

Figure S1 The conserved motif identified in the moso bamboo GRF family.

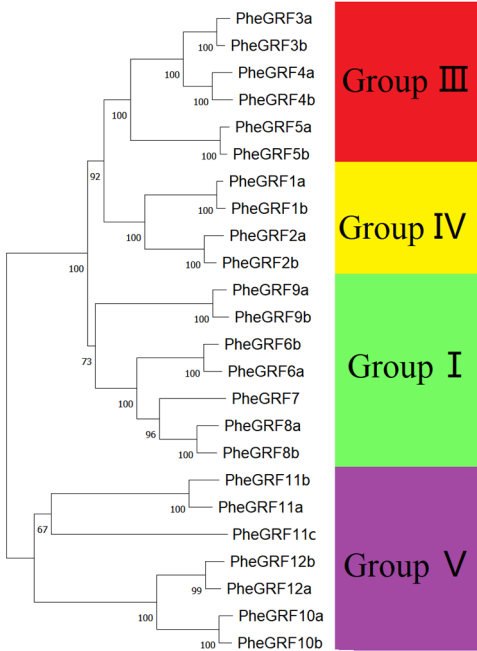


Figure S2 A neighbor-joining tree was constructed based on the alignment of full-length amino acid sequences of PheGRF protein.

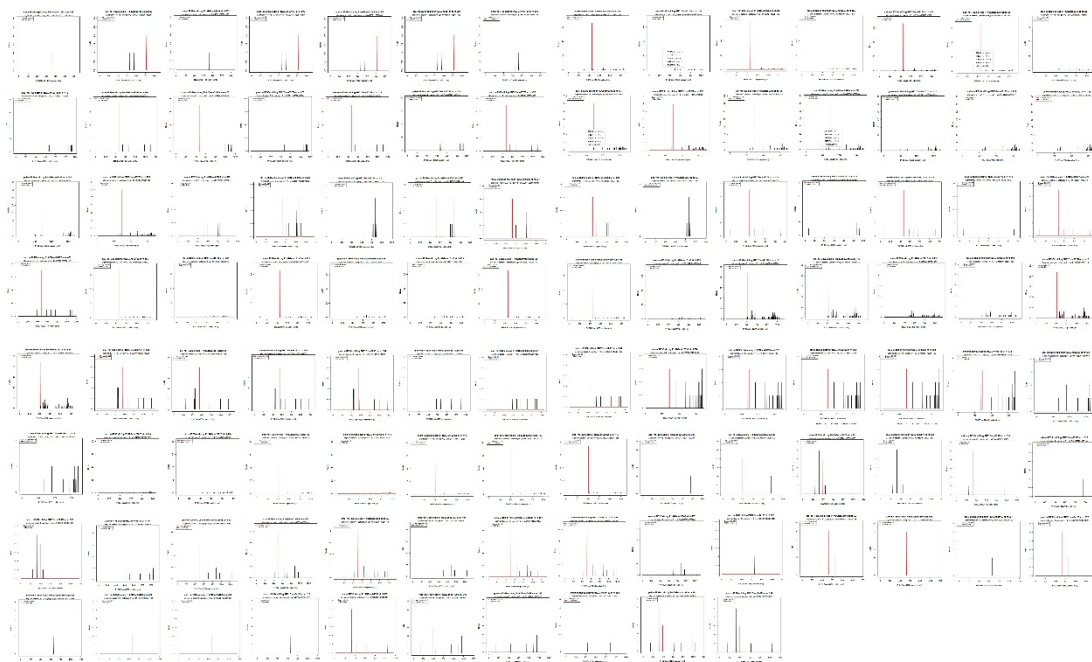


Figure S3 Splicing sites prediction based on degradation group sequencing.

