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1 Contribution of *sox9b* to pigment cell formation in medaka fish

2

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13

14 Abstract

15 SoxE-type transcription factors, Sox10 and Sox9, are key regulators of the development  
16 of neural crest cells. Sox10 specifies pigment cell, glial, and neuronal lineages, whereas  
17 Sox9 is reportedly closely associated with skeletogenic lineages in the head, but its  
18 involvement in pigment cell formation has not been investigated genetically. Thus, it is  
19 not fully understood whether or how distinctly these genes as well as their paralogs in  
20 teleosts are subfunctionalized. We have previously shown using the medaka fish *Oryzias*  
21 *latipes* that pigment cell formation is severely affected by the loss of *sox10a*, yet  
22 unaffected by the loss of *sox10b*. Here we aimed to determine whether Sox9 is involved  
23 in the specification of pigment cell lineage. The *sox9b* homozygous mutation did not  
24 affect pigment cell formation, despite lethality at the early larval stages. By employing  
25 *sox10a*, *sox10b*, and *sox9b* mutations, compound mutants were established for the  
26 *sox9b* and *sox10* genes and pigment cell phenotypes were analyzed. Simultaneous loss  
27 of *sox9b* and *sox10a* resulted in the complete absence of melanophores and  
28 xanthophores from hatchlings and severely defective iridophore formation, as has been  
29 previously shown for *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutants, indicating that Sox9b as well  
30 as Sox10b functions redundantly with Sox10a in pigment cell development. Notably,  
31 leucophores were present in *sox9b*<sup>-/-</sup>; *sox10a*<sup>-/-</sup> and *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutants,  
32 but their numbers were significantly reduced in the *sox9b*<sup>-/-</sup>; *sox10a*<sup>-/-</sup> mutants. These  
33 findings highlight that Sox9b is involved in pigment cell formation, and plays a more  
34 critical role in leucophore development than Sox10b.

35

36 Keywords: medaka fish, *Oryzias latipes*, SoxE transcription factor, melanophore,  
37 melanocyte, iridophore, xanthophore, leucophores, cell fate, functional redundancy

38

39

40 Introduction

41 Sry (sex determining region Y)-box (Sox) proteins are high-mobility group (HMG)  
42 transcription factors that regulate various developmental processes in animals (Wegner,  
43 1999). The Sox family, characterized by the presence of an HMG-type DNA binding  
44 domain in the N-terminus and a transactivation domain in the C-terminal, includes the  
45 SoxE subfamily, comprising Sox8, Sox9, and Sox10 (Wegner, 1999). Sox9 and Sox10 have  
46 emerged as key regulators of neural crest cells (NCCs); expression of these are  
47 overlapping in NCCs, but expression of Sox9 precedes that of Sox10 in frogs, chicks, mice,  
48 and others (Simoes-Costa & Bronner, 2015).

49

50 Sox10 specifies pigment cell, as well as neural cell in neural crest derivatives: glial cells  
51 In the peripheral nervous system (Kuhlbrodt et al., 1998; Weider & Wegner, 2017),  
52 sensory neurons (Carney et al., 2006; Delfino-Machin et al., 2017), and enteric neurons  
53 (Elworthy, Pinto, Pettifer, Cancela, & Kelsh, 2005). In mice, Sox10 activates *Mitf*  
54 expression, and *Mitf* in turn promotes melanocyte differentiation by driving *Dopa*  
55 *chrome tautomerase* expression, and thereby melanin synthesis (Hou, Arnheiter, &  
56 Pavan, 2006).

57

58 In general, teleosts, including zebrafish, have three types of pigment cells, melanophores,  
59 iridophores, and xanthophores, but a few species, including medaka (Japanese rice fish),  
60 contain leucophores as an additional fourth type (Hashimoto, Goda, & Kelsh, 2021). To  
61 date, all pigment cell types are believed to originate from the common stem cell,  
62 chromatoblasts, which are derived from NCCs, although there is ongoing controversy  
63 about the exact identity of these progenitors (see Nikaido et al.,  
64 doi.org/10.1101/2021.06.17.448805). Since Sox10 loss-of-function in zebrafish *sox10<sup>-/-</sup>*  
65 (*colorless*) mutants results in severe depletion of all pigment cell types (Dutton et al.,  
66 2001; Kelsh, 2006), Sox10 activity is vital for fate specification of each pigment cell type.

67

68 Sox9 may be best known as a regulator of chondrocyte differentiation (Lefebvre, 2019).  
69 For instance, Sox9 inactivation in the neural crest lineage results in severe craniofacial  
70 defects in mice (Mori-Akiyama et al., 2003). Sox9 functions as an early neural crest  
71 specifier, and its expression is maintained in migratory NCCs within the branchial arches,  
72 reflecting its crucial role in cartilage formation (Mori-Akiyama et al., 2003). In zebrafish,

73 both *sox9b* and *sox10* are expressed in early NCCs, and thus in the progenitors of all  
74 pigment cells (Hashimoto et al., 2021). Thus, it is conceivable that both Sox9 and Sox10  
75 might have partially redundant functions in the development of one or more pigment  
76 cell types. In frogs, overexpression of Sox9 or Sox10 has equivalent effects on neural  
77 crest formation (Taylor & Labonne, 2005). Overexpression of Sox9 induces the formation  
78 of melanophores and rescues neural crest formation in zebrafish *sox10<sup>-/-</sup>* (*colorless*)  
79 mutant embryos (Lee et al., 2016). Similarly, in zebrafish, injection of a fruit fly or  
80 lamprey *soxE* expression plasmid partially rescues melanogenesis in *sox10<sup>-/-</sup>* (*colorless*)  
81 mutant embryos (Lee et al., 2016). More directly, Greenhill and colleagues have reported  
82 that zebrafish *sox10<sup>-/-</sup>* (*colorless*) mutants occasionally exhibit residual melanin  
83 expression (Greenhill, Rocco, Vibert, Nikaido, & Kelsh, 2011). They showed that  
84 morpholino-mediated knockdown of Sox9b suppressed the expression of residual  
85 melanin. These findings suggest that Sox9b is a component of the gene regulatory  
86 network, not only for early neural crest specification, but also for pigment cell  
87 development, perhaps through supportive action of Sox10.

