

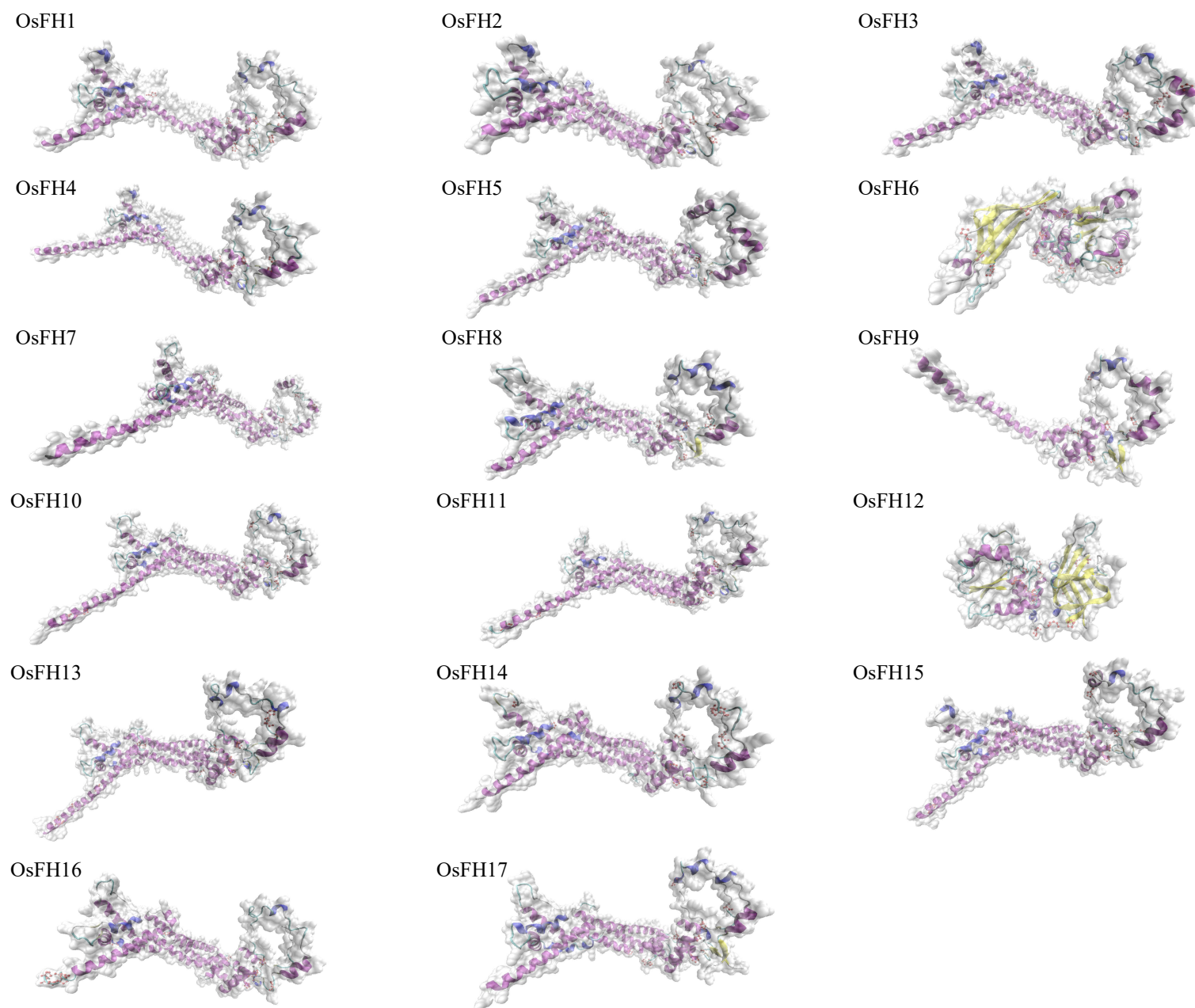


Fig. S1 Prediction of the tertiary structure of rice FORMIN proteins. Yellow represents the β -sheet, purple represents the alpha helix, blue represents the short alpha helix, gray represents the unstructured chain, cyan represents the loop chain

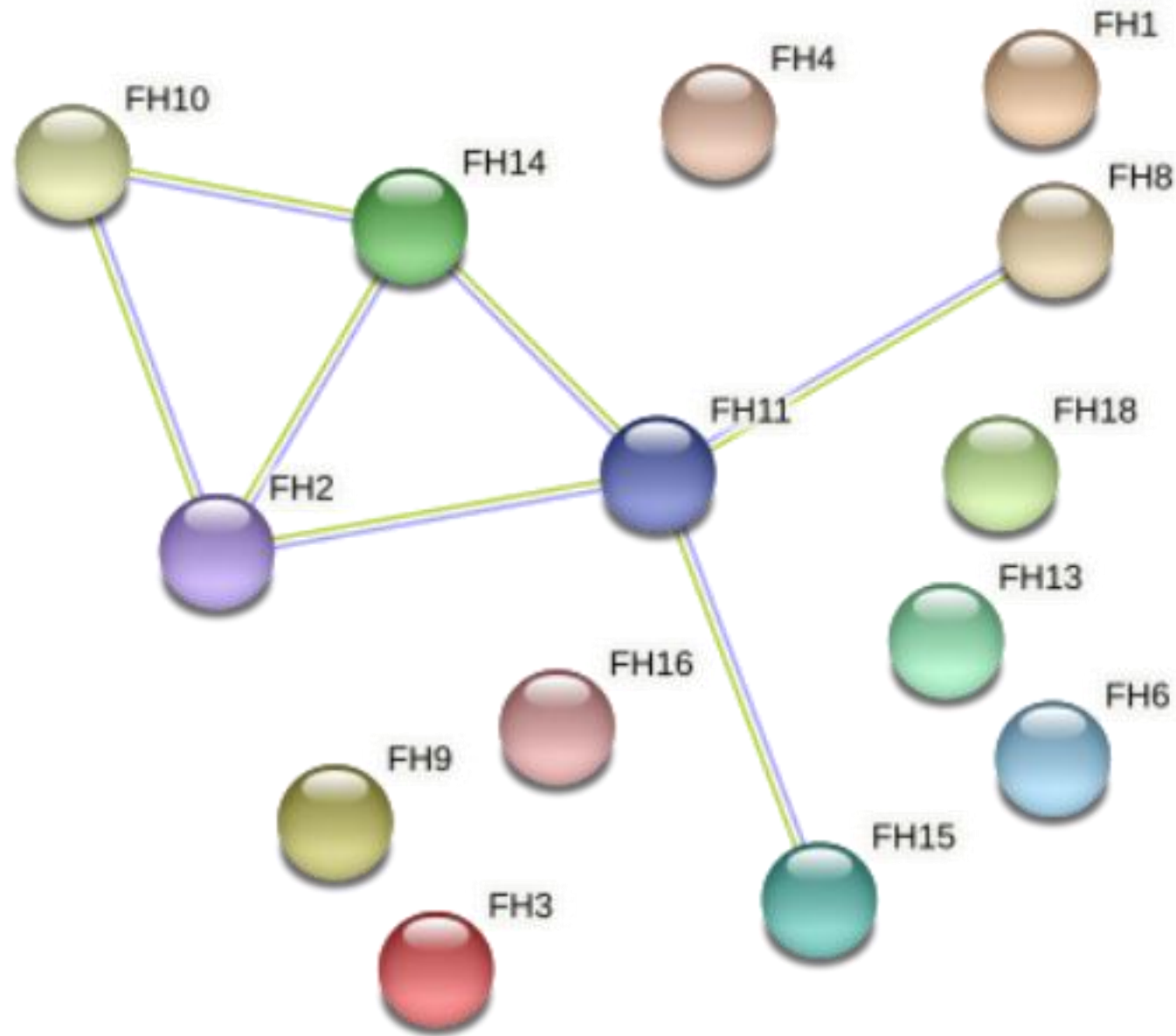


Fig. S2 The protein-protein interaction network as analyzed by String software. An edge was drawn with up to two differently colored lines that represent the existence of the two types of evidence used in predicting the associations. A green line indicates neighborhood evidence, and a blue line indicated co-occurrence evidence

