Updated phylogeny of Chikungunya virus suggests lineage-specific RNA architecture

– Supplement –

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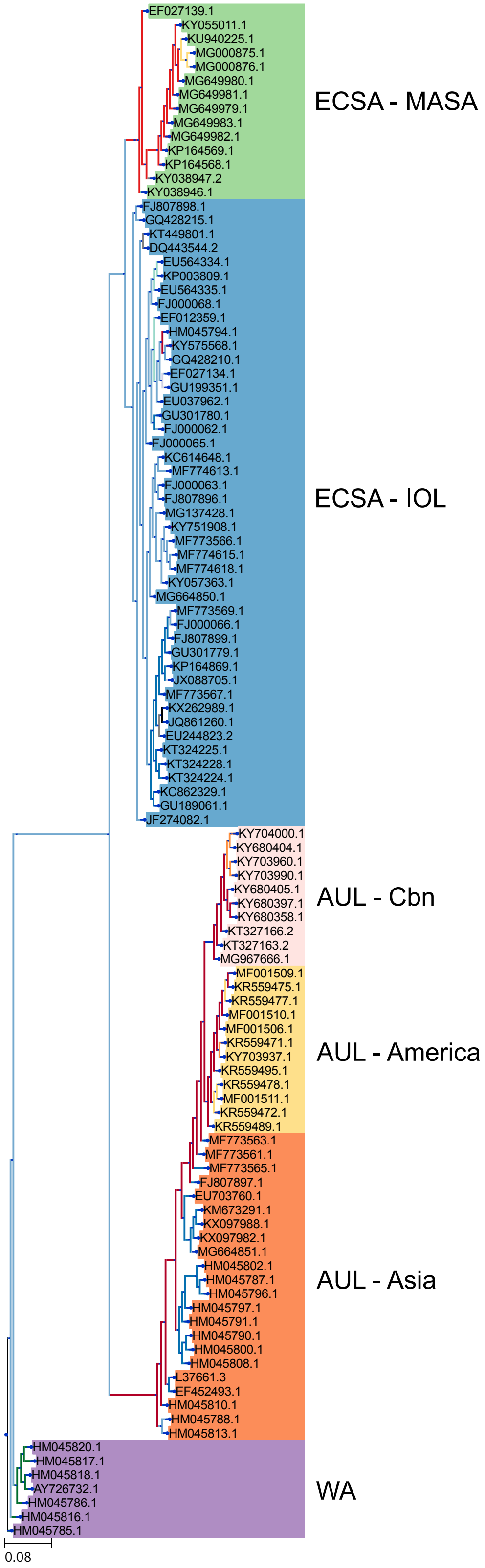

Fig. 1. Maximum-Likelihood phylogenetic tree based on a manually curated alignment of 111 complete CHIKV 3'UTRs. Color coding of the tree based on Fig. 1 in main text. Leaves are colored according to lineage, with UTRs harbouring the duplication event in the AUL-American lineage are colored separately.