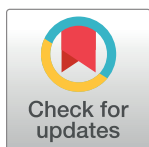


CORRECTION

## Correction: Endomicroscopic and Transcriptomic Analysis of Impaired Barrier Function and Malabsorption in Environmental Enteropathy

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There is an error in [Table 3](#). The sign of the fold expression is reversed and the log2Ratio is inverted. The errors arose through mixing up group A and B.



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### OPEN ACCESS

**Citation:** Kelly P, Besa E, Zyambo K, Louis-Auguste J, Lees J, Banda T, et al. (2022) Correction: Endomicroscopic and Transcriptomic Analysis of Impaired Barrier Function and Malabsorption in Environmental Enteropathy. *PLoS Negl Trop Dis* 16(6): e0010505. <https://doi.org/10.1371/journal.pntd.0010505>

**Published:** June 2, 2022

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**Table 3. Differentially expressed genes in 4 biopsies from duodenum with multiple plumes seen by confocal laser endomicroscopy compared to 4 with minimal plumes.**

| Gene ID   | Gene name/function  | Functional group                                | Locus                 | log2Ratio | Fold change | Probability score |
|-----------|---|---|-----------------------|-----------|-------------|-------------------|
| 1671      | Human defensin 6  | Paneth cell antimicrobial peptides              | 479                   | 2.17316   | 4.505       | 0.826343          |
| 1670      | Human defensin 5  |   | 449                   | 1.92632   | 3.788       | 0.813815          |
| 5068      | Reg 3 $\alpha$  |   | 1117                  | 1.87921   | 3.676       | 0.80937           |
| 7033      | Trefoil factor 3; epithelial repair peptide                                 | Epithelial repair peptide                       | 1054                  | 2.16378   | 4.464       | 0.820769          |
| 327657    | Serpin 9; protease inhibitor  | Anti-proteolytic                                | 1851                  | 12.8255   | 7143        | 0.857051          |
| 27290     | SPINK 4; protease inhibitor   |   | 386                   | 4.41835   | 21.28       | 0.872211          |
| 3934      | Lipocalin 2; iron sequestration   | Cation uptake and sequestration from pathogens  | 840                   | 2.18948   | 4.566       | 0.81402           |
| 4057      | Lactotransferrin; antimicrobial peptide and iron sequestration              |   | 2593                  | 5.38692   | 41.67       | 0.80093           |
| 4891      | Solute carrier family 11, member 2 (DMT-1); iron, manganese and zinc uptake |   | 4424                  | 1.84634   | 3.610       | 0.804259          |
| 55600     | Intelectin 1; lactoferrin receptor  |   | 386                   | 3.6465    | 12.5        | 0.834541          |
| 1179      | Chloride channel accessory 1  | Nutrient and electrolyte transport, not cations | 3123                  | 3.4113    | 10.64       | 0.827942          |
| 29802     | Pre-B lymphocyte 3  | Immune function and inflammation                | 602                   | 4.7429    | 27.03       | 0.815015          |
| 2353      | c-fos; AP-1 subunit   |   | 2158                  | -2.765478 | 0.147       | 0.854176          |
| 2354      | fos B; AP-1 subunit   |   | 3776                  | -7.030998 | 0.008       | 0.892508          |
| 10578     | granulysin; cytotoxic cell effector molecule                                |   | 995                   | -2.736818 | 0.150       | 0.80525           |
| 3127      | HLA-DR $\beta$ 5; antigen presentation                                      |   | 1171                  | -2.412484 | 0.188       | 0.842403          |
| 3627      | chemokine C-X-C ligand 10; chemokine, interferon- $\gamma$ pathway          |   | 1227                  | -2.902382 | 0.134       | 0.807325          |
| 1543      | Cytochrome P450, family 1, subfamily A, no 1                                |   | Xenobiotic metabolism | 2608      | -2.364329   | 0.194             |
| 139728    | CaM kinase; PNCK  | Role or function unclear in this context        | 1888                  | 3.69906   | 12.99       | 0.805404          |
| 1843      | Dual specificity phosphatase 1  |   | 2040                  | -1.946366 | 0.258       | 0.806404          |
| 692203    | Small nucleolar RNA, C/Dbox 88B   |   | 97                    | 12.4208   | 5555.6      | 0.820723          |
| 100861532 | unknown function  |   | 13357                 | 3.20998   | 9.259       | 0.822118          |
| 260436    | chromosome 4, ORF7  |   | 573                   | 7.68911   | 208.3       | 0.937805          |

The **Probability** shown is derived from RKPM-normalised values using NOIseq (non-parametric) computation of signal to noise ratio, and using a standard threshold, q, of 0.8 which corresponds to an odds ratio of 4:1 that the gene is differentially expressed. Values of Probability shown indicate the probability that a given transcript is differentially expressed; higher values indicate greater probability of differential expression; values greater than 0.8 are accepted as significant [29].

<https://doi.org/10.1371/journal.pntd.0010505.t001>

## Reference

1. Kelly P, Besa E, Zyambo K, Louis-Auguste J, Lees J, Banda T, et al. (2016) Endomicroscopic and Transcriptomic Analysis of Impaired Barrier Function and Malabsorption in Environmental Enteropathy. *PLoS Negl Trop Dis* 10(4): e0004600. <https://doi.org/10.1371/journal.pntd.0004600> PMID: 27050312