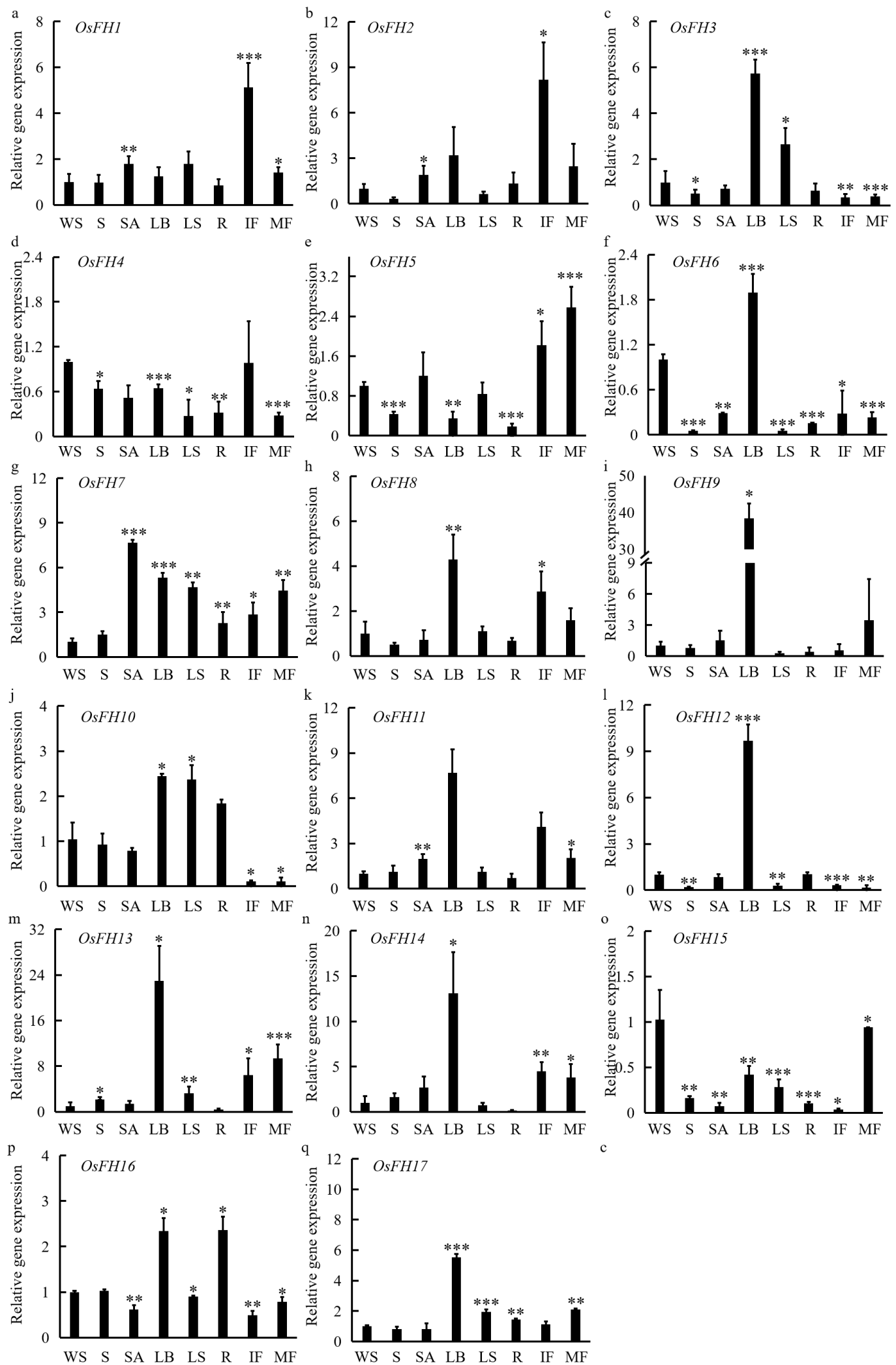


Fig. S3 Gene expression profiling of the rice *FORMIN* genes in eight different tissues or organs. Tissues or organs, include whole seedings (WS), shoots (S), shoot apices (SA), leaf blades (LB), leaf sheaths (LS), roots (R), immature flowers (IF) and mature flowers (MF). Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

