

Supporting information for online publication

Genotyping-by-sequencing reveals the impact of a restocking programme on wild common carp (*Cyprinus carpio*) populations of the southern Caspian basin

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Supplementary Table 1. Population differentiation statistic according to exact G test and Fisher's method (above diagonal) and related P values (below diagonal) based on 17,828 SNP markers on *C. carpio*.

	Anzali	Anzali-wetland	Miankaleh	Gomishan	Farmed population
Anzali	--	116293.1	96132.3	92725.9	70593.03
Anzali-wetland	0.001	--	62431.5	66731.2	119726.584
Miankaleh	0.001	0.001	--	59982.2	98648.2
Gomishan	0.001	0.001	0.03	--	91637.5
Farmed population	0.001	0.001	0.001	0.001	--

Supplementary Table 2. Results of the population assignment test in *C. carpio* across the southern basin of the Caspian Sea, based on 17,828 SNPs obtained from Genotyping-by-Sequencing.

Individual	Current	Inferred	Lik_ratio
GFO-18-sorted	Anzali	Anzali-wetland	7243.643
GFO-19-sorted	Anzali	Anzali-wetland	7717.398
GFO-22-sorted	Anzali	Anzali-wetland	9317.301
GFO-3-sorted	Anzali	Gomishan	2984.914
GFO-4-sorted	Anzali	Gomishan	3292.677
GFO-5-sorted	Anzali	Farmed	1998.821
GFO-6-sorted	Anzali	Gomishan	3991.871
GFO-62-sorted	Miankaleh	Anzali-wetland	2092.202
GFO-69-sorted	Miankaleh	Anzali-wetland	2300.603
GFO-72-sorted	Miankaleh	Gomishan	3229.731
GFO-73-sorted	Miankaleh	Anzali-wetland	2699.644
GFO-74-sorted	Miankaleh	Anzali-wetland	2162.869
GFO-75-sorted	Miankaleh	Gomishan	4394.753
GFO-76-sorted	Miankaleh	Gomishan	2234.092
GFO-77-sorted	Miankaleh	Anzali-wetland	2718.994
GFO-78-sorted	Miankaleh	Gomishan	3189.063
GFO-79-sorted	Miankaleh	Gomishan	2332.305
GFO-80-sorted	Miankaleh	Anzali-wetland	2259.345
GFO-81-sorted	Miankaleh	Gomishan	2987.443
GFO-82-sorted	Miankaleh	Gomishan	3885.508

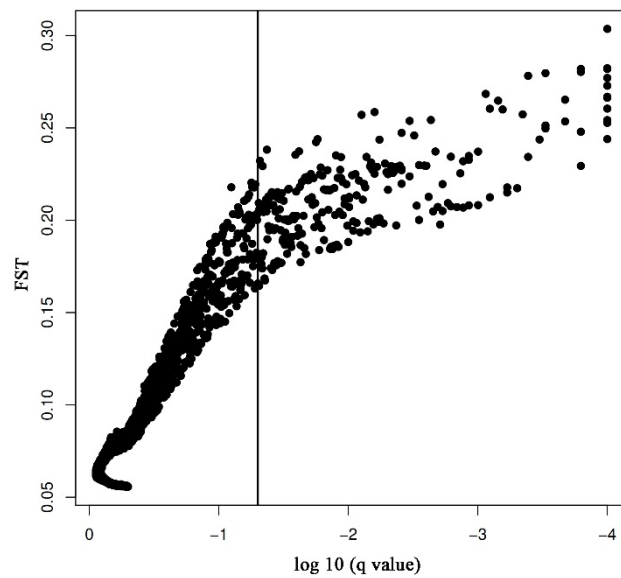
GFO-84-sorted	Miankaleh	Gomishan	3202.637
GFO-119-sorted	Gomishan	Farmed	9727.148
GFO-147-sorted	Gomishan	Farmed	1825.85
GFO-122-sorted	Farmed	Gomishan	2751.963
GFO-127-sorted	Farmed	Gomishan	2488.378

Supplementary Table 3. Candidate genes under selection. Only loci with Log10(PO)>2 are shown.

Gene abbreviation / ID	Chromosomal position of outliers
<i>cpne9</i>	NC_031736.1: 858687; NC_031736.1: 858692; NC_031736.1: 858781; NC_031736.1: 858810
<i>ldah</i>	NC_031729.1: 8336104; NC_031729.1: 8336120; NC_031729.1: 8336196
<i>LOC109046319</i>	NC_031738.1: 12654647; NC_031738.1: 12654656; NC_031738.1: 12654844
<i>LOC109048805</i>	NC_031742.1: 3215333; NC_031742.1: 3215335
<i>LOC109058795</i>	NW_017538061.1: 183609
<i>LOC109061054</i>	NW_017538162.1: 620718; NW_017538162.1: 620721; NW_017538162.1: 620742
<i>LOC109066538</i>	NW_017538306.1: 550997
<i>LOC109068350</i>	NW_017538839.1: 26129; NW_017538839.1: 26149; NW_017538839.1: 26157; NW_017538839.1: 26162
<i>LOC109075554</i>	NW_017540992.1: 371537
<i>LOC109080829</i>	NW_017542367.1: 449887
<i>LOC109086801</i>	NW_017545228.1: 66338
<i>LOC109096896</i>	NC_031697.1: 10389072
<i>LOC109098077</i>	NC_031716.1: 13374368
<i>LOC109104259</i>	NC_031726.1: 3458633; NC_031726.1: 3458674
<i>LOC109107456</i>	NC_031729.1: 2488860
<i>srp68</i>	NC_031728.1: 7725480
<i>sytl2a</i>	NC_031716.1: 7348375

Supplementary Figure 1. A) Outliers found through Bayescan analysis. The X axis indicates $\log_{10}$ (q value) and the Y axis shows the F_{ST} values. **B)** Number of private alleles identified by the Population program of Stacks2.3b in different populations of *C. carpio*.

A



B

