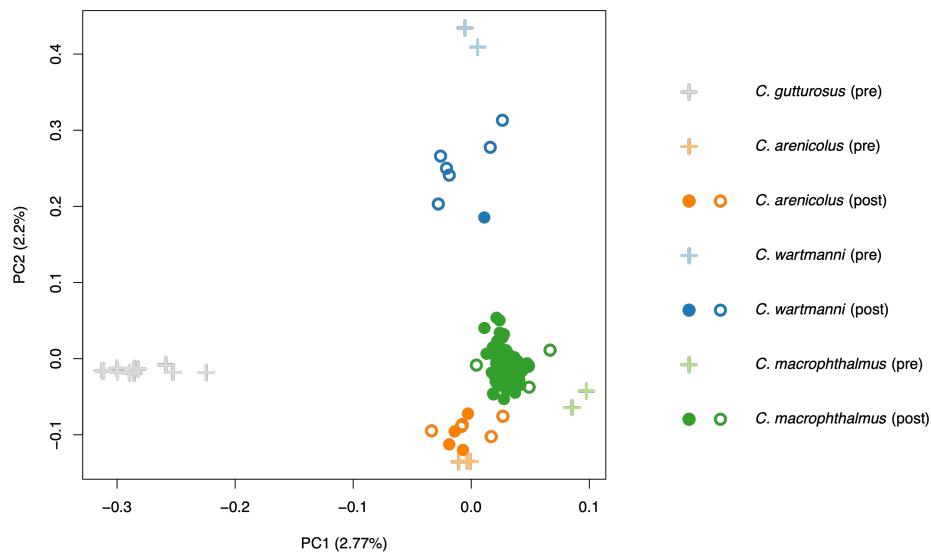
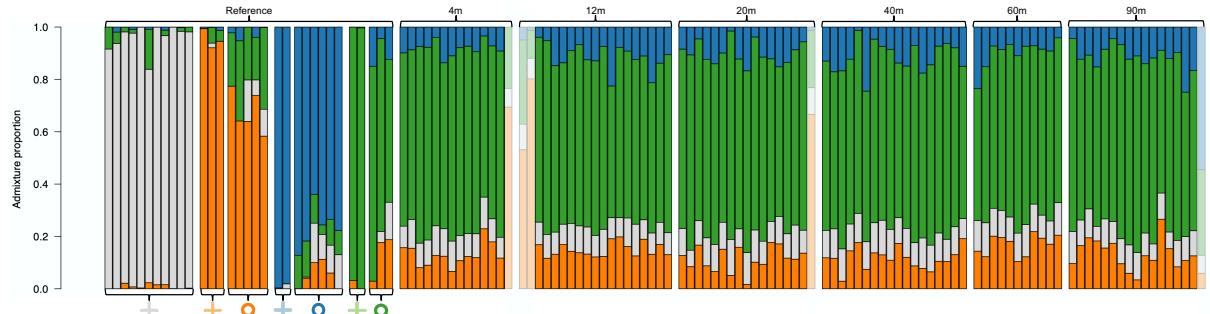


