

Supplementary Material

Transcriptomic Insights into the Development of Olecranon Honey Peach Fruits Using Two Different Planting Methods

Table S1. Number of reads after filtering rRNA and low quality.

Sample	Total	Total Mapped (%)	Unique Mapped (%)	Multiple Mapped (%)	Unmapped (%)
SBY-15 WAP-1	42541336	40800694 (95.91%)	38467898 (90.42%)	2332796 (5.48%)	1740642 (4.09%)
SBY-15 WAP-2	43174984	41392591 (95.87%)	39628288 (91.79%)	1764303 (4.09%)	1782393 (4.13%)
SBY-15 WAP-3	43806834	42272572 (96.50%)	40083531 (91.50%)	2189041 (5.00%)	1534262 (3.50%)
SBY-17 WAP-1	44608108	42734335 (95.80%)	40920730 (91.73%)	1813605 (4.07%)	1873773 (4.20%)
SBY-17 WAP-2	43666686	42153086 (96.53%)	40395874 (92.51%)	1757212 (4.02%)	1513600 (3.47%)
SBY-17 WAP-3	43830956	42327860 (96.57%)	40791703 (93.07%)	1536157 (3.50%)	1503096 (3.43%)
SBY-19 WAP-1	44932540	43148515 (96.03%)	41570745 (92.52%)	1577770 (3.51%)	1784025 (3.97%)
SBY-19 WAP-2	43577092	42166417 (96.76%)	40584588 (93.13%)	1581829 (3.63%)	1410675 (3.24%)
SBY-19 WAP-3	43988468	42602058 (96.85%)	41110825 (93.46%)	1491233 (3.39%)	1386410 (3.15%)
SJH-15 WAP-1	44651486	42944073 (96.18%)	40956827 (91.73%)	1987246 (4.45%)	1707413 (3.82%)
SJH-15 WAP-2	43702964	42352772 (96.91%)	40250124 (92.10%)	2102648 (4.81%)	1350192 (3.09%)
SJH-15 WAP-3	44374164	42973631 (96.84%)	39845089 (89.79%)	3128542 (7.05%)	1400533 (3.16%)
SJH-17 WAP-1	48229486	46333093 (96.07%)	44023571 (91.28%)	2309522 (4.79%)	1896393 (3.93%)
SJH-17 WAP-2	43281486	41823141 (96.63%)	39857854 (92.09%)	1965287 (4.54%)	1458345 (3.37%)
SJH-17 WAP-3	44490636	43036222 (96.73%)	40125924 (90.19%)	2910298 (6.54%)	1454414 (3.27%)
SJH-19 WAP-1	46124438	44286230 (96.01%)	41912799 (90.87%)	2373431 (5.15%)	1838208 (3.99%)

SJH-19 WAP-2	44858728	43371335 (96.68%)	40608694 (90.53%)	2762641 (6.16%)	1487393 (3.32%)
SJH-19 WAP-3	44125870	42703010 (96.78%)	39934132 (90.50%)	2768878 (6.27%)	1422860 (3.22%)

Table S2. Comparing the numbers of DEGs of ‘SJH’ and ‘SBY’.