88

89 While zebrafish has a single *sox10* gene, medaka has two teleost paralogs of *sox10*,  
90 *sox10a*, and *sox10b*, and their simultaneous loss results in defects of melanophore,  
91 iridophore, and xanthophore specification, as seen in zebrafish *sox10* mutants (Nagao et  
92 al., 2018). Surprisingly, the number of leucophores, which are absent in zebrafish, was  
93 unaffected in medaka, although their distribution was shifted to the head (Nagao et al.,  
94 2018). Thus, although leucophores are proposed to share a progenitor with  
95 xanthophores (Kimura et al., 2014; Nagao et al., 2014), these findings suggest that  
96 leucophore fate may be less dependent on Sox10a and Sox10b than xanthophore fate.  
97 This finding led to the hypothesis that residual SoxE activity may promote leucophore  
98 fate in medaka.

99

100 To address this possibility, we first investigated the expression of candidate *soxE* genes,  
101 *sox8*, *sox9a*, and *sox9b*, in the neural crest. Based on the results, phenotypic analyses of  
102 medaka *soxE* mutants were conducted, comparing *sox10a<sup>-/-</sup>*, *sox9b<sup>-/-</sup>* double, and *sox10a<sup>-/-</sup>*  
103 *sox10b<sup>-/-</sup>*; *sox9b<sup>-/-</sup>* triple mutants. We found that *sox9b* acted on pigment cell fate  
104 specification in a manner comparable to that of *sox10b*. Additionally, the effect of *sox9b*  
105 in leucophore specification was stronger than that of *sox10b*. Thus, this study uncovered

106 a previously unappreciated function of Sox9 in vertebrate pigment cell development.

107

108 Materials and Methods

109 Ethics

110 The animal work in this study was approved by the Nagoya University Animal Experiment  
111 Committee and was conducted in accordance with the Regulations on Animal  
112 Experiments at Nagoya University.

113

114 Medaka strains

115 The Nagoya strain of the medaka fish *Oryzias latipes* was used as the wild type (WT). The  
116 *sox9b*<sup>K136X</sup> TILLING mutant was a gift from Prof. M. Tanaka, Nagoya University (Nakamura  
117 et al., 2012). The *sox10a*<sup>E2del16</sup> and *sox10b*<sup>E1del7</sup> mutant strains have been described  
118 previously (Nagao et al., 2018). The *sox10a*<sup>E2del16/E2del16</sup>, *sox10b*<sup>E1del7/E1del7</sup>, and  
119 *sox9b*<sup>K136X/K136X</sup> mutants are considered null mutants (Nakamura et al., 2012, Nagao et  
120 al., 2012) (see Suppl. Fig. 1), and are therefore designated as *sox10a*<sup>-/-</sup>, *sox10b*<sup>-/-</sup>, and  
121 *sox9b*<sup>-/-</sup>, respectively. The *sox10a*<sup>-/-</sup> mutants hatched and survived at approximately 9–  
122 10 days post fertilization (dpf) but died thereafter. The *sox10b*<sup>-/-</sup> mutants appeared  
123 normal throughout their lives. Some of the *sox9b*<sup>-/-</sup> mutants, but not all, hatched and  
124 survived at approximately 9–10 dpf, but died thereafter.

125

126 Mating

127 Homozygotes for single, double, or triple *soxE* mutations were obtained by crossing  
128 heterozygotes for the corresponding mutation(s).

129

130 Genotyping

131 Mutations in *sox10a*, *sox10b*, and *sox9b* were detected using polymerase chain reaction  
132 fragment length polymorphism by polyacrylamide gel electrophoresis (PAGE), as  
133 previously described (Nagao et al., 2018; Nakamura et al., 2012). To detect the 16 bp  
134 *sox10a*<sup>E2del16</sup> deletion mutation, the following primer set was used: 5'-  
135 CTCCCTCTAGGCTGCTGAACGAGA-3' and 5'-GAGACCCTGCGCCACATTGTGAT-3'. For the  
136 *sox10b*<sup>E1del7</sup> 7 bp deletion mutation, the following primer set was used to amplify  
137 genomic DNA fragments: 5'-GAATTCAATGTCCAGGGAGGAGCAGAGCCT-3' and 5'-  
138 GTCGTCGGATTTGGCGGAAGAACA-3'. These fragments were subsequently digested with

139 *MspI* (New England Bio Labs, Beverly MA, USA), which only cuts the WT allele, and then  
140 separated using PAGE. To detect the *sox9b*<sup>K136X</sup> point mutation, the following primer set  
141 was used: 5'-GTGCATTAGAGACGCGGTGTCCCAAGTGCT-3' and 5'-  
142 TAAGGAGCCTCCAAAGTTTTCCAAGAGTTC-3'. The resulting DNA fragments were digested  
143 with *PvuII* (New England Bio Labs, Beverly MA, USA), which only cuts the mutant allele.  
144

#### 145 Whole mount *in situ* hybridization and plastic sectioning

146 Whole mount *in situ* hybridization and plastic sectioning were performed as previously  
147 described (Nagao et al., 2014). The digoxigenin (Roche Diagnostics GmbH, Mannheim,  
148 Germany)-labeled antisense riboprobe was synthesized from the plasmid harboring full-  
149 or partial-length open reading frame of *sox10a*, *sox10b*, *sox9a*, *sox9b* or *sox8* cDNA using  
150 SP6 or T7 polymerase (Promega, Madison, WI, USA) after restriction enzyme digestion  
151 (New England Bio Labs, Beverly MA, USA). For plastic sectioning, the stained samples  
152 were embedded in Technovit 8100 (Heraeus Kulzer, Wehrheim, Germany) and  
153 sectioned at 10 µm-thickness.  
154

#### 155 Microscopy

156 Melanophores were subjected to a combination of bright and dark-field illumination  
157 under a stereomicroscope (MZ APO, Leica Microsystems, Wetzlar, Germany).  
158 Leucophores and iridophores were identified in a dark field. Xanthophores were  
159 identified by detecting their autofluorescence using UV light exposure with a DAPI filter  
160 (Imager.D1, Carl Zeiss, Oberkochen, Germany).  
161

#### 162 Results and Discussion

163 To identify candidate *soxE* gene(s) involved in pigment cell development, the *sox8*, *sox9a*,  
164 and *sox9b* expression patterns were examined using *in situ* analysis. During the early to  
165 mid-somite stages, when pigment cell progenitors are established in the trunk, *sox9b*  
166 shows *in situ* signals highly similar to those of *sox10a* and *sox10b* (Fig. 1). *sox9b* mRNA  
167 was observed in the premigratory NCCs and migrating cells, most prominently between  
168 somites and the neural tube, while *sox9a* mRNA showed little evidence of localized  
169 expression and *sox8* mRNA was observed mostly in the placode, somite, and neural tube.  
170 Thus, *sox9b* was identified as a strong candidate for residual SoxE activity underlying  
171 medaka pigment cells, especially leucophores, and fate specification in the absence of