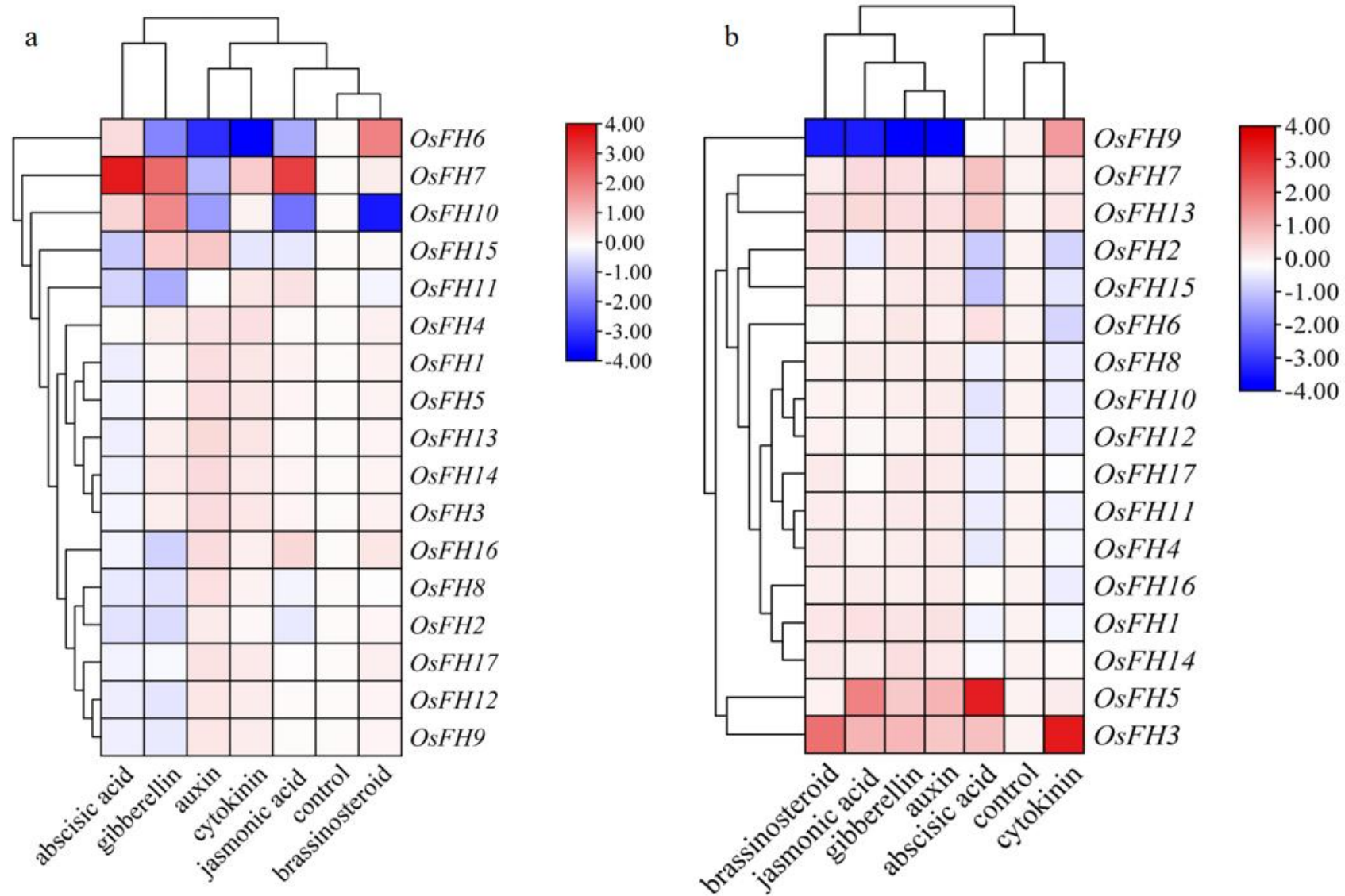


Fig. S4 Expression profiles of rice *FORMIN* genes responding to phytohormone treatment. Expression profiles of *OsFHs* in the rice shoot a) or in the rice root b) under different phytohormone treatments. The data used in the figure were obtained from the Xpro database. All red represents up-regulated genes, and blue is for down-regulated ones

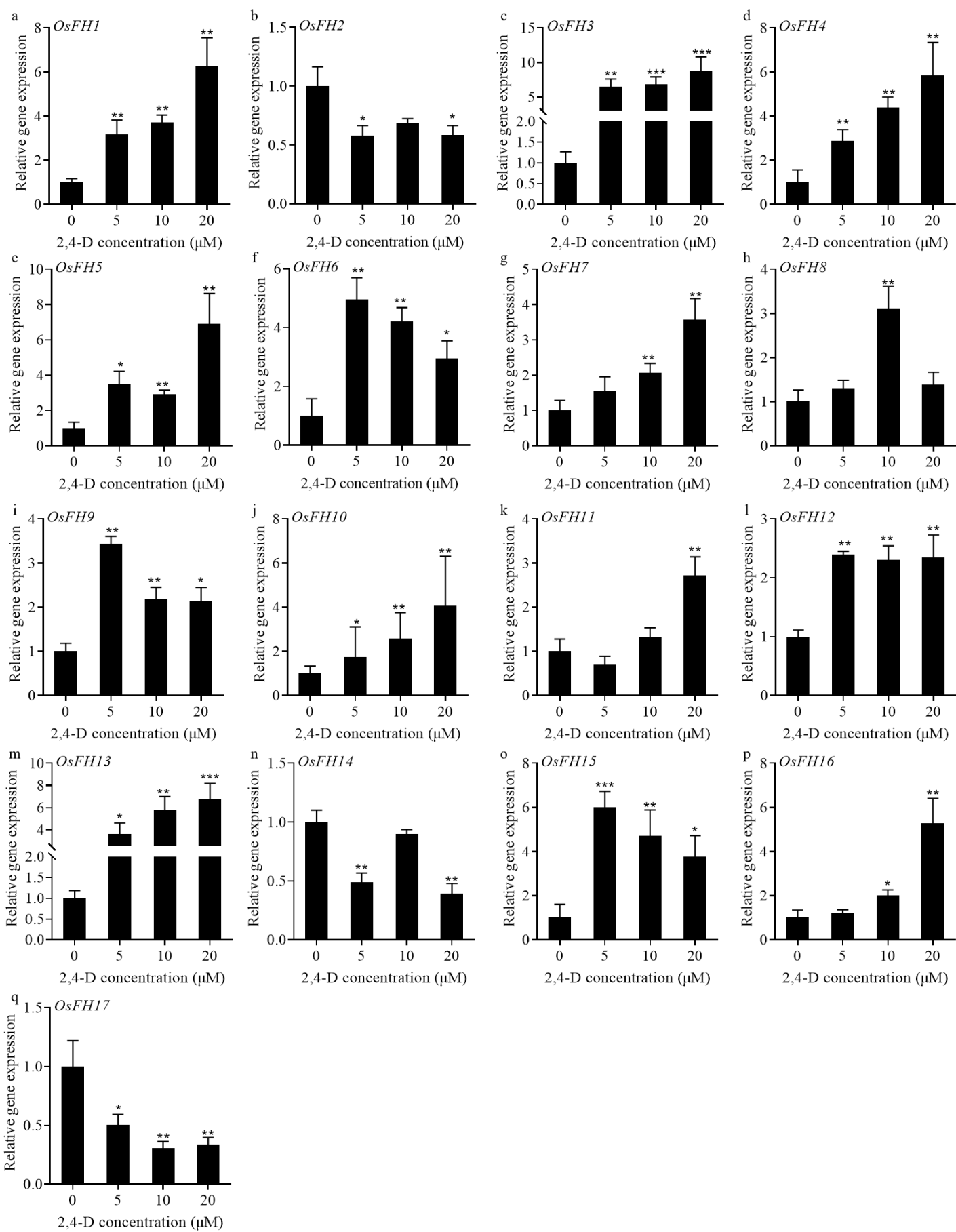


Fig. S5 Expression patterns of *FORMIN* genes in the shoot of rice under IAA treatment. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

