Supplementary Information

Molecular mechanisms of tannin accumulation in Rhus galls and genes involved in plant-insect interactions

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Figure S1. Utilization of tannic acid derived from gallnut of *R. chinensis*. A. Medicine (synergist); B. Leatherworking; C. Textile printing; D. Mineral separation; E. Oil exploration.

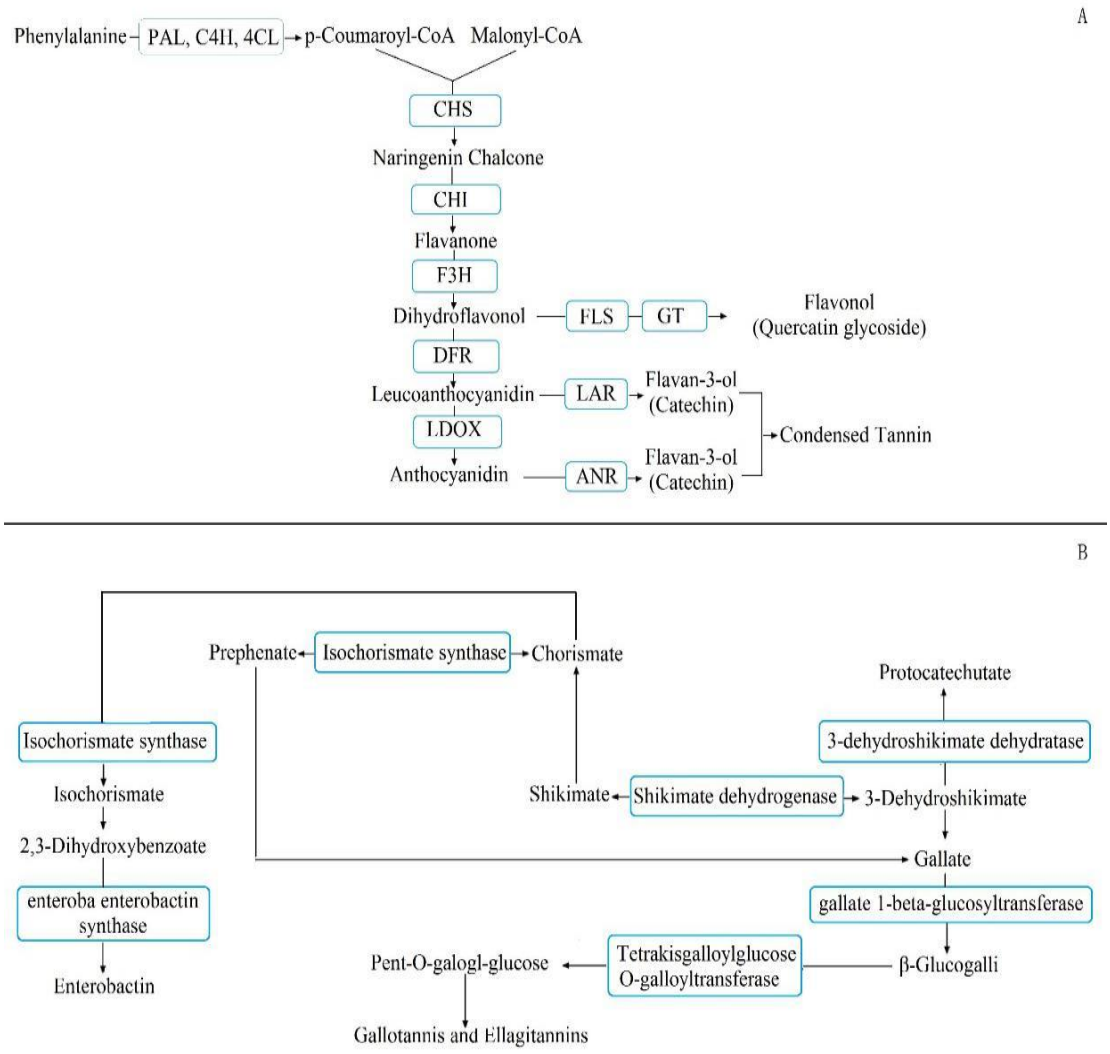

Figure S2 The pathways of Tannins biosynthesis. A. The procession of condensed tannin biosynthesis, PAL (phenylalanine ammonialyase); C4H (cinnamate 4-hydroxylase); 4CL (4-coumarate CoA ligase); CHS (chalcone synthase); DFR (dihydroflavonol 4-reductase); LAR (leucoanthocyanidin reductase); ANR (anthocyanidin reductase); **B. The procession of gallotannin biosynthesis.**

