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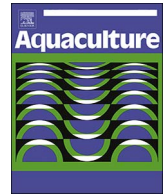
TEAD3, implicated by association to grilsing in Atlantic salmon

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ABSTRACT

With the recent finding that the vestigial-like family member 3 (*Vgll3*) gene is associated with early maturation, we decided to re-examine previously reported quantitative trait loci (QTL) and genome wide association (GWA) studies, involved with early maturation, to see if *Vgll3* was the source of any of these associations. Using a TaqMan assay for *Vgll3*, we were able to verify that a prominent QTL for early maturation was indeed associated with *Vgll3*. Next, we used *Vgll3* genotypes as a cofactor to re-examine for any additional QTLs or GWAs. Several were found at the chromosome-wide significance level. By examining interacting partners of *Vgll3* from other organisms, we identified several candidate genes that may interact with *Vgll3* in Atlantic salmon and effect early maturation. The location of these genes were determined from the genome sequence, while markers near QTL were examined to see if they were near any *Vgll3* interacting genes. In this way, we identified *TEAD3* as a putative gene also influencing early maturation in Atlantic salmon. A TaqMan assay was used to genotype *TEAD3*. These genotypes appear to be associated with early maturation.

1. Introduction

New Brunswick Atlantic salmon farming generated an estimated $250 million CAD in 2002 (McClure et al., 2007). Of this, between $11–$24 million CAD was estimated to be lost due to early maturation (known as grilsing in Atlantic salmon) (McClure et al., 2007). Typically, the loss in revenue from early maturation has to do with the flesh quality degradation that accompanies maturation (Aksnes et al., 1986). Understanding why some fish mature earlier than others offers Atlantic salmon producers a potential mechanism where they may be able to reduce these losses.

Variation of age at maturity may benefit a species in the wild. The variation in age at maturation can preserve genetic diversity by maintaining alleles that would be detrimental if only a single age at maturation existed. This variation may also increase the number of potential spawners during a single year, which would help maintain genetic diversity (Saunders and Schom, 1985). The diversity maintained by multiple life-histories may also make Atlantic salmon more able to adapt to different environments (e.g. low-flow and high-flow streams, reviewed in (Fleming, 1996)) and potentially explains part of the reason why they have been successful at colonizing so many locations.

The mechanism maintaining variation in age at maturity is likely complex, but may reflect a balance between male mating strategies

(Fleming, 1996; Gross, 1985). Larger males tend to have an aggressive mating style, fighting for mating opportunities; while the smaller males often use a strategy of wait and sneak-in (Gross, 1985). In environments where there are many large males, a sneak fertilization may be a highly effective strategy of reproduction, but when there are many small fish trying to sneak-in, fighting may be more effective (Fleming, 1996; Gross, 1985).

Genetic variation associated with age at maturity has been seen in quantitative trait loci (QTL) and genome wide association (GWA) studies (Gutierrez et al., 2015, 2014; Johnston et al., 2014). More recently, two research groups have posited that the vestigial-like family member 3 (*Vgll3*) gene may partially regulate the timing of maturity in Atlantic Salmon (Ayllon et al., 2015; Barson et al., 2015). This makes *Vgll3* a focus for possible use in marker assisted selection to reduce the number of early maturing individuals.

The homologs of the *Vgll3* gene have been studied extensively in other organisms. In *Drosophila*, *vestigial* was found to be involved in wing formation (Kim et al., 1996). Later, it was found that another protein, scalloped (a homolog of *transcription enhancer factor-1* in vertebrates), was needed in wing formation and that the proteins of these two genes interacted to do so (S. Paumard-Rigal, 1998; Simmonds et al., 1998). Simmonds et al. (1998), suggested that *vestigial* was a tissue-specific co-factor of the transcription factor *scalloped*.

In vertebrates, three *vestigial* homologs were characterized that all

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contain a *transcription enhancer factor-1* (TEF-1 commonly referred to as *TEAD* genes) interacting domain (Maeda et al., 2002). The vestigial homologs appear to form heterodimers with TEF-1 (Maeda et al., 2002). This interaction appeared to play a role in skeletal muscle differentiation in a mouse model (Maeda et al., 2002). Again, suggesting that the *vestigial* homologs act as transcriptional co-factors. It has also been shown that vertebrate TEF-1 shares enough similarity with *Drosophila* scalloped, that TEF-1 can be substituted for scalloped and still have wingblade development (Deshpande et al., 1997). Similarly, human vestigial homologs can also be substituted for vestigial in *Drosophila* and wing development will still continue (Vaudin et al., 1999).

Early estimates of the number of *TEF-1* genes in mammalian genomes was three to five (Kaneko and DePamphilis, 1998). It was shown that each gene contains a TEA DNA (TEAD) binding domain, with nearly identical amino acid sequence. This allows each of them to bind conserved non-coding DNA elements (Kaneko and DePamphilis, 1998). Expression of these genes varies from tissues, but nearly every tissue expresses at least one *TEAD* gene. These observations led researchers to conclude that in order for *TEAD* genes to differentially regulate genes in separate tissues, there must a mechanism for ubiquitous TEAD proteins to only bind a subset of the possible conserved non-coding DNA elements (Kaneko and DePamphilis, 1998). All these pieces of evidence support the idea that *TEAD* genes and *vestigial* homologs (*Vgll*1–4) are involved in regulating transcription in both vertebrates and invertebrates, and that *vestigial* homologs are tissue-specific co-factors for the more general *TEF-1*.

More recently, four *TEAD* genes and four *VGLL* genes have been characterized in vertebrates (reviewed in (Pobbati and Hong, 2013)). Along with the TEA DNA binding domain, each of the *TEAD* genes also contains a transactivation domain, allowing them to interact with several coactivators, including: yes-associated protein (YAP/TAZ), Myb-binding protein 1A (p160), and Vgll (Pobbati and Hong, 2013). *TEAD1* and *TEAD2* appear to be especially important for differentiation in cardiac muscle, *TEAD4* is vital for placental development, and major functions for *TEAD3* have yet to be elucidated (Pobbati and Hong, 2013). In mammals, *Vgll1* and *Vgll4* are expressed in multiple tissues, *Vgll2* is mainly expressed in skeletal muscle, and *Vgll3* expression is found almost entirely in the placenta (Pobbati and Hong, 2013).

An interesting feature of the interplay between *TEAD* and *Vgll* genes is the ability of TEAD proteins to be able to bind multiple coactivators. In the Hippo signaling pathway, involved in cell proliferation and differentiation, TEAD proteins interact with YAP/TAZ to stimulate cell growth and proliferation (reviewed in Ashraf and Pervaiz, 2015). YAP/TAZ may be activated by external stimuli such as reactive oxygen species (Ashraf and Pervaiz, 2015). Competition for the TEAD transactivation domain, may create a dynamic interplay between YAP/TAZ and Vgll. Variation in any of these genes may alter the dynamic between YAP/TAZ and Vgll; this is highlighted in various cancers (Ashraf and Pervaiz, 2015).