172 Sox10a and Sox10b. Therefore, we further investigated the role of *sox9b*.

173

174 To determine whether *sox9b* functions in pigment cell development in medaka, a *sox9b*  
175 loss-of-function mutant, *sox9b*<sup>K136X</sup>, was used. This mutant had a nonsense mutation in  
176 exon 2 and was predicted to generate a truncated Sox9b protein lacking the C-terminus  
177 of the HMG DNA-binding domain and the transactivation domain (Suppl. Fig. 1)  
178 (Nakamura et al., 2012). The homozygous mutant *sox9b*<sup>-/-</sup> exhibited normal  
179 pigmentation at the hatching stage (Fig. 2, A1, A3, and A6 vs. B1, B3, and B6 for  
180 leucophores; A2 and A4 vs. B2 and B4 for melanophores; A5 and A7 vs. B5 and B7 for  
181 iridophores; and A8 vs. B8 for xanthophores; see also Suppl. Table 1), apparently with a  
182 severe defect in jaw formation (Suppl. Fig. 2).

183

184 As previously shown by Nagao et al. (2018) (Nagao et al., 2018), although the medaka  
185 *sox10b*<sup>-/-</sup> single mutant shows no overt pigment cell phenotype, *sox10a*<sup>-/-</sup> single mutant  
186 hatchlings show a reduction in all pigment cell types except for leucophores (Fig. 2, A1,  
187 A3 and A6 vs. C1, C3, and C6) compared to that of WT siblings (Fig. 2, A2 and A4 vs. C2  
188 and C4 for melanophores; A7 vs. C7 for iridophores [those in the iris of A5 and C5 look  
189 unaltered]; and A8 vs. C8 for xanthophores). The *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutants  
190 showed a more severe reduction in the numbers of melanophores (Fig. 2, E2 and E3),  
191 iridophores (Fig. 2, E4 and E6), and xanthophores (Fig. 2, E7), but retained leucophores  
192 in the dorsal head region (Fig. 2, E5). Thus, while *sox10b* was dispensable for pigment  
193 cell development, it acted redundantly with *sox10a* in pigment cell specification. To  
194 determine whether *sox9b* functions redundantly in a similar manner to *sox10b*, *sox10a*<sup>-/-</sup>  
195 *sox9b*<sup>-/-</sup> double mutants were studied. Simultaneous loss of Sox10a and Sox9b resulted  
196 in almost complete absence of melanophores, iridophores, and xanthophores, in  
197 addition to a severe reduction in leucophores in the trunk, although some double  
198 mutants retained a considerable number of leucophores in the head (Fig. 2):  
199 Melanophores (D2 and D3) and xanthophores (D7) were absent from the body surface,  
200 iridophores were lost from the dorsal surface of the yolk (D6), but occasionally remained  
201 partially in the iris (D4), while leucophores remained in the head to anterior trunk region  
202 with numbers varying between individuals (D1 and D5). These phenotypes are  
203 reminiscent of those in *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutants (Fig. 2 E1 and E5, Suppl. Fig.  
204 3). The *sox10b*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> double mutants showed no apparent pigment cell phenotypes,



205 but showed defective jaw formation, presumably attributed to Sox9b loss.

206

207 Next, the number of leucophores over the dorsal surface of the head and the dorsal  
208 midline of the body were quantified in the *sox9b*<sup>-/-</sup> single mutant and the *sox10a*<sup>-/-</sup>;  
209 *sox9b*<sup>-/-</sup> and *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutants (Fig. 3). Compared to that of the wild-  
210 type Nagoya strain, *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> double mutant larvae exhibited a significant  
211 reduction in leucophore numbers, while *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> double mutant or *sox9b*<sup>-/-</sup>  
212 single mutant larvae were indistinguishable from WT. These data suggested that  
213 leucophore specification required SoxE activity, with greater dependence on Sox9b than  
214 Sox10b.

215

216 Finally, whether leucophores differentiated in the absence of *sox10a*, *sox10b*, and *sox9b*  
217 was determined. Triple heterozygous fish were crossed, and out of their offspring, more  
218 than 200 embryos without melanophores were collected, which represent the  
219 population at least doubly homozygous for *sox10a* and either *sox10b* (Fig. 4, A) or *sox9b*  
220 (Fig. 4, B), and presumably contained triple homozygotes of these *soxE* genes. Assuming  
221 that a third mutation of either *sox9b* or *sox10b* may be homozygous in a Mendelian  
222 fashion, the *soxE* triple homozygosity was expected to appear in approximately one  
223 quarter of the 200 embryos obtained. At 6 dpf, when leucophores had become visible in  
224 siblings, the presence of leucophores in the embryos was determined and the embryos  
225 were genotyped. *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup>; *sox9b*<sup>+/-</sup> compound mutants retained leucophores  
226 on the dorsal head region (Fig. 4, C), while *sox10a*<sup>-/-</sup>; *sox10b*<sup>+/-</sup>; *sox9b*<sup>-/-</sup> compound  
227 mutants also retained leucophores (Fig. 4, D), but in a few cases, there were few or no  
228 leucophores (Fig. 4, E). Importantly, no triple homozygotes were observed at 6 dpf,  
229 although the double homozygous embryos (> 200) examined should have included  
230 approximately one-quarter triple homozygotes, assuming that they were viable. We  
231 further collected and genotyped more than one hundred 2 dpf-embryos without  
232 melanophores, obtained from a cross of triple heterozygous fish. Again, no triple  
233 homozygotes were found in these embryos, so it was concluded that the triple  
234 homozygous mutation must be lethal during early developmental stages.

235

236 In conclusion, this study revealed that, in medaka, Sox9b plays a role in pigment cell  
237 specification to an extent similar to that of Sox10b. By considering the severity of

238 pigment cell phenotypes in the single and compound mutants, we concluded that while  
239 Sox10a is a pivotal player in pigment cell specification, both Sox10b and Sox9b  
240 functioned in a partially redundant manner to Sox10a. For melanophore, iridophore, and  
241 xanthophore specification, Sox10b and Sox9b appeared to be equally important. In  
242 contrast, for leucophore specification, Sox9b appeared to be more influential than  
243 Sox10b. Finally, analysis of the triple *soxE* compound mutants revealed that only those  
244 with *sox9b* and *sox10a* homozygosity occasionally show an absence of leucophores.  
245 Furthermore, this analysis suggests an essential role of *soxE* in viability of the early  
246 embryo, which may shed light on a new function of *soxE* in early embryogenesis.

