59.1, and
269 KH.L59.12) in the notochord lineages (A7.3, A8.5, and AM) (see supplementary link; Fig 4) (Winkley
270 et al., 2021). It is puzzling however that the binding site is also enriched in the epidermal lineage, in
271 which read counts for *Zic-r.b* transcripts are negligible throughout the stages analysed in this study (see
272 supplementary link; Fig 4). Finally, binding sites of a variety of ETS-domain transcription factors were
273 found enriched in a-line neural genes (aN>aE) and in those in the mesoderm (notochord) lineage
274 (AM>AN) (Winkley et al., 2021). This is consistent with acquisition of these fates requiring ERK
275 signals (Hudson et al., 2003; Yasuo and Hudson, 2007), which, as described above, can control ETS-
276 domain transcription factors by direct phosphorylation (Yang et al., 1996).

277 Overall, at this stage of development, the TFBS enrichment is unique for each lineage, including
278 for the two neural lineages, consistent with the distinct ontologies of the two neural lineages. However,
279 we observed that binding sites for both *Zic-r.b* and *Otx* are enriched in differentially expressed genes in
280 both neural lineages.

281

282 **Conclusion**

283 In this study, we show that neural cells become transcriptionally more similar to each other than they
284 are to their early segregating sister lineages by the neural plate stage of development (Fig 2). We identify
285 a set of both known and novel genes which are enriched in the two neural lineages (Fig 4). Among the
286 shared set of genes are several which are also reported to be expressed in the CNS of vertebrates, such

287 as *Noggin*, *ZCCHC24*, *miR-124*, *Celf*, *Zic* and possibly *miR-219*, suggesting an evolutionary important
288 gene set (Kang et al., 2012; Knecht et al., 1995; McMahon et al., 1998; Vidyanand et al., 2017; Wu et
289 al., 2019). In terms of regulation, *Zic-r.b* and *Otx* binding sites are enriched in differentially expressed
290 genes of both neural lineages, suggesting an early generic requirement for these factors in neural fates.
291 Otherwise the enrichment of transcription factor binding sites is unique in each lineage consistent with
292 their different ontologies and specification mechanisms. We suspect that our list of shared enriched
293 genes may be an underestimate since the number of cells analysed in any given comparison was small
294 and read counts often showed high variance across cells, e.g. the case of *Otx* (S1 Fig). The identification
295 of known markers, however, such as *CELF3/5/6*, *Zic-r.b* and *Pans/miR-124* indicates that the strategy
296 used is justifiable.

297

298 **Materials and Methods**

299 *Ascidian embryo culture and basic methods*

300 We used *Ciona robusta* for dissection and sequencing analysis. General culture and methods of ascidians
301 are published in (Sardet et al., 2011). Embryos were dissected on a 1.5% agarose-coated dish with a fine
302 glass ‘hair’ smeared with cellular debris. A single isolated cell was transferred in 0.5µl of seawater into
303 a 0.2ml PCR tube containing 9µl RNase-free water. After visual inspection of the presence of the cell
304 under stereomicroscope, 1µl of 10x Reaction buffer (SMARTer Ultra Low Input RNA Kit, Takara Bio)
305 was added and the tube was vortexed immediately and stored at -80°C before being processed for library
306 preparation. For all *in situ* hybridisation (ISH) analysis, *Ciona intestinalis* was used following the
307 published protocol (Hudson, 2020). DIG-labelled probes were made from the following cDNA clones:
308 GC32e02 (KH.C7.140); GC11m08 (KH.C14.33); GC31n24 (KH14.310); GC03h09 (KH.C4.90);
309 GC27k22 (KH.C12.562) (Satou et al., 2002). The probe for KH.L18.113 was synthesised from PCR
310 fragments amplified from VES105_E20 (Gilchrist et al., 2015) using the following PCR primers:
311 KH.L18.113-F : ATACAAGCAACTCAACCAACGC; KH.L18.113-R :
312 CTCACTATAGGGTATCTTGGTCGTTTCGTC; T7-probe :
313 ggccTAATACGACTCACTATAGGG. For *miR-124* detection, specific locked nucleic acid (LNA)
314 probes doubly-labelled with digoxigenin were purchased from Qiagen and ISH was conducted following
315 the published protocol (Chen et al., 2011). ISH was not attempted for KH.C11.540, KH.C1.29 or
316 KH.C7.59.

317

318 *Library preparation and sequencing*

319 Indexed Illumina libraries were prepared using Nextera XT kits (Illumina) from cDNAs generated with
320 SMARTer Ultra low input RNA kit (Takara Bio) according to manufacturers’ instructions. Sequencing
321 was conducted in the UCA GenomiX genomics platform (Sophia Antipolis, France) using Illumina
322 NextSeq500 system. For each library, single end 75bp reads were obtained with sequencing depth of
323 around 8 million reads per cell.

