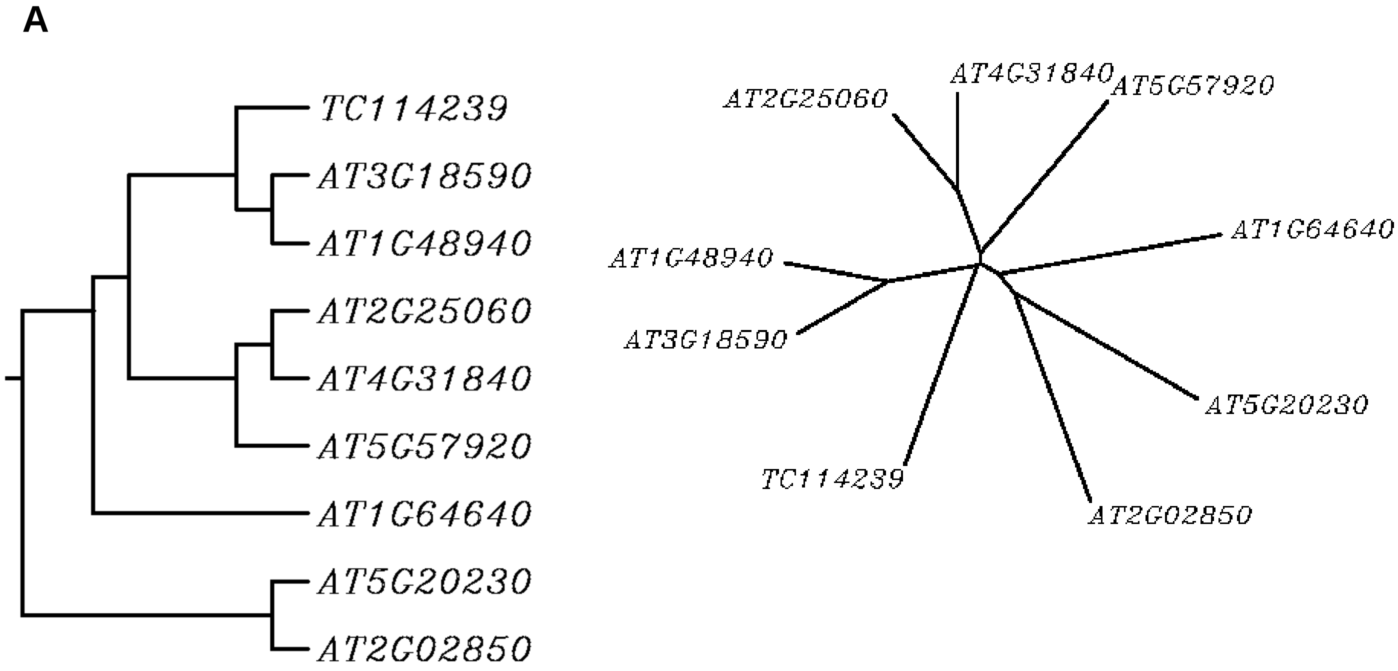


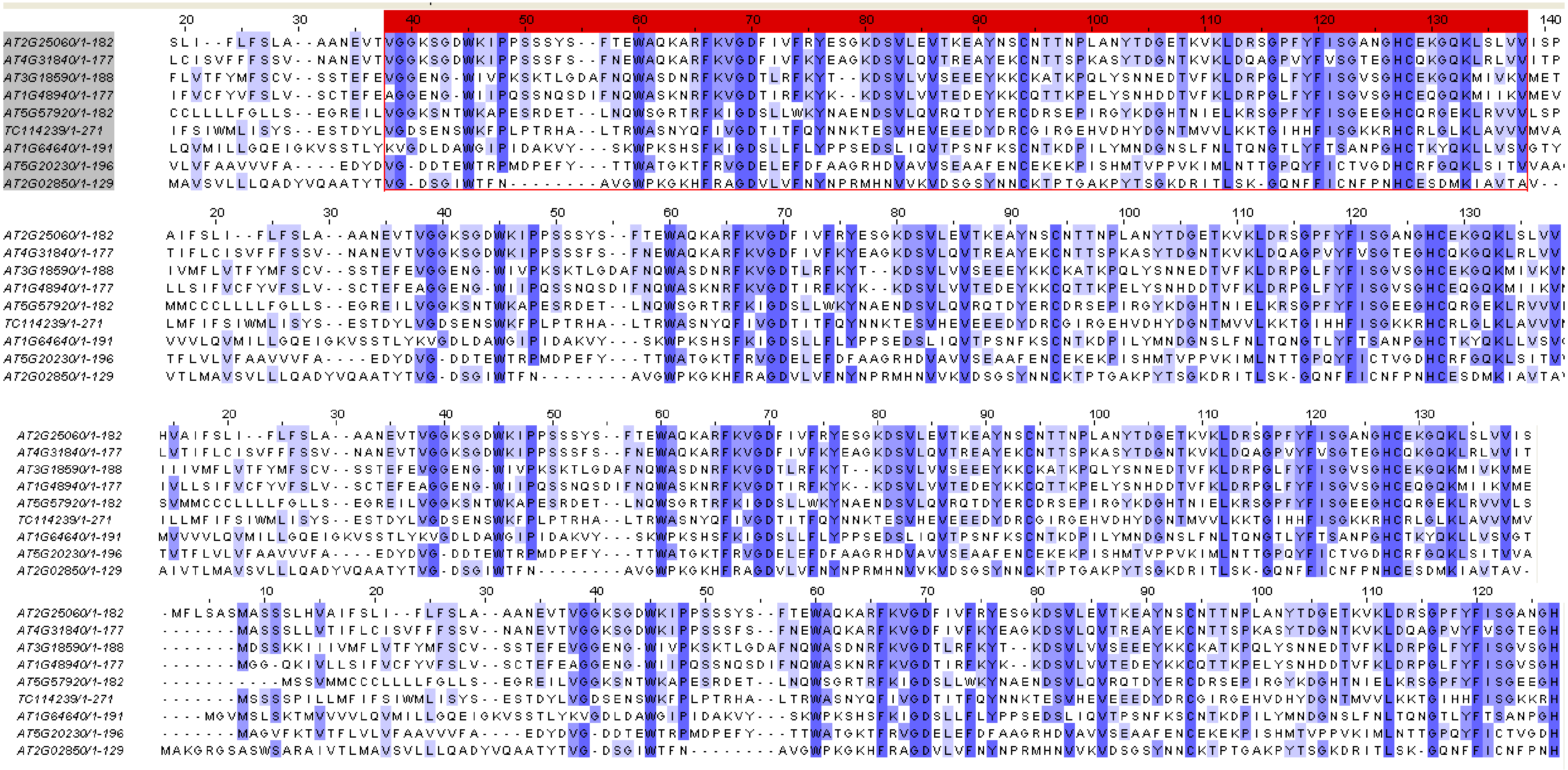
N-J tree unrooted

N-J tree

At5g57920 (*AtENOD20)*

Supplemental Figure S4 A

B



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                     20        30        40        50        60        70        80        90        100       110       120       130       140
AT2G25060/1-182     SLI--FLFSLA--AANEVTVGGKSGDWKIPPSSSYS--FTEWAQKARFKVGDFIVFRYESGKDSVLEVTKEAYNSCNTTNPLANYTDGETKVKLDRSGPFYFISGANGHCEKGQKLSLVVISP
AT4G31840/1-177     LCISVFFFSSV--NANEVTVGGKSGDWKIPPSSSFS--FNEWAQKARFKVGDFIVFKYEAGKDSVLQVTREAYEKCNTTSPKASYTDGNTKVKLDQAGPVYFVSGTEGHCQKGQKLRLVVITP
AT3G18590/1-188     FLVTFYMFSCV--SSTEFEVGGENG-WIVPKSKTLGDAFNQWASDNRFKVGDTLRFKYT--KDSVLVVSEEEYKKCKATKPQLYSNNEDTVFKLDRPGLFYFISGVSGHCEKGQKMIVKVMET
