Variation in the genomic basis of parallel phenotypic and ecological divergence in benthic and pelagic morphs of Icelandic Arctic charr (*Salvelinus alpinus*)

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Data accessibility: Data and R code is archived on Dryad and Zenodo (DOI:https://doi.org/10.5061/dryad.05qfttf58). All R code is also archived on Github (https://github.com/PhDMattyB/Icelandic_Charr_Genomics).

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Supplementary tables and figures:

Table S1. Outlier loci identified using pcadapt and Bayescan within each population and were subsequently removed to account for selection in fastsimcoal2.

Population	**Pcadapt outliers**	**Bayescan outliers**	**Total outliers removed**
Galtabol	40	0	40
Svínavatn	41	12	53
Þingvallavatn	16	437	453
Vatnshlíðarvatn	5	0	5

Table S2. AIC model comparison of divergence history models across four polymorphic populations of Icelandic Arctic charr. Models with the lowest AIC and ΔAIC indicate the best fit between the observed and expected site frequency spectra. IM = Isolation by migration; CIM = Change in isolation by migration; SC = Secondary contact; MT = Morph type. The digit refers to the number of morphs within each demographic analysis.

Population	**Model**	**AIC**	**ΔAIC**
Galtaból	2IM	10779.2	887.4
	CIM	9891.8	0
	2SC	10655.2	763.4
Svínavatn	2IM	4147.5	236.1
	CIM	3911.4	0
	2SC	3936.1	24.7
Þingvallavatn	3IM	5329.6	22494
	3IM_MT	5254.7	2174.5
	3_SC	3080.2	0
	3_SC_MT	5358.5	2278.3
Vatnshlíðarvatn	2IM	1440.8	0
	CIM	1450.7	9.9
	2SC	1445.1	4.3

Table S3. Test of phenotypic parallelism in body shape among five benthic-pelagic morph pairs across four polymorphic populations of Icelandic Arctic charr. Bolded values indicate significant differences in benthic-pelagic divergence trajectories. The angles of divergence vectors are shown above the diagonal while the magnitude of body shape differences are shown below the diagonal.

Benthic-pelagic morph pair	G: Benthic-pelagic	S: Benthic-pelagic	T: Benthic 1-pelagic	T: Benthic 2-pelagic	V: Benthic-pelagic
G: Benthic-pelagic	-	2.60	1.21	0.88	**0.05**
S: Benthic-pelagic	0.043	-	2.47	2.80	2.66
T: Benthic 1-pelagic	0.017	0.035	-	0.33	1.16
T: Benthic 2-pelagic	0.014	0.034	0.0046	-	0.83
V: Benthic-pelagic	0.0067	0.037	0.012	0.0091	-

Table S4. ANOVA tests to compare mean Fst values between trait associated RDA outliers and neutral SNPs as well as between the three different RDA outlier types for four benthic-pelagic morph pairs from three Icelandic lakes.

Comparison	Morph pair		Df	Sum.sq	Mean.sq	F-value	p-value
RDA outliers vs Neutral SNPs	G: Benthic-pelagic	Value	1	1.159	1.1585	932.1	<0.001
		Residuals	14185	17.613	0.0012		
	S: Benthic-pelagic	Value	1	28.18	28.181	32873	<0.001
		Residuals	14185	12.16	0.001		
	T: Benthic 1-pelagic	Value	1	15.80	15.801	29448	<0.001
		Residuals	14198	7.62	0.001		
	T: Benthic 2-pelagic	Value	1	12.33	12.332	23414	<0.001
		Residuals	14200	7.479	0.001		
RDA outlier types	G: Benthic-pelagic	Value	2	15.68	7.842	235.2	<0.001
		Residuals	412	13.74	0.033		
	S: Benthic-pelagic	Value	2	0.043	0.022	0.268	0.765
		Residuals	317	25.65	0.081		
	T: Benthic 1-pelagic	Value	2	0.002	0.0008	0.012	0.988
		Residuals	299	20.17	0.067		
	T: Benthic 2-pelagic	Value	2	0.43	0.215	2.754	0.065
		Residuals	300	23.45	0.782		

Table S5. Number of overlapping 200 Kb windows across all benthic and pelagic morph pairs with significant trait associated outlier loci. Above the diagonal indicates the number of shared outlier 200Kb regions associated with morphology, resource use, and both traits combined, respectively. Below the diagonal indicates the number of Fst outlier loci and 200Kb Fst outlier regions that are shared across morph pairs.

