

Supplementary figures

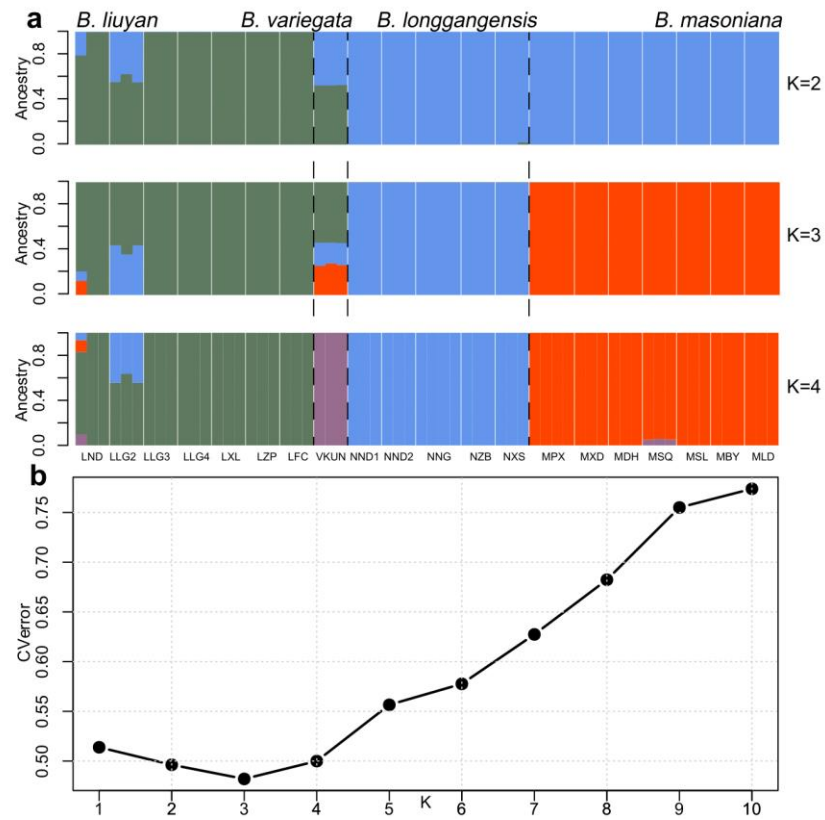


Figure S1 (a) Results of genetic clusters from K=2 to K=4 based on nuclear SNP dataset of the *Begonia masoniana* complex. **(b)** Cross-validation plot for K=1-10 obtained with ADMIXTURE. Each vertical bar represents an individual, with different colors representing one of the genetic ancestries.

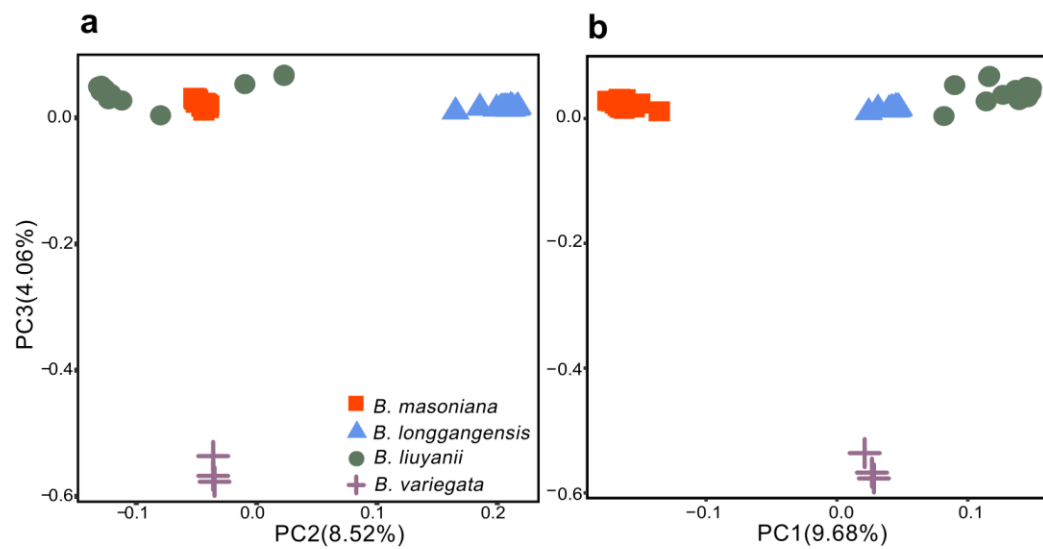


Figure S2 Principal component analysis (PCA) of the four *Begonia* species based on nuclear SNPs.

