

# **Identification of the Candidate Proteins Related to Oleic Acid Accumulation during Peanut (*Arachis hypogaea* L.) Seed Development through Comparative Proteome Analysis**

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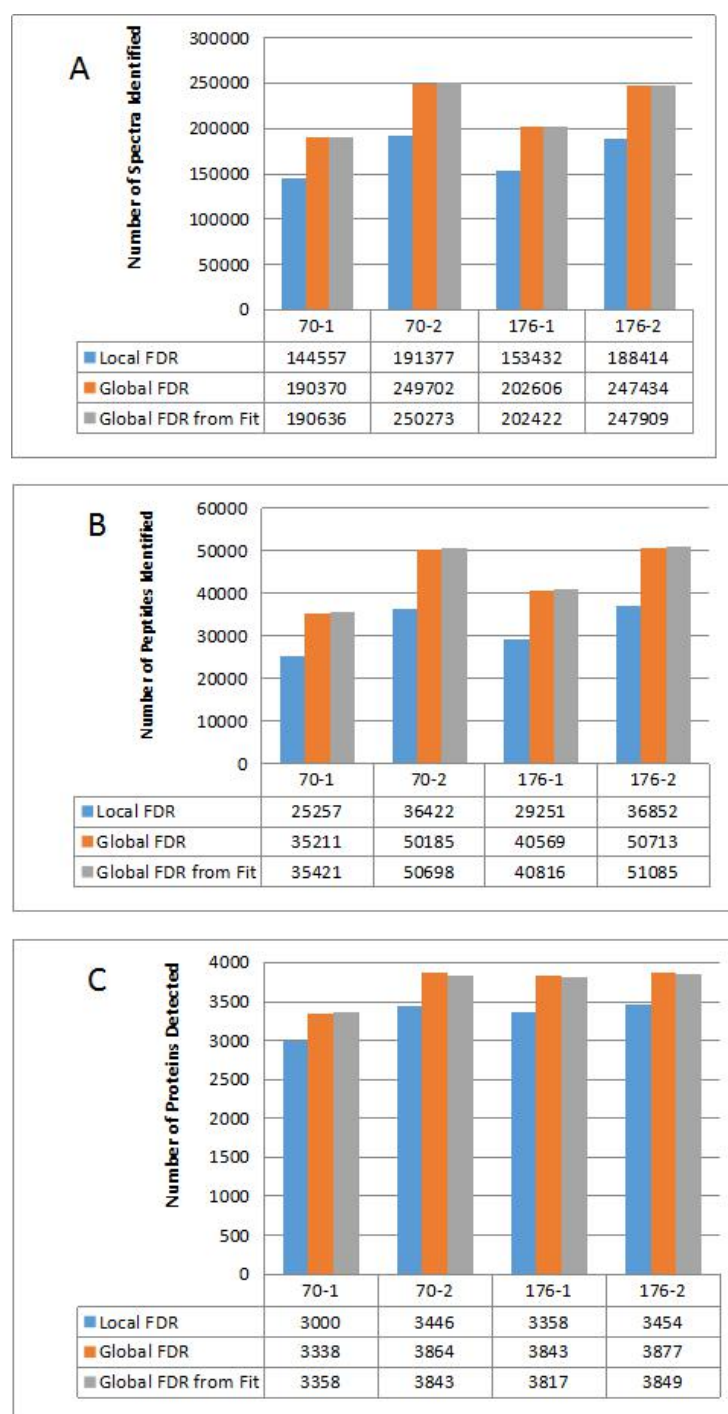


Figure S1. Results of mass spectrometry analysis and protein identification. A-C, Number statistics of spectra, peptides, and proteins in the samples from different biological replicate.