As previously stated, genetic variation in *Vgll3* in Atlantic salmon appears to partially control the timing of when a salmon will return to fresh water (age at maturity). Based on previous research, a likely hypothesis is that Vgll3 does so by interacting with a TEAD protein. The genetic variation in *Vgll3*, associated with age at maturation, (Ayllon et al., 2015; Barson et al., 2015) is not found in the Vg_Tdu super family domain of Atlantic salmon's *Vgll3*-based on a comparison of the *Vgll3* sequence to the conserved domain database (Marchler-Bauer et al., 2015). This suggests that the variation does not disrupt binding of the *TEAD* and *Vgll3* genes.

We suspected that if variation in the *Vgll3* gene could influence age at maturity in Atlantic salmon, then variation in a *Vgll3* interacting gene may also alter timing of maturation. We used samples and datasets from Gutierrez et al. (2014) and Gutierrez et al. (2015), first to determine if *Vgll3* was responsible for any of the QTL or GWA's in these studies. Next, we used these datasets and new *Vgll3* genotype information to identify possible interacting QTL. The Atlantic salmon genome was

used to identify if any of the markers near QTL were physically linked to binding partners of Vgll3.

2. Materials and methods

2.1. Population and dataset

Five Atlantic salmon families utilized by Gutierrez et al. (2014) were used for QTL analysis, GWA analysis, and association testing. These families are from the Mowi strain and were bred for Mainstream Canada (now Cermaq) as part of their broodstock program (Gutierrez et al., 2014). Fertilization occurred in late 2005, the fry from these families were pooled in February 2006, and phenotypes were scored as late as 2009 (Gutierrez et al., 2014). An additional 160 individuals (80 Grilse and 80 Non-Grilse) and 192 parents from the 2005 broodstock year were utilized in a GWA analysis. These individuals were originally a part of a GWA study conducted by Gutierrez et al. (2015). Genotype information was also collected by Gutierrez et al. (2014) and Gutierrez et al. (2015).

2.2. Genotyping Vgll3

Two genotyping assays were used to interrogate the *Vgll3* genotypes of all of the individuals (Fig. 1). The preliminary assay utilized restriction fragment length polymorphisms (RFLP) to determine if variation existed at the same loci found in previous research (Ayllon et al., 2015; Barson et al., 2015). Once both variants were identified in the population, a TaqMan assay was used for all of the samples.

For the RFLP assay, the following reagents were used to amplify two segments of the *Vgll3* gene on chromosome 25 of the Atlantic salmon genome in a 10 μL reaction:

200 nM primer
    Amino Acid 54 Assay
    Forward Primer: TGA TCG TTG TGG TGC TGA CTA
    Reverse Primer: AGC CCT GGA GAA ATG CTC ATC
    Amino Acid 323 Assay
    Forward Primer: TCC TGC CTG GTG TGA AGA CT
    Reverse Primer: AGA AAC GTA GAC ATG GGA GAG AG
1 × PCR Buffer with Mg2 + (Applied Biological Materials Inc.)
200 μM dNTP Mix (Applied Biological Materials Inc.)
1 U Taq DNA Polymerase (Applied Biological Materials Inc.)

An initial denaturation of 95 °C for 5 min was followed by 35 rounds of 95 °C for 30 s, 62.5 °C for 30 s, and 72 °C for 30 s. This was followed by a final extension at 72 °C for 10 min. The 10 μL PCR product was then digested either using *Nla*III (amino acid 54) or *Ale*I (amino acid 323), for 4 h using 5 units per reaction at 37 °C. This was followed by a heat-inactivation of 80 °C for 30 min. The reaction was then loaded onto a 1.5% agarose gel and ran for 40 min at 110 V and scored for markers.

The same amino acid positions of the *Vgll3* gene were verified using a TaqMan assay. For amino acid position 54 of the *Vgll3* gene on chromosome 25 of the Atlantic Salmon, the following primers were used to amplify the segment around the amino acid and the following probes were used to verify the allele at that position:

Forward Primer: CTC CCT CTC TCT CGG TCT ATT T
Reverse Primer: CGC TGC TGT TGC TGT CT
Probe (C): /5HEX/CAGC + A + C + GGAG + CA/3IABkFQ/
Probe (T): /56-FAM/AC + AGC + A + T + GGA + GC/3IABkFQ/

For amino acid position 323 of the *Vgll3* gene, the following primers and probes were used:
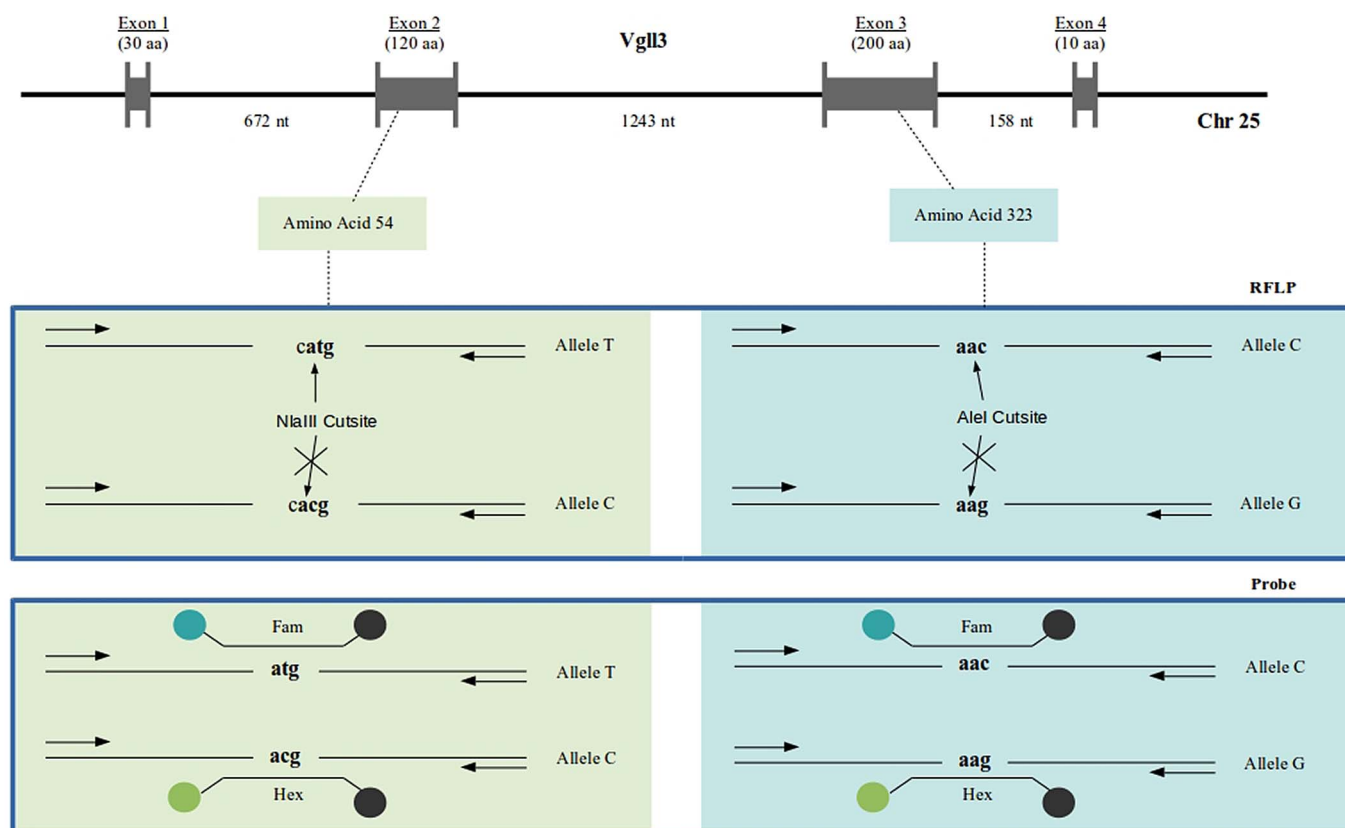
Forward Primer: AGA GCC AGG GA TAC ACA

