

Supporting Information

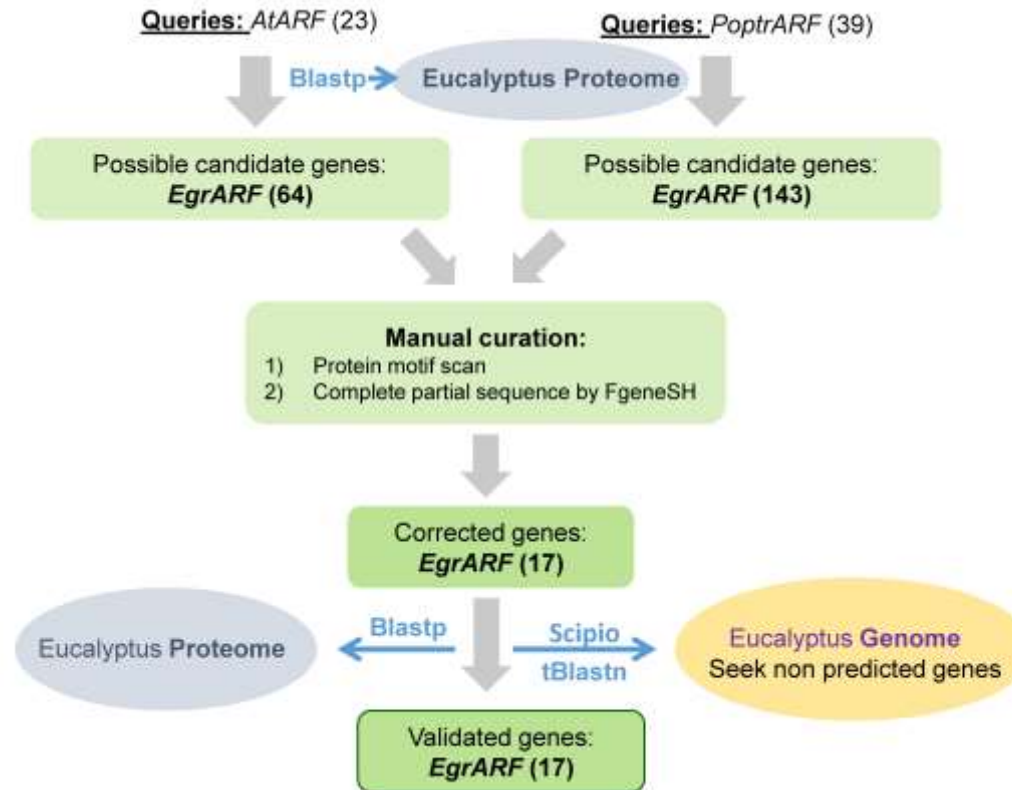


Figure S1 Procedure used for identifying ARF genes in *Eucalyptus grandis*. Arabidopsis ARF protein sequences were used to search their orthologs in the predicted Eucalyptus proteome by using in BLASTP. Sixty-four Eucalyptus proteins identified in this initial search were further examined by manual curation using protein motif scanning and the FgeneSH program to complete partial sequences. Redundant and invalid genes were eliminated based on gene structure, integrity of conserved motifs and EST support. Manual curation resulted in 17 complete Eucalyptus ARF protein sequences. These 17 protein sequences were used in two subsequent additional searches: first, a BLASTP search against the Eucalyptus proteome to identify exhaustively all divergent Eucalyptus ARF gene family members and, second, tBLASTn searches against the Eucalyptus genome for any possible unpredicted genes. To confirm our findings, we used poplar ARF proteins and repeated the complete search procedure described above and obtained identical results.

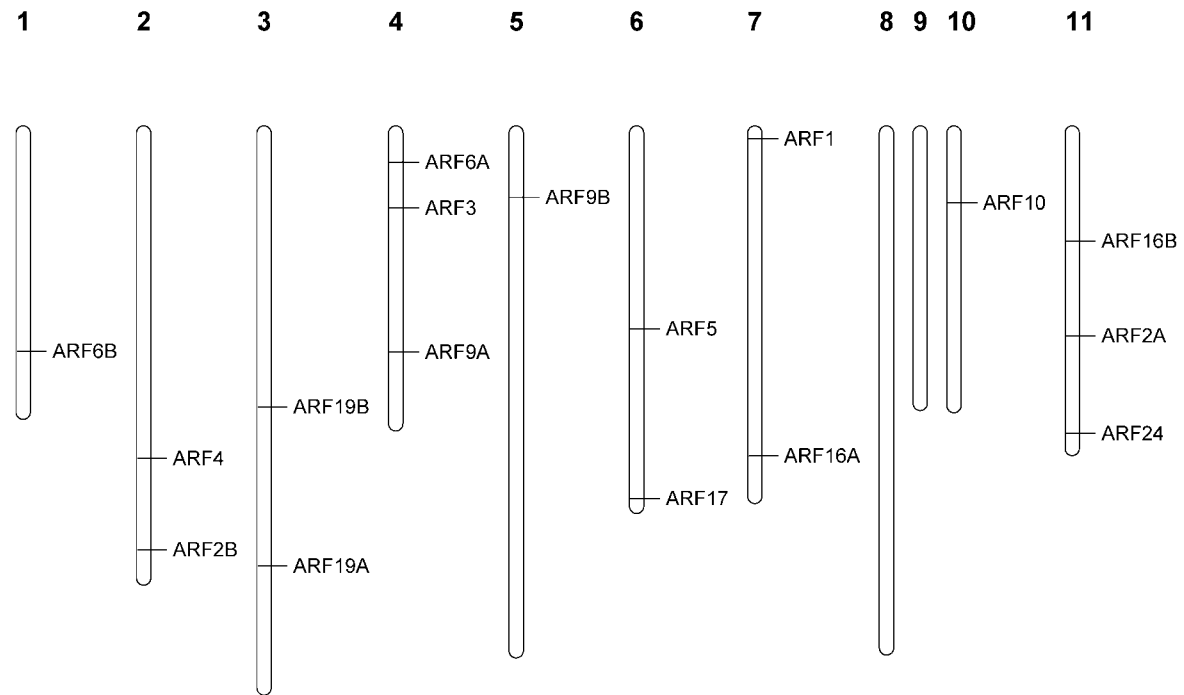


Figure S2 Locations of the 17 EgrARF genes on the 11 *Eucalyptus grandis* chromosomes.

AtARF5	MMASLSCV	EDKMKT	SCL	VNGGGT	ITTT	SQSTLLEEMKLLK	---	DQSG	TRKPV	---	INSELWHACAGPLVCLPQV	GSLVYYF	SGHSE	QVAVSTR	RR	SATTQV	PNYPNL	PSQ	---	LMCOV	HNVT	LHAD	KDS	SDEIYA	QMS	129	
EgrARF5	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	136
AtARF8	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	97	
EgrARF6B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	102	
AtARF6	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	100	
EgrARF6A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	98	
EgrARF19B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	108	
AtARF19	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	97	
AtARF7	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	98	
EgrARF19A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	97	
EgrARF24	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	110	
EgrARF2B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	102	
AtARF2	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	135	
EgrARF2A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	105	
AtARF1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	96	
EgrARF1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	99	
AtARF11	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	117	
AtARF18	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	100	
AtARF9	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	87	
EgrARF9A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	88	
EgrARF9B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	94	
AtARF13	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	99	
AtARF14	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF23	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF15	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF20	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF21	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF12	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF22	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	101	
AtARF4	MEFDLN	ETIAE	VEEEN	DDVG	VGGG	TRIDK	GRLGIS	PSSSS	CSSG	SSSSSSST	GSA	S---	---	---	---	---	---	---	---	---	---	---	---	---	---	138	
EgrARF4	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	130	
AtARF3	MGG	LIDL	NVME	TEED	ET	QQT	PSSAS	GSVS	PTSS	SSAS	VS	SVSS	NSAGG	---	---	---	---	---	---	---	---	---	---	---	---	121	
EgrARF3	MIDL	N	VEDDE	PSSGS	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	122	
AtARF16	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	87	
EgrARF16B	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	90	
EgrARF16A	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	100	
AtARF10	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	78	
EgrARF10	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	84	
AtARF17	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	86	
EgrARF17	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	112	
1.	10.	20.	30.	40.	50.	60.	70.	80.	90.	100.	110.	120.	130.	140.	150.												



DNA-binding domain

AtARF5	LQPVHS	-----LRDVFVPVDFG	-----MLRGSKH	-PTEFFCKTLTASD	STSHGGFV	PRRAAEKLFPP	LDYSA	PPPTQELVVRDL	LHENTW	TFRHIYR	GOPKRHL	LLTTG	--WSLFVGS	KRLRAGD	SVLFI	RDEKS	QLMVG	256															
EgrARF5	LQPVNS	-----EKDVFVPVDFG	-----LRPSKH	-PSEFFCKTLTASD	STSHGGFV	PRRAAEKLFPP	LDYSA	PPPTQELVVRDL	LHNDW	TFRHIYR	GOPKRHL	LLTTG	--WSLFVGA	KRLRAGD	SVLFI	RDEKS	QLMVG	262															
AtARF8	LQPLTP	-----EEQKTFVPIEL	-----G-IPSKQ	-PSNYFCKTLTASD	STSHGGFV	PRRAAEKVFPP	LDYTLQPPA	QELIARDL	LHDV	EKWFRIYR	GOPKRHL	LLTTG	--WSVFS	AKRLVAGD	SVLFI	RNEKN	QLFLGI	224															
EgrARF6B	LQPLSP	-----QEOKDLYLLPAEL	-----G-TPSKQ	-PTNYFCKTLTASD	STSHGGFV	PRRAAEKVFPP	LDYSQPPA	QELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	AKRLVAGD	SVLFI	RNEKN	QLLLGI	230															
AtARF6	LQPLNA	-----QEOKDLYLLPAEL	-----G-VPSRQ	-PTNYFCKTLTASD	STSHGGFV	PRRAAEKVFPP	LDYSQPPA	QELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	AKRLVAGD	SVLFI	RNEKN	QLLLGI	227															
EgrARF6A	LQPLSP	-----QEOKDLYLLPAEL	-----G-SPSKQ	-PTNYFCKTLTASD	STSHGGFV	PRRAAEKVFPP	LDYSLQPPA	QELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	AKRLVAGD	SVLFI	RNEKN	QLLLGI	225															
EgrARF19B	LQPVPS	-----FDKCALLRSDL	-----ALKTKP	-QPDFCKTLTASD	STSHGGFV	PRRAAEKLFPP	LDYSLQPPA	QELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSLFV	GKRLFAGD	SVLFI	RDDK	QLLLGI	235															
AtARF19	LQPVNK	-----YDRCALLASDM	-----GLKLNKQ	-PTEFFCKTLTASD	STSHGGFV	PRRAAEKLFPP	LDYSLQPPA	QELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	VTKRFLVAGD	SVLFI	RDEKS	QLMLGI	224															
AtARF7	LQPVNK	-----YDRCALLASDM	-----GLKLNKQ	-PNEFFCKTLTASD	STSHGGFV	PRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	VTKRFLVAGD	SVLFI	RDKA	QLLLGI	225															
EgrARF19A	LQPVSK	-----YDQCALLASDM	-----GLKQSRQ	-PTEFFCKTLTASD	STSHGGFV	PRRAAEKLF	PALDFM	OPPCQELIARDL	LHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	VTKRFLVAGD	SVLFI	RDEKS	QLLLGI	224															
EgrARF24	LIPBEAK	-----VSTPPRD	-----NTRFVFKILTQSD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	VTKRFLVAGD	SVLFI	RDEKS	QLLLGI	226																
EgrARF2B	LLPVFN	-----QDETAVKETE	-----HPLPRP	-RVHSECKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSLFV	SKKLVAGD	DAFIF	LRG	ENGELRVG	229															
AtARF2	LLPEAN	-----QENAEKEAP	-----LPPPFRF	-QVHSECKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	SKKLVAGD	DAFIF	LRG	ENGELRVG	262															
EgrARF2A	LLPEAN	-----QEDSLDKEPP	-----PPPPFRF	-KVHSECKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	SKKLVAGD	DAFIF	LRG	ENGELRVG	232															
AtARF1	LLPELD	-----QSEPTSPDAP	-----VQEPK	-TVHSECKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	SKKLVAGD	DAFIF	LRG	ENGELRVG	225															
EgrARF1	LLPEPE	-----QKEVTPDPP	-----LLEPPRC	-KVHSECKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	SKKLVAGD	DAFIF	LRG	ENGELRVG	222															
AtARF11	LQPEED	-----QSEPTSLDPP	-----LVEPAK	-TVDSFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSTFV	TSKRLVAGD	DAFV	FLR	GETGDLRVG	243															
AtARF18	LQPEED	-----QSEPTSLDPP	-----IVGPTKQ	-EFHSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSTFV	TSKRLVAGD	DAFV	FLR	GETGDLRVG	226															
AtARF9	LIPVGT	-----EVDPEMSPDS	-----PPELQRP	-KVHSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSTFV	TSKRLVAGD	DAFV	FLR	GETGDLRVG	214															
EgrARF9A	LLPEAP	-----QSEPMSPDY	-----LLEPPRP	-RVHSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSTFV	TSKRLVAGD	DAFV	FLR	GETGDLRVG	214															
EgrARF9B	LIPAGN	-----LMEPTSPDV	-----SAETPRT	-RVHSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSTFV	TSKRLVAGD	DAFV	FLR	GETGDLRVG	220															
AtARF13	LMPDIT	-----EVMTHNTT	-----MDTRRP	-IVYFSEKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	224															
AtARF14	LMPDIT	-----QVVIPTQN	-----Q-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	224															
AtARF23	LMPDIT	-----QVVIPTEN	-----E-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	221															
AtARF15	LMPDIT	-----VSNLQVVIPTQN	-----E-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	229															
AtARF20	LMPDIT	-----QVVIPTQS	-----E-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	220															
AtARF21	LMPDIT	-----QVVIPTQS	-----E-NRFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	224															
AtARF12	LMPDIT	-----QVVIPTQN	-----E-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	224															
AtARF22	LMPDIT	-----QVVIPTQN	-----E-NQFRP	-LVNSEFVKILTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GTPQRHM	FTSGGG	SVFAT	KRLVAGD	DAFV	FLR	GETGDLRVG	222															
AtARF4	LLPLQE	-----FSMLNGE	KEVKELGGEER	-----NGSSV	KR-TPHM	FCKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSLFV	SKKLVAGD	DAFV	FLR	GETGDLRVG	275													
EgrARF4	LLPQLE	VGLDSEGRAL	E-LGV	DENDI	-----GGSP	RS-TPHM	FCKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSVFS	QKNLV	SGDA	VFL	FRG	DELRLGI	267											
AtARF3	LLPESE	-DIERKVR	EGIIDV	GGEDY	-----EVLK	RSN-TPHM	FCKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSAFV	NKLV	SGDA	VFL	FRG	DELRLGI	257											
EgrARF3	LVPERE	-QIEH	KLREGD	NEIDLDE	DEI	-----EP	AVKSS-TPHM	FCKTLTASD	STSHGGFV	LRRAAEKLF	PALDFM	OPPCQELVAKD	IHDNE	WKFRHIYR	GOPKRHL	LLTTG	--WSAFV	NKLV	SGDA	VFL	FRAS	DELRLGI	259										
AtARF16	LIPLKD	-----DEYVD	HEYGD	GEDSN	-----GF	ESNE-KTP	SFAKTLTQSD	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TILAKD	VHGD	VKFRHIYR	GTPRRHL	LLTTG	--WSNFV	NKLV	AGD	IVFM	RAENG	DLCVGI	218								
EgrARF16B	LVP LTS	-----SEPDF	GDDGIG	-----GL	QSDG	DKPAS	FAKTLTQSD	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TILAKD	VHGD	VKFRHIYR	GTPRRHL	LLTTG	--WSNFV	NKLV	AGD	IVFM	RAENG	DLCVGI	219								
EgrARF16A	LMPMRS	-----DEYH	HLDD	GGSL	-----GK	GTEN	LEKVAS	FAKTLTQSD	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TIVAKD	VHGES	WKFRHIYR	GTPRRHL	LLTTG	--WGNFV	NKLV	AGD	IVFM	RAENG	DLCVGI	230							
AtARF10	LLPLPG	-----NDL	LDEN	AVGL	LPSSD	-----G	NGNGKE-KPAS	FAKTLTQSD	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TIVAKD	VHGES	WKFRHIYR	GTPRRHL	LLTTG	--WSTFV	NKLV	AGD	IVFM	RAENG	DLCVGI	213							
EgrARF10	LVP LPN	-----TELDF	EDRA	EAAA	-----G	SDNE-KPAS	FAKTLTQSD	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TIVAKD	VHGES	WKFRHIYR	GTPRRHL	LLTTG	--WSTFV	NKLV	AGD	IVFM	RAENG	DLCVGI	215								
AtARF17	LQPMTO	-----QQTPT	NYR	FG	FD	-----G	VDVDDNN-KVT	FAKLITP	SANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TIVAKD	VHGES	WKFRHIYR	GTPRRHL	LLTTG	--WSK	FVNS	KLV	AGD	SVFM	MKSAD	EMF	IGV	217					
EgrARF17	LRFV	VVH-----P	GA	LQ	ESP	-----A	R	GN	PEEK	IVS	FAL	ITL	PS	DANNGG	GFV	PRYCAET	IFPR	LDYSA	PPVQ	TIVAKD	VHGES	WKFRHIYR	GTPRRHL	LLTTG	--WSK	FVNS	KLV	AGD	SVFM	MKSAD	EMF	IGV	240