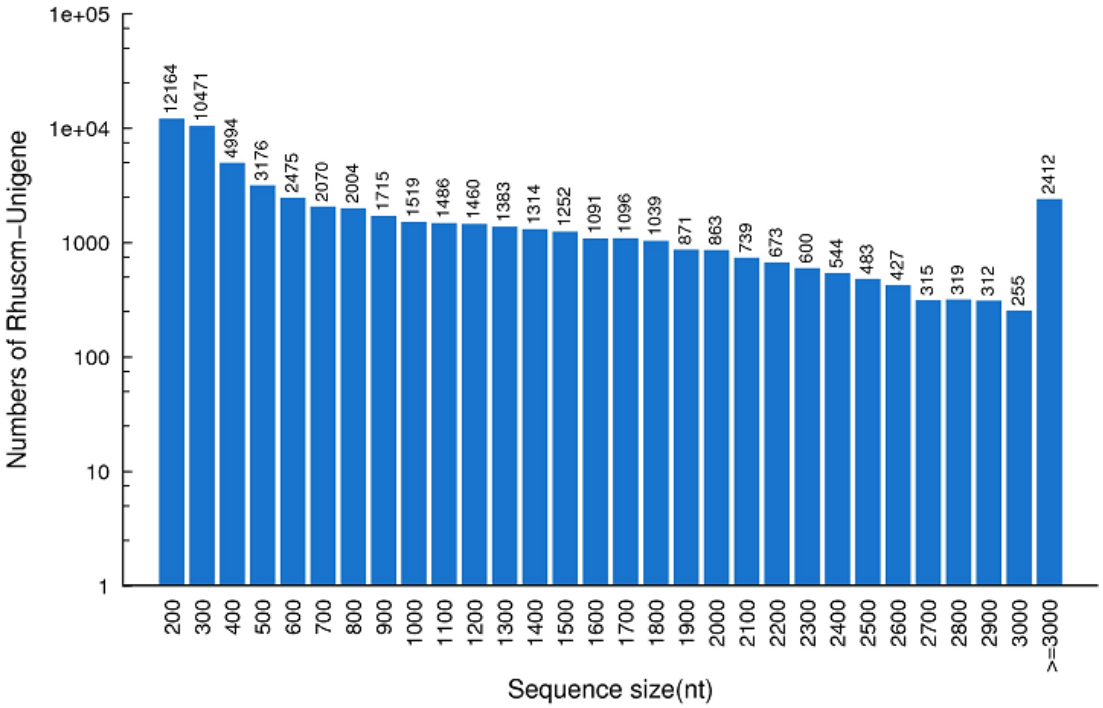

Figure S3 Length distribution of unigenes of *R. chinensis*

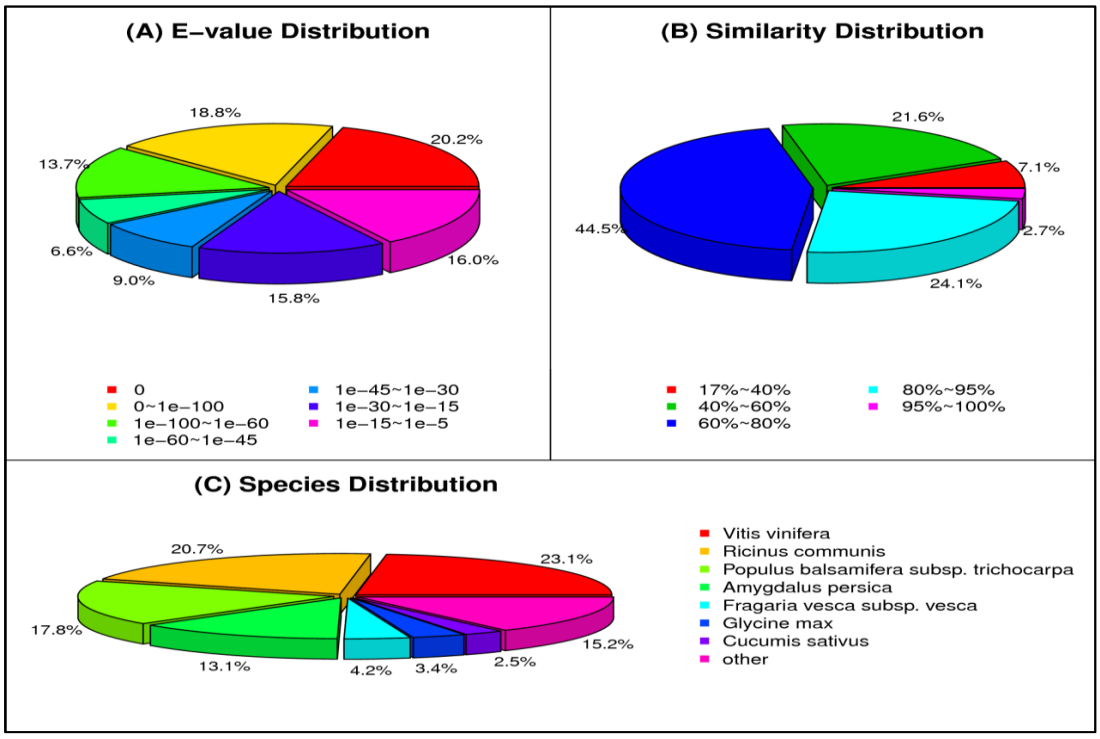

Figure S4. Data of Nr classification. (A) The E-value distribution of the result of Nr annotation. (B) The similarity distribution of the result of Nr annotation. (C) The species distribution of the result of Nr annotation.

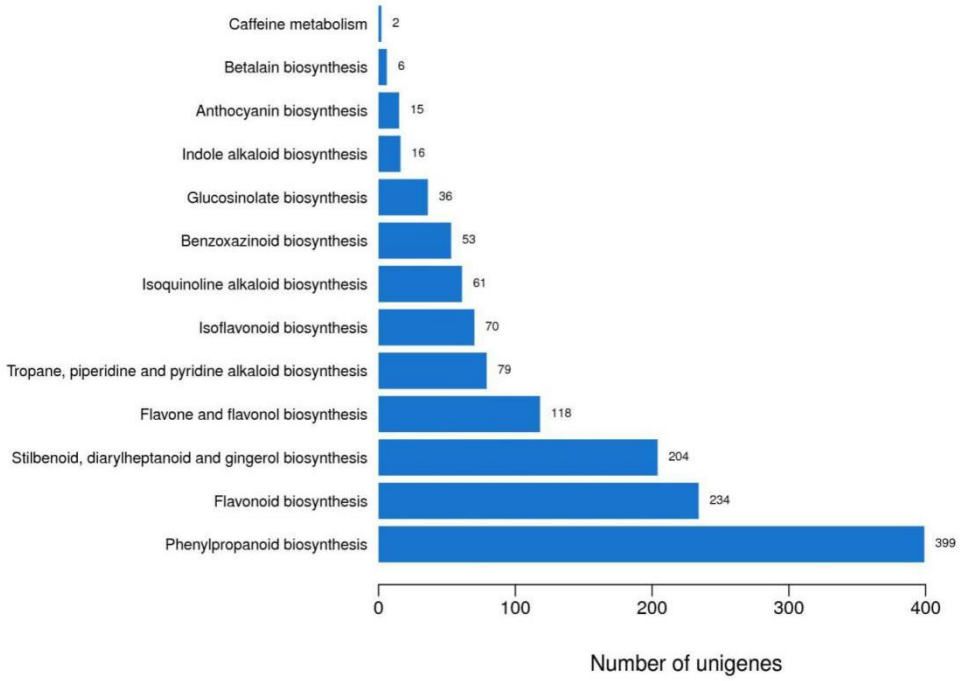

Figure S5. Pathway on biosynthesis of other secondary metabolites by KEGG. X-axis is the number of unigenes which annotated each pathway and y-axis is the sub-pathway.

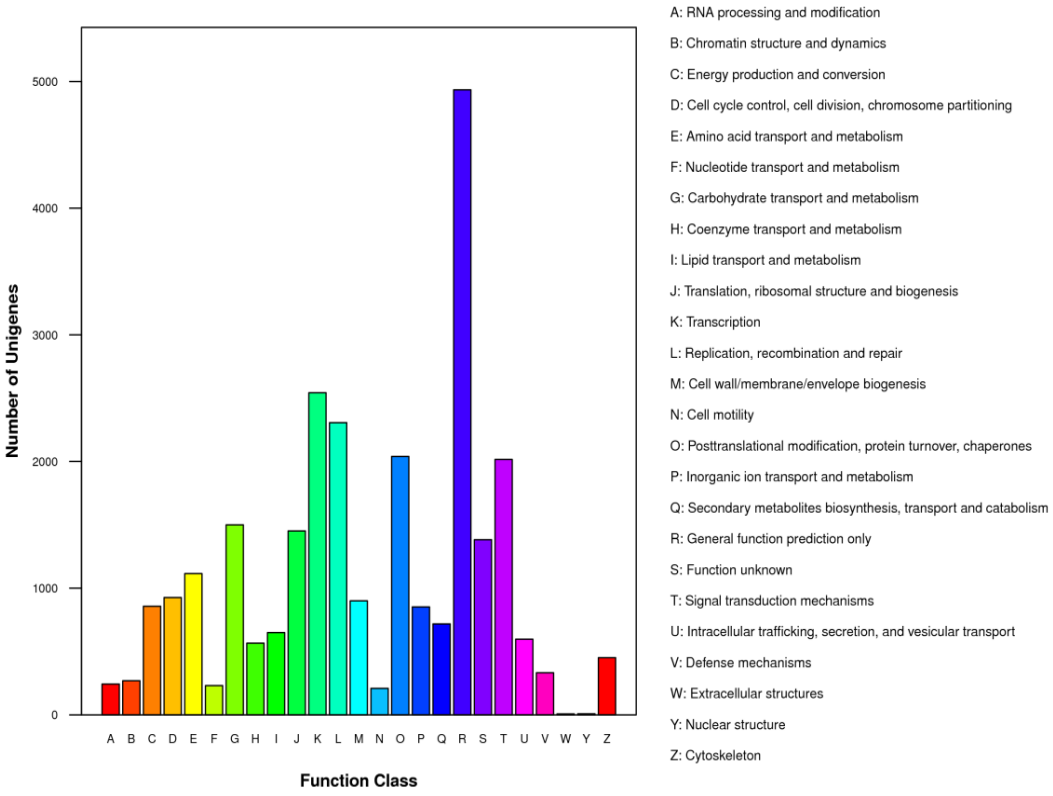

Figure S6. COG function classification of Unigenes. The horizontal coordinates are function classes of COG and the vertical coordinates are numbers of Unigenes in one class. The notation on the right is the full name of the functions in X-axis.

