

Figure S1. Sampling diagram of trunk parts of *E. grandis*. 1) represented the DBH, which is 1.4 m from the ground; 2) represented the middle part of the trunk, about 10.5 m from the ground. 3) represented the upper part of the trunk, which is about 21.0 m from the ground.

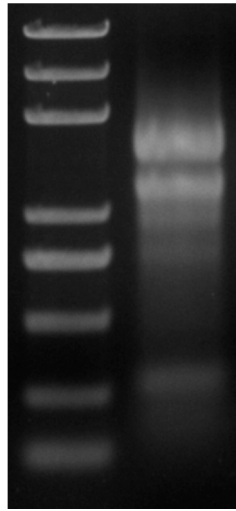


Figure S2. Total RNA extraction from *E. grandis* immature xylem
M2Kb, molecular marker2000 bp

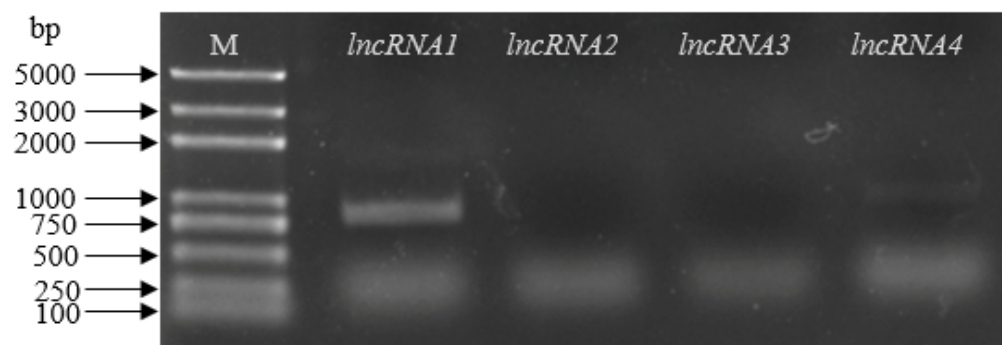


Figure S3. Electrophoresis for PCR product of *lncRNA1* and *lncRNA4* cloning

Table S1. Primer sequence of target gene qPCR

Gene		Primer 5'-3'
XM_010040005.2	F	TCCGATGCCCAAGTTTCTCC
	R	ATCCCAACCCGAATACCCAG
NM_001302719.1	F	AGAATGAACTCGGACAAAAGCC
	R	AATGGGGAACGCACACTCA
XM_010058963.2	F	GGCACCGAGTCCGAAATAGA
	R	AACATCCAAGCCACAGCGAA
XM_010048758.2	F	AACAGAACAAGCACAAAGCACC
	R	TGACCATAAGATGAGACTGGGAAC
XM_010046732.2	F	GTTGCTTCGGTGGTCATTGG
	R	TGTTTCGTTGGGGTTGGGAC
XM_010030508.2	F	GGGTATGGCTCTTTGGCTGT
	R	GTCTGTGTTGTTGTTGCGGT
XR_001980078.1	F	TAGACACACGCTATGCTGCC
	R	ACACTCGGTGCGACAAATGA
XR_001985124.1	F	ACAACTCAAATCCCAATCCACC
	R	CCTTCTTCAGCACTCCTCACT
XR_727233.2	F	TGAATGAAAGGAGCAGCCAGA
	R	CGGCAAGGTGAAAGCAGTT
XR_720796.2	F	CTGCCCCCTCCTATGTTGTC
	R	GGCTCTCTTCCCATCCTGTATC
TCONS_00028436	F	CCAGTCCTCGCCCTGTTCT
	R	TGCTTCTCTTTGTCTGGGTTCA
TCONS_00034287	F	GCTTCTGTAGTTTCGTCTCGTC
	R	GCCCTTTTCTCAGCACATTC
TCONS_00074394	F	CGAGCCAAACAAGCACACAA
	R	ACCCATCGTCGGATTTCTTC
TCONS_00003650	F	AGCGAGATTGGGAAGAACGG
	R	TCAAAGGACAAGGTGGACAGA
TCONS_00003171	F	GTTTATTCCCTTATGCTGGCTTG
	R	CCACGGTCTCCTAACCCTTG

Table S2. Primer sequence

Gene	Primer 5'-3'
EglnR1(XR_001980078.1)	F <u>ACGGGGGACTCTTGACCATGGGTTTGACTTGATAACGCTGTG</u>
	R <u>CTGGTCACCAATTCACACGTGAAAACGATAAAAGTCGTGTGGA</u>
EglnR2(XR_720796.2)	F <u>ACGGGGGACTCTTGACCATGGACCCGACGGAGCGCCTGGCCC</u>
	R <u>CTGGTCACCAATTCACACGTGCAAGCCAACGTACTTACGCTT</u>
EglnR3(XR_727233.2)	F <u>ACGGGGGACTCTTGACCATGGCGACGAAGAAGAAAACGGAG</u>
	R <u>CTGGTCACCAATTCACACGTGTGCAGATTATAATACAATACA</u>
EglnR4(XR_001985124.1)	F <u>ACGGGGGACTCTTGACCATGGCCATGCCGAAAAACAGGTGAA</u>
	R <u>CTGGTCACCAATTCACACGTGTATTATTACTTAAAATATTGG</u>

The underlined part represents the gene sequence, and the underlined part is the connector sequence used for cloning.