324

325 ***Computational analysis***

326 *Ciona robusta* sequences and annotation were taken from the GHOST database ([http://ghost.zool.kyoto-](http://ghost.zool.kyoto-u.ac.jp/download_kh.html)
327 [u.ac.jp/download_kh.html](http://ghost.zool.kyoto-u.ac.jp/download_kh.html)) - specific files used are named below.

328

329 *(1) Read mapping & counts*

330 Reads were aligned to the *Ciona* genome using STAR (version 2.7.10a) with the ‘--quantMode
331 GeneCounts’ option to quantify reads per gene (Dobin et al., 2013). Exon annotation was taken from
332 the KH.KH.Gene2013.gff3 file reprocessed for compatibility with STAR gene/exon format.
333 ReadsPerGene files were merged to a single gene by cell type raw count matrix.

334

335 The count matrix of raw reads is available at http://github.com/rcply/ciona_sc/

336

337 *(2) Differential expression analysis*

338 The raw count matrix was analysed using DESeq2 (Love et al., 2014). Two outlier cells were consistent
339 outliers and excluded from further analysis (A6115 and A87r5). Comparisons were performed using
340 count matrices restricted to the particular stage (e.g. only cells from the 32-cell stage). To deal with
341 batch and animal specific effects reflecting data collection constraints, comparisons involving the 16-,
342 32- and 64-cell stages included an animal of origin term in their design formula. DESeq2 alpha was 0.01
343 and log fold change cutoff 0.0. lfcShrink was performed using ‘ashr’.

344 The PCA plot data were first subjected to Variance Stabilizing Transformation (using the ‘vst’
345 function) followed by the plotPCA function of the DESeq2 package, using the default top 500 genes by
346 row variance.

347 The cluster tree of cell types was produced from within the Seurat package (Stuart et al., 2019),
348 using the BuildClusterTree function with a PCA reduction (from Seurat) with dimensions 1 to 12.

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350 The code for these tests is accessible at https://github.com/rcply/ciona_sc/

351

352 *(3) miR-124 target site enrichment*

353 3’UTR exons were taken from the KH_Ciona_2013.fa file using annotation in the
354 KH.KH.Gene2013.gff3 file. Transcripts were processed individually. For each transcript exons labelled
355 as ‘three_prime_UTR’ were concatenated and the complete UTR sequence reverse complemented
356 where necessary. These sequences were searched for the ‘7mer-m8’ (GTGCCTTn) and ‘7mer-A1’
357 (nTGCCTTA) *mir-124* target sequences (which together also cover the ‘8mer’ sequence), taken from
358 (Chen et al., 2011). Sequence identifiers were sorted for redundancy at the locus (i.e. gene) level. This
359 resulted in a list of 873 potential *mir-124* targets. Chi-square tests were performed on the intersection of
360 this list with the 4 neural plate stage cell-type differential expression lists.

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(4) *Transcription factor binding site enrichment*

We searched regions of the *Ciona* genome 1kb upstream of gene start sites based on the KH.KHGene2013.gff3 annotation, after first filtering to remove low complexity regions as defined by nseg (Wootton and Federhen, 1993) (<https://github.com/jebrosen/nseg>). Transcription factor binding site models (n=745) were taken from the profile weight matrix (PWM) data described in (Jolma et al., 2013). Although these data are not derived from *Ciona*, transcription factor specificity is generally well conserved over longer evolutionary timescales (Nitta et al., 2015). Because of its recognised importance in early neural differentiation, we manually added the *Ciona* ZicL (Zic-r.b) binding motif taken from data in Figure 2 of (Yagi et al., 2004). PWM searches were performed using the MOODS software library (Korhonen et al., 2017), with a false positive rate of 0.0001. Exactly overlapping matches to the same PWM on forward and reverse strands (i.e. palindromic sites) were counted as one match.

For each pairwise cell comparison, a set of ‘real’ genes was taken as those with significant DESeq2 p_adj values. For each PWM, the number of binding sites in the ‘real’ set and the number of binding sites in the remaining set were compared using a nested Poisson model to determine if they occurred at a significantly different rate in the ‘real’, with a P-value adjustment for testing multiple PWMs. For PWMs with an adjusted P-value more significant than 0.05, we also generated 100 permuted ‘real’ sets and excluded PWMs where the P value from the ‘real’ set was ever found to be less significant than any permuted value, to exclude cases where this model is inappropriate - these sites are marked FALSE in S3 Table.

For visualization purposes, we generated plots of the total number of binding sites for a particular PWM from 10,000 randomly sampled sets of genes of the same size as the DESeq2 ‘real’ set for a particular comparison. We fit a normal distribution to these plots and mark the true number of binding sites for the real set.

The code for these tests is accessible at https://github.com/rcply/ciona_sc/.

