Coordinated Lipid Mobilization During Seed Development and Germination in Peanut (*Arachis hypogaea* L.)

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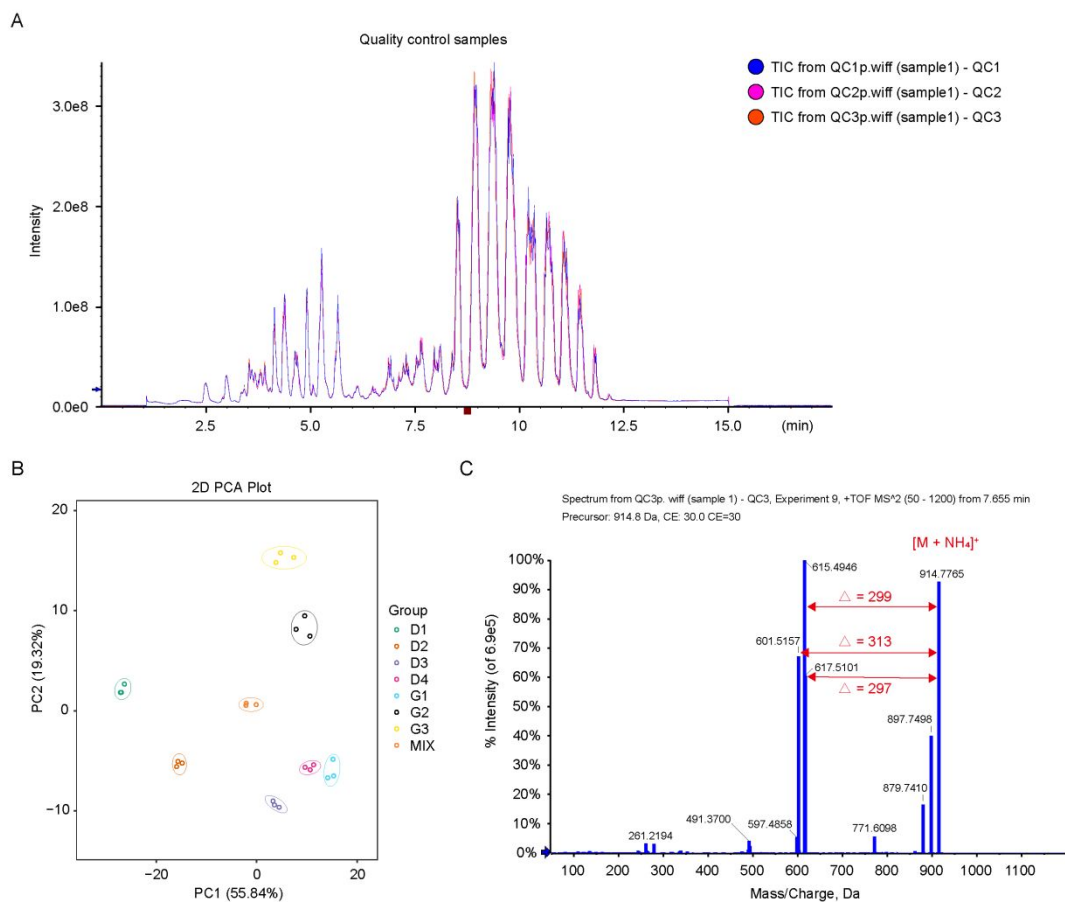
Supplementary

Fig. S1. Qualitative and quantitative analysis of lipidomic analysis of peanut large-seed. (A) Multi peak diagram of lipid quality control detection. (B) Seed sample principal component pca plot. Coordinates principal component, and percentage indicates the value of the principal component's contribution to sample variance. (C) LC-MS/MS PI scanning mass spectrum with a target ion m/z 914.8 [$C_{57}H_{100}O_7$+NH_4] for hydroxylated-TAG (18:1_C18:2_C18:2-OH).
