

Table S1 List of primers sequences of the selected genes for RT-qPCR

Gene	Gene ID	Nucleotide sequences for primers	Product size (bp)
TGA	c42668_g1_i1	CAGCCAAAGCAATCAAGCGT TCAACCTGCTTTTCCTCGCT	138
SAUR	c12931_g1_i1	CTCTCCGCACTTTCCCTCAC ACTGCCTCAACATCTGTCGG	111
SAUR	c58902_g1_i1	TCCATGACCCGCTCGAAAA ATGGAGCGGTTTCGTCGTAAG	147
PR1	c42413_g1_i1	GCGGCACCTTTGTTATCTGC CAATCATCACCTCACGCACG	114
KAO	c27636_g1_i1	GGGTATCCCGTTGCCATGAA TTCATGGCTGGTGGTTGGAG	117
KAO	c15090_g1_i1	CTCCTGGTGATATGGGCTGG AAATCGCTCGTCGTCCATCA	109
GA3ox-2	c10824_g1_i1	GTCAGCGGCCTCCAGATTTT TAATATGCGTCGGAGGGCTG	202
GA3ox-2	c49690_g1_i1	GGTCTTACCCGAGTGTGCTC TGTGCCAAGATACTCGCTCC	176
SQLE	c26224_g1_i1	TGAGACGCAACCTCTGCAAT ACCAAACAGCGAATCTCGGA	166
MVD	c28767_g2_i1	TCGTGCCTGTGATGTTGAGG AGCAGCAGAGGAAGCCAATC	130

Table S2 Number of differentially expression genes (DEGs) in GO pathways

GO Slim	Category	Description	DEGs	p-value
GO:0008150	Biological Process	biological_process	76	0.07373607
GO:0009653	Biological Process	anatomical structure morphogenesis	36	0.5275879
GO:0016043	Biological Process	cellular component organization	109	0.6072271
GO:0009987	Biological Process	cellular process	541	0.8646903
GO:0016265	Biological Process	death	13	0.1086476
GO:0009790	Biological Process	embryo development	3	0.9994034
GO:0040007	Biological Process	growth	10	0.9955565
GO:0008152	Biological Process	metabolic process	772	5.37E-06
GO:0007275	Biological Process	multicellular organismal development	64	0.9574919
GO:0009791	Biological Process	post-embryonic development	41	0.7425556
GO:0040029	Biological Process	regulation of gene expression, epigenetic	6	0.9946273
GO:0000003	Biological Process	reproduction	27	0.9999384
GO:0009628	Biological Process	response to abiotic stimulus	62	0.07916062
GO:0009607	Biological Process	response to biotic stimulus	36	0.006537785
GO:0009719	Biological Process	response to endogenous stimulus	31	0.3881356
GO:0009605	Biological Process	response to external stimulus	48	0.006930599
GO:0006950	Biological Process	response to stress	111	0.0132773
GO:0003700	Biological Process	sequence-specific DNA binding transcription factor activity	13	0.7734611
GO:0006810	Biological Process	transport	141	0.2919744
GO:0005575	Cellular Component	cellular_component	25	0.4133736
GO:0005623	Cellular Component	cell	413	0.3359327
GO:0005737	Cellular Component	cytoplasm	302	0.05007433
GO:0005856	Cellular Component	cytoskeleton	8	0.9851101
GO:0005829	Cellular Component	cytosol	26	0.9986052
GO:0005783	Cellular Component	endoplasmic reticulum	13	0.9704135
GO:0005768	Cellular Component	endosome	2	0.9991664
GO:0030312	Cellular Component	external encapsulating structure	31	8.08E-06
GO:0005576	Cellular Component	extracellular region	82	7.98E-24
GO:0005615	Cellular Component	extracellular space	1	0.3264089
GO:0005794	Cellular Component	Golgi apparatus	10	0.9921006
GO:0005622	Cellular Component	intracellular	368	0.605164
GO:0016020	Cellular Component	membrane	261	0.003589111
GO:0005739	Cellular Component	mitochondrion	20	0.9999995
GO:0005654	Cellular Component	nucleoplasm	1	0.9974909

