Figure S1. Gene models and expression. (A) The gene models of the SPT4 and SPT5 genes are adapted from the Arabidopsis database (http://www.arabidopsis.org/). Coding sequences are indicated by light blue boxes, UTRs in dark blue, while introns are depicted as lines. The positions of T-DNA insertions are also indicated. (B) The transcript levels of the four genes in various tissues are displayed using the AtGenExpress tool (http://jsp.weigelworld.org/expviz/expviz.jsp) based on a large set of public microarray transcript profiling data.

```
                                    C  C                C  C
ScSPT4     --------------------------M-SSERACMLCGIVQTTNEFNRDGCPNCQGIF
HsSPT4     -----------------MALETVPKDL-RHLRACLLCSLVKTIDQFEYDGCDNCDAYL
DmSPT4     -----------------MAFDAIPKDL-RGLRACLVCSLVKSFDQFETDGCENCEEFL
AtSPT4-2   ----------------MGSAPAQIPTSFGHELRACLRCRLVKTYDQFRDAGCENCP-FF
AtSPT4-1   ----------------MGEAPAQIPTSFGHELRACLRCRLVKTYDQFRDSGCENCP-FF
Pt-SPT4    ----------------MGSAAAQIPTSFGHELRACLRCRLVKTYDQFRESGCENCP-FF
VvSPT4     -----------------MSNAAQIPTSFGHELRACLRCRLVKTYDQFRESGCENCP-FF
OsSPT4     MRGGGGGGGGDGMMDDGP--KYAQIPTSFGHELRACLRCRLVKTYDQFMEQGCENCP-FL
ZmSPT4     MRGGG----GGGMMDDEERVGHAEIPTSFGPELRACLRCRLVKTYDQFRENGCENCP-FL
                                     ***: * :*:: ::*    ** **      :

                                    ↓
ScSPT4     EEAGV--STMECTSPSFEGLVGMCKPTKSWVAKWLSVDHSIAGMYAIKVDGRLPAEVVEL
HsSPT4     QMKGNREMVYDCTSSSFDGIIAMMSPEDSWVSKWQRVSNFKPGVYAVSVTGRLPQGIVRE
DmSPT4     RMKNNKDNVYDHTSNNFDGIIALTTPTDSWVAKWQRLSRFTRGIYAISVSGTLPQSTLRD
AtSPT4-2   KMEEDHERIVEVTTPNFNGIISVMDPSRSWAARWLRIGKFAPGCYTLAVSEPLPEEMQHL
AtSPT4-1   KIEDDHERIVDVTTPNFNGIISMMDPRRSWAARWLRIGKFAPGCYTLAVSEALPEEMQFI
Pt-SPT4    KMDEDHERVVDCTTPNFTGIISVMDPSRSWAARWLRIGRFVPGCYTLAVSEALPEDLQNL
VvSPT4     KMDEDHERVVDCTTPNFNGIISMMDPSRSWAARWLRIGRFVPGCYTLAVSEALPEDLQNL
OsSPT4     DMERDHDNVVNCTTPNFTGIISVMDPGRSWAARWLRIGKFIPGCYTLAVAEELPEEYQSV
ZmSPT4     EMDREHDNVVNCTTPNFTGIISLMDPSRSWAARWLRIGRFIPGCYTLAVSEELPEEYQGI
            : *: .* *::.:   *  **.::*  :  .   * *:: *    **

ScSPT4     LP----HYKPRDGSQVE
HsSPT4     LKSRGVAYKSRDTAIKT
DmSPT4     MKNRGIVYKSRDRSQR-
AtSPT4-2   CQEERVQYVLPKRM---
AtSPT4-1   CQQARVQYVPPKRI---
Pt-SPT4    CEDERVPYIPPKRV---
VvSPT4     CEEERVQYVPPKR----
OsSPT4     CQDNNVQYFPPKRV---
ZmSPT4     CQDNNVQYVPPKRV---
                   *     .
```
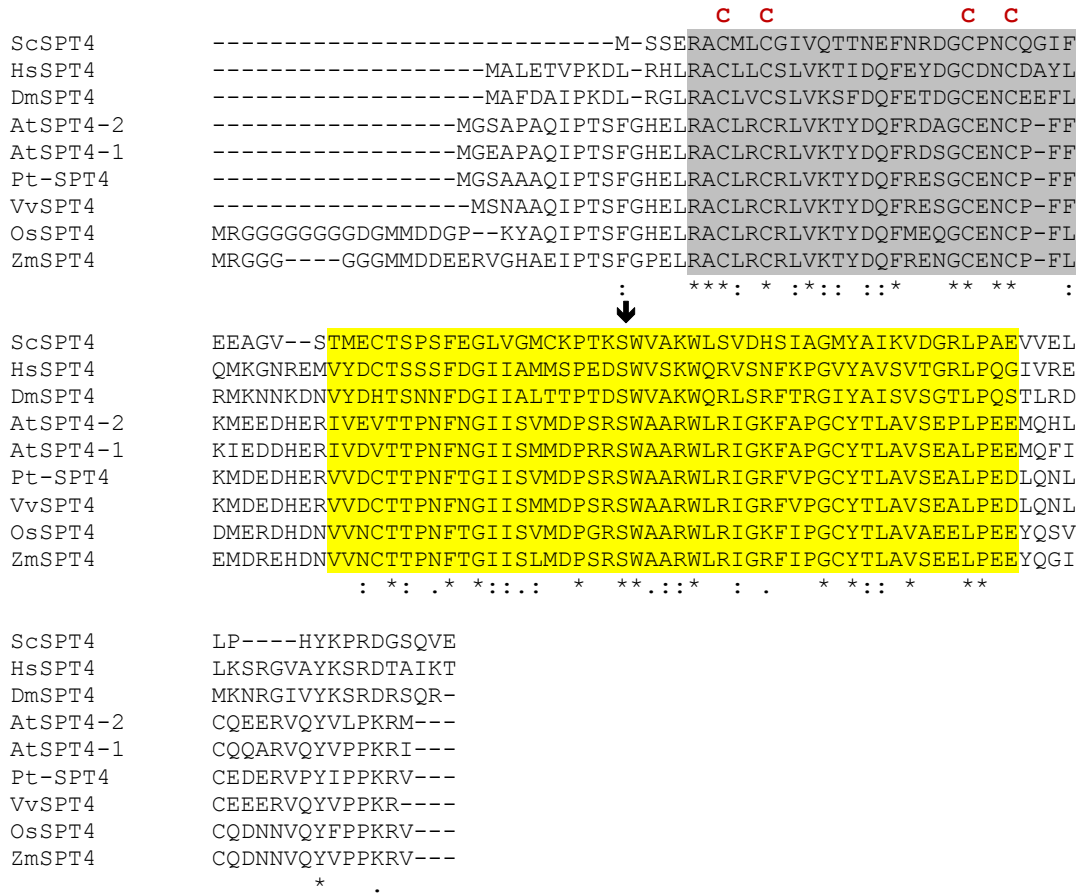
Figure S2. Amino acid sequence alignment of SPT4 of different species. The alignment was generated using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/) and the SPT4 amino acid sequences of *Sacharomyces cerevisiae* (Sc), *Homo sapiens* (Hs), *Drosophila melanogaster* (Dm), the dicot species *Arabidopsis thaliana* (At), *Populus trichocarpa* (Pt) , *Vitis vinifera* (Vv) and the moncot species *Oryza sativa* (Os) and *Zea mays* (Zm). The Zinc-binding motif is highlighted in grey and the NGN-binding domain mediating the interaction with SPT5 in yellow. The four Cys residues forming the Zinc finger are depicted in red on top of the sequences, and the Ser residue critical for SPT5-interaction is indicated by an arrow (9). Asterisks below the sequences indicate invariant residues, while (:) indicate residues that are highly conserved. When compared to their orthologs from other organisms, for instance, SPT4-2 shares 27.4%, 35.8% and 67.2% amino acid sequence identity with its yeast, human and rice relatives, respectively.

```
ScSPT5      MSDNSDTNVSMQDHDQQFADPVVVPQSTDTKDENTSDKDTVDSGNVTTTESTERAESTSN
HsSPT5      MSDSEDSN----------------------------------------------------
DmSPT5      MSDSEVSN----------------------------------------------------
AtSPT5-1    MSQYS-------D-----------------------------------------------
AtSPT5-2    MPRSRDEDDELDGDY--------------------------------------------E
PtSPT5      MARRRDEDDDLEDEE--------------------------------------------Y
VvSPT5      MPRRRHDDD---DDD--------------------------------------------L
OsSPT5      MSRGSREEED----------------------------------------------EEEVY
ZmSPT5      MARRGHDDDDDEVDEEE---------------------------------------EEDAY
            *

ScSPT5      IPPLDGEEKEAKSEPQQPEDNAETAATEQVSSSNGPATDDAQATLNTDSSEANEIVKKEE
HsSPT5      ---FSEEED---------------------------------------------SERSSD
DmSPT5      ---MSDSGSEDGSI--SNK-SQRSARSKSRSRSRSGSRGS--RSVSRSRSR-SQSGHSRS
AtSPT5-1    ------------------------------------------------------------
AtSPT5-2    ALDLEEEEEEDEEE--EEE-RGR----G-----------------------------GG
PtSPT5      EEQEEQLMDEEEEY--EEE-EEE----D-----------------------------RG
VvSPT5      EPEEDDVLDDDEDY--EDE-DVG----------------------------------V
OsSPT5      DS----EEEEEEG--EVE-ERG----GKR--SRGG---------------------G
ZmSPT5      DLDDDEDEDEEDDY--EEE-TRR----GKA--SRGG-GG---------------AKSG


ScSPT5      GSDERKRPREEDTKNSDGDTKDEGDNKDEDDDEDDDDDDDDEDDDDE-------------
HsSPT5      GEEA---EVDEERRSAA------GSEKEEEPEDE-EEEEEEEEYDEEEE-----------
DmSPT5      GSES---PQRRDNRGKS------DESGEEEEPP-GEDIDSEEYDEEEN-----------
AtSPT5-1    --------------------DDYSHEDDSEM-EDEDEEDEYEPRSSRKGRSGKKRGR
AtSPT5-2    GSR-----RKRGRSNFI------DDYAEEDSQEE-D--DDDEDYGSS-----------R
PtSPT5      AAI-----KKRRRSDFI------DDIAEEEDEEE-DDDDDDEDYGGG------------G
VvSPT5      GSS-----RKRSRSEFI------DDVAEEDDDED--DDDDDEDFGGS-----------R
OsSPT5      GGG-----KWSGVESFI------DDAASEDEDEE-EEEDDDEDYVGGG-----------
ZmSPT5      GGR-----KRSREDNFI------DDSAIEDEDDE-D-----DDGGGR-PR----------
                              .    *:  .           ::

ScSPT5      -------APTKRRRQERNRFLDIEAEVSDDEDEDEDEEDSELVRE---------GFITH-
HsSPT5      ----EEDDDRPPKKPRHGGFILDEADVDDEYEDEDQWE--DGAEDILEKEEIEASNIDN-
DmSPT5      ----DDHPRKKKKKERFGGFIIDEAEVDDEVDEDDEWE--EGANEIGIVG----NEIDE-
AtSPT5-1    SNSDSDGRRGSKKKSSGSAFIDWEVEVDDDVEDDDDDVDVEDGKQQLKFGDFSLCFIVS-
AtSPT5-2    GGKGA---ASKRKKPSASIFLDREAHQVDDEDEEEE----DEAED---------DFIVD-