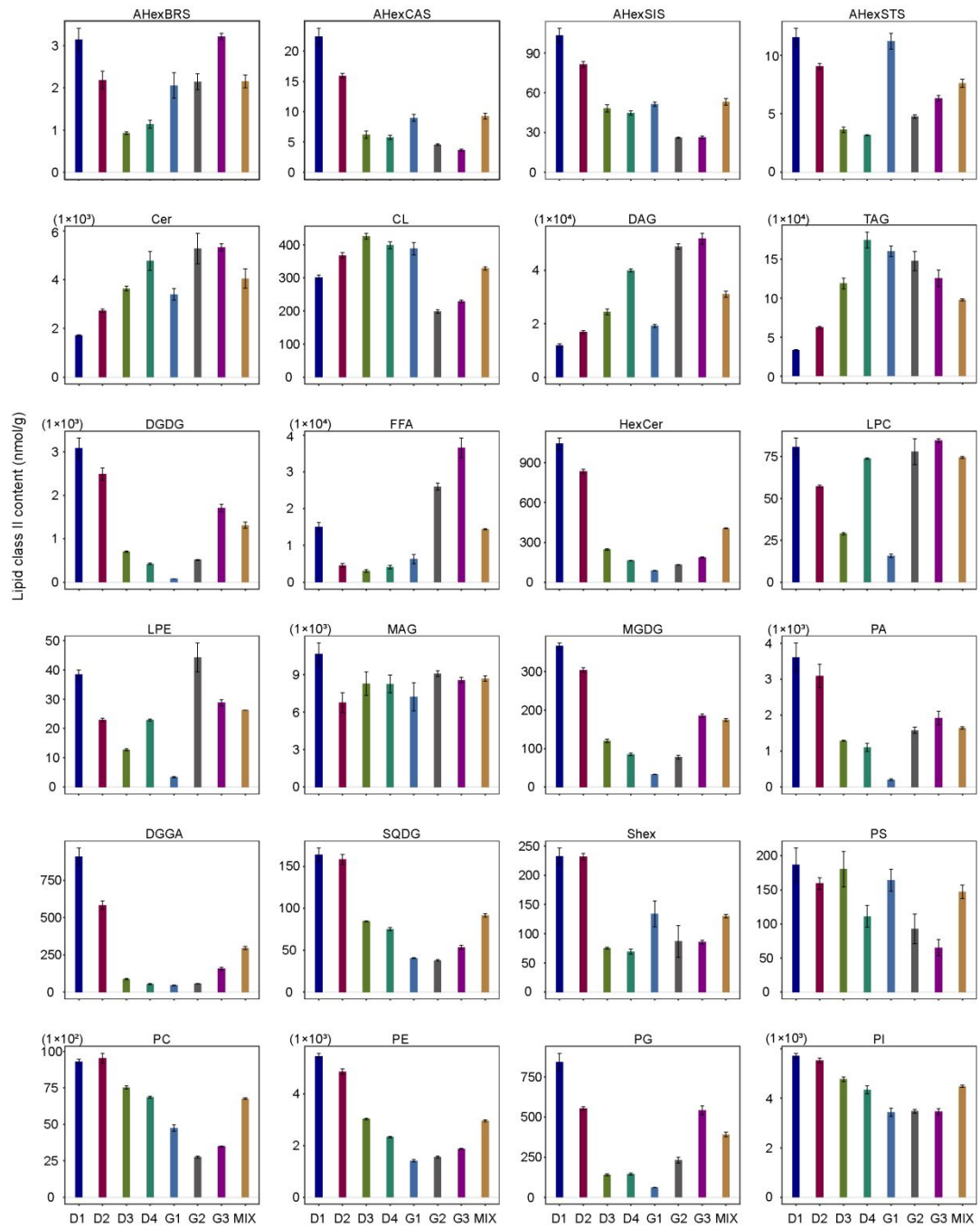
Fig. S2. Content analysis of 24 sub-classes lipids in different stages.
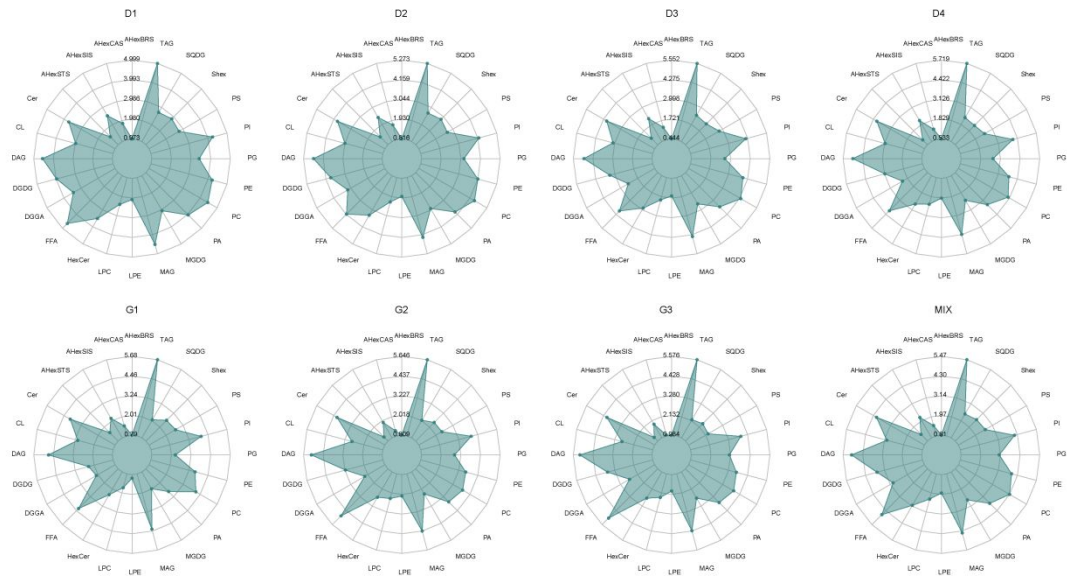
Fig. S3. Content analysis of 24 sub-classes lipids in same stage.
