Supplemental Figure 1. Tendril-less leaf phenotype of allele *tl-pet*.

Arrow marks an extended petiolule supporting a narrow leaflet.

Supplemental Figure 2 ClustalW2 sequence alignment used to estimate tree in Figure 3.

```
                      *         20         *         40         *         60         *         80
CR962121_7 : ----------------------------MN----HQDQMMLMSQLFPAC-----EYTQIIS--------------QQGEKK :  30
CR962121_5 : ----------------------------MN----HQDQMMLMSQLFPAC-----EYTQIIS--------------QQGEKK :  30
At4g36740  : ----------------------------MN-YTVDDQNMAFISQLYPD------VYTQIV---------------QPGEVK :  31
At2g18550  : ----------------------------MNNQNVDDHNLLLISQLYPN------VYTPLVPQ-------------QGGEAK :  34
At5g66700  : ----------------------------MDHGRLMDDQMMLGSQVYPYTTQPQNSHCIIVNQ-------------IDGGEE :  40
Tl_Pisum   : ----------------------------MDWNTDTTVPFVP--------PPGSSLS--------------FFYNYNNYNYS :  31
Tl_Lens_cu : ----------------------------MDWNTDSTVPFVP--------PPGSSLS--------------FFYNYNSYNYS :  31
Tl_Lathyru : ----------------------------MDWNNERAVPFVP--------PPASSLS--------------FFYNYNNYNYS :  31
Tl_Vicia_n : ----------------------------MDWNTDTTVPFVP--------PPGSSLS--------------FFYNYNSYNYS :  31
Tl_Vicia_s : ----------------------------MDWNTDSTVPFVP--------PPGSSLS--------------FFYNYNNYDYS :  31
AC139525_2 : ----------------------------MEWNGN-TRSFVP--------QPESSLS--------------FLYNYNQCSYQ :  30
At5g03790  : ----------------------------MEWSTTSNVENVRVAFMPPPWPESSSFN--------------SLHSFNFDPYA :  39
At2g36610  : ----------------------------MEYWSSSFIDGA----------SSSSFI--------------SPF-YNFDHFS :  28
At2g46680  : ----------------------------MTEGGE--YSPAMMSAEPFLTMKK----------------------------- :  22
At3g61890  : ----------------------------MEEGDF--FNCCFSEISSGMTMNK----------------------------- :  22
AC174358_2 : ----------------------------MEYSQYSSYSAEAGEEETYTTSSI----------------------------- :  24
At1g27050  : ----------------------------MENSDTDSEVFFWFQNQNQNHSHKFPSSCFPPS--------SHSAFYGSSSMI :  45
At5g53980  : ----------------------------MENS----------QSQGKN--------------------------------- :  10
AC145165_1 : ----------------------------MKRLNNTSDSFSTPLITISP--STEEHSPRNK-------------HVYGMEFQ :  38
TC106805   : ----------------------------MKRLG-SSDSLG-ALMTICP--TTEEESPRNN-------------QVYGREFQ :  36
CU024864_1 : ----------------------------MKRFN-NSETMA-SLLSMYQ--SKEVDVDQRNE--------A---KGYSEEFQ :  38
At4g40060  : ----------------------------MKR-LSSSDSMC-GLIS----TSTDEQSPR---------------GYG-SNYQ :  31
At2g22430  : ---------------------------MMKR-LSSSDSVG-GLISLCPTTSTDEQSPR---------------RYGGREFQ :  37
At5g65310  : ----------------------------MKRSRGSSDSLS-GFLPIRHSTTDKQISPRPTT--------TGFLYSGAGDYS :  44
At1g69780  : ----------------------------MSCNN-GMSFFPSNFMIQTSYEDDHPHQSPSLAPLLPSCSLPQDLHGFA-SFL :  51
At1g26960  : ----------------------------MSCNNNGLAFFPENFSLQNHHQEEEDH--------------PQLLQDFH-GFL :  38
CT571261_1 : --------------------------------MHEMAFFQANFMLQTPHHHDDHHQPSSLN-----SILPQDYHGGP-SFL :  43
AC136974_2 : -----------------------------------MAFPPPHSFMFNPHEDHDQLPSTSLN--TFPSFPPQHFQQGA-PFL :  43
TC103795   : -----------------------------------MKIIIMKTYFLLQLLLTPILPFHLIN--TFKGSGSN---GGA-SFM :  40
At5g15150  : --------------MYMYEEERNNINNNQEGLRLEMAFPQHGFMFQQLHEDNAHHLPSPTS---LPSCPPHLFYGGGGNYM :  64
At3g01220  : --------------MYVFDP------TTEAGLRLEMAFPQHGFMFQQLHEDNSQDQ--------LPSCPPHLFNGGG-NYM :  52
CR954197_2 : ----------------------------MAGGKLFGGS-------NMSLLLQNERLP------CTSEVLESLWVHTPASFQ :  40
TC100666   : ----------------------------MAGGRVFSNGPANISNINMNILLQNQQQTPRGN--SSQQPLDSLFLSSSASFF :  51
TC94592    : ----------------------------MESGRLYFDSSACRGNNMNMLFLGN--------------------ADLGFRG- :  32
At3g01470  : ----------------------------MESNSFFFDPSASHGN--SMFFLGN--------------------LNPVVQGG :  31
At4g37790  : MGLDDSCNTGLVLGLGLSPTPNNYNHAIKKSSSTVDHRFIRLDPSLTLSLSGESYKIKTGAGAGDQICRQTSSHSGISSFS :  81
                                         m

                     *       100         *       120         *       140         *       160
CR962121_7 : PK---PRRKRSKK--------------------------NKGGENSANDMNKKRKLSDEQVNILEENFGNEHKLESEK--- :  79
CR962121_5 : PK---PRRKRSKK--------------------------NKGGENSANDMNKKRKLSDEQVNILEENFGNEHKLESEK--- :  79
At4g36740  : QP---KRRRKKTKGS----------------------VASADG---GNGLFRKRKLTDEQVNMLEMSFGDEHKLESER--- :  81
At2g18550  : PT---RRRKRKSKSV----------------------VVAEEGENEGNGWFRKRKLSDEQVRMLEISFEDDHKLESER--- :  87
At5g66700  : SKPVKRRRKRRSKGSS---------------------ATNEEDVAEIGGMLRKRKLTDEQVNMLEYSFGNEHKLESGR--- :  97
Tl_Pisum   : GIEASEAALGETQQR----------LLPVIDDETNKINNGKDYREKKKTKNKKNKLTSNQVDALERSFHEEIKLDPER--- :  99
Tl_Lens_cu : GIERSEAALGETQQR----------LLPAIDDETNKINNGKDHREKKKTKTKKNKLTSNQVDALERSFNEEIKLDPER--- :  99