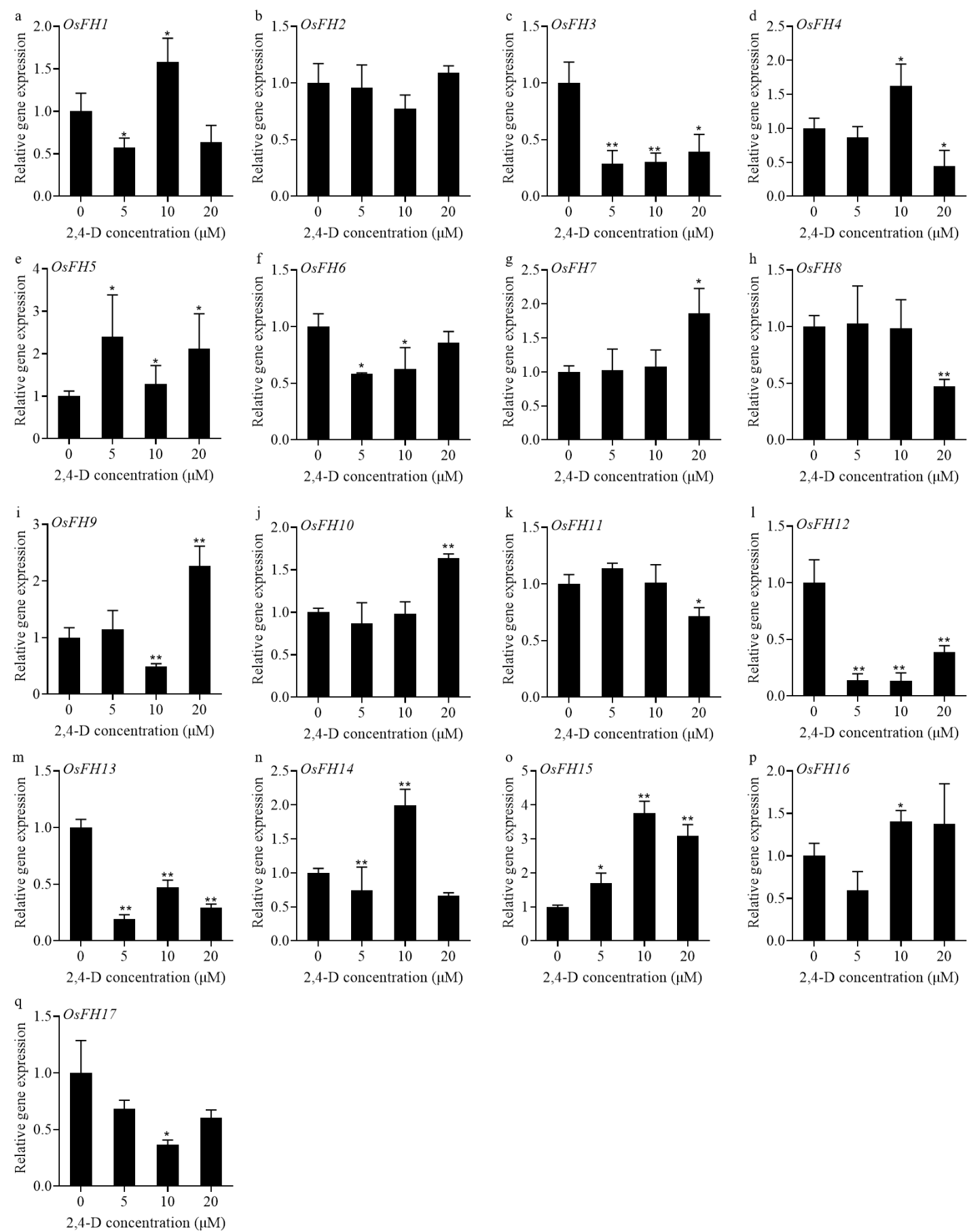


Fig. S6 Expression patterns of *FORMIN* genes in the root of rice under IAA treatment. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

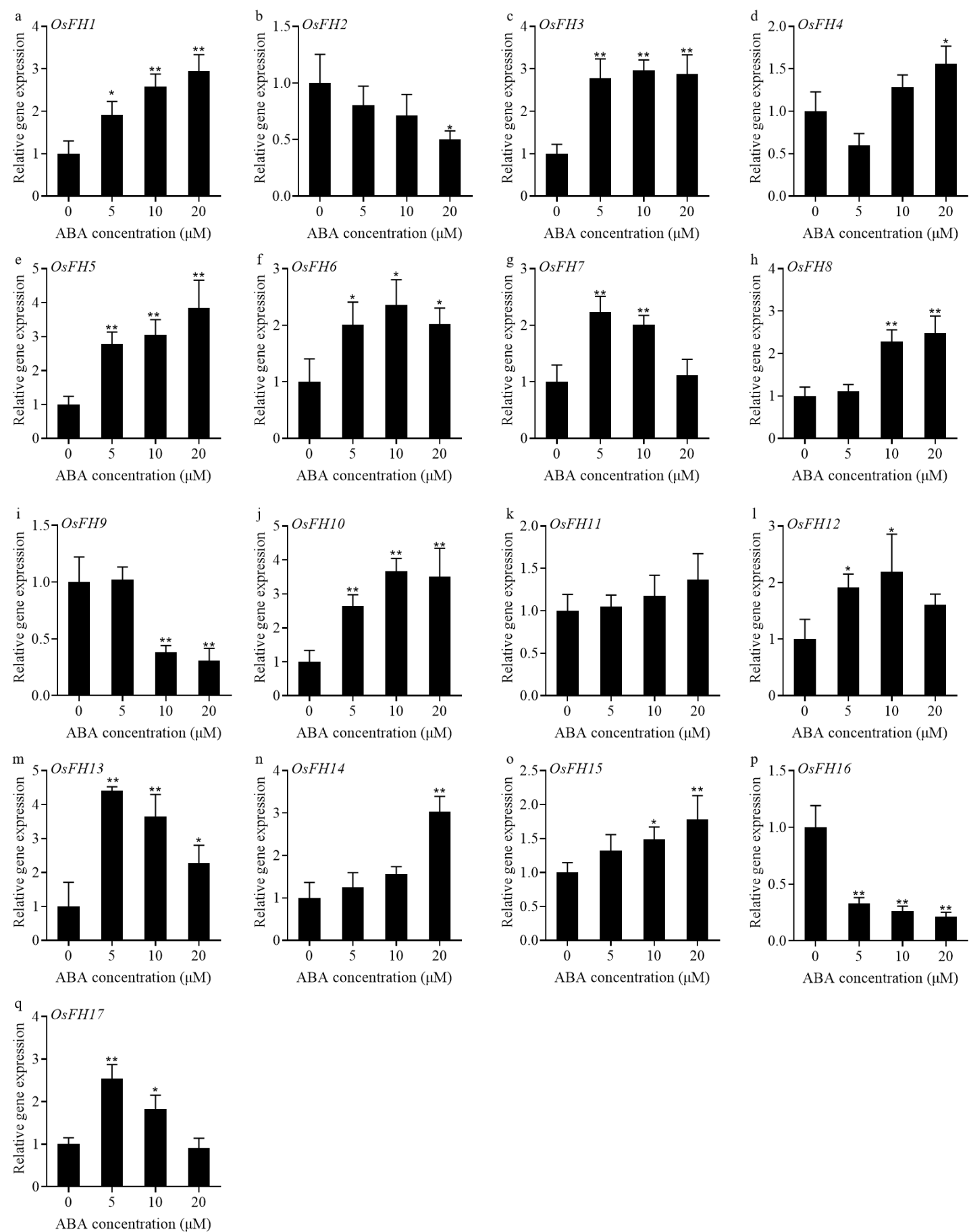


Fig. S7 Expression patterns of *FORMIN* genes in the shoot of rice under ABA treatment. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