The percentage of variation explained by each principal component is shown in parentheses.

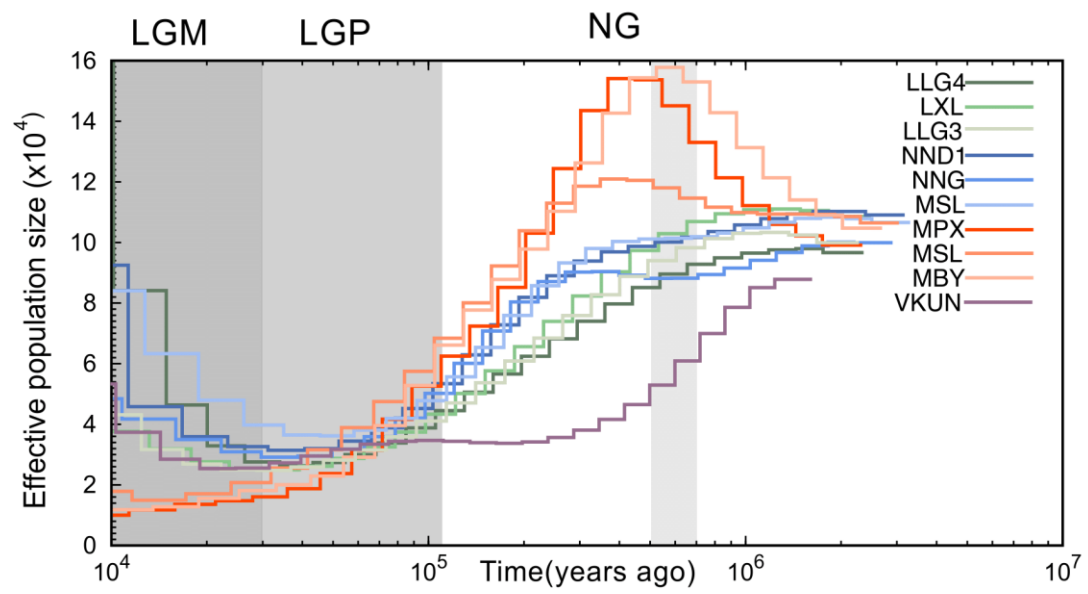


Figure S3 Demographic history inferred by the pairwise sequentially Markovian coalescent (PSMC) model for three populations within the *Begonia masoniana* complex.

