

Supplementary material

Figure A2. Results of linkage disequilibrium (LD) analyses for single nucleotide polymorphisms (SNPs) within seven Z-linked loci sampled from grey teal (above diagonal) and chestnut teal (below diagonal). Only SNPs within the same locus were in significant LD after a correction for the false discovery rate (black boxes) (Benjamini & Hochberg 1995). Evidence of LD between pairs of SNPs from different loci was weak ($P \leq 0.05$) and not significant after a correction (grey boxes). Crosshatches indicate pairwise comparisons that were not possible as a result of the SNP being fixed in that species.

!

!

Literature Cited

Benjamini Y, Hochberg Y (1995) Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B*, **57**, 289-300.

Kuhner MK (2006) LAMARC 2.0: maximum likelihood and Bayesian estimation of population parameters. *Bioinformatics*, **22**, 768-770.

Peters JL, Roberts TE, Winker K, McCracken KG (2012) Heterogeneity in genetic diversity among non-coding loci fails to fit neutral coalescent models of population history. *PLoS One*, **7**, e31972.

Peters JL, Zhuravlev Y, Fefelov I, Logie A, Omland KE (2007) Nuclear loci and coalescent methods support ancient hybridization as cause of mitochondrial paraphyly between gadwall and falcated duck (*Anas* spp.). *Evolution*, **61**, 1992-2006.