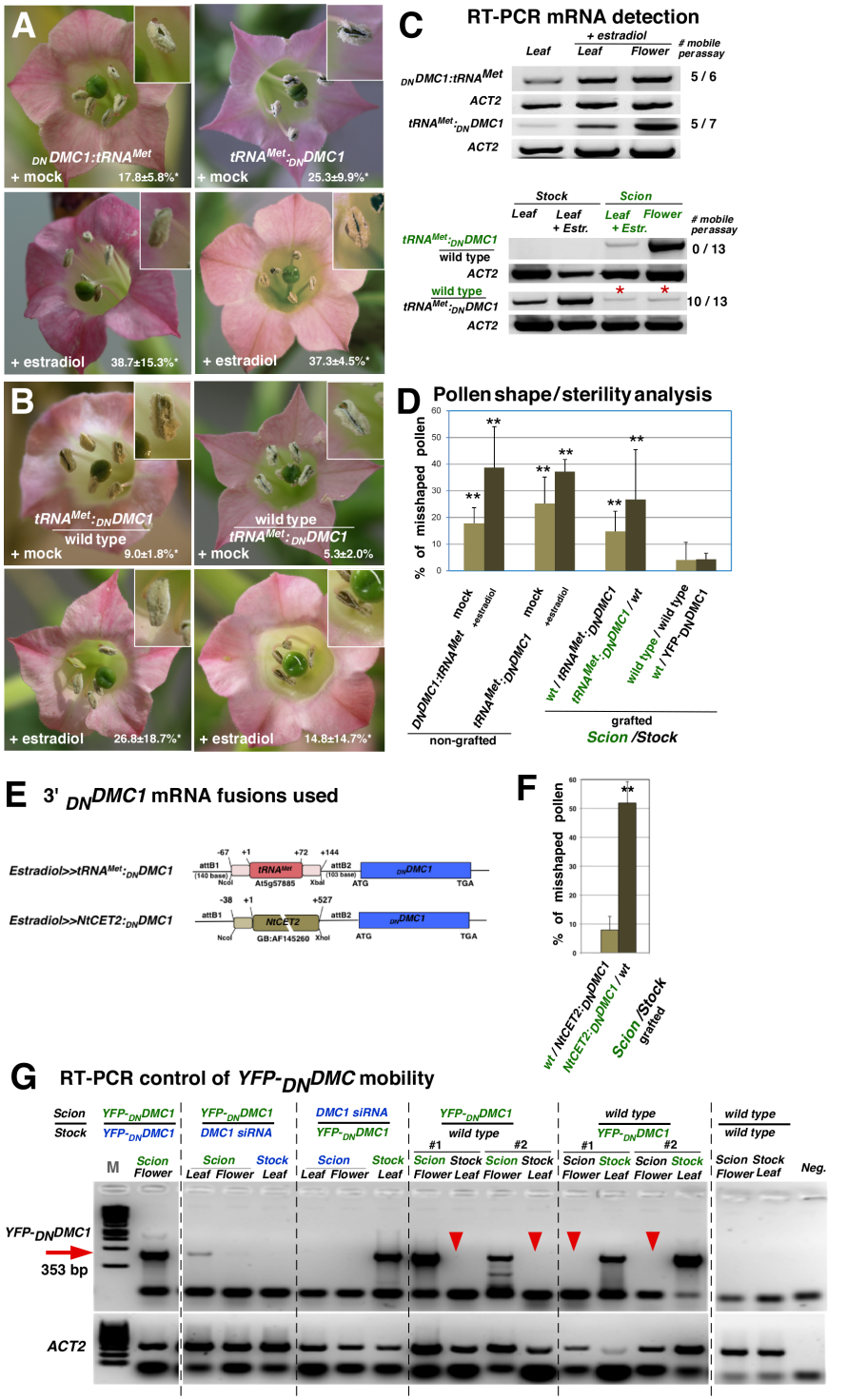
Supplemental Data. Zhang et al. (2016). Plant Cell 10.1105/tpc.15.01056

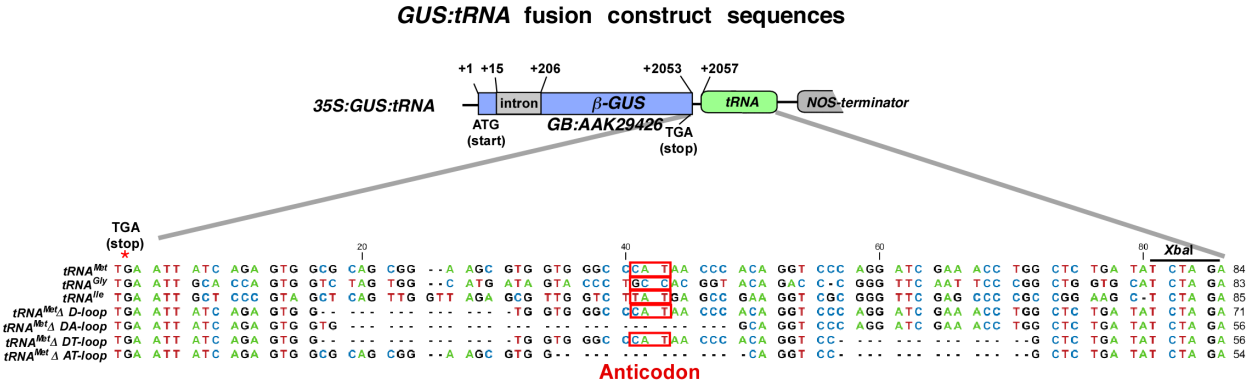
Supplemental Figure 1



Supplemental Figure 1. *tRNA^{Met}:$_{DN}$DMC1* movement into flowers and pollen phenotype.
(**A**) Upper panel: Flowers of non-grafted transgenic plants supported by *$_{DN}$DMC1:tRNA^{Met}* and *tRNA^{Met}:$_{DN}$DMC1* are fertile when mock treated. Lower panel: Application of estradiol inducing *$_{DN}$DMC1:tRNA^{Met}* and *tRNA^{Met}:$_{DN}$DMC1* expression resulted in partially sterile anthers suggesting production of the dominant negative $_{DN}$DMC1 protein.