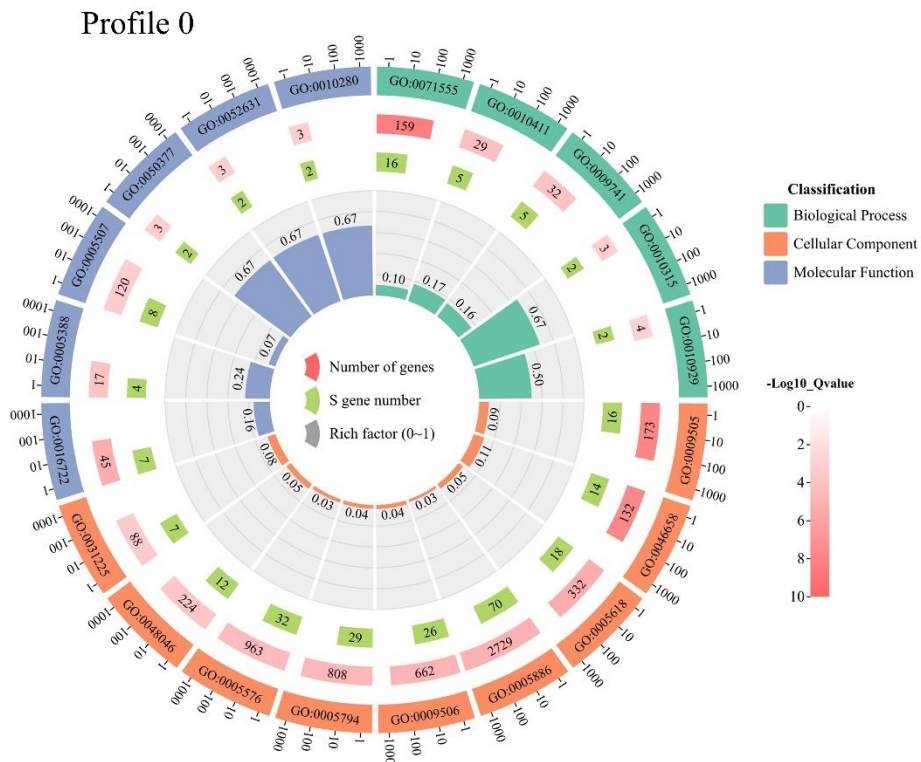
	UP	DOWN
SJH-17 WAP vs. SJH-15 WAP	326	493
SJH-19 WAP vs. SJH-17 WAP	329	765
SBY-17 WAP vs. SBY-15 WAP	1070	1191
SBY-19 WAP vs. SBY-17 WAP	2688	2129
SJH-15 WAP vs. SBY-15 WAP	743	1022
SJH-17 WAP vs. SBY-17 WAP	1837	2485
SJH-19 WAP vs. SBY-19 WAP	504	1630

*Log2(FC)≥1, Q≤0.05

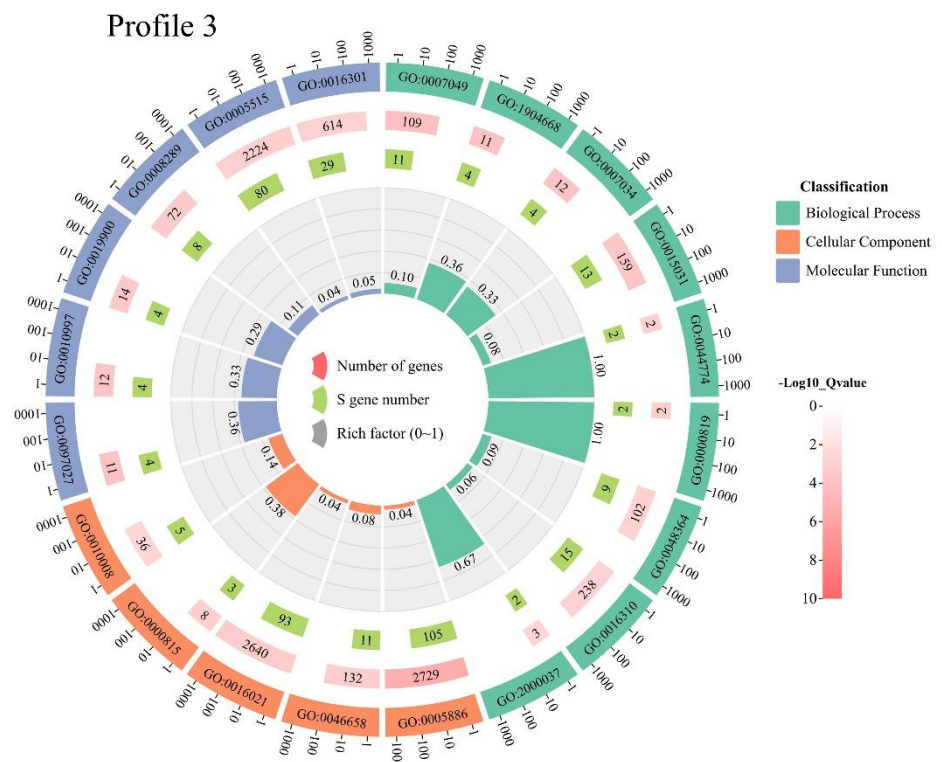
Table S3. Pairs of primers used to amplify the targeting genes by qPCR.