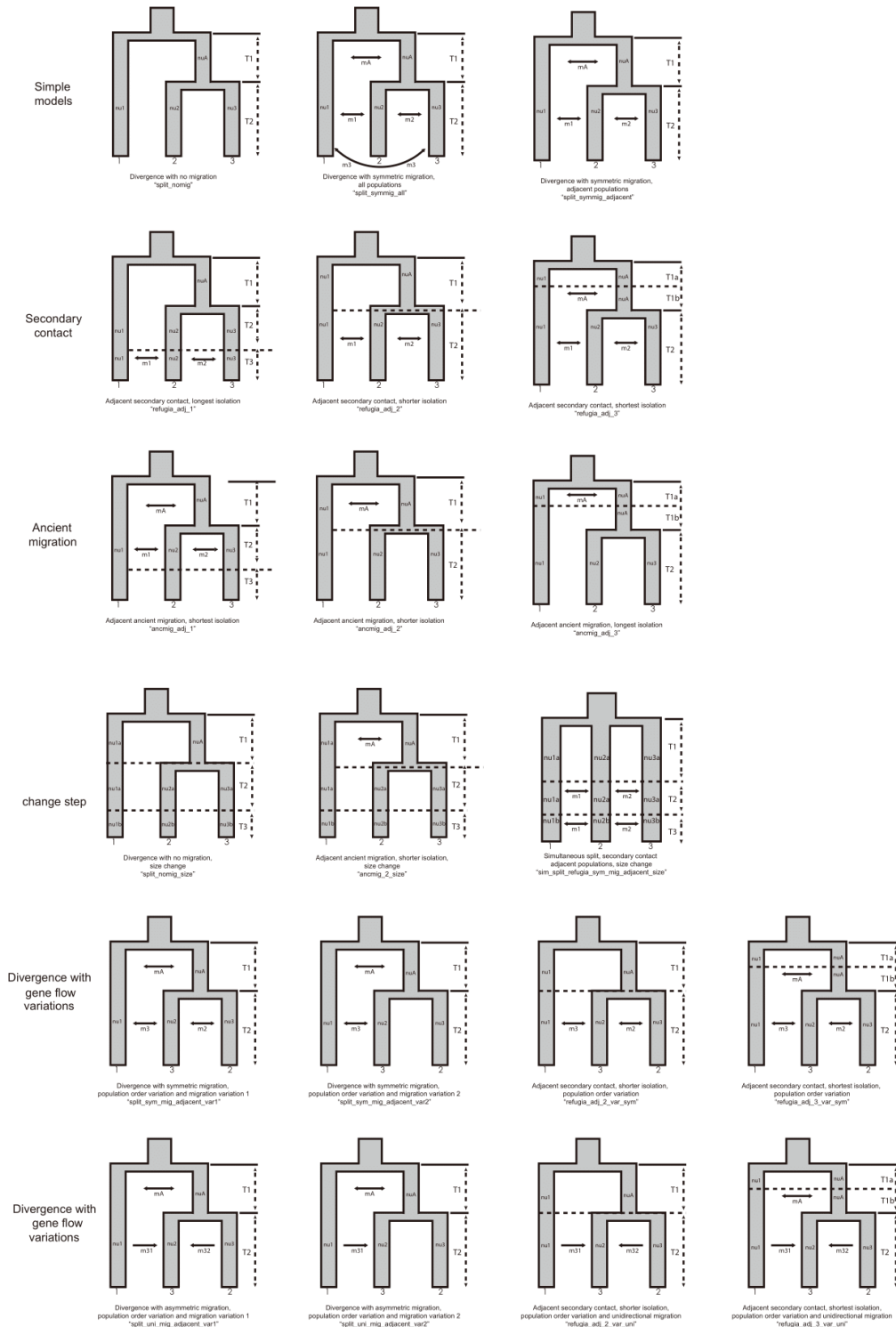


Figure S4 Demographic models of *dadi* tested for species divergence among *B. liuyanii*, *B. longgangensis*, and *B. masoniana*. Nu, population size; T, time points; m, migrations. Solid lines depict migration directions. Dashed lines with arrows represent time intervals. Dashed lines represent the interspecies isolation. The numbers 1, 2, and 3 under the bars represent *B. liuyanii*, *B. longgangensis*, and *B. masoniana*, respectively.