Fig. 1. Structure of *Vgll3* and genotype assays. The *Vgll3* gene in Atlantic salmon is composed of four exons and 360 amino acids. To determine the genotypes that were previously shown to be associated to age at maturation in Atlantic salmon, two different assays were used. The first assay was RFLP and the second was a TaqMan assay.

Reverse Primer: GAT ATC CAT GGG TGT GTG TAG AG
Probe (G): /5HEX/TG + TGA + A + G + ACA + GAGG/3IABkFQ/
Probe (C): /56-FAM/TGTGA + A + C + ACA + G + AGG/3IABkFQ/

PrimeTime Gene Expression Master Mix (1×) was used with the primers (500 nM), and probes (150 nM) to amplify DNA samples (~25 ng) using an initial denaturation period of 3 min at 95 °C and 40 cycles of denaturation at 95 °C for 5 s and annealing/extensions at 60 °C for 30 s. The genotypes for amino acid position 54 and position 323 were nearly identical (data not shown) and so only the results from positions 54 were reported.

2.3. QTL and GWA analyses

Using custom Perl scripts and LepMap2 (Rastas et al., 2015), *Vgll3* was added to the genetic map produced by (Lien et al., 2011) and used by Gutierrez et al. (2014). Then genotype and map information was converted to GridQTL (Seaton et al., 2006) format using Perl scripts and a sib-pair analysis was ran for the five families. The sib-pair analysis was ran either using sex as a fixed-effect or not and with *Vgll3* as a co-factor or not. A chromosome-wide significance level was chosen for the QTL analysis instead of an experiment-wide significance level. The lower threshold was chosen because we were interested in specific loci and the corrections for multiple testing would likely be too conservative at the experiment-wide significance level.

Similar to the QTL analysis, Perl scripts were used to convert genotype, pedigree, and phenotype information from Gutierrez et al. (2014) and Lien et al. (2011) to a format accepted by GenABEL (Aulchenko et al., 2007) in the R environment (R Core Team, 2015). In GenABEL, problematic markers were removed using the function check.markers. Next, kinship was estimated by the ibs function with the

weight variable set to freq. This information was used to estimate a polygenic model of age at maturity. Then a GRAMMAS genome wide analysis was performed using the polygenic relationship model with a permutation test of 1000 to identify the significance level. This model included sex as a factor influencing age at maturity and either included *Vgll3* information or this was left out to see if *Vgll3* was influencing other candidate associations.

2.4. Genotyping TEAD3

To identify variants in the *TEAD3* gene, the sequence of this gene was downloaded from the NCBI (XM_014133832.1), and was aligned to an Atlantic salmon RNA-seq dataset from the NCBI SRA database (SRR1422850); with the max target sequence set to 5000. These alignments were downloaded as a SAM file and visualized with IGV (Robinson et al., 2011; Thorvaldsdóttir et al., 2013). The nucleotide position 2306 of XM_014133832.1 appeared to be variable (C vs. G). An allele-specific PCR assay was designed for this location (Fig. 2).

200 nM primer
Forward Primers:
2306(C) GTG CCT TTC TCC AAA GAC ATC
2306(G) GTG CCT TTC TCC AAA GAC ATG
Reverse Primer:
TCA TGC TAT GCC CTT GCT GT
1× CoralLoad (Qiagen)
1× PCR Buffer with Mg2 + (Applied Biological Materials Inc.)
200 μM dNTP Mix (Applied Biological Materials Inc.)
1 U Taq DNA Polymerase (Applied Biological Materials Inc.)

An initial denaturation of 95 °C for 5 min was followed by 30 rounds of 95 °C for 30 s, 60.5 °C for 30 s, and 72 °C for 30 s. This was followed by a final extension at 72 °C for 1 min. The reaction was then loaded
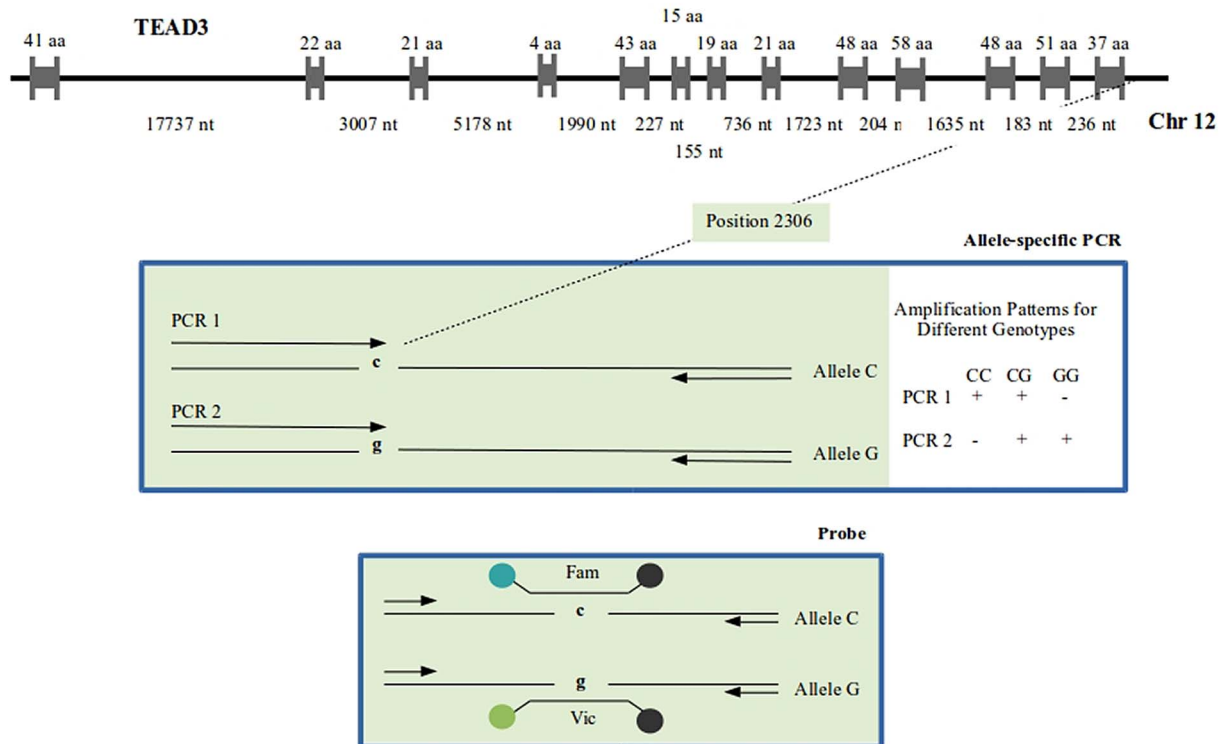
Fig. 2. Structure of *TEAD3* and genotype assays. The *TEAD3* gene in Atlantic salmon is composed of 13 exons and 428 amino acids. An allele-specific PCR was used to assay nucleotide variation near the end of the gene and a TaqMan assay was used to verify these results.

onto a 1.5% agarose gel and electrophoresed for 40 min at 110 V. The genotype information was collected for the five families and the 80 grilse and 80 non-grilse individuals.