(5) *mir-124 target site enrichment*

3’UTR exons were taken from the KH_Ciona_2013.fa file using annotation in the KH.KHGene2013.gff3 file. Transcripts were processed individually. For each transcript exons labelled as ‘three_prime_UTR’ were concatenated and the complete UTR sequence reverse complemented where necessary. These sequences were searched for the ‘7mer-m8’ (GTGCCTTn) and ‘7mer-A1’ (nTGCCTTA) *mir-124* target sequences (which together also cover the ‘8mer’ sequence), taken from (Chen et al., 2011). Sequence identifiers were sorted for redundancy at the locus (i.e. gene) level. This resulted in a list of 873 potential *mir-124* targets. Chi-square tests were performed on the intersection of this list with the 4 neural plate stage cell-type differential expression lists.

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644 **Figure captions**

645 **Fig 1. Two distinct developmental lineages for *Ciona* larval CNS: a-line and A-line.**

646 (A) Drawing of the larval CNS enlarged within the larvae outline. The tail is truncated (indicated by the
647 square). The larval CNS is derived from a-line cells (pink), which make up the anterior part of the
648 sensory vesicle and A-line cells (orange) which make up much of the remaining CNS. The dorsal most
649 row of cells from the posterior sensory vesicle to the tip of the tail arises from the b-lineage (not
650 coloured). SV: sensory vesicle; TG: trunk ganglion; NC: nerve cord. (B) Isolated cells from each stage
651 were coloured with a- and A-line neural lineages in pink and orange, epidermis in dark grey, mesoderm
652 in light blue and endoderm in purple. Black lines connecting two given cells indicate their sister
653 relationship. Note that cells of the neural plate stage embryo were isolated as pairs of two sister cells.
654 n= number of each particular cell type sequenced. (C) The presence of expected differentially expressed
655 genes (“cell 1>cell 2” indicates a set of genes enriched in cell 1) confirmed correct identification and
656 isolation of the cells. *Zic.r-b* is a multi-copy gene (KH.S816.1, KH.S816.2, KH.S816.4, KH.L59.1, and
657 KH.L59.12).

658

659 **Fig 2. Transcriptional trajectories during the course of neural lineage segregation.**

660 (A) Principal component analysis (PCA) of the cells (left). Count data per gene were variance stabilizing
661 transformed (vst in DESeq2, see methods) and the 500 genes with greatest variance used for the basis
662 of the PCA. Each point represents a single cell following the key on the right side that indicates its
663 identity. Schematic drawing (right) represents the transcriptional trajectories of the different lineages
664 analysed. (B) Cluster tree of the cell types (see methods for details). With the exception of aN and AN,
665 the closest neighbour of all neural lineage precursors is its corresponding early diverging sister lineage
666 cell. Note that, at the 16-cell stage, the a5.3 and A5.1 cells have no sampled sister cell types of the same
667 lineage. Neural lineages are represented by red branches. eG: early gastrula; ect: ectoderm; mesend;
668 mesoendoderm (cf. Fig 1).

669

670 **Fig 3. Hierarchical clustering of larval stage neural cell types.**

671 In order to highlight their respective lineage origins, the larval neural cell clusters defined in Cao et al,
672 2019 are renamed as follows (“A” for A-line neural lineage, “a” for a-line neural lineage, “b” for b-line
673 neural lineage, and “P” for peripheral nervous system): A01 *KCNB1*+ motor ganglion; A02 *GLRA1*+
674 motor ganglion; A03 *AMD*+ motor ganglion; A04 *VP*+ pSV; A05 *VP-R*+ SV; A06 *GSTM1*+ SV; A07
675 MHB; A08 Tail nerve cord (A); A09 Ependymal cells; A10 *GLGB*+ pSV; A11 Trunk nerve cord (A);
676 A12 *Pax2/5/8-A*+ neck; a13 *Arx*+ pro-aSV; a14 *Aristaless*+ aSV; a15 *Opsin1*+, *PTPRB*+ aSV; a16 *Rx*+
677 aSV; a17 *FoxP*+ aSV; a18 *Opsin1*+, *STUM*+ aSV; a19 *Lhx1*+ GABAergic neurons; a20 *Lox5*+ aSV;
678 a21 *Lhx1*+, *Bsh*+ aSV; a22 *Eminens*; a23 *Six3/6*+ pro-aSV; a24 *Hedgehog2*+ SV; a25 Coronet cells;
679 a26 Pigment cells; b01 Tail nerve cord (b); b02 *Arx*+ nerve cord (b); b03 Trunk nerve cord (b); b04
680 *FoxD-b*+ cells; P01 Glia cells; P02 pATENs; P2b PSCs related; P03 Collocytes; P04 PSCs; P05 CESNs;

681 P06 RTENs; P07 aATENs; P08 BTNs; P09 *Dll-A+* ANB (anterior neural boundary); P10 *Pitx+* ANB
682 (anterior neural boundary). Furthermore, neural cell clusters of the A-line origin are marked with orange
683 dots while those of the a-line origin with pink dots. The transcriptome dataset used in this analysis was
684 generated in Cao et al, 2019.