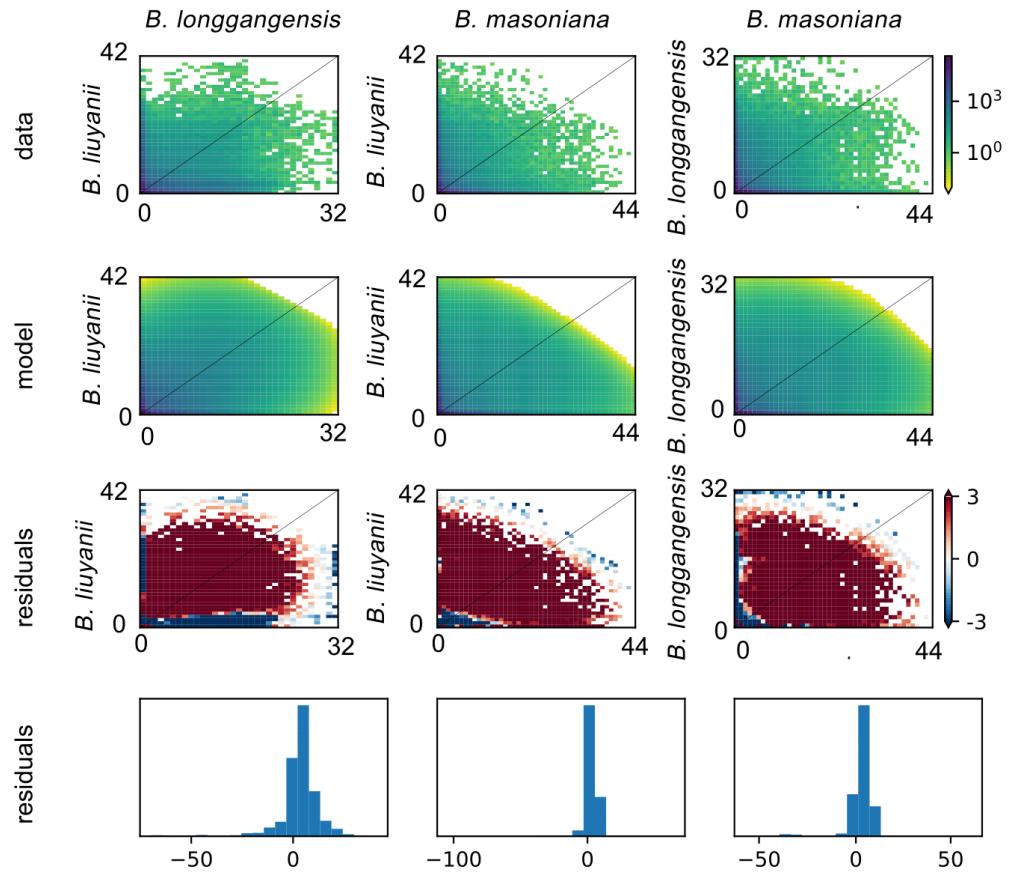


Figure S5 Goodness-of-fit evaluation of the best demographic model inferred by *dadi*. Comparisons include pairwise 2D-SFS for the data, the model, and the resulting residuals for each species combination.

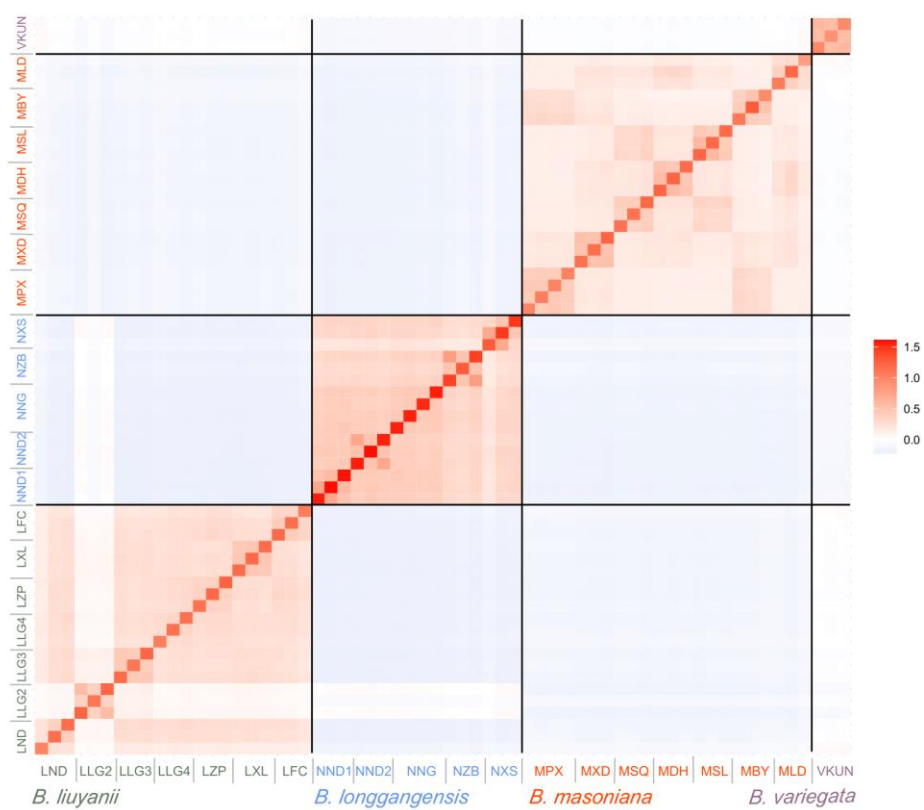


Figure S6 The kinship relationships among all individuals of the *Begonia masoniana* complex.

