

Figure S1. Phenotype of *NTT* and *STK* overexpression lines. Early flowering plants of *35S::NTT* (A) or *35S::STK* (C) overexpression lines. Fruits of the *35S::NTT* (B) and *35S::STK* (D) overexpression lines. E, Plants of the *35S::NTT 35S::STK* double overexpression line, which do not produce fruits. Scale bars = 1 cm in A, C and E; 0.2 cm in B and D.

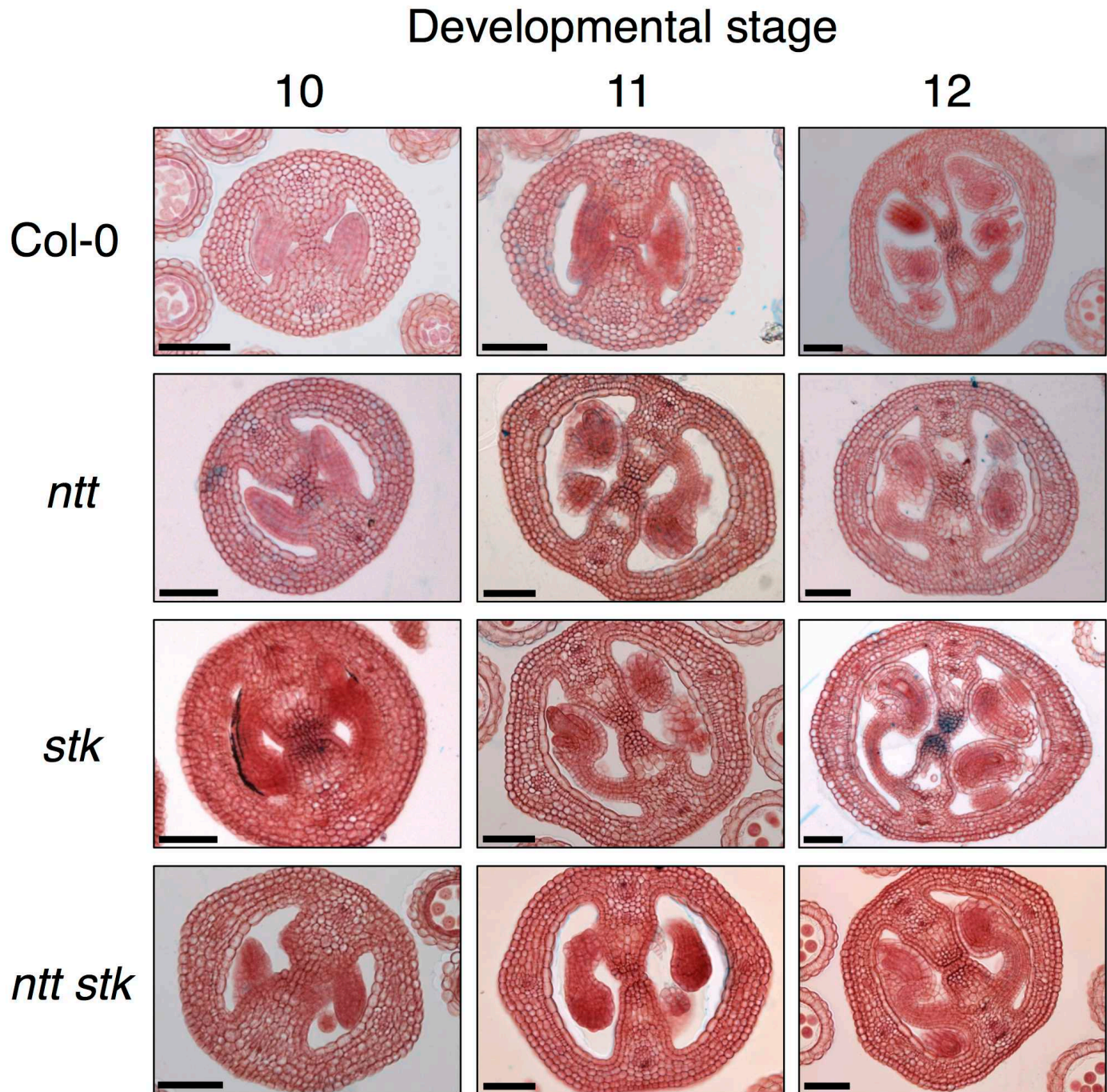


Figure S2. Transverse sections of stage 10–12 gynoecia of Col-0, *ntt*, *stk* and *ntt stk* double mutant. Scale bars = 50 μ m.

