SUPPLEMENTAL MATERIAL

Name	Nucleotide sequence
PtTrxClotfor	5'CCCC**CCATGG**CTACAGTAAAGTTGGTGGATGCA3'
PtTrxClotrev	5'CCCC**GGATCC**TTAATTCCCAGAAACAAGGGC3'
PtTrxClotRTfor	5'CCCC**CCATGG**CTACAGTAAAGTTGGTGGATGCA3'
PtTrxClotRTrev	5'CCCC**GGATCC**TTAATTCCCAGAAACAAGGGC3'
PtTrxClotGFPrev	5'CCCCGGATCCTTCCCAGAAACAAGGGC3'
PtTrxlike1RTfor	5'CCCCC**CCATGG**CTGAGGATAATACAAAGAAA3'
PtTrxlike1RTrev	5'CCCCC**GGATCC**TTACGAATGCAACCACAAGCG3'
PtTrxlike1GFPfor	5'CCCCCCATGGAGGATAATACAAAG3'
PtTrxlike1GFPrev	5'CCCCGGATCCGAATGCAACCACAAGCG3'
PtTrxlike2.1for	5'CCCCC**CCATGG**CTACCAGGCCAACC3'
PtTrxlike2.1rev	5'CCCCC**GGATCC**TTATACGAATTTCTGGATCAT3'
PtTrxlike2.1C45Sfor	5'TCTTGGTGCCGGAAATCCATTTATTTGAAGCCA3'
PtTrxlike2.1C45Srev	5'TGGCTTCAAATAAATGGATTTCCGGCACCAAGA3'
PtTrxlike2.1R43G/K44Pfor	5'ATGGCTTCTTGGTGCGGGCCATGCATTTATTTGAAG3'
PtTrxlike2.1R43G/K44Prev	5'CTTCAAATAAATGCATGGCCCGCACCAAGAAGCCAT3'
PtTrxlike2.1RTfor	5'CGTGACTTGTCAGTATTAAGT3'
PtTrxlike2.1GFPfor	5'CCCCCCATGGCTTCTAAGATCTTACAGAAC3'
PtTrxlike2.1GFPrev	5'CCCCGGATCCAAGGTACCCTCATTTTC3'
PtTrxlike2.2RTfor	5'CGTGACTTGTCAGTATTAAGT3'
PtTrxlike2.2RTrev	5'CCCC**GGATCC**TCACAAGGTATCCTCATTTTCAATC3'
PtTrxlike2.3RTfor	5'AAGCATTCCTTGTCAAAACCC3'
PtTrxlike2.3RTrev	5'CCCC**GGATCC**TCACAAGGTATCCTCATTTTCAATC3'
PtTrxlilium1.1RTfor	5'TCAAACCCGGCAACAC3'
PtTrxlilium1.1RTrev	5'GGGTTTTCTCCTCTGAGTC3'
PtTrxlilium1.2for	5'CCCC**CCATGG**CTTCGGTTGTGGCTCAG3'
PtTrxlilium1.2rev	5'CCCC**GGATCC**TCATCTCCCCGAAATGGC3'
PtTrxlilium1.2RTfor	5'GTTTCTTCTAATGTTGG3'
PtTrxlilium2.1RTfor	5'ATAAGAGGATCTCTCTTTC3'
PtTrxlilium2.1RTrev	5'GCAACGGGCTGTGTTGTG3'
PtTrxlilium2.2for	5'CCCC**CCATGG**CTGAAACTGACCAACCG3'
PtTrxlilium2.2rev	5'CCCC**GGATCC**TTATGTAGATCCTGCTGT3'
PtTrxlilium2.2RTfor	5'TAAGAATTTATCCTCTCTTATA3'
PtTrxlilium2.2RTrev	5'GCAACGGGCTGTGTTGTG3'
PtTrxlilium3for	5'CCCC**CCATGG**CTAAGGCAAAATTCCCCTCT3'
PtTrxlilium3rev	5'CCCC**GGATCC**TTAGGTGTCTTGAGCTGC3'
PtTrxlilium3S87Pfor	5'CGCACTTCTTGTGGACCCTGCAAGTATATAGAG3'
PtTrxlilium3S87Prev	5'CTCTATATACTTGCAGGGTCCACAAGAAGTGCG3'
PtTrxlilium3S84Wfor	5'GATTTTTATCGCACTTGGTGTGGAAGCTGCAAG3'
PtTrxlilium3S84Wrev	5'CTTGCAGCTTCCACACCAAGTGCGATAAAAATC3'
PtTrxlilium3S84W/S87Pfor	5'TATCGCACTTGGTGTGGACCATGCAAGTAT3'
PtTrxlilium3S84W/S87Prev	5'ATACTTGCATGGTCCACACCAAGTGCGATA3'

