Table 1. Suppl. Details of *BnAux/IAA*, *BnARF*, and *BnLBD* genes and their homologues in other species. *Q* - ratio of sequence similarity, CDS - coding sequence.

Gene	Genbank number	CDS [bp]	Predicted protein(aa)	Homologous genes			Group
				Gene	Accession	Q [%]	
BnIAA1	KR076511	951	316	*MnIAA26*	XP_010098149.1	60	IAA-II
BnIAA2	KR076512	774	257	*MnIAA13*	XP_010105210.1	65	IAA-II
BnIAA3	KR076513	1068	355	*MnIAA9*	XP_010104556.1	85	IAA-I
BnIAA4	KR076514	1059	352	*MnIAA9*	XP_010105114.1	84	IAA-I
BnIAA5	KR076515	1062	353	*MnIAA27*	XP_010098105.1	71	IAA-I
BnIAA6	KR076516	957	318	*MnIAA27*	XP_010107373.1	70	IAA-I
BnIAA7	KR076517	735	244	*RcIAA16*	XP_010102292.1	75	IAA-I
BnIAA8	KR076518	738	245	*RcIAA16*	XP_007050421.1	63	IAA-I
BnIAA9	KR076519	591	196	*MnIAA3*	XP_010102293.1	76	IAA-I
BnIAA10	KR076520	603	200	*MnIAA4*	XP_010087759.1	68	IAA-I
BnIAA11	KR076521	588	195	*MnIAA3*	XP_010102293.1	61	IAA-I
BnIAA12	KR076522	600	199	*MnIAA17*	XP_010110305.1	77	IAA-I
BnIAA13	KR076523	756	251	*PmIAA14*	XP_008224185.1	73	IAA-I
BnIAA14	KR076524	777	258	*MnIAA29*	XP_010090614.1	60	IAA-II
BnIAA15	KR076525	963	320	*MnIAA18*	XP_010095461.1	51	IAA-II
BnIAA16	KR076526	576	191	*PmIAA6*	XP_010110304.1	71	IAA-I
BnARF1	KR072635	2751	916	*MnARF6*	XP_010090447.1	90	ARF-III
BnARF2	KR072636	2829	942	*MnARF6*	XP_010106165.1	90	ARF-III
BnARF3	KR072637	2043	680	*MdARF1*	XP_008378943.1	82	ARF-Ia
BnARF4	KR072638	2028	675	*MdARF9*	XP_008341793.1	71	ARF-Ia
BnARF5	KR072639	2106	701	*MnARF18*	XP_010100721.1	75	ARF-Ia
BnARF6	KR072640	2520	839	*MnARF2*	XP_010099050.1	85	ARF-Ia
BnARF7	KR072641	2403	800	*MnARF4*	XP_010104118.1	84	ARF-II
BnARF8	KR072642	2112	703	*MnARF18*	XP_010107532.1	90	ARF-IV
BnARF9	KR072643	2061	686	*TcARF19*	XP_007009852.1	68	ARF-IV
BnARF10	KR072644	2130	709	*MnARF18*	XP_010089974.1	81	ARF-IV
BnARF11	KR072645	3342	1113	*MnARF5*	XP_010106948.1	85	ARF-III
BnARF12	KR072646	2610	869	*MnARF19*	XP_010089663.1	93	ARF-III
BnARF13	KR072647	2847	948	*MnARF5*	XP_010095167.1	86	ARF-III
BnARF14	KR072648	2172	723	*MnARF3*	XP_010111164.1	81	ARF-II
BnLBD1	KR076527	540	179	*PmLOB1*	XP_008233120.1	75	LBD-Ia
BnLBD2	KR076528	573	190	*CaLOB25*	XP_008230551.1	70	LBD- Ia
BnLBD3	KR076529	666	221	*VvLOB6*	XP_002266137.1	71	LBD- Ia
BnLBD4	KR076530	573	190	*TcLOB*	XP_010067552.1	64	LBD- Ia
BnLBD5	KR076531	783	260	*CaLOB22*	XP_004510487.1	40	LBD- Ia
BnLBD6	KR076532	693	230	*TcLOB31*	XP_008345767.1	66	LBD- Ia