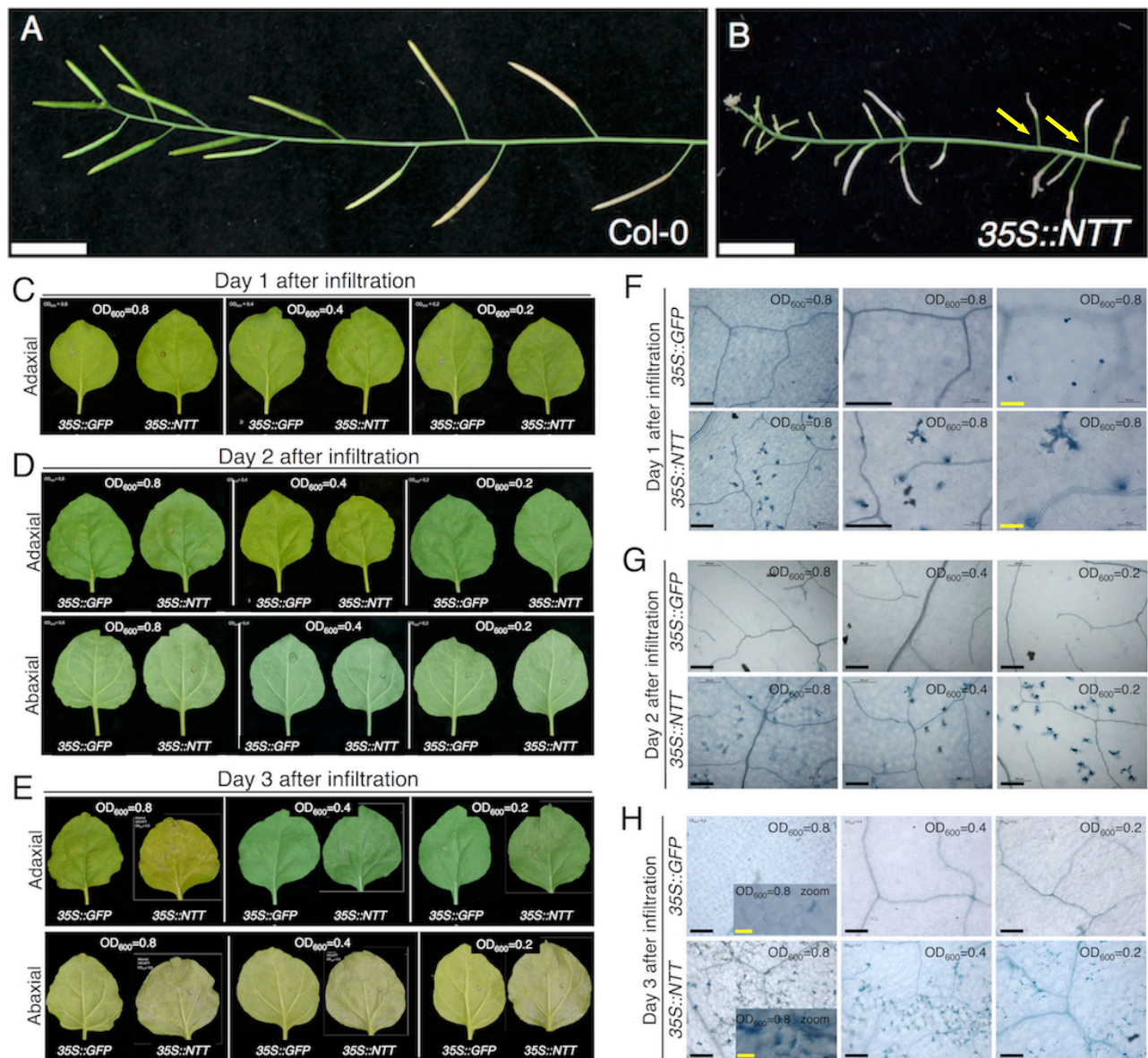


Figure S3. *NTT* accelerates senescence and promotes cell death. A-B, Fruit senescence in *Col-0* (A) and *35S::NTT*; no senescence is observed in pedicels (yellow arrows) (B). C-H, *NTT* can trigger transcriptional responses leading to cell death. Analysis of cell death caused by *NTT* or *GFP* transient expression in Nicotiana leaves. *GFP* expression was used as a negative control (note: no leaf damage was observed when *STK* alone was infiltrated in the BiFC experiment, while *NTT* alone or together *NTT* and *STK* it was observed). Overview of Nicotiana leaves 1 day (C), 2 days (D) and 3 days (E) after agro-infiltration. Detection of dead cells using the trypan blue staining in Nicotiana leaves 1 day (F), 2 days (G) and 3 days (H) after agro-infiltration. Bars represent 1 cm in A,B; in F-H, black bars represent 200 μ m and yellow bars 50 μ m.

