Supplementary Materials: Verification of SNPs Associated with Growth Traits in Two Populations of Farmed Atlantic Salmon

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Supplementary Table 1. The markers selected from GWA analysis for verification.

Sources	Marker ID	*p*-value *	Marker and Flanking Sequence
Top 0.5% SNPs in growth traits	AX87956267	2.37×10^{-3} (L)/ 1.45×10^{-3} (W)	CCATGTAGTTTTTGCATTCCAAAAGATCTTGCTGC**M**AAGAGCTAATGATTATTACAGATATTATGTTATTT
	AX88290778	7.27×10^{-4} (L)/ 1.03×10^{-3} (W)	TGGCACTTTTCAAATATTGAATTGGAATTTCAATT**M**ATGTCCTGAATTGACCATGGCTCTGGATAGAAACT
	AX87963258	1.65×10^{-5} (L)/ 1.42×10^{-4} (W)	CCTGTATGAGGGCAGCGAATGCTGGGTTCTGGAGG**Y**TGGCATGAATACCTAGGAGAGAGAATGGTTGTATT
	AX88270804	1.32×10^{-3} (L)/ 6.96×10^{-4} (W)	TCAGAGGTCTCGCTGGCGTCTCGTGAGACAGAGAG**R**GGGTCGTTCCGCCACTGGGAGGTGAAAGAGGGCAA
	AX87944147	5.45×10^{-5} (L)/ 2.78×10^{-5} (W)	CAGAGAGAGGGAGACCAGCGAGAGGGACACCAGAA**M**AAAAAGAAGGGAGGAAATTGAAGATGTTGCGGCGG
	AX87934338	7.30×10^{-5} (L)/ 6.41×10^{-5} (W)	ATTTAGCCACAGGGCCTATCCTCCCATCCTTAGAC**Y**GGCAGAGAGAGATGTAGGGAGACAAAGGCCTTTCA
	AX87992121	2.67×10^{-4} (L)/ 9.54×10^{-5} (W)	GAGCACTCCAACATTAATTTATTCAGGCATATTTA**M**CAGGACAAAGAGCAGAGGCCAGACCCTCCCGCCAC
	AX87943138	4.82×10^{-4} (L)/ 1.17×10^{-4} (W)	CACTTCAAGAGTTTACACGAAAAGTTGTTCTTATT**R**CGGAAATTGCCTATTGAGCTTTCCTATTCATGTAT
Chr. 20	AX87998237	5.70×10^{-2} (L)/ 4.85×10^{-2} (W)	GCAATGGAGGATGGAGATAATGGTTATGGAGATGG**Y**ATGGAGCTGGAGAAGGAACTGAGTCAGGAAGAGAG
	AX88289827	1.84×10^{-2} (L)	TGGAATTGCCCCCATACACTAATTACAAATGAAAG**M**GGTCTCTAATCTGGTGCTTGTCCCTTTGTAGTGTC
Top 0.5% in weight	AX87888225	9.96×10^{-5}	AATCTGACAGCGGTTCTTTCTTTTACCCAGTCGGA**S**AGGCCTCCTGGCTGGGGGTGCAAGGGCAGTTCACA
	AX88223695	1.24×10^{-4}	GCCCTATCAGAGAGAAGGGGGGGTGATGATAACAA**Y**GAGGTAGCTTTTTCAATCAACAATCACTCTTTTTA
	AX87959413	1.25×10^{-4}	CCCTTCATCGTATGGACTGACCATAAAAACCTGAC**Y**TACATCCAGACCGCCAAACGTCTGAACTCCCGGCA
Top 0.5% in length	AX88141678	5.45×10^{-5}	AGTTTTGGCTGGGGTAAGTAAAGGATACTTTCCAA**R**TATTTATCTTTTTTTAGAAGGCCTACTCTAATTTA
	AX87959512	9.13×10^{-5}	CCCTTTCAAGCACACCTTTCTCAATAACCTGTGGC**Y**AGTTATTCACAATTTTTGATGAAGAAATAAGGTTT
	AX88083269	1.02×10^{-4}	TTCCAGAAGATCCAAGAGCTGATAGATGACAAGCA**R**GCTCTGGTGTTTGTTCTCATCGATGAGGTAAAGCA

* The *p*-value was given in Tsai *et al.* [14]. W, body weight; L, body length. The shadow is used to distinguish different sources of markers utilized in this study. The bold letter are the single nucleotide polymorphism used in this study.

Supplementary Table 2. The marker ID, *p*-value estimated by the GWA analysis, putative gene and flanking sequence of two informative SNPs. The results were given in Tsai *et al.* [14].

Marker	Genotype	# No of Fish	Weight (g, SE)	Length (mm, SE)
AX88141678	G/G	22	128.58 (5.20)	225.50 (3.48)
	A/G	240	115.26 (1.58)	216.93 (1.06)
	A/A	362	109.16 (1.22)	211.82 (0.81)
		PVE	0.06	0.07
		p-value	4.12×10^{-4}	5.45×10^{-5}
AX88270804	G/G	153	119.25 (2.11)	218.54 (1.42)
	A/G	355	110.98 (1.08)	213.69 (0.72)
	A/A	116	106.25 (2.52)	210.50 (1.69)
		PVE	0.05	0.04
		p-value	1.32×10^{-3}	6.69×10^{-4}