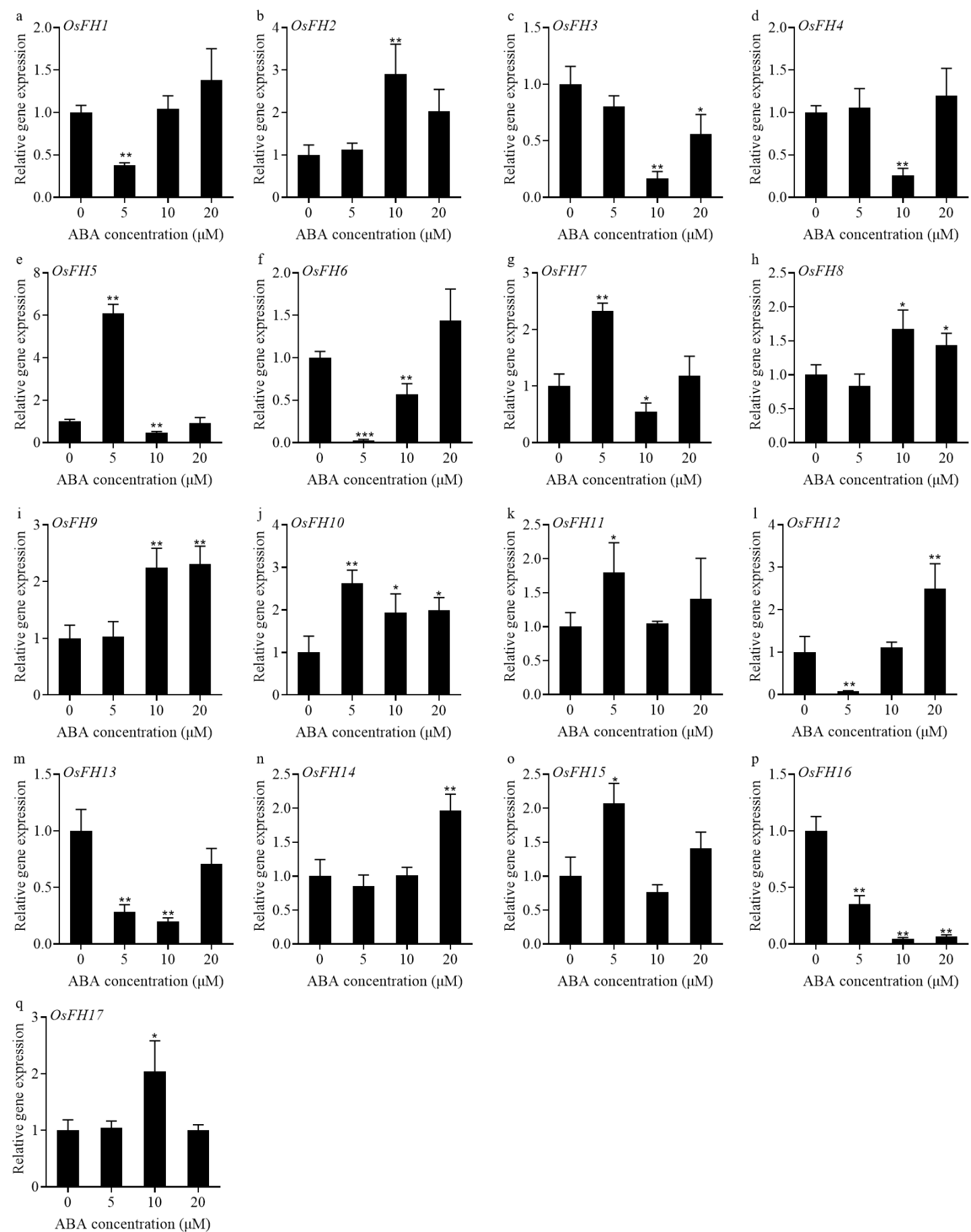


Fig. S8 Expression patterns of *FORMIN* genes in the root of rice under ABA treatment. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

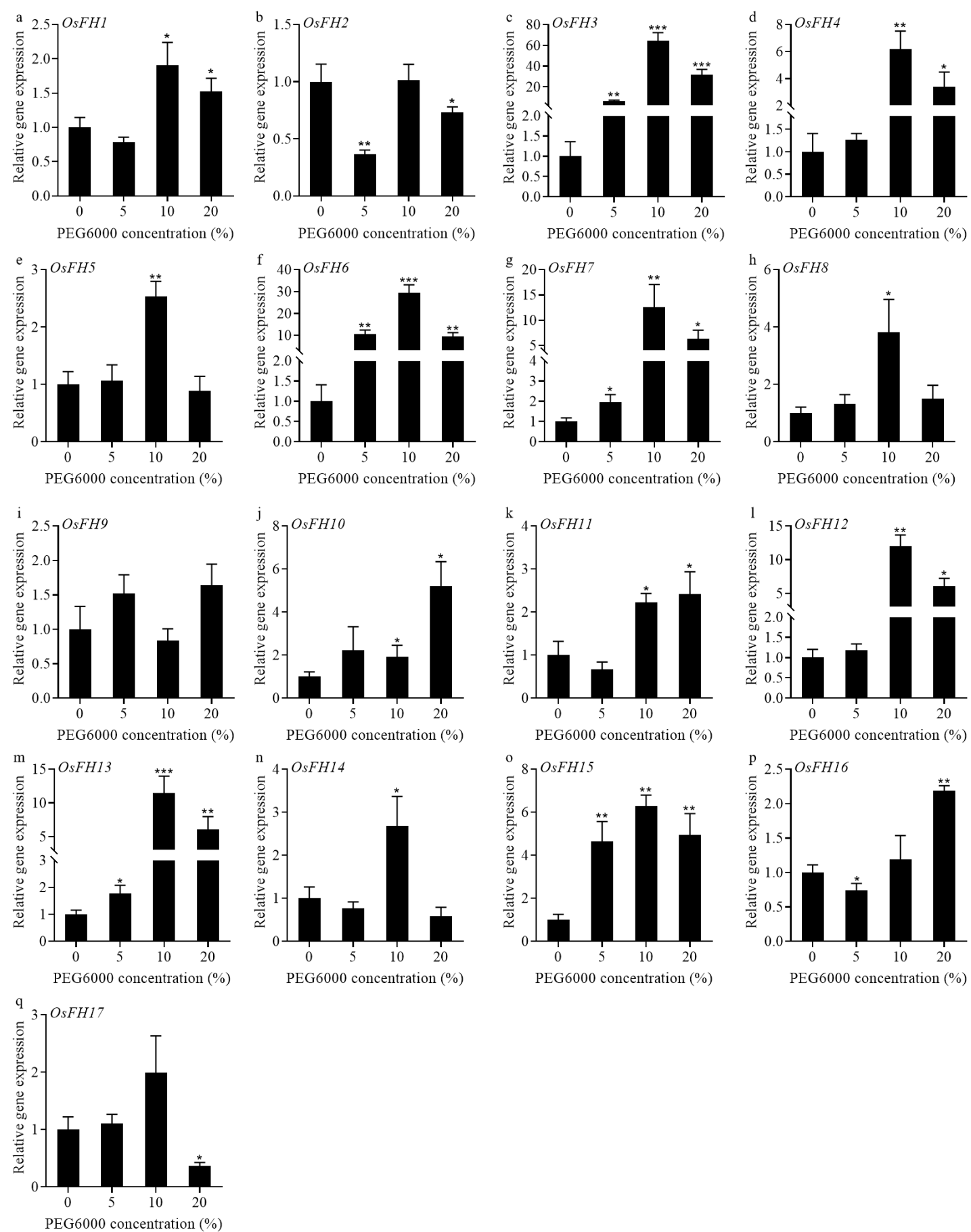


Fig. S9 Expression levels of Rice *FORMIN* genes under PEG6000 treatment in the shoot. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

