Appendix contents

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S**upplementary Figure Legends**

Figure S1. Expression pattern of cell-type specific AGO1 lines. (A) Columella; *ACR4*::*GFP*:*AGO1*. **(B)** Stele; *SHR*::*GFP*:*AGO1*. **(C)** Endodermis; *SCR*::*GFP*:*AGO1*. **(D)** Cortex; *CO2*::*GFP*:*AGO1*. **(E)** Epidermis; *WER*::*GFP*:*AGO1*. Scale Bars = 50 μM.

Figure S2. Small RNA blot confirmation of RNA sequencing results. Input (left panels) and Immunoprecipitated (right panels) cell-type specific AGO1 probed for multiple different miRNA's listed on the right. NT(-) non-transformed with FLAG antibody added. NT(+) lysate were adjusted to ~ ¼ concentration and immunoprecipitated with native AGO1 antibody as a 'whole root' control. U6 is used as a loading control. The images used in the figures for the main text are repeated here. miR163, miR167, miR171 and miR173 are shown in Figure 1F. miR396 in Figure 4B. miR169 in Figure 5A. miR165/166 in Figure 6A.

Figure S3. RNA secondary structure of three new miRNA precursors. Structures were made using miRPlant software. Shown in red are the mature AGO1 loaded miRNA's.

Figure S4. Expression Pattern of HYL1 and specific effect of *hyl1-2* mutation on miRNA abundance. (A) Confocal images of two independent HYL1 translational fusions driven by the native promoter. **(B)** Representative miRoot browser snap shots of *HYL1* in WT and *hyl1* mutant. **(C)** RNA gel blot analysis of a set of hypomorphic miRNA biogenesis mutants. Probes are shown on the right and U6 serves as a loading control.

Figure S5. Polysome Profiling as a method to assay miRNA targeting.
qRT-PCR on miRNA targets on total RNA from WT or *hyl1-2* mutants or total (35S) polysome immunoprecipitations on the same backgrounds. **(A)** *SPL10*^{miR156} **(B)** *TCP4* ^{miR319} **(C)** *ARF17*^{miR160} **(D)** *CUC1* ^{miR164} **(E)** *PHB* ^{miR165} **(F)** *NF-YA2* ^{miR169} **(G)** *MYB65* ^{miR165} **(H)** *CSD2* ^{miR398}. Error Bars represent +/- SD of three biological replicates.

Figure S6. Cell-type specific markers as assessed by polysome mRNAseq. Normalized read counts of **(A)** *ACR4* **(B)** *SHR* **(C)** *SCR* **(D)** *CO2* **(E)** *WER* and **(F)** *GL2* in each cell-type specific polysome library. Values are the mean of two biological replicates from WT lines. Also shown are miRoot browser snapshots of representative transcripts.

Figure S7. Assembly of the miRoot brower. To facilitate single-cell exploration of the root-tip's miRNA biology, the F:AGO1-IP and F:RPL18-IP sequencing data-sets were integrated into a user-friendly browser coined miRoot, designed to operate on desk computers, tablets or smartphones. Cell-specific signals for single miRNAs (WT background) or single mRNA translatomes (WT/*hyl1-2* backgrounds) are queried in miRoot via a virtual root interface where colored patterns of various intensities reflect the relative pan-layer signals' strengths. The interface was designed by graphic cell layer deconvolution (Adobe Illustrator) based upon authentic high-resolution photographs of WT versus *hyl1-2* root tips, as depicted in (**A**). The virtual root depictions therefor take into account the characteristics of *hyl1-2* compared to WT root-tips, including cellularly disorganized columella and quiescent center, enlarged stele, and defects in the anticlinal-*versus*-periclinal division rates of epidermal cells. The layers were then digitalized and assembled to reconstitute the virtual root interfaces. In the **miRNA-query** miRoot setting shown in (**B**, blue square on the top), all currently known Arabidopsis miRNAs (miRbase v.21) may be interrogated primarily via their numeric identifier; the plethora of new miRNAs discovered is this study, isomiRs and targets thereof will be incorporated at later stages. Upon miRNA query, all known matching miR-5p/3p and paralogs (a, b, c, d…) are displayed in a pulldown menu alongside the sequence of the mature miRNA guide strand (blue rectangle). We stress that miRoot displays signal intensities for AGO-loaded *i.e.* functional miRNAs, that are relative to one another between cell layers. The cross-layer signals of the miR156 isoform **a,** strand **5p** are depicted here as an example. Root images are exported in an Adobe Illustrator® CS6-compatible format via the save option (blue square).

In the **transcript-query** miRoot setting shown in (**C,** blue square on the top), the full, curated Arabidopsis transcriptome (TAIR10) may be interrogated via gene

identification number (e.g. *AT1G69170* here), gene describer (e.g. SBP-domain transcription factor) or gene name (e.g. *SPL6*). In its most simplified implement, miRoot can thus be used as a root-tip layer-specific translatome analyzer. We have verified that its performances are at least on par with those of the cell-specific root translatome available from the eFP bowser (Bailey-Serres group at UCR). All plant miRNA targets predicted and/or validated so far display extended miRNA:target site complementarity such that they constitute a highly predictable subset of the Arabidopsis transcriptome. In the example shown in (**C**) the miR156 target $SPL6^{miR156}$ was queried and, thus, the colored maps obtained in (**A**) for the miR156**a** and (**C**) for $SPL6^{miR156}$ can be compared visually. Here mutually-exclusive patterns of AGO1-loaded miR156a, on the one hand, and $SPL6^{mir156}$ accumulation on the other, are observed, as expected from a direct, cell-autonomous plant miRNA-target interaction. Note that the stele signals do not show, however, this mutually-exclusive pattern and this will be addressed in points **F**-onward.

miR156 belongs to an extended family of paralogs (**a-b-c-d-e-f-g-h-i**) displaying each single-nucleotide polymorphisms that may refine targeting of specific SPL transcripts. Some of these paralogs are much less expressed and loaded into AGO1 than others, however, yet miRoot will display layer-specific patterns regardless of signal intensity. This might be confusing when visually analyzing the respective contributions of isoforms to target regulation as illustrated in panel (**D**) with miR156**a** signal and miR156**g**. The raw values (squared in blue) show that the signal intensity for paralog **a** is two-orders-of magnitude higher than that of paralog **g**. The scale option (blue square and inlay) solves this issue by allowing signal normalization between any number of miRNA paralogs subjected to the option, with the values being recalculated relative to the paralog displaying the highest-intensity signal. Panel (**E**) illustrates how rescaling highlights the near-background AGO1-loading signal of miR156 paralog **g** across root cell layers. Signal rescaling of all miR156 paralogs likewise identified that, in addition to **g**, paralogs **h** and **I** have no significant contribution to root-tip gene regulation (not shown). miR156 paralogs **a-b-c-d-e-f-g** display similar AGO1-loading signals in each root-tip layer, and since they are all involved, in principle, transcript targeting, it might be desirable to measure their bulk contribution to $SPL6^{miR156}$ regulation in each cell layer. As shown in (**F**) miRoot allows signal accretion via

the “add to sum-group” option (the blue rectangle shows that any miRNA paralog can be selectively removed from the sum-group at any time). A “Sum-Group” is then generated (blue rectangle, top right corner) upon which the “create” option allows signal aggregation in each individual layer, as depicted here in the grey zone for miR156**a-b-c-d-e-f-g**. Note that signal accretion can also be useful to reconstitute the inferred bulk regulation conferred by paralogous miRNA displaying distinct spatial AGO1-loading patterns and/or different signal intensities. It was used, for instance, in this study, with miR164**a/b** and miR164**c** as shown in fig. S10C.

Importantly, miRoot also enables removal of single/multiple layers and concurrent re-calculation of relative signal intensities across the remaining cell files. This option notably enables exclusion of the stele, of which none of the four intrinsic layers was individually resolved by SHR:F::AGO1-IPs, as discussed in the main text. miRoot will thus artificially assign often elevated and single-layer signals to the other stele layers. Because the stele represents a major fraction of the root, this can create exaggerated signals potentially masking/undermining those of adjacent cell files, since all signals are relative to each-others. (**F-G**) illustrate this phenomenon with elevated stele-derived signals from each miR156 paralogs **a-f** (~35,000 Normalized read counts/paralog, panel B) resulting, upon accretion, in a total signal of ~213,000 Normalized read counts (panel F, blue square). As shown in **(G,** blue rectangle), these elevated signals barely contribute to *SPL6*^{mir156} transcript regulation in the whole stele (1.3 folds-change in *hyl1* versus WT). Accordingly, no significant change in *SPL6*^{mir156} accumulation is observed in the stele in the WT compared to *hyl1* backgrounds (**C**). This suggests that the strong stele miR156 signals originate mainly from a single, as yet undefined stele cell-type, and are diluted in the others. By contrast, for instance, the epidermis-derived miR156**a-f** signals (green square), contribute significantly to *SPL6*^{mir156} control in this layer, given the 4.5 folds-change in *hyl1* versus WT transcript accumulation observed (**G**). Panel (**H-I**) shows how the stele removal option used on both the miR156**a-f** (**H**) and *SPL6*^{mir156} (**I**) miRoot outputs resolves the caveat and provides, upon recalculation of relative signal intensities across all adjacent layers, a more accurate view of the spatial *SPL6*^{mir156} regulation. In particular, the epidermal miR156 **a-f** pool now clearly stands out as the dominant

contributor to this spatial regulation (compare **B-C** to **H-I**). These adjustments thereby contribute to refine the mutually-exclusive pattern observed initially (**B-C**). As expected, the *SPL6*^{mir156} translatome signal is elevated in all layers in the *hyl1* background, and in the epidermis in particular. This optional layer-removal feature is also useful to focus analyses of layer-specific regulations, as was done in the case of *GRF2* regulation by miR396a (Figure 3H-J).

Figure S8. Contrasted loading of miR and miR* across cell-layers. Brower snapshot of miR824-5p (miR) and miR824-3p (miR*) demonstrating differential loading across different cell types.

Figure S9. Cell-type specific regulation of MYB transcription factors by miR159. (**A**) Layer-specific normalized read counts of miR159 paralogs a-b-c from AGO1-IP-deep-Seq and independent northern analysis. Lower panel: scaled, layer-specific AGO1-IP signal of each miR159 paralog and sum thereof calculated via miRoot (**B**) Representative confocal images of *pmiR159a::H2B:GFP* and *pmiR159b::H2B:GFP* transcriptional fusions. (**C**) Representative confocal images of *pMYB33::H2B:GFP* and p*MYB65::H2B:GFP* transcriptional fusions. (**D**) miRoot snapshots of layer-specific translatome signals for *MYB33* (left) and *MYB65* (right) in WT *versus hyl1* backgrounds. **(E)** Expression pattern of *MYB33* genomic fusion in WT or *hyl1* backgrounds. **(F)** Relative expression of *MYB33* as assessed by qRT-PCR in different cell types after cell-type specific polysome immunoprecipitation in WT an *hyl1* backgrounds. The top graph represents raw values per cell layer and on the bottom adjusted for each cell layer with WT for each set at 1 and mutant adjusted relatively within each cell layer. **(G)** The same as shown in (F) but for *MYB65*. **(H)** Generic scheme demonstrating the principles of miRNA-mediated buffering. Scale bars represent 50μM. Error bars represent +/- SD of two biological replicates. The same blot in panel A is shown in Figure 1F.

Figure S10. miR397-directed regulation of Lac4 across contiguous developmental stages.

(A) Representative confocal images of *LAC4* transcriptional (left) and translational (right) fusions. MZ,TZ,EZ,DZ: meristematic, transition, elongation,

differentiation zone. (**B**) miRoot snapshots of layer-specific translatome signals for *LAC4*. **(C)** Scheme demonstrating special and temporal miRNA-mediated gene regulation revealed by cell-type specific profiling. Scale bars: 50μM. Polysome signals are Log values of reads per 10 million, and AGO1-IP miRNA values are normalized read counts.