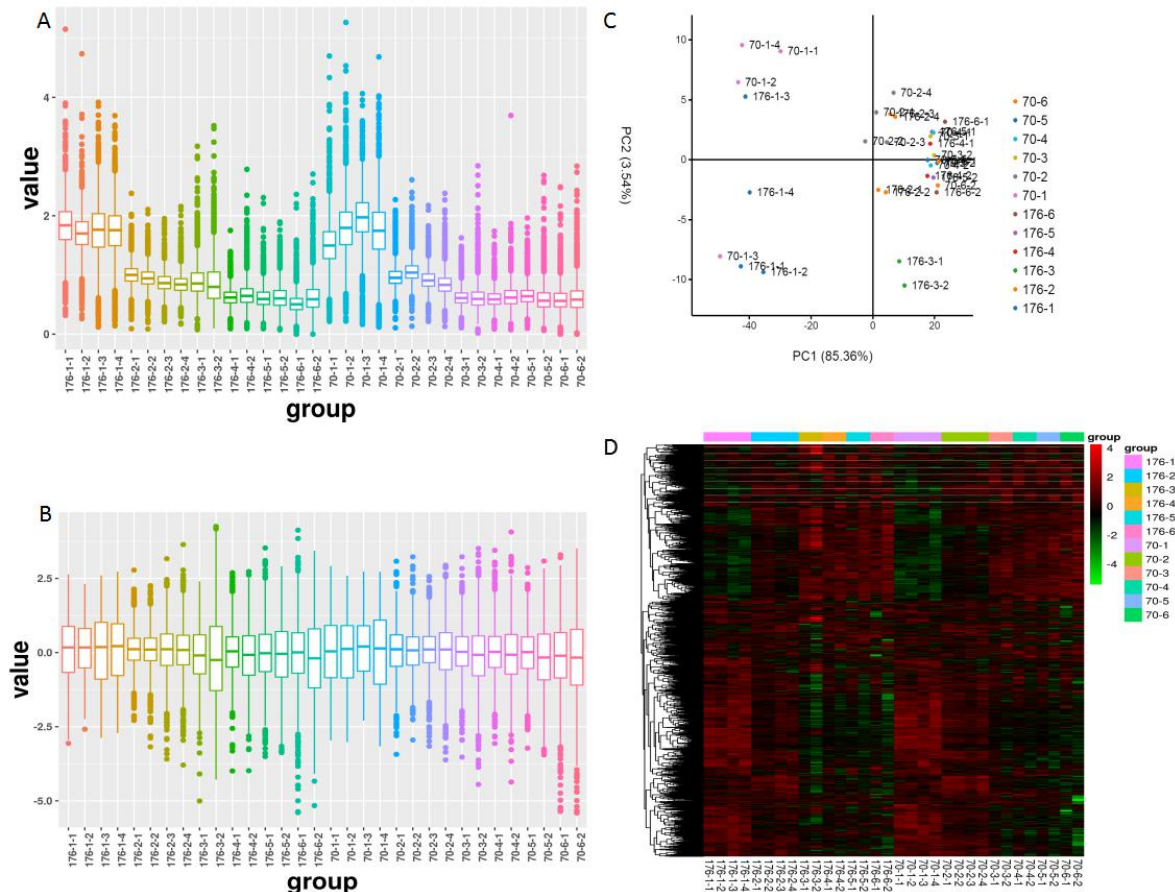


Figure S2. Quality control of experimental data. A-B, normalization treatment of experimental data. C, Principal component analysis (PCA) of different samples from different biological replicate. D, Heatmap represented the level expression of total differentially expressed proteins across the comparable samples Kainong70 and Kainong176.

