

Figure S1 Root morphology of two *Brassica napus* genotypes (D4-15, D2-1) in response to N availability in the hydroponic environments. Fifteen-day-old plants were transferred to a nutrient solution lacking N. After a further 15 days, N was re-supplied to the solution. The number of root tips (A), root surface area (B), root volume (C) and average root diameter (D) were measured after 0, 1, 3, 5, 7, 9 and 15 days of N starvation and 1, 3 and 5 days after N resupply (R timepoints). Bars indicate means \pm SE (n = 3). The effects of genotype, days and the interaction between genotype and days were analyzed using two-way ANOVA with the Tukey HSD post hoc test (# P < 0.05; NS, not significant). Statistical comparisons among different time points were made using one-way ANOVA with the Tukey HSD post hoc test (* P < 0.05).

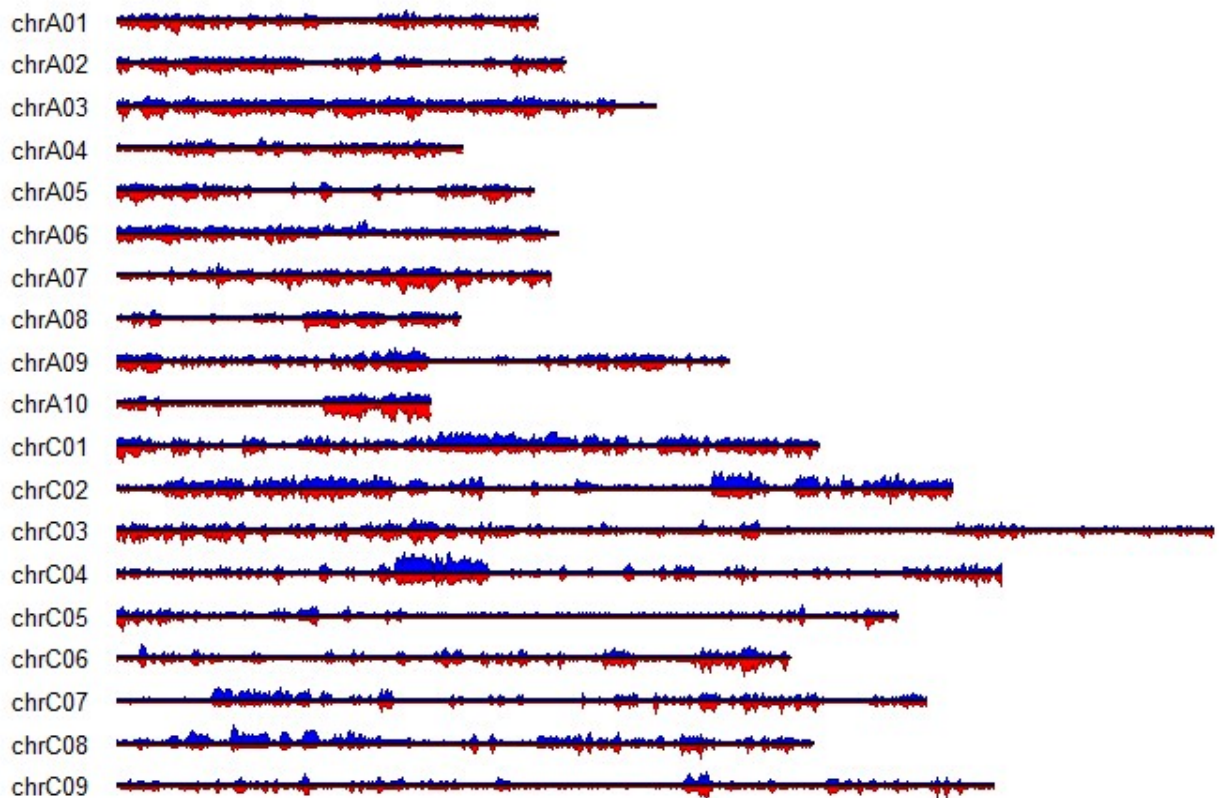
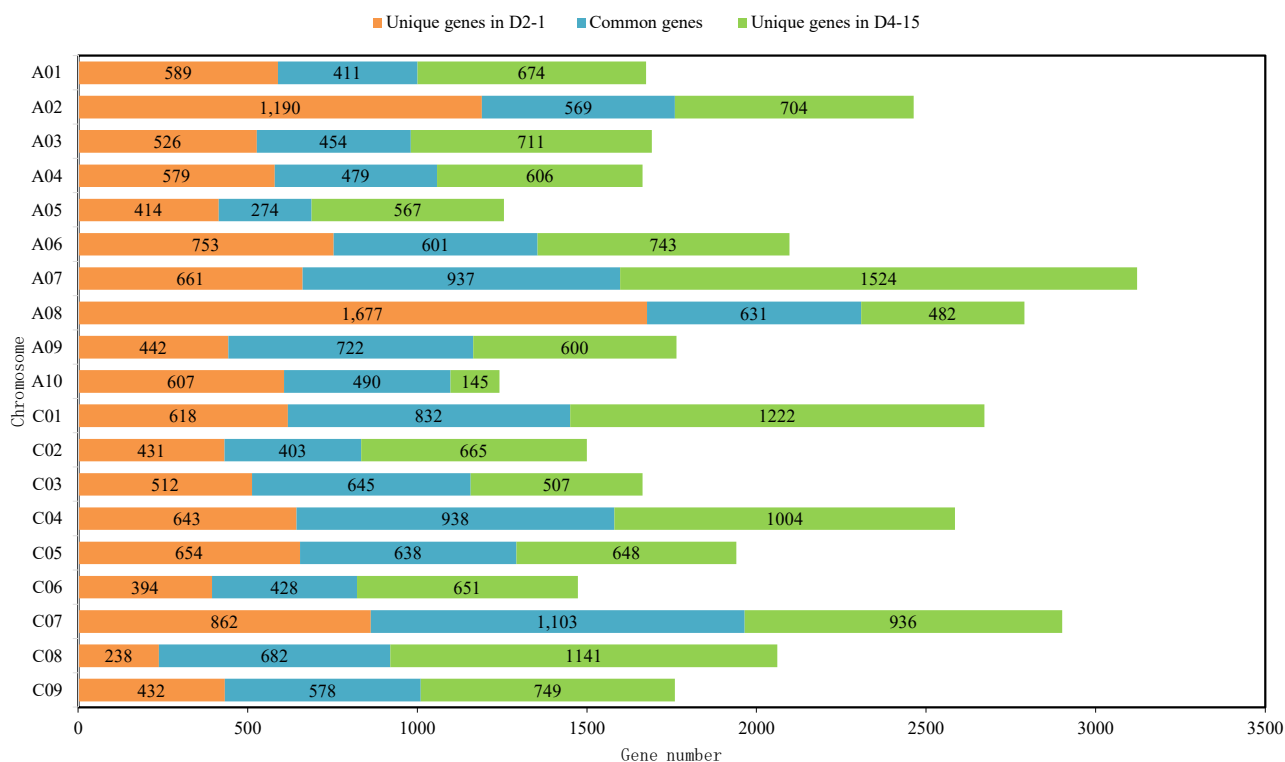
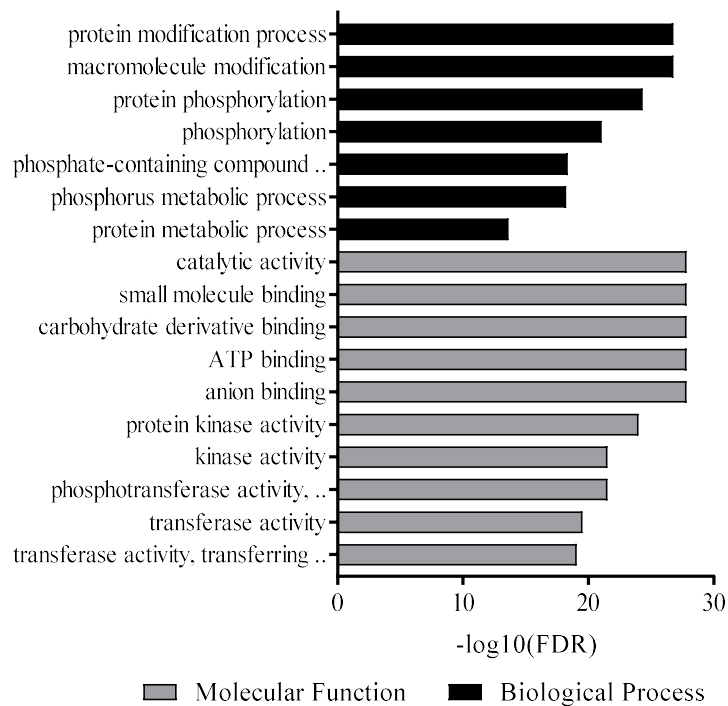
A**B**