B3 domain

DNA-binding domain

AtARF5	RRANRC	-----	TALP	SSV	LSADS	-----	MHIGVLA AAAHAAT	ANR	PFLIFYNP	-----	RACPAEFV	PLAKYRKAICG	QLSVGMRFGMMF	ETED	SGK	340														
EgrARF5	RRANRC	-----	TTLP	SSV	LSTD	-----	MHIGILAAAHAAT	RS	SFTIFYNP	-----	RACPSEFVI	PLVKYRKAVYGR	IRISVGMRFGMMF	ETEE	SGK	346														
AtARF8	RHATRP	-----	OTIVP	SSV	LSSDS	-----	MHIGLLAAAHAHA	AIN	SCTVFFHP	-----	RASQSEFVI	QLSKYIKAVFHR	IRISVGMRFRMLF	ETEE	SSV	308														
EgrARF6B	RRANRP	-----	OTVMP	SSV	LSSDS	-----	MHIGLLAAAHAHA	AIN	SRTIFYNP	-----	RASPSEFVI	PLAKYVKAVYH	IRVSVGMRFRMLF	ETEE	SSV	314														
AtARF6	RRANRP	-----	OTVMP	SSV	LSSDS	-----	MHLGLAAAHAHA	AIN	SRTIFYNP	-----	RASPSEFVI	PLAKYVKAVYH	IRVSVGMRFRMLF	ETEE	SSV	311														
EgrARF6A	RRANRP	-----	OTVMP	SSV	LSCDS	-----	MHLGLAAAHAHA	AIN	SRTIFYNP	-----	RASPSEFV	ISLAKYIKAVYH	IRVSVGMRFRMLF	ETEE	SSV	309														
EgrARF19B	RRANRC	-----	PTNLS	SSV	LSSDS	-----	MHIGLLAAAHAHA	AIN	SPTIFYNP	-----	CFALRASP	SEFVIPLAKYVKAVYS	NIQISLGMFRFMMF	ETED	SGT	324														
AtARF19	RRANRC	-----	TPTLS	SSV	LSSDS	-----	MHIGLLAAAHAHA	AIN	SPTIFYNP	-----	RASPSEFV	VLAKYINKALYA	QVSLGMFRFMMF	ETED	CGV	307														
AtARF7	RRANRC	-----	QPALS	SSV	LSSDS	-----	MHIGVLA AAAHA	NAN	SPTIFYNP	-----	RAAPAEFV	VPLAKYTKAMYA	QVSLGMFRFRMIF	ETEE	CGV	308														
EgrARF19A	RRANRC	-----	QPALS	SSV	LSSDS	-----	MHIGLLAAAHAHA	AIN	SPTIFYNP	-----	RWASPSEF	VIPLAKYINKAFYT	QVSLGMFRFMMF	ETEE	GV	308														
EgrARF24	RRLMKS	-----	OTTIS	SSI	LSGHS	-----	MRHGLLASALH	AVST	GMTFTVYK	-----	WACTSGFI	IGYQYVKAMAN	DYSIGKFRFRMQ	FED	LCE	309														
EgrARF2B	RRAMRC	-----	LNNVP	SSI	MPSHS	-----	MHIGVLATAWHA	IST	GMTFTVYK	-----	RTSPAEFI	IPFDKYIEAKF	DYSIGMFRFMT	FE	EEAPE	312														
AtARF2	RRAMRC	-----	QGNVP	SSV	LSSH	-----	MHLGLVATAWHA	IST	GMTFTVYK	-----	RTSPSEFVI	PFDQYMSLVKN	NYISIGMFRFKMR	FE	EEAPE	345														
EgrARF2A	RRAMKC	-----	QGNVS	PSV	TSSH	-----	MHLGLVATAWHA	IST	GMTFTVYK	-----	RISPAEFI	IPYDQYMSLKK	NYISIGMFRFKMR	FE	EEAPE	315														
AtARF1	RRHMRC	-----	OTNIP	SSV	TSSH	-----	MHIGVLA TAAHA	IT	GTIFSVFK	-----	RTSRSE	-----	LEAKTQ	KLSVGMFRFKMR	FE	EEAPE	297													
EgrARF1	RRLMRC	-----	OSNMP	SSV	TSSH	-----	MHLGLVATAWHA	IAI	GTLSVFK	-----	RTSRSEFVI	SLNKYLEARAH	KLSIGMFRFKMR	FE	EEAPE	308														
AtARF11	RRLAKC	-----	OSTMP	ASV	TSSQS	-----	MRLGLVATASH	AVT	TTIFVVK	-----	RI	SQFIISVNKYMMAMKN	GFSLGMRYRMR	FE	EEAPE	324														
AtARF18	RRLARH	-----	OSTMP	TSV	TSSQS	-----	MHLGLVATASH	AVR	TTIFVVK	-----	RI	SQFIVGVNRYMEAIKH	GFSLGRFRMR	FE	EEAPE	307														
AtARF9	RRANLC	-----	OSNMP	SSV	TSSH	-----	MHLGLVATARHA	IQ	KTMFIVYK	-----	RTSQFI	ISLNKYLEAMSN	KFSVGMFRFKMR	FE	EGED	SPE	295													
EgrARF9A	RRMARC	-----	OSTMP	ASV	LSSQS	-----	MHLGLVATASH	AVQ	TLFVVYK	-----	RTSQFI	ISLNKYLEAVNN	KFSVGMFRFKMR	FE	EGED	SPE	295													
EgrARF9B	KRVARC	-----	OSNMP	SSV	TSSQS	-----	MHLGLVATASH	AVT	TLFVVYK	-----	RTSQFI	ISLNKYLEALNN	KFTVGMFRFKMR	FE	EGED	SPE	301													
AtARF13	RRAKHC	-----	OGHIP	SSV	TSANC	-----	MQHGVATSVVNA	FRK	TCMFNVYK	-----	SSSQFV	ISYDKRFVDAMNN	NYIVGSRFRMQ	FE	EGD	FSE	305													
AtARF14	RRAGHC	-----	QGNIP	SSI	VSID	-----	MRHGIIASAKH	AFD	NCMFIVYK	-----	RS	SQFIVSYDKFLD	VVNN	KFNVGSRFTMR	FE	EGDD	FSE	305												
AtARF23	R-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	222														
AtARF15	RRARHC	-----	QGNIP	SSI	VSID	-----	MRHGVIASAKH	AFD	NCMFIVYK	-----	RS	SQFIVSYDKFLD	AVNN	KFNVGSRFTMR	FE	EGDD	FSE	310												
AtARF20	RRARHC	-----	QGNIP	SSI	VSID	-----	MRHGVIASAKH	ALD	NCIFIVYK	-----	SIRS	SQFIVSYDKFLD	AMNN	KFIVGSRFTMR	FE	EGDD	FSE	303												
AtARF21	RRARHC	-----	QGNIP	SSI	VSID	-----	MRHGVIASAKH	AFD	NCIFIVYK	-----	RS	SQFIVSYDKFLD	AVNN	KFNVGSRFTMR	FE	EGDD	FSE	305												
AtARF12	RRARHC	-----	QGNIP	SSI	VSID	-----	MRHGVIASAKH	AFD	NCMFIVYK	-----	RS	SQFIVSYDKFLD	AVNN	KFNVGSRFTMR	FE	EGDD	FSE	305												
AtARF22	RRAGHC	-----	QGNIP	SSI	VSID	-----	MRHGVIASAKH	AFD	NCMFIVYK	-----	RS	SQFIVSYDKFLD	AVNN	KFNVGSRFTMR	FE	EGDD	FSE	303												
AtARF4	RRARP	-----	RNGLP	DSI	TEKNS	-----	CSNILSLVAN	AVS	TKSMHFVYSP	-----	RATHAEFVI	PYKYIT	IRS	PVCI	TRFRMR	FE	EMDD	SPE	357											
EgrARF4	RRARHP	-----	RNVLP	GST	VGEQN	-----	MCPAVLSAVAS	AVS	TKSVHFVYSP	-----	RASHAEFV	VPYQYKYLK	INN	VICIGTR	FKMR	VD	DDAPE	350												
AtARF3	RRASCI	-----	EGTAA	LSA	QYNQN	-----	MNHNNSFEVA	HS	VFSISYNP	-----	KASWNF	FIIPAPKFLV	VDY	PCFI	GMRFKAR	VE	SEDA	SE	340											
EgrARF3	RRAIQV	-----	KGASA	FPS	LCIQ	-----	LNQSALMDV	PKAVSLGIA	FSVYDP	-----	RASSSEFLI	PARRFFK	ILNQ	TLAP	GMRFKMR	FE	EAED	TAE	342											
AtARF16	RRAKRGI	IGNGPEYSAGWN	PIGGSCG	YSSL	LREDE	-----	SNLRRSNC	SLADR	KGVTAESVIEAATLAI	SRP	FEVVYYP	-----	RASTSEFC	KALDARAAMRI	PWC	GMRFKMA	FE	ETED	SSR	334										
EgrARF16B	RRAKRG	-----	IGSGPESSSGWN	PVGGNC	CAVPYGGFAF	-----	LIEDENKLI	TNGHGN	CMSGNGSLMGK	KRVTP	EAUV	EAASL	AANGHP	FEVVYYP	-----	RASTPEFC	VKSLVKTAMQI	RWCP	GMRFKMA	FE	ETED	SSR	345							
EgrARF16A	RRAKRGI	GIGGNDNACGWN	SASGNFG	-----	GYSMFA	REGS	NL	-----	MQKGC	-----	GGEFRRK	VIGESV	LQAATL	AAKQ	QPF	FEVVYYP	-----	RAGTPEFF	VRASSV	TAMQV	QWCS	GMRFKM	FE	ETED	ASR	345				
AtARF10	RRAKRGL	SGSNAGSDNP	YPGFS	GFLR	-----	DDESTTT	TKLMM	KRNG	-----	NNDGNAAT	GRV	VEA	VAEVARA	ACQAF	FEVVYYP	-----	RASTPEFC	VKAADVRSAMRI	RWC	GMRFKMA	FE	ETED	SSR	332						
EgrARF10	RRAKRG	IGGESQA	AWSSGGG	SCVP	-----	QFGGFSM	-----	LLRE	EEKILMRNA	ANAG	CDGGFR	GGKGR	VRVQ	SEVIEA	ALAAK	QPF	FEVVYYP	-----	RASTPEFC	VKASVKAAMRI	QWCS	GMRFKMA	FE	ETED	SSR	339				
AtARF17	RRITP	ISSSDG	SSY	GGDEY	NGYY	-----	SSV	-----	AKEDD	-----	GPSK	KTFR	RSNG	LTA	EAVLDA	INRA	SQGLP	FEVVYYP	-----	AAGWSEFV	VRAEDVES	BMSM	YWP	GTR	VKMAM	FE	ETED	SSR	329	
EgrARF17	RRAVRNS	QVDCARWRE	QIGGRLKVE	-----	ESGLRD	GFSRNG	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	RAESDFV	VKAER	VEEALKS	LWTA	GMR	KMA	VE	EAED	CSR	346



