

## 1    **Supporting Information**

## 2    **Supplementary Figures**

3    Fig. S1. Linear and geometric morphometric traits measured in this study. We set 19 landmarks  
4    (red circles) and measured 17 linear traits (blue bars) as well as throat color (blue circle). See Tab.  
5    1 for trait abbreviations. Suction proxy (SucP) is the distance along the body axes from the  
6    anterior-most point of the premaxillary bone to the junction of dorsal and head scales.

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Fig. S2. Variation in linear morphometric traits among males grouped by habitat and throat color.  
a) Residuals of 16 size-corrected linear traits, see Tab. 1 for abbreviations. Nearshore / red-throated males tend to be on average larger-headed and deeper-bodied and show a larger dorsal fin (Tab. 1).  
b) PCA for the 16 size-corrected linear traits with individuals grouped by throat color and nest habitat. c) Body size distribution of males sampled in 2007, 2013 and 2015. Nearshore / red-throated males tend to be on average larger than offshore / orange males (Tab. 1). Differences in body size between years are likely due to variation in sampling dates and growth rates depending on different winter conditions in these years.

Fig. S3. Variation in body shape among males grouped by habitat and throat color, showing a trend for shorter heads and more slender bodies in offshore / orange males. Grey outlines show body shape at PC/CV=0 and black outlines the respective values indicated by the axis label. a) & b) Principal component analysis results of male overall shape variation. PC axes 2 and 3 are shown, as the first PC axes reflects bending. c) & d) Canonical variance analysis results of male overall shape variation for males grouped into nearshore vs. offshore (c) and red vs. orange (d) males.

Fig. S4. Stomach content and stable isotope data for males from 2007. a) Stomach contents: Offshore / orange males tended to have more copepods and cladocerans, as well as more stickleback eggs in their stomachs, while nearshore / red stickleback had more chironomids and isopods, in line with their proximity to terrestrial habitats. b) & c) Carbon depletion (b) tends to be stronger in nearshore / red stickleback and they tend to occupy an on average higher trophic position (c) than offshore / orange males, however these differences are not significant (Tab. 1).

# 31    **Supplementary Tables**

32    Table S1. Candidate genes in genomic islands with functions relevant to phenotypic differentiation among Jordeweiher stickleback males.

Island	Gene name	Gene	Ensembl*	Relevant GO terms / GO super-terms
C.2a	insulin-like growth factor 1b receptor	igf1rb	14729	camera-type eye-development, photoreceptor cell maintenance
C.2a	LEO1 homolog, Paf1/RNA polymerase II complex component	leo1	14999	melanocyte differentiation
C.2b	cyclic nucleotide gated channel beta 1a	cngb1a	17581	visual perception
C.2b	forkhead box B1a	foxb1a	17597	visual learning
C.3	RAB18B, member RAS oncogene family	rab18b	16395	eye development
C.3	forkhead box C1a	foxc1a	16468	camera-type eye-development
H.11	recoverin a	rcvrna	14486	cone photoresponse recovery
H.11	granulin a	grna	14616	neural retina development
H.11	ribosomal protein L27	rpl27	14635	erythrocyte differentiation
HC.12	ATPase, H <sup>+</sup> transporting, lysosomal accessory protein 1b	atp6ap1b	11378	eye pigment granule organization, melanosome organization, retina development in camera-type eye, retinal pigment epithelium development
HC.12	premelanosome protein b	pmelb	11605	developmental pigmentation, melanosome organization
HC.14	ribosomal protein L7a	rpl7a	15957	embryonic eye morphogenesis
H.16	gap junction protein, alpha 3	gja3	1367	post-embryonic eye morphogenesis
H.16	intraflagellar transport 88 homolog	ift88	1380	eye photoreceptor cell development, photoreceptor cell maintenance
HC.18	RAB32a, member RAS oncogene family	rab32a	11637	melanosome organization
HC.18	ribosomal protein S7	rps7	11913	nucleate erythrocyte
C.18b	opsin 8, group member b	opn8b	12337	G-protein coupled photoreceptor activity, phototransduction
C.20c	glyceraldehyde-3-phosphate dehydrogenase	gapdh	10219	nucleate erythrocyte
C.20c	Ras interacting protein 1	rasip1	10504	nucleate erythrocyte
C.20c	interleukin 11a	il11a	10508	retinal ganglion cell
C.20c	recoverin 2	rcvrn2	10601	cone photoresponse recovery
C.20c	PRP31 pre-mRNA processing factor 31 homolog (yeast)	prpf31	11464	retina development in camera-type eye
C.20c	PRP3 pre-mRNA processing factor 3 homolog (yeast)	prpf3	11792	retina development in camera-type eye
H.21a	RAB18A, member RAS oncogene family	rab18a	1694	eye development
H.21a	Kruppel-like factor 6a	klf6a	1778	erythrocyte maturation

