

Supplementary Table and Figures

Table S1. The list of RT-PCR Primers.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')	Function
<i>AcJAZ1</i>	CTTTGGACGTATGCTGCAGA	TCTGCAGCATACGTCCAAAG	RT-qPCR
<i>AcJAZ2</i>	TCGCAGCTCACAATCTTCTAC	GAGCTTGCAGAGCGAACTAT	RT-qPCR
<i>AcJAZ3</i>	TTGTAGCCTCTTGAGCCAATAC	CTCATTCGTCCCTTCCTTGTT	RT-qPCR
<i>AcJAZ4</i>	ACAAGGTGGGTCTCTCTCTAA	CAGCATTCTCTGAGGGTTTCT	RT-qPCR
<i>AcJAZ5</i>	GCAGCGGAAGCAAGTAATGGAG	CTCGCGATTGGCAGCTCTC	RT-qPCR
<i>AcJAZ6</i>	GGTTCGGTTCCATCCTCTTC	CGGTGCACCTTCCACTAAAC	RT-qPCR
<i>AcJAZ7</i>	TCTGCCTCCGACTTGGTAT	GATGGCTCTTGCCTGAATCT	RT-qPCR
<i>AcJAZ8</i>	CTCGGTCACCCCCGAAAAG	GAGGGCTACCTCCTTGCGAAC	RT-qPCR
<i>AcJAZ9</i>	GCAGCAGCAACAGCAGCAGC	CATTTCTCGTCTCGCCATCGATA	RT-qPCR
<i>AcJAZ10</i>	CGATTCGCTCTTCGACTCATC	CACACCTCCCAACAGTAATAG	RT-qPCR
<i>AcJAZ11</i>	AGGGCATTGAGAGGTACGA	ACTCTGTGCGGCAAGTTTAT	RT-qPCR
<i>AcJAZ12</i>	CTCCGTTTCCCCCGAAAAG	CTACCTGAGAGCAACCTCCTTCC	RT-qPCR
<i>AcJAZ13</i>	GGTAAGGTCGAGGAATTGATGCG	CTTTCCTCCTTTTCGCGAGG	RT-qPCR
<i>AcJAZ14</i>	CAGCAGCAGCAGCAGCGGG	CTCCATTTCTCGCTCGCCATC	RT-qPCR
<i>AcPP2A</i>	TTGTCATCGCTTCCTCCAAG	GTGTTGTCCACCACAGTATGA	RT-qPCR
<i>AcJAZ4</i>	cacgggggactctagaATGGAGCGGGATTTTTT GGG	tcccgggagcggtaccTTAGAGAGAGAGA TGGAGAGAGAGAG	BiFC
<i>AcJAZ5</i>	cacgggggactctagaATGTGAAGGCCGCCGC C	tcccgggagcggtaccTTAGGTGGTCAACC TTTCCTTGCGCC	BiFC
<i>AcJAZ13</i>	cacgggggactctaga ATGGAGAGGGAAAAAACCAAC	tcccgggagcggtacc CTACAAACGAAGCTCATGTTC	BiFC
<i>AcMYC2</i>	cacgggggactctaga ATGATGGAGGCCTTCATG	tcccgggagcggtacc CTACCTGCAAGGAGAGGG	BiFC
<i>AcNINJA</i>	cacgggggactctaga ATGGAGGACGAAAATGGCCTC	tcccgggagcggtaccGTTTTGGGCCGATG CTGCTG	BiFC
<i>AcJAM1</i>	cacgggggactctaga ATGGTGATGGGGAGGCTATG	tcccgggagcggtaccCTGCGACTGGGACT GCGAC	BiFC