PtSPT5      GGGGGGGGRKQKGKKRRGSEFFDDIAQVASDD-DEEE----EDAED---------DFIVDD
VvSPT5      RG------SHRAKRRSGSEFLDLEAAVDSDE-EEEE----EDGED---------DFIVD-
OsSPT5      -----GGR--ARKRKRASILIDDMAQVDDEEEEEED-------------GEFEDGFID-D
ZmSPT5      ----------KKGGGGVRGFFDEEAQVDEDEEEEDE----GEGED---------DFIN-D
                      ::    .    .:  ::::                          *

ScSPT5      -GDDEDDEASAPGARRDDRLHRQLDQDLNKTSEEDAQRLAKELRERYGRSSSKQYRAA--
HsSPT5      VV-L--DEDRSGA---------RRLQN-LWR-DQREEELGEYYMKKYAKSSVGETVYG-G
DmSPT5      LGPT--ARDIEIR---------RRGTN-LWD-TQKEDEIEEYLRKKYADESIAKRHFGDG
AtSPT5-1    GEADLPNEDSDHRR----QYYQRGFHP-HEE---DVDELEKRTLERLSTKYA---KDD-Y
AtSPT5-2    NGTDLPDERGDR------RYE-RRFLP-RDENDEDVEDLERRIQERFSSRH----HEE-Y
PtSPT5      HGADLPDEASGR------RMH-RPLLS-REDDQEDVEALERSIQARYAKSM----HSE-Y
VvSPT5      AGAELPDEDDGQ------RMRRRPLLP-QEDEQEDFEALERKIQERYGKSS----HAE-Y
OsSPT5      TRADDPDQDVGRSS----R---RHPSS-MLDEEEDVDALVKLIHDRYIIPSS---HFV-D
ZmSPT5      AGADLPDEDVVRGS----R---RHSIP-MRDEEEDIDEMERQVRERYARST----HIE-Y
                  .                :              : :.    :

ScSPT5      --AQDGYVPQRFLLPSVDTATIWGVRCRPGKEKELIRKLLKKKFNLDRAMGKKKLKILSI
HsSPT5      SDELSDDITQQQLLPGVKDPNLWTVKCKIGEERATAISLMRKFIA--YQFTDTPLQIKSV
DmSPT5      GEEMSDEITQQTLLPGIKDPNLWMVKCRIGEEKATALLLMRKYLT--YLNTDDPLQIKSI
AtSPT5-1    ELDDVNDVDQQALLPSVRDPKLWLVKCAIGREREVAVCLMQKIVD-----RGSEFKIRSA
AtSPT5-2    D-EEATEVEQQALLPSVRDPKLWMVKCAIGREREVAVCLMQKFID-----RGADLQIRSV
PtSPT5      D-EETTEVEQQALLPSVRDPKLWMVKCAIGRERETAVCLMQKYID-----KGSELQIRSV
VvSPT5      D-EETTEVEQQALLPSVRDPKLWMVKCAIGHEREAAVCLMQKSID-----KGPEVQIRSA
OsSPT5      DDDGVTEVEQQALLPSVKDPKLWMVKCAIGHERETAICLMQKSID-----T-PDLQIKSV
ZmSPT5      G-EEAAEVEQQALLPSVKDPKLWMVKCAIGHERETAICLMQKFID-----R-SDLQIKSV
                 : *: ***.:  .:* *:* *.*:     *::* .         .:* *
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                              ↓
ScSPT5    FQRDNYTGRIYIEAPKQSVIEKFCNGVPDIYI--SQKLLIPVQELPLLLKPNKSDDVALE
HsSPT5    VAPEHVKGYIYVEAYKQTHVKQAIEGVGNLRLGYWNQQMVPIKEMTDVLKVV-KEVANLK
DmSPT5    IAPEGVKGYIYLEAYKQTHVKTCIDNVGNLRMGKWKQEMVPIKEMTDVLKVV-KEQVGLK
AtSPT5-1  IALDHLQNYVYIEADMEAHVKEAIKGMRNIYA-NQKILLVPIKEMTAVLSVE-SKAIDLS
AtSPT5-2  VALDHLKNFIYVEADKEAHVKEAIKGMRNIYA-NQKILLVPIRMTDVLSVE-SKAIDLS
PtSPT5    VALDHLKNYIYIEADKEAHVREACKGLRNIFG--QKIMLVPIREMTDVLSVE-SKVIDLS
VvSPT5    IALDHLKNYIYIEADKEAHVKEACKGLRNIYA--QKVMLVPIREMTDVLSVE-SKAVDLS
OsSPT5    LALDHLKNYIYVEAYKEAHVKEACKGVRNIFA-SRKVTLVPIREVADVLSVQ-SKSTDIS
ZmSPT5    VALDHLKNYIYVEAEKEAHVKEACKGLRNIYA-SAKITLVPIKEMADVLSVE-SKSVDLS
          .   :      :*:**  :: :.   . : ::     :  ::*::*: :*.  .. :.

ScSPT5    EGSYVRIKRGIYKGDLAMVDQISENNLEVMLKIVPRLDYGKFDEIDPTTQ-QRKSRRPTF
HsSPT5    PKSWVRLKRGIYKDDIAQVDYVEPSQNTISLKMIPRIDYDRIKARMSLKD---WFAKRKK
DmSPT5    VKQWVRLKRGLYKDDIAQVDYVDLAQNQVHLKLLPRIDYTRMRGALRTTATESDDSKRKK
AtSPT5-1  RDSWVRMKLGIYKGDLAQVDVDNVRKRVTVKLIPRIDLQALANKLEGT----ENVK-KK
AtSPT5-2  RDTWVRMKIGTYKGDLAKVVDVDNVRQRVTVKLIPRIDLQALASKLDGR----EVSK-KK
PtSPT5    RDTWVRMKIGTYKGDLAKVVDVDNVRQRVTVKLIPRIDLQALANKLEGR----EAPK-KK
VvSPT5    RNTWVRMKIGTYKGDLAKVVDVDNVRQRVTVQLIPRIDLQALANKLEGR----EVVT-KK
OsSPT5    INTWVRMKLGAYKGDLAKVVDVDDVHQKVTVKLIPRIDLQALANKFDGL----KVVKEKK
ZmSPT5    RDSWVRMKLGIYKGDLAKVVDVDNVRQRVDVKLIPRIDLQALASKLEGR----DIVK-KK
           :**:* * ** *:* *  :.  . : :::::**:*    :           .

ScSPT5    AHRAPPQLFNPTMALRLDQANLYKRD----DRHFTYKNEDYIDGYLYKSFRIQHVETKNI
HsSPT5    FKRPPQRLFDAEKIRSLGGDV-----ASDGDFLIFEGNRYSRKGFLFKSFAMSAVITEGV
DmSPT5    KRRPAAKPFDPEAVRAIGGEV-----HSDGDFLLFEGNRYSRKGFLYKNFTMSAILSDGV
AtSPT5-1  AFAPPPRFMNIDEARELHIRVEHRRDPMTGDYFENIGGMLFKDGFLYKKVSTKSIAAQNV
AtSPT5-2  AFVPPPRFMNIDEARELHIRVERRRDHMTGDYFENIGGMLFKDGFHYKQVSLKSITVQNV
PtSPT5    AFVPPPRFMNVDEARELHIRVERRRDPMTGDYFENIGGMLFKDGFLYKTVSMKSISAQNI
VvSPT5    AFKPPPRFMNVEEAREMHIRVERRRDPMTGDYFENIGGMMFKDGFLYKTVSMKSISVQNI
OsSPT5    SFVPPPKLFSANEAR----------NRDSGEYYEMVDGLKFKDGFLHKTFSIKSISAHNI
ZmSPT5    AFVPPPRFFNIDEAREMHIRVERRRDKESGEYFEWVDNLKFKDGFLYKSVSTKSIHKSNI
           : :.                :          : .*: .*  . .:   :

ScSPT5    QPTVEELARFGSKEGAVDLTSVSQSIKKAQAAKVTFQPGDRIEVLNGEQRGSKGIVTRTT
HsSPT5    KPTLSELEKFEDQPEGIDLEVVTEST-GK-EREHNFQPGDNVEVCEGELINLQGKILSVD
DmSPT5    KPTLAELERFEESPEEVNLEIMGTVKDDP-TMAHSFSMGDNVEVCVGDLENLQAKIVAID
AtSPT5-1  TPTFDELERFKRPNENGEIDFVDESTLFANRKKGHFMKGDAVIVIKGDLKNLKGWIEKVD
AtSPT5-2  TPTFDELEKFNKPSENGEGDFGGLSTLFANRKKGHFMKGDAVIVIKGDLKNLKGWVEKVD
PtSPT5    KPSFDELEKFRSPGENGDGDVASLSTLFANRKKGHFMKGDAVIVVKGDLKSLKGWVEKVD
VvSPT5    QPTFDELEKFRTPGETEDGDMASLSTLFANRKKGHFMKGDAVIIVKGDLKNLKGWVEKVE
OsSPT5    QPSFDELEKFREPDNDINEDAASLSTLFTNRKKGHFMKGDSVIVIKGDLKNLEGYVEKAE
ZmSPT5    QPTFDELEKFKKPGDDMNGDMASLSTLFANRKKGHFMKGDAVIVIKGDLKNLEGWVEKVE
          *:. ** :*           :             *  ** : : *:    :. :

ScSPT5    KDIATI--KLNGFTTPLEFPISTLRKIFEPGDHVTVINGEHQGDAGLVLMVEQGQVTFMS
HsSPT5    GNKITIMPKHEDLKDMLEFPAQELRKYFKMGDHVKVIAGRFEGDTGLIVRVEENFVILFS
DmSPT5    GTMITVMPKHQDLKDPLIFKASELRKYFKTGDHARVLAGRYEGETGLIIRVEPTRVVLVS
AtSPT5-1  EENVLIRSEMKDLPNPIAVNGRELCKYFEPGNFVKVVSGIHEGGTGMIVKVDQHMLIILS
AtSPT5-2  EENVLIRSEVKGLPDPLAVNERELCKYFEPGNHVKVVSGTHEGATGMVVKVDQHVLIILS
PtSPT5    EENVHIRPEMKGLPKTLAVNEKELCKYFEPGNHVKVVSGTHEGVTGMVVKVEQ-------
VvSPT5    EENVHIRPEMKGLPKTLAVNEKELCKYFEPGNHVKVVSGTQEGATGMVVKVEGHVLIILS
OsSPT5    DATVHIRSKLPGLLNTLVFNEGDLCKCFNPGDHVKVVSGVQEGATGLVVKVEGHVLIILS
ZmSPT5    DETVHIRPKISDLPKTLAFNEKELCKYFKPGDHVKVISGVQEGATGMVVKVEGHVLIILS
          :  :    :   : .     * * *: *:.. *: *   :* :*::: *:

ScSPT5    TQTSREVTITANNLSKSIDTTA---TSSEYALHDIVELSAKNVACIIQAGHDIFKVIDET
HsSPT5    DLTMHELKVLPRDLQLCSETASGVDVGGQHEWGELVQLDPQTVGVIVRLERETFQVLNMY
DmSPT5    DLTNHELEVLPRDLQLCSDVATGVDCLGQFQWGDMVQLDSQNVGVIVRLERENFHVLGMN
AtSPT5-1  DTTKEHICVFADHVAKSAEVTKGVTKIGDYELHDLVILSDFSFGVILKLDSEAIQILKGV
AtSPT5-2  DTTKEHVRVFADHVVESSEVTTGVTKIGDYELHDLVLLDNLSFGVIIRLENEAFQVLKGV
PtSPT5    -----HIRVFADDVVESSEVTTGVTKIGDYELHDLVLLDNMSFGLIIRVESEAFQVLKGV
