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Corrigendum

Corrigendum to "A novel salmonid myoD gene is distinctly regulated during development and probably arose by duplication after the genome tetraploidization" [FEBS Lett. 580 (2006) 4996–5002]^{\Leftrightarrow}

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An unfortunate mistake occurred when preparing Fig. 1 and Supplementary information Fig. 1. The regions highlighted as basic and helix–loop–helix were incorrectly placed. Fig. 1 and Supplementary information Fig. 1 are shown correctly below with original legends.

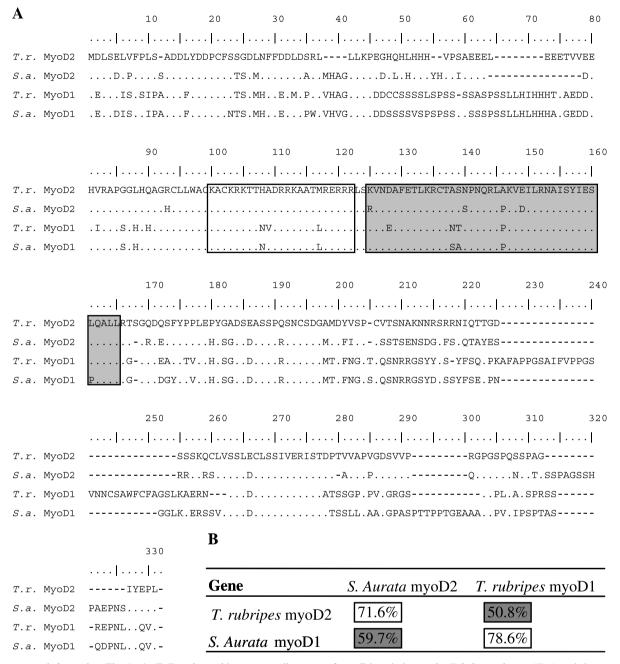
	10 20 30 40 50 60 70
smyoDlc tmyoDlc btmyoDlc smyoDlb tmyoDlb smyoDla tmyoDla	I Y I Y I Y I
	LYY
smyoDlc tmyoDlc btmyoDlc smyoDlb tmyoDlb smyoDla tmyoDla	80 90 100 110 120 130 140 WACKACKRKTTNTDRRKAATMRERRRLG KVNDAFENLKRCTSNNPNORLPKVEILRNAISYIESLQSLLR
smyoDlc tmyoDlc btmyoDlc smyoDlb tmyoDlb smyoDla tmyoDla	150 160 170 180 190 200 210 GQDGE-NYYPSLEHYNGDSDASSPRSNCSDGMMEYNAPTCTSARRSSYESSYFAETPNADARSKKNAVIS
smyoDlc tmyoDlc btmyoDlc smyoDlb tmyoDlb smyoDla tmyoDla	220 230 240 250 260 270 280

Fig. 1. Amino acid alignment of smyoD1c (DQ317527), tmyoD1c (EST: CX137438), btmyoD1c (DQ366710), smyoD1b (AJ557150), tmyoD1b (TmyoD2) (Z46924), smyoD1a (AJ557148), and tmyoD1a (TmyoD1) (Z46924). Amino acid sequences identical to smyoD1c are indicated by a dot. Gaps are shown as a dash. Stars identify identical sequences globally and colons represent conserved amino acid substitutions. The basic (light grey) and helix–loop–helix (dark grey) domains are shown.

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Supplementary information Fig. 1. A. Full amino acid sequence alignment of myoD2 orthologues in *Takifugu rubripes (T.r.)* and *Sparus aurata* (*S.a.*) with their myoD1 paralogues. Accession numbers are: *T.r.* myoD2 (NM_001040062), *S.a.* myoD2 (AF478569), *T.r.* myoD1 (AY445316) and *S.a.* myoD1 (AF478568). The basic (white boxes) and HLH domains (grey boxes) are shown. B. Percentage identities of the same sequences as in A. Note that paralogues are more dissimilar than orthologues (grey and white boxes, respectively). Sequences were aligned using emboss:needle and the Blosum62 matrix (http://www.ebi.ac.uk/emboss/align/).