BnLBD7	KR076533	714	237	*PmLOB29*	XP_008235796.1	65	LBD- Ia
BnLBD8	KR076534	771	256	*VvLOB29*	XP_002263533.1	57	LBD- Ia
BnLBD9	KR076535	705	234	*PtLOB33*	XP_002316271.1	67	LBD- Ia
BnLBD10	KR076536	540	179	*VvLOB4*	XP_002264049.2	78	LBD- Ia
BnLBD11	KR076537	567	188	*CaLOB4*	XP_004505337.1	81	LBD- Ia
BnLBD12	KR076538	549	182	*MdLOB12*	XP_008363768.1	79	LBD- Ia
BnLBD13	KR076539	711	236	*VvLOB15*	XP_002279029.1	77	LBD- Ia
BnLBD14	KR076540	858	285	*PmLOB15*	XP_010067592.1	59	LBD- Ia
BnLBD15	KR076541	930	309	*MdLOB41*	XP_008348114.1	65	LBD-II
BnLBD16	KR076542	720	239	*CsLOB38*	XP_006466482.1	68	LBD-II

Table 2 Suppl. Primers of ramie *GAPDH* gene (endogenous control) and *Aux/IAA*, *ARF*, and *LBD transcription factors* used for RT-qPCR..

Gene	Forward primer	Reverse primer
BnIAA1	GACAAATATTAGCAGTGGTGGCA	GTATATTCTCCACTTCCGTCCAGT
BnIAA2	GAGAGACTAAGGATCAAGCAGCA	CTCATGATTCGGAGCCTTTTCAC
BnIAA3	GAGCGTTGTATGTTAAGGTCAGC	CCATCTCTGTCCTCATACGTCAG
BnIAA4	CTACAAGAAAGATCCCGTCCGAC	TCTACCTTCCTTAAATACGGAGC
BnIAA5	GGAAAAGGCTCTGTGTTGTTCTC	TTGGAAGCAGGAGGACTAGTATG
BnIAA6	TCAAGATCTACGGCAGTTACACG	ACCAACTAGCATCCAATCACCAT
BnIAA7	TTCAGCTCTTTCACTATCGGGTT	CATCACCAACAAGCATCCAATCC
BnIAA8	AAATGTTCAGTTCCTTCAGCACC	CCTCCTTTCCTTTCATTATGCGC
BnIAA9	AAGAGAGCTTTGCCAATTGACAC	ATGCTGACCTTTACGTAGATCCC
BnIAA10	CCCAACAACAGCAACAAGAAACT	CCCTGAAATCTCTGCCTCTGAAT
BnIAA11	GTCTTTTCCAGCTCACAATTGGG	CCAAGTCCTCTAGCTTCTGATCC
BnIAA12	GATGAATCTAGTGCAACCAAGCC	TTGAAGAGCAATGAGAAGGTGTT
BnIAA13	TGCTAAGTGTGAACGAGAGAGAT	GGAAGGGTTTTGTCTTTGTTGCT
BnIAA14	TAGAGATCATCAGCAGGACGAGA	GAGAGCAAGTTGTGTTTAAGCGT
BnIAA15	ACAGCTTCCAATTGCATGAAAGT	TACAGAATTACCATCGCAACGGA
BnIAA16	GGAAGGTCTAGGGTTGGAAATCA	CATGCTGACTTTGACGTACACTT
BnARF1	CCAAATTCAGCAGCTACCATGAG	CGGCGACAGTATTTTGATACACC
BnARF2	CTTCATCCGACGTTTCCCAAATC	AGTACACTCTGACCAGCACTAGA
BnARF3	TTCTGAGAGGTGAAAACGGAGAG	CAGAAAAGAGTGTGCCAGTTGAG
BnARF4	ACTCAGTCACACGATACAACACA	GCCAACGGATAAACTTTTGCTCT
BnARF5	CACAGAAGGGACAAAGCAAACAA	CATCACGTCATTCTCATTGTCGG
BnARF6	TGTCATGTCGAACCAAGCTCATA	ATTCCCTGCTTGTGAACCTTAGT
BnARF7	ACCTACAAAATCAACCCCTCACA	TACTCCATCCTGTAGTGAGCAGA
BnARF8	TACCAACATTTCCCGGCAATCTA	GACTGGAAATAGACCTGACTGCA
BnARF9	TGTTTACGCGAAGATTAGGCTTG	CACAGTATCGAGGGACAGAGAAC
BnARF10	GAGCCATGTTCTTTACCATGACG	TCGAATTCCAGTCATCCATGTCC
BnARF11	CGATGCTCAAATTCCCAACTACC	AAGCAACGCATCCTTATCAACAG
BnARF12	CAGCACAATACAGCAGAGTTTCC	CCGCCACAGTTAGAGAGTAAGTT
BnARF13	GATAAAGGCCCCGGAGATCTAAG	GCTGGAATCCTTGCTCTATCTCA
BnARF14	ATGACGAATTTGACCAATGCCTG	TCTGTAATTGCTCGGTTTGTGTG
BnLBD1	AATTGGAGACGACGAGGGCTAA	ACACACTAAAGTTGTAGCCATCA
BnLBD2	TCATCATCATCATCATCAAGCCC	TACCTCCATCACCTAACGATCTG
BnLBD3	GGTGAACTCGCTGGCCTAC	GAGATGAGGTTGATGCCGAGA
BnLBD4	AGCAATGTGAGCAAGATCCTGA	GAAGTGTTGTTGTTGTTGTTGGC
BnLBD5	TCGTCAAAGAATCTGGCCCC	CTGATAGCCTGTTGAAGTGAAAA
BnLBD6	GGAAGTGCGTGAAGGGGTG	TTCACTACCTGTTGTTGGAGAGC