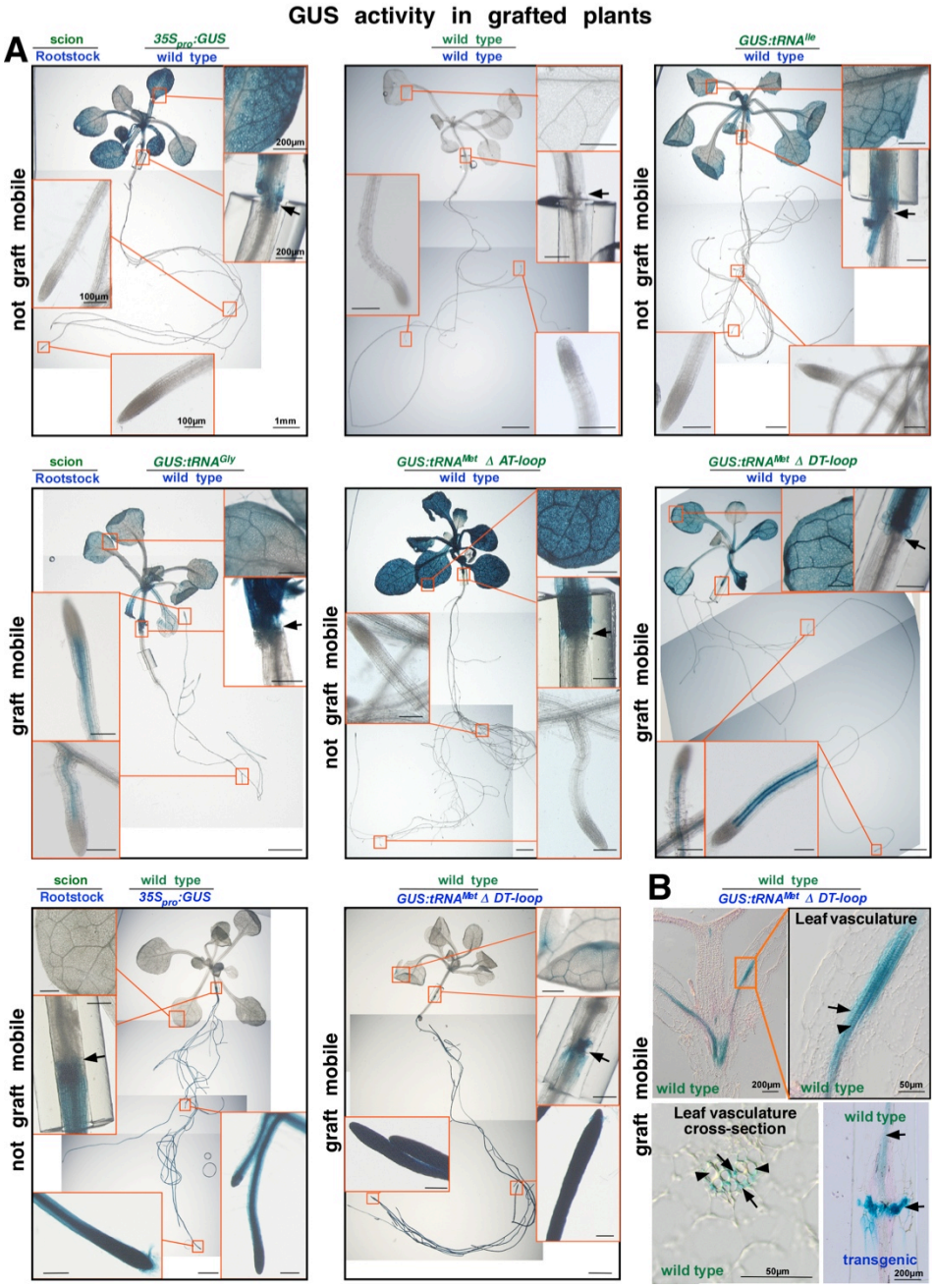
(**B**) Upper panel: Grafted *tRNA^{Met}:$_{DN}$DMC1* / wild-type or wild-type / *tRNA^{Met}:$_{DN}$DMC1* plants showed partial sterile pollen production when mock treated. Lower panel: After application of estradiol onto grafted *tRNA^{Met}:$_{DN}$DMC1* / wild-type or wild-type / *tRNA^{Met}:$_{DN}$DMC1* plants formation of aberrant pollen / sterile anthers in wild-type flowers suggest *tRNA^{Met}:$_{DN}$DMC1* mRNA transport and expression of the truncated DMC1 protein in wild-type male organs. (**C**) RT-PCR assays on poly(A)-RNA samples from transgenic *$_{DN}$DMC1*:*tRNA^{Met}* (n=6) and *tRNA^{Met}:$_{DN}$DMC1* (n=7) tissues indicate presence of fusion transcripts in both transgenic and in wild-type scion flowers (red asterisks) suggesting mobility of the *tRNA^{Met}:$_{DN}$DMC1* fusion transcript over graft junctions. The number of grafted plants tested is shown on the right. *ACTIN2 (ACT2)* specific RT-PCR was used as a positive control. (**D**) Statistical analysis of misshapen pollen appearing on grafted plants (Supplemental Table 1). Compared to mock treated control grafts production of misshaped pollen was significantly higher in estradiol treated *$_{DN}$DMC1*:*tRNA^{Met}* and *tRNA^{Met}:$_{DN}$DMC1* transgenic plants and in wild-type scions supported by *tRNA^{Met}:$_{DN}$DMC1*. (**E**) Schematic drawing of the *$_{DN}$DMC1* RNA fusion constructs. (**F**) Statistical analysis of misshapen pollen appearing on *CET2*:*$_{DN}$DMC1 /* wild-type grafted plants indicate lack of misshapen pollen appearing on wild-type flowers suggesting that neither the fusion transcript nor the encoded $_{DN}$DMC1 protein is not transferred from stock to scion. (**G**) RT-PCR assays on poly(A)-RNA samples from grafted YFP-$_{DN}$DMC1 transgenic plants. Red arrowheads indicate lack of detectable transcript in wild-type plant parts. Asterisks indicate statistically significant differences against controls using Chi-square test of independence of variables in a contingency table. Biological replicates: n>8. Error bars indicate S.D.. For details and number of independent transgenic *$_{DN}$DMC1:tRNA^{Met}* or *tRNA^{Met}:$_{DN}$DMC1* lines used in the grafting experiments see Supplemental Table 1.