Island	Gene name	Gene	Ensembl*	Relevant GO terms / GO super-terms
H.21a	ATP-binding cassette, sub-family A (ABC1), member 4a	abca4a	2000	visual perception
H.21a	cyclic nucleotide gated channel beta 3	cngb3	2128	visual perception
H.21b	nephronophthisis 3	nphp3	3823	visual perception

33 \*Ensembl-Gene ID, e.g. ENSGACG000000001778 shown as 1778.

34 Table S2. Table of QTLs and outlier regions identified in previous studies overlapping with genomic islands from this study. PVE: percentage of variance  
 35 explained, OutR: outlier region.

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
QTL	chrII	1,554,409	5,248,887	associated marker $\pm$ 1 Mb	body shape	landmark x23	9.5	C.2a	Rogers <i>et al.</i> 2012
QTL	chrII	2,554,409	13,504,821	1.5-LOD region as reported	feeding	row 2 joint raker number	5.3	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	2,554,409	13,504,821	1.5-LOD region as reported	feeding	row 3 epi raker number	6.4	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	2,554,409	21,574,761	1.5-LOD region as reported	feeding	joint raker number	4.7	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	2,554,409	21,574,761	1.5-LOD region as reported	body shape	non-ray-bearing postanal pterygiophore number	5.5	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	4,086,475	7,655,992	1.5-LOD region as reported	feeding	epibranchial 1 length	6.7	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	4,248,797	21,574,761	1.5-LOD region as reported	feeding	opercle width	7.5	C.2a	Miller <i>et al.</i> 2014
QTL	chrII	4,786,748	21,574,761	1.5-LOD region as reported	defence	dorsal spine 2 length	3.9	C.2a	Miller <i>et al.</i> 2014
QTL	chrIII	4,622,006	16,690,554	1.5-LOD region as reported	feeding	premaxilla length	3.7	C.3, H.3	Miller <i>et al.</i> 2014
QTL	chrVII	26,760,481	30,314,299	associated marker $\pm$ 1 Mb	body shape	landmark x25	12.8	H.7	Rogers <i>et al.</i> 2012
QTL	chrVII	26,760,481	30,314,299	associated marker $\pm$ 1 Mb	body shape	landmark x24	13.3	H.7	Rogers <i>et al.</i> 2012
QTL	chrVII	26,882,412	30,850,397	1.5-LOD region as reported	feeding	premaxilla length	3.9	H.7	Miller <i>et al.</i> 2014
QTL	chrVII	27,760,481	30,850,397	1.5-LOD region as reported	feeding	opercle width	5.4	H.7	Miller <i>et al.</i> 2014
QTL	chrVII	27,760,481	30,850,397	1.5-LOD region as reported	feeding	dentary height	5.7	H.7	Miller <i>et al.</i> 2014
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	complete vs. reduced pelvis		H.7	Shapiro <i>et al.</i> 2004
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	pelvis asymmetry	13.5	H.7	Shapiro <i>et al.</i> 2004
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	ascending branch height	22.2	H.7	Shapiro <i>et al.</i> 2004
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	pelvic girdle length	27.8	H.7	Shapiro <i>et al.</i> 2004
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	pelvic spine length	43.7	H.7	Shapiro <i>et al.</i> 2004
QTL	chrVII	28,313,620	30,314,299	associated marker $\pm$ 1 Mb	defence	mendelian pelvic locus		H.7	Cresko <i>et al.</i> 2004
QTL	chrX	3,320,834	8,666,776	1.5-LOD region as reported	feeding	dorsal toothplate 1 tooth number	4.2	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	8,666,776	1.5-LOD region as reported	feeding	dorsal toothplate 2 tooth number	7.6	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	12,662,644	1.5-LOD region as reported	feeding	ventral toothplate tooth number	3.6	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	12,662,644	1.5-LOD region as reported	body shape	last postanal pterygiophore position	4.4	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	12,662,644	1.5-LOD region as reported	defence	serration number on dorsal spine 2	6.1	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	12,662,644	1.5-LOD region as reported	defence	serration area on dorsal spine 2	6.7	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,320,834	16,084,203	1.5-LOD region as reported	feeding	all raker number	3.0	C.10	Miller <i>et al.</i> 2014
QTL	chrX	3,962,473	16,084,203	1.5-LOD region as reported	feeding	joint raker number	4.4	C.10	Miller <i>et al.</i> 2014
QTL	chrX	5,838,691	7,839,293	associated marker $\pm$ 1 Mb	feeding	tooth number	3.3	C.10	Cleves <i>et al.</i> 2014
QTL	chrX	6,287,740	16,084,203	1.5-LOD region as reported	feeding	row 6 joint raker number	6.4	C.10	Miller <i>et al.</i> 2014
QTL	chrX	6,838,691	16,084,203	1.5-LOD region as reported	feeding	row 7 hypo raker number	5.5	C.10	Miller <i>et al.</i> 2014

