

Table S1: AVTRV and ITR sequences used in phylogenetic analyses and sequences

Fish species	Genes	Sequence ID	Fish species	Genes	Sequence ID
<i>Dicentrarchus labrax</i>	V2B1	DLAgn_00092800	<i>Lepisosteus oculatus</i>	ITR	ENSDARP00000050113_1
	V2B2	DLAgn_00089180		V2B	ENSLACP00000015306_1
	V2A1	DLAgn_00131190		V1A	ENSGACP00000004706_1
	V2A2	DLAgn_00125320		V2A	ENSGACP00000014075_1
	V1A1	DLAgn_00209950	<i>Gallus gallus</i>	V2C	JH591411.1
	V1A2	DLAgn_00170900		V2C	ENSGALG00000009497
	V2C	DLAgn_00207720		V1A	ENSGALG00000009808
	ITR1	DLAgn_00093190		OTR	ENSGALG00000003138
	ITR2	DLAgn_00093990		V1B	ENSGALG00000000788
<i>Oreochromis niloticus</i>	V1Aa	XM_003443925.5		V2C	ENSMGAG00000009257
	V2A1	XM_003448162.5	<i>Danio rerio</i>	V2C	ENSDARG00000076690
	V2B2	XM_003442789.5		ITR1	ENSDARG00000033956
	V2B1	XM_025907435.1		V2B	ENSDARG00000076797
	ITR1	XM_003441444.5		ITR2	ENSDARG00000044175
	ITR2	XM_003448399.3		V2A1	ENSDARG00000029219
				V2A2	ENSDARG0000007436
<i>Gasterosteus aculeatus</i>	V2C	ENSGACG00000018884	<i>Latimeria chalumnae</i>	V1Aa	ENSDARG00000077083
	V2A1	ENSGACG00000008681		ITR	ENSLACG00000018362
	V2A2	ENSGACG00000010636		V1B	ENSLACG00000013680
	V1Aa	ENSGACG00000003589		V1A	ENSLACG00000014523
	V1Ab	ENSGACG00000000737		V2A	ENSLACG00000014898
	V2B	ENSGACG00000000754		V2B	ENSLACG00000013474
	ITR1	ENSGACG00000000914	<i>Oryzias latipes</i>	ITR1	ENSORLGG00000000719
<i>Xiphophorus maculatus</i>	V1Aa	ENSXMAG00000017820		V2B	ENSORLGG00000001494
	ITR2	ENSXMAG00000016299		ITR2	ENSORLGG00000003297
	ITR1	ENSXMAG00000001524		V1Aa	ENSORLGG00000002126
	V2A1	ENSXMAG00000010783		V2A1	ENSORLGG00000007088
	V2A2	ENSXMAG00000009554		V2A2	ENSORLGG00000016671
	V2C	ENSXMAG00000009218		V1Ab	ENSORLGG00000017245
	V2B(1)	ENSXMAG00000001906	<i>Takifugu rubripes</i>	V2B	ENSTRUG00000001010
	V2B(2)	ENSXMAG00000002230		V2A2	ENSTRUG00000000643
<i>Anolis carolinensis</i>	V2A	ENSACAG000000021016		V2A1	ENSTRUG000000015164
	V2C	ENSACAG000000000005		V1Ab	ENSTRUG000000016314
	V1A	ENSACAG000000000443		V1Aa	ENSTRUG000000006025
	V1B	ENSACAG000000012849			

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<i>Anolis carolinensis</i>	OTR	ENSACAG00000011241	<i>Takifugu rubripes</i>	ITR2	SINFRUG00000140687
<i>Xenopus tropicalis</i>	OTR	ENSXETG00000001441		ITR1	ENSTRUG00000003223
	V2A	ENSXETG000000014233	<i>Mus musculus</i>	OTR	ENSMUSG000000049112
	V2C	ENSXETG000000015741		V1A	ENSMUSG000000020123
	V1A	ENSXETG000000018781		V2A	ENSMUSG000000031390
	V1B	ENSXETG000000005930		V1B	ENSMUSG000000026432
<i>Homo sapiens</i>	V1B	ENSG00000198049	<i>Ciona intestinalis</i>	VPR	ENSCING000000006620
	OTR	ENSG00000180914	<i>Octopus vulgaris</i>	OPR	AB158496.1
	V1A	ENSG00000166148		CTR1	AB158493.1
	V2A	ENSG00000126895		CTR2	AB158495.1