Supplemental Figure 2



Supplemental Figure 2. tRNA sequences fused to the 3'UTR of *GUS*.
Alignment of tRNA sequences fused to the *GUS* coding DNA sequence. The *GUS* sequence harboring an intron was fused with *tRNA*^{Met} (CAU), *tRNA*^{Gly} (GCC), *tRNA*^{Ile} (TAT) and deletion variants of *tRNA*^{Met} (CAU) named *tRNA*^{Met} Δ*D*, Δ*DA*, Δ*DT*, and Δ*AT*. The length of tRNA sequences (counted from the *GUS* ATG start codon) is indicated at the right. Asterisks indicate the *GUS* TGA stop codon. Red boxes indicate the anticodon sequence of the cloned tRNAs.

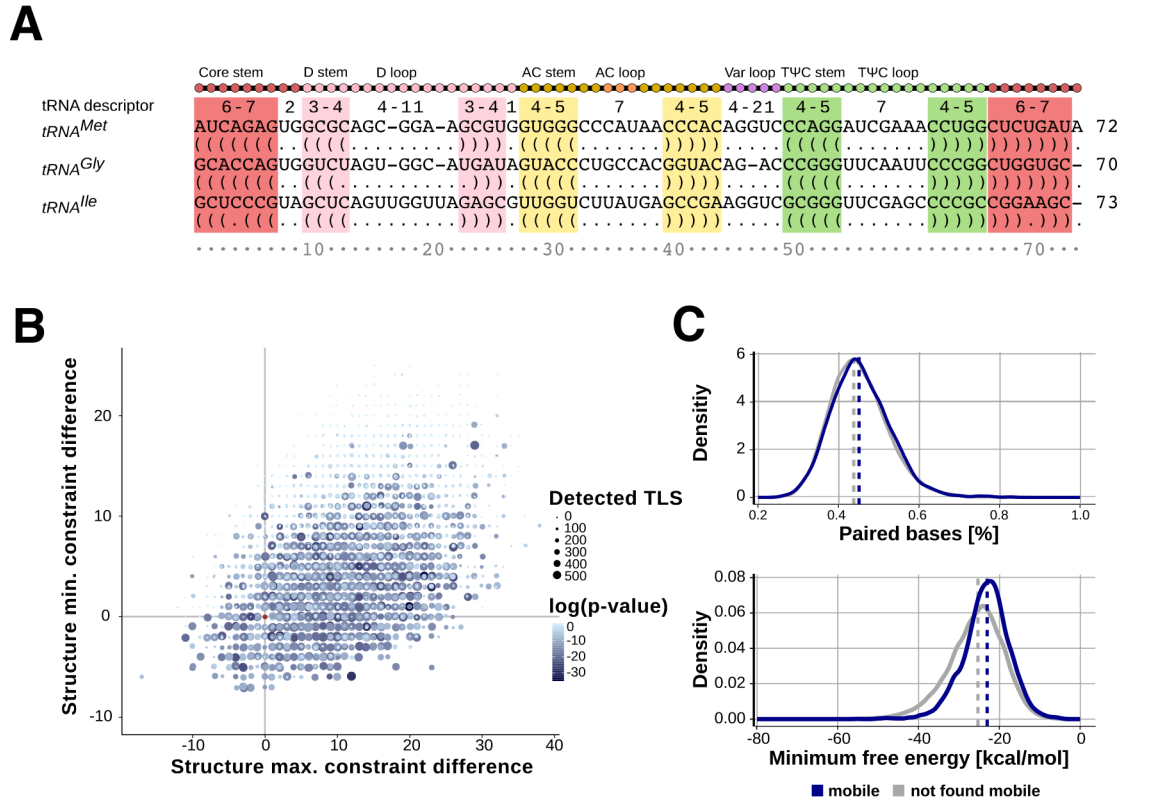
Supplemental Figure 3



Supplemental Figure 3. Images of hypocotyl-grafted wild-type / *GUS:tRNA* transgenic plants.