Target Genes		Sequence (5'-3')	Product Size
ncbi_18789554	F	TCGTTGGGGTGGAGAATGTT	157bp
	R	AACAGGGGGAATCAATGCCA	
ncbi_18777071	F	GACGACGATTGCTTTGTTGCT	163bp
	R	GACTGAAGGGGTAAACCACGG	
ncbi_18770520	F	TACACCGTCTTCCTGCCTCT	105bp
	R	AACAGCAGAATCTCCACTCTCG	
ncbi_18791135	F	GCACTAAGAGAGTGGAGGGC	135bp
	R	GCCCGTTAGACTGGGACAAA	
ncbi_18774451	F	ATGGCCCTGAGATCGCTTAC	108bp
	R	CAGCAAGCTCAACCGCGTTA	
ncbi_18767223	F	TTGCCCTTCTCTCCAGGTATG	103bp
	R	TGTTTGGCTTCATCACCGCT	
ncbi_18788353	F	GCAATGGGGCCTACTGGAAA	124bp
	R	GCAACGGATTGGGATAAGTAGGA	
ncbi_18769018	F	ATGGTCAGCTATCAGGAACCG	188bp
	R	ACCCTTCAATGTGACTGGGC	
ncbi_18768307	F	TCTCACCGACTTGGGTTTCA	111bp
	R	TTCCGGATTTGGTCCAGTCG	
ncbi_18772722	F	GTTTCTACAGCAAGCGGGTG	165bp
	R	CAACCAGTCTAGGGCTCCAC	
ncbi_18778944	F	CCTATGGCGAGGAGGATTCTG	180bp
	R	TCCACGCAACACTCCCATAC	
ncbi_18792321	F	GCGCAAATACTCGACAACGG	172bp
	R	AACCCAACGAGGACAGATAGT	
Actin	F	AGCAGAGCGATTCCGTTGTCC	153bp
	R	CCTCCACTCAGCACTATGTTACCAT	

