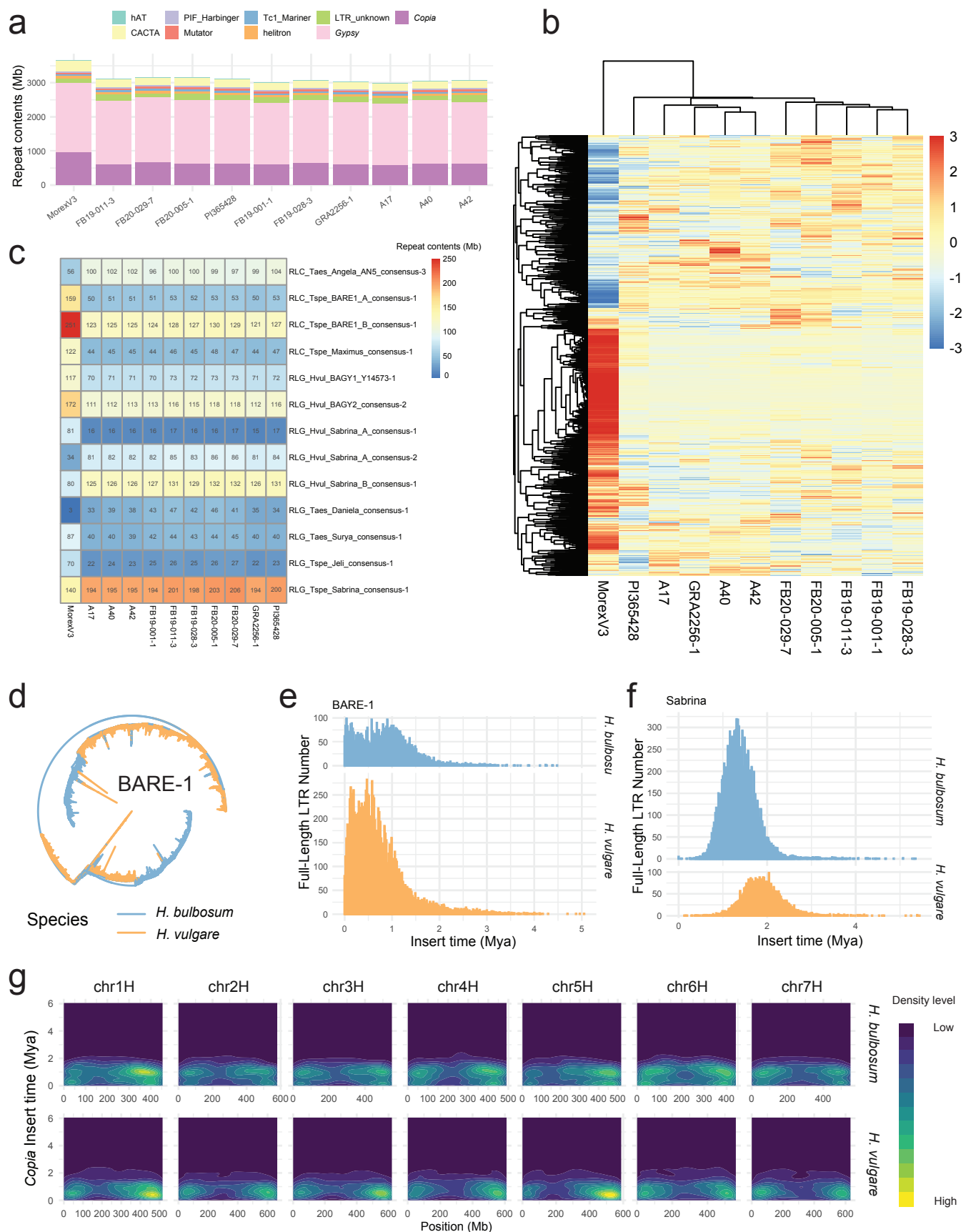




Extended Data Figure 7: Evolution of TEs in *H. bulbosum* and *H. vulgare*. (a) Size and composition of the repetitive portion of the *H. bulbosum* and *H. vulgare* genomes. Haplotype 1 of each *H. bulbosum* genome is shown. (b) Heatmap constructed from a matrix tabulating the abundance of 989 TE representatives from the TREP database. (c) Subsets of abundance matrix for the 13 most variable TE representatives. Numbers in the boxes and the color code refer to the cumulative lengths of TE sequences assigned to each representative per haplotype. (d) Approximately maximum-likelihood phylogenetic trees for all full-length BARE-1 elements in *H. vulgare* and *H. bulbosum*. (e) Distribution of the insertion times of all full-length BARE-1 elements in *H. vulgare* and *H. bulbosum*. (f) Distribution of the insertion times of all full-length Sabrina elements in *H. vulgare* and *H. bulbosum*. (g) Two-dimensional density plot showing the relationship between insertion time and genomic position of *Copia* elements.