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
QTL	chrXII	498,629	9,007,257	associated marker $\pm$ 1 Mb	body shape	landmark y12	9.0	HC.12	Rogers <i>et al.</i> 2012
QTL	chrXII	498,629	9,007,257	associated marker $\pm$ 1 Mb	body shape	body depth	9.0	HC.12	Rogers <i>et al.</i> 2012
QTL	chrXII	498,629	9,007,257	associated marker $\pm$ 1 Mb	body shape	landmark y6	11.0	HC.12	Rogers <i>et al.</i> 2012
QTL	chrXII	3,528,005	15,130,396	1.5-LOD region as reported	feeding	opercle neck width	8.4	HC.12	Miller <i>et al.</i> 2014
QTL	chrXII	3,528,005	19,667,912	1.5-LOD region as reported	feeding	dorsal toothplate 1 width	5.2	HC.12	Miller <i>et al.</i> 2014
QTL	chrXII	3,830,036	11,751,243	1.5-LOD region as reported	feeding	ceratobranchial 4 length	3.5	HC.12	Miller <i>et al.</i> 2014
QTL	chrXII	3,830,036	19,667,912	1.5-LOD region as reported	feeding	dentary height	6.9	HC.12	Miller <i>et al.</i> 2014
QTL	chrXII	3,830,195	5,551,755	1.5-LOD region as reported	feeding	dorsal toothplate 2 width	4.4	HC.12	Miller <i>et al.</i> 2014
QTL	chrXII	4,551,614	6,551,755	associated marker $\pm$ 1 Mb	body shape	landmark x25	11.1	HC.12	Rogers <i>et al.</i> 2012
QTL	chrXII	5,551,749	15,130,396	1.5-LOD region as reported	feeding	premaxilla length	3.7	HC.12	Miller <i>et al.</i> 2014
QTL	chrXIV	1	12,440,728	1.5-LOD region as reported	feeding	in-lever 1 of articular length	5.3	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	9,939,598	1.5-LOD region as reported	feeding	epibranchial 1 length	4.0	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	ceratobranchial 1 length	3.5	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	ceratobranchial 4 length	3.6	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	ceratobranchial 5 length	3.7	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	premaxilla length	3.8	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	articular length	3.9	HC.14	Miller <i>et al.</i> 2014
QTL	chrXIV	2,698,856	15,188,529	1.5-LOD region as reported	feeding	premaxilla height	5.2	HC.14	Miller <i>et al.</i> 2014
QTL	chrXVI	16,413,003	18,202,793	1.5-LOD region as reported	feeding	medial gill raker length	6.0	H.16	Glazer <i>et al.</i> 2015
QTL	chrXVI	16,413,003	18,202,793	1.5-LOD region as reported	feeding	lateral gill raker length	6.3	H.16	Glazer <i>et al.</i> 2015
QTL	chrXVI	16,413,003	18,202,793	1.5-LOD region as reported	feeding	middle gill raker length	9.1	H.16	Glazer <i>et al.</i> 2015
QTL	chrXVII	763,556	16,509,762	associated marker $\pm$ 1 Mb	body shape	landmark x25	9.5	C.17	Rogers <i>et al.</i> 2012
QTL	chrXVII	2,058,474	5,290,116	1.5-LOD region as reported	feeding	ceratobranchial 1 length	3.7	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	5,290,116	1.5-LOD region as reported	feeding	ceratobranchial 3 length	4.1	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	5,290,116	1.5-LOD region as reported	feeding	hypo raker number	5.1	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	15,509,762	1.5-LOD region as reported	feeding	dentary height	4.6	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	15,509,762	1.5-LOD region as reported	feeding	ceratobranchial 2 length	4.9	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	15,509,762	1.5-LOD region as reported	feeding	dentary length	7.5	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	2,058,474	20,254,136	1.5-LOD region as reported	feeding	middle raker spacing	3.3	C.17	Miller <i>et al.</i> 2014
QTL	chrXVII	4,466,582	17,136,436	1.5-LOD region as reported	feeding	ventral tooth plate tooth number	7.3	C.17	Ellis <i>et al.</i> 2015
QTL	chrXVIII	5,070,409	12,934,334	1.5-LOD region as reported	feeding	ventral tooth plate intertooth spacing	9.9	HC.18	Ellis <i>et al.</i> 2015
QTL	chrXVIII	7,613,260	15,688,949	1.5-LOD region as reported	feeding	all raker number	2.8	HC.18, C.18a, C.18b	Miller <i>et al.</i> 2014
QTL	chrXVIII	9,393,393	12,520,434	1.5-LOD region as reported	body shape	frontal width	3.8	HC.18	Miller <i>et al.</i> 2014



Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
QTL	chrXVIII	9,393,393	14,194,268	1.5-LOD region as reported	feeding	ceratobranchial 1 length	2.9	HC.18, C.18a, C.18b	Miller <i>et al.</i> 2014
QTL	chrXVIII	11,520,276	13,520,434	associated marker $\pm$ 1 Mb	body shape	body shape:dorsal extent of the ascending branch of the pelvis (x)	4.5	HC.18, C.18a, C.18b	Albert <i>et al.</i> 2008
QTL	chrXVIII	11,520,276	13,520,434	associated marker $\pm$ 1 Mb	body shape	body shape:dorsal extent of ectocorocoid (x)	5.5	HC.18, C.18a, C.18b	Albert <i>et al.</i> 2008
QTL	chrXVIII	11,520,276	13,520,434	associated marker $\pm$ 1 Mb	body shape	body shape:posterior extent of ectocorocoid (x)	5.7	HC.18, C.18a, C.18b	Albert <i>et al.</i> 2008
QTL	chrXVIII	11,520,276	13,520,434	associated marker $\pm$ 1 Mb	body shape	body shape:anterior extent of ectocorocoid (y)	5.7	HC.18, C.18a, C.18b	Albert <i>et al.</i> 2008
QTL	chrXVIII	11,520,276	13,520,434	associated marker $\pm$ 1 Mb	body shape	body shape:posterior extent of premaxilla (x)	6.3	HC.18, C.18a, C.18b	Albert <i>et al.</i> 2008
QTL	chrXX	3,763,571	15,500,733	1.5-LOD region as reported	feeding	lateral gill raker length	6.5	C.20b, C.20c, C.20d	Glazer <i>et al.</i> 2015
QTL	chrXX	3,806,402	15,047,247	1.5-LOD region as reported	feeding	gill raker number adult	11.5	C.20b, C.20c, C.20d	Glazer <i>et al.</i> 2014
QTL	chrXX	3,806,402	19,341,384	1.5-LOD region as reported	feeding	gill raker number adult	9.7	C.20b, C.20c, C.20d	Glazer <i>et al.</i> 2014
QTL	chrXX	3,831,311	16,942,924	associated marker $\pm$ 1 Mb	defence	pelvic girdle length	11.7	C.20b, C.20c, C.20d	Rogers <i>et al.</i> 2012
QTL	chrXX	4,831,311	7,907,076	1.5-LOD region as reported	feeding	all raker number	18.1	C.20b, C.20c	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	11,260,235	1.5-LOD region as reported	feeding	row 1 raker number	8.6	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	11,260,235	1.5-LOD region as reported	feeding	branchial arch 1 raker number	11.0	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	12,244,188	1.5-LOD region as reported	defence	anal spine length	6.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	12,244,188	1.5-LOD region as reported	feeding	branchial arch 2 raker number	13.6	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	12,244,188	1.5-LOD region as reported	feeding	odd row raker number	15.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	12,244,188	1.5-LOD region as reported	feeding	cerato raker number	25.3	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	body shape	frontal width	3.2	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	defence	dorsal spine 2 area	4.7	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 2 raker number	7.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	dorsal toothplate 2 tooth number	7.6	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	dorsal toothplate 1 tooth number	8.8	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 4 raker number	10.2	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 4 cerato raker number	11.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 5 raker number	11.6	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 6 cerato raker number	11.7	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 3 raker number	12.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	lateral raker spacing	12.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 5 cerato raker number	13.0	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 9 cerato raker number	13.2	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 2 cerato raker number	13.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 7 cerato raker number	13.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 6 raker number	13.7	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 1 cerato raker number	14.3	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	middle raker spacing	14.8	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	even row raker number	16.4	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	body shape	supraoccipital crest width	16.6	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	row 3 cerato raker number	16.9	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,175,213	1.5-LOD region as reported	feeding	branchial arch 3 raker number	17.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	16,433,340	1.5-LOD region as reported	feeding	row 8 raker number	7.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	defence	dorsal spine 3 length	3.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	feeding	premaxilla height	4.5	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	feeding	ventral toothplate width	5.0	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	body shape	vertebrae number	5.2	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	defence	serration number on dorsal spine 2	8.0	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	feeding	branchial arch 4 raker number	8.1	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	4,831,311	18,002,157	1.5-LOD region as reported	defence	serration area on dorsal spine 2	9.0	C.20b, C.20c, C.20d	Miller <i>et al.</i> 2014
QTL	chrXX	6,027,562	15,047,247	1.5-LOD region as reported	feeding	gill raker number adult	22.4	C.20b, C.20c, C.20d	Glazer <i>et al.</i> 2014
QTL	chrXX	6,907,076	8,907,472	associated marker $\pm$ 1 Mb	body shape	landmark y27	9.3	C.20c	Rogers <i>et al.</i> 2012
QTL	chrXX	8,194,876	18,002,157	1.5-LOD region as reported	feeding	ventral toothplate tooth number	5.4	C.20d	Miller <i>et al.</i> 2014
QTL	chrXXI	1,811,555	3,811,729	associated marker $\pm$ 1 Mb	body shape	landmark y26	10.0	H.21a	Rogers <i>et al.</i> 2012
QTL	chrXXI	1,811,555	3,811,729	associated marker $\pm$ 1 Mb	body shape	landmark y25	10.6	H.21a	Rogers <i>et al.</i> 2012
QTL	chrXXI	1,811,555	3,811,729	associated marker $\pm$ 1 Mb	defence	plate number in aa f2s	23.2	H.21a	Colosimo <i>et al.</i> 2004
QTL	chrXXI	2,811,555	9,041,896	1.5-LOD region as reported	body shape	third predorsal pterygiophore position	5.4	H.21a	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	defence	dorsal spine 2 length	3.0	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	ceratobranchial 1 length	3.0	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	hypo raker number	4.2	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	ceratobranchial 3 length	4.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	body shape	frontal width	4.9	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	defence	dorsal spine 1 length	5.0	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	in-lever 2 of articular length	5.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	articular length	5.8	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	ceratobranchial 4 length	5.9	H.21a, H.21b	Miller <i>et al.</i> 2014