Tl_Lathyru : GIEAGEAALGETQQR----------LLPVIDDETKMINNGKECQKKKKSKNKKNKLTSNQVDALERSFHEEIKLEPER--- :  99
Tl_Vicia_n : GIEASEGALGETQQR----------LLPVIDDDPNKINNGKDNREKKKAKNKKNKLTSNQVDALERSFHEEIKLDPER--- :  99
Tl_Vicia_s : GIEASEGALAETQQR----------LLPVIDDDPNKINNGKDHRDKKKAKNKKNKLTSNQVDALERSFHEEIKLDPER--- :  99
AC139525_2 : GM--MEVKHQDWTDT----------MFPEMEK---MMKYG--NQEKKK------RLTSEQMESLESSFQEEIKLDPQR--- :  85
At5g03790  : GNSYTPG-DTQTGP-----------VISVPESEKIMNAYRFPNN--NNEMIKKKRLTSGQLASLERSFQEEIKLDSDR--- : 103
At2g36610  : GNQDNRCLGTMMGAQQ--------DILHVP-LAMVESGYGEESNSFNGQEKKKKKMTSEQLKFLERSFQEEIKLNPDRKMK : 100
At2g46680  : ------------------------------------------MKKSNHNKNNQRRFSDEQIKSLEMMFESETRLEPRK--- :  58
At3g61890  : ------------------------------------------KKMK--KSNNQKRFSEEQIKSLELIFESETRLEPRK--- :  56
AC174358_2 : ------------------------------------------SSMRKKKNKNTKRFTDEQIKSLETMFETETRLEPRK--- :  60
At1g27050  : NTETATMDE-----------------------------EDVCESYMMREITKKRKLTPIQLRLLEESFEEEKRLEPDR--- :  94
At5g53980  : ---------------------------------------------------KKKRLTQDQVRQLEKCFTMNKKLEPDL--- :  37
AC145165_1 : SMML-----DGFEEE------------------GCVEETGHH-------SEKKRRLRVDQVKALEKNFEVENKLEPER--- :  86
TC106805   : SMM------EGLDEE------------------GCVDEPG----------QKKRRLSVDQVKALEKNFEVENKLEPDR--- :  80
CU024864_1 : AML------DRLEQE------------------DSYEDGSPM-------LEKKRRLGYDQVKALEKSFELDNKLEPER--- :  85
At4g40060  : SML------EGYDED------------------ATLIEEYSGNHHHMGLSEKKRRLKVDQVKALEKNFELENKLEPER--- :  85
At2g22430  : SML------EGYEEE------------------EEAIVEERG---HVGLSEKKRRLSINQVKALEKNFELENKLEPER--- :  88
At5g65310  : QMF------DALEDD------------------GSLEDLGGVGHASSTAAEKKRRLGVEQVKALEKNFEIDNKLEPER--- :  98
At1g69780  : GKRSPMEGCCDLETG---------------NNMNG-EEDYSDD--GSQMGEKKRRLNMEQVKTLEKNFELGNKLEPER--- : 111
At1g26960  : GKRSPMNNVQGFCN----------------LDMNG-DEEYSDD--GSKMGEKKRRLNMEQLKALEKDFELGNKLESDR--- :  97
CT571261_1 : GKRC-MSFSSGIELG---------------EEANIPEEDLSDD--GSQAGEKKRRLNMEQVKTLEKSFELGNKLEPER--- : 103
AC136974_2 : LKKS-MSFS-GIENKCHDH-----------HEVHGD-DELSDD-GFQSGEKKIRLNLDQVQALEKSFEFGNKLDPER--- : 106
```

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TC103795   : MKRS-MSFS-GIESNHINTNK-------CDELMHGDEDQLSDEEGYSQMGEKKKRLSLEQVKALEKSFEIGNKLEPER--- : 109
At5g15150  : MNRS-MSFTGVSDHHHLTQKSPTTTNNMNDQDQVGEEDNLSDDGSHMMLGEKKKRLNLEQVRALEKSFELGNKLEPER--- : 141
At3g01220  : MNRS-MSLMNVQEDHNQTLD----------------EENLSDDGAHTMLGEKKKRLQLEQVKALEKSFELGNKLEPER--- : 113
CR954197_2 : GSNSVVNFENGGGSN-----RVVTDRPFFQQLEKEENCGDEDYEACYHQQGKKRRLSSEQVQFLEKSFEVENKLEPDR--- : 113
TC100666   : GSRSMVSFEDVQG-------RKRRNRSFFGGFDLDEN-GEDEMDEYFHQSEKKRRLSVDQVQFLEKSFEEDNKLEPER--- : 121
TC94592    : --RSMMSMEEGSK-----------RRPFFSSP--DELYDEEYYEE--QSPEKKRRLTSEQVHMLEKSFEEENKLEPER--- :  93
At3g01470  : GARSMMNMEETSK-----------RRPFFSSP--EDLYDDDFYDD--QLPEKKRRLTTEQVHLLEKSFETENKLEPER--- :  94
At4g37790  : SGRVKREREISGGDGEE-------EAEETTERVVCSRVSDDHDDEEGVSARKKLRLTKQQSALLEDNFKLHSTLNPKQ--- : 152
                                                                 k 4    Q   LE  F     L p

                    *       180         *       200         *       220         *       240
CR962121_7 : -----KDRLAMELGLDPRQVAVWFQNRRARWKNKKLEEEYFSLKKNHESTILEKCLLETKM-------LKLREQLSEAEKE : 148
CR962121_5 : -----KDRLAMELGLDPRQVAVWFQNRRARWKNKKLEEEYFSLKKIHESTILEKCLLETKLREQHSEALKLREQLSEAEKE : 155
At4g36740  : -----KDRLAAELGLDPRQVAVWFQNRRARWKNKRLEEEYNKLKNSHDNVVVDKCRLESEV-------IQLKEQLYDAERE : 150
At2g18550  : -----KDRLASELGLDPRQVAVWFQNRRARWKNKRVEDEYTKLKNAYETTVVEKCRLDSEV-------IHLKEQLYEAERE : 156
At5g66700  : -----KEKIAGELGLDPRQVAVWFQNRRARWKNKKLEEEYAKLKNHHDNVVLGQCQLESQI-------LKLTEQLSEAQSE : 166
Tl_Pisum   : -----KMKLSAELGLQPRQVAVWFQNRRTRWKTKQLEHSYDVLK--------------QENQKLQEEVMVLKEKLKEKSDC : 161
Tl_Lens_cu : -----KMKLSAELGLQPRQVAVWFQNRRTRWKTKQLEHSYDVLK--------------QENQKLQEEVIELKEKLKEKSDF : 161
Tl_Lathyru : -----KMKLSAELGLQPRQVAVWFQNRRTRWKTKQLEHSYDVLK--------------QENQKLQEEVMELKEKLKEKSDG : 161
Tl_Vicia_n : -----KMKLSAELGLQPRQVAVWFQNRRTRWKTKQLEQSYDVLK--------------QENQKLQDEVMELKEKLKEKADC : 161
Tl_Vicia_s : -----KMKLSAELGLQPRQVAVWFQNRRTRWKTKQLEQDYDVLK--------------QENQKLQDEVMTLKEKLKEKGDC : 161
AC139525_2 : -----KMKLSKELGLQPRQIAIWFQNRRARWKTKQLEHLYDSLRHQFEVVS-------KEKQQLQDEVMKLKAMLKEQGNS : 154
At5g03790  : -----KVKLSRELGLQPRQIAVWFQNRRARWKAKQLEQLYDSLRQEYDVVS-------REKQMLHDEVKKLRALLRDQGLI : 172
At2g36610  : LNPDRKMKLSKELGLQPRQIAVWFQNRKARWKNKQLEHLYESLRQEFDIVS-------REKELLQEELIQLKSMIREDSSC : 174
At2g46680  : -----KVQLARELGLQPRQVAIWFQNKRARWKSKQLETEYNILRQNYDNLASQFESLKKEKQALVSELQRLKEATQKKTQE : 134
At3g61890  : -----KVQVARELGLQPRQVAIWFQNKRARWKTKQLEKEYNTLRANYNNLASQFEIMKKEKQSLVSELQRLNEEMQRPKEE : 132
AC174358_2 : -----KLQLARELGLQPRQVAIWFQNKRARWKSKQLEREYNKLQNSYNNLASKFESMKKERQTLLIQLQKLNDLIQKPIEQ : 136
