



Supplementary Material

Molecular Evolutionary and Expression Pattern Analysis of *AKR* Genes Shed New Light on *GalUR* Functional Characteristics in *Brassica rapa*

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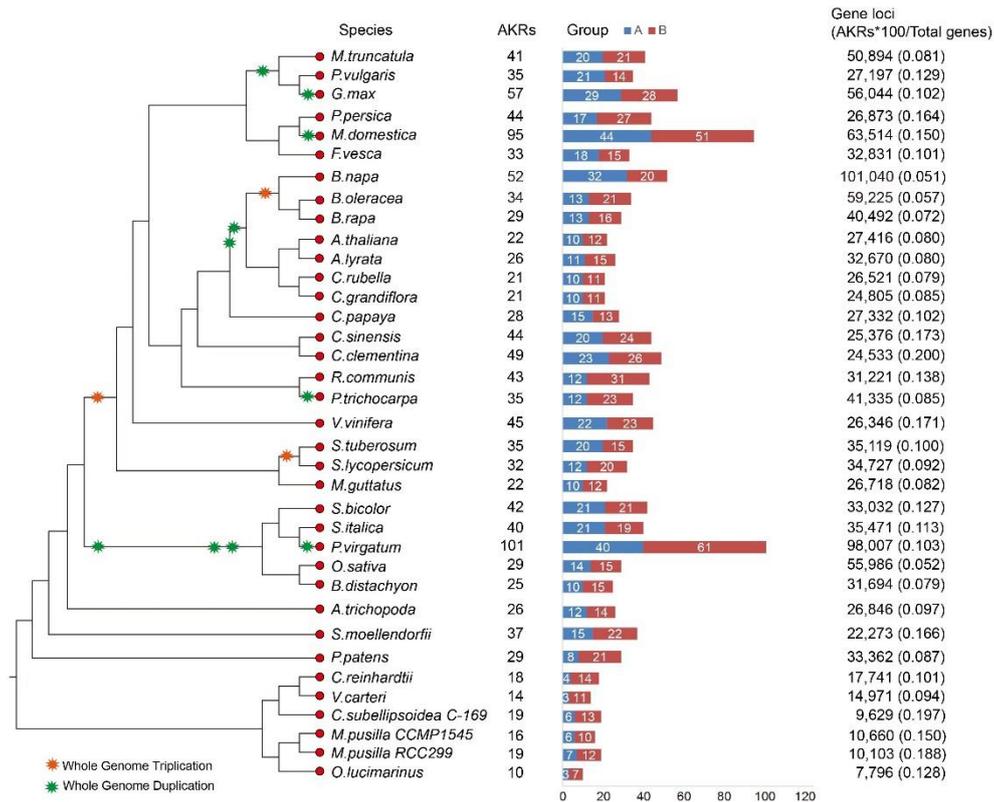


Figure S1. Distribution of number statistics of aldo-keto reductase (AKR) genes in plant species.

From left to right: (i) phylogenetic relationship of all selected species; (ii) the numbers of AKR genes in every species; (iii) the numbers of group A and B AKR genes; (iv) the percentage of AKR genes occupy all genes of every species.