VvSPT5    DTTKEHLRVFADDVVESSEVTSGVTRIGDYELHDLVLLDNLSFGVIIRVESEAFQVLKGV
OsSPT5    DTTKEHIRVFADHVVESSEVTTGLTRIGDYELHDLVLLGWKKKHFRQENLYRTFHILKGE
ZmSPT5    DTTKEHIRVFADHVVESSEITTGITRIGDYELHDLVLLDNLSFGVIIRVEAEAFQVLKGV
          .: :   .:  . : :      .:.  ::* *  .      .       ::::
```

```
ScSPT5     GKVSTITKGSILSKINTARARVSSVDANGNEIKIGDT--IVEKVGSRREGQVLYIQTQQI
HsSPT5     GKVVTVRHQAV--TRKKDNRFAVALDSEQNNIHVKDIVKVIDGPHSGREGEIRHLFRSFA
DmSPT5     GKCIECKPTAL--HKRKENRHTVALDADQNQIRRRDVVKVMEGPHAGRSGEIKHLYRSLA
AtSPT5-1   PDSSEVSIVKASEIKYKIWKKINVQDRYKNVVAVKDVVRVIEGPSKGKQGPVVQIYKGVL
AtSPT5-2   PDRPEVALVKLREIKCKLEKKINVQDRYKNVIAVKDDVRVIEGPSKGKQGPVKHIYKGVL
PtSPT5     TERAEVALVRLREIKCKIEKKTNVQDRYKNTVSVKDVVRIIDGPCKGKQGPVEHIYRGVL
VvSPT5     PDRPEVVLVKLREIKFKIDKRVNVQDRFKNTVSVKDVVRILDGPCKGKQGPVEHIYKGVL
OsSPT5     PDKPELVLVKLREIKSKIYRRTSAKDRSSNIVSTKDVVRVIEGACKVESKGLWNIYTEEY
ZmSPT5     PDRPEVVLVKLREIKSKIERRSSAKDRSNNIISAKDVVRVVEGACKGKQGPVEHIHKGML
              .           .       *    * :    *     :::      ..  :  :

ScSPT5     FVVSKKIVENAGVFVVNPSNVEAVASKDNM-LSNKM--DLSKMNPEIISKMGPPSSKTFQ
HsSPT5     FLHCKKLVENGGMFVCKTRHLVLAGGSKPRDVTNFTVGGFAPM-SPRISSPMHPSAGGQR
DmSPT5     FLHCRMYTENGGIFVCKTRHLQLAGGSKTTVSNAGIVGGLGFM-SPRIQSPMHPSGGR--
AtSPT5-1   FIHDRHNLEHTGFICTRCSSCVLAGG----------------NFKTPALVPPSPRRFQ
AtSPT5-2   FIYDRHHLEHAGFICAKCTSCIVVGGSRSGANRNGGDS-LSRYGNFKAPAPVPSSPGRFQ
PtSPT5     FIYDRHHLEHAGYICAKSHSCIVIGGSRSNGDRN-GDS-YSRLGSFKT-PRVPPSPRRFP
VvSPT5     FIYDRHHLEHAGFICAKSHSCVVVGGSRSNADRS-GDS-FSRFANLRTPPRVPESPRRFP
OsSPT5     FLFMIVTTLNIQALSVQAHNH-----ASLLGDQLGMGTVDPRFGAFRSSARILQSPGRLP
ZmSPT5     FIYDRHHLEHAGFICAKAQSCLLVGGSTGGRRGNGMDTADARLDALRSSASILQSPGRLP
           *:        .   : .                                         *

ScSPT5     QP----IQ-----------SRGGREVALGKTVRIRSAGYKGQLGIVKDVNGDKATVELHS
HsSPT5     GGFGSPGGGSGGMSRG---RGRRDNELIGQTVRISQGPYKGYIGVVKDATESTARVELHS
DmSPT5     ---GARGGARGGRGGF---RVTRDREILGKTIKISGGPYKGAVGIVKDATESTARVELHT
AtSPT5-1   RADMGYNPGAGGRHQGG-RGRRGDDHLVGTYVKIRLGPFKGYSGRLVEVKDKLVRVELEA
AtSPT5-2   RGRGGGYNNSGGRHGGG-RGR-GDDSLLGTTVKIRLGPFKGYRGPVVEVKGNSVRVELEM
PtSPT5     RG--GPPFDSGGRNRGG-RG--GHDALVGTTIKVRQGPFKGYRGRVVDIKGQFVRVELES
VvSPT5     RG--GRPMDSGGRHRGG-R---GHDSLIGSTIKIRQGPFKGYRGRVVDVNGQSVRVELES
OsSPT5     PK--APHTNYGRRFGGRDHGGKHDTLVNRCIKIKSGPYKGYRGRVKEMTGALVRVELDS
ZmSPT5     PR--GPNMNYGGRFGGG-RGGRGYDALVGKCIKIKSGPYKGYRGRVKEVTGALVRVELDS
                             :   :::  . :**  *  : :  .  . ***.

ScSPT5     KNKHIT-------IDKHKLTYYNREGGEG--ITYDELVNRRGRVPQ-ARMGPSYVSAPRN
HsSPT5     TCQTIS-------VDRQRLTTVGSRRPGGMTSTYGRTP-------MYGSQTPMYG-----
DmSPT5     SCQTIS-------VDRNHIAIVGVTGKEGSVSTYGRTPAR---TPGYGAQTPSYT-----
AtSPT5-1   KIVTVE---------RKAISDM--------TDNVVAT--------------PQYN-----
AtSPT5-2   KIVT---------VDRGAISDNV-A-----TTPFRDT--------------SRYS-----
PtSPT5     QMKVVTGKYSSMSVDRSHISDNVVV-----STPYRDA-------------PRYG-----
VvSPT5     QMKVVT-------VDRNQISDNVAV-----ATPYRDA-------------PRYG-----
OsSPT5     LMKVVA-------VKREDIADTATV-----ATPFG-E-------------SHNS-----
ZmSPT5     LMKIVT-------VKRDDIADTPTV-----ATPFR-E-------------PRYS-----
                         :  ::

ScSPT5     MATGGIAAGAAATSSGLSGGMTPGWSSF----DGGKTPAVNAHGGSG-----------GG
HsSPT5     --S--------GSRTPMYGSQTPLQDGSRTPHYGSQTPLHDGSRTPAQSGAWDPNNPNTP
DmSPT5     -AA--------GSKTPLVGSQTPNWDTDRTPYGTMTPSHDGSMTPR-HGAWDPTANTTP
AtSPT5-1   --M--------GSQTPMHPSRTPLHPCMTPMRHSGATPIHDGMRTPMRGRAWNPYMPMSP
AtSPT5-2   --M--------GSETPMHPSRTPLHPYMTPMRDSGATPIHDGMRTPMRDRAWNPYTPMSP
PtSPT5     --M--------GSETPMHPSRTPLRPYMTPMRDSGATPIHDGMRTPMRDRAWNPYAPMSP
VvSPT5     --M--------GSETPMHPSRTPLHPYMTPMRDVGATPIHDGMRTPMRDRAWNPYAPMSP
OsSPT5     --W--------GNETPVHPSRTPLRPFQTPLRDPGATPVPNGMRTPMPSRAWA---PMSP
ZmSPT5     --L--------GGETPMHPSRTPHHAYQTPMRDPGATPIHDGMRTPMRSRAWA---PMSP
                .  : :  . **           **  :.

ScSPT5     GVSSWGGASTWGGQGNGGASAWGGAGGGASAWGGQGTGATSTWGGASAWGNKSSWGGAST
HsSPT5     SRAEEEYEYAFDDEPTPSPQAYGGTP----------NPQTPGYPDPSS------PQVNPQ
DmSPT5     ARNN-DFDYSLE-EPSPSPG-----Y----------NPSTPGY-----------QMTSQ
AtSPT5-1   PRDNWED---------GNPGSWGT------------------------------------
AtSPT5-2   PRDNWED---------GNPGSWG-TS----------P-------------------Q
PtSPT5     PRDNWED---------GNPGSWG-TS----------P-------------------Q
VvSPT5     PRDNWEE---------GNPDSWVTTS----------P-------------------Q
OsSPT5     PRLAL--------------GW--------------------------------Q
ZmSPT5     PRDNWED---------GNPATWG-SS----------P-------------------A
```

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ScSPT5    WASGGESNGAMSTWGGTGDRSAYGGAS---TWGGNNNNKS------TRDGGASAWGNQDD
HsSPT5    YNPQ--TPGTPAMYNTD-QFSPYAAPSPQGSYQPSPSPQSYHQVAPSPAG--YQNTHS--
DmSPT5    FAPQ--TPGTL--YGSDRSYSP--------FNPSPSP----------------------
AtSPT5-1  -------------------SPYEAATPGSDWGSSTPGRSSYRDAGTPINNA--------
AtSPT5-2  YQPG--SP----------PSRAYEAPTPGSGWASTPGG--SYSDAGTPRDHGSAYANA--
PtSPT5    YQPG--SP----------PSGTYEAPTPGSGWASTPGG--NYSEAGTPRDSSSAYANA--
VvSPT5    YQPG--SP----------PSRTYEAPTPGSGWASTPGG--NYSEAGTPRDSTPAYANV--
OsSPT5    SMPG--TP----------VPQPHEAPTPGSGWAVTPGV--SFGD---------ASGKN--
ZmSPT5    YQPG--TP----------QARPYEAPTPGSGWANTPGV--SFNDAPTPRD---NYANA--
                                             :    .

ScSPT5    GNRSAWNNQ-----------GNKSNY-----GG---------------------NSTWG
HsSPT5    --PASYHPTPSPMAYQASPSPSPVGYSPMTPGAPSPGGYNPH----TPGSGIEQNSSDWV
DmSPT5    ------APSPYPVGYM--NTPSPSTYSPNTPGGIPQSPYNPQ----TPGASLDSSMGDWC
AtSPT5-1  -----------NA--PSPMTPSSTSYLPTTPGGQAMTPGT-DLDVMSLDI-GGDAE-TRF
AtSPT5-2  --PSPYLPST-PG---QPMTPSSASYLPGTPGGQPMTPGT-GLDVMSPVI-GGDAE-AWF
PtSPT5    --PSPYLPST-PG--GQPMTPSSASYLPGTPGGQLMTPGTNGLDMMSPVI-GGDGEGPWF
VvSPT5    --PSPYLPST-PG--GQPMTPNSVSYLPGTPGGQPMTPGT-GVDVMSP-I-GGEQEGPWF
OsSPT5    --PSSYATPT-PS--GQPMTPNPASYLPSTPGGQPMTLGYIEMDIMSPAI-GEEGGRNWL
ZmSPT5    --PSPYVPST-PV--GQPMTPNSASYLPGTPGGQPMTPGNAGMDMLSPII-GGDGEVAWL
                        .       *         *.