685

686 **Fig 4. Genes whose transcripts are enriched in both neural lineages at neural plate stage.**

687 Graphs show normalized transcript counts in the a-line neural (pink), a-line epidermis (green), A-line
688 neural (blue) or A-line mesoderm (purple) at the neural plate stage. In all cases the comparisons between
689 aN and aE and between AN and AM show statistically significant up regulation (see text for details).
690 Note logarithmic y-axes. Individual data points are represented as dots.

691

692 **Fig 5. Spatial expression pattern of selected neural-enriched genes at early gastrula and neural
693 plate stages.**

694 For all genes analysed, except for *Noggin (NOG)*, expression in both neural lineages was confirmed. A=
695 expression detected in A-line neural cells; a= expression detected in a-line neural cells; eg= early
696 gastrula stage; npl= 6-row neural plate stage.

697

698 **Fig 6. Transcription factor-binding site identification and enrichment analyses indicate distinct
699 regulatory inputs to activate neural plate stage genes between the two neural lineages.**

700 Binding motif sequence logos are on the left column with names of corresponding transcription factors.
701 The red line in each histogram indicates the observed number of TF sites in the 1kb upstream region of
702 the set of significantly ‘up’ lists of genes. Numbers of genes are analysed: 131 for aN vs aE; 220 for aE
703 vs aN; 98 for AN vs AM; 120 for AM vs AN (e.g., “aN vs aE” indicates a set of genes up-regulated in
704 aN compared to aE). The distributions show the total number of sites from the same number of genes
705 drawn randomly (10,000 trials) from the *Ciona* gene set. Dotted lines represent 3 standard deviations
706 above the mean of each fitted normal distribution (blue lines). See methods for more details.

707

708 **Supporting information**

709 **S1 Fig. Expression of *Otx* at neural plate stage.**

710 Although there is clear separation between the expression levels in AN and AM (right hand side, blue,
711 purple), this is less obvious in aN vs aE (left hand side, green, red) owing to the high variability of aE
712 counts (note log scale).