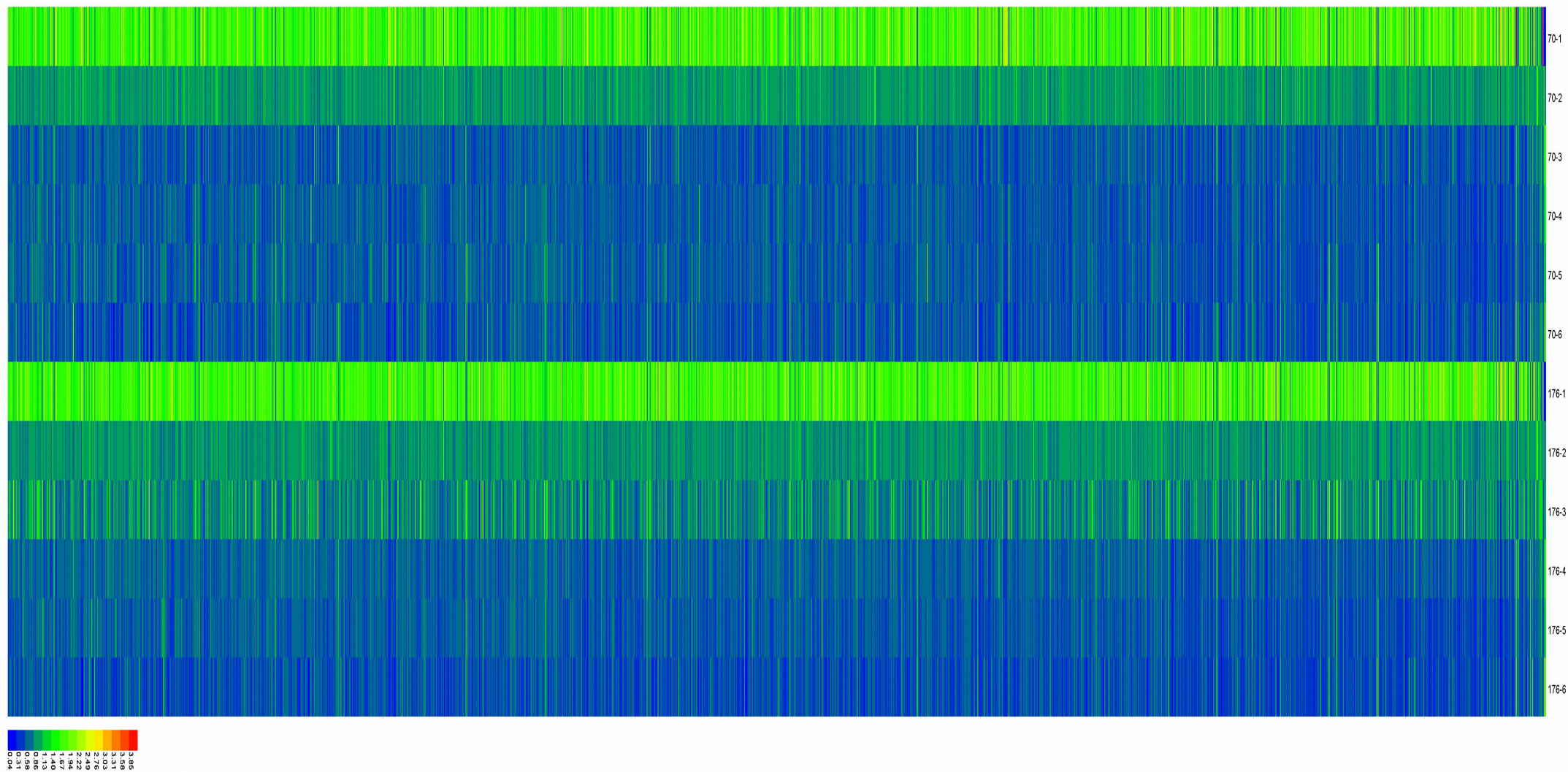


Figure S3. Heatmap displayed the expression levels of identified DEPs in both peanut cultivars. The number (70-1, 70-2,....., 176-6) in the heatmap indicated the samples came from 6 development stages (1-6) in normal-oleate cultivar Kainong70 (70) and high-oleate cultivar Kainong176(176).

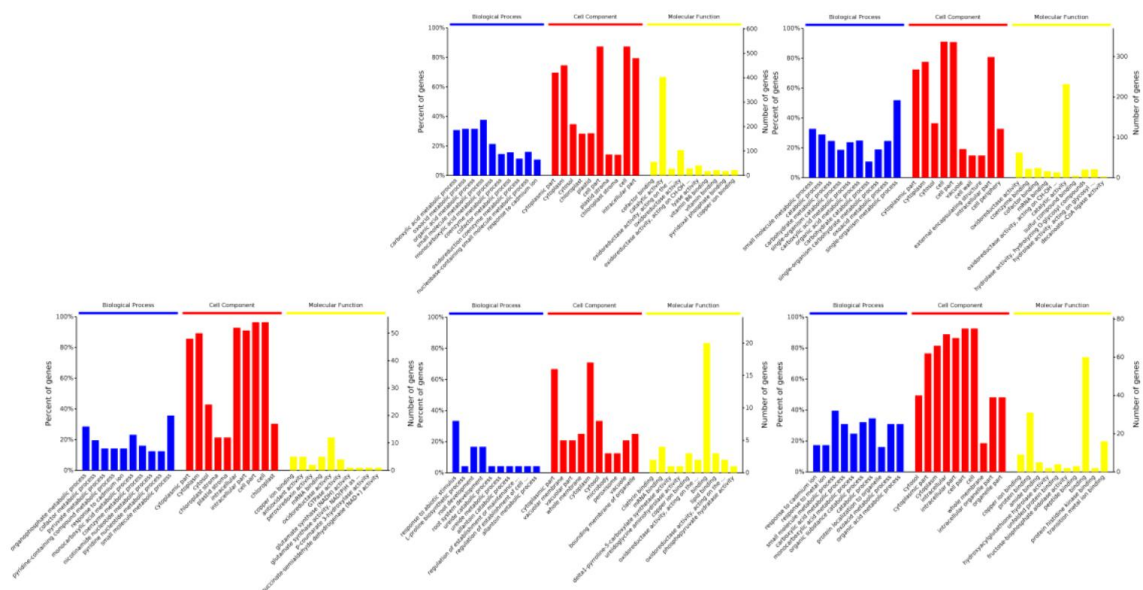


Figure S4. Histogram showing GO classification of DEPs at each stage of seed development in low-oleate variety Kainong70.

