

Table S1. Primers used for qRT-PCR validation

Gene_ID	Forward primer (5'-3')	Reverse primer (5'-3')
Glyma.03G219000	CTAGATTGCAGGGATGCCAAG	TCCCACCATTGTTTCTGAGCATA
Glyma.13G267800	TTACTGCGTCGAGTTTGCCA	ACGATGATTGTGCAGGACGA
Glyma.09G238300	GGCACTCTTTGCCATTTCCA	TCCTCGAGCATTGTGATGGG
Glyma.18G035000	ACTGGACACAAGGTGACGAA	TCACGCCGAACTTGGGAGAT
Glyma.12G183400	AGGACCATTTTAATTGTTGGAGCC	AGCTGATTTGGCATCCGAAG
Glyma.11G222600	GCCAAAGTGGAATCCACGAC	CCATGTCTCTTCTCCTGCCG
Glyma.18G061100	CACCAAGAAACATGCCGCAA	GCCCATTCTCAATTCGCCC
Tubulin	GGAGTTCACAGAGGCAGAG	CACTTACGCATCACATAGCA

Table S2. The quality and concentration measurements of RNA sample

Number	Hpi	Sample number	Repeat	RIN	Concentration (ng/μL)
1	0h	NN-0h-1	1	7.3	615
2	0h	NN-0h-2	2	7.2	633
3	0h	NN-0h-3	3	7.3	669
4	0h	KF-0h-1	1	6.9	1038
5	0h	KF-0h-2	2	7.1	346
6	0h	KF-0h-3	3	6.5	209
7	6h	NN-6h-1	1	6.4	639
8	6h	NN-6h-2	2	6.2	981
9	6h	NN-6h-3	3	6.3	1065
10	6h	KF-6h-1	1	6.7	948
11	6h	KF-6h-2	2	6.8	1002
12	6h	KF-6h-3	3	6.4	735
13	48h	NN-48h-1	1	6.7	1089
14	48h	NN-48h-2	2	7.3	603
15	48h	NN-48h-3	3	7.3	615
16	48h	KF-48h-1	1	7.7	488
17	48h	KF-48h-2	2	7.7	669
18	48h	KF-48h-3	3	7.6	488
19	5d	NN-5d-1	1	6.6	440
20	5d	NN-5d-2	2	6.7	450
21	5d	NN-5d-3	3	7.4	428
22	5d	KF-5d-1	1	7.1	388
23	5d	KF-5d-2	2	7.3	434
24	5d	KF-5d-3	3	7.1	394