BnLBD7	ATGACTCAGGAACAGTAAACCCT	AGACGTTTTCATCCGGGATTAGG
BnLBD8	TCAAAGACCCCATTTACGGATGT	TGTCTTCCATTGTTGTGCCTTTC
BnLBD9	TTCGCTCCTTATTTCTGCTACGA	TTGGAGGGCAAAGATATGAGCAA
BnLBD10	CCAATCCGGCTACCAATTACAAC	CATGACCACAAAGACTCTCCCAT
BnLBD11	CCGCCTGCAAGCTTCTCC	GCTACTCACTGCATCCCCTC
BnLBD12	GTGTTCGCTCCTTATTTTCCCTC	CATTCGCTTCGTACACCAAACTG
BnLBD13	CGGAACCATAAACACCATCACG	TCTTAATCTCACATTCGCTTCGT
BnLBD14	TGGGACTAATATCAGCCTTGCAG	ATGAAGAGAGACCAAAGCAGCAT
BnLBD15	CAAGGGGTGTAGCGAGAACTG	GATCCTCCCGCATGCCTC
BnLBD16	GTCTTCGTCGCCAAGTTCTTC	CCAGTTCCCCGTCCACAG
GAPDH	TGGAAGAATCGGTAGGTTGG	CTGTCACTGTTTTTGGCGTC

Table 3 Suppl. Information on Aux/IAA, ARF and LBD transcription factors in mulberry.

MGD number	GenBank number	Nucleotide [bp]	Predicted protein [aa]	Family
Morus003649	EXC15862.1	1407	468	Aux/IAA
Morus004500	EXB40150.1	861	286	Aux/IAA
Morus005886	EXB60287.1	864	287	Aux/IAA
Morus008968	EXC33724.1	690	229	Aux/IAA
Morus011267	EXC04075.1	1209	402	Aux/IAA
Morus012561	EXB26568.1	600	199	Aux/IAA
Morus013888	EXB44470.1	603	200	Aux/IAA
Morus015873	EXB46013.1	816	271	Aux/IAA
Morus016103	EXC03899.1	1137	378	Aux/IAA
Morus016329	EXB29840.1	612	203	Aux/IAA
Morus016332	EXB29843.1	915	304	Aux/IAA
Morus017323	EXB89357.1	582	193	Aux/IAA
Morus019458	EXC25824.1	570	189	Aux/IAA
Morus019459	EXC25825.1	618	205	Aux/IAA
Morus024574	EXB93235.1	774	257	Aux/IAA
Morus024575	EXB93236.1	570	189	Aux/IAA
Morus025533	EXC01157.1	1137	378	Aux/IAA
Morus026239	EXB74542.1	1035	344	Aux/IAA
Morus026283	EXB74586.1	981	326	Aux/IAA
Morus001564	EXC48061.1	1839	612	ARF
Morus003135	EXC24693.1	1989	662	ARF
Morus004087	EXB38182.1	3435	1144	ARF
Morus005124	EXB58397.1	2823	940	ARF
Morus005202	EXB76510.1	2814	937	ARF
Morus008052	EXB38688.1	2076	691	ARF
Morus008055	EXB38691.1	1869	622	ARF
Morus008224	EXC12830.1	3360	1119	ARF
Morus010971	EXB80401.1	2001	666	ARF
Morus011422	EXB39505.1	2709	902	ARF
Morus012709	EXC08253.1	3108	1035	ARF
Morus013151	EXB81210.1	2478	825	ARF
Morus014401	EXB98559.1	2439	812	ARF
Morus015046	EXC30555.1	2253	750	ARF
Morus020450	EXC34681.1	2139	712	ARF
Morus023490	EXB83883.1	2088	695	ARF
Morus024385	EXC16214.1	2076	691	ARF
Morus000182	XP_010092590.1	627	208	LBD

