Supplementary Figure

The L467F-F508del Complex Allele Hampers Pharmacological Rescue of Mutant CFTR by Elexacaftor/Tezacaftor/Ivacaftor in Cystic Fibrosis Patients: The Value of the Ex Vivo Nasal Epithelial Model to Address Non-Responders to CFTR-Modulating Drugs

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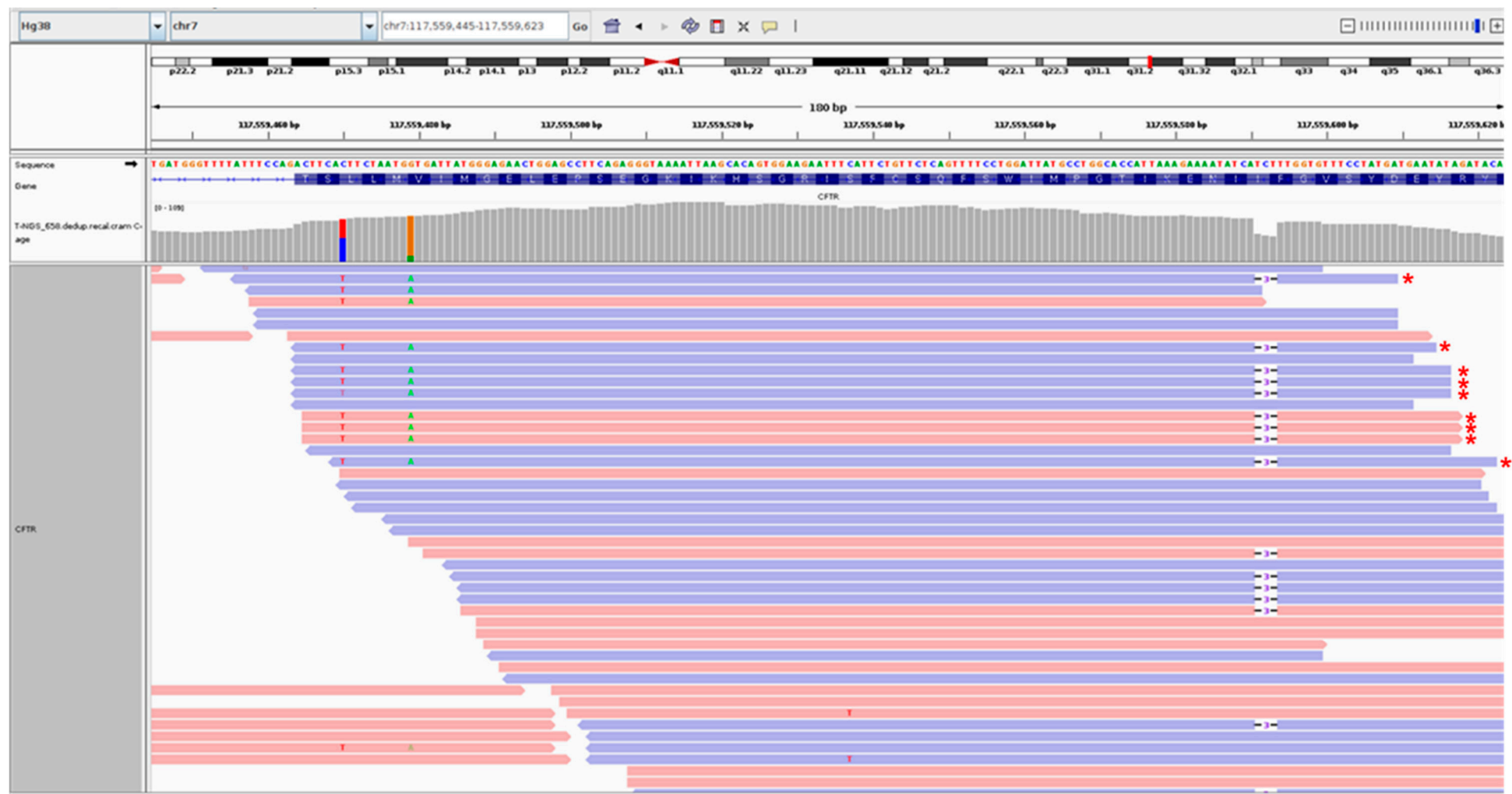[‡] These authors contributed equally as last authors.

Figure S1. The L467/F508del complex allele and the Gaslini exome genomic database. Genomic window spanning a region of the *CFTR* exon 11 generated by the Integrative Genomics Viewer (IGV) and displaying the BAM alignment track mapped read-segments per reference sequence (GRCh38/hg38). Red asterisks indicate the reads showing the mismatch positions corresponding to the presence of the L467F (T, red) and F508del (-3-) variants in *cis* in the same sequence fragment. A further mismatch (A, green) in cis with the two variants corresponds to the presence of the V470M polymorphism