Table S3. Filtering and quality testing of raw data

sample	RawDates	CleanDates(%)	CleanReads	AF-N (%)	AF-Q20 (%)	AF-Q30 (%)	AF-GC (%)
N-0h-1	38316550	38203520(99.71%)	38203520	0.00%	97.92%	93.84%	44.62%
N-0h-2	37389334	37262492(99.66%)	37262492	0.00%	97.69%	93.34%	44.77%
N-0h-3	39840346	39719024(99.70%)	39719024	0.00%	97.79%	93.56%	44.60%
K-0h-1	38429302	38317066(99.71%)	38317066	0.00%	97.80%	93.56%	44.37%
K-0h-2	38871420	38758548(99.71%)	38758548	0.00%	97.90%	93.76%	44.41%
K-0h-3	50947114	50782582(99.68%)	50782582	0.00%	97.97%	93.91%	44.25%
N-6h-1	52702614	52528690(99.67%)	52528690	0.00%	97.80%	93.54%	44.83%
N-6h-2	37122540	36979958(99.62%)	36979958	0.00%	97.74%	93.42%	43.95%
N-6h-3	36221774	36076218(99.60%)	36076218	0.00%	97.25%	92.37%	44.12%
K-6h-1	47652768	47497958(99.68%)	47497958	0.00%	97.70%	93.19%	44.06%
K-6h-2	41321860	41186074(99.67%)	41186074	0.00%	97.90%	93.71%	43.94%
K-6h-3	36336686	36209812(99.65%)	36209812	0.00%	97.72%	93.31%	44.12%
N-48h-1	45270514	45138286(99.71%)	45138286	0.00%	97.98%	93.92%	44.07%
N-48h-2	41960744	41837188(99.71%)	41837188	0.00%	97.95%	93.83%	43.93%
N-48h-3	43879010	43760292(99.73%)	43760292	0.00%	97.97%	93.86%	44.23%
K-48h-1	46262956	46102148(99.65%)	46102148	0.00%	97.87%	93.67%	44.62%
K-48h-2	40720914	40573796(99.64%)	40573796	0.00%	97.25%	92.32%	44.77%
K-48h-3	45122878	44982208(99.69%)	44982208	0.00%	97.71%	93.36%	44.70%
N-5d-1	46440676	46286008(99.67%)	46286008	0.00%	97.82%	93.57%	44.08%
N-5d-2	41224732	41092568(99.68%)	41092568	0.00%	97.69%	93.31%	44.15%
N-5d-3	43119928	42987632(99.69%)	42987632	0.00%	97.87%	93.71%	44.15%
K-5d-1	50233860	50082364(99.70%)	50082364	0.00%	97.82%	93.59%	44.32%
K-5d-2	44085528	43952372(99.70%)	43952372	0.00%	97.77%	93.45%	44.00%
K-5d-3	48974382	48824674(99.69%)	48824674	0.00%	97.85%	93.61%	44.14%

Tables S4. Statistics of RNA-Seq map

Sample	Clean_Reads	Total_Mapped	Multiple_Mapped	Uniquely_Mapped
N-0h-1	38203520	36192502(95.35%)	1688525(4.45%)	34503977(90.90%)
N-0h-2	37262492	35181039(94.88%)	1586732(4.28%)	33594307(90.60%)
N-0h-3	39719024	36989707(93.73%)	1736765(4.40%)	35252942(89.33%)
K-0h-1	38317066	35607895(93.39%)	1817255(4.77%)	33790640(88.62%)
K-0h-2	38758548	36685819(95.10%)	1861236(4.82%)	34824583(90.28%)
K-0h-3	50782582	47808806(94.69%)	2417617(4.79%)	45391189(89.90%)
N-6h-1	52528690	48760437(95.19%)	2789599(5.45%)	45970878(89.75%)
N-6h-2	36979958	34876231(95.17%)	1609790(4.39%)	33266441(90.77%)
N-6h-3	36076218	34232308(95.58%)	1556419(4.35%)	32675858(92.60%)
K-6h-1	47497958	45397359(96.10%)	2148356(4.55%)	43249003(91.55%)
K-6h-2	41186074	39600001(96.72%)	1710267(4.18%)	37889734(92.54%)
K-6h-3	36209812	34419177(95.87%)	1544653(4.30%)	32874524(91.56%)
N-48h-1	45138286	43039495(96.55%)	1807590(4.05%)	41231905(92.49%)
N-48h-2	41837188	40387971(97.05%)	1661573(3.99%)	38726398(93.06%)
N-48h-3	43760292	42293820(97.10%)	1692433(3.89%)	40601387(93.22%)
K-48h-1	46102148	44608553(96.98%)	1578563(3.43%)	43029990(93.55%)
K-48h-2	40573796	39071783(96.54%)	1404365(3.47%)	37667418(93.07%)
K-48h-3	44982208	43348990(96.71%)	1636656(3.65%)	41712334(93.06%)
N-5d-1	46286008	44301782(95.96%)	1338265(2.90%)	42963517(93.07%)
N-5d-2	41092568	39384574(96.09%)	1091398(2.66%)	38293176(93.42%)
N-5d-3	42987632	41032401(95.70%)	1132225(2.64%)	39900176(93.06%)
K-5d-1	50082364	48123969(96.37%)	1468040(2.94%)	46655929(93.43%)
K-5d-2	43952372	42067168(96.14%)	1293181(2.96%)	40773987(93.18%)
K-5d-3	48824674	46509905(95.16%)	1526710(3.14%)	44983195(92.47%)