ScSPT5    GH---------------------------------------------------------
HsSPT5    TTDIQVKVRDTYLDTQVVGQTGVIRSV-TGGMCSVYLKDSE--KVVSISSEHLEPIT PTK
DmSPT5    TTDIEVRIHT-HDDTDLVGQTGIIRTV-SNGVCSVFLRQED--RSVSIVSEHLAPVL PCN
AtSPT5-1  IPGILVNVHKAGEDRN----PGVIRDVLPDGSCVVALGHRGEGETIRATQNKVSLVC PKK
AtSPT5-2  MPDILVDIHKAGEDTD----VGVIRDV-SDGTCKVSLGSSGEGDTIMALPSELEIIP PRK
PtSPT5    IPDILVTVHRTADESA----VGVIREVLQDGSCKIVLGAHGNGETITALPSEIEMVV PRK
VvSPT5    MPDILVHIRRPGEENT----LGVIREVLPDGTYRVGLGSSGGGEIVTVLHAEIDAVA PRK
OsSPT5    LPDVLVNVLREGYDTT----CGVVKEVLPDGSCRVALGSSGSGDEITAFPNEFEVVK PKK
ZmSPT5    LPDVLVNVLRGGD-DG----PGVVREVLGDGSCRVALGSSGNGDVVTVLANEVEVIR PKK


ScSPT5    ----------------------------------------------------------
HsSPT5    NNKVKVILGEDREATGVLLSIDGE DGIVRMDL---DEQLKILNLRFLGKLLEA-
DmSPT5    GDEFKIIYGDDRESVGRVLSKDGD VFVCR--I---NEEIKLLPINFLCKMKSID
AtSPT5-1  NERVKILGGKYCGSTAKVIGEDGQ DGIVKLDE---SLDIKILKLTILAKLVHE-
AtSPT5-2  SDRVKIVGGQYRGSTGKLIGIDGS DGIVKIDD---NLDVKILDLALLAKFVQP-
PtSPT5    SDKIKILGGAHRGATGKLIGVDGT DGIVKLED---TLDVKILDMVILAKLAQM-
VvSPT5    SDKIKIMGGAHRGATGKLIGVDGT DGIVKVDD---TLDVKILDMVLLAKLVQP-
OsSPT5    NDKLKIMSGSWRGLTGKLLGVDGS DGIVKVDGLETTDQTKILDTAILGKLAA--
ZmSPT5    SDRIKILNGNFRGYTGKLIGIDGS DGIVRLDE---TYEVKILDMVILAKLAT--
```

Figure S3. Amino acid sequence alignment of SPT5 of different species. The alignment was generated using Clustal Omega (http://www.ebi.ac.uk/Tools/msa/clustalo/) and the SPT5 amino acid sequences of *Sacharomyces cerevisiae* (Sc), *Homo sapiens* (Hs), *Drosophila melanogaster* (Dm), the dicot species *Arabidopsis thaliana* (At), *Populus trichocarpa* (Pt) , *Vitis vinifera* (Vv) and the moncot species *Oryza sativa* (Os) and *Zea mays* (Zm). The acidic N-terminal domain is highlighted in yellow, the NGN domain mediating the interaction with SPT4 (and RNAPII) in grey, and the KOW domains in blue. The (putative) phosphorylated Thr residues of the C-terminal repeats (CTR) are indicated in red, and the Glu residue within the NGN domain that is critical for SPT4-interaction is indicated by an arrow (9). Asterisks below the sequences indicate invariant residues, while (:) indicate residues that are highly conserved. When compared to their orthologs from other organisms, for instance, SPT5-2 is to 22.9%, 34.4% and 54.0% identical to its yeast, human and rice relatives, respectively.
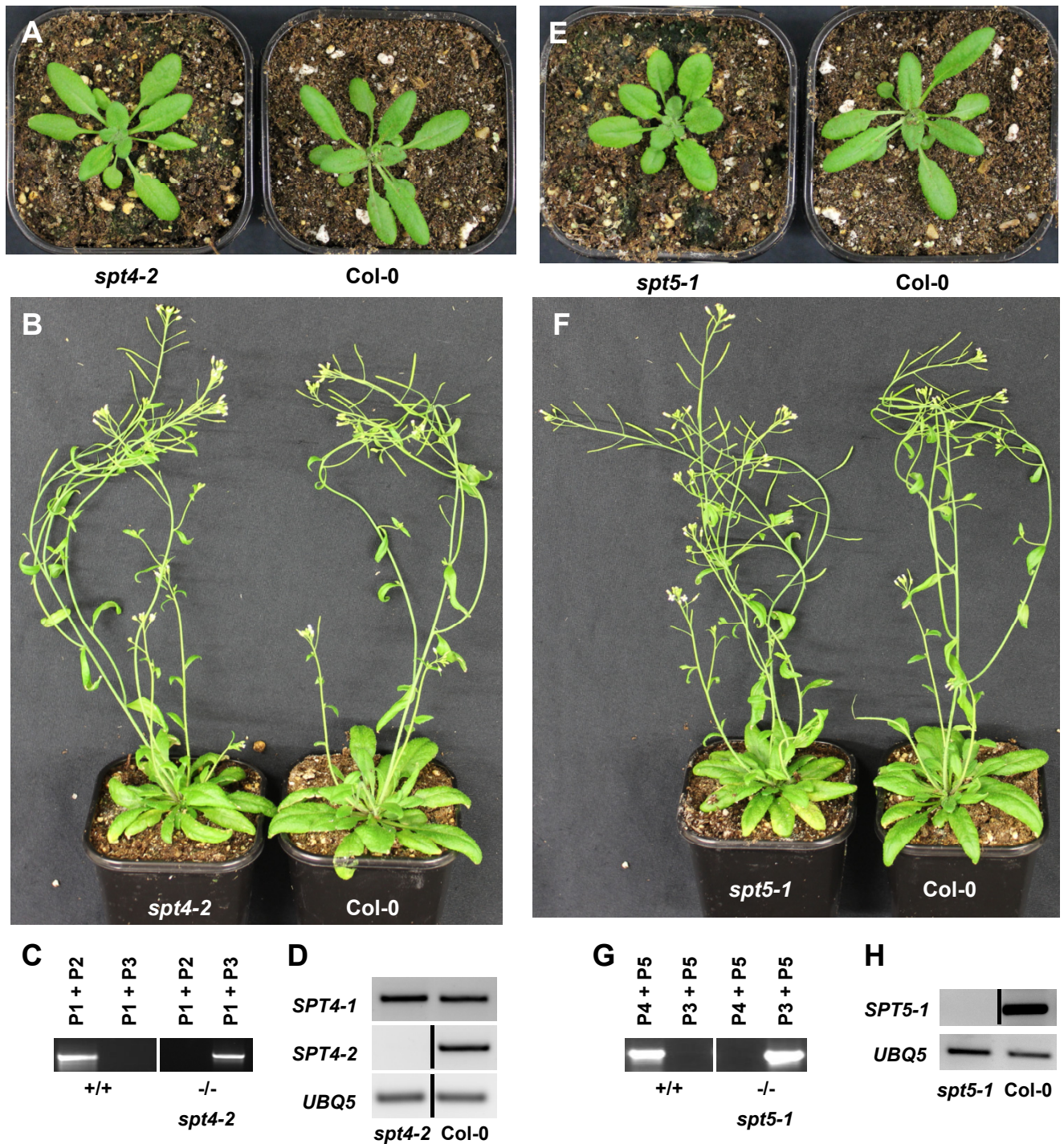
Figure S4. Plants that do not express *SPT4-2* or *SPT5-1* are viable. *spt4-2* plants (SAIL_262_E06) at 21 DAS (A) and 35 DAS (B) develop similar to Col-0 control plants. (C) Genotyping of segregating plants by PCR with the indicated primers (cf. Fig. S1). Shown are results for a wild type plant (left) and a plant homozygous for the T-DNA insertion (*spt4-2*, right). In *spt4-2* plants no transcript of the *SPT4-2* gene is detectable by rtPCR in RNA isolated from seedlings, while the transcripts of the *SPT4-1* gene and of the reference gene *UBQ5* are present approximately at wild type levels (D). *spt5-1* plants (SAIL_1297_A11) at 21 DAS (E) and 35 DAS (F) develop similar to Col-0 control plants. We noticed that the leaves of *spt5-1* plants display a somewhat more round shape than Col-0 leaves, but whether this observation is caused by the lack of *SPT5-1* expression requires further experimentation. (G) Genotyping of segregating plants by PCR with the indicated primers (cf. Fig. S1). Shown are results for a wild type plant (left) and a plant homozygous for the T-DNA insertion (*spt5-1*, right). In *spt5-1* plants no transcript of the *SPT5-1* gene is detectable by rtPCR in RNA isolated from stamen, while the transcript of the reference gene *UBQ5* is readily detectable (H).

Figure S5. Induced expression of a SPT5-2 RNAi construct affects plant growth. (A) Transcript level of *SPT5-2* and *UBQ5* as determined by rt-PCR in untransformed Col-0 and various independent transformed lines expressing the SPT5-2 RNAi construct under control of an estradiol-inducible system. The application of estradiol is indicated by (+), while the untreated controls are indicated by (-). (B) The images depict each 10 seedlings that are grown in liquid MS medium in the absence of estradiol, or that were treated with estradiol. (D) Fresh-weight (FW) of seedlings grown in liquid MS medium with or without estradiol. FW of each line was normalised to the mock treatment. Relative FW was analysed using a one-way ANOVA and error bars indicate SD of two replicates. Data sets marked with asterisks are significantly different from Col-0 as assessed by Dunnett's multiple comparison test: * $P < 0.05$, ** $P < 0.01$. The experiment was performed twice with similar results. (D) Seedlings grown on solid MS medium in the absence (-) or presence (+) of estradiol.