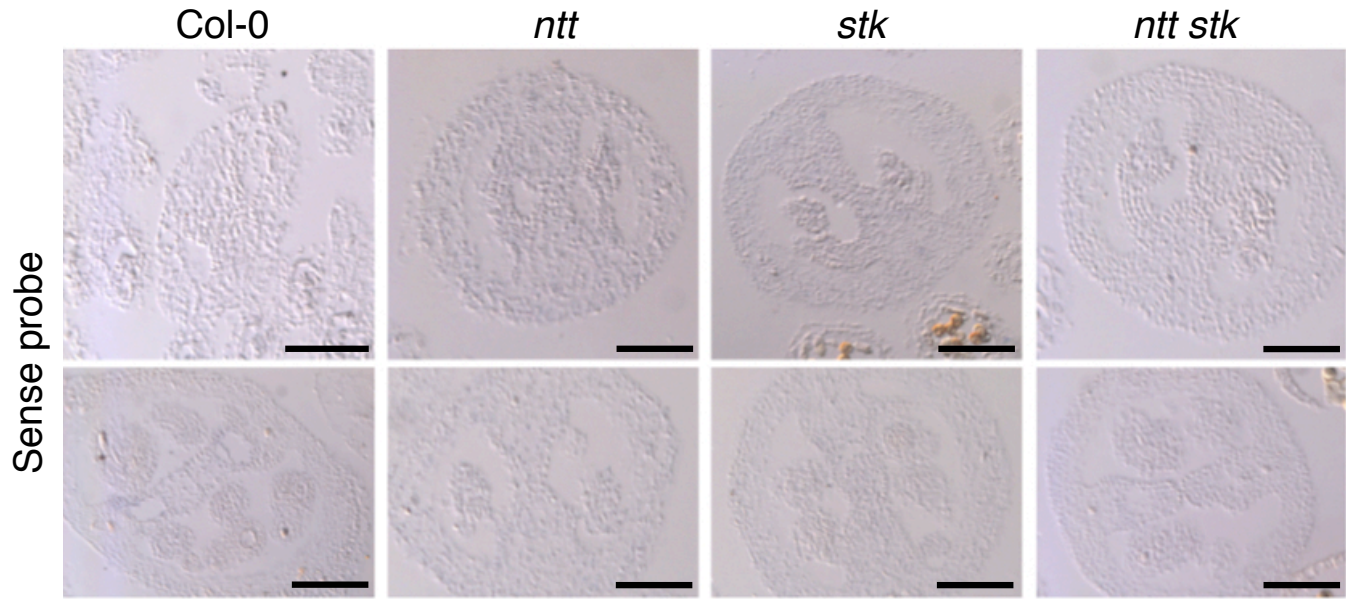


Figure S4: Sense probe controls for the *In situ* hybridization detection of *AT3G26140* (Glycosyl Hydrolase) in the gynoecium. The four genetic backgrounds are shown. Scale bars = 50 μm.

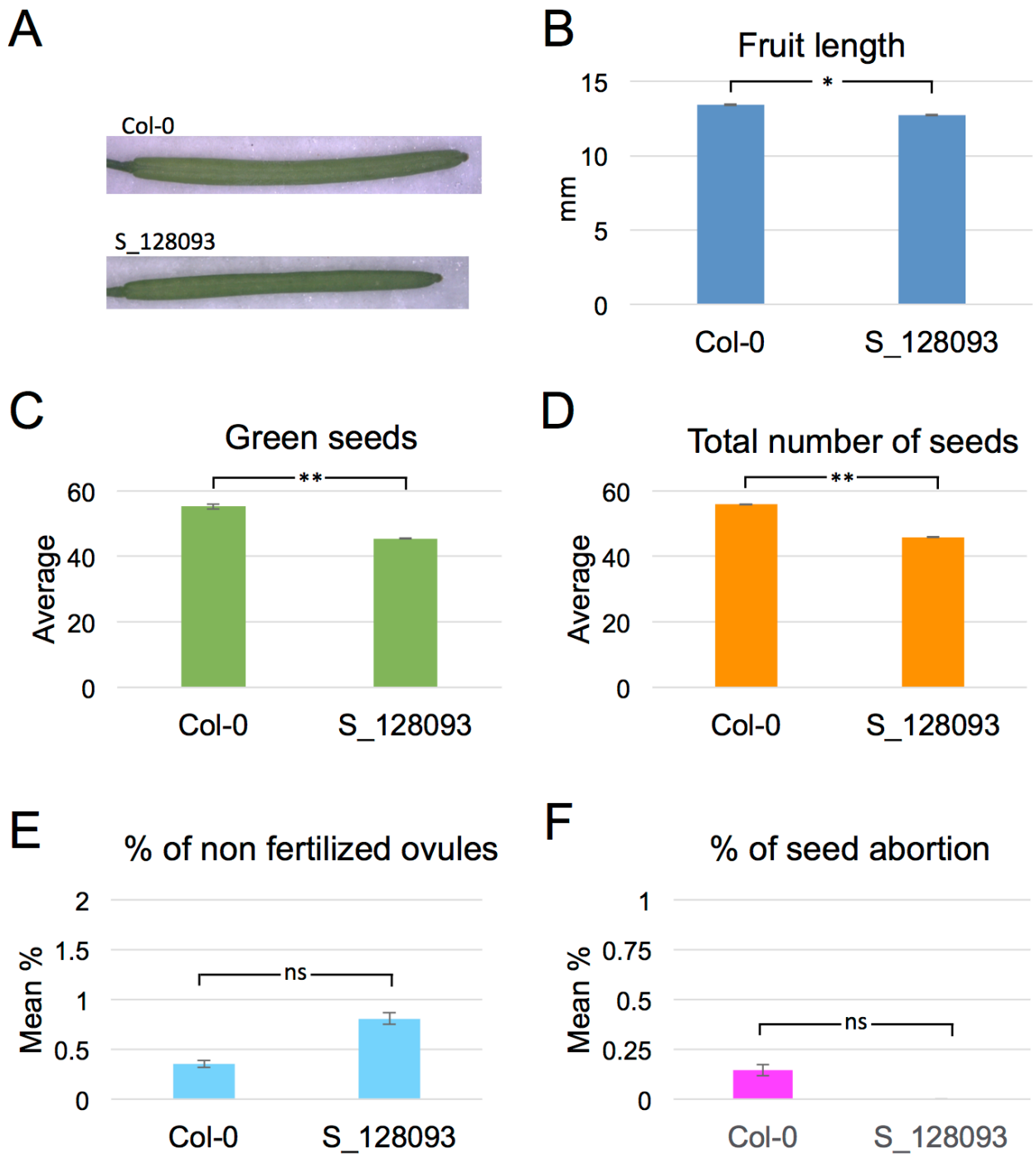


Figure S5. Analysis of At3g26140 (glycosyl hydrolase) insertional line. A, Overview of fruits of Col-0 and S_128093 line. Analysis of fruit length (B), number of green seeds (C), total number of seeds (D), % of non fertilized ovules (E) and seed abortion (F). Statistical analyses were performed using a T-test, $p < 0.01$ (*) or $p < 0.001$ (**).