Auxin response factor (ARF) domain

DNA-binding domain

AtARF5 RR-YMGITVIGISDLDPLRWPGSKWRNLQVWDEP-GCNDKPTRVSPWDIETPESLFI F--PSLTSLGKLRQLHPSYFACETEWGSLIKRPLIR-----VPSDANGIMPYA 440
 EgrARF5 RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-GCGDKQNRVSPWDIETPESLFI F--PSLTSLALKRPLHTGF-----MGGETEWGSLVVKRPLIQVPPGGGMNLLPFASVPNLCSEQLIKM-----IMKPPQPIVNH P 472
 AtARF8 RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 EgrARF6B RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 AtARF6 RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 EgrARF6A RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 EgrARF19B RR-FMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 AtARF19 RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGDRPSRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 AtARF7 RR-YMGITVIGISDLDPLRWPGSKWRNLQVWDEP-AAGDRPSRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 EgrARF19A RR-YMGITIGISDLDPLRWPGSKWRNLQVWDEP-TAGERQPRVSLWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 EgrARF24 QR-LGGTVVIGIEDLDPVRWPGSKWRNLQVWDEP-SKICPCERVSPWDIESLDDP--GKKQAVLPTSLKRRTRPCSLQ-----LDWPTFVMDDESQW-----SVAPKRSQRQ-P 408
 EgrARF2B QR-FSGTIVIGIEDVDPVRWPGSKWRNLQVWDEP-TSIRHPRDRVSPWNIEPAVTAPD-----NLPASRPKRPRASMS-----SSTDSSVRMREGPLGN-----GTDPPADIGF-S 409
 AtARF2 QR-FTGITVIGIEESDPRWPKSKWRSLKVRWDEP-SSIPRPDRVSPWKVEPALAPPALS-FVPMSPRKRPRSNIA P-----SSPSSMLTREG-----ITKANMDPLPAS 442
 EgrARF2A QR-FTGITVIGIEDADPKGWRDITKWRSLKVRWDEP-SAIPRPDRVSPWKVEPALAPPALS-FVPMSPRKRPRSNIA P-----SSPSSMLTREG-----ITKANMDPLPAS 442
 AtARF1 KR-FSGTIVIGQENKSSVWHDSEWRSLKVRWDEP-SSVFRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 389
 EgrARF1 RR-FSGTIVIGQENKSSVWHDSEWRSLKVRWDEP-SSIMRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF11 RI-FTGITVIGISDLDPLRWPGSKWRNLQVWDEP-SSIQRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF18 RI-FTGITVIGISDLDPLRWPGSKWRNLQVWDEP-TTVQRPDKVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF9 RR-YSGTIVIGKDCSP-HWKDSKWRCLVHWDEP-ASISRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 EgrARF9A RR-FSGTIVIGVEDISS-QWTDKWRSLKVRWDEP-ASVFRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 EgrARF9B RR-FSGTIVIGVEDISS-QWTDKWRSLKVRWDEP-ASVFRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF13 KR-YDGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-SFPLRPNOVSPWDIEHLTPWSNVS-RSSFLKNKRREVNE-----IGSSSSHLLP-P 387
 AtARF14 RR-FSGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-SFPLRPNOVSPWDIEHLTPWSNVS-RSSFLKNKRREVNE-----IGSSSSHLLP-P 387
 AtARF23 ----- 222
 AtARF15 RR-YFGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-ASFLRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF20 RR-YFGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-ASFLRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF21 RR-YFGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-ASFLRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF12 RR-CFGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-TSFGPKKVVSPWDIEHLTPWSNVS-RSSFLKNKRREVNE-----IGSSSSHLLP-P 387
 AtARF22 RR-YFGTIVIGVNDMSP-HWKDSKWRSLKVRWDEP-ASFLRPDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF4 RR-CAGVTVIGVCDLDPVRWPGSKWRNLQVWDEP-FVSDHQERVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 EgrARF4 KR-CTGVVTRIGDLDPLRWPGSKWRNLQVWDEP-ITNGHQDRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 AtARF3 RR-SPGIISGISDLDPLRWPGSKWRNLQVWDEP-VANGHQQRVSPWELVPLVANSIPSSQ-QPPQQRNKRPRPPGL-----PSPATGPS-----GPVTPDGVVK-- 390
 EgrARF3 RR-HSGLIANISDMDPVRWPGSKWRNLQVWDEP-VEPDRGSRICPWEIEPLTTFPMYP-SLFPRLRKRPPHAGTSSSLPDGRGDLGSLTWRGCG-----GGEQQGLLPLNYPSVGLFPWMQQRLLDSQMGTDNNQQYQAMLAA 444
 AtARF16 ISWFMGTVAQVADPIRWPNSPWRLLQVWDEP-DLLQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 EgrARF16B ISWFMGTVAQVADPIRWPNSPWRLLQVWDEP-DLLQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 EgrARF16A ISWFMGTVAQVADPIRWPNSPWRLLQVWDEP-DLLQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 AtARF10 ISWFMGTVAQVADPIRWPNSPWRLLQVWDEP-DLLQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 EgrARF10 ISWFMGTVAQVADPIRWPNSPWRLLQVWDEP-DLLQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 AtARF17 ITWFGIVSSVYQETG-PWRGSPWKQLQITWDEP-EILQNVKRVSPWLVVLSNMPPIHL-SFSPRKKLRPLPHHPDF-----PDLGHFP-----LDQIPVPPFPFN 434
 EgrARF17 MTWHGIVSSVYQETG-PWRGSPWKQLQITWDEP-EAMQDKRSVNPWQVSEIGFSPSLDSV-----YPPVKKLRVPLRSALG-----REGSGHFPDMS 434
 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600



NLS

DNA-binding domain

AtARF5	PSASNTSGQEQLNSQMSAP-----AKPENSTLSCSSGRVQHGLEQSMEQ-----	555
EgrARF5	VLNQVPSTSTGELPEENIAS-----GPSSQNHNLNHPILLNQNGQIQSQACSWPP-----	616
AtARF8	NLPQQNMRQEVSNQPAQQQ-----QLQPPDQNAVLNAFKMQNGHLQ-----	547
EgrARF6B	PSYNDQRQQQHQHQPPQQS-----QQFNHTSLQQMPNITITLQYQYGSIGSQSSSLP-----AISQSQQN	579
AtARF6	QQQQLSQQQQQLSQQQQQQAVLGVPEETHQPSQAQSQSNNHLQQQQQVVDNHNPSASAAVVSAMSQFGSASQPPNTSPLQSMSTSLCHQQSFSDTNGG-----	615
EgrARF6A	PSQFALASQSHATSLQTPS-----LCQQL	575
EgrARF19B	PDQSSSLPMPDNQIQLOMIQKLLQQQQQQQSLLAQQSALQCPHTHPQLQEQRQHDPVVSQSFKSMVTSQMLEMPQSTANSFSQPNIIQQIQKNNSQLNVRFSNLQQPKFOEQSGLLPEMVGHMGLPQISTSHASASASMLTGAAG	753
AtARF19	PNQPTGFSQSQLQQSMLPTGAKMTHQININSMGNKGLSQMTSFAQEMFPQQOLEMHNSSQLLRNQEQSSLHSLQNLSONPQQLQMQQQSSKPPSQQLQLQLLQKLQQQQQQSIPPVSSSLQPLSALQTTQSHQLQQLSSQNQQP	696
AtARF7	PLQSHSHPPQQQLQHKLQQLQVFNQQLYNGQAAAOHQSQGASTHHLQPLVSGSMASSVITPPSSSLNQSFOQQQQSKLQQAHHHLGASTSQSSVITSTKSSNLMSAPPQPTQFSRQVEQQPPGLNGQNLQQLLQQAHAHQAAQ	736
EgrARF19A	PLNGGGVVTSNQFPSQMVQQSALYSQLQQQQQQQLLTTQNAFSPSPSILGINKVPVHPTSVSQSKFQSQMEQQQPSLLQRHQQQPMQMPPSSLLQQ-----SWTQRAQPQLQPLPQVLQNLSEQQIQLQLQKLQQ	702
EgrARF24	D-----	446
EgrARF2B	NTWVPQLVQEAATLNLVPPDS-----GTFHHRHGLFSSFLRRDSEITKRAKKQ-----NSAETKTDL	516
AtARF2	ENWMSSARHEPTYTDLLSGF-----GTNIDPSHGQRIPFYDHSSSPMPAKRILSDSEGKFDY-----	553
EgrARF2A	VSHGFSLSEQSSAANPARK-----HLVDQGRKFHII	522
AtARF1	KSPFVSIQSAF-----	426
EgrARF1	GPSAALSQYTVN-----	445
AtARF11	-----	435
AtARF18	P-----	412
AtARF9	SV-----	423
EgrARF9A	PQTEGDRQFSPSVC-----	437
EgrARF9B	GGWLPSPCLSVSPNILPDAV-----DDSKSVSA	460
AtARF13	S-----	424
AtARF14	P-----	428
AtARF23	-----	222
AtARF15	P-----	433
AtARF20	P-----	412
AtARF21	P-----	428
AtARF12	P-----	428
AtARF22	P-----	426
AtARF4	RFPRVLQGEICSLKSFPPF-----AGFSPA	547
EgrARF4	RFPRVLQGEICTLKSLLTK-----PEYNLGTWCKSSSLSCSSFG-----	548
AtARF3	GFHKVLQGE-----	483
EgrARF3	GFQMPFSRNGCSALSQGSND-----	490
AtARF16	P-----	473
EgrARF16B	HSIRSMRTSNQPRMH-----	504
EgrARF16A	PLNHTSVSTRFSRGAFFG-----	501
AtARF10	LNLSSYTGNKHL-----	478
EgrARF10	PHSRSSNSITKDNTQ-----	498
AtARF17	PP-----	463
EgrARF17	-----	461
760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	