At1g27050  : -----KLWLAEKLGLQPSQVAVWFQNRRARYKTKQLEHDCDSLKASYAKLKTDWDILFVQNQTLKSKVQFLNRLTSHYFQE : 170
At5g53980  : -----KLQLSNQLGLPQRQVAVWFQNKRARFKT-------QSLEVQHCTLQSKHEAALSDKAKLEHQVQFL---------- :  96
AC145165_1 : -----KEKLAIELGLQPRQVAVWFQNRRARWKTKQLERDYGVLKANYDALKLKFDAIAQDNKAFHKEIKELKSKLGE---- : 158
TC106805   : -----KVKLAQELGLQPRQVAVWFQNRRARWKTKQLERDYGVLKANYDALKLNCEDLQRDKETLLKEVKELKSRLQI---- : 152
CU024864_1 : -----KVKLAEDLGLQPRQVSIWFQNRRARTKTKQLERDYSVLKSNFDVLKVEYTNLQQENETLTRKLRELKAKLLR---- : 157
At4g40060  : -----KTKLAQELGLQPRQVAVWFQNRRARWKTKQLEKDYGVLKGQYDSLRHNFDSLRRDNDSLLQEISKIKAKVNG---- : 157
At2g22430  : -----KVKLAQELGLQPRQVAVWFQNRRARWKTKQLEKDYGVLKTQYDSLRHNFDSLRRDNESLLQEISKLKTKLNGGGGE : 164
At5g65310  : -----KVKLAQELGLQPRQVAIWFQNRRARWKTKQLERDYGVLKSNFDALKRNRDSLQRDNDSLLGQIKELKAKLNVEGVK : 174
At1g69780  : -----KMQLARALGLQPRQIAIWFQNRRARWKTKQLEKDYDTLKRQFDTLKAENDLLQTHNQKLQAEIMGLKNREQTES-- : 185
At1g26960  : -----KLELARALGLQPRQIAIWFQNRRARSKTKQLEKDYDMLKRQFESLRDENEVLQTQNQKLQAQVMALKSREPIES-- : 171
CT571261_1 : -----KMQLARALNLQPRQVAIWFQNRRARWKTKQLEKDYDVLKRQYDAIKLDNDALQAQNQKLQAEILALKNREPTES-- : 177
AC136974_2 : -----KVQLAKALGLQPRQIAIWFQNRRARCKTKQLENEYEVLKKKFEAVKDENDALKVHNQKLQGELEALKSKDWCEGGT : 182
TC103795   : -----KMQLAKALGLQPRQVAIWFQNRRARWKTKQLEKEYEVLKKQFDSLKADNNTLKAQNNKLHAELQTLKKRDCFENGT : 185
At5g15150  : -----KMQLAKALGLQPRQIAIWFQNRRARWKTKQLERDYDSLKKQFDVLKSDNDSLLAHNKKLHAELVALKKHDRKES-- : 215
At3g01220  : -----KIQLAKALGMQPRQIAIWFQNRRARWKTRQLERDYDSLKKQFESLKSDNASLLAYNKKLLAEVMALKNKECNEG-- : 187
CR954197_2 : -----KVQLAKELGLQPRQVAIWFQNRRARFKTKQLEKDYGTLKASFDSLKDDYDNLLQENDKLKEEVNSLKNKLIPRDKE : 189
TC100666   : -----KTKLAKDLGLQPRQVAIWFQNRRARWKTKQLEKDYDSLNDGYESLKTEYDNLLKEKDRLQSEVASLTEKVLEREKQ : 197
TC94592    : -----KTQLAKKLGLQPRQVAVWFQNRRARWKTKQLERDYDVLKSSYDSLLSTYDSINKENEKLKSEVVSLNEKLQV---- : 165
At3g01470  : -----KTQLAKKLGLQPRQVAVWFQNRRARWKTKQLERDYDLLKSTYDQLLSNYDSIVMDNDKLRSEVTSLTEKLQG---- : 166
At4g37790  : -----KQALARQLNLRPRQVEVWFQNRRARTKLKQTEVDCEFLKKCCETLT-------DENRRLQKELQDLKALKLSQPFY : 221
                  K  6   Lg6qprQ6a6WFQN44aR K  q e  y  L                    l      6

                   *       260         *       280         *       300         *       320
CR962121_7 : IQRLREP-----NSSSSTSSISQFMEVVDPQFHD-EFEVNHIYNDD----------------------------------- : 188
CR962121_5 : IQRLREPFERVTSSSSSTSSMSQSVEVVDPPFLG-EFGVDNGYDDD----------------------------------- : 200
At4g36740  : IQRLAERVEGGSSNSPISSSVSVEAN-ETPFFGDYKVGDDGDDYDH----------------------------------- : 195
At2g18550  : IQRLAKRVEGTLSNSPISSSVTIEANHTTPFFGDYDIGFDGEADEN----------------------------------- : 202
At5g66700  : IRKLSERLEEMPTNSS-SSSLSVEAN-----NAPTDFELAPETNYN----------------------------------- : 206
Tl_Pisum   : RTQTFGDETVESPLEGLGWREIEGYKPYPNSHNQQGSTSSIQQA------------------------------------- : 205
Tl_Lens_cu : RTQTFGNETVESPLEGLEWREIEGYEPYPNSHNQHGSTSSIQQA------------------------------------- : 205
Tl_Lathyru : RTQTFGDETVESPLEGLGWREIEGYEPYPNSHNQQGSTSSIQQA------------------------------------- : 205
Tl_Vicia_n : RTQTFGDETVESPLEGLGWREIEGYNPYPSTYNQQGTSSSTQQA------------------------------------- : 205
Tl_Vicia_s : RTQAFGDETVESPLEGLGWREIEGYNPYPSCYNQQGTTSSTQQA------------------------------------- : 205
AC139525_2 : CGRMQGYYTEMSVEETETVESTSEAALRCSNREVKGKIHQQLNI------------------------------------- : 198
At5g03790  : KKQISAGTIKVSGEE-DTVEISSVVVAHPRTENMNANQITGGNQ------------------------------------- : 215
At2g36610  : KKKQ-------------TWEKACS--------------------------------------------------------- : 185
At2g46680  : EERQCSGDQAVVALSSTHHESENEENRRRKPEEVRPEMEMKDDKGHHGVMCDHHDYEDDDNG-----------------YS : 198
At3g61890  : KHHECCGDQGLALSSST--ESHNG----------KSEPEGRLDQG--SVLCNDGDYN------------------------ : 175
AC174358_2 : SQSSSQVKEAKSMESASENGGRNK-----CEAEVKPSPSMERSEHVLDVLSDD--------------------------D : 185
At1g27050  : SVQNFDDTFKQVDLLKEKLKMQENLETQSIERKRLGEEGSSVKSDNTQYSEEEGLENQYSFP-----------------EL : 234
At5g53980  : ---------------------QDELKRARNQLALFTNQDSPVDNSNLGSCDEDHDD------------------------- : 131
AC145165_1 : -EEKST---INVLVKEELTMLESCDEDKHN---PSSETSNPSSESKDHLDYDCIINNNDVGIGE---------------TS : 217
TC106805   : -QEENTTTESDVCVKEELITLQ---ESENT---ASDETAILRSDSKD-LNNDCFKNGDGV--------------------A : 205
CU024864_1 : -VESNE------LEKEVECPISRGIERGGS---ESNSSGIIKEES----NVDSPMCFNGS--------------------- : 203
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At4g40060  : -EEDNNNNKAITEG----VKEEEVHKTDSI---PSSPLQFLEHSSGFNYRRSFTDLRDLLP-------------------- : 210
At2g22430  : -EEEEENNAAVTTESDISVKEEEVSLPEKITEAPSSPPQFLEHSDGLNYR-SFTDLRDLLPL-----------------KA : 226
At5g65310  : GIEENGALKAVEANQSVMANNEVLELSHRS---PSPPPHIPTDAPTSELA---FEMFSIFP-------------------- : 229
At1g69780  : INLNKE-TEGSCSN-RSDNSSDNLRLDISTAPPSNDSTLTGGHPPPPQTVGRHFFPPSPATA------------------- : 245