Figure S11. Selective expression gradients of miR164 family targets dictated by limiting miRNA concentration (A) Confocal images of *pmiR164a*::*mVENUS-N7* (left), *pmiR164b*::*H2B*:*GFP* (middle) and *pmiR164c*::*mVENUS-N7* (right). **(B)** Normalized miR164a-c read counts and independent northern analysis. **(C)** Browser snapshot of AGO1:miR164a-b (left) and miR164c (right) accumulation. **(D)** Endodermis and cortex focused accumulation of miR164 paralogues a-b (left), c (centre) and sum of the two is shown on the right. **(E)** Browser snapshots of total polysome transcripts for NAC1 in WT and *hyl1* mutants. **(F)** The same as shown in (D) but for NAC6. **(G**) Focused miRoot analysis of the *NAC1* translatome signal in WT *versus hyl1* endodermis/cortex and predicted sequence alignment between miR164a/b-c and *NAC1* (target). (**H**) Same as (G) but for *NAC6*. **(I)** Representation of principles of gene regulation mediated by gradients and base-pairing of miRNA:target combinations across cell layers. A portion of the blot shown in Figure S2 is shown here in panel (B) *: statistically significant upregulation based on two biological replicates with a fdr of <0.05. Scale bars represent 50μM. All miRNA levels are represented as Normalized read counts per million and Polysome sequencing is shown as LOG(RP10M).

Figure S12. Translational repression of GRF's by miR396 in the columella. (A) miRoot browser images of *GRF3* polysome profiling in WT and *hyl1* highlighting only the Columella. Also shown is the normalized read count values for each background. **(B)** Expression of translational fusion of either WT *GRF3* (left) or resistant (*rGRF3*-right) GFP reporters. **(C)** MiRoot browser images of *GRF1* polysome profiling in WT and *hyl1* highlighting only the Columella. Also shown is the normalized read count values for each background. Scale for miRoot are LOG(ReadsPer10Million) and the graphs are normalized read counts. **(D)**

MiRoot browser snapshot of *PLT2* transcript levels within the Columella. Error bars are +/- SD of two biological replicates. Scale bars represent 50μM.

Figure S13. Non-cell autonomous accumulation and activity of miR165/166. **(A)** Normalized read counts of miR165 and miR166. Representation of the sum of miRNA165a/166b accumulation. **(B)** Confocal images of miR165a and miR166b transcriptional activity. miRoot browser shapshots in WT and *hyl1* mutants of miR165/166 targets **(C)** *PHV* **(D)** *REV* and **(E)** *AtHB15.* Log scales (RP10M) are shown.

Figure S14. Non-cell autonomous accumulation and activity of miR160 (**A**) Representative confocal images of *pmiR160(a/b/c)::H2B:GFP* transcriptional fusions. (**B**) Northern analysis of AGO1-loaded miR160. (**C**) miRoot snapshots of layer-specific translatome signals for *ARF173* in WT *versus hyl1* backgrounds.

Figure S15. Maintenance of cell specific and autonomous AGO1 accumulation and molecular confirmation of miR395 induction upon Sulfur starvation. (A) Cell-type specific expression of *GFP*::*AGO1* translational fusions upon SO4- starvation **(B)** Western blot analysis of miR395 transcriptional reporter lines under normal (+) and SO4 starvation (-) conditions. Coomassie blue (CB) staining serves as a loading control **(C)** RNA gel blot analysis of RNA from the same roots sampled in (B) showing induction of miR395 under each experimental condition. U6 serves as a loading control. Scale Bars represent 50μM.

Figure S16. Non-cell autonomous activity of miR395. miRoot browser shots of miR395 targets **(A)** *APS4* **(B)** *APS1* **(C)** *SULTR2;1* in WT and *hyl1* backgrounds. Scales are LOG values of RP10M.

Figure S17. Binding miRNA duplexes within the epidermis. (A) *pWER*::*GFP*:*P19* confocal image demonstrating the cell-autonomy of P19 within the epidermis. **(B)** Western blots of two independent IPs that were performed corresponding to; left the RNA used in (C) and right RNA used in (D). Coomassie

Blue (CB) serves as a loading control for the input. **(C)** RNA gel blot analysis of IPed epidermal specific guide strand miRNAs as indicated by the probes of the right. U6 serves as a loading control for the input. **(D)** RNA gel blot analysis of independently IPed epidermal specific star (*) strand miRNAs as indicated on the right and also the guide strand for miR396. U6 serves as a loading control for the input. Scale bar represents 50μM.

Fig. S18. Sequestering miR395 by Stele specific P19 expression. (A) Western blot analysis of p*SHR*::*HA*:*P19* IPs under normal (+) and sulfur starved conditions (-). Coomassie blue (CB) staining serves as a loading control for the input. **(B)** RNA gel blot analysis of *pSHR*::*HA*:*P19* IPs under normal (+) and sulfur starved conditions (-). miR159 serves as a negative control for SO4- specific induction of miR395 and U6 serves as a loading control. The images in (B) are also used in Figure 7.

Figure S19. Expression and movement of pri/miRNA163. (A) Confocal images of *pmiR163*::*H2B*:*mCHERRY*. **(B)** Browser shots of polysome bound primiR163 in either WT (left) or *hyl1*. **(C)** Brower shot of mature miR163 accumulation. Scale bars represent 50μM. Scales for browser images are Normalized read counts.

Figure S20. Movement of miR160 within mature leaf tissue. (A) Cross section of leaf and the cell types isolated using the meselect technique. Vasculature is circled and lower epidermis is shaded in red. **(B)** Western blot analysis of whole leaf and meselect separated vasculature and epidermis. Two independent lines each of *pmiR160a*::*H2B*:*GFP*, *pmiR160b*::*H2B*:*GFP* and *pmiR160c*::*H2B*:*GFP* are shown. After GFP detection the membrane was stripped and detection of ACTIN2 was performed to demonstrate that protein isolated using the technique were amenable to antibody detection. Coomassie blue (CB) serves as a form of loading control. **(C)** RNA gel blot analysis of whole leaf, vasculature or epidermis isolated from either WT or *hyl1* mutant plants. Probes are given on the right and U6 serves as a loading control. Note some of portions of this figure are the same images as shown in the main text as Figure 7.

Figure S21. Promoter activity of APS4. *pAPS4*::*H2B*:*GFP* transcriptional fusions in either WT or *hyl1* backgrounds under either normal (SO4+) or Sulfur starvation conditions (SO4-) are shown.

Table S1. Mapping statistics for deep sequencing of cell-type specific AGO1 bound miRNAs.

Table S2. Normalized Read counts for all known miRNAs in cell-type specific AGO1 libraries.

Table S3. List and statistics of new miRNAs identified in cell-type specific AGO1 libraries.

Table S4. Mapping statistics for RNAseq of cell-type specific polysome bound mRNAs in WT and *hyl1* backgrounds.

Table S5. Differential analysis of RNAseq of cell-type specific polysome bound mRNAs in WT and *hyl1* backgrounds.

Table S6. List of oligonucleotides used in this study.

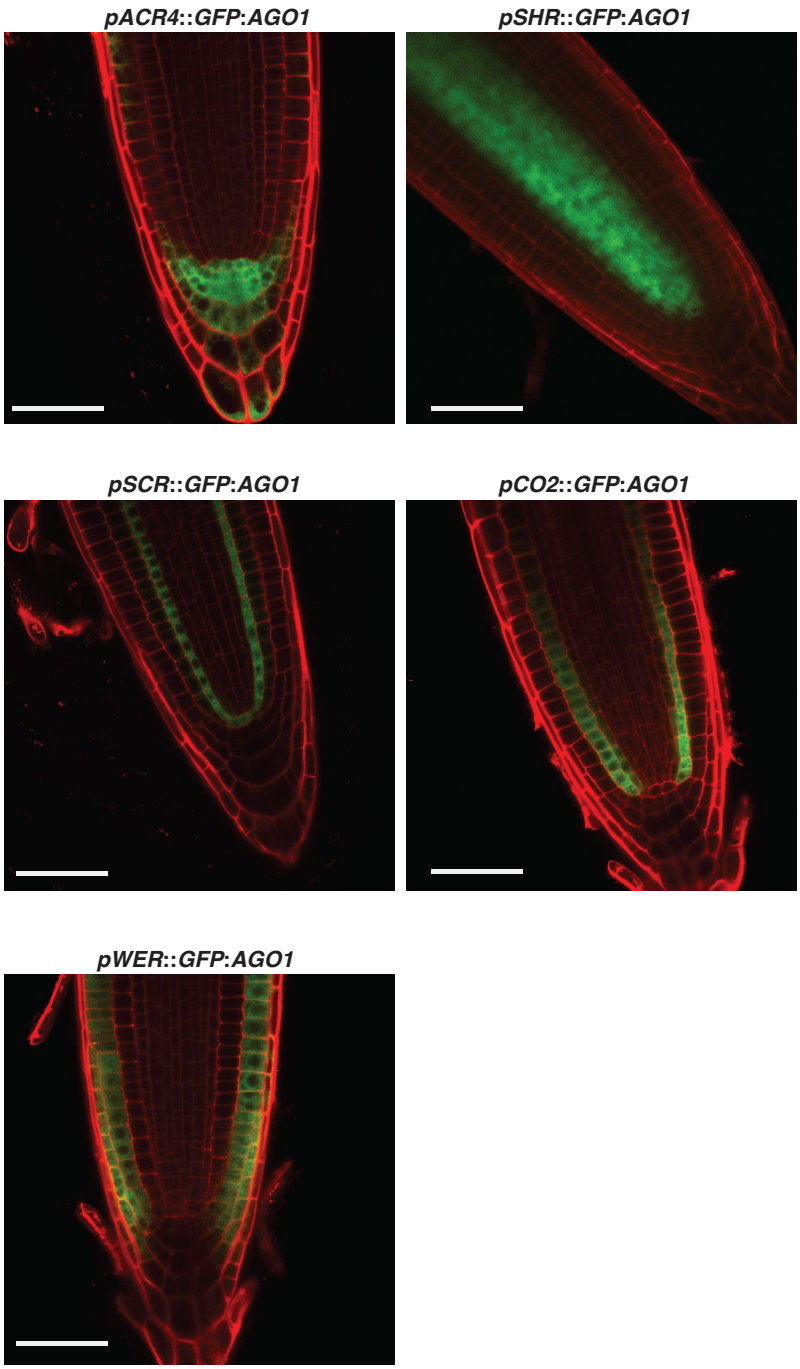
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Figure S1

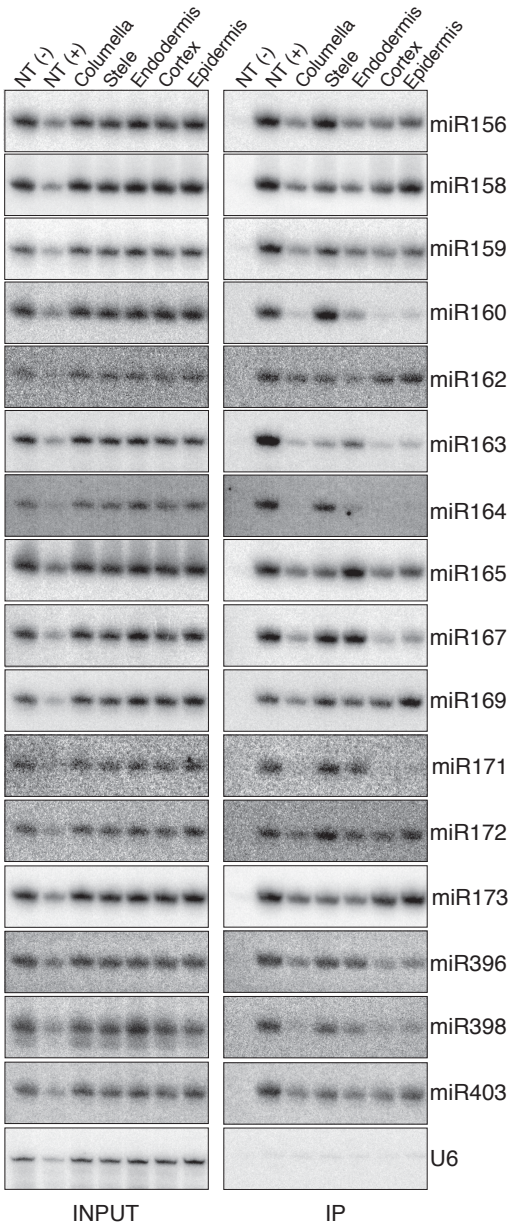
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Figure S2

