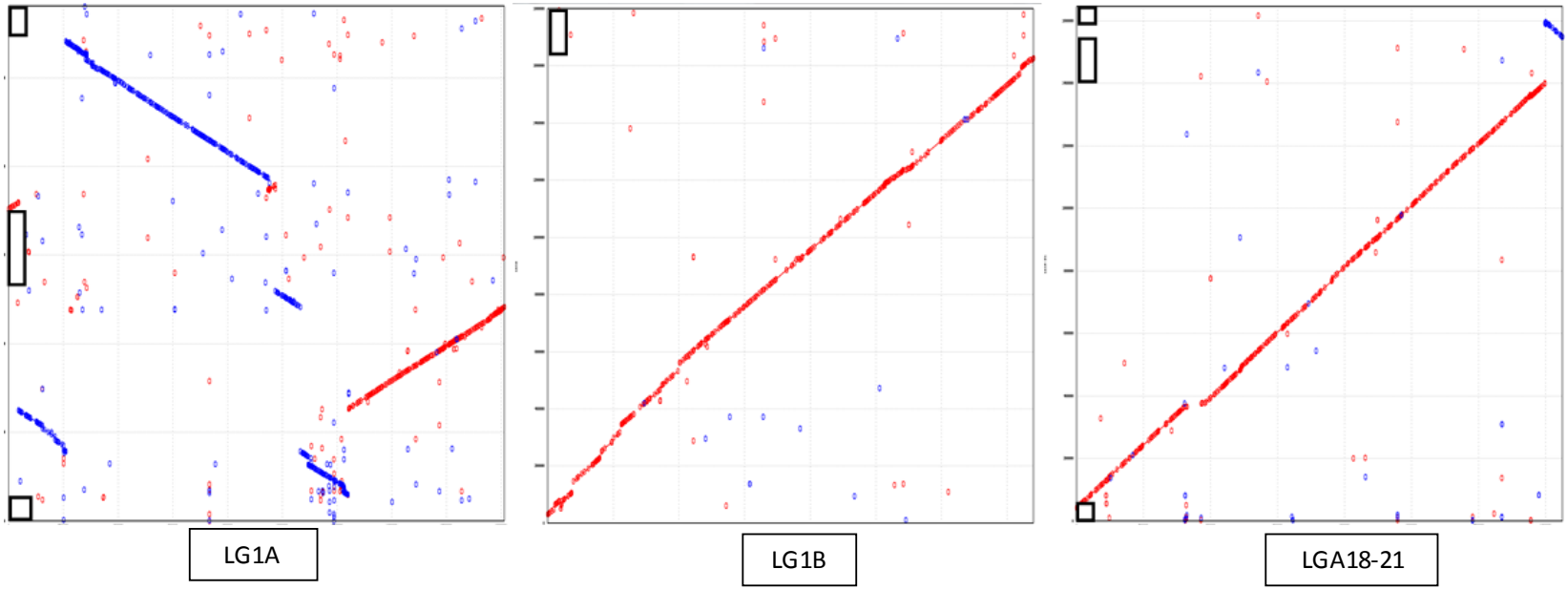
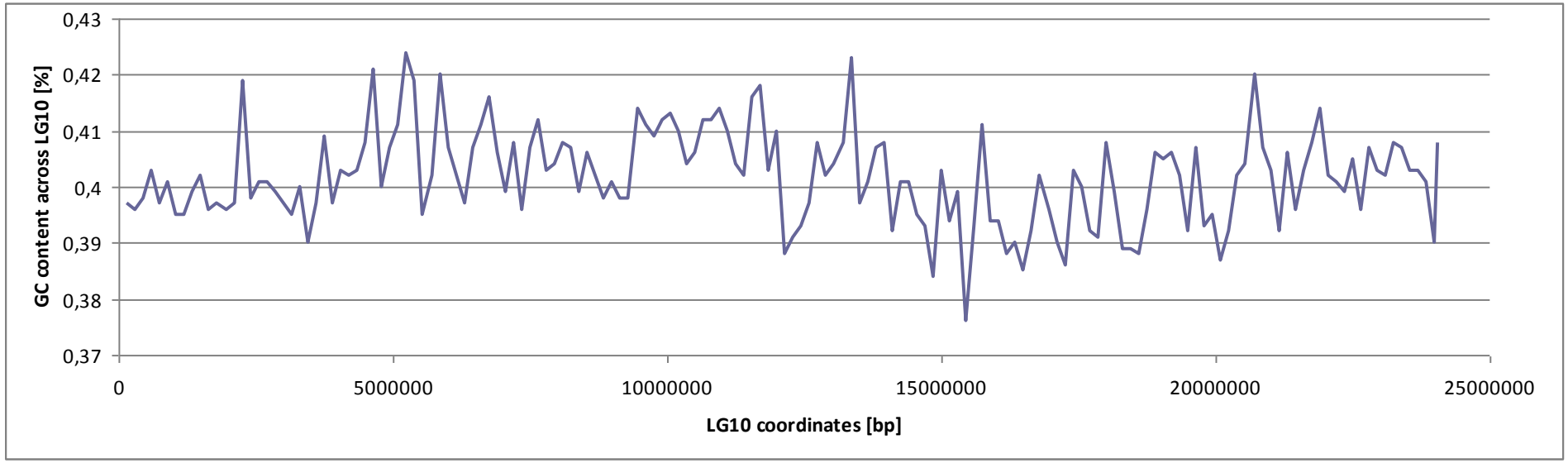
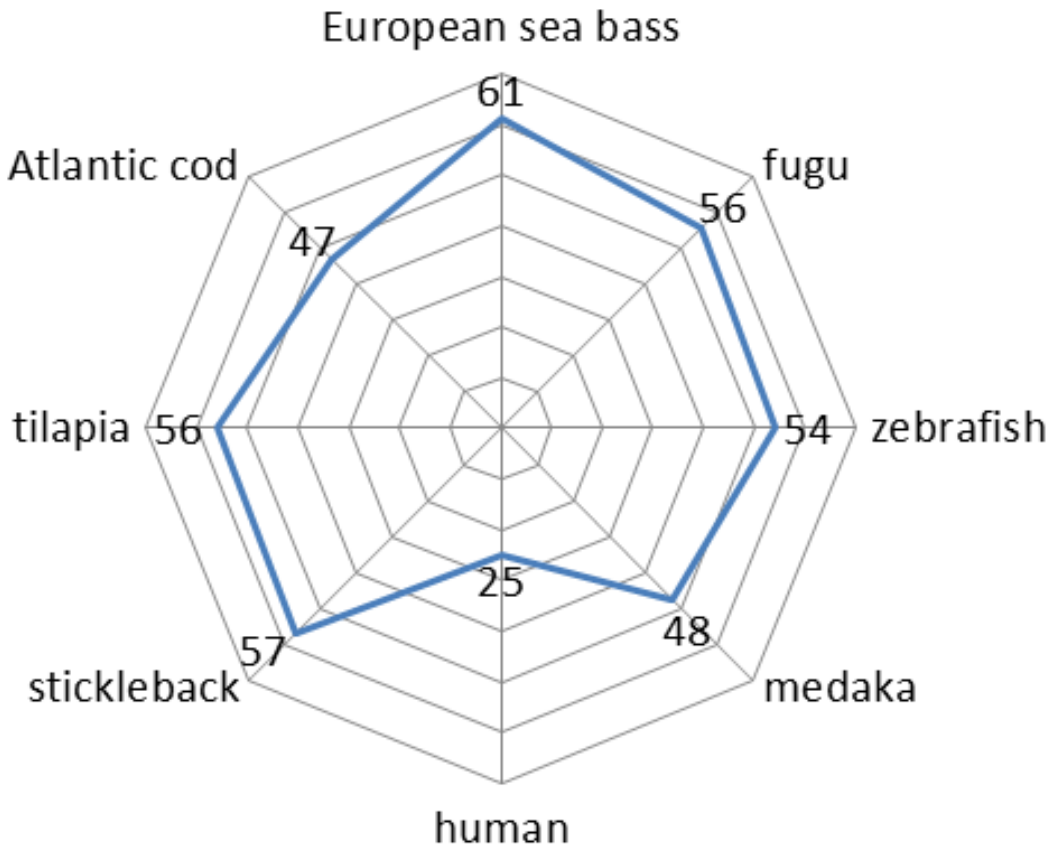
Supplementary Figures