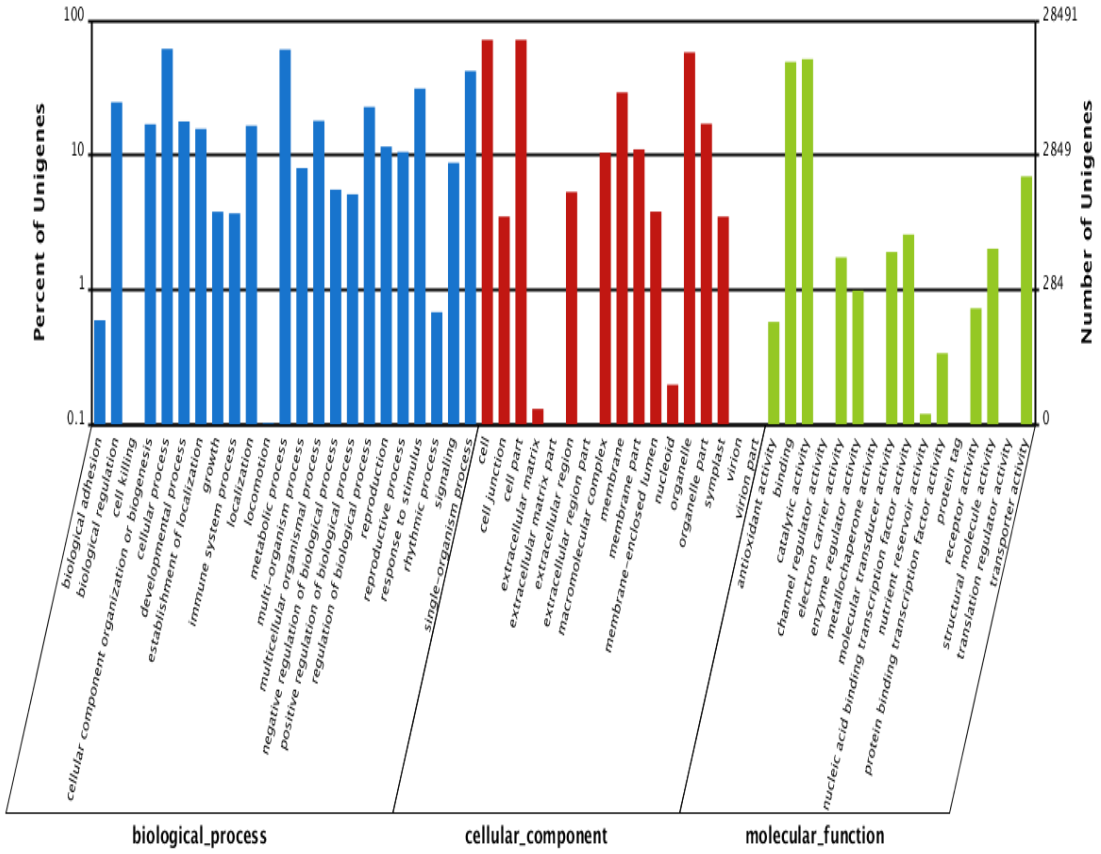

Figure S7. GO classification analysis of Unigenes in All-Unigene. GO functions is showed in X-axis. The right Y-axis shows the number of genes which have the GO function, and the left Y-axis shows the percentage.

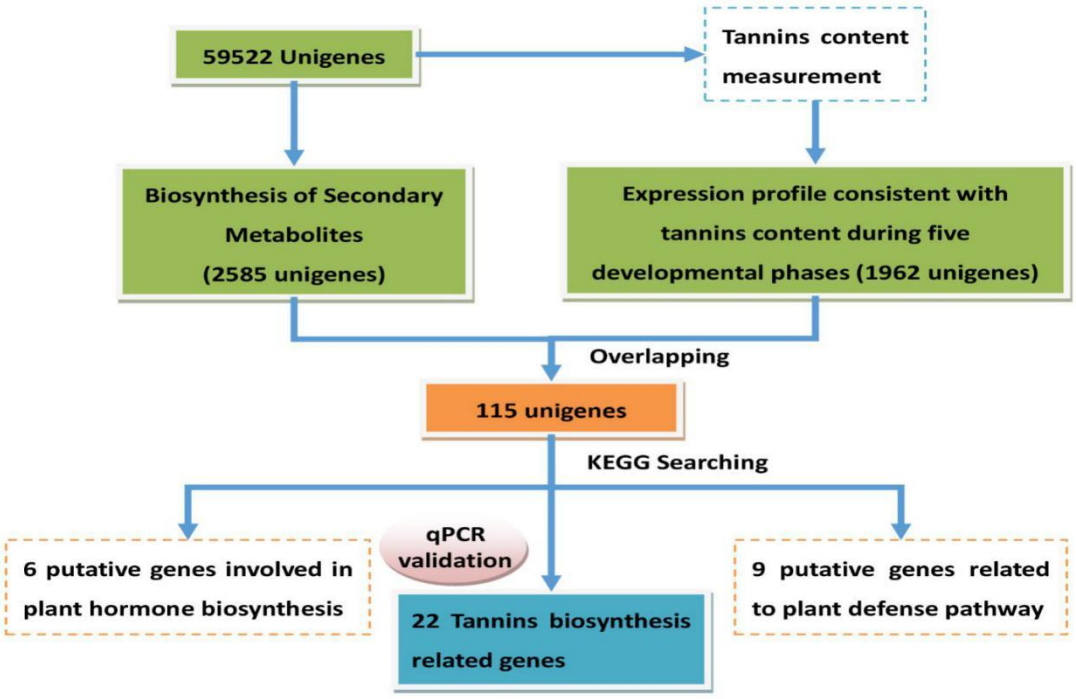

Figure S8. Selective strategy of putative genes related to condensed tannin biosynthesis, plant defense and hormone pathway from the whole unigenes of transcriptome data.

