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Fig.S1 The dry weight, chlorophyll content, number of lateral roots and root to shoot ratio in two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

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Fig.S2 The soluble sugar and free amino acids content in foliar and roots of two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

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Fig.S3 The nitrogen assimilation enzyme activities (NR,GS and GOGAT) in foliar and roots of two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

Fig.S4 Length distribution of Fraxinus mandschurica unigenes

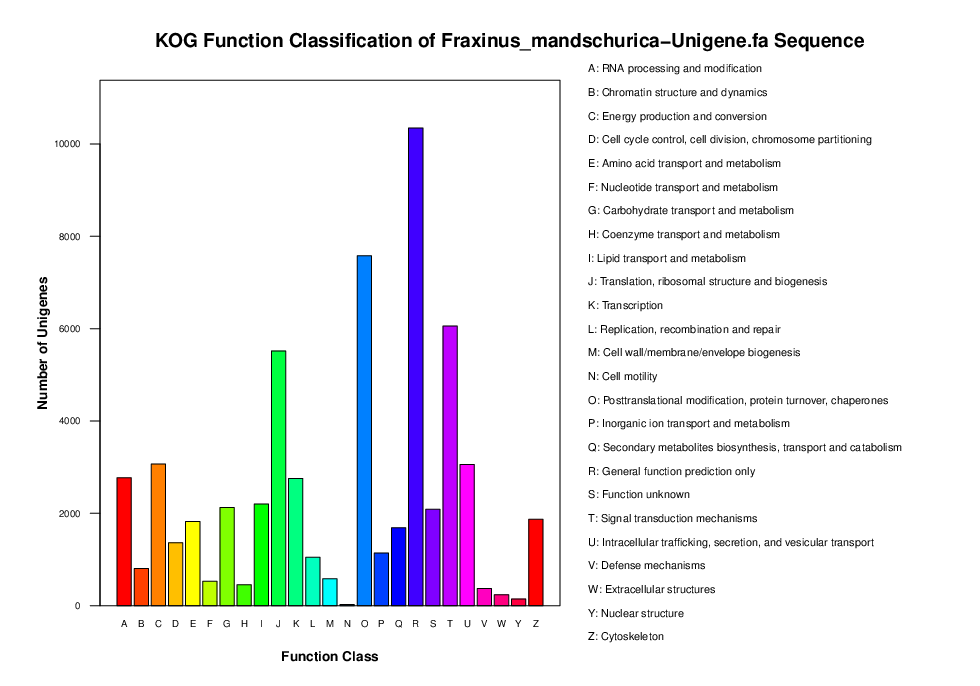


Fig.S5 Histogram of clusters orthologous groups (KOG) classification, a total of 35879 unigenes with lengths more than 300 bp were divided into 25 KOG categories.