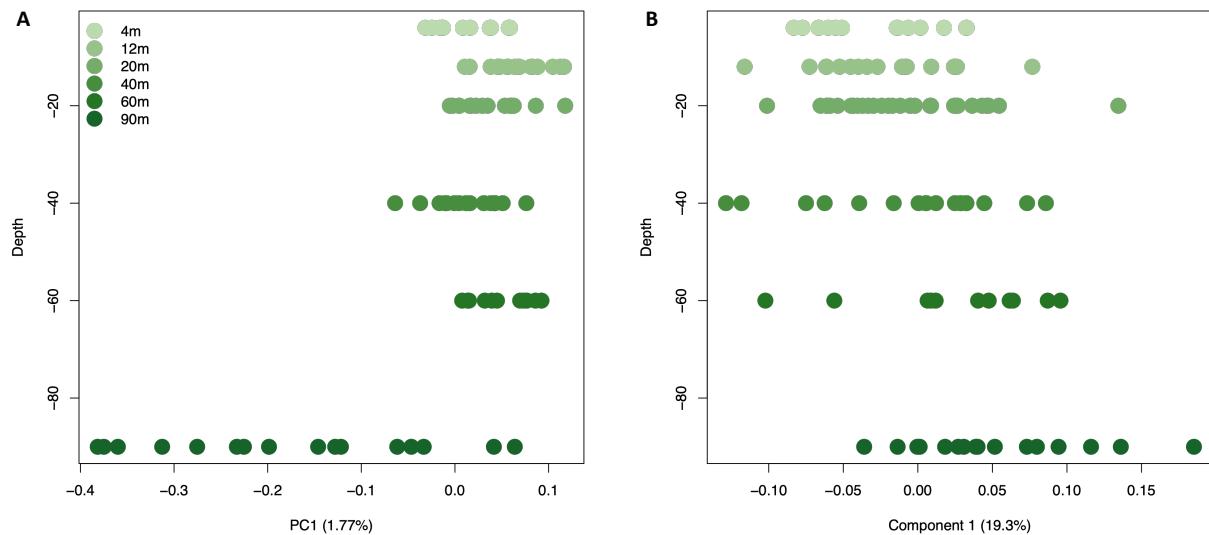
Supplementary Information



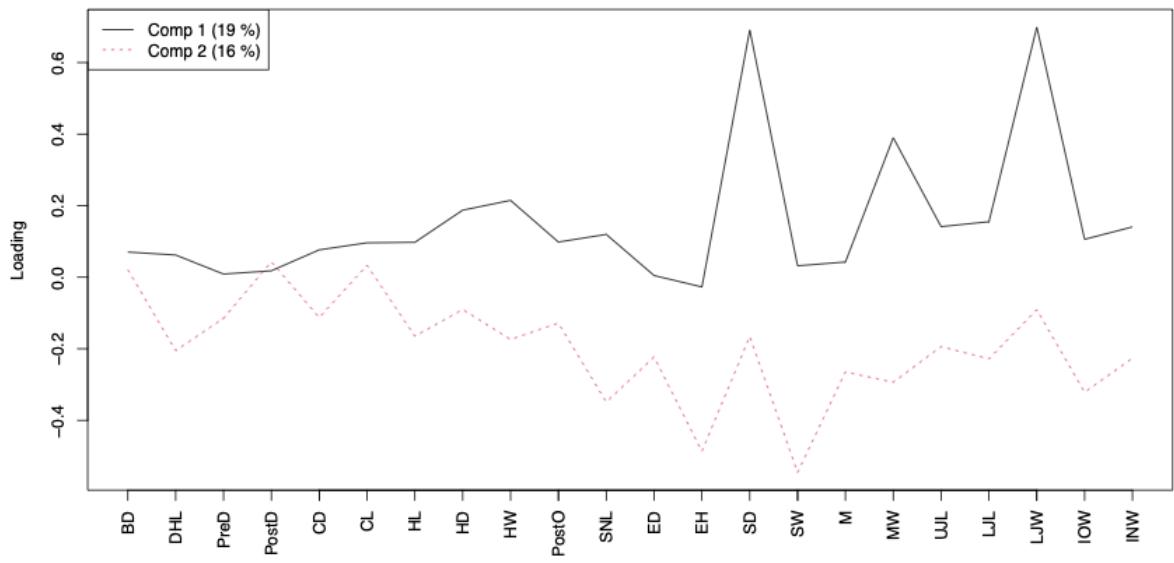
Supplementary Figure 1: PCA including all available Lake Constance samples. Grey is *C. gutturosus*, blue is *C. wartmanni*, green is *C. macrophthalmus* and orange is *C. areniculus* (see legend to the right). Pre-eutrophication samples from Frei et al. (2022) are indicated with crosses, post-eutrophication samples are indicated with circles. Filled circles are samples caught in the depth transect sampling of this study, empty circles are from Frei et al. (2022).



Supplementary Figure 2: Structure analysis, using all depth transect samples and all samples used in Frei et al. (2022). Grey is *C. gutturosus*, blue is *C. wartmanni*, green is *C. macrophthalmus* and orange is *C. arenicola*. Reference samples from Frei et al. (2022) are divided into pre-eutrophication (crosses) and post-eutrophication (empty circles) samples. Samples are grouped into the six spawning depth populations, and individuals that were assigned to *C. wartmanni* or *C. arenicola* are shaded.



Supplementary Figure 3: **A)** Principal component 1 of the genomic PCA against depth including all caught *C. macrophthalmus* individuals. There was a significant correlation of PC1 with depth ($\rho=-0.37$, $p=0.0003$). **B)** Component 1 of the partial least squares analysis against depth. There was a significant correlation of component 1 with depth ($\rho=-0.44$, $p=2e-6$).