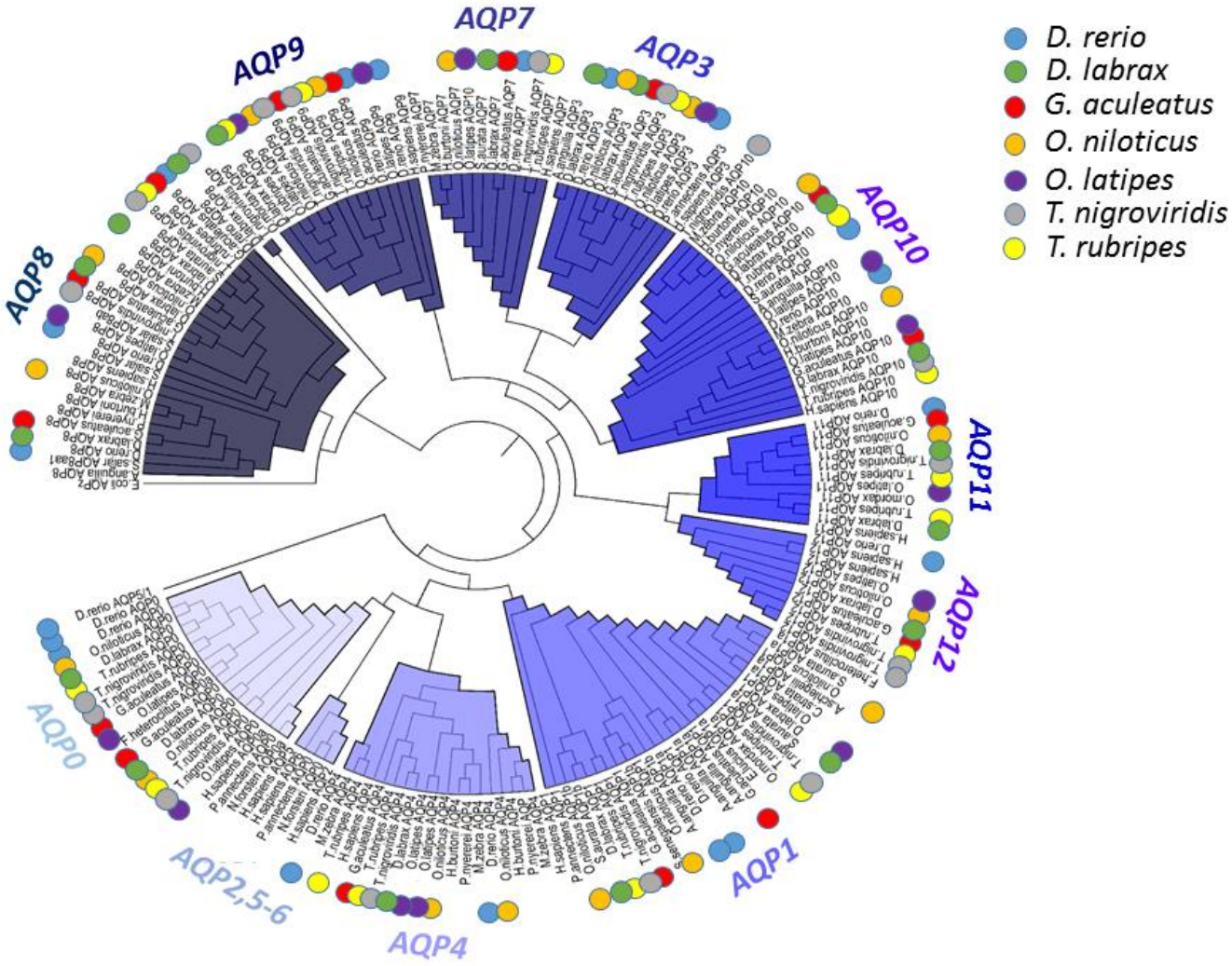
Supplementary Figure 1: Comparison of the new chromosomal sequences to the old version assembly of 3 chromosomes produced by the BAC mapping approach. By comparing the sequences from the BAC and the WGS approach for the three seabass chromosomes that have been sequenced by mapping BAC-ES to the *G. aculeatus* genome, we found that two of them have been similarly assembled between the BAC and the WGS approach (LG1B and LG18-21). Interestingly, all chromosomal groups assembled from the WGS data have more contig sequence assigned to the chromosome (rectangles at the chromosome vertical axis of the plots) in comparison to the BAC approach, which is due to the fact that gaps in the comparative BAC map resulted in sequencing gaps. For LG1A, the differences in long-range continuity between BAC and WGS strategy might be due to a long gap in the comparative BAC map in the middle of the chromosome that led to scaffolding problems. The missing sequence in this region maps to a megabase sized, unordered piece of the *G. aculeatus* genome named “scaffold_27”. Therefore, BAC clones mapping to this region were not included in the chromosomal BAC pools.



