

Supplementary Table S4. Microsatellite and SNP analysis of SALTAS broodstock families in which the sex-determining gene resides on Ssa06 (AS-4). Markers are arranged in order corresponding to their placement on the female European Atlantic salmon linkage map (See Phillips *et al.* 2009 for nomenclature) www.asabase.org. The seven families originally analyzed are highlighted yellow.

Marker	2009_XX ¹																45	44	47	41	42	43	46							
Ssa02	21	18	39	40	30	02	15	26	10	24	03	06	36	07	11															
Ssa1077BSFU			18/24 (1.4)					6/23 (0)			7/14 (0)																			
Ssa0055BSFU	² 25/33 ⁴ (2.0)	9/17 (0)		8/18 (0)	13/25 (0)	11/18 (0.1)	7/16 (0.1)	15/22 (0.6)		6/16 (0)		11/21 (0)	6/16 (0)	10/32 (0)				11/16 (0.5)	12/14 (1.7)											
Ssa0183BSFU			17/24 (0.9)			8/18 (0)								21/32 (0.7)	10/13 (0.9)		7/11 (0.2)	9/11 (1.0)												
Ssa202DU															4/13 (0.4)					5/12 (0.1)	10/12 (1.3)									
Ssa0233BSFU								7/21 (0)																						
Ssa1265BSFU																														
Ssa0182ECIG																														
Ssa06																				total	Ssa06	LOD	theta							
OMM5037	31/32 (7.7)																	15/15 (4.5)	10/10 (3.0)	11/11 (3.3)	14/15 (2.9)	13/13 (3.9)	12/12 (3.6)	12/12 (3.6)	118/120	OMM5037	31.7	0.02		
Ssa0074ECIG				25/25 (7.5)				17/21 (1.9)			14/14 (4.2)	21/21 (6.3)	20/21 (4.6)												97/102	Ssa0074ECIG	22	0.05		
Ssa0376BSFU			23/25 (4.5)	18/18 (5.4)	25/25 (7.5)			21/23 (4.0)	20/21 (4.6)	14/16 (3.2)	14/14 (4.2)			32/32 (9.6)	13/13 (3.9)	15/15 (4.5)	11/11 (3.3)	11/11 (3.3)	15/16 (3.2)	14/14 (4.2)	12/12 (3.6)	13/13 (3.9)			271/279	Ssa0376BSFU	68.2	0.03		
Ssa0789BSFU		16/16 (2.9)	23/25 (4.5)				14/16 (3.2)									14/14 (4.2)	11/11 (3.3)	10/10 (3.0)	14/15 (2.9)	14/14 (4.2)	11/11 (3.3)	13/13 (3.9)			140/145	Ssa0789BSFU	34.2	0.03		
Ssa0043BSFU																11/13 (1.5)	5/5 (1.5)	10/10 (3.0)	14/16 (3.2)		11/11 (3.3)	13/13 (3.9)			64/68	Ssa0043BSFU	13.9	0.06		
Ssa0103aECIG				19/19 (5.4)																						19/19	E15190_1379	5.7	0	
Ssa0142BSFU																13/13 (3.9)	11/11 (3.3)	11/11 (3.3)	14/15 (2.9)	14/14 (4.2)	12/12 (3.6)	7/7 (2.1)			82/83	Ssa0142BSFU	22.6	0.01		
Ssa0350BSFU																4/4 (1.2)	11/11 (3.3)	11/11 (3.3)	15/16 (3.2)	14/14 (4.2)	12/12 (3.6)	5/5 (1.5)	72/73		Ssa0350BSFU	19.7	0.01			
Ssa1299BSFU						17/18 (3.7)		22/23 (5.1)									11/11 (3.3)	11/11 (3.3)			12/12 (3.6)	12/12 (3.6)			85/87	Ssa1299BSFU	22.1	0.02		
Ssa0752BSFU																10/10 (3.0)	10/10 (3.0)				11/11 (3.3)	13/13 (3.9)			44/44	Ssa0752BSFU	12.6	0		
Ssa03																														
Ssa0649BSFU																														
Ssa0343BSFU				6/19 (0.6)																										
OMM1272			11/24 (0)																											
Ssa0017BSFU								8/22 (0.3)				8/15 (0)																		
ESTNV_29224_109																														
Ssa0368BSFU	18/34 (0)	9/17 (0)					9/16 (0.1)			14/17 (1.7)		10/21 (0)	8/21 (0.3)	17/31 (0.1)							8/14 (0.1)	9/12 (0.7)								
Ssa0818BSFU				11/25 (0.1)	10/20 (0)			6/21 (0.9)						7/12 (0.1)		3/10 (0.4)	4/11 (0.2)	8/16 (0)												
Ssa0212BSFU																														
Ssa0516BSFU																														
OMM5019																														
OMM1267																														
SsaD144																														
OMM5037/2																														
Ssa0676BSFU																														

¹Family (2009 year class where family ID's are given as XX, values below). ²Chromosome number shown in Ssa0X. ³Number of offspring for which genotype/phenotype agree / number of offspring for which genotype/phenotype disagree. ⁴LOD score corresponding to the ratio of correct genotype/phenotype matches:incorrect genotype/phenotype matches in a given family.