Erratum to: Molecular identification of species and ploidy of *Carassius* fishes in Lake Biwa, using mtDNA and microsatellite multiplex PCRs

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Unfortunately, Fig. 2 contains an error (the sequence of the primer “CytbGengoroL”). The correct figure is given below.

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	580	590	600	610	620	630	640	650
	CCGCTACTGTTATCCACCTACTG CytbNigoroL							
cb1	TGCGCTACTGTTATCCACCTACTGTTTCTTCACGAAACAGGATCAAACAACCCCATCGGGCTGAACTCGGACGCAGACA							
cb2								
cb3								
cb4								
cc1	A.....T.....C.....G..G..G..T.....AT.A.....							
cc2	A.....T.....C.....G..G..G..T.....AT.A.....							
cc3	A.....T.....C.....G..G..G..T.....T..AT.A.....							
cc4	A.....T.....C.....G..G..G..T.....AT.A.....							
	660	670	680	690	700	710	720	730
cb1	AAATTTCTTTCCACCCATACTTTTCTTACAAAGACCTCCTTGGGTTCTGTAATTATACTACTAGCCCTTACACTCCTGGCA							
cb2	A.....							
cb3	A.....							
cb4								
cc1	T.....A.....T.....G.....T.....C.....G.....							
cc2	A.....T.....G.....T.....C.....G.....							
cc3	A.....T.....G.....T.....C.....G.....							
cc4	A.....T.....G.....T.....C.....							
	740	750	760	770	780	790	800	810
	ACCCAGCTAATCCTCTGGTC CytbGengoroL							
cb1	TTGTTTTCCCAAACCTTTTAGGAGACCCAGAAAACCTTCACCCAGCCAATCCCCTGGTTACTCCCTCCTACATTAAACC							
cb2	..A.....							
cb3	..A.....							
cb4								
cc1	..A..C.....T.....T.....C..C..G.....							
cc2	..A..C.....T.....T.....C..C..G.....							
cc3	..A..C.....T.....T.....C..C..G.....							
cc4	..A..C.....T.....T.....C..C..G.....							
	820	830	840	850	860	870	880	890
cb1	AGAGTGATATTTCTATTGCTATGCCATCCTCCGATCAATCCCCAACAAACTAGGAGGAGTTCTTGCACTACTGTTCT							
cb2	A.....							
cb3								
cb4								
cc1	T.....A.....T.....A.....T.....							
cc2	T.....A.....T.....G.....A.....T.....							
cc3	T.....A.....T.....G.....A.....T.....							
cc4	T.....A.....T.....A.....T.....							
	900	910	920	930	940	950	960	970
cb1	CTATCCTTGTAAGTAGTAGTACCCCTGCTACACACCTCGAAACAACGAGGACTAACATTTGCGCCGATCACCCAATTT							
cb2	..C.....A.....							
cb3	A.....							
cb4								
cc1	..C.....A..G.....A.....A.....G..C.....A.....G.....							
cc2	..C.....A..G.....A.....A.....G..C.....A.....G.....							
cc3	A..G.....A.....A.....G..C.....A.....G.....							
cc4	..C.....A..G.....A.....A.....G..C.....A.....G.....							
	980	990	1000	1010	1020	1030	1040	1050
cb1	CTATTTTGAACCTTTAGTCGCAGACATGATTATCCTAACATGAATTGGAGGAATACCAGTAAACACCCATTTATTATCAT							
cb2	G.....							
cb3	G.....							
cb4	G.....							
cc1	G.....							
cc2	G.....							
cc3	A.....G.....							
cc4	G.....							
	1060	1070	1080	1090	1100	1110	1120	1130
cb1	TGGACAAATCGCATCCGTCTTATATTTGCACTATTCTCTGTTCTCTTCCCACTAGCAGGATGATTAGAAAAATAAGCAC							
cb2	C.....							
cb3	G.....							
cb4								
cc1	C.....G.....G.....C.....T..C.....G.....C.....							
cc2	C.....G.....G.....C.....T..C.....G.....C.....							
cc3	C.....G.....G.....C.....T..C.....G.....C.....							
cc4	C.....G.....G.....C.....T..C.....G.....C.....							
	1140							
cb1	TGAAATGAGCT							
cb2								
cb3								
cb4								
cc1								
cc2								
cc3								
cc4								

Fig. 2 Sequences and locations of the two haplotype-specific primers designed in this study (cytbNigoroL for *Carassius buegeri* and its polyploid, and cytbGengoroL for *C. cuvieri*), with aligned sequences of the mitochondrial cytochrome *b* gene of four selected haplotypes

from *C. buegeri* (or its polyploid) and *C. cuvieri* from Lake Biwa. Nucleotides identical to the first sequence are denoted by dots. Nucleotide positions are numbered according to the whole cytochrome *b* gene (1,141 bp)