The genotypes at the 2306 position of the *TEAD3* gene were verified using a TaqMan assay.

Forward Primer: GAT GGC AAC CAA GTG CCT
Reverse Primer: CAG AGT GGC TGG CAA CTG
Probe (G): TCC AAA GAC ATG TAT TGA T
Probe (C): TCC AAA GAC ATC TAT TGA T

TaqMan® Genotyping Master Mix (1×) was used with TaqMan assay solution (1×) to amplify DNA samples (~25 ng) using an initial denaturation period of 10 min at 95 °C and 40 cycles of denaturation at 95 °C for 15 s and annealing/extensions at 60 °C for 60 s.

2.5. Statistical analysis

A custom Perl script was written to perform a permutation test because many of the expected values calculated for a chi-square analysis were below five (i.e. it violates the assumptions of the chi-square analysis). For this permutation test: the allele frequencies were determined from the observed data, two random distributions were then created from the allele frequency (and the observed total count), and a chi-square value was calculated by comparing these two random distributions. The chi-square value calculation was one permutation, and represents an expected value if the genotypes were randomly distributed for both categories (i.e. there was not an association with the genotypes and categories).

The chi-square value calculation was repeated 20,000 times (2 million for the combined genotype analysis) in order to find the distribution of expected chi-square values if the data was randomly distributed based on the observed allele frequencies and the observed total count. The observed chi-square value was then calculated and compared to the distribution. A *p*-value was assigned to the comparison based on the percentage of random chi-square values that had a greater chi-square value than the observed chi-square value (one-tailed).

Six comparisons were made in this manner. The male grilse were compared to male non-grilse for the *Vgll3*, *TEAD3*, and combined genotypes. There were no female grilse, so a comparison was performed between the 2 sea-winter and 3 sea-winter females for all genotypes. The 80 grilse and 80 non-grilse had an infrequent minor allele frequency (~8%) and were not analyzed for this reason.

In order to test if there was a significant interaction between the *TEAD3* and *Vgll3* loci, a logistic regression was performed in PLINK (version 1.9) (Purcell et al., 2007) using the – logistic interaction and – condition commands. To use the logistic regression analysis, maturation was treated as a binary trait. A simple logistic regression analysis, without covariates and interaction terms, was also performed to verify that treating the trait as binary, gave similar results as the permutation tests.

3. Results

When evaluating five Atlantic salmon families for QTLs, sex was included as a fixed-effect and *Vgll3* genotype information was used as a co-factor. The result of this analysis can be seen in Fig. 3. Four QTL were significant at the chromosome-wide significance level. On chromosome 25, the most significant marker was near 53 cM and not the *Vgll3* marker, which is at ~50 cM. When *Vgll3* is removed as a co-factor, there is no change in position of the most significant marker. These results are different from Gutierrez et al. (2014), likely due to the inclusion of all markers instead of the subset of markers that were polymorphic in all families used in that study.

When using all of the datasets for a GWA analysis (Fig. 4), again the most significant marker on chromosome 25 was not *Vgll3* (position 28,653,293), but a marker near it (position 27,031,877). It should be noted that *Vgll3* was removed during quality control, but if quality control was not used, *Vgll3* still was not the most significant marker. When the *Vgll3* genotype was used in the GRAMMAS model, markers on
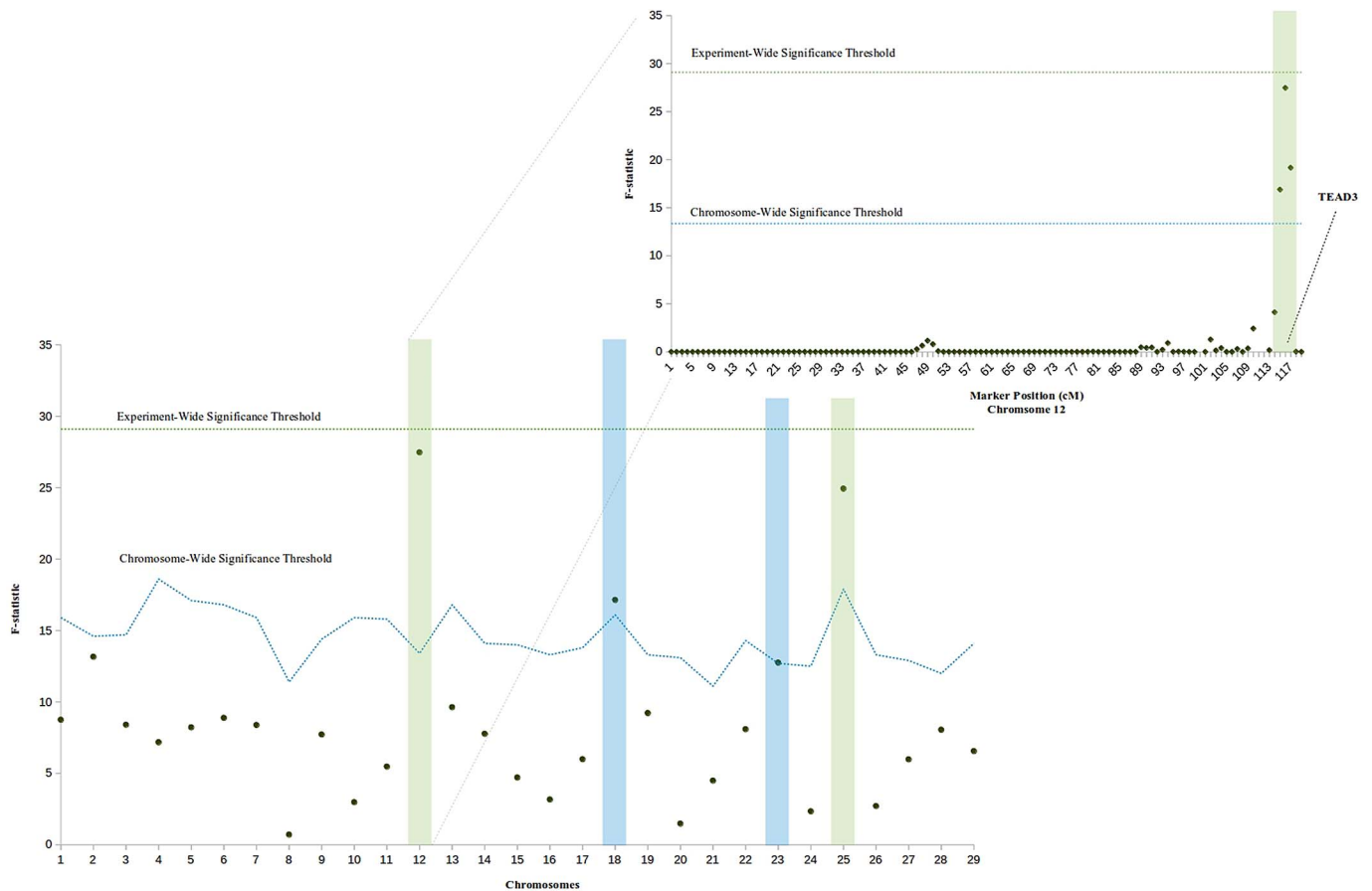
Fig. 3. QTL analysis of grilsing in five families. This figure depicts a QTL analysis for all families and all chromosomes. This was a re-analysis of data presented in Gutierrez et al. (2014). Sex was used as a fixed-effect and the *Vgll3* gene was used as a co-factor. The lower, dashed line indicates the chromosome-wide significance level (determined through a permutation test with 1000 permutations) and the upper represents the experiment-wide significance threshold. The most significant markers are plotted per chromosome. *Vgll3* was included in this re-analysis as a marker, but was not the most significant marker on chromosome 25. It was located close to the most significant marker, however. The insert shows a finer scale of the QTL analysis for all families on chromosome 12. The approximate location of the *TEAD3* gene is also shown.