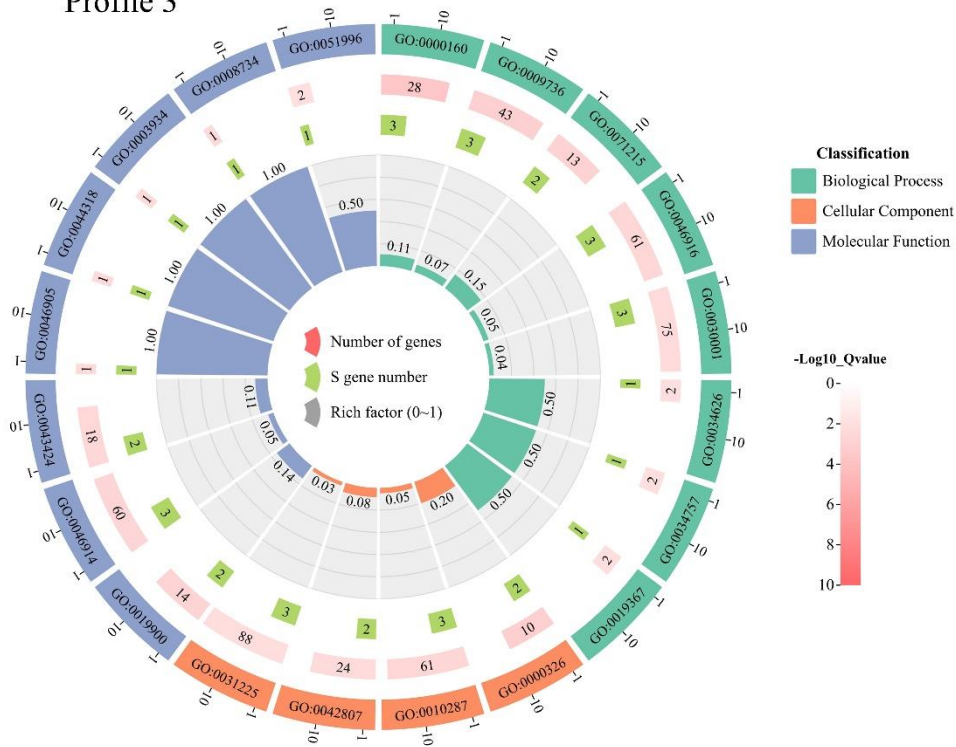
a



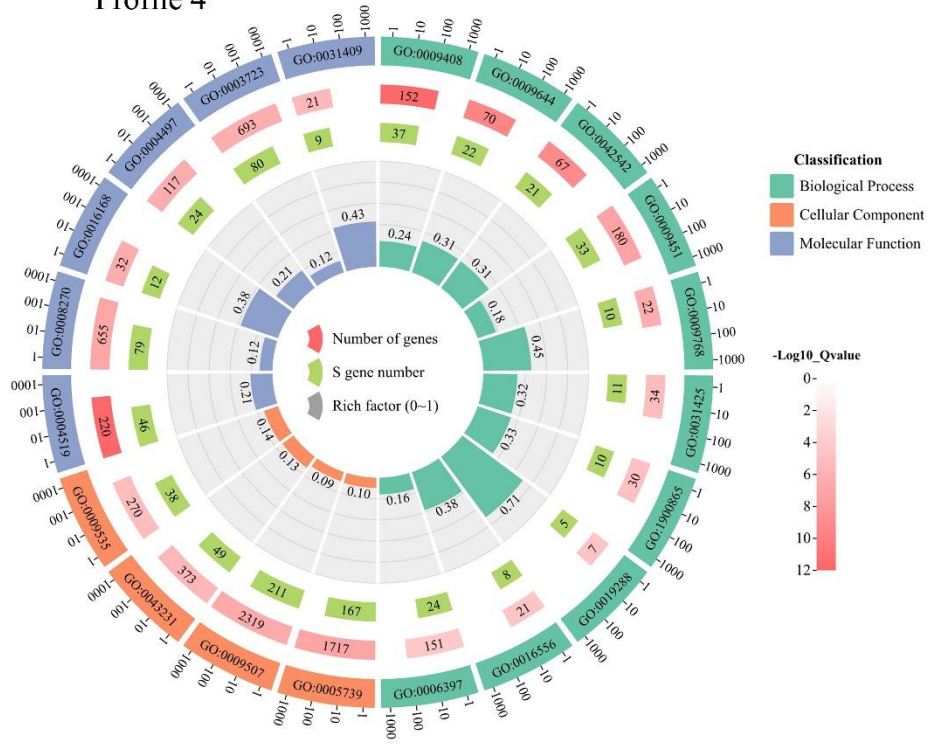
b



Profile 3



Profile 4



Profile 7

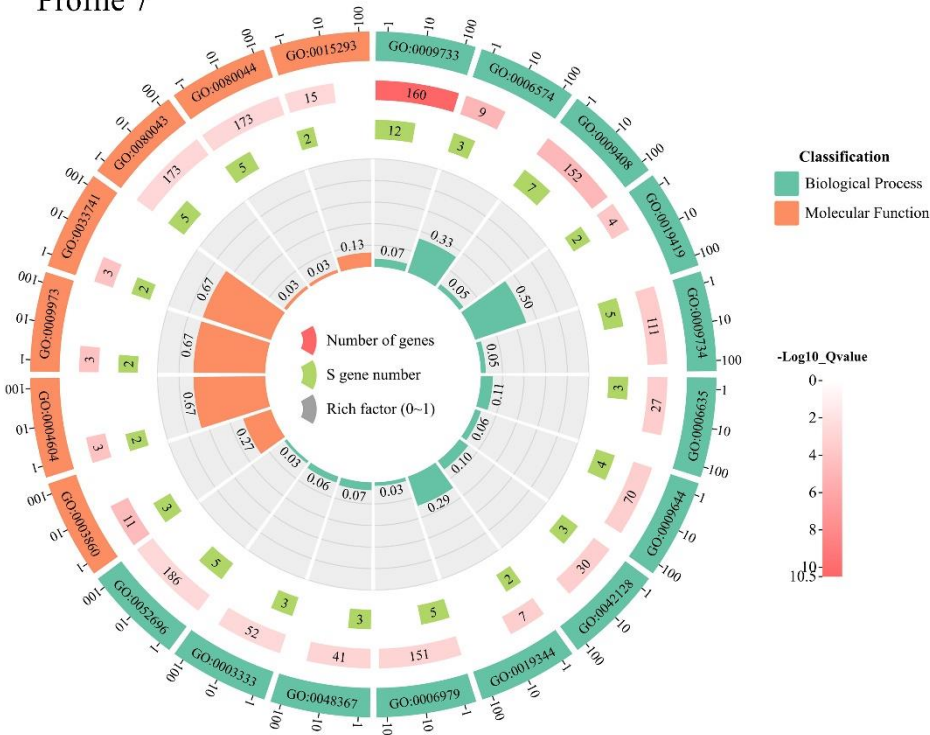
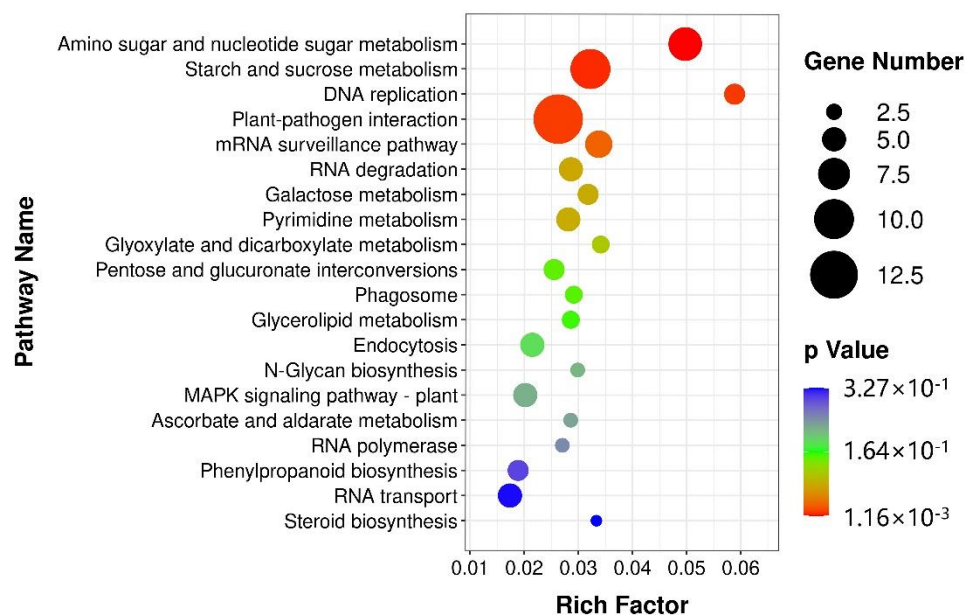


Figure S1. GO enrichment circle plot based on the clustering analysis results in Figure 6. (a) ‘SJH’ enrichment circle plot of up and downregulated profiles, and profiles 0 and 3 are downregulated enrichment circle plots and profile 7 is the upregulated enrichment circle plot. (b) ‘SBY’ enrichment circle enrich plot of up and downregulated profiles, and profile 3 is the downregulated enrichment circle plot, while profile 4 is the upregulated enrichment circle plot. The outermost circle color indicates the GO terms classification, while the character indicates the GO terms code. The color of the second outer circle indicates the q-value, and the number represents the number of background genes. The number in the third circle indicates the number of genes mapped to the GO term. The innermost circle color indicates the GO classification, while the number indicates the rich factor.