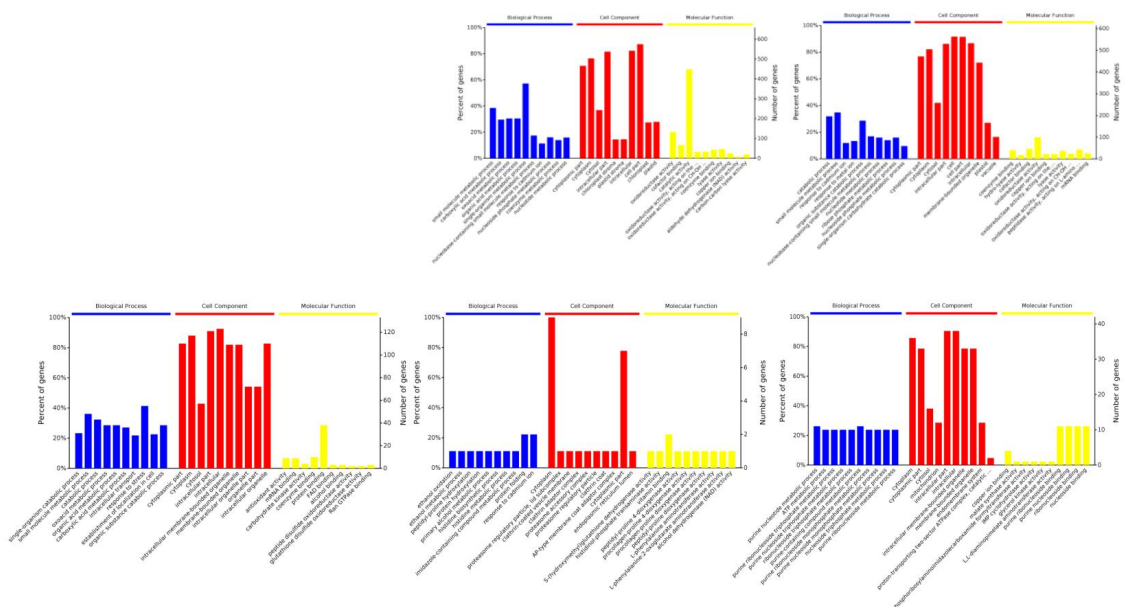


Figure S5. Histogram showing GO classification of DEPs at each stage of seed development in high-oleate variety Kainong176.