(**A**) Example images of *Arabidopsis thaliana* Col-0 plants that were hypocotyl grafted. The presented wild-type (Col-0) / transgenic plant graft combinations are indicated above. Magnified images of leaf areas, root tips, and graft junction (arrows) are indicated by orange rectangles. Blue colored tissues in the shown plant parts indicate presence of GUS activity. (**B**) Micrographs of thin sections made on a paraffin-embedded grafted plant. Wild type was grafted with *GUS:tRNA^{Met} ΔDT* transgenic stocks. GUS enzymatic activity (blue color) was detected in vascular cells of wild-type leaves and wild-type hypocotyl in cells associated to the vasculature (arrows). Arrowheads indicate xylem vessels.

Supplemental Figure 4

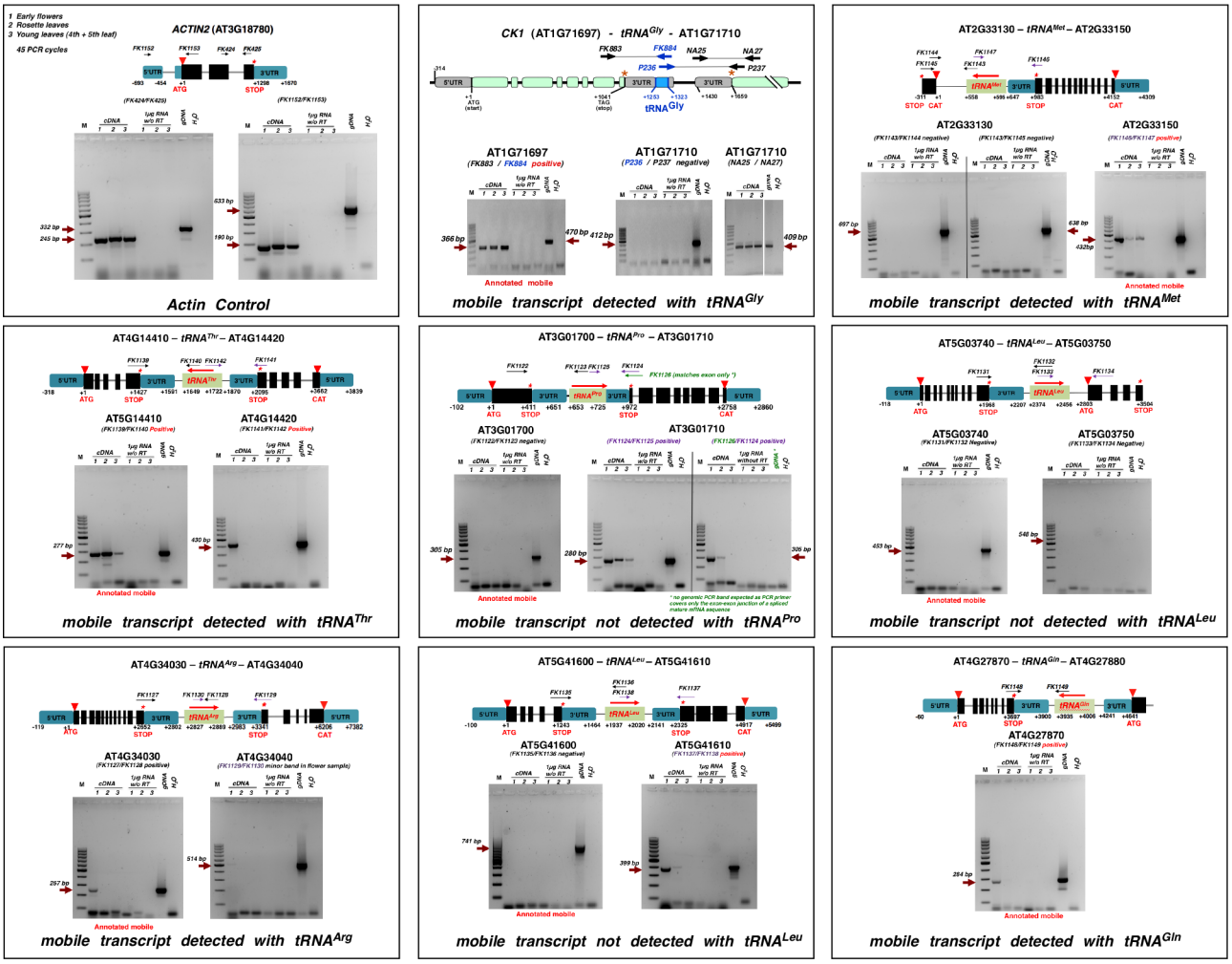


Supplemental Figure 4. Computational analysis of tRNA-like sequences (TLS) present in mobile mRNAs.

