Reply to: “SLC40A1-R178G or R178Q and ferroportin disease? A call for vigilance in mutation reporting”

To the Editor:
We appreciate the observation by Dr. Wallace uncovering our error in citing unwittingly the nomenclature of amino acid alteration of the mutation g.963G>A (according to the NCBI reference sequence NM_014585) of SLC40A1 gene, as R178G (Arg178Gly) instead of R178Q (Arg178Gln). An Erratum has already been submitted in concern to our initial publication [1]. We have to emphasize that all the data presented in both our initial publication describing this alteration and in the Letter to the Editor [2] are absolutely correct. At the time of the submission of the initial publication in Blood Cells Molecules and Diseases, this alteration (R178Q) was really novel, as the paper of Cunat et al. [3] had not appeared in the literature. Unfortunately, a database of ferroportin gene (SLC40A1) mutations is not yet available. It would be worthy such a database to be established for SLC40A1, as it is the rule for other genes of clinical interest. Very usefully, a formal and detailed review of the incoming alterations is provided by such databases.

To the end, we have recently performed a detailed bioinformatic analysis in order to assess whether this alteration is likely to be deleterious and, if possible, to determine which aspects of protein function are affected. For this purpose, we used two different software packages, namely SIFT (Sorting Intolerant From Tolerant; available at: http://sift.bii.a-star.edu.sg/) and PolyPhen2 (available at: http://genetics.bwh.harvard.edu.pha2/) and we determined that the R178Q mutation is rather deleterious for protein function (intolerant on SIFT analysis with a probability score 0.00, and probably damaging on PolyPhen2 analysis: sensitivity score 0.00, specificity score: 1.00), causing the emergence of the classical ferroportin disease.

We honestly apologize for our mistake. Such mistakes would be really avoided using the cDNA numbering position rather than nucleotide positions obtained from NCBI reference sequences (that are regularly updated) and the presentation of amino acid substitutions by both three letter and single letter codes, as it is rightly proposed by Dr. Wallace.

Conflict of interest
The authors declared that they do not have anything to disclose regarding funding or conflict of interest with respect to this manuscript.

References