Table S2. Prediction of subcellular localization of AcJAZ proteins

AcJAZs	DeepLoc analysis: scores				Prediction	MULocDeep analysis: scores				Prediction
	Nucleus	Cytoplasm	Membrane	Peroxisome		Nucleus	Cytoplasm	Membrane	Peroxisome	
AcJAZ1	0.5712	0.0113	0.0385	0.2126	Nucleus	0.8517	0.1329	0.0024	0.0024	Nucleus
AcJAZ2	0.9938	0.0061	0	0	Nucleus	0.7764	0.0575	0.0022	0.0018	Nucleus
AcJAZ3	0.6793	0.0101	0.0779	0.1179	Nucleus	0.7206	0.0926	0.0011	0.0019	Nucleus
AcJAZ4	0.8810	0.0103	0.0929	0.0027	Nucleus	0.5278	0.1691	0.0045	0.0018	Nucleus
AcJAZ5	0.9470	0.0397	0.0102	0.0005	Nucleus	0.7679	0.0023	0.001	0.0051	Nucleus
AcJAZ6	0.9894	0.0103	0.0002	0	Nucleus	0.8423	0.1112	0.0019	0.0016	Nucleus
AcJAZ7	0.9908	0.009	0.0001	0	Nucleus	0.8001	0.1192	0.0022	0.0021	Nucleus
AcJAZ8	0.9970	0.0427	0.0002	0	Nucleus	0.8963	0.0418	0.0026	0.0019	Nucleus
AcJAZ9	0.9951	0.0022	0.002	0.0001	Nucleus	0.7391	0.1236	0.0019	0.0018	Nucleus
AcJAZ10	0.9929	0.0069	0.0001	0	Nucleus	0.4406	0.0091	0.0021	0.0015	Nucleus
AcJAZ11	0.9998	0.0002	0	0	Nucleus	0.7853	0.1372	0.0042	0.0019	Nucleus
AcJAZ12	0.9999	0.0001	0	0	Nucleus	0.8354	0.041	0.0424	0.0024	Nucleus
AcJAZ13	0.8363	0.0509	0.0584	0.0059	Nucleus	0.5198	0.0331	0.0025	0.0074	Nucleus
AcJAZ14	0.9921	0.0025	0.0036	0.0001	Nucleus	0.9323	0.0292	0.0043	0.0018	Nucleus

Table S3. Prediction of subcellular localization of OsJAZ proteins.

OsJAZs	DeepLoc analysis: scores				Prediction	MULocDeep analysis: scores				Prediction
	Nucleus	Cytoplasm	Membrane	Peroxisome		Nucleus	Cytopla sm	Membr ane	Mitocho ndrion	
OsJAZ1	0.9958	0.004	0.0002	0.0001	Nucleus	0.6839	0.2866	0.0019	0.0037	Nucleus
OsJAZ2	0.9917	0.008	0.0001	0.0001	Nucleus	0.9943	0.0395	0.0012	0.0016	Nucleus
OsJAZ3	0.9307	0.065	0.0019	0.0008	Nucleus	0.477	0.2956	0.0179	0.0012	Nucleus
OsJAZ4	0.9754	0.023	0.0003	0.0007	Nucleus	0.1322	0.6674	0.0077	0.0024	Cytoplasm
OsJAZ5	0.7923	0.196	0.0038	0.0022	Nucleus	0.7517	0.1888	0.001	0.0022	Nucleus
OsJAZ6	0.9861	0.014	0	0.0001	Nucleus	0.793	0.0267	0.0017	0.0065	Nucleus
OsJAZ7	0.9360	0.029	0.0105	0.0132	Nucleus	0.7086	0.0904	0.0009	0.1257	Nucleus
OsJAZ8	0.8515	0.046	0.0312	0.0357	Nucleus	0.4382	0.374	0.001	0.093	Nucleus
OsJAZ9	0.9799	0.017	0.0007	0.0019	Nucleus	0.3738	0.3097	0.0009	0.0108	Nucleus
OsJAZ10	0.7663	0.174	0.0369	0.0024	Nucleus	0.2317	0.2242	0.0036	0.3879	Mitochondrion
OsJAZ11	0.7008	0.275	0.0108	0.0011	Nucleus	0.5993	0.2065	0.0009	0.0037	Nucleus
OsJAZ12	0.6676	0.1444	0.0896	0.0215	Nucleus	0.3619	0.1213	0.0017	0.1828	Nucleus
OsJAZ13	0.9643	0.024	0.0052	0.0018	Nucleus	0.1703	0.0196	0.0015	0.2418	Mitochondrion
OsJAZ14	0.7302	0.207	0.0224	0.021	Nucleus	0.3191	0.2839	0.0014	0.035	Nucleus
OsJAZ15	0.9984	0.001	0.0001	0.0001	Nucleus	0.7406	0.0087	0.0008	0.0163	Nucleus

