

Supporting information

Table S1. Values of selected explanatory variables for each lake sampled for this study on Brook Charr in Québec, Canada. For details description of the variables and their complete names see Table 2 in the main text.

Reserve	Lake	TotalHa	SinceMeanYear	MeanFishStock	NbStockEv	Depth	LakeSize	MeanTemp	MeanpH	MeanO2
Mastigouche	Abénakis (ABE)	1914.8	23.8	957.4	10	5.2	5.0	17.7	6.8	6.8
Mastigouche	Arbout (ARB)	380.0	37.8	316.7	6	8.1	5.0	18.7	6.7	6.7
Mastigouche	Chamberlain (CHA)	958.3	27.8	1916.7	9	9.9	18.0	18.4	6.8	8.1
Mastigouche	Cougouar (COU)	1668.8	30.0	953.6	14	10.8	8.0	18.7	6.9	8.1
Mastigouche	Deux-étapes (DET)	3647.2	22.1	2039.1	22	19.3	12.3	19.4	6.8	6.7
Mastigouche	Gélinotte (GEL)	1652.0	9.8	1032.5	8	5.8	5.0	16.9	6.0	6.5
Mastigouche	Grignon (GRI)	845.8	14.9	2086.3	11	19.4	29.6	19.5	6.7	7.7
Mastigouche	Jones (JON)	467.9	31.8	1637.5	8	15.2	28.0	19.9	6.8	7.8
Mastigouche	Ledoux (LED)	3956.2	33.0	13550.0	4	15.3	13.7	20.2	6.8	7.8
Mastigouche	Lemay (LEM)	913.7	37.2	2908.5	6	13.4	19.1	20.3	6.9	7.7
Portneuf	Amanites (AMA)	1108.9	16.0	261.0	35	12.3	8.0	22.2	6.7	6.7
Portneuf	Caribou (CAR)	570.0	3.5	259.0	11	12.2	5.0	23.4	6.7	6.8
Portneuf	Daphnies (DAP)	424.0	7.9	385.0	11	7.9	10.0	22.5	6.8	7.7
Portneuf	Duhamel (DUH)	1404.9	24.8	1769.0	27	24.7	34.0	22.40	6.7	6.2
Portneuf	Méhot (MET)	4660.5	11.1	981.0	38	15.5	8.0	24.5	6.7	6.8
Saint-Maurice	À la Truite (TRU)	1814.5	40.9	1684.9	7	8.0	6.5	21.3	6.2	4.8
Saint-Maurice	Brown (BRO)	114.5	44.8	7812.5	4	25.9	273.0	20.5	7.6	5.8
Saint-Maurice	Brûlot (BRU)	246.9	44.0	666.7	3	2.8	8.1	19.4	6.5	5.7
Saint-Maurice	Corbeil (COR)	526.3	45.0	2500.0	2	7.8	9.5	20.6	7.2	5.3
Saint-Maurice	Gaspard (GAS)	258.6	44.5	1500.0	2	13.9	11.6	20.4	7.6	5.1
Saint-Maurice	Maringouins (MAR)	1072.6	35.4	415.6	16	2.6	6.2	19.5	7.1	5.4
Saint-Maurice	Melchior (MEL)	454.6	44.5	1000.0	2	10.8	4.4	19.9	6.9	4.9
Saint-Maurice	Milord (MIL)	1174.5	26.1	3428.1	16	3.1	46.7	20.0	7.4	5.7
Saint-Maurice	Perdu (PER)	2292.7	36.1	3166.8	16	15.2	22.1	19.9	6.9	5.9
Saint-Maurice	Porc-Épic (POE)	1648.2	41.0	741.7	6	4.1	2.7	18.6	6.5	5.4
Saint-Maurice	Portage (POR)	1044.0	30.2	4451.3	11	8.9	46.9	20.9	7.2	5.2
Saint-Maurice	Soucis (SOU)	2803.7	39.0	750000.0	1	29.3	267.5	19.4	7.4	5.3
Saint-Maurice	Tempête (TEM)	3784.0	27.8	2056.5	23	22.9	12.5	19.8	6.6	5.4
Saint-Maurice	Vierge (VIE)	208.3	47.5	593.5	2	6.6	5.7	20.9	6.6	5.2

Table S2. Detailed methods, options and values for each filter used to identify SNPs for this study on Brook Charr in Québec, Canada.