713

714 **S1 Table. DESeq2 results.**

715 **S2 Table. Shared neural genes.**

716 **S3 Table. Enriched transcription factor binding sites.**

717

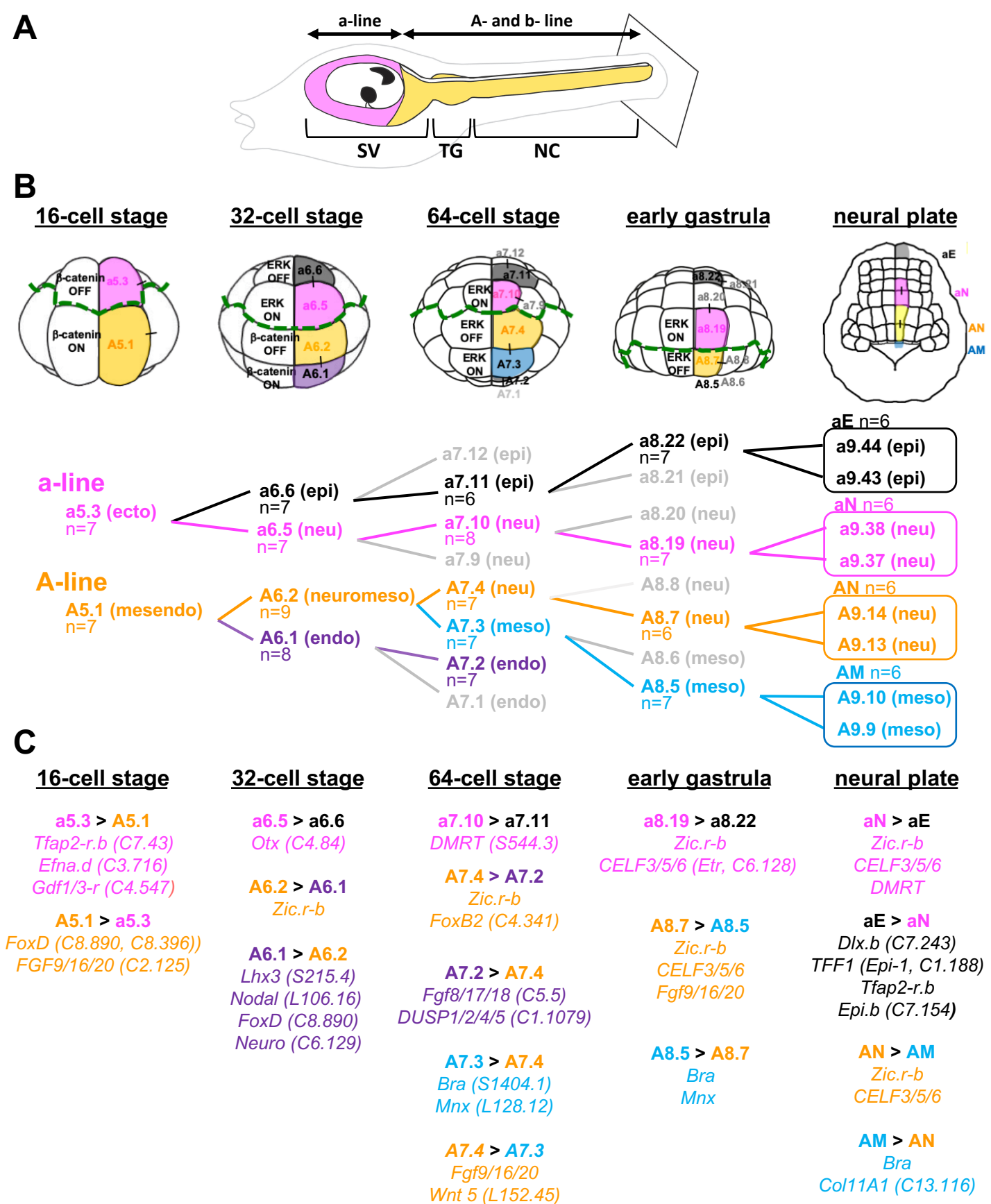
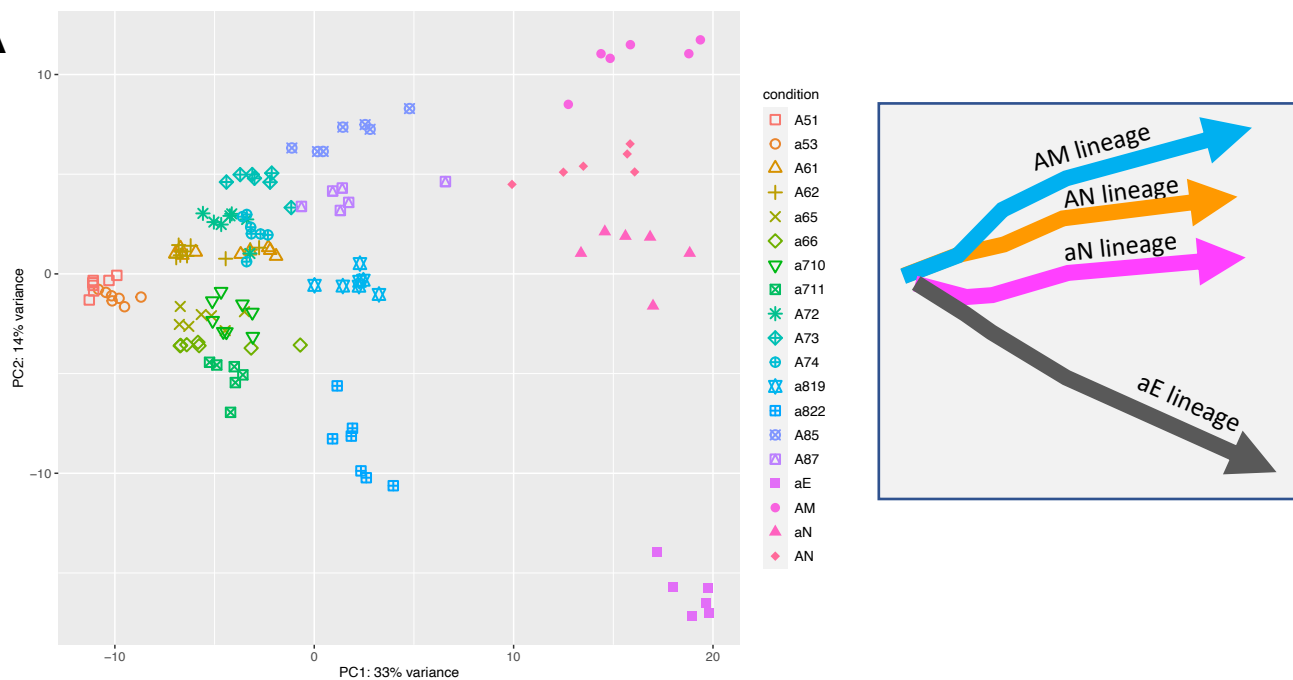
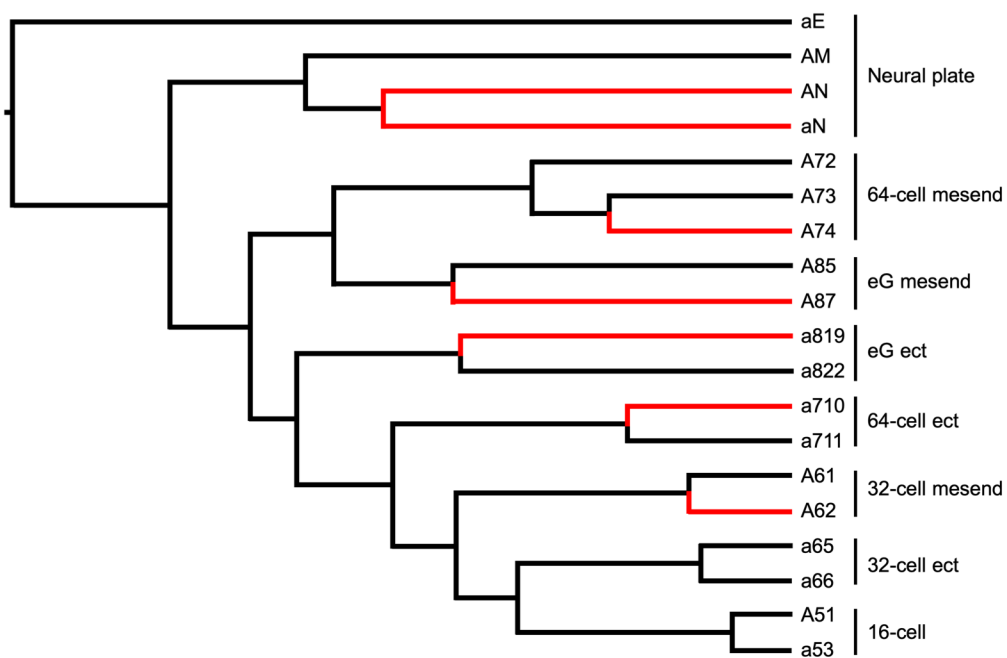


