

Table S1. Primers of 15 DEGs

| Gene | Accession Number | Forward Primer (5'-3') | Reverse Primer (5'-3') |
|----------------|------------------|------------------------|------------------------|
| ACT | LOC106312299 | TGGTTGGGATGGGACAGAAG | AATGCCGTGCTCAATAGGGT |
| ncbi_106295500 | LOC106295500 | ATCGGTTACCTCGACATT | TCACAGCAGGATCATTACA |
| ncbi_106300718 | LOC106300718 | TCAAAGGGAATCAGCAAA | TTACCGCTCAAGAAACCA |
| ncbi_106296668 | LOC106296668 | AATTCTACCACGACCTCA | CCACCGTATTCATCTTCTA |
| ncbi_106318388 | LOC106318388 | CTTCTTACCGTGGCTTCA | TACCCATCTCATCCTTTCTT |
| ncbi_106328411 | LOC106328411 | AAACGAAGCATCCCAAGA | TGAGCCATTCCCAGAGTA |
| ncbi_106311920 | LOC106311920 | AACAATCGGACAAGTCGC | CCATAACCCAATCACTGCTA |
| ncbi_106308421 | LOC106308421 | GAGTGCCCTGGTGTGTC | GTGGTCGGGAAGGTAAGA |
| ncbi_106342634 | LOC106342634 | TTCTCCCAATCTCACCAA | GAACTCCCAACCTTCCCT |
| ncbi_106295962 | LOC106295962 | TGGCGTGGGACAAATAAA | TGGAGTGCCTGAGGAAGG |
| ncbi_106322682 | LOC106322682 | TTACAGAGGGGTGAGACAGA | AACCACGCATCCTAAAAGCA |
| ncbi_106321330 | LOC106321330 | TTCTATGGAACCCACAACGA | AGACATCAGGACAGGACGAC |
| ncbi_106318387 | LOC106318387 | TCCTTTCACTGCTTCTTACC | CACCCATCTCATCCTTTCTT |
| ncbi_106307722 | LOC106307722 | ATCTGAAGGAGAACGGTAGC | GGAGGATGAGGAAGAAAAAC |
| ncbi_106331458 | LOC106331458 | AGAGTCGTCCTCGCCCTTCA | TTGGTTCCTTGGCCTTCGTA |
| ncbi_106309520 | LOC106309520 | CTCCTTCTTTCCCATCTCAT | GGCTTTCTTCATTTTCGTTTC |

Table S2. Summary of sequencing reads after filtering.

| Sample | Raw reads | Clean reads | Mapped reads | Clean bases | Q20 | Q30 | GC(%) |
|--------|------------|-------------|--------------|---------------|--------|--------|--------|
| CK-1 | 47,163,946 | 47,083,950 | 91.01% | 7,027,200,604 | 97.72% | 93.23% | 47.73% |
| CK-2 | 46,732,296 | 46,648,346 | 91.20% | 6,963,869,670 | 97.94% | 93.80% | 47.78% |
| CK-3 | 39,426,234 | 39,356,652 | 91.26% | 5,880,297,602 | 97.83% | 93.51% | 47.82% |
| LS-1 | 49,853,254 | 49,763,488 | 91.21% | 7,429,483,537 | 97.82% | 93.48% | 47.79% |
| LS-2 | 41,652,914 | 41,579,822 | 91.40% | 6,206,694,348 | 97.96% | 93.86% | 47.77% |
| LS-3 | 42,222,764 | 42,149,418 | 91.78% | 6,289,724,527 | 98.20% | 94.45% | 47.64% |
| DS-1 | 35,736,340 | 35,668,084 | 90.90% | 5,326,895,587 | 97.87% | 93.61% | 47.59% |
| DS-2 | 40,381,950 | 40,311,228 | 91.17% | 6,018,110,169 | 98.10% | 94.21% | 47.54% |
| DS-3 | 54,259,602 | 54,160,188 | 90.62% | 8,081,888,288 | 97.62% | 93.01% | 47.57% |
| LDS-1 | 41,642,550 | 41,553,578 | 91.46% | 6,202,801,083 | 97.75% | 93.29% | 47.97% |
| LDS-2 | 40,914,856 | 40,840,248 | 91.23% | 6,098,610,869 | 98.04% | 94.03% | 47.74% |
| LDS-3 | 41,000,918 | 40,925,494 | 90.74% | 6,110,689,061 | 97.85% | 93.59% | 47.54% |

[Figure S1]

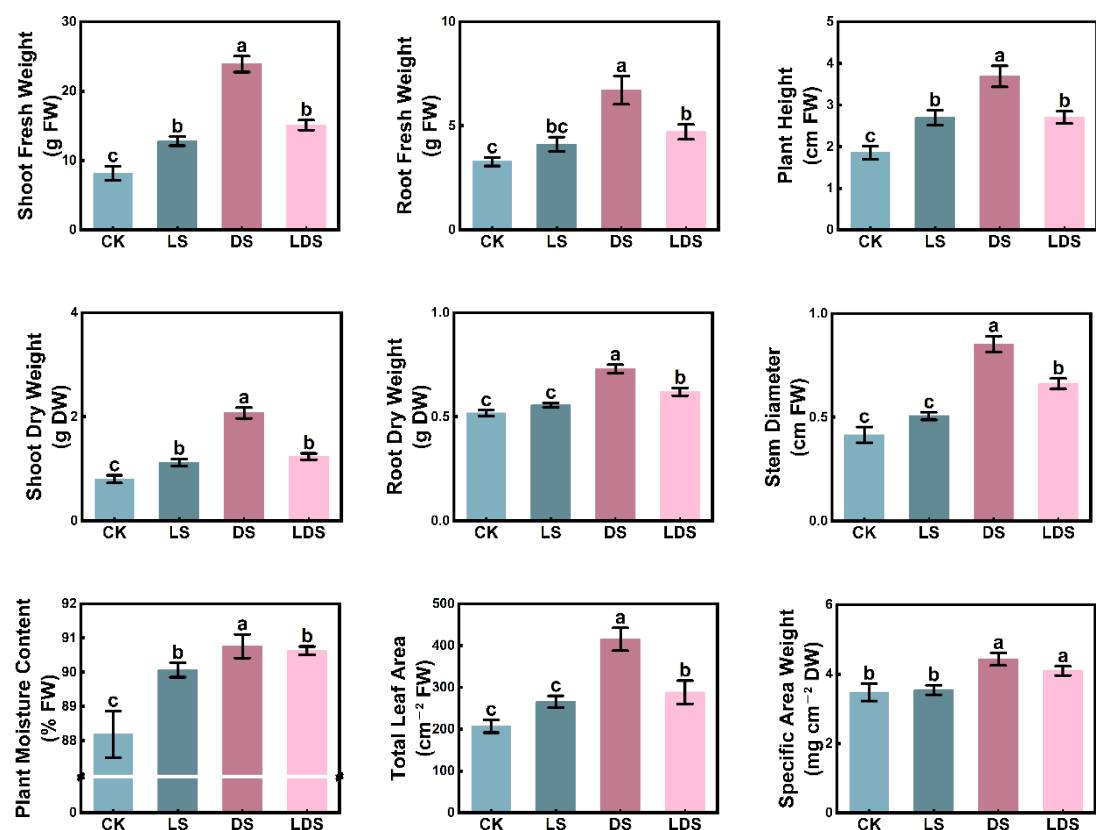


Figure S1. the morphology and biomass of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation

[Figure S2]