Fig. S1 Sequence logos in selected regions of mammalian and fish V1a/V1a1 compared to *D. labrax* V1a1 (first two lines), mammalian and fish V1a/V1a2 compared to *D. labrax* V1a2 (third and fourth line) and mammalian and fish OTR/ITR1 compared to *D. labrax* ITR1. Black asterisks indicate putative OXT/AVP ligand binding amino acids in mammalian receptors (Chini and Fanelli, 2000; Koehbach et al., 2013). Red asterisks indicate important residues for AVT binding (Acharjee et al., 2004; Chini and Fanelli, 2000). Red boxes show important residues for oxytocin ligand selectivity, binding and signaling (Koehbach et al., 2013). Green boxes show amino acid differences between *D. labrax* V1a1 and V1a2. Sequence numbering corresponds to the human OXTR sequence (Accession no. NP_001341583.1).

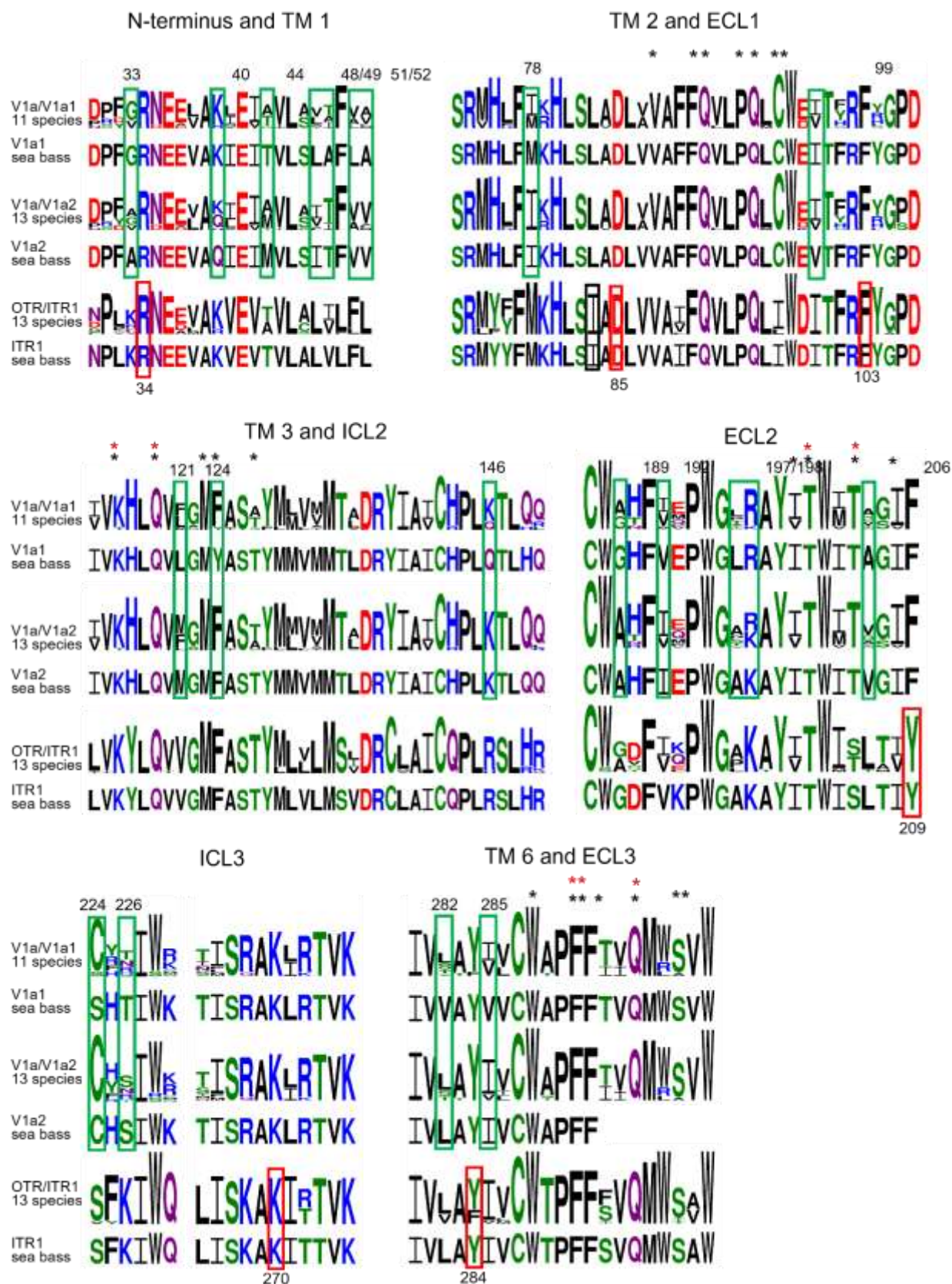