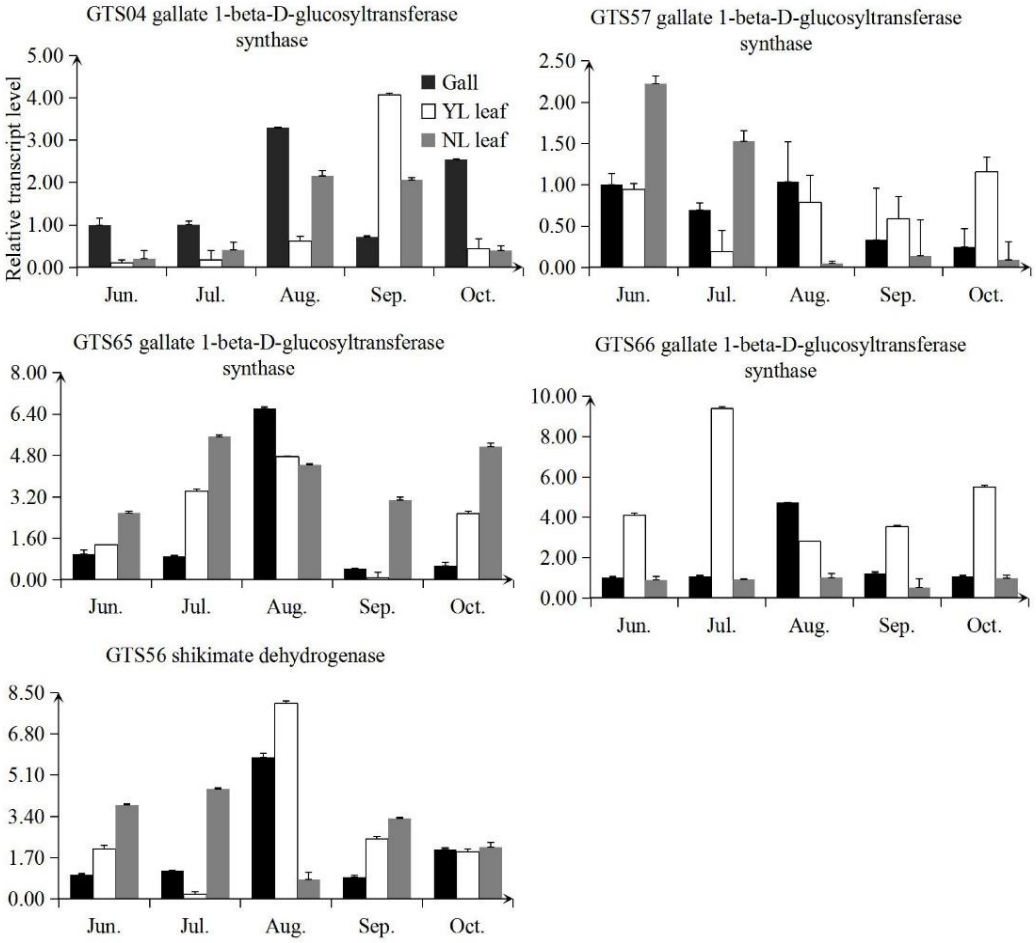

Figure S9. qPCR analyses of changes in transcript abundance of 5 putative genes related to gallotannin biosynthesis of *R. chinensis* in different developmental stage showing similar levels in gallnut than in leaf.

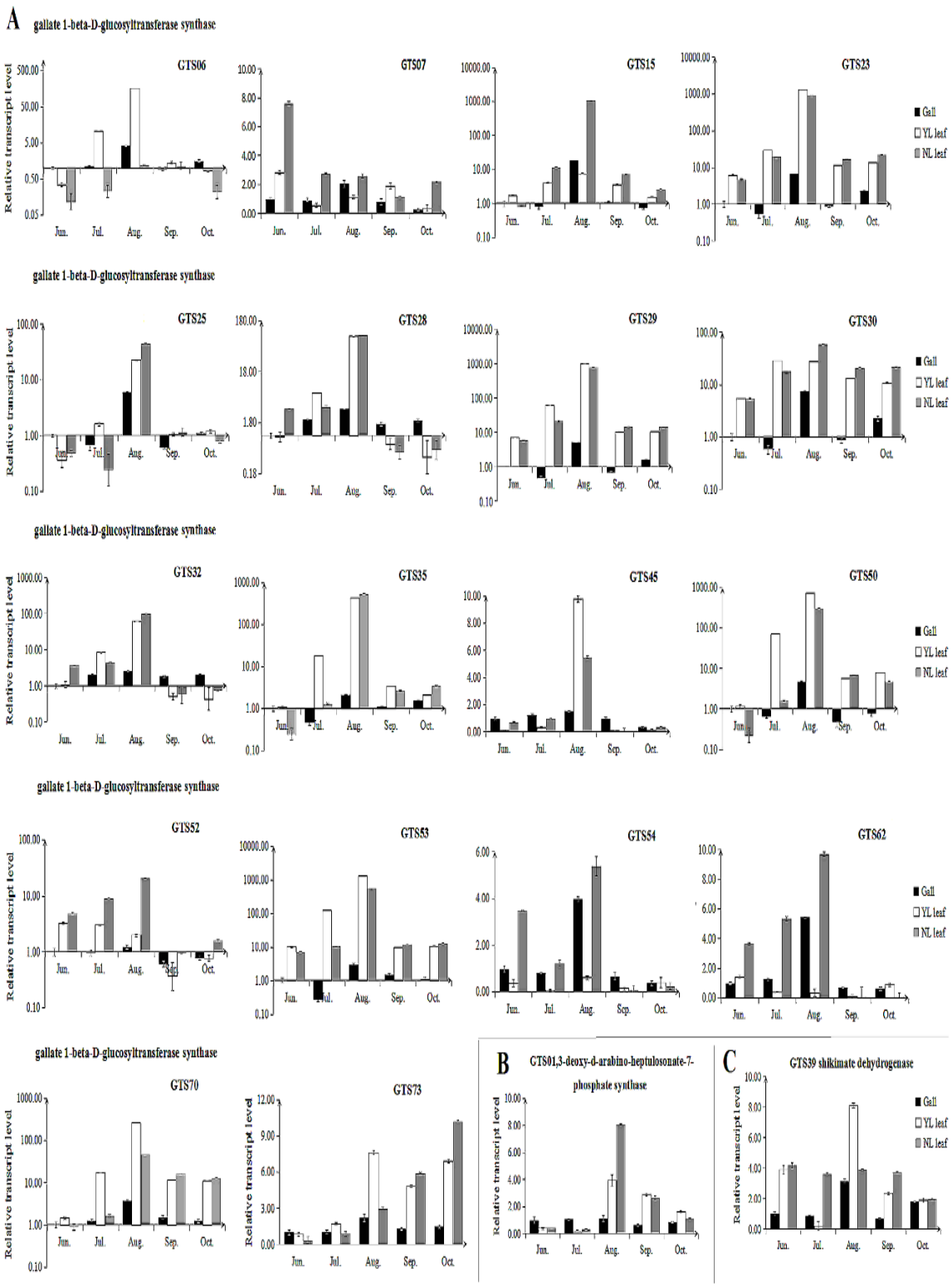

Figure S10. qPCR analyses of changes in transcript abundance of 20 putative genes related to gallotannin biosynthesis of *R. chinensis* in different developmental stage show higher levels in leaf than in gallnut.

Table S1 The weight percentage of tannin in gallnut during different developmental stage of *Rhus chinensis*

	Jun.21	Jul.26	Aug.8	Aug.18	Aug.28	Sep.10	Sep. 24	Oct.12
1	0.3882	0.7075	0.7279	0.7005	0.6823	0.6825	0.6559	0.5937
2	0.3736	0.5819	0.7621	0.7179	0.6538	0.6536	0.5874	0.5840
3	0.3883	0.6780	0.7537	0.7224	0.7083	0.6769	0.6419	0.5871
Ave.	0.3834	0.6558	0.7479	0.7136	0.6815	0.6710	0.6284	0.5883
SE	0.0085	0.0657	0.0178	0.0116	0.0273	0.0153	0.0362	0.0049

Table S2 The weight percentage of tannin in leaf during different developmental stage of *R. chinensis*

	Jun.21	Jul.26	Aug.8	Aug.18	Aug.28	Sep.10	Sep. 24	Oct.12
1	0.0272	0.0317	0.0389	0.0170	0.0280	0.0335	0.0361	0.0303
2	0.0293	0.0301	0.0435	0.0233	0.0314	0.0276	0.0435	0.0332
3	0.0275	0.0457	0.0646	0.0200	0.0338	0.0338	0.0423	0.0303
Ave.	0.0280	0.0359	0.0490	0.0201	0.0311	0.0316	0.0406	0.0313
SE	0.0019	0.0086	0.0137	0.0032	0.0029	0.0035	0.0040	0.0017

Table S3 The weight percentage of condensed tannin in gallnut during different developmental stage of *Rhus chinensis*

	Jun.21	Jul.26	Aug.8	Aug.18	Aug.28	Sep.10	Sep. 24	Oct.12
1	0.68%	0.36%	0.31%	0.38%	1.19%	0.70%	0.55%	1.77%
2	0.64%	0.35%	0.30%	0.35%	0.95%	0.63%	0.55%	1.79%
3	0.78%	0.34%	0.32%	0.37%	1.05%	0.65%	0.47%	1.86%
Ave.	0.70%	0.37%	0.32%	0.42%	0.90%	0.67%	0.39%	1.92%
SE	0.07%	0.01%	0.01%	0.01%	0.12%	0.03%	0.05%	0.05%