Table S5. Comparison of regional statistics

sample	Exon (%)	Intron (%)	Intergenic (%)
N-0h-1	33800232(93.39%)	1619608(4.47%)	772662(2.13%)
N-0h-2	32927610(93.59%)	1540904(4.38%)	712525(2.03%)
N-0h-3	34564181(93.44%)	1600245(4.33%)	825281(2.23%)
K-0h-1	33320175(93.58%)	1560920(4.38%)	726800(2.04%)
K-0h-2	34327145(93.57%)	1678575(4.58%)	680199(1.85%)
K-0h-3	44696720(93.49%)	2188078(4.58%)	924008(1.93%)
N-6h-1	45046813(92.38%)	2300996(4.72%)	1412628(2.90%)
N-6h-2	32190829(92.30%)	1925311(5.52%)	760091(2.18%)
N-6h-3	31764263(92.79%)	1796985(5.25%)	671060(1.96%)
K-6h-1	42144693(92.84%)	2456920(5.41%)	795746(1.75%)
K-6h-2	36660504(92.58%)	2231523(5.64%)	707974(1.79%)
K-6h-3	31853472(92.55%)	1886689(5.48%)	679016(1.97%)
N-48h-1	39325921(91.37%)	2819083(6.55%)	894491(2.08%)
N-48h-2	36939425(91.46%)	2684301(6.65%)	764245(1.89%)
N-48h-3	38771504(91.67%)	2757887(6.52%)	764429(1.81%)
K-48h-1	41021592(91.96%)	2861983(6.42%)	724918(1.63%)
K-48h-2	36031145(92.22%)	2421721(6.20%)	618917(1.58%)
K-48h-3	39980804(92.23%)	2681519(6.19%)	686667(1.58%)
N-5d-1	4035203(91.08%)	3163120(7.14%)	788459(1.78%)
N-5d-2	35991346(91.38%)	2732169(6.94%)	661059(1.68%)
N-5d-3	37444850(91.26%)	2859885(6.97%)	727666(1.77%)
K-5d-1	44124107(91.69%)	3182650(6.61%)	817212(1.70%)
K-5d-2	38318240(91.09%)	2932403(6.97%)	816525(1.94%)
K-5d-3	42427428(91.22%)	3246867(6.98%)	835610(1.80%)

Table S6. Function of candidate genes

Gene ID	Pathway	Description	GO Fuction
<i>Glyma.03G219000</i>	Plant hormone signal transduction; MAPK signaling pathway – plant	protein phosphatase 2C 37	catalytic activity; protein serine; threonine phosphatase activity
<i>Glyma.09g238300</i>	Unknown	gibberellin-regulated protein 4-like [Arachis ipaensis]	Unknown
<i>Glyma.11G222600</i>	Plant hormone signal transduction; MAPK signaling pathway – plant	protein phosphatase 2C 37	catalytic activity/protein serine; threonine phosphatase activity
<i>Glyma.12G183400</i>	Peroxisome; Cutin, suberine and wax biosynthesis	fatty acyl-CoA reductase 3 [Glycine max]	fatty-acyl-CoA reductase (alcohol-forming) activity
<i>Glyma.13G267800</i>	Folate biosynthesis	gamma-glutamyl hydrolase isoform X1 [Glycine max]	catalytic activity; omega peptidase activity
<i>Glyma.18G035000</i>	Plant hormone signal transduction; MAPK signaling pathway – plant	protein phosphatase 2C 37	catalytic activity; protein serine/threonine phosphatase activity
<i>Glyma.18G061100</i>	Metabolic; Biosynthesis of secondary metabolites; Alanine, aspartate and glutamate metabolism	asparagine synthetase 1	asparagine synthase (glutamine-hydrolyzing) activity