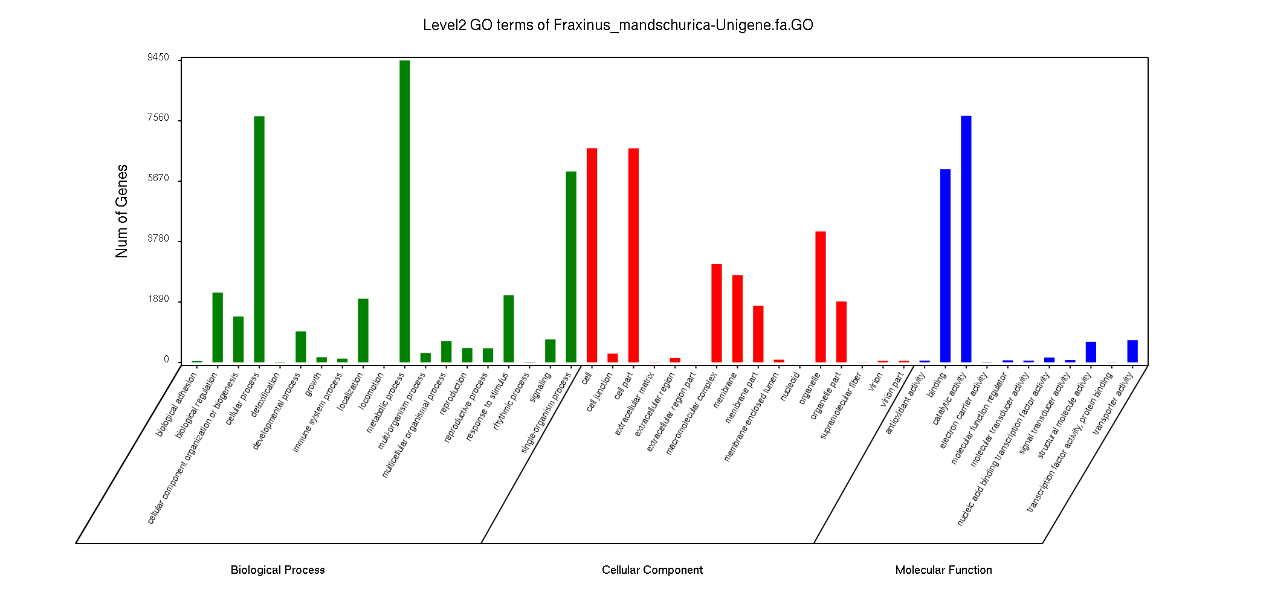


Fig.S6 Functional annotation of assembled sequences based on gene ontology (GO) categorization, 16,028 unigenes were grouped into the three main GO domains: “cellular component”, “molecular function”, and “biological process”.

