

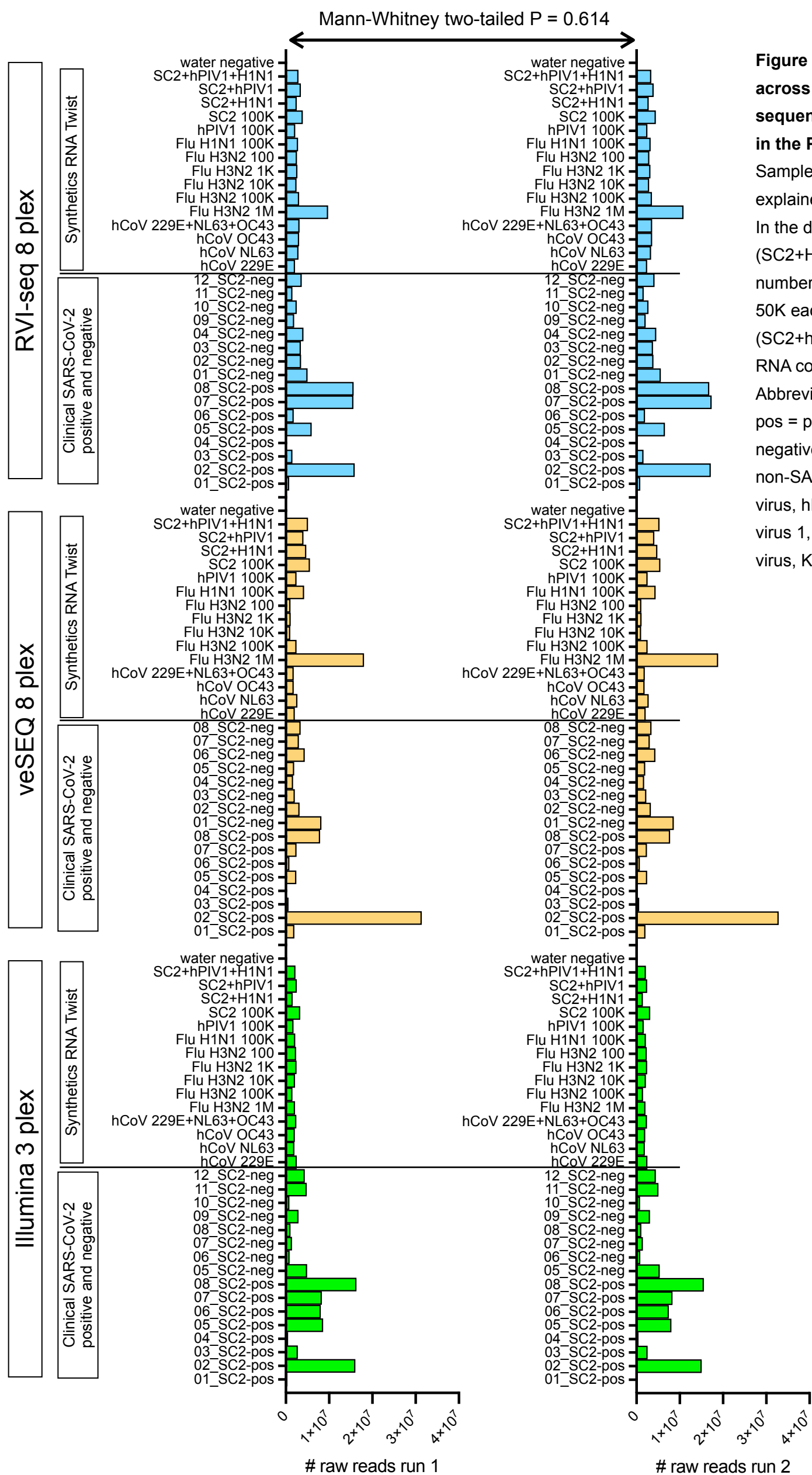


Figure S2 - Number of raw reads across the two replicated sequencing runs were very similar in the Pilot 1 experiment

Sample types and sequence IDs are explained in **Extended Data Table 1**. In the double mix samples (SC2+H1N1 and SC2+hPIV1), the number of RNA copies added was 50K each, and in the triple mix sample (SC2+hPIV1+H1N1), the number of RNA copies added was 33K each. Abbreviations: SC2 = SARS-CoV-2, pos = positive for SARS-CoV-2, neg = negative for SARS-CoV-2, hCoV = non-SARS-CoV-2 human corona virus, hPIV = human parainfluenza virus 1, H3N2 and H1N1 = influenza A virus, K = thousand