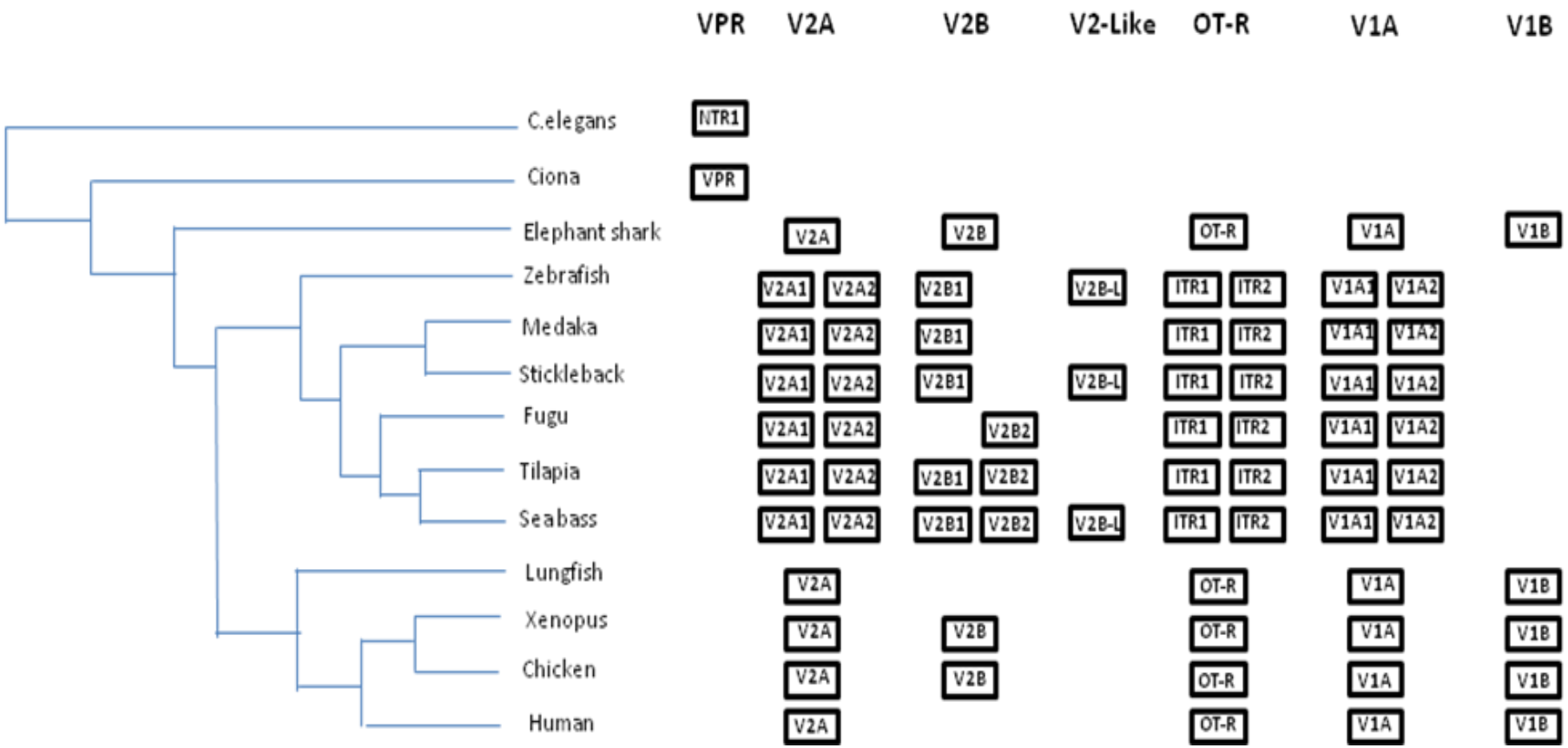
Supplementary Figure 2: Distribution of GC content along seabass chromosome 10. Similar unpatterned GC contents were found across all chromosomes (not shown).



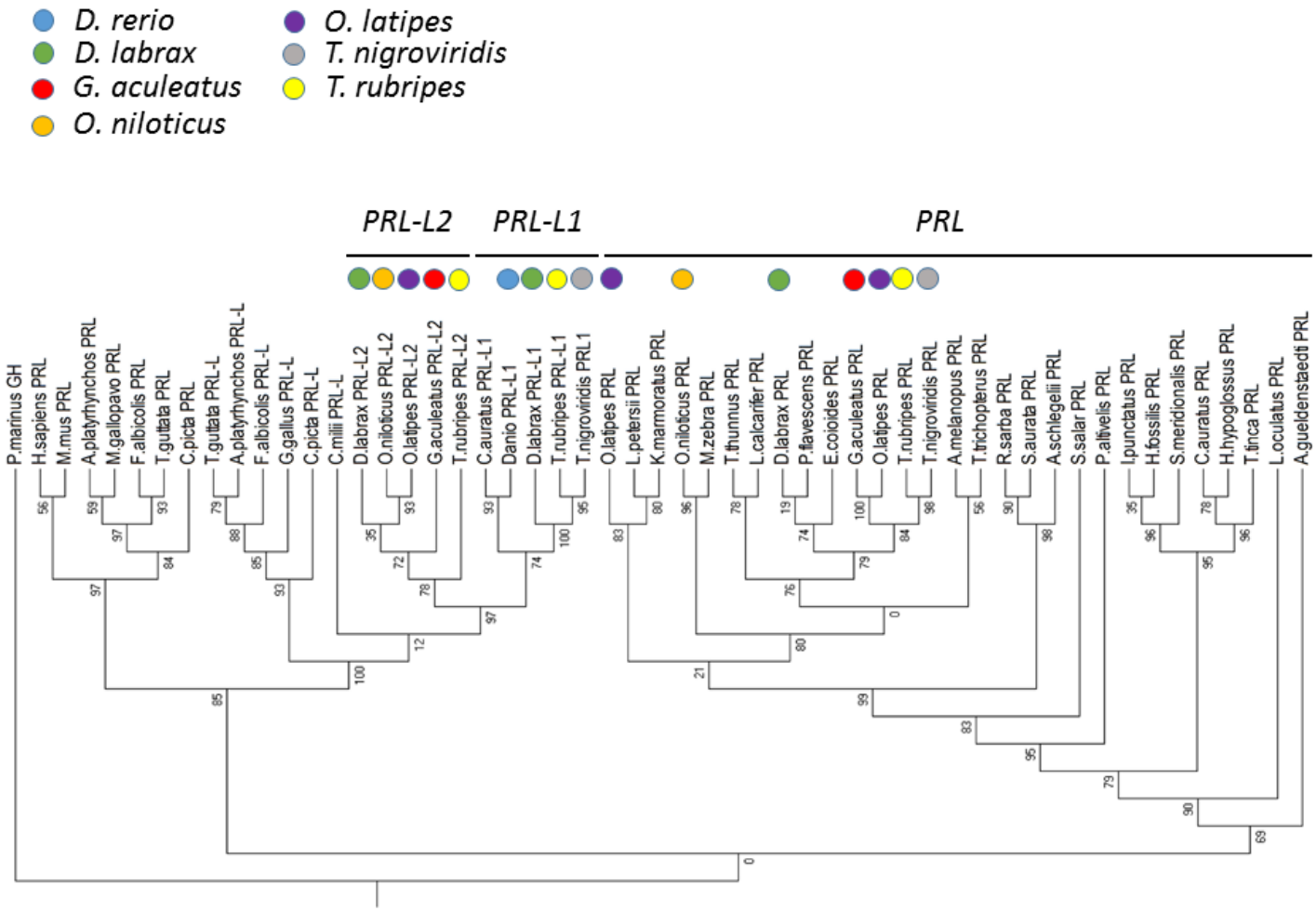
Supplementary Figure 3: Claudin genes numbers across several teleosts and human genomes.