Morus002082	XP_010088541.1	852	283	LBD
Morus003679	XP_010099606.1	627	208	LBD
Morus003750	XP_010110147.1	675	224	LBD
Morus005107	XP_010106242.1	786	261	LBD
Morus005283	XP_010086870.1	759	252	LBD
Morus005793	XP_010103038.1	390	129	LBD
Morus005914	XP_010086954.1	714	237	LBD
Morus006407	XP_010091043.1	921	306	LBD
Morus006937	XP_010087532.1	540	179	LBD
Morus008640	XP_010103788.1	921	306	LBD
Morus009777	XP_010111893.1	504	167	LBD
Morus009778	XP_010111894.1	684	227	LBD
Morus009779	XP_010111895.1	720	239	LBD
Morus009899	XP_010105431.1	876	291	LBD
Morus011165	XP_010099465.1	534	177	LBD
Morus012304	XP_010087059.1	603	200	LBD
Morus013233	XP_010109898.1	960	319	LBD
Morus013514	XP_010092196.1	534	177	LBD
Morus013700	XP_010088495.1	624	207	LBD
Morus014124	XP_010108453.1	693	230	LBD
Morus014422	XP_010104136.1	675	224	LBD
Morus014552	XP_010102497.1	549	182	LBD
Morus014650	XP_010103761.1	747	248	LBD
Morus016263	XP_010093051.1	516	171	LBD
Morus020555	XP_010108819.1	510	169	LBD
Morus022437	XP_010092842.1	723	240	LBD
Morus022439	XP_010092844.1	732	243	LBD
Morus023484	XP_010100715.1	522	173	LBD
Morus025355	XP_010096608.1	711	236	LBD
Morus025918	XP_010098482.1	552	183	LBD
Morus027282	XP_010090051.1	834	277	LBD

Table 4 Suppl. Basic information on unigenes obtained from three previous transcriptome databases.