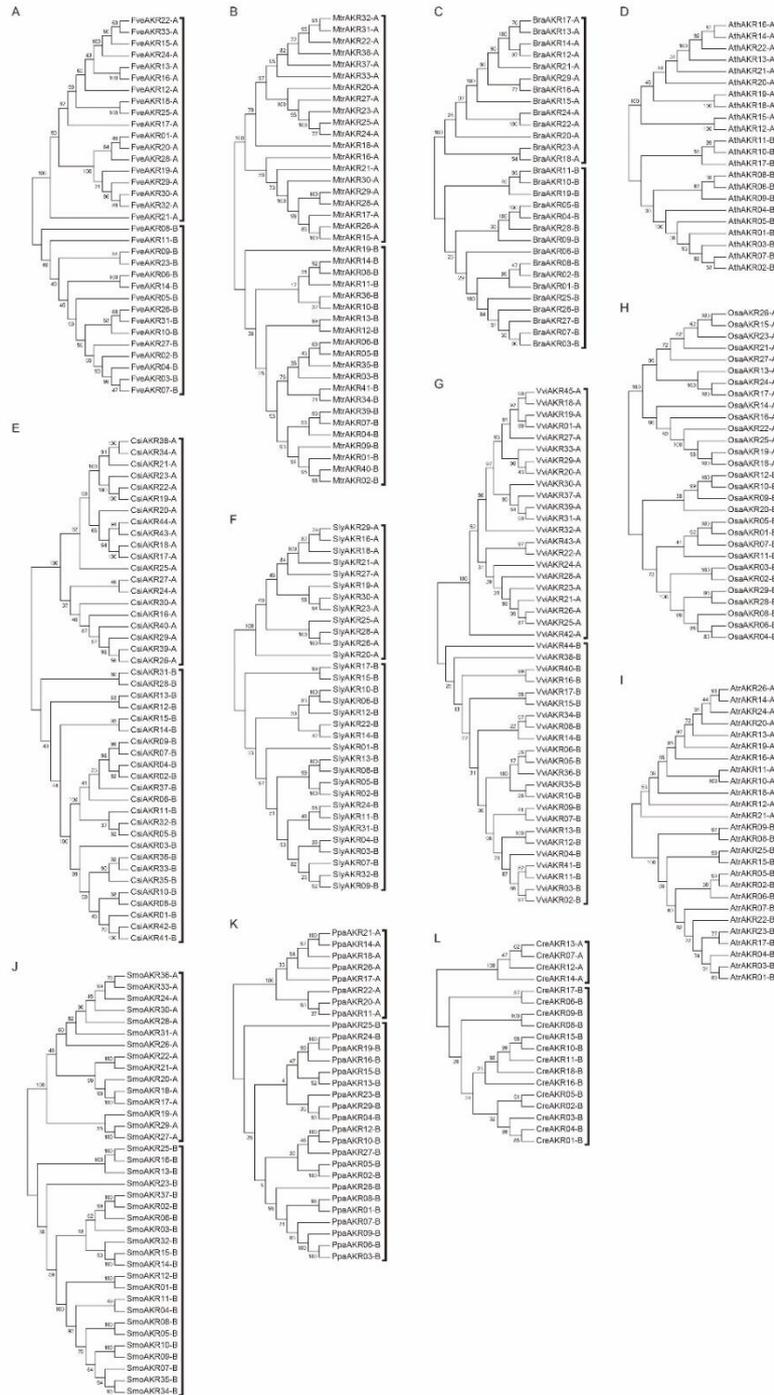


Figure S2. Phylogenetic trees of aldol-keto reductase (AKR) proteins of the selected plant species for PAML analysis

A: *Fragaria vesca*; B: *Medicago truncatula*; C: *Brassica rapa*; D: *Arabidopsis thaliana*; E: *Citrus sinensis*; F: *Solanum lycopersicum*; G: *Vitis vinifera*; H: *Oryza sativa*; I: *Amborella trichopoda*; J: *Selaginella moellendorffii*; K: *Physcomitrella patens*; L: *Chlamydomonas reinhardtii*.