AtARF5	-----ASQVT-----TSTVCNEEKVNQLLQKPGASSVVOAQDCLDITHQIQYQSDPFGFLETDDELTSQVSSSFQSLAGSYKQPFILSSQDSSAVVLVDSINSPLFHDVW-----	657
EgrARF5	---QPLQIPIA-----DSNVLHGSSPFVNPDELMFSSSTNKSVAALIRSPGPFISCGSQDPSATFGDPVQGLPLISQELWDHQGINLRFPSQGDQITPLPEQDPSSSLCGISNSV-----	721
AtARF8	---WQQSEMP-----SPSMKSDFTDSSNKFATTASPASGDGNLLNFSITGQSVLPEQLTTEGWSPKASNTFSEPLSLPQAYPG-----KSLALEPGNFPQ-----	635
EgrARF6B	IFEDGMENPIV-----ASDVSQPMQILSISRDGSSQLLSVNGSDSMISSSLLKKQNSVEPHLLSEAAHCILPQVEQLATHTTNVSEFANYLPPFPGREYSAYPGATDPQSS-----	686
AtARF6	-----NNPI-----SPLHTLLSNFSQDESSQLLHLTRTNSAMTSSGWPFSKRPVAVDSSFOHSGAGNNTNQSVLEQLGQSHTSNVPPNAVSLPPFPGRECSIEQEGSASDPH-----	716
EgrARF6A	SFSDSTGNPVT-----SPVVSPLQTLGSGFTQDGSTHHLNLPRTNSSVSPSSWPSKRAAIESLVPSSGQORVLPQMDQLGPPQNNLSPSSVSLPPFPGRECLDQEVTDVQSH-----	682
EgrARF19B	GPSVTTDDMPCASASGONCANIVQSMNCRPHRSASISEDMSQSTATFWNPSALETIGSNGNMMKDFQPKPDVKPSLDVSKGQNGQFFSAQTYLNGATTQTDYLDASSSTTSVCL-----	870
AtARF19	LAHGNNSPAS---IFMQPPQIQVSPQQQGQMSNKNLVAAGRSHSGHTDGEAPSCSTSPSANNTGHDNVSPTNFLSRNQQQQAASVVSASDSVFERASNPVQELYTKTESRISQGM-----	810
AtARF7	QIFQSSLLEQPHIQFQLLQRLQOQQQQQFLSPQSQLEPHHQLSQQLQQLPTLSQGHQFPSSCTNNGLSLQPPQMLVSRPQEKQNPVVGGVKAYSGLIDGGDAPSSSTSPTNNCQISSGFLNRSQSGPAILLPDAATDMSGNLVQDL-----	886
EgrARF19A	QQQHQQQLPNP-----AGPLLQPLQOQQQQQQHQQQVVLPQNM-----PLSQQLVCSNLPTPALLPQPSPNPHLYGQOKALTAVRALSGLTDGDPSCSTSPS--TNNC-----	803
EgrARF24	-----VMPAN-----STSWEARITTFETKDDNE-----KTLAQINR-----FGKC-----	480
EgrARF2B	IPSPGSVRQGP-----SLNMLGSGIVASLENESRQQQSL-----GNVKGDTKREMNSGNCFLPMHSPSLAQQLKANG-----NGSC-----	589
AtARF2	---LANQWQMI-----HSGLSLKLHESPKVPAATDASLOGRCNVKYEYVVLNGLSTENAGGNWPIRPRALNVEEVVNAQAQAQAREQVTKPFTIQEETAKRE-----GNC-----	654
EgrARF2A	GNHWSMIPSSL-----SLNLSERNRNSLHGNDMHSPOGIGKYSGSKEYPVVHGQRVEQP HQNWVMRPMSPHFNFPHASESISKSPYAQQH-----EAIKAKGNC-----	619
AtARF1	---WPTNADSA-----AESFASAFNNESTEK-----KQTN-----GNVC-----	457
EgrARF1	---WPSHMETI-----TDPCTPVNGKESSEK-----RESC-----GSGC-----	476
AtARF11	-----KSVFSSGLQCKITEAPV-----TSSC-----	456
AtARF18	-----SLERT-----SGGYSSNNSFKPETPPP-----PTNC-----	438
AtARF9	-----SNVAK-----DSTLNDQMVSPEVQK-----KPET-----TANY-----	451
EgrARF9A	---GWPLI-----SSSLMHSKPKRNEPKVEL-----AEKPERPTSC-----	470
EgrARF9B	LPVPCRHPIAH-----PSSLNNEMLPNPAEDGK-----KVEP-----TSSC-----	496
AtARF13	-----LLAIP-----NENVNSDQMIOPRKEDI-----TEA-----TTSC-----	454
AtARF14	-----VQPMA-----KLNANNVVTPIEENI-----TINA-----VASF-----	456
AtARF23	-----	222
AtARF15	---VQPMP-----KRNANNQMVVTQIEENI-----TTKA-----GTNF-----	462
AtARF20	---VQPMP-----KLNANNQMVVTQIEENI-----TTKA-----VTNF-----	441
AtARF21	---VQPMP-----KLNANNQMVVTQIEENI-----TTKA-----GTNF-----	457
AtARF12	---VQPMP-----KLNANNQMVTEMEENI-----TTKT-----GTNF-----	457
AtARF22	---VQPMP-----KLNANNQMVVTQIEENI-----TTKT-----GTNF-----	455
AtARF4	AAPNPFAYQAN-----KSSYPPLALHGIRSTHVPYQN-----PYNA-----GNCSS-----	588
EgrARF4	---VHQAP-----KYHFQDVKSSESLSQKVY-----FPYNDILKSSQD-----RTRCS-----	587
AtARF3	---TVPAY-----SITDHRQHGLSQRNIW-----CG-----	507
EgrARF3	---RFGLPVS-----SVQVSSPSSVLMFHQPSRK-----SNR-----SSLC-----	524
AtARF16	---PPPPS-----SLOLSPSLGLRNIIDTRNEKGFCE-----LTMGTTPCNDTKSK-----KSHI-----	519
EgrARF16B	---KSSSDDDI-----STLLTMTNYGKVFKKLE-----EVKK-----PPQL-----	537
EgrARF16A	---AFEDN-----NNSISCLLRMGISEN-----SKENFEKKS-----	532
AtARF10	---SPAMF-----LSSFNPRHHHYQARDSE-----NSNNISCSLTMGNPAMVQDKKSVGSKVTHQF-----	532
EgrARF10	---GSESL-----SCVLTMGNCSSQSEKS-----GDEK-----KHKF-----	527
AtARF17	-----	463
EgrARF17	-----DASRAFGLVNYVDENPP-----MYTC-----	482

..... 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050



AtARF5	-----DTQLNGLKFDQFSPLMQODLYASQNICMSNSTS-----	-----NILDPPISNTVLDDFCAIKDIDFQNHPSGCLVGNNTS	729
EgrARF5	-----CLKDLSAESNNQSGIYSCNLNDASNGGSSAIDPFS-----	-----ISSAILDDFCTIKDGFPPNLSDCLVGNFS	784
AtARF8	-----NPSLFGVDPDSGLFLPSTVPRFASSSGDAEAS-----	-----PMSL	671
EgrARF6B	-----LLFGVNIDSTSLMMQNGMQHLRNIQSEHDSLS-----	-----VFPGTSNFASVAG	731
AtARF6	-----SHLLFGVNIDSSLLMPNGMSNLRISGIEGCDST-----	-----TLPPFSSNFNN	761
EgrARF6A	-----LLFGVNLEPSSLLMQNGISSLRVAVGESDSTS-----	-----MPFPSNYISNSGA	727
EgrARF19B	-----SQSDAHIQQNNSSVSYNQSMFLFRDTSQDREVQADIRSSVFPSS-----	-----NADVQAGIPVNSDSMFGKGMVGLGKGFANDVPSAGILLADYDNK	957
AtARF19	-----NMKAGEHFRFKSAVTDQIDVSTAGTTYCPDVVG-----	-----PVQQQTFFLPSPFGFDGDCQSHHPRNNLAFPGNLEAVTSDPLY	887
AtARF7	-----YKSDMRLLKQELVGCQKSKASLIDHOLEASASGTSYGLDGGE-----	-----NNRQQNFLAPTFGLDQDSRNLGGANVDNCFVVDITLLSRGYD	971
EgrARF19A	-----HIPSNNFLCKNQVAQPVVLVGDSSLIIEPMNHLEHQMKEPDARIKHELPPSSKGHDLKQKASVITDPLEVSSSATSCLDAMAAQONFSLPTFCLESDVQSQPRNTSPPFAANIDNLAADLLSRGFDSQKDLQNLSTYGGG	943	
EgrARF24	-----KVFGVSLADD-TSELPSL-----	-----	497
EgrARF2B	-----KLFGLISLMSGTVA TESDNHGHVGSQKPVLQSN-----	-----LVDVSEPNVLGSPKIC	637
AtARF2	-----RLFGIPLTNNMNGTDSMSTQRNNLNDAAGLTQ-----	-----IASPKVQDLS	697
EgrARF2A	-----KLFGIPLVSNPVMKASAVSVRSATNVFTDHVD-----	-----SPSQAHGFR	661
AtARF1	-----RLFGFELVENVNVDECFSAASVSGAVAVDQPV-----	-----PSNEFDSGQQSEPLNI	505
EgrARF1	-----RLFGVQLLDSAKKESLSVTLAAGQRDDDKTAL-----	-----SVDD	512
AtARF11	-----RLFGFDLTSKPPASATIPH-----	-----DKQL	478
AtARF18	-----SYRLFGFDLTSNSPAPIPQD-----	-----	458
AtARF9	-----RLFGIDLMSSSLAVPEEKTA PMR PINISKPTM-----	-----DSHS	487
EgrARF9A	-----RLFGIDLINHSSNSQQVDRRLTVQPLDGSAGIN-----	-----ETHTPGNAPAAD	514
EgrARF9B	-----RLFGIDLINHTLSSPPSDKGFQSMCVSTATT-----	-----EGHVQMALSTAD	540
AtARF13	-----LLFGVDLTKVSKSKDSIC-----	-----PIES	476
AtARF14	-----RLFGVSLATPSVIKDPVE-----	-----QIGL	478
AtARF23	-----	-----	222
AtARF15	-----RLFGVSLATPPVIKDPPIE-----	-----QIGS	484
AtARF20	-----RLFGVSLATPLVIKDPPIE-----	-----EIGS	463
AtARF21	-----RLFGVTLDTPPMIKDPIK-----	-----QIGS	479
AtARF12	-----RLFGVTLDTPPVIKDPIE-----	-----EIGS	479
AtARF22	-----RLFGVSLVTPSVIKDPIE-----	-----EIGS	477
AtARF4	-----GPPSRAINFGEETRKFDQAQNEGGLPNNVTADLFP-----	-----KIDMMG	628
EgrARF4	-----DSTNFLREVASVRSLRVQNEAIERTKVDVRNLES-----	-----ICHSPNFGD	630
AtARF3	-----PFQNSLRILPPSVSSSPSS-----	-----VLLTNSNS	535
EgrARF3	-----NTLPWDEKLSSPMKVS-----	-----FGGT	544
AtARF16	-----VLFGLLILPEEQISEKGS-----	-----TDTANI	543
EgrARF16B	-----VLFGKPIILTEQQISLSNSATTTTTTASPVRTS-----	-----SEEKIDKTGSFPDGP	584
EgrARF16A	-----HILLFGQLILVDQQNSSESSGDTTGRCSSGEGNQE-----	-----RMSNSS	572
AtARF10	-----VLFGQPIILTEQQVMNRKR-----	-----	550
EgrARF10	-----LLFGQPIILTEQQISRGRSGCDVVSDVVSGRGS-----	-----TDGNT	564
AtARF17	-----QLFTNNFLSLPDLGKVS-----	-----T	482
EgrARF17	-----NIFGNNVVKPKPKICTDL-----	-----NIGS	504
1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200		



