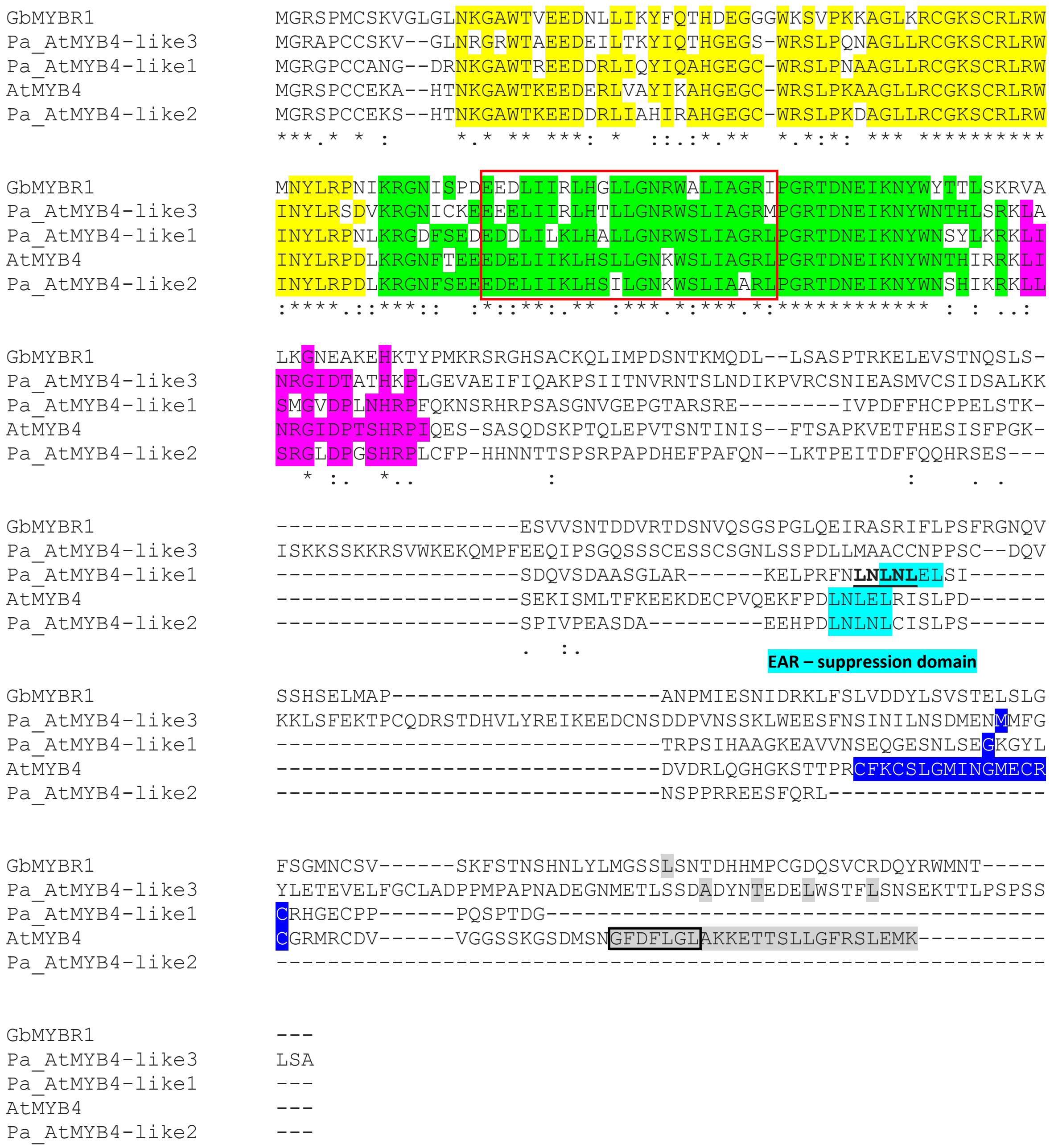
Figure S3 Alignment of *Arabidopsis thaliana* MYB4 (AtMYB4), *Gingko biloba* MYB GbMYBR1) and all MYB4-like copies from *Picea abies* (Pa)