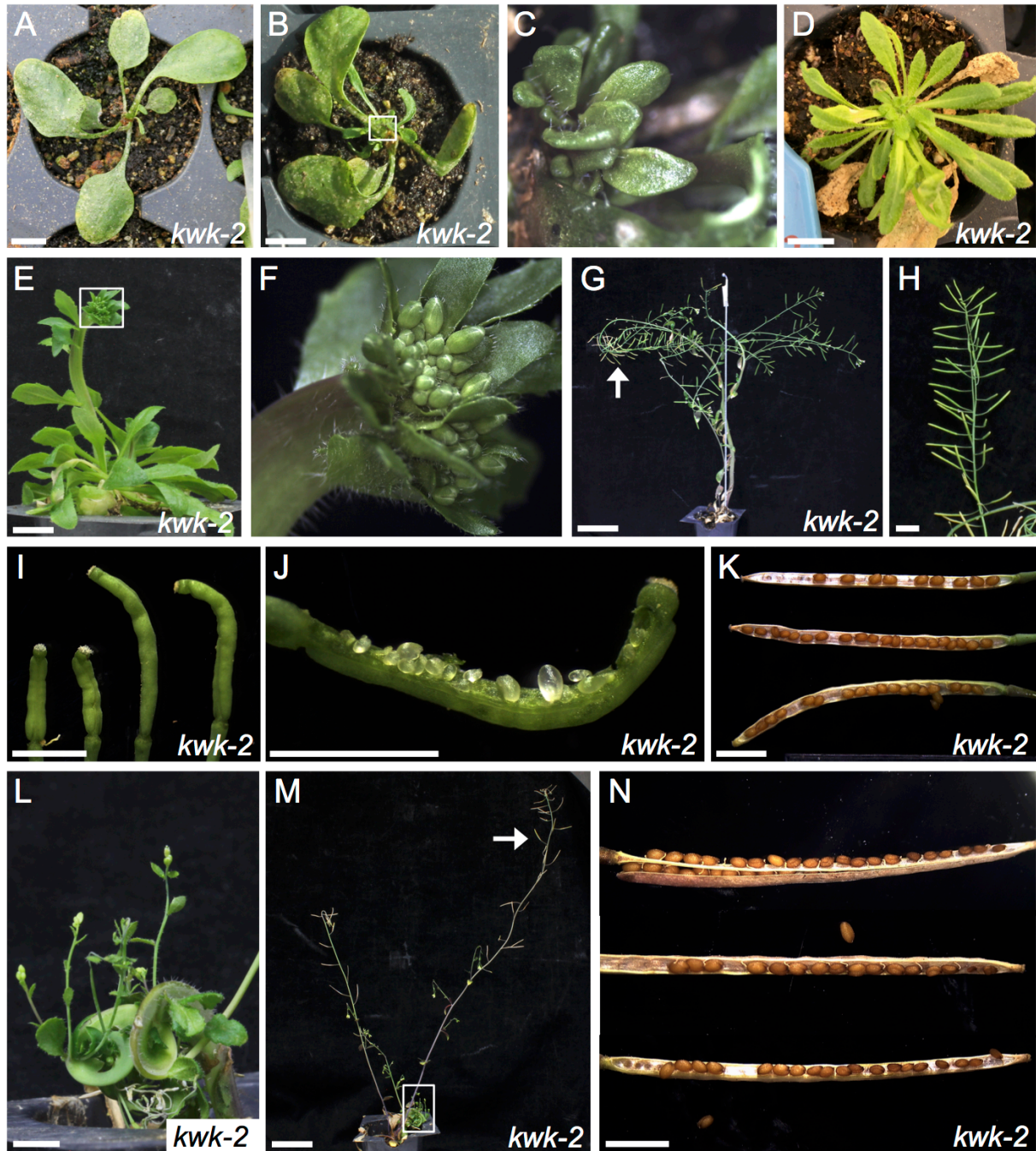


Figure S6. *kwk/abcg15* mutant phenotype in the Col-0 background.

A-N, Examples of *kwk-2* mutant plants severely affected in development. Young plant (A) affected in SAM development, producing few leaves (B), lateral growth is observed in older plant (D), C is a close-up of boxed region in B. E-F, The main inflorescence is affected producing abnormal fruits (I) with severe defects in ovule development (J). Secondary inflorescences seem to grow normally (G). H, a close-up of shoot marked in G with an arrow, the seed-set and development of these fruits (K) is similar to WT, but phyllotaxis is affected. L,M, Another plant with similar phenotypes, main shoot is severely affected (L is a close-up of boxed region in M). Secondary shoots (arrow in M) produce normal fruits (N). Scale bars = 1 cm in A-E and H; 5 cm in G and M; and 2 mm in I-K and N.

Figure S7. ARACNe-based coexpression network.