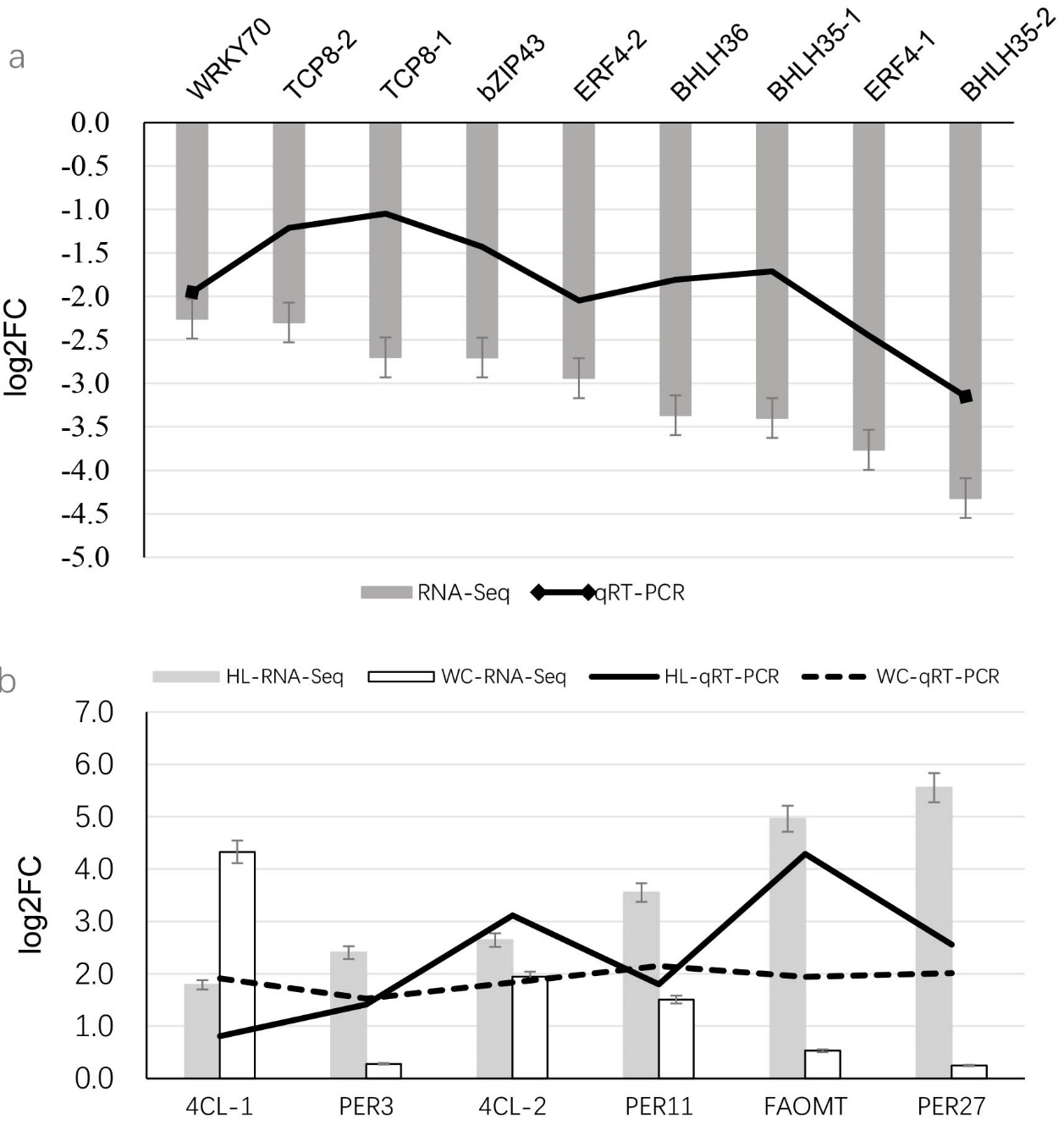


Fig.S7 The relative expression levels of (a) nine DEGs identified in the comparison CP1 and (b) six DEGs identified in the comparison CP4 and CP5 between RNA-Seq and qRT-PCR. The genes relative expression levels were determined by 2-ΔΔCT as expressed, and were normalized to the expression level of TU.

