Genome Medicine

ERRATUM

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Erratum to: Illuminating uveitis: metagenomic deep sequencing identifies common and rare pathogens

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Erratum

It has come to our attention that there is an error in Fig. 3a for this article [1]. The correct version of Fig. 3a can be found below. The red markers now reflect the sequence differences. The text is correct. There was also a row omitted in Additional file 1: Table S1. The revised version can be found below.

Additional file

Additional file 1: Table S1. List of nucleotide substitutions identified in subject 6's RV genome. The patient's RV genome was aligned with the Stuttgart strain (GenBank DQ388280.1). A nucleotide change was considered a substitution only if the change was present in ≥ 4 reads or in 80% of the total reads at that nucleotide position. (PDF 120 kb)

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Reference
1. Doan T, Wilson MR, Crawford ED, Chow ED, Khan LM, Knopp KA, O'Donovan BD, Xia D, Hacker JK, Stewart JM, Gonzales JA, Archarya NR, DeRisi JL. Illuminating uveitis: metagenomic deep sequencing identifies common and rare pathogens. Genome Med. 2016;8:106.

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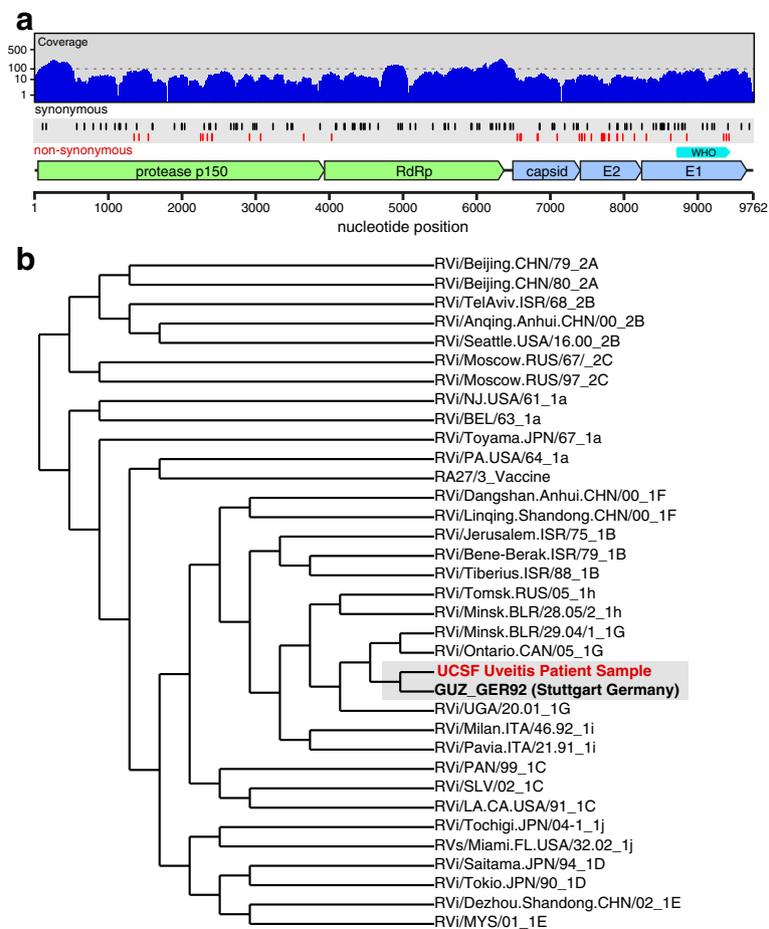
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Fig. 3 Identification of rubella virus (*RV*) by metagenomic deep sequencing (MDS). **a** Illustrates how the 9688 nucleotide paired-end sequence reads obtained from sequencing the RNA extracted from subject 6's aqueous fluid aligned to the most closely matched RV genome (GenBank DQ388280.1): 99.3% of the total RV genome is represented. Positions of synonymous (*black vertical lines*) and non-synonymous (*red vertical lines*) variants are shown. Of the 149 substitutions, 107 were synonymous and 42 were non-synonymous. Of the 42 non-synonymous mutations, 25 occurred within the coding region for the E1 and E2 glycoproteins. Per unit length, the number of non-synonymous mutations in the E1 and E2 proteins was 6.3-fold higher than in the non-structural proteins. The *cyan marker* above the E1 gene represents the 739-nucleotide sequence window recommended by the World Health Organization (*WHO*) for RV genotyping. **b** Phylogenetic analysis of subject 6's RV strain obtained from MDS with 32 WHO reference strains, GUZ_GER92 (Stuttgart strain), and the RV27/3 vaccine strain, demonstrating that the subject's RV sequence was most closely related to the genotype 1G viruses and not the vaccine strain