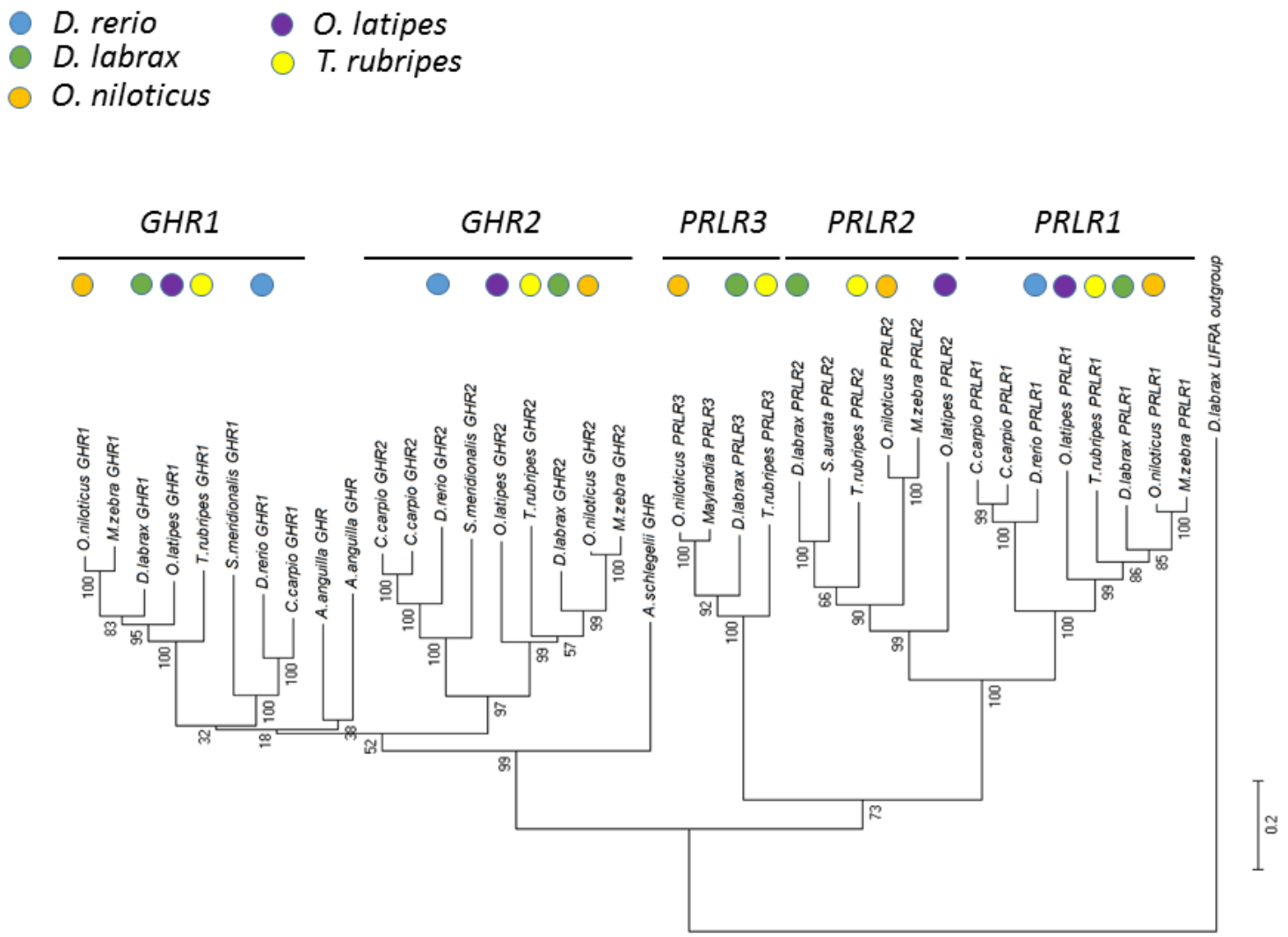
Supplementary Figure 4: Phylogeny of aquaporin gene family showing the number of duplicates found in the genomes of seabass and six other fully sequenced fish species.



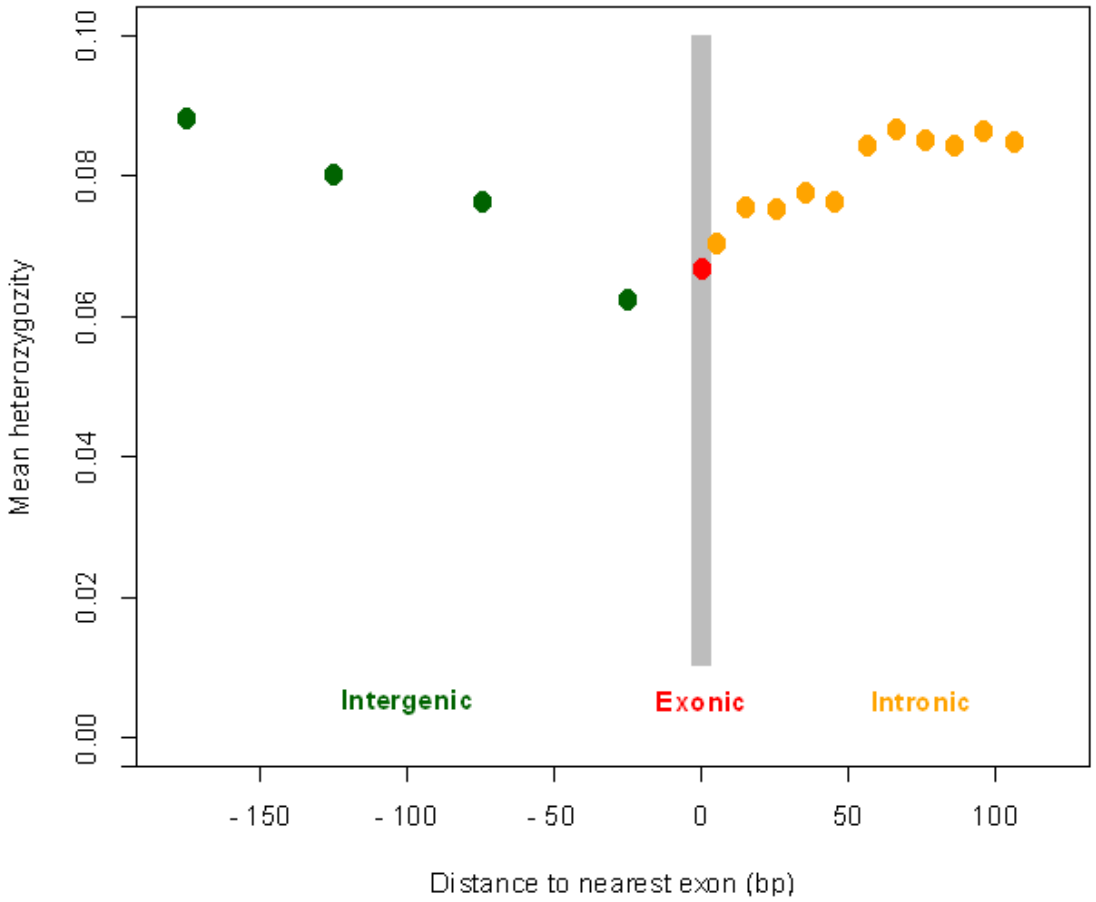
Supplementary Figure 5: Model for vasopressin receptors gene duplications in Deuterostomes