Figure S3

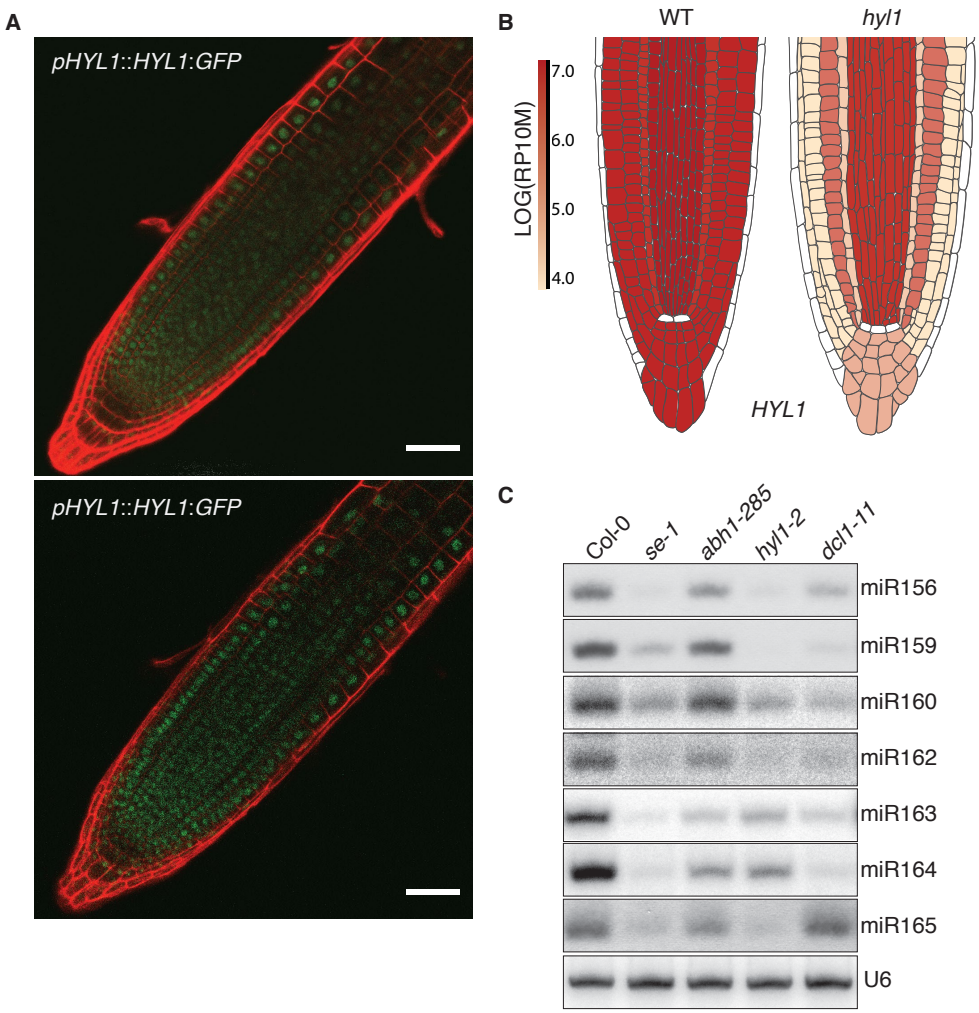
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Figure S4

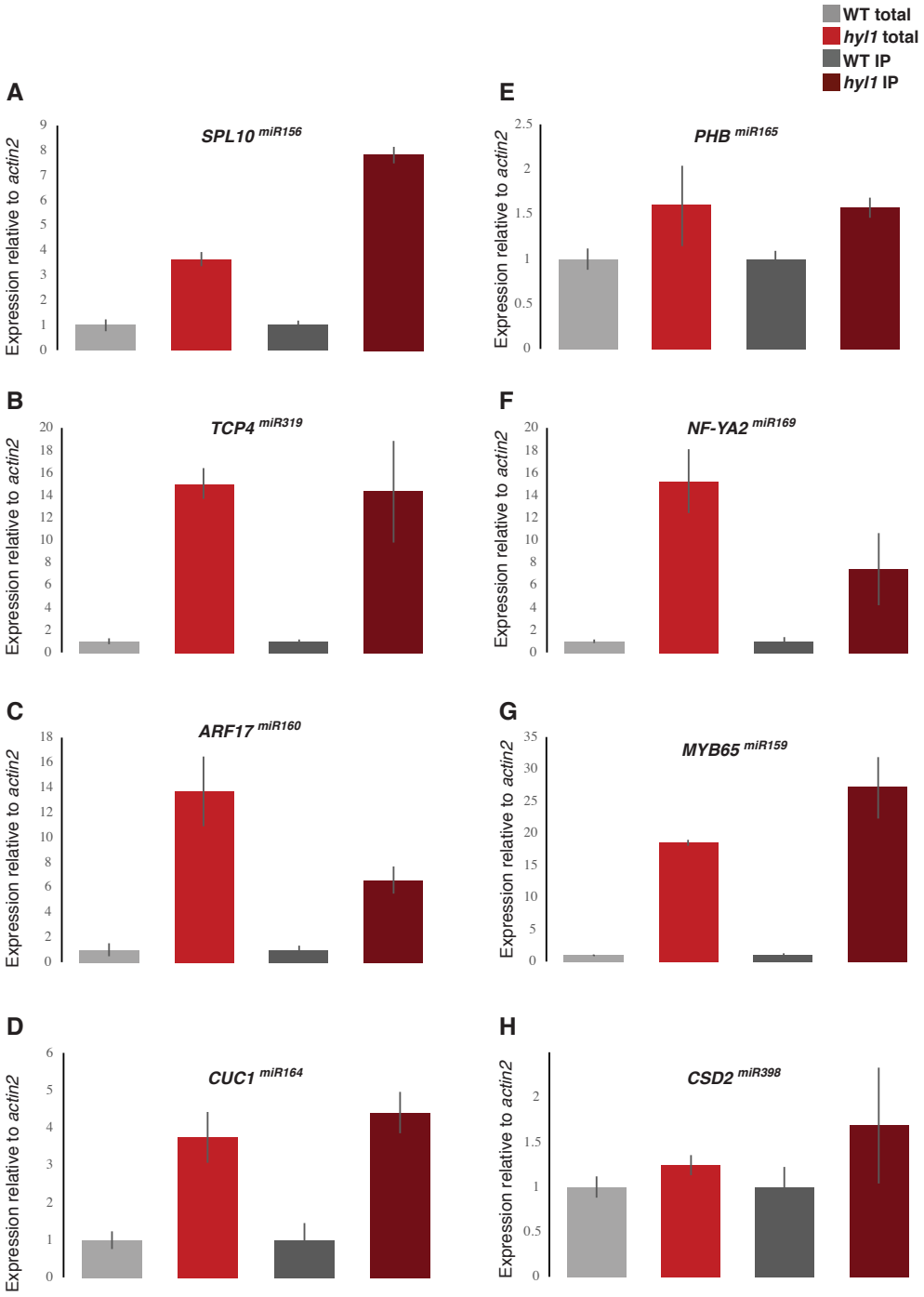
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Figure S5

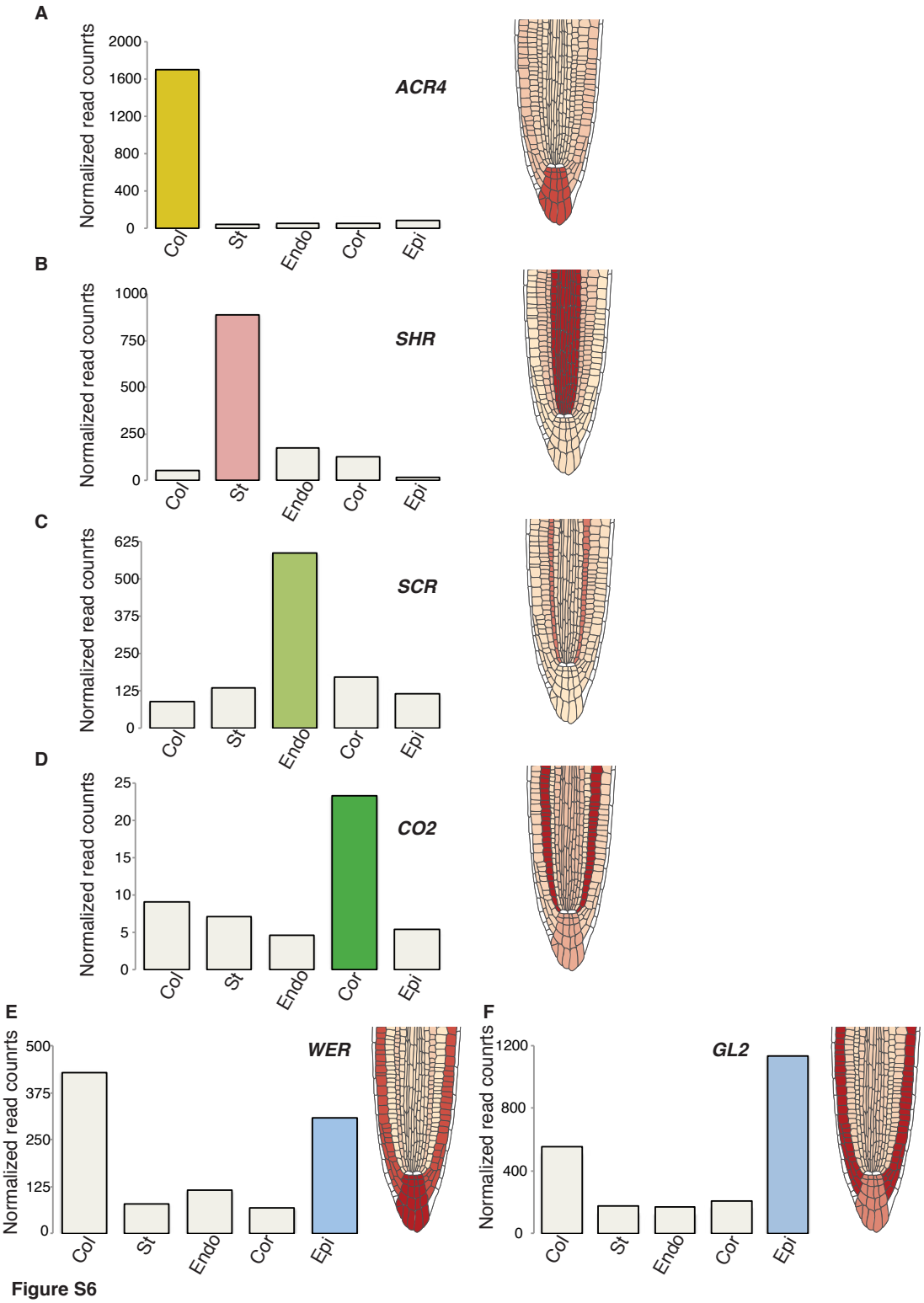
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Figure S6