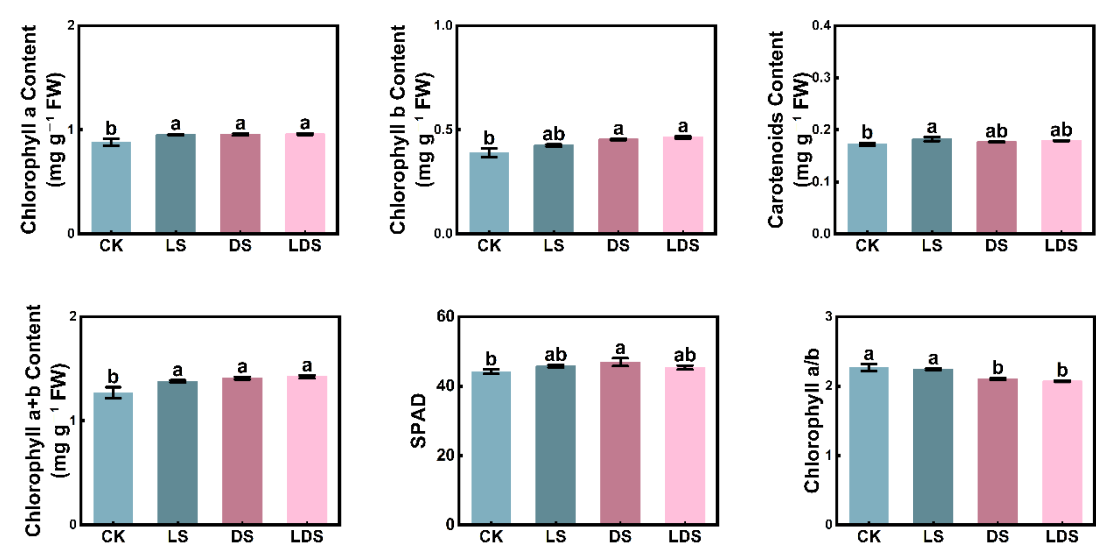


Figure S2. the pigment content of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation

[Figure S3]

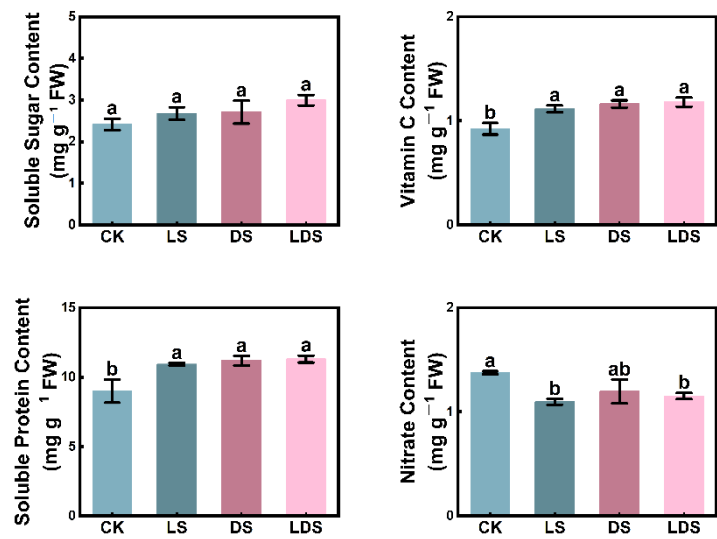


Figure S3. the nutritional quality content of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation

[Figure S4]

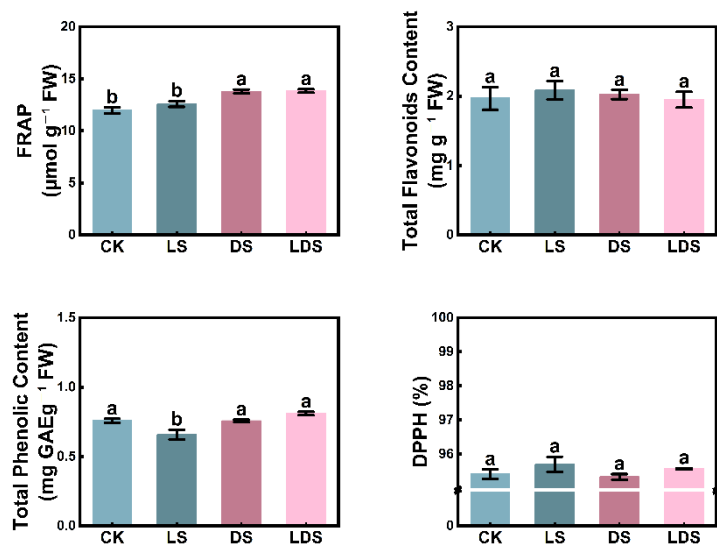


Figure S4. the antioxidant capacity and compounds of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation

[Figure S5]

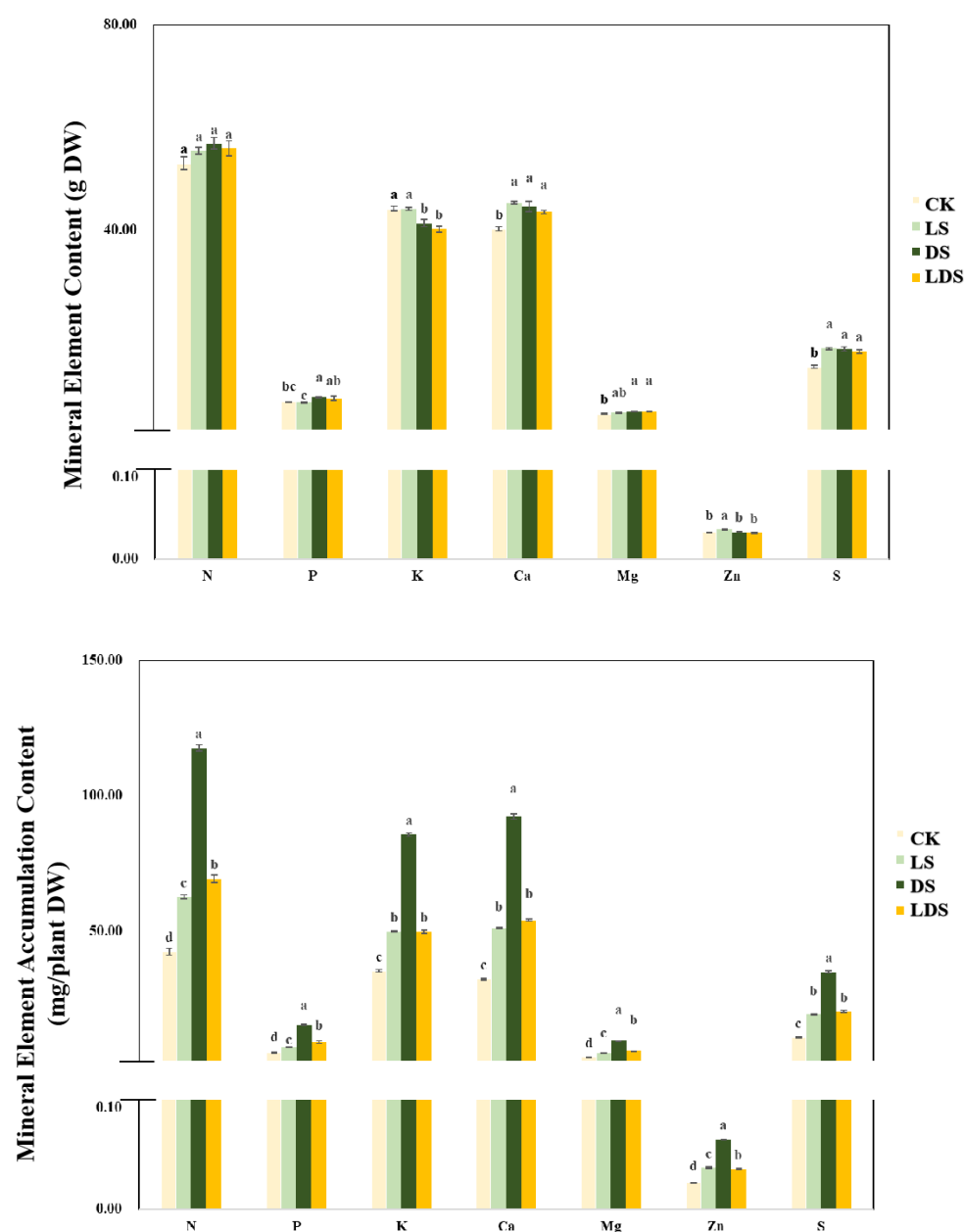


Figure S5. Mineral element and mineral element accumulation contents of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation