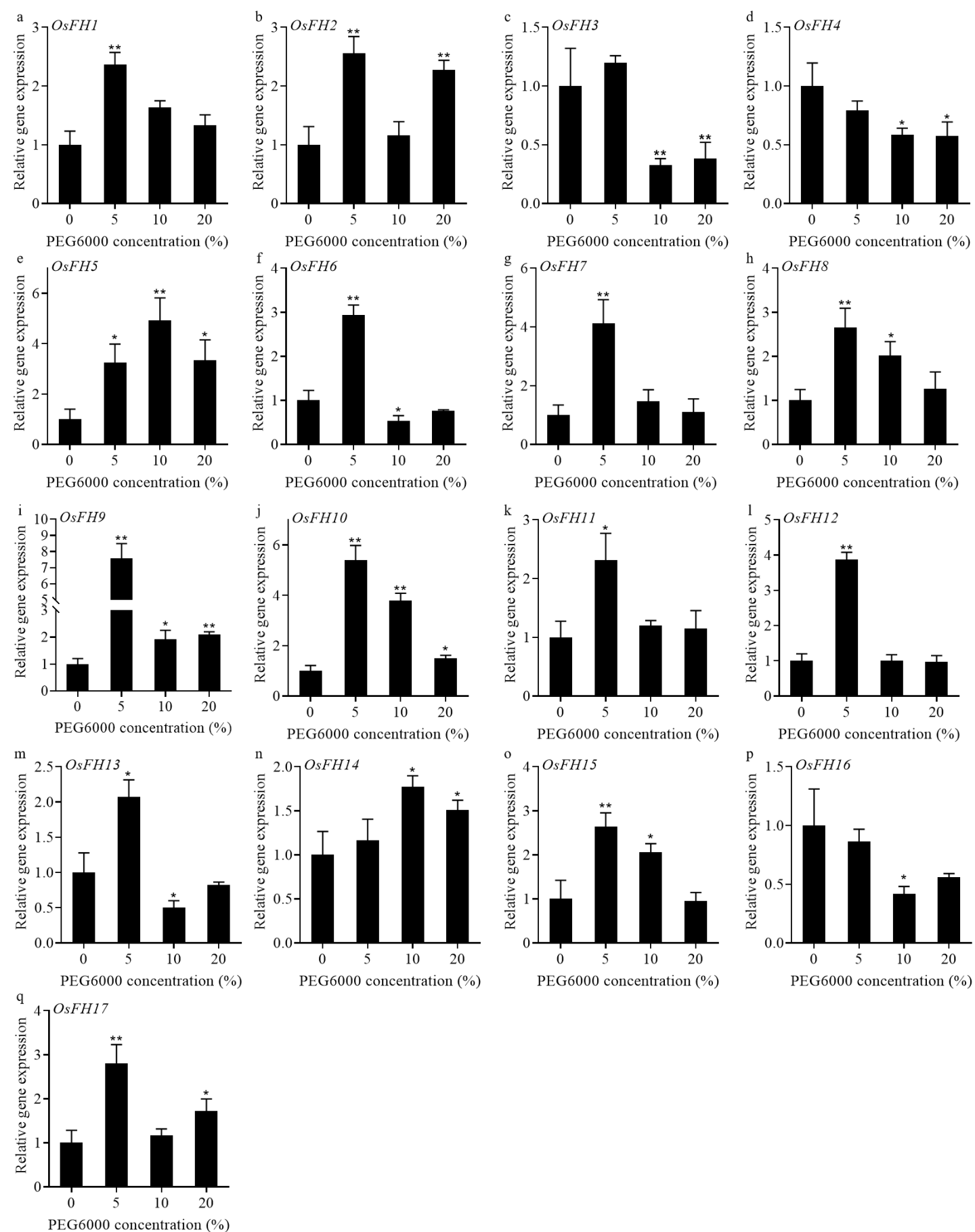


Fig. S10 Expression levels of Rice *FORMIN* genes under PEG6000 treatment in the root. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

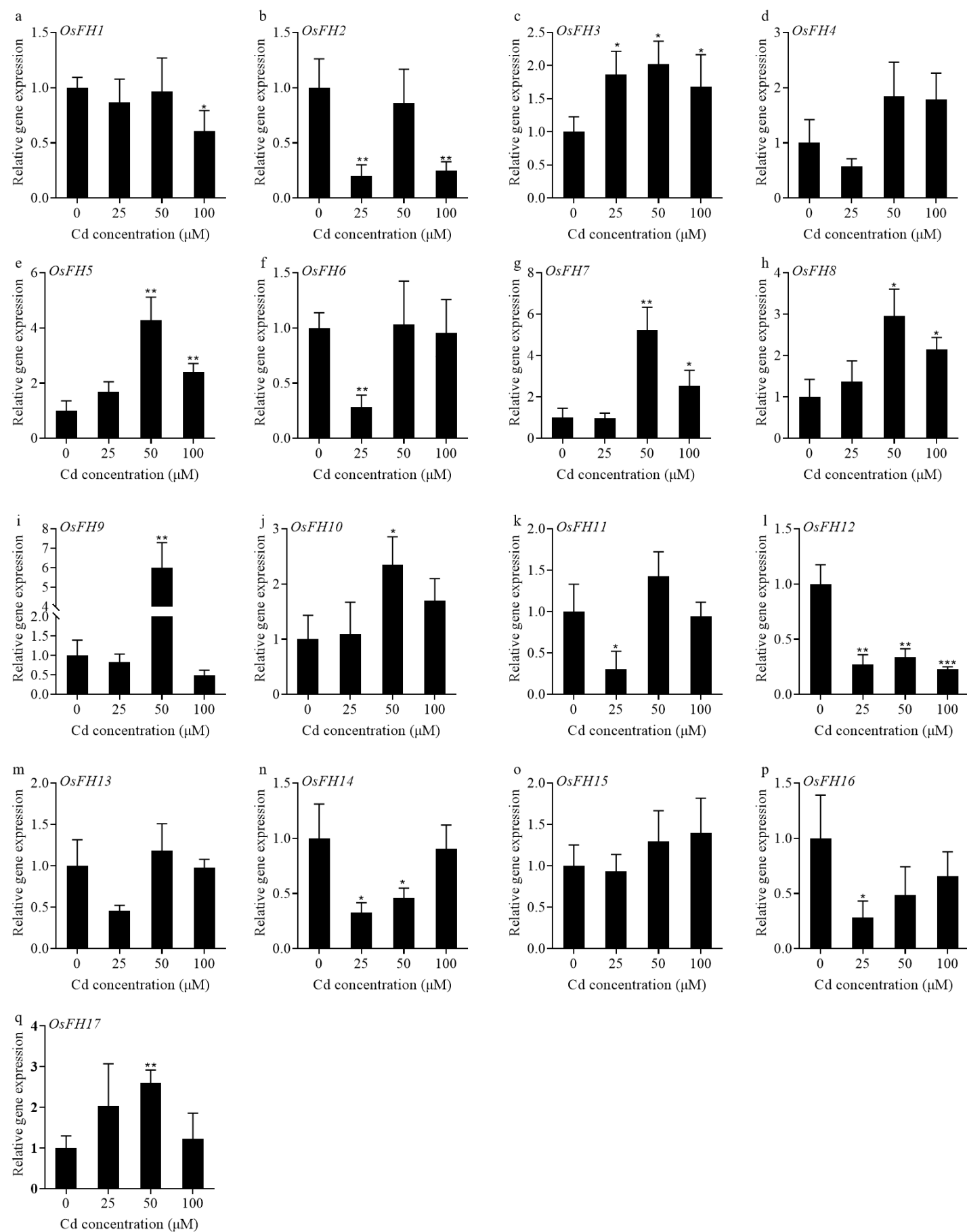


Fig. S11 Expression levels of Rice *FORMIN* genes under Cd treatment in the shoot. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

