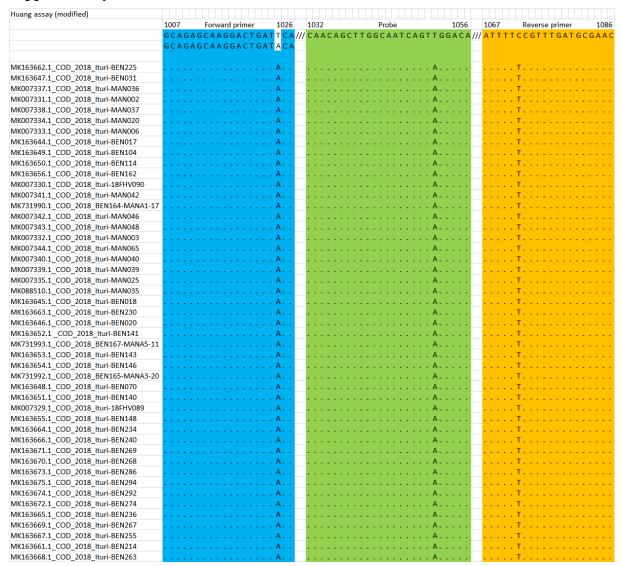
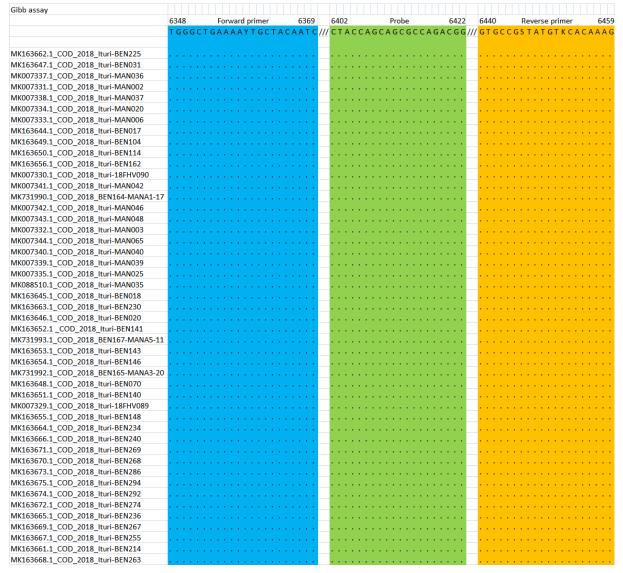
## Supplementary



**Figure S1.** Primers and probe described in the Huang et al. assay (and supplementary forward primer [this study]) matched against the multiple alignment dataset (nucleoprotein gene) representing EBOV strains during the 2018 outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo. Y = C/T; S = C/G; K = G/T. Nucleotide positions refers to the sequence of Zaire ebolavirus genome (GenBank accession number MK007339).



**Figure S2.** Primers and probe described in the Gibb et al. assay matched against the multiple alignment dataset (glycoprotein gene) representing EBOV strains during the 2018 outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo. Y = C/T; S = C/G; K = G/T. Nucleotide positions refers to the sequence of Zaire ebolavirus genome (GenBank accession number MK007339).