[Figure S6]

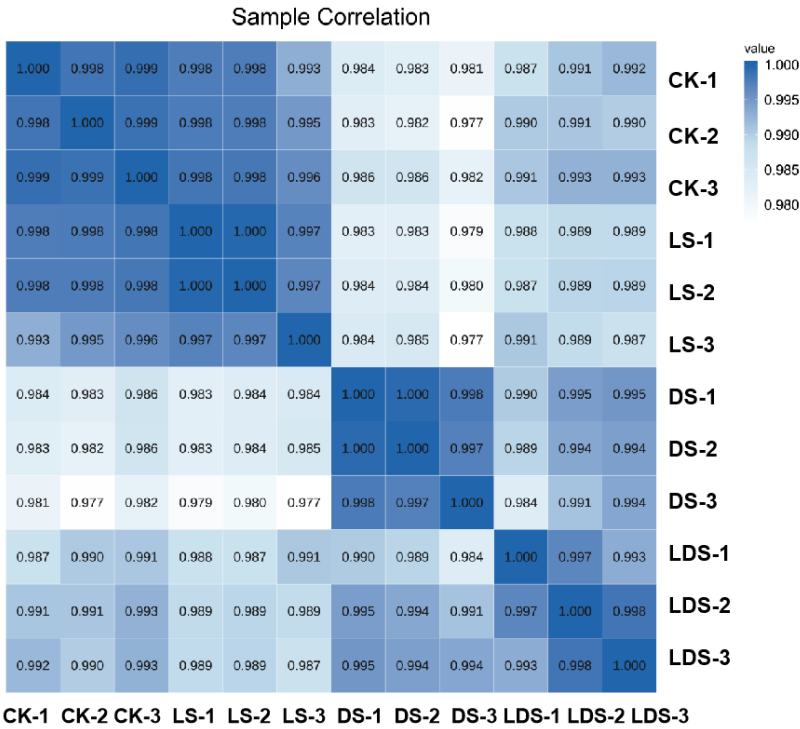


Figure S6. Pearson correlation coefficients of 12 datasets.

[Figure S7]

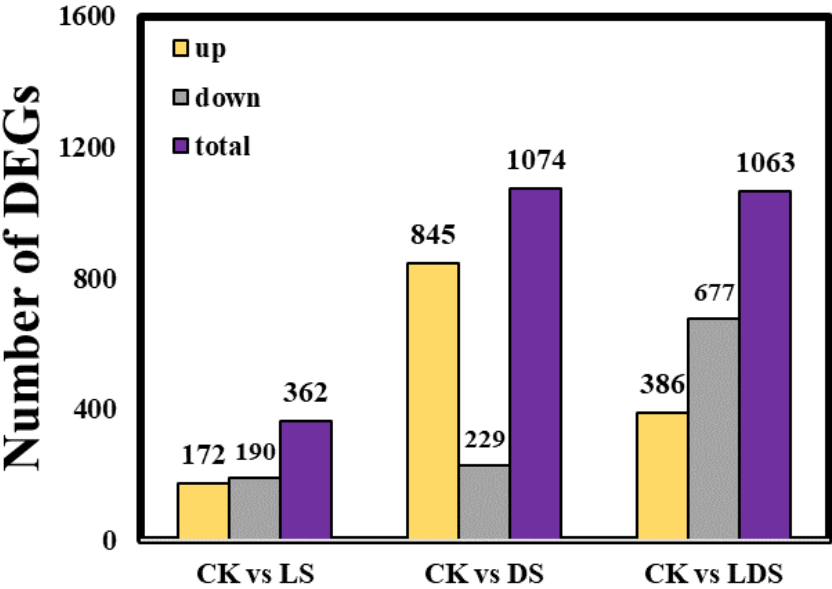


Figure S7. The DEGs among different comparison groups.

[Figure S8]

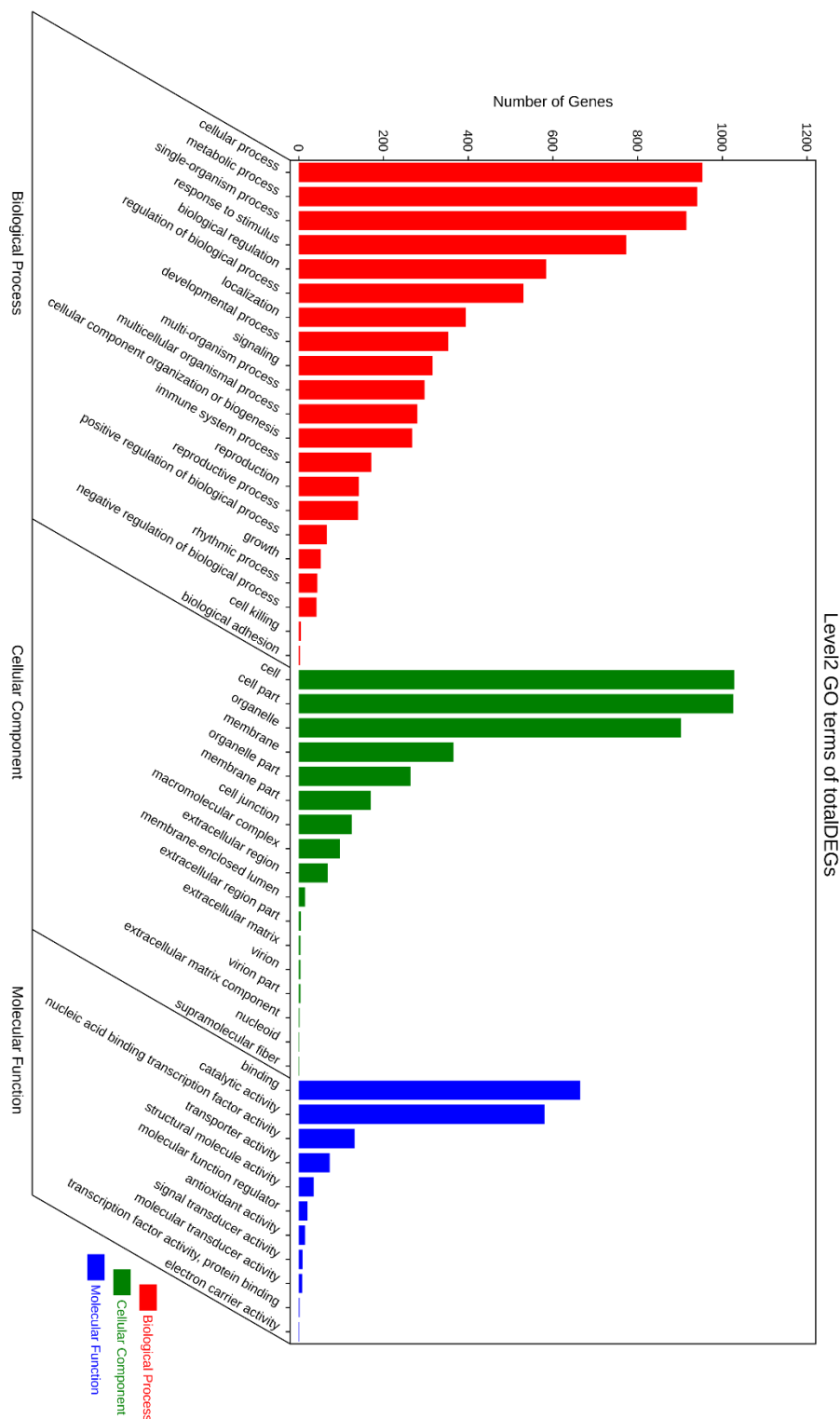


Figure S8. GO enrichment of 2047 DEGs.