Table S4. The *cis*-acting abiotic responsive elements in Pineapple *JAZ* genes.

Gene name	Abiotic responsive elements									
	ABRE ¹	MeJA ²	WRE ³	ERE ⁴	DRE ⁵	SARE ⁶	LTRE ⁷	GIRE ⁸	AURE ⁹	TC-rich ¹⁰
<i>AcJAZ1</i>	14	4	3	4	0	2	0	1	0	0
<i>AcJAZ2</i>	2	6	3	3	0	0	2	0	0	0
<i>AcJAZ3</i>	12	4	2	2	0	0	1	0	0	1
<i>AcJAZ4</i>	13	4	1	2	1	0	0	0	0	0
<i>AcJAZ5</i>	12	4	4	2	0	0	0	1	1	0
<i>AcJAZ6</i>	4	4	4	26	0	0	2	0	0	0
<i>AcJAZ7</i>	15	2	4	1	1	1	1	1	0	0
<i>AcJAZ8</i>	5	2	1	1	0	0	4	2	0	0
<i>AcJAZ9</i>	10	4	2	4	1	1	0	0	0	0
<i>AcJAZ10</i>	3	4	3	0	5	3	0	0	1	0
<i>AcJAZ11</i>	0	4	3	0	0	0	0	0	1	0
<i>AcJAZ12</i>	4	8	2	23	0	1	1	0	0	0
<i>AcJAZ13</i>	1	2	4	2	0	1	0	1	0	1
<i>AcJAZ14</i>	9	2	0	3	1	0	0	0	0	0

Note: ¹Abscisic acid responsive elements; ²MeJA-responsive elements; ³Wound responsive elements; ⁴Ethylene responsive elements; ⁵Drought responsive elements; ⁶Salicylic responsive elements; ⁷Low-temperature responsive elements; ⁸Gibberellin-responsive elements; ⁹Auxin-responsive elements; ¹⁰Defense and stress responsive elements.

Table S5. *MYC2* genes in pineapple

No.	Gene ID	Bit score	E-value
1	Aco018875.1	498	5.00E-169
2	Aco018208.1	158	3.00E-42
3	Aco026873.1	137	8.00E-38
4	Aco010845.1	135	2.00E-33
5	Aco005839.1	122	1.00E-29
6	Aco030901.1	103	3.00E-23
7	Aco007275.1	102	9.00E-23
8	Aco012028.1	92	2.00E-19
9	Aco029228.1	82	4.00E-17

Table S6. *JAM1* genes in pineapple.

No.	Gene ID	Bit score	E-value
1	Aco005839.1	186	3.00e-51
2	Aco030901.1	84.3	4.00e-17
3	Aco007275.1	83.6	8.00e-17
4	Aco000272.1	82.4	4.00e-17
5	Aco015882.1	81.6	6.00e-17
6	Aco002246.1	80.5	1.00e-16
7	Aco031432.1	79.3	2.00e-16
8	Aco022880.1	77	8.00e-15

Table S7. *NINJA* genes in pineapple.