At1g26960  : INLNKE-TEGSCSD-RSENISGDIR------PPEIDSQFALGHPP------------------------------------ : 208
CT571261_1 : INLNKE-TEGSSSN-RSENSS-EIKLDMSRTPASDSPLSTHQHTTS-----RTFFPPS---A------------------- : 228
AC136974_2 : KYLMKE-TEGSWSN-GSDNSL-NINLDLSRTQALNSSVSSQNGRNL-----ISLLPTSLN--------------------- : 234
TC103795   : ISLKKE-NEGSWSN-GSDNSS-DMNLDLSRT------------------------PNSLK--------------------- : 218
At5g15150  : AKIKREFAEASWSNNGSTENNHNNNSSD-----ANHVSMIKDLFPS----------------------------------- : 256
At3g01220  : NIVKRE-AEASWSNNGSTENSSDINLEMPRETITTHVNTIKDLFPS----------------------------------- : 232
CR954197_2 : --KVNSEDKSSPEAINSPHNNIDPMDIISITNSENGSKMSLPN-MVLKCKQEDANSAKSDVLDSDSPHCNDG----NNLSS : 263
TC100666   : EGKFKQGESETKEFLKEPTINKPLVDSVSEGEGSKLSIVEASNNNNNNNKLEDISSARSDILDCESPRYTDGVLETCDSSY : 278
TC94592    : --QAKDMLEEPLSEKKADPLPVDIAQIFSIKVDDHMSSGSVGS----AVVDESSPRVVGVIVDSVDSYFPADNYAGCVAPI : 240
At3g01470  : --KQETANEPPGQVPEPNQLDPVYINAAAIKTEDRLSSGSVGS----AVLDDDAP----QLLDSCDSYFPS------IVPI : 231
At4g37790  : MHMPAATLTMCPSCERLGGGGVGGDTTAVDEETAKGAFSIVTKP------------------------------------- : 265


                  *       340         *       360         *       380         *       400
CR962121_7 : ----------------------------------------------------------------VFFMPDATYYFNGQE-W : 204
CR962121_5 : ----------------------------------------------------------------VFFMPNETCYYNGME-W : 216
At4g36740  : ----------------------------------------------------------------LFYPVPENSYIDEAE-W : 211
At2g18550  : ----------------------------------------------------------------LLYSP---DYIDGLD-W : 215
At5g66700  : ----------------------------------------------------------------IPFYMLDNNYLQSMEYW : 223
Tl_Pisum   : -----------------------------------------------------------------AEGYINSSFIVEDFDS : 221
Tl_Lens_cu : -----------------------------------------------------------------AEGYMNNSFIVEDFDS : 221
Tl_Lathyru : -----------------------------------------------------------------AEGYINSSFIVEDFDS : 221
Tl_Vicia_n : -----------------------------------------------------------------AEGYINNSFIVEDFDS : 221
Tl_Vicia_s : -----------------------------------------------------------------AEGYINSSFIVEDFDS : 221
AC139525_2 : -----------------------------------------------------------------DEG--NCSFNLEDYNI : 212
At5g03790  : -----------------------------------------------------------------VYGQYNNPMLVASSGW : 231
At2g36610  : --------------------------------------------------------------------------------- :   -
At2g46680  : NNIKREYFGGFEEEPDH---------------------------------------------LMNIVEPAD-SCLTSSDDW : 233
At3g61890  : NNIKTEYFG-FEEETDHE--------------------------------------------LMNIVEKADDSCLTSSENW : 211
AC174358_2 : TSIKVEYFG---LEDETG--------------------------------------------LMNFAEHAD-GSLTSPEDW : 218
At1g27050  : AVLGFYYDPTLTASNLRQ--------------------------------------------EPLKVTCADQMTQIQISDV : 271
At5g53980  : -----------------------------------------------------------------QVVVFDELYACFVSNG : 147
AC145165_1 : SLFPVDLKDGSSDSDS---------SAISSSGVLQSQQHLLLSP----------ESSS----MNCFQYQKSYHVKMEEHNF : 275
TC106805   : SLFPADFKDGSSDSDSSAILNEESNAAISSSGVLQN-HNFLMSPGSSSLKFNCSESSSPSSMSNCFQFQTQF-VKMEEHNF : 284
CU024864_1 : --LPSSMINLVHYYDS--------------RGSQEN------------------------------VFQNQF-MRMEEQNF : 237
At4g40060  : --NSTVVEAGSSDSCD-------------SSAVLNDETSSDNGRLT----------PPVTVTGGSFLQFVKTEQTEDHEDF : 266
At2g22430  : AASSFAAAAGSSDSSD-------------SSALLNEESSS-NVTVA----------APVTVPGGNFFQFVKMEQTEDHEDF : 283
At5g65310  : --RTENFRDDPADSSD-------------SSAVLNEEYSPNTVEAAG-------AVAATTVEMSTMGCFSQFVKMEEHEDL : 288
At1g69780  : -TTTTTTMQFFQNSSSG-----------------------------------------------QSMVKEEN-SISNMFCA : 277
At1g26960  : ---TTTTMQFFQNSSSE-----------------------------------------------QRMVKEEN-SISNMFCG : 238
CT571261_1 : -RPSSGIAQLFQTSSRPEI----------------------------------------QCQKIDQMVKEE--SLSNMFCG : 266
AC136974_2 : ---PNNIPQLLQFTSRP-------------------------------------------------DIQDE--NFSSMFHN : 261
TC103795   : ---PTSMTQLLQCSSKS-------------------------------------------------DLQDE--SFCNMFNN : 245
At5g15150  : ---SIRSATATTTSTHID----------------------------------------------HQIVQDQDQGFCNMFNG : 288
At3g01220  : ---SIRSS-AHDDDHHQN----------------------------------------------HEIVQEES--LCNMFNG : 261
CR954197_2 : FIEPT-DSDFSQDEEDNDN-------------------------------------------LSHNLLTLPCLPKVEDVCY : 300
TC100666   : VFEPEYQSDLSQDEED------------------------------------------------HNLLPPYIFTKLEDVNY : 311
TC94592    : ERVQSEEDDGSDDGRN--------------------------------------------------YFDVFVASETEQHNH : 271
At3g01470  : Q-DNSNASDHDNDRSC--------------------------------------------------FADVFVPTTSPSHDH : 261