Figure S2 Overview of the polymorphic genes in the whole genome of D4-15 and D2-1 compared to that of *Damor-bzh*. Venn diagram showed the number of polymorphic genes identified between D4-15 and *Damor-bzh* (red), and between D2-1 and *Damor-bzh* (blue). Chromosomal distributions (B) of the polymorphic genes were displayed. The density of polymorphic genes per 100 kb between D2-1 and *Damor-bzh* was showed in blue color, and the density of polymorphic genes per 100 kb between D4-15 and *Damor-bzh* was showed in red color.

A



B



C

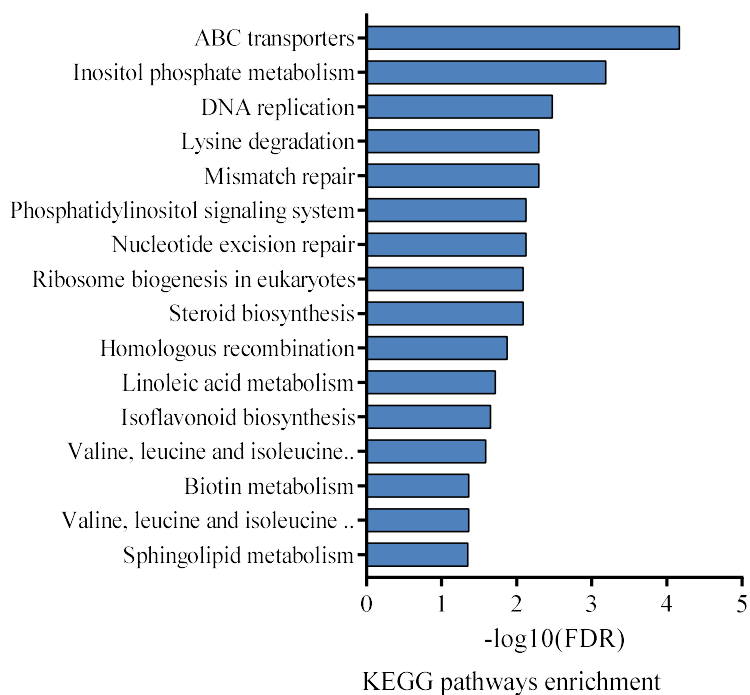


Figure S3 Chromosomal distribution and annotation of the polymorphic genes in the whole genome of D4-15 and D2-1. A, chromosomal distribution of the unique and common polymorphic genes. B, the gene ontology (GO) and KEGG pathway analysis of the genes with sequence variation in the genomic level between D4-15 and D2-1.