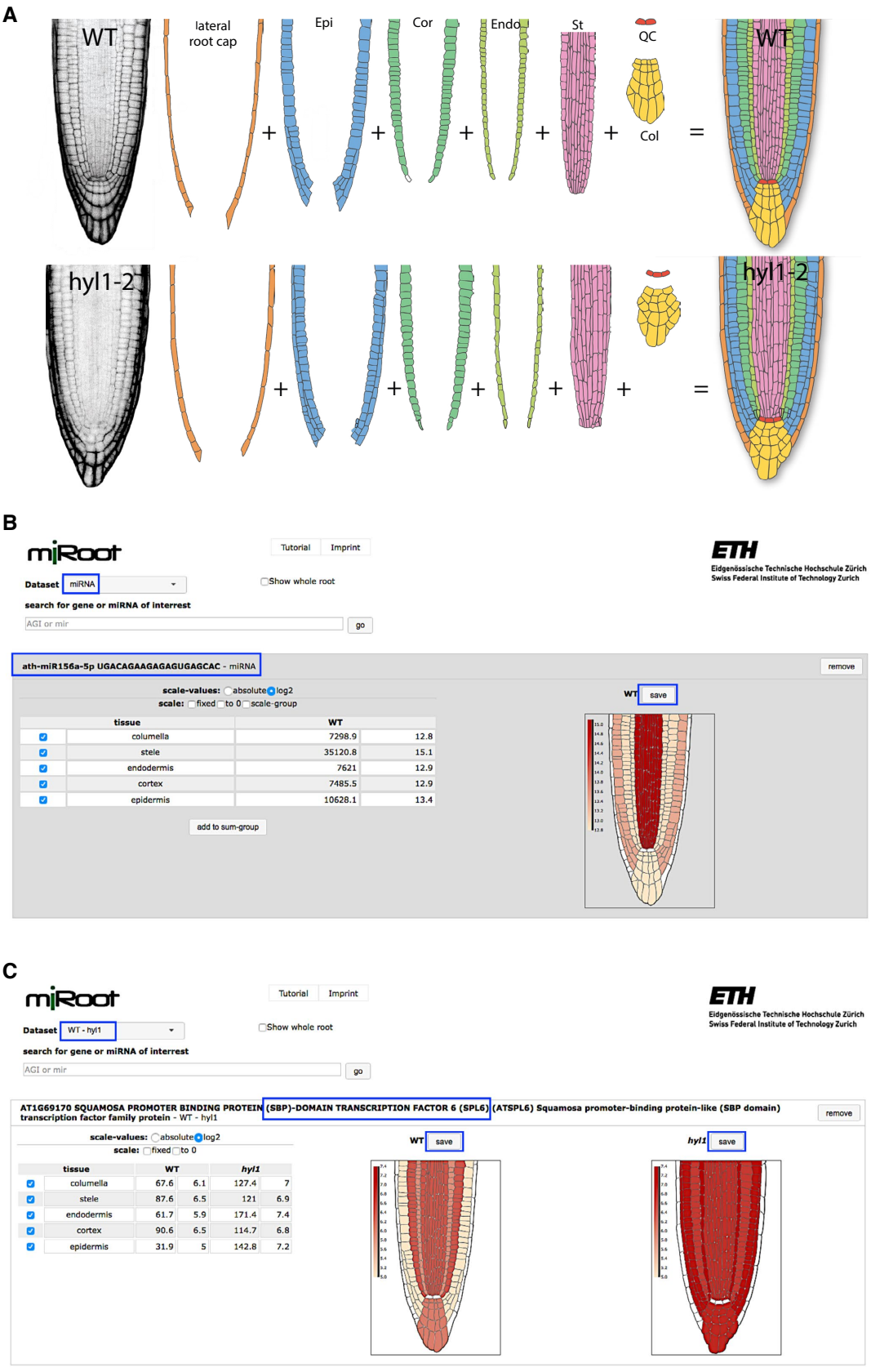

Figure S7 (continued on next page)

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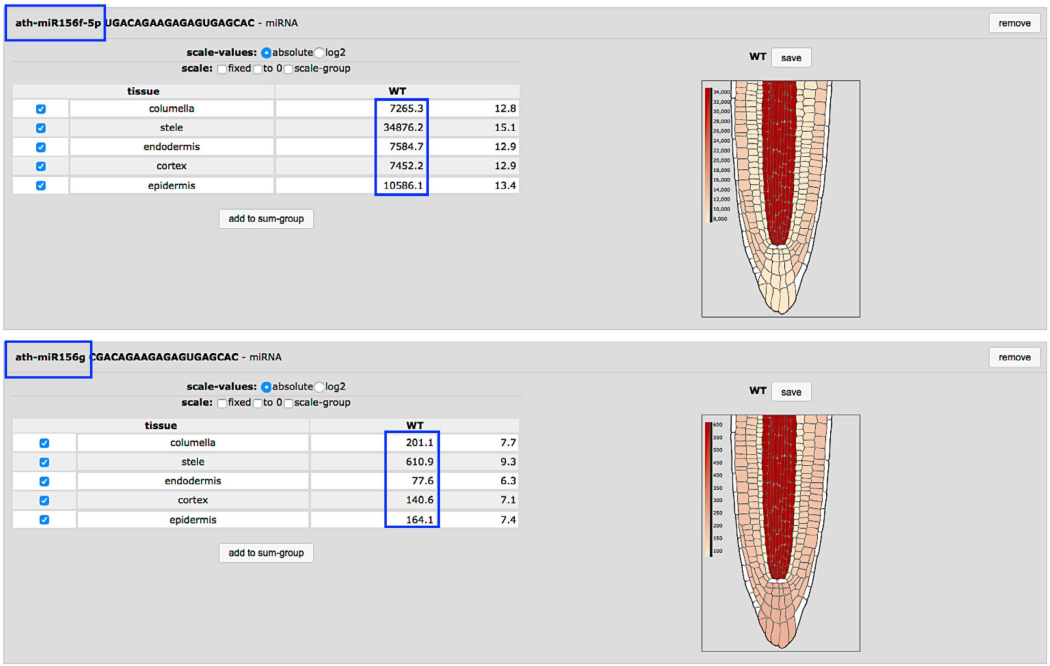

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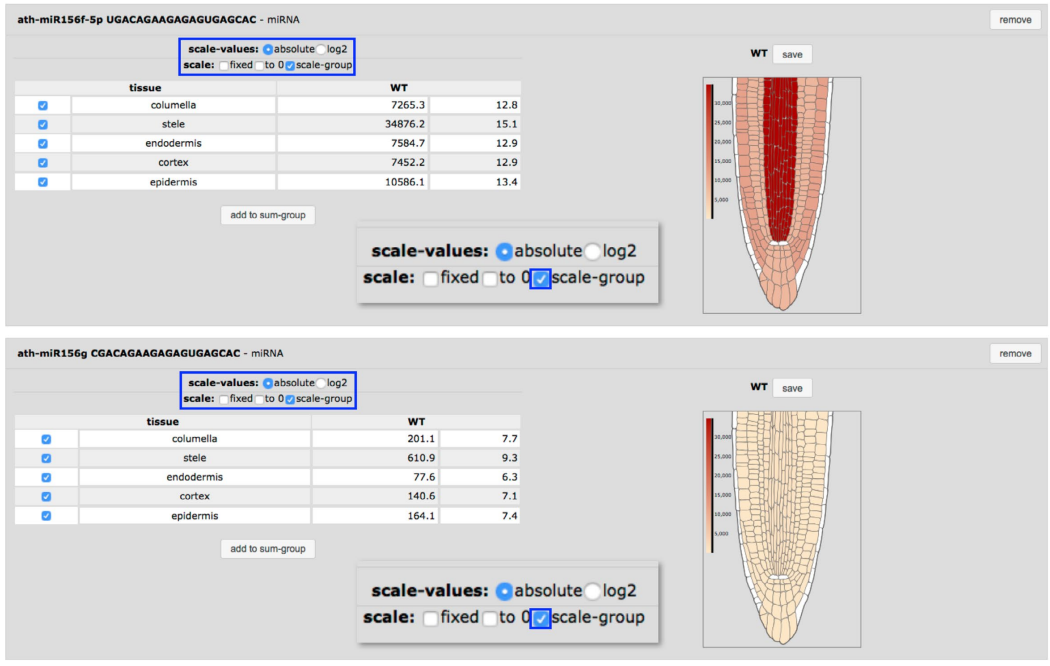

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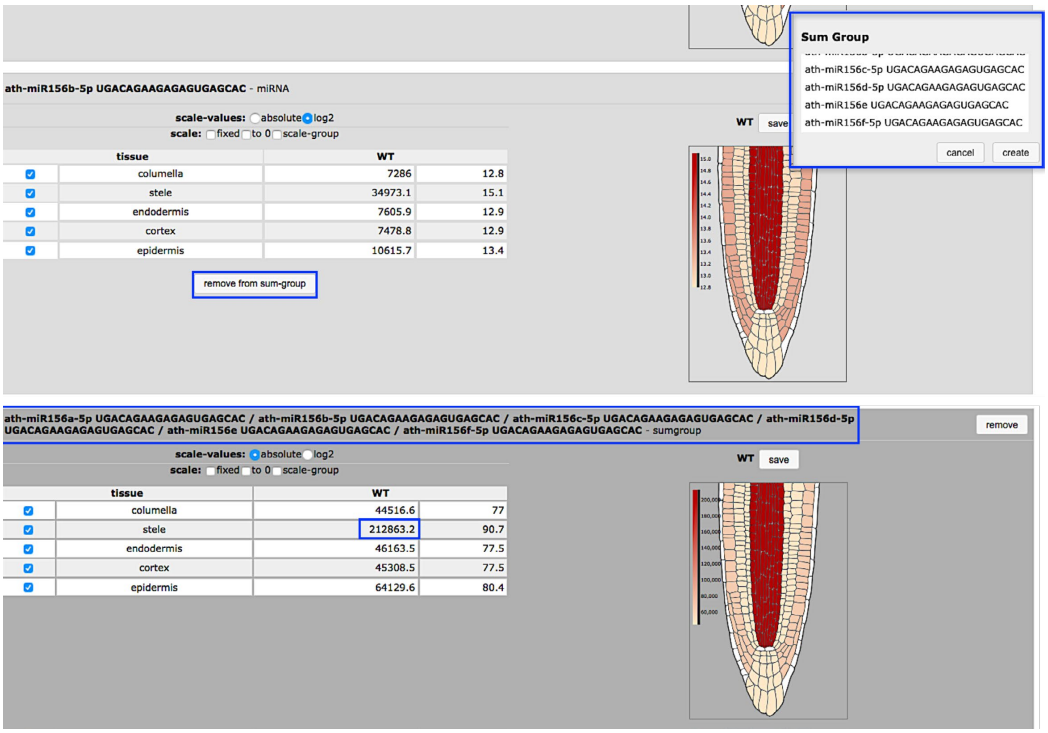

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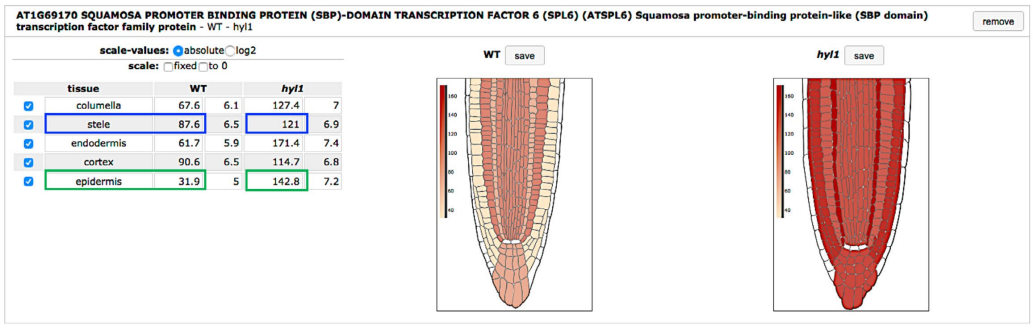