---

GO:0005634	Cellular Component	nucleus	40	1
GO:0005777	Cellular Component	peroxisome	9	0.3181969
GO:0009536	Cellular Component	plastid	205	5.29E-29
GO:0005840	Cellular Component	ribosome	24	0.8736675
GO:0009579	Cellular Component	thylakoid	113	3.81E-54
GO:0005773	Cellular Component	vacuole	39	0.9992188
GO:0003674	Molecular Function	molecular_function	37	4.83E-12
GO:0005488	Molecular Function	binding	458	0.4993076
GO:0004872	Molecular Function	receptor activity	6	0.360004
GO:0005198	Molecular Function	structural molecule activity	24	0.8542385

---

Table S3 The number of differentially expression genes (DEGs) in KEGG pathways

Category	Pathway	DEG
Metabolism	Overview	22
Metabolism	Carbohydrate metabolism	54
Metabolism	Energy metabolism	62
Metabolism	Lipid metabolism	30
Metabolism	Nucleotide metabolism	4
Metabolism	Amino acid metabolism	42
Metabolism	Metabolism of other amino acids	15
Metabolism	Glycan biosynthesis and metabolism	1
Metabolism	Metabolism of cofactors and vitamins	14
Metabolism	Metabolism of terpenoids and polyketides	18
Metabolism	Biosynthesis of other secondary metabolites	29
Metabolism	Xenobiotics biodegradation and metabolism	20
Genetic Information Processing	Transcription	1
Genetic Information Processing	Translation	6
Genetic Information Processing	Folding, sorting and degradation	10
Environmental Information Processing	Membrane transport	5
Environmental Information Processing	Signal transduction	24
Cellular Processes	Transport and catabolism	4
Cellular Processes	Cell growth and death	12
Cellular Processes	Cell communication	1
Organismal Systems	Immune system	4
Organismal Systems	Endocrine system	14
Organismal Systems	Circulatory system	1
Organismal Systems	Digestive system	4
Organismal Systems	Excretory system	1
Organismal Systems	Nervous system	6
Organismal Systems	Development	3
Organismal Systems	Environmental adaptation	12

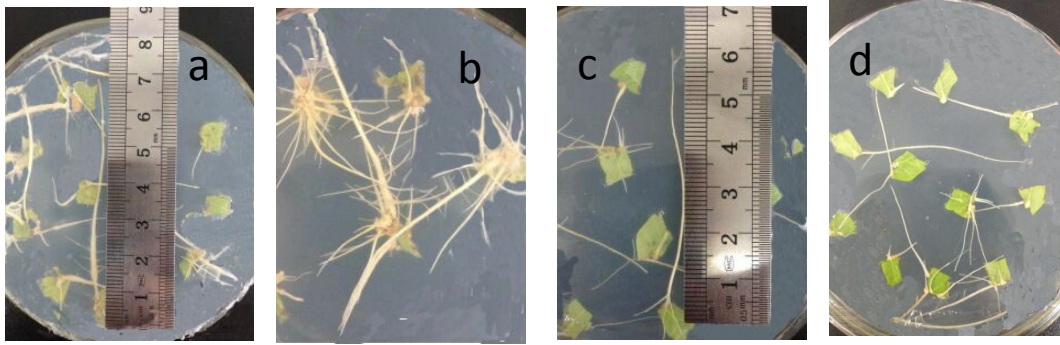


Figure S1. The figures of ARs were induced from young leaves of neem on MS medium supplement with different concentrations of IBA. The figure a and b were supplement with  $0.5 \text{ mg L}^{-1}$  IBA, and the figure c and d were supplement with  $1.5 \text{ mg L}^{-1}$  IBA.

