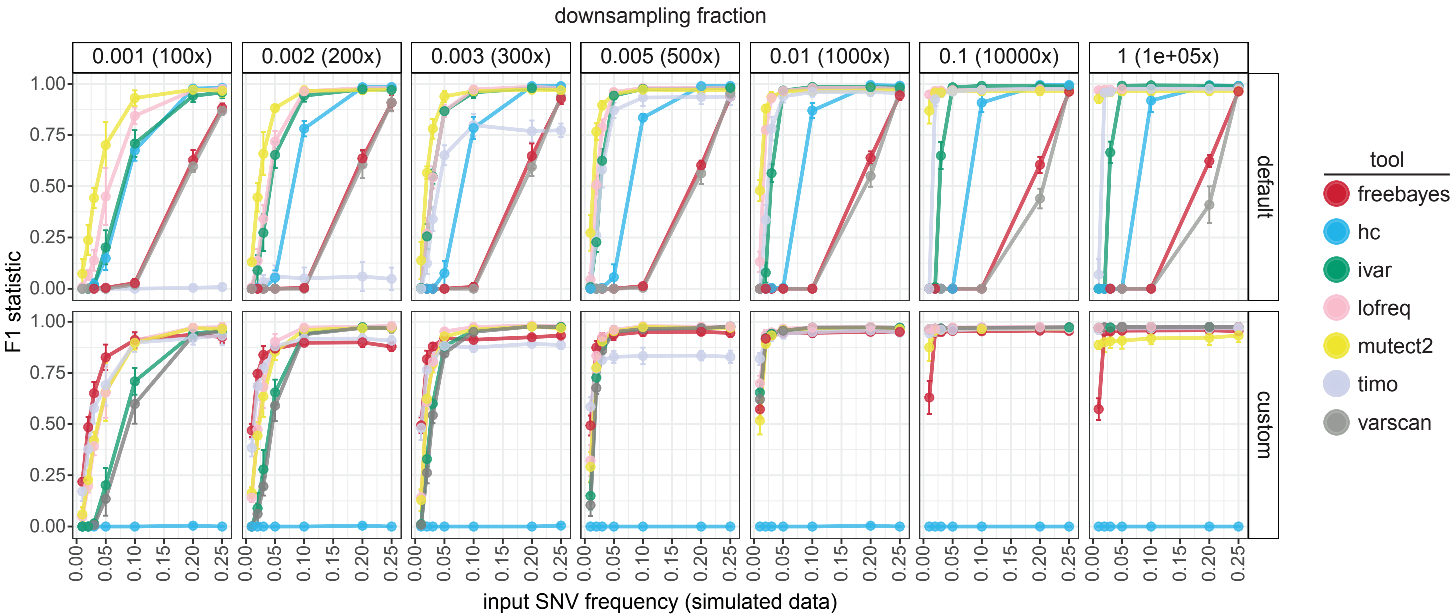

Figure S2. Variant caller performance using default and custom parameters on simulated data. F1 statistic for each variant caller across a range of downsampling fractions (0.001-1, expected read depth: 100x-100,000x) and allele frequencies (0.01-0.25, 1-25%). Values shown are mean and standard deviation across the four viruses (A/H1N1, A/H3N2, B/Victoria, SARS-CoV-2) using default (top), or custom (bottom) input parameters (Table S1). Color represents the variant caller used.