Carboxy-terminal dimerization domain

AtARF5	FAQDVQSQITSASFAD-----SQAFSRQDFPDNSGGTGTSSSNVDFDDCCLRQN--KGGSSWQKIATPRVRTYTKVQV-KTG-SVGRSIDVTFKDYEEELKSAIECMFGLG--GLLTHPQSSGWKLIVVDYESDVLVGGDDPW	860
EgrARF5	SSQDVQSQITSASLAD-----SQAFSRQDFPDNSGGTSSSNV-----DFDESSILKNSTWQQVAPMRTYTKVQV-KAG-SVGRSIDVTFNFRNYEELLSAIEYMFGLG--GLLNDPRGSGWKLIVVDYENDVLVGGDDPW	910
AtARF8	TDSGFQNSLYSCMQDT-----THELLHGA-----GQINS-----SNQTKNFVKVYV-KSG-SVGRSLDITRFSSYHELREELGKMPFAIE--GLLEDPLRSGWQLVFDKENDILLGGDDPW	772
EgrARF6B	TEFPHNSDMATPSSCID-----ESGFLOSS-----ENVQV-----VNPPTRTTFVKVHV-KSG-TFGRSLDITKFFSSYDELRSELARMPGLE--GOLEDPQRSGWQLVFDRENILLGGDDPW	833
AtARF6	DFSGNLAMTTPSSCID-----ESGFLOSS-----ENLGS-----ENPQSNTFVKVYV-KSG-SFGRSLDITKFFSSYHELRSELARMPGLE--GOLEDPVRSGWQLVFDRENILLGGDDPW	863
EgrARF6A	DFAPNPSVAPPGGIDD-----SGFLQSPH-----NLNGV-----NVPTRTTFVKVYV-KSG-SFGRSLDITKFFSSYHELRSELARMPGLE--GOLEDPVRSGWQLVFDRENILLGGDDPW	828
EgrARF19B	EPQQLSSSMVQSFQVSDVAFNLMESALNESTLVSRG-----PWGPA-----APQFQRMRTTFVKVYV-KRG-AVGRSVDITRYSGYDELKQDLARRFGIE--GOLEDGQKVGWKLIVVDHENDILLVGGDDPW	1074
AtARF19	SQKDFQNLVFNNGTNRDIEITELSSAAISSQSFGLPSIPFKPGCSNEVG-----GINDSGIMNNGGLWPNGTQRMRTYTKVQV-KRG-SVGRSIDVTRYSGYDELRRDLARMPGLE--GOLEDPLTSDWKLIVVDHENDILLVGGDDPW	1025
AtARF7	SQKDLQNLMSNYGGVTNDIGTEMSTSAVRTQSGVFNVPAINSD-----LAVNDAGVLGGGLWPAQTQRMRTYTKVQV-KRG-SVGRSIDVNRRYRGYDELRRDLARMPGLE--GOLEDPQTSWKLIVVDHENDILLVGGDDPW	1104
EgrARF19A	TPRDIETELSTAASIS-----SQSFGVPS-----MPFKAGCSNDVAINDTGLVNG-----GIWSSQTQRMRTYTKVQV-KRG-SVGRSIDITRYSGYDELRRDLARMPGLE--GOLEDPHRTDWKLIVVDHENDILLVGGDDPW	1065
EgrARF24	-----QVSN-----SSLSLSS-----SVPEL-----SKS-----SDFYQVI--INETSRRGRPADLRFKGYDKFIHGLDQLFYFG--GNLIGR--SSGHWVKCTDDNGDSVPIRDYN--	584
EgrARF2B	LKIAFSPFIAYGEGQGR-----FSSSEQVH-----RDVGG-----KHAVSTRSCKIKVH-KDIPVGRSVDLRFHGYSELITELDEIFDFN--GDLVAP--SKEWLIVTFDDEGDMMLVGGDDPW	741
AtARF2	QSKGSKSTNDHREQGR-----PFQINNVH-----PKDAQ-----TKTNSRSRCKFKVH-KOGIALGRSVDLRFQNYEELVABLDRLDFEFN--GELMAP--KDWLIVYDDENDMMMLVGGDDPW	800
EgrARF2A	LDQPMPEFLNAANGDD-----LVANSLEKEK-----LFQNSQPENRDVHHRVQASSTRSCTKVQV-KOGIALGRSVDLAKFNSYDELRAELDQLFEFG--GELMNP--RSNWLIVYNDDEGDMMLVGGDDPW	776
AtARF1	NQSDIPSS-----GSGDDPE-----KSLRSRQP-----ESRSRQIRSCIKVH-MOGSAVGRAIDLRFSECYEDLFFKLEEMFDIK--GELLES--TKKQVVYDDEDDMMVGGDDPW	601
EgrARF1	DSKEHQEPSCVNHDFE-----PSACYDPE-----KSCPNSSQ-----DLGSRQIRCTIKVH-MOGIAGRAVLAQFRSEYEDLLMRFEEMFEIG--GELCGS--MRKQVVYDDEDDMMVGGDDPW	619
AtARF11	ISVDSNISDSTTKQD-----PNSNSPK-----EQKQV-----TSTRSRIKVVQV-MOGTAVGRAVDLTLRSYDELILKELEKMFIE--GELSP--KDKWAVTFDDEGDRMLVGGDDPW	577
AtARF18	-----KQPMDTCCGAAK-----CQFPIPT-----SMSEQ-----KKQTSRSRRTKVQV-MOGIAGRAVDLTLRSYDELILKELEEMFEIQ--GOLLA--RDKWIVVTFDDEGDMMLAGDDPW	555
AtARF9	DPKSEISK-VSEKKQ-----EPAEGSPK-----EVQSK-----SSSTRSRRTKVQV-MOGVPVGRAVDLNLALGYNELIDLEKLFDIK--GELRS--RNQWEIVTFDDEGDMMLVGGDDPW	587
EgrARF9A	SQQKSVVLKTSKEIIP-----KQSVVSK-----EIRSK-----QSCSTTARSRIKVVQV-MOGVAVGRAVDLTFMEFYDQLIDLEEMFEIK--GELRP--RNKWEIVTFDDEGDMMLVGGDDPW	617
EgrARF9B	SDQKCDIQKASEEVQV-----RQMQLGK-----EGQTK-----QICST--RSRRTKVQV-MOGMAVGRAVDLTMLEGYQLMNELEEMFDLK--GQLQS--RDKWEIVTFDDEGDMMLGGDDPW	641
AtARF13	CKKSLPQ-----DKKFDQ-----TQPLRSRK-----EVQST-----EPNFT--RSRIKVH-MOGVAISRAVDLTMHGGYNLIQKLELEELFDLK--DELRD--RNQWEIVTFNNEGAEMLVGGDDPW	574
AtARF14	EISRLTQ-----EKKFGQ-----SQILRSPT-----EIQSK-----QFSST--RTCTKVQV-MOGVTIGRAVDLSVLNGYDQLILELEKLFDLK--GQLQA--RNQWEIAFTNNEEDKMLVGGDDPW	576
AtARF23	-----	222
AtARF15	DISKLTE--GKKFGQ-----SQTLRSP-----KIQSK-----QFSSTRCTKVQV-MOGVTIGRAVDLSVLNGYDQLILELEKLFDLK--GQLQT--RNQWKIIFGSDDEMLVGGDDPW	582
AtARF20	DISKLTE--GKKFGQ-----SQTLRSP-----EIQSK-----QFSSTRCTKVQV-MOGVTIGRAVDLSVLNGYDQLILELEKLFDLK--GQLQT--RNQWKIAFTDSDGYEMLVGGDDPW	561
AtARF21	DISKLTE--RKKFGQ-----SQTLRSP-----EIQSK-----QFSSTRCTKVQV-MOGVTIGRAVDLSVLNGYDQLILELEKLFDIK--GQLQT--RNQWKIAFTSDGYEMLVGGDDPW	577
AtARF12	EISKLTE--GKKFGL-----SQTLRSP-----EIQNK-----QFSSTRCTKVQV-MOGVTIGRAVDLSVLNGYDQLILELEKLFDIK--GQLQT--RNQWEIAFTDSDDKMLVGGDDPW	577
AtARF22	EISKLTE--GKKFGQ-----SQTLRSP-----EIQSK-----QFSSTRCTKVQV-MOGVTIERAVDLSVLNGYDQLILELEELFDLK--GQLQT--RNQWEIAFTDSDDKMLVGGDDPW	575
AtARF4	KQRGSELNMNASSGCK-----LFGFSLPV-----ETPAS-----KPSSSKRCTKVH-KOGSQGRAIDLRLNGYDQLMELERLNME--GLLRDP--EKGWRIYTFDSDNMMVGGDDPW	732
EgrARF4	SQRAQANGSIDSLLSG-----CKLGYPL-----IAEAPTS-----TLGNSKRSCIKVH-KOGLNVLGRAIDLRLNSYQDLLNLERLFSME--GLLRDP--DKGWRIYTFDSDNMMVGGDDPW	736
AtARF3	PNGRLED--HHGGSGR-----CRLFGLPL-----GVRD-----TDETTAVASAIYAVQVGNMKGASVQSNHHS--GRD-----IYAMR--DMLL-----DIAL-----	608
EgrARF3	SPLGLLNEENRLSFPH-----SSILLPSE-----GVVS-----EDMAPPLKSSCRLF--GISLTEGRDVSHEKVSMSSSLRNG--EPLFGHI--GE-----NFHPKANVSRVVGSS--	633
AtARF16	EKTQISSGGSNQNGVA-----GREFSSD-----EGSPCKSKV-----HDASGLETGCKVVF--MESEDDVGRITLDSVLGSYEEELSRKLSDMFGIK--KSEMLS--SVLVRDASGAIKYGAEFFP	647
EgrARF16B	DSARQOSG-QREQOSS-----CEGLRVEH-----DKHQV-----EMACSEIHGCKVVF--IASDDVGRITLDSVLGASVDELCRKLTFDMFGIE--NSQ--SLARHVLVYRDSKGAEKRIKGEFPY	684
EgrARF16A	EGSRNNVLYYNGTVES-----SSDGFTG-----IRRDR-----ASDLDTGTGCKVVF--MESENVGRITLDSVLGSYDELYRNLRDMFGIN--GSERLS--KVLVYSDAAGAIKAGDEFP	672
AtARF10	-FLEEAEAEEEKGLV-----ARGLTWNY-----SLQGL-----ETGCKVVF--MESEDDVGRITLDSVLGSYQELRYRKLAEFMFIERSDLLT-----HVVYRDANGVIKRIKGEFP	644
EgrARF10	GKPKFLSDGVGSLTKQA-----GAFGLWRH-----GFETS-----ELGLETGCKVVF--MESEDDVGRITLDSVLGSYDELYRKLGMFPGIE--RSEMPSS--HVLVYRDAAGTVKRIKGEFP	663
AtARF17	EMMNFSGSPSDNLSFN-----SNTNLLSS-----GNDLV-----GNRGPLSKKVNSIQ-----LFGKIITVEHSESSPAESSLCE--ED--GSKES--SDNETQLSLSHAPP	569
EgrARF17	SASELSTDSFSS-----WHSFGLEI-----SNGQCNTSK-----IGVVSIIQLFKGTIHAMKPAESNLD-----GVVSPSSDGSKRPGVITVQLSEPOLGPFEEF	590

.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



domain III

domain IV

Carboxy-terminal dimerization domain

AtARF5 EEFVGCVR CIRILSPTEVQQMSEEGMKLLNSAGINDLKTSVS ----- 902
EgrARF5 EEFVGCVR CIRILSPVEVQQM-----SEEGMKLLNSAGQVV-----NATTS----- 952
AtARF8 E----- 773
EgrARF6B QEFVNNVWYIKILLSPEHVQL-----GKQGINPANSVPRQAL----- 870
AtARF6 PEFVSSVWCIKILSPQEVQQM-----GKRGLLELLNSAPSSMNVDKLPSNGNCDDFGNRSDPRNLGNGIASVGGSFNV 935
EgrARF6A PEFVNSVWCIKILSPQEVQQMGKLDLELLNSIPVQRHSNGGC-----DFETNRQDSRTINSGLPSVGLDYGTL 897
EgrARF19B EDFVNCVRCIKILSPQEVQQM-----SLDGDPTNTLTPNQAC-----SSSDGCV----- 1119
AtARF19 EEFVNCVQNIKILLSVEVQQM-----SLDGDLAALPTTNOAC-----SETDSGNAWKVHYEDTSAASFNR 1086
AtARF7 EEFVNCVQSIKILLSAEVQQM-----SLDGNFAGVPVTNOAC-----SGGDSGNAWRGHYDDNATSFNR- 1164
EgrARF19A EEFVTVCQSVKILLSSTEVEQQM-----SLDGDLLGLVPTPNQAS-----SGTDSGNAWRGDLISR----- 1119
EgrARF24 REFVSMIHQGLICPKEEQVK-----QGAHLM----- 611
EgrARF2B EEFQGMVKHIFIYSKEEVKRM-----APRPLVFKSEESISPKT-----SHKRYSGGI----- 787
AtARF2 QEFCCMVRKIFIYTKEEVVKM-----NPGTLCRSEEEAVVT-----EGSDAKDAKSASNPLSLSSAGNS- 859
EgrARF2A QEFQGVIRKIFIYTRREEVQKM-----KPGTISAKDEDNLVMD-----EGVFSKMTSDTLPSASDPKNC- 835
AtARF1 NEFCGMVRKIFIYTPREEVKL-----SPKNKLAVNARMQLKA-----DAEENGTTEGRSSMAGSR----- 657
EgrARF1 NEFCSMAKKIYIYTTEEVKRL-----LPKIKLPEVEDVGPANG-----GSDVAVNTDDRSSVVGSGC----- 675
AtARF11 NEFCMAKKLFIYPSDEVKKM-----RSKSLLDGDKGTIVNLE-----SDQRTVHV----- 622
AtARF18 NEFCMAKKIFIYSSDEVKKM-----TTKLISSSLENEEYV-----NESFENRSG----- 602
AtARF9 PEFQNMVKRIFIWKSKEEVKRM-----TPGNQLRMLLREVEIT-----LTTSTKTDNHSN----- 636
EgrARF9A PEFQNMARRIFIWSSQDVKKM-----SPGSRLEPVSSVEEEGSLA----- 656
EgrARF9B PEFQNMVRRIFICSSQDVKKM-----SAKSKLPVSSVQEEGT-----VISSESADN----- 687
AtARF13 PEFQNMAKRIFICSKEEIKKM-----KLNKFFQPESKALIS-----SDVPPNVTDN----- 621
AtARF14 PEFQNMVKKIFIYKKEEVKNL-----KSRKSLSS----- 605
AtARF23 ----- 222
AtARF15 PEFQNMVKRIYIQRR----- 598
AtARF20 PEFQNMVKKILIYSKEEVKNL-----KSSKSLSS----- 590
AtARF21 PEFQNMVKKILIYSKEEVKNL-----KSSKSLSS----- 606
AtARF12 PEFQNMVKKIFIQKRR----- 593
AtARF22 PEFQNMVKKILIFKRGQKLE-----VQ----- 598
AtARF4 HDFCNVVWKIHLYTKEEVENA-----NDDNKCLEQAALMME-----ASKSSSVSQPSSPTITRV----- 788
EgrARF4 HEFCDDVVTKIHLYTQEEVEKMTGMSIDDTQSCLDQAPLMME-----ASKSSSVQPPDGPTVVRL----- 797
AtARF3 ----- 608
EgrARF3 ---NCFRVLDPVSDVLFD-----VAS----- 653
AtARF16 SEFLKTAARRLTILTEQGESV-----VV----- 670
EgrARF16B SDFIRTAARRLTILLNSSNGV-----GS----- 707
EgrARF16A SDFLKTAKRLTIAGYAMKLI----- 692
AtARF10 SDFMKAHKRLTIKMDIGGDNV-----RKTWITGIRTEGENGLD-----ASTKTGPLSIFA----- 693
EgrARF10 SDFMRTAKRLTIFMDSAGRST-----GRTELLGRRNAENGFD-----STTKAGPLSTYA----- 712
AtARF17 -----SVPKHSNSNAGSS-----SQG----- 585
EgrARF17 ECEVQAMGCRYIVVQVCSLQY-----IYPAVFIOQRNLCD----- 626
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....



Supplementary Figure 3. Multiple sequence alignment of predicted amino acid sequences of *EgrARF* and *AtARF* proteins. The multiple sequence alignment was obtained with muscle and manual correction. The highly conserved domains and nuclear localization signals (NLSs) of ARF proteins were noted on the bottom of the alignment with different colours. The amino acid position was given on the right of each sequence.