Steps	Parameters	Value	
Adapter removal (Cutadapt v1.8.1)	AGATCGGAAGAGCGGG		
	Maximum error tolerance for barcodes recognition (e)	0.2	
STACKS workflow (v1.40)	Minimum length, reads shorter than <i>N</i> bases are discarded (m)	80	
	<i>process_radtags</i> (v1.40)	Enzymes	PstI & MspI
		Truncate final read length (bp) to this value (t)	80
		Rescue barcodes and RAD-tags (r)	True
		Clean data, remove any read with an uncalled base (c)	True
	Mapping (Gmap-Gsnap 2015-12-31.v9)	Discard reads with low quality scores (q)	True
		Maximum number of mismatches	5
		Minimum coverage	0.90
	Trimming .sam files (samtools v1.2)	Indel penalty	2
		Remove MAPQ with a value under <i>N</i>	5
<i>pstacks</i> (v1.40)	Only includes reads with none of the bits set in INT set in FLAG	4 & 1797	
	Minimum depth of coverage to report a stack (m)	4	
	Alpha	0.05	
<i>cstacks</i> (v1.40)	Model type	snp	
	Base catalog matching on genomic location (g)	True	
	Number of mismatches allowed between sample tags when generating the catalog (n)	1	
<i>sstacks</i> (v1.40)	Specify K-mer size for matching between catalog loci	Automatic	
	Base catalog matching on genomic location (g)	True	
	Minimum percentage of individuals in a population required to process a locus (r)	0.5	
<i>population</i> (v1.40)	Minimum number of populations a locus must be present in (p)	2	
	Minimum stack depth required for individuals at a locus (m)	4	
	R analysis (v3.2.3)		
<i>stackr</i> (summary_haplotypes)	Filtering for loci with more than 2 alleles	True	
Custom filtering script	Minimum allele coverage (c)	0	
	Maximum allele coverage (C)	400	
	Minimum depth, minimum copy number of an allele (m)	5	
	Maximum allelic imbalance (l)	4	
	Minimum genotype likelihood (l)	6	
	Minimum percentage of individual genotyped for each locus	0.70	
	Minor allele frequency (global and population)	0.1	
	Max number of SNPs authorized per locus	6	
Number of SNPs kept per locus	1		

Table S3. Pearson correlation matrix of pairwise correlation coefficients for environmental parameters and stocking intensity variables included in this study on Brook Charr in Québec, Canada. Bold values indicate significant correlation ($\alpha = 0.05$). * are significant after Bonferroni correction. The description of the variables presented in this table can be found in Table 2 in the main text.

	LakeSize	TotalHa	SinceMeanYear	MeanFishStock	NbStockEv	Depth	MeanTemp	MeanpH	MeanO2
LakeSize									
TotalHa	-0.01								
SinceMeanYear	0.23	-0.27							
MeanFishStock	0.68*	-0.22	0.13						
NbStockEv	-0.23	0.5	-0.59	-0.21					
Depth	0.62*	0.36	-0.05	0.46	0.2				
MeanTemp	-0.02	0.08	-0.3	-0.09	0.46	0.22			
MeanpH	0.56	-0.2	0.34	0.3	-0.18	0.28	0.12		
MeanO2	-0.19	0.09	-0.51	-0.17	0.18	0.09	-0.05	-0.2	