247

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251

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255

256

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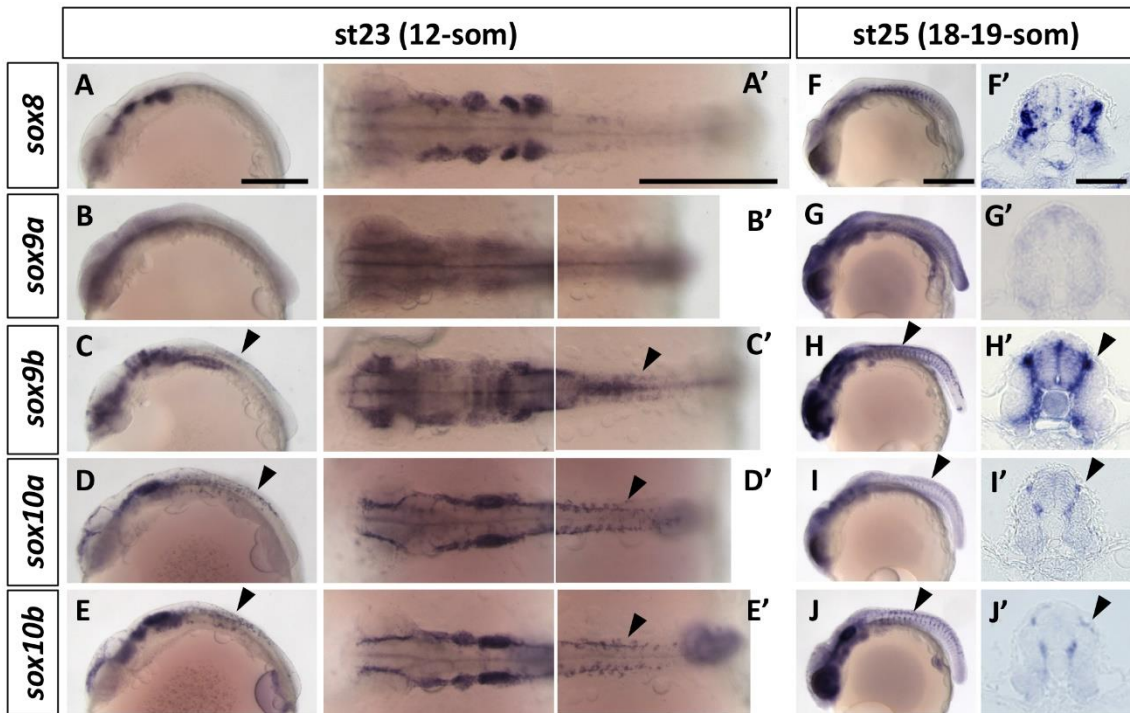
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320

321 Figure legends



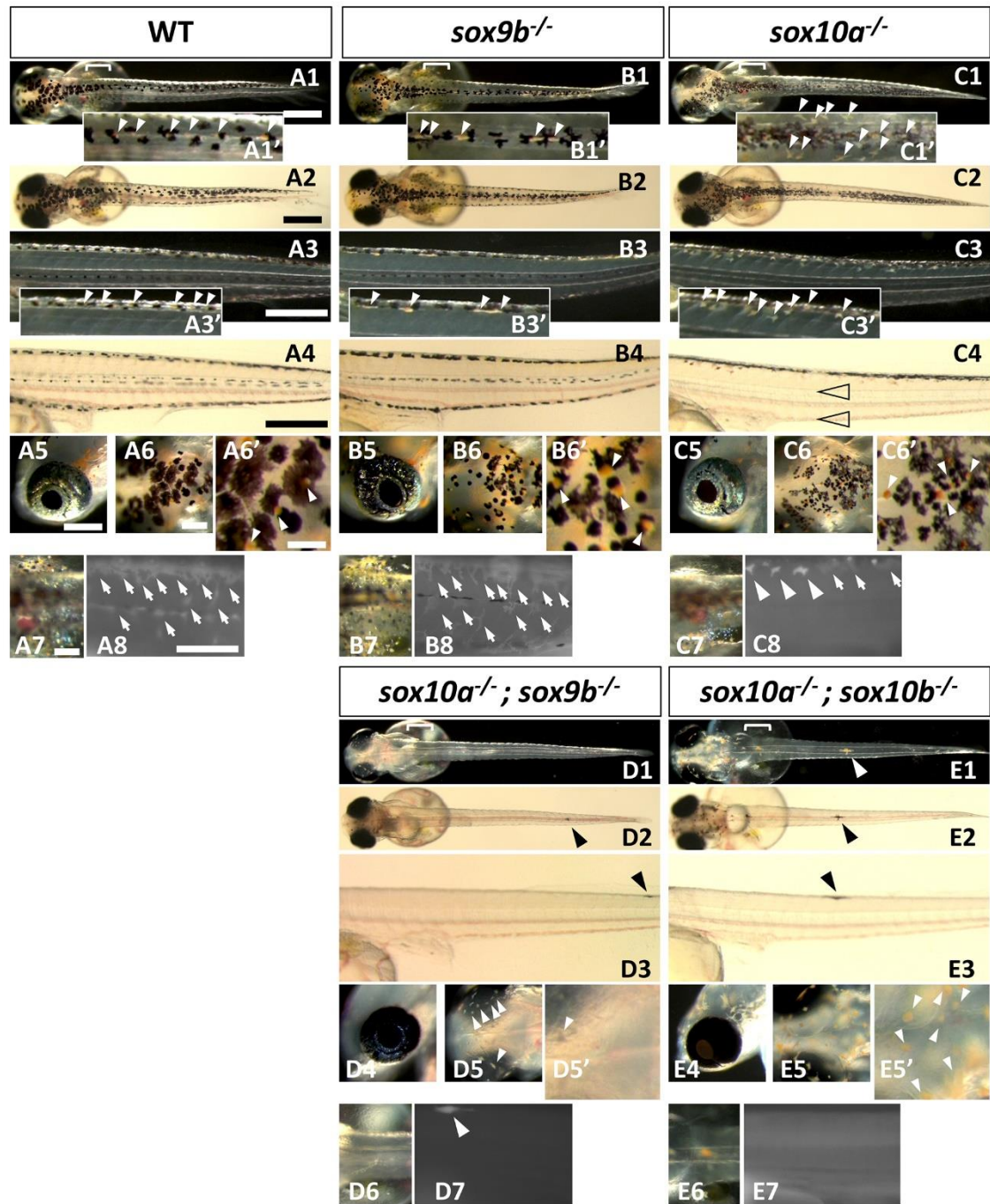
322

323 Fig. 1 Expression pattern comparison of the *soxE*-group genes

324 *In situ* hybridization of *sox8* (A, F), *sox9a* (B, G), *sox9b* (C, H), *sox10a* (D, I), and *sox10b* (E,  
 325 J) mRNAs at stage 23 (12-somites, A to E) and stage 25 (18–19-somites, F to J) in wild-  
 326 type (WT) embryos. Arrowheads indicate signals in the premigratory neural crest cells  
 327 (NCCs). *sox9b*, *sox10a*, and *sox10b* mRNA expression is detected in the NCCs, in contrast  
 328 to *sox8* and *sox9a*.

