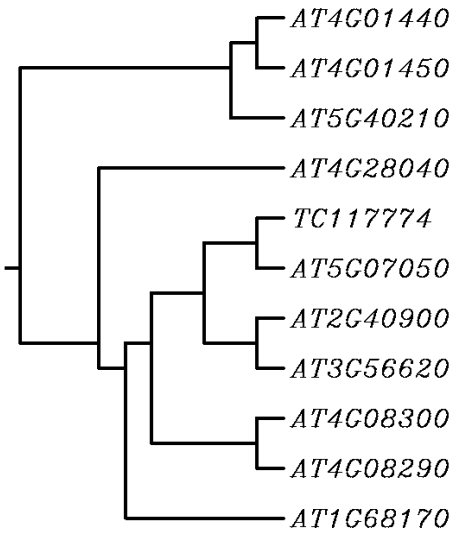
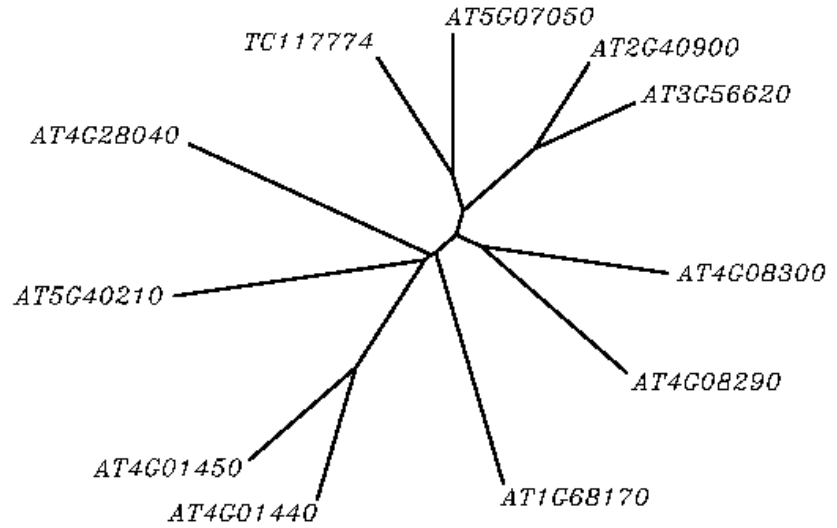