AT1G48940/1-177     IFVCFYVFSLV--SCTEFEAGGENG-WIIPQSSNQSDIFNQWASKNRFKVGDTIRFKYK--KDSVLVVTEDEYKKCQTTKPELYSNHDDTVFKLDRPGLFYFISGVSGHCEQGQKMIIKVMEV
AT5G57920/1-182     CCLLLLFGLLS--EGREILVGGKSNTWKAPESRDET--LNQWSGRTRFKIGDSLLWKYNAENDSVLQVRQTDYERCDRSEPIRGYKDGHTNIELKRSGPFYFISGEEGHCQRGEKLRVVVLSP
TC114239/1-271      IFSIWMLISYS--ESTDYLVGDSENSWKFPLPTRHA--LTRWASNYQFIVGDTITFQYNNKTESVHEVEEEDYDRCGIRGEHVDHYDGNTMVVLKKTGIHHFISGKKRHCRLGLKLAVVVMVA
AT1G64640/1-191     LQVMILLGQEIGKVSSTLYKVGDLDAWGIPIDAKVY---SKWPKSHSFKIGDSLLFLYPPSEDSLIQVTPSNFKSCNTKDPILYMNDGNSLFNLTQNGTLYFTSANPGHCTKYQKLLVSVGTY
AT5G20230/1-196     VLVFAAVVVFA----EDYDVG-DDTEWTRPMDPEFY---TTWATGKTFRVGDELEFDFAAGRHDVAVVSEAAFENCEKEKPISHMTVPPVKIMLNTTGPQYFICTVGDHCRFGQKLSITVVAA
AT2G02850/1-129     MAVSVLLLQADYVQAATYTVG-DSGIWTFN--------AVGWPKGKHFRAGDVLVFNYNPRMHNVVKVDSGSYNNCKTPTGAKPYTSGKDRITLSK-GQNFFICNFPNHCESDMKIAVTAV--