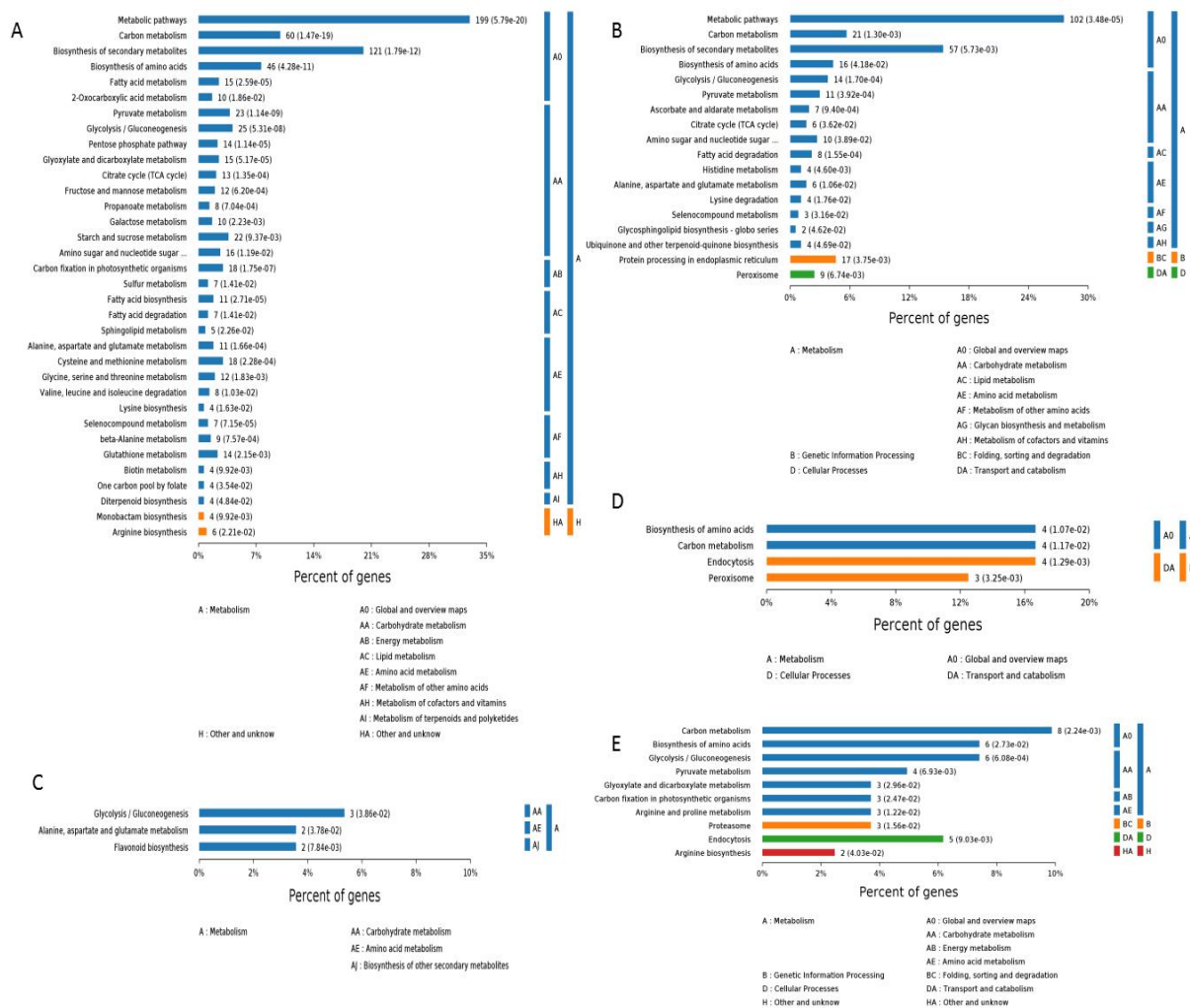


Figure S6. KEGG pathway enrichment of DEPs during the seed development in low-oleate variety Kainong70. From A to E represented the 70-2VS70-1, 70-3VS70-2, 70-4VS70-3, 