

CORRECTION

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Correction to: Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia

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Correction to: *BMC Genomics* (2020) 21:5
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Following the publication of this article [1], it was noted that due to a typesetting error the figure legends were paired incorrectly. The figure legends for Figs. 1, 2, 3, 4 and 5 were wrongly given as captions for Figs. 2, 3, 4, 5 and 1 respectively.

The correct figures and captions have been included in this Correction, and the original article has been corrected.

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1. Kamau E, et al. Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia. *BMC Genomics*. 2020;21:5. <https://doi.org/10.1186/s12864-019-6400-z>.

The original article can be found online at <https://doi.org/10.1186/s12864-019-6400-z>

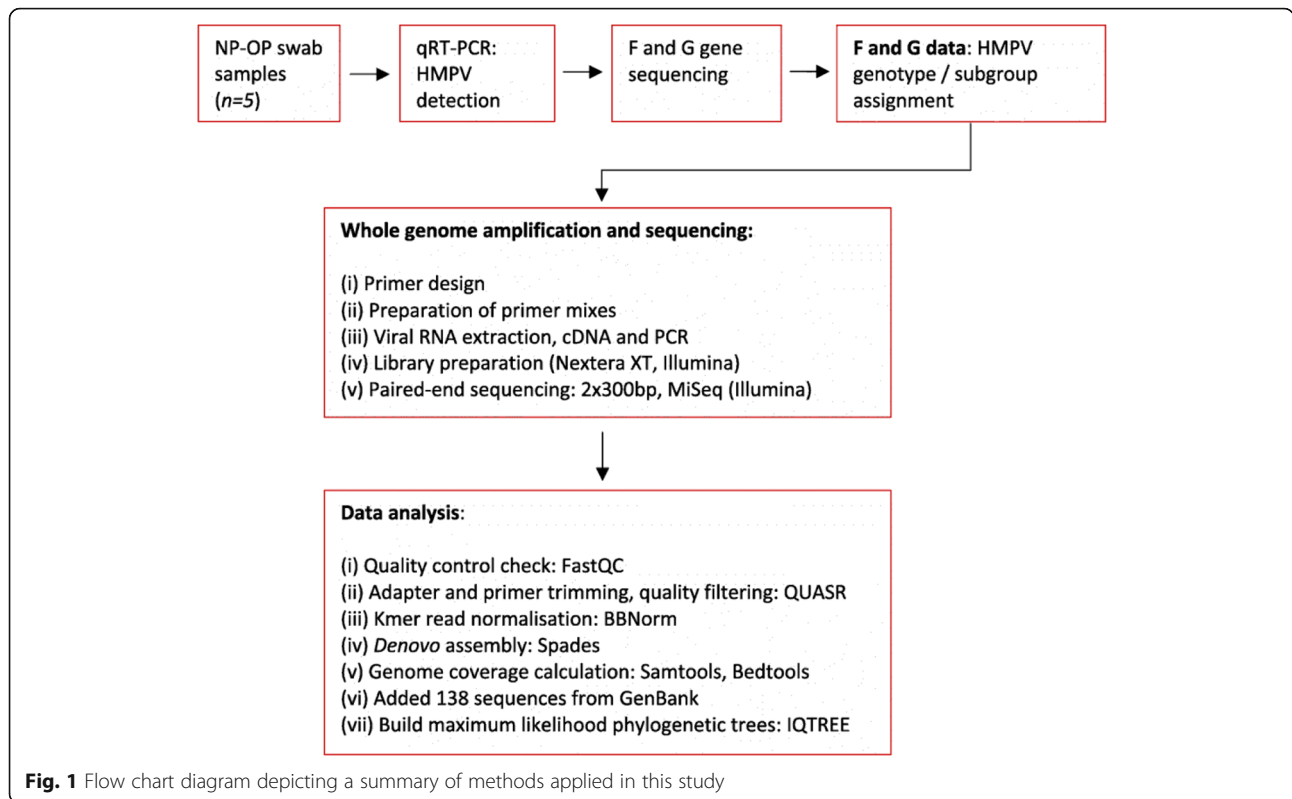
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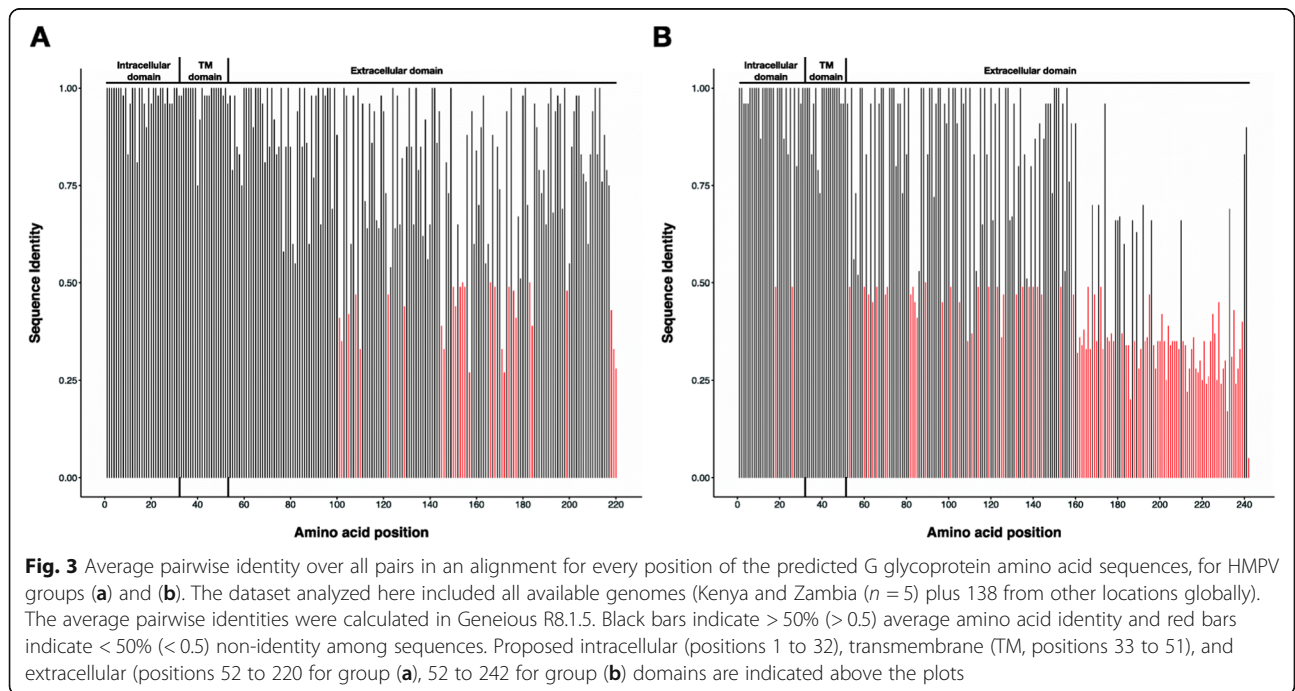
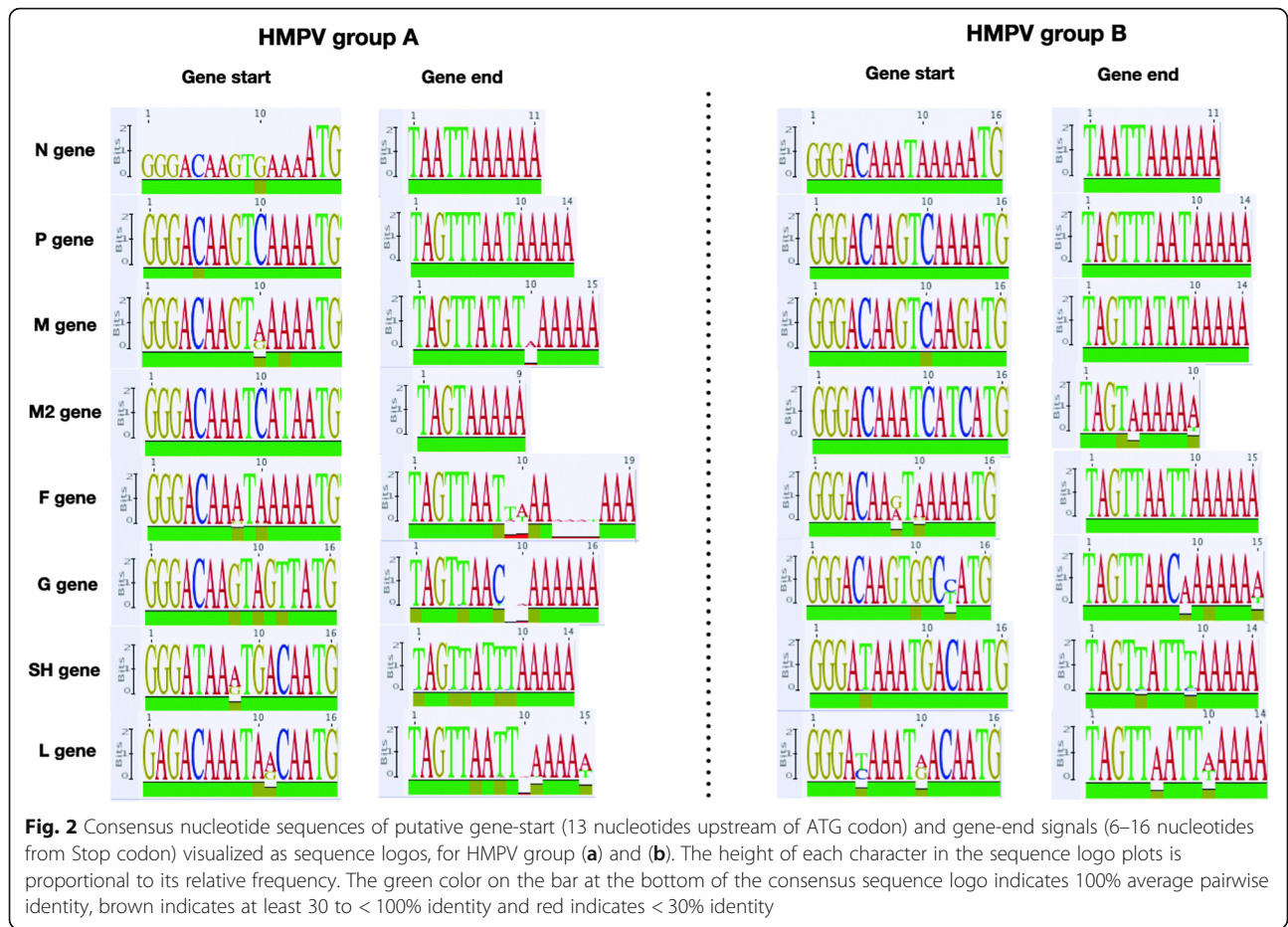
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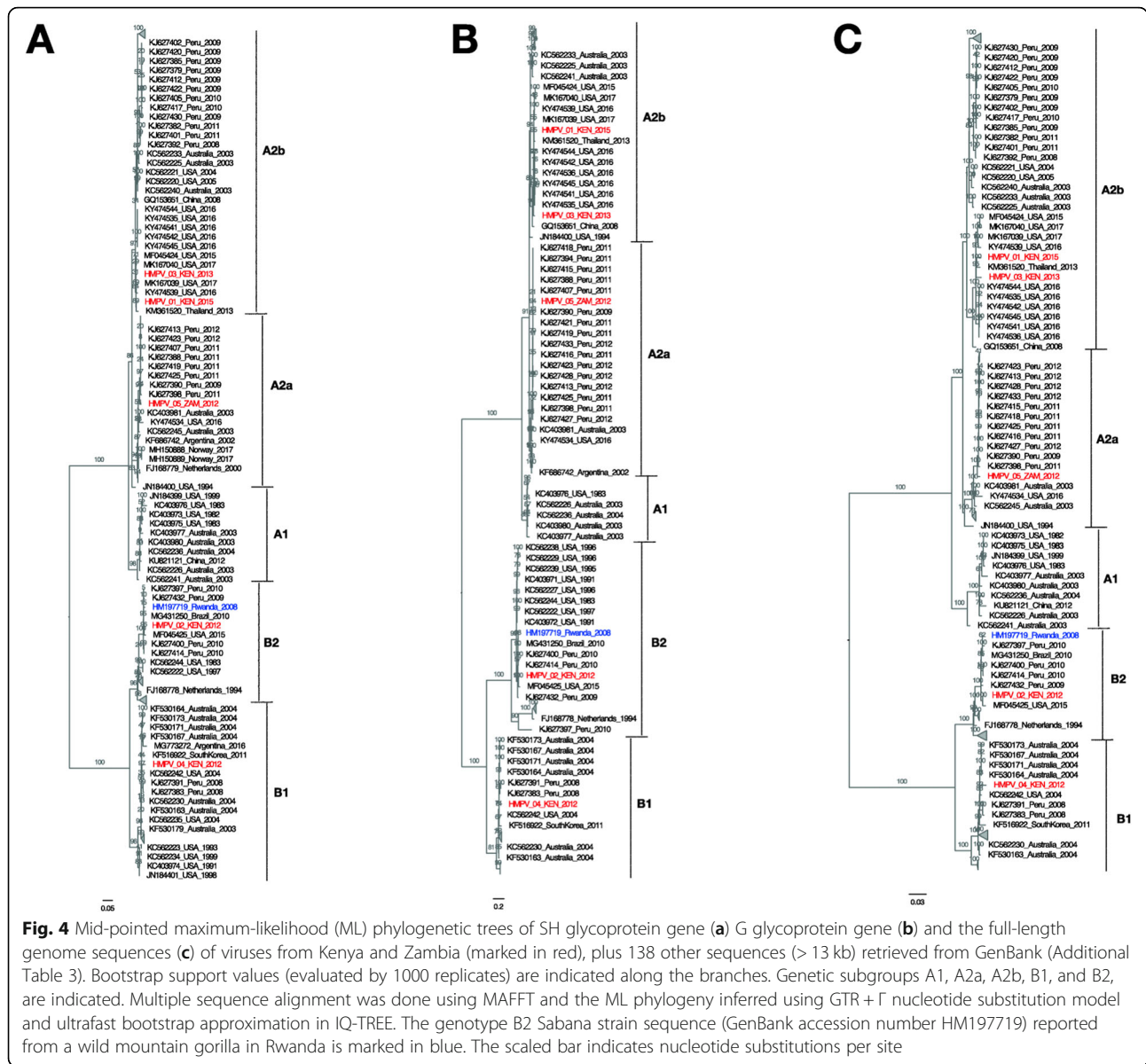