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GbMYBR1              MGRSPMCSKVGLGLNKGAWTVEEDNLLIKYFQTHDEGGGWKSVPKKAGLKRCGKSCRLRW
Pa_AtMYB4-like3      MGRAPCCSKV--GLNRGRWTAEEDEILTKYIQTHGEGS-WRSLPQNAGLLRCGKSCRLRW
Pa_AtMYB4-like1      MGRGPCCANG--DRNKGAWTREEDDRLIQYIQAHGEGC-WRSLPNAAGLLRCGKSCRLRW
AtMYB4               MGRSPCCEKA--HTNKGAWTKEEDERLVAYIKAHGEGC-WRSLPKAAGLLRCGKSCRLRW
Pa_AtMYB4-like2      MGRSPCCEKS--HTNKGAWTKEEDDRLIAHIRAHGEGC-WRSLPKDAGLLRCGKSCRLRW
                     ***.* * :     *.* ** ***: *  ::.:*.**  *.*:*: *** **********

GbMYBR1              MNYLRPNIKRGNISPDEEDLIIRLHGLLGNRWALIAGRIPGRTDNEIKNYWYTTLSKRVA
Pa_AtMYB4-like3      INYLRSDVKRGNICKEEEELIIRLHTLLGNRWSLIAGRMPGRTDNEIKNYWNTHLSRKLA
Pa_AtMYB4-like1      INYLRPNLKRGDFSEDEDDLILKLHALLGNRWSLIAGRLPGRTDNEIKNYWNSYLKRKLI
AtMYB4               INYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLI
Pa_AtMYB4-like2      INYLRPDLKRGNFSEEEDELIIKLHSILGNKWSLIAARLPGRTDNEIKNYWNSHIKRKLL
                     :****.::***::  :*::**:.** :***.*:***.*:************ : :  ..:

GbMYBR1              LKGNEAKEHKTYPMKRSRGHSACKQLIMPDSNTKMQDL--LSASPTRKELEVSTNQSLS-
Pa_AtMYB4-like3      NRGIDTATHKPLGEVAEIFIQAKPSIITNVRNTSLNDIKPVRCSNIEASMVCSIDSALKK
Pa_AtMYB4-like1      SMGVDPLNHRPFQKNSRHRPSASGNVGEPGTARSRE--------IVPDFFHCPPELSTK-
AtMYB4               NRGIDPTSHRPIQES-SASQDSKPTQLEPVTSNTINIS--FTSAPKVETFHESISFPGK-
Pa_AtMYB4-like2      SRGLDPGSHRPLCFP-HHNNTTSPSRPAPDHEFPAFQN--LKTPEITDFFQQHRSES---
                       * :.  *..          :                           :    . .

GbMYBR1              -------------------ESVVSNTDDVRTDSNVQSGSPGLQEIRASRIFLPSFRGNQV
Pa_AtMYB4-like3      ISKKSSKKRSVWKEKQMPFEEQIPSGQSSSCESSCSGNLSSPDLLMAACCNPPSC--DQV
Pa_AtMYB4-like1      -------------------SDQVSDAASGLAR------KELPRFNLNLNLELSI------
AtMYB4               -------------------SEKISMLTFKEEKDECPVQEKFPDLNLELRISLPD------
Pa_AtMYB4-like2      -------------------SPIVPEASDA---------EEHPDLNLNLCISLPS------
                                        .  :.

GbMYBR1              SSHSELMAP---------------------ANPMIESNIDRKLFSLVDDYLSVSTELSLG
Pa_AtMYB4-like3      KKLSFEKTPCQDRSTDHVLYREIKEEDCNSDDPVNSSKLWEESFNSINILNSDMENMMFG
Pa_AtMYB4-like1      ------------------------------TRPSIHAAGKEAVVNSEQGESNLSEGKGYL
AtMYB4               ------------------------------DVDRLQGHGKSTTPRCFKCSLGMINGMECR
Pa_AtMYB4-like2      ------------------------------NSPPRREESFQRL-----------------

GbMYBR1              FSGMNCSV------SKFSTNSHNLYLMGSSLSNTDHHMPCGDQSVCRDQYRWMNT-----
Pa_AtMYB4-like3      YLETEVELFGCLADPPMPAPNADEGNMETLSSDADYNTEDELWSTFLSNSEKTTLPSPSS
Pa_AtMYB4-like1      CRHGECPP------PQSPTDG---------------------------------------
AtMYB4               CGRMRCDV------VGGSSKGSDMSNGFDFLGLAKKETTSLLGFRSLEMK----------
Pa_AtMYB4-like2      ------------------------------------------------------------

GbMYBR1              ---
Pa_AtMYB4-like3      LSA
Pa_AtMYB4-like1      ---
AtMYB4               ---
Pa_AtMYB4-like2      ---
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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.