Table S4 The weight percentage condensed tannin in leaf during different developmental stage of *R. chinensis*

	Jun.21	Jul.26	Aug.8	Aug.18	Aug.28	Sep.10	Sep. 24	Oct.12
1	6.63%	10.21%	12.86%	8.65%	6.57%	8.05%	10.38%	11.64%
2	5.36%	9.67%	12.29%	9.12%	6.78%	8.29%	9.99%	11.68%
3	5.34%	9.24%	12.34%	7.79%	6.06%	7.42%	11.08%	10.69%
Ave.	5.78%	9.71%	12.50%	8.52%	6.47%	7.92%	10.48%	11.34%
SE	0.74%	0.48%	0.31%	0.68%	0.37%	0.45%	0.55%	0.56%

Table S5 Output statistics of sequencing

Samples	Total Raw Reads	Total Clean Reads	Total Clean Nucleotides (nt)	Q20 percentage	N percentage	GC percentage
Rhuscm	86,165,236	80,033,622	7,203,025,980	97.85%	0.00%	43.73%

Table S6 Statistics of assembly quality

	Sample	Total Number	Total Length(nt)	Mean Length(nt)	N50	Total Consensus Sequences	Distinct Clusters	Distinct Singletons
Contig	Rhuscm	88,592	43,027,436	486	1224	-	-	-
Unigene	Rhuscm	59,522	52,899,372	889	1675	59,522	15,125	44,397

Table S7. RPKM of 81 putative genes related to gallotannin biosynthesis

Gene name	Jun.	Jul.	Aug.	Sept.	Oct.	Average	Functional categories
GTS38	286.62	459.01	295.53	192.21	418.97	330.47	
GTS17	110.79	202.42	244.97	81.79	136.13	155.22	
GTS43	139.36	145.16	103.95	114.59	261.29	152.87	
GTS22	75.28	158.56	155.61	80.14	119.59	117.84	
GTS63	31.36	86.94	41.88	39.41	247.34	89.39	
GTS15	29.66	107.54	270.72	6.71	21.84	87.29	
GTS30	62.91	71.56	209.98	13.70	32.90	78.21	
GTS27	24.10	21.42	223.27	12.25	25.20	61.25	
GTS23	50.83	43.13	129.54	6.25	35.20	52.99	
GTS58	36.07	28.49	143.29	27.43	21.77	51.41	
GTS67	58.90	66.30	35.16	32.40	57.46	50.04	
GTS53	30.16	22.21	82.57	5.44	51.33	38.34	
GTS04	10.19	12.56	12.76	40.67	82.41	31.72	
GTS35	35.21	6.14	53.60	10.82	36.99	28.55	
GTS41	32.56	6.48	51.70	13.89	37.60	28.45	
GTS11	11.07	14.04	16.05	38.60	52.48	26.45	
GTS66	19.31	16.89	30.71	20.79	40.96	25.73	UDP-glucose
GTS14	8.83	4.06	88.54	2.34	12.26	23.21	
GTS42	23.34	25.31	17.45	18.91	17.49	20.50	
GTS70	14.24	14.17	21.05	15.46	32.23	19.43	
GTS18	13.58	20.24	22.43	29.90	9.37	19.10	
GTS45	15.78	14.61	16.41	25.75	16.24	17.76	
GTS52	18.53	14.38	24.96	11.05	3.66	14.52	
GTS50	11.90	1.78	25.47	5.37	16.00	12.10	
GTS32	14.55	0.08	17.75	7.77	8.27	9.68	
GTS29	12.73	4.58	19.74	2.61	4.40	8.81	
GTS77	3.82	8.69	2.53	21.17	3.71	7.98	
GTS25	7.09	11.40	12.85	5.17	3.28	7.96	
GTS65	4.52	13.12	4.40	2.47	12.63	7.43	
GTS31	10.56	9.07	7.19	5.12	4.92	7.37	
GTS54	7.71	0.00	3.06	16.59	0.00	5.47	
GTS06	9.34	0.02	3.16	0.00	12.22	4.95	
GTS73	4.75	0.63	1.50	9.28	5.34	4.30	

GTS36	3.81	1.97	4.15	6.08	4.83	4.17	
GTS55	2.43	2.60	2.17	1.19	11.06	3.89	
GTS28	0.00	18.02	0.86	0.14	0.14	3.83	
GTS83	1.79	1.49	0.76	0.37	12.40	3.36	
GTS76	7.70	1.27	1.06	2.31	3.10	3.09	
GTS82	3.02	1.74	5.99	0.33	3.79	2.97	
GTS85	3.70	1.88	0.79	2.22	0.71	1.86	
GTS78	0.31	0.91	0.93	1.21	3.32	1.34	
GTS07	0.28	0.14	0.00	0.00	5.97	1.28	
GTS68	1.75	1.63	0.25	0.30	0.62	0.91	UDP-glucose
GTS71	1.73	0.00	1.06	1.63	0.00	0.88	
GTS74	0.00	0.40	2.29	0.00	0.81	0.70	
GTS10	508.34	225.79	283.61	426.71	21.16	293.12	
GTS13	258.63	127.14	162.74	288.85	21.55	171.78	
GTS39	48.56	32.20	77.15	32.16	43.43	46.70	
GTS26	29.73	43.68	65.98	20.08	52.54	42.40	Shikimate dehydrogenase
GTS56	19.89	29.27	18.90	48.81	25.44	28.46	
GTS51	7.33	0.73	11.86	12.49	51.10	16.70	
GTS44	9.10	2.52	11.48	6.46	8.97	7.71	
GTS49	5.03	0.25	6.50	6.39	13.92	6.42	
GTS60	4.44	2.75	3.47	10.60	6.07	5.47	
GTS33	0.96	0.93	7.37	3.48	0.82	2.71	
GTS16	11.09	11.99	10.27	12.31	14.14	11.96	
GTS46	7.55	6.16	5.66	7.38	3.44	6.04	
GTS19	1.88	6.18	7.02	4.23	1.82	4.23	
GTS64	4.67	2.48	1.09	4.57	1.20	2.80	isochorismate
GTS69	5.64	3.00	1.02	3.01	0.50	2.63	synthase
GTS75	3.12	2.00	0.57	2.81	0.64	1.83	synthase
GTS79	2.89	1.73	0.66	0.65	0.11	1.21	
GTS84	0.70	0.80	1.28	0.46	1.13	0.87	
GTS09	0.47	1.38	0.00	0.78	0.53	0.63	
GTS59	97.03	188.33	63.48	13.93	50.30	82.61	
GTS24	10.38	17.57	34.38	20.19	7.02	17.91	chorismate mutase
GTS37	7.49	5.92	7.44	3.32	3.69	5.57	
GTS80	0.36	1.07	0.36	0.71	0.00	0.50	
GTS12	1526.07	2515.44	2447.76	4405.86	2139.91	2607.01	
GTS40	138.32	204.95	277.22	83.42	91.40	159.06	3-deoxy-d-arabino-heptulosonate-7-phosphate synthase
GTS48	106.45	109.16	48.06	86.01	28.93	75.72	
GTS34	48.29	112.16	53.85	45.67	17.94	55.58	
GTS61	61.05	87.78	14.44	56.82	11.28	46.27	
GTS01	13.96	4.70	4.85	2.96	2.18	5.73	
GTS20	126.09	137.69	191.76	333.14	78.90	173.52	3-dehydroquinate
GTS21	83.43	124.74	136.90	255.80	54.20	131.01	synthase (DHQ
GTS72	4.64	5.71	2.13	0.00	0.51	2.60	synthase)