70-5VS70-4, and 70-6VS70-5, respectively.

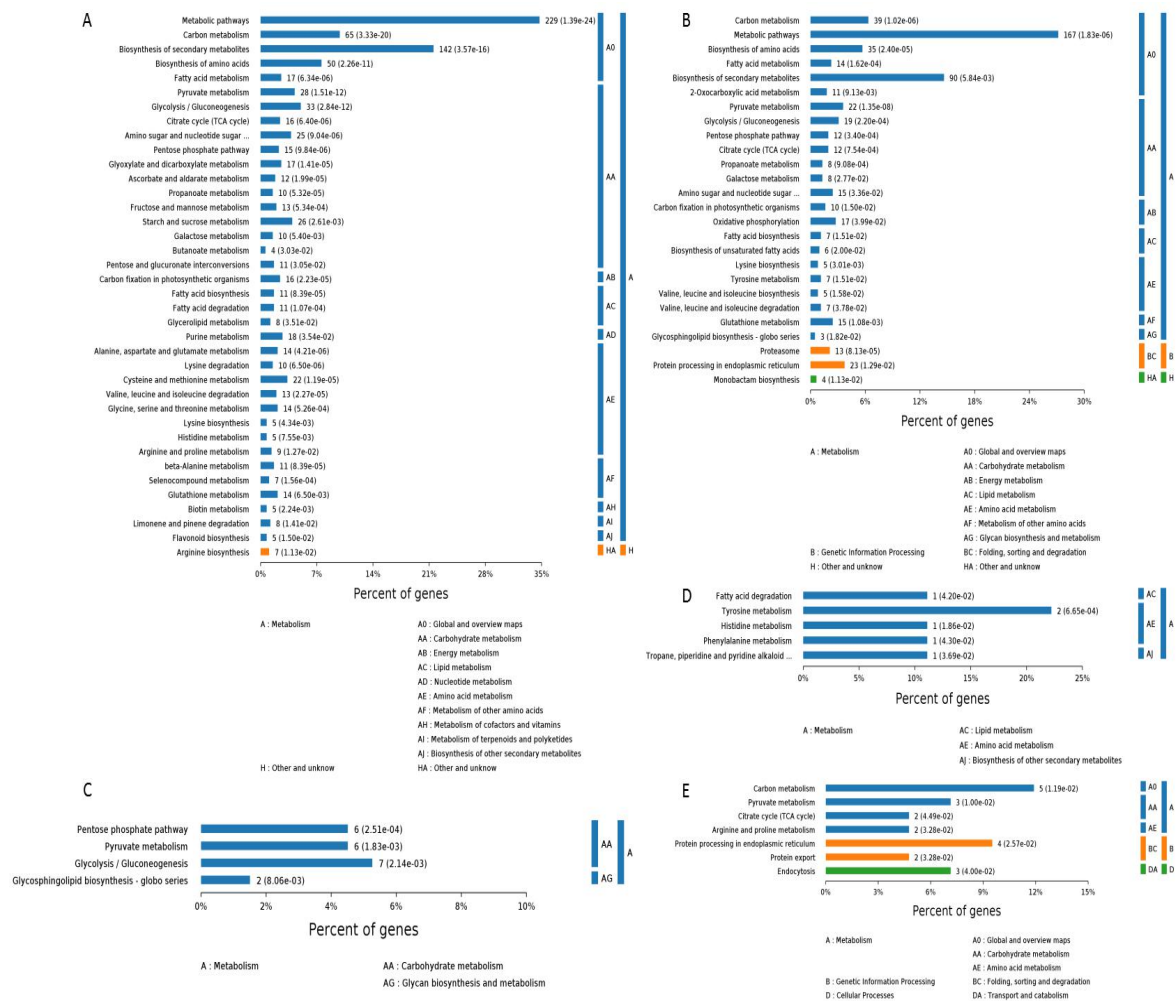
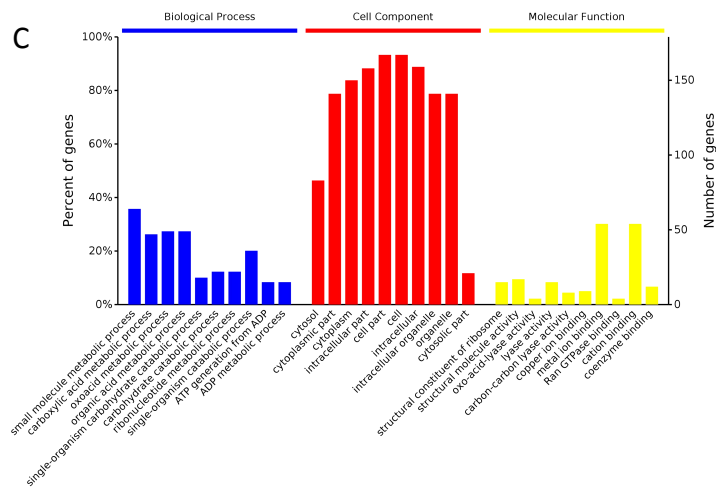
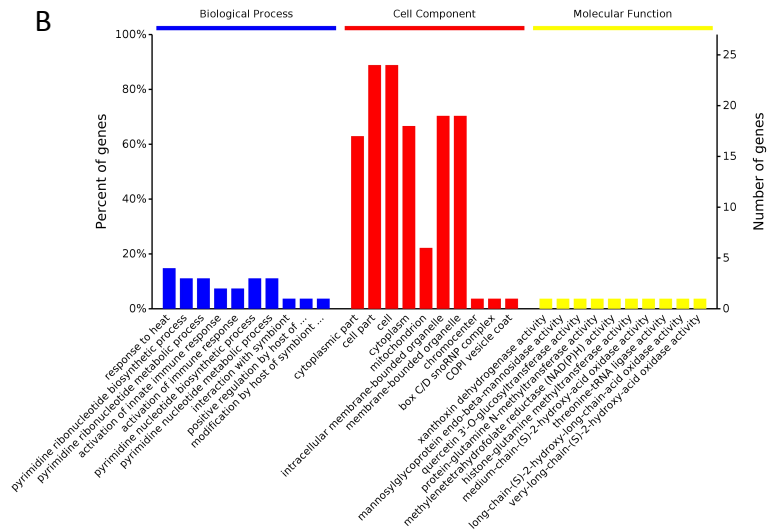
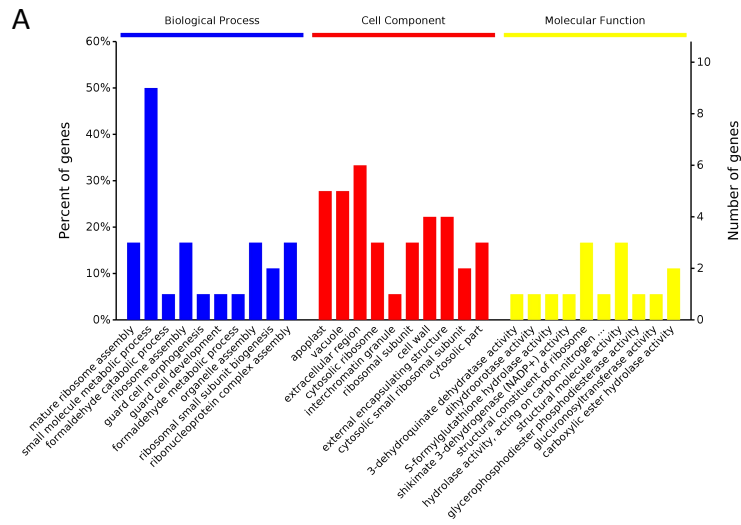


