

Figure 1-figure supplement 2

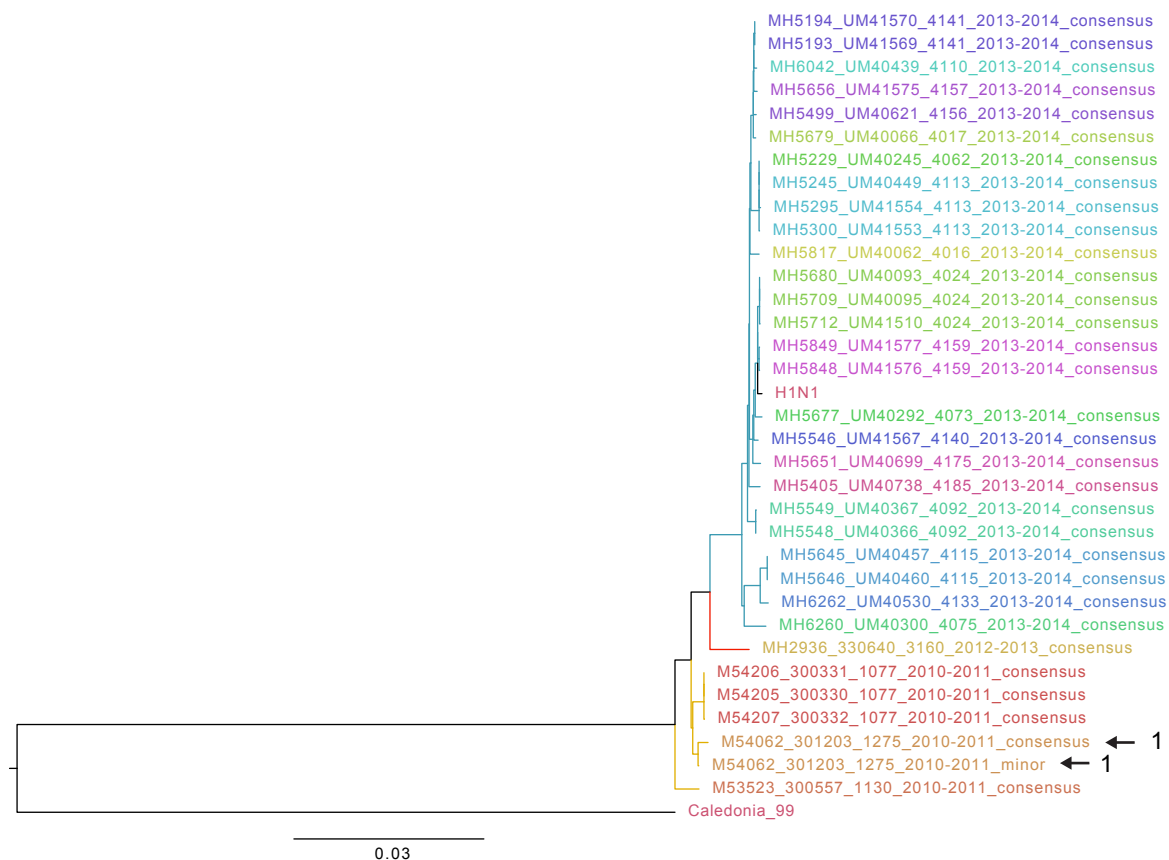


Figure 1-figure supplement 2. Approximate maximum likelihood trees of the concatenated coding sequences for high quality H1N1 samples. The branches are colored by season; the tip identifiers are colored by household. Arrows with numbers indicate consensus and putative minor haplotypes for samples with greater than 10 iSNV. Trees were made using FastTree (Price et al. 2010). “Caledonia” refers to A/New Caledonia/20/1999(H1N1). “H1N1” refers to sequence from a plasmid clone derived from a clinical sample corresponding to A/California/07/2009.