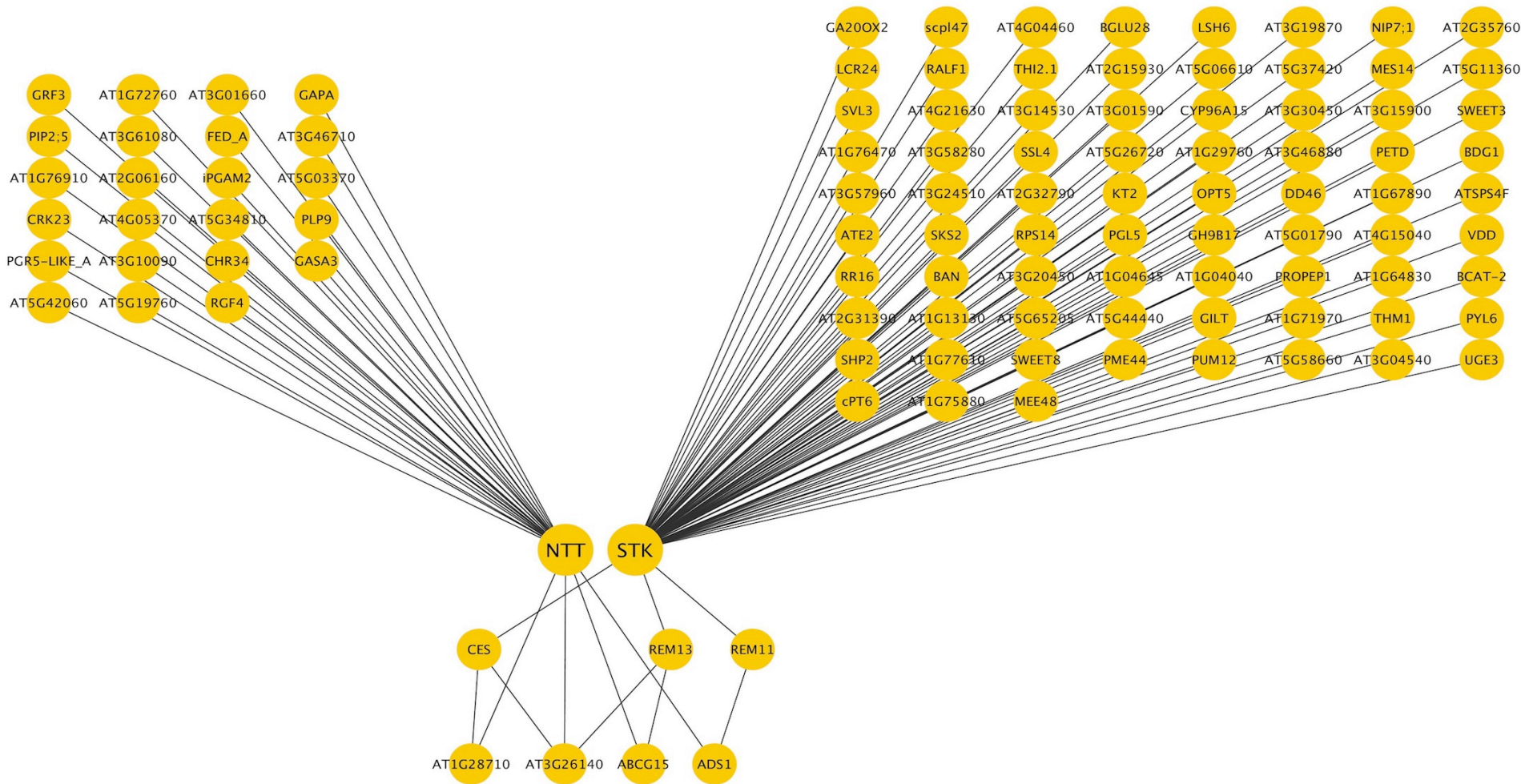


Table S1. Results of tested interactions in the Y2H assays.

The + simbol indicates yeast growth and blue intensity in LacZ assays.

- indicates no growth or no staining.

BD clone (AG ID)	BD clone (alias)	AD clone (AG ID)	AD clone (alias)	Selection medium 1		Selection medium 2	
				SD-ADE	LacZ	SD-HIS	LacZ
AT3G57670	NTT	AT1G77850	ARF17	+++	+++	+++	+++
AT3G57670	NTT	AT4G29080	IAA27	+++	+++	+++	+++
AT3G57670	NTT	AT3G57670	NTT	+++	+++	+++	+++
AT3G57670	NTT	AT4G00870	bHLH14	+++	+++	+++	+
AT3G57670	NTT	AT4G18960	AG	+++	-	+++	+++
AT3G57670	NTT	AT1G31140	GOA	+++	-	+++	+++
AT3G57670	NTT	AT4G09960	STK	+++	-	+++	+++
AT3G57670	NTT	AT4G37750	ANT	+	+	+++	+++
AT3G57670	NTT	AT2G37630	AS1	+	+	+++	+++
AT3G57670	NTT	AT2G21230	DKM	+	+	+++	+++
AT3G57670	NTT	AT1G19220	ARF19	+++	+++	-	-
AT3G57670	NTT	AT5G37020	ARF8	-	-	+++	+++
AT3G57670	NTT	AT4G17460	JAB	+++	+++	-	-
AT3G57670	NTT	AT1G70510	KNAT2	+++	+++	-	-
AT3G57670	NTT	AT2G46870	NGA1	+++	+++	-	-
AT3G57670	NTT	AT1G24260	SEP3	-	-	+++	+++
AT3G57670	NTT	AT2G27990	PNF	-	-	+++	+
AT3G57670	NTT	AT1G59750	ARF1	-	-	+++	+
AT3G57670	NTT	AT5G41410	BEL1	-	-	+++	+
AT3G57670	NTT	AT3G61970	NGA2	-	-	+	+
AT3G57670	NTT	AT2G45190	FIL	+++	+	-	-
AT3G57670	NTT	AT5G60450	ARF4	+	+	-	-
AT3G57670	NTT	AT3G15170	CUC1	+	+	-	-
AT3G57670	NTT	AT5G16560	KAN	+	+	-	-
AT3G57670	NTT	AT3G51060	STY1	+	+	-	-
AT3G57670	NTT	AT3G50330	HEC2	+	-	-	-
AT3G57670	NTT	AT3G61830	ARF18	-	-	-	-
AT3G57670	NTT	AT1G69180	CRC	-	-	-	-
AT3G57670	NTT	AT5G53950	CUC2	-	-	-	-
AT3G57670	NTT	AT2G33860	ETT	-	-	-	-
AT3G57670	NTT	AT5G67060	HEC1	-	-	-	-
AT3G57670	NTT	AT1G23380	KNAT6	-	-	-	-
AT3G57670	NTT	AT1G01030	NGA3	-	-	-	-
AT3G57670	NTT	AT1G68640	PAN	-	-	-	-
AT3G57670	NTT	AT2G34710	PHB	-	-	-	-
AT3G57670	NTT	AT3G54220	SCR1	-	-	-	-
AT3G57670	NTT	AT4G36260	STY2	-	-	-	-
AT3G57670	NTT	AT2G17950	WUS	-	-	-	-
AT3G57670	NTT	AT4G08150	BP	-	-	-	-
AT3G57670	NTT	AT5G02030	RPL	+	-	+++	+
AT3G57670	NTT	AT1G62360	STM	+++	+++	-	-
AT3G57670	NTT	AT5G60910	FUL	+++	-	+++	+++
AT3G57670	NTT	AT3G58780	SHP1	+++	-	+++	+++
AT3G57670	NTT	AT2G42830	SHP2	+++	-	+++	+++

* Reported in Marsch-Martínez, N. *et al.* (2014) *Plant J*, **80**, 69-81.

