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Corrigendum

Corrigendum to “A molecular analysis of neurogenic placode and cranial sensory ganglion development in the shark, *Scyliorhinus canicula*” [Dev. Biol. 304 (2007) 156–181]

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It has come to the attention of the authors that, owing to a computer file mix-up, the partial cDNA sequence submitted to GenBank as *Scyliorhinus canicula Eya4* (accession number EF185886) was incorrect. Although the text of the article and the *Eya4* expression data are unaffected, this sequence was used to prepare the *Eya4*-related information presented in [Fig. 1](#), [Tables 1 and 2](#), and [Supplementary Fig. 5](#). The GenBank submission has been corrected (accession number EF185886.2) and corrected versions of the above-named figures and tables are provided here. The authors sincerely apologise for this mistake and for any inconvenience this may have caused.

The authors would like to acknowledge the invaluable assistance of James Blundell in preparing the corrected figures and tables.

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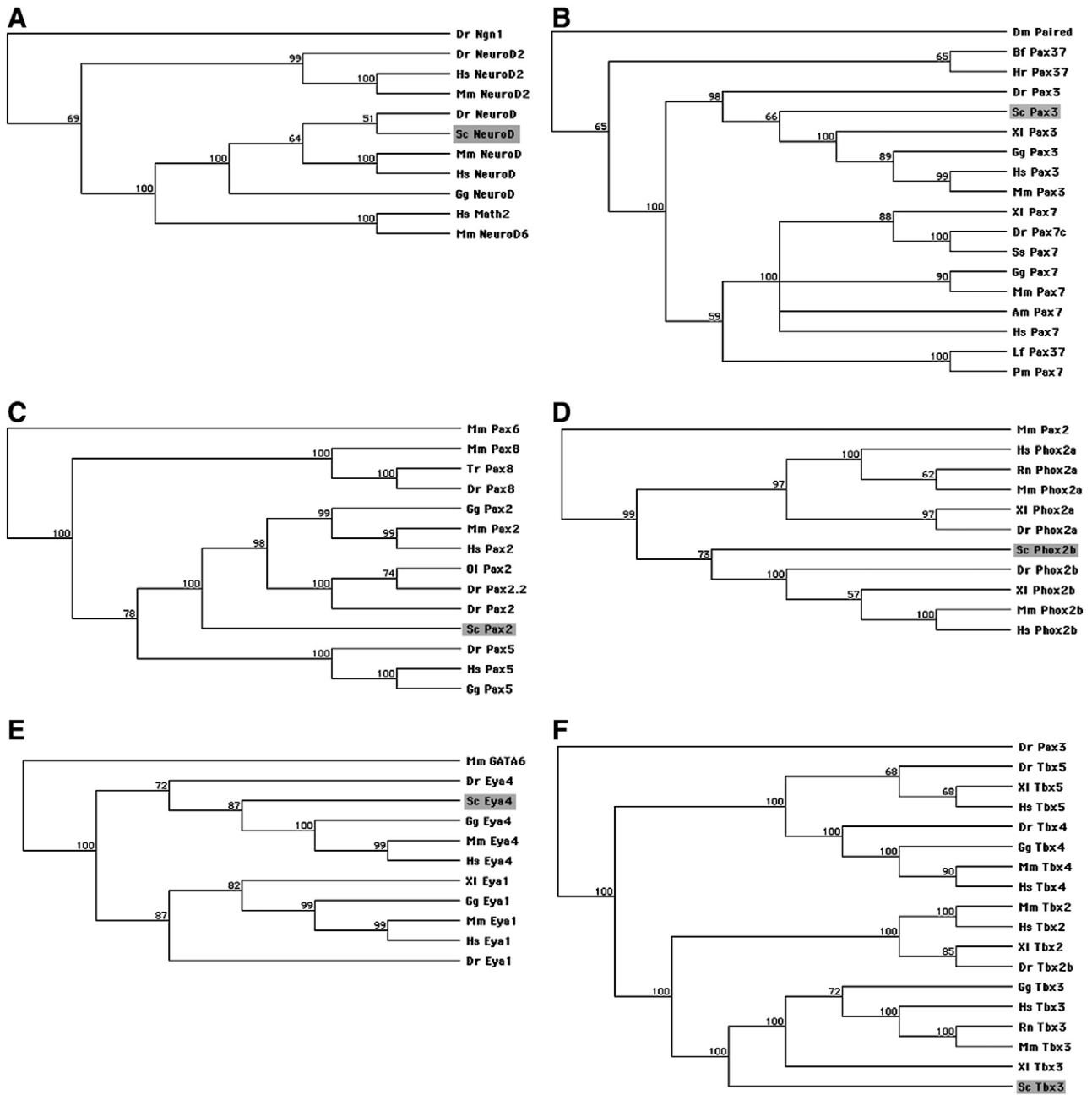


Fig. 1. Phylogenetic trees, constructed in MacVector using the neighbor-joining method, of predicted protein sequences confirming the identity of cloned fragments of six *S. canicula* transcription factors (shaded box in each tree). Figures adjacent to nodes indicate percentage bootstrap support values. (A) NeuroD. (B) Pax3. (C) Pax2. (D) Phox2b. (E) Eya4. (F) Tbx3. Species abbreviations: Am, *Ambystoma mexicanum*; Bf, *Branchiostoma floridae*; Cf, *Canis familiaris*; Ci, *Ciona intestinalis*; Dm, *Drosophila melanogaster*; Dr, *Danio rerio*; Fr, *Fugu rubripes*; Gg, *Gallus gallus*; Hr, *Halocynthia roretzi*; Hs, *Homo sapiens*; Lf, *Lampetra fluviatilis*; Mm, *Mus musculus*; Ol, *Oryzias latipes*; Pm, *Petromyzon marinus*; Rn, *Rattus norvegicus*; Sc, *Scyliorhinus canicula*; Ss, *Salmo salar*; Tr, *Takifugu rubripes*; Xl, *Xenopus laevis*.