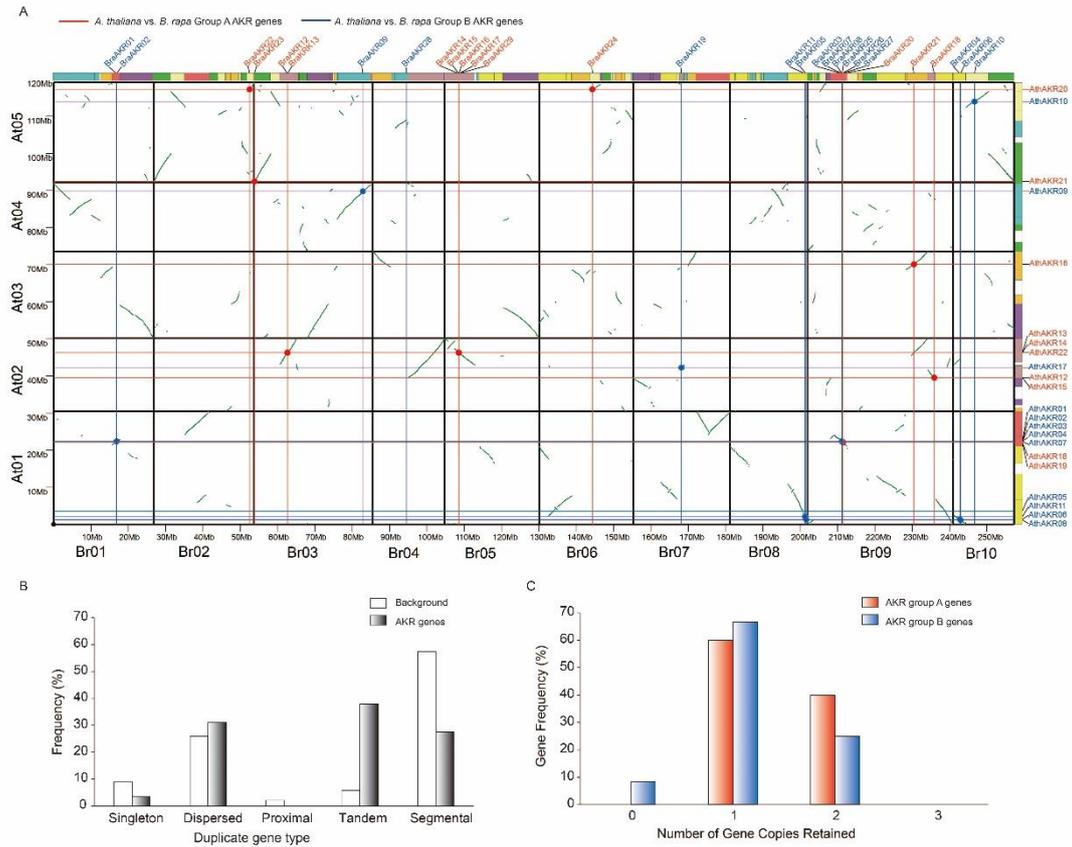


Figure S3. Aldo-keto reductase (AKR) homologous genes in segmental syntenic regions of the *Brassica rapa* and *Arabidopsis thaliana* genomes and their duplication types in *B. rapa*. (A) Conserved collinear blocks of genes (green irregular lines) are shown between the 10 *B. rapa* chromosomes (horizontal axis) and the five *A. thaliana* chromosomes (vertical axis). Red and green dots indicate group A and B AKR homologs in the two species. (B) The different duplicated types (singleton, dispersed, proximal, tandem and segmental) were counted in *B. rapa*. Open boxes indicate the whole genome level. (C) Copy numbers of group A and B AKRs after genome triplication and fractionation in *B. rapa*.

