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.

Figure S1 Alignment of *Arabidopsis thaliana* MYB3 (AtMYB3), *Gingko biloba* MYB (GbMYBR1) and all MYB3-like copies from *Picea abies* (Pa)

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Pa_AtMYB3-like3      MGRPQSCS-----GLKLRKGAWTSEEDLLLKKCIEVHGE-GSWPLLPQKTGLQRSGKSCR
AtMYB3               MGRSPCCE-----KAHMNKGAWTKEEDQLLVDYIRKHGE-GCWRSLPRAAGLQRCGKSCR
Pa_AtMYB3-like4      MGRSPSCSSYSKHEDGLNRGAWTAGEDKILSEYVKTHGV-GRWRSLPKKAGLRRCGKSCR
Pa_AtMYB3-like2      MGRSPCCS-----KEGLNRGAWTKTEDIILCEYIRIHGD-GGWRTLPKKAGLKRCGKSCR
Pa_AtMYB3-like5      MGRS-CCS-----KEGLNRGAWSRKEDMILSEYIRIHGD-GGWTNLPQRAGLKRCGKSCR
GbMYBR1              MGRSPMCS---KVGLGLNKGAWTVEEDNLLIKYFQTHDEGGGWKSVPKKAGLKRCGKSCR
Pa_AtMYB3-like1      MGRAPCCA-----KVGLNKGAWSAEEDSLLGKYIQTHGE-GNWRSLPKKAGLRRCGKSCR
                     ***.  *         :..***:  ** :* . .  *.  * *  :*. :**.*.*****

Pa_AtMYB3-like3      LRWLNYLSPNVKRGNISEDEELLIIRMHRLLGNRWALIAGRIPGRSDNEIKNYWNTHLSK
AtMYB3               LRWMNYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKR
Pa_AtMYB3-like4      LRWLNYLRPDIKRGNISFEEEELIIRLYRLLGNRWALISGRLPGRTDNEIKNYWNTHLSK
Pa_AtMYB3-like2      LRWLNYLRPDIKRGGISPDEEELIIRLHRLLGNRWSLIAGRLPGRTDNEIKNYWNTCLSK
Pa_AtMYB3-like5      LRWTNYLRPDIKLGNISPDEDELIIRMHRLLGNRWSLIAGRLPGRTDNEIKNYWNTRLSK
GbMYBR1              LRWMNYLRPNIKRGNISPDEEDLIIRLHGLLGNRWALIAGRIPGRTDNEIKNYWYTTLSK
Pa_AtMYB3-like1      LRWLNYLRPCIKRGNITADEEELIIRMHALLGNRWSIIAGRVPGRTDNEIKNYWNTNLSK
                     *** *** * :* *.:: :*: ***.:: ****.*::*:**:***:******** * :..

Pa_AtMYB3-like3      KVNRSRSDD--------------------------FNCNKENVVQTLTSEEGKGGQEIG-
AtMYB3               KLLSRGIDPNSHRLINESVVSPSSLQND--------VVETIHLDFSGPVKPEPVREEIG-
Pa_AtMYB3-like4      KVRMGESDPRFQNLCK-----RRDVPPYPNYDEDIYASQNAPVKTTGV----RYGRAVA-
Pa_AtMYB3-like2      KLLLSMNKSQSKVT-KNVKSTSKSSPVQNR------VFKTTPVKVTTAV---RLSETIR-
Pa_AtMYB3-like5      KL-LSIDDSQSKSTARNLETSSKSPPPPPN-----HVFKTTPIKITTAV---KFSETVG-
GbMYBR1              RVALKGNEAKEHKTYPMKRSRGHSACKQ-------LIMPDSNTKMQDLLSASPTRKELE-
Pa_AtMYB3-like1      KLAVRGIDPKTHKKVTTDSINRASDRFNQRKGGKLYDCSQRSQRLERNVV--RAGQSTGL
                     .:     .

