

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	<i>DLAgn_00092800</i>	<i>Lepisosteus oculatus</i>	ITR	<i>ENSDARP00000050113_1</i>
	V2B2	<i>DLAgn_00089180</i>		V2B	<i>ENSLACP00000015306_1</i>
	V2A1	<i>DLAgn_00131190</i>		V1A	<i>ENSGACP00000004706_1</i>
	V2A2	<i>DLAgn_00125320</i>		V2A	<i>ENSGACP00000014075_1</i>
	V1A1	<i>DLAgn_00209950</i>		V2C	<i>JH591411.1</i>
	V1A2	<i>DLAgn_00170900</i>		<i>Gallus gallus</i>	<i>ENSGALG00000009497</i>
	V2C	<i>DLAgn_00207720</i>		V1A	<i>ENSGALG00000009808</i>
	ITR1	<i>DLAgn_00093190</i>		OTR	<i>ENSGALG00000003138</i>
	ITR2	<i>DLAgn_00093990</i>		V1B	<i>ENSGALG00000000788</i>
<i>Oreochromis niloticus</i>	V1Aa	<i>XM_003443925.5</i>	<i>Danio rerio</i>	V2C	<i>ENSMGAG00000009257</i>
	V2A1	<i>XM_003448162.5</i>		V2C	<i>ENSDARG00000076690</i>
	V2B2	<i>XM_003442789.5</i>		ITR1	<i>ENSDARG00000033956</i>
	V2B1	<i>XM_025907435.1</i>		V2B	<i>ENSDARG00000076797</i>
	ITR1	<i>XM_003441444.5</i>		ITR2	<i>ENSDARG00000044175</i>
	ITR2	<i>XM_003448399.3</i>		V2A1	<i>ENSDARG00000029219</i>
<i>Gasterosteus aculeatus</i>	V2C	<i>ENSGACG00000018884</i>	<i>Latimeria chalumnae</i>	V2A2	<i>ENSDARG00000007436</i>
	V2A1	<i>ENSGACG00000008681</i>		V1Aa	<i>ENSDARG00000077083</i>
	V2A2	<i>ENSGACG00000010636</i>		ITR	<i>ENSLACG00000018362</i>
	V1Aa	<i>ENSGACG00000003589</i>		V1B	<i>ENSLACG00000013680</i>
	V1Ab	<i>ENSGACG00000000737</i>		V1A	<i>ENSLACG00000014523</i>
	V2B	<i>ENSGACG00000000754</i>		V2A	<i>ENSLACG00000014898</i>
	ITR1	<i>ENSGACG00000000914</i>		V2B	<i>ENSLACG00000013474</i>
<i>Xiphophorus maculatus</i>	V1Aa	<i>ENSXMAG00000017820</i>	<i>Oryzias latipes</i>	ITR1	<i>ENSORLG00000000719</i>
	ITR2	<i>ENSXMAG00000016299</i>		V2B	<i>ENSORLG00000001494</i>
	ITR1	<i>ENSXMAG00000001524</i>		ITR2	<i>ENSORLG00000003297</i>
	V2A1	<i>ENSXMAG00000010783</i>		V1Aa	<i>ENSORLG00000002126</i>
	V2A2	<i>ENSXMAG00000009554</i>		V2A1	<i>ENSORLG00000007088</i>
	V2C	<i>ENSXMAG00000009218</i>		V2A2	<i>ENSORLG00000016671</i>
	V2B(1)	<i>ENSXMAG00000001906</i>		V1Ab	<i>ENSORLG00000017245</i>
	V2B(2)	<i>ENSXMAG00000002230</i>		Takifugu rubripes	<i>ENSTRUG00000001010</i>
<i>Anolis carolinensis</i>	V2A	<i>ENSACAG00000021016</i>		V2A2	<i>ENSTRUG0000000643</i>
	V2C	<i>ENSACAG00000000005</i>		V2A1	<i>ENSTRUG00000015164</i>
	V1A	<i>ENSACAG0000000443</i>		V1Ab	<i>ENSTRUG00000016314</i>
	V1B	<i>ENSACAG00000012849</i>		V1Aa	<i>ENSTRUG00000006025</i>