chromosome 25 were no longer significantly associated with age at maturity. The remaining significant markers appeared anomalous since surrounding markers did not show any association with age at maturity. Association with surrounding markers might be expected because of linkage disequilibrium.

Of the four QTL, only the one on chromosome 12 was located near a potential binding partner of *Vgll3*. This QTL was located at 115 cM and the marker located at this position aligned to position 75,694,886 on chromosome 12. *TEAD3* meanwhile is located at position 79,047,649, which is closer to markers near 117 cM (78,652,735 to 79,202,674) of the genetic map (Fig. 3). This association was not seen in the GWA analysis. Johnston et al. (2014), found a GWA relatively near this location (chromosome 12, position 61,511,101) for sea-winter age. Pedersen et al. (2013), found a QTL on chromosome 12 for parr maturation, which was the most significant QTL for that trait.

To see if *TEAD3* was associated with age at maturity, the five families were genotyped for a SNP in *TEAD3*. Using a permutation test, the male genotypes were significantly different ($p = 0.046$) between grilse and non-grilse individuals; suggesting that there is an association between this genotype and age at maturity in males. The genotypes for the various phenotype categories are shown in Figs. 5, 6, and 7 for the five families genotyped for *Vgll3*, *TEAD3*, and for both genotypes. Allele frequencies for *Vgll3* and *TEAD3* are shown in Fig. S1.

In Fig. 5, it can be seen that 3% of the grilse were homozygous for the *Vgll3* "CC" genotype, while 29% of the 2SW males had the "CC" genotype. In Fig. 7, it can be seen that 55% of the male grilse have a "CT × GG" haplotype, which is 36% more than the "CT × GG"

haplotype seen in 2SW males. The difference between the two categories appears greater than that between the categories when considering a single gene (Figs. 5 and 6). The *p*-value for the combined genotypes is also smaller for the combined analysis, and may suggest that the genotypes are more predictive in combination.

In order to determine if there was a significant interaction between the two loci, a logistic regression analysis was performed and included *TEAD3* as a cofactor and an interaction coefficient between the *TEAD3* and *Vgll3* loci. The interaction term was not significant ($p = 0.95$) and suggests that the interaction does not affect the phenotype more than would be expected by the linear addition of each loci independently. For this analysis, the phenotype was treated as a binary trait. To determine if this would influence the association between the phenotype and genotypes, another regression analysis was performed without cofactor or interaction terms. Only *Vgll3* was significantly associated in the logistic regression analysis ($p = 0.013$), but *TEAD3* had a low *p*-value ($p = 0.064$) similar to the permutation test.

