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Author Correction: Full-length RNA-Seq of the *RHOH* gene in human B cells reveals new exons and splicing patterns

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Correction to: *Scientific Reports* https://doi.org/10.1038/s41598-024-79307-0, published online 16 November 2024

The original version of this Article contained errors in the Introduction, Results, Discussion and Conclusion sections.

In the Introduction,

"We first named these genes X1, 1a, X2, 1b, X3, and X4 (Table S1, for accession numbers)."

now reads:

"We first named these exons X1, 1a, X2, 1b, X3, and X4 (Table S1, for accession numbers)."

In the Results section, under the subheading 'NanoString analysis of B cells allowed the discovery of potential new *RHOH* exons',

"On the basis of our previous work using a 5′Race-PCR[4] approach, "priming" inside the RhoH gene encoding an exon allowed the upstream identification of new exons. "

now reads:

"On the basis of our previous work using a 5′Race-PCR[4] approach, "priming" inside the RhoH encoding exon allowed the upstream identification of new exons. "

"Therefore, we designed 18 pairs of probes for EST1-8 and Uni1-3 for 6 out of the 7 *RHOH* exons we had previously identified; exons 1–4, 6, and 7; and the *RHOH* 3′-UTR as a control."

now reads:

"Therefore, we designed 18 pairs of probes for EST1-8 and Uni1-3 for 6 out of the 7 *RHOH* exons we had previously identified: exons 1-4, 6, 7, and the *RHOH* 3′-UTR as a control."

Under the subheading 'Full-length mRNA-Seq analysis of the *RHOH* gene in B cells',

"Thus, among the 18 *RHOH* mRNA molecules described above, 11 might be templates for RhoH protein synthesis (T01–05, T22–27), and 7 (T06–07–08, T20–21, T28–29) known exons have never been detected before. Specifically, the T06–07–08 transcript, which exhibited a large split of exon 7, was weakly expressed, while the T20 and T21 genes without any exon 7 sequence were notably expressed, all of which eliminate the possibility of RhoH protein synthesis."

now reads:

"Thus, among the 18 *RHOH* mRNA molecules described above, 11 might be templates for RhoH protein synthesis (T01–05, T22–27), and 7 (T06–07–08, T20–21, T28–29) containing known exons have never been

detected before. Specifically, the T06–07–08 transcripts, which exhibited a large split of exon 7, were weakly expressed, while the T20 and T21 mRNAs without any exon 7 sequence were notably expressed, all of which eliminate the possibility of RhoH protein synthesis."

"Second, we detected 5 new *RHOH* exons, which led to the generation of 18 new transcripts that did not contain RhoH, which encodes exon 7 or exon 6 (Fig. 4). "

now reads:

"Second, we detected 5 new *RHOH* exons, which led to the generation of 18 new transcripts that did not contain exon 6 nor RhoH encoding exon 7 (Fig. 4)."

"Among the 11 *RHOH* transcripts with new exons that started from exon 2 (T09–19), T09 contained a new single exon that was never predicted before; we named this gene EX3B, which was spliced to exon 2."

now reads:

"Among the 11 *RHOH* transcripts with new exons that started from exon 2 (T09–19), T09 contained a new single exon that was never predicted before; we named this exon EX3B, which was spliced to exon 2."

"The T35 and T36 transcripts contained exon 5 and were named EX5B1–2. Remarkably, these cells exhibited two larger sizes, EX5B1 and EX5B2 (Fig. 4, Tables S1 and S3). "

now reads:

"The T35 and T36 transcripts contained exon 5 which was named EX5B1-2. Remarkably, it exhibited two larger sizes, EX5B1 and EX5B2 (Fig. 4, Tables S1 and S3)."

Under the subheading 'Quantitative analysis of *RHOH* transcript pattern variation during B-cell differentiation',

"In contrast, the expression of most of the mRNAs starting from exon 4 did not vary upon differentiation, except for T20, which contained exon 4 alone and had a greater size and presented a 5.7-fold decrease in expression after PMA treatment."

now reads:

"In contrast, the expression of most of the mRNAs starting from exon 4 did not vary upon differentiation, except for T20, which contained exon 4 alone with a greater size and presented a 5.7-fold decrease in expression after PMA treatment."

Under the subheading 'Potential protein/peptide formation from *RHOH* mRNA molecules',

"First, transcript T09, which contains the rather large EX3B gene, presented 2 possible ORFs, p5- and p6-ORF, starting inside EX3B or EX2, respectively, that generated 4 peptides."

now reads:

"First, transcript T09, which contains the rather large EX3B exon, presented 2 possible ORFs, p5- and p6-ORF, starting inside EX3B or EX2, respectively, that generated 4 peptides."

In the Discussion section, under the subheading 'Annotation mistakes',

"Our publication refers to the sequence of the first described *RHOH* mRNA[4], named this mRNA Z35225, whereas the number in the EMBL database is Z35227 (in the EMBL database, Z35225 refers falsely to a bacterial DNA for ribosomal spacer sequence; see Table S1)."

now reads:

"Our publication refers to the sequence of the first described *RHOH* mRNA[4], named this mRNA Z35225, whereas the number in the EMBL database is Z35227 (in the EMBL database, Z35225 refers to a bacterial DNA for ribosomal spacer sequence; see see Table S1)."

Under the subheading 'Splicing-polyA sites',

"In our perseverance in the discovery of new elements arising from the *RHOH* full-length RNA-Seq, we observed at the 3′ extremity of the gene that some of the 7′ ends of the exons mapped close to polyadenylation sites (Fig. S4)."

now reads:

"In our perseverance in the discovery of new elements arising from the *RHOH* full-length RNA-Seq, we observed at the 3' extremity of the gene that some exon terminations mapped to polyadenylation sites (Fig. S4)."

Under the subheading 'Potential peptides',

"Such synthesis could be initiated by noncanonical codons, as suggested here (Table S4), or by human genes[35,36,37]."

now reads:

"Such synthesis could be initiated by noncanonical codons, as suggested here (Table S4), or reported in other human genes[35,36,37]."

Under the subheading 'Outlook',

"Full-length mRNA sequencing of the *RHOH* gene allowed us to identify new exons and new transcripts to show quantitative discrimination of these transcripts in B-cell lines across differentiations and, more promisingly, new fusion transcripts involving the *RHOH* and *LINC02265* genes."

now reads:

"Full-length mRNA sequencing of the *RHOH* gene allowed us to identify new exons and new transcripts to show quantitative discrimination of these transcripts in B-cell lines across differentiation and, more promisingly, new fusion transcripts involving the *RHOH* and *LINC02265* genes."

In the Conclusion section,

"Targeted RNA-Seq analysis of the *RHOH* gene led to the discovery of more genes than we knew about this gene in human B cells."

now reads:

"Targeted RNA-Seq analysis of the *RHOH* gene led to the discovery of more exons than we knew about this gene in human B cells."

In the legend of Table 1, the sentence "Significant values are in italics." was removed. In addition,

"One of these mutations started from exon 2 (T06-07a–08), and the other started from exon 4 (T20-21; T28-29)."

now reads:

"One of these versions started from exon 2 (T06-07–08), and the other started from exon 4 (T20-21; T28-29)."

The original Article has been corrected.

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