Supplemental Table I. Primers used for cloning, RT PCR and site-directed mutagenesis. The *Nco*I and *Bam*HI restriction sites are underlined and the mutagenic bases are in bold characters. The primers used for expression studies are indicated RT (for RT PCR experiments). Primers used for GFP experiment are indicated GFP (for green fluorescent protein experiment). The primers used for cloning possess restriction sites underlined.

A

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PtClot          MTVKLVDATISSFGSVFEKFKA--EAPKNKVNLILFLADNDPSTNLSWCPDCVRAEPVIL 58
AtClot          MTLKKVDANPSTLESSLQELKSD-ETSRSKINFILFLADNDPTTGQSWCPDCVRAEPVIY 59
OsClot          MTVEKVDATVADFDAHFDKLFAAGDDAEGKVKLLLFLADRDASSNQTWCPDCNVAEPVIY 60
                **:: ***  : : : :::: :  :    *::::***** * ::  :*****  *****

PtClot          KKLEALP----DDVALLRAYVGDRPTWRNPQHPWRVDSRFKLKGVPTLISWENDAVKGRL 114
AtClot          KTLEEFP----EEVKLIRAYAGDRPTWRTPAHPWRVDSRFKLTGVPTLVRWDGDSVKGRL 115
OsClot          DRVEAAAKGKEKDVVLLRAYVGDKPTWRDPAHPWRADPRFRLTGVPTLIRWENGAAAARL 120
                  :*        :* *:*** **:**** * **** * **:* *****: *:  :   **

PtClot          EDYEAHLEHKINALVSGN- 132
AtClot          EDHQAHLPHLILPLLAPST 134
OsClot          GDDEAHLADKVDAVVNAAN 139
                 * :***   :  ::
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B

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PtTrx-like1      MEDN--TKKGLDGTGLELPVNL--HGNLKSASSDQSHLQILHDIKSSNTPAVINYGASWC 56
OsTrx-like1      MEEGEAKKTGLEGTGLSLPGSS--HGNLRSAGSDQQLKQMLDSLKSSKSPAVINYGASWC 58
AtTrx-like1      -----MRKQESEGANLEFESKSNDNGNVKIAPNDQSFLTILDDIKSSKSPAVINYGASWC 55
                       *   :*: * :      :**:: *  **    :*  :***::***********

PtTrx-like1      RVCSQILPAFCQLSNNFPKLSFVYADIDECPETTQHIRYTPTFHFYRDGERVDEMFGAGE 116
OsTrx-like1      RVCSQILPPFCRFSNEFKNLTFIYADIDECPETTQNIRYTPTFHFYRDGEKVDEMLGTGE 118
AtTrx-like1      GVCSQILPAFRKLSNSFSKLKFVYADIDECPETTRHIRYTPTFQFYRDGEKVDEMFGAGE 115
                 *******  * ::** * :* *:***********::*******:******:****:*:**

PtTrx-like1      ERLHDRLWLHS 127
OsTrx-like1      ERLHDRLWLHS 129
AtTrx-like1      QRLHDRLWLHS 126
                 :**********
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C

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PtTrx-like2.1      MSVLAANPHVL-YREVQYHNKDQQQQLWSGGGVGSSLLLSQRTSFGCSWFDGR-NKDLCK 58
AtTrx-like2.1      MAALASNPQML-TRQAHGNKKE---QLWRK----ESLNLEKKCGFCVSVYS---NEKLGR 49
OsTrx-like2.1      MALIAPSPRVLRAREAPAAGALQPPAAACSTVAGGGGAAGRPLGMWSGGGGGGGGKGRRR 60
PtTrx-like2.2      MSKILQNPPSLRLLSSNSIPR----DLSILS--IPCQNPSILISKKLS-PGKFILPGK-I 52
PtTrx-like2.3      MSKILHSPPSLRFLSPNSIPRDPSRDLSVLSSTISCPNPAISIFKKLSSPGKFNLPGK-N 59
AtTrx-like2.2      MSEIVNLSSSLRSLNPKISPLVP--PYRQTSSSFSRPRN----FKYHSFTDKICLAAERI 54
                   *: :      *