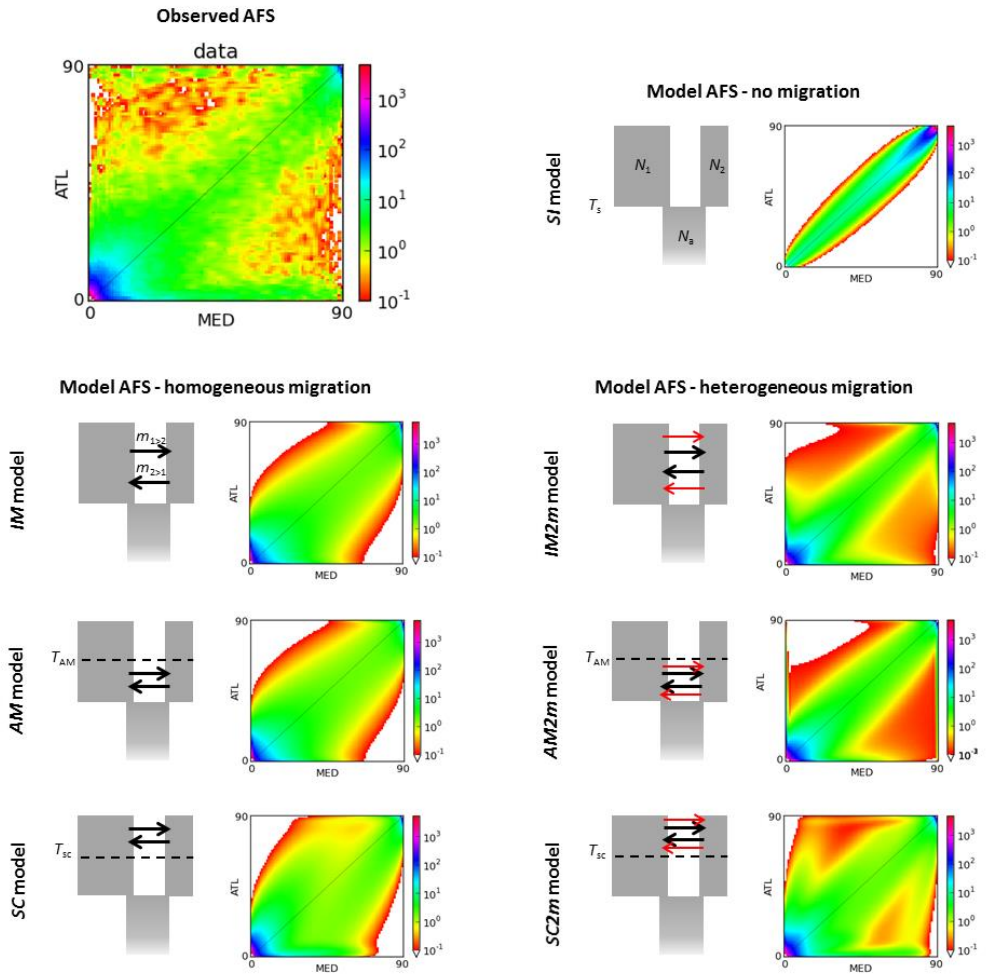
Supplementary Figure 6: Phylogeny of prolactin and prolactin-like genes in teleost fishes.



Supplementary Figure 7: Position of prolactin receptor-like genes (*PRLR*) in the other somatotropin receptors' phylogeny



Supplementary Figure 8: Mean expected heterozygosity in seabass as a function of the physical distance to nearest exon.



Supplementary Figure 9: Results of model fitting for seven alternative models of divergence. *SI* is the strict isolation model. *IM* is the Isolation-with-Migration model, *AM* the Ancient Migration model, and *SC* is the Secondary Contact model. All three models of divergence-with-gene-flow were implemented using one, shared migration rate in each direction ($m_{1>2}$, $m_{2>1}$) across the genome (homogeneous migration), or with two categories of migration rates in each direction across the genome (heterogeneous migration).

Supplementary Tables

Supplementary Table 1: Summary statistics of sequencing data, detailed for each sequencing strategy.

Technology	**SANGER (ABI3730xl)**		**ROCHE/454 pyrosequencing**		**Illumina GAIIx**		
Read type (insert size)	PLASMID (1-4 kbp)	BAC ES (100 - 200 kbp)	454 SINGLE END	454 MATE-PAIRS (10 - 30 kbp)	PE (200-350 bp)	PE (400-600 bp)	PE (800-1000 bp)
Read number	2,968,230	102,690	5,887,597	1,008,190	133,762,688	63,667,334	6,400,112
Average length (bp)	678	669	422	183	86	99	96
Total length (bp)	2,011,428,197	68,701,876	2,483,714,938	184,071,015	11,483,791,419	6,283,880,364	614,423,708
Approximate coverage (if genome size is 763Mb)	2.6	0.1	3.3	0.2	15.1	8.2	0.8

Supplementary Table 2: Contigs and scaffolds summary statistics at different stages of the seabass genome assembly.

	CA6.1	**Split scaffolds** (if no 20 kb mate pair coverage)	**BAMBUS scaffolder** (20 kb mates+BACends)	**Assembled chromosomal groups** (including information from RH map, linkage map and synteny)
Contig number	48,076	46,509	46,509	22,145
Contigs total length (bp)	686,341,209	670,105,629	670,105,629	575,169,980
Contig length average	14,276	14,408	14,408	25,973
Largest Contig (bp)	505,692	505,692	505,692	505,692
N50 Contig length (bp)	53,106	53,190	53,190	62,381
weak/degen contigs total length (bp)	94,680,694	110,916,274	110,916,274	
Scaffold number	18,496	18,902	16,830	24
Scaffolds total length (bp)	691,920,969	675,293,870	675,418,190	578,977,601
Scaffold length average (bp)	37,409	35,726	40,132	24,124,067
Largest scaffold (bp)	4,747,568	4,744,412	17,900,694	32,612,477
N50 Scaffold length (bp)	803,503	610,830	5,087,423	26,215,200

Supplementary Table 3: Statistics of gene annotation in the seabass genome

Number of sequences:	**Chromosomal sequences**	**Unordered sequences**	**All sequences**
Genes	21,038	5,681	26,719
Exons	215,177	27,906	243,083
Coding exons	207,883	26,736	234,619
Introns	194,139	22,225	216,364
5-prime UTR > 9bp	10,762	1,676	12,438
3-prime UTR > 9bp	14,190	2,426	16,616
Both UTRs > 9 bp	10,266	1,110	11,376

Assembly coverage:	**Chromosomal sequences**	**Unordered sequences**	**All sequences**	**Fraction of all sequences**	**Average size**
Genes total (bp)	316,349,781	30,407,051	346,756,832	51.30%	12,978
Coding exons total (bp)	35,644,056	5,531,610	41,175,666	6.09%	169
Intron total (bp)	258,620,115	22,737,198	281,357,313	41.63%	1,199
5-prime UTR	4,155,321	760,516	4,915,837	0.73%	395
3-prime UTR	20,898,758	2,266,352	23,165,110	3.43%	1,394

Functional annotation:	**Chromosomal sequences**	**Unordered sequences**	**All sequences**
Genes with description	20,170	5,263	25,433
Genes with assigned symbol	18,279	2,961	21,240
Genes without description, symbol and peptide larger 99 aa	456	410	866

Supplementary Table 4: Summary of transcriptome sequences generated for gene annotation of the seabass genome.
Four libraries constructed with 4 pools of 2 tissues from 14 individuals were generated, totalizing 19 Gb of sequences.