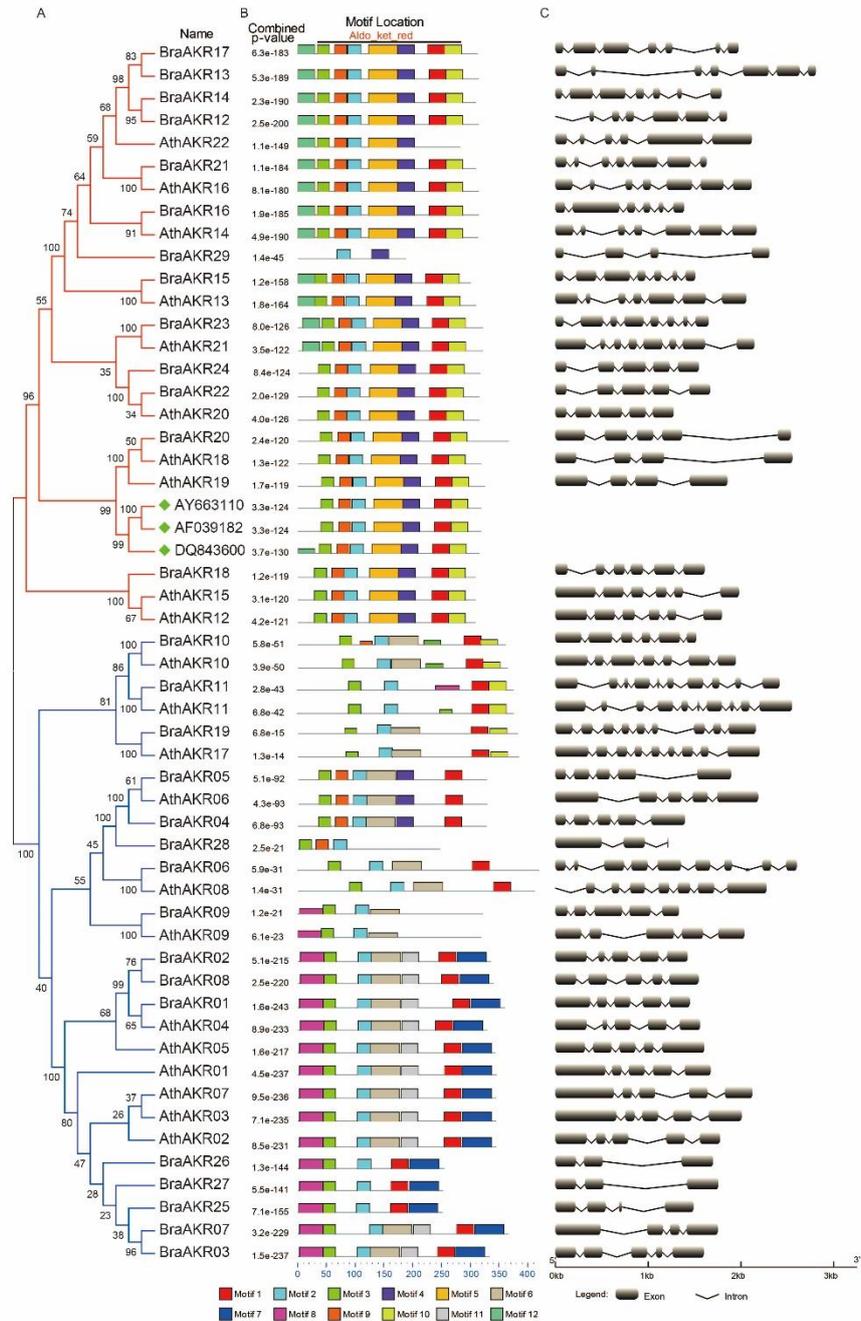


Figure S4 An analytical view of the aldo-keto reductase (AKR) gene family in *Brassica rapa* and *Arabidopsis thaliana*.

(A) Protein maximum-likelihood (ML) tree: this tree was constructed using the ML method, and bootstrap values were calculated with 1000 replications. Group A AKRs are colored red and group B AKRs are colored blue. (B) Protein structure: the search for the common motifs shared among the AKRs proteins of each group was performed using MEME; the clade situation was in the bottom. (C) Gene structure: the exons are highlighted by black boxes; introns are shown as broken lines.