PtTrx-like2.1      KNSK-------RDLKVAASWPGMTRPTSVEMEPIDDSHHLDKILLQAHELSQPIIIDWMA 111
AtTrx-like2.1      SHME-------KEWRLKAFWSNIAQPTTLEMEPINNVEELDAVLSHARQLSQPIIIEWMA 102
OsTrx-like2.1      ERGD-------GMLRAEAYFWDVSKP--VEMEEIDSMEKLDDALRWSVENKQPIIIDWMA 111
PtTrx-like2.2      HGFEGGNGIFHAWSQEGSLQEVDDSPVSFELEPIYSESQFDRVIAEAQQLVESVIIVWCV 112
PtTrx-like2.3      RDFR-------AWSQEGPLQEVDDSPVSFELEPIYSESQFDRVIAEAQQLEESVIIVWCV 112
AtTrx-like2.2      RAVD-------IQKQDGGLQELDDSPVSVELGPICGESHFDQVMEDAQKLGESVVIVWMA 107
                             :          *   *:  *     :*  :  : :  : ::* *

PtTrx-like2.1      SWCRKCIYLKPKLEKLAAEYDTKIKFYCVDVNKVPQALVKRGNISKMPTIQLWKDGEMKA 171
AtTrx-like2.1      SWCRKCIYLKPKLEKLAAEYNNRAKFYYVDVNKVPQTLVKRGNISKMPTIQLWKEDEMKE 162
OsTrx-like2.1      SWCRKCIYLKPRLEKIAGEFPG-VRFYFVDVNKVPQTVVKRGNITKMPTIQLWKDGEWAA 170
PtTrx-like2.2      VWCRKCIYLKPKLEKLAADYNRRLRFYCVNVNNIPHKLVARAGVTKMPTIQLWKDSKKQA 172
PtTrx-like2.3      VWCRKCIYLKPKLEKLAADYYRRSRFYRVDVNNVPHKLVTRAGVTKMPTIQLWKDSKKQA 172
AtTrx-like2.2      AWCRKCIYLKPKLEKLAAEFYPRLRFYHVDVNAVPYRLVSRAGVTKMPTIQLWRDGQKQA 167
                    **********:***:* ::    :** *:** :*  :* *  ::********:: :

PtTrx-like2.1      EVIGGHKAWLVMEEVREMIQKFV-- 194
AtTrx-like2.1      EVIGGHKGWLVIEEVRELINKFV-- 185
OsTrx-like2.1      EVIGGHKAWLVMDEVREMIQKHK-- 193
PtTrx-like2.2      EVIGGHKAYLVINEVREMIENEGTL 197
PtTrx-like2.3      EVIGGHKAYLVINEVREMIENEDTL 197
AtTrx-like2.2      EVIGGHKAHFVVNEVREMIENDSIT 192
                   *******  :*::****:*::
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D

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PtTrx-lilium1.1       -MTEVLSKTNLFSSGNYQTRQHNTISVFTKSCRLKGFPSRVKPQGLRSQISRSSSCSDFY 59
AtTrx-lilium1.1       -MTEVISKTSLFLGACGNHHRVDDFSFSPVSFGGFGLKKSFSCLKLKSQKPLR---SVFY 56
OsTrx-lilium1.1       -MAEALCSGSVASP-CGEVGVGFAAGLVRGAAAAAALAESVPIGGYSS-------KSTFP 51
OsTrx-lilium1.2       -MAATAAQAVAVKG-SVAVPPCGSRGRRRGAVASVRMAAAAATSALRIGR-----RSPFL 53
AtTrx-lilium1.3       MATDSFIKLNPISFNRARFDLRDFAGISPKSISSLCCISPR----LIS-------CNHFS 49
AtTrx-lilium1.2       MDAISSLGTNCVLSGVSPFSQENQSKSKLSPFMSLDLKEHP----MAS--------ADFT 48
                        :                                                      *

PtTrx-lilium1.1       GKRVVVHGNQSKPRRGYLPQASVVALTGLKLKYAKKWWEKGLQPNMREVTSAQDLVDSLM 119
AtTrx-lilium1.1       GKQIVFGDSQDESFR---RSSAITAQTTLRIGTAQKWWEKGLKDNMREISSAQELVDSLT 113
OsTrx-lilium1.1       SGRVALTERKARPLPR--NLEAAHGQMNLTIGKAMRWWEKCLQPNMREIESAQDLADSLL 109
OsTrx-lilium1.2       GGRLAVGPRRSRPVPR--NLVAPV-QMNLAFAKATKWWEKGLQPNMREVESAQDLVDSLT 110
AtTrx-lilium1.3       PRTLISGENGNILFSKKKIPAFVRCQTSLGIGRNQKWWEKELKPNMKSVTSPQDLVVSLR 109
AtTrx-lilium1.2       NQTLTAFSSSS-------ASPFQAKTSSIGMSRGMRWWEKSTNHNMLEIQSANHLVDSLL 101
                         :                        : :    :****  : **  : * : *  **