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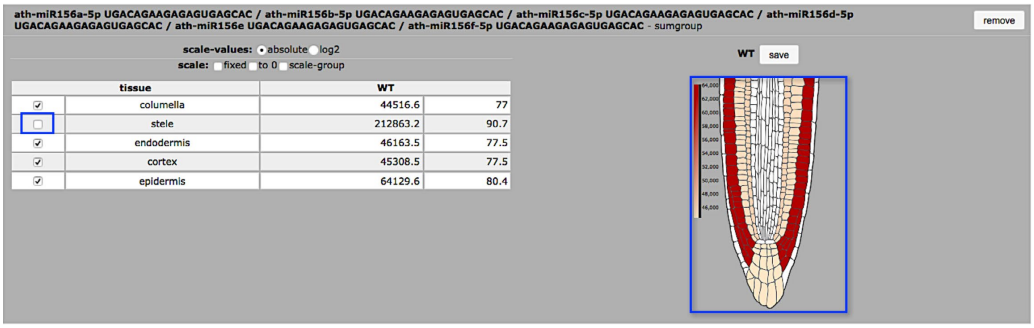
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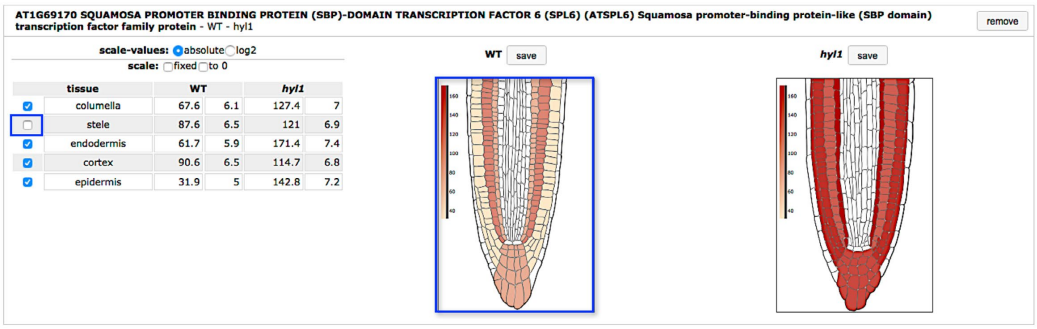
I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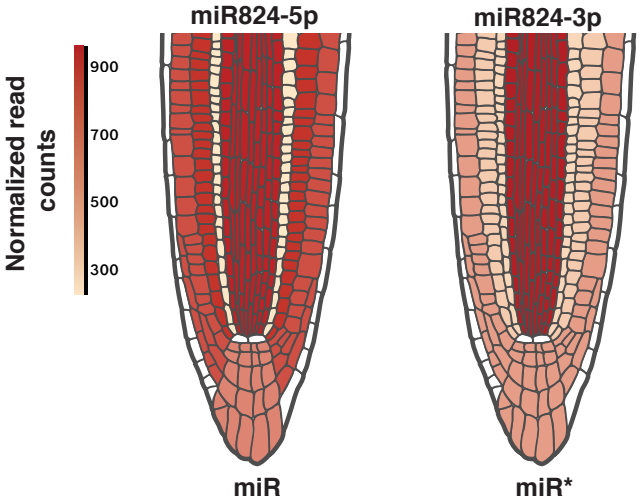
hyl1 save

Figure S7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700
500
300
miR
miR*

Figure S8

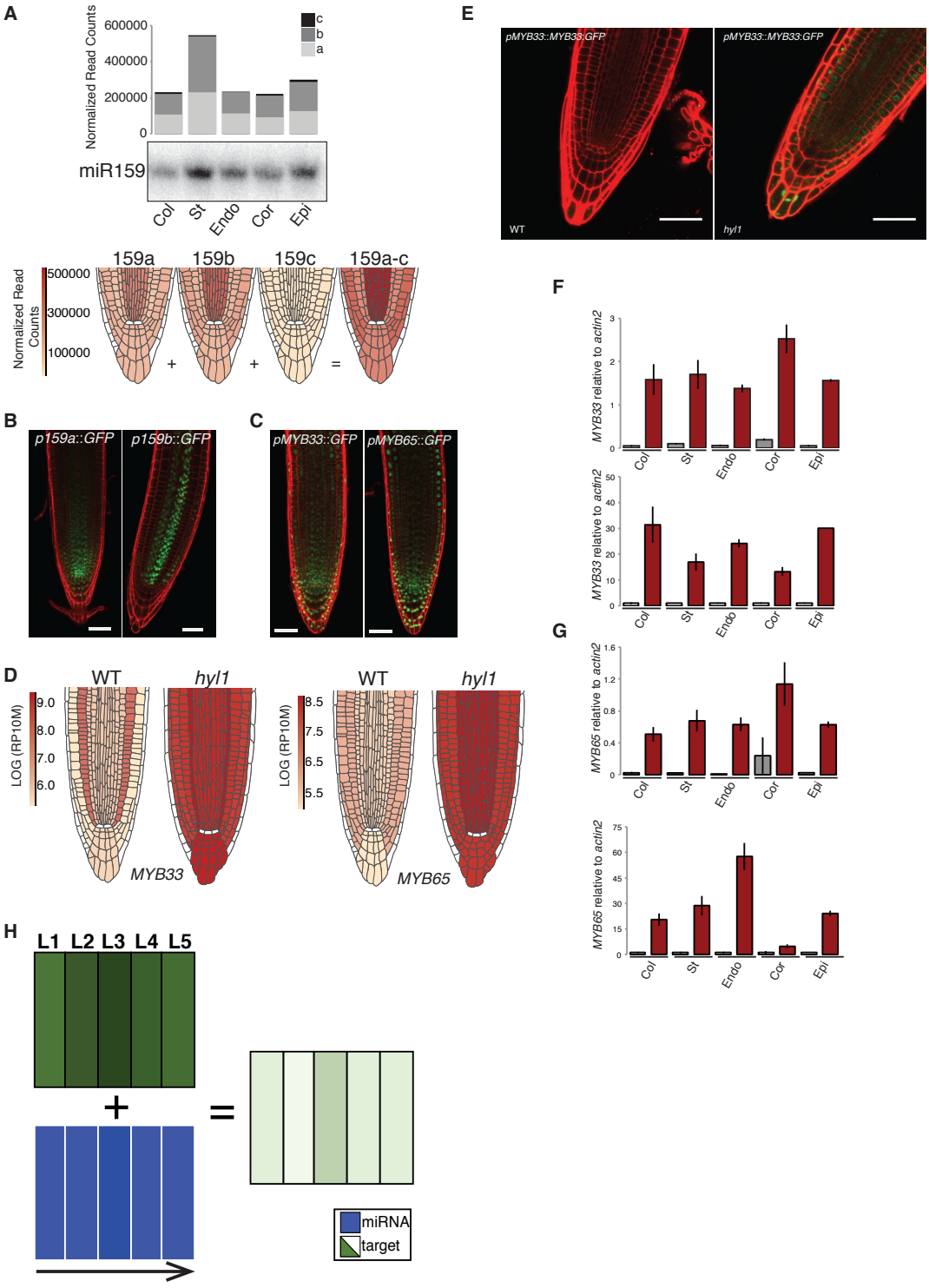
A
Normalized Read Counts
600000
400000
200000
0
c
b
a
miR159
Col
St
Endo
Cor
Epi
159a
159b
159c
159a-c
Normalized Read Counts
500000
300000
100000
+
+
=
B
p159a::GFP
p159b::GFP
C
pMYB33::GFP
pMYB65::GFP
D
WT
hyl1
LOG (RP10M)
9.0
8.0
7.0
6.0
MYB33
WT
hyl1
LOG (RP10M)
8.5
7.5
6.5
5.5
MYB65
E
pMYB33::MYB33:GFP
pMYB33::MYB33:GFP
WT
hyl1
F
MYB33 relative to actin2
Col
St
Endo
Cor
Epi
MYB33 relative to actin2
G
MYB65 relative to actin2
MYB65 relative to actin2
H
L1 L2 L3 L4 L5
+
=
miRNA
target

Figure S9

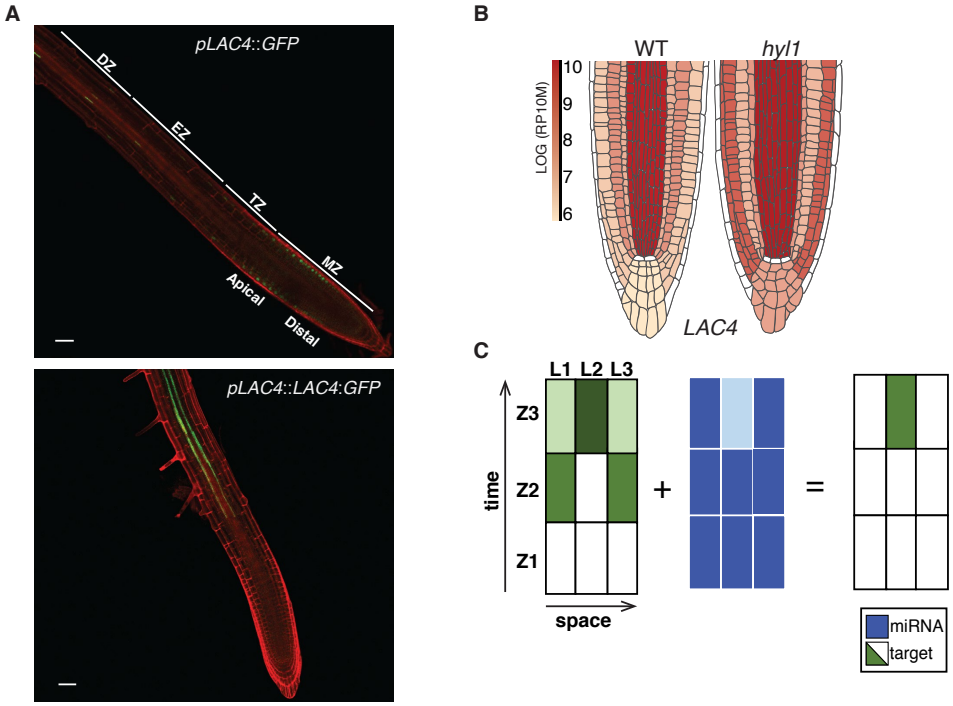
A
pLAC4::GFP
DZ
EZ
TZ
MZ
Apical
Distal
pLAC4::LAC4:GFP
B
WT
hyl1
LOG (RP10M)
10
9
8
7
6
LAC4
C
L1 L2 L3
Z3
Z2
Z1
time
space
+
=
miRNA
target