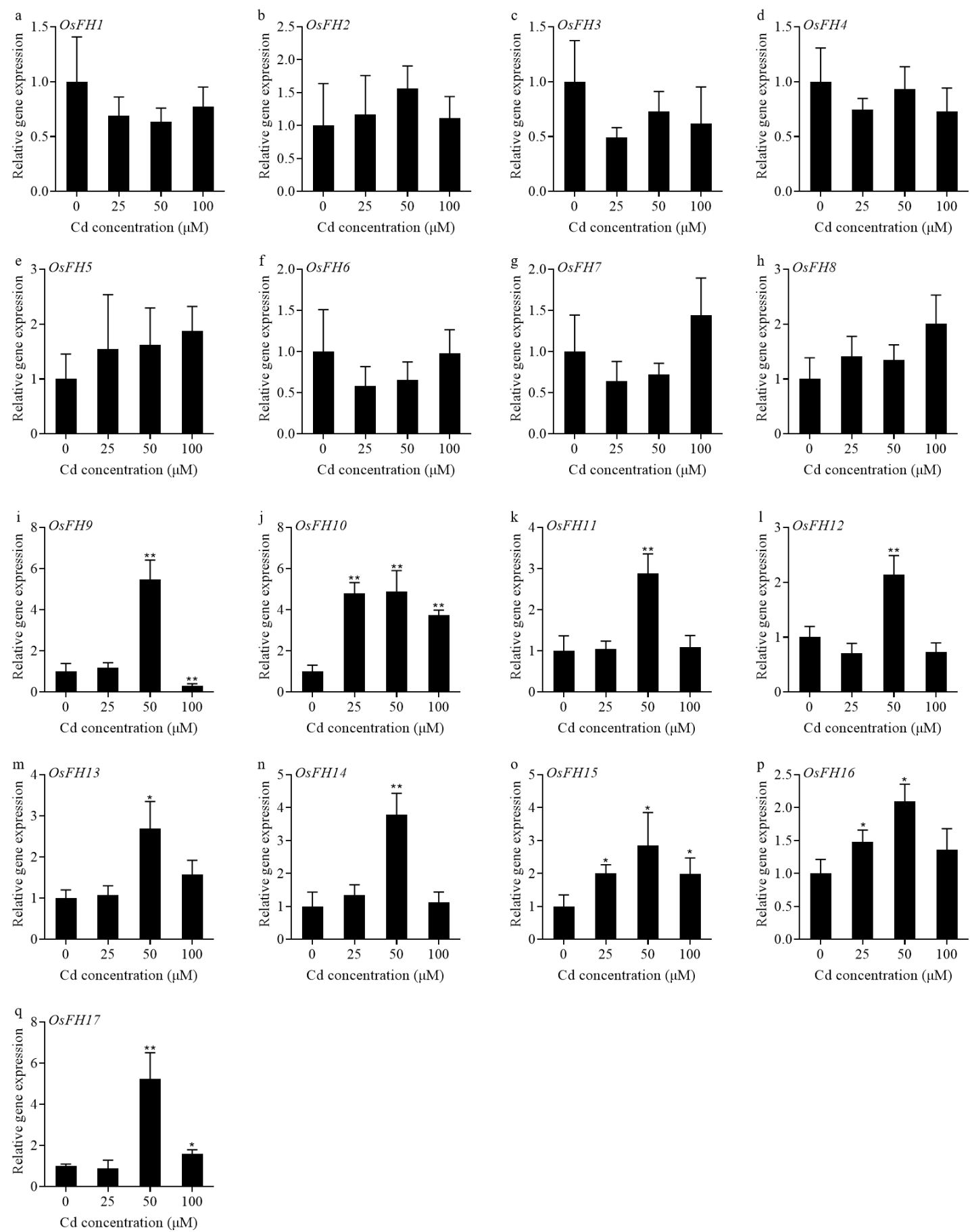


Fig. S12 Expression levels of Rice *FORMIN* genes under Cd treatment in the root. Data are the mean $\pm$ SD for three biological replicates. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t-test

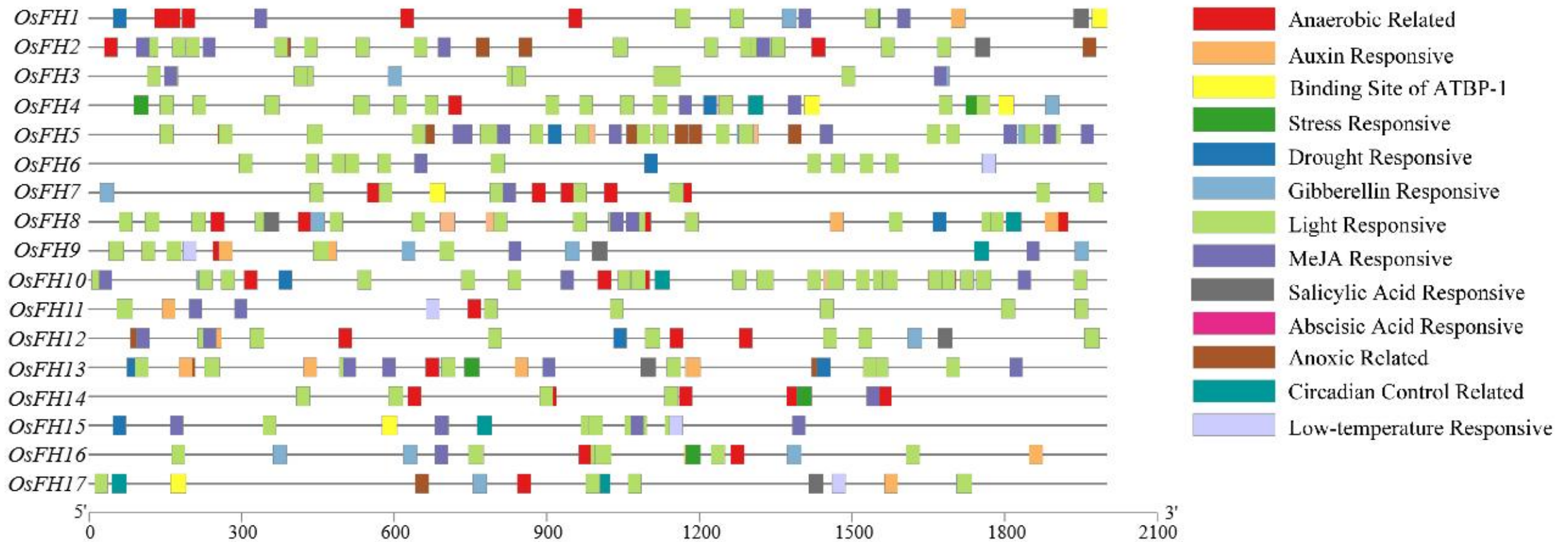


Fig. S13 Cis-acting element analysis in *OsFHs* promoter regions. Positional distribution of predicted Cis-regulatory element on *OsFHs* promoters were shown as vertical bars. Promoter sequences (–2000 bp) of seventeen *OsFHs* genes were analyzed by using PlantCARE. Legend depicts the colour of individual cis-acting elements