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	body shape	total postanal pterygiophore number	5.9	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	body shape	last postdorsal pterygiophore position	6.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	dorsal toothplate 1 width	6.5	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	ceratobranchial 5 length	6.5	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	defence	dorsal spine 3 length	6.7	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	premaxilla length	7.2	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	dentary length	7.2	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	ventral toothplate length	10.7	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	premaxilla height	12.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,811,555	13,187,908	1.5-LOD region as reported	feeding	epibranchial 1 length	15.5	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	2,969,125	4,969,333	associated marker $\pm$ 1 Mb	defence	lateral plate number	10.0	H.21a	Peichel <i>et al.</i> 2001
QTL	chrXXI	2,969,333	9,021,249	associated marker $\pm$ 1 Mb	defence	lateral plate-b qtl		H.21a	Cresko <i>et al.</i> 2004
QTL	chrXXI	3,930,309	5,930,456	associated marker $\pm$ 1 Mb	feeding	tooth plate area	14.7	H.21a	Cleves <i>et al.</i> 2014
QTL	chrXXI	4,642,714	14,055,502	1.5-LOD region as reported	feeding	epibranchial 1 length	6.7	H.21a, H.21b	Erickson <i>et al.</i> 2014
QTL	chrXXI	4,930,309	13,187,908	1.5-LOD region as reported	feeding	dorsal toothplate 1 tooth number	7.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	4,939,045	6,939,294	associated marker $\pm$ 1 Mb	feeding	tooth spacing	7.3	H.21a	Cleves <i>et al.</i> 2014
QTL	chrXXI	5,777,108	13,187,908	1.5-LOD region as reported	feeding	epibranchial 1 length	9.3	H.21a, H.21b	Erickson <i>et al.</i> 2014
QTL	chrXXI	5,939,045	13,187,908	1.5-LOD region as reported	body shape	last postanal pterygiophore position	12.3	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	5,939,045	13,187,908	1.5-LOD region as reported	feeding	dorsal toothplate 2 width	15.4	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	5,939,045	13,187,908	1.5-LOD region as reported	feeding	ventral toothplate tooth number	26.2	H.21a, H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	6,709,145	9,264,690	95% confidence interval as reported	feeding	tooth number	31.5	H.21a	Cleves <i>et al.</i> 2014
QTL	chrXXI	7,914,244	13,187,908	1.5-LOD region as reported	feeding	ventral toothplate width	23.6	H.21b	Miller <i>et al.</i> 2014
QTL	chrXXI	8,072,478	12,912,828	1.5-LOD region as reported	feeding	ventral tooth plate tooth number	13.5	H.21b	Ellis <i>et al.</i> 2015
QTL	chrXXI	9,041,658	13,187,908	1.5-LOD region as reported	feeding	dorsal toothplate 2 tooth number	7.8	H.21b	Miller <i>et al.</i> 2014
OutR	chrII	4,879,721	4,895,041	exact region as reported				C.2a	Feulner <i>et al.</i> 2015
OutR	chrII	4,968,220	4,994,219	exact region as reported				C.2a	Feulner <i>et al.</i> 2015
OutR	chrII	5,130,902	5,156,901	exact region as reported				C.2a	Feulner <i>et al.</i> 2015
OutR	chrII	22,113,185	23,708,229	outlier microsat $\pm$ 1 Mb				C.2b	Mäkinen <i>et al.</i> 2008
OutR	chrII	23,642,336	23,672,335	exact region as reported				C.2b	Feulner <i>et al.</i> 2015
OutR	chrIII	7,925,000	9,936,000	outlier microsat $\pm$ 1 Mb				C.3	DeFaveri <i>et al.</i> 2011
OutR	chrIII	10,209,638	10,288,125	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,256,795	10,270,838	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,260,001	10,270,000	exact region as reported				H.3	Feulner <i>et al.</i> 2015