Table S2. ARACNe-based coexpression network of *NTT* and *STK*.Coexpression network: genes connected to *NO TRANSMITTING TRACT (NTT)*

<i>AGI ID</i>	<i>GENE ALIAS</i>	<i>BRIEF DESCRIPTION</i>	<i>SOURCE</i>
AT3G30350	RGF4	uncharacterized protein	[Source:EMBL;Acc:AEE77635.1]
AT5G38480	GRF3	14-3-3-like protein GF14 psi	[Source:EMBL;Acc:AED94323.1]
AT3G63200	PLP9	PATATIN-like protein 9	[Source:EMBL;Acc:AEE80447.1]
AT3G54820	PIP2;5	putative aquaporin PIP2-5	[Source:EMBL;Acc:AEE79295.1]
AT4G09600	GASA3	gibberellin-regulated protein 3	[Source:EMBL;Acc:AEE82770.1]
AT3G10090		40S ribosomal protein S28-1	[Source:EMBL;Acc:AEE74858.1]
AT5G42060		DEK, chromatin associated protein	[Source:EMBL;Acc:AED94761.1]
AT5G19760		Mitochondrial substrate carrier family protein	[Source:EMBL;Acc:AED92746.1]
AT1G72760		protein kinase-like protein	[Source:EMBL;Acc:AEE35369.1]
AT4G23310	CRK23	putative cysteine-rich receptor-like protein kinase 23	[Source:EMBL;Acc:AEE84737.1]
AT5G03370		acylphosphatase	[Source:EMBL;Acc:AED90593.1]
AT3G61080		protein kinase-like protein	[Source:EMBL;Acc:AEE80151.1]
AT1G76910		uncharacterized protein	[Source:EMBL;Acc:AEE35902.1]
AT3G26650	GAPA	glyceraldehyde-3-phosphate dehydrogenase A	[Source:EMBL;Acc:AEE77191.1]
AT2G21450	CHR34	chromatin remodeling 34	[Source:EMBL;Acc:AEC07179.1]
AT3G01660		S-adenosylmethionine-dependent methyltransferase domain-containing protein	[Source:EMBL;Acc:AEE73700.1]
AT4G05370		BCS1 AAA-type ATPase	[Source:EMBL;Acc:AEE82510.1]
AT3G46710		putative disease resistance RPP13-like protein 2	[Source:EMBL;Acc:AEE78196.1]
AT4G22890	PGR5-LIKE_A	Transmembrane protein present in thylakoids	[Source:EMBL;Acc:AEE84674.1]
AT3G08590	iPGAM2	2,3-biphosphoglycerate-independent phosphoglycerate mutase 2	[Source:EMBL;Acc:AEE74651.1]

Coexpression network: genes connected to *SEEDSTICK* (*STK*) (page 1)

AGI ID	GENE ALIAS	BRIEF DESCRIPTION	SOURCE
AT2G42830	SHP2	agamous-like MADS-box protein AGL5	[Source:EMBL;Acc:AEC10174.1]
AT5G18000	VDD	VERDANDI protein	[Source:EMBL;Acc:AED92494.1]
AT1G61720	BAN	anthocyanidin reductase	[Source:EMBL;Acc:AEE33879.1]
AT2G40670	ARR16 (RR16)	two-component response regulator ARR16	[Source:EMBL;Acc:AEC09862.1]
AT5G22980	scpl47	carboxypeptidase	[Source:EMBL;Acc:AED93104.1]
AT1G04040		HAD superfamily, subfamily IIIB acid phosphatase	[Source:EMBL;Acc:AEE27649.1]
AT1G72260	THI2.1	thionin 2.1	[Source:EMBL;Acc:AEE35295.1]
AT1G77610		EamA-like transporter	[Source:EMBL;Acc:AEE36000.1]
AT2G15930		uncharacterized protein	[Source:EMBL;Acc:AEC06449.1]
AT1G13130		Cellulase (glycosyl hydrolase family 5) protein	[Source:EMBL;Acc:AEE28973.1]
AT4G26590	ATOPT5 (OPT5)	oligopeptide transporter 5	[Source:EMBL;Acc:AEE85224.1]
AT5G24420	PGL5	6-phosphogluconolactonase 5	[Source:EMBL;Acc:AED93309.1]
AT3G20450		B-cell receptor-associated protein 31-like protein	[Source:EMBL;Acc:AEE76381.1]
AT4G33220	PME44	pectinesterase 44	[Source:EMBL;Acc:AEE86192.1]
AT1G10070	BCAT-2	branched-chain-amino-acid aminotransferase 2	[Source:EMBL;Acc:AEE28539.1]
AT5G58660		oxidoreductase, 2OG-Fe(II) oxygenase family protein	[Source:EMBL;Acc:AED97082.1]
AT2G32790		ubiquitin-conjugating enzyme E2 D/E	[Source:EMBL;Acc:AEC08742.1]
AT3G58280		phospholipase-like protein (PEARL1 4) with TRAF-like domain	[Source:EMBL;Acc:AEE79763.1]
AT1G07090	LSH6	uncharacterized protein	[Source:EMBL;Acc:AEE28076.1]
AT1G64830		aspartyl protease-like protein	[Source:EMBL;Acc:AEE34295.1]
AT2G31390		fructokinase	[Source:EMBL;Acc:AEC08541.1]
AT3G11240	ATE2	arginine-tRNA protein transferase 2	[Source:EMBL;Acc:AEE75019.1]
AT5G65205		Rossmann-fold NAD(P)-binding domain-containing protein	[Source:EMBL;Acc:AED98017.1]
AT5G37420		uncharacterized protein	[Source:EMBL;Acc:AED94186.1]
AT3G04540		defensin-like protein 44	[Source:EMBL;Acc:AEE74094.1]
AT2G44460	BGLU28	beta glucosidase 28	[Source:EMBL;Acc:AEC10422.1]