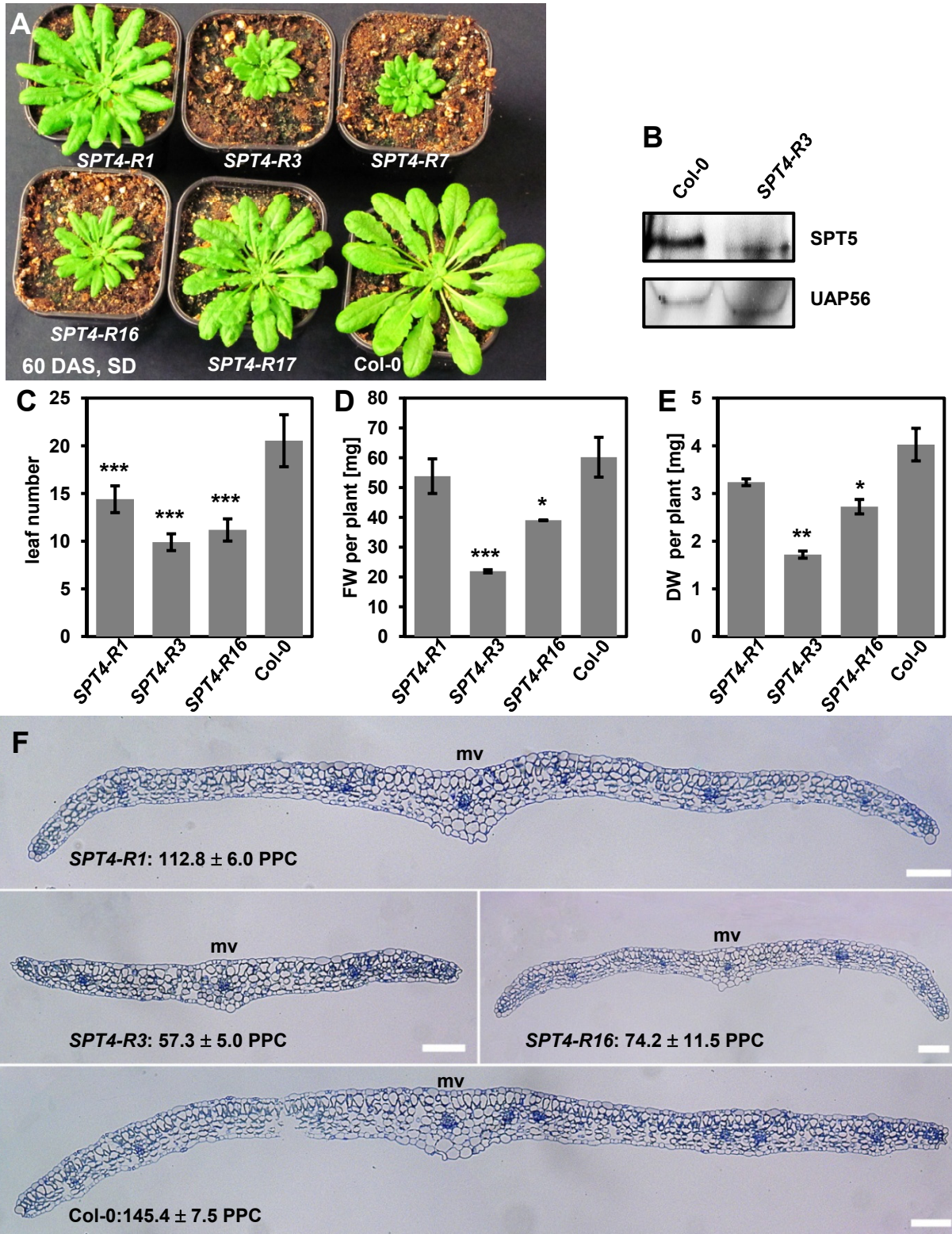
Figure S6. SPT4-RNAi lines exhibit reduced growth. (A) Col-0 and different RNAi lines 60 DAS, short day, soil grown. (B) Immunoblot analysis of nuclear extracts of SPT4-R3 and Col-0 plants probed with anti-SPT5 and as a reference with an antibody against RNA helicase UAP56 (28). (C-E) Quantification of total leaf number (35 DAS, long day, soil grown), fresh weight and dry weight (21 DAS, long day, grown on solid MS) of Col-0 and different RNAi plants. Leaf number, fresh/dry weight were analysed using a one-way ANOVA. Error bars indicate SD of at least 10 plants (C) and of two independent experiments with at least 35 plants per experiments (D,E). Data sets marked with asterisks are significantly different from Col-0 as assessed by Dunnett's multiple comparrison test: * P < 0.05, ** P < 0.01 or *** P < 0.001. The experiment in (C) was performed at least three times with similar results. (F) Microscopic images of transverse sections of 12 DAS leaves. Average palisade parenchyma cell (PPC) numbers across the leaf are indicated (n≥4). Scale bars represent 100 µm.
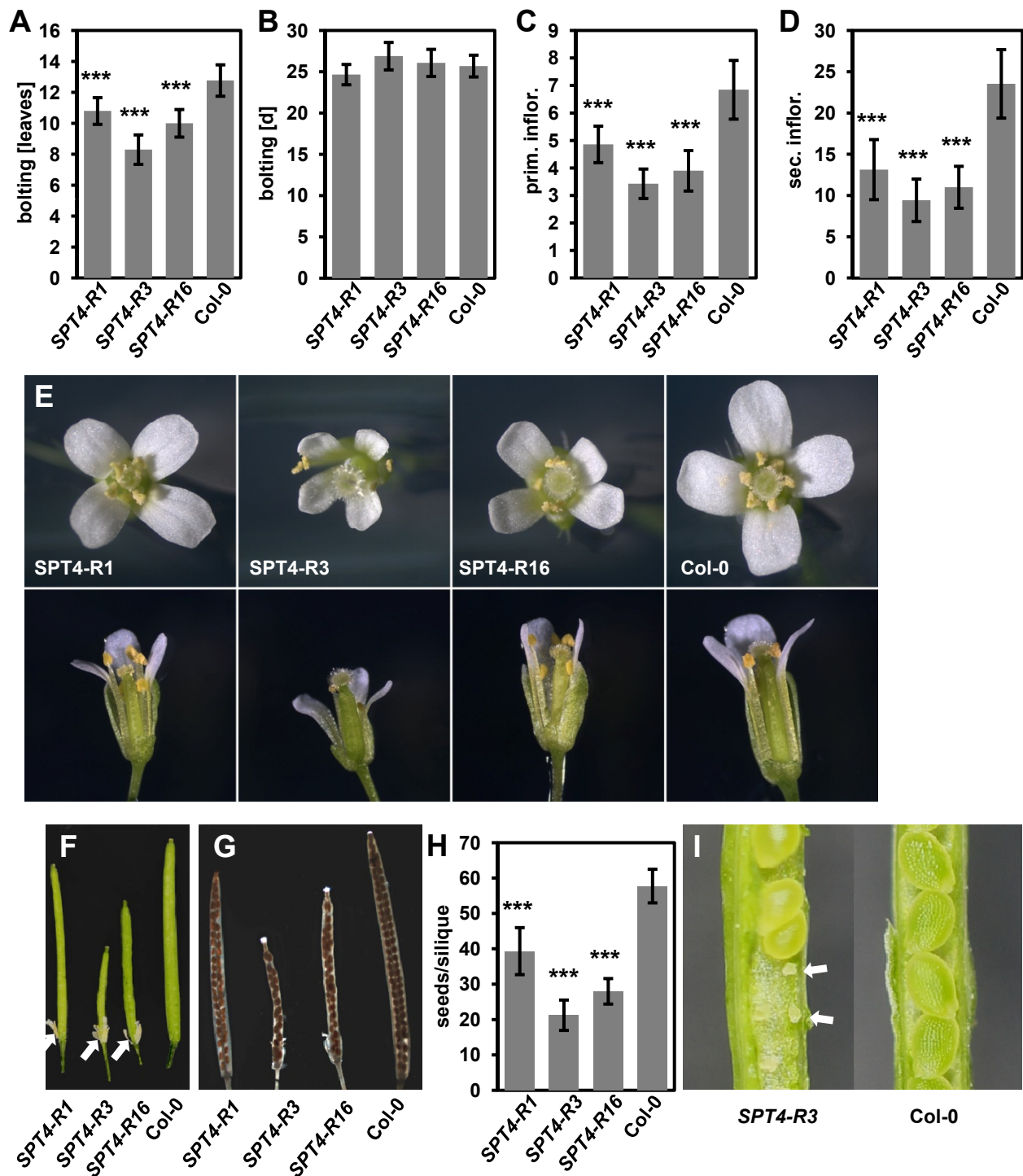
Figure S7. Reproductive defects of SPT4-RNAi plants relative to Col-0. Bolting of plants was scored by counting the total number of leaves (A) and by determining the time of bolting in DAS (B). The number of primary (C) and secondary (D) inflorescences was scored at 15 Days after bolting. Leaves at bolting, prim. and sec. inflorescences were analysed using a one-way ANOVA. Error bars indicate SD of at least 10 plants. Data sets marked with asterisks are significantly different from Col-0 as assessed by Dunnett's multiple comparison test: * $P < 0.05$, ** $P < 0.01$ or *** $P < 0.001$. Each experiment was performed at least three times with similar results. (E) Flowers were documented from top (top row) and from side of opened flowers (bottom row). Documentation of freshly harvested elongated siliques (F) with arrows indicated the defect in shedding floral organs, and cleared siliques illustrate the number of seeds produced (G). (H) Average number of seeds per silique. Seeds per siliques were analysed using a one-way ANOVA. Error bars indicate SD of at least 16 siliques. Data sets marked with asterisks are significantly different from Col-0 as assessed by Dunnett's multiple comparison test: * $P < 0.05$, ** $P < 0.01$ or *** $P > 0.001$. (I) Open siliques, illustrating fully developed seeds and ovules that did not develop in an SPT4-R3 silique (indicated by arrows).
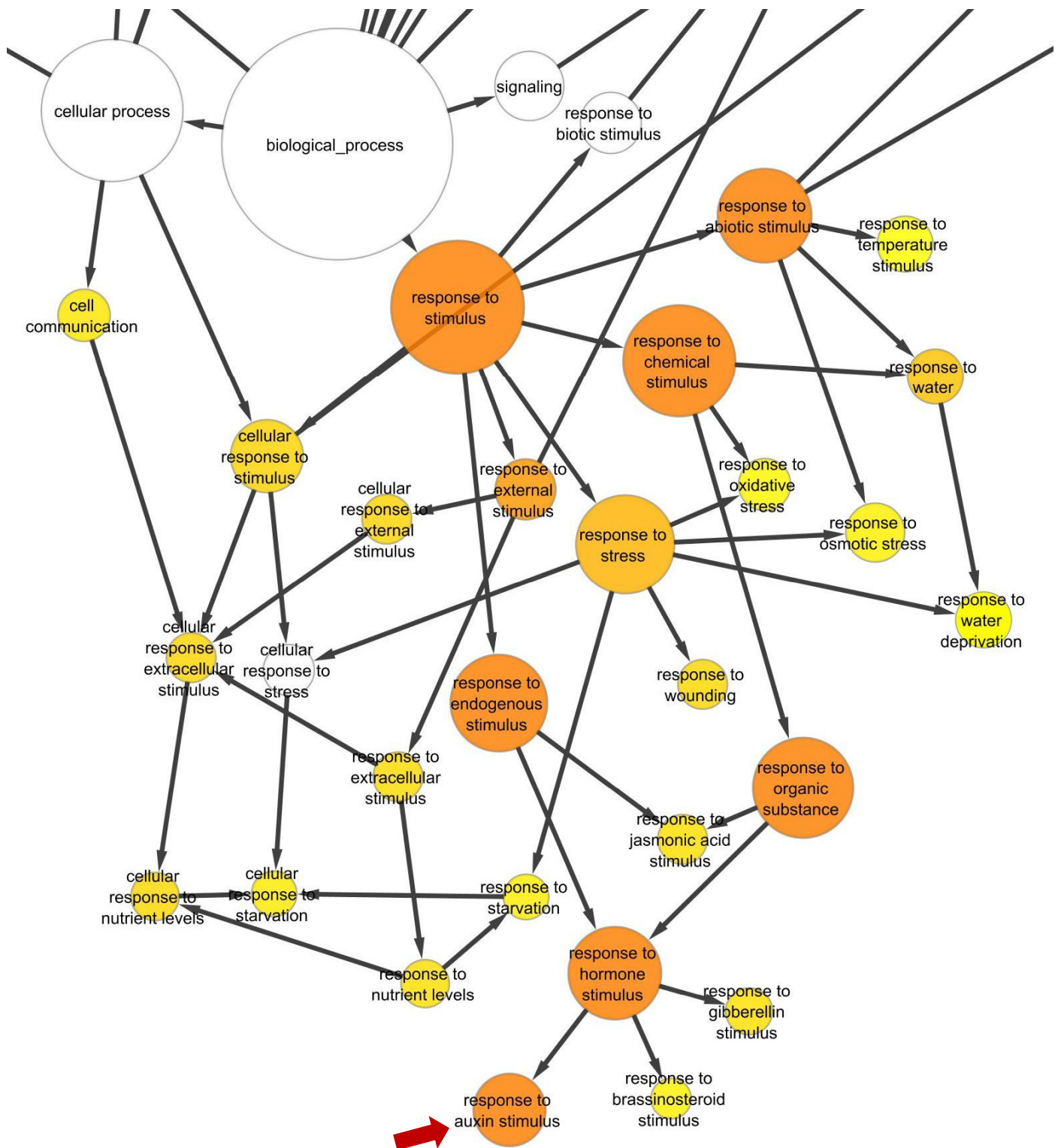
Figure S8. Gene ontology analysis of genes differntially expressed in SPT4-R3 relative to Col-0. The analysis was performed in Cytoscape using the BiNGO plugin version (Maere et al., 2005; Shannon et al., 2003). GO categories were identified that were significantly overrepresented among the differentially expressed genes >2-fold down-regulated. The different grades of orange of the circles correspond to the level of significance of the overrepresented GO category (P < 0.05). The size of the circles is proportional to the number of genes in each category. An arrow indicates the category of auxin-related genes that are primarily discussed here. Note that for clarity, only the part of the entire network related to the stimulus responsive categories is shown.