Table S3. Primer sequences of positive control test

Name	Primer 5'-3'
Carrier identification primer NPTII-F	ATGGGGATTGAACAAGATGGAT
Carrier identification primer NPTII-R	AGAACTCGTCAAGAAGGCG
lncRNA1 Specific primers GSP-F	ACGGGGGACTCTTGACCATGGGTTTGACTTGATAACGCTGTG
lncRNA1 Specific primers GSP--R	CTGGTCACCAATTCACACGTGAAAACGATAAAGTCGTGTGGA
lncRNA4 Specific primers GSP-F	ACGGGGGACTCTTGACCATGGCCATGCCGAAAAACAGGTGAA
lncRNA4 Specific primers GSP--R	CTGGTCACCAATTCACACGTGTATTATTACTTAAAATATTGG

Table S4. Genome comparative statistics

Sample	Total reads	Unmapped reads	Unique mapped reads	Multiple Mapped reads	Mapping ratio
lnc-Eg-1-1	70483482	24333767 (34.52%)	45549467 (64.62%)	600248 (0.85%)	65.48%
lnc-Eg-1-2	74001308	24243744 (32.76%)	49139752 (66.40%)	617812 (0.83%)	67.24%
lnc-Eg-1-3	92610992	27699495 (29.91%)	64135663 (69.25%)	775834 (0.84%)	70.09%
lnc-Eg-2-1	71071034	25913896 (36.46%)	44588760 (62.74%)	568378 (0.80%)	63.54%
lnc-Eg-2-2	80106116	27588617 (34.44%)	51861927 (64.74%)	655572 (0.82%)	65.56%
lnc-Eg-2-3	81976276	28491700 (34.76%)	52862820 (64.49%)	621756 (0.76%)	65.24%
lnc-Eg-3-1	66293004	20222163 (30.50%)	45530175 (68.68%)	540666 (0.82%)	69.50%
lnc-Eg-3-2	83054758	30310117 (36.49%)	52093301 (62.72%)	651340 (0.78%)	63.51%
lnc-Eg-3-3	76564332	26099385 (34.09%)	49865059 (65.13%)	599888 (0.78%)	65.91%

Table S5. Statistics on the number of transcripts

Sample name	Known transcripts	New transcripts	Total transcripts
Eg-1	3111 (42.24%)	3034	6145
Eg-2	3145 (42.70%)	3085	6230
Eg-3	3184 (43.23%)	3198	6382

Table S6. Filtering statistics of each sample data

sample	clear reads	clear tags
mir-Eg-1-1	19195506 (100%)	17188379 (93.5914%)
mir-Eg-1-2	11284354 (100%)	9717184 (90.0907%)
mir-Eg-1-3	14029273 (100%)	12424446 (92.5181%)
mir-Eg-2-1	15835441 (100%)	14023205 (91.6934%)
mir-Eg-2-2	14707836 (100%)	12913710 (91.1709%)
mir-Eg-2-3	15196301 (100%)	13856645 (94.6872%)
mir-Eg-3-1	13768037 (100%)	12451928 (94.0469%)
mir-Eg-3-2	13297013 (100%)	12222468 (95.1670%)
mir-Eg-3-3	12778590 (100%)	11772059 (95.7422%)

Table S7. The tag statistics of samples, compared with the genome

sample	total	match	ratio(%)
mir-Eg-1-1	17188379	10198736	59.34
mir-Eg-1-2	9717184	5409417	55.67
mir-Eg-1-3	12424446	6539559	52.63
mir-Eg-2-1	14023205	8422141	60.06
mir-Eg-2-2	12913710	8701828	67.38
mir-Eg-2-3	13856645	7150397	51.60
mir-Eg-3-1	12451928	7195374	57.79
mir-Eg-3-2	12222468	6598773	53.99
mir-Eg-3-3	11772059	5787837	49.17

Table S8. Statistics of known miRNA number and tag abundance identified in each sample

sample	total	miRNA num	tags uniq	tags total	ratio(%)
mir-Eg-1-1	17188379	306	12337	1855844	10.80%
mir-Eg-1-2	9717184	228	7293	925292	9.52%
mir-Eg-1-3	12424446	249	7837	821287	6.61%
mir-Eg-2-1	14023205	272	9970	1139684	8.13%
mir-Eg-2-2	12913710	172	7254	1846069	14.30%
mir-Eg-2-3	13856645	233	7596	884420	6.38%
mir-Eg-3-1	12451928	283	10326	979617	7.87%
mir-Eg-3-2	12222468	206	7232	916688	7.50%
mir-Eg-3-3	11772059	190	6490	863884	7.34%

Table S9. The number of novel miRNA identified in each sample and the abundance statistics of tag

sample	total	miRNA number	tags uniq	tags total	Ratio (%)
mir-Eg-1-1	17188379	3508	3857	137817	0.80%
mir-Eg-1-2	9717184	3020	3175	55776	0.57%
mir-Eg-1-3	12424446	3376	3621	50850	0.41%
mir-Eg-2-1	14023205	3329	3604	103383	0.74%
mir-Eg-2-2	12913710	1644	1783	104857	0.81%
mir-Eg-2-3	13856645	3466	3715	51609	0.37%
mir-Eg-3-1	12451928	3288	3564	103357	0.83%
mir-Eg-3-2	12222468	3365	3634	60721	0.50%
mir-Eg-3-3	11772059	3197	3397	43359	0.37%

Table S10. Predictive statistics of all miRNA target gene loci

Sample_name	miRNA_number	target_gene_number	target_site_number
mir-Eg-1-1	1125	4677	7681
mir-Eg-1-2	933	3856	6770
mir-Eg-1-3	981	3811	6074
mir-Eg-2-1	1065	4398	6934
mir-Eg-2-2	603	2424	3936
mir-Eg-2-3	982	3422	5648
mir-Eg-3-1	1025	3872	6208
mir-Eg-3-2	976	3729	6480
mir-Eg-3-3	886	3146	5305

Table S11. Statistics on new predictive targeting relationships of circRNAs

小 RNA 数目	靶基因数目 (环状 RNA)	靶向关系数目
4347	3871	250104