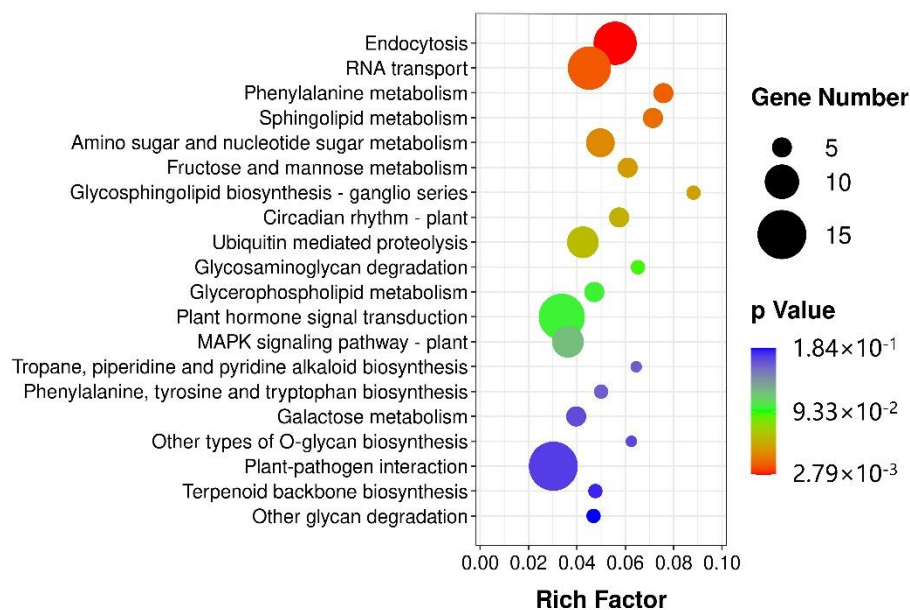
a

Profile 0 Top 20 of KEGG Enrichment

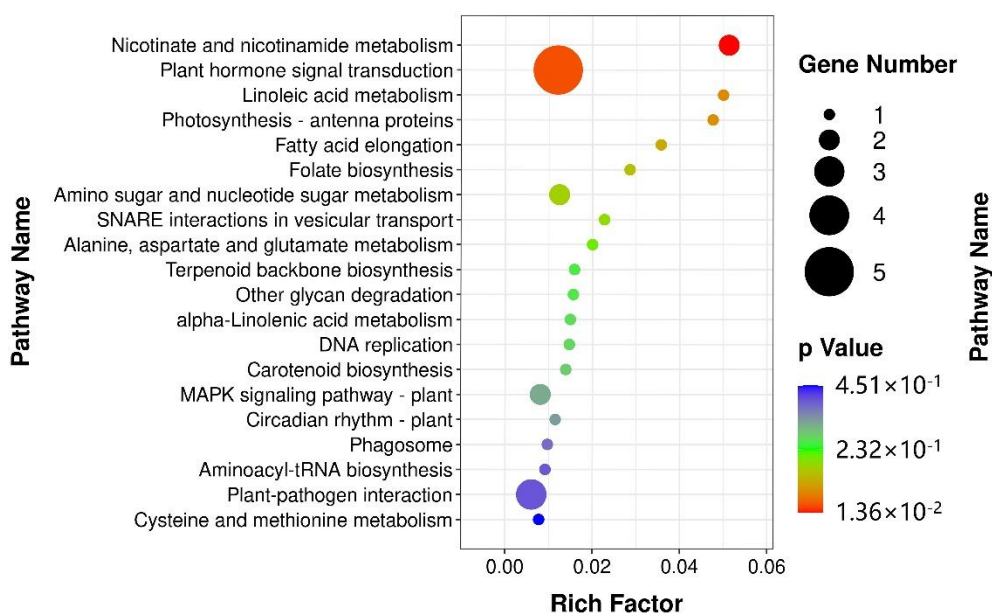


b

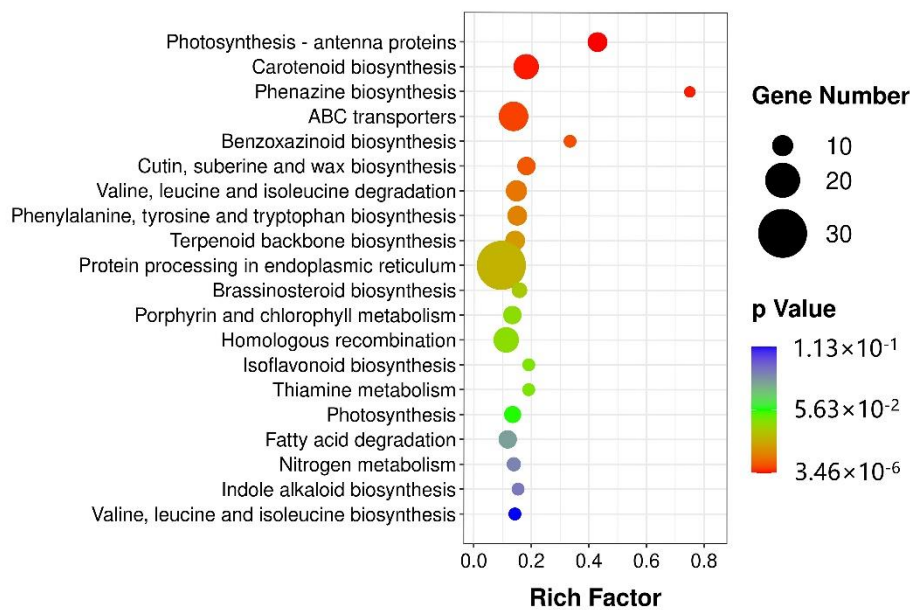
Profile 3 Top 20 of KEGG Enrichment



Profile 3 Top 20 of KEGG Enrichment



Profile 4 Top 20 of KEGG Enrichment



Profile 7 Top 20 of KEGG Enrichment

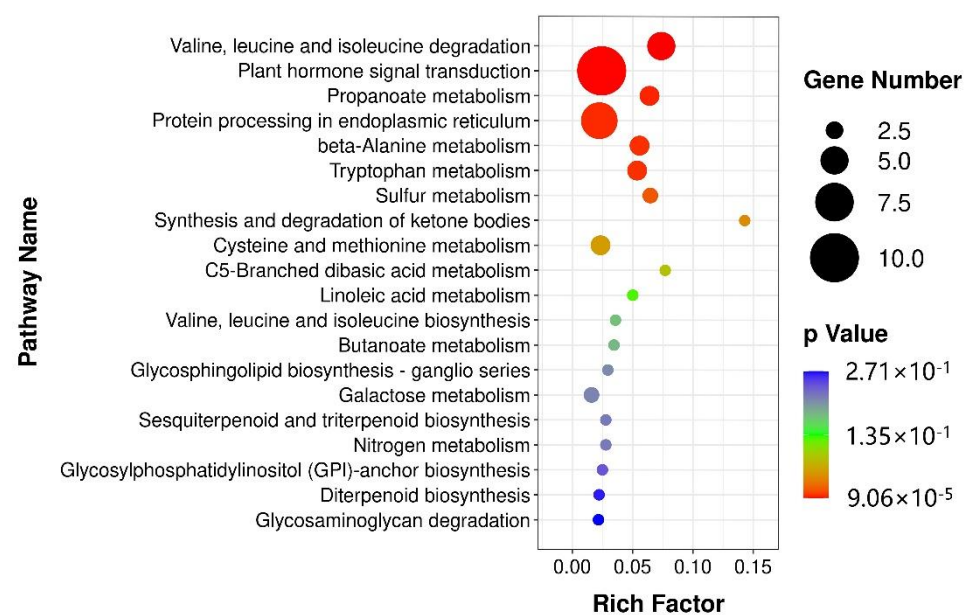


Figure S2. KEGG enrichment bubble diagram based on the clustering analysis results in Figure 6. (a) ‘SJH’ bubble diagram of up and downregulated profiles, and profiles 0 and 3 are down-regulated enrichment bubble diagram and profile 7 is the upregulated enrichment bubble diagram. (b) ‘SBY’ bubble diagram of up and downregulated profiles, and profile 3 is the downregulated enrichment bubble diagram, while profile 4 is the upregulated enrichment bubble diagram. The color of each circle and the size indicate the p -value and the number of genes mapped to the pathway, respectively.