Tissue (number of fish)	**Number of reads** (*CASAVA*)	**Cleaned read-pairs** (*Trimmomatic*)	**Cleaned bases**	**Mapped reads** (*TopHat*)
Liver (3)	24,346,576	24,322,906	4,843,728,650	40,135,177
Liver (3)	23,032,898	23,022,547	4,586,809,602	33,974,188
Intestine (4)	25,630,146	25,161,013	4,844,714,333	34,309,342
Intestine (4)	24,250,509	23,869,642	4,651,095,519	40,922,353

Supplementary Table 5: Annotation of the seabass mtDNA genome and similarity with the striped bass (*Morone saxatilis*)

Name	Type	Minimum	Maximum	Length	Direction	Similarity
tRNA-Phe	tRNA	1	68	68	forward	78.82%
rRNA 12S	rRNA	69	1026	958	forward	88.18%
rrnS gene	gene	69	1026	958	forward	88.18%
tRNA-Val	tRNA	1029	1100	72	forward	87.50%
rRNA 16S	rRNA	1101	2800	17	forward	85.33%
rrnL gene	gene	1101	2800	17	forward	85.33%
tRNA-Leu	tRNA	2887	2960	74	forward	80.54%
ND1 gene	gene	2961	3935	975	forward	72.68%
tRNA-Ile	tRNA	3940	4009	70	forward	84.57%
tRNA-Gln	tRNA	4009	4079	71	reverse	87.32%
tRNA-Met	tRNA	4079	4149	71	forward	92.39%
ND2	gene	4150	5194	1045	forward	79.80%
tRNA-Trp	tRNA	5195	5267	73	forward	72.88%
tRNA-Ala	tRNA	5269	5337	69	reverse	73.91%
tRNA-Asn	tRNA	5339	5411	73	reverse	85.21%
L strand origin of replication rep origin	rep_origin	5412	5444	33	forward	73.53%
tRNA-Cys	tRNA	5445	5512	68	reverse	70.88%
tRNA-Tyr	tRNA	5513	5582	70	reverse	87.14%
COX1 gene	gene	5584	7134	1551	forward	73.44%
tRNA-Ser	tRNA	7135	7205	71	reverse	64.51%
tRNA-Asp	tRNA	7222	7292	71	forward	75%
COX2 gene	gene	7298	7988	691	forward	70.82%
tRNA-Lys	tRNA	7989	8062	74	forward	95.14%
ATP8 gene	gene	8067	8234	168	forward	78.50%

ATP6 gene	gene	8225	8908	684	forward	78.60%
COX3 gene	gene	8908	9692	785	forward	73.86%
tRNA-Gly	tRNA	9693	9764	72	forward	85%
ND3 gene	gene	9765	10113	349	forward	70.09%
tRNA-Arg	tRNA	10114	10182	69	forward	100%
ND4L gene	gene	10183	10479	297	forward	70.30%
ND4 gene	gene	10473	11853	1381	forward	67.96%
tRNA-His	tRNA	11854	11922	69	forward	89.57%
tRNA-Ser	tRNA	11923	11991	69	forward	68.70%
tRNA-Leu	tRNA	11997	12069	73	forward	87.67%
ND5 gene	gene	12070	13911	1842	forward	64.82%
tRNA-Glu	tRNA	14272	14340	69	reverse	79.70%
CYTB gene	gene	14345	15485	1141	forward	70.18%
tRNA-Thr	tRNA	15486	15556	71	forward	94.93%
tRNA-Pro	tRNA	15556	15625	70	reverse	87.14%
control region D-loop	D-loop	15626	17576	1950	forward	
ND6 gene	gene	17577	18095	519	reverse	80%
Tandem repeat 17 pb	repeat_region	16112	16179	68	forward	
Tandem repeats 48 pb	repeat_region	16206	16637	432	forward	
Tandem repeats 48 pb (variants)	repeat_region	16638	16733	96	forward	
Tandem repeat 48 pb	repeat_unit	16734	16781	48	forward	
Tandem repeats 48 pb (variants)	repeat_region	16782	16973	192	forward	
Control region (D-loop)	D-loop	18096	18253	157	forward	

Supplementary Table 6: Summary statistics of the different types of repetitive elements in the seabass genome.

Type of repeats	All sequences		Sequence assigned to chromosomes		Unordered sequences	
Sine	4044377	0.60%	2770467	0.48%	1273910	1.31%
Line	17859437	2.64%	9251430	1.60%	8608007	8.88%
LTR	4254880	0.63%	1539066	0.27%	2715814	2.80%
DNA	28341507	4.19%	21802767	3.77%	6538740	6.75%
Simple	12257952	1.81%	9426978	1.63%	2830974	2.92%
low complexity	5635934	0.83%	4742868	0.82%	893066	0.92%
Satellite	3309911	0.49%	1535002	0.27%	1774909	1.83%
RNA	1419305	0.21%	84397	0.01%	1334908	1.38%
Other	1127250	0.17%	566955	0.10%	560295	0.58%
Unknown	66865035	9.89%	54683761	9.44%	12181274	12.57%
Total	145115588	21.47%	106403691	18.38%	38711897	39.93%

Supplementary Table 7: Statistics for whole genome alignments of teleost species against the seabass genome assembly. The species were ordered by similarity with seabass.

Aligned species	***O. niloticus***	***G. aculeatus***	***T. rubripes***	***O. latipes***	***T. nigroviridis***	***G. morhua***	***D. rerio***
seabass sequence covered by colinear regions	579,237,436 (86.68%)	568,385,867 (85.05%)	524,324,456 (78.46%)	530,564,057 (79.39%)	510,465,800 (76.39%)	346,641,017 (51.87%)	243,220,222 (36.40%)
largest colinear region	4,682,506	7,784,832	3,739,309	3,741,975	2,524,371	2,265,684	664,057
N50 colinear region length	886,981	996,379	589,013	575,643	495,766	224,518	89,075
seabass sequence covered by alignment blocks	171,342,748 (25.64%)	138,015,935 (20.65%)	84,121,215 (12.59%)	78,537,826 (11.75%)	73,418,610 (10.99%)	30,196,195 (4.52%)	18,886,208 (2.83%)
largest alignment block	17,527	17,548	17,114	11,608	11,552	17,369	17,113
N50 alignment block length	453	384	288	282	275	193	178
average % nucleotide identity of alignment blocks	79.07%	78.64%	78.88%	78.30%	78.73%	78.44%	76.46%

Supplementary Table 8: **Total number of gene copies for the five expanded gene families which may have played a role in adaptation to euryhalinity.** FW: freshwater, BW: brackish water, SW: sea water.