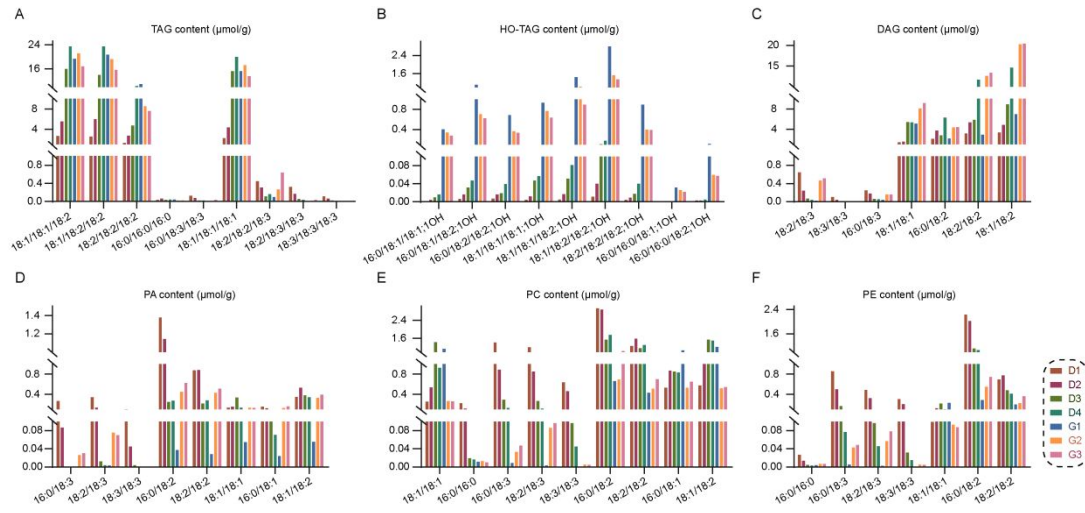
Fig. S4. Lipid content in TAG, HO-TAG, DGA, PA, PC and PE with 16:0, 18:1, 18:2, and 18:3.

Fig. S5. Analysis of main characteristics of DALs. (A) The classification and percentage of DALs. (B) The proportion of DALs in GL. (C) The proportion of DALs in GP. (D) The content and change trend of the top three lipids in GL and GP in each period. (E) The number and change trend of the top three lipids in GL and GP in each period.

Pearson correlation between samples

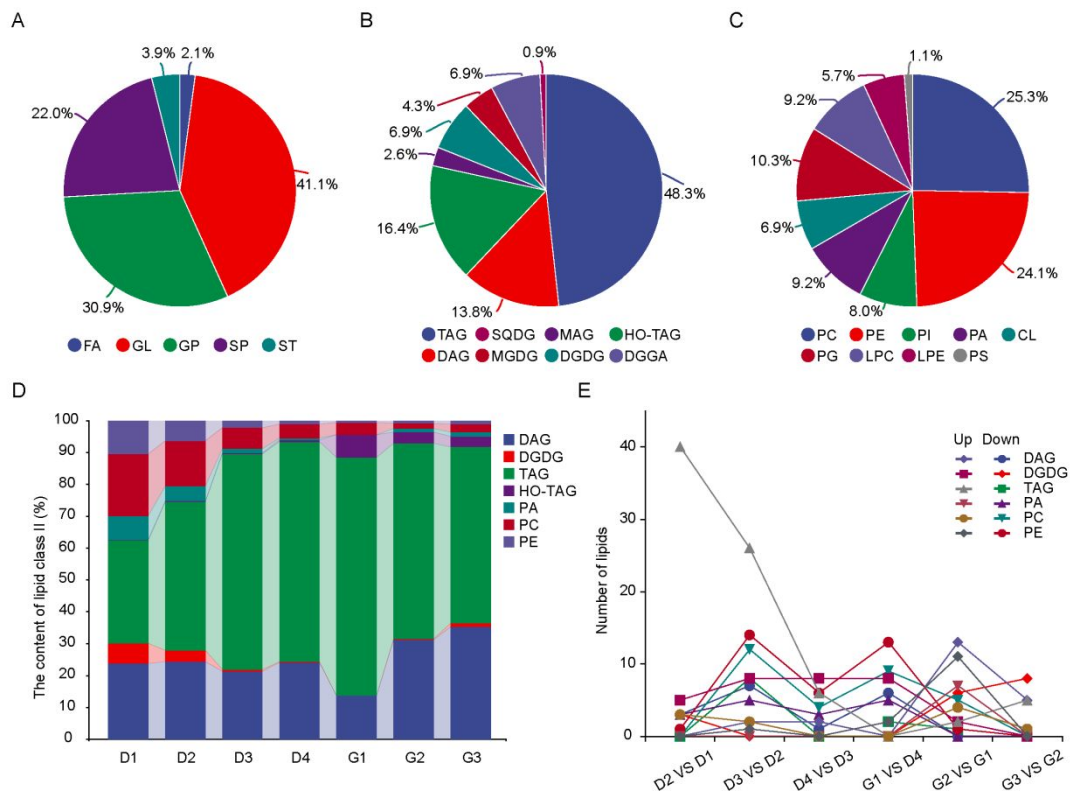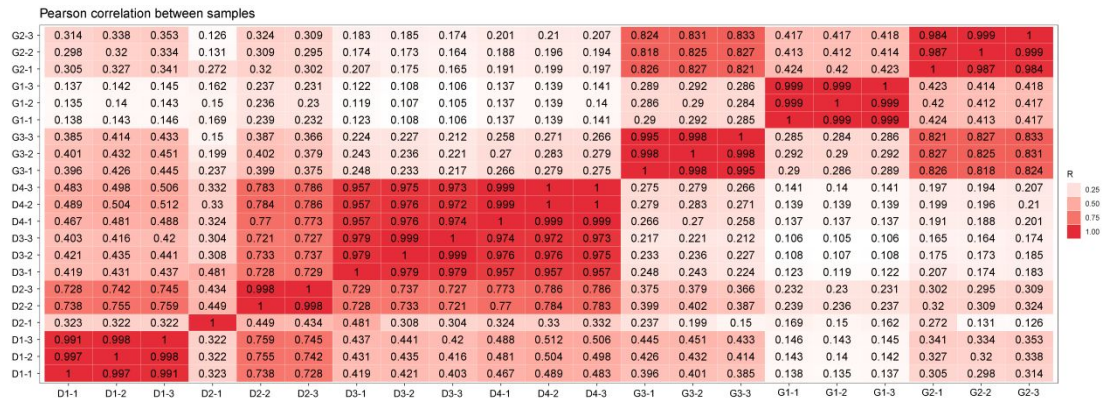|	D1-1	D1-2	D1-3	D2-1	D2-2	D2-3	D3-1	D3-2	D3-3	D4-1	D4-2	D4-3	G3-1	G3-2	G3-3	G1-1	G1-2	G1-3	G2-1	G2-2	G2-3
G2-3	0.314	0.338	0.353	0.126	0.324	0.309	0.183	0.185	0.174	0.201	0.21	0.207	0.824	0.831	0.833	0.417	0.417	0.418	0.984	0.999	1
G2-2	0.298	0.32	0.334	0.131	0.309	0.295	0.174	0.173	0.164	0.188	0.196	0.194	0.818	0.825	0.827	0.413	0.412	0.414	0.987	1	0.999
G2-1	0.305	0.327	0.341	0.272	0.32	0.302	0.207	0.175	0.165	0.191	0.199	0.197	0.826	0.827	0.821	0.424	0.42	0.423	1	0.987	0.984
G1-3	0.137	0.142	0.145	0.162	0.237	0.231	0.122	0.108	0.106	0.137	0.139	0.141	0.289	0.292	0.286	0.999	0.999	1	0.423	0.414	0.418
