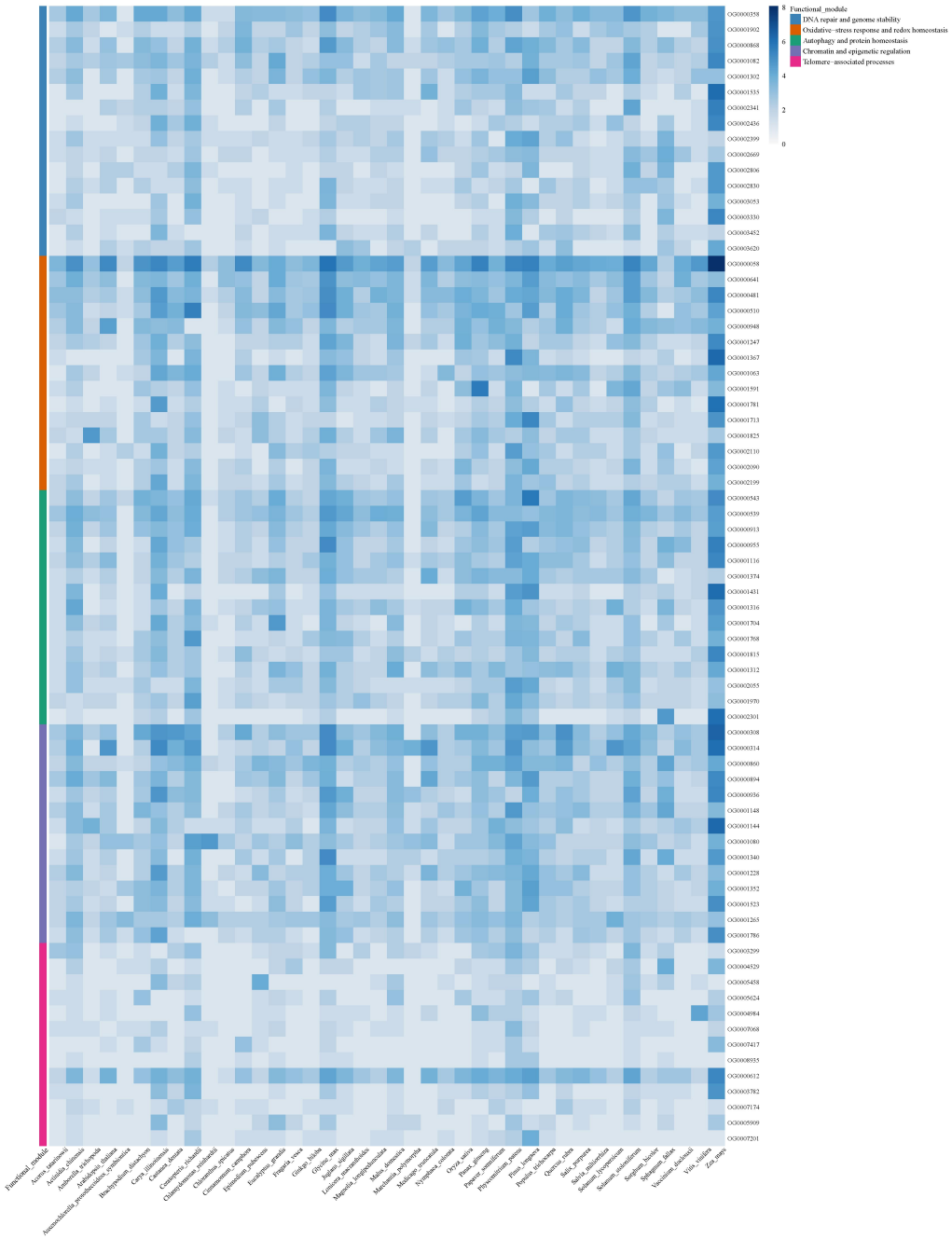

Figure S7. Copy-number conservation of representative core orthogroups across plant species. Representative orthogroups were selected from five longevity-relevant functional modules: DNA repair and genome stability, oxidative-stress response and redox homeostasis, autophagy and protein homeostasis, chromatin and epigenetic regulation, and telomere-associated processes. The colored annotation bar at the left identifies the functional module associated with each orthogroup. Orthogroups were selected according to the number of species with available annotations, annotation support, and representation within each functional module. Darker colors indicate higher copy numbers, whereas light colors indicate low or zero copy number. Because all displayed orthogroups are defined as core orthogroups, differences among species primarily reflect lineage-specific gene duplication, gene-loss patterns, and variation in gene-model annotation rather than absence from the core orthogroup set.