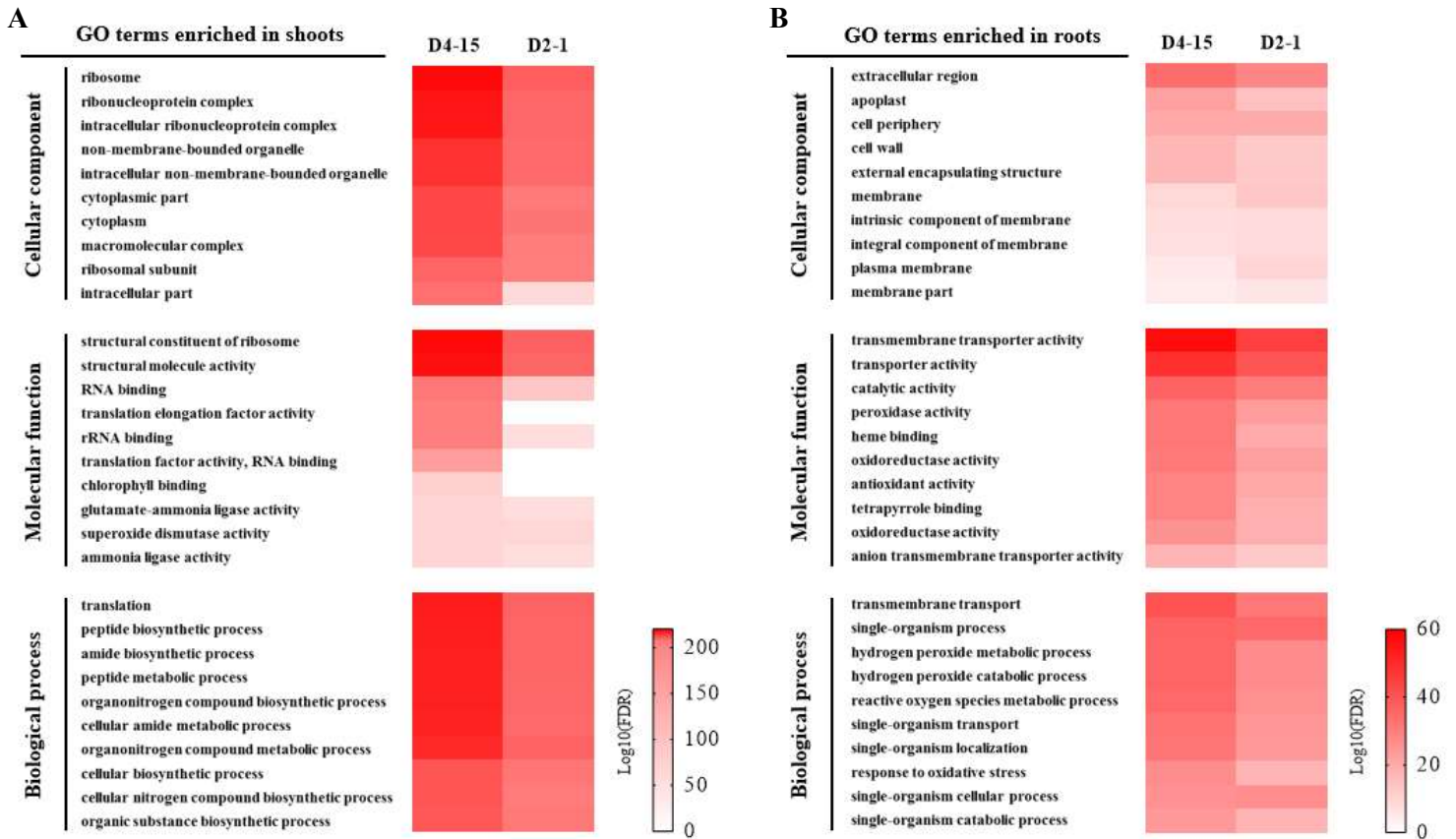


Figure S4 Comparative gene ontology (GO) enrichment analysis of differentially expressed genes (DEGs) in D4-15 and D2-1. Cellular component, molecular function and biological process of the DEGs in shoots (A) and roots (B) of D4-15 and D2-1 were displayed based on the pairwise comparisons of D2-1_{-N}/D2-1_{+N}, D4-15_{-N}/D4-15_{+N}, respectively. Colored panels indicated the *P* values of each GO term.