[Figure S9]

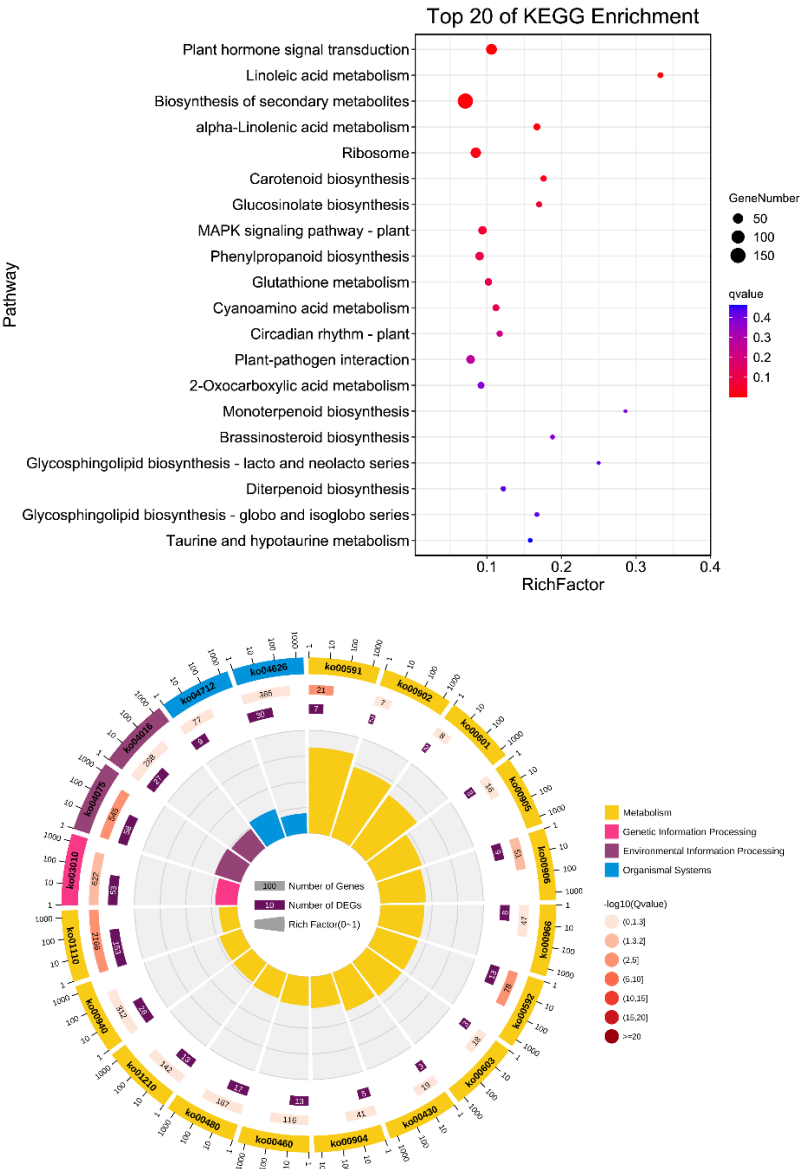


Figure S9. Top 20 KEGG pathways enrichment of 2047 DEGs.

[Figure S10]

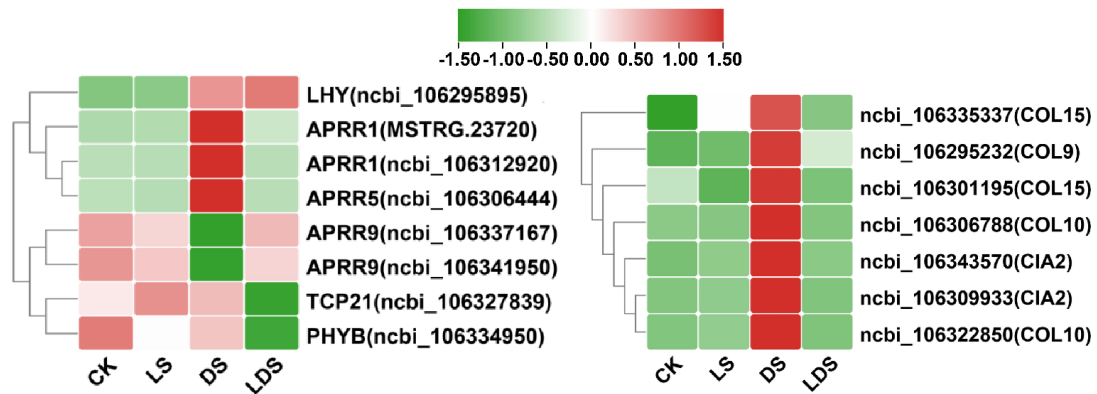


Figure S10. Expression of DEGs related to circadian rhythm – plant pathway.

[Figure S11]

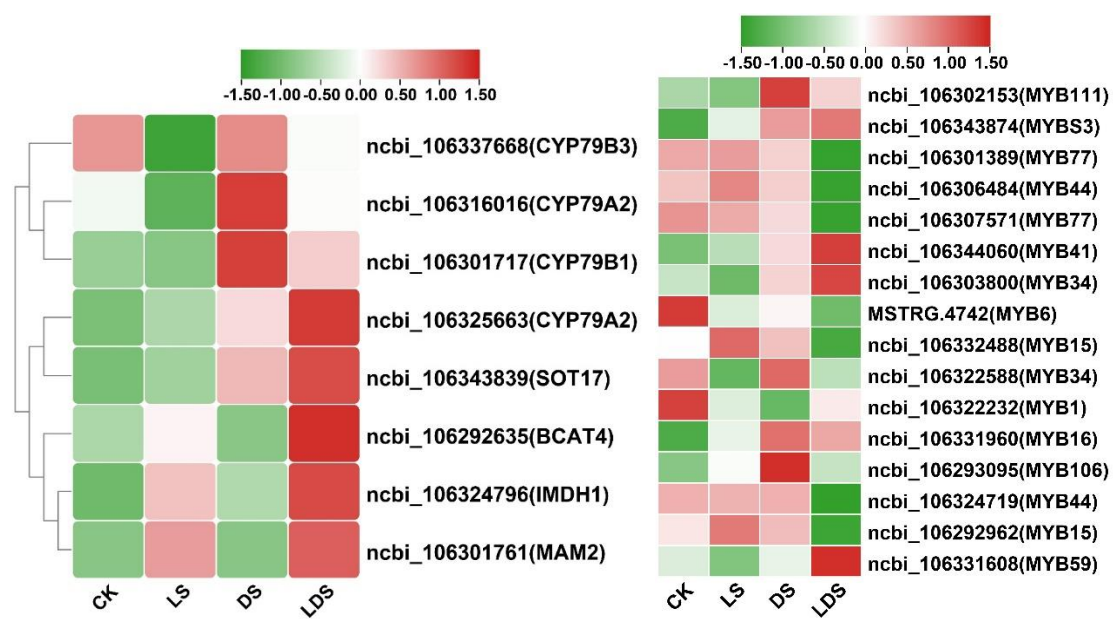


Figure S11. Expression of DEGs related to Glucosinolate biosynthesis pathway and MYB family

[Figure S12]