At4g37790  : -------------------------------------------------------------------------RFYNPFTN : 273


                 *       420         *       440         *       460         *       480
CR962121_7 : INV------------------------------------------------------------------------------ : 207
CR962121_5 : ISLYM---------------------------------------------------------------------------- : 221
At4g36740  : MSLYI---------------------------------------------------------------------------- : 216
At2g18550  : MSQFM---------------------------------------------------------------------------- : 220
At5g66700  : DGLYV---------------------------------------------------------------------------- : 228
Tl_Pisum   : VS-LHQECHWPELP---YYP------------------------------------------------------------- : 237
Tl_Lens_cu : VS-LHQECHWPELP---YFP------------------------------------------------------------- : 237
Tl_Lathyru : VS-LHQECHWPELP---YYP------------------------------------------------------------- : 237
Tl_Vicia_n : VS-LHQECHWPELP---YYP------------------------------------------------------------- : 237
Tl_Vicia_s : VS-LHQECHWPELP---YYP------------------------------------------------------------- : 237
AC139525_2 : NNNVPLLPYWPAAVPYNYHP------------------------------------------------------------- : 232
At5g03790  : PS----------------YP------------------------------------------------------------- : 235
At2g36610  : --------------------------------------------------------------------------------- :   -
At2g46680  : RGFKSDTTTLLDQSSNNYP-WRDFWS------------------------------------------------------- : 258
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At3g61890  : GGFNSDS--LLDQSSSNYPNWWEFWS------------------------------------------------------- : 235
AC174358_2 : SAFESND--LLGQSSCDYQ-WWDFWS------------------------------------------------------- : 241
At1g27050  : TEPASSAHKKIEVTQRSSSMSRKRDKPYTNRHTPARISKRRRPWAPSSSEHDEIIDKPITKPPPPPALVVMGLPANCSVLE : 352
At5g53980  : HGSSSTSWV------------------------------------------------------------------------ : 156
AC145165_1 : LSADEACNFFSDEQAPTLQWYCP-DQWS----------------------------------------------------- : 302
TC106805   : LSADETCDFFSDEQPPTLQWYCS-EEWN----------------------------------------------------- : 311
CU024864_1 : LSNSELFSFFSVDQSPTL--------------------------------------------------------------- : 255
At4g40060  : LSGEEACGFFSDEQPPSLHWYSASDHWT----------------------------------------------------- : 294
At2g22430  : LSGEEACEFFSDEQPPSLHWYSTVDHWN----------------------------------------------------- : 311
At5g65310  : FSGEEACKLFADNE----QWYCS-DQWNS---------------------------------------------------- : 312
At1g69780  : MDDHS--GFWPWLDQQQYN-------------------------------------------------------------- : 294
At1g26960  : IDDQS--GFWPWLDQQQYN-------------------------------------------------------------- : 255
CT571261_1 : MDDQA--GFWPWLEQQHFN-------------------------------------------------------------- : 283
AC136974_2 : IDEHQ--NLWPWA-------------------------------------------------------------------- : 272
TC103795   : IDEQQ--SLWPWTDHQQHQFR------------------------------------------------------------ : 264
At5g15150  : IDETTSASYWAWPDQQQQHHNHHQFN------------------------------------------------------- : 314
At3g01220  : IDETTPAGYWAWSDPNHNHH-HHQFN------------------------------------------------------- : 286
CR954197_2 : DDPHENSCNFGFPVEDQTFCFWPY--------------------------------------------------------- : 324
TC100666   : SDPPHNSTSYGFQEEDHHQALWPWSY------------------------------------------------------- : 337
TC94592    : EE-------------GEALNWWGNMYYVA---------------------------------------------------- : 287
At3g01470  : H--------------GESLAFWGWP-------------------------------------------------------- : 272
At4g37790  : PSAAC---------------------------------------------------------------------------- : 278


                *        500        *        520        *        540        *        560
CR962121_7 : --------------------------------------------------------------------------------- :   -
CR962121_5 : --------------------------------------------------------------------------------- :   -
At4g36740  : --------------------------------------------------------------------------------- :   -
At2g18550  : --------------------------------------------------------------------------------- :   -
At5g66700  : --------------------------------------------------------------------------------- :   -
Tl_Pisum   : --------------------------------------------------------------------------------- :   -
Tl_Lens_cu : --------------------------------------------------------------------------------- :   -
Tl_Lathyru : --------------------------------------------------------------------------------- :   -
Tl_Vicia_n : --------------------------------------------------------------------------------- :   -
