

CORRECTION

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Correction to: Deploying new generation sequencing for the study of flesh color depletion in Atlantic Salmon (*Salmo salar*)

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Correction to: *BMC Genomics* 22, 545 (2021)
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Following publication of the original article [1], it was reported that an incorrect image was published as Fig.6. The correct Fig. 6 is included in this Correction and the original article has been corrected.

The original article can be found online at <https://doi.org/10.1186/s12864-021-07884-9>.

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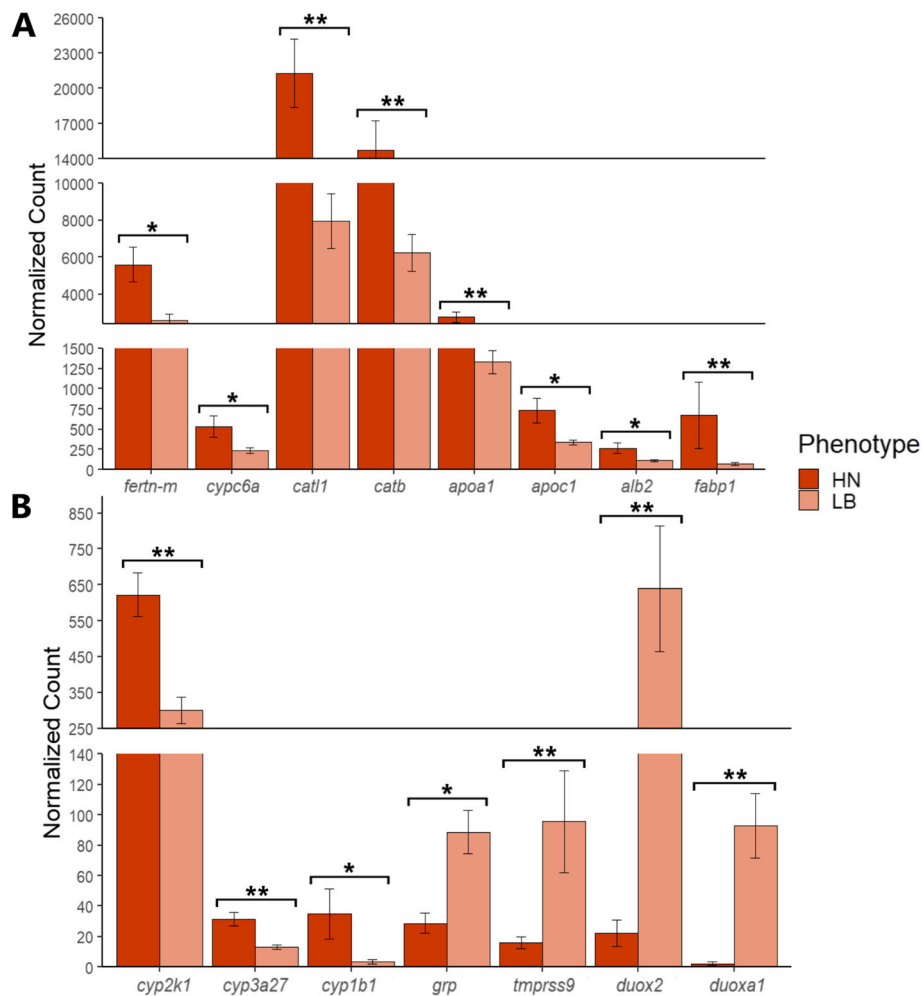


Fig. 6 Analysis comparing HN and LB phenotypes. Subset of DEGs of interest identified in the transcriptomes from the two library preparations. **A** Expression pattern of eight genes identified in the QuantSeq library: ferritin-m (*ferrn-m*), involved in iron ion transport; cytochrome c oxidative subunit 6 A mitochondrial-like (*cypc6a*), involved in oxidation-reduction process; cathepsin L1 (*catl1*) and cathepsin B (*catb*) involved in apoptosis and muscle degradation; apolipoprotein A1 (*apoa1*), apolipoprotein C1 (*apoc1*), serum albumin 2 (*alb2*), fatty acid-binding protein 1 (*fabp1*) involved in lipid metabolism; **B** Expression pattern of seven genes identified in the TruSeq library: cyp450 gene family *cyp2k1*, *cyp3a27* and *cyp1b1*, involved in oxidation-reduction process; gastrin-releasing peptide (*grp*) involved in regulation of feeding, and *tmprss9*, dual oxidase 2-like (*duox2*), dual oxidase maturation factor 1-like (*duoxa1*) involved in SNP analysis. Asterisks (* and **) indicate significant difference between the HN and LB phenotypes at $P < 0.05$ and $P < 0.01$, respectively

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