

Development and Evaluation of a Hybrid Capture-Based NGS Panel for Comprehensive Detection of Respiratory Pathogens

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Supplementary Figure S1. Correlation between RT-PCR Ct values and genome coverage in individual pathogens

Violin plots illustrating the distribution of genome coverage ($>10\times$ depth) obtained from NGS data in relation to RT-PCR Ct values for individual pathogens. Only pathogens with ≥ 5 clinical samples are displayed. Each dot represents an individual sample. Horizontal lines represent medians, as in Figure 6. Viral pathogens are shown in panel a, and bacterial pathogens are depicted in panel b. Created with BioRender.com.