	D. labrax	***T. rubripes***	***T. nigroviridis***	***D. rerio***	***O. latipes***	***G. aculeatus***	***O. niloticus***	***G. morhua***
claudin	61	56	51	54	48	57	56	47
aquaporin	18	16	18	18	14	16	18	19
OTX/AVT receptor	9	7	5	7	8	7	8	7
PRL/PRL-like	3	3	2	2	3	2	2	2
PRLR	3	3	2	2	2	3	3	2
TOTAL	**94**	**85**	**78**	**83**	**75**	**85**	**87**	**77**
Habitat	SW/BW	SW	FW/BW	FW	FW/BW	FW/BW/SW	FW/BW	SW
Halinity	euryhaline	stenohaline	euryhaline	stenohaline	euryhaline	euryhaline	euryhaline	stenohaline
Salinity tolerance	FW-SW	BW (25% SW) -SW	FW-SW	FW-BW (25‰)	FW-SW	FW-SW	FW-SW	BW (9ppt)-SW
References		Lee et al., 2005	Lin et al., 2004	Uliano et al., 2010	Inoue & Takei, 2002	Shimada et al., 2011	Schofield et al., 2011	Larsen et al., 2012

Lee, K. M., Kaneko, T. & Aida, K. (2005). Low-salinity tolerance of juvenile fugu Takifugu rubripes. Fisheries Science 71, 1324-1331.
Lin, C. H., Tsai, R. S. & Lee, T. H. (2004). Expression and distribution of Na, K-ATPase in gill and kidney of the spotted green pufferfish, Tetraodon nigroviridis, in response to salinity challenge. Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology 138, 287-295.
Uliano, E., Cataldi, M., Carella, F., Migliaccio, O., Iaccarino, D. & Agnisola, C. (2010). Effects of acute changes in salinity and temperature on routine metabolism and nitrogen excretion in gambusia (Gambusia affinis) and zebrafish (Danio rerio). Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology 157, 283-290.
Inoue, K. & Takei, Y. (2002). Diverse Adaptability in Oryzias Species to High Environmental Salinity. Zoological Science 19, 727-734.
Shimada, Y., Shikano, T. & Merilä, J. (2011). A High Incidence of Selection on Physiologically Important Genes in the Three-Spined Stickleback, Gasterosteus aculeatus. Molecular Biology and Evolution 28, 181-193.
Schofield, P.J., Peterson, M.S., Lowe, M.R., Brown-Peterson, N.J. and Slack, W.T. (2011). Survival, growth and reproduction of non-indigenous Nile tilapia, Oreochromis niloticus (Linnaeus1758). I. Physiological capabilities in various temperatures and salinities. Marine and Freshwater Research 62, 439–449.
Larsen, P. F., Nielsen, E. E., Meier, K., Olsvik, P. A., Hansen, M. M. & Loeschcke, V. (2012). Differences in Salinity Tolerance and Gene Expression Between Two Populations of Atlantic Cod (Gadus morhua) in Response to Salinity Stress. Biochemical Genetics 50, 454-466.

Supplementary Table 9: **Summary of tree branches exhibiting signatures of positive selection in gene-trees constructed for seabass aquaporin gene duplications.** In bold are evidenced branches involving seabass gene copies.

Locus[a]	**Branch**[b]	**Corrected p-value**[c]	**ω^{+}**[d]	**Pr [$\omega=\omega^{+}$]**[e]
NM_001114910 *AQP8*	**Node 93**[f]	0.001	10000	0.14
XM_003973563 *AQP7*	**Node 23**[f]	0.011	472.18	0.30

[a] Putative orthologous locus in zebrafish/takifugu and the corresponding protein
[b] Branch under episodic diversifying selection at $p \leq 0.05$.
[c] The p-value for episodic selection at this branch corrected for multiple testing using the Holm-Bonferroni method
[d] The ω value inferred for positively selected sites long this branch.
[e] The proportion of sites inferred to be evolving at ω+ along this branch
[f] Node 93 refers to the separation of seabass AQP8 (DLAGN_00189570) and zebrafish AQP8 (NM_001114910) genes; Node 23 refers to the separation of seabass AQP7 (DLAGN_00090530) and zebrafish AQP7 (NM_199910) genes.

Supplementary Table 10: **Summary of tree branches exhibiting signatures of positive selection in gene-trees constructed for seabass vasopressin receptors gene duplications. In bold are evidenced branches involving seabass gene copies.**

Locus[a]	**Branch**[b]	**Corrected p-value**[c]	**ω^{+d}**	**Pr [$\omega=\omega^{+}$]**[e]
NM_001301114 *V1A2*	**Node 5**[f]	< 0.0001	171.73	0.12
NM_001297676 *V1A1*	Node 6[f]	0.017	7.76	0.18
NM_001297676 *V1A1*	**Node 7**[f]	0.001	36.21	0.13
XM_001922007 *V2A1*	**Node 48**[f]	0.000	720.47	0.20
XM_001922007 *V2A1*	**Node 50**[f]	0.017	3333.85	0.13
ENSDARP00000119491 *V2B-L*	**DLAGN_00207720_V2B-L**	0.030	482.81	0.04

[a] Putative orthologous locus in zebrafish and the corresponding protein
[b] Branch under episodic diversifying selection at $p \leq 0.05$.
[c] The p-value for episodic selection at this branch corrected for multiple testing using the Holm-Bonferroni method
[d] The ω value inferred for positively selected sites long this branch.
[e] The proportion of sites inferred to be evolving at ω+ along this branch
[f] Node 5 refers to the separation of seabass V1A2 (DLAGN_00170900) and takifugu V1A2 (ENSTRUP00000041717) genes; Node 6 refers to the separation of zebrafish V1A1 (NM_001297676) and other teleost V1A1 genes; Node 7 refers to the separation of seabass V1A1(DLAGN_00209950) and takifugu (ENSTRUP00000014647) V1A1 genes; Node 48 refers to the separation of fish V2A2 genes and V2A1 genes; Node 50 refers to the separation of seabass V2A1 (DLAGN_00125320) and takifugu V2A1 (ENSTRUP00000001533) genes.

Supplementary Table 11: **Summary of tree branches exhibiting signatures of positive selection in gene-trees constructed for seabass prolactin gene duplications.** In bold are evidenced branches involving seabass gene copies.

Locus[a]	**Branch**[b]	**Corrected p-value**[c]	**ω^{+}**[d]	**Pr [$\omega=\omega^{+}$]**[e]
NM_181437 *PRL 1*	***Node 10***[f]	0.019	10000	0.38
NM_001162854 *PRL-L*	**Node 28**[f]	0.039	1187.75	0.12

[a] Putative orthologous locus in zebrafish and the corresponding protein
[b] Branch under episodic diversifying selection at $p \leq 0.05$. Italicized putative duplicated genes in the seabass genome. Locus names are as in the seabass genome browser.
[c] The p-value for episodic selection at this branch corrected for multiple testing using the Holm-Bonferroni method
[d] The ω value inferred for positively selected sites long this branch.
[e] The proportion of sites inferred to be evolving at ω+ along this branch
[f] Node 10 refers to the separation of teleost fish PRL and the spotted gar PRL gene; Node 28 refers to the separation of seabass PRL-L2 (LG6) and takifugu rubripes PRL-L2 (XM_003967630) novel gene duplicates.

Supplementary Table 12: **Summary of tree branches exhibiting signatures of positive selection in gene-trees constructed for seabass prolactin receptor gene duplications.** In bold are evidenced branches involving seabass gene copies.