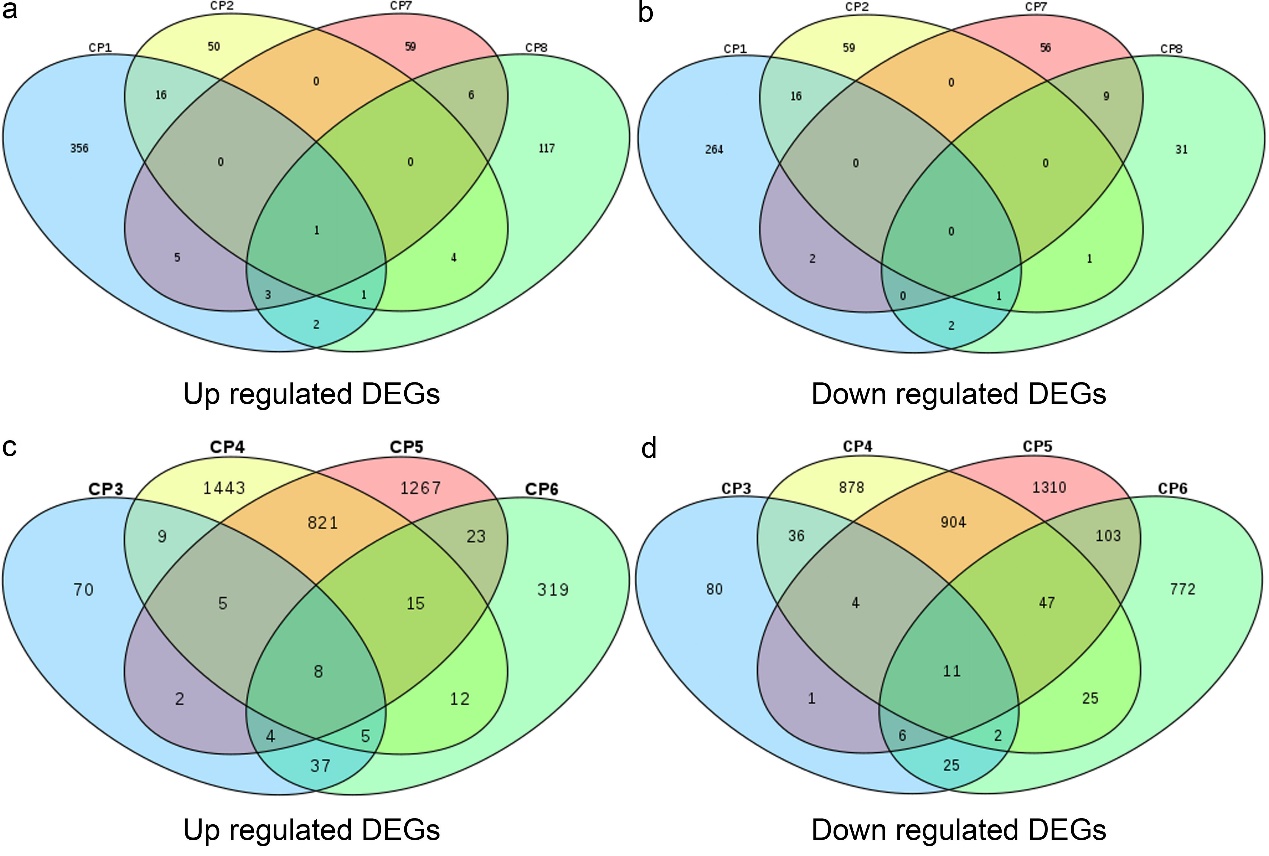


Fig.S8 A Venn diagram describing overlaps among differentially expressed genes (DEGs) in HL and WC. **a**. Up-regulated gene in folium and root; **b**. Down-regulated gene in folium and root; **c**. Up-regulated gene in folium and root under nitrogen deficiency; **d**. Down-regulated gene in folium and root under nitrogen deficiency.

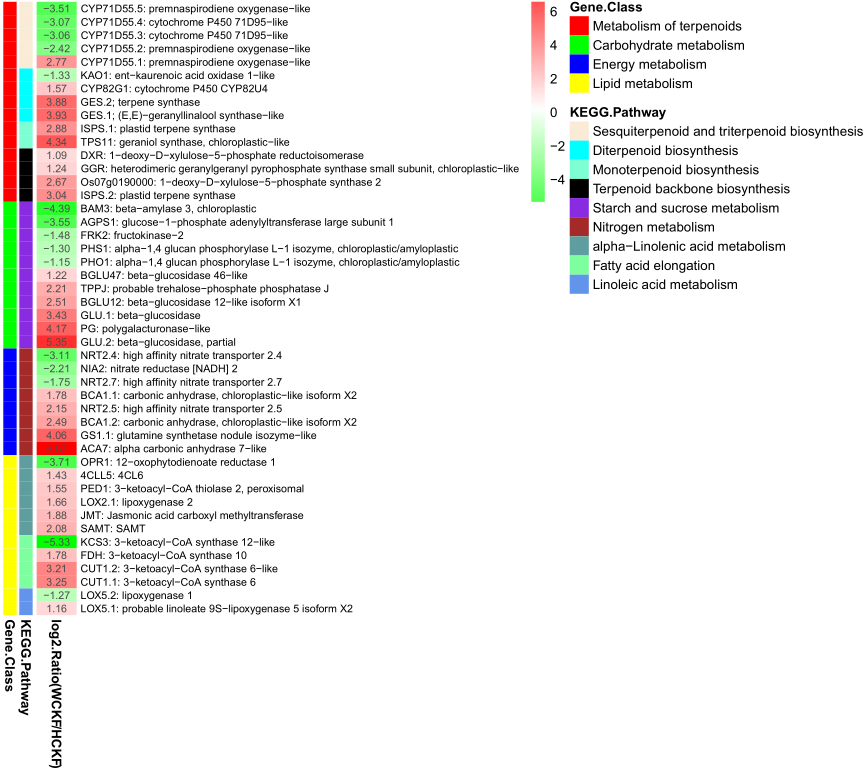


Fig.S9 Nine significantly enriched KEGG pathways for HL vs. WC in foliar under complete nitrogen