                        20        30        40        50        60        70        80        90        100       110       120       130
AT2G25060/1-182     AIFSLI--FLFSLA--AANEVTVGGKSGDWKIPPSSSYS--FTEWAQKARFKVGDFIVFRYESGKDSVLEVTKEAYNSCNTTNPLANYTDGETKVKLDRSGPFYFISGANGHCEKGQKLSLVV
AT4G31840/1-177     TIFLCISVFFFSSV--NANEVTVGGKSGDWKIPPSSSFS--FNEWAQKARFKVGDFIVFKYEAGKDSVLQVTREAYEKCNTTSPKASYTDGNTKVKLDQAGPVYFVSGTEGHCQKGQKLRLVV
AT3G18590/1-188     IVMFLVTFYMFSCV--SSTEFEVGGENG-WIVPKSKTLGDAFNQWASDNRFKVGDTLRFKYT--KDSVLVVSEEEYKKCKATKPQLYSNNEDTVFKLDRPGLFYFISGVSGHCEKGQKMIVKV
AT1G48940/1-177     LLSIFVCFYVFSLV--SCTEFEAGGENG-WIIPQSSNQSDIFNQWASKNRFKVGDTIRFKYK--KDSVLVVTEDEYKKCQTTKPELYSNHDDTVFKLDRPGLFYFISGVSGHCEQGQKMIIKV
AT5G57920/1-182     MMCCCLLLLFGLLS--EGREILVGGKSNTWKAPESRDET--LNQWSGRTRFKIGDSLLWKYNAENDSVLQVRQTDYERCDRSEPIRGYKDGHTNIELKRSGPFYFISGEEGHCQRGEKLRVVV
TC114239/1-271      LMFIFSIWMLISYS--ESTDYLVGDSENSWKFPLPTRHA--LTRWASNYQFIVGDTITFQYNNKTESVHEVEEEDYDRCGIRGEHVDHYDGNTMVVLKKTGIHHFISGKKRHCRLGLKLAVVV
AT1G64640/1-191     VVVLQVMILLGQEIGKVSSTLYKVGDLDAWGIPIDAKVY---SKWPKSHSFKIGDSLLFLYPPSEDSLIQVTPSNFKSCNTKDPILYMNDGNSLFNLTQNGTLYFTSANPGHCTKYQKLLVSV
AT5G20230/1-196     TFLVLVFAAVVVFA----EDYDVG-DDTEWTRPMDPEFY---TTWATGKTFRVGDELEFDFAAGRHDVAVVSEAAFENCEKEKPISHMTVPPVKIMLNTTGPQYFICTVGDHCRFGQKLSITV
AT2G02850/1-129     VTLMAVSVLLLQADYVQAATYTVG-DSGIWTFN--------AVGWPKGKHFRAGDVLVFNYNPRMHNVVKVDSGSYNNCKTPTGAKPYTSGKDRITLSK-GQNFFICNFPNHCESDMKIAVTA

