



### Additional file 3 – Conifer MYB phylogeny based on partial sequences using a 31 amino acids region

The 31 amino acid region in the R3 MYB domain (shown in box) is present in all the MYB used here. The phylogenetic tree was based on an alignment derived using the Clustal W program and the neighbour-joining method (1000 Bootstraps). The bar indicates an evolutionary distance of 0.1%. *Mus musculus* MmMYBA were not used as out group but as landmark. Pg: *Picea glauca*, Pm: *Picea mariana*, At: *Arabidopsis thaliana*, Pt: *Pinus taeda*, Cp: *Chamaecyparis pisifera*, Co: *Chamaecyparis obtusa*, Jr: *Juniperus rigida*, Ts: *Thuja standishii*, Td: *Thuja dolabrata*, Ss: *Sequoia sempervirens*, Mg: *Metasequoia glyptostroboides*, Td: *Taxodium distichum*, Gl: *Glyptostrobus lineatus*. PmMYB sequences come from Xue *et al.* [12], PtMYB1 and PtMYB4 from Patzlaff *et al.* [10, 11] and *Cupressaceae* MYB sequences of the down phylogenetic clade from Kusumi *et al.* [34].