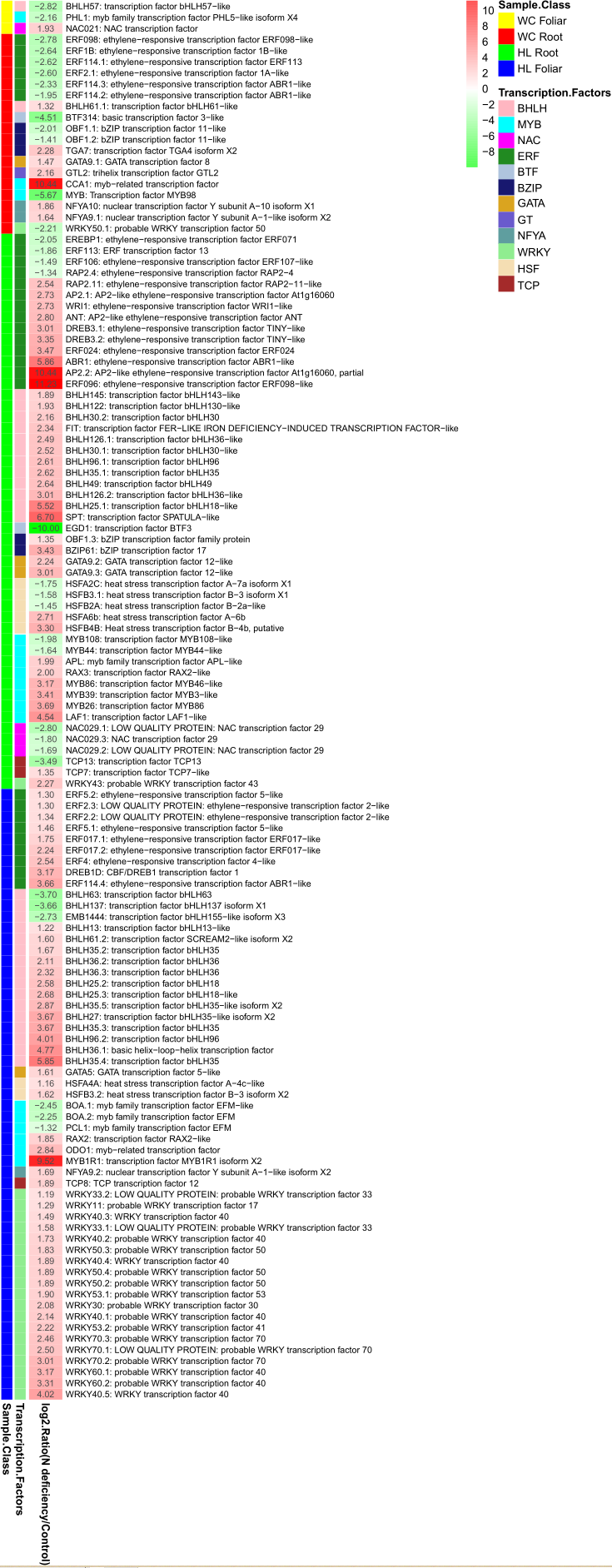


Fig.S10 The DEGs related to transcription factors unique to HL and WC in response to nitrogen deficiency.