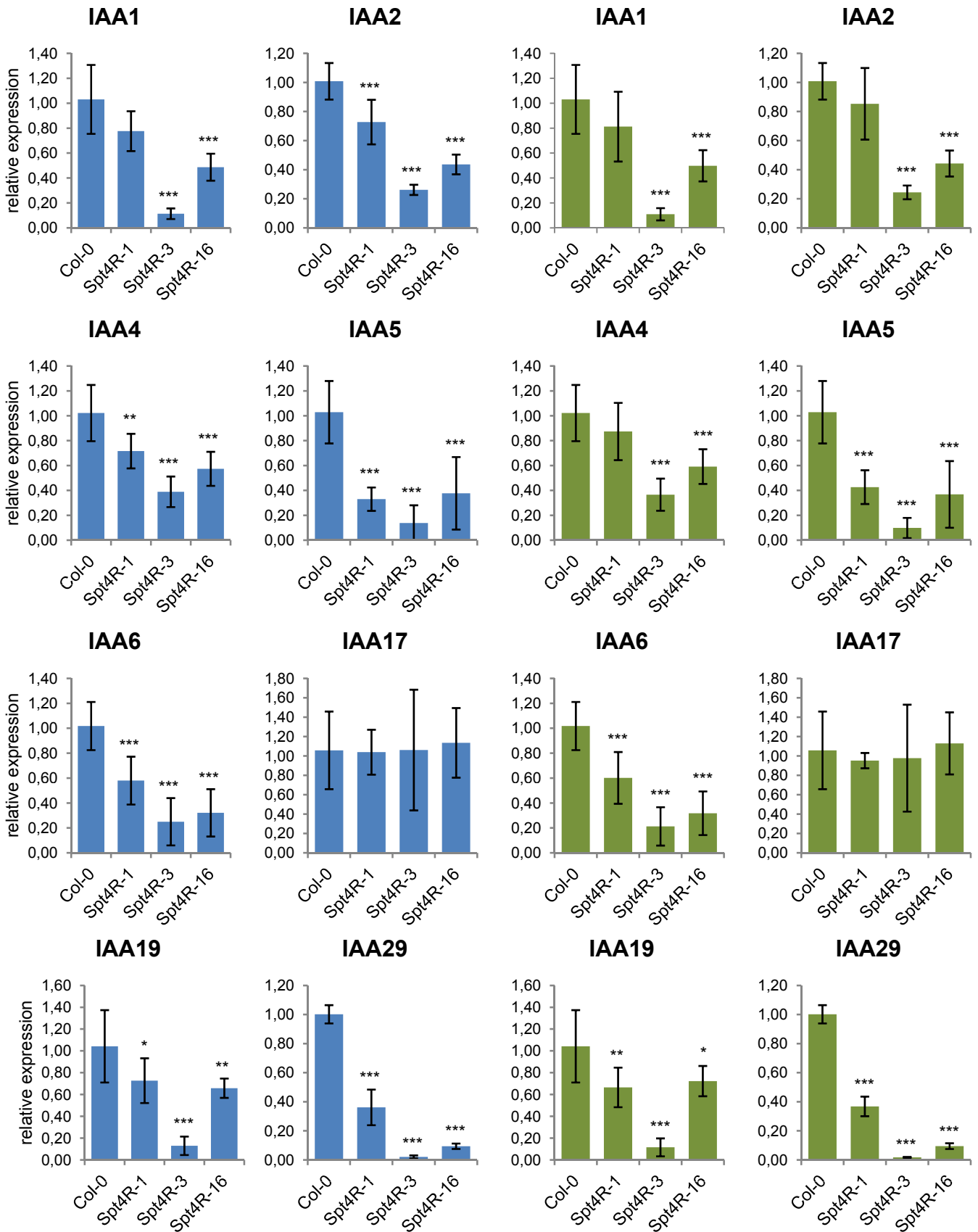
Figure S9. Real-time qPCR analysis of transcript levels of *AUX/IAA* genes. Quantitative rtPCR analysis of the SPT4-RNAi plants relative to Col-0 using as a reference *ACT8* (blue bars) or *EF1a* (green bars). Relative expression was analysed using a one-way ANOVA. Error bars indicate SD of at least three biological and three technical replicates. Data sets marked with asterisks are significantly different from wild-type as assessed by Dunnett's multiple comparison test: * P < 0.05, ** P < 0.01 or *** P < 0.001.
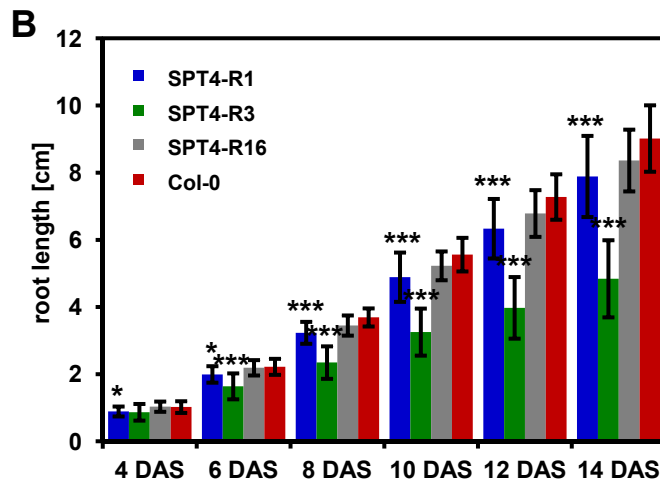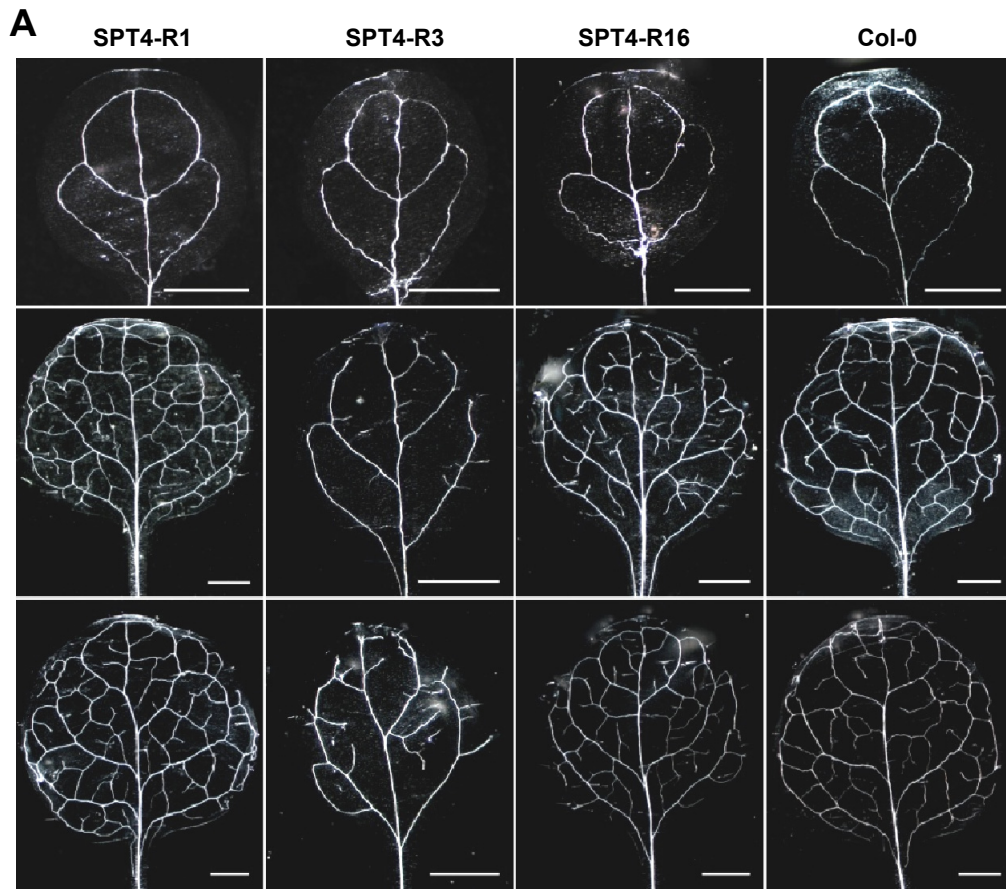
Figure S10. Leaf vein patterning, root growth and lateral root number of SPT4-RNAi plants relative to Col-0. (A) Vein pattern of cleared leaves of the indicated plant lines. Representative leaves of 26d old plants are shown: Cotyledon (top), first leaf (middle) and second leaf (bottom), and size bars indicate 1 mm. (B) The length of the primary root of plants grown on MS medium was measured at the indicated DAS. Root lenght was analysed using a one-way ANOVA. Error bars indicate SD of at least 14 plants. Data sets marked with asterisks are significantly different from Col-0 as assessed by Dunnett's multiple comparison test: * $P < 0.05$, ** $P < 0.01$ or *** $P > 0.001$. The experiment was performed three times with similar results.