                          20        30        40        50        60        70        80        90        100       110       120       130
AT2G25060/1-182     HVAIFSLI--FLFSLA--AANEVTVGGKSGDWKIPPSSSYS--FTEWAQKARFKVGDFIVFRYESGKDSVLEVTKEAYNSCNTTNPLANYTDGETKVKLDRSGPFYFISGANGHCEKGQKLSLVVIS
AT4G31840/1-177     LVTIFLCISVFFFSSV--NANEVTVGGKSGDWKIPPSSSFS--FNEWAQKARFKVGDFIVFKYEAGKDSVLQVTREAYEKCNTTSPKASYTDGNTKVKLDQAGPVYFVSGTEGHCQKGQKLRLVVIT
AT3G18590/1-188     IIIVMFLVTFYMFSCV--SSTEFEVGGENG-WIVPKSKTLGDAFNQWASDNRFKVGDTLRFKYT--KDSVLVVSEEEYKKCKATKPQLYSNNEDTVFKLDRPGLFYFISGVSGHCEKGQKMIVKVME
AT1G48940/1-177     IVLLSIFVCFYVFSLV--SCTEFEAGGENG-WIIPQSSNQSDIFNQWASKNRFKVGDTIRFKYK--KDSVLVVTEDEYKKCQTTKPELYSNHDDTVFKLDRPGLFYFISGVSGHCEQGQKMIIKVME
AT5G57920/1-182     SVMMCCCLLLLFGLLS--EGREILVGGKSNTWKAPESRDET--LNQWSGRTRFKIGDSLLWKYNAENDSVLQVRQTDYERCDRSEPIRGYKDGHTNIELKRSGPFYFISGEEGHCQRGEKLRVVVLS
TC114239/1-271      ILLMFIFSIWMLISYS--ESTDYLVGDSENSWKFPLPTRHA--LTRWASNYQFIVGDTITFQYNNKTESVHEVEEEDYDRCGIRGEHVDHYDGNTMVVLKKTGIHHFISGKKRHCRLGLKLAVVVMV
AT1G64640/1-191     MVVVVLQVMILLGQEIGKVSSTLYKVGDLDAWGIPIDAKVY---SKWPKSHSFKIGDSLLFLYPPSEDSLIQVTPSNFKSCNTKDPILYMNDGNSLFNLTQNGTLYFTSANPGHCTKYQKLLVSVGT
AT5G20230/1-196     TVTFLVLVFAAVVVFA----EDYDVG-DDTEWTRPMDPEFY---TTWATGKTFRVGDELEFDFAAGRHDVAVVSEAAFENCEKEKPISHMTVPPVKIMLNTTGPQYFICTVGDHCRFGQKLSITVVA
AT2G02850/1-129     AIVTLMAVSVLLLQADYVQAATYTVG-DSGIWTFN--------AVGWPKGKHFRAGDVLVFNYNPRMHNVVKVDSGSYNNCKTPTGAKPYTSGKDRITLSK-GQNFFICNFPNHCESDMKIAVTAV-

                             10        20        30        40        50        60        70        80        90        100       110       120
AT2G25060/1-182     -MFLSASMASSSLHVAIFSLI--FLFSLA--AANEVTVGGKSGDWKIPPSSSYS--FTEWAQKARFKVGDFIVFRYESGKDSVLEVTKEAYNSCNTTNPLANYTDGETKVKLDRSGPFYFISGANGH
AT4G31840/1-177     -------MASSSLLVTIFLCISVFFFSSV--NANEVTVGGKSGDWKIPPSSSFS--FNEWAQKARFKVGDFIVFKYEAGKDSVLQVTREAYEKCNTTSPKASYTDGNTKVKLDQAGPVYFVSGTEGH
AT3G18590/1-188     -------MDSSKKIIIVMFLVTFYMFSCV--SSTEFEVGGENG-WIVPKSKTLGDAFNQWASDNRFKVGDTLRFKYT--KDSVLVVSEEEYKKCKATKPQLYSNNEDTVFKLDRPGLFYFISGVSGH
AT1G48940/1-177     -------MGG-QKIVLLSIFVCFYVFSLV--SCTEFEAGGENG-WIIPQSSNQSDIFNQWASKNRFKVGDTIRFKYK--KDSVLVVTEDEYKKCQTTKPELYSNHDDTVFKLDRPGLFYFISGVSGH
AT5G57920/1-182     -----------MSSVMMCCCLLLLFGLLS--EGREILVGGKSNTWKAPESRDET--LNQWSGRTRFKIGDSLLWKYNAENDSVLQVRQTDYERCDRSEPIRGYKDGHTNIELKRSGPFYFISGEEGH
TC114239/1-271      -------MSSSSPILLMFIFSIWMLISYS--ESTDYLVGDSENSWKFPLPTRHA--LTRWASNYQFIVGDTITFQYNNKTESVHEVEEEDYDRCGIRGEHVDHYDGNTMVVLKKTGIHHFISGKKRH
AT1G64640/1-191     ----MGVMSLSKTMVVVVLQVMILLGQEIGKVSSTLYKVGDLDAWGIPIDAKVY---SKWPKSHSFKIGDSLLFLYPPSEDSLIQVTPSNFKSCNTKDPILYMNDGNSLFNLTQNGTLYFTSANPGH
AT5G20230/1-196     -------MAGVFKTVTFLVLVFAAVVVFA----EDYDVG-DDTEWTRPMDPEFY---TTWATGKTFRVGDELEFDFAAGRHDVAVVSEAAFENCEKEKPISHMTVPPVKIMLNTTGPQYFICTVGDH
AT2G02850/1-129     MAKGRGSASWSARAIVTLMAVSVLLLQADYVQAATYTVG-DSGIWTFN--------AVGWPKGKHFRAGDVLVFNYNPRMHNVVKVDSGSYNNCKTPTGAKPYTSGKDRITLSK-GQNFFICNFPNH
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Supplemental Figure S4 B