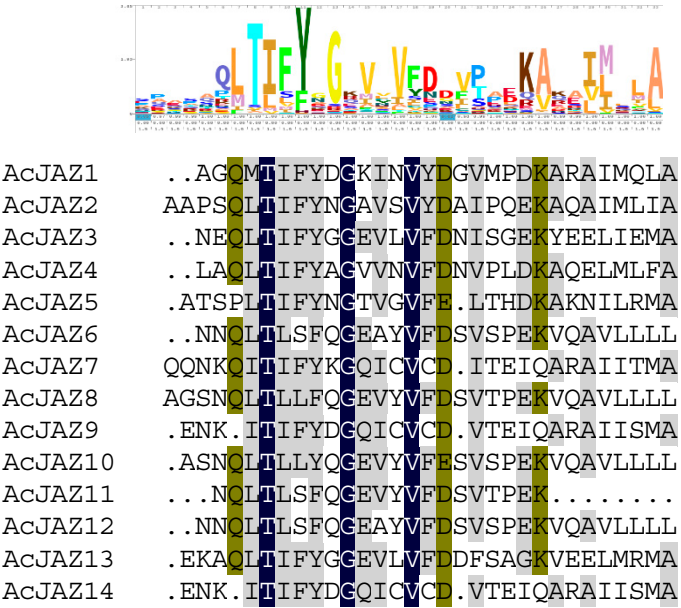
No.	Gene ID	Bit score	E-value
1	Aco006735.1	210	8e-62
2	Aco017364.1	72.0	5e-14
3	Aco012414.1	66.2	7e-12
4	Aco003903.1	63.5	3e-11
5	Aco004854.1	60.5	4e-10

Table S8. BiFC identification of protein-protein interactions among central regulators of the JA-signaling pathway in pineapple.

<div>-YFP^N \ -YFP^C</div>	YFP ^C	AcJAZ4	AcJAZ5	AcJAZ11	AcJAZ13
YFP ^N	-	-	-	-	-
AcMYC2	-	-	+	-	+
AcNINJA	-	-	+	-	+
AcJAZ4	-		+	-	+
AcJAM1	-	-	+	-	+

Note: “+” means detected fluorescence signal from the protein-protein interaction by BiFC analysis; “-” represents no fluorescence signal detected from the vector pairs.

(a)



(b)

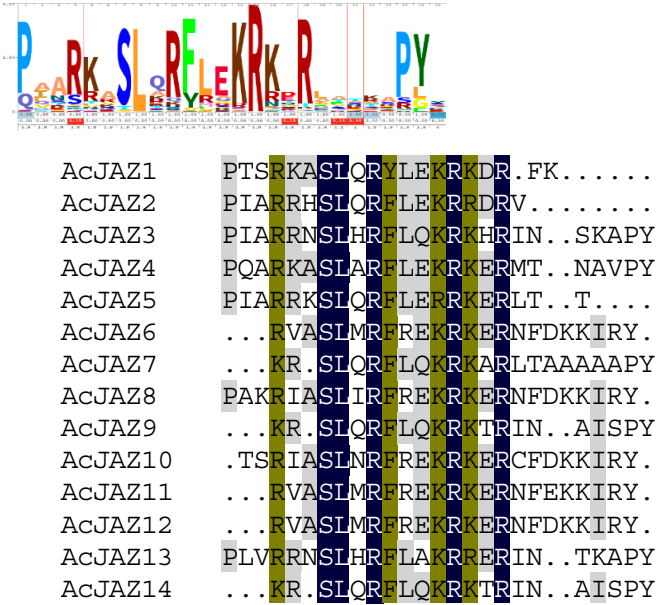


Figure S1. The alignment of 14 AcJAZ proteins showed the tify motif and Jas domain. (a) tify motif. (b) Jas domain.