Figure S10

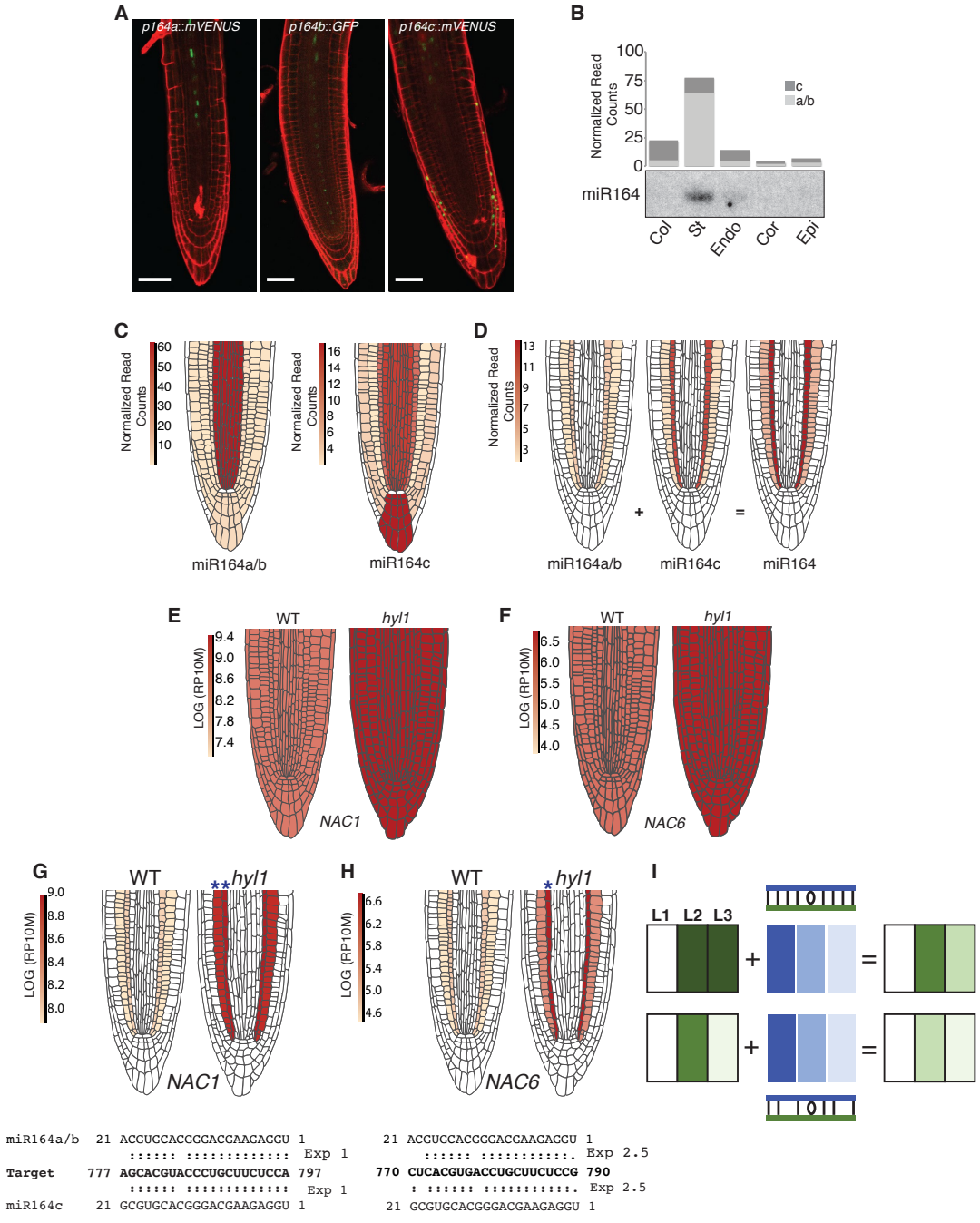
A
p164a::mVENUS
p164b::GFP
p164c::mVENUS
B
Normalized Read Counts
100
75
50
25
0
c
a/b
miR164
Col
St
Endo
Cor
Epi
C
Normalized Read Counts
60
50
40
30
20
10
miR164a/b
16
14
12
10
8
6
4
miR164c
D
Normalized Read Counts
13
11
9
7
5
3
miR164a/b
+
miR164c
=
miR164
E
WT
hyl1
LOG (RP10M)
9.4
9.0
8.6
8.2
7.8
7.4
NAC1
F
WT
hyl1
LOG (RP10M)
6.5
6.0
5.5
5.0
4.5
4.0
NAC6
G
WT
hyl1
LOG (RP10M)
9.0
8.8
8.6
8.4
8.2
8.0
NAC1
H
WT
hyl1
LOG (RP10M)
6.6
6.2
5.8
5.4
5.0
4.6
NAC6
I
L1 L2 L3
+
=
+
=
miR164a/b 21 ACGUGCACGGGACGAAGAGGU 1
::::::: ::::::::::::: Exp 1
Target 777 AGCACGUACCCUGCUUCUCCA 797
::::::: ::::::::::::: Exp 1
miR164c 21 GCGUGCACGGGACGAAGAGGU 1
21 ACGUGCACGGGACGAAGAGGU 1
::::::: :::::::::::. Exp 2.5
770 CUCACGUGACCUGCUUCUCCG 790
: ::::::: :::::::::::. Exp 2.5
21 GCGUGCACGGGACGAAGAGGU 1

Figure S11

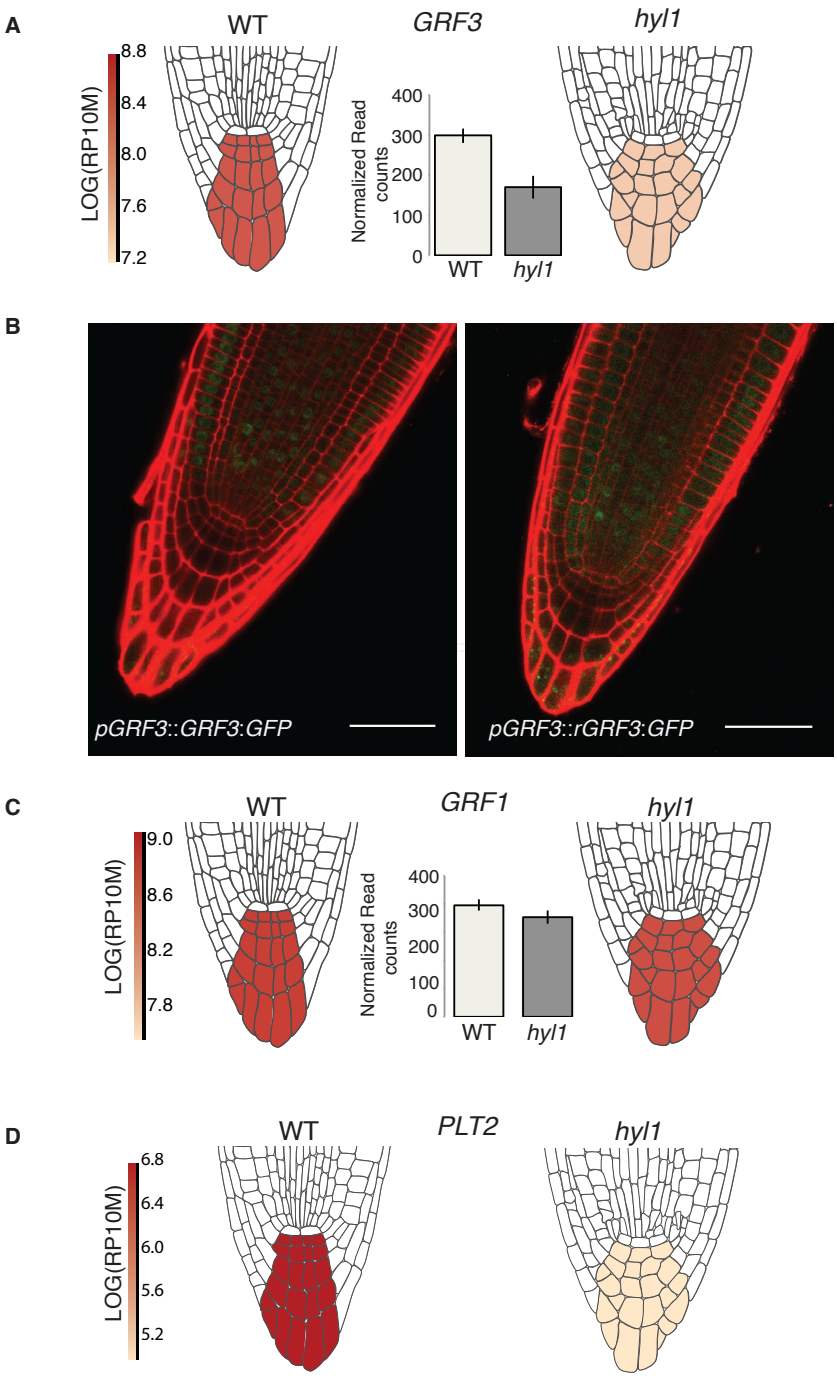
A
WT
GRF3
hyl1
LOG(RP10M)
8.8
8.4
8.0
7.6
7.2
Normalized Read counts
400
300
200
100
0
WT
hyl1
B
pGRF3::GRF3:GFP
pGRF3::rGRF3:GFP
C
WT
GRF1
hyl1
LOG(RP10M)
9.0
8.6
8.2
7.8
Normalized Read counts
400
300
200
100
0
WT
hyl1
D
WT
PLT2
hyl1
LOG(RP10M)
6.8
6.4
6.0
5.6
5.2

Figure S12

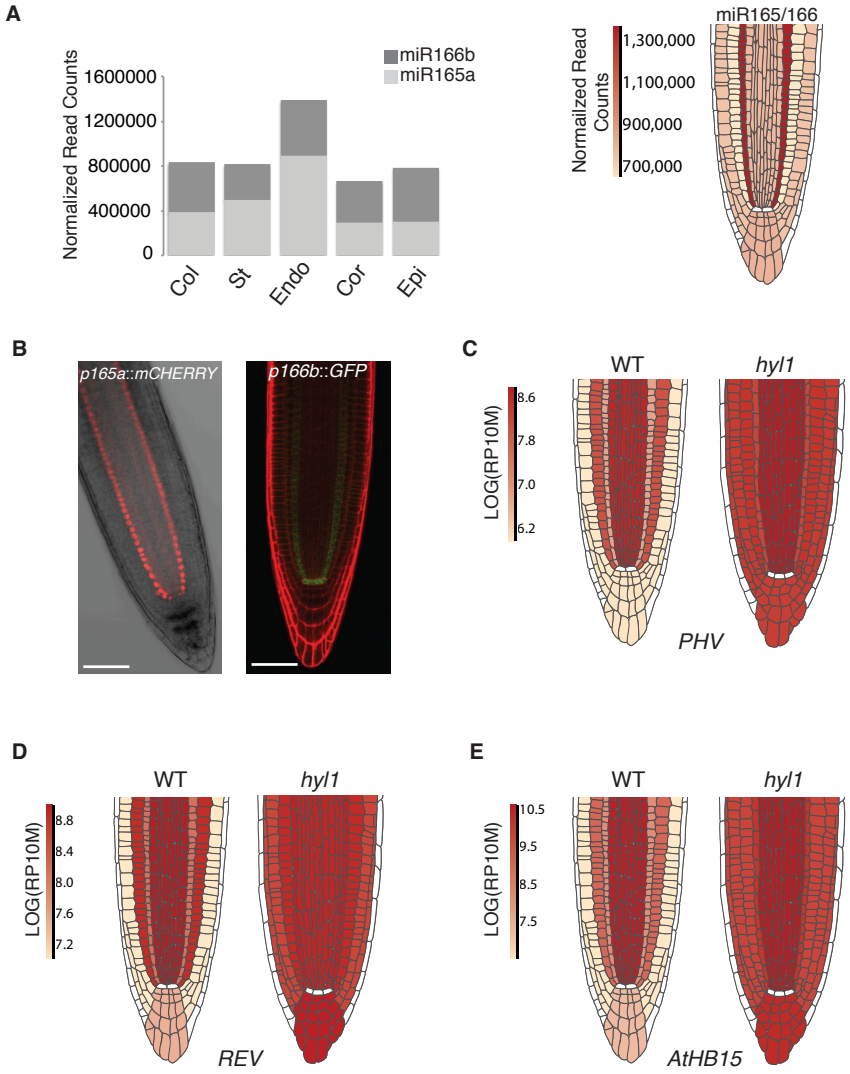
A
Normalized Read Counts
1600000
1200000
800000
400000
0
miR166b
miR165a
Col
St
Endo
Cor
Epi
miR165/166
Normalized Read Counts
1,300,000
1,100,000
900,000
700,000
B
p165a::mCHERRY
p166b::GFP
C
WT
hyl1
LOG(RP10M)
8.6
7.8
7.0
6.2
PHV
D
WT
hyl1
LOG(RP10M)
8.8
8.4
8.0
7.6
7.2
REV
E
WT
hyl1
LOG(RP10M)
10.5
9.5
8.5
7.5
AtHB15