Gene	Unigene identified from three databases			CDS	Overlapped length [bp]	Nt [bp]
	unigene in database 1	unigene in database 2	unigene in database 3			
BnIAA1	comp80455_c1_seq2_12	isotig08005_19	comp37534_c1	complete	1050	1403
BnIAA2	comp71911_c0_seq1_17	isotig13778_17	comp30758_c1	complete	822	886
BnIAA3	comp84374_c0_seq1_30	contig01096_3	comp35932_c0	complete	456	2250
BnIAA4	comp28464_c0_seq1_14	isotig08637_32	comp27595_c0	complete	672	1184
BnIAA5	comp73203_c0_seq1_24		comp36448_c1	complete	1068	1530
BnIAA6	comp68352_c0_seq1_33	isotig09503_31	comp29348_c0	complete	957	2179
BnIAA7	comp82563_c2_seq1_8	HS0W81S01ARJPK_8	comp31086_c0	complete	110	1283
BnIAA8	comp69622_c0_seq1_6	HRX1MBH01D4MPY_3	comp36496_c2	complete	83	1588
BnIAA9	comp67354_c0_seq1_20	isotig01677_17	comp28931_c0	complete	624	898
BnIAA10	comp59054_c0_seq1_8	isotig11418_23	comp37569_c6	complete	588	826
BnIAA11	comp80500_c0_seq1_9	isotig15752_14	comp32517_c0	complete	663	931
BnIAA12	comp40669_c0_seq1_9	isotig13023_5	comp25059_c0	complete	615	1064
BnIAA13			comp36308_c0	complete		3608
BnIAA14	comp67519_c0_seq2_19	HRMYNUX02IZRT5_5		complete	478	849
BnIAA15	comp75140_c0_seq1_5	HRX1MBH02JAWXQ_3	comp29571_c1	complete	498	1424
BnIAA16	comp122320_c0_seq1_4	isotig12891_13	comp22653_c0	complete	468	785
	comp85522_c0_seq1_13	HS0W81S02EB2YY_9	comp20706_c0	partial	531	826
	comp40669_c0_seq1_9	isotig13023_5	comp25059_c0	partial	615	1064
	comp63047_c0_seq1_8		comp37092_c1	partial	313	668
		HS0W81S02E0AXU_1		partial		363
			comp16384_c0	partial		525
			comp36418_c3	partial		3609
BnARF1	comp85660_c1_seq3_31	isotig06912_77	comp36011_c4	complete	2775	3937
BnARF2		isotig06932_25		complete		2826
BnARF3	comp66622_c0_seq2_49	isotig07064_13	comp34650_c0	complete	2070	3589
BnARF4	comp81604_c0_seq1_17	isotig03306_83	comp34808_c0	complete	2055	2813
BnARF5	comp83272_c0_seq1_40	isotig07417_45	comp37075_c3	complete	2133	2380
BnARF6	comp80459_c0_seq1_21	HRX1MBH02IBUYC_2	comp34353_c3	complete	109	4004
BnARF7	comp78488_c0_seq4_22	isotig07123_60	comp31401_c1	complete		3044
BnARF8	comp79913_c0_seq2_51	isotig11410_15	comp36497_c0	complete	714	3112
BnARF9		isotig07826_16	comp32433_c0	complete	1367	2321
BnARF10	comp82952_c0_seq2_50	isotig03472_24	comp33311_c0	complete	1884	3019
BnARF11	comp82578_c0_seq1_30	isotig03902_37	comp34057_c1	complete	1914	4436
BnARF12	comp81801_c0_seq2_33	isotig06881_30	comp33685_c2	complete	1300	4270
BnARF13	comp83441_c0_seq1_64	isotig06993_32	comp35067_c0	complete	2874	3472
BnARF14	comp55752_c0_seq5_41	isotig06999_59	comp32001_c2	complete	2079	3014
	comp77752_c0_seq11_9	isotig13112_21	comp34290_c0	partial	578	3543
	comp8950_c0_seq1_16			partial		1590

		HS0W81S01APSXA_6		partial		261
		HS0W81S02EZRZ1_2		partial		255
		HRX1MBH01D5GOR_5		partial		582
		HS0W81S01BR78S_3		partial		351
		isotig06828_23		partial		705
BnLBD1	comp72081_c0_seq1_11		comp22599_c0	complete	289	729
BnLBD2	comp75436_c0_seq1_5	HRMYNUX02GV5AJ_1		complete	205	570
BnLBD3	comp960250_c0_seq1_3	isotig15238_12	comp602129_c0	complete	103	783
BnLBD4	comp26823_c0_seq1_4		comp36793_c1	complete	423	837
BnLBD5			comp19689_c0	complete		1076
BnLBD6	comp69818_c0_seq1_7		comp27487_c0	complete	813	839
BnLBD7	comp80444_c0_seq1_6			complete		729
BnLBD8	comp78815_c0_seq1_17			complete		825
BnLBD9	comp198839_c0_seq1_7			complete		711
BnLBD10	comp52152_c0_seq2_14	isotig12329_18	comp30988_c0	complete	356	861
BnLBD11	comp78524_c0_seq2_34	isotig06310_15	comp33631_c1	complete	498	1200
BnLBD12	comp117146_c0_seq1_6		comp22500_c0	complete	576	880
BnLBD13	comp33524_c0_seq1_16		comp5079_c0	complete	705	872
BnLBD14	comp79710_c0_seq2_21		comp25575_c0	complete	510	1036
BnLBD15	comp83429_c0_seq1_6	isotig11401_5	comp31295_c0	complete	1074	1873
BnLBD16	comp73599_c0_seq2_18	isotig11716_16	comp38508_c0	complete	774	1419
	comp41170_c0_seq1_5	isotig15923_5	comp27395_c0	partial	570	648
	comp785_c0_seq1_2	HRX1MBH02JB4W6_12	comp20993_c0	partial	57	1006
	comp241816_c0_seq1_2		comp23838_c2	partial	255	255
	comp62997_c0_seq3_6		comp23838_c0	partial	324	434
	comp72243_c0_seq1_11		comp19810_c0	partial	263	405
	comp60910_c0_seq1_15		comp37137_c0	partial	444	672
		isotig15151_7	comp37137_c1	partial	236	764
	comp70802_c0_seq1_12			partial		582
	comp54465_c0_seq1_9			partial		255
		isotig08996_2		partial		303
		HS0W81S02EYKL3_6		partial		246
			comp2170_c0	partial		488