Figure S7. KEGG pathway enrichment of DEPs during the seed development in high-oleate variety Kainong176. From A to E represented the 176-2VS176-1, 176-3VS176-2, 176-4VS176-3, 176-5VS176-4, and 176-6VS176-5, respectively.





proteins in Kainong176 VS Kainong70 under the different development stage. From A to F represented the 20(stage1), 30(stage2), 40(stage3), 50(stage4), 60(stage5), and 70(stage6) DAF (days after flowering), respectively. Most top 10 terms were displayed in the biological process, cell component, and molecular function process, respectively.

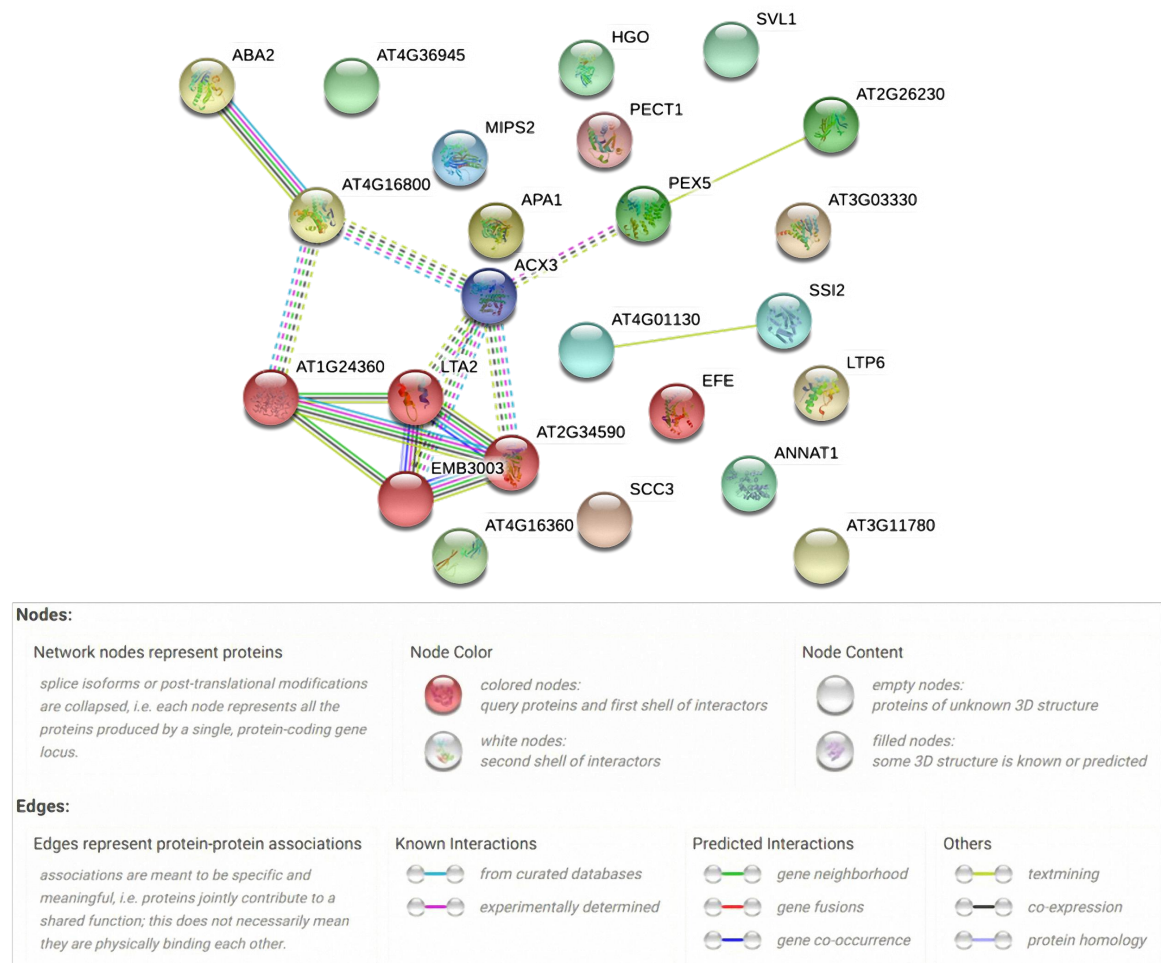


Figure S9. STRING predicted the interacting network of 28 DEPs regarding FA synthesis and metabolism using their homologous genes in *Arabidopsis*. In the STRING network, the nodes represented the proteins; and the results in the nodes represented the predicted 3D structures of proteins. The lines represented the associated relationship between the linked proteins, different line colors indicated evidence of the interaction between the linked proteins, different line colors indicated evidence of the interaction between the linked proteins. For example, blue and pink solid line indicated the curated database and experimentally determined real protein-protein associated evidence, but the dotted lines represented the putative interaction evidence based on bioinformatics analysis of database, and the network was clustered to a specified MCL inflation parameter.