G1-2	0.135	0.14	0.143	0.15	0.236	0.23	0.119	0.107	0.105	0.137	0.139	0.14	0.286	0.29	0.284	0.999	1	0.999	0.42	0.412	0.417
G1-1	0.138	0.143	0.146	0.169	0.239	0.232	0.123	0.108	0.106	0.137	0.139	0.141	0.29	0.292	0.285	1	0.999	0.999	0.424	0.413	0.417
G3-3	0.385	0.414	0.433	0.15	0.387	0.366	0.224	0.227	0.212	0.258	0.271	0.266	0.995	0.998	1	0.285	0.284	0.286	0.821	0.827	0.833
G3-2	0.401	0.432	0.451	0.199	0.402	0.379	0.243	0.236	0.221	0.27	0.283	0.279	0.998	1	0.998	0.292	0.29	0.292	0.827	0.825	0.831
G3-1	0.396	0.426	0.445	0.237	0.399	0.375	0.248	0.233	0.217	0.266	0.279	0.275	1	0.998	0.995	0.29	0.286	0.289	0.826	0.818	0.824
D4-3	0.483	0.498	0.506	0.332	0.783	0.786	0.957	0.975	0.973	0.999	1	1	0.275	0.279	0.266	0.141	0.14	0.141	0.197	0.194	0.207
D4-2	0.489	0.504	0.512	0.33	0.784	0.786	0.957	0.976	0.972	0.999	1	1	0.279	0.283	0.271	0.139	0.139	0.139	0.199	0.196	0.21
D4-1	0.467	0.481	0.488	0.324	0.77	0.773	0.957	0.976	0.974	1	0.999	0.999	0.266	0.27	0.258	0.137	0.137	0.137	0.191	0.188	0.201
D3-3	0.403	0.416	0.42	0.304	0.721	0.727	0.979	0.999	1	0.974	0.972	0.973	0.217	0.221	0.212	0.106	0.105	0.106	0.165	0.164	0.174
D3-2	0.421	0.435	0.441	0.308	0.733	0.737	0.979	1	0.999	0.976	0.976	0.975	0.233	0.236	0.227	0.108	0.107	0.108	0.175	0.173	0.185
D3-1	0.419	0.431	0.437	0.481	0.728	0.729	1	0.979	0.979	0.957	0.957	0.957	0.248	0.243	0.224	0.123	0.119	0.122	0.207	0.174	0.183
