

Erratum

Erratum à l'article / Erratum to the article
“The Kazusa cDNA project for identification
of unknown human transcripts”
[C. R. Biologies 326 (2004) 959–966]

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Disponible sur Internet le 14 août 2004

Une coquille s'est glissée dans l'article de Takahiro Nagase, Reiko Kikuno, Osamu Ohara, intitulé *The Kazusa cDNA project for identification of unknown human transcripts*, C. R. Biologies 326 (2003) 959–966.

Les légendes des Figs. 1 et 2 ont été inversées. Nous les rétablissons ci-après. Nous prions ces auteurs ainsi que nos lecteurs de bien vouloir excuser cette erreur.

A misprint slipped into the article by Takahiro Nagase, Reiko Kikuno, Osamu Ohara, entitled The Kazusa cDNA project for identification of unknown human transcripts, C. R. Biologies 326 (2003) 959–966.

The captions of Figs. 1 and 2 have been reversed the order. Correct captions are restored hereafter. We apologize to these authors and our readers for this mistake.

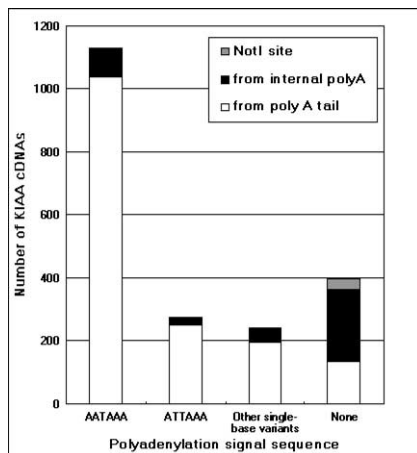


Fig. 1. Integrity of the 3'-end of the KIAA cDNAs. The integrity of the 3'-end of each of the KIAA cDNAs, which have the corresponding genomic sequence entries in a human genome database of the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>), was assessed according to the previous report [13]. In brief, the KIAA cDNA sequences were examined in terms of canonical polyadenylation signals (AATAAA, ATTA AAA, and other single-base variants of AATAAA) usually observed within 30-nucleotides upstream of the 3'-end of the complete cDNA. In addition, the appearance of a poly(A) stretch within 10 nucleotides just downstream of the 3'-end of the cDNA on the genome was also checked to ascertain whether the cDNAs synthesized by internal priming were primed from an internal poly(A) stretch or actual poly(A) tail. Some cDNAs without any polyadenylation signal sequence have a Not I site at the 3'-end. These 3'-end Not I sites most likely originate from internal Not I site of cDNAs. The number of these clones is indicated as 'Not I site' in this figure.

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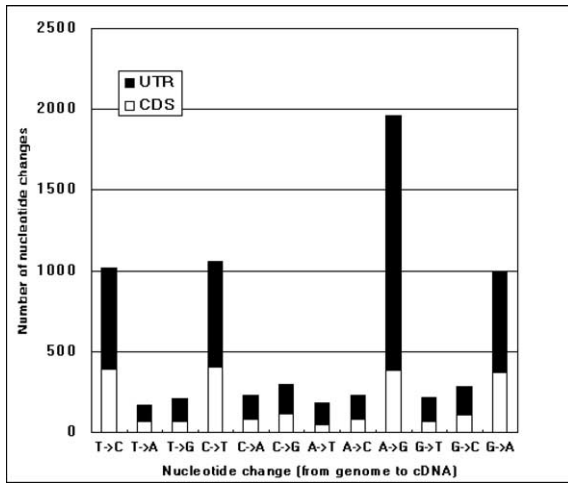


Fig. 2. Comparison of the KIAA cDNA sequences with the corresponding genomic sequences. KIAA cDNA sequences were compared with their corresponding genomic sequences. In this figure, only single nucleotide differences between them are accounted. Types of nucleotide differences are shown along the horizontal line as (the residue in the genomic entry) → (the residue in the KIAA cDNA sequence). The nucleotide differences that occurred in CDS (assigned by GeneMark program [11]) and untranslated region (UTR) are displayed as open and filled bars.