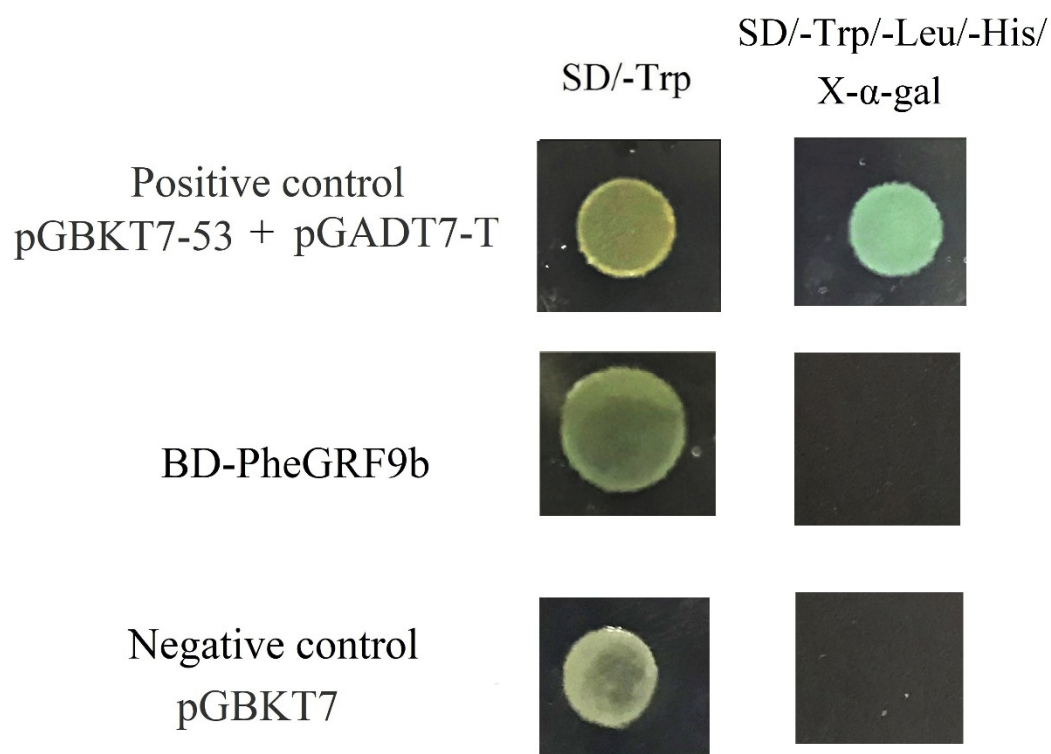


Figure S4 PheGRF9a self-transcription activation assay

Table S1 The Ka/Ks ratio of moso bamboo GRF gene pairs.