Tl_Vicia_s : --------------------------------------------------------------------------------- :   -
AC139525_2 : --------------------------------------------------------------------------------- :   -
At5g03790  : --------------------------------------------------------------------------------- :   -
At2g36610  : --------------------------------------------------------------------------------- :   -
At2g46680  : --------------------------------------------------------------------------------- :   -
At3g61890  : --------------------------------------------------------------------------------- :   -
AC174358_2 : --------------------------------------------------------------------------------- :   -
At1g27050  : LKSRFEIYGSISRIRIHKDGIGSVSYRTAESAEAAIAGSHEPSFGISIDSKKLEVVWATDPLVKWKEGVTAGEGKERTSSF : 433
At5g53980  : --------------------------------------------------------------------------------- :   -
AC145165_1 : --------------------------------------------------------------------------------- :   -
TC106805   : --------------------------------------------------------------------------------- :   -
CU024864_1 : --------------------------------------------------------------------------------- :   -
At4g40060  : --------------------------------------------------------------------------------- :   -
At2g22430  : --------------------------------------------------------------------------------- :   -
At5g65310  : --------------------------------------------------------------------------------- :   -
At1g69780  : --------------------------------------------------------------------------------- :   -
At1g26960  : --------------------------------------------------------------------------------- :   -
CT571261_1 : --------------------------------------------------------------------------------- :   -
AC136974_2 : --------------------------------------------------------------------------------- :   -
TC103795   : --------------------------------------------------------------------------------- :   -
At5g15150  : --------------------------------------------------------------------------------- :   -
At3g01220  : --------------------------------------------------------------------------------- :   -
CR954197_2 : --------------------------------------------------------------------------------- :   -
TC100666   : --------------------------------------------------------------------------------- :   -
TC94592    : --------------------------------------------------------------------------------- :   -
At3g01470  : --------------------------------------------------------------------------------- :   -
At4g37790  : --------------------------------------------------------------------------------- :   -


               *        580        *        600        *        620
CR962121_7 : -------------------------------------------------------------- :   -
CR962121_5 : -------------------------------------------------------------- :   -
At4g36740  : -------------------------------------------------------------- :   -
At2g18550  : -------------------------------------------------------------- :   -
At5g66700  : -------------------------------------------------------------- :   -
Tl_Pisum   : -------------------------------------------------------------- :   -
Tl_Lens_cu : -------------------------------------------------------------- :   -
```

```
Tl_Lathyru : -------------------------------------------------------------- :   -
Tl_Vicia_n : -------------------------------------------------------------- :   -
Tl_Vicia_s : -------------------------------------------------------------- :   -
AC139525_2 : -------------------------------------------------------------- :   -
At5g03790  : -------------------------------------------------------------- :   -
At2g36610  : -------------------------------------------------------------- :   -
At2g46680  : -------------------------------------------------------------- :   -
At3g61890  : -------------------------------------------------------------- :   -
AC174358_2 : -------------------------------------------------------------- :   -
At1g27050  : SSKLLRPVMPLRKHGRSSRLASAIVNPRSDNTKGISGDGGISSPATTSEVKQRNIVTYDDIV : 495
At5g53980  : -------------------------------------------------------------- :   -
AC145165_1 : -------------------------------------------------------------- :   -
TC106805   : -------------------------------------------------------------- :   -
CU024864_1 : -------------------------------------------------------------- :   -
At4g40060  : -------------------------------------------------------------- :   -
At2g22430  : -------------------------------------------------------------- :   -
At5g65310  : -------------------------------------------------------------- :   -