Benthic-pelagic morph pair	G: Benthic-pelagic	S: Benthic-pelagic	T: Benthic 1-pelagic	T: Benthic 2-pelagic
G: Benthic-pelagic	—	0, 0, 2	0, 0, 1	0, 0, 0
S: Benthic-pelagic	265, 12	—	0, 0, 2	0, 0, 0
T: Benthic 1-pelagic	187, 8	186, 7	—	1, 0, 3
T: Benthic 2-pelagic	185, 4	185, 4	281, 18	—
V: Benthic-pelagic	216, 11	236, 11	168, 5	171, 4

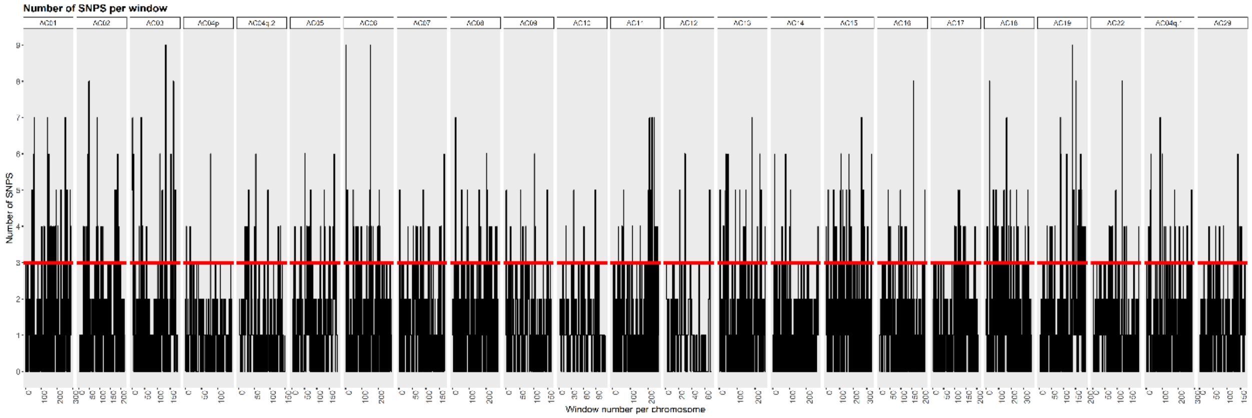

Figure S1. SNP density across the Arctic charr genome for a common set of 14,187 SNPs across four polymorphic populations of Icelandic Arctic charr. The red line indicates a cut off of three SNPs per 200Kb sliding window.

