

Table S1. Bioinformatics analysis of positive clones

Clone	Orthologous		Protein weight/kDa	Subcellular		Theoretical pI	Number of amino acids
	<i>Betula</i>	Protein		localization			
	<i>platyphylla</i> gene	name		MultiLoc	WoLF		
	No.				PSORT		
C1	CCG025282.1	BpARF19	126474.3	nucl	nucl	6.01	1130
C2	CCG023520.1	BpIAA7	26919.5	nucl	nucl	8.52	243
C3	CCG016662.1	BpHSP90	37370.4	cyto	cyto,cysk	9.24	342

Notes: nucI, nucleus; cyto, cytoplasm; cysk; cytoskeleton.

Table S2. Statistics table of sequencing data

Sample	Obtained Reads	Obtained Bases(G)	Q30(%)	GC(%)
NT-1	20,089,887	5.76	95.99	48.23
NT-1	21,837,212	6.15	96.54	47.94
NT-1	23,445,110	6.73	95.87	47.84
OE-1	30,862,461	8.81	96.36	48.29
OE-2	26,874,823	7.79	96.11	47.93
OE-3	24,180,069	6.99	96.06	48.01
RE-1	28,633,405	8.17	96.1	47.74
RE-2	26,158,426	7.49	96.13	48.95
RE-3	28,320,129	8.15	96.18	48.32

Table S3. Characteristics of *BpARF* genes in *B. platyphylla*

Gene	GenBank accession No.	A/ R	Domains	Predicted protein (aa)	Molecular weight (kDa)	Theoretical pI	Up/ downregulated in transgenic line
BpARF1	MG254848	R	B3, MR, PB1	642	71837.93	5.44	up
BpARF2	MG254849	R	B3, MR, PB1	773	86004.70	6.04	down
BpARF3	MG254850	R	B3, MR	748	81807.15	6.39	up
BpARF4	MG254851	R	B3, MR, PB1	771	85492.06	6.35	up
BpARF5	MG254852	A	B3, MR, PB1	933	103140.27	5.02	up
BpARF6	MG254853	A	B3, MR, PB1	917	102267.91	6.33	down
BpARF7	MG254854	A	B3, MR, PB1	1615	179000.83	5.52	up
BpARF8	MG254855	A	B3, MR, PB1	666	74648.63	5.82	down
BpARF9	MG254856	R	MR, PB1	276	30742.98	5.17	up
BpARF10	MG254857	R	B3, MR,	713	78320.53	8.09	up
BpARF11	MG254858	R	B3, MR,	702	76964.15	6.36	up
BpARF12	MG254859	R	B3, MR, PB1	577	64120.94	6.09	up
BpARF13	MG254860	R	PB1	91	10587.33	4.43	No change
BpARF14	MG254861	R	B3, MR, PB1	597	66889.24	6.06	up
BpARF15	MG254862	R	PB1	131	14787.59	8.37	No change
BpARF16	MG254863	R	B3, MR,	592	65240.44	6.04	up
BpARF17	MG254864	R	B3, MR,	356	40087.18	5.22	No change
BpARF18	MG254865	R	B3, MR, PB1	608	67203.72	5.90	up
BpARF19	MG254866	A	B3, MR, PB1	834	92033.39	5.81	up
BpARF20	MG254867	A	B3, MR, PB1	1083	119859.55	6.21	down
BpARF21	MG254868	A	B3, MR, PB1	810	89654.40	5.93	down
BpARF22	MG254869	R	MR, PB1	484	54351.41	6.61	up
BpARF23	MG254870	R	PB1	105	11974.52	4.64	up
BpARF24	MG254871	R	PB1	74	8357.69	10.15	No change
BpARF25	MG254872	R	B3, MR	688	76266.98	6.22	down

A: activator ARF; R: repressor ARF; B3: DNA-binding domain; MR: middle region; PB1: Phox and Bem1 domain.

Table S4. The list of primers used in qRT-PCR to verified the RNA-seq

Gene name	Gene ID in birch	Forward primer	Reverse primer
ALD2	birch_GENE_10018389	CCCAACATCTGATTAACGGGC	GGACATCTTTGGCCATGGTC
AUX1	birch_GENE_10024474	GAGCTTTAGCTAGGCTCCCTGT	GCCCAGCCTCCTATGAATG
AUX5	birch_GENE_10015123	GGTCCGACCAAGCTAGTGCTAT	ATGCAGAGGGAAGCGTCAGTG
CUC3	birch_GENE_10016566	CAAGGAGGTCTACAGTACTGC	CCATTCCTCCTTACACGTGTG
CYCD5.1	birch_GENE_10019666	CTCGCTTGGATGCCATTGAG	CATCCGATATTCCGATAGGGCC
CDC20.2	birch_GENE_10024083	GTATTGATGAGGAAGATGGCCC	GATAAGACCGTCCATTCTCC
GH3.6	birch_GENE_10025767	GGAGGACACTGCTGTATAGC	GTTTGTGTAAGGGTCATAGGGCC
HDZ1	birch_GENE_10021965	TAGTGCATCTGGAACGACCAC	TGAACCCAGTCGACAGCAGTTC
NAC35	birch_GENE_10011582	GAAAGTATCGGAACGGGGATC	CATGATGAGGCAAGCGATACTCG
SAUR21	birch_GENE_10028928	CGTTGGAGAGAGCGAAAAG	CTTACCAAAGTCACCAGGGCAC
SAUR37	birch_GENE_10009388	TACAGCCAGATAAGCCCAACGT	GTCTTGTTGCCCCACGTACAC
ORR9	birch_GENE_10019204	CCATGTTCTCGCTGTTGATG	CATAGCCTGTCATTCCCGGCAT
ARR5	birch_GENE_10026690	CGTGGATAGTGGAAGAAGAG	CCGGCTTTACTATGAAATCCTC
WUSCHEL	birch_GENE_10030531	GGAATTGTATCGACGTGGGACT	CAAATACTGTCCTACTTGCCCC
TCP11	birch_GENE_10010554	AGTTCTCCGACCGGAAAGTCTC	ACTCGATTGTCTCGCCGTCTGAG
ARG7	birch_GENE_10027864	CAAGGAGGGAGACGATTGGATC	GAGCAAGTCCTTGTTGGGTTGG
REV1	birch_GENE_10009894	GTCTGGTTCCAGAATCGCAG	CATCAGTAGTTGCCACTGACGC
TCP5	birch_GENE_10014059	GACAGGCATAGCAAAGTTTGC	GAAGGGGTGGGAGCTTGTCAT
YUCCA4	birch_GENE_10020487	GAGGGTTCGAACTCAGGACTTG	GTGTCTGCAAAGGTCCAAGC
PIN6	birch_GENE_10002923	CTCCCCAACACACTCGTCATG	GATTGACCCAGCTGTGTCAGG