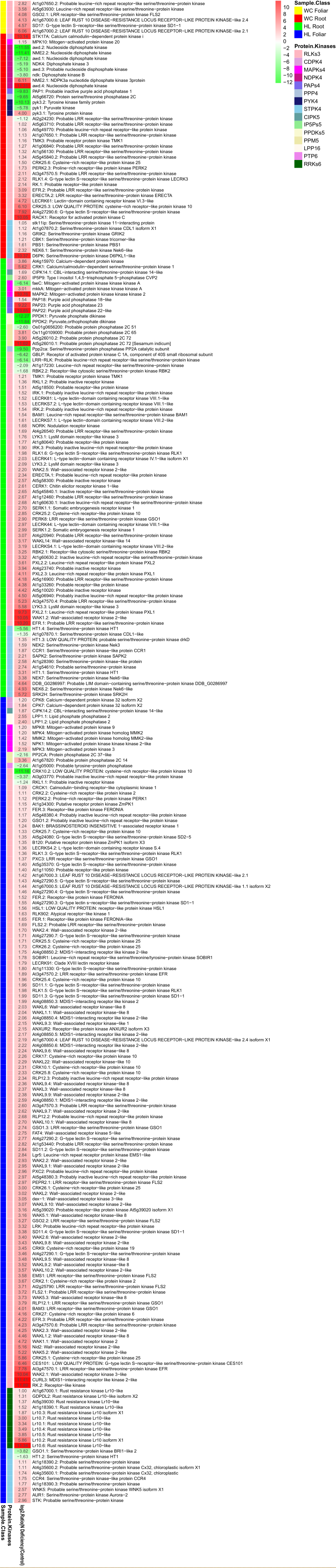


Fig.S11 The DEGs related to protein kinases unique to HL and WC in response to nitrogen deficiency.

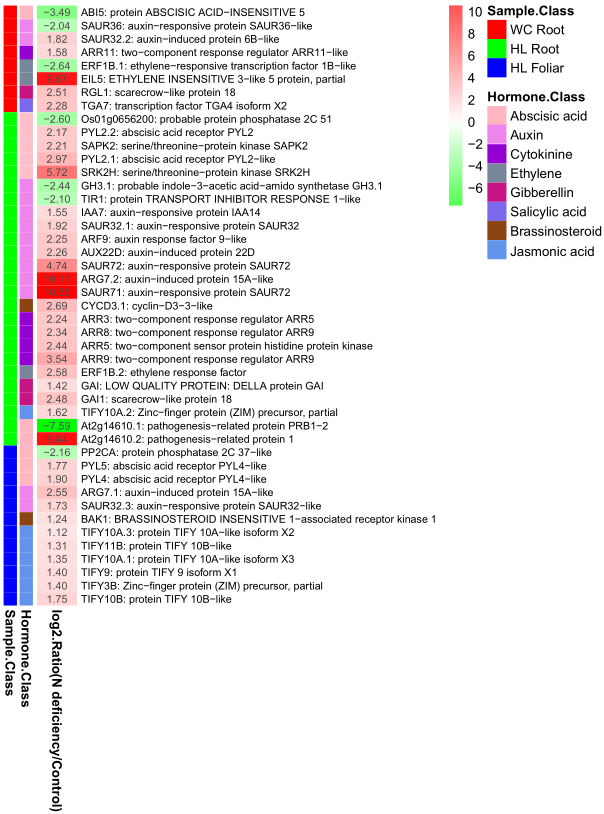


Fig.S12 The DEGs related to plant hormone signal transduction unique to HL and WC in response to nitrogen deficiency.

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Fig.S13 The lignin content in root of two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

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Fig.S14 The content of endogenous ABA and GA in foliar and root of two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

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Fig.S15 The content of endogenous IAA and ZR in foliar and root of two Fraxinus mandshurica provenances, WC and HL, under complete nitrogen and nitrogen deficiency. Each data point represents the average of three replicates, and nine seedlings were used for each treatment. Error bars represent mean ± SE. Different lowercase letters indicate significant differences at P<0.05.