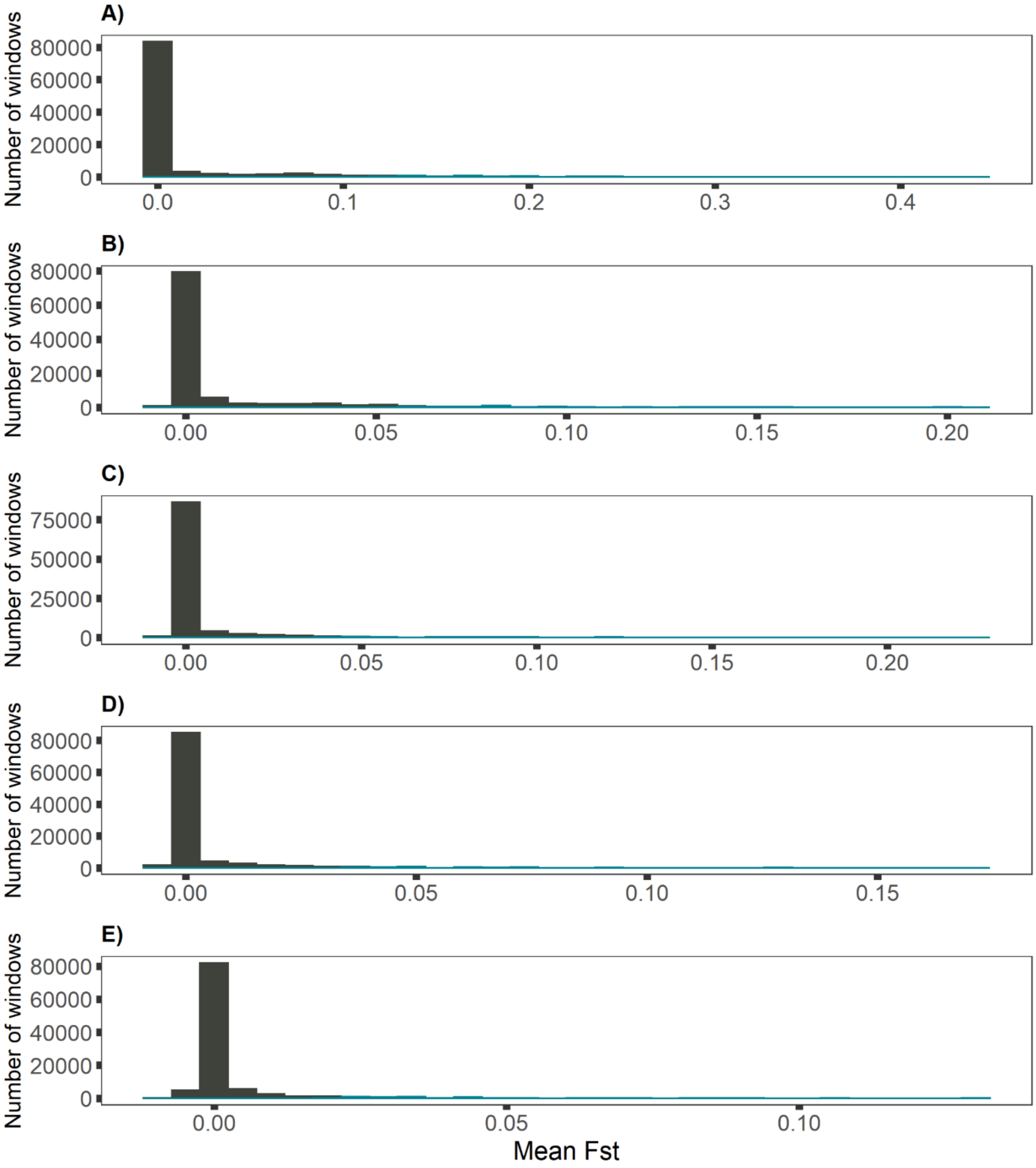

Figure S2. Fst distributions of 200Kb windows across the genome of polymorphic populations of Icelandic Arctic charr. Neutral windows are shown in grey and Fst outlier windows are shown in blue. A) Galtaból, B) Svínavatn, C) Þingvallavatn: Benthic 1 – pelagic, D) Þingvallavatn: Benthic 2 – pelagic, E) Vatnshlíðarvatn