Coexpression network: genes connected to *SEEDSTICK* (page 2)

AGI ID	ALIAS	BRIEF DESCRIPTION	SOURCE
AT5G01790		uncharacterized protein	[Source:EMBL;Acc:AED90392.1]
AT1G29760		Putative adipose-regulatory protein (Seipin)	[Source:EMBL;Acc:AEE31126.1]
AT4G12960	GILT	Gamma interferon responsive lysosomal thiol (GILT) reductase family protein	[Source:EMBL;Acc:AEE83207.1]
AT4G14080	MEE48	putative glucan endo-1,3-beta-glucosidase A6	[Source:EMBL;Acc:AEE83368.1]
AT3G19870		uncharacterized protein	[Source:EMBL;Acc:AEE76302.1]
AT1G33990	ATMES14	methyl esterase 14	[Source:EMBL;Acc:AEE31655.1]
AT1G03680	ATHM1 (THM1)	thioredoxin M1	[Source:EMBL;Acc:AEE27596.1]
AT5G56510	APUM12 (PUM12)	pumilio 12	[Source:EMBL;Acc:AED96775.1]
AT4G15040		Subtilisin-like serine endopeptidase family protein	[Source:EMBL;Acc:AEE83544.1]
AT3G20520	SVL3	protein SEUSS-like 3	[Source:EMBL;Acc:AEE76390.1]
AT3G57960		Emsy N Terminus (ENT) domain-containing protein	[Source:EMBL;Acc:AEE79724.1]
AT1G71970		uncharacterized protein	[Source:EMBL;Acc:AEE35259.1]
AT2G40330	PYL6	abscisic acid receptor PYL6	[Source:EMBL;Acc:AEC09815.1]
AT5G51810	GA20OX2	gibberellin 20 oxidase 2	[Source:EMBL;Acc:AED96129.1]
AT4G29285	LCR24	defensin-like protein 163	[Source:EMBL;Acc:AEE85613.1]
AT5G44440		FAD-binding and BBE domain-containing protein	[Source:EMBL;Acc:AED95109.1]
AT5G11360		Interleukin-1 receptor-associated kinase 4 protein	[Source:EMBL;Acc:AED91665.1]
AT3G14530		geranylgeranyl diphosphate synthase 9	[Source:EMBL;Acc:AEE75535.1]
AT5G53190	SWEET3	Nodulin MtN3 family protein	[Source:EMBL;Acc:AED96320.1]
AT2G34520	RPS14	small subunit ribosomal protein S14	[Source:EMBL;Acc:AEC08984.1]
ATC00730	PETD	photosynthetic electron transfer D	[Source:TAIR;Acc:ATCG00730]
AT3G46880		uncharacterized protein	[Source:EMBL;Acc:AEE78214.1]
AT3G24510		defensin-like protein 259	[Source:EMBL;Acc:AEE76910.1]
AT5G40260	SWEET8	protein RUPTURED POLLEN GRAIN 1	[Source:EMBL;Acc:AED94527.1]
AT5G26720		uncharacterized protein	[Source:EMBL;Acc:AED93572.1]

Coexpression network: genes connected to *SEEDSTICK* (page 3)

AGI ID	ALIAS	BRIEF DESCRIPTION	SOURCE
AT1G76470		Rossmann-fold NAD(P)-binding domain-containing protein	[Source:EMBL;Acc:AEE35846.1]
AT3G15900		uncharacterized protein	[Source:EMBL;Acc:AEE75744.1]
AT1G75880		GDSL esterase/lipase EXL1	[Source:EMBL;Acc:AEE35769.1]
AT4G10120	ATSPS4F	sucrose-phosphate synthase	[Source:EMBL;Acc:AEE82845.1]
AT1G63180	UGE3	UDP-glucose 4-epimerase	[Source:EMBL;Acc:AEE34065.1]
AT4G21630		Subtilase family protein	[Source:EMBL;Acc:AEE84483.1]
AT1G67890		PAS domain-containing protein tyrosine kinase	[Source:EMBL;Acc:AEE34716.1]
AT3G51420	SSL4	strictosidine synthase-like 4 protein	[Source:EMBL;Acc:AEE78790.1]
AT5G51480	SKS2	Monocopper oxidase-like protein SKS2	[Source:EMBL;Acc:AED96089.1]
AT1G02900	ATRALF1	rapid alkalization factor 1	[Source:EMBL;Acc:AEE27494.1]
AT4G04460		phytepsin	[Source:EMBL;Acc:AEE82391.1]
AT1G57750	MAH1	cytochrome P450, family 96, subfamily A, polypeptide 15	[Source:EMBL;Acc:AEE33459.1]
AT3G01590		glucose-6-phosphate 1-epimerase	[Source:EMBL;Acc:AEE73693.1]
AT2G35760		uncharacterized protein	[Source:EMBL;Acc:AEC09157.1]
AT1G04645		self-incompatibility protein S1-like protein	[Source:EMBL;Acc:AEE27728.1]
AT2G40540	TRK2 (KT2)	potassium transporter 2	[Source:EMBL;Acc:AEC09846.1]
AT5G06610		uncharacterized protein	[Source:EMBL;Acc:AED91042.1]
AT5G64900	PROPEP1	elicitor peptide 1	[Source:EMBL;Acc:AED97966.1]
AT1G64670	BDG1	alpha/beta-hydrolase domain-containing protein	[Source:EMBL;Acc:AEE34272.1]
AT4G39000	GH9B17	endoglucanase 23	[Source:EMBL;Acc:AEE87006.1]
AT1G22015	DD46	putative beta-1,3-galactosyltransferase 5	[Source:EMBL;Acc:AEE30185.1]