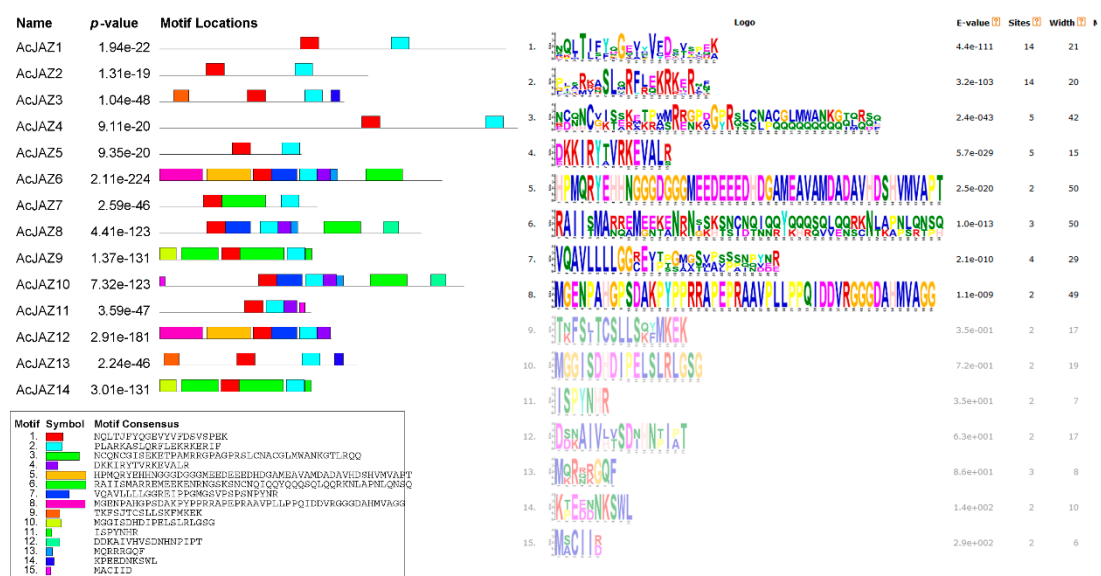


Figure S2. Motif logos of AcJAZs. The height of letters within the logos represents the relative frequency of the specific amino acids.