Table S1. Auxin-related genes differentially expressed in SPT4-R3 relative to Col-0

Probe set ID	Sig log ratio	Fold[a] change	p-value	AGI[b]	Gene, description[2]
249719_at	2.48	5.56	0.00008	At5g35735	auxin-responsive family protein
253253_at	1.81	3.50	0.00002	At4g34750	response to auxin stimulus
249606_at	1.81	3.50	0.00006	At5g37260	RVE2 (REVEILLE 2); DNA binding / transcription factor
266839_at	1.61	3.05	0.00000	At2g25930	ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor
247643_at	1.60	3.03	0.00003	At5g60450	ARF4 (AUXIN RESPONSE FACTOR 4); transcription factor
246133_at	1.31	2.47	0.00008	At5g20960	AAO1 (ARABIDOPSIS ALDEHYDE OXIDASE 1); aldehyde oxidase/ indole-3-acetaldehyde oxidase
255479_at	1.30	2.46	0.00000	At4g02380	SAG21 (SENESCENCE-ASSOCIATED GENE 21)
256829_at	1.14	2.20	0.00001	At3g22850	similar to auxin down-regulated protein ARG10
247013_at	1.12	2.17	0.00104	At5g67480	BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator
251436_at	-1.00	-2.01	0.00009	At3g59900	ARGOS (AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE)
247979_at	-1.03	-2.04	0.00025	At5g56750	auxin transport
250972_at	-1.04	-2.06	0.00009	At5g02840	LCL1 (LHY/CCA1-like 1); DNA binding / transcription factor
254758_at	-1.05	-2.07	0.00041	At4g13260	YUC2 (YUCCA2); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ oxidoreductase
264598_at	-1.08	-2.11	0.00038	At1g04610	auxin biosynthetic process
247726_at	-1.12	-2.17	0.00008	At5g59430	TRP1 (TELOMERIC REPEAT BINDING PROTEIN 1); DNA binding / double-stranded telomeric DNA binding
258402_at	-1.13	-2.18	0.00000	At3g15450	similar to auxin down-regulated protein ARG10
254926_at	-1.13	-2.19	0.00029	At4g11280	ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase
267092_at	-1.14	-2.21	0.00008	At2g38120	AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter
245244_at	-1.15	-2.22	0.00005	At1g44350	ILL6; IAA-amino acid conjugate hydrolase/ metallopeptidase
264025_at	-1.15	-2.22	0.00002	At2g21050	auxin mediated signaling pathway
258797_at	-1.21	-2.31	0.00005	At3g04730	IAA16; transcription factor
245947_at	-1.27	-2.41	0.00059	At5g19530	ACL5 (ACAULIS 5); spermine synthase/ thermospermine synthase
254746_at	-1.27	-2.42	0.00003	At4g12980	auxin-responsive protein, putative

262951_at	-1.29	**-2.44**	**0.00026**	At1g75500	secondary cell wall biogenesis, positive regulation of auxin metabolic process
264323_at	-1.32	**-2.50**	**0.00014**	At1g04180	auxin biosynthetic process
263890_at	-1.35	**-2.55**	**0.00006**	At2g37030	response to auxin stimulus
263656_at	-1.41	**-2.66**	**0.00080**	At1g04240	SHY2 (SHORT HYPOCOTYL 2); transcription factor; IAA3
265454_at	-1.48	**-2.79**	**0.00002**	At2g46530	ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor
253061_at	-1.56	**-2.95**	**0.00001**	At4g37610	BT5 (BTB AND TAZ DOMAIN PROTEIN 5); protein binding / transcription regulator
249109_at	-1.62	**-3.08**	**0.00027**	At5g43700	ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor; IAA4
265806_at	-1.62	**-3.08**	**0.00003**	At2g18010	response to auxin stimulus
267461_at	-1.63	**-3.09**	**0.00000**	At2g33830	dormancy/auxin associated family protein
253103_at	-1.63	**-3.10**	**0.00034**	At4g36110	response to auxin stimulus
263433_at	-1.67	**-3.18**	**0.00001**	At2g22240	MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase
253908_at	-1.69	**-3.23**	**0.00005**	At4g27260	WES1; indole-3-acetic acid amido synthetase
261766_at	-1.77	**-3.41**	**0.00010**	At1g15580	IAA5 (INDOLE-3-ACETIC ACID INDUCIBLE 5); transcription factor
248163_at	-1.84	**-3.58**	**0.00278**	At5g54510	DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase
266830_at	-1.86	**-3.64**	**0.00012**	At2g22810	ACS4 (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 4); 1-aminocyclopropane-1-carboxylate synthase
252965_at	-2.19	**-4.55**	**0.00000**	At4g38860	response to auxin stimulus
245593_at	-2.23	**-4.69**	**0.00000**	At4g14550	IAA14 (INDOLE-3-ACETIC ACID INDUCIBLE 14); protein binding / transcription factor/ transcription repressor
253794_at	-2.31	**-4.95**	**0.00001**	At4g28720	auxin biosynthetic process
257766_at	-2.36	**-5.14**	**0.00001**	At3g23030	IAA2 (INDOLE-3-ACETIC ACID INDUCIBLE 2); transcription factor
247925_at	-2.50	**-5.65**	**0.00000**	At5g57560	TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase
259790_s_at	-2.50	**-5.68**	**0.00001**	At1g29430	response to auxin stimulus
259332_at	-2.63	**-6.20**	**0.00009**	At3g03830	response to auxin stimulus
259783_at	-2.66	**-6.33**	**0.00001**	At1g29510	SAUR68 (SMALL AUXIN UPREGULATED 68)
260152_at	-2.73	**-6.63**	**0.00000**	At1g52830	IAA6 (INDOLE-3-ACETIC ACID 6); transcription factor
245276_at	-2.77	**-6.81**	**0.00001**	At4g16780	ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor
258399_at	-2.80	**-6.97**	**0.00000**	At3g15540	IAA19 (INDOLE-3-ACETIC ACID INDUCIBLE 19); transcription factor
257506_at	-2.81	**-7.03**	**0.00000**	At1g29440	response to auxin stimulus
245397_at	-3.07	**-8.42**	**0.00001**	At4g14560	IAA1 (INDOLE-3-ACETIC ACID INDUCIBLE); protein binding / transcription factor

259784_at	-3.17	-9.01	0.00000	At1g29450	response to auxin stimulus
259787_at	-3.21	-9.28	0.00001	At1g29460	response to auxin stimulus
248801_at	-3.41	-10.61	0.00000	At5g47370	HAT2; DNA binding / transcription factor/ transcription repressor
259331_at	-3.45	-10.89	0.00001	At3g03840	response to auxin stimulus
259773_at	-3.46	-11.02	0.00000	At1g29500	response to auxin stimulus
250012_x_at	-4.48	-22.35	0.00000	At5g18060	response to auxin stimulus
253423_at	-4.62	-24.61	0.00000	At4g32280	IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor

[a]only genes are shown, whose transcript levels were ≥2-fold up- or down-regulated (highlighted in pink and blue, respectively) in SPT4-R3 relative to Col-0.

[b]*AUX/IAA* genes are highlighted in green.

Table S2. Mass spectrometry results of the SPT4-GS affinity purification

AGI	#IPs[a]	mass [kDa]	Mascot mean score	description[b]
At4g08350	5	115.3	2115.30	SPT5-2
At5g04290	5	157.9	1103.76	SPT5L
At5g63670	5	13.4	330.78	SPT4-2
At5g08565	5	13.4	223.97	SPT4-1
At5g13680	5	146.5	176.90	ELO2
At1g02080	4	269.7	712.05	CCR4-NOT subunit 1
At4g19210	3	68.3	319.52	ABC transporter E family member 2
At2g42520	3	67.6	297.93	DEAD-box ATP-dependent RNA helicase 37
At5g50320	3	63.1	222.10	ELO3
At3g62530	3	38.1	127.45	armadillo/beta-catenin-like repeat-containing protein
At1g53165	2	76.5	461.20	map 4 kinase alpha1
At4g35800	2	204.9	393.60	NRPB1
At1g32380	2	43.3	318.15	ribose-phosphate pyrophosphokinase 2
At5g27970	2	180.4	259.06	armadillo/beta-catenin-like repeat-containing protein
At5g43780	2	52.1	251.81	sulfate adenylyltransferase
At2g02740	2	29.7	140.00	ssDNA-binding transcriptional regulator
At1g79530	2	44.8	122.45	glyceraldehyde 3-phosphate dehydrogenase
At5g53460	1	242.7	2953.00	NADH-dependent glutamate synthase
At3g46740	1	89.1	760.84	protein TOC75-3
At4g21710	1	134.9	667.08	NRPB2
At4g11820	1	51.1	604.11	hydroxymethylglutaryl-CoA synthase
At3g21140	1	42.8	528.56	Pyridoxamine 5'-phosphate oxidase family protein
At1g80070	1	275.3	501.99	Pre-mRNA-processing-splicing factor
At5g60790	1	66.8	428.71	ABC transporter F family member 1
At1g36160	1	251.6	412.81	acetyl-CoA carboxylase 1
At3g15220	1	76.3	389.84	putative protein kinase
At4g31490	1	106	350.33	coatomer subunit beta-2
At2g27040	1	102.8	329.86	argonaute 4
At1g33410	1	169.3	245.44	suppressor of auxin resistance1 protein (SAR1)
At3g09840	1	89.3	237.59	cell division control protein 48-A
At3g05680	1	226.8	220.79	embryo defective 2016
At1g72560	1	111.4	202.00	protein PAUSED (mediates nuclear export of tRNAs)
At2g41040	1	28.9	197.31	S-adenosyl-L-methionine-dependent methyltransferases
At3g48860	1	54.1	188.57	uncharacterized protein
At1g05460	1	113.3	188.41	RNA helicase SDE3
At5g03540	1	72.3	188.07	exocyst subunit exo70 family protein A1
At1g14850	1	159.9	178.50	nucleoporin 155
At3g05040	1	133.1	175.07	HASTY
At1g69220	1	124.5	169.50	putative serine/threonine kinase
At1g27595	1	104.9	165.16	symplekin
At5g36230	1	49.3	158.10	armadillo/beta-catenin-like repeat-containing protein
At4g38600	1	82.6	157.17	E3 ubiquitin-protein ligase UPL3

At2g41220	1	177.6	144.76	ferredoxin-dependent glutamate synthase precursor
At2g18960	1	104.2	141.64	H(+)-ATPase 1
At1g78900	1	68.8	138.58	V-type proton ATPase catalytic subunit A
At2g46280	1	36.3	133.01	eukaryotic translation initiation factor 3 delta subunit
At2g07698	1	85.9	130.15	F-type H+-transporting ATPase subunit alpha
At5g64270	1	141.4	127.50	putative splicing factor
At1g50360	1	129.9	127.36	P-loop containing nucleoside triphosphate hydrolase-like protein
At1g53500	1	75.2	119.68	UDP-glucose 4,6-dehydratase
At1g45000	1	44.7	117.48	AAA-type ATPase family protein
At1g21170	1	122.6	115.96	Exocyst complex component SEC5
At2g02560	1	134.8	108.73	cullin-associated NEDD8-dissociated protein 1
At5g26830	1	80.9	107.43	threonyl-tRNA synthetase
At4g00800	1	211.9	103.21	transducin family protein / WD-40 repeat family protein

[a]numbers indicate in how many out of a total of 5 experiments the respective protein was identified.
[b]proteins discussed in this report are highlighted in yellow.

