



Extended Data Figure 8: Relationships between *H. bulbosum* populations. (a) Positions of the 10 pangenome accessions in PCA diversity space. (b) Geographic map showing the origins of 260 accessions subjected to genotyping-by-sequencing. Information was aggregated at the country level. Map source (<https://maps.stamen.com/>) (c) Neighbor-joining tree constructed from a genome-wide SNP matrix (nuclear genome) of 32 *H. bulbosum* haplotypes and one *H. vulgare* genome. Geographic origins and ploidy are color-coded (d) Maximum likelihood (ML) tree constructed from the whole chloroplast genomes of the 32 *H. bulbosum* and one *H. vulgare*. The wheat chloroplast genome was included as an outgroup. (e) Population trajectory as inferred by PSMC of the Libyan diploid PI365428, diploids from other countries, autotetraploids, and synthetic heterozygotes between the Libyan diploid and other diploid and tetraploid haplotypes. (f) Genetic distance of PI365428 to other populations. (g) Heatmap showing the identity-by-state (IBS) distance matrix between 270 *H. bulbosum* and 3 *H. vulgare* genomes. (h) Genetic distance of the Greek tetraploid populations.