

Heatmap showing the correlation of gene expression between 12 samples. The samples are grouped into three clusters: Ctrl (ctrl_1 to ctrl_6), Dark (dark_1 to dark_6), and Arahy (Arahy.HS5Z9Z to Arahy.T2CQE4). The color scale ranges from -2.50 (blue) to 2.00 (red).

Sample	ctrl_1	ctrl_2	ctrl_3	ctrl_4	ctrl_5	ctrl_6	dark_1	dark_2	dark_3	dark_4	dark_5	dark_6
Arahy.HS5Z9Z	0.5	0.5	1.5	2.0	0.5	0.5	0.5	0.5	0.5	1.5	0.5	1.5
Arahy.NNA8KD	0.0	0.0	1.0	1.0	1.0	0.0	1.5	1.0	2.0	0.0	1.0	1.0
Arahy.D04KR2	0.0	0.5	1.5	0.0	0.0	0.0	0.5	0.5	0.5	1.5	0.5	0.5
Arahy.7E2TSQ	0.5	0.5	0.5	0.5	0.0	0.0	1.5	0.5	0.5	1.5	1.5	0.0
Arahy.PM8GQZ	0.0	0.5	0.5	0.5	2.0	0.0	0.5	0.5	0.5	1.5	1.5	0.5
Arahy.F3Y113	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Arahy.A3SZXW	0.5	0.5	1.5	1.5	2.0	0.5	0.5	0.5	1.5	1.5	1.5	0.5
Arahy.T2CQE4	0.0	0.5	1.5	1.5	2.0	0.5	0.5	0.5	1.5	1.5	1.5	0.5

(A)

Aradu.T66QJ
Arahy.A3SZXW
Arahy.T2CQF4
AtPHYB
AtPHYD
AtPHYE
Arahy.F3Y113
Aradu.H9LWJ
Arahy.PM8GQZ
AtPHYC
AtPHYA
Arahy.D04KR2
Aradu.E3ZED
Arahy.7E2TSQ
Aradu.G6IAK
Arahy.NNA8KD
Arahy.HS5Z9Z

(B)

Aradu.G6IAK
Aradu.E3ZED
Aradu.H9LWJ
Aradu.T66QJ

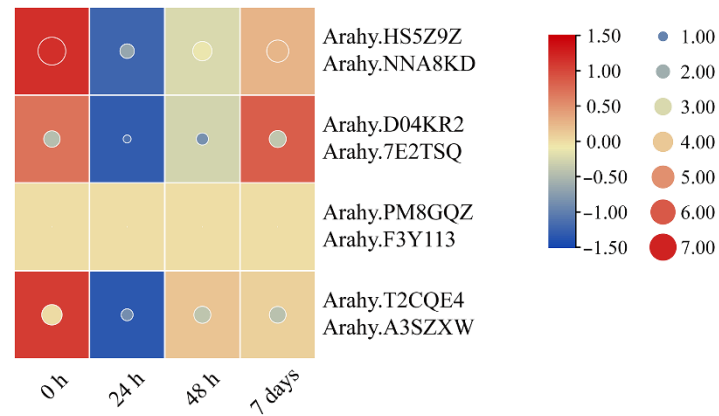
ctrl drought

(C)

Aradu.G6IAK
Aradu.E3ZED
Aradu.H9LWJ
Aradu.T66QJ

ctrl_1 ctrl_2 3day_1 3day_2 6day_1 6day_2 9day_1 9day_2

Supplementary Figure S2. Expression profiling of *PHY* genes in wild peanut under abiotic stress. **(A)** Phylogenetic analysis of *PHY* genes from *Arachis duranensis* (AA) *Arachis hypogaea* (AABB) and *Arabidopsis thaliana*. **(B)** Expression profiling of *PHY* genes under drought treatment. **(C)** Expression profiling of *PHY* genes under nematode infection. Transcriptome data for *Arachis duranensis* under drought and nematode treatment were obtained from Peanutbase. The square color scale of heatmap indicates FPKM values following row normalization, with maximal and minimal expression denoted by red and blue, respectively. The circular color scale indicates raw FPKM values, where the area subtended by each circle is directly proportional to the expression level.



Supplementary Figure S3. Expression profiling of *PHY* genes in cultivated peanut under drought treatment. Young peanut seedlings were treated with 15% PEG6000 solution for 24h, 48h and 7days. The square color scale of heatmap indicates RPKM values following row normalization, with maximal and minimal expression denoted by red and blue, respectively. The circular color scale indicates raw RPKM values, where the area subtended by each circle is directly proportional to the expression level.