4. Discussion

While researching the mechanisms governing age at maturation has fairly apparent applications in aquaculture (i.e. marker assisted selection), less obvious benefits may be to conservation efforts. As described in 1. Introduction, various ages at maturity may benefit a species by preserving genetic diversity that would otherwise be lost due to environmental constraints (e.g. low-flow and high-flow streams). Conservation efforts which monitor age at maturity may be more
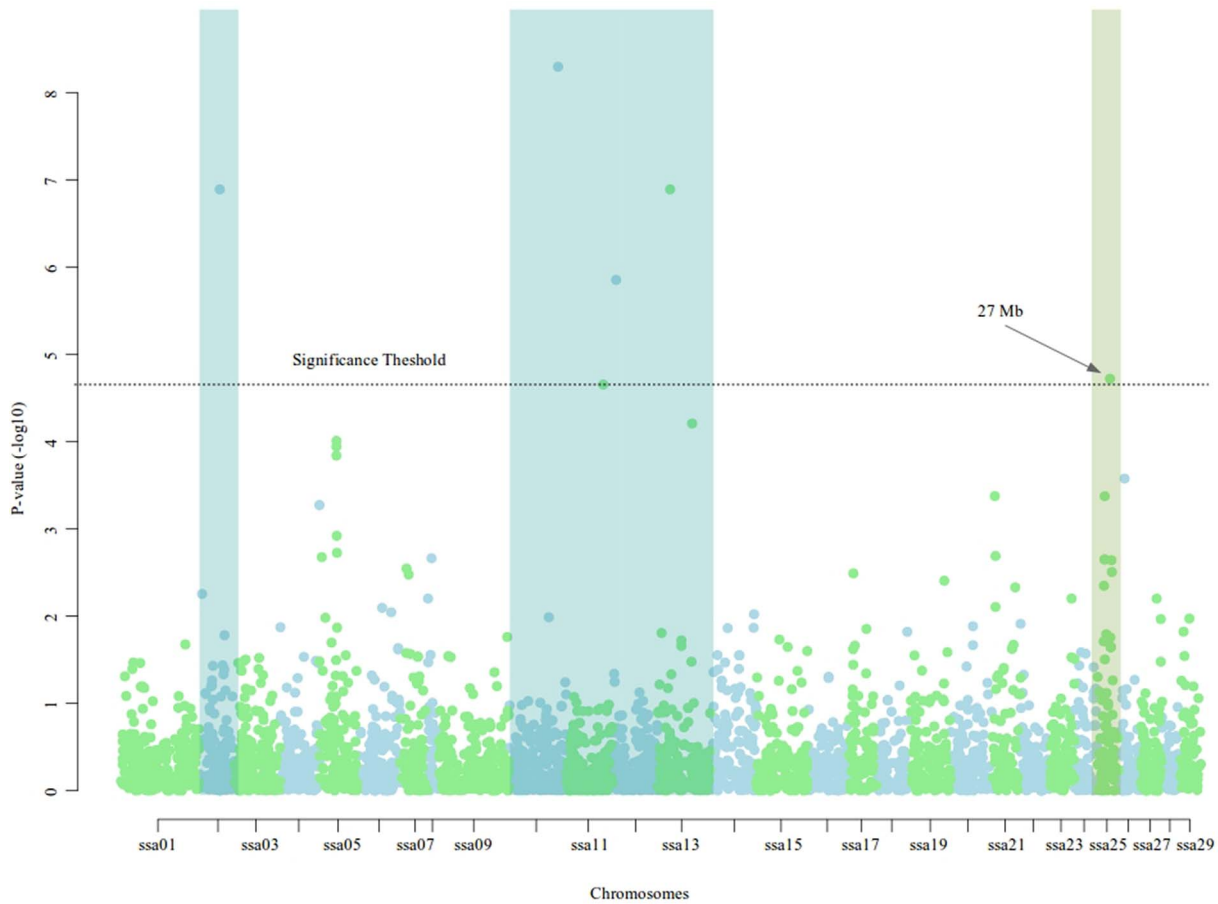
Fig. 4. Genome wide analysis of grilsing from Cermaq (mainstream) dataset. This was a re-analysis of data presented in Gutierrez et al. (2015). *Vgll3* was added as a marker in this analysis, but was filtered during quality control. When quality control was removed, *Vgll3* did not show the strongest association. The *Vgll3* gene is close to the most associated marker on chromosome 25.
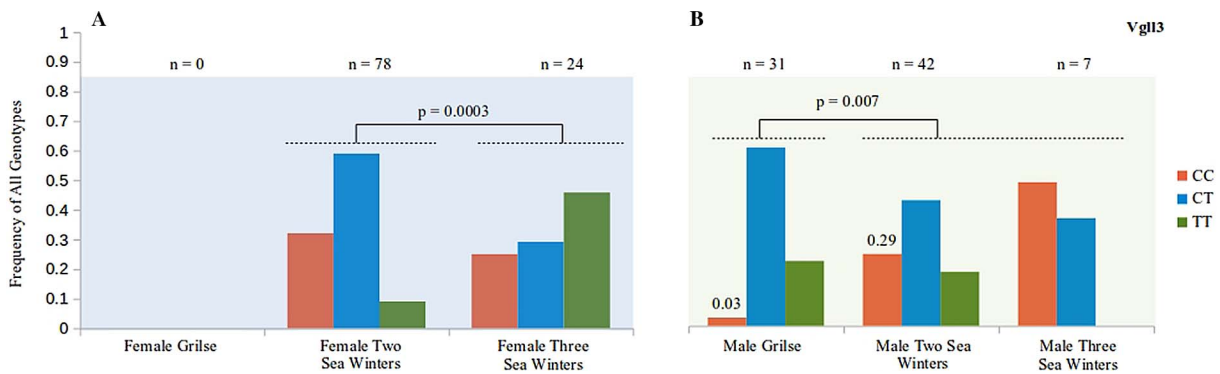

Fig. 5. Frequency of *Vgll3* genotypes in the family dataset. A) Females in the five families and the frequency of the CC, CT, and TT genotypes. The females are divided into sub-categories of grilse (G), maturing after two-sea winters (2SW), and maturing after three-sea winters (3SW). B) Males in the five families and the frequency of the three genotypes. The males are divided into the same sub-categories as the females. A permutation test was used to determine significance (*p*-values are shown).

effective than otherwise for this reason. Genotyping for markers related to age at maturity offers a convenient and cost-effective means of this type of monitoring; as well as a means for selection against undesirable maturation ages in aquaculture.

With the discovery that *Vgll3* was associated with age at maturity, the question of how it might do so now remains to be discovered. Based on previous research on *vestigial* and other *Vgll* genes in other verte-brates, a logical hypothesis is that it does so by interacting with a *TEAD* gene. Here we tested if variation in *TEAD* genes might also be involved with determining age at maturity, and we found evidence suggesting that *TEAD3* is involved.

Previous evidence that Vgll and TEAD proteins physically interact, implicates transcription initiation from the Vgll3/TEAD3 putative complex playing a role in determining age at maturation. There are some preliminary studies done with pigs that may illuminate what types of genes might be activated by TEAD3 in Atlantic salmon. Evidence from several quantitative trait loci (QTL) analyses, led re-searchers to suggest that the accumulation of androstenone in pigs was related to the *TEAD3* gene (Lee et al., 2005; Quintanilla et al., 2003; Robic et al., 2012, 2011). Because of the conservation that has been seen with *TEAD* genes (i.e. human TEAD protein substitution in *Dro-sophila* still producing wings), one could speculate that *TEAD3* may play
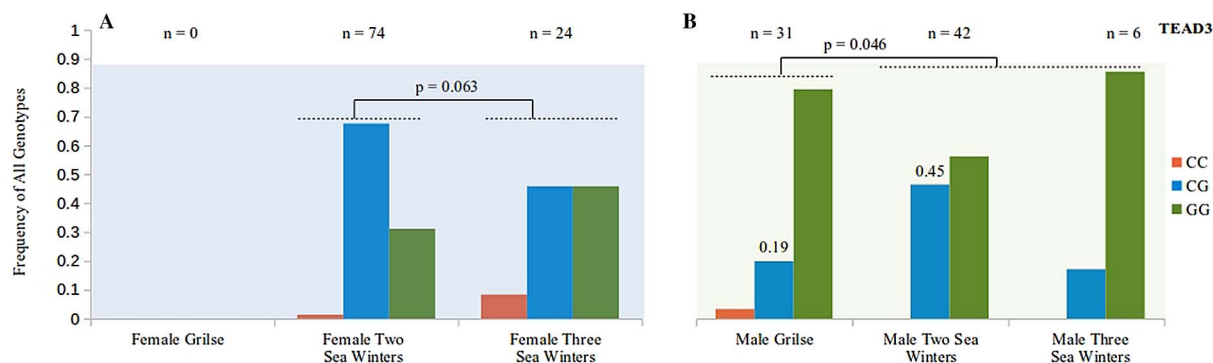
Fig. 6. Frequency of *TEAD3* genotypes in the family dataset. A) Females in the five families and the frequency of the CC, CG, and GG genotypes. The females are divided into sub-categories of grilse (G), maturing after two-sea winters (2SW), and maturing after three-sea winters (3SW). B) Males in the five families and the frequency of the three genotypes. The males are divided into the same sub-categories as the females. A permutation test was used to determine significance (*p*-values are shown).

