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CORRECTION

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Correction to: Quantitative trait loci for resistance to *Flavobacterium psychrophilum* in rainbow trout: effect of the mode of infection and evidence of epistatic interactions

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Correction to: Fraslin et al. *Genet Sel Evol* (2018) 50:60

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After publication of this work [1], we noted that there was an error in Table 3 Line 4: ^bOmy2_{Omy3} should be ^bOmy21_{Omy3}.

The correct Table 3 is included here.

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Table 3 Results of QTL analysis using the model M2 for resistance trait following injection or immersion challenges

Infection route	QTL	LRTmax	Position (cM)	CI (95%)	Increase in survival rate		Resistance origin		P value fixed effect	P value interaction
					Fixed_R (%)	Fixed_S (%)	Fixed_R	Fixed_S		
IMMERSION	Omy17 _{Omy3}	13.97*	61	0–92	38	7	AP2	AP2	***	NS
	Omy25a _{Omy3}	10.41*	4	0–35	10	18	B57	B57	***	NS
<i>Type 1 interaction</i>										
INJECTION	^a Omy3 _{Omy29}	15.27**	89	46–105	16	47	AP2	AP2	***	***
IMMERSION	^b Omy21 _{Omy3}	15.35**	97	63–104	4	39	B57	B57	***	***
	^b Omy3 _{Omy21}	40.73***	87	82–93	20	55	AP2	AP2	***	***
	^c Omy3 _{Omy2}	35.66***	87	81–94	17	44	AP2	AP2	***	***
INJECTION	^a Omy29.2 _{Omy3}	14.85*	23	8–49	5	48	B57	AP2	***	*
	Omy17 _{Omy25a}	15.85**	73	53–79	11	53	AP2	B57	***	***
IMMERSION	Omy7.2 _{Omy21}	11.48*	7	0–103	5	31	AP2	B57	***	***
<i>Type 2 interaction</i>										
INJECTION	^d Omy25a _{Omy3}	25.49***	14	10–18	53	16	B57	B57	***	*
	^d Omy3 _{Omy25a}	35.35***	89	86–92	59	22	AP2	AP2	***	***
	Omy26 _{Omy29}	11.75*	18	0–34	30	26	AP2	AP2	***	***
INJECTION	Omy17 _{Omy29}	18.29***	74	58–92	47	11	AP2	B57	***	***
IMMERSION	Omy24 _{Omy2}	12.71*	4	0–19	20	1	B57	AP2	***	***
<i>Type 3 interaction</i>										
IMMERSION	Omy7.1 _{Omy2}	16.42**	61	32–87	19	19	B57	AP2	***	***

The table presents chromosome-wide or genome-wide significant QTL detected for STATUS using model M2; Reciprocal interactions could be tested only for QTL detected in the first STATUS analysis (model M1); LRTmax = maximum of likelihood ratio test; Position in the genetic map in centimorgans (cM); CI = confidence interval; Chromosome-wide significant = * $P \leq 0.01$; Genome-wide significant = *** $P \leq 0.05$ or **** $P \leq 0.01$; P values for fixed effect and interaction corrected with Benjamini–Hochberg method: Non-significant = NS; * P value ≤ 0.05 ; *** P value ≤ 0.001

^a The reciprocal interaction could not be tested as a new QTL (Omy29.2_{Omy3}-QTL) was detected with the reciprocal model

^{b,d} Reciprocal models for QTL pairs

^c The QTL in the reciprocal model (Omy2_{Omy3}-QTL) was only suggestive ($P \leq 0.05$) at the chromosome-wide level

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