Gene 1	Location	Gene 2	Location	Duplication types	Ka	Ks	Ka/Ks
PH02Gene03768.t1 (PheGRF4a)	hic_scaffold_3:86189727	PH02Gene08777.t1 (PheGRF4b)	hic_scaffold_17:18671790	WGD	0.035096	0.141917	0.247302
PH02Gene02258.t2 (PheGRF3a)	hic_scaffold_23:12865011	PH02Gene10190.t3 (PheGRF3b)	hic_scaffold_24:61167988	WGD	0.033063	0.066159	0.499757
PH02Gene23215.t2 (PheGRF5a)	hic_scaffold_6:6514485	PH02Gene29026.t2 (PheGRF5b)	hic_scaffold_8:1707627	WGD	0.030261	0.096972	0.31206
PH02Gene03385.t2 (PheGRF2a)	hic_scaffold_8:14186770	PH02Gene02620.t1 (PheGRF2b)	hic_scaffold_6:15130344	WGD	0.055414	0.153787	0.360331
PH02Gene34199.t1 (PheGRF1a)	hic_scaffold_17:6504498	PH02Gene33579.t1 (PheGRF1b)	hic_scaffold_3:97165941	WGD	0.023117	0.143991	0.160542
PH02Gene32022.t1 (PheGRF11a)	hic_scaffold_10:52546653	PH02Gene45969.t1 (PheGRF11b)	hic_scaffold_4:30356073	WGD	0.022526	0.144882	0.155475
PH02Gene01931.t1 (PheGRF12a)	hic_scaffold_23:16329922	PH02Gene00590.t1 (PheGRF12b)	hic_scaffold_24:58027198	WGD	0.046145	0.101135	0.45627
PH02Gene01484.t1 (PheGRF10a)	hic_scaffold_3:82398027	PH02Gene03343.t1 (PheGRF10b)	hic_scaffold_17:22455120	WGD	0.021573	0.146075	0.147682
PH02Gene15670.t1 (PheGRF9a)	hic_scaffold_15:79050765	PH02Gene26381.t1 (PheGRF9b)	hic_scaffold_21:28883675	WGD	0.037645	0.138642	0.271527
PH02Gene26399.t1 (PheGRF6a)	hic_scaffold_21:19016635	PH02Gene06203.t1 (PheGRF6b)	hic_scaffold_15:86449468	WGD	0.040375	0.147348	0.274009
PH02Gene06385.t2 (PheGRF8a)	hic_scaffold_7:51518367	PH02Gene34169.t1 (PheGRF8b)	hic_scaffold_15:24940152	WGD	0.061216	0.107567	0.569103
PH02Gene02258.t2 (PheGRF3a)	hic_scaffold_23:12865011	PH02Gene08777.t1 (PheGRF4b)	hic_scaffold_17:18671790	WGD	0.127392	0.430448	0.295951
PH02Gene03768.t1 (PheGRF4a)	hic_scaffold_3:86189727	PH02Gene02258.t2 (PheGRF3a)	hic_scaffold_23:12865011	WGD	0.136772	0.444735	0.307535
PH02Gene03768.t1 (PheGRF4a)	hic_scaffold_3:86189727	PH02Gene10190.t3 (PheGRF3b)	hic_scaffold_24:61167988	WGD	0.131	0.435394	0.300878
PH02Gene10190.t3 (PheGRF3b)	hic_scaffold_24:61167988	PH02Gene08777.t1 (PheGRF4b)	hic_scaffold_17:18671790	WGD	0.119446	0.441194	0.270733
PH02Gene33803.t1 (PheGRF7)	hic_scaffold_12:32116354	PH02Gene26399.t1 (PheGRF6a)	hic_scaffold_21:19016635	Dispersed	0.399799	2.003109	0.199589
PH02Gene33803.t1 (PheGRF7)	hic_scaffold_12:32116354	PH02Gene06203.t1 (PheGRF6b)	hic_scaffold_15:86449468	Dispersed	0.397698	2.168189	0.183424
PH02Gene06385.t2 (PheGRF8a)	hic_scaffold_7:51518367	PH02Gene33803.t1 (PheGRF7)	hic_scaffold_12:32116354	Dispersed	0.298967	1.037966	0.288031

Table S2 The accession numbers of the GRFs from each species.

Species name	Gene name	ID	Accession number
<i>Vigna unguiculata</i>	VunGRF	Vun004052	\
<i>Arabidopsis thaliana</i>	AtGR6	AT2G06200.1	AY060586
<i>Arabidopsis thaliana</i>	AtGR1	AT2G22840.1	AY102634
<i>Arabidopsis thaliana</i>	AtGR3	AT2G36400.1	AY102636
<i>Arabidopsis thaliana</i>	AtGR9	AT2G45480.1	AY074647
<i>Arabidopsis thaliana</i>	AtGR5	AT3G13960.1	AY102638
<i>Arabidopsis thaliana</i>	AtGR4	AT3G52910.1	AY102638
<i>Arabidopsis thaliana</i>	AtGR8	AT4G24150.1	AL109619
<i>Arabidopsis thaliana</i>	AtGR2	AT4G37740.1	AK176432
<i>Arabidopsis thaliana</i>	AtGR7	AT5G53660.1	AK176109
<i>Oryza sativa subsp. japonica</i>	OsGRF10	LOC_Os02g45570.1	AK108170
<i>Oryza sativa subsp. japonica</i>	OsGRF4	LOC_Os02g47280.1	AK063983
<i>Oryza sativa subsp. japonica</i>	OsGRF1	LOC_Os02g53690.1	AF201895
<i>Oryza sativa subsp. japonica</i>	OsGRF9	LOC_Os03g47140.1	AK058659
<i>Oryza sativa subsp. japonica</i>	OsGRF6	LOC_Os03g51970.1	AK073578
<i>Oryza sativa subsp. japonica</i>	OsGRF12	LOC_Os04g48510.1	AK110934
<i>Oryza sativa subsp. japonica</i>	OsGRF3	LOC_Os04g51190.1	FJ546693
<i>Oryza sativa subsp. japonica</i>	OsGRF5	LOC_Os06g02560.1	AK103508