Table S3. Oligonucleotide primers used in this study and construction of plasmids

#	primer	use	plasmid	restr. site
P1	ATGGGAAGCGCACCAGCT	Genotyping, T-DNA insertion *spt4-2* (At5Gg63670)		
P2	CATCGACCATTCCACAAGATT	Genotyping, T-DNA insertion *spt4-2* (At5g63670)		
P3	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC	Genotyping, T-DNA insertion SAIL LB (*spt4-2*, *spt5-1* and *spt5-2-4*)		
P4	GGGAACCCGGGATCATGGGGA	Genotyping, T-DNA insertion *spt5-1* (At2g34210)		
P5	TGGGGTCACTCATGAACTAACTTGGC	Genotyping, T-DNA insertion *spt5-1* (At2g34210)		
	GTTCATAGGCGAAGCATCATGA	Genotyping, T-DNA insertion *spt5-2-1* (At4g08350)		
	GGTGACTTCTGAGAACCAATCT	Genotyping, T-DNA insertion *spt5-2-1* (At4g08350)		
	TGCATTCTTCACTGGTCTGCTGCAC	Genotyping, T-DNA insertion *spt5-2-2* (At4g08350)		
	ACCTCCAGAGTCCCGCATTGGA	Genotyping, T-DNA insertion *spt5-2-2* (At4g08350)		
	CTTGGCTAAGGCCAGGTC	Genotyping, T-DNA insertion *spt5-2-3* (At4g08350)		
	TTGTGTTGCACTTGTTCCCAG	Genotyping, T-DNA insertion *spt5-2-3* (At4g08350)		
	AGGAAATCAAGCCAAACCATG	Genotyping, T-DNA insertion *spt5-2-4* (At4g08350)		
	TGGTGGTAGTTACTCGGATGC	Genotyping, T-DNA insertion *spt5-2-4* (At4g08350)		
	ATTTTGCCGATTTCGGAAC	Genotyping, T-DNA insertion SALK LBb1.3 (*spt5-2-1, 2, 3*)		
	TCACATGCGTTTCGGCAGAA	Genotyping, T-DNA insertion SPT4RNAi		
	GAAGAGCCAATTAAGATAAAACGTTGAATGTA	Genotyping, T-DNA insertion SPT4RNAi		
	TGGGCTGCAGGTCGAGGCTA	Genotyping, T-DNA insertion SPT5RNAi activator unit		
	CGCAAGACCCTTCCTCTATA	Genotyping, T-DNA insertion SPT5RNAi activator unit		
	TGGGCTGCAGGTCGAGGCTA	Genotyping, T-DNA insertion SPT5RNAi responder unit		
	TCCTCATGCCCTTGATTGCCTCTT	Genotyping, T-DNA insertion SPT5RNAi responder unit		
	AACCCGGGTCACATGCGTTTCGGCAGAA	Insertion of *SPT4-2* (At5g63670) CDS in pFGC5941	pFGC5941-SPT4-2	XbaI, SwaI
	AATCTAGAATGGGAAGCGCACCAGCT	Insertion of *SPT4-2* (At5g63670) CDS in pFGC5941	pFGC5941-SPT4-2	XmaI, SwaI
	AATTTCTAGAGGCGCGCCTATATGTTGAAGCAGACAAGG	Insertion of *SPT5-2* (At4g08350) CDS in pFGC5941	pFGC5941-SPT5-2	XbaI, AscI
	AATTGGATCCATTTAAATGTTGGTGTAACATTCTGAACAG	Insertion of *SPT5-2* (At4g08350) CDS in pFGC5941	pFGC5941-SPT5-2	BamHI, SwaI
	CACCGGCGCGCCGAGCTCGGTACCCGACGAG	Insertion of UBQ10-Promotor (At4g05320) in pMDC150	pMDC150-UBQP	Gateway® cloning
	GGCGCGCCCTGTTAATCAGAAAAACTCAG	Insertion of UBQ10-Promotor (At4g05320) in pMDC150	pMDC150-UBQP	Gateway® cloning
	CACCTACATTTACAATTACCATGG	Insertion of SPT5-RNAi in pMDC160 or pMDC221	pMDC160/221-SPT5RNAi	Gateway® cloning
	GTCTTAATTAACTCTCTAGA	Insertion of SPT5-RNAi in pMDC160 or pMDC221	pMDC160/221-SPT5RNAi	Gateway® cloning
	TTGGGCCCAACAATGGGAAGCGCACCAGCTCAGATTC	Insertion of *SPT4-2* (At5g63670) CDS in pCambia2300-GS	pCambia2300-SPT4-2-GS	SmaI

	TTGAGCTCTCACATGCGTTTCGGCAGAACAT	Insertion of *SPT4-2* (At5g63670) CDS in pCambia2300-GS	pCambia2300-SPT4-2-GS	SacI
	AATTGGATCCACTCCAATGCGGGACTCTGGAGC	Insertion of *SPT5-2* (At4g08350) C-terminal CDS in pQE9	pQE-SPT5-2C	BamHI
	AATTCTGCAGTCACGGTTGCACAAACTTGGCTAATAAGG	Insertion of *SPT5-2* (At4g08350) C-terminal CDS in pQE9	pQE-SPT5-2C	XhoI
	AATTGGTACCATGCCGCGAAGCAGAGACGAAG	Insertion of *SPT5-2* (At4g08350) N-terminal CDS in pBC-SK	pBC-SK-SPT5-2N	KpnI
	AATGAGCTCCCAGCTTACTGGCTAGTGCC	Insertion of *SPT5-2* (At4g08350) N-terminal CDS in pBC-SK	pBC-SK-SPT5-2N	SacI
	AATTGGTACCATGGATCGCAAGGGAAAGGG	Insertion of *SPT5-L* (At5g04290) N-terminal CDS in pBC-SK	pBC-SK-SPT5-LN	KpnI
	AATTGAGCTCGGACAGTAACTCCCCCACCAT	Insertion of *SPT5-L* (At5g04290) N-terminal CDS in pBC-SK	pBC-SK-SPT5-LN	SacI
	ATGGGAGAAGCGCCTGCC	Expression of *SPT4-1* (At5g08565)		
	ACTTCCATTCATAACCTCCATC	Expression of *SPT4-1* (At5g08565)		
	ATGGGAAGCGCACCAGCT	Expression of *SPT4-2* (At5g63670)		
	CATCGACCATTCCACAAGATT	Expression of *SPT4-2* (At5g63670)		
	AACTTCCTACTTACCTACCACACCCG	Expression of *SPT5-1* (At2g34210)		
	GGCTCACTTTGTTCTGTGTCGCTC	Expression of *SPT5-1* (At2g34210)		
	CAGATAATGTTGCGACAACACCGTTTAG	Expression of *SPT5-2* (At4g08350)		
	CTGATATTGAGGACTCGTTCCCC	Expression of *SPT5-2* (At4g08350)		
	GAAGGCGAAGATCCAAGACAAGGAA	Expression of *UBQ5* (At3g62250)		
	GGAGGACGAGATGAAGCGTCGA	Expression of *UBQ5* (At3g62250)		
	TCGTTTGGGATTACCCGGAGCA	qRT-PCR, *IAA1* (At4g14560)		
	TTGTGTTTTTGCAGGAGGAGGA	qRT-PCR, *IAA1* (At4g14560)		
	CCTCCTACCAAAACTCAAATCGTTGG	qRT-PCR, *IAA2* (At3g23030)		
	GAGATCGATCTTGCGAAGGTAAGGA	qRT-PCR, *IAA2* (At3g23030)		
	TCTCTGTGGGAGAGTACTTTGAGAGA	qRT-PCR, *SHY2/IAA3* (At1g04240)		
	GCACGTACATATGAACATCTCCCATG	qRT-PCR, *SHY2/IAA3* (At1g04240)		
	CCAGGGACAGAAGAAACTGTTTCTTG	qRT-PCR, *IAA4* (At5g43700)		
	CCAACAATCTGAGCCTTTGGAGGA	qRT-PCR, *IAA4* (At5g43700)		
	GGATGCTTGCTGGAGATGTTCCTT	qRT-PCR, *IAA5* (At1g15580)		
	CTGTAAGGCTCACTCACATTCACATG	qRT-PCR, *IAA5* (At1g15580)		
	AGTCACGGTTCTTGAGAATCTCTTCG	qRT-PCR, *IAA6* (At1g52830)		
	AGGTACATCTCCGACGAGCATCC	qRT-PCR, *IAA6* (At1g52830)		
	ATCTACGACTCATGACGTCGTGACT	qRT-PCR, *IAA17* (At1g04250)		
	ATCACGTTCTTCCGGTATGATCTCAC	qRT-PCR, *IAA17* (At1g04250)		
	CCTCCTACCAAAACTCAAATCGTTGG	qRT-PCR, *IAA19* (At3g15540)		
	GAGATCGATCTTGCGAAGGTAAGGA	qRT-PCR, *IAA19* (At3g15540)		
	GGGGATGTTACATGGAAGATCTTTGC	qRT-PCR, *IAA29* (At4g32280)		
	GGTCCGATTTGAACGCCTATCCTT	qRT-PCR, *IAA29* (At4g32280)		
	TGCTGGTCGTGACCTTACTGATTACC	qRT-PCR, *Actin8* (At1g49240)		

TCTCCATCTCTTGCTCGTAGTCGACA	qRT-PCR, *Actin8* (At1g49240)		
CTCACATTTTCGTAGCCGCAAGAC	qRT-PCR, *EF1α* (At5g60390)		
GATCAAGTGACCAGTTGTGGTCGAT	qRT-PCR, *EF1α* (At5g60390)		
TTGGGAAATACTGTAATAAGCTTCCT	ChIP qPCR, At3g02260-1		
TCCATGTGTTATTCTAATGATGTGCT	ChIP qPCR, At3g02260-1		
ACCGCCTTTCCCTCTTTGTCGT	ChIP qPCR, At3g02260-2		
GTCTCAAAGCGTAGCTTGCCAGA	ChIP qPCR, At3g02260-2		
AGATGGTTTCGGGGAGGAAAATCAC	ChIP qPCR, At3g02260-3		
GCTTCTCTTTCGACAGGCCAGAG	ChIP qPCR, At3g02260-3		
CAGGCGTTATCTCTTGAACCATTGC	ChIP qPCR, At3g02260-4		
TACTTGCTGTAGCCACACTCGTTG	ChIP qPCR, At3g02260-4		
CAAACCCAAGAAACCGGTCCACA	ChIP qPCR, At3g02260-5		
GAGTTGATTTCGTCGAGCCACGA	ChIP qPCR, At3g02260-5		
CCAACACATTTACGTTCACACAAACC	ChIP qPCR, At3g02260-6		
TTAATTCAAACGCGACGAGTTTAACCAT	ChIP qPCR, At3g02260-6		
ATGGGCTTAACCTTAAGGACACAGAG	ChIP qPCR, *IAA1*-5' (At4g14560)		
GAGCAGATTCTTCTGTTGAGTCGTTG	ChIP qPCR, *IAA1*-5' (At4g14560)		
GGATGTTGGTCGGTGATGTTCCA	ChIP qPCR, *IAA1*-3' (At4g14560)		
GTTTTTGCCTCGACCAAAAGGTGT	ChIP qPCR, *IAA1*-3' (At4g14560)		
GGGAGAGATGTGGCAGAGAAGATG	ChIP qPCR, *IAA19*-5' (At3g15540)		
CCTTCTCAGCGTCACCACCAGA	ChIP qPCR, *IAA19*-5' (At3g15540)		
CATATTTGTGCAGGTGTGGCCTTG	ChIP qPCR, *IAA19*-3' (At3g15540)		
TAGAACATACCCCCAAGGTACATCAC	ChIP qPCR, *IAA19*-3' (At3g15540)		
GACGAAGCTGCCTTAGAAATGGAGT	ChIP qPCR, *IAA29*-5' (At4g32280)		
GGTACCCAAACAAGACGCAGCA	ChIP qPCR, *IAA29*-5' (At4g32280)		
TAGAGATCGACCGTGTGCATATACAAG	ChIP qPCR, *IAA29*-3' (At4g32280)		
TAGAAGAATAGAGGAAAAAGATCGAGTGGA	ChIP qPCR, *IAA29*-3' (At4g32280)		