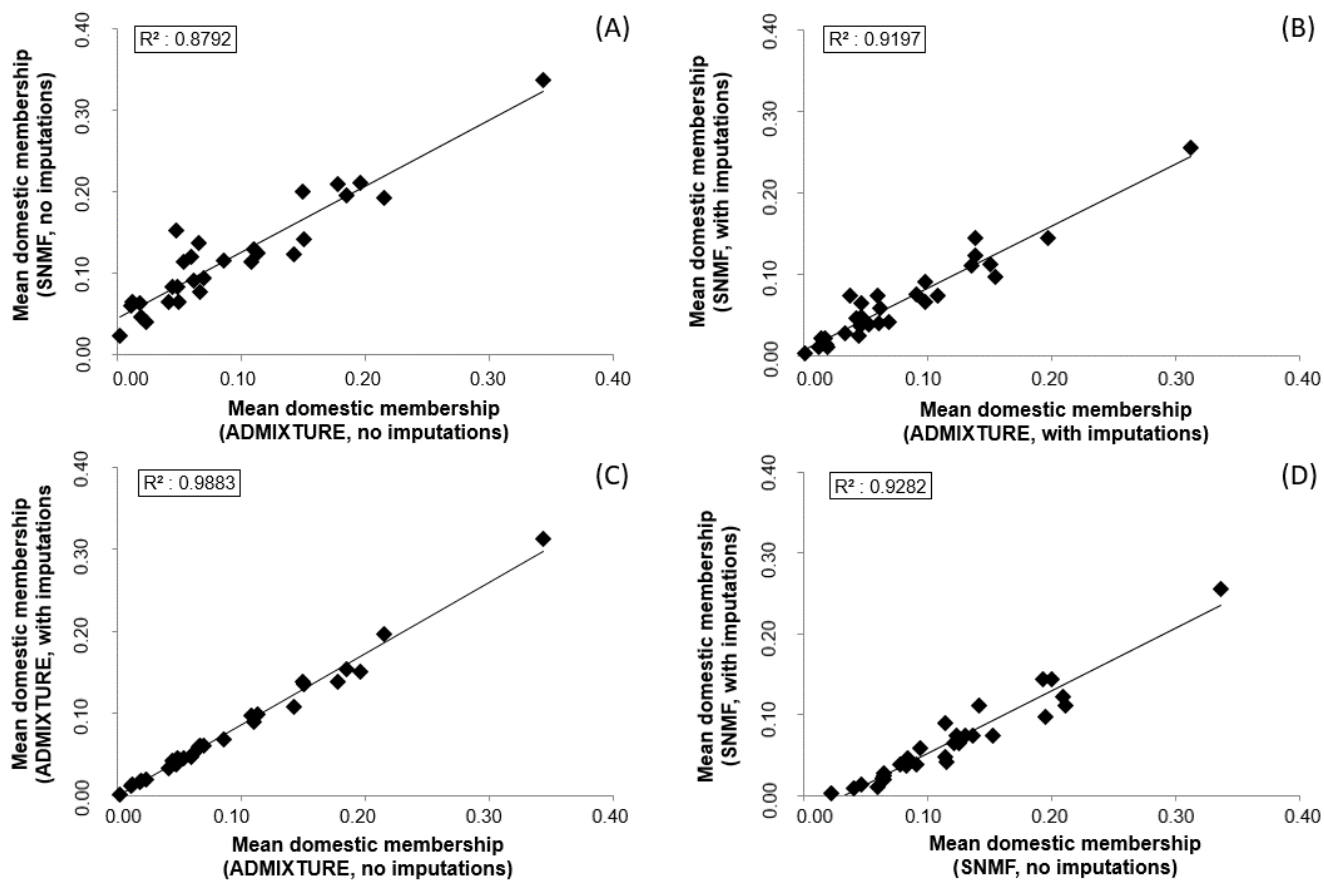
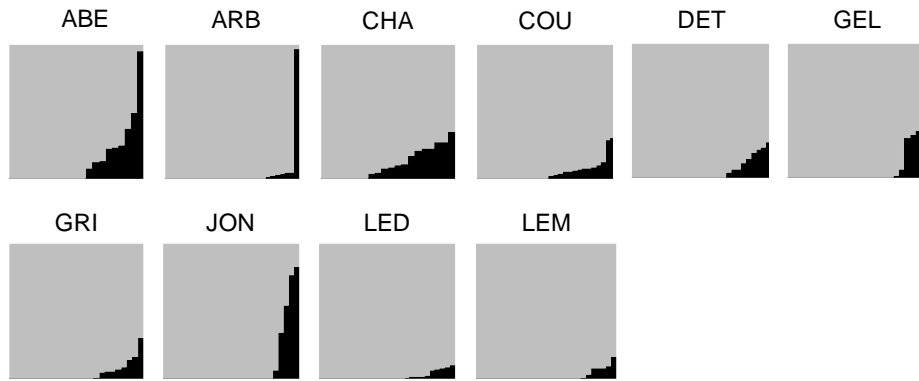
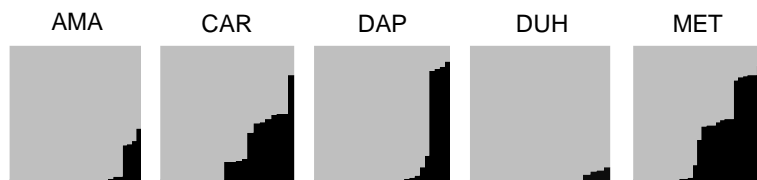