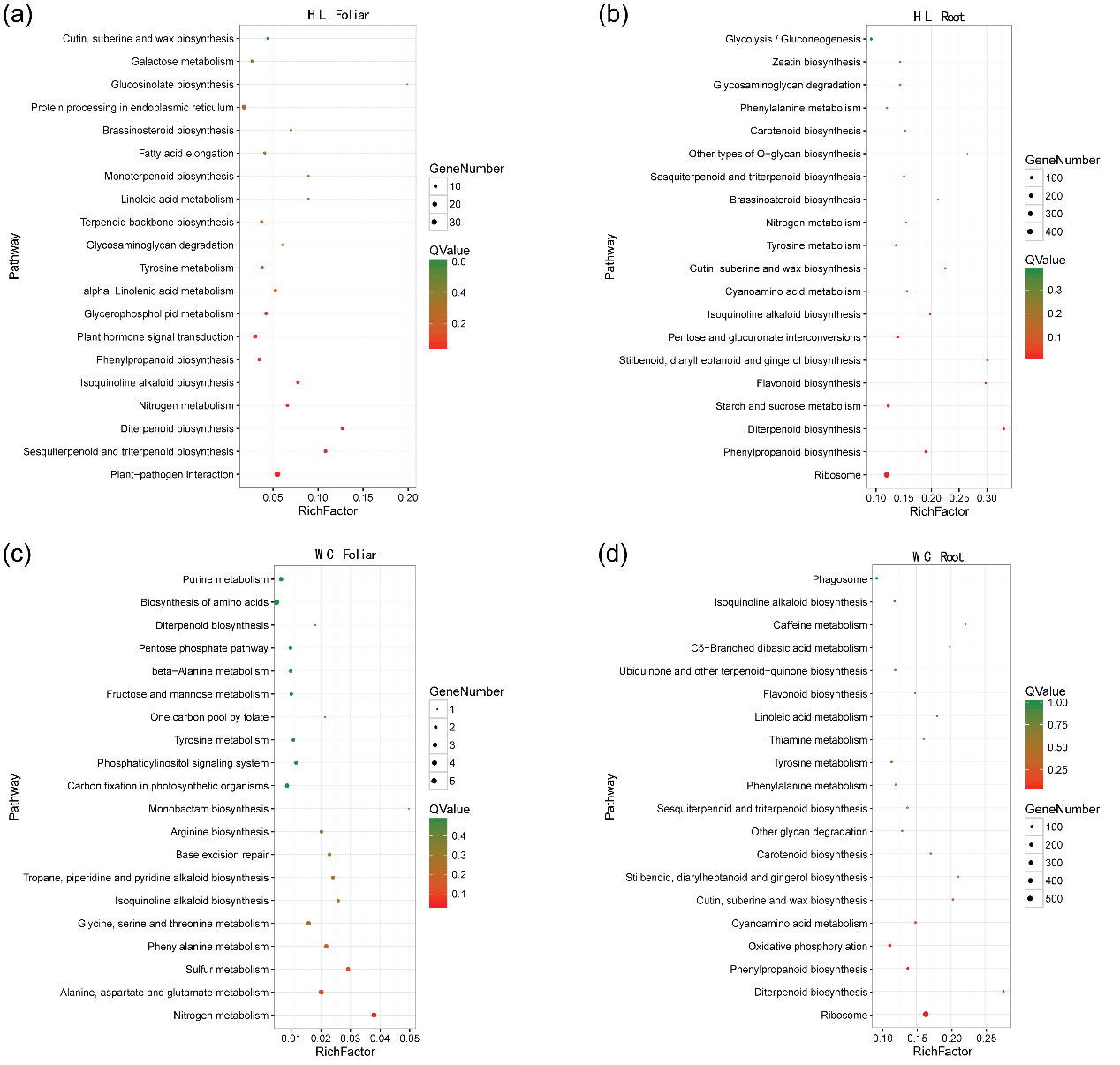


Fig.S16 Top20 of pathway enrichment between complete nitrogen and nitrogen deficiency in HL foliar (a), HL root (b), WC Foliar (c) and WC root (d).