Author Correction: Genetic variants identified in novel candidate genes for anorexia nervosa and analysis of molecular pathways for diagnostic applications

K. DONATO, M.C. MEDORI, A. MACCHIA, S. CECCHIN, M.R. CECCARINI, T. BECCARI, V. GATTA, L. STUPPIA, V. BENFATTI, L. DALLA RAGIONE, P. CHIURAZZI, C. MICHELETTI, K. DHULI, G. MADEO, G. BONETTI, G. MARCEDDU, M. BERTELLI

MAGISNAT, Atlanta Tech Park, Peachtree Corners, GA, USA

Correction to: Eur Rev Med Pharmacol Sci 2023; 27 (6 Suppl): 77-88 –DOI: 10.26355/eurrev_202312_34692-published on December 18, 2023.

After publication and following some post-publication concerns, the authors have applied the following corrections to the galley proof.

- The conflict of interest section has been amended as follows:

K. Donato is employee at MAGI EUREGIO and MAGISNAT. G. Marceddu is employee at MAGI EUREGIO. M. Bertelli is president of MAGI EUREGIO, MAGISNAT, and MAGI's LAB. M.C. Medori, A. Macchia, S. Cecchin, C. Micheletti, K. Dhuli, G. Madeo, G. Bonetti are employees at MAGI's LAB. M. Bertelli, M.R. Ceccarini, and P. Chiurazzi are patent inventors (US20220362260A11). M. Bertelli, P.E. Maltese, G. Marceddu, and S. Cecchin are patent inventors (US20230173003A1). M. Bertelli, K. Dhuli, and P.E. Maltese are patent inventors (WO2022079498A1). M. Bertelli, K. Donato, M.C. Medori, M.R. Ceccarini, T. Beccari, P. Chiurazzi, C. Micheletti, K. Dhuli, G. Bonetti, G. Marceddu are patent applicants (Application Number: 18/466.879). The remaining authors have no conflict of interest to disclose.

- Since the current study shares the same NGS panel for the genetic analysis as the study cited in Ref. 5 (Ceccarini MR, Precone V, Manara E, Paolacci S, Maltese PE, Benfatti V, Dhuli K, Donato K, Guerri G, Marceddu G, Chiurazzi P, Dalla Ragione L, Beccari T, Bertelli M. A next generation sequencing gene panel for use in the diagnosis of anorexia nervosa. Eat Weight Disord 2022; 27: 1869-1880), the authors amend the following sentence:

"A subset comprising 163 genes from a dedicated Next-Generation Sequencing (NGS) panel was analyzed[5]"
in
"A subset comprising 163 genes from a dedicated Next-Generation Sequencing (NGS) panel, previously used in the study by Ceccarini et al[5], was analyzed".
The authors clarify that the analyzed patients of the two articles are completely independent.

- To clarify the data reported in Table II, the authors amend the following sentence:

"Genetic variants identified in the AN population are reported in Table II."
In
"The genomic sequencing NGS was performed in all 135 patients recruited in the study. After obtaining the raw data, based on the ACMG guidelines, the results were filtered, and Table II reports the variants considered Pathogenic (P), likely pathogenic (LP), and Variable with Uncertain Significance (VUS), 61 patients in total".

- Consequently, to improve clarity, the legend of Table II has been amended as follows:

Genetic variants identified in 61 patients out of the total 135 patients analyzed by NGS.

There are amendments to this paper. The Publisher apologizes for any inconvenience this may cause.