(**A**) tRNA structure descriptor and structural alignment of *tRNA*^{Met}, *tRNA*^{Gly}, and *tRNA*^{Ile}. The numbers indicate the accepted descriptor ranges of structural elements (stem and loops). Note that the tRNA descriptor does not recognize the structure of the *tRNA*^{Ile} which did not confer mobility when fused to GUS. (**B**) Evaluation of parameter space for the tRNA descriptor constraints. Given a tRNA descriptor model, we tested for enrichment of TLS in mobile relative to non-mobile predicted gene transcripts. The default tRNA descriptor (indicated by a red circle at coordinate origin, p=0.001) indicates an enriched number of hits in mobile transcripts in comparison to non-mobile transcripts. Departure from the default tRNA descriptor parameters is expressed by the sum over differences of the constraint values for the minimum element length (y-axis) as well as by the sum over the maximum element length differences (x-axis). Out of 20,000 produced descriptors, 13,598 that have less than 5,000 gene hits to the non-mobile dataset (excluding tRNA genes) were plotted. Coloring is according to p-values resulting from the counts of motif hits to mobile versus non-mobile transcript sequences (Fisher's exact test), point sizes indicate the number of hits to mobile transcripts. Increasing minimum stem and loop lengths in the RNA structure models result in lower numbers of matches in the mobile transcript dataset. Similarly, relaxing maximum length constraints results in larger number of false positive matches in the non-mobile dataset and, thus, motif hits to mobile versus non-mobile transcripts get less significant. (**C**) Degree of structuredness associated with the predicted structure of the 150 nt 3'-terminal sequence region of mobile (n=3,606) vs. non-mobile (n=23,132) predicted mRNAs. Upper graph shows structuredness in terms of number of predicted paired bases. Lower graph in terms of predicted minimum free energy (MFE). The vertical dashed lines denote the medians of the two distributions.

Supplemental Figure 5

RT-PCR detection of di-cistronic tRNA transcripts



Supplemental Figure 5. RT-PCR assays confirming the presence of di-cistronic poly(A)-RNA:tRNA transcripts in wild-type *A. thaliana* flowers and leaves.

The upper left panel shows a control for the performed poly(A) RT-PCR assays (45 cycles) and used RNA samples. *ACTIN2* (AT3G18780) specific primers were used to evaluate presence of transcripts and potential genomic DNA (gDNA) contamination prior to assaying mRNA:tRNA di-cistronic transcription of seven selected graft-mobile mRNAs. For this purpose an RT-reaction for all primer combinations was performed in parallel without adding reverse transcriptase (1 µg RNA w/o RT). gDNA was used as a positive control for the primer combinations and PCR reactions. In each panel schematic drawings of the genomic loci indicate gene arrangements and distances to neighboring tRNA loci according to TAIR10. Arrows and primer ID numbers indicate PCR primer matching sites and identity (see Supplemental Table 2). Red arrows indicate expected PCR bands and size. RNA samples were harvested from wild-type *A. thaliana* (Col-0) plants. Sample 1: early inflorescences; Sample 2: mature rosette leaves, both from plants grown on soil in the greenhouse; Sample 3: 4th and 5th leaf from ~3 weeks old seedlings grown under controlled conditions on 1x MS medium. For an overview of the results see Figure 4C and Supplemental Data Set 2.

Supplemental Table 1. Pollen shape analysis of wild-type, transgenic, and grafted plants.

	Scion / Stock	# of plants with visual pollen sterility (# of plants)	# independent lines	# of pollen analyzed (# plants)	% misshapen pollen	P - value	Significance
	hpDMC1 siRNA	10 (10)	3	5101 (10)	78.08 ± 10.86 %	0.0	***
Controls	**wild type**	0 (10)	3	5365 (10)	7.51 ± 2.59 %	-	ns
	YFP-$_{DN}$ DMC1	0 (6)	3	947(4)	3.27 ± 1.84 %	-	ns
	wild type / wild type (before estradiol induction)	0 (12)	3	1187(7)	4.04 ± 3.00%	-	ns
	wild type / wild type (after estradiol induction)	0 (6)	3	643 (6)	3.27 ± 3.96%	-	ns
Control grafts	**wild type /** YFP-$_{DN}$ DMC1	0 (8)	3	1068 (4)	5.62 ± 3.10 %	-	ns
	YFP-$_{DN}$DMC1 **/ wild type**	0 (6)	2	3664 (5)	5.84 ± 1.31 %	-	ns
	YFP-$_{DN}$DMC1 **/ YFP-**$_{DN}$ DMC1	0 (6)	4	824 (3)	4.13 ± 2.83 %	-	ns
	wild type / $_{DN}$*DMC1:tRNA*^{Met} (before estradiol induction)	0 (6)	3	239 (3)	3.35 ± 1.32 %	-	ns
	wild type / $_{DN}$*DMC1:tRNA*^{Met} (after estradiol induction)	11 (17)	8	1525 (6)	14.23 ± 7.60 %	3.76e-24	***
$_{DN}$***DMC1: tRNA***^{Met} **grafts**	$_{DN}$*DMC1:tRNA*^{Met} / **wild type** (before estradiol induction)	3 (6)	3	416 (3)	13.94 ± 2.28 %	3.78e-10	***
	$_{DN}$*DMC1:tRNA*^{Met} / **wild type** (after estradiol induction)	16 (19)	9	2331 (8)	38.65± 22.46 %	7.52e-270	***
	YFP:$_{DN}$DMC1 / $_{DN}$*DMC1:tRNA*^{Met} (after estradiol induction)	2 (5)	2	374 (1)	10.96 ± 0.00 %	0.00417	**
	wild type / $_{DN}$*DMC1:BEL5* (before estradiol induction)	0 (4)	2	433 (2)	8.08 ± 0.76 %	0.51261	ns
	wild type / $_{DN}$*DMC1:BEL5* (after estradiol induction)	10 (14)	4	1398 (10)	19.67 ± 14.33 %	3.60e-65	***
$_{DN}$***DMC1:BEL5*** **grafts**	$_{DN}$*DMC1:BEL5* / **wild type** (before estradiol induction)	3 (4)	2	243 (2)	21.40 ± 6.92 %	9.04e-65	***
	$_{DN}$*DMC1:BEL5* / **wild type** (after estradiol induction)	12 (14)	6	1200 (5)	30.92 ± 7.56 %	8.43e-221	***