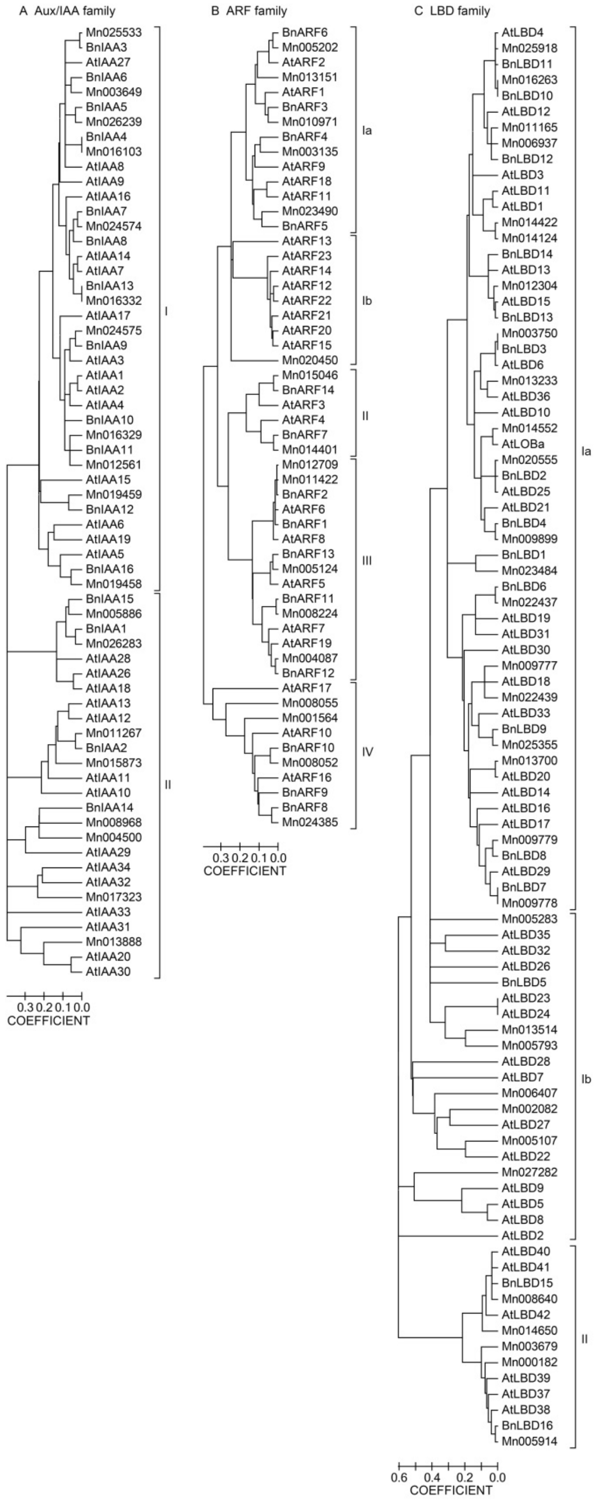

Fig. 1 Suppl. Phylogenetic analysis of *Arabidopsis*, mulberry, and ramie proteins in Aux/IAA family (*A*), ARF family (*B*) and LBD family (*B*). These gene families are from *A. thaliana* (*At*), *B. nivea* (*Bn*) and *M. notabilis* (*Mn*). A neighbor-joining phylogenetic tree was constructed for Aux/IAA, ARF and LBD proteins using *MEGA 5.0* software (Tamura *et al.* 2011). The most parsimonious tree with bootstrap values from 1 000 trials was used.