Coexpression network core

<i>AGI ID</i>	<i>GENE ALIAS</i>	<i>BRIEF DESCRIPTION</i>	<i>SOURCE</i>
AT1G06080	ADS1	delta-9 acyl-lipid desaturase 1	[Source:EMBL;Acc:AEE27937.1]
AT1G28710		nucleotide-diphospho-sugar transferase domain-containing protein	[Source:EMBL;Acc:AEE31018.1]
AT3G26140		Cellulase (glycosyl hydrolase family 5) protein	[Source:EMBL;Acc:AEE77125.1]
AT5G60140	REM11	AP2/B3 domain-containing transcription factor	[Source:EMBL;Acc:AED97284.1]
AT3G46770	REM13	AP2/B3 domain-containing transcription factor	[Source:EMBL;Acc:AEE78203.1]
AT1G25330	HAF/CES	Transcription factor bHLH75	[Source:EMBL;Acc:AEE30607.1]
AT3G21090	ABCG15	ABC transporter G family member 15	[Source:EMBL;Acc:AAM13053.1]

Table S3. Primer list.

GENE ALIAS	GENE ID	EXPERIMENT	PRIMER NAME	SEQUENCE	FRAGMENT LENGTH (bp)
<i>Glycosyl Hydrolase</i>	AT3G26140	ChIP-qPCR	RT 1982 (FW carg3)	CGTGTTTGATTGAATACACCACCCT	172
			RT 1983 (REV carg3)	AACAAATCCTATGTTACTCAATCATAGCTT	
			RT 2631 (FW NTT-binding site)	AGAGCTAAGACGCATGTTTTGC	136
			RT 2632 (FW NTT-binding site)	ACACGCCAGCTTCACTCTTT	
		qRT-PCR	SdF1027	GTCCGATCACGACACGTAAA	198
			SdF1028	GTCGATTCCAAACTCGCTAAGA	
<i>ABCG15</i>	AT3G21090	ChIP-qPCR	SdF632 (At3g26140_probe_FW)	CACCCTTAGATCCAACCAAGGTC	193
			SdF633 (At3g26140_probe_REV)	GAGGCTGAGATGGTCTCCCC	
		qRT-PCR	RT 2070 (FW cargos 10-11)	CTTGTGGCTTGTCACTTGTGG	106
			RT 2071 (REV cargos 10-11)	ATCTTTGACCTTTGCACCACT	
			RT 2627 (FW NTT-binding site)	GACTTGCTTCAATTTTAGTGGCT	159
			RT 2628 (REV NTT-binding site)	TCGTCGGACAAAACTCTAAACTC	
<i>ADS1</i>	AT1G06080	ChIP-qPCR	SdF1029	AGATGAGCCGTGGAGCGTAT	100
			SdF1030	CCGTTTAGCCTTTGGAGCAA	
		qRT-PCR	RT 2072 (FW cargos 3-4)	AGGATGAGGTATCGATGGTTGC	124
			RT 2073 (REV cargos 3-4)	TGTATGTGGTGGACCAAGCA	
			RT 2633 (FW NTT-binding site)	CCGTTAGGTTTTGGTCACAGTC	163
			RT 2634 (REV NTT-binding site)	TTTACGGGTGGGTCCTCCAT	
<i>Nucleotide-diphospho-sugar transferase</i>	AT1G28710	ChIP-qPCR	SdF1023	TGTCCATTTCTCTGTCTCTTG	269
			SdF1024	TAGGACTATGTGGGTCCCTATC	
		qRT-PCR	RT 2130 (FW cargos 4-7)	TGGTGTTACATCCAAATCCGGT	156
			RT 2131 (REV cargos 4-7)	CGCAAAGAGAAGAGCAACGG	
			RT 2629 (FW NTT-binding site)	AATCGAACTGGGTCATCGACTT	134
			RT 2630 (REV NTT-binding site)	TCGGAATGCCCTTTGACTT	
<i>ACTIN2</i>		qRT-PCR	SdF1033	CCGCGGCTACAATCTTACTT	210
			SdF1034	AGCCTCATGTGCTACCATTTTC	
<i>ACTIN7</i>	AT5G09810	ChIP-qPCR	SdF1161	AATCACAGCACTTGCACC	100
			SdF1162	ATTCTTGACCTGCCTC	
<i>NTT</i>	AT5G09810	ChIP-qPCR	RT_045 (FW act7)	CGTTTCGCTTTCTTAGTGTTAGCT	132
			RT_046 (REV act7)	AGCGAACGGATCTAGAGACTCACCTTG	
<i>NTT</i>	AT3G57670	<i>NTT::GUS</i> line	S314	ATAATCGATCCGTGGAGCCAATATAGGTCGAAC	1216
			S318	TCTCCATGGTGAAGAGAGAGAGAGGAAGAGAAAGG	