Supplementary Figure 4: Loadings of each trait of the partial least squares regression analysis (Figure 1D and Supplementary Figure 3B). All 22 morphometric traits and their loading on component 1 and 2 of the partial least squares regression analysis. The three traits with highest (positive) loadings on component 1 are LJW (lower jaw width), SD (snout depth) and MW (mouth width). The three traits with highest (negative) loadings on component 2 are SW (snout width), EH (eye height) and SNL (snout length).

Supplementary Table 1: D-statistic results for the test of introgression during eutrophication from *C. gutturosus* into each of the spawning depth populations. The table includes the ordering of the populations on the four-taxon topology used for the ABBA BABA test, as well as the resulting D values, Z-scores and p-values of the block-jackknife approach in 5 Mb blocks.

D	Z	P-value	P1	P2	P3	Outgroup
0.02	5.81	0.00	<i>C. macrophthalmus</i> pre (n=2)	4m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)
0.01	4.78	0.00	<i>C. macrophthalmus</i> pre (n=2)	12m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)
0.02	5.97	0.00	<i>C. macrophthalmus</i> pre (n=2)	20m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)
0.02	6.31	0.00	<i>C. macrophthalmus</i> pre (n=2)	40m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)
0.02	5.46	0.00	<i>C. macrophthalmus</i> pre (n=2)	60m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)
0.01	4.19	0.00	<i>C. macrophthalmus</i> pre (n=2)	90m	<i>C. gutturosus</i> pre (n=11)	<i>S. salar</i> (n=1)

Supplementary Table 2: D-statistic results for the test of introgression during eutrophication from *C. wartmanni* into each of the spawning depth populations. The table includes the ordering of the populations on the four-taxon topology used for the ABBA BABA test, as well as the resulting D values, Z-scores and p-values of the block-jackknife approach in 5 Mb blocks.

D	Z	P-value	P1	P2	P3	Outgroup
0.01	2.82	0.00	<i>C. macrophthalmus</i> pre (n=2)	4m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)
0.01	3.72	0.00	<i>C. macrophthalmus</i> pre (n=2)	12m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)
0.01	4.05	0.00	<i>C. macrophthalmus</i> pre (n=2)	20m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)
0.01	4.54	0.00	<i>C. macrophthalmus</i> pre (n=2)	40m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)
0.01	3.72	0.00	<i>C. macrophthalmus</i> pre (n=2)	60m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)
0.01	2.43	0.02	<i>C. macrophthalmus</i> pre (n=2)	90m	<i>C. wartmanni</i> pre (n=2)	<i>S. salar</i> (n=1)

Supplementary Table 3: D-statistic results for the test of introgression during eutrophication from *C. arenicolus* into each of the spawning depth populations. The table includes the ordering of the populations on the four-taxon topology used for the ABBA BABA test, as well as the resulting D values, Z-scores and p-values of the block-jackknife approach in 5 Mb blocks.

D	Z	P-value	P1	P2	P3	Outgroup
0.00	0.52	0.60	<i>C. macrophthalmus</i> pre (n=2)	4m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)
0.00	-0.56	0.57	<i>C. macrophthalmus</i> pre (n=2)	12m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)
0.00	-0.52	0.60	<i>C. macrophthalmus</i> pre (n=2)	20m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)
0.00	-0.48	0.63	<i>C. macrophthalmus</i> pre (n=2)	40m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)
0.00	-0.19	0.85	<i>C. macrophthalmus</i> pre (n=2)	60m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)
0.00	-1.47	0.14	<i>C. macrophthalmus</i> pre (n=2)	90m	<i>C. arenicolus</i> pre (n=3)	<i>S. salar</i> (n=1)

Supplementary Table 4: Genes overlapping with any candidate SNP under selection between shallow and deep water (n=107), and their respective best Blast hits with an annotation of the genome of *Salmo salar*.