**A**



*N-J tree*



*N-J tree unrooted*

**MtN21**

**B**

20 30 40 50 60 70 80 90 100 110 120 130 140  
 TC117774/1-394 ENSKPYFAMILQFGYAGMNIITKLSLNGGMSHYVLLVYRHAFAFATAIAPFAIIFEW--KDQPKIIFSVFMQILLLALLGPVIDQNFYYAGLKLTSPTFFSCAMSNMLPAMTFVMAVLCRMEIVNLKK  
 AT5G07050/1-402 TSSKPYFAMILSLQFGYAGMNIITKLSLNTGMSHYVLLVYRHAFAFATAIAPFAFFER--KAQPKIIFSIQMQLFLLGLLGPVIDQNFYYMGLKYTSPFFSCAMSNMLPAMTFILAVLFRMEMLDLKK  
 AT2G40900/1-394 ESAKPYFAMVCLQFGYAGMNLVTKVLDORGMSHYVLLVYRHAFAFATAIAPFALLSER--KVRSKMTFFPIFMQIFVLLALLGPVIDQNLYYIGLKLTSPTFFSAVSNIVPAITIIILATLFRMEKVMRK  
 AT3G56620/1-377 ESAKPYFAMVCLQFGYAGMNLVTKVLDORGMSHYVLLVYRHAFAFATAIAPFALLSER--KVRPKMTFFPIFMQIFVLLALLGPVIDQNLYYAGLKLTSPTFFAGAVTNIVPALTFIISICRMEKVMRK  
 AT4G08300/1-373 DKLKPIAIIISLQFGYAGMYIITMVSFKHGMNHWILATYRHHVATIVIAFFALILER--KIRPKMTWPLFLRILALGFLLEPLLDQNLYYIGMKATSATYSSAFVNALPAITFIMAVIFRIETVNLKK  
 AT4G08290/1-384 HKLRPYLLMIFLQFGAAGTYIVIMATLNQGNRYVIVYRNLVAALVLAPFALIFER--KVRPKMTLSVLWKIMALGFLLEPVLDDGFGYLGMMNMTSATYTSAMNIIPLSVTFIIAWILRMEKVNIAE  
 AT1G68170/1-356 --MKDITAMVVVQIATAGLNIFFKLAMEDGNNPVLVAYRLLFATLFMIFICFIFQR--KKRPEFTCRMLLALLSGLLGVVIPSILITIGLALTSATFSAAGVLTPLVTFIFAALLRMEKVMRSLG  
 AT4G01440/1-365 -KWTPIVIMVMINSALGGLANLAVKLVLDGGMNMSIATYRLAISTLFLAIAFFWER--KTRPTLTNLNLVQLFFSALVGSALTYFFLLGLSYTSATLACAFISMTPAITFVMALIFRVEKLNKMSKAGMVMGALICIGALLTMYKGVPL  
 AT4G01450/1-361 -KWAPMIVLIVSNMILAGMVNALVKKVLDGGINHMMVIAIYRGLISTLFLVAYFWER--KTRPKLTLISICQLFVSALFGASLMQYFLLGLSYTSATLGSFAFWAIMPSLTFVMALIFGFEKLSLKT  
 AT5G40210/1-339 -DGMVILTAMVVTEFSNVGNTLVKAATSKGLSPFVVLVYSYTFGSLLLPLTFFSFRS-RSLPPLTFSILCNMGLGLI-ASAFDILGNYGKIYSSPTLSSAMSNVPAFTFILA VVFRMENISLGGKAVLWGLK  
 AT4G28040/1-359 SKYKAVLALVLDQFISAGVALFVTKAAFMEGLNPTFVYVYRQAIATLFLICISFISAWRKENKPSLGVRGFWVVALTAVIGVTVDNAYFKGIDLSSSMACAMTNLIPAVTFIISIVGFEKIRRS

50 60 70 80 90 100 110 120 130 140 150 160  
 TC117774/1-394 GMSHYVLLVYRHAFAFATAIAPFAIIFEW--KDQPKIIFSVFMQILLLALLGPVIDQNFYYAGLKLTSPTFFSCAMSNMLPAMTFVMAVLCRMEIVNLKCLRCAKVIIGTILTVAGAMLMTLYKGPVL  
 AT5G07050/1-402 TGMSHYVLLVYRHAFAFATAIAPFAFFER--KAQPKIIFSIQMQLFLLGLLGPVIDQNFYYMGLKYTSPFFSCAMSNMLPAMTFILAVLFRMEMLDLKKLWCAKVIAGTVVTVAGAMLMTIYKGGPIV  
 AT2G40900/1-394 RGMSHYVLLVYRHAFAFATAIAPFALLSER--KVRSKMTFFPIFMQIFVLLALLGPVIDQNLYYIGLKLTSPTFFSAVSNIVPAITIIILATLFRMEKVMRKVRCLVVMGTLTVVGSILMIFYKGPFI  
 AT3G56620/1-377 RGMSHYVLLVYRHAFAFATAIAPFALLSER--KVRPKMTFFPIFMQIFVLLALLGPVIDQNLYYAGLKLTSPTFFAGAVTNIVPALTFIISICRMEKVMRKAIVGTVVTVLIVV6ALMLLIFKIPLI  
 AT4G08300/1-373 HGMNHWILATYRHHVATIVIAFFALILER--KIRPKMTWPLFLRILALGFLLEPLLDQNLYYIGMKATSATYSSAFVNALPAITFIMAVIFRIETVNLKKTSLAKVIIGTAITVGGAMVMTLYKGPPI  
 AT4G08290/1-384 DGMNPSVLVAYRLLFATLFMIFICFIFQR--KKRPEFTCRMLLALLSGLLGVVIPSILITIGLALTSATFSAAGVLTPLVTFIFAALLRMEKVMRSLGSSVGLAKVFTLFGVGGALVFIYRGLIEI  
 AT1G68170/1-356 GGVNHMMVIAIYRGLISTLFLAIAFFWER--KTRPTLTNLNLVQLFFSALVGSALTYFFLLGLSYTSATLACAFISMTPAITFVMALIFRVEKLNKMSKAGMVMGALICIGALLTMYKGVPL  
 AT4G01440/1-365 GGINHMMVIAIYRGLISTLFLVAYFWER--KTRPKLTLISICQLFVSALFGASLMQYFLLGLSYTSATLGSFAFWAIMPSLTFVMALIFGFEKLSLKTIGYGVVLTGLISLVGGLLTMYQIPL  
 AT5G40210/1-339 KGLSPFVVLVYSYTFGSLLLPLTFFSFRS-RSLPPLTFSILCNMGLGLI-ASAFDILGNYGKIYSSPTLSSAMSNVPAFTFILA VVFRMENISLGGKSSVAVLWGLTILSIIIGALVTVLYHGPML  
 AT4G28040/1-359 EGLNPTFVYVYRQAIATLFLICISFISAWRKENKPSLGVRGFWVVALTAVIGVTVDNAYFKGIDLSSSMACAMTNLIPAVTFIISIVGFEKIRRSKMSKAVKVIIGTVCGGAMAMTFLRGPKL