Fish species	Genes	Sequence ID	Fish species	Genes	Sequence ID
<i>Anolis carolinensis</i>	OTR	<i>ENSACAG00000011241</i>	<i>Takifugu rubripes</i>	ITR2	<i>SINFRUG00000140687</i>
<i>Xenopus tropicalis</i>	OTR	<i>ENSXETG0000001441</i>		ITR1	<i>ENSTRUG0000003223</i>
	V2A	<i>ENSXETG00000014233</i>	<i>Mus musculus</i>	OTR	<i>ENSMUSG00000049112</i>
	V2C	<i>ENSXETG00000015741</i>		V1A	<i>ENSMUSG00000020123</i>
	V1A	<i>ENSXETG00000018781</i>		V2A	<i>ENSMUSG00000031390</i>
	V1B	<i>ENSXETG00000005930</i>		V1B	<i>ENSMUSG00000026432</i>
<i>Homo sapiens</i>	V1B	<i>ENSG00000198049</i>	<i>Ciona intestinalis</i>	VPR	<i>ENSCING0000006620</i>
	OTR	<i>ENSG00000180914</i>	<i>Octopus vulgaris</i>	OPR	<i>AB158496.1</i>
	V1A	<i>ENSG00000166148</i>		CTR1	<i>AB158493.1</i>
	V2A	<i>ENSG00000126895</i>		CTR2	<i>AB158495.1</i>

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).

### N-terminus and TM 1

33	40	44	48/49	51/52
V1a/V1a1 11 species	DPFGRNEEVAKIEITAVLALTFXO			
V1a1 sea bass	DPFGRNEEVAKIEITAVLALFA			
V1a/V1a2 13 species	DPFGRNEEVAKIEITAVLALTFV			
V1a2 sea bass	DPFGRNEEVAKIEITAVLALTFV			
OTR/ITR1 13 species	NPLKRNEEVAKVEVAVLALVLFL			
ITR1 sea bass	NPLKRNEEVAKVEVTVLALVLFL			
	34			

### TM 2 and ECL1

78	*	**	***	99
SRMHLFMKHLSLADLxVAFFQVLPQLC	EV	IT	FR	YYPD
SRMHLFMKHLSLADLVVAFFQVLPQLC	WE	IT	FR	YYPD
SRMHLFMKHLSLADLxVAFFQVLPQLC	EV	IT	FR	YYPD
SRMHLFMKHLSLADLVVAFFQVLPQLC	WE	IT	FR	YYPD
SRMYYFMKHLSIAVVAFQVLPQLI	DIT	FR	YYPD	
SRMYYFMKHLSIAVVAFQVLPQLI	DIT	FR	YYPD	
	85			103

### TM 3 and ICL2

* * 121 124 *	146			
V1a/V1a1 11 species	TKHLQVEGMFASTYMLMMTLDRYIAICHPLKTLQQ			
V1a1 sea bass	IVKHLQVLMGMFASTYMMVMMTLDRYIAICHPLKTLHQ			
V1a/V1a2 13 species	TKHLQVEGMFASTYMLMMTLDRYIAICHPLKTLQQ			
V1a2 sea bass	IVKHLQVLMGMFASTYMMVMMTLDRYIAICHPLKTLQQ			
OTR/ITR1 13 species	LVKYLQVVGMFASTYMLMMTS DRCLAI CQPLRSLSHR			
ITR1 sea bass	LVKYLQVVGMFASTYMLVMSVDRCLAI CQPLRSLSHR			

### ECL2

189 190 197 198 *	*	*	206							
CW	AHFTEP	PGRAY	T	T	GIF					
CW	GHFTEP	WGLRAY	IT	WT	AGIF					
CW	AHFTEP	PGRAY	T	T	GIF					
CW	AHFTEP	WGAKAY	IT	WT	VGIF					
CW	GDFK	P	GA	Y	T	T	S	I	T	Y
CW	GDFVKP	WGAKAY	IT	WT	S	L	T			

### ICL3

224 226				
V1a/V1a1 11 species	CYTIVL	TSRAKLRTVK		
V1a1 sea bass	SHTIWK	TISRAKLRTVK		
V1a/V1a2 13 species	CYTIVL	TSRAKLRTVK		
V1a2 sea bass	CHSIWK	TISRAKLRTVK		
OTR/ITR1 13 species	SFKIWQ	LISKAKIRTVK		
ITR1 sea bass	SFKIWQ	LISKAKITTVK		
	270			

### TM 6 and ECL3

282 285 *	**	***	*	**			
IV	Y	T	V	APFF	TyQMW	Sv	
IV	Y	WV	C	APFF	TVQM	W	
IV	Y	T	V	APFF	TyQMW	Sv	
IV	Y	T	V	C	TPFF	FVQM	S
IV	Y	T	V	C	TPFF	FVQM	S
IV	Y	T	V	C	TPFF	SVQM	SAW

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.

