

Figure S4 Alignment of *Arabidopsis thaliana* MYB4 (AtMYB4), *Ginkgo biloba* MYB (GbMYB1) and all MYB4-like copies from *Pinus taeda* (Pt)

GbMYB1	-----MGRSPMCNSKVGLG	LNGAWTVEEDNL	LIKYFQT	HDEGG	
Pt_AtMYB4-like1	-----MARAPCCPIG	-DRNKGAWTREEDDKL	IQYIQT	HGE-C	
Pt_AtMYB4-like3	-----MGRAPCANC	-DRSKGAWTKEEDDR	LTQYIQA	HGE-C	
Pt_AtMYB4-like5	-----MGRSPCCCEKA	-HTNKGAWSK	QVLIAYIRAHG	E-C	
AtMYB4	-----MGRSPCCCEKA	-HTNKGAWTKEEDER	VAYIKAHGE	C	
Pt_AtMYB4-like6	-----MKR-----		KLLIKGFD	AH	
Pt_AtMYB4-like4	MSLFPLSLPSGIPVVA	VAVFLSMKMRKYSCCEKA	-HTKKGAWTQ	QEDARIVAYIQA	HGE-C
Pt_AtMYB4-like2	-----MGRTPCCEKG-	HTNKGAWTKEEDDR	LIAHRAHGE	C	

GbMYB1	GWKSVPKKAGLKRGGKSCRLRWNNYLRPNI	KRGNISPD E DLII R LH G LLGNRWA I AGF
Pt_AtMYB4-like1	G WNSLPKAAGL R CGKSCRLRWNNYLRPQL	KRGNFSE E DD D IL L KL H ALLGNKWSLIA G
Pt_AtMYB4-like3	CWRSLPKAAGL R CGKSCRLRWNNYLRPDL	KRGNFSE E DD D IL L KL H ALLGNKWSLIA G
Pt_AtMYB4-like5	CWRSLPKAAGL R CGKSCRLRWNNYLRPDL	KRGNFSE E DD D IL L KL H ALLGNKWSLIA S
AtMYB4	CWRSLPKAAGL R CGKSCRLRWNNYLRPDL	KRGNFTEEE E EL L KL H LLGNKWSLIA G
Pt_AtMYB4-like6	----- L KRGNFSEEE E EL L KL H LLGNKWSLIA G	
Pt_AtMYB4-like4	G WRYLPKAAGL R CGKSCRLRWNNYLRPDL	KRGNFSEEE E EL L KL H LLGNKWSLIA A
Pt_AtMYB4-like2	RWRSLPKAAGL R CGKSCRLRWNNYLRPDL	KRGNFSEEE E EL L KL H IT I GNKWSLIA A

GbMYB1	IPGRTDNEIKNYWYITLSKRVALKCNEAKEHTKYPMKRSRGHSACKQLIMPDSNTKMQDLS
Pt_AtMYB4-like1	IPGRTDNEIKNYWNSLKRKLISMGVDPLTHR--PFQKICRHR--
Pt_AtMYB4-like3	IPGRTDNEIKNYWNSLKRKLISMGVDPLTRR--PFQRNSRH--
Pt_AtMYB4-like5	IPGRTDNEIKNYWNTTHIKRKLLKEKGIDPNTHL--PILPDHGS--
AtMYB4	IPGRTDNEIKNYWNTTHIKRKLLINRGIDPTSHR--P1QESSAS--
Pt_AtMYB4-like6	LEGRGNGEIKNHWSIMRKRLSSRGLHPQTHR--SLRPPHNS--
Pt_AtMYB4-like4	MAGRRTDNEIKNYWNTTHIKRKLLSSRGLDPQTHR--SLCPPHNS--
Pt_AtMYB4-like2	LEGRRTDNEIKNYWNSHIKRKLLSERGIDPRSHR--PLCPPSNT--