GTS62	0.28	0.81	0.82	0.01	0.87	0.56
GTS03	1.82	0.00	0.48	0.00	0.00	0.46
GTS02	0.15	0.00	0.30	0.01	0.00	0.09

Table S8. Twenty-two putative genes related to tannin biosynthesis

No.	Gene name	KEGG Orthology	Enzyme	Pathway
1	TS-1	K00224	leucoanthocyanidin reductase	flavonoid biosynthesis
2	TS-2	K06892	leucoanthocyanidin dioxygenase	
3	TS-3	K13082	bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase	
4	TS-4	K05277	leucoanthocyanidin dioxygenase	
5	TS-5	K13229	leucoanthocyanidin dioxygenase	
6	TS-6	K06892	leucoanthocyanidin dioxygenase	
7	TS-7	K05279	flavonol 3-O-methyltransferase	flavone and flavonol biosynthesis
8	TS-8	K05280	flavonoid 3'-monooxygenase	
9	TS-9	K01904	4-coumarate--CoA ligase	
10	TS-10	K01904	4-coumarate--CoA ligase	
11	TS-11	K01904	4-coumarate--CoA ligase	
12	TS-12	K10526	4-coumarate--CoA ligase	
13	TS-13	K10526	4-coumarate--CoA ligase	
14	TS-14	K13493	anthocyanidin 3-O-glucosyltransferase	anthocyanin and flavanone biosynthesis
15	TS-15	K10775	phenylalanine ammonia-lyase	
16	TS-16	K13267	flavonoid 6-hydroxylase	isoflavonoid biosynthesis
17	TS-17	K13267	flavonoid 6-hydroxylase	
18	TS-18	K13258	2-hydroxyisoflavanone dehydratase	
19	TS-19	K13258	2-hydroxyisoflavanone dehydratase	
20	TS-20	K13258	2-hydroxyisoflavanone dehydratase	

21	TS-21	K13258	2-hydroxyisoflavanone dehydratase	
22	TS-22	K13258	2-hydroxyisoflavanone dehydratase	

Table S9. Fifteen putative genes related to plant defense system and hormone biosynthesis

No.	Gene name	KEGG Orthology	Enzyme	Pathway
1	PD-1	K01183	chitinase	plant antibacterial activity
2	PD-2	K15563	chitinase	
3	PD-3	K01183	chitinase	
4	PD-4	K01183	chitinase	
5	PD-5	K00517	cytochrome P450	cuticle, tethered layer and wax synthesis
6	PD-6	K13407	cytochrome P450	
7	PD-7	K11818	cytochrome P450	
8	PD-8	K15086	(3S)-linalool synthase	plant terpenoid synthesis
9	PD-9	K00511	squalene monooxygenase	
10	PHS-1	K00227	lathosterol oxidase	plant hormone synthesis
11	PHS-2	K10760	adenylate isopentenyltransferase (cytokinin synthase)	
12	PHS-3	K12619	adenylate isopentenyltransferase (cytokinin synthase)	
13	PHS-4	K10760	adenylate isopentenyltransferase (cytokinin synthase)	
14	PHS-5	K10760	adenylate isopentenyltransferase (cytokinin synthase)	
15	PHS-6	K05282	gibberellin 20-oxidase	

Table S10 The quantitative PCR primers of 12 candidate genes in gallnut of *R. chinensis*

Gene ID	Primer sequence	Tm	Gene length
TS-18	AATGTTGACTGTTTGGTGAGGG	59	111
	GGAAAGTATTATCGTCTCGTCGTT	59.3	
TS-19	GAAATGGACCTGAAACTTGGC	58.8	125
	GACTAATCCGATTGACCCGAC	58.5	
TS-15	TAGTTCCTCCTCAAAGGCTCC	57.9	212
	TTCACCCATCAAGGTTCTGC	58.1	
TS-2	GGAGGATACAGTGCGGGTTT	58.9	153
	CAATGCGAATTACAAGAGCGT	58.4	
TS-4	AAGAATCCCCATTCACGACA	57	181
	TTCCAGAGCGATACATCAAGC	58.5	
TS-14	TGTATGCCTTGTTTCACTGACC	57.7	72
	TTGCACCCCAACTTTCCA	57.4	
TS-8	AACAGGCATACAGGCGAGAT	57.2	182
	TGCAGCAGGCAAGTTCATAG	57.9	
TS-9	AGAGCCTGTTTTCTGTTTCGTC	58.1	164
	TTACTGGGTTCCAAAGTCCGT	58.8	
PD-1	CTGTTTTGGATGGGATTGACTT	58.4	137
	AGGAAATGGACACTGAGGAGC	58.2	
PD-8	CCCTTCACCCTGTGTTCTAATC	58	219
	TTTTCAGCCAGTGCTACGG	57.1	
PHS-1	TGTTGTCAAGAAGGTGGTTTACTAT	57.4	106
	TTTCCATGCTTCTGACATCTGT	57.3	
PHS-2	TAACTCAGCCCGTCATTTCTTT	58.7	71
	GTGGGACATATTTGGATTTTGC	58.9	
Actin	CATCACTCATCGGTATGGAAGC	59.6	164
	AGTGATTTCCTTGCTCATACGGT	59.9	

Dataset S1. The amino acid sequences translated by the twenty-two putative genes related to condensed tannin biosynthesis in gallnuts of *R. chinensis* after aphids feeding.

TS-1

M G K S K V L V V G A T G Y I G R R I V K A S L A Q G H T T Y V L Q R P E I G L D I E K I Q M L L S F K Q E G A I L V E G S F S D H K S L V D A V K K V D V V I C T M S G *

TS-2

M K I L S L E L G L R E N H L Q N A F G G E N I G A C L R V N F Y P K C P Q P D L T L G L S S H S D P G G L T M L L P D D Q V A G L Q V R K G D N W I T V K P A K H A F I V N I G D Q I Q V L S N A N Y K S V E H R V I V N P E Q E R V S L A F F Y N P K S D I P I E P V K E L V T P D K P A L Y P P M T F D E Y R L F I R L R G P R G K S Q V D S M K S P K C Y *

TS-3

G T L G I L K A C V N S K T V K R V V Y T S S A S A V T F S S N D Q E I V D E I V H G V T *

TS-4

M N K L Q S W P E P I V R V Q S L S E S G L N K I P E R Y I K P S T E R P S F S S E N G I D H H N V N I P I I D L A G L F Q D D Q N V R A Q I I S Q V N M A C R E W G F F Q I L N H G V R P E L M D Q A R E T W R Q F F H A P M E L K Q A Y A N S P K T Y E G Y G S R L G V E K G A I L D W R D Y Y F L *

TS-5

M A A Y D R R K E V E E F D S S K I G V K G L S D S S I T S I P K I F I H P P E T L S T L K S S Q D D T T I T I P V I D L A K I N S P V D R P N I I Q Q V K E A A K S W G F F Q V I N H G I D L S V V E N T I Q A V K S F H E Q P A E M K A K F Y K R E E K S G V M Y A S N N D L Y R S K A A S W H D Y L Q V W M S P E K A K E E D I P E I C R R E A V A W D F H A Q M V G E E V M E L L C E G L G L E A G K F K E L T F S E S R L F V G I Y Y P S C P Q P D L T L G L T P H T D P G A L T V L L Q N Q V P G L Q I K H G D Q W V N V K P L H G S L T I N I G D F L Q I I S N G E Y N S V Q H R V L A N T W E E P R I S V V M F L N V T K W E G S G S H G P L P E L I S A E K P A V Y R K F T K E E Y Y D N F Y S K G L D S K S L I D K L K L *