329 Scale bars: (A, A', F) 0.2 mm, also applied to B, C, D, E, B', C', D', E', G, H, I, and J; (F') 20  
 330  $\mu$ m, also applied to G', H', I, and J'.

331



332

333 Fig. 2 Pigment cell phenotypes of *soxE* mutants

334 Pigments of wild-type (WT) and mutant hatchlings were observed at 7 days post  
 335 fertilization (dpf). (A1–A8) WT, (B1–B8) *sox9b*<sup>-/-</sup> mutants, (C1–C8) *sox10a*<sup>-/-</sup> mutants, (D1–  
 336 D7) *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> mutants, and (E1–E7) *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> mutants. Magnified  
 337 images are numbered with a prime ('). Arrows indicate xanthophores, and arrowheads  
 338 indicate leucophores. The square brackets in A1, B1, C1, D1, and E1 indicate where A7,  
 339 B7, C7, D6, and E6 correspond to.

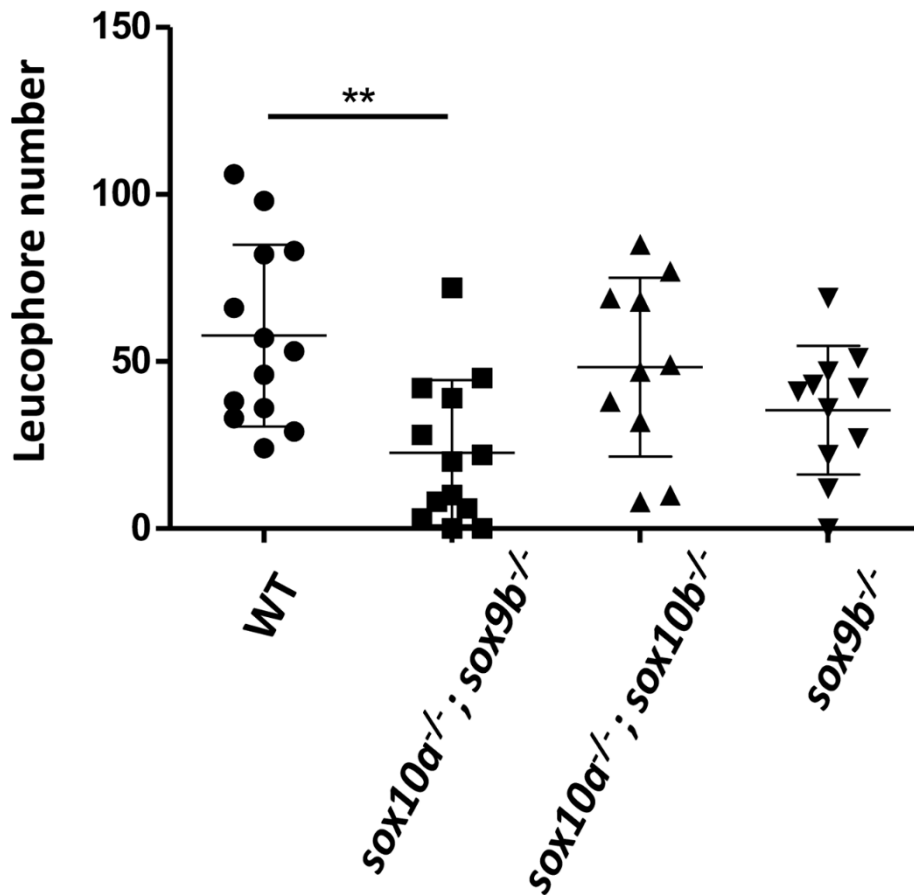
340 In the WT hatchlings, melanophores and black cells are observed dorsally in the head  
341 and form three horizontal stripes (dorsal, lateral, and ventral) at the trunk (A1, 2, 4, and  
342 6). Leucophores, which appear yellowish to orange (A1, 3, and 6) in emitted light and  
343 blackish or brownish in transmitted light (A2 and 4), are also in the head and along the  
344 dorsal and ventral stripes and are associated with melanophores. In contrast,  
345 iridophores, shiny cells, are in the iris and dorsally on the yolk sac (A5 and 7) and  
346 xanthophores are evident on the lateral surface of the body through emission of  
347 autofluorescence under UV light (A8).

348 *sox9b*<sup>-/-</sup> mutant hatchlings appear normal in pigmentation. Melanophores are scattered  
349 on the head and form three stripes on the body (B1, 2, 4, and 6); leucophores are  
350 associated with melanophores all along the dorsal and ventral stripes (B1, 3, and 6);  
351 iridophores are observed both in the iris and on the yolk sac (B5 and 7); xanthophores  
352 are located laterally on the body (B8). In *sox10a* mutants, melanophores are severely  
353 reduced in the lateral and ventral stripes, more severely in the posterior body (C1, 2, 4;  
354 open arrowheads in C4 indicate the absence of two stripes (lateral and ventral) of  
355 melanophores), and xanthophores are nearly absent (C8), while leucophores and  
356 iridophores are unaffected (C1, 3, and 6, and C5 and 7, respectively).

357 In the *sox10a; sox9b* and *sox10a; sox10b* double homozygous null mutants, similar  
358 pigment cell phenotypes are observed. Melanophores and xanthophores are completely  
359 lost (D1, 2, 3, 5, E1, 2, 3, 5, and D7, E7, respectively), whereas leucophores are nearly  
360 absent from the body (D1 and E1) but remain in the head in considerable numbers (D5  
361 and E5), while iridophores are lost from the yolk sac (D6 and E6), but remain in the iris  
362 in residual numbers (D4 and E4).

363 Scale bars: A1–5, 0.5 mm, also applied to B1–5, C1–5, D1–4, and E1–4; A6–8, 0.25 mm,  
364 also applied to B6–8, C6–8, D5–7, and E5–7.