D2-3	0.728	0.742	0.745	0.434	0.998	1	0.729	0.737	0.727	0.773	0.786	0.786	0.375	0.379	0.366	0.232	0.23	0.231	0.302	0.295	0.309
D2-2	0.738	0.755	0.759	0.449	1	0.998	0.728	0.733	0.721	0.77	0.784	0.783	0.399	0.402	0.387	0.239	0.236	0.237	0.32	0.309	0.324
D2-1	0.323	0.322	0.322	1	0.449	0.434	0.481	0.308	0.304	0.324	0.33	0.332	0.237	0.199	0.15	0.169	0.15	0.162	0.272	0.131	0.126
D1-3	0.991	0.998	1	0.322	0.759	0.745	0.437	0.441	0.42	0.488	0.512	0.506	0.445	0.451	0.433	0.146	0.143	0.145	0.341	0.334	0.353
D1-2	0.997	1	0.998	0.322	0.755	0.742	0.431	0.435	0.416	0.481	0.504	0.498	0.426	0.432	0.414	0.143	0.14	0.142	0.327	0.32	0.338
D1-1	1	0.997	0.991	0.323	0.738	0.728	0.419	0.421	0.403	0.467	0.489	0.483	0.396	0.401	0.385	0.138	0.135	0.137	0.305	0.298	0.314

R
0.25
0.50
0.75
1.00

Fig. S6. Correlation analysis of transcriptome data. The darker the color, the higher the correlation, and the closer the number is to 1.
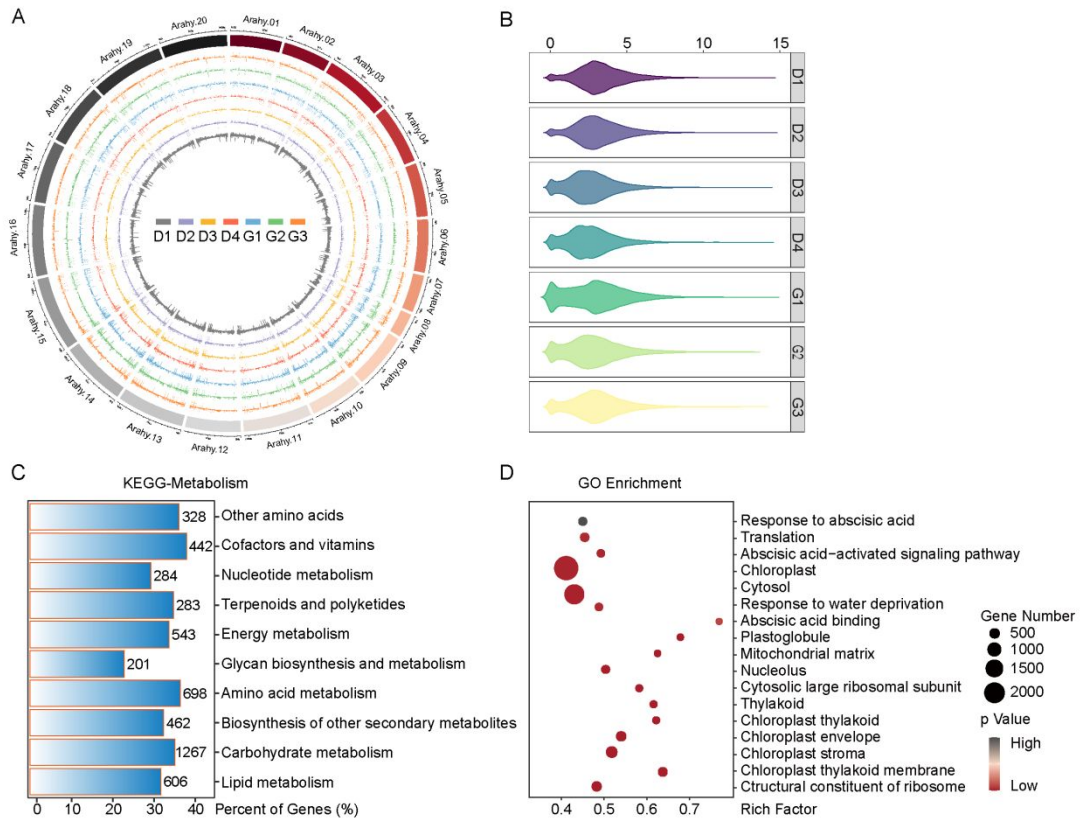
Fig. S7. The expression analysis of DEGs. (A) Circle Diagram of the expression of all DEGs. (B) The violin plot showing biological repeat. (C) The analysis of KEGG pathways of all DEGs. (D) The analysis of GO functional annotation of all DEGs.