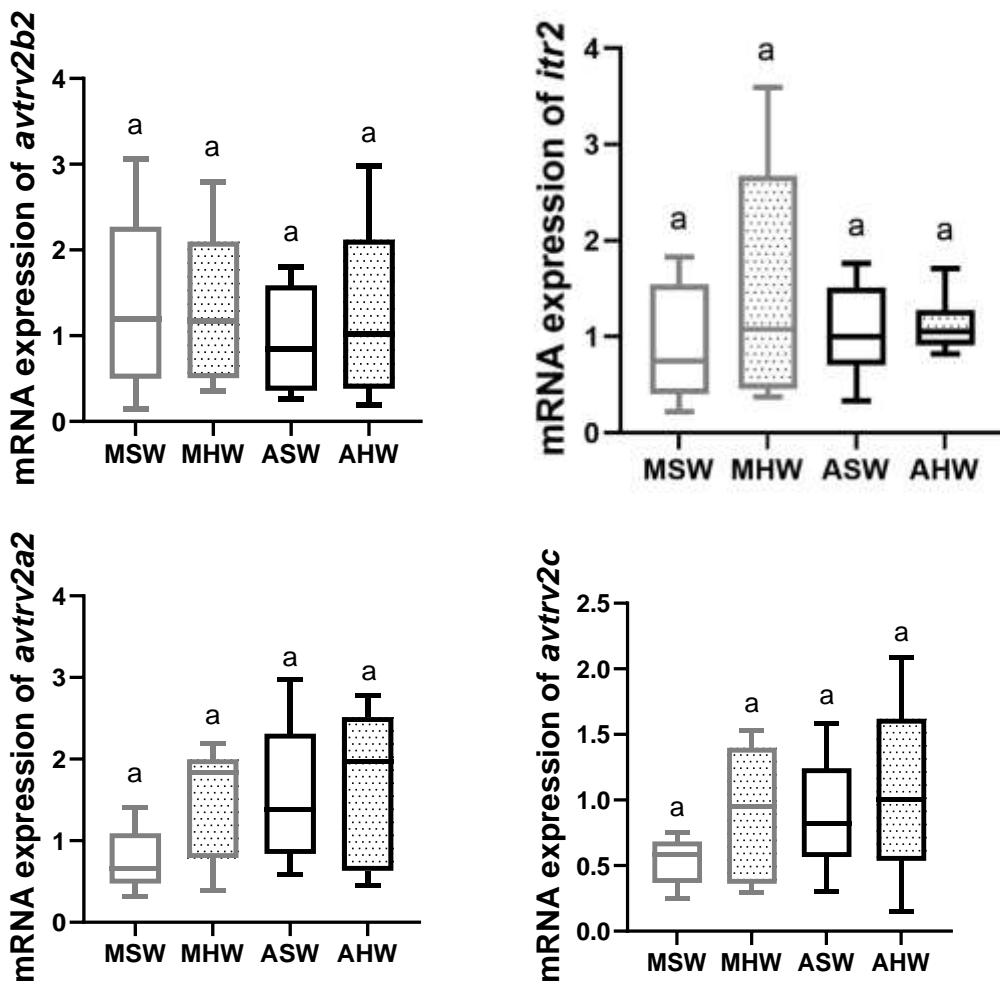


Fig. S3 Relative *avtrv2a1*, *avtrv2a2*, *avtrv2b2*, *avtrv2c* and *itr2* mRNA expression were measured in the posterior intestines of Mediterranean (M) and Atlantic (A) European sea bass maintained in seawater (SW) and hypersaline water (HW). Different letters denote significant differences between 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.