365



366

367 Fig. 3 Quantitation of leucophore numbers in *sox10a*; *sox9b* and *sox10a*; *sox10b* double  
 368 homozygous mutants

369 Leucophores on the head and along the dorsal midline were counted for wild-type (WT),  
 370 *sox10a*; *sox9b* double mutants, and *sox10a*; *sox10b* double homozygous mutants.

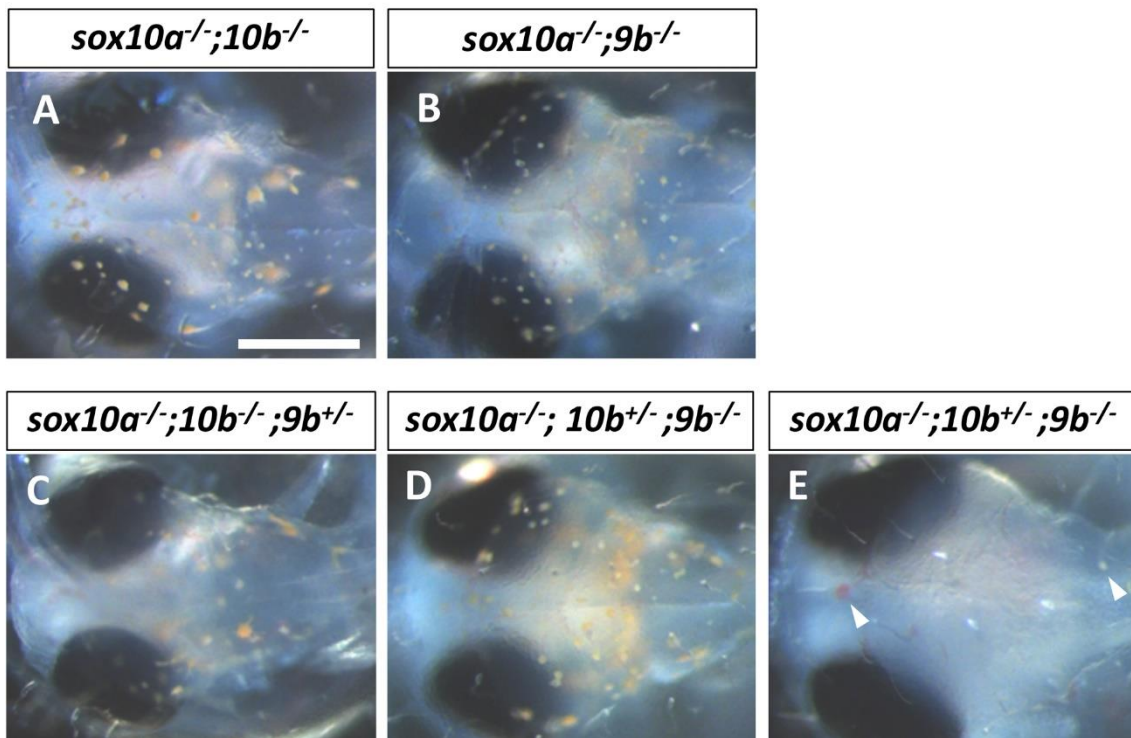
371 Compared to WT, the counts are significantly reduced in the *sox10a*; *sox9b* double  
 372 mutants ( $p = 0.0029319$ ), but not in the *sox10a*; *sox10b* double mutants ( $p = 0.7828484$ ).

373 Please note that the counts in *sox9b* single homozygous mutants are not significantly  
 374 different from those in WT ( $p = 0.1215848$ ). \*\*Significance was tested using one-way

375 ANOVA and Tukey HSD. Plot graphs were drawn using PRISM software (version 5).

376





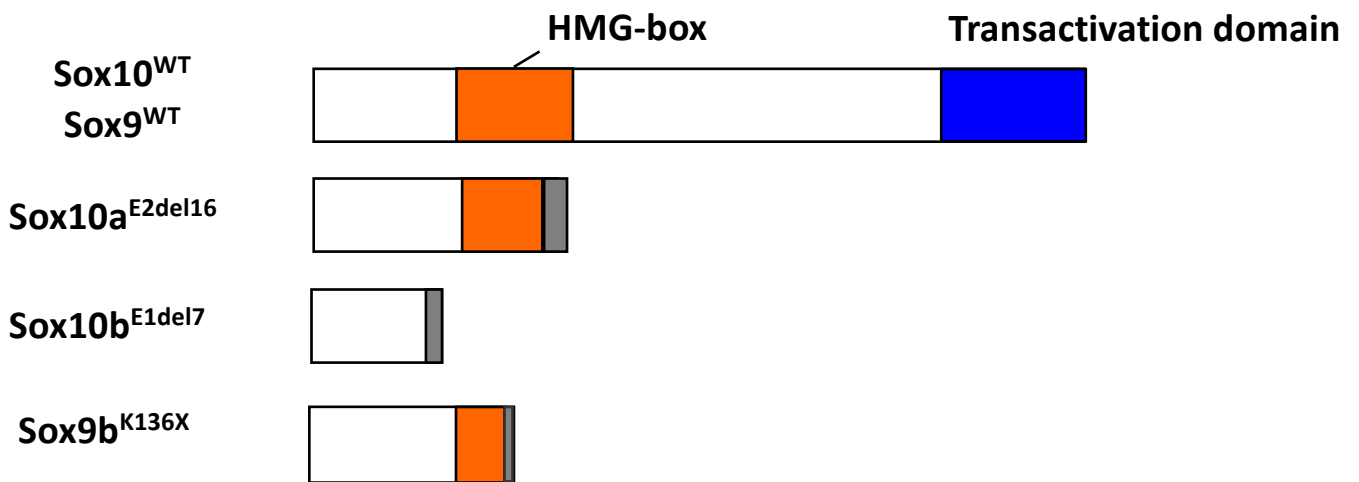
377

378 Fig. 4 Leucophore phenotype in the compound *sox10a*; *sox10b*; *sox9b* triple mutants  
 379 The 5-day post fertilization (dpf) embryos were obtained from *sox10a*; *sox10b*; *sox9b*  
 380 triple heterozygous parents. Those without melanophores, which are presumably at  
 381 least doubly homozygous for *soxE* mutations (*sox10a* and either *sox10b* or *sox9b*), were  
 382 photographed and genotyped. As previously described, most double mutants, *sox10a<sup>-/-</sup>*;  
 383 *sox10b<sup>-/-</sup>* (A) and *sox10a<sup>-/-</sup>*; *sox9b<sup>-/-</sup>* (B) have a considerable number of leucophores on  
 384 their heads. The *sox10a<sup>-/-</sup>*; *sox10b<sup>-/-</sup>*; *sox9b<sup>+/-</sup>* (C) and *sox10a<sup>-/-</sup>*; *sox10b<sup>+/-</sup>*; *sox9b<sup>-/-</sup>* (D)  
 385 compound mutants retained a few leucophores. In a few cases, *sox10a<sup>-/-</sup>*; *sox10b<sup>+/-</sup>*;  
 386 *sox9b<sup>-/-</sup>* embryos have little or no leucophores. The mutant in (E) has two leucophores  
 387 on the head (indicated by arrowheads). Importantly, there are no triple homozygous  
 388 survivors of *sox10a*, *sox10b*, and *sox9b* in the 2 dpf or 5 dpf offspring of the *sox10a*;  
 389 *sox10b*; *sox9b* triple heterozygous parents.