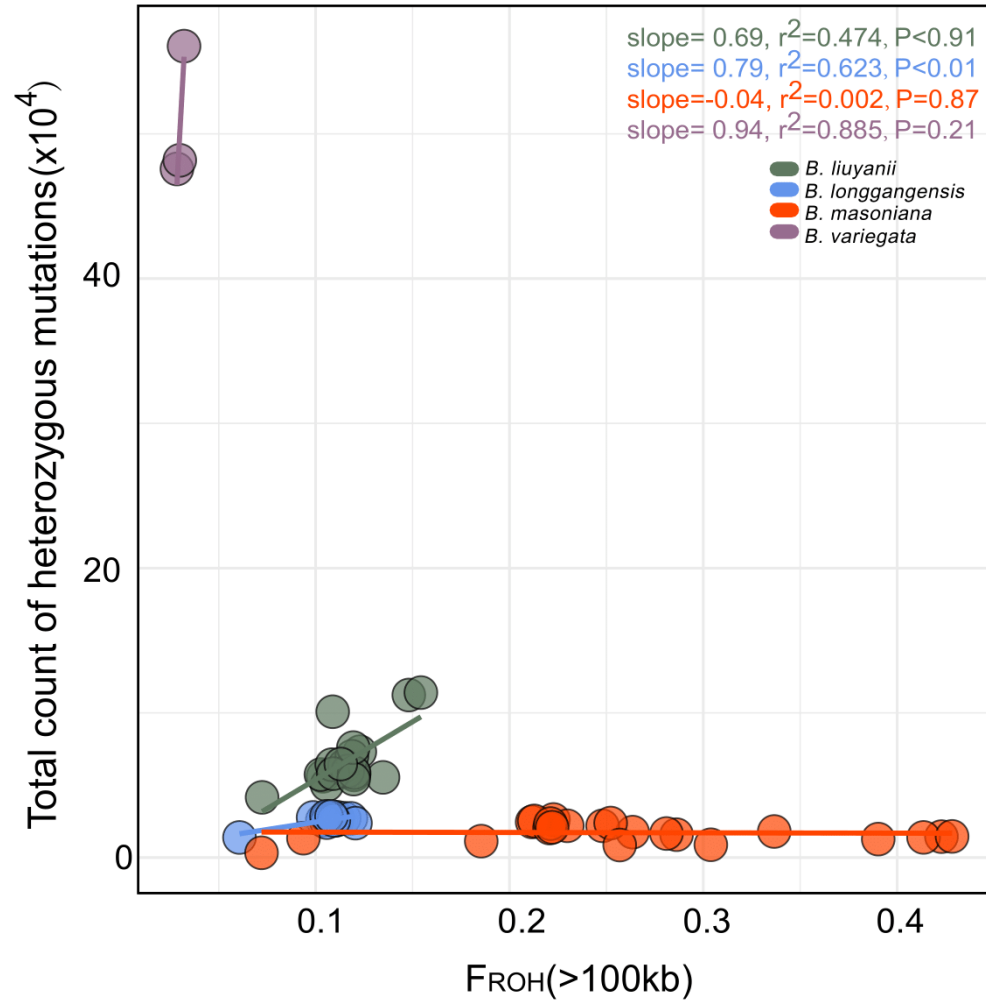


Figure S7 Correlation between genome-wide F_{ROH} and total count of heterozygous deleterious sites.