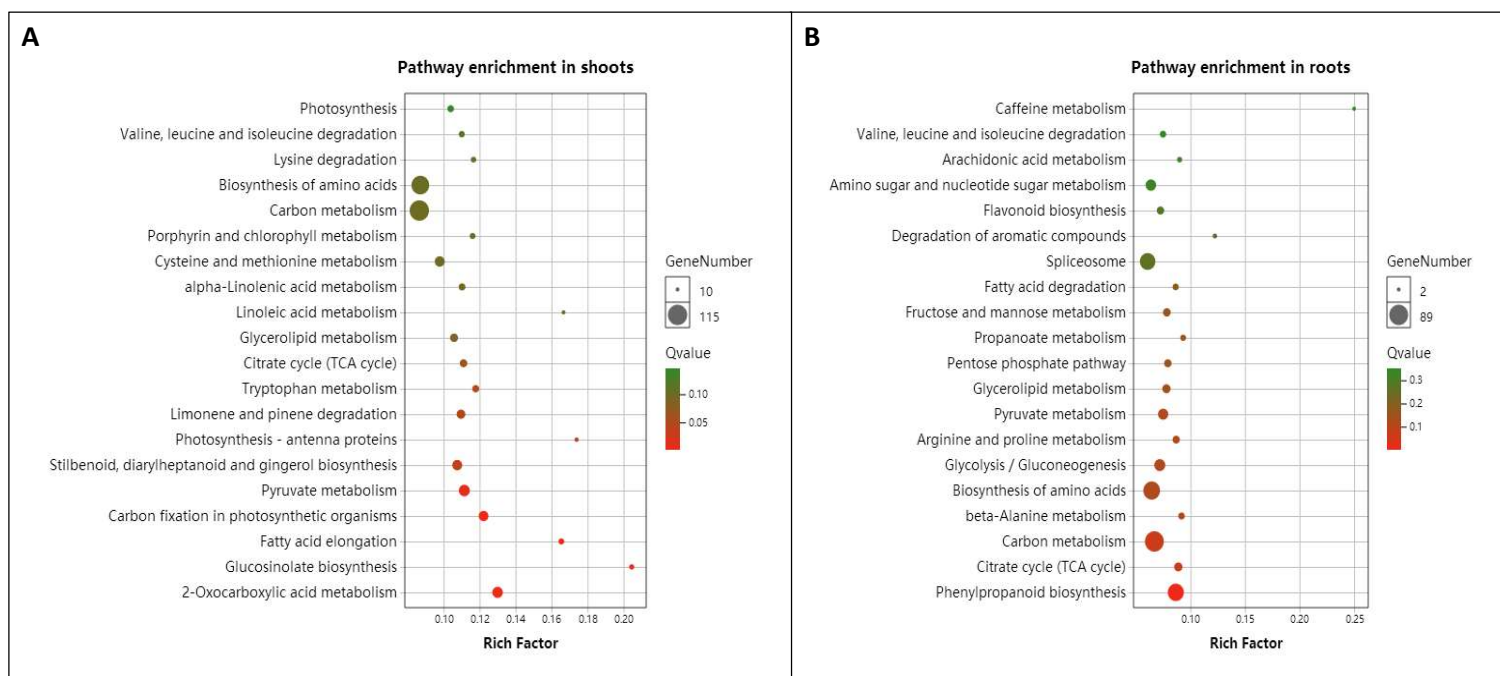
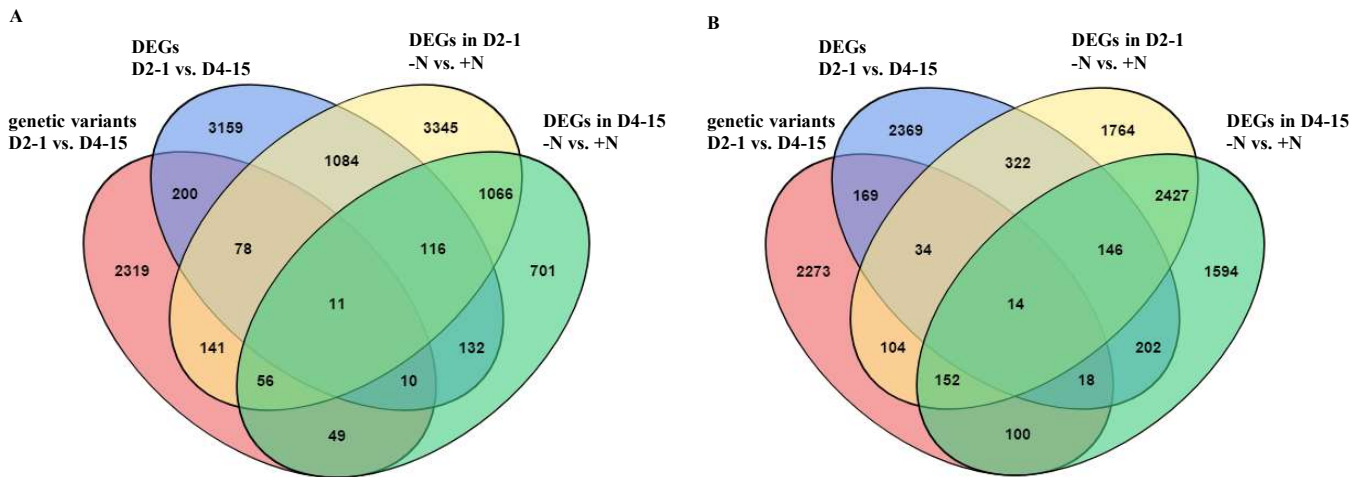


Figure S5 KEGG pathway analysis of differentially expressed genes (DEGs) in D4-15 and D2-1. The top 20 enriched pathways of DEGs in D4-15 in comparison with D2-1 in shoots (A) and roots (B) under N starvation conditions were shown. The X-axis indicated the enrichment factor. The dot color and size indicated the Q value and gene number as shown on the right.