***tRNA^{Met}:$_{DN}$DMC1* grafts**	**wild type** / *tRNA^{Met}:$_{DN}$DMC1* (before estradiol induction)	0 (4)	2	398 (2)	5.28 ± 2.02 %	-	ns
	wild type / *tRNA^{Met}:$_{DN}$DMC1* (after estradiol induction)	14 (21)	4	2291 (8)	14.80 ± 14.73 %	2.42401e-27	***
	tRNA^{Met}:$_{DN}$DMC1 / **wild type** (before estradiol induction)	2 (4)	2	332 (3)	9.04 ± 1.78 %	0.01835	*
	tRNA^{Met}:$_{DN}$DMC1 / **wild type** (after estradiol induction)	18 (22)	6	4540 (12)	26.81 ± 18.68 %	1.34e-177	***
Non-grafted transgenic plants	*$_{DN}$DMC1:tRNA^{Met}* (before estradiol induction)	3 (6)	6	723 (2)	17.48 ± 5.83 %	4.10e-22	***
	$_{DN}$DMC1:tRNA^{Met} (after estradiol induction)	6 (6)	6	555 (4)	38.74 ± 15.32 %	3.92e-115	***
	$_{DN}$DMC1:BEL5 (before estradiol induction)	2 (5)	5	709 (4)	5.92 ± 2.61 %	-	ns
	$_{DN}$DMC1:BEL5 (after estradiol induction)	5 (5)	5	313 (3)	56.87 ± 6.24 %	1.77e-175	***
	tRNA^{Met}:$_{DN}$DMC1 (before estradiol induction)	3 (6)	6	637 (2)	25.27 ± 9.91 %	5.15e-56	***
	tRNA^{Met}:$_{DN}$DMC1 (after estradiol induction)	5 (6)	6	287 (3)	37.28 ± 4.45 %	1.29e-84	***

Asterisks indicate statistical significance regarding the enhanced number of misshaped pollen against wild-type control using Chi-square test of independence of variables in a contingency table (ns - not significant, * p-value ≤ 0.05, ** p-value ≤ 0.01, *** p-value ≤ 0.001)

Supplemental Table 2. Oligonucleotides used in the study.

Construct	Primer sequences	Purpose / Size of PCR fragment
$_{DN}$*DMC1:BEL5*	FK868-F 5' GATGCTCCGAATCTCGCTGA 3'	
	FK869-R 5'-GTTGCTTGCTGCTGGTGAAG 3'	491 bp
$_{DN}$*DMC1: tRNA*^{Met}	FK868-F 5' GATGCTCCGAATCTCGCTGA 3'	
	FK851-R 5'-TTCCGCTGCGCCACTCTGATT 3'	260 bp
DMC1: tRNA^{Met}	FK868-F 5' GATGCTCCGAATCTCGCTGA 3'	
	FK851-R 5'-TTCCGCTGCGCCACTCTGATT 3'	260 bp
tRNA^{Met}*:*$_{DN}$*DMC1*	FK774-F 5' ATAACCCACAGGTCCCAG 3'	
	FK771-R 5' TTCCATTCCCTCCTTTCA 3'	422 bp
YFP- $_{DN}$DMC1	FK938-F 5' CCCGACAACCACTACCTGAG 3'	
	FK858-R 5' TCATCGAGAGCTTGACACCCTGT 3'	353 bp
Actin (GB: X69885)	FK422-F 5' CACCGGTATTGTGTTGGACTC 3'	
	FK423-R 5' AGGACCTCAGGACAACGGAAACG 3'	303 bp
ACTIN2 (At3g18780)	FK424-F 5' GGAAGGATCTGTACGGTAAC 3'	245 bp
	FK425-R 5' TGTGAACGATTCCTGGACCT 3'	
BP T-DNA insertion verification primer for *CHOLINE KINASE 1 (CK1)* mutant	FK907-F 5' ATTTTGCCGATTTCGGAAC 3'	504-804 bp
LP primer salk_023420	FK908-R 5' TGGTTCATTACAGGAGAACCG 3'	1096 bp
RP primer salk_023420	FK909-F 5' TTTGTGAATCTCAGGGAATGC 3'	BP+RP 504-804 bp
LP primer salk_070759	FK914-R 5' AGCAGCCATCTCACAAAAGTG 3'	1012 bp
RP primer salk_070759	FK915-R 5' TCTAAAACGCGTTTTGCAAAC 3'	BP+RP 492-792 bp
CK1:*tRNA*^{Gly} detection	FK883-F 5' CTATGGGGAATCATCTCGGG 3'	331 bp
	FK884-R 5' CACTAGACCACTGGTGCTTC 3'	
CK1:*tRNA*^{Gly} *detection*	FK883-F 5' CTATGGGGAATCATCTCGGG 3'	392 bp
	FK992-R 5' CCGTGGCAGGGTACTATCAT 3' '	
CK1-tRNA^{Gly} mobility detection specific for *ck1.2* (salk_023420)	FK883-F 5' CTATGGGGAATCATCTCGGG 3'	309 bp
	FK962-R 5' GTAGACTATATATTGTGGTGTAAAC 3'	