Fig. 7. Frequency of *Vgll3* and *TEAD3* genotypes in the family dataset. A) Females in the five families and the frequency of the various combinations of genotypes. The females are divided into sub-categories of grilse (G), maturing after two-sea winters (2SW), and maturing after three-sea winters (3SW). B) Males in the five families and the frequency of the three genotypes. The males are divided into the same sub-categories as the females. A permutation test was used to determine significance (*p*-values are shown).
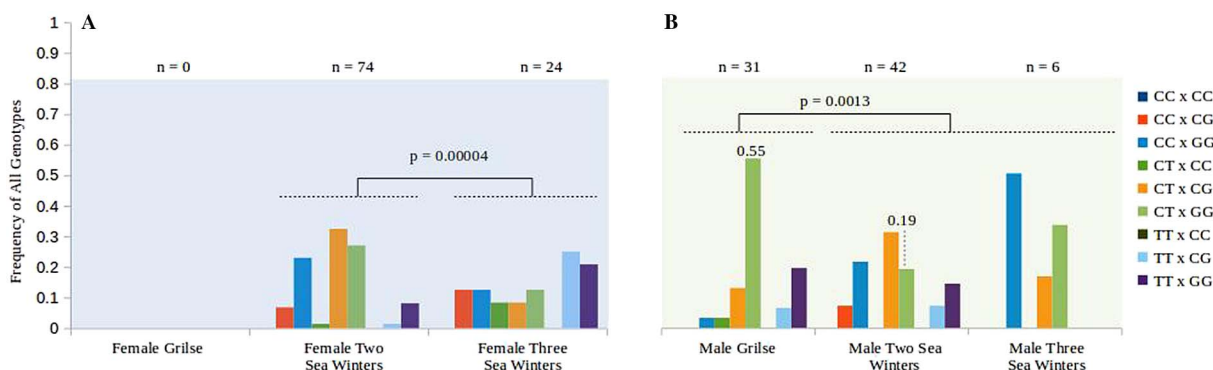
a similar role in Atlantic salmon. With the generation of these hypotheses, an avenue of research can now be explored to further refine our understanding of age at maturation.

An interesting note about the position of the QTL and GWA analyses was that the *Vgll3* marker was not the most significant marker in the datasets, even though it was close to the most significant marker on chromosome 25. Phenotyping and genotyping errors may explain the position discrepancy. Another note of interest is that the *TEAD3* genotype was unlikely to be the causative variant since it was randomly chosen based on sequence alignments that were unrelated to age at maturation rather than from sequences from individuals with variation in the age at maturation phenotype. It is more likely that this particular variant is in linkage disequilibrium with the causative mutation.

A few lines of investigation that may be fruitful to pursue in the future include: 1) confirming Vgll3 and TEAD3 interact, 2) identifying in which tissues they occur, and 3) performing QTL analyses in other populations to understand if *TEAD3* influences age at maturation in other populations.

Supplementary data to this article can be found online at http://dx. doi.org/10.1016/j.aquaculture.2017.06.026.

References

Aksnes, A., Gjerde, B., Roald, S.O., 1986. Biological, chemical and organoleptic changes during maturation of farmed Atlantic salmon, *Salmo salar*. Aquaculture 53, 7–20. http://dx.doi.org/10.1016/0044-8486(86)90295-4.

Ashraf, A., Pervaiz, S., 2015. Hippo circuitry and the redox modulation of hippo components in cancer cell fate decisions. Int. J. Biochem. Cell Biol. 69, 20–28. http://dx. doi.org/10.1016/j.biocel.2015.10.001.

Aulchenko, Y.S., de Koning, D.-J., Haley, C., 2007. Genomewide rapid association using mixed model and regression: a fast and simple method for genomewide pedigree-based quantitative trait loci association analysis. Genetics 177, 577–585. http://dx. doi.org/10.1534/genetics.107.075614.

Ayllon, F., Kjærner-Semb, E., Furmanek, T., Wennevik, V., Solberg, M.F., Dahle, G., Taranger, G.L., Glover, K.A., Almén, M.S., Rubin, C.J., Edvardsen, R.B., Wargelius, A., 2015. The vgll3 locus controls age at maturity in wild and domesticated Atlantic salmon (*Salmo salar* L.) males. PLOS Genet. 11, e1005628. http://dx.doi.org/10. 1371/journal.pgen.1005628.

Barson, N.J., Aykanat, T., Hindar, K., Baranski, M., Bolstad, G.H., Fiske, P., Jacq, C., Jensen, A.J., Johnston, S.E., Karlsson, S., Kent, M., Moen, T., Niemelä, E., Nome, T., Næsje, T.F., Orell, P., Romakkaniemi, A., Sægrov, H., Urdal, K., Erkinaro, J., Lien, S., Primmer, C.R., 2015. Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature 528, 405–408. http://dx.doi.org/10.1038/ nature16062.

Deshpande, N., Chopra, A., Rangarajan, A., Shashidhara, L.S., Rodrigues, V., Krishna, S., 1997. The human transcription enhancer factor-1, TEF-1, can substitute for *Drosophila* scalloped during wingblade development. J. Biol. Chem. 272, 10664–10668. http://dx.doi.org/10.1074/jbc.272.16.10664.

Fleming, I.A., 1996. Reproductive strategies of Atlantic salmon: ecology and evolution. Rev. Fish Biol. Fish. 6, 379–416. http://dx.doi.org/10.1007/BF00164323.

Gross, M.R., 1985. Disruptive selection for alternative life histories in salmon. Nature 313, 47–48. http://dx.doi.org/10.1038/313047a0.

Gutierrez, A.P., Lubieniecki, K.P., Fukui, S., Withler, R.E., Swift, B., Davidson, W.S., 2014. Detection of Quantitative Trait Loci (QTL) related to grilsing and late sexual maturation in Atlantic salmon (*Salmo salar*). Mar. Biotechnol. (NY) 16, 103–110. http:// dx.doi.org/10.1007/s10126-013-9530-3.

Gutierrez, A.P., Yáñez, J.M., Fukui, S., Swift, B., Davidson, W.S., 2015. Genome-Wide Association Study (GWAS) for growth rate and age at sexual maturation in Atlantic

salmon (*Salmo salar*). PLoS One 10, e0119730. http://dx.doi.org/10.1371/journal.
pone.0119730.

Johnston, S.E., Orell, P., Pritchard, V.L., Kent, M.P., Lien, S., Niemelä, E., Erkinaro, J.,
Primmer, C.R., 2014. Genome-wide SNP analysis reveals a genetic basis for sea-age
variation in a wild population of Atlantic salmon (*Salmo salar*). Mol. Ecol. 23,
3452–3468. http://dx.doi.org/10.1111/mec.12832.

Kaneko, K.J., DePamphilis, M.L., 1998. Regulation of gene expression at the beginning of
mammalian development and the TEAD family of transcription factors. Dev. Genet.
22, 43–55. http://dx.doi.org/10.1002/(SICI)1520-6408(1998)22:1<43::AID-
DVG5>3.0.CO;2-7.

Kim, J., Sebring, A., Esch, J.J., Kraus, M.E., Vorwerk, K., Magee, J., Carroll, S.B., 1996.
Integration of positional signals and regulation of wing formation and identity by
Drosophila vestigial gene. Nature 382, 133–138. http://dx.doi.org/10.1038/
382133a0.