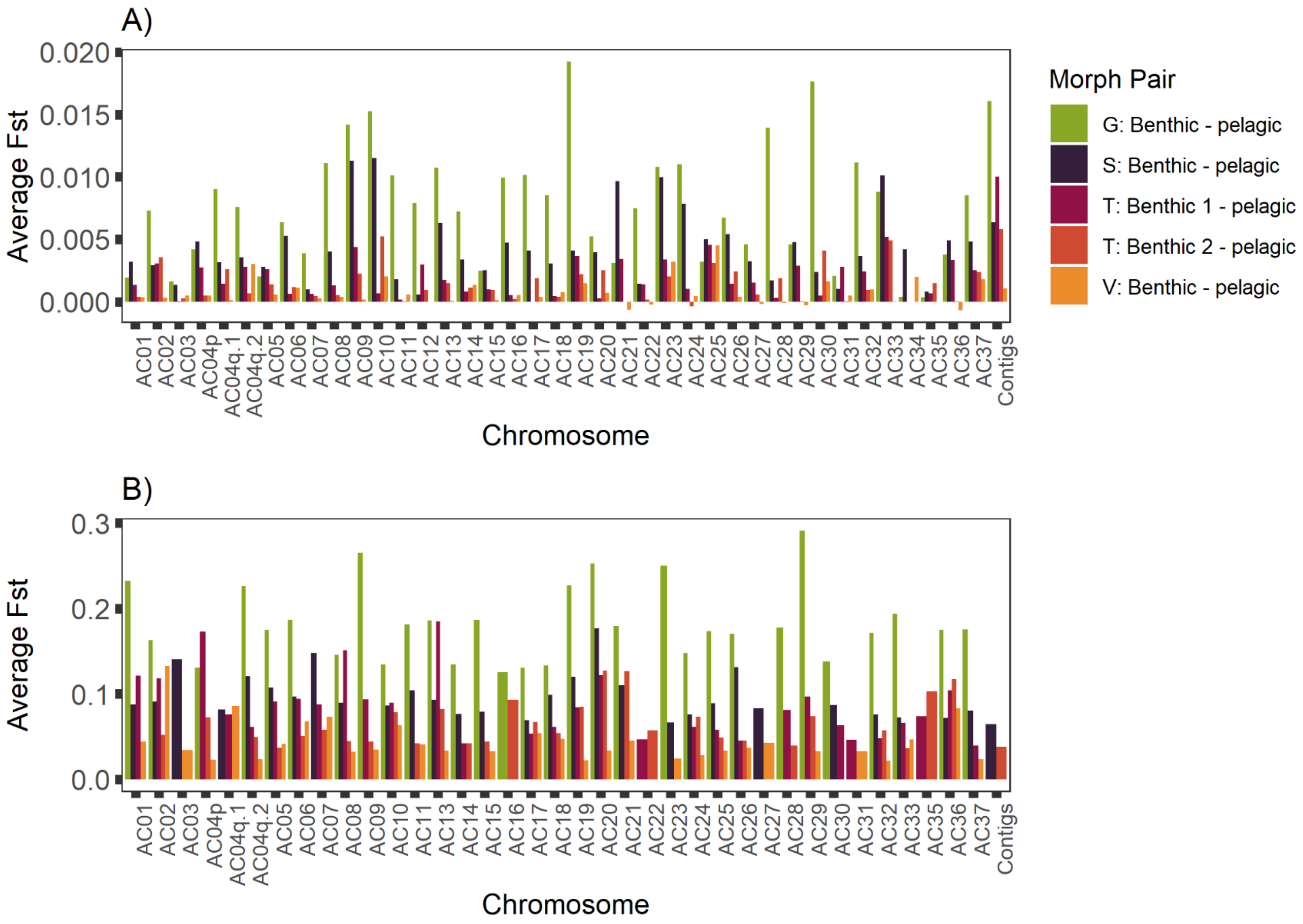

Figure S3. Average Fst values for 200Kb outlier windows per chromosome for each sympatric benthic and pelagic morph pair of Icelandic Arctic charr. A) Average Fst values of neutral 200Kb windows. B) Average Fst values of outlier 200Kb windows.

