

CORRIGENDUM

The ocular albinism type 1 protein, an intracellular G protein-coupled receptor, regulates melanosome transport in pigment cells

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Human Molecular Genetics 2008, 17, 3487–3501.
doi: 10.1093/hmg/ddn241

The Authors wish to make a correction to the genotype indicated for two melanocyte cell lines developed and characterized in the study above. Indeed, during a recent RNAseq analysis, we realized that the previously indicated *Oa1*^{+/+} and *Oa1*^{-/-} melanocyte lines are actually *Oa1*^{+/-} and *Oa1*^{-/-}, i.e. they are wild type and *Oa1*-KO, respectively, as originally reported, but they are both male, rather than female (Figures 1-2). These new findings do not affect any of the major conclusions of the original manuscript, since even in the remote possibility that the sex could impact on the physiopathology of isolated melanocytes in culture, the published work contains several other independent controls (analysis of wild type and *Oa1*-KO mouse retinas; analysis of *Oa1*-KO melanocytes transiently transfected or stably transduced with vectors for wild type or mutant *OA1*)

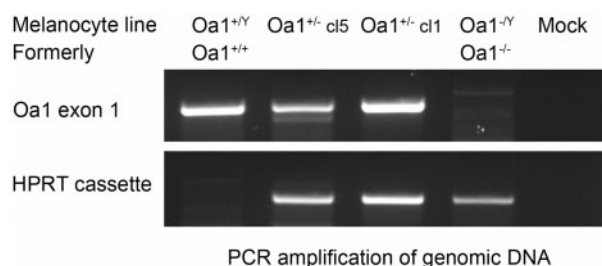


Figure 1. PCR from genomic DNA to confirm the HPRT cassette insertion at the *Oa1* locus in the indicated melanocyte cell lines. As described in the manuscript, heterozygous *Oa1*^{+/-} were subcloned and tested for *Oa1* expression, to select clones expressing *Oa1* from the wild type X chromosome.

[†]The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

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supporting the reliability of the results. The genotypes will also be corrected in the Wellcome Trust Functional Genomics Cell Bank website, through which these cell lines are presently available (<https://www.sgu.ac.uk/depts/anatomy/pages/Dot/Cell%20bank%20holdings.htm#melanocytes>).

The RNAseq analysis and additional validation experiments were performed by A Palmigiano and MV Schiaffino, both authors of the original manuscript.

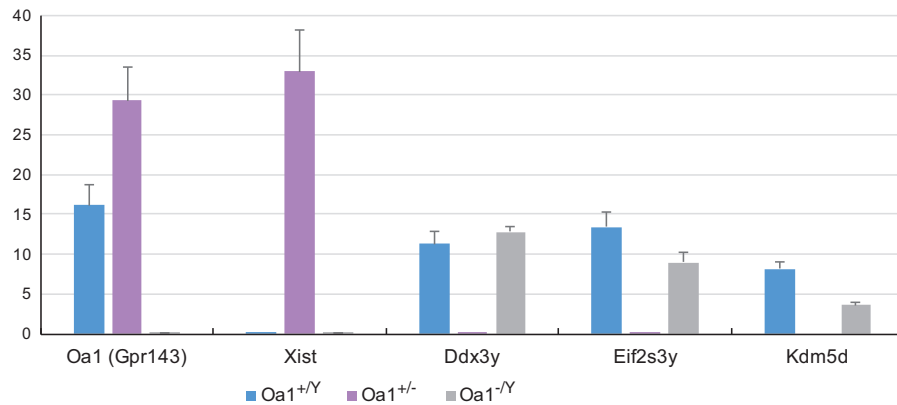


Figure 2. Expression levels of Oa1 (Gpr143), Xist (X-inactive specific transcript), and three Y specific genes (Ddx3y, Eif2s3y, Kdm5d), obtained by RNAseq analysis and normalized for transcript length and total number of reads (RPKM). Mean \pm SD of 3 independent samples for each melanocyte cell line.