390 Notably, leucophores appear yellowish to orange at this stage.

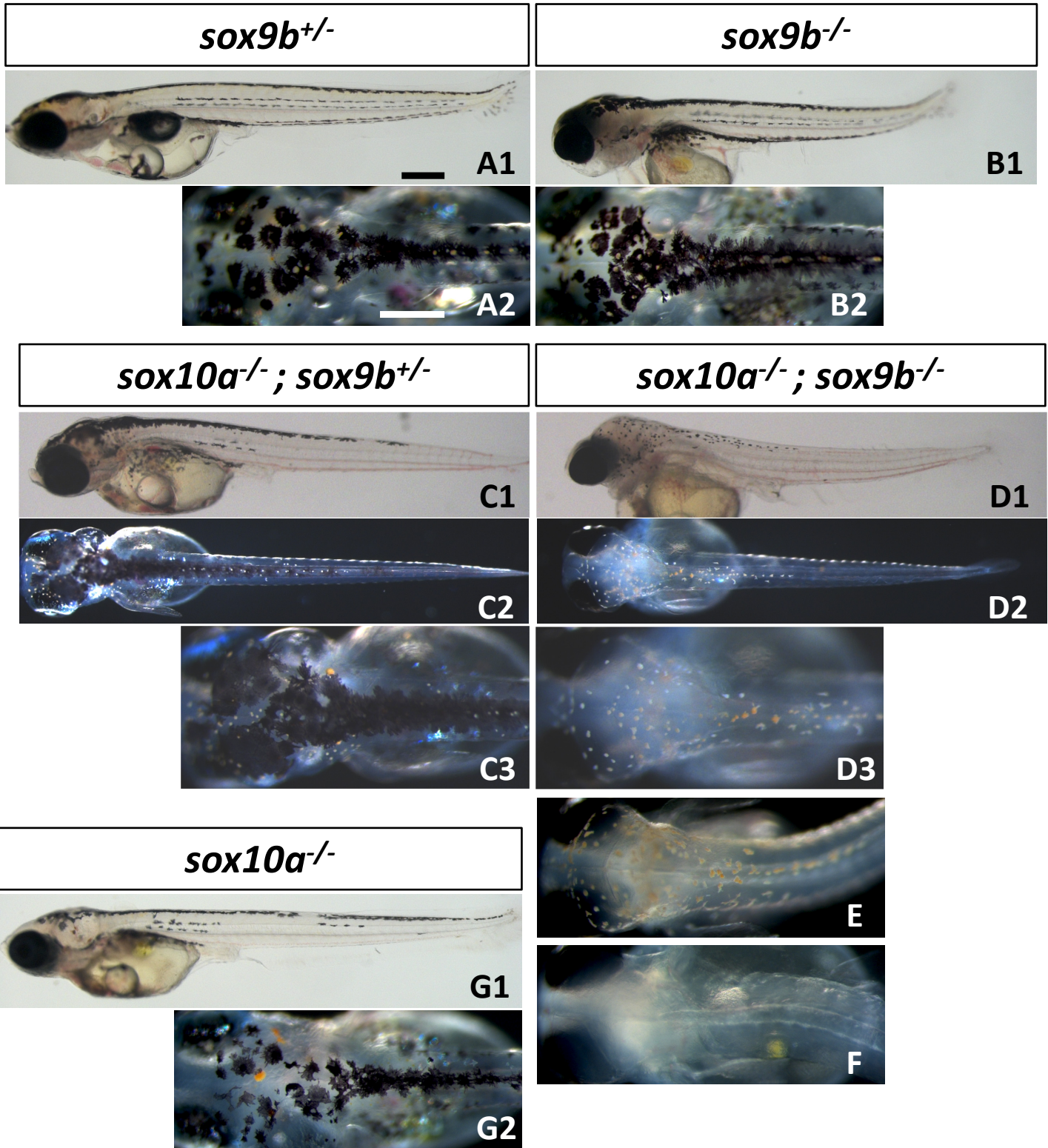
391 Scale bars: (A) 0.5 mm, also applied to B, C, D, and E.

392



Suppl. Fig. 1 Schematic of predicted primary structures of WT and mutant Sox9b, Sox10a and Sox10b proteins.

None of the mutant Sox proteins has a complete HMG-type DNA binding domain (red) nor a transactivation domain (blue). Gray box indicates a de novo amino acid sequence following the frame-shift due to the deletion or point mutation.