PtTrx-lilium1.1       NAGDQLVVVDFFSPGCGGCKALHPKICQLAEMNPDVQFLQVNYEEHKSMCYSLNVHVLPF 179
AtTrx-lilium1.1       NAGDKLVVVDFFSPGCGGCKALHPKICQFAEMNPDVQFLQVNYEEHKSMCYSLGVHVLPF 173
OsTrx-lilium1.1       NAGDKLVVVDFFSPGCGGCRALHPKIAQLAEKNPEVLFLQVNYEKHKSMCYSLHVHVLPF 169
OsTrx-lilium1.2       NAGDNLVIVDFFSPGCGGCRALHPKICQIAEQNPDVLFLQVNYEEHKSMCYSLHVHVLPF 170
AtTrx-lilium1.3       NAGDKLVVVDFFSPSCGGCKALHPKICKIAEKNPEVEFLQVNYEEHRSLCQSLNIHVLPF 169
AtTrx-lilium1.2       NAGDRLVVLDFYSPGCGGCKSLHPKICQLAETNPNVMFLKVNQEELRTMCHGLNVHVLPF 161
                      **** **::**:** ****::***** ::** **:* **:** *: :::*  * :*****

PtTrx-lilium1.1       FRFYRGAHGRLCSFSCTNATIKKFKDALAKHTPERCSLGPTKGLEEKELVALAANKDLSF 239
AtTrx-lilium1.1       FRFYRGSQGRVCSFSCTNATIKKFRDALAKHGPDRCSLGPTKGLEEKELVALAANKELNF 233
OsTrx-lilium1.1       FRFYRGAQGRVSSFSCTNATIKKFKDALAKHGPDRCGLGPAKGLEESELMALAINRDLNF 229
OsTrx-lilium1.2       FRFYRGAQGRLCSFSCTNATIKKFRDALAKHKPDRCSLGPTRGLEESELLALAANNDLQF 230
AtTrx-lilium1.3       FRFYRGSSGRVCSFSCTNATIRKFKEALEKHGREQCSIGETKGLEEKELVAMAANKDLSF 229
AtTrx-lilium1.2       FKFYRGAEGKVCSFSCTIATINKFKKALDKHGSERCSLGDAKGLDEKELAALASVGELKM 221
                      *:****: *:: ***** *** **: ** **  ::* :* ::**:* ** *:*   :* :

PtTrx-lilium1.1       TYTPKPVQPAPVPAEEEVAPTAGPSHSDRGLPLPLPITSSKSAQDSEEKTLVSSGR--- 295
AtTrx-lilium1.1       TYTPK-----PVPVEKEAATPD----SNPSLPVPLPSMSS-----NDEKTLVSAGR--- 275
OsTrx-lilium1.1       TYTPNQ---DLVPIADALLKEAA---APGGPWLPLPATATQLFIQGSENSLLSSGR--- 279
OsTrx-lilium1.2       NYTKKP---ELVPSGECRSCQEL---DCGTTRF-LPRKPCQQV--------------- 266
AtTrx-lilium1.3       DYKPTS-----CGNIQEQKKKE----------IFLPKSPTFNKQKEVEHSLLLVSPAPA 273
AtTrx-lilium1.2       NSLTMH----QASNIGYKTEEQY------------------------QTMVL------ 245
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E

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PtTrx-lilium2.1       MADVVG--LPSFRSLRVPSYLL---ASNNSTSLQPLLSHNQINFSDKRIS---------L 46
PtTrx-lilium2.2       MAVVVGL-LPSFRSLGFPSSLLTSFASSNPISLQPLLSHKHISFSDIRIYPLLYSSAATA 59
AtTrx-lilium2         MAGVVRLTTTSVQAIRVSSSFSSFATALNP--LQPCLPPNSNLNSDKRLRLLSSSPSCSS 58
OsTrx-lilium2         MAEALLP-LPRRLVVTASTPACSSASSSTSPSPHCLLSRANPR---------------P 43
                      **  :         :   :      ::      :  *