Locus[a]	**Branch**[b]	**Corrected p-value**[c]	**ω^{+d}**	**Pr [$\omega=\omega^{+}$]**[e]
XM_004074724 *PRLR1*	*DLAGN_00083540_PRLR1*	*< 0.0001*	*10000.00*	*0.05*
XM_005459179 *PRLR2*	*DLAGN_00121350_PRLR2*	*< 0.0001*	*174.45*	*0.10*
XM_005459179 *PRLR2*	NM_001279622_TILAPIA_PRLR2	*< 0.0001*	*23.01*	*0.15*
XM_003966644 *PRLR3*	**Node 7**[f]	*0.012*	*31.70*	*0.09*
XM_005459179 *PRLR2*	**Node 13**[f]	0.016	*7703.89*	*0.08*
XM_003966644 *PRLR3*	DLAGN_00136380_PRLR3	0.020	*12.06*	*0.10*

[a] Putative orthologous locus in zebrafish/medaka/takifugu and the corresponding protein
[b] Branch under episodic diversifying selection at $p \leq 0.05$. Italicized putative duplicated genes in the seabass genome. Locus names are as in the seabass genome browser.
[c] The p-value for episodic selection at this branch corrected for multiple testing using the Holm-Bonferroni method
[d] The ω value inferred for positively selected sites long this branch.
[e] The proportion of sites inferred to be evolving at ω+ along this branch
[f] Node 7 refers to the separation of seabass PRLR3 (DLAGN_00136380) and Tilapia PRLR3 (XM_005459179) genes; Node 13 refers to the separation of seabass PRLR2 (DLAGN_00121350) and tilapia PRLR2 (NM_001279622) genes.

Supplementary Table 13: **Summary of tree branches exhibiting signatures of positive selection in gene-trees constructed for seabass-specific recent duplications.** In bold are evidenced branches involving seabass gene copies.

Locus[a]	**Branch**[b]	**Corrected p-value**[c]	**ω^{+}**[d]	**Pr [$\omega=\omega^{+}$]**[e]
ENSORLG00000006910 Unknown protein	***DLAGN_00143800***	0.000	408.77	0.04
ENSORLG00000006910 Unknown protein	ENSONIG00000009239	0.018	3.49	0.35
ENSDARG00000016345 *NCOA5*	**Node 13**[f]	0.001	3540.31	0.02
ENSDARG00000016345 *NCOA5*	***DLA_LG1A_007760***	0.039	10000.00	0.01
ENSORLG00000004029 *ACP2*	***DLA_LG24_002230***	< 0.0001	9999.43	0.05
ENSDARG00000061672 si:ch73-334d15.1	ENSGACG00000004476	0.015	16.95	0.02
ENSDARG00000061672 si:ch73-334d15.1	***DLAGN_00105480***	0.028	20.16	0.05
ENSDART00000104504 *fetuin B*	**DLAGN_00145680_680**	< 0.0001	136.43	0.07

[a] Putative orthologous locus in zebrafish/medaka and the corresponding protein

[b] Branch under episodic diversifying selection at $p \leq 0.05$. Italicized putative duplicated genes in the seabass genome. Locus names correspond to names in the seabass genome browser.

[c] The p-value for episodic selection at this branch corrected for multiple testing using the Holm-Bonferroni method

[d] The ω value inferred for positively selected sites along this branch. To check for potential inflation of ω values due to low numbers of synonymous substitutions, uncorrected percentages of synonymous substitutions were estimated in relevant pairwise sequence comparisons. Values ranged from 0.055 (5.5% uncorrected) to 0.125 (12.5%) between recent duplicates in seabass (absolute number of synonymous changes ranged between 12 and 30).

[e] The proportion of sites inferred to be evolving at ω+ along this branch

[f] Node 13 refers to the origin of seabass duplicated genes at this locus (split LG1A_007760/LG1A_007750)

Supplementary Table 14: **Origin of the 103 samples of the seabass used for the RAD sequencing experiment.**

Species	Basin	Country	Location	Longitude	Latitude	Date	Sample size
D. labrax	Mediteranean Sea	France	Mauguio	43.578899	4.028435	10/1/2011	25
D. labrax	Mediteranean Sea	France	Palavas	43.516564	3.939257	9/25/2012	15
D. labrax	Mediteranean Sea	Algeria	Annaba	36.930683	7.804985	7/1/2012	10
D. labrax	Atlantic Ocean	Portugal	Mondego	40.139515	-8.758678	11/28/2011	31
D. labrax	Atlantic Ocean	France	Biarritz	43.501001	-1.618137	6/18/2003	19
D. punctatus	Mediteranean Sea	Tunisia	El Biban	33.25247	11.238899	2005	3

Supplementary Table 15: **Results of model fitting for seven alternative models of divergence**. *SI* is the strict isolation model. *IM* is the Isolation-with-Migration model, *AM* the Ancient Migration model, and *SC* is the Secondary Contact model. All three models of divergence-with-gene-flow were implemented using one, shared migration rate in each direction (m_{12}, m_{21}) across the genome (homogeneous migration), or with two categories of migration rates in each direction across the genome (heterogeneous migration).

Model	k	MLE	AIC	Δi	*L*(Mi|y)	wi	Theta	nu1	nu2	m12	m21	me12	me21	Ts	Tps	P	O
SI	4	-29993,2	59994,3	36674,9	0	0	9897	16,2760	0,4519	-	-	-	-	0,0624	-	-	0,9900
IM	6	-21070,9	42153,8	18834,4	0	0	5931,6	2,9108	0,3094	0,4490	8,4505	-	-	0,6916	-	-	0,9793
AM	7	-21071,10	42156,2	18836,8	0	0	5925,1	2,9107	0,3097	0,4491	8,4452	-	-	0,6943	0,0000	-	0,9789
SC	7	-17012,4	34038,7	10719,3	0	0	6204,2	2,8178	0,2781	1,1983	16,8157	-	-	0,5180	0,0476	-	0,9795
IM2M	9	-15030,2	30031,5	6712,04	0	0	5555,9	2,6122	0,5031	3,2216	26,6674	0,2852	1,7767	0,8781	-	0,6579	0,9779
AM2M	10	-15210,2	30440,4	7121,03	0	0	5258,9	3,0583	0,4789	0,0000	29,7270	0,2365	2,0261	0,9427	0,0002	0,6502	0,9751
SC2M	10	-11649,7	23319,41	0	1	1	6018,80	2,3569	0,472	9,0584	45,018	1,431	8,938	0,634	0,027	0,645	0,9770

k The number of free parameters in the model
MLE maximum likelihood estimate over 20 independent runs
AIC Akaike Information Criterion
Δ_i Difference in AIC between model i and the best model (*SC2M*)
***L*(M$_i$\|y)** Relative likelihood of model i compared to the best model (*SC2M*)
w_i Akaike weight of model i compared to the best model (*SC2M*)
Theta Theta parameter for the ancestral population before split ($\theta = 4N_{ref}\mu$), with N_{ref} being the effective size of the ancestral population, and μ the per-site mutation rate per generation.
nu1 The effective size of the Atlantic lineage population
nu2 The effective size of the Mediterranean lineage population
m12 The neutral movement of genes from the Mediterranean to the Atlantic lineage in units of $2N_{ref}m_{2>1}$ generations
m21 The neutral movement of genes from the Atlantic to the Mediterranean lineage in units of $2N_{ref}m_{1>2}$ generations
me12 The effective migration rate of “genomic-island” genes from the Mediterranean to the Atlantic lineage
me21 The effective migration rate of “genomic-island” genes from the Atlantic to the Mediterranean lineage
Ts The time of split in units of $2N_{ref}$ generations
Tps The time of migration stop (*AM* model) or start (*SC* model) post-split in units of $2N_{ref}$ generations
P The proportion of the genome experiencing reduced effective migration rate compared to freely exchanged genes
O The proportion of correctly orientated SNPs when inferring ancestral allelic states using *D. punctatus* as an outgroup species