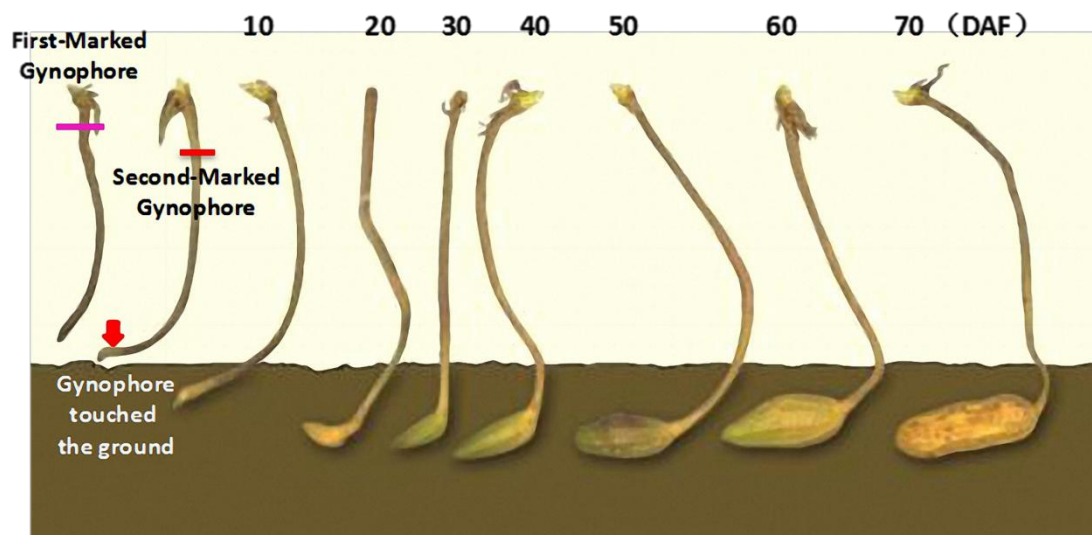


Figure S10. The process of marked gynophore during peanut seed development. We made a cartoon to explain the process of seeds collection in two peanut cultivars, but the picture was downloaded from a website ([www.baidu.com](http://www.baidu.com)) just for explain the question, not for commercial use.

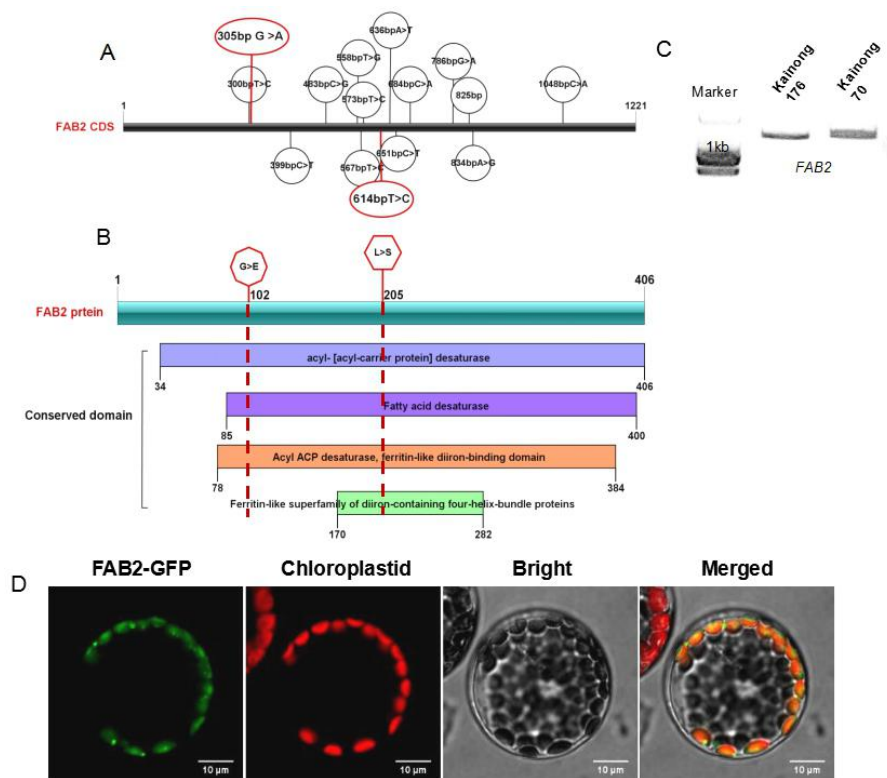


Figure S11. Recent study results of *FAB2*. A, 16 mutant site of bases in high-oleic cultivar Kainong176 compared with Kainong70. B, protein structure of *FAB2* in Kainong176. C, *FAB2* coding sequences were detected by agarose gel electrophoresis in different cultivars. D, subcellular localization of *FAB2-GFP* in protoplast cell of *Arabidopsis*.

Table S5. CT-value of *AhI8S* in the real-time PCR reaction.

	Cycle Time (CT)	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5	Stage 6	CT Mean (stage)
CT(Kainong70)	Repeat 1	21.69733429	21.84574127	20.15601921	20.2365818	20.55398369	20.8539772	20.89060624
	Repeat 2	21.29128265	21.69669533	20.08484459	20.65895844	20.20822525	21.11344147	20.84224129
	Repeat 3	21.28997612	21.68653107	20.29577255	21.00416756	19.81446457	20.53738022	20.77138201
	CT Mean (repeat)	21.42619769	21.74298922	20.17887878	20.63323593	20.1922245	20.83493296	20.83474318
CT(Kainong176)	Repeat 1	20.93497086	20.20988655	19.75986481	19.52990913	20.94015503	20.60691452	20.33028348
	Repeat 2	20.11518478	20.18793106	19.44475746	19.96493912	20.76073647	20.71387291	20.19790363
	Repeat 3	20.95371056	20.0320816	19.24794006	19.79506874	21.26062584	21.3200779	20.43491745
	CT Mean (repeat)	20.6679554	20.14329974	19.48418744	19.76330566	20.98717244	20.88028844	20.32103486