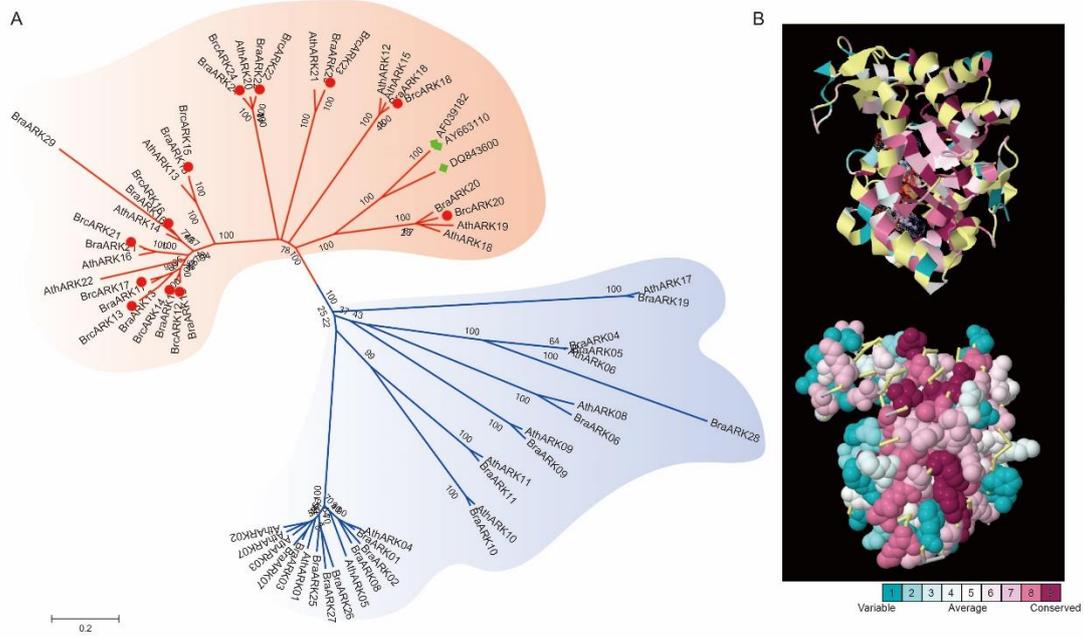


Figure S5. Phylogenetic tree of cloned aldo-keto reductase (AKR) genes and conserved evolution of AKR-3D.

(A) Phylogenetic tree among cloned AKR genes and *A. thaliana* and *B. rapa* AKR genes. Red represents the cloned genes and green represents GalUR genes. (B) Crystal structure of the putative AKR protein based on PDB:3H7U model. Residues are colored according to their levels of conservation. The score is 1 to 9 as blue to purple, which represents viable to conserve.