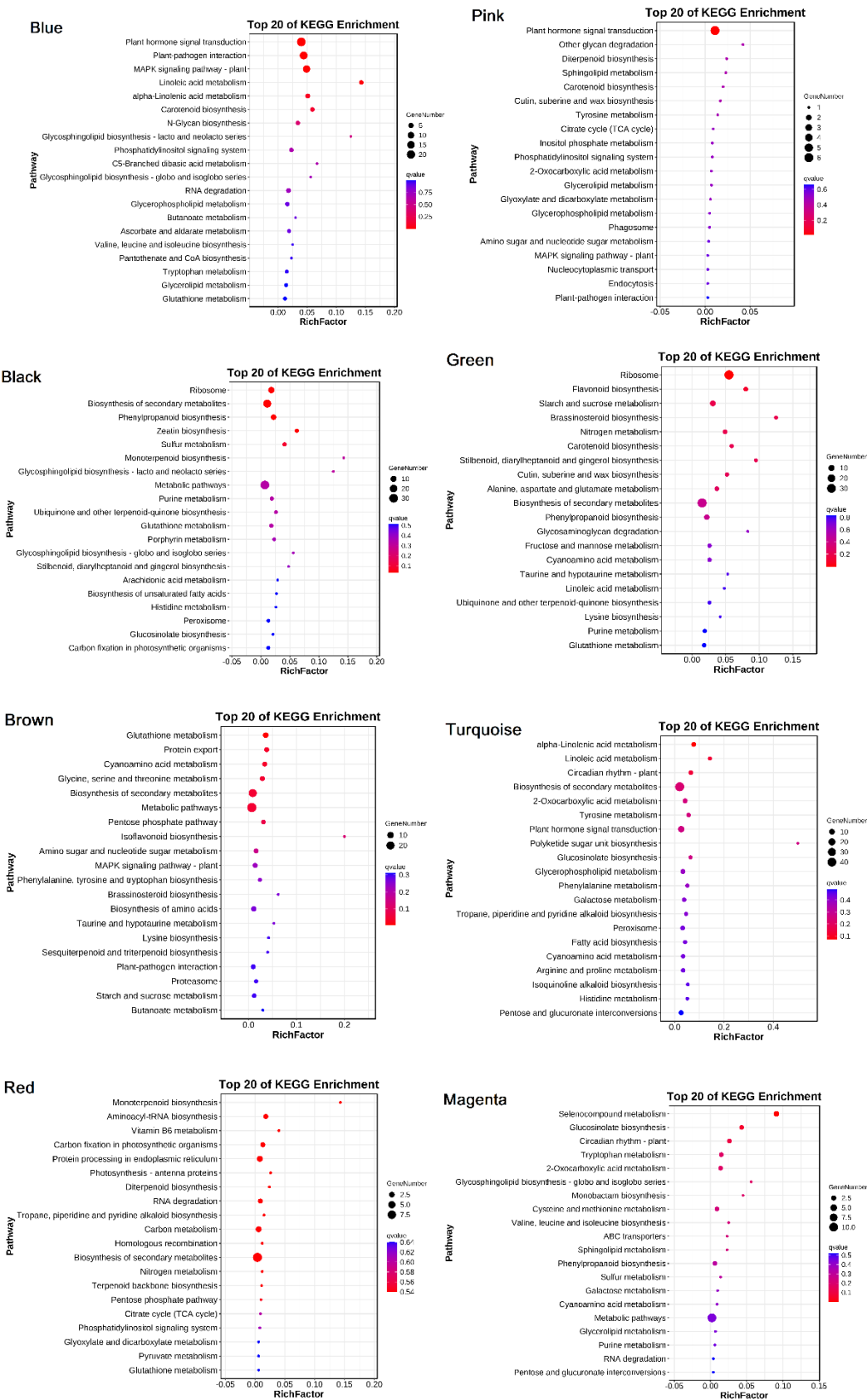


Figure S12. Top 20 KEGG enrichment pathways of 8 modules

[Figure S13]

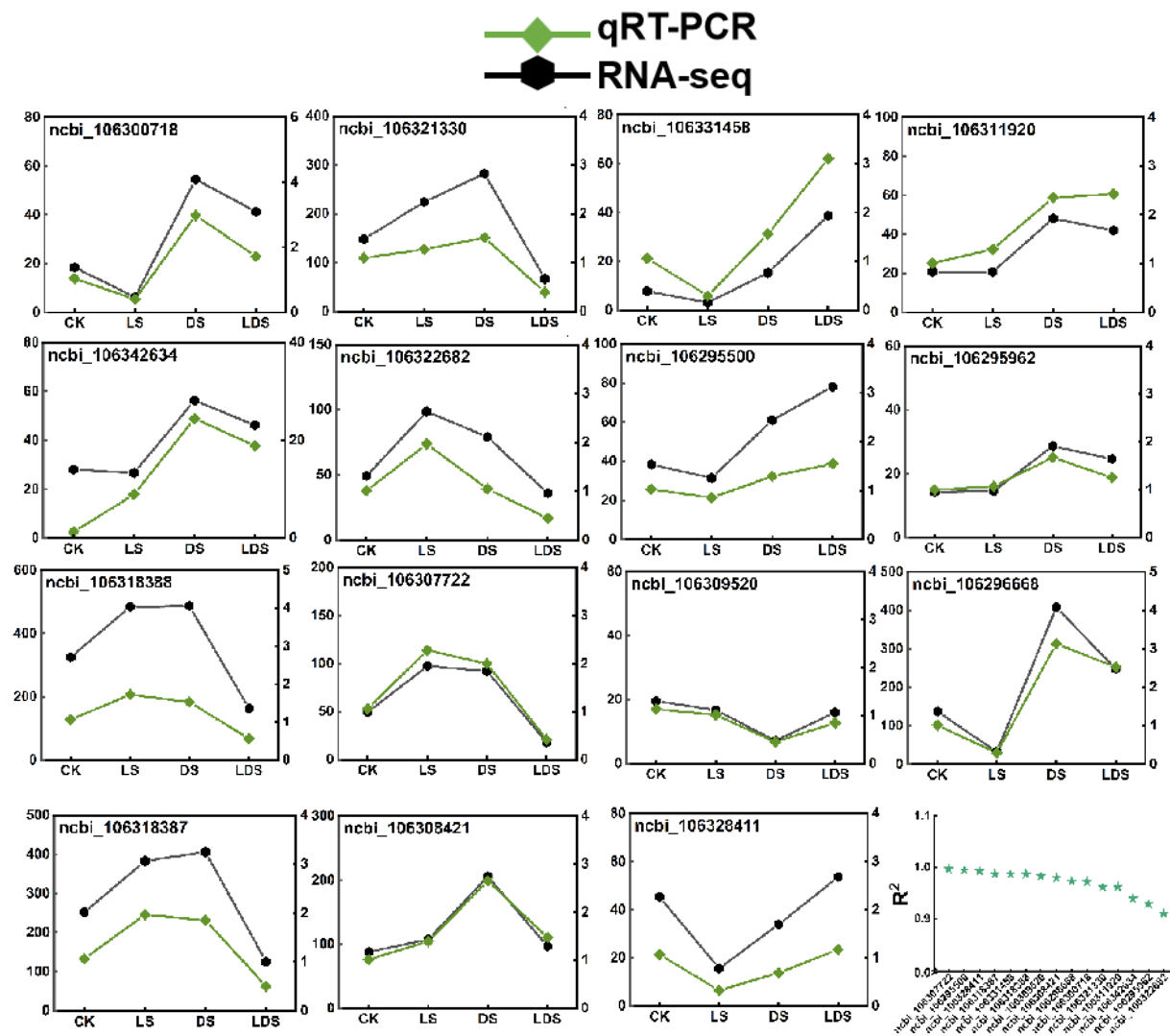


Figure S13. Correlation coefficients between the qRT-PCR and RNA-seq results.

