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Impact of the influenza protein PB1-F2 on the biochemical composition of human epithelial cells revealed by synchrotron Fourier transform infrared spectromicroscopy

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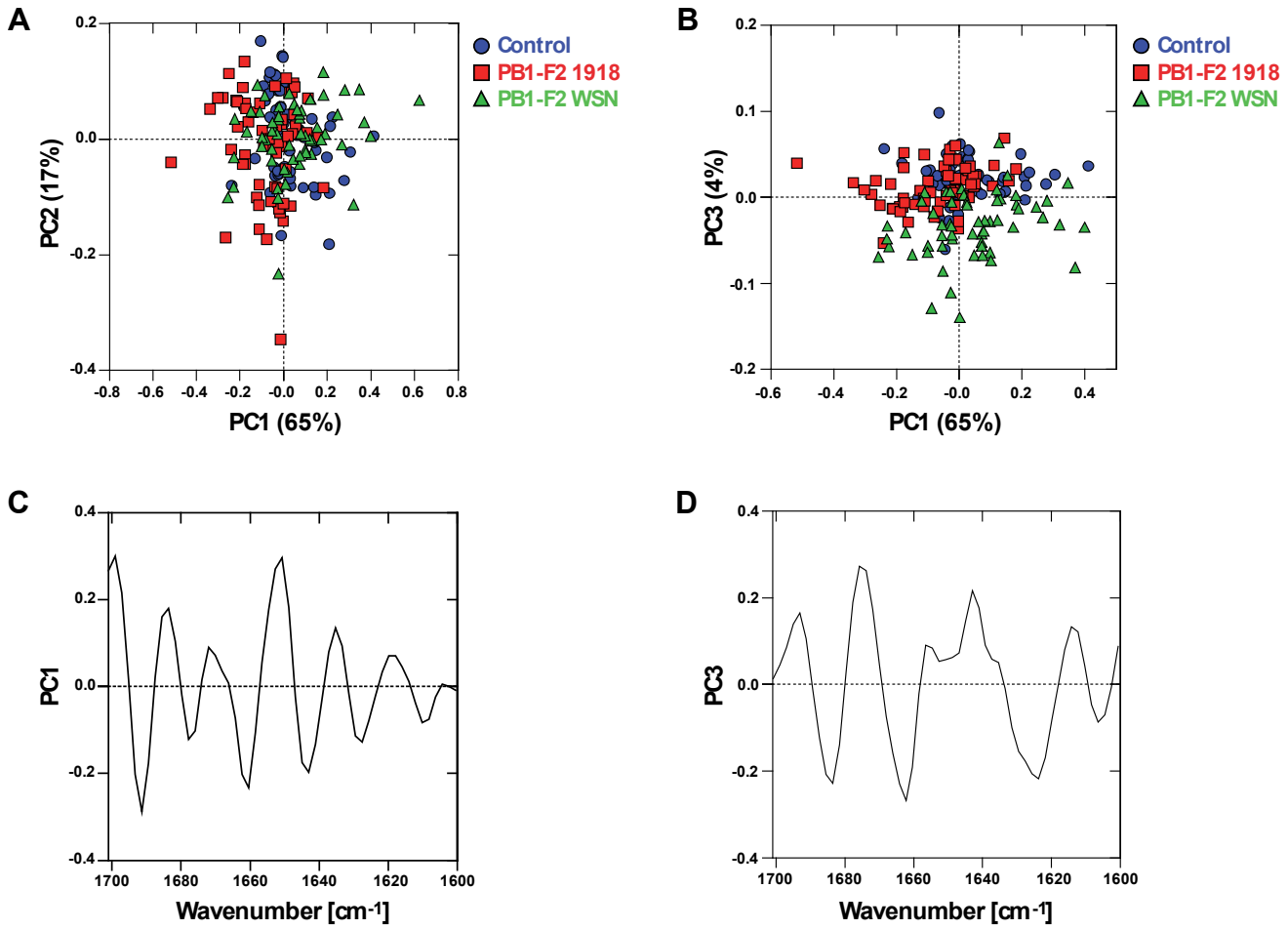

Figure S1. sFT-IR spectromicroscopy analysis of control-, PB1-F2 WSN- and PB1-F2 1918-transfected HEK293T cells in the amide I region. PCA score plots of PC1 against PC2 (A) and PC1 against PC3 (B) for IR spectra in the 1700–1600 cm^{-1} region of the spectrum. Numbers in brackets correspond to the percentage of the total variance explained by each PC. Each blue circle, red square and green triangle represent a single-cell IR spectrum collected from empty-vector (control)-, PB1-F2 1918- and PB1-F2 WSN-transfected HEK293T cells, respectively. (C and D) Loading plots indicating the influence of the variables (i.e. wavenumber here) that are taken into account in the determination of PC1 (C) and PC3 (D) by PCA. PC1, PC2 and PC3 account for 65 %, 17 % and 4 % of the total explained variance, respectively. Despite that the PC1 axis partially separate the PB1-F2 1918 cluster from the control cluster, and that the PC3 axis clearly separate the PB1-F2 WSN cluster from the two other clusters, the corresponding loading plots are difficult to interpret. Consequently, no specific signature of protein secondary structures can be assigned to PB1-F2-transfected cells based on amide I region.

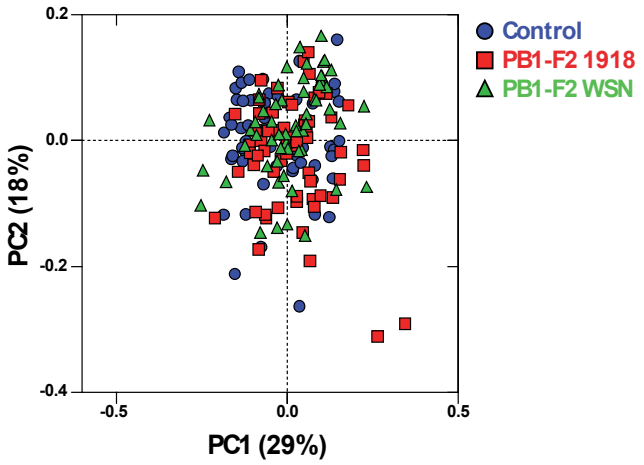

Figure S2. sFT-IR spectromicroscopy analysis of control-, PB1-F2 WSN- and PB1-F2 1918-transfected HEK293T cells in the CH_2/CH_3 region. PCA score plot of PC1 against PC2 for IR spectra in the 3100–2800 cm^{-1} region of the spectrum. Numbers in brackets correspond to the percentage of the total variance explained by each PC. Each blue circle, red square and green triangle represent a single-cell IR spectrum collected from empty-vector (control)-, PB1-F2 1918- and PB1-F2 WSN-transfected HEK293T cells, respectively.