TS-6

M E A K V L Q K L Q Y P T W V D L D K F Q R K P S G S V R F S R R M R E E K R V Q V L I S A H M Q P S I T S N R N R S V T S E I S C T F Q G F P A S I L E P G G F H A P L D E A L I L K N K S Q E I E P Y L D G R C I Y L V G M M G S G K T T V G K V L S G V L G Y S F F D S D T L I E Q A V G G T T V T D I F K L Y G E G F F R D K E T E V L R K L S I M H R L V V S T G G G A V T R P I N W K Y M R N G I S V F L D V P L E A L A Q R I A A V G T N S R P L L H H E S G D A Y T K A L K R L S T L W E E R S R A Y E N A N A R V C L E N I A A K L G H R D V S A L T P A T I A I E A L E Q I E H F L K E E G E M P F *

TS-7

M E E M K F L K L V V K E T LR L H P P A P L L V P R E C R E K C V I N G F D I P I K T R V I V N A W A I G R D P E Y W S E P E I F N P E

TS-8

L A G F N I S D L F P S I N F L Q W I T K S Q V E K L H Q E A D R I V E K I I N E H K K G Q A P L N I D K S E E A E D L

TS-9

M A A S D S E I V K D F R F F R V Y K D G R V Q L S F P P F V K A T V P P S D D P V T G V Q S K D V T I S S E P P V S A R I F I P K V T D P K Q K F P L L F Y V H G G G F C I M S A F A P G Y H S F C S T I S A Q A G A I V V S V E Y G L F P D R P I P A C Y E D S W A A L Q W V A S H V S G N G P E P C L N D H A D F N K V F I S G V S A G G N I S H T L A F R V G S I G L P G V K V V G V I L V H P Y F G G T G D D E M W L F M C P N N G G L Q D P R L K P P A E D L A K L G C A R V L I F

V A E K D H L N V V G K N Y L E D L K K S G W S G S V E L F E S Y G E G H V F H M L S P E S E K A V E L T N K F V S F L K Q D *

TS-10

M I P R Y I Q N G F F L F I K R I E V T S L S S M A S T D S E I V N E F R F F R V Y K D G R V E L F S P P C P K V P P S A D P V T G V R S K D V T I S S E P L V S A R I F I P K L S D P N Q K F P L L F L V H G G G F C I M S A F A P R Y H L F C N T V S A Q A G A I V V S V E Y G L F P D R P I P A C Y E D S W A A L Q W V A S H V S G N G P E T W L N D H A D F G K V F I G G D S A G G N I S H T L S F R V G S I G L V G V K V V G V I L I H P Y F G G T E D D E M W L Y M N P S N S G L Q D P R L K P P L E D L A K F G C E R V L I F V A E K D H L NT P G K D Y Y E D L K K S G W*

TS-11

M A S S T D S E I A K E F P F F R V Y K D G R V E L F R P H W D K I P P S D D P I T G V R S K D V T I S S E P P V S A R I F I P K L T S P T Q K F P L L L Y V H G G G F S M L S A F S P Q Y H N F C S T V S A L A G V I V V S V E Y G L F P A R P I P A C Y E D S W A A L Q W V A S H V N G N G P D P W L N D H A N F S K V F I G G D S A G G N I S H T L A F R V G S I G L P G M K V D G V I L V H P Y F G G T E D D Q M W L Y M N P T N G G L Q D P R L K P P A E D L G K L G C E R V L I F V A E K D H L Y T P G K D Y H E D L K K S G W G G E V E L V E N H G E E H C F H F H D P K Y E K A V E L T N K F V S F I K Q D *

TS-12

M D S T Q P E I A Y D F S P M L I V Y K D G T V N R L T G N D I V P T S L D P K T N V K S K D V V Y S P E N G L S V R L Y I P K T V S Q N Q K L P L L V Y F H G G G G F C I E S P F S P P Y H N Y L N S L V A E A N I V V V S V Q Y R R A P E H H L P C A Y D D S W T A L K W V A S H V N G S G P E D W L N S H A D F E K V F F S G D S A G A N I A H R M G I K H G L E K L E G V N V E G I V L C H P Y F W G N E A V A N E T A D E N R R K F V E A L W R F T Y P E T T G C D D L W V N P A V D P N L A K L G C R R V L V L V A E K D L L C A R G W Y Y H Q K L K E S G W G G D V E V V E T N G E Q H V F H L F N P G C E N A K A M I K K T A D F Y N N

TS-13

M D S S T N E V A H E Y L P Y F R A Y K D G R V E R F F G S D R V P V S L D G S Q N G V C S K D V V I V S E T G L S A R I F I P A G A T K P G Q K L P L V V Y Y H G G G F F M G T P F C S A Y N N S V S S L A A K A N A I A V S V D Y R L A P E H Y V P V A Y E D S W A A L K W V A S H C N G E G P E A W L N N Y A D F H R V F L A G D S A G G N M V H N M A I Q A S V E D L N G V K L S G I C L I Q P Y F G R Q D G G V D K W W T F V C P T T S G S D D H R I N P S V D S R L S S L R C N R V L I C V A E K D N L K E R G L F Y D E T L R D S E W V G E V E I A E T E G E D H V F H L F N P N S E K A V A L L E K I A S F I N Q *

TS-14

L E S I C E G V P M I C M P C F T D Q R V N A R Y V S D V W K V G
V Q L E N G L D R E N I D R T I R R L M V E K E G E E I R G R I L C
L K E K A N I C L R Q G G S S S E S L

TS-15

W R N C K T L N A L L S T L H L F V E T F T E T I S K I G I N Q E G I
T V G L T S F F Q V Q I N V M A W H R A T K K V E D M S F N M S T
A S A V F L E E I R P K E F T S *

TS-16

M N S S A I R Y N E E K E E S F A Y A I Q L V T G S V L P M T L K A
A I D L D I F E I I A K A G P G A K L S A S E I A S R M S A Q N K D A
P M M V D R I L R L L S S H S V L T C Y V V G L E R L Y S L A P V S
K Y F V H D Q N G V S L G P F M A L I Q D K V F M D S W A Q L K D
A V L E G G V P F D R V H G T H A F E Y P G L D A R F N Q V F N T A
M F N H T T I V I N E I L K V Y K G F E S I K Q L V D V G G G L G I T
L K A I T S R Y P H V T A I N F D L P H V I Q H A P Q N P G V E H V
G G D M F E S V P K G D A I F M K W I L H D W S D E H C L K L L K
N C Y K S I P E D G K V I V V E G I L P V M A E T K V T S K G V S Q
M D V V M M T Q N P G G K E R T K H E F M A L A T A A G F S G I R
Y E C F V C N F W V M E F Y K *

TS-17

M E A F S W V V L A T A W L A A L V F L K R I S T S W R Q S L N S I
P G P K P W P I I G N L N L I G P L P H Q S L H K L A Q K Y G S I M Q
L K F G S F P V V V A S S A E M A K L F L R T H D H I F A S R P P T
A A G K Y T T Y N Y L N I T W A P Y G P Y W R Q G R K M Y L A E L
F S S K R L E S Y E Y I R V E E L R D S M S R L Y A L S G K P I V L K
D H L S R F T L S I I S R I V L G K K Y F C V S K S E T S V V T L E E
F Q E M M D E L F L L N G V I N I G D W I P W M D F L D L Q G Y V
K R M K V L K K R L D R F H D H V F D E H K S K R E G V K D F E A
K D M V D L L L R L A D D P N F D A K L T S D S I K G F T Q D L I A
G G T D T A A T T V E W A M S E

