Consumers and environmentalists are increasingly concerned about the potential dangers of genetically modified organisms (GMOs). Yet, some of the criticisms of transgenic plants and animals also apply to artificially selected breeds. In animals, strains selected for high production efficiency may be more susceptible to behavioural, physiological and immunological disfunctions, and many of the genetic changes accumulated in breeding strains are simply unknown. Incomplete knowledge of accumulated heritable differences in breeding strains is of particular concern for the conservation of wild salmonid populations. As one example, the problem of farmed Atlantic salmon escapees has taken alarming proportions, with many hundreds of thousands, and sometimes up to a few millions farmed salmon escaping annually from their sea cages. Gene flow from artificially-selected salmon for aquaculture production to wild populations may lead to outbreeding depression, whereby the adaptive fitness of the wild offspring in subsequent generations, is reduced. A better knowledge of evolutionary changes induced by selective breeding is therefore crucial for assessing the consequences of genetic interactions between wild and escaped farmed salmon. Evolutionary changes may strongly depend on alterations in gene regulation and the microarray (DNA chips) technology offers the possibility of scanning transcription differences at many thousands of genes between farmed and wild salmon. In this paper, I will illustrate how such new “postgenomics” tools may i) provide evidence for the role of selection in driving rapid evolutionary changes, ii) identify specific gene functions that have been altered by the process of selection, and iii) allow to quantify the extent of outbreeding depression resulting from the hybridization between artificially and wild organisms.