Table S2. Primers used for amplifying and sequencing of the mtDNA region of coregonids analyzed in this study. The position numbers for primers refer to the complete sequence of the *C. lavaretus* mitochondrial DNA (NCBI acc. AB034824); T_A–annealing temperature; C($MgCl_2$)–concentration of $MgCl_2$ in the reaction mixture.

Primer name	Position, bp	Sequence (5'-3')	Direction	T_A (C°)	C (MgCl2), mM	Source	Comment
LGL381	1987–2010	ACC CCG CCT GTT TAC CAA AAA CAT	forward	53	1.5	[75, 76]	for PCR-RFLP and sequencing
ND1pr1Rv	2571–2593	TCA CGT AGA CTT TAA TCG TTG A	reverse	53	1.5	[77]	for PCR and sequencing
ND1pr2Fr	2549–2568	CCG CTA TTA AGG GTT CGT TT	forward	51	2	[77]	for PCR and sequencing
ND1pr2Rv	3096–3113	CAT AAG GTA AGT GCG AGT GTT	reverse	51	2	[77]	for PCR and sequencing
ND1pr3Fr	3061–3080	CCC TTC CTA TTC CTC GCT AC	forward	51	2	[77]	for PCR and sequencing
ND1pr3Rv	3547–3568	GCG TAT TTA TGA GGA GAT GTT	reverse	51	2	[77]	for PCR and sequencing
ND1pr4Fr	3477–3501	ACT AGT CTC TGG GTT TAA TGT AGA A	forward	53	1.5	[77]	for PCR and sequencing
LGL563	4019–4037	GGT TCA TTA GTG AGG GAA GG	reverse	53	1.5	[76]	for PCR-RFLP and sequencing
ND1_3fw-cs	3061–3080	CCC TTC CTG TTC CTC GCT AC	forward	51	2	[26]	for PCR and sequencing; least cisco, when ND1pr3Fr does not work
ND1_3rv-csal	3547–3568	GCG TAT TTA TGA GAA GGA TGT T	reverse	51	2	[26]	for PCR and sequencing; vendace and least cisco, when ND1pr3Fr does not work
ND1_4fw-calb	3475–3499	GAA CTA GTC TCT GGC TTT AAT GTA G	forward	54	2	[26]	for PCR and sequencing; vendace, when ND1pr4Fr does not work
ND1_4fw-cta	3475–3499	GAA CTA GTC TCT GGA TTT AAT GTA G	forward	54	2	[26]	for PCR and sequencing; ciscoes, when ND1pr4Fr does not work
ND1_3rv-whf	3547–3568	GCG TAT TTA TGA GGA GGA TGT T	reverse	51	2	Present study	for PCR and sequencing; whitefish, when ND1pr4Fr does not work
ND1_4fw-whf	3475–3499	GAA CTA GTC TCT GGT TTT AAT GTA G	forward	51	2	Present study	for PCR and sequencing; whitefish, when ND1pr3Rv does not work

All PCRs were carried out in 20 µL of buffer manufactured by SinEnzyme (Russia, www.sibenzymeus.com) containing 60 mM Tris-HCl (pH 8.5 at 25°C), 25 mM KCl, 1.5 mM MgCl2, 10 mM 2-mercaptoethanol, 0.1% Triton X-100. The amplification mixture contained about 300 ng of total cell DNA, X mM MgCl2 (see in this Table); 200 nmol each of four deoxyribonucleotides, 10 pmol of forward and reverse primers, and 0.5–1.0 U of Taq

polymerase (SibEnzyme, Russia). The amplification programs in all cases involved a stage of initial denaturation of DNA 4 min at +95°C; 31 cycles of DNA fragment amplification: 30 s at +95°C, 30 s at specific for primers TA (see in this Table), and +72°C for 50 s, as well as a final chain elongation stage at +72°C for 5 min.