

Gene ontology (GO) enrichments were developed using the five clusters identified by the hierarchical clustering analysis of the group of 526 DE genes, using the agriGO platform [42]. These genes were obtained from comparison between LB and SB segregants, in the FTS and B68 stages.



Figure S1A

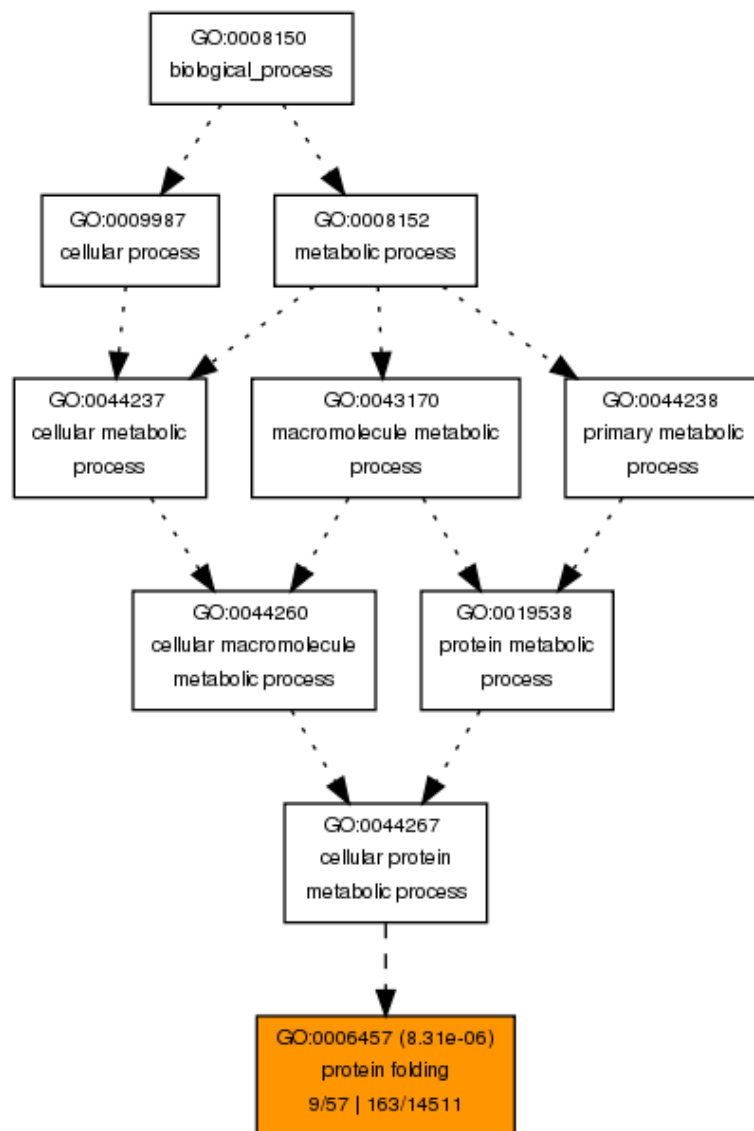


Figure S1B

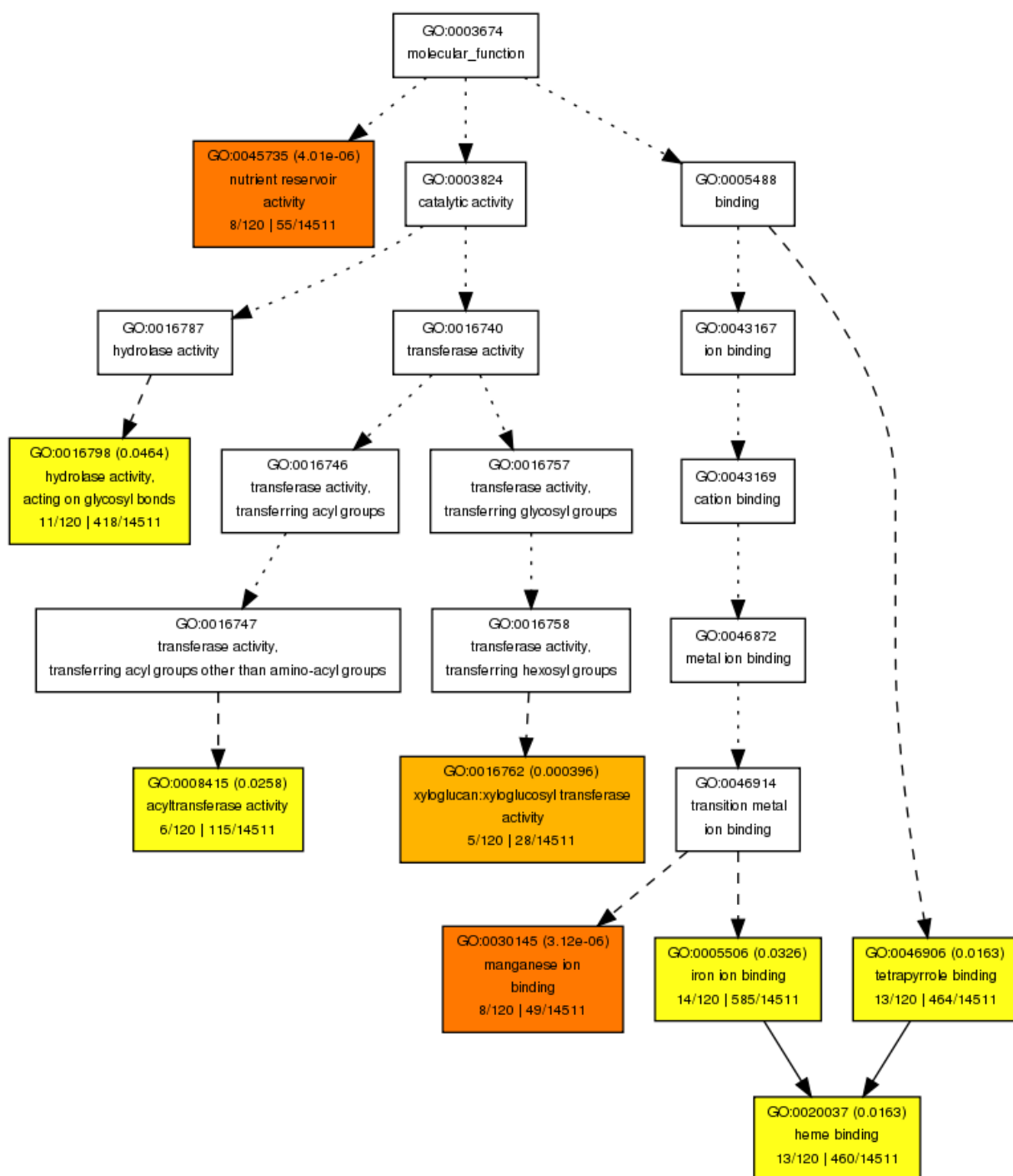


Figure S1C

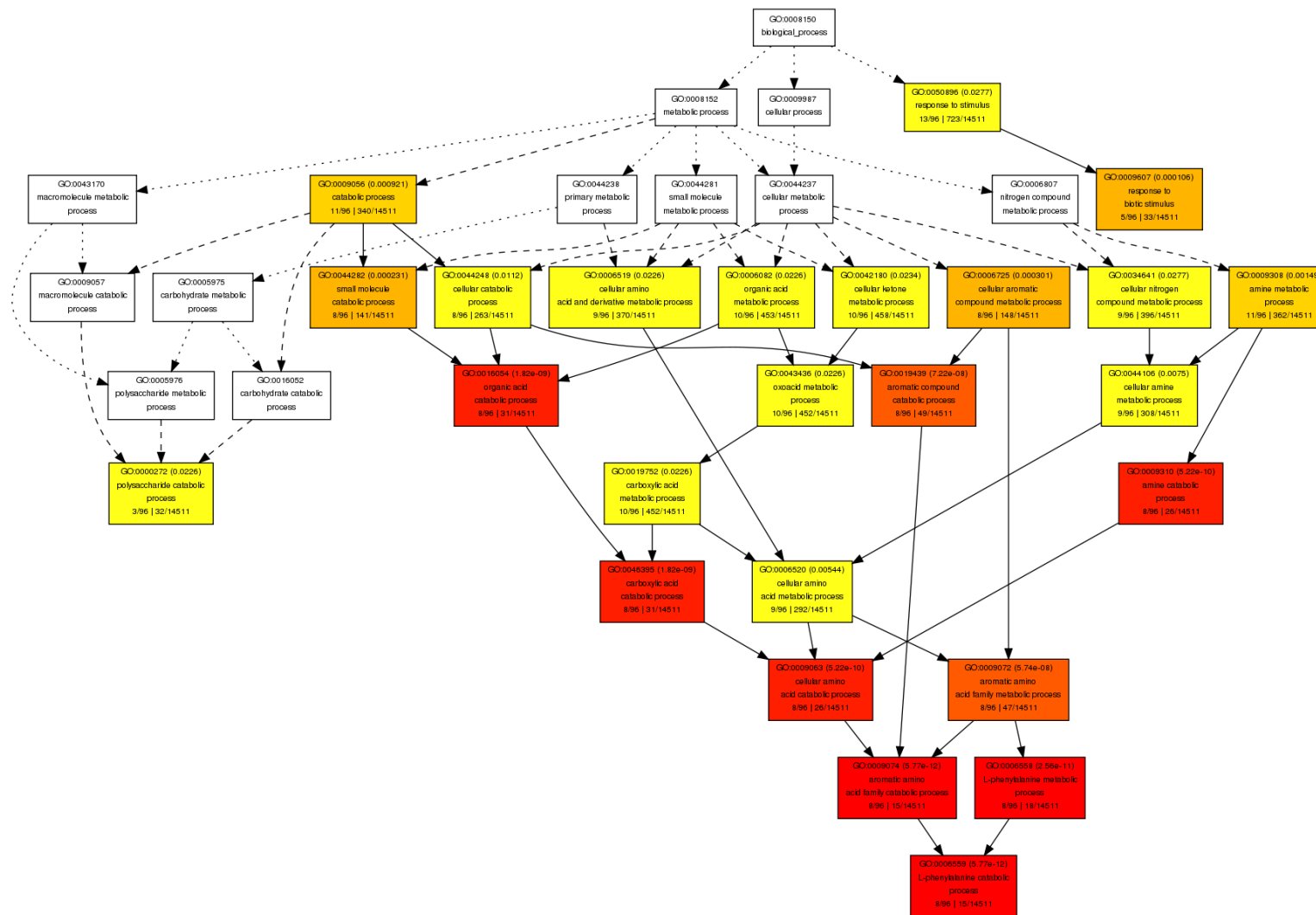


Figure S1D

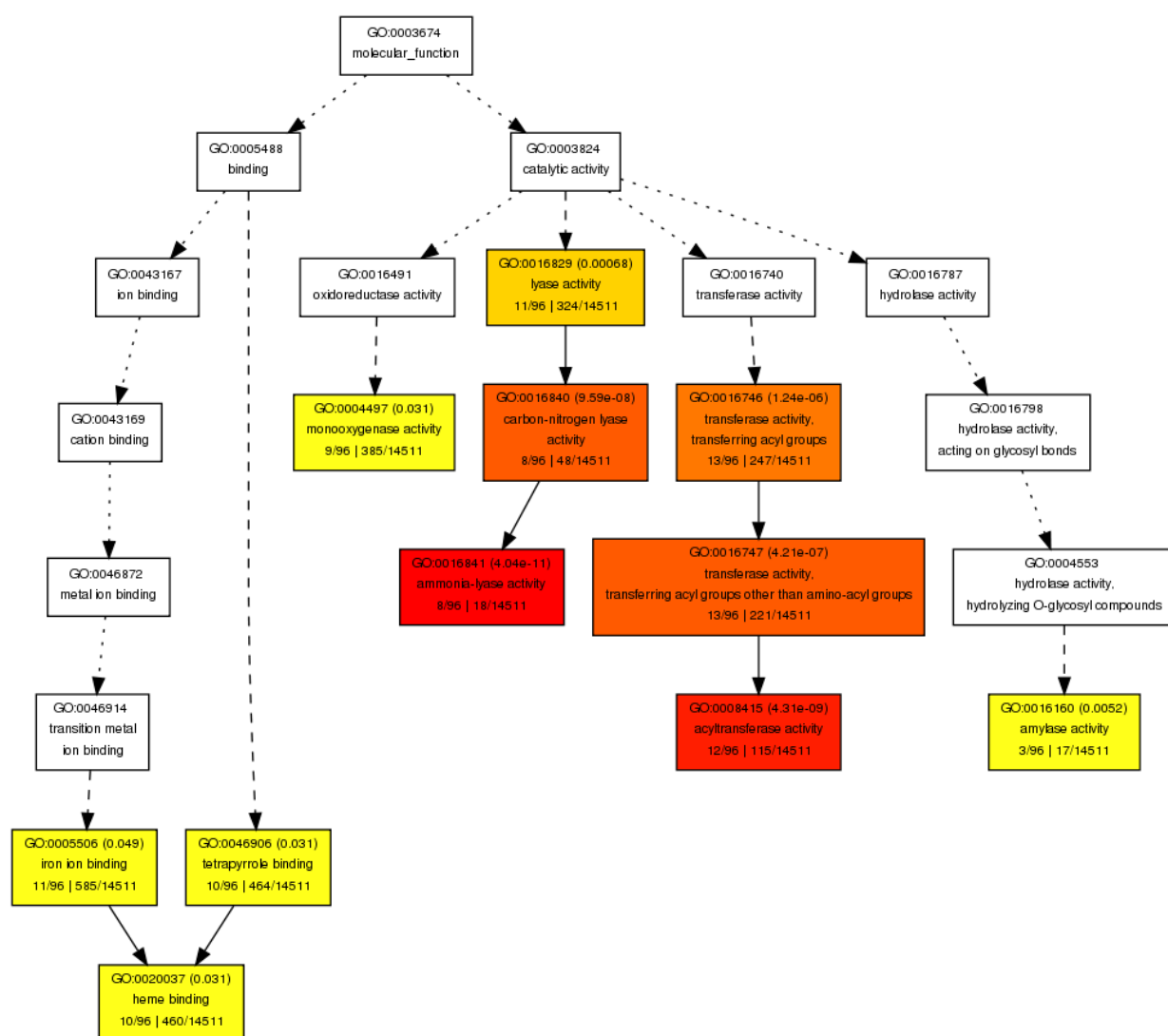


Figure S1E