PtTrx-lilium2.1       SRFSSS-----------PRDQFLSFKVHATVAET-DQPKWWERNAGPNMIDIHSTDEFLS 94
PtTrx-lilium2.2       SRFSFS-----------RRKQLLSFKVHATVAET-DQPKWWEKNAGPNMIDIHSTEEFLR 107
AtTrx-lilium2         SHYHPSSGLGSHLPLRRPKSQVVRVKVDENVAET-EPPKWWERNA-PNMVDIHSTEEFLS 116
OsTrx-lilium2         PRLAAP-----------SPPRHRRLKAHAAVSDKSEQPKWWEKNAGPNMIDIHSTQEFLD 92
                       :                :    *    *::  : *****:** ***:*****:***

PtTrx-lilium2.1       ALSQAEDRLVIVEFYGTWCASCRALFPKLCRTAEDHPEILFLKVNFDENKPMCKSLNVKV 154
PtTrx-lilium2.2       ALSEAGDRLVIVEFYGTWCASCRALFPKLCRTAEEHPEILFLKVNFNENKPMCRSLNVKV 167
AtTrx-lilium2         ALSGAGERLVIVEFYGTWCASCRALFPKLCKTAVEHPDIVFLKVNFDENKPMCKSLNVRV 176
OsTrx-lilium2         ALRDAGDRLVIVEFYGTWCGSCRALFPRLCRTAVENPDILFLKVNFDENKPMCKRLNVKV 152
                      **  * :************ *******:**:** ::*:*:******:******: ***:*

PtTrx-lilium2.1       LPYFHFYRGAHGQLESFSCSLAKFQKIKDSIEMHNTARCSIGPPKGVGELTLESVSASQD 214
PtTrx-lilium2.2       LPYFHFYRGAHGQLESFSCSLVKFQKIKDAIEMHNTARCSIGPPKAVGELTLESISAPQD 227
AtTrx-lilium2         LPFFHFYRGADGQLESFSCSLAKFQKIKDAIQLHNTDRCSLGPAKVPEGLTLA------- 229
OsTrx-lilium2         LPYFHFYRGADGQLEAFSCSLAKFQKLKDAIAVHNTARCSIGPPVGVGDVLDS----PEE 208
                      **:******* ****:***** ****:**:* :*** ***:**      :

PtTrx-lilium2.1       KPVGST-- 220
PtTrx-lilium2.2       KTAGST-- 233
AtTrx-lilium2         KPAASS-- 235
OsTrx-lilium2         KPAEASPR 216
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F

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PtTrx-lilium3       MEKARTFLLQLQQHIDCGGSLNVVMQKQNILYSKASFG-FGRNPDRQLDCRIPCVAPSML 59
AtTrx-lilium3       ----MTPLLWF--------CFKILIFDSNLQISHCSYHGYSGLTSR---GGINTVENHRW 45
OsTrx-lilium3       ----------------------MITASLLPLPATSSSSGRRSLP---PPTTTFPRPPP 33
                                          :    :     :

PtTrx-lilium3       PCRGNEKSCLMKAKFPSITKYAGLNFPKNNVASRPGRIKAVVDENPGELSDEDDDLCPVD 119
AtTrx-lilium3       VWHNNG----VRLSFP--RAESSINITMGCTLQR-GIAKSLSQENLVELSDENDDLCPVE 98
OsTrx-lilium3       PLRRHR-------HLSSSSSSASSTESDGGGGSTNGSLPGLP---PVVVEEEEEEFCPVE 83
                      : :         :      :             *    :       : :*::::***:

PtTrx-lilium3       CVREFKTDEEFLRILEKAKETDSLVVVDFYRTSCGSCKYIEQGFAKLCKGSGDQEAAVTF 179
AtTrx-lilium3       CVTEFKTDDELLSVLEKSKETNSLVVVDFYRTACGSCKYIEQGFSKLCKQSGDQEAPVIF 158
OsTrx-lilium3       CVTEFKTEEELARVLERAKATGALVVVDFFRPSCGSCKYIEQGFMKLCKGSGDHGSSVVF 143
                    ** ****::*:  :**::* * :******:* :*********** **** ***: : * *

