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ERRATUM

Erratum to: Novel method for genotyping clinical herpes simplex virus type 1 isolates

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Unfortunately, Fig. 1 was published incorrectly in the original publication of the article. The correct version of Fig. 1 is given below:

The online version of the original article can be found under doi:10.1007/s00705-015-2568-y.

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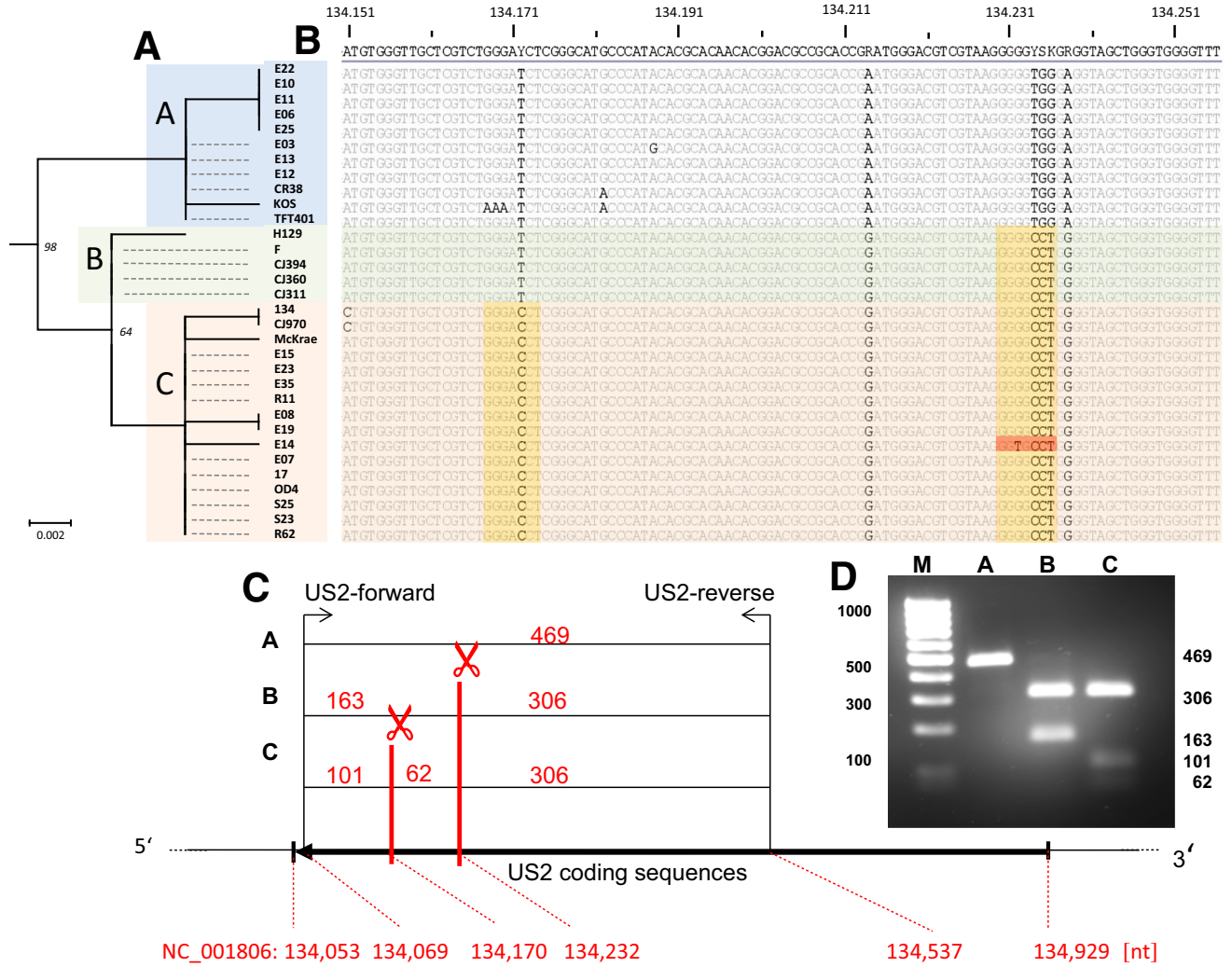

Fig. 1 Phylogenetic analysis of US2 as a basis for a novel HSV-1 genotyping method. **(A)** Phylogenetic tree constructed from 32 aligned amino acid sequences of HSV-1 US2 from NCBI GenBank (MEGA6 software using maximum-likelihood, the JTT-model and 500 bootstrap replicates). Three groups with high bootstrap support (italic letters) were identified and designated as A (blue), B (green) and C (ochre). **(B)** 105-nt window of the aligned coding sequence from US2 highlighted according to the group segregation of (A) and *Eco*O109I recognition sites (highlighted in golden colour). A single polymorphism in the *Eco*O109I recognition site was observed for strain E14 (highlighted in red). **(C)** Schematic illustration (forward primer starts at 134,069 and reverse primer ends at 134,537) and **(D)** results of agarose gel electrophoresis of the three HSV-1 US2 genotypes based on RFLP analysis of an amplified 469-bp DNA fragment using *Eco*O109I (✂). Genotype A, no cleavage, 469-bp fragment; genotype B, cleavage into 306-bp and 163-bp fragments; genotype C, cleavage into 306-bp, 101-bp and 62-bp fragments