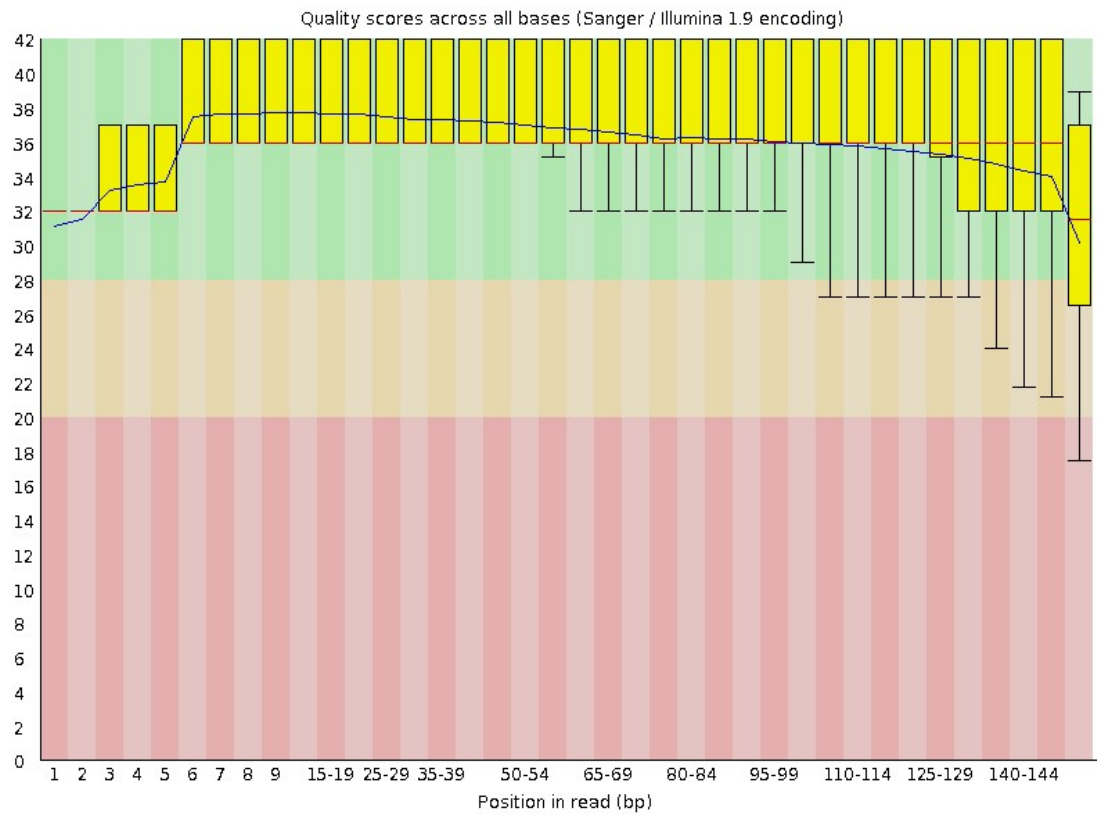


Figure S2. **Quality scores across all bases.** The X axis represents the position of bases in reads (5'-3'), while the Y axis represents the quality (Q) value of bases. Generally speaking, the quality of bases is better than the both ends.

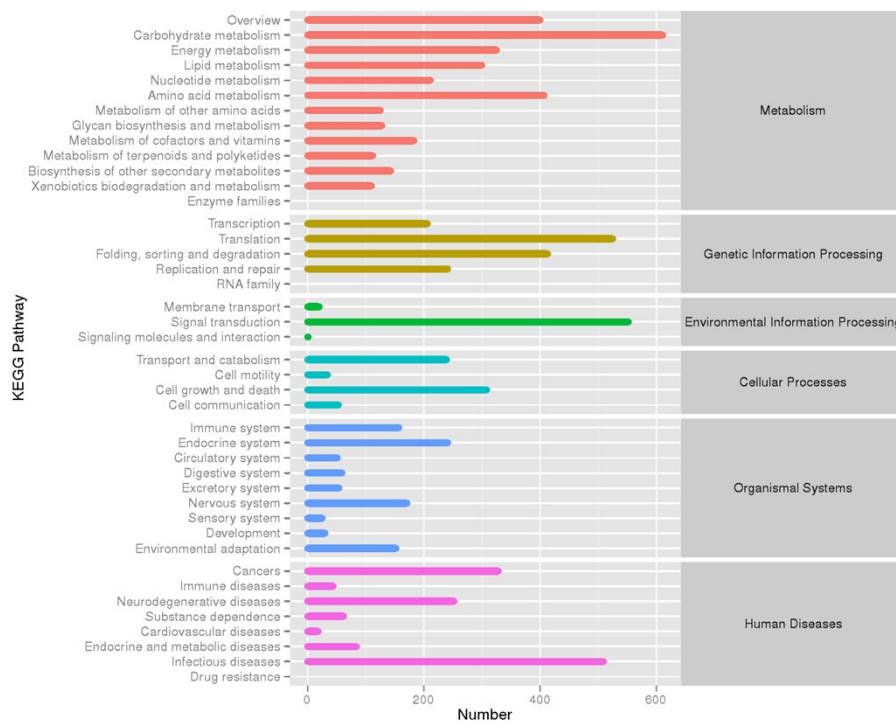


Figure S3. **KEGG pathway assignments.** Among NR unigene sequences, 5,380 transcripts were assigned to KEGG pathways by KASS analysis.