Name	Accession number	Alternative splicing	Name	Accession number	Alternative splicing
EgrARF1	Eucgr.G00076.1		AtARF1	AT1G59750.1	
	Eucgr.G00076.2			AT1G59750.2	
	Eucgr.G00076.3			AT1G59750.3	
	Eucgr.G00076.4			AT1G59750.4	
EgrARF2A	Eucgr.K02197.1		AtARF2	AT5G62000.1	
	Eucgr.K02197.2			AT5G62000.2	
	Eucgr.K02197.3			AT5G62000.3	
	Eucgr.K02197.4			AT5G62000.4	
	Eucgr.K02197.5				
EgrARF2B	Eucgr.B03551.1				
	Eucgr.B03551.2				
EgrARF3	Eucgr.D00588.1		AtARF3	AT2G33860	
	Eucgr.D00588.2				
EgrARF4	Eucgr.B02480.1		AtARF4	AT5G60450	
	Eucgr.B02480.2		Δ AtARF4		
	Eucgr.B02480.3				
EgrARF5	Eucgr.F02090.1		AtARF5	AT1G19850	
EgrARF6A	Eucgr.D00264.1				
	Eucgr.D00264.2				
EgrARF6B	Eucgr.A02065.1		AtARF6	AT1G30330	
	Eucgr.A02065.2				
	Eucgr.A02065.3				
			AtARF7	AT5G20730.1	
				AT5G20730.2	
				AT5G20730.3	
			AtARF8	AT5G37020.1	
				AT5G37020.2	
EgrARF9A	Eucgr.D01764.1		AtARF9	AT4G23980.1	
EgrARF9B	Eucgr.E00888.1				AT4G23980.2
	Eucgr.E00888.2				
EgrARF10	Eucgr.J00923.1		AtARF10	AT2G28350	
				AT2G46530.1	
			AtARF11	AT2G46530.2	
				AT2G46530.3	
			AtARF12	AT1G34310	
				AT1G34170.1	
			AtARF13	AT1G34170.2	
				AT1G34170.3	
			AtARF14	AT1G35540	
			AtARF15	AT1G35520	
EgrARF16A	Eucgr.G02838.1		AtARF16	AT4G30080	
EgrARF16B	Eucgr.K01240.1				
EgrARF17	Eucgr.F04380.1		AtARF17	AT1G77850	
			AtARF18	AT3G61830	
EgrARF19A	Eucgr.C03293.1		AtARF19	AT1G19220	
	Eucgr.C03293.2				
EgrARF19B	Eucgr.C02178.1				
	Eucgr.C02178.2				
			AtARF20	AT1G35240	
			AtARF21	AT1G34410	
			AtARF22	AT1G34390	
			AtARF23	AT1G43950	
EgrARF24	Eucgr.K03433.1				

Figure S4 Comparative analysis of predicted ARF alternative variants between *Eucalyptus grandis* and *Arabidopsis thaliana*. The alternative spliced protein sequences were extracted from Phytozome except for AtARF4 (obtained from Finet et al. (2013), the motif structures were predicted by Pfam (<http://pfam.xfam.org/>)).

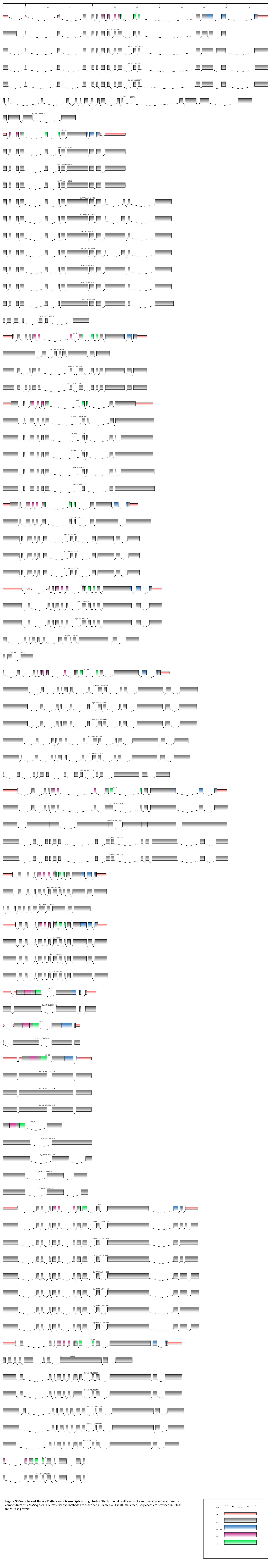
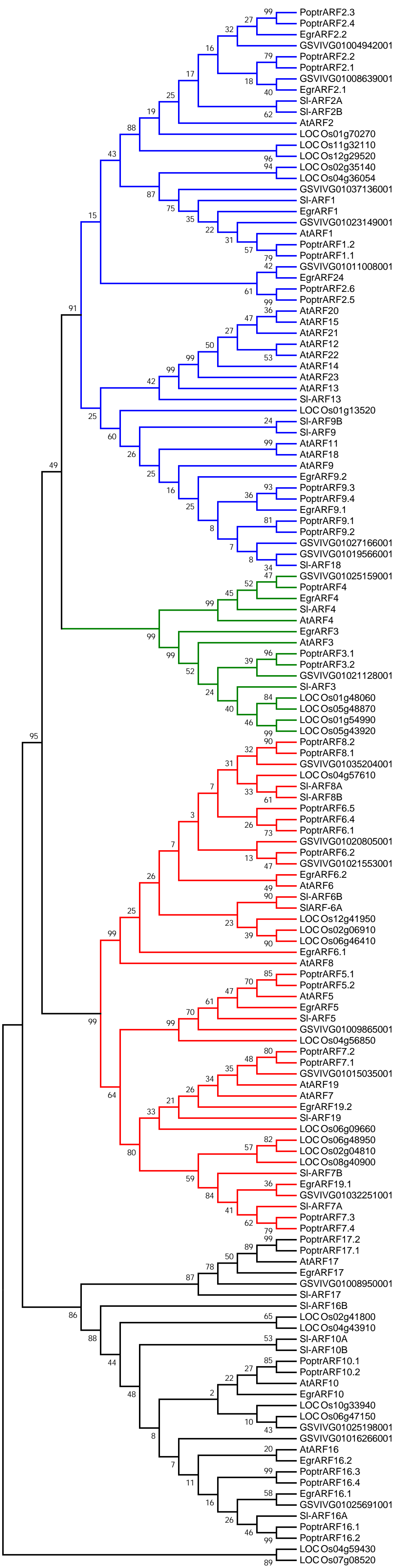


Figure S5 Structure of the ARF alternative transcripts in *E. globulus*. The *E. globulus* alternative transcripts were obtained from a compendium of RNASeq data. The material and methods are described in Table S4. The illumina reads sequences are provided in File S1 in the FastQ format.



I

III

II

IV

Figure S6 Comparative Phylogenetic relationships between ARF proteins from poplar, Eucalyptus, grapevine, Arabidopsis, tomato and rice. Full-length protein sequences were aligned using the Clustal_X program. The phylogenetic tree was constructed by using the MEGA5 program and the neighbour-joining method with predicted full-length ARF proteins. Bootstrap supports are indicated at each node.

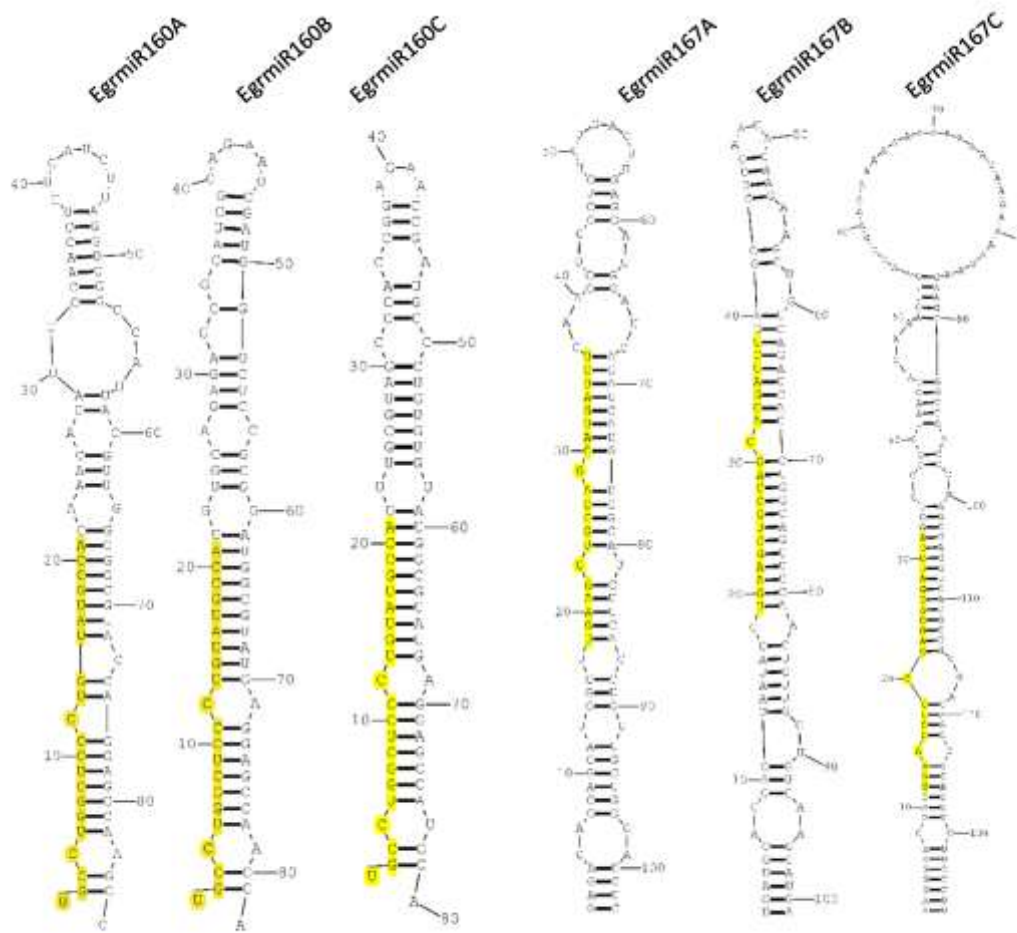


Figure S7 Predicted stem-loop structures of three EgrmiR160 and three EgrmiR167. The part of the stem-loop from which the mature microRNA derives is highlighted in yellow.

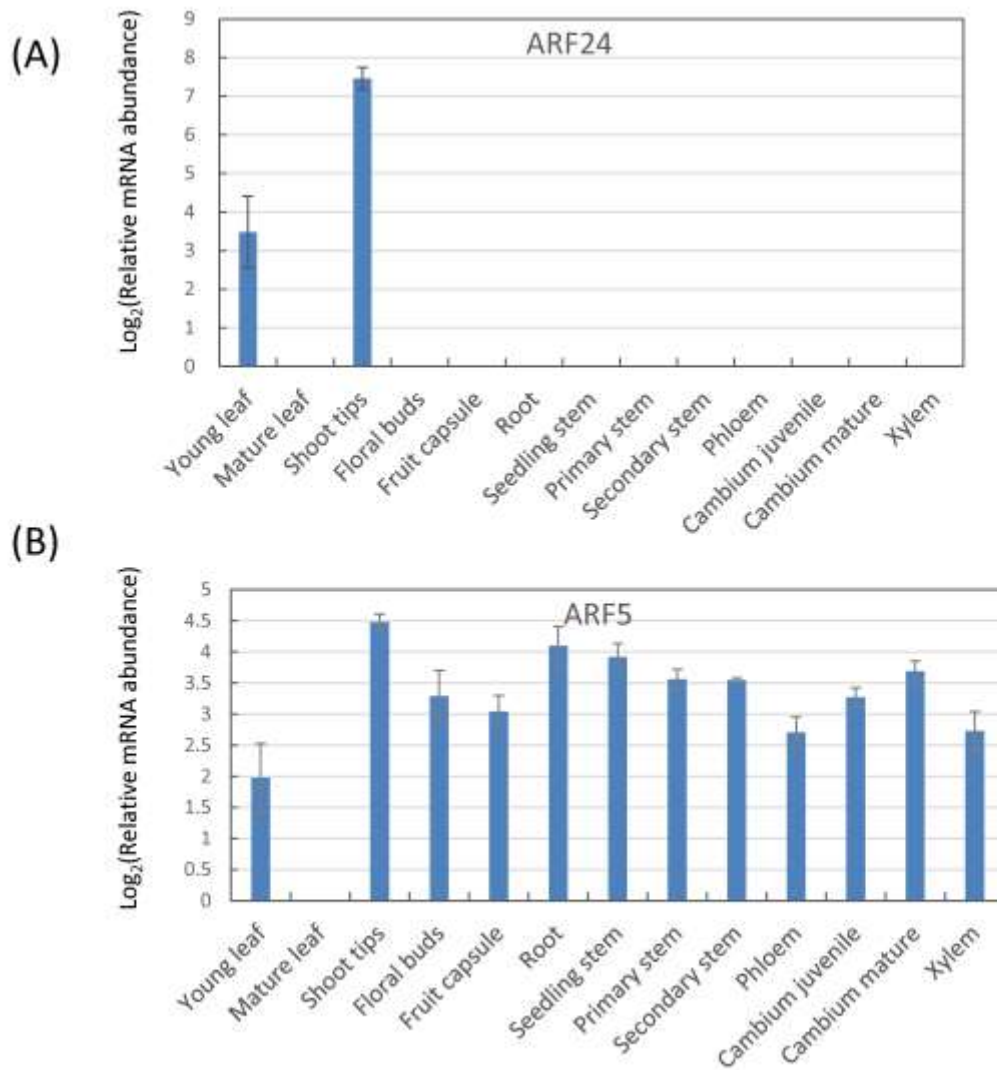


Figure S8 Expression profiles of EgrARF5 and EgrARF24 in various organs and tissues. Relative mRNA abundance of EgrARF5 and EgrARF24 was compared to expression in the control sample of mature leaves and in vitro plantlets, respectively. Error bars indicate the SE of mean expression values from three independent experiments.

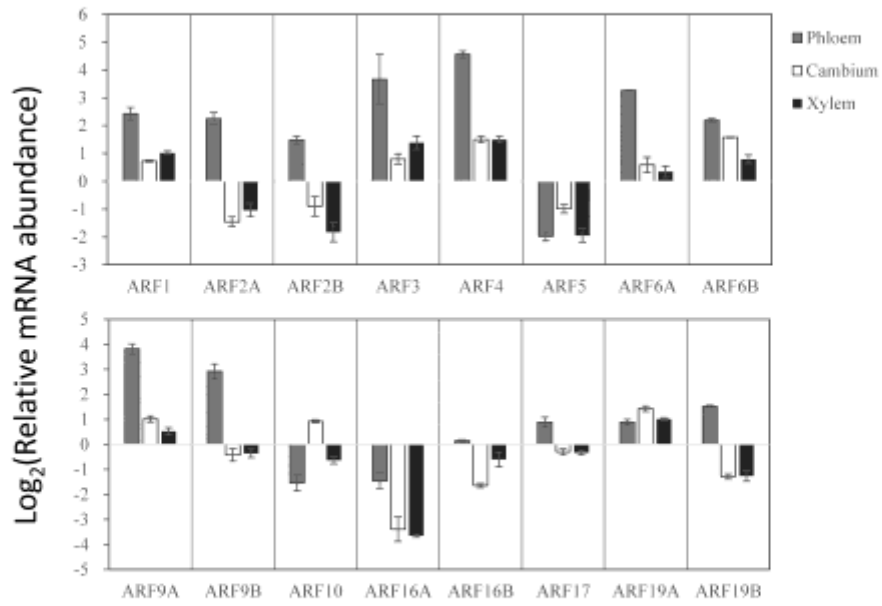


Figure S9 Expression profiles of EgrARF genes in tissues involved in secondary growth. Relative mRNA abundance was compared to expression in the control sample (in vitro plantlets).