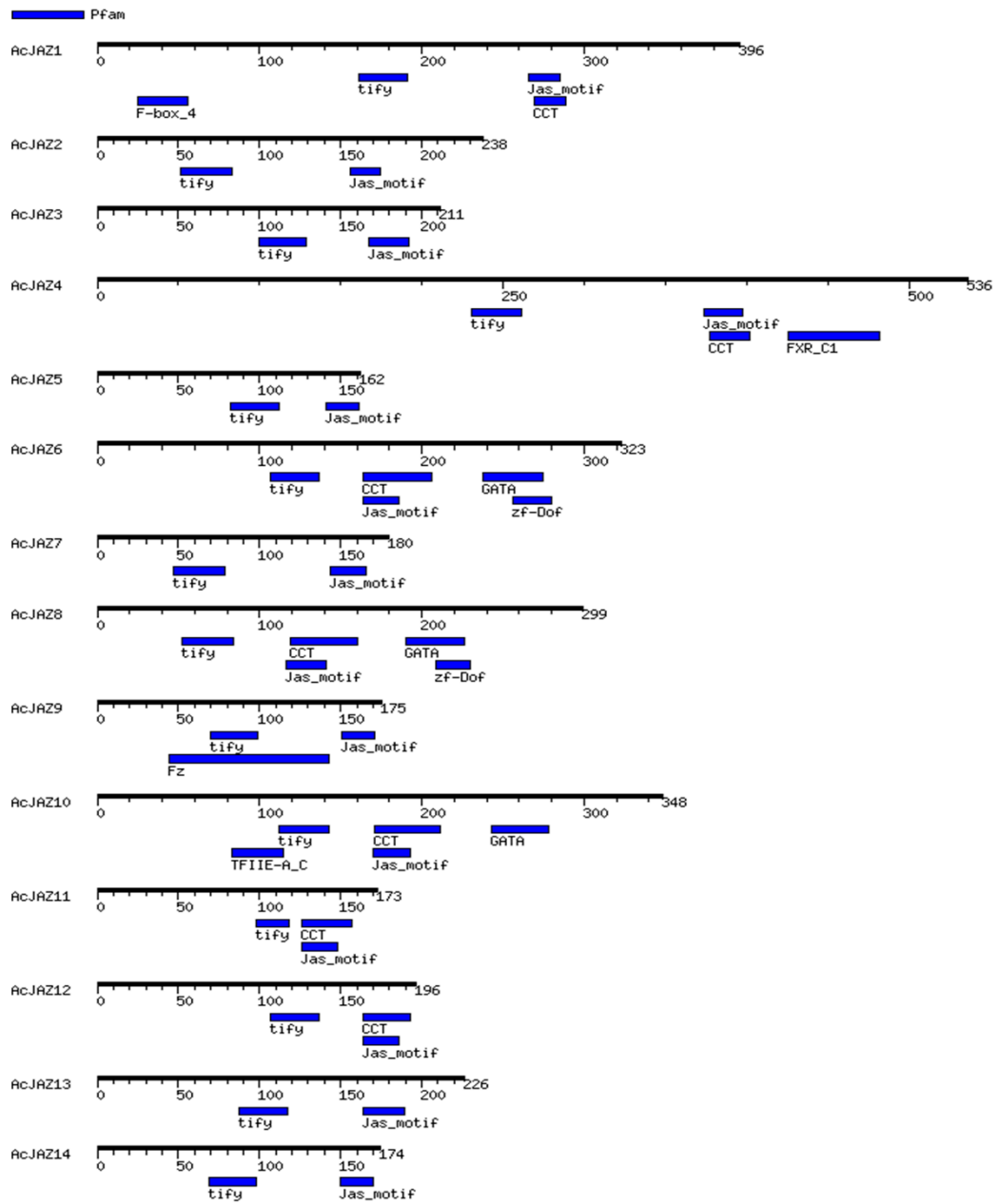


Figure S3. Motifs in AcJAZ identified by Pfam.

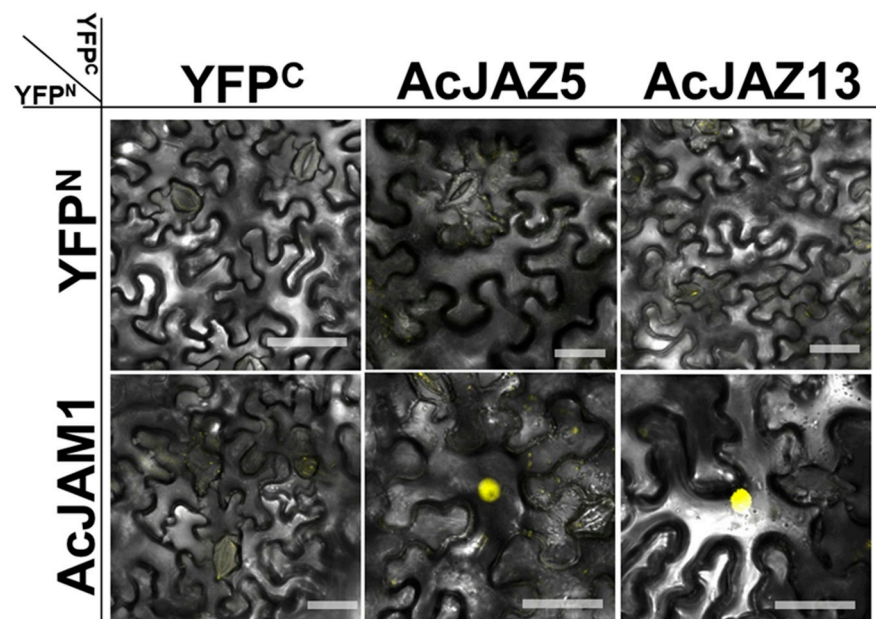


Figure S4. The protein-protein interactions among central regulators of the JA-signaling pathway in pineapple (continued).
Bar=50μm.