Gene name Alpine whitefish genome assembly (De-Kayne et al., 2020)	E value	Perc. identical	Accession	Description
snap_masked-PGA_scaffold11_203_contigs_length_63881516-processed-gene-283.13	2.00E-116	77.38	NP_001136192.1	RNA polymerase II subunit A C-terminal domain phosphatase SSU72
maker-PGA_scaffold11_203_contigs_length_63881516-snap-gene-418.12	0	89.89	XP_014023237.2	phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta-like
maker-PGA_scaffold11_203_contigs_length_63881516-snap-gene-480.10	0	85.07	XP_013987572.1	disks large-associated protein 4 isoform X1
maker-PGA_scaffold12_167_contigs_length_57740044-augustus-gene-463.9	3.00E-14	100	XP_045579496.1	gamma-aminobutyric acid receptor subunit beta-1 isoform X3
maker-PGA_scaffold14_173_contigs_length_55641933-snap-gene-414.19	0	97	XP_013997625.1	nucleoporin NUP188
maker-PGA_scaffold14_173_contigs_length_55641933-snap-gene-446.9	0	92.08	XP_013999495.2	lamin-B1
maker-PGA_scaffold15_168_contigs_length_54025139-augustus-gene-331.8	0	87.41	XP_045563145.1	kinesin-like protein KIF2A isoform X5
maker-PGA_scaffold15_168_contigs_length_54025139-snap-gene-398.18	0	85.17	XP_014026493.1	tenascin isoform X1
maker-PGA_scaffold17_183_contigs_length_51949489-snap-gene-114.25	0	87.47	XP_045562700.1	ARF GTPase-activating protein GIT2a isoform X2
maker-PGA_scaffold18_164_contigs_length_59907985-augustus-gene-424.0	0	87.9	XP_045544677.1	mucin-17
maker-PGA_scaffold19_147_contigs_length_54335267-snap-gene-386.8	0	91.1	XP_014004818.1	phosphatidylinositol 3-kinase regulatory subunit gamma-like isoform X1
maker-PGA_scaffold23_167_contigs_length_50329371-snap-gene-199.0	0	92.39	XP_014001415.2	laminin subunit beta-2 isoform X2
maker-PGA_scaffold23_167_contigs_length_50329371-snap-gene-487.17	1.00E-154	88.26	XP_045548802.1	FYVE, RhoGEF and PH domain-containing protein 1 isoform X1
maker-PGA_scaffold24_152_contigs_length_51033154-snap-gene-280.12	0	90.94	XP_014047632.1	rho-associated protein kinase 2 isoform X3
maker-PGA_scaffold24_152_contigs_length_51033154-snap-gene-396.16	0	85.99	XP_014051926.1	intersectin-2 isoform X1
maker-PGA_scaffold25_179_contigs_length_50922480-snap-gene-111.6	4.00E-156	87.74	XP_014025515.2	harmonin-like isoform X2
maker-PGA_scaffold26_192_contigs_length_48683376-snap-gene-73.17	0	87.65	XP_045545764.1	rap guanine nucleotide exchange factor 1 isoform X1
maker-PGA_scaffold26_192_contigs_length_48683376-snap-gene-229.16	0	91.17	XP_013984216.1	rab9 effector protein with kelch motifs
maker-PGA_scaffold26_192_contigs_length_48683376-snap-gene-381.32	0	72.26	XP_014051430.1	platelet-derived growth factor receptor beta
maker-PGA_scaffold28_172_contigs_length_4897775-snap-gene-133.10	2.00E-142	68.62	XP_014065728.2	consortin-like
maker-PGA_scaffold28_172_contigs_length_4897775-snap-gene-260.13	0	86.12	XP_014066184.1	protein jagged-2-like isoform X1
maker-PGA_scaffold29_157_contigs_length_48675208-snap-gene-407.12	0	84.5	XP_013991973.1	serine--tRNA ligase, cytoplasmic-like
maker-PGA_scaffold30_165_contigs_length_48446552-snap-gene-119.2	3.00E-73	72.61	XP_014034412.1	ras-related protein Rab-26
snap_masked-PGA_scaffold30_165_contigs_length_48446552-processed-gene-161.4	1.00E-36	92.31	XP_014034785.1	cGMP-dependent protein kinase 1 isoform X2
maker-PGA_scaffold30_165_contigs_length_48446552-snap-gene-177.15	2.00E-108	85.02	XP_014034899.2	mitochondrial import inner membrane translocase subunit Tim23

maker-PGA_scaffold33_143_contigs_length_40727438-augustus-gene-264.4	0.00E+00	94.94	XP_014014854.1	unnamed protein product
maker-PGA_scaffold38_206_contigs_length_33962415-snap-gene-84.0	3.00E-175	86.6	XP_014062081.1	EH domain-binding protein 1-like isoform X7
maker-PGA_scaffold38_206_contigs_length_33962415-snap-gene-286.7	0.00E+00	78.07	XP_014012100.1	phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform X1
maker-PGA_scaffold4_243_contigs_length_45591172-snap-gene-365.20	0.00E+00	84.47	XP_045559993.1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 isoform X3
maker-PGA_scaffold7_351_contigs_length_68138733-snap-gene-159.14	0.00E+00	98.25	XP_013998328.2	homeobox protein DLx5a-like