At1g69780  : -------------------------------------------------------------- :   -
At1g26960  : -------------------------------------------------------------- :   -
CT571261_1 : -------------------------------------------------------------- :   -
AC136974_2 : -------------------------------------------------------------- :   -
TC103795   : -------------------------------------------------------------- :   -
At5g15150  : -------------------------------------------------------------- :   -
At3g01220  : -------------------------------------------------------------- :   -
CR954197_2 : -------------------------------------------------------------- :   -
TC100666   : -------------------------------------------------------------- :   -
TC94592    : -------------------------------------------------------------- :   -
At3g01470  : -------------------------------------------------------------- :   -
At4g37790  : -------------------------------------------------------------- :   -
```

Supplemental Table 1. Comparison of species richness in legume lineages composed of climbing plants and sister non-climbing groups. Adapted from (Gianoli, 2004) with species numbers estimated according to (Lewis et al., 2005).

Climbing plant taxa	number of spp.	sister group (non-climbing)	number of spp.
Papilionoideae			
Fabeae	330	Trifolieae	250
Papilionoideae			
Milletioid/phaseoloid clade	2647	Indigofereae	768

Supplemental Table 2. Confirmed *tendril-less* alleles

Line no.	Allele no.	Background	Author of allele	Mutagen	Isogenic or not	Mutation
JI 1194	wt	Marx isoline			yes	
JI 1197	*tl-w*, (*tl-1*)		(de Vilmorin, 1910)	spontaneous		3 bp insertion
JI 31	wt	Witham Wonder			no	
JI 32	*tl-pet*, (*tl-2*)		(Lamm, 1957)	spontaneous		SNP
	wt	Sprint x WL1018 F1			not analysed	
	tl-x, (*tl-3*)		(Gorel et al., 1994; Berdnikov et al., 1999)	7 krad gamma rays		not analysed
	wt	SGE			not analysed	
SGE0812	*tl-na*, (*tl-4*)		(Rozov, 2006)	EMS		not analysed
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 1081/6	*tl-5*		this paper	FN 20 Gy		deletion
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN	*tl-6*		this paper	FN 20 Gy		deletion

1132/1						
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 1167/3	*tl-7*		this paper	FN 20 Gy		deletion
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 1347/6	*tl-8*		this paper	FN 20 Gy		deletion
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 1484/1	*tl-9*		this paper	FN 20 Gy		deletion
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 2086/3	*tl-10*		this paper	FN 20 Gy		deletion
JI 2822	wt	JI15xJI399, RIL 39			yes	
FN 1770/4	*tl-11*		this paper	FN 20 Gy		Not analysed
JI 516	wt	Maro			yes	
JI 1373	*tl-12*		this paper	spontaneous		1908 bp deletion
JI 2224	wt	Ramonski 77			yes	
JI 3128	*tl-13*	I/101	(Vassileva, 1979), this paper	20 krad gamma rays, 1725rad/min		deletion
	wt	Kazanski			Not analysed	

	tl-14	VIII/11	(Vassileva, 1979), this paper	20 krad gamma rays, 2000rad/min		Not analysed
	wt	Iregi-5			Not analysed	
	tl-15	V/10	(Vassileva, 1979), this paper	5 krad gamma rays, 49rad/min		Not analysed
JI 3131	wt	Iregi-5			very closely related	
JI 3130	*tl-16*	V/243	(Vassileva, 1979), this paper	0.25 krad FN + 0.2 % EMS		deletion
5839	wt	Torsdag				
MC1a/1	*tl-17*		this paper	EMS	yes	SNP
JI 3253	wt	Cameor				
M3 4092-1	*tl-18*		this paper	EMS	yes	SNP

Allelism notes. *tl-1* is the original de Vilmorin mutant, known as *tl-white*, or *tl-w*, after the listing in (White, 1917). Allelism tests for *tl-pet* (Lamm, 1957) and *tl-na* (Rozov, 2006) were conventional crossings to *tl-w*, where the authors reported a tendril-less F1 progeny plant. Homozygous lethal *tl-x* (Gorel et al., 1994; Berdnikov et al., 1999) was determined to be allelic by the authors because it was generated by mutagenesis of a heterozygous *Tl/tl-1* F1 seed, which yielded a plant with tendril-less branches ie. branches "homozygous" at the *tl* locus *tl-w*/*tl-x*. Conventional allelism tests were done for all JIC FN *tl* mutants, either prior to molecular analysis, as crosses to *tl-w* line JI 1197 (*tl-5*, *tl-6*, *tl-7*, *tl-8*, *tl-9*, *tl-10*), or later, as a cross to *tl-w* line JI 1201 (*tl-11*). Others listed were found to be allelic after molecular analysis, either by sequencing (*tl-1* confirmed, *tl-12*, *tl-17* and *tl-18*), or by identification as a deletion mutant by absence of a *Tl* PCR marker (Vassileva alleles *tl-13* and *tl-16* and JIC FN alleles, *tl-5*, *tl-6*, *tl-7*, *tl-8*, *tl-9*, *tl-10* confirmed). Vassileva alleles *tl-14* (VIII/11) and *tl-15* (V/10) were crossed to *tl-13* (I/101) and F1 progeny were reported as tendril-less (Vassileva, 1979), therefore our molecular identification of the *tl-13* allele also confirms alleles *tl-14* and *tl-15*.