Construction of *GUS-tRNA fusion* forward primer	FK963-F 5' CTAG CCATGG TAGATCTGAGG 3'	
Construction of *GUS- tRNA^{Gly}* reverse primer	FK944-R 5' GCG CGG TGA CCT GCA CCA GCC GGG AAT TGA ACC CGG GTC TGT ACC GTG GCA GGG TAC TAT CAT GCC ACT AGA CCA CTG GTG CAA TTC ACA CGT GAT GGT GAT GGT G 3'	Size of GUS-Gly tRNA 2141 bp
Construction *of GUS- tRNA^{Met}* reverse primer	FK945-R 5' GCG CGG TGA CCT ATC AGA GCC ACC TT CGA TCC TGG GAC CTG TGG GTT ATG GGC CCA CCA CGC TTC CGC TGC GCC ACT CTG ATA ATT CAC ACG TGA TGG TGA TGG TG 3'	Size of GUS-Met tRNA 2141 bp
Construction *GUS- tRNA^{Ile}* reverse primer	FK946-R 5' GCG CGG TGA CCG CTT CCG GCG GGG CTC GAA CCC GCG ACC TTC GGC TCA TAA GAC CAA CGC TCT AAC CAA CTG AGC TAC GGG AGC AAT TCA CAC GTG ATG GTG ATG GTG 3'	Size of GUS-Met tRNA 2142 bp
Construction *GUS- tRNA^{Met} D loop deletion (dD)* reverse primer	FK948-R 5' GCG CGG TGA CCT ATC AGA GCC AGG TTT CGA TCC TGG GAC CTG TGG GTT ATG GGC CCA CCA CCA CTC TGA TAA TTC ACA CGT GAT GGT GAT GGT G - 3'	Size of GUS-Met tRNA dD 2128 bp
Construction *of GUS- tRNA^{Met} D Anticodon loop deletion (dDA)* reverse primer	FK950-R 5' GCG CGG TGA CCT ATC AGA GCC AGG TTT C GAT CCT GGG ACC TGC CAC CAC TCT GAT AAT TCA CAC GTG ATG GTG ATG GTG 3'	Size of GUS-Met tRNA dDT 2113 bp
Construction *GUS- tRNA^{Met} D and TΨC loop deletion (dDT)* reverse primer	FK949-R 5' G CGC GGT GAC CTA TCA GAG CGG ACC TGT GGG TTA TGG GCC CAC CAC CAC TCT GAC AAT TCA CAC GTG ATG GTG ATG GTG 3'	Size of GUS-Met tRNA dDA 2113 bp
Construction *GUS- tRNA^{Met} Anticodon and TΨC loop deletion (dAT)* reverse primer	FK947-R 5' GC GCG GTG ACC TAT CAG AGC GGA CCT GCC ACG CTT CCG CTG CGC CAC TCT GAT AAT TCA CAC GTG ATG GTG ATG GTG 3'	Size of GUS-Met tRNA dAT 2111 bp
Adding *tRNA^{Met}* + XbaI +*BstEII* reverse primer	FK951-R 5' gcgc GGTGACC TCTAGA TATCAGAGC 3'	
Adding *tRNA^{Gly}* + XbaI +*BstEII* reverse primer	FK952-R 5' gcgc GGTGACC TCTAGA TGCACC 3'	
Adding *tRNA^{Ile} XbaI +BstEII* reverse primer	FK953-R 5' gcgc GGTGACC TCTAGA GCTTCCGG 3'	

GUS RNA mobility test	FK1091-F 5' CAACAGCTTCCGGACCGCAC 3'	428 bp
	FK1092-R 5' GATTGAGCGCGATGACGTCA 3'	
GUS:*tRNA^{Met}* mobility	FK1079-F 5' CGAGTACTACCAGGCGAACC 3'	316 bp
	FK1081-R 5' CAGAGCCAGGTTTCGATCCTG 3'	
GUS:*tRNA^{Gly}* mobility	FK1079-F 5' CGAGTACTACCAGGCGAACC 3'	281 bp
	FK1086-R 5' GCAGGGTACTATCATGCCAC 3'	
GUS:*tRNA^{Ile}* mobility	FK1080-F 5' ACCACGTCGTGTTCGATGAG 3'	272 bp
	FK1085-R 5' GGCTCATAAGACCAACGCTC 3'	
Construction *of GUS*:*tRNA^{Met} D loop deletion (dD)* reverse primer	FK1079-F 5' CGAGTACTACCAGGCGAACC 3'	316 bp
	FK1081-R 5' CAGAGCCAGGTTTCGATCCTG 3'	
GUS:*tRNA^{Met} D and TΨC* loop deletion (dDT) mobility verification	FK1080-F 5' ACCACGTCGTGTTCGATGAG 3'	255 bp
	FK1083-R 5' GTTATGGGCCCACCACCACTC 3'	

