

Article

# Diversity and Complexity of Internally Deleted Viral Genomes in Influenza A Virus Subpopulations with Enhanced Interferon-Inducing Phenotypes

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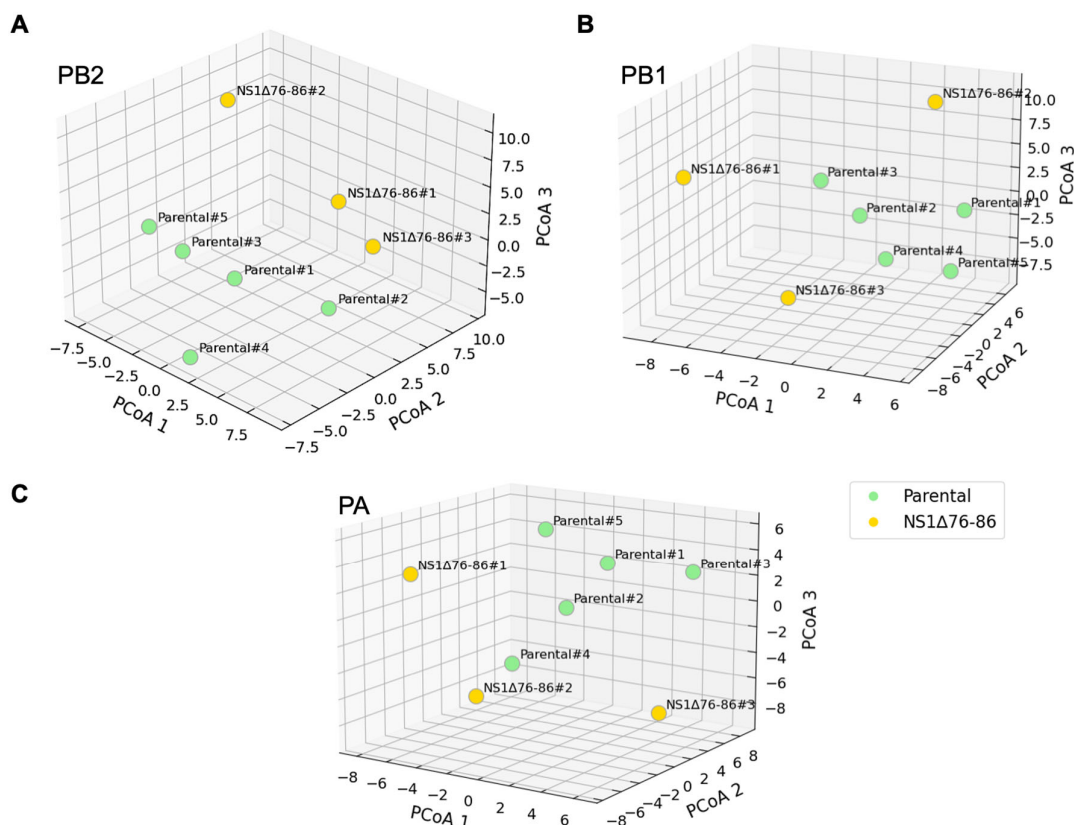
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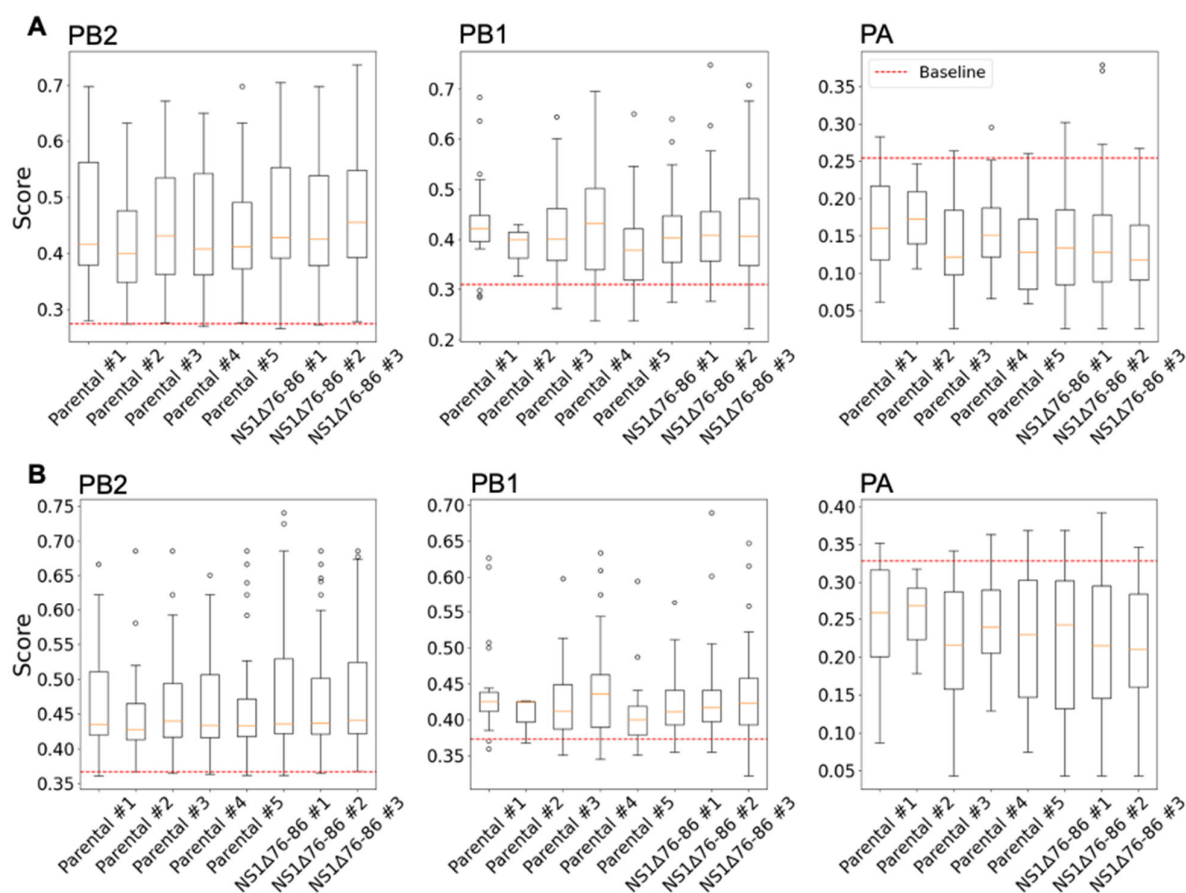
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**Supplementary Figure S1.** Principal component analysis (PCoA) based on Euclidean distances among the abundance of ID vRNA and the break and rejoin sites for PB2 (A), PB1 (B), and PA (C)-derived ID vRNAs detected in parental (green) and NS1Δ76-86 (golden) clones. The NS1Δ76-86 clones appeared to have greater separation from each other than the parental clones.



**Supplementary Figure S2.** Prediction of the disordered nature of putative viral polypeptides encoded by the ID vRNAs from each plaque-purified clone. No significant differences were observed between the average IUPred3 (**A**) and ANCHOR2 (**B**) values among the viral clones with distinct IFN-inducing phenotypes. Red dotted lines represent the mean value estimated for the intact PB2, PB1, or PA viral proteins.