

Comparing genomic signatures of domestication in two Atlantic salmon (*Salmo salar* L.) populations with different geographical origins

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© 2018 The Authors. *Evolutionary Applications* published by John Wiley & Sons Ltd. Selective breeding and genetic improvement have left detectable signatures on the genomes of domestic species. The elucidation of such signatures is fundamental for detecting genomic regions of biological relevance to domestication and improving management practices. In aquaculture, domestication was carried out independently in different locations worldwide, which provides opportunities to study the parallel effects of domestication on the genome of individuals that have been selected for similar traits. In this study, we aimed to detect potential genomic signatures of domestication in two independent pairs of wild/domesticated Atlantic salmon populations of Canadian and Scottish origins, respectively. Putative genomic regions under divergent selection were investigated using a 200K SNP array by combining three different statistical methods based either on allele frequencies (LFMM, Bayescan) or haplotype d