Fig. 4 Mid-pointed maximum-likelihood (ML) phylogenetic trees of SH glycoprotein gene (a) G glycoprotein gene (b) and the full-length genome sequences (c) of viruses from Kenya and Zambia (marked in red), plus 138 other sequences (> 13 kb) retrieved from GenBank (Additional Table 3). Bootstrap support values (evaluated by 1000 replicates) are indicated along the branches. Genetic subgroups A1, A2a, A2b, B1, and B2, are indicated. Multiple sequence alignment was done using MAFFT and the ML phylogeny inferred using GTR + Γ nucleotide substitution model and ultrafast bootstrap approximation in IQ-TREE. The genotype B2 Sabana strain sequence (GenBank accession number HM197719) reported from a wild mountain gorilla in Rwanda is marked in blue. The scaled bar indicates nucleotide substitutions per site

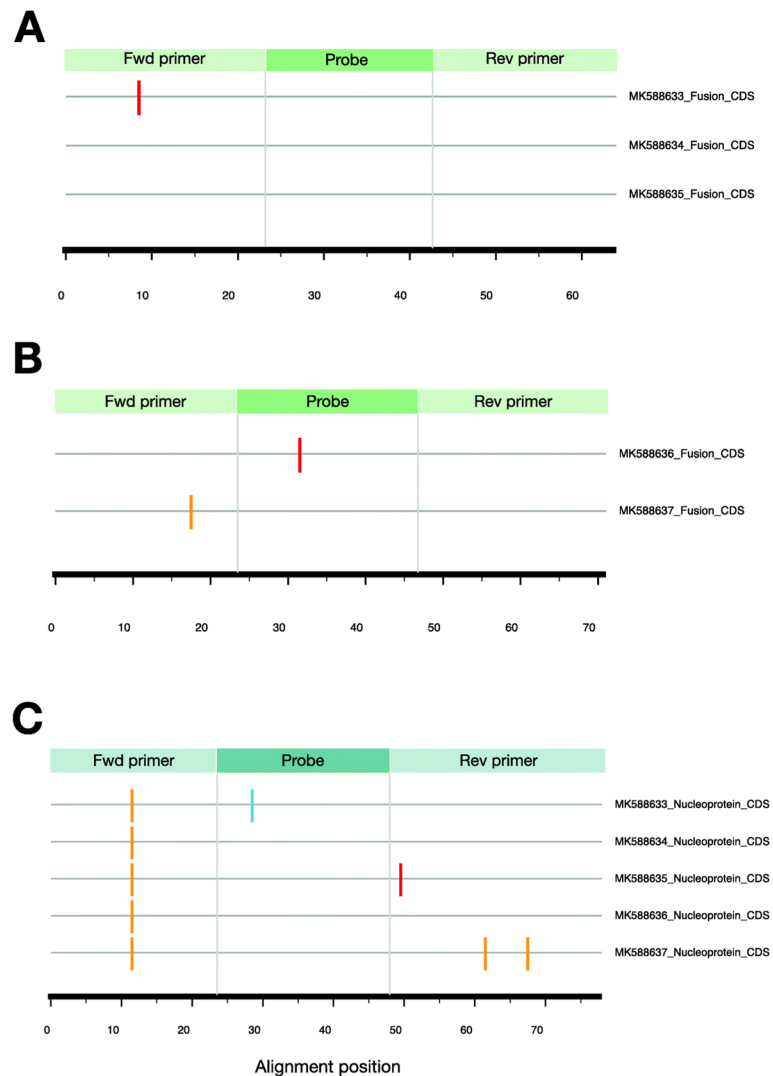


Fig. 5 Mismatches between the rRT-PCR diagnostic primers and probes and their expected binding sites in the five genomes from Kenya and Zambia. ‘Fwd primer’ = Forward primer and ‘Rev primer’ = Reverse primer. Two rRT-PCR assays were used for HMPV detection. The colored bars in the figure indicate nucleotide differences (mismatches) between (a) three HMPV-A genomes and HMPV-A specific primers and probes targeting fusion gene, (b) two HMPV-B genomes and HMPV-B specific primers and probes also targeting fusion gene, and (c) all five genomes reported here and specific primers and probes targeting nucleoprotein gene. The sequences of the rRT-PCR primers and probes checked against the African HMPV genomes are listed in Additional file 7: Table S4