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
OutR	chrIII	10,298,113	10,326,112	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,423,312	10,498,345	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,600,650	10,625,505	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,626,713	10,750,873	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,805,589	10,830,135	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrIII	10,849,624	10,934,254	exact region as reported				H.3	Feulner <i>et al.</i> 2015
OutR	chrVII	28,101,770	30,101,909	outlier microsat $\pm$ 1 Mb				H.7	Mäkinen <i>et al.</i> 2008
OutR	chrVII	29,357,287	30,850,397	outlier microsat $\pm$ 1 Mb				H.7	Mäkinen <i>et al.</i> 2008
OutR	chrXI	14,309,864	16,310,001	outlier microsat $\pm$ 1 Mb				H.11	DeFaveri <i>et al.</i> 2011
OutR	chrXI	16,359,445	17,646,579	outlier microsat $\pm$ 1 Mb				H.11	Kaeuffer <i>et al.</i> 2011
OutR	chrXII	4,329,168	18,644,933	exact region as reported				HC.12	Feulner <i>et al.</i> 2015
OutR	chrXII	5,330,664	5,365,913	exact region as reported				HC.12	Feulner <i>et al.</i> 2015
OutR	chrXII	5,756,782	5,777,305	exact region as reported				HC.12	Marques <i>et al.</i> 2016
OutR	chrXVII	4,945,848	4,971,907	exact region as reported				C.17	Feulner <i>et al.</i> 2015
OutR	chrXVIII	334,676	15,953,870	exact region as reported				HC.18, C.18a, C.18b	Feulner <i>et al.</i> 2015
OutR	chrXX	1	1,570,921	outlier microsat $\pm$ 1 Mb				C.20a	DeFaveri <i>et al.</i> 2011
OutR	chrXX	618,036	639,311	exact region as reported				C.20a	Jones <i>et al.</i> 2012
OutR	chrXX	654,064	660,088	exact region as reported				C.20a	Jones <i>et al.</i> 2012
OutR	chrXX	669,147	672,859	exact region as reported				C.20a	Jones <i>et al.</i> 2012
OutR	chrXX	674,015	686,169	exact region as reported				C.20a	Jones <i>et al.</i> 2012
OutR	chrXX	1,569,221	18,771,174	exact region as reported				C.20b, C.20c, C.20d	Feulner <i>et al.</i> 2015
OutR	chrXX	3,830,764	12,260,847	outlier microsat $\pm$ 1 Mb		species diagnostic marker		C.20b, C.20c, C.20d	Malek <i>et al.</i> 2012
OutR	chrXX	5,229,935	5,265,934	exact region as reported				C.20b	Feulner <i>et al.</i> 2015
OutR	chrXX	5,534,011	5,536,418	exact region as reported				C.20b	Jones <i>et al.</i> 2012
OutR	chrXX	5,537,509	5,539,221	exact region as reported				C.20b	Jones <i>et al.</i> 2012
OutR	chrXX	5,738,160	5,776,342	exact region as reported				C.20b	Feulner <i>et al.</i> 2015
OutR	chrXX	5,880,398	5,885,735	exact region as reported				C.20b	Jones <i>et al.</i> 2012
OutR	chrXX	6,030,687	6,034,687	exact region as reported				C.20b	Jones <i>et al.</i> 2012
OutR	chrXX	6,082,919	6,233,437	exact region as reported				C.20b	Feulner <i>et al.</i> 2015
OutR	chrXX	6,929,309	6,940,558	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	6,980,238	7,007,237	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	6,987,798	7,014,797	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	6,993,687	7,003,686	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,029,059	7,075,058	exact region as reported				C.20c	Feulner <i>et al.</i> 2015