GbMYBR1	LSASPTRKELEVNSTNQSLSESVVSNDDVRTDSNVQSGSPGLQEIRASRIFLPSFRGNQW-
Pt_AtMYB4-like1	-----DQPLSE-----NVSE-----PEIASSGKF---VQDFFHCF-
Pt_AtMYB4-like3	-----DLSLPE-----KVEV-----PEIARPREI--VENFFHS-F-
Pt_AtMYB4-like5	-----FGSSNE-----NHVF-----SKRSRCKPSEV-LTDFQQ-
AtMYB4	-----QDKSKPTQLEPVTSNT-----INISFTSAPK--VETFHEISIS-
Pt_AtMYB4-like6	-----STTLNSPPPP-DHQI-----LAFESRRRAE--IADFFQL--
Pt_AtMYB4-like4	-----NSTLSSPSVP-EHEI-----SPLQNPNRTAD--IADFFQQ-
Pt_AtMYB4-like2	-----TSLSWSAP----DREF-----PAIQNLRTP--ITDFQH--

GbMYBR1	SSHSELMAPANPMIESNI DRKLFSLVDDYLSVTEL S LGESGMNCNSVSKFS-----
Pt_AtMYB4-like1	SELSVESAQLSNAAGGSLARDGQ---PD--- LNLNL DLD GLTVTCPSI IHSEG-----
Pt_AtMYB4-like3	SELCGDQEVSQDSAASES LARDE---PST LNLNL ELSINASVMHVAKEP-----
Pt_AtMYB4-like5	-QTPGGTTSVVLKVIKAQN DHDYD---KD---VNLDLSITLPSLCSQSSGSSSRELSSG-----
AtMYB4	FPGKSEKISMLTFKEEKDEC P VQEKFPD--- LNLNL RISLPFDVDRLQGHG----KSTT-----
Pt_AtMYB4-like6	--EGLKSSPIESA ASTDEEHPC---PD---INLDLCMGLSSNSAPA-----
Pt_AtMYB4-like4	--DRSERSPVENAA CKEEEH---PD--- LNLNL CISLPSNSTLAAN-----
Pt_AtMYB4-like2	--NRSESSPILPAAPDAEED---PD--- LNLNL CISLPSNSSPAANTA---QS-----

GbMYBR1 -TNSHNLYL**M**GSSLSNTDHMPGCDQSVCRDQYRWMNT
Pt_AtMYB4-like1 -KQNVVNSEQGENDLGEGMGYLAYHSGEAPMPLLRL
Pt_AtMYB4-like3 ILKS**K**PGEEEGA**G**RPFDKEGYLFRRYEECPVKGSSLRL
Pt_AtMYB4-like5 RLSND**T**CQDDHKE**K**I**C**CHIGLRTVGESECCSG-CWD
AtMYB4 PRCFKS**L**U**G**MING**M**ECRC**R**GRMRCDVVGGSSKGSDMSN **GFDLGLAKKETTSILLGFRSLEM**
Pt_AtMYB4-like6
Pt_AtMYB4-like4 -RAMDANSNSGLGVWCH-TGPQINS DPRCENRYCERNS**FTEID**SSSGSIHG**I****LDLQI**SAL
Pt_AtMYB4-like2 RKTVDNSLNGSSEVCPVGLQINYGKYCDSGYCEQNASCFSQFRLV

GbMYB1	---
Pt_AtMYB4-like1	---
Pt_AtMYB4-like3	---
Pt_AtMYB4-like5	---
AtMYB4	K--
Pt_AtMYB4-like6	---
Pt_AtMYB4-like4	GVQ
Pt_AtMYB4-like2	---

R2 – DNA binding domain is highlighted in yellow.

R3 – DNA binding domain is highlighted in green.

bHLH binding motif – Indicated by red box.

C1 motif – Highlighted in pink.

EAR – Suppression domain is highlighted in light blue (which comprises part of the C2 motif).

Alternative EAR domain in Pt_AtMYB4-like1, Pt_AtMYB4-like3, Pt_AtMYB4-like4 and Pa_AtMYB4-like1 are marked with box and, bold and underlined.

Zinc-finger motif – Highlighted in dark blue (C3 motif).

C4 motif – Highlighted in grey. The GY/FDFLGL motif is indicated by black box.