Figure S13

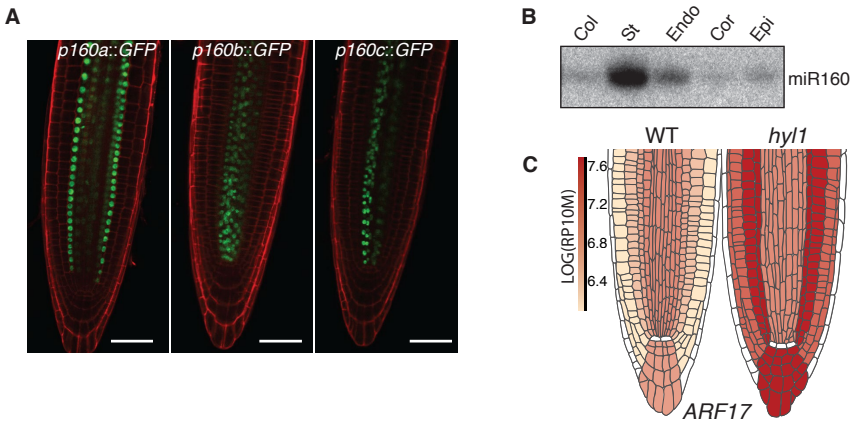
A
p160a::GFP
p160b::GFP
p160c::GFP
B
Col
St
Endo
Cor
Epi
miR160
C
WT
hyl1
LOG(RP10M)
7.6
7.2
6.8
6.4
ARF17

Figure S14

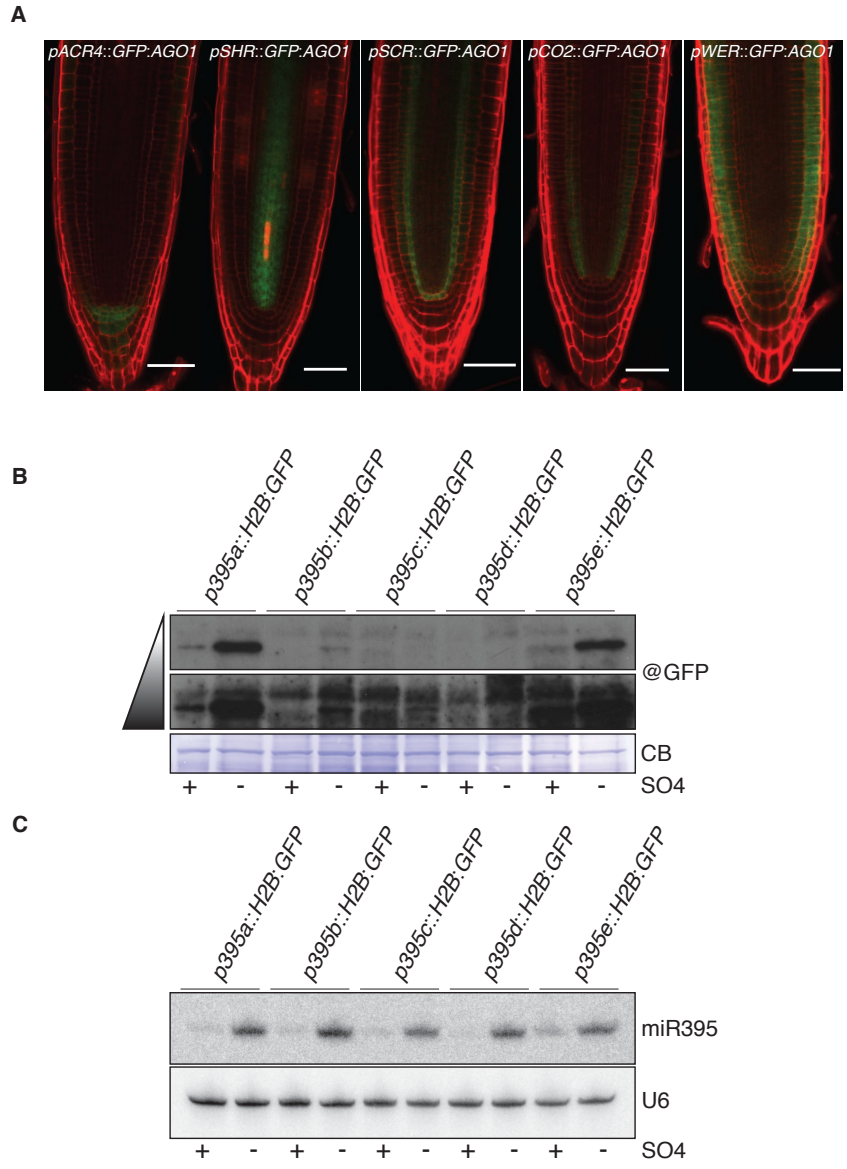
A
pACR4::GFP:AGO1
pSHR::GFP:AGO1
pSCR::GFP:AGO1
pCO2::GFP:AGO1
pWER::GFP:AGO1
B
p395a::H2B:GFP
p395b::H2B:GFP
p395c::H2B:GFP
p395d::H2B:GFP
p395e::H2B:GFP
@GFP
CB
+ - + - + - + - + -
SO4
C
p395a::H2B:GFP
p395b::H2B:GFP
p395c::H2B:GFP
p395d::H2B:GFP
p395e::H2B:GFP
miR395
U6
+ - + - + - + - + -
SO4

Figure S15

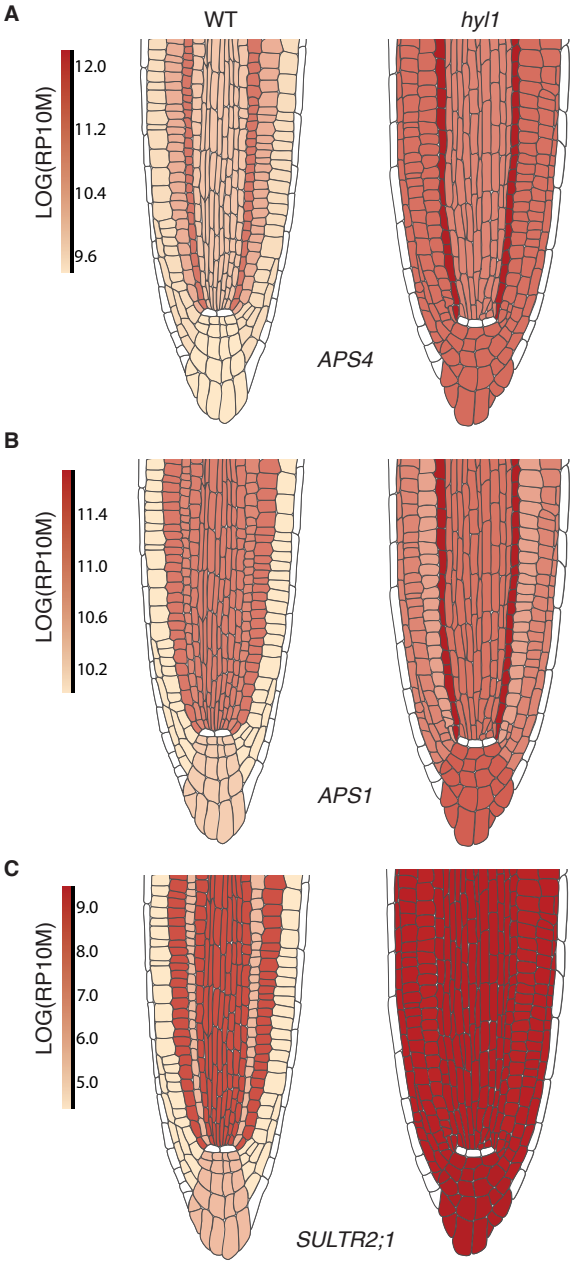
A
WT
hyl1
LOG(RP10M)
12.0
11.2
10.4
9.6
APS4
B
LOG(RP10M)
11.4
11.0
10.6
10.2
APS1
C
LOG(RP10M)
9.0
8.0
7.0
6.0
5.0
SULTR2;1

Figure S16

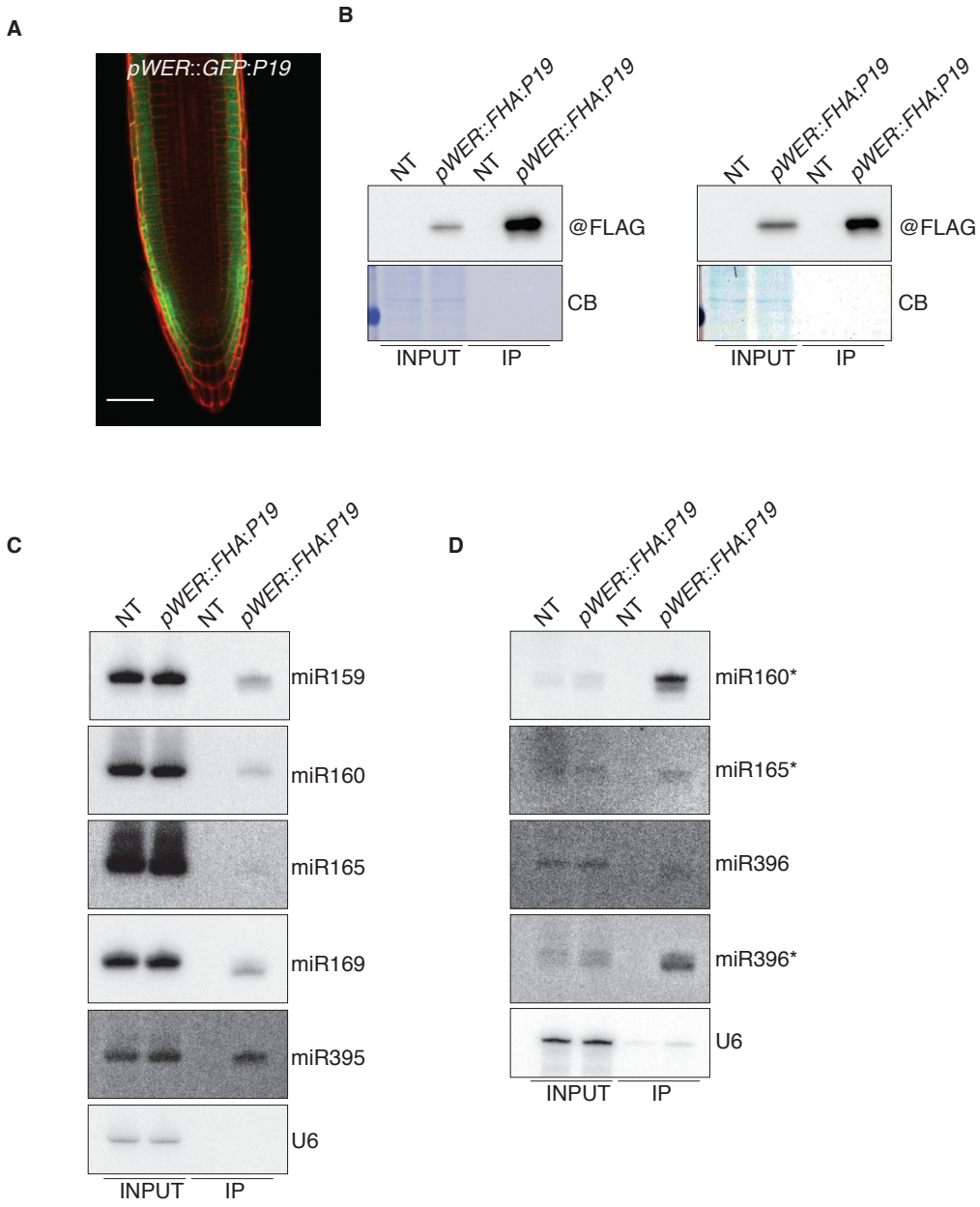
A
pWER::GFP:P19
B
NT
pWER::FHA:P19
NT
pWER::FHA:P19
@FLAG
CB
INPUT
IP
C
miR159
miR160
miR165
miR169
miR395
U6
D
miR160*
miR165*
miR396
miR396*
U6

Figure S17

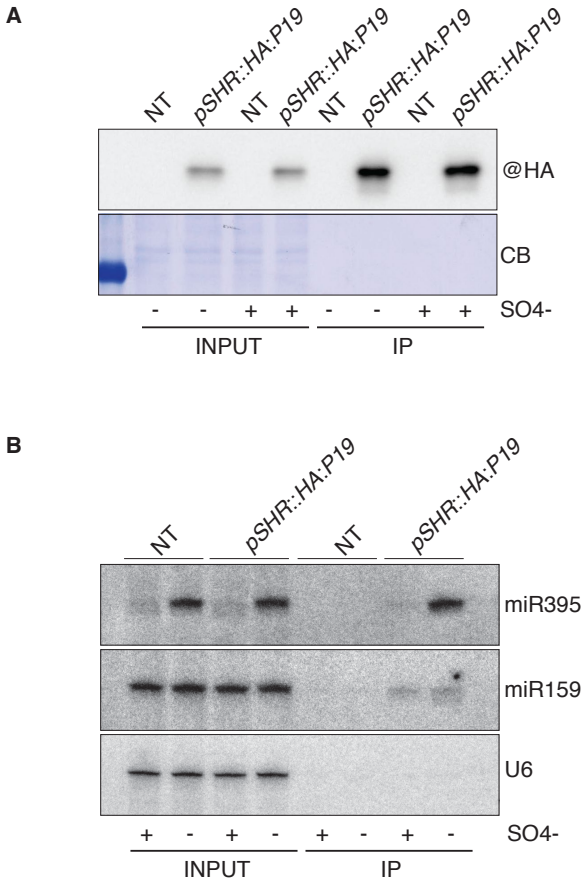
A
NT
pSHR::HA:P19
NT
pSHR::HA:P19
NT
pSHR::HA:P19
NT
pSHR::HA:P19
@HA
CB
- - + + - - + + SO4-
INPUT
IP
B
NT
pSHR::HA:P19
NT
pSHR::HA:P19
miR395
miR159
U6
+ - + - + - + - SO4-
INPUT
IP

Figure S18

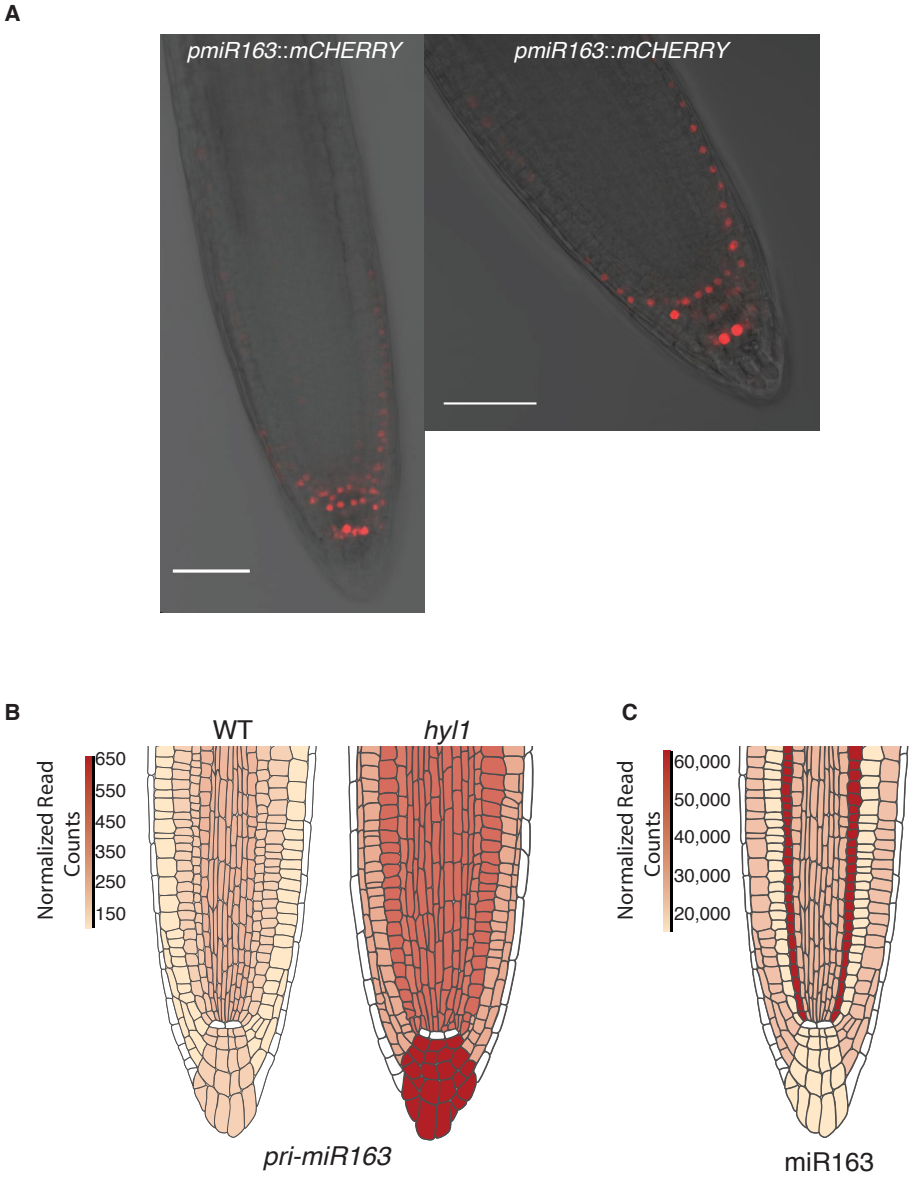
A
pmiR163::mCHERRY
pmiR163::mCHERRY
B
WT
hyl1
Normalized Read Counts
650
550
450
350
250
150
pri-miR163
C
Normalized Read Counts
60,000
50,000
40,000
30,000
20,000
miR163

Figure S19

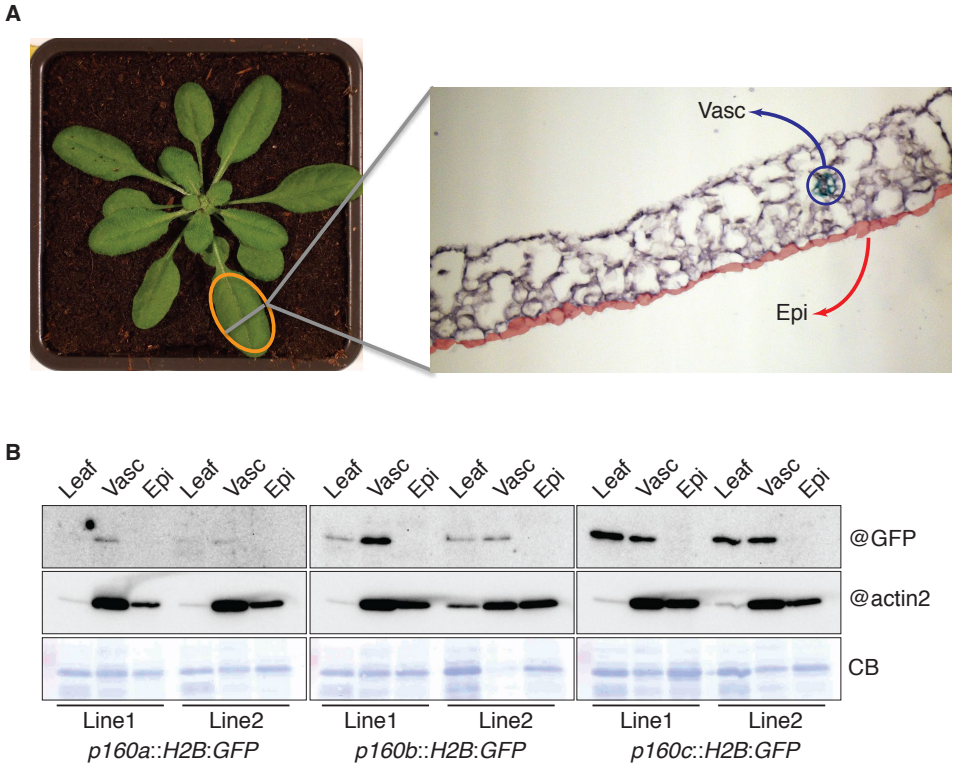
A
Vasc
Epi
B
Leaf
Vasc
Epi
@GFP
@actin2
CB
Line1
Line2
p160a::H2B:GFP
p160b::H2B:GFP
p160c::H2B:GFP
C
miR160
miR159
miR171
U6
WT
hyl1

Figure S20

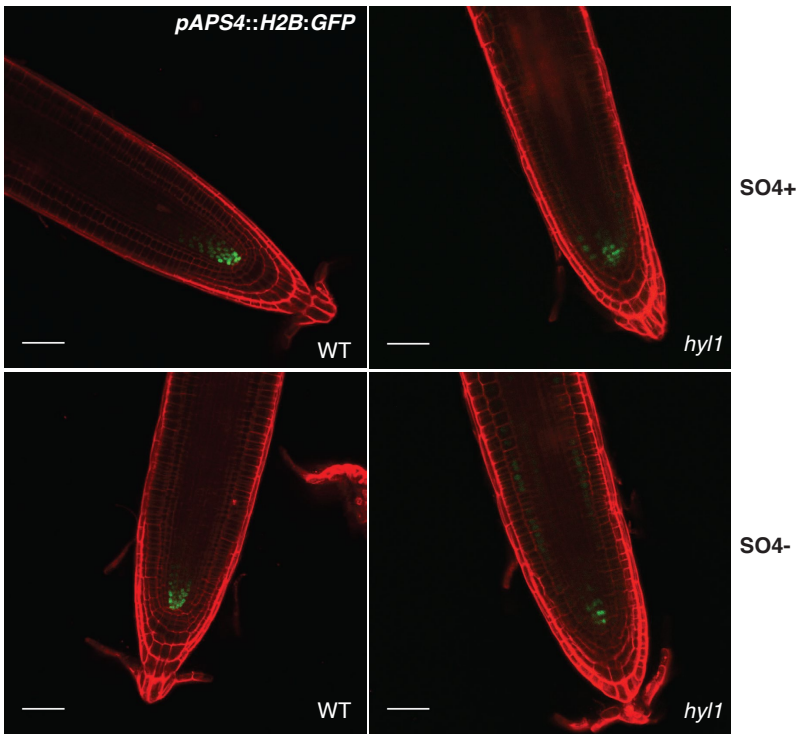

Figure S21

Appendix Table 1

lib	raw reads 15-#	mapped reads	% mapped reads	tRNA precursor re	tRNA precursor reads
GYK.2(AGO1)	18547490	16799853	90.58	13492335	80.31
GYK.3(ACR4)	17599135	15522843	88.20	10168756	65.51
GYK.4(SHR)	24998562	21453974	85.82	17461625	81.39
GYK.5(SCR)	21787779	19595676	89.94	15709545	80.17
GYK.6(CO2)	19666086	16409688	83.44	11956425	72.86
GYK.7(WER)	29909684	25655350	85.78	19796913	77.16

Appendix Table 2

Name	GYK2(AGO1)	GYK3(ACR4)	GYK4(SHR)	GYK5(SCR)	GYK6(CO2)	GYK7(WER)	miRNA_id	miRBaseV21_sequence	chromosome	positions	strand	miRBase_id	IR10_sequen	arged_positi	enlarged_sequences
ath-miR156a-3p	73.21	30.92	98.82	38.78	21.94	36.64	**ath-miR156a-3p**	GCUCACUGCUCUUUCUGUCAGA	Chr2	76470-10676	-	IMAT003186	TGCTCTTTCT	76468-10676	TGCTCTTTCTGTCAGATT
ath-miR156a-5p	20109.43	7298.87	35120.83	7620.99	7485.53	10628.11	**ath-miR156a-5p**	UGACAGAAGAGAGUGAGCAC	Chr2	76534-10676	-	IMAT000016	GAAGAGAGTG	76532-10676	AAGAGAGTGAGCACAC
ath-miR156b-3p	2448.24	847.46	2929.76	1126.27	503.36	336.58	**ath-miR156b-3p**	UGCUCACCUCUCUUUCUGUCAGU	Chr4	75004-15075	+	IMAT003186	CCTCTCTTTCT	75002-15075	CCTCTCTTTCTGTCAGTTG
ath-miR156b-5p	20065.08	7286.04	34973.13	7605.