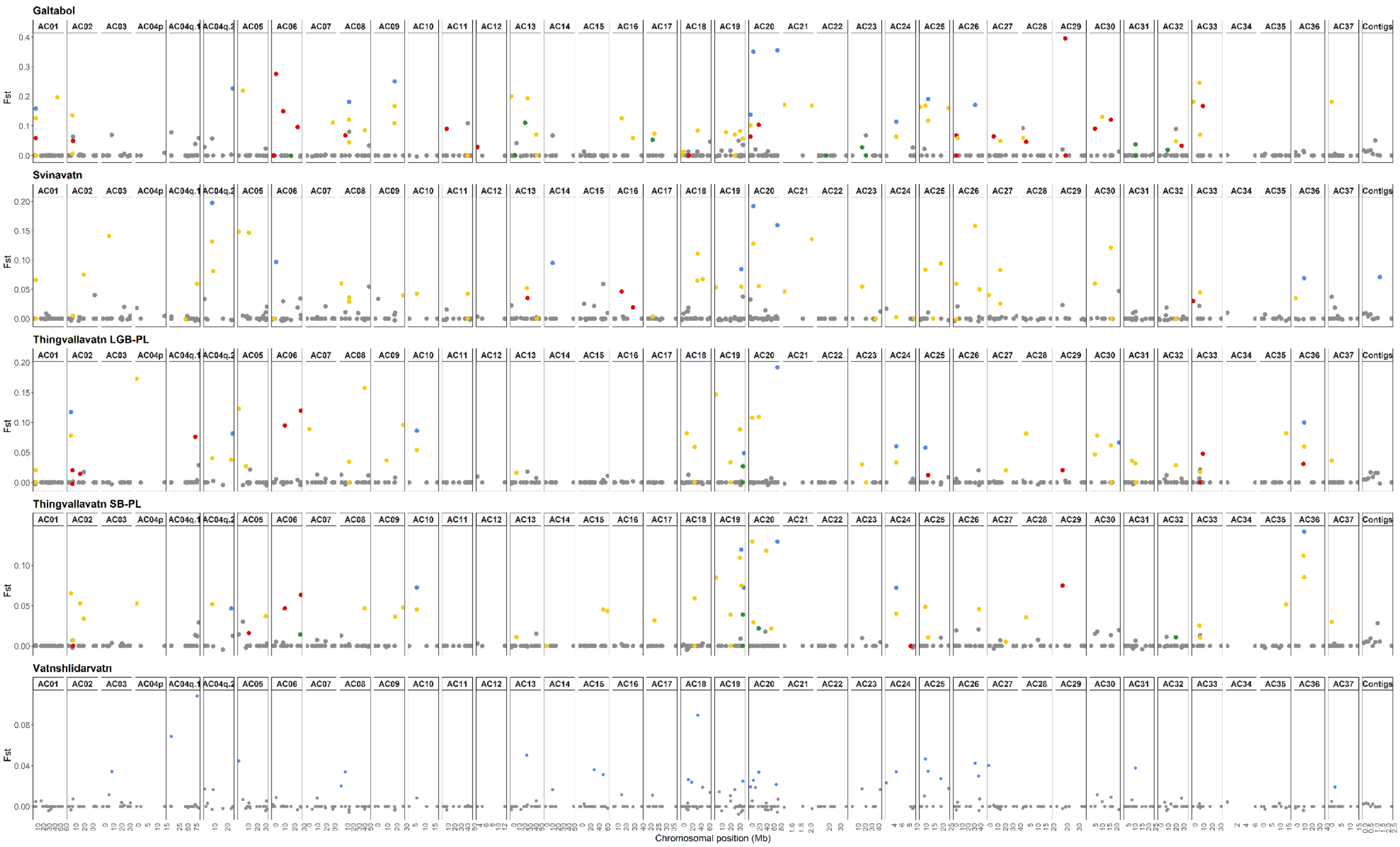

Figure S4. Genomic divergence within 200Kb windows along chromosomes of sympatric benthic and pelagic morphs of Icelandic Arctic charr. Colouration of different points distinguishes neutral windows from outliers as well as the different outlier types. Neutral windows are shown in grey, FST outliers are shown in light blue, shared FST outliers are shown in dark blue, morphological RDA outliers are shown in red, resource use RDA outliers are shown in green, and overlapping RDA outliers are shown in yellow. A) Galtaból. B) Svínavatn. C) Þingvallavatn: benthic 1 – pelagic, D) Þingvallavatn: benthic 2 – pelagic, E) Vatnshlíðarvatn.

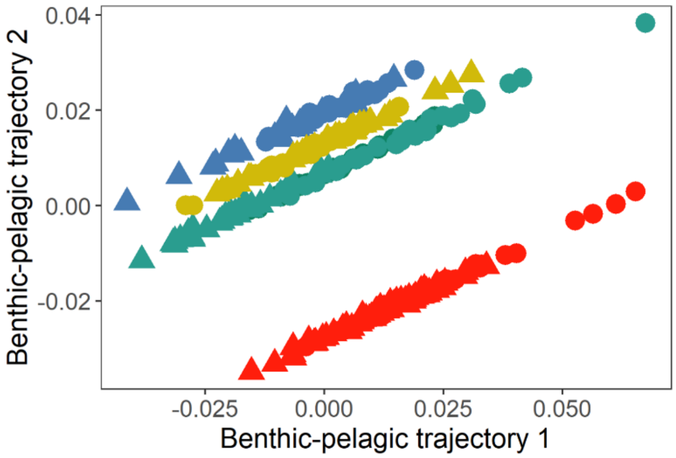

Figure S5. Phenotypic divergence trajectories across five benthic and pelagic morph pairs of Arctic charr from four geographically separated lakes in Iceland. Galtaból is shown in blue; Svínavatn in red; Þingvallavatn in green, and Vatnshlíðarvatn in yellow. Circles and Triangles represent benthic and pelagic morphs, respectively. Phenotypic divergence trajectories for each benthic and pelagic morph pair. All partial warp and uniform component scores were projected onto PC1 and PC2, the major axes of phenotypic variation, with all populations combined. Divergence trajectories were then calculated by summarizing the covariance between PC1 and PC2 for further tests of parallelism.