Lee, G.J., Archibald, A.L., Law, A.S., Lloyd, S., Wood, J., Haley, C.S., 2005. Detection of
quantitative trait loci for androstenone, skatole and boar taint in a cross between
large white and Meishan pigs. Anim. Genet. 36, 14–22. http://dx.doi.org/10.1111/j.
1365-2052.2004.01214.x.

Lien, S., Gidskehaug, L., Moen, T., Hayes, B.J., Berg, P.R., Davidson, W.S., Omholt, S.W.,
Kent, M.P., 2011. A dense SNP-based linkage map for Atlantic salmon (*Salmo salar*)
reveals extended chromosome homeologies and striking differences in sex-specific
recombination patterns. BMC Genomics 12, 615. http://dx.doi.org/10.1186/1471-
2164-12-615.

Maeda, T., Chapman, D.L., Stewart, A.F.R., 2002. Mammalian vestigial-like 2, a cofactor
of TEF-1 and MEF2 transcription factors that promotes skeletal muscle differentia-
tion. J. Biol. Chem. 277, 48889–48898. http://dx.doi.org/10.1074/jbc.M206858200.

Marchler-Bauer, A., Derbyshire, M.K., Gonzales, N.R., Lu, S., Chitsaz, F., Geer, L.Y., Geer,
R.C., He, J., Gwadz, M., Hurwitz, D.I., Lanczycki, C.J., Lu, F., Marchler, G.H., Song,
J.S., Thanki, N., Wang, Z., Yamashita, R.A., Zhang, D., Zheng, C., Bryant, S.H., 2015.
CDD: NCBI's conserved domain database. Nucl. Acids Res. 43, D222–D226. http://dx.
doi.org/10.1093/nar/gku1221.

McClure, C.A., Hammell, K.L., Moore, M., Dohoo, I.R., Burnley, H., 2007. Risk factors for
early sexual maturation in Atlantic salmon in seawater farms in New Brunswick and
Nova Scotia, Canada. Aquaculture 272, 370–379. http://dx.doi.org/10.1016/j.
aquaculture.2007.08.039.

Paumard-Rigal, S., 1998. Specific interactions between vestigial and scalloped are re-
quired to promote wing tissue proliferation in *Drosophila melanogaster*. Dev. Genes
Evol. 208, 440–446. http://dx.doi.org/10.1007/s004270050201.

Pedersen, S., Berg, P.R., Culling, M., Danzmann, R.G., Glebe, B., Leadbeater, S., Lien, S.,
Moen, T., Vandersteen, W., Boulding, E.G., 2013. Quantitative trait loci for pre-
cocious parr maturation, early smoltification, and adult maturation in double-back-
crossed trans-Atlantic salmon (*Salmo salar*). Aquaculture 410–411, 164–171. http://
dx.doi.org/10.1016/j.aquaculture.2013.06.039.

Pobbati, A.V., Hong, W., 2013. Emerging roles of TEAD transcription factors and its
coactivators in cancers. Cancer Biol. Ther. 14, 390–398. http://dx.doi.org/10.4161/
cbt.23788.

Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A.R., Bender, D., Maller, J.,
Sklar, P., de Bakker, P.I.W., Daly, M.J., Sham, P.C., 2007. PLINK: a tool set for whole-
genome association and population-based linkage analyses. Am. J. Hum. Genet. 81,
559–575. http://dx.doi.org/10.1086/519795.

Quintanilla, R., Demeure, O., Bidanel, J.P., Milan, D., Iannuccelli, N., Amigues, Y.,
Gruand, J., Renard, C., Chevalet, C., Bonneau, M., 2003. Detection of quantitative
trait loci for fat androstenone levels in pigs. J. Anim. Sci. 81, 385–394.

R Core Team, 2015. R: A Language and Environment for Statistical Computing. R
Foundation for Statistical Computing, Vienna, Austria.

Rastas, P., Calboli, F.C.F., Guo, B., Shikano, T., Merilä, J., 2015. Construction of ultra-
dense linkage maps with Lep-MAP2: stickleback F2 recombinant crosses as an ex-
ample. Genome Biol. Evol. evv250. http://dx.doi.org/10.1093/gbe/evv250.

Robic, A., Fève, K., Larzul, C., Billon, Y., van Son, M., Liaubet, L., Sarry, J., Milan, D.,
Grindflek, E., Bidanel, J.P., Riquet, J., 2011. Expression levels of 25 genes in liver and
testis located in a QTL region for androstenone on SSC7q1.2. Anim. Genet. 42,
662–665. http://dx.doi.org/10.1111/j.1365-2052.2011.02195.x.

Robic, A., Larzul, C., Grindflek, E., Chevillon, P., Hofer, A., Fève, K., Iannuccelli, N.,
Milan, D., Prunier, A., Riquet, J., 2012. Molecular characterization of the porcine
TEAD3 (TEF-5) gene: examination of a promoter mutation as the causal mutation of a
quantitative trait loci affecting the androstenone level in boar fat. J. Anim. Breed.
Genet. 129, 325–335. http://dx.doi.org/10.1111/j.1439-0388.2011.00979.x.

Robinson, J.T., Thorvaldsdóttir, H., Winckler, W., Guttman, M., Lander, E.S., Getz, G.,
Mesirov, J.P., 2011. Integrative genomics viewer. Nat. Biotech. 29, 24–26. http://dx.
doi.org/10.1038/nbt.1754.

Saunders, R.L., Schom, C.B., 1985. Importance of the variation in life history parameters
of Atlantic salmon (*Salmo salar*). Can. J. Fish. Aquat. Sci. 42, 615–618. http://dx.doi.
org/10.1139/f85-080.

Seaton, G., Hernandez-Sanchez, J., Grunchec, J.A., White, I., Allen, J., De Koning, D., Wei,
W., Berry, D., Haley, C., Knott, S., 2006. GridQTL: A Grid Portal for QTL Mapping of
Compute Intensive Datasets. In: Proceedings of the 8th World Congress on Genetics
Applied to Livestock Production (Belo horizonte, Brazil). 8th World Congress of
Genetics Applied to Livestock Production [WCGALP], Belo Horizonte, Brazil (13-18
August).

Simmonds, A.J., Liu, X., Soanes, K.H., Krause, H.M., Irvine, K.D., Bell, J.B., 1998.
Molecular interactions between vestigial and scalloped promote wing formation in
Drosophila. Genes Dev. 12, 3815–3820. http://dx.doi.org/10.1101/gad.12.24.3815.

Thorvaldsdóttir, H., Robinson, J.T., Mesirov, J.P., 2013. Integrative Genomics Viewer
(IGV): high-performance genomics data visualization and exploration. Brief.
Bioinform. 14, 178–192. http://dx.doi.org/10.1093/bib/bbs017.

Vaudin, P., Delanoue, R., Davidson, I., Silber, J., Zider, A., 1999. TONDU (TDU), a novel
human protein related to the product of vestigial (vg) gene of *Drosophila melanogaster*
interacts with vertebrate TEF factors and substitutes for Vg function in wing forma-
tion. Development 126, 4807–4816.