Figure S1. Comparisons of the results obtained with the software ADMIXTURE and SNMF ran with or without imputations for this study on Brook Charr in Québec, Canada. (A) Mean domestic membership obtained with SNMF without imputations as a function of the mean domestic membership obtained with ADMIXTURE without imputations. (B) Mean domestic membership obtained with SNMF with imputations as a function of mean domestic membership obtained with ADMIXTURE with imputations. (C) Mean domestic membership obtained with ADMIXTURE with imputations as a function of the mean domestic membership obtained with ADMIXTURE without imputations. (D) Mean domestic membership obtained with SNMF with imputations as a function of mean domestic membership obtained with SNMF without imputations. Black diamonds represent sampled lakes.

Mastigouche



Portneuf



Saint-Maurice

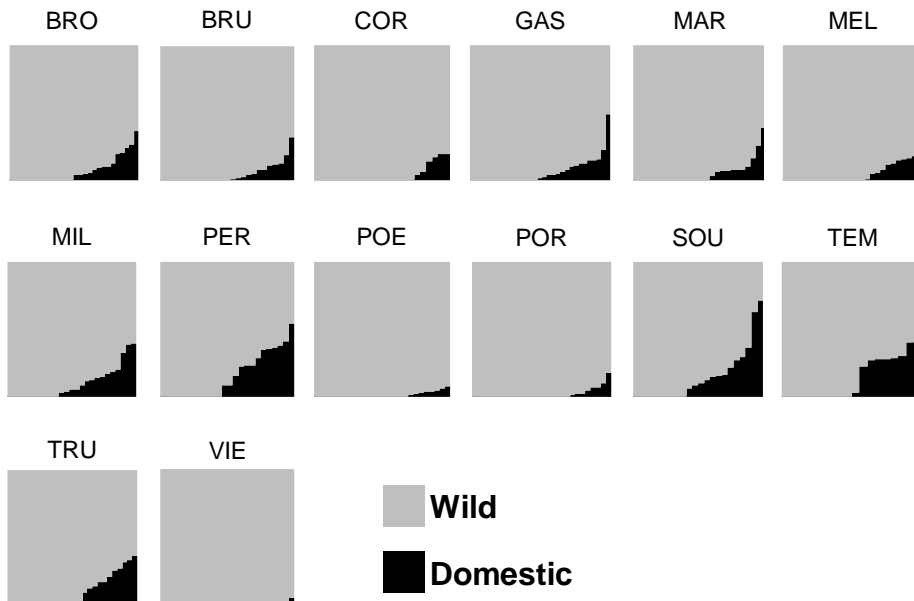


Figure S2. Bayesian individual clustering results for each lake (classified by wildlife reserve) of this study on Brook Charr in Québec, Canada. Columns represent proportion of membership of each individual to each cluster and rang from 0 to 100%.