PtTrx-lilium3       LKHNVIDEYDEQSEVAERLRIKTVPLFHFYKKGVLVESFPTRDKERILGAILKYTSPAAQ 239
AtTrx-lilium3       LKHNVVDEYDEQSEVAERLRIKAVPLFHFYKNGVLLESFATRDKERIDAAILKYTSSES- 217
OsTrx-lilium3       LKHNVIDEYDEQSEVADRLRIKVVPLFHFYKNGVLLEAFATRDKERIIAAIQKYTAPSSP 203
                    *****:**********:***** ********:***:*:* *******  ** ***:  :

PtTrx-lilium3       DT--------- 241
AtTrx-lilium3       ----------
OsTrx-lilium3       PAESEEPSQEG 214
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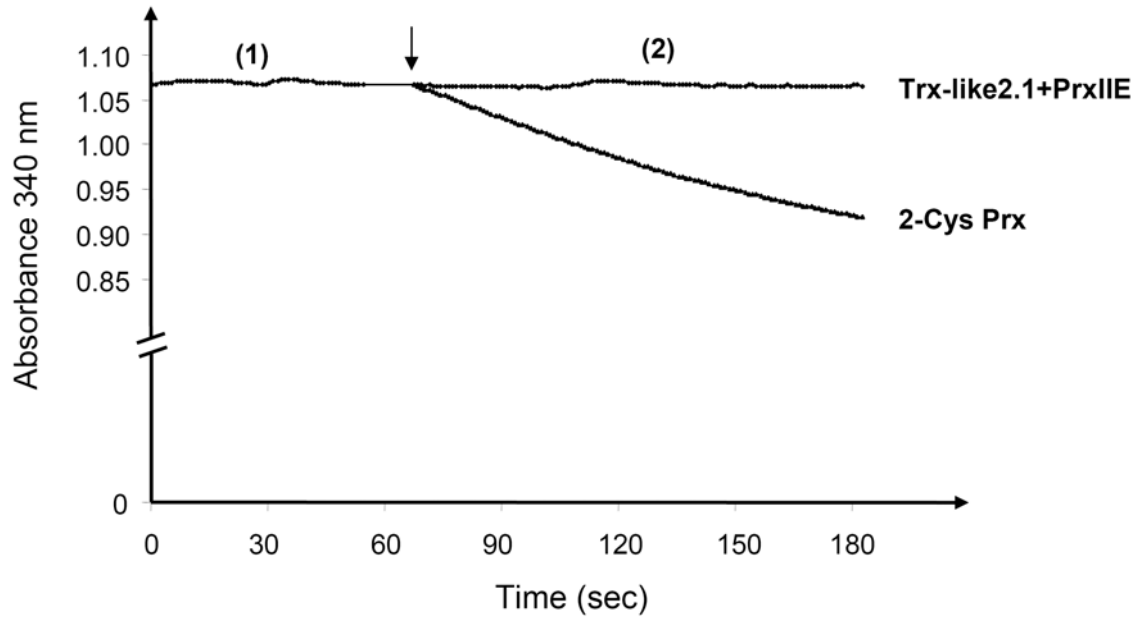
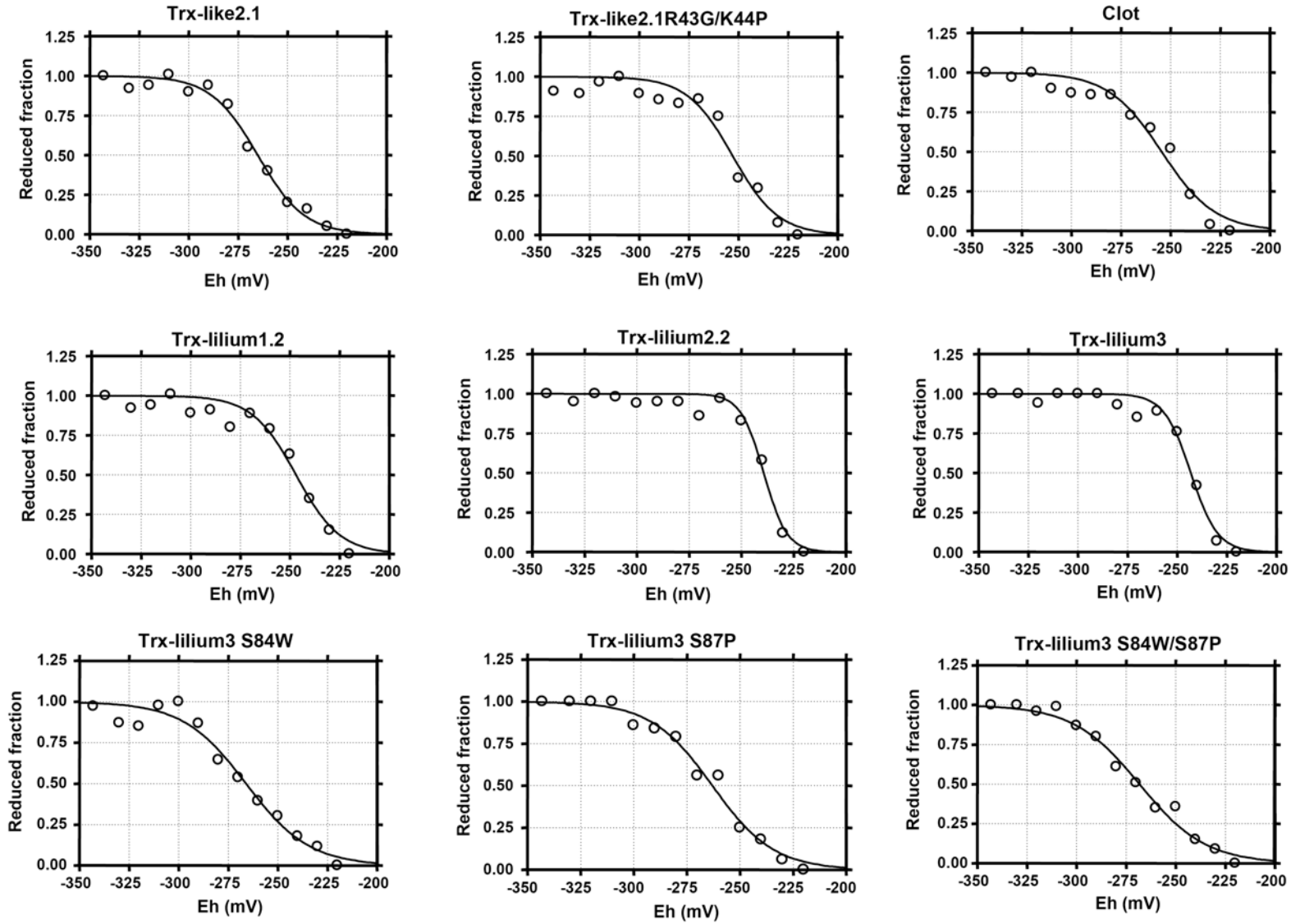
Supplemental Figure 1: Amino acid sequence comparison of atypical Trx families.