GUS:*tRNA*^{Met} *D and Anticodon* loop deletion *(dDA)* mobility verification	FK1079-F 5' CGAGTACTACCAGGCGAACC 3'	274 bp
	FK1084-R 5' GATCCTGGGACCTGCCAC 3'	
GUS:*tRNA*^{Met} *Anticodon and TΨC loop deletion (dAT)* reverse primer	FK1079-F 5' CGAGTACTACCAGGCGAACC 3'	292 bp
	FK1082-R 5' GCTGCGCCACTCTGATAATTC 3'	
GUS / NOS terminator RNA mobility RT-PCR primer	FK1099-F 5' AGAACGCTAGCCATCACCATC 3'	127 bp
	FK1100-R 5' GCCAAATGTTTGAACGATCGGG 3'	
GUS / NOS terminator mobility RT-PCR primer	FK1099-F 5' AGAACGCTAGCCATCACCATC 3'	135 bp
	FK1090-R 5' GCAAGACCGGCAACAGGAT 3'	
ACTIN2 RT-qPCR (AT3G18780)	FK1097-F 5' TCCCTCAGCACATTCCAGCAGAT 3'	69 bp
	FK1098-F 5' AACGATTCCTGGACCTGCCTCATC 3'	
UBQ10 RT-qPCR (AT4G05320)	FK1095-F 5' CACACTTCACTTGGTCTTGCGT 3'	61 bp
	FK1096-R 5' TAGTCTTTCCGGTGAGAGTCTTCA 3'	
CK1 primer used in RT-qPCR shown in Figure 4F	FK1105-F 5' ATCTTCTGGGGACTATGGGGA 3'	126 bp
	FK1106-R 5' TCATCCTTCAAGAAGCAAAGGC 3'	
CK1 primer used in RT-qPCR (equivalent results as with FK1096 and FK1105)	FK1107-F 5' TCATACACGCCAGAACTCTTTC 3'	198 bp
	FK1108-R 5' CCAACCGATACTTATCCATCTCTA 3'	
AT3G01700-*tRNA*^{Pro} di-cistronic poly(A) RT-PCR	FK1122-F 5' CCGGATTCTTCATCTTCTCTCTCT 3'	305 bp
	FK1123-R 5' CCTAAGCGAGAATCATACCACTAGACC 3'	
tRNA^{Pro}-AT3G01710 di-cistronic poly(A) RT-PCR	FK1124-F 5' GTTACAGTAGCAGAGAGGTCTTACA 3'	280 bp
	FK1125-R 5' CGAGTTCAATTCTCGGAATGCC 3'	
tRNA^{Pro}-AT3G01710 di-cistronic poly(A) RT-PCR	FK1126-F 5' CAACAGACCAAACTAAGAAAGCTC 3'	305 bp
	FK1125-R 5' CGAGTTCAATTCTCGGAATGCC 3'	
AT4G34030-*tRNA*^{Arg} di-cistronic poly(A) RT-PCR	FK1127-F 5' CCTTTAGAAGATACTCGATTTGGTGTC 3'	257 bp
	FK1128-R 5' GTCTGATTAGAAGTCAGACGCCT 3'	
tRNA^{Arg}-AT4G34040 di-cistronic poly(A) RT-PCR	FK1129-F 5' CGACATAAAAGCACCGTTCC 3'	514 bp
	FK1130-R 5' GGCCCAATGGATAAGGCGT 3'	
AT5G03740-*tRNA*^{Leu} di-cistronic poly(A) RT-PCR	FK1131-F 5' CAGTGCAGCTGCTTGAGAAGA 3'	453 bp
	FK1132-R 5' GTCTTCCCCCTTAACCACTCG 3'	
tRNA^{Leu}-AT5G03740 di-cistronic poly(A) RT-PCR	FK1133-F 5' GGTTTGCCCGAGTGGTTAAG 3'	548 bp
	FK1134-R 5' GACAAGGTGCAGCTTCTTTGA 3'	
AT5G41600-*tRNA*^{Leu} di-cistronic poly(A) RT-PCR	FK1135-F 5' CTCTGAACAAGAAGAAGGATTAAGG 3'	741 bp
	FK1136-R 5' CCTTAGACCACTCGGCCATC 3'	

tRNA^{Leu}-AT5G41610 di-cistronic poly(A) RT-PCR	FK1137-F 5' GACTTCTACGGATAAAGACTCTGA 3'	399 bp
	FK1138-R 5' TCTAAGGCGCCAGACTCAAG 3'	
AT4G14410-*tRNA*^{Thr} dicistronic poly(A) RT-PCR	FK1139-F 5'GCCTCCTGCTGCTTAAACTCT 3'	277 bp
	FK1140-R 5' GTAAGCGGGAGGTCTTGAGT 3'	
tRNA^{Thr}-AT4G14420 dicistronic poly(A) RT-PCR	FK1141-F 5' GCTCCAAAGGCAAAAGCAAAC 3'	430 bp
	FK1142-R 5' AACGGGTGCTCTAACCAACT 3'	
AT2G33130-*tRNA*^{Met} di-cistronic poly(A) RT-PCR	FK1143-F 5' GCTAGCGCGTAGGTCTCATA 3'	638 bp
	FK1144-R 5' GAAGCAAAGCTGCCGAGATG 3'	
AT2G33130-*tRNA*^{Met} di-cistronic poly(A) RT-PCR	FK1143-F 5' GCTAGCGCGTAGGTCTCATA 3'	697 bp
	FK1145-R 5' TTCTCCACCGTCCATGCAAT 3'	
tRNA^{Met}-AT2G33150 di-cistronic poly(A) RT-PCR	FK1146-F 5' CGCTCGCTAGAGAGGACCAT 3'	432 bp
	FK1147-R 5' GACCTACGCGCTAGCCAACT 3'	
AT4G27870-tRNA^{Gln} di-cistronic poly(A) RT-PCR	FK1148-F 5' CTGAAACTGAATCTTGCCTGGAG 3'	284 bp
	FK1149-R 5' GGACTCTGAATCCAGTAACCCG 3'	
AT1G171710-tRNA^{Gly} di-cistronic poly(A) RT-PCR	P237-F 5' GGACTTGTAGCCGTTCTCGT 3'	
	P236-R 5' ATGATAGTACCCTGCCACGG 3'	
AT1G171710 poly(A) RT-PCR	NA27-F 5' GGGAAAGGAATGAGGTTGGT 3'	
	NA25-R 5' TGGATGTAAAATGTTCTTGATTTC 3'	
ACTIN2 (At3g18780) poly(A) RT-PCR	FK1152-F 5' ACTTTCATCAGCCGTTTTGA 3'	190 bp
	FK1153-R 5'ACGATTGGTTGAATATCATCAG 3'	