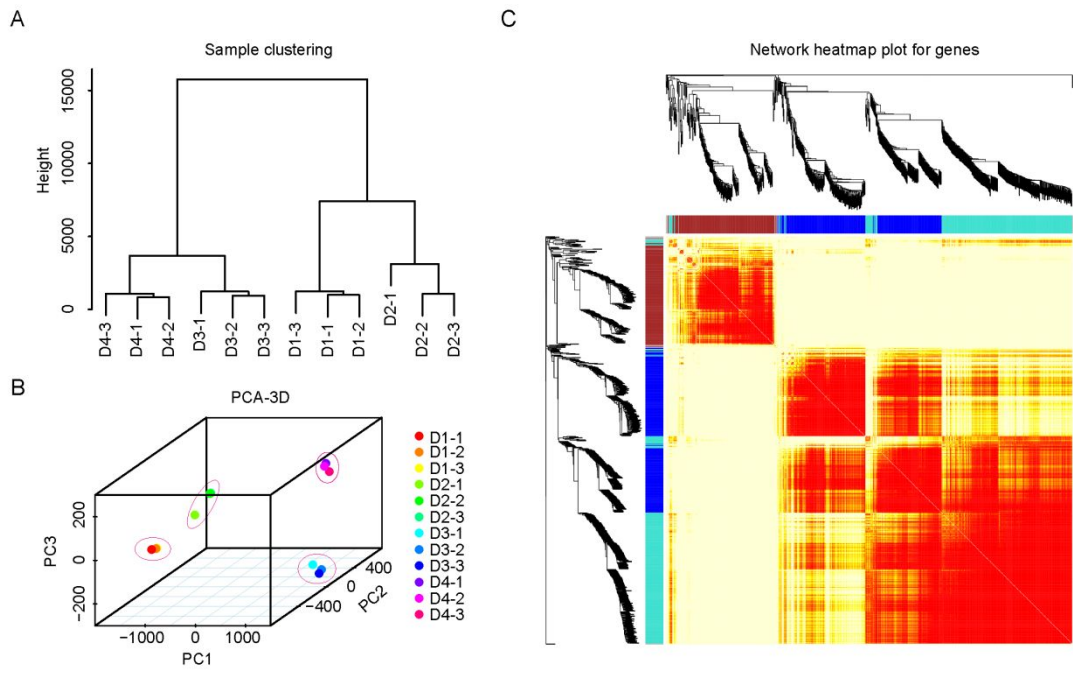
Fig. S8. The quality control analysis for WGCNA of DEGs and DALs in de-velopment. (A) Transcriptome data cluster diagram. (B) The PCA-3D for transcrip-tome data. (C) WGCNA module correlation analysis.
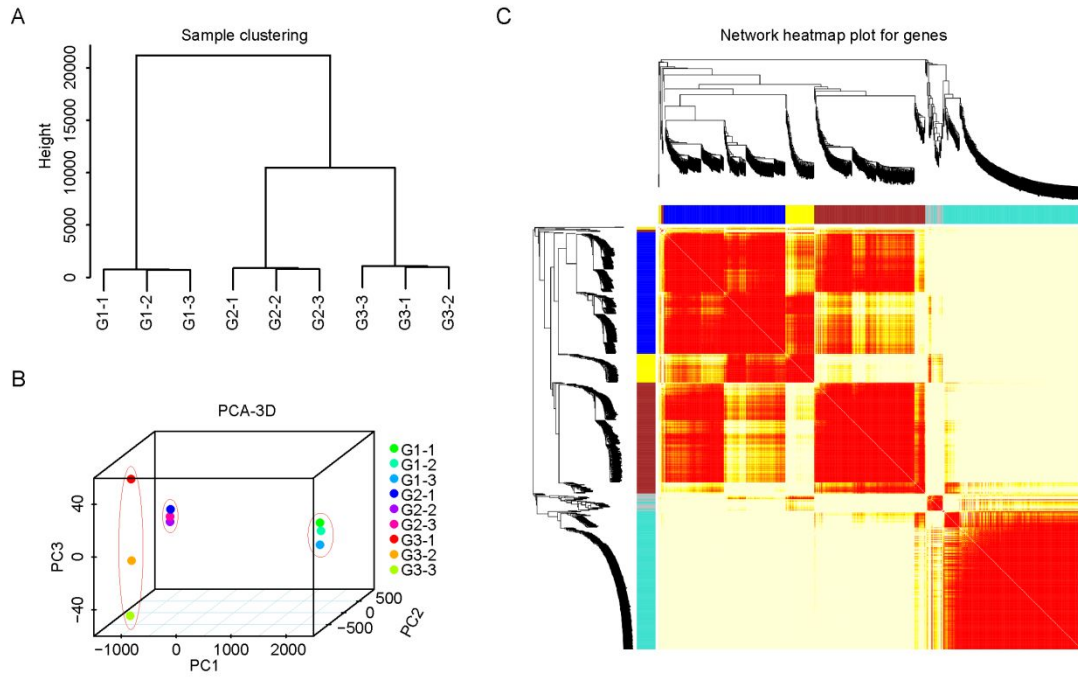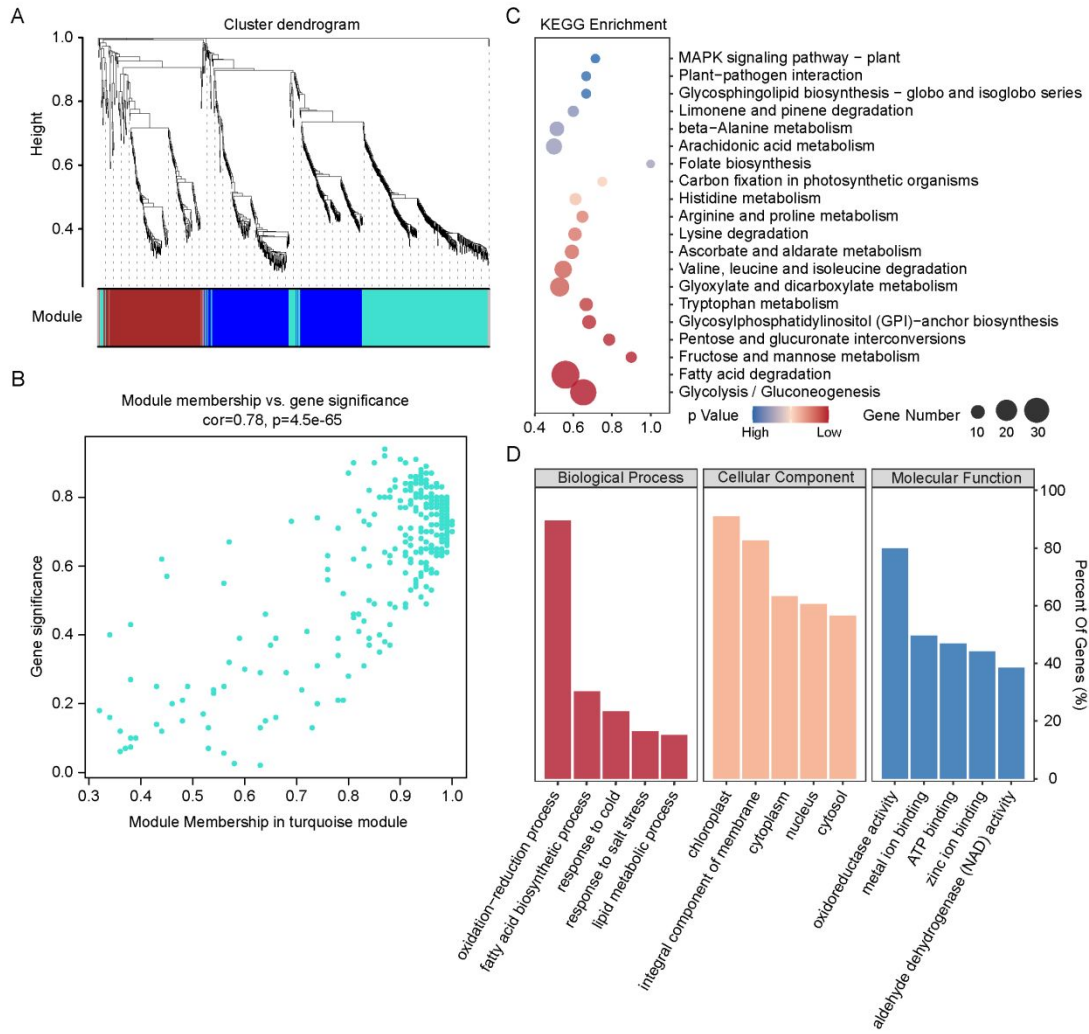
Fig. S9. The quality control analysis for WGCNA of DEGs and DALs in ger-mination. (A) Transcriptome data cluster diagram. (B) The PCA-3D for transcrip-tome data. (C) WGCNA module correlation analysis.

Fig. S10. Turquoise module gene analysis for development. (A) Hierarchical clustering tree. (B) Significance of Turquoise module genes. (C) KEGG analysis for Turquoise module genes. (D) GO functional annotation for Turquoise module genes.