Pa_AtMYB3-like3      A----ENYSSH----SQPKSR-------ISINTDHNQHADM-----------LEEPSTG-
AtMYB3               MVNNCESSGTT-----------------------------------------SEKDYG-
Pa_AtMYB3-like4      ELENFDSYNPD----HVPDTHDGSTQEGLKAADDHVVEIDT---SKSWSQL-LLEHCMGD
Pa_AtMYB3-like2      PKGSMNGYGCS----NRSSDEAFKLCN-AKETTNS---------SKSWCDL-LGNDTEG-
Pa_AtMYB3-like5      PK-RCNGYGRS----NCSSAEAIKLCN-IKENTNSIPHDDSEHIVFDMTDVNLLETEAG-
GbMYBR1              VSTN-QSLSES----VVSNTDDVRTDSNVQSGSPGLQEIRASRI--------FLPSFRGN
Pa_AtMYB3-like1      VIPNVHNLKADLKGQYIAGPREIQSSNSIRSSSPINTPIQPKSNDFMQPQP-VVSSDAGK
                           .                                                    *

Pa_AtMYB3-like3      --------LTKCQSYRNTPTEQTDLIHFDYKFSCQNSA--DDLFQAGNCSAS----D---
AtMYB3               ----------NEEDWVLNLELSVG---PSYRY--------ESTRKVSVVDSA--------
Pa_AtMYB3-like4      YQYDRLQPNASSSAVQLPPQLSVNLSCPRFIFDLPQRSHTDSKKKQITMDGAFEIEN---
Pa_AtMYB3-like2      --------RISNSSMSLALERSPN----SYYFGTDAATLADSLLDLNELSSP----D---
Pa_AtMYB3-like5      --------NCTSAIWSLEEERSPH----SYYFAVDTATLDESLSELNVLSSP----D---
GbMYBR1              Q-------VSSHSELMAPANPMIESNIDRKLFSLVD----DYLSVSTELSLGFSGMN---
Pa_AtMYB3-like1      QTDDSTVYCSSDSAASCALIDHLSSEDDDQYLSLEGNSNECYSHTVAEESGTLKSSNPQT
                                .      EAR – suppression domain                .

Pa_AtMYB3-like3      -----CSETEILQQLLHPCSDMEEYWR-----EVHGDAQLFAFDSV-------------W
AtMYB3               --------------------ESTRRWGSELFGAHESDAVCLCCRIG-----------LFR
Pa_AtMYB3-like4      -----LE-------LLDQEKGRNQDWVCQG--GESHDGTTSQEQRG-----------MPR
Pa_AtMYB3-like2      -----CS-------LLSPPSNCSADFGLQ---DFCGEPVTLTAEANEFEVVSSDQSIMQR
Pa_AtMYB3-like5      -----CN-------LLYSASGSSTDFELE---EFYREAATLATGIN--------------
GbMYBR1              -----CS-------VSKFSTNSHNLYLMGS--SLSNTDHHMPCGDQ-----SVCRDQYRW
Pa_AtMYB3-like1      HSEAICDSRERDNGGPVQKHDQFPEYDVFSFFDVRNAENEICCNDDQWVHEQEMPQLHSW
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Pa_AtMYB3-like3      NMV-------------------------------------------------------
AtMYB3               NESCRNCRVSDVRTH-------------------------------------------
Pa_AtMYB3-like4      DLGRA-ESRSQLQDHGSRSSPS------------------------------------
Pa_AtMYB3-like2      DKGFTVLDDQGIEEFYDHTQPLDWIHELDYIEKSSPRALSFLLLESEDEREEKLGDHTQI
Pa_AtMYB3-like5      DSVFT-----------------------------------------------------
GbMYBR1              MNT-------------------------------------------------------
Pa_AtMYB3-like1      DNQIDDQGKEHFGSHVNNDVTAMSWEASFWF-----------------------------

Pa_AtMYB3-like3      ----
AtMYB3               ----
Pa_AtMYB3-like4      ----
Pa_AtMYB3-like2      PDVV
Pa_AtMYB3-like5      ----
GbMYBR1              ----
Pa_AtMYB3-like1      ----
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