Fig. S2 Relative *avtrv2b2*, *avtrv2a2*, *avtrvc* and *itr2* mRNA expression were measured in the anterior intestines of Mediterranean (M) and Atlantic (A) European sea bass maintained in seawater (SW) and hypersaline water (HW). Different letters denote significant differences between groups (two-way ANOVA followed by Tukey's test, $P < 0.05$, $N = 11$). Data are represented as the median, first and third quartile (box), minimum and maximum values.

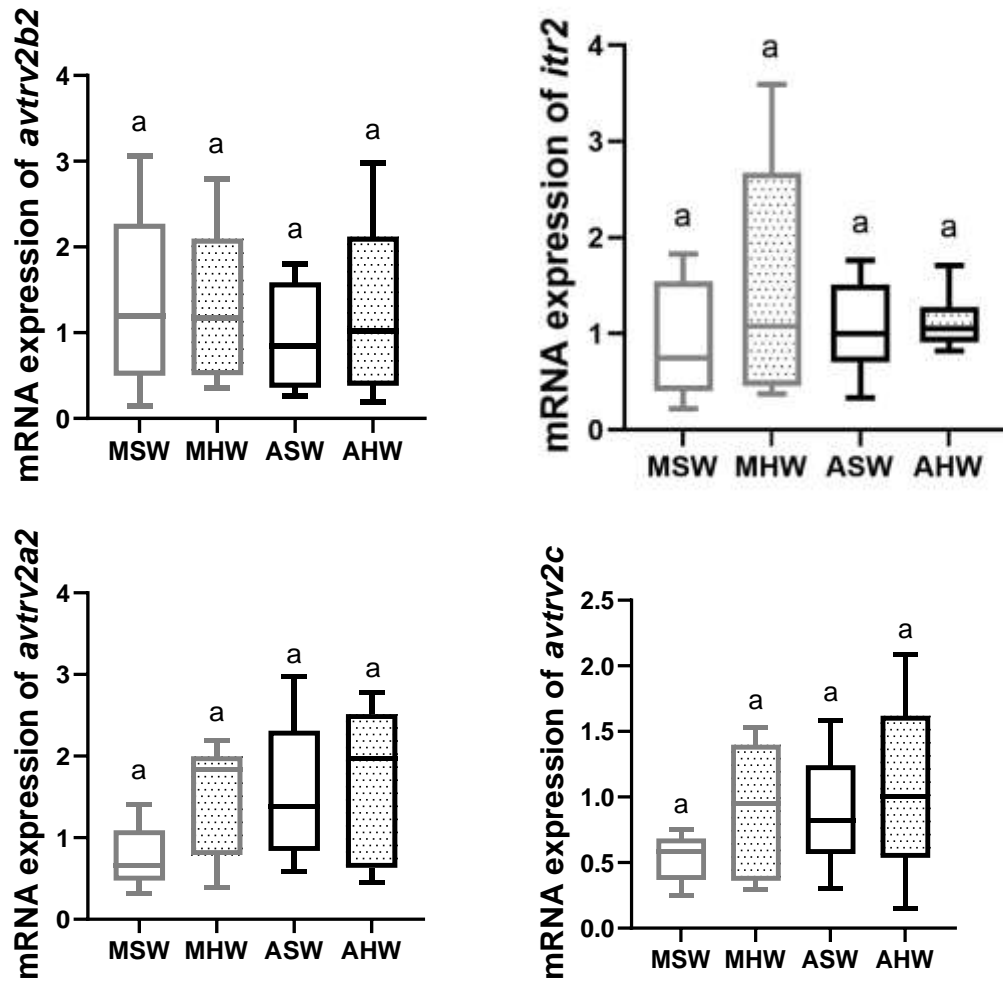


Fig. S3 Relative *avtrv2a1*, *avtrv2a2*, *avtrv2b2*, *avtrv2c* and *itr2* mRNA expression were measured in the posterior intestines of Mediterranean (M) and Atlantic (A) European sea bass maintained in seawater (SW) and hypersaline water (HW). Different letters denote significant differences between groups (two-way ANOVA followed by Tukey's test, $P < 0.05$, $N = 11$). Data are represented as the median, first and third quartile (box), minimum and maximum values.