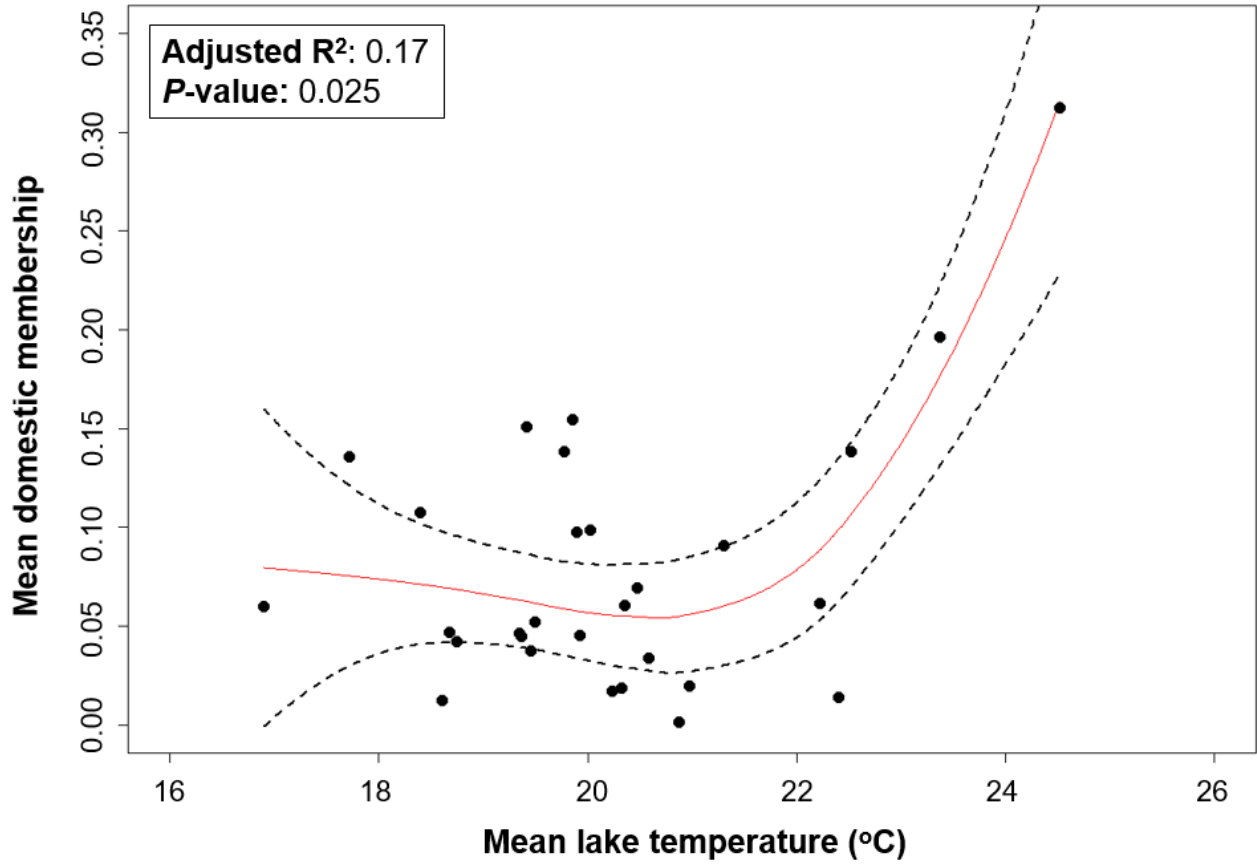


Figure S3. Mean domestic membership observed in each lake as a function of the mean temperature for this study on Brook Charr in Québec, Canada.