200 210 220 230 240 250 260 270 280 290 300 310 320  
 TC117774/1-394 KDNWFLGSIILLIATLAWSSLFVLQAKAIEITYKNHQTLTSLICFFGTILAFATLLIMENK-DSVMTIGWDMNLLAAAYAGIVTSSIIYYIDGLVIKKGPVFATFSPLMMIIVAIMGFFILAEQL  
 AT5G07050/1-402 DKEFLKGSILLIFATLAWASLFVLQAKILKTYAKHQLSLTTLICFISLTLQAVAVTFVMEHN-PSAWRIGWDMNLLAAAYAGIVASSIIYYVQGVIMKKGKPVFATFSPLMMIIVAVMGSVFLAEKI  
 AT2G40900/1-394 TADYLKAAVFLLLASLSWASFFVLQAAATLKKYSAH-LSMSTMVCFMGTQLQSLALAFVMEHN-PSALNIGFDMNLLAAAYAGIMSSIIAYYVQGLMMQRKGPVFTAFNPLIVVIVSIMSFFVLGGQI  
 AT3G56620/1-377 GEDYLKATVFLLLIASFSWASFFVLQAAATLKKYSSH-LSLSTMVCFMGTQLQSTALTVMFEPN-LSAWNIGFDMNLLASAYAGIMSSIIAYYVQGMMTKQKSVIIVTAFNPLVVIIGSIIIGFLILNQTL  
 AT4G08300/1-373 DQNVVVTGLAVMGSITTWAGFFILQSFLLKYPAE-LSLVMWICAMGTVLNTIASLIMVVD-VSAWKVGMDSGTLAAVYSGVVCSGMAYYIQSIVIRERGPVFTSFSFPMCMIIATFLGLVLAEKI  
 AT4G08290/1-384 HNNWVVGTLILLGCVAVSGFVVLQSIITKYPAD-LSLSALICLAGAVQSFVALVVERH-PSGAVGWDARLFAPLYTIVSSGITYYVQGMVMKTRGPVFTAFNPLCMILVALIASFILHEQI  
 AT1G68170/1-356 HHSILGALLVFGGNIISLWFLLVQKISKQFGGP-YWNATLNMNMGVVVAMLVLCWEHD-LDEWRLGNIRLLIYAYAILISGMVVAVNAWCIERGPLFVSVPVGLVIVALVGSFLLDLDEL  
 AT4G01440/1-365 PENWIIIGCVLLFAGSSCFGSMWMLDAKVNKYPCC-YSTTVLSFFGTIQCALLSLIKSRD-ITAWILTDKLDIVTIVYAGAVAQGLCTVGSWCIIRKRPITETSIFTFVGLIFATLDFDLIHRQI  
 AT4G01450/1-361 HENWIIKGFLLGLVGLVFSWMLDAKINVKYPCC-YSTVILSVFGLQCALLSLIKTRH-LEDWILRDELTIITVVIAGVVAQGMCTVGMWCIKQGGPVVSSSPVVLMSATVDFLILHREI  
 AT5G40210/1-339 HSDWIIIGGLLALQYILVSVYLVMAHTMGRYPSA-VVVTLVHNVCIADVCAFVSLLAEKDNPKAWVIRFDITLITVVATGILNSGYVVIHT-WAVSHKGPVYLSMFKPLSILIAAVSTFIFLQESL  
 AT4G28040/1-359 NTAWLLGCFLLISTFAWSLWLILQVPIASHCPDH-LYTSACTCFIATIASFLVALALGNTHLPPWKLDSFLKLSCCIYSSGFQA-ISFFLDAWIVSQKGPVSALFNPLSAVIVTFFGALYKKEQT