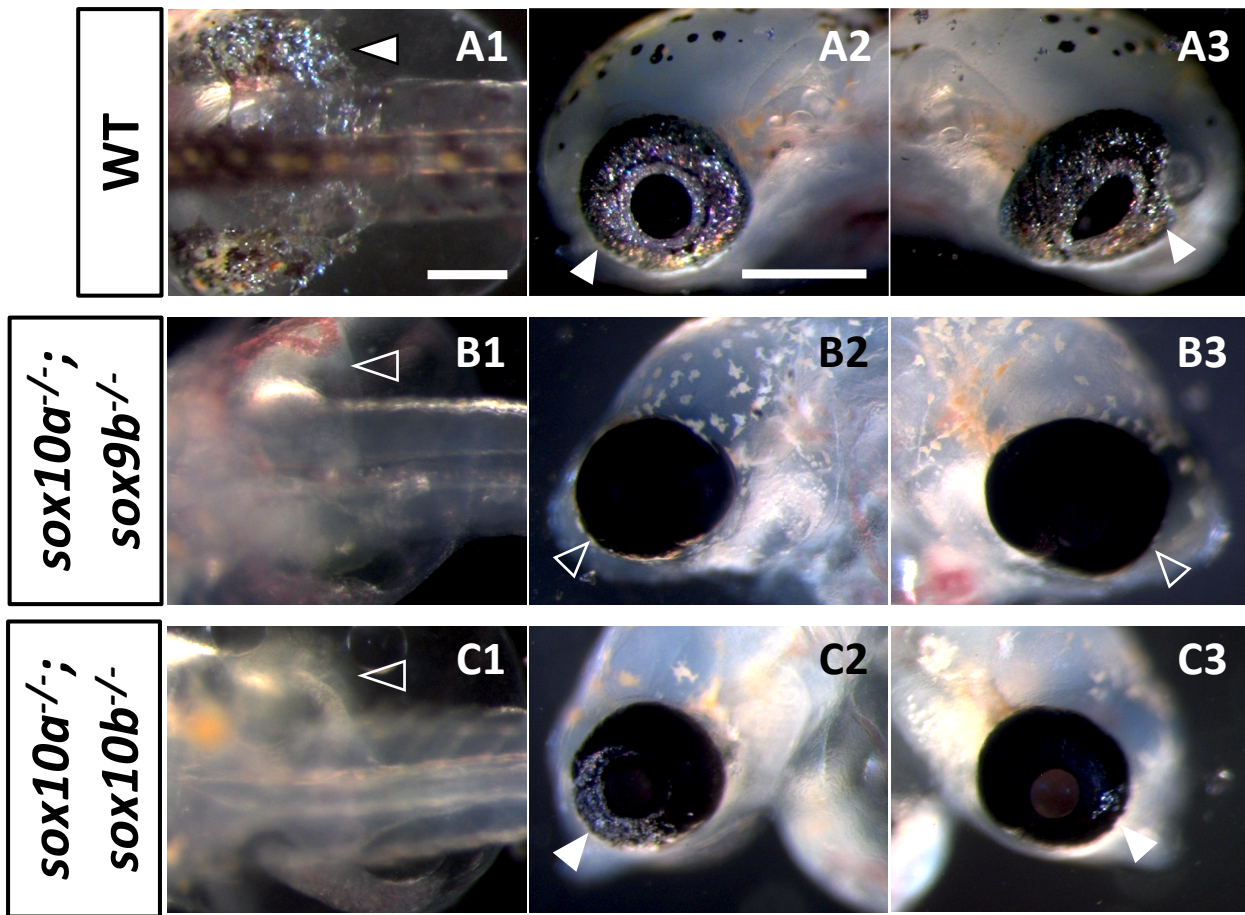
Suppl. Fig. 2 Phenotype in the compound *sox10a*; *sox9b* mutants (A1-A2) *sox9b*<sup>+/-</sup> mutant. (B1-B2) *sox9b*<sup>-/-</sup> mutant. (C1-C3) *sox10a*<sup>-/-</sup>; *sox9b*<sup>+/-</sup> mutant. (D1-D3, E, F) *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> mutants. (G1-G2) *sox10a*<sup>-/-</sup> mutant. 9dpf larva.

Pigmentation looks normal in *sox9b* heterozygote (A1, 2) and homozygote (B1, 2) while *sox9b* homozygote shows defective jaw formation and body elongation (B1).

In the *sox10a*<sup>-/-</sup>; *sox9b*<sup>+/-</sup> mutant, melanophores are mostly lost from the two ventral stripes (C1), and leucophores are reduced posteriorly in the tail region (C2, 3). In the *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> mutant, melanophores are completely absent (D1), and location of leucophores become severely shifted to the anterior (D2, 3). Two additional *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> mutants are shown: one retains abundant leucophores on the head (E) as also seen in the individual in D3, while the other has none of these (F), suggesting considerable variation in leucophore number (formation) in this genotype. Loss of *sox10a* alone results in partial but not complete absence of melanophores (G1, 2).

Please note that leucophores look yellowish to orange at this stage.

Scale bars: (A1-2) 0.5 mm, also applied to B1-2, C1-3, D1-3, E, F and G1-2.



Suppl. Fig. 3 Iridophore phenotype in *sox10a*; *sox9b* and *sox10a*; *sox10b* mutants (A1-A3) WT. (B1-B3) *sox10a*<sup>-/-</sup>; *sox9b*<sup>-/-</sup> mutant. (C1-C3) *sox10a*<sup>-/-</sup>; *sox10b*<sup>-/-</sup> mutant. Iridophores on the dorsal yolk (A1) are lost in the *sox10a*; *sox9b* (B1) and the *sox10a*; *sox10b* (C1) double homozygous mutants. Iridophores in the iris (A2, 3) are sometimes partially retained in the double homozygous mutants: almost complete absence in the *sox10a*; *sox9b* homozygote (B2, 3); partial retainment in the *sox10a*; *sox10b* homozygote (C2, 3). Compare these phenotypes with those in Fig.1 D4, E4.

White arrowheads indicate the presence of iridophores. White-outlined arrowheads indicate the absence of iridophores.

Please note that leucophores look yellowish to orange at this stage.

Scale bars: (A1) 0.25 mm, also applied to B1 and C1; (A2) 0.5 mm, also applied to A3, B2-3 and C2-3.

Supplementary Table 1. Summary of pigment cell phenotypes in *soxE* compound mutants

<i>sox10a</i>	<i>sox10b</i>	<i>sox9b</i>	Melanophore	Xanthophore	Iridophore	Leucophore
+/+	+/+	+/+	Forms three stripes (dorsal, lateral, and ventral) in the trunk; dorsally in the head	Dorso-laterally scattered over the trunk; dorsally in the head	On the dorsal surface over the yolk sac; in the iris	Along the trunk dorsal midline; dorsally in the head
+/+	+/+	-/-				
+/+	-/-	+/+				
+/+	-/-	-/-				
-/-	+/+	+/+	Severely reduced in the lateral and ventral stripes; more severely reduced in the posterior body; relatively unaffected in the head	Reduced in the posterior body; relatively unaffected in the head	Apparently unaffected	Reduced in the posterior body; relatively increased in the head
-/-	-/-	+/+	Absent	Absent	Absent from the yolk sac; absent or a few in the iris	Nearly absent from the trunk; increased in the head
-/-	+/+	-/-	Absent	Absent	Absent from the yolk sac; absent or a few in the iris	Nearly absent from the trunk; increased in the head Note that the total leucophore number is significantly smaller than that in the above genotype ( <i>sox10a</i> <sup>-/-</sup> ; <i>sox10b</i> <sup>-/-</sup> ; <i>sox9b</i> <sup>+/+</sup> ).

The wild-type phenotypes and locations of pigment cells focused on in this study (at 7 days post fertilization, hatching stage) are shown in the second row.