Table S1. Primers used for qRT-PCR analysis

Gene Name	Gene ID	Direction	Primer Sequences	Length of product
<i>OsFH1</i>	<i>Os01g0897700</i>	Primer-F	CCCAATGATGCCACAGTTG	455
		Primer-R	TCAAGGTGATGATGCTGAAG	
<i>OsFH2</i>	<i>Os04g0461800</i>	Primer-F	CGCACCGAAACAGCAGAGCAG	219
		Primer-R	TCGATCATCTTCTCGTCCAGCC	
<i>OsFH3</i>	<i>Os10g0119300</i>	Primer-F	TCCAAACTGAGAGTGTTTGC	246
		Primer-R	CTTGTTGTTTCTAGCTCGAG	
<i>OsFH4</i>	<i>Os10g0347800</i>	Primer-F	GACCTTAGTAAAGATGGCTC	238
		Primer-R	CATTCTGTTCCTGTCTC	
<i>OsFH5</i>	<i>Os07g0596300</i>	Primer-F	CGCTCTCCGCAAATCTTCC	171
		Primer-R	AGTAATCCCCTGTACTCATCCTC	
<i>OsFH6</i>	<i>Os08g0280200</i>	Primer-F	TCTGTCAAAGTTTCAAGTGCCG	229
		Primer-R	GGGATGGAAATGATGAAAGGTC	
<i>OsFH7</i>	<i>Os02g0794900</i>	Primer-F	TCAAGAAACCGCCCGATGG	102
		Primer-R	CTGCAACACCTCTTATGTGG	
<i>OsFH8</i>	<i>Os03g0204100</i>	Primer-F	CAACAACGGGAGCACGTCAATGCG	311
		Primer-R	TGGCGATGTTCTGCGCCTTCTTGG	
<i>OsFH9</i>	<i>Os08g0431200</i>	Primer-F	GCATTCCCAAGGATGGAGGT	108
		Primer-R	CTTCAATTCAGTGCAAGCTCC	
<i>OsFH10</i>	<i>Os02g0161100</i>	Primer-F	CGCCATCTTTCTTCTGGACCAG	162
		Primer-R	TTCCGTGGAATGACTCGATAAC	
<i>OsFH11</i>	<i>Os07g0545500</i>	Primer-F	GCCTCATCTCTGTGCAGCTC	147
		Primer-R	CCAATCCACACTTGACCCATG	
<i>OsFH12</i>	<i>Os04g0245000</i>	Primer-F	CTGGTTTCAGGCTTGTCTCCC	183
		Primer-R	GCCAACCGCCTTTCTCACAATG	
<i>OsFH13</i>	<i>Os07g0588200</i>	Primer-F	TTGCCTTCGAGAGAGTGATG	293
		Primer-R	TCGGATGATCTCTTTAACCACG	
<i>OsFH14</i>	<i>Os05g0104000</i>	Primer-F	AGGGAGGTGTGCTTACTGG	178
		Primer-R	TAAGCTCTTCCTCATTGGTG	
<i>OsFH15</i>	<i>Os09g0517600</i>	Primer-F	TGCAACCAGGAGAACAAGGTG	270
		Primer-R	CGCAAATGGTATCGCAAGCAC	
<i>OsFH16</i>	<i>Os02g0739100</i>	Primer-F	GCAGGCAATCGGATGAATGC	256
		Primer-R	ATGGACCCTGACTTGTGGAG	
<i>OsFH17</i>	<i>Os04g0100300</i>	Primer-F	CGCCATTCAAGAAGTCGCC	106
		Primer-R	TTTGATTGGCAGTAACTTTGT	

Table S2. The protein-protein interaction of FORMINs analyzed by using String software

Node1	Node2	Node1 accession	Node2 accession	Node1 annotation	Node2 annotation	Score
<i>OsFH10</i>	<i>OsFH14</i>	Q6H7U3	Q0DLG0	Formin-like protein 10	Formin-like protein 14	0.541
<i>OsFH10</i>	<i>OsFH2</i>	Q6H7U3	Q7XUV2	Formin-like protein 10	Formin-like protein 2	0.448
<i>OsFH11</i>	<i>OsFH14</i>	Q0D5P3	Q0DLG0	Formin-like protein 11	Formin-like protein 14	0.516
<i>OsFH11</i>	<i>OsFH15</i>	Q0D5P3	Q69MT2	Formin-like protein 11	Formin-like protein 15	0.44
<i>OsFH11</i>	<i>OsFH2</i>	Q0D5P3	Q7XUV2	Formin-like protein 11	Formin-like protein 2	0.427
<i>OsFH11</i>	<i>OsFH8</i>	Q0D5P3	Q10Q99	Formin-like protein 11	Formin-like protein 8	0.454
<i>OsFH14</i>	<i>OsFH10</i>	Q0DLG0	Q6H7U3	Formin-like protein 14	Formin-like protein 10	0.541
<i>OsFH14</i>	<i>OsFH11</i>	Q0DLG0	Q0D5P3	Formin-like protein 14	Formin-like protein 11	0.516
<i>OsFH14</i>	<i>OsFH2</i>	Q0DLG0	Q7XUV2	Formin-like protein 14	Formin-like protein 2	0.496
<i>OsFH15</i>	<i>OsFH11</i>	Q69MT2	Q0D5P3	Formin-like protein 15	Formin-like protein 11	0.44
<i>OsFH2</i>	<i>OsFH10</i>	Q7XUV2	Q6H7U3	Formin-like protein 2	Formin-like protein 10	0.448
<i>OsFH2</i>	<i>OsFH11</i>	Q7XUV2	Q0D5P3	Formin-like protein 2	Formin-like protein 11	0.427
<i>OsFH2</i>	<i>OsFH14</i>	Q7XUV2	Q0DLG0	Formin-like protein 2	Formin-like protein 14	0.496
<i>OsFH8</i>	<i>OsFH11</i>	Q10Q99	Q0D5P3	Formin-like protein 8	Formin-like protein 11	0.454

Table S3. *OsFHs* expression pattern analysis based on Gene Expression Atlas database

Gene	Experiment accession	Experimental treatment comparison	log 2 fold change	Adjusted p-value
OsFH1	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'shoot' at '24 hour'	-2	0.004648416
OsFH1	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '1 hour'	1	0.0438788
OsFH13	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'shoot' at '24 hour'	-1.3	0.000344835
OsFH15	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'shoot' at '24 hour'	-3.3	0.00038457
OsFH16	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '24 hour'	3.8	1.71813E-68
OsFH16	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '1 hour'	3	1.72086E-45
OsFH2	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '24 hour'	-3.4	0.017469971
OsFH3	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '1 hour'	-1	0.030209891
OsFH7	E-MTAB-4306	cadmium sulfate; 50 micromolar' vs 'none' in 'root' at '24 hour'	1.5	8.57007E-08
OsFH16	E-MTAB-4994	drought environment' vs 'normal watering'	1.2	2.64333E-07
OsFH2	E-GEOD-41647	drought environment' vs 'control' in 'tolerant to drought environment' at '6 hour'	-1.8	1.81266E-05
OsFH2	E-GEOD-41647	drought environment' vs 'control' in 'tolerant to drought environment' at '3 hour'	-1.6	5.21116E-05
OsFH2	E-GEOD-41647	drought environment' vs 'control' in 'susceptible to drought environment' at '6 hour'	-1.4	1.76322E-05
OsFH7	E-GEOD-41647	drought environment' vs 'control' in 'susceptible to drought environment' at '3 hour'	1.5	9.78703E-05
OsFH7	E-GEOD-41647	drought environment' vs 'control' in 'tolerant to drought environment' at '6 hour'	1.5	0.015583454
OsFH7	E-GEOD-41647	drought environment' vs 'control' in 'susceptible to drought environment' at '6 hour'	1.3	0.01919221
OsFH13	E-MTAB-3230	PEG Stress' vs 'normal' in 'Wild Type'	1.6	0.004586795
OsFH13	E-MTAB-3230	PEG Stress' vs 'normal' in 'Mutant'	1.2	9.4582E-06
OsFH6	E-MTAB-3230	PEG Stress' vs 'normal' in 'Mutant'	-1.3	4.91311E-05
OsFH6	E-MTAB-3230	PEG Stress' vs 'normal' in 'Wild Type'	-1	0.015008153