Fig 1

A**B****Fig 2**

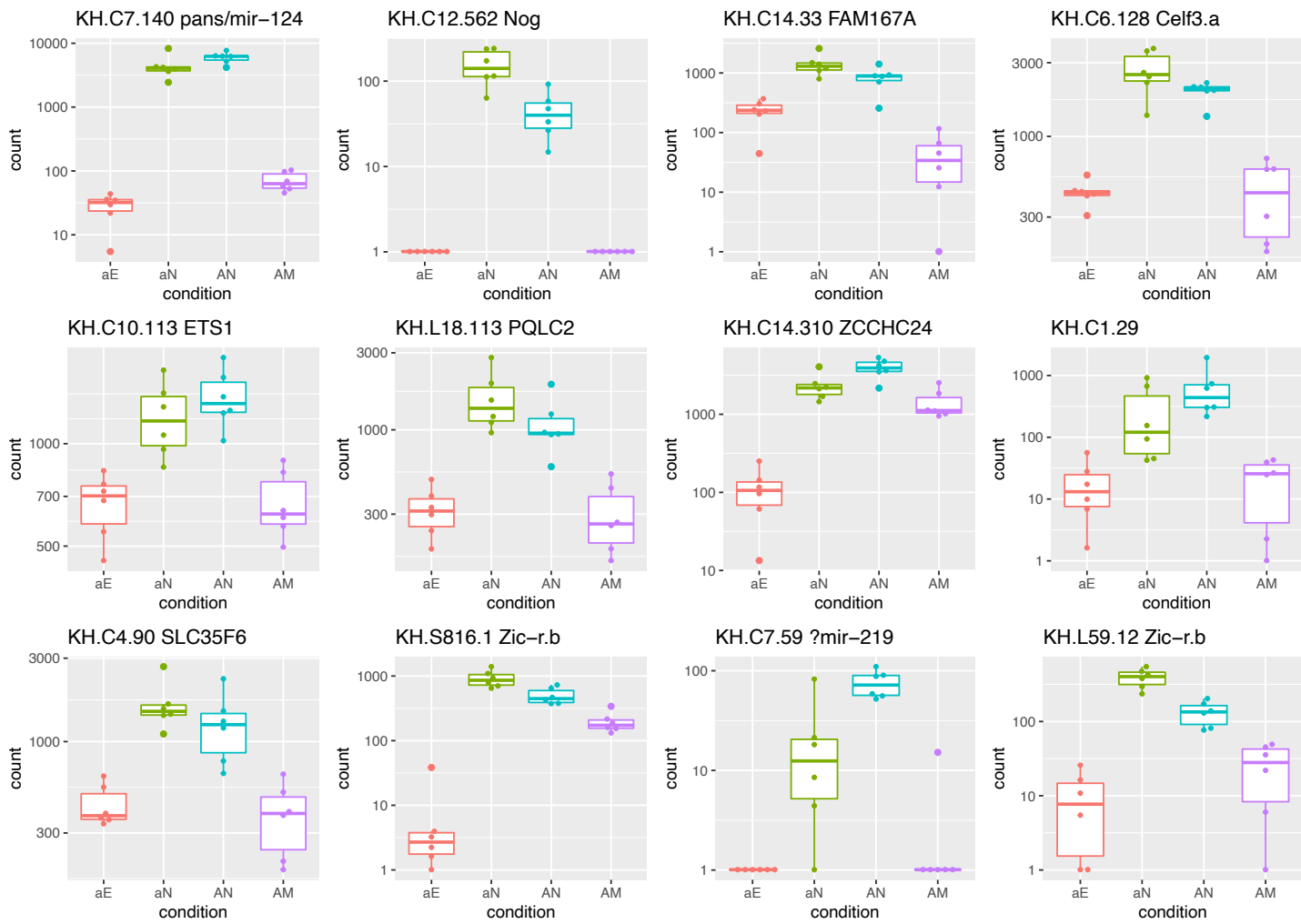


Fig 4

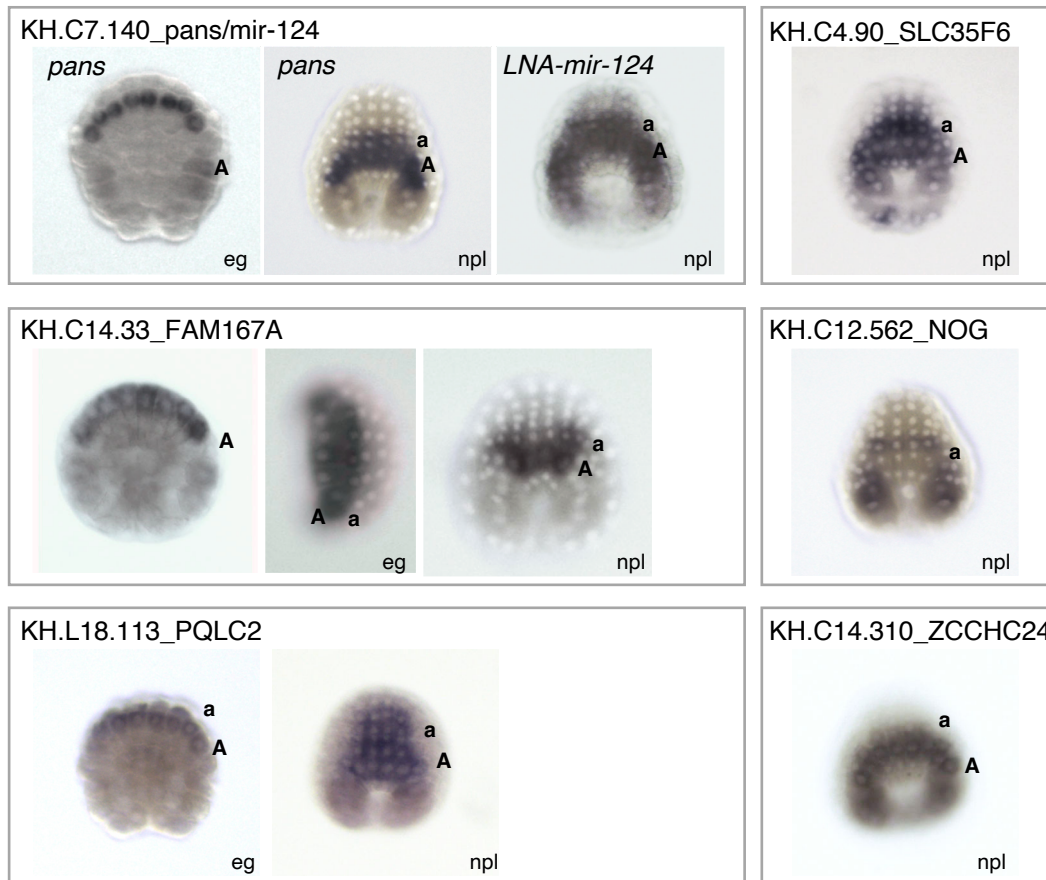