[Figure S14]

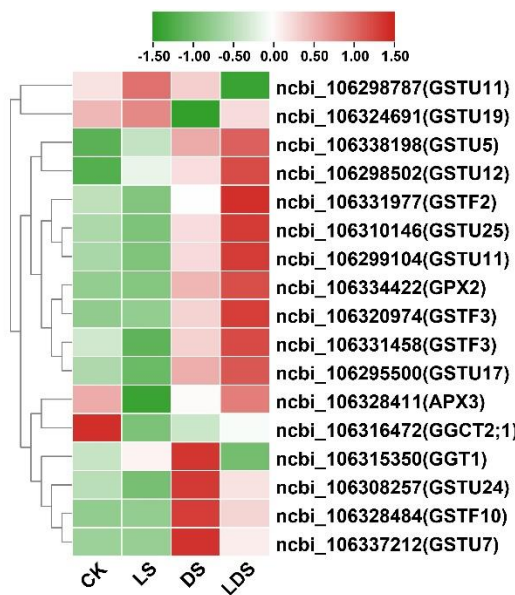


Figure S14. Expression of DEGs related to Glutathione pathway

[Figure 1]

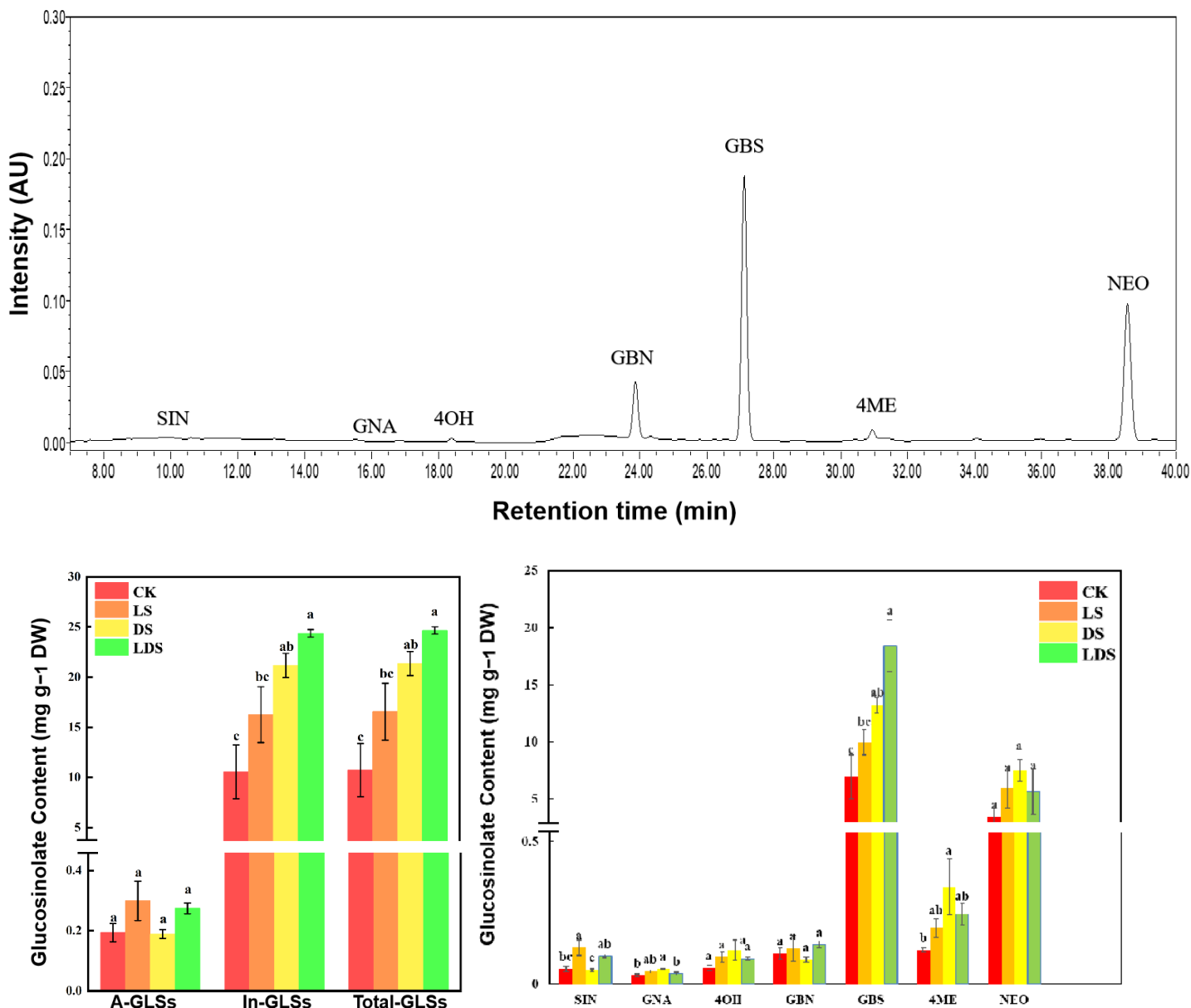


Figure 1. Glucosinolate content of kale under different UV-A treatments. Different lowercase letters reveal significant differences ($p < 0.05$), according to Duncan's test. Vertical bars indicate the standard margin of error. "LS" = Light-UVA Supplementation, "DS" = Dark-UVA Supplementation, "LDS" = Light/Dark-UVA Supplementation. SIN = sinigrin, GNA = gluconapin, 4OH = 4-hydroxyglucobrassicin, GBS = glucobrassicin, GBN = glucobrassicinapin, NEO = neoglucobrassicin, 4ME = 4-methoxyglucobrassicin, In-GLSs = Indolic Glucosinolate, A-GLSs = Aliphatic Glucosinolates..

[Figure 2]