References not in the main text:

Berdnikov, V.A., Gorel, F.L., Bogdanova, V.S., Kosterin, O.E., Trusov, Y.A., and Rozov, S.M. (1999). Effect of a substitution of a short chromosome segment carrying a histone H1 locus on expression of the homeotic gene *Tl* in heterozygote in the garden pea *Pisum sativum* L. Genet. Res. **73:** 93-109.

Gorel, F.L., Berdnikov, V.A., and Temnykh, S.V. (1994). A deletion covering the *Tl* locus in *Pisum sativum*. Pisum Genetics **26:** 16-17.

Rozov, S. (2006). A new allele at the *Tl* locus - tl^{na}. Pisum Genetics **38:** 15-16.

White, O.E. (1917). Studies of inheritance in *Pisum*. II. The present state of knowledge of heredity and variation in peas. Proc. Am. Philos. Soc. **56:** 487-588.

Supplemental Table 3. Epistasis of *uni* over *tl*. T-test of unifoliolate plants segregating in combined F2 populations; FN1210/1 (*uni*/*uni*) x FN1081/6 (*tl*/*tl*), FN1210/1 (*uni*/*uni*) x FN1132/1 (*tl*/*tl*) and FN1210/1 (*uni*/*uni*) x FN2086/3 (*tl/tl*), n = 188. Results for plants with tendrils are not included in the table. Leaflet counts were made when plants were four weeks old. Tl marker scores: 1 = PCR band present, corresponding to *Tl Tl* homozygotes and *Tl tl* heterozygotes, 0 = PCR band absent, corresponding to homozygous *tl tl* deletion mutants.

plant phenotype	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni
Tl marker score	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total no. leaflets/plant	9	8	8	9	8	10	8	9	8	9	8	8	8	8
plant phenotype	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni
Tl marker score	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Total no. leaflets/plant	8	9	9	8	8	8	9	10	8	10	9	8	9	8
plant phenotype	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni
Tl marker score	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Total no. leaflets/plant	8	8	8	9	9	9	8	9	9	8	9	9	8	7
plant phenotype	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni	uni			
Tl marker score	1	1	1	1	1	1	1	1	1	1	1			
Total no. leaflets/plant	10	8	8	8	9	7	9	10	8	8	9			

t-test, leaflet number	
n (tot)	53
mean	8.51
variance	0.52
Stdev	0.72
SEM	0.10
popvar	0.55
exp var(mean) pop n=39	0.01
exp var(mean) pop n=14	0.04
est var diff (mean)	0.05
obs diff	0.11
t	0.48
P	0.631
v	51

Supplemental Table 4. Primer and adapter sequences

Piimers and adapters used in marker screening:	
*Pst*I adapter 1	5’-CTCGTAGACTGCGTACATGCA-3’,
*Pst*I adapter 2	5’-TGTACGCAGTCTAC-3’.
*Mse*I adapter 1	5’-GACGATGAGTCCTGAG-3’,
*Mse*I adapter 2	5’- TACTCAGGACTCAT-3’.
*Pst*I primer	5’-GACTGCGTACATGCAG(A/C/G/T)-3’,
*Mse*I primer	5’-GATGAGTCCTGAGTAA(A/C/G/T)-3’.
Sequencing primers:	
34R9	5’-GTGTATTGACTGCATCCTTCGGTG -3’
34R8	5’-GTTAGTTGTGTATATTGATATTGAGTG -3’
34F8REV	5’-CACATGTCAATTTCAAATGAGTTAC -3’
34F7REV	5’-GCACTTCATACCACACTTCGATTC -3’
TLHD5’	5’-GGAGTAGATTACACCCAAAAGAGAG -3’
TLHD5'REV	5’-CTCTCTTTTGGGTGTAATCTACTCC -3’
TLHDF1	5’-GATTACCGAGAGAAGAAGAAGAC -3’
TLHDF2	5’-AAGAAGAATAAATTAACAAGTAACCAAG -3’
34cDNA5’	5’-GAAAATCAGAAACTTCAAGAAGAGG -3’
TLHD3'nest	5’-CTCACAAGCCACACACG -3’
TLHD3’	5’-CGGATAATGGGAGTAGTGGAG -3’
Primers used in PCR cloning experiments:	
TLHDcDNA5’-1	5’- GAGACAACACCCTTTGATCC -3’
34cDNA3’	5’- GTCTTCAAACGACTAATACCTAACTACTAG -3’
TLHD5'nest	5’-GAGAGACACTGTTTACCGTACG -3’
TLHD3'nest2	5’- CAAACACCTCACAAGCCACAC-3’

RT-PCR primers:	
ologo T primer	5’-GACTCGAGTCGACATCG(T)$_{17}$-3’
TLHDF1	5’- GATTACCGAGAGAAGAAGAAGAC-3’
34F1	5’- GTTGAATGCTACTTGTTGATCC-
PsAGO1	5’-TTCTACCTCTGTGCTCATGCG-3’
PsAGO2	5’-CCTCGAATTTCATGAATTGCC-3’.
Quantitative PCR primers:	
PsTIF	5’-CTAGGTGGAAGACTAAGCAGC-3’
PsTIspanR	5’-GCTTTTCCTTCAACACCATAACCTC-3’.
PsActF	5’-CACAATTGGCGCTGAAAGAT-3’
PsActR	5’-TAATTGAGTTAAATGTCGTCTCATGGAT-3’
RACE PCR primers:	
34F6	5’-GAACAAAGGGTACTGTGGTATCAG -3’
34F6adj	5’-AGAAGAACCTGGAGGAGGAAC-3’
34PstextR1	5’- GATACATCAACAGTTCTTTCATTG-3’
Primers for probe amplification for RNA *in situ* hybridization:	
34cDNA5’	5’- GAAAATCAGAAACTTCAAGAAGAGG-3’
34cDNA3’	5’- GTCTTCAAACGACTAATACCTAACTACTAG-3’