The alignments of Clot (A), Trx-like1 (B), Trx-like2 (C), Trx-lilium1 (D), Trx-lilium2 (E) and Trx-lilium3 (F) protein families were performed with ClustalW from sequences retrieved in phytozome (http://www.phytozome.net/) for *Populus trichocarpa* (Pt), *Arabidopsis thaliana* (At) and *Oryza sativa* (Os). The strictly conserved amino acids are marked by an asterisk while other conservative amino acid changes are indicated by a colon. Accession numbers are as follows: PtClot (POPTR_0001s23270), AtClot (At5g42850), OsClot (Os06g21550), PtTrx-like1 (POPTR_0006s12500), OsTrx-like1 (Os04g47260), AtTrx-like1 (At3g53220), PtTrx-like2.1 (POPTR_0016s05950), PtTrx-like2.2 (POPTR_0010s23260), PtTrx-like2.3 (gw1.VIII.1056.1), AtTrx-like2.1 (At5g06690), AtTrx-like2.2 (At5g04260), OsTrx-like2.1 (Os02g53400), PtTrx-lilium1.2 (POPTR_0013s05790), PtTrx-lilium2.1 (POPTR_0006s15520), PtTrx-lilium1.1 (POPTR_0019s04750), PtTrx-lilium2.2 (POPTR_0018s07010), PtTrx-lilium3 (POPTR_0014s02920), AtTrx-lilium1.1 (At1g08570), AtTrx-lilium1.2 (At5g61440), AtTrx-lilium1.3 (At2g33270), AtTrx-lilium2 (At4g29670), AtTrx-lilium3 (At1g07700), OsTrx-lilium1.1 (Os07g48510), OsTrx-lilium1.2 (Os03g21000), OsTrx-lilium2 (Os05g11090), OsTrx-lilium3 (Os02g35900). Note that for this alignment the poplar sequences used are those from the *Populus trichocarpa* sequenced genome, and that a few variations can exist between poplar species.