Figure S1 A, B, C, D, E. GO enrichment of five clusters identified in hierarchical clustering of 526 DE genes, derived from comparison between LB and SB segregants. A. GO categories over-represented in Cluster 1 (Biological Process); **B.** GO categories over-represented in Cluster 3 (Biological Process); **C.** GO categories over-represented in Cluster 4 (Molecular Function); **D.** GO categories over-represented in Cluster 5 (Biological Process); **E.** GO categories over-represented in

Cluster 5 (Molecular Function). Biological Process and Molecular Function categories are shown, and only significantly over-represented categories were considered ($p < 0.05$ and $FDR < 0.05$). The analysis was performed using the online agriGO tool and the GO complete category. The boxes contain the GO number, the p-value (in parentheses), the category description, the number of genes in each category associated with the GO term versus the total of query genes and the number of genes in each category out of 14,511 genes of the reference genome of *Vitis vinifera* (PN40024, 12X.v1), with associated GO terms. The arrows indicate the relationships among the GO categories, as follows: black solid arrows mean that a GO category is also included in the other one; red solid arrows mean that one GO category positively regulates the other; green solid arrows mean that the GO category negatively regulates the other; black dashed arrows indicate that there are two significant nodes related to the GO category; and black dotted arrows indicate that only one significant node is related to the GO category.