Fig 5

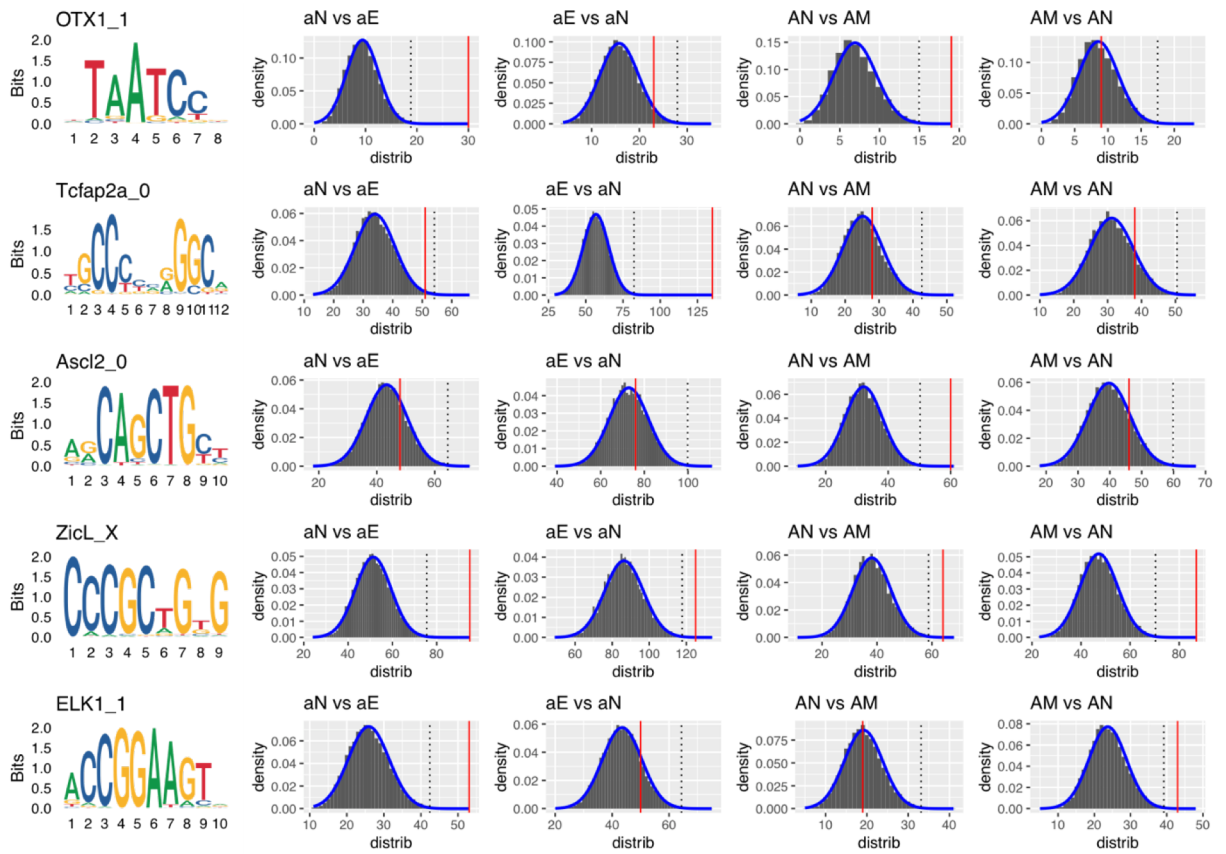
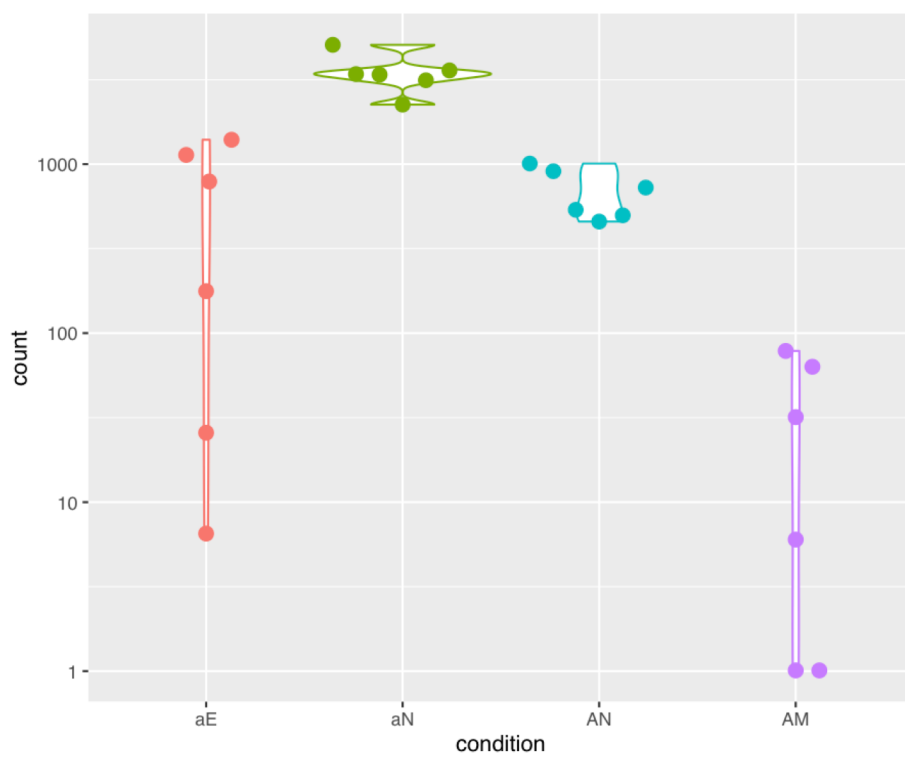


Fig 6



S1 Fig