230 240 250 260 270 280 290 300 310 320 330 340  
 TC117774/1-394 DAKAIETYKNHQTLTSLICFFGTILAFATLLIMENK-DSVMTIGWDMNLLAAAYAGIVTSSIIYYIDGLVIKKGPVFATFSPLMMIIVAIMGFFILAEQLFGSVIGSILVVIIGLSVLLWGGK-  
 AT5G07050/1-402 DAKILKTYAKHQLSLTTLICFISLTLQAVAVTFVMEHN-PSAWRIGWDMNLLAAAYAGIVASSIIYYVQGVIMKKGKPVFATFSPLMMIIVAVMGSVFLAEKIFLGGVIGAVLIVIGLVALWGGK-  
 AT2G40900/1-394 QAAATLKKYSAH-LSMSTMVCFMGTQLQSLALAFVMEHN-PSALNIGFDMNLLASAYAGIMSSIIAYYVQGLMMQRKGPVFTAFNPLIVVIVSIMSFFVLGGQIYLGQVIGVVVLLWGGKAVLWGGK-  
 AT3G56620/1-377 QAAATLKKYSSH-LSLSTMVCFMGTQLQSTALTVMFEPN-LSAWNIGFDMNLLASAYAGIMSSIIAYYVQGMMTKQKSVIIVTAFNPLVVIIGSIIIGFLILNQTLGGVLMGAILVGGVCTVWGGK-  
 AT4G08300/1-373 DSFTLKKYPAE-LSLVMWICAMGTVLNTIASLIMVVD-VSAWKVGMDSGTLAAVYSGVVCSGMAYYIQSIVIRERGPVFTSFSFPMCMIIATFLGLVLAEKIHLGSIIGAVIFVFGVYVWGGK-  
 AT4G08290/1-384 DSITIKTYPAD-LSLSALICLAGAVQSFVALVVERH-PSGAVGWDARLFAPLYTIVSSGITYYVQGMVMKTRGPVFTAFNPLCMILVALIASFILHEQIHFCVIGGAVIAAGLYMVMVGGK-  
 AT1G68170/1-356 DVKISKQFGGP-YWNATLNMNMGVVVAMLVLCWEHD-LDEWRLGNIRLLIYAYAILISGMVVAVNAWCIERGPLFVSVPVGLVIVALVGSFLLDLDELHLSIGTVIIGALYILWAGK-  
 AT4G01440/1-365 DAKVNKYPCC-YSTTVLSFFGTIQCALLSLIKSRD-ITAWILTDKLDIVTIVYAGAVAQGLCTVGSWCIIRKRPITETSIFTFVGLIFATLDFDLIHRQIFLGSVGGVVIIFGLYIFLLGK-  
 AT4G01450/1-361 DAKINVKYPCC-YSTVILSVFGLQCALLSLIKTRH-LEDWILRDELTIITVVIAGVVAQGMCTVGMWCIKQGGPVVSSSPVVLMSATVDFLILHREIYLGSVIGSVVVVIIGLYIFLWRS-  
 AT5G40210/1-339 MAHTMGRYPSA-VVVTLVHNVCIADVCAFVSLLAEKDNPKAWVIRFDITLITVVATGILNSGYVVIHT-WAVSHKGPVYLSMFKPLSILIAAVSTFIFLQESLYLGSVMGGLISIGFMYLWGGK-  
 AT4G28040/1-359 DVPVIAASHCPDH-LYTSACTCFIATIASFLVALALGNTHLPPWKLDSFLKLSCCIYSSGFQA-ISFFLDAWIVSQKGPVSALFNPLSAVIVTFFGALYKKEQTYLGSLLBALAILGLYILWGGK-

**Supplemental Figure S5 B**