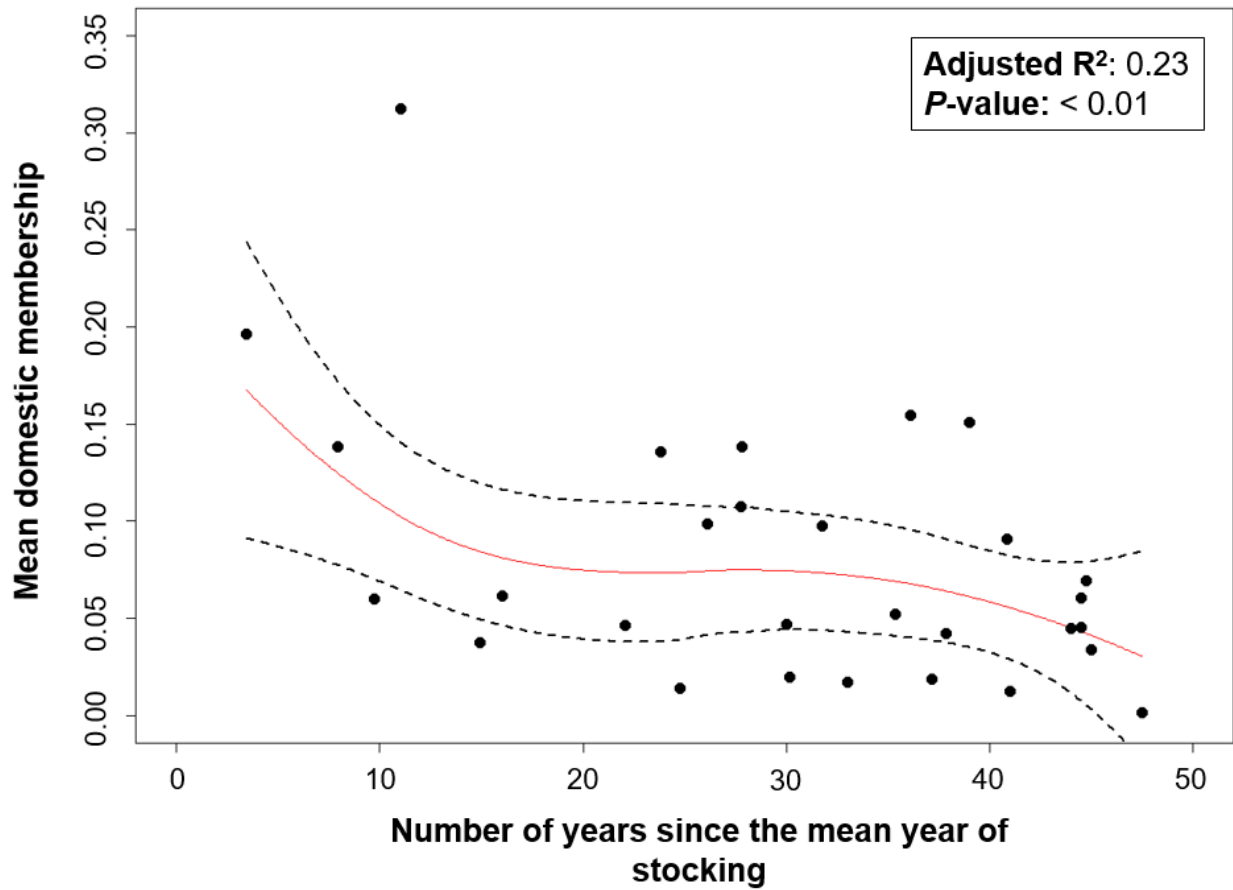


Figure S4. Mean domestic membership observed in each lake as a function of the number of years since the mean year of stocking for this study on Brook Charr in Québec, Canada