Corrections:

Figure 6 legend:

Comparison of adaptive substitutions per codon per year between measles (yellow), four influenza strains (A/H3N2, A/H1N1pdm, B/Vic, and B/Yam- shown in shades of red), OC43 lineage A (dark teal), OC43 lineage B (light teal), and 229E (dark blue). The polymerase, receptor-binding domain, and membrane fusion domain for influenza strains are PB1, HA1, and HA2. For both human coronaviruses (HCoVs), they are RdRp, S1, and S2, respectively. For measles, the polymerase is the L gene, the receptor-binding protein is the H gene, and the fusion protein is the F gene. Error bars show 95% bootstrap percentiles from 100 bootstrapped data sets.