



**Figure S5** Joint site frequency spectra (SFS) for clades A1, A2, and C. Total numbers of derived allele counts are shown for all three pairwise comparisons of clades. The vast majority of variation is located along the x and y-axis indicating that most variation is clade-specific. Only a small percentage of total variation is shared between clades and may therefore represent ancestral diversity, introgression, or convergent evolution.