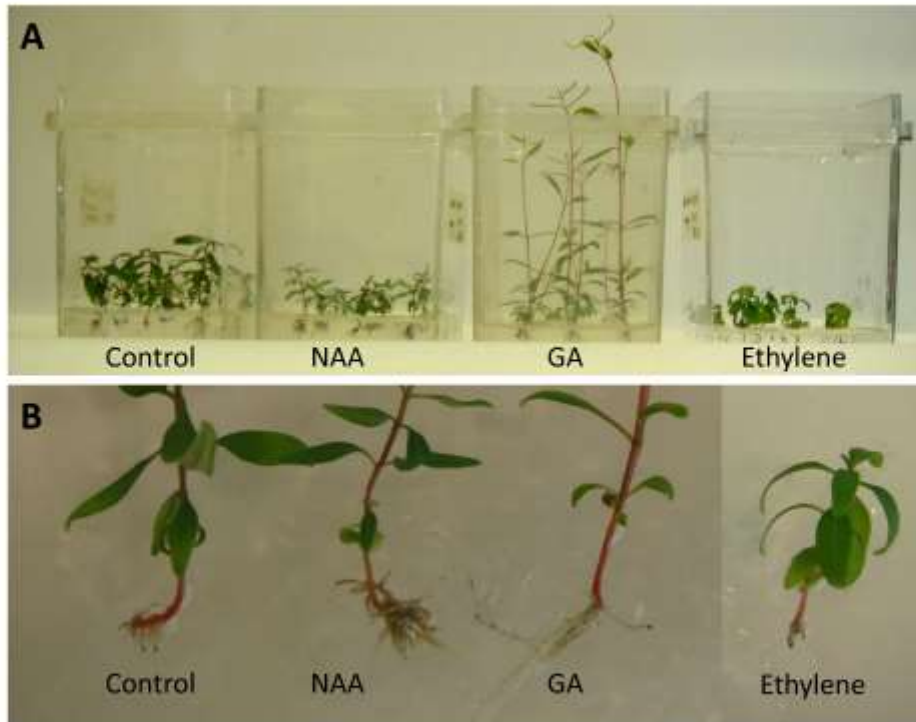


Figure S10 Young *Eucalyptus grandis* trees phenotypes in response to various long-term hormonal treatments. 10 mM NAA, or 20 mM gibberellic acid or 100 mM ACC were added to the medium of 65-d-old young tree, and phenotypes were observed 14 days later.

Table S1. The primers for *EgrARF* genes and reference genes used in qRT-PCR experiments

Name	Accession No.	Forward 5'-3'	Reverse 5'-3'	Efficiency
<i>ARF1</i>	Eucgr. G00076.1	TTTAAGAGCGCTGTGGTTCTCTG	AAGCATCAGCAAACGCACCTTG	1.90
<i>ARF2A</i>	Eucgr. K02197.1	GGCATGCCATTTCTACAGGAACC	TCAGCAGGGCTTATCCTAGGTTTG	1.97
<i>ARF2B</i>	Eucgr. B03551.1	ATTGAGGGCTGAACCAGAGACC	TGGTTAGGCACCGGAAGCAAAG	1.95
<i>ARF3</i>	Eucgr. D00588.1	ACATATATACCGGGCAGGACAGC	TCTCCGGTTTACAAATGCACTCC	1.94
<i>ARF4</i>	Eucgr. B02480.1	AGCTGTCGCTAGTGCTGTATCC	AACTCTGCATGGCTTGCCCTTG	1.96
<i>ARF5</i>	Eucgr. F02090.1	GCACATGGCAACAGCAAGTAGC	ATCGACCTTCCGACTGATCCTG	1.97
<i>ARF6A</i>	Eucgr. D00264.1	TGAGCTTGCTCGCATGTTTAGCC	TGTCACAAACTCCGGCCAAGG	1.89
<i>ARF6B</i>	Eucgr. A02065.1	GCTGGCAGCTTGTATTTGTAGACC	CCACACATTGTTGACGAACTCCTG	1.88
<i>ARF9A</i>	Eucgr. D01764.1	TCCAAAGCAGTCTGTGGTTTCACC	ATGCGACTCCTTGCACTGGTAG	1.87
<i>ARF9B</i>	Eucgr. E00888.1	GTGACTCGTTCGTGTTCTTAAGGG	TGACGAGCAACTCGTTTCACTCC	2.00
<i>ARF10</i>	Eucgr. J00923.1	TAGCAGGGCGTGTGCTGTTATC	AATCCGGACGCTTGCCTTTCTC	1.90
<i>ARF16A</i>	Eucgr. G02838.1	AGGGACATGTTCCGCATAAACGG	AATAGCACCGGCAGCATCTGAG	1.84
<i>ARF16B</i>	Eucgr. K01240.1	CTCAGAAATCGGCCACTGCAAAG	TGAGGCAAGCAACGAGAGATCG	1.97
<i>ARF17</i>	Eucgr. F04380.1	ATGGAGGTGGTGGTGAATGCAG	AAACCACCTCGAACGGCAATCC	1.85
<i>ARF19A</i>	Eucgr. C03293.1	TCAGTTTCAAGCGGATGAGAAGCC	AAGGACAGCCACTCTGGGTTAG	1.78
<i>ARF19B</i>	Eucgr. C02178.1	TCAAACAGGACCTGGCTCGTAG	CGAACACAGTTCACGAAGTCTC	1.93
<i>ARF24</i>	Eucgr. K03433.1	TCCAGCGACTTTGTGCAGGTTATC	AGCCTTTGAATGGGCTGAGGTC	1.92
<i>EF-1α</i>	Eucgr. B02473.1	ATGCGTCAGACTGTGGCTGTTG	TTGGTCACCTTGCTCCACTTG	1.84
<i>SAND</i>	Eucgr. B02502.1	TTGATCCACTTGGGACAAGGC	TCACCCATTGACATACACGATTGC	2.11
<i>PP2A1</i>	Eucgr. B03386.1	TCGAGCTTTGGACCGCATACAAG	ACCACAAGAGGTCACACATTGGC	1.98
<i>PP2A3 5' end</i>	Eucgr. B03031.1	CGGAAGAAGTGGGTGTGTTT	CACAGAGGGTCTCCAATGGT	2.03
<i>PP2A3 3' end</i>	Eucgr. B03031.1	CAGCGGCAAACTTGAAGCG	ATTATGTGCTGCATTGCCAGTC	2.02
<i>IDH 5' end</i>	Eucgr. F02901.1	AATCGACCTGCTTCGACCCTTC	TCGACCTTGATCTTCTCGAAACCC	1.92
<i>IDH 3' end</i>	Eucgr. F02901.1	TGCTGTGGCAGCTGAACTCAAG	ATGTTGTCCGCCAGTCACCTAC	1.86

Table S2. Protein identity matrix between EgrARF and AtARF

	EgrARF1	EgrARF2A	EgrARF2B	EgrARF3	EgrARF4	EgrARF5	EgrARF6A	EgrARF6B	EgrARF9A	EgrARF9B	EgrARF10	EgrARF16A	EgrARF16B	EgrARF17	EgrARF19A	EgrARF19B	EgrARF24
AtARF1	0.622	0.388	0.399	0.239	0.31	0.244	0.251	0.257	0.471	0.446	0.226	0.222	0.216	0.194	0.203	0.208	0.309
AtARF2	0.39	0.593	0.495	0.23	0.297	0.226	0.249	0.246	0.361	0.345	0.193	0.185	0.181	0.164	0.206	0.203	0.268
AtARF3	0.244	0.22	0.242	0.462	0.326	0.192	0.196	0.205	0.247	0.23	0.195	0.197	0.187	0.206	0.153	0.157	0.23
AtARF4	0.298	0.28	0.295	0.31	0.578	0.226	0.231	0.247	0.282	0.286	0.198	0.193	0.195	0.168	0.201	0.202	0.24
AtARF5	0.242	0.247	0.247	0.195	0.224	0.593	0.342	0.349	0.235	0.232	0.181	0.176	0.181	0.156	0.311	0.302	0.2
AtARF6	0.243	0.247	0.244	0.18	0.22	0.337	0.691	0.656	0.238	0.235	0.181	0.168	0.18	0.143	0.369	0.349	0.197
AtARF7	0.196	0.216	0.208	0.147	0.186	0.293	0.32	0.332	0.187	0.183	0.148	0.145	0.147	0.115	0.59	0.415	0.159
AtARF8	0.263	0.235	0.254	0.197	0.236	0.334	0.518	0.541	0.266	0.251	0.191	0.189	0.194	0.166	0.329	0.317	0.214
AtARF9	0.435	0.347	0.367	0.224	0.273	0.232	0.247	0.25	0.586	0.584	0.236	0.218	0.213	0.195	0.208	0.193	0.3
AtARF10	0.221	0.196	0.206	0.184	0.192	0.165	0.183	0.188	0.235	0.229	0.601	0.477	0.493	0.292	0.154	0.158	0.205
AtARF11	0.449	0.356	0.357	0.224	0.271	0.235	0.253	0.25	0.522	0.488	0.238	0.229	0.227	0.204	0.198	0.202	0.341
AtARF12	0.347	0.285	0.298	0.214	0.243	0.193	0.208	0.212	0.397	0.369	0.206	0.214	0.209	0.191	0.169	0.172	0.312
AtARF13	0.344	0.271	0.286	0.2	0.236	0.189	0.204	0.207	0.391	0.374	0.188	0.202	0.192	0.172	0.159	0.164	0.289
AtARF14	0.357	0.285	0.308	0.213	0.247	0.2	0.21	0.218	0.412	0.385	0.2	0.208	0.205	0.187	0.169	0.173	0.317
AtARF15	0.343	0.278	0.29	0.209	0.24	0.193	0.208	0.213	0.393	0.368	0.205	0.217	0.208	0.196	0.167	0.171	0.3
AtARF16	0.214	0.178	0.2	0.197	0.196	0.166	0.185	0.179	0.227	0.217	0.525	0.58	0.525	0.318	0.151	0.152	0.197
AtARF17	0.179	0.149	0.155	0.171	0.141	0.139	0.138	0.139	0.177	0.162	0.284	0.276	0.291	0.421	0.113	0.123	0.167
AtARF18	0.449	0.348	0.354	0.227	0.283	0.225	0.252	0.256	0.519	0.486	0.233	0.229	0.225	0.204	0.201	0.197	0.335
AtARF19	0.207	0.215	0.214	0.161	0.199	0.318	0.346	0.354	0.198	0.195	0.164	0.156	0.16	0.129	0.604	0.448	0.169
AtARF20	0.351	0.283	0.297	0.21	0.249	0.196	0.212	0.218	0.399	0.381	0.204	0.216	0.211	0.196	0.17	0.172	0.309
AtARF21	0.357	0.283	0.295	0.21	0.249	0.198	0.212	0.221	0.398	0.375	0.205	0.214	0.212	0.191	0.175	0.176	0.308
AtARF22	0.356	0.284	0.299	0.211	0.24	0.195	0.208	0.212	0.407	0.382	0.201	0.209	0.202	0.188	0.17	0.173	0.307
AtARF23	0.163	0.13	0.138	0.14	0.119	0.088	0.094	0.098	0.176	0.161	0.106	0.116	0.108	0.127	0.073	0.074	0.155

