Corrigendum: Identification of Rare PB2-D701N Mutation from a Patient with Severe Influenza: Contribution of the PB2-D701N Mutation to the Pathogenicity of Human Influenza

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A corrigendum on

Identification of Rare PB2-D701N Mutation from a Patient with Severe Influenza: Contribution of the PB2-D701N Mutation to the Pathogenicity of Human Influenza

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In the original article, there was a mistake in Supplementary Table 1 as published. The first entry (A/Aragon/270/2014) had the Identification number pending. The corrected Supplementary Table 1 has been updated on the original article with the Identification number KY887997 (GISAID EPI_ISL_257783).

In the original article, there was an error. A sentence regarding methodology was missing.

A correction has been made to ASSOCIATION OF PB2-701N WITH VIRAL PATHOGENICITY IN THE INFECTED PATIENT section, Paragraph 1:

Primary viral isolation was performed for further genome analysis of this virus. Virus was amplified by one passage in MDCK cells at low multiplicity of infection using the titrated virus isolated from the original clinical sample. Total viral RNA was isolated from purified virions as previously described (Rodriguez et al., 2013), and full genome sequence was determined by next-generation sequencing with TruSeq v3 chemistry and 50 bp single reads on an Illumina HiSeq 2000. **FASTQ sequences were aligned against the influenza (A/California/04/09) genome**. To determine the consensus sequence of the virus, coverage and nucleotide composition of aligned reads were analyzed. Nucleotide positions with an identity of $\geq 75\%$ were considered. Samtools mpileup (Li et al., 2009) and in-house php scripts were used.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way.

The original article was updated with the corrections.

REFERENCES

Rodriguez, A., Falcon, A., Cuevas, M. T., Pozo, F., Guerra, S., Garcia-Barreno, B., et al. (2013). Characterization *in vitro* and *in vivo* of a pandemic H1N1 influenza virus from a fatal case. *PLoS ONE* 8:e53515. doi: 10.1371/journal.pone.0053515

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., et al. (2009). The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25, 2078–2079. doi: 10.1093/bioinformatics/btp352

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.