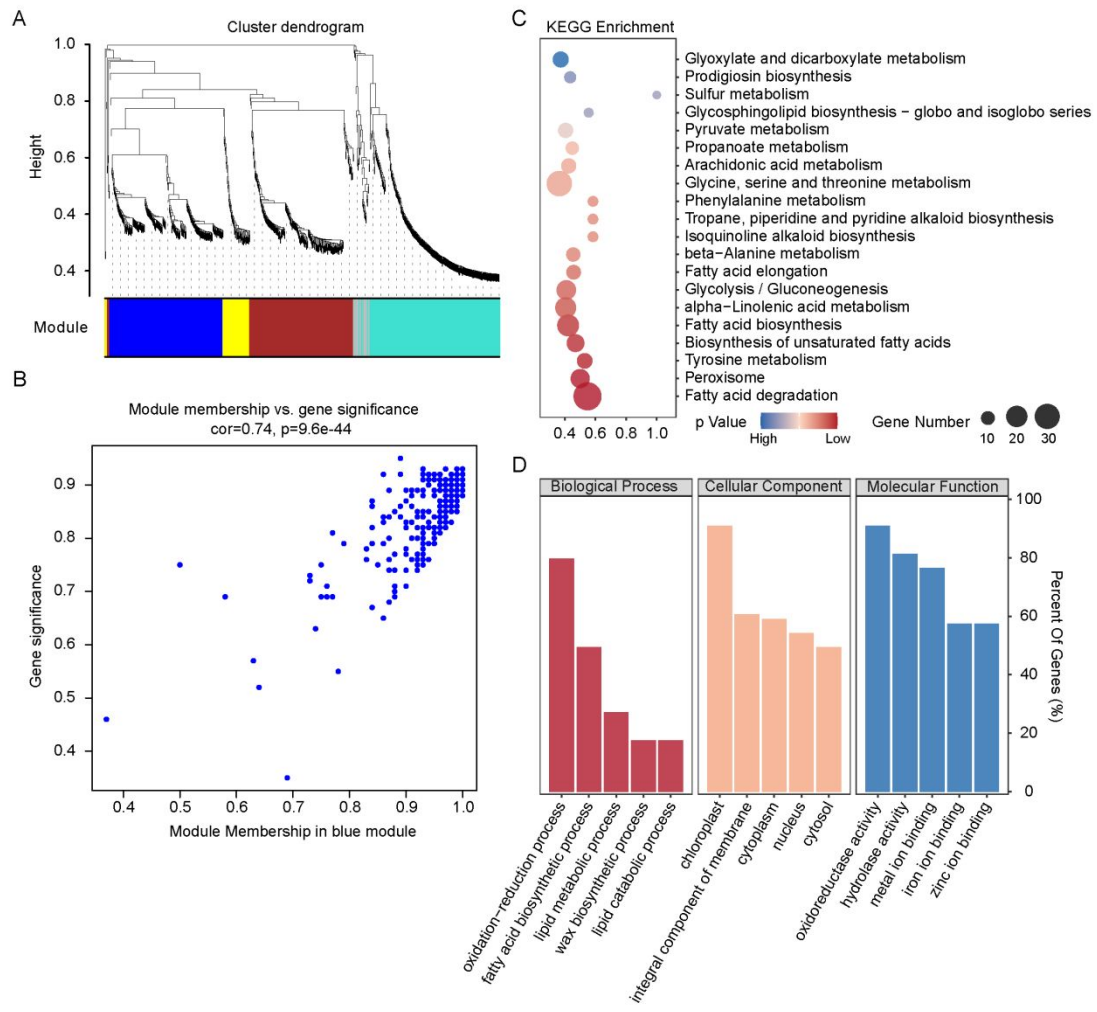
Fig. S11. Blue module gene analysis for germination. (A) Hierarchical cluster-ing tree. (B) Significance of Blue module genes. (C) KEGG analysis for Blue mod-ule genes. (D) GO functional annotation for Blue module genes.
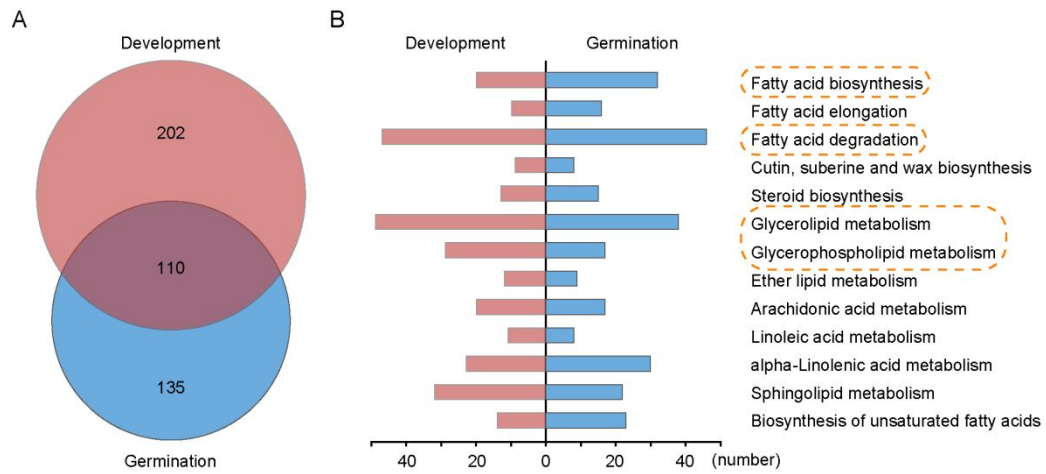
Fig. S12. Development and germination modular gene contrasts. (A) Venn di-agram for modular gene. (B) KEGG analysis for Development and germination modular gene.