Type	Chrom.	Start	End	Confidence interval	Trait category	Trait	PVE	Overlapping island	Reference
OutR	chrXX	7,338,374	7,360,411	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,357,075	7,420,074	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,691,924	7,794,108	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,754,461	7,817,481	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,886,470	7,921,469	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	7,899,308	7,905,715	exact region as reported				C.20c	Jones <i>et al.</i> 2012
OutR	chrXX	7,924,665	7,937,687	exact region as reported				C.20c	Jones <i>et al.</i> 2012
OutR	chrXX	7,939,687	7,942,187	exact region as reported				C.20c	Jones <i>et al.</i> 2012
OutR	chrXX	7,955,271	8,000,270	exact region as reported				C.20c	Feulner <i>et al.</i> 2015
OutR	chrXX	8,003,537	10,004,159	outlier microsat $\pm$ 1 Mb				C.20c, C.20d	Mäkinen <i>et al.</i> 2008
OutR	chrXXI	4,900,560	4,918,709	exact region as reported				H.21a	Jones <i>et al.</i> 2012
OutR	chrXXI	4,920,167	4,928,691	exact region as reported				H.21a	Jones <i>et al.</i> 2012
OutR	chrXXI	5,361,805	5,378,230	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	5,573,572	5,684,081	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	5,655,189	5,676,188	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	5,664,149	5,674,148	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	5,768,854	5,951,853	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	6,100,266	6,276,857	exact region as reported				H.21a	Feulner <i>et al.</i> 2015
OutR	chrXXI	6,868,953	6,951,952	exact region as reported				H.21a	Feulner <i>et al.</i> 2015

36 Note that the genomic coordinates are based on the re-assembly reference genome (Glazer et al. 2015).