Table S3. Protein identity matrix among EgrARF

	EgrARF1	EgrARF2A	EgrARF2E	EgrARF3	EgrARF4	EgrARF5	EgrARF6A	EgrARF6B	EgrARF9A	EgrARF9B	EgrARF10	EgrARF16A	EgrARF16B	EgrARF17	EgrARF19A	EgrARF19B	EgrARF24
EgrARF1	ID	0.389	0.411	0.246	0.29	0.247	0.261	0.267	0.503	0.471	0.237	0.245	0.233	0.2	0.208	0.206	0.329
EgrARF2A	0.389	ID	0.515	0.222	0.276	0.247	0.261	0.262	0.372	0.371	0.202	0.204	0.206	0.167	0.215	0.218	0.296
EgrARF2B	0.411	0.515	ID	0.233	0.285	0.252	0.265	0.266	0.387	0.388	0.211	0.205	0.204	0.166	0.218	0.218	0.317
EgrARF3	0.246	0.222	0.233	ID	0.363	0.197	0.196	0.2	0.237	0.241	0.21	0.207	0.202	0.18	0.165	0.164	0.226
EgrARF4	0.29	0.276	0.285	0.363	ID	0.225	0.236	0.235	0.281	0.285	0.214	0.21	0.21	0.166	0.194	0.188	0.242
EgrARF5	0.247	0.247	0.252	0.197	0.225	ID	0.371	0.379	0.236	0.242	0.185	0.18	0.192	0.15	0.32	0.328	0.203
EgrARF6A	0.261	0.261	0.265	0.196	0.236	0.371	ID	0.678	0.263	0.265	0.191	0.187	0.193	0.155	0.35	0.337	0.217
EgrARF6B	0.267	0.262	0.266	0.2	0.235	0.379	0.678	ID	0.268	0.266	0.194	0.197	0.203	0.162	0.361	0.358	0.224
EgrARF9A	0.503	0.372	0.387	0.237	0.281	0.236	0.263	0.268	ID	0.668	0.238	0.236	0.239	0.198	0.21	0.208	0.321
EgrARF9B	0.471	0.371	0.388	0.241	0.285	0.242	0.265	0.266	0.668	ID	0.224	0.223	0.228	0.189	0.207	0.203	0.301
EgrARF10	0.237	0.202	0.211	0.21	0.214	0.185	0.191	0.194	0.238	0.224	ID	0.564	0.577	0.302	0.166	0.166	0.202
EgrARF16A	0.245	0.204	0.205	0.207	0.21	0.18	0.187	0.197	0.236	0.223	0.564	ID	0.556	0.301	0.162	0.156	0.204
EgrARF16E	0.233	0.206	0.204	0.202	0.21	0.192	0.193	0.203	0.239	0.228	0.577	0.556	ID	0.311	0.164	0.165	0.214
EgrARF17	0.2	0.167	0.166	0.18	0.166	0.15	0.155	0.162	0.198	0.189	0.302	0.301	0.311	ID	0.125	0.135	0.199
EgrARF19A	0.208	0.215	0.218	0.165	0.194	0.32	0.35	0.361	0.21	0.207	0.166	0.162	0.164	0.125	ID	0.476	0.159
EgrARF19E	0.206	0.218	0.218	0.164	0.188	0.328	0.337	0.358	0.208	0.203	0.166	0.156	0.165	0.135	0.476	ID	0.163
EgrARF24	0.329	0.296	0.317	0.226	0.242	0.203	0.217	0.224	0.321	0.301	0.202	0.204	0.214	0.199	0.159	0.163	ID

Table S4 Comparison of the number of alternative transcripts predicted in phytozome for *E. grandis* to those found in *E. globulus* in a large compendium transcriptomic data

Gene name	<i>E. grandis</i>	<i>E. globulus</i>
<i>EgrARF1</i>	4	6
<i>EgrARF2A</i>	5	11
<i>EgrARF2B</i>	2	3
<i>EgrARF3</i>	2	5
<i>EgrARF4</i>	3	4
<i>EgrARF5</i>	1	4
<i>EgrARF6A</i>	2	6
<i>EgrARF6B</i>	3	4
<i>EgrARF9A</i>	1	2
<i>EgrARF9B</i>	2	3
<i>EgrARF10</i>	1	1
<i>EgrARF16A</i>	1	1
<i>EgrARF16B</i>	1	3
<i>EgrARF17</i>	1	4
<i>EgrARF19A</i>	2	7
<i>EgrARF19B</i>	2	6
<i>EgrARF24</i>	1	1

These numbers include the primary transcripts

Material and Methods for Alternative splicing validation

TopHat and Cufflink Suite (Trapnell et al. 2012), currently used for differential gene and transcript expression analysis of RNA-seq experiments, were used to validate the *Eucalyptus ARF* genes (*E. grandis* genome v162 annotation).

Ten developing xylem (DX) RNA-Seq libraries were produced and sequenced FASTERIS SA (Genève, CH; www.fasteris.com). RNA-Seq libraries were prepared from ten equimolar pools of high quality individual total RNA: a) four seasonal libraries produced from total RNA extracted from DX samples collected in 2008 on three ramets of non-related tree genotypes at Herdade do Zambujal, Pegões (Portugal) [February 26 th (Feb), May 23rd (May), September 5th (Sep) and December 3rd (Dec)] (Carocha et al., unpublished); b) four pulp yield pools (five trees by pool) obtained by pooling the total RNA from samples

Table S5. The number of *EgrARF24* orthologs in other species

Species	Number of orthologs*
<i>Brassica rapa</i>	0
<i>Gossypium raimondii</i>	2
<i>Malus domestica</i>	2
<i>Medicago truncatula</i>	0
<i>Citrus sinensis</i>	1
<i>Citrus clementina</i>	1
<i>Prunus persica</i>	1
<i>Solanum lycopersicum</i>	0
<i>Manihot esculenta</i>	0
<i>Ricinus communis</i>	0
<i>Linum usitatissimum</i>	0
<i>Phaseolus vulgaris</i>	1
<i>Glycine max</i>	2
<i>Cucumis sativus</i>	0
<i>Fragaria vesca</i>	1
<i>Arabidopsis lyrata</i>	0
<i>Capsella rubella</i>	0
<i>Thellungiella halophila</i>	0
<i>Carica papaya</i>	1
<i>Theobroma cacao</i>	1
<i>Solanum tuberosum</i>	0
<i>Mimulus guttatus v1.1</i>	0
<i>Aquilegia coerulea</i>	1
<i>Sorghum bicolor</i>	0
<i>Setaria italica</i>	0
<i>Panicum virgatum</i>	0
<i>Brachypodium distachyon</i>	0
<i>Selaginella moellendorffii</i>	0
<i>Populus trichocarpa</i>	2
<i>Arabidopsis thaliana</i>	0
<i>Zea mays</i>	0
<i>Oryza sativa</i>	0
<i>Vitis vinifera</i>	1
<i>Eucalyptus grandis</i>	1

*The number of *EgrARF24* orthologs in other species are counted in phytozome by using "Filter homologs" with a cut off E value 1.0E-50

Table S6. Potential small RNAs which target for *EgrARF* genes

Small RNA gene	Small RNA sequence (5' -3')	Length h	Genomic location	Predicted small RNA gene sequences (5' -3')
MIR160				
<i>EgrMIR160a</i>	UGCCUGGCUCCUGUAUGCCA	21	scaffold_4:29,715,926..29,716,011	TGCCTGGCTCCCTGTATGCCACAAACATATTCCAACCTTTCATCTTAGGTTGGCCATTACGTTG GTGGCGTACCAGGAGCCAAGCC
<i>EgrMIR160b</i>	UGCCUGGCUCCUGUAUGCCA	21	scaffold_7:46392610..46392691	TGCTTGGCTCCTCATAACGCATCCGCGGAGACCATCGATTCTCCGATGCGCTCTGACATGG CATAACAGGAGCCAGGCA
<i>EgrMIR160c</i>	UGCCUGGCUCCUGUAUGCCA	21	scaffold_10:12063249..12063328	TGCATGGCTCCTCATAACGCATACACACAGGCCATCGGTTCTCCGGTGGGCTACGCAAATGGCA TACAGGAGCCAGGCA
MIR167				
<i>EgrMIR167a</i>	UGAAGCUGCCAGCAUGAUCU	20	scaffold_8:49,907,076..49,907,178	GAGATGCCAGCAACAGGTGAAGATGCCACATGATCTGATCCATCCTCAAGTCAAAGAGGGAGGT TGAGATCATGCTGGCAGCTTCAACCGATGCTGGTCTCTC
<i>EgrMIR167b</i>	UGAAGCUGCCAGCAUGAUCU	20	scaffold_8:62,733,419..62,733,519	TCATGCTTCACAGCAACAGTTGAAACTGCCAGATGATCTGACAGCTTCTTCTATTGAAGGCTCA GATCATGCTGGCAGCTTCAGCTATTAGTGGTGCATGA
<i>EgrMIR167c</i>	UGAAGCUGCCAGCAUGAUCUA	21	scaffold_11:42,258,705..42,258,841	AAGGGAACGAGTGAAGCTGCCAGCATGATCTAGCTCCGGCTAACTGAAAACCTCAACCGAAAA AAAAAAAAAACAAGAAAAGAAGAAGTGGTTAACCTAGCTAGGTCATGCTGCGACAGCCTCACT TTCTTGACCTTGTAAGACCTTTTCTTGACCTTGTAAGACCCCTCCGTTCCCGCCCGTCACT
<i>EgrTAS3</i>	UUCUUGACCUUGUAAGACCUU	21	scaffold_8:58712106..58712287	TCTCCTCCGGCCCCGGGCTCTGAATCGCGAGTGAGCGATGTAGAGTACGGTCGCTGCCTTCC CCTTCCCACTCACTTCTCCTTCTGTCTATCCCTCCTGAGCTACTC

Table S7. Small RNAs target site prediction of *EgrARF* genes

miRNA Acc.	Target Acc.	Expectation ^a (E)	Target Accessibility ^b (UPE)	Alignment	Inhibition ^c	Multiplicity ^d
UGCCUGGCUCCUGUAUGCCA EgrmiR160	Eucgr. J00923.1 EgrARF10	0	20.2	miRNA 20 CCGUAUGUCCUCGGUCCGU 1 : : : : : : : : : : : : : : : Target 1804 GGCAUACAGGGAGCCAGGCA 1823	Cleavage	1
UGCCUGGCUCCUGUAUGCCA EgrmiR160	Eucgr. G02838.1 EgrARF16A	0	20.2	miRNA 20 CCGUAUGUCCUCGGUCCGU 1 : : : : : : : : : : : : : : : Target 1435 GGCAUACAGGGAGCCAGGCA 1454	Cleavage	1
UGCCUGGCUCCUGUAUGCCA EgrmiR160	Eucgr. K01240.1 EgrARF16B	1	22.4	miRNA 21 ACCGUAUGUCCUCGGUCCGU 1 : : : : : : : : : : : : : : : Target 2095 UGGUAUGCAGGGAGCCAGGCA 2115	Cleavage	1
UGCCUGGCUCCUGUAUGCCA EgrmiR160	Eucgr. F04380.1 EgrARF17	0.5	18.0	miRNA 21 ACCGUAUGUCCUCGGUCCGU 1 : : : : : : : : : : : : : : : Target 1218 UGGCAUGCAGGGAGCCAGGCA 1238	Cleavage	1
UGAAGCUGCCAGCAUGAUCUA EgrmiR167	Eucgr. D00264.1 EgrARF6A	3.5	22.2	miRNA 20 UCUAGUACGACCGUCGAAGU 1 : : : : : : : : : : : : : : : Target 2416 AGAUCAGGCUGGCAGCUUGU 2435	Cleavage	1
UGAAGCUGCCAGCAUGAUCUA EgrmiR167	Eucgr. A02065.1 EgrARF6B	3.5	23.4	miRNA 20 UCUAGUACGACCGUCGAAGU 1 : : : : : : : : : : : : : : : Target 3043 AGAUCAGGCUGGCAGCUUGU 3062	Cleavage	1
UUCUUGACCUUGUAAGACCUU EgrTAS3	Eucgr. K02197.1 EgrARF2A	3.5	17.3	miRNA 21 UUC CAGAAUGUCCAGUUCUU 1 : : : : : : : : : : : : : : : Target 1249 AGGAUCUUGCAAGGUCCAGAA 1269	Cleavage	1
UUCUUGACCUUGUAAGACCUU EgrTAS3	Eucgr. B03551.1 EgrARF2B	1.5	18.5	miRNA 21 UUC CAGAAUGUCCAGUUCUU 1 : : : : : : : : : : : : : : : Target 1641 AAGCCUUGCAAGGUCAAGAA 1661	Cleavage	1
UUCUUGACCUUGUAAGACCUU EgrTAS3	Eucgr. D00588.1 EgrARF3	0.5	20.5	miRNA 21 UUC CAGAAUGUCCAGUUCUU 1 : : : : : : : : : : : : : : : Target 1641 AAGGUCUUGCAAGGUCAAGAA 1661	Cleavage	1
UUCUUGACCUUGUAAGACCUU EgrTAS3	Eucgr. B02480.1 EgrARF4	0.5	24.1	miRNA 21 UUC CAGAAUGUCCAGUUCUU 1 : : : : : : : : : : : : : : : Target 1631 AAGGUCUUGCAAGGUCAAGAA 1651	Cleavage	1

^aThe complementarity score between small RNA and their target transcript, if its score is greater than 4 it will be discarded

^bThe energy required to open (unpair) secondary structure around target site on target mRNA, The less energy means the more possibility that small

^cThe principle of the miRNA function, cleave mRNA or inhibits the translation of target genes

^dThe number of small RNA target sites on each mRNA

collected at Carregal Fundeiro, Abrantes (Portugal), from 10 trees with very contrasting pulp yields in the coded AxB mapping population, and 10 trees with very contrasting pulp yields in a natural variation panel; c) two libraries from samples collected from an adult tree and a juvenile one, (same genotype) at Herdade do Zambujal, Pegões (Portugal). Sampling procedures and RNA extraction were described, respectively in Paux et al. (2004) and Cassan- Wang et al. (2012). All samples were kindly provided by RAIZ Institute (Portugal).

The TruSeq™ SBSv5 sequencing kit (Illumina) was used for library sequencing, using the Illumina Hi-Seq 2000 instrument, on a multiplex runs with 1x100nt+7(index) cycles. For each RNA-Seq library, adaptors removal and a successive quality and contaminants (ribosomal sequences) filters were applied. The resulting filtered high quality reads were then mapped to the *E. grandis* genome sequence v162 using TopHat v1.3.1. Cufflinks v1.1.0 was used to determine the potential coding regions and their intron-exon structures. Finally, Cuffcompare v1.1.0 were then used to compare the assembled multiple libraries Cufflinks transcripts to the *E. grandis* v162 gene annotations.

The sequences of the Illumina reads from RNA Seq used to predict the *E. globulus* alternative transcripts are provided in FastaQ format in supplementary File S1.

REF:

Cole Trapnell, Adam Roberts, Loyal Goff, Geo Pertea, Daehwan Kim, David R Kelley, Harold Pimentel, Steven L Salzberg, John L Rinn & Lior Pachter (2012) Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. Nature Protocols 7: 562–578