TS-18

M A A G N D I D D L P K N A A N Y T A L T P L W F L E R A A T V H P
S R A S L I H G S V R Y T W H Q T Y Q R C R R F A S A L S R R S V G
L G S T V A V I A P N V P A L Y E A H F G V P M A G A V L N S V N I
R L N A Q T I A F L L G H S A S A V V M V D Q E S F S V A E E A L K
I M E E K S K G N F K P P I L I V I G D E S C D P K V L E Y A L G R G
A I E Y E K F L E T G D P E F A W K P P Q D E W Q S I A L G Y T S G
T T A S P K G V V L S H R G A Y V M S M S G A L I W G L N E G A V
Y L W T L P M F H C N G W C Y T W S L A A L C G T N I C L R Q V T
A K A V Y S A I A K Y G V T H F C A A P V V L N T I V N A S P E D T
I L P L P H V V N V M T A G A A P P Q S V L F S M S Q K G F R V T H
T Y G L S E T Y G P S T V C A W K P E W N S L P P E T Q A R L N S R
Q G V R Y I G L E F L D V I D T R T K K P V P A D G K T I G E I V L G

G N S V M K G Y L K N P K A N E E A F A D G W F H S G D L G V K H
P D N Y I E I K D R S K D I I I S G G E N I S S L E V E N L L Y L H P
A I L E A S V V A R P D E R W G E S P C A F I T L K Q G A D K D E P
R L A E D I M K F C R E K M P A Y W V P K S V I F G P L P K T A T G
K I Q K H I L R A K A K E M G P V K R S K L *

TS-19

M E V Q A K P Q E E L I I Y R S K L P D I Y I P N H L P L H S Y C F E
N I A Q V A S R P C L I N G S T G D V Y T Y S D V E L T A R K I A S
G L N K L G I Q Q Y D V I M L L L P N F P E F I L S F L G A S Y R G A
I V T A A N P L C T P A E I S K Q A E A S N A K L I I T Q A C Y V D K
V K A L S E K R D V K I M C I D A A P D G C L H F S E L T Q A D E N
D L P E V K F N P D D V V A L P Y S S G T T G L P K G V M L T H K G
L V T S V A Q Q V D G E N P N L Y F H S E D V I L C V L P L F H I Y
A L N S I F L C G L R A G A S I L L M Q R F E I N S L L Q L I Q R Y K
V T V A P M V P P I V L A I A K S P D V D K H D M S S I R F I K S G A
A P L G K E L E D S V R A K F P N A T L G Q G Y G M T E A G P V L A
M G L A F A K H P F P I K P G A C G T V V R N A E M K I I D P D T G
A Y L P R N Q P G E I C I R G D Q I M K G Y L N D Q E A T K R T I D
S D G W L H T
G D I G Y I D D D D E L F I V D R L K E L I K Y K G F Q V A P A E L
E A M L L T H S S I S D A A V V P M K D D Q A G E V P V A F V V K A
K D S Q I T E D E V K Q F I S K Q V V F Y K R I N R V F F I D A I P K
A P S G K I L R K D L R A K L A A G L P N *

TS-20

M E G T I R C S A N Y V P L S P I S F L E R S A I V Y R D R L S V V Y
E D V K Y T W K E T H Q R C I K L A S A L A D L G I S R G D V V A A
L A P N I P A M Y E L H F G V P M A G A V L C T L N V R H D S A M
V A V L L K H S E A K I I F V D H Q L L D T A R A A V E I L A K S T T
K L P L L V I I P E C S T V R N P I P A H E N L E Y E S L L A K G I L
D F E V R R P K D E W D P I S L N Y T S G T T S S P K G V I Y S H R
G A Y L N S L A V A L L N E M S S M P T Y L W C V P M F H C N G W
C L T W A V A A Q G G T N V C L R I V N A K G I F D N V A R Y K V
T H L G G A P T V L N M I V N A A A G E R R P L P G K V V V M T G
G A P P P P Q V L F S M E E L G F V V T H S Y G L T E T Y G P G T V
C T W K P E W D S L P R E A Q A K I K A R Q G L H H L G M E E V D
I K D P V T M K S V P P D A K T M G E A M F R G N T V M N G Y L K
N S K A T Q D A F N G G W Y R
S G D L G V K H P D G Y I E L K D R S K D I I I S G G E N I S T I E V
E S V L F S H P S V L E A A V V G R P D D H W G E T P C A F V K L K
D G C D A S S E E L I K Y C R S R L P H F M A P R T I V F Q D L P K
T S T G K T Q K F V L R E K A K A M G S I S K Q R S S K L *

TS-21

M E G T I R C S A N Y V P L S P I S F L E R S A I V Y R D R L S V V Y
E D V K Y T W K E T H Q R C I K L A S A L A D L G I S R G D V V A A

L A P N I P A M Y E L H F G V P M A G A V L C T L N V R H D S A M
V A V L L K H S E A K I I F V D H Q L L D T A R A A V E I L A K S T T
K L P L L V I I P E C S T V R N P I P A H E N L E Y E S L L A K G I L
D F E V R R P K D E W D P I S L N Y T S G T T S S P K G V I Y S H R
G A Y L N S L A V A L L N E M S S M P T Y L W C V P M F H C N G W
C L T W A V A A Q G G T N V C L R I V N A K G I F D N V A R Y K V
T H L G G A P T V L N M I V N A A A G E R R P L P G K V V V M T G
G A P P P P Q V L F S M E E L G F V V T H S Y G L T E T Y G P G T V
C T W K P E W D S L P R E A Q A K I K A R Q G L H H L G M E E V D
I K D P V T M K S V P P D A K T M G E A M F R G N T V M N G Y L K
N S K A T Q D A F N G G W Y R
S G D L G V K H P D G Y I E L K D R S K D I I I S G G E N I S T I E V
E S V L F S H P S V L E A A V V G R P D D H W G E T P C A F V K L K
D G C D A S S E E L I K Y C R S R L P H F M A P R T I V F Q D L P K
T S T G K T Q K F V L R E K A K A M G S I S K Q R S S K L *

TS-22

M E Q R S L H T D P K S G F N S L T K T F H S L K A P V H L P P E N
A F L S A A E Y A F S L R A T S P W P D D S V A L V N S I T G Q R I S
Y S E F G H R T K S L A A Y L Q K V T Q L S K H D V A F V L S P N S
I Q V P I L Y F S L L S L G V I I S P A N P V A T E S E I Y G Q I Q L S
K P V I A F A R S S T V H K L P K L K H Q T I L I D S P E F E S M M V
S S K H E F K H V K L S Q S D P A A I M Y S S G T T G K V K G V M L
T H R N F I A Q T A I N S A A W K M S E K R E S P S A M L F T T P Y
F H I F G F F Y S I R S V A L S E K A V V M D R F D W K N M L K A V
Q E F S V T H V A L T P P V V V K L S K D G S T D D Y D L S S L E T
V I C G A A P L G K E A I A A F T S R F P K V M L V Q A Y G L T E S
T A A V A R T I G L E E N M K W G S T G K L Y A G F E A K V V D P
E T S D A L P P C K E G E L W I R G P T I M K G Y V G D P E A T S A
T L V C D G W M R
T G D L C Y I D E N G F L F I V D R L K E L I K Y K G Y Q V A P A E
L E Q V L I S H P Q V A D A A V I P Y P D K E T G Q V P M A F V V R
Q P Q S T L N E T E I M D F V A K Q V A P Y K K I R R V A F I N S I P
K S A A G K I L R K D L I R K F V L P P P A S S R L *