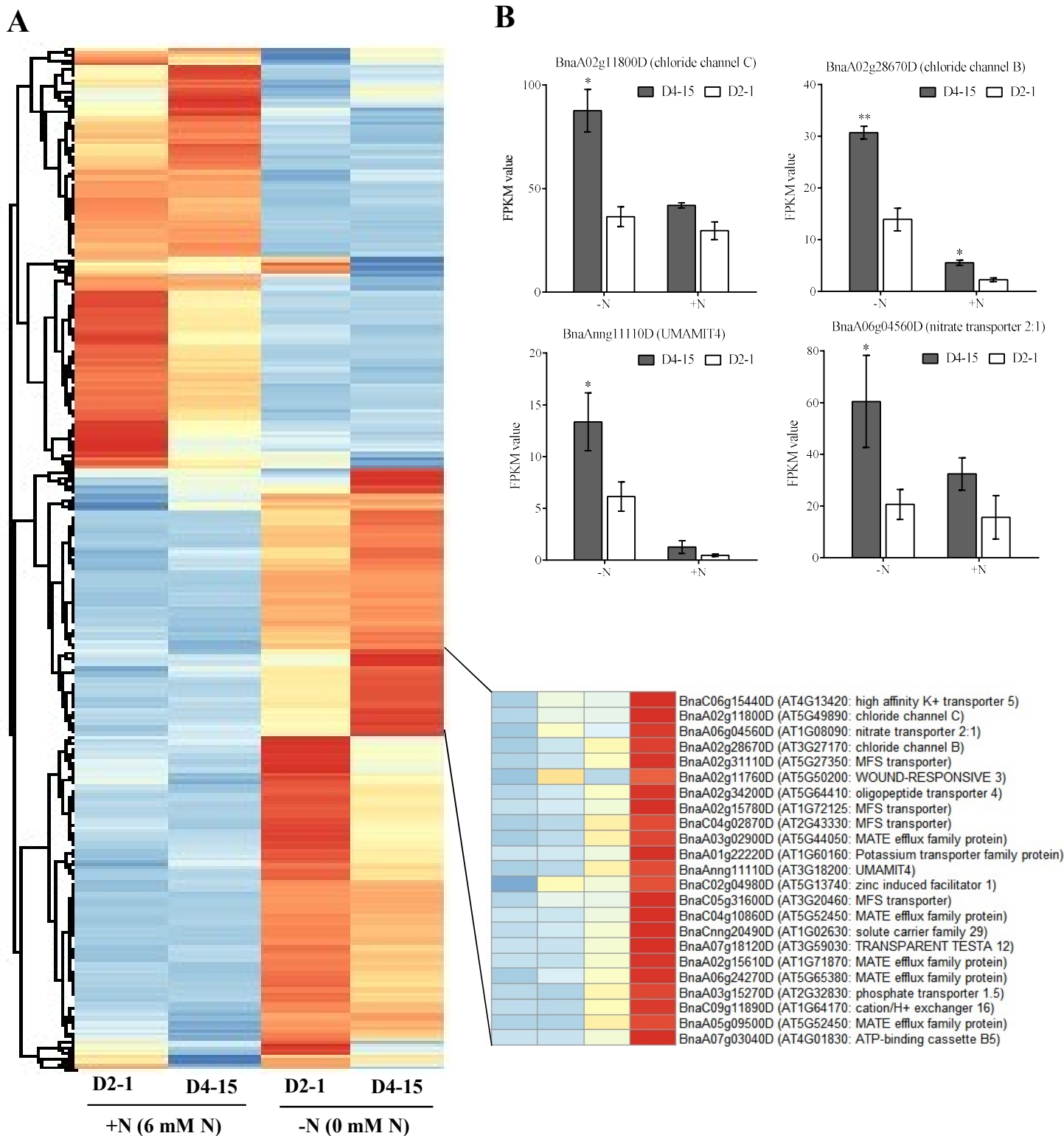


Figure S7 Transporter genes identified using RNA-seq in roots of D4-15 and D2-1 under +N (6 mM N) and -N (0 mM N) treatments. (A) Heat maps of all the transporter genes. (B) FPKM values of the four selected genes.