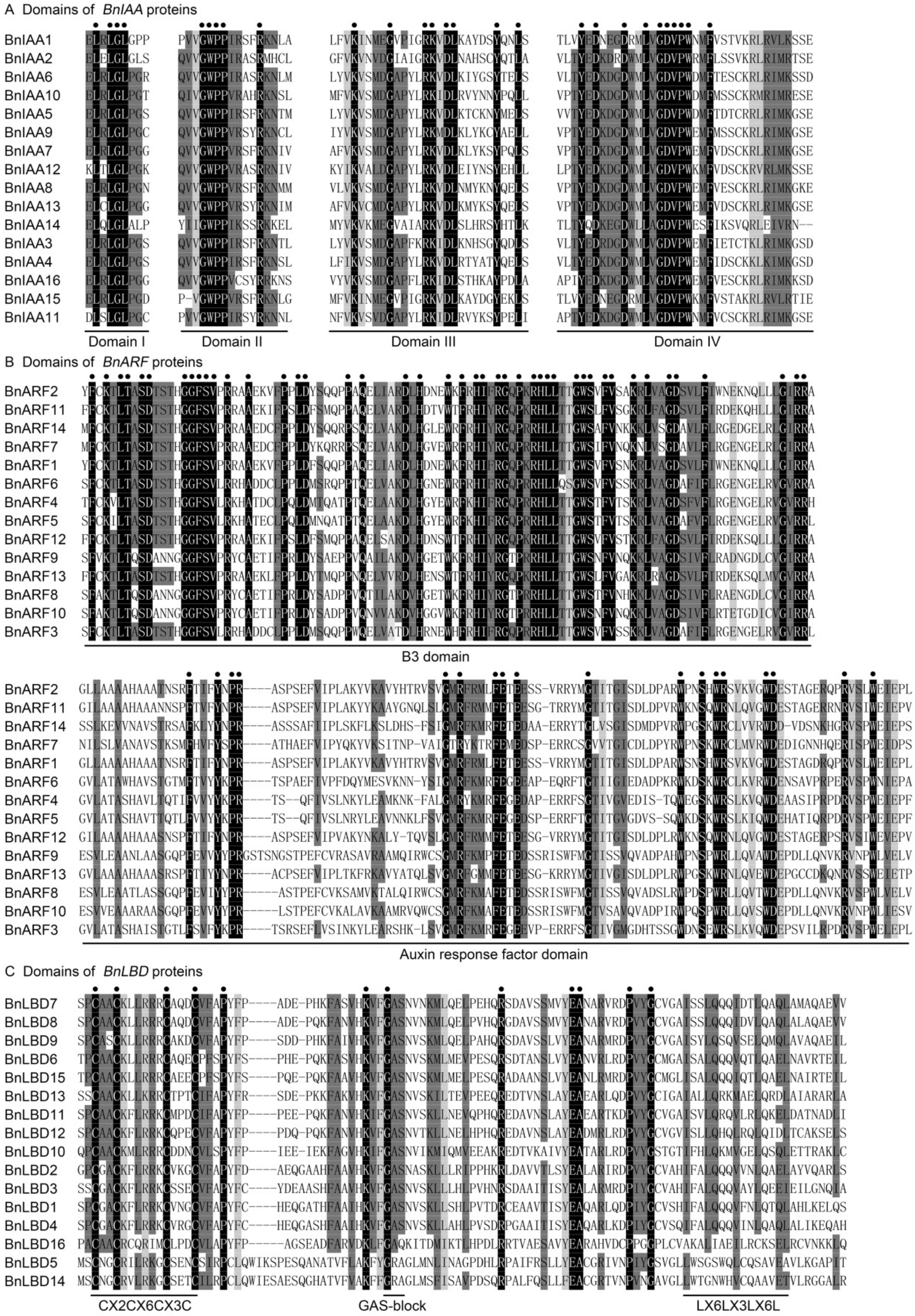

Fig. 2 Suppl. Conserved functional domains of *BnIAA* (*A*), *BnARF* (*B*), and *BnLBD* (*C*) proteins. Conserved amino acids are highlighted with *spots*.