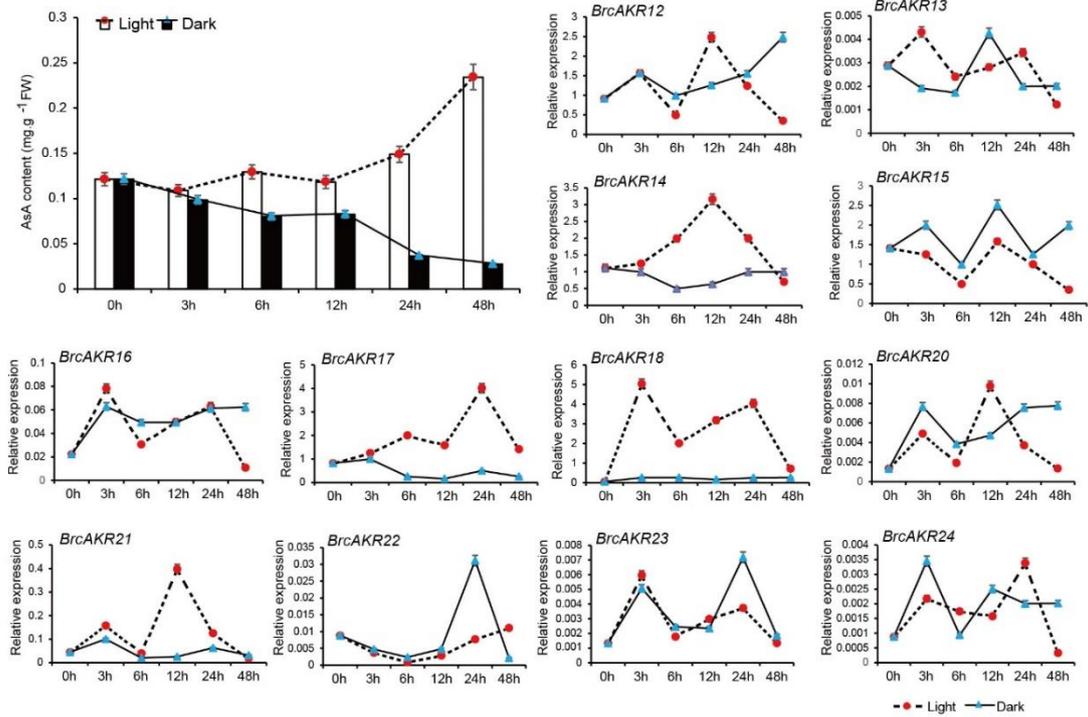


Figure S6. Effect of light on the ascorbic acid (AsA) level and the expression patterns of aldo-keto reductase (AKR) genes in Pak-Choi leaves.

Bar chart indicate AsA levels. line charts: Transcript levels of AKR genes. For each sample, transcript levels were normalized with those of actin (control). Data are the mean values \pm SD of three individual experiments (n = 3).

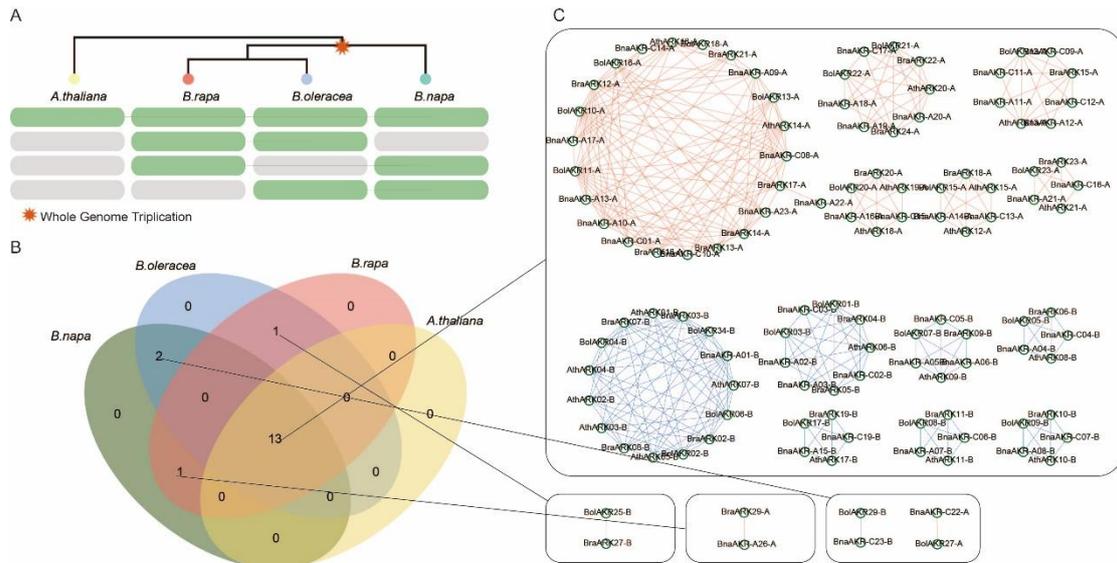


Figure S7. Relationship of aldo-keto reductase (AKR) homologous genes among *Arabidopsis thaliana*, *Brassica rapa*, *Brassica oleracea* and *Brassica napus*.

All of 17 cluster among AKR homologous genes were deduce by OrthoMCL program. (A) The distribution of AKR homologs clusters; (B) Venn diagram of AKR homologs relationship; (C) The interrelation network of AKR orthologs. The group A and B AKR orthologs gene pairs are highlighted by red and blue, respectively.