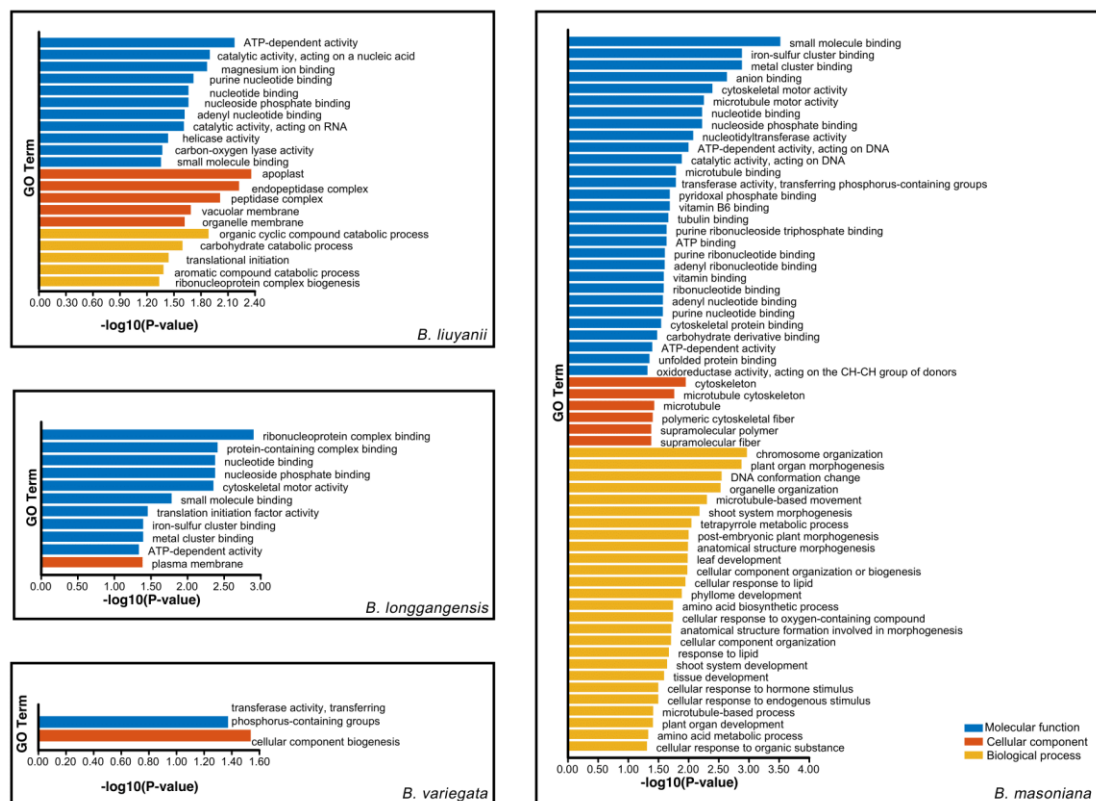


Figure S8 Enrichment of the GO pathway for loss-of-function (LOF) homozygous mutations.

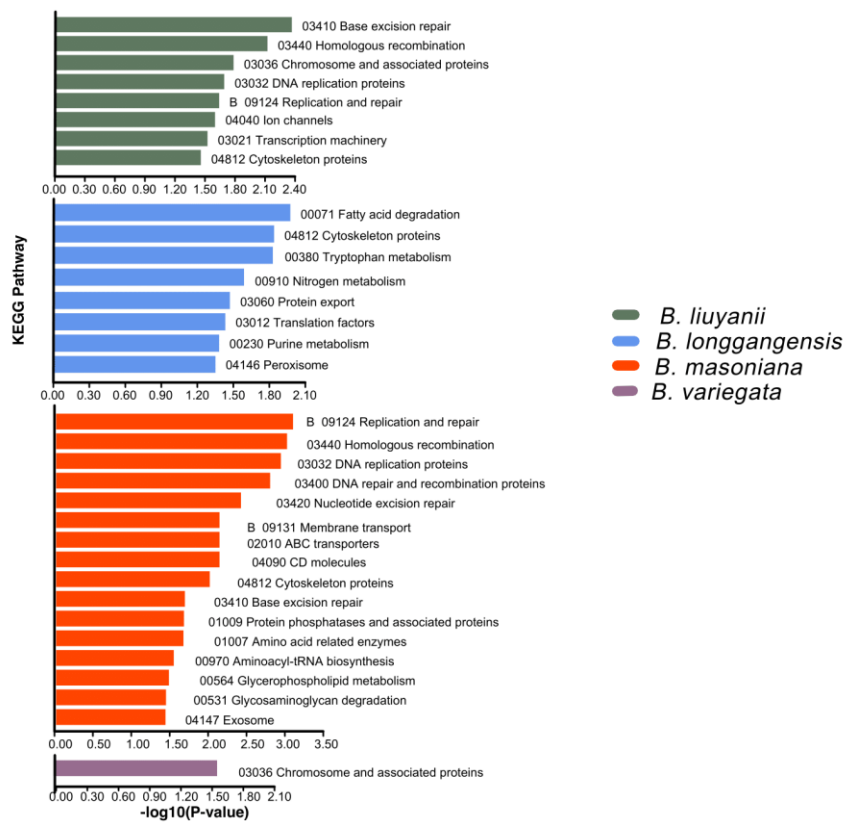


Figure S9 Enrichment of the KEGG pathway for loss-of-function (LOF) homozygous mutations.