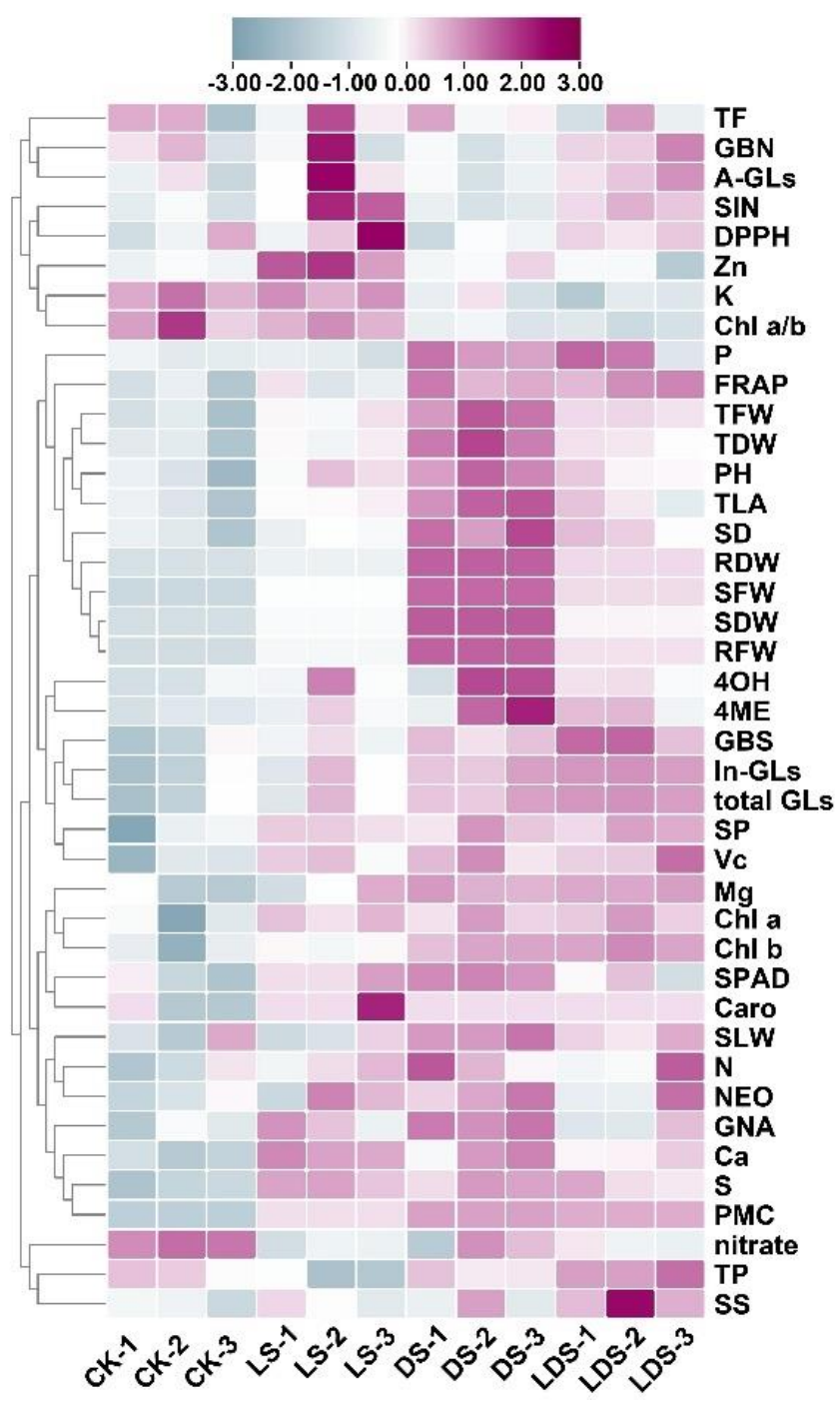


Figure 2. Cluster heatmap analysis summarizing the morphology and quality of kale in supplemental UV-A light treatments and CK. A false-color scale with purple as an increased parameter while blue represents a decreased parameter was used to visualize the results. “LS” = Light-UVA Supplementation, “DS” = Dark-UVA Supplementation, “LDS” = Light/Dark-UVA Supplementation, “PMC” = plant moisture content, “SAW” = specific area weight, “PH” = plant height, “TFW” = total fresh weight, “RDW” = root dry weight, “SD” = stem diameter, “SFW” = shoot fresh weight, “RFW” = root fresh weight, “SDW” = shoot dry weight, “RFW” = root fresh weight, “TDW” = total dry weight, “TLA” = total leaf area, “TP” = total phenolic, “SS” = Soluble sugar, “TF” = total flavonoids, “SP” = soluble protein, “Vc” = Vitamin C, the full name of all GLS variants has been described in Figure 1.

[Figure 3]

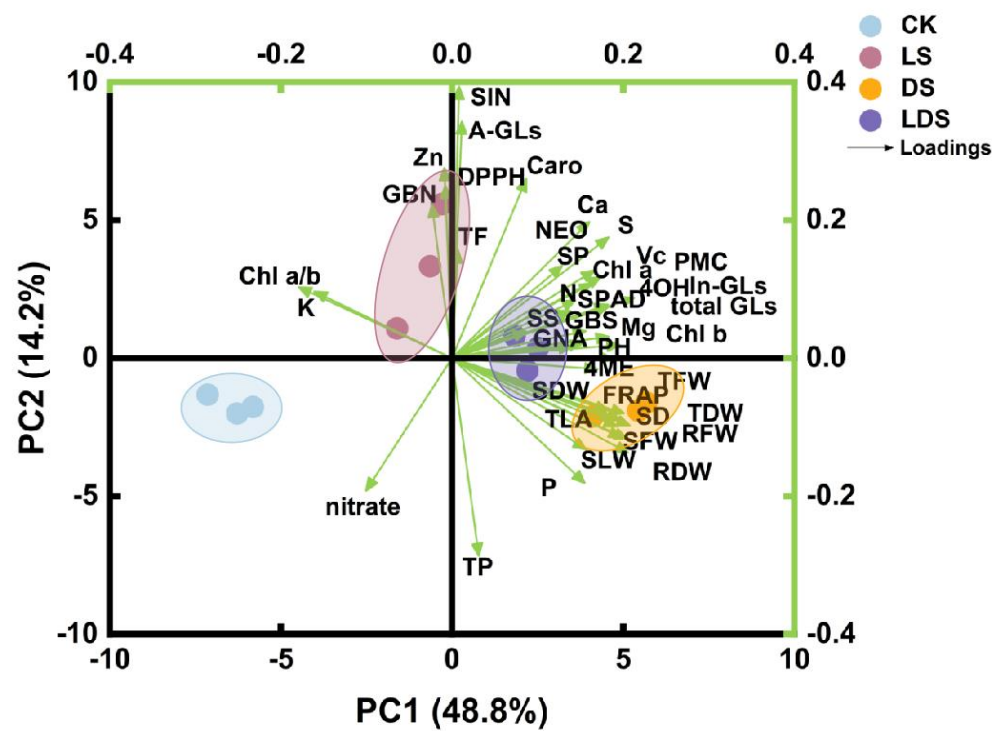


Figure 3. Multivariate principal component analysis presented the relationship between indexes among 4 treatments. The full name has been described in Figure 2. “LS” = Light-UVA Supplementation, “DS” = Dark-UVA Supplementation, “LDS” = Light/Dark-UVA Supplementation

[Figure 4]

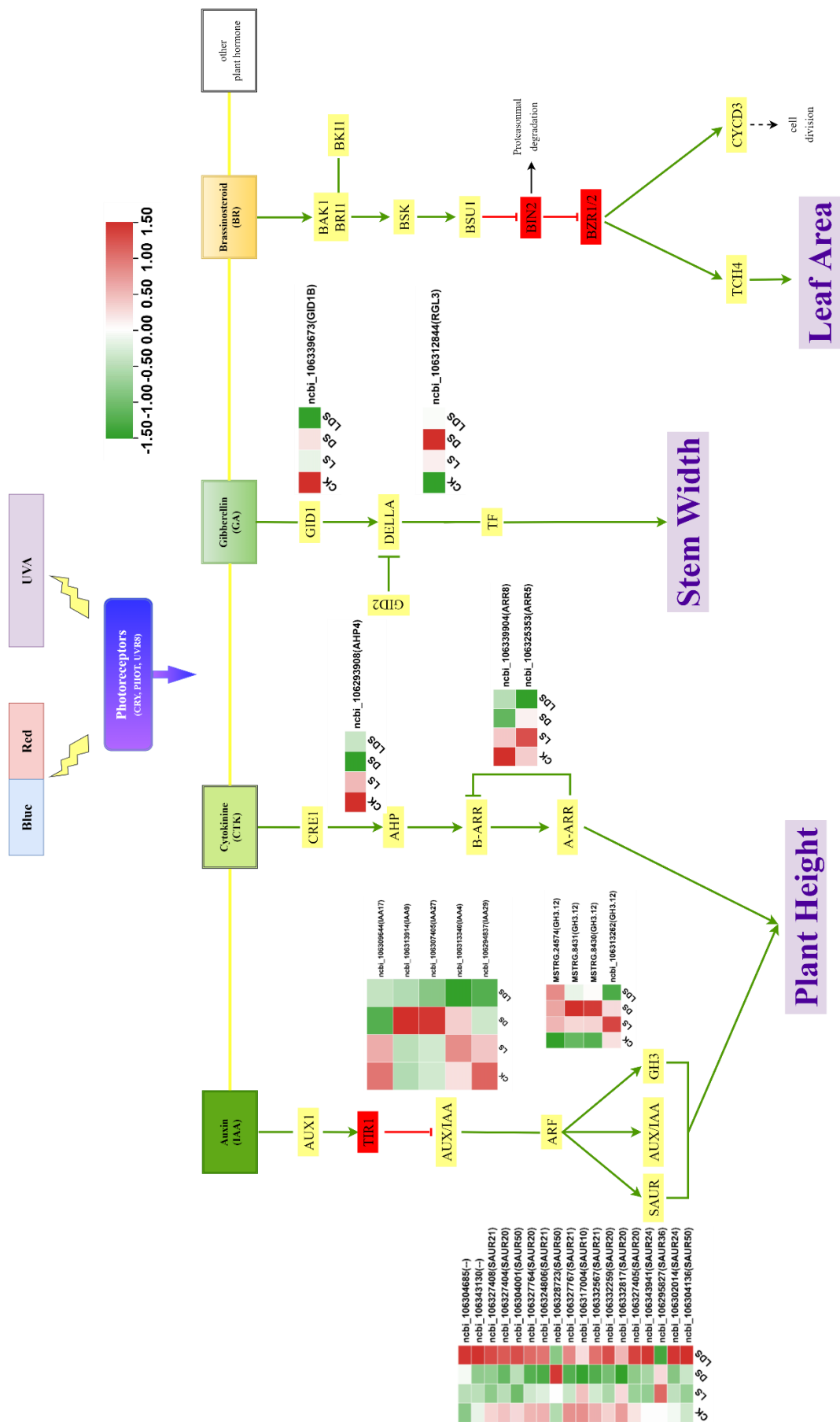


Figure 4. Expression of DEGs on plant hormone signal transduction pathway. Made by diagrams.net. “LS” = Light-UVA Supplementation, “DS” = Dark-UVA Supplementation, “LDS” = Light/Dark-UVA Supplementation