<i>Oryza sativa subsp. japonica</i>	OsGRF2	LOC_Os06g10310.1	CT836198
<i>Oryza sativa subsp. japonica</i>	OsGRF11	LOC_Os07g28430.1	CT836198
<i>Oryza sativa subsp. japonica</i>	OsGRF8	LOC_Os11g35030.1	AK103055
<i>Oryza sativa subsp. japonica</i>	OsGRF7	LOC_Os12g29980.1	AK103055
<i>Phyllostachys edulis</i>	PheGRF12b	PH02Gene00590.t1	\
<i>Phyllostachys edulis</i>	PheGRF10a	PH02Gene01484.t1	\
<i>Phyllostachys edulis</i>	PheGRF12a	PH02Gene01931.t1	\
<i>Phyllostachys edulis</i>	PheGRF3a	PH02Gene02258.t2	\
<i>Phyllostachys edulis</i>	PheGRF2b	PH02Gene02620.t1	\
<i>Phyllostachys edulis</i>	PheGRF10b	PH02Gene03343.t1	\
<i>Phyllostachys edulis</i>	PheGRF2a	PH02Gene03385.t2	\
<i>Phyllostachys edulis</i>	PheGRF4a	PH02Gene03768.t1	\
<i>Phyllostachys edulis</i>	PheGRF6b	PH02Gene06203.t1	\
<i>Phyllostachys edulis</i>	PheGRF8a	PH02Gene06385.t2	\
<i>Phyllostachys edulis</i>	PheGRF4b	PH02Gene08777.t1	\
<i>Phyllostachys edulis</i>	PheGRF3b	PH02Gene10190.t3	\
<i>Phyllostachys edulis</i>	PheGRF9a	PH02Gene15670.t1	\
<i>Phyllostachys edulis</i>	PheGRF11c	PH02Gene22646.t2	\
<i>Phyllostachys edulis</i>	PheGRF5a	PH02Gene23215.t2	\
<i>Phyllostachys edulis</i>	PheGRF9b	PH02Gene26381.t1	\
<i>Phyllostachys edulis</i>	PheGRF6a	PH02Gene26399.t1	\
<i>Phyllostachys edulis</i>	PheGRF5b	PH02Gene29026.t2	\
<i>Phyllostachys edulis</i>	PheGRF11a	PH02Gene32022.t1	\
<i>Phyllostachys edulis</i>	PheGRF1b	PH02Gene33579.t1	\
<i>Phyllostachys edulis</i>	PheGRF7	PH02Gene33803.t1	\
<i>Phyllostachys edulis</i>	PheGRF8b	PH02Gene34169.t1	\
<i>Phyllostachys edulis</i>	PheGRF1a	PH02Gene34199.t1	\
<i>Phyllostachys edulis</i>	PheGRF11b	PH02Gene45969.t1	\

Table S3 Primers used for qRT-PCR.

Name	Primer
PH02Gene02258.t2F	GAGGGAGCCACTGTCTTTCT
PH02Gene02258.t2R	CAGAGGTTGCCATCGGAATG
PH02Gene03343.t1F	GAGAAAGAAGCCGACTCGC
PH02Gene03343.t1R	AGTAGCGGTAGATGAGCACC
PH02Gene10190.t3F	GGAGCGACTTTGTGACTGTC
PH02Gene10190.t3R	CGGAATGGAGATCGAGAGCT
PH02Gene23215.t2F	ACGGCAGCAAGTACTCTCTT
PH02Gene23215.t2R	TGATGGCTCAAGGTGGGAAT
PH02Gene26399.t1F	CCTATCATCGGCCTCCACAT
PH02Gene26399.t1R	CTTGCTTCCATGGTGCTGTT
TIP41F	AAAATCATTGTAGGCCATTGTCTG
TIP41R	ACTAAATTAAGCCAGCGGGAGTG