Supplemental Figure 2. Assessment of poplar Trx-like2.1 reduction by Arabidopsis NTRc.
The reduction of Trx-like2.1 by AtNTRc was evaluated using a coupled assay linked to the spectrophotometric detection of NADPH oxidation at 340 nm. NADPH, 1.5 µM NTRc and 100 µM H2O2 were initially incubated for 1 min (1). As indicated by the arrow, the *A. thaliana* 2-Cys Prx (2 µM) used as a control, or a mixture of Trx-like2.1 (10 µM) and PrxIIE (2 µM) have then been added to the cuvette (2). The consumption of NADPH comcomitant to the reduction of hydrogen peroxide was followed as a function of time.

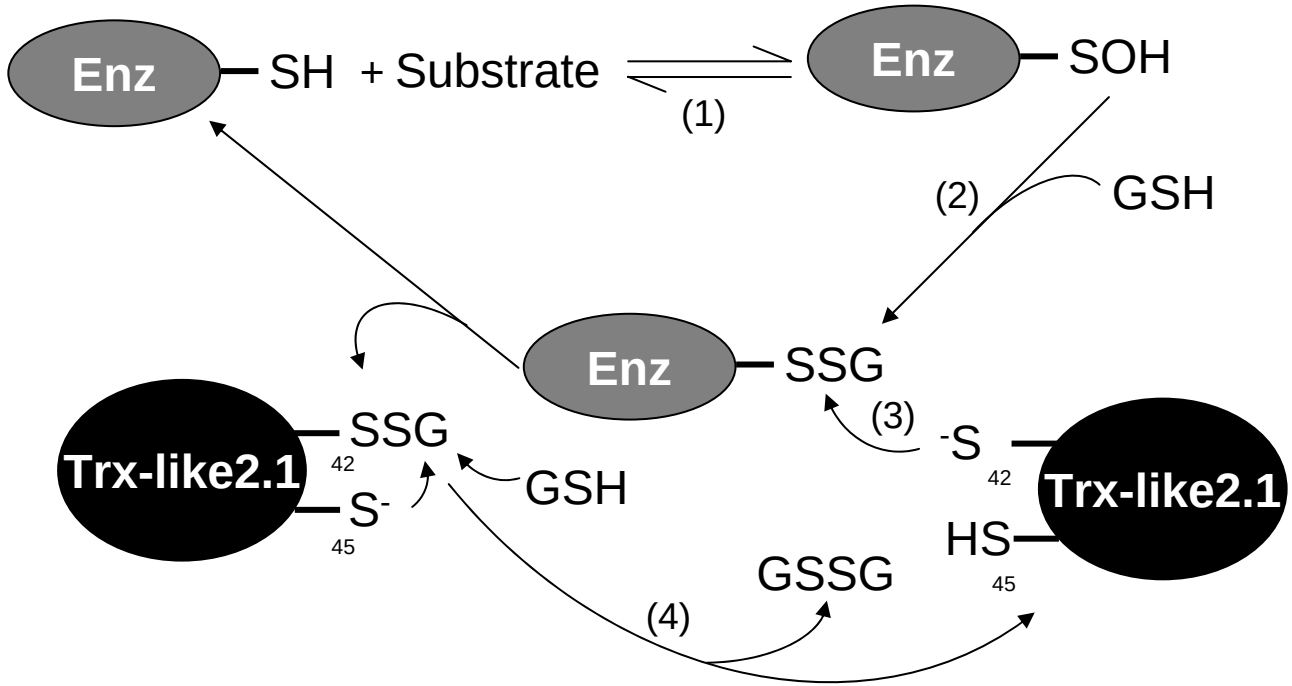
Suppl Figure 2



Supplemental Figure 3. Redox midpoint potentials of Trxs-like and -lilium.

The titrations were carried out using a total DTT concentration of 2 mM in the redox buffer and with a redox equilibration time of 2 h. Free protein thiols are labeled by mBBr. Values are the means ± S.D. of three independent experiments.

Suppl Figure 3



Supplemental Figure 4. Proposed mechanism for the glutathione- and Trx-like2.1-dependent regeneration of target proteins using a single catalytic cysteine.

The first step consists of substrate reduction with the concomitant release of 1 mol of product and the formation of a stable sulfenic acid intermediate on the catalytic Cys (1). The sulfenic acid is then attacked by GSH leading to the release of one molecule of water and to the formation of a glutathione adduct (2), which is subsequently attacked by the catalytic cysteine of Trx-like2.1 (3). The glutathionylated form of Trx-like2.1 is likely reduced by another GSH molecule (4).

Suppl Figure 4