[Figure 5]

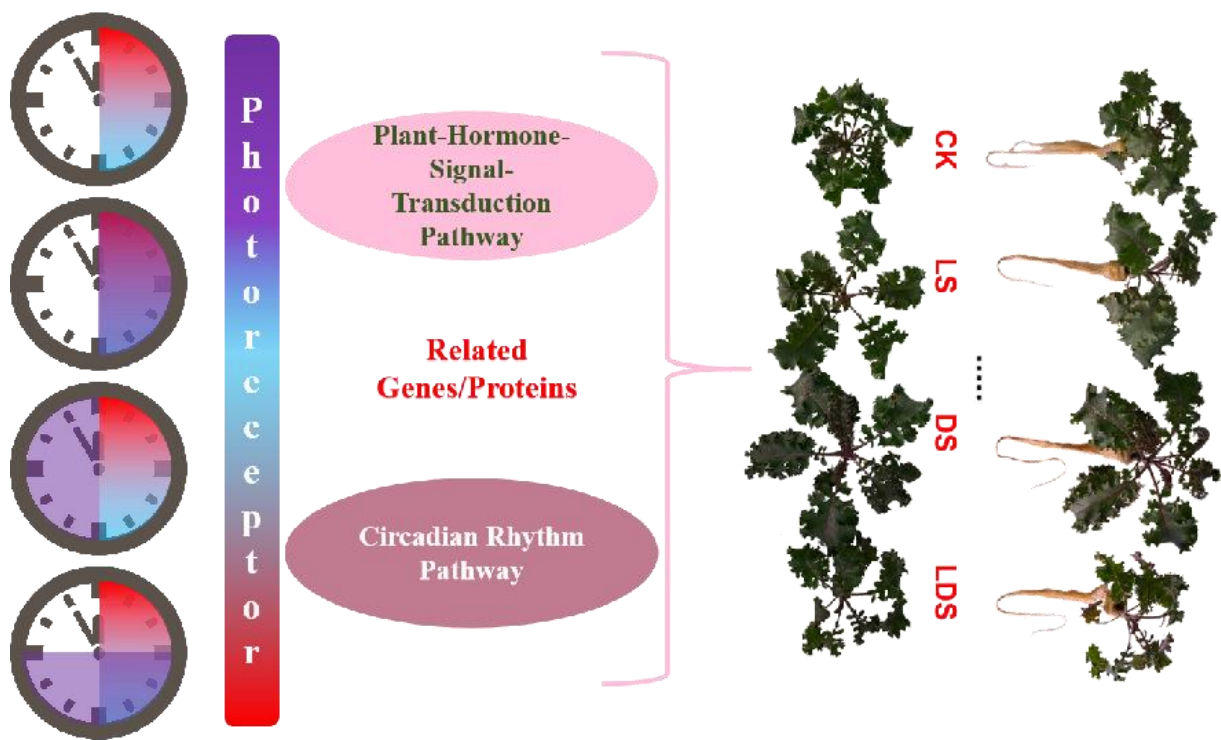


Figure 5. Key regulatory pathways/genes responded to different UV-A supplementation of kale. “LS” = Light-UVA Supplementation, “DS” = Dark-UVA Supplementation, “LDS” = Light/Dark-UVA Supplementation

[Figure 6]

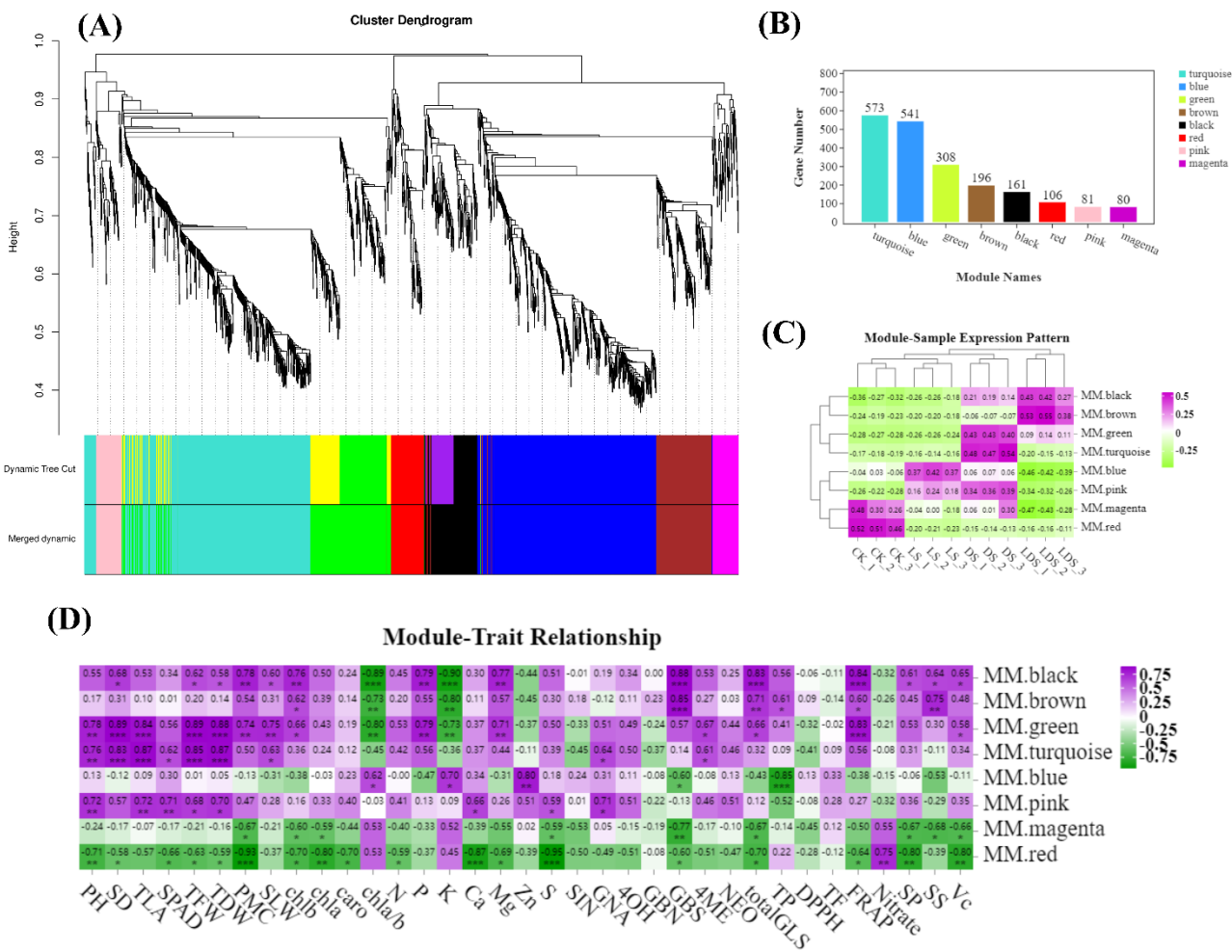


Figure 6. WGCNA of 2047 DEGs. (A) Cluster dendrogram indicating 8 modules of co-expressed genes by WGCNA. (B) Gene numbers of different modules. (C) Module-Sample expression patterns. (D) Module-trait correlations. p values were shown as: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. The full name of the traits has been described in Figure 2. The color scale shows correlations from positive (purple) to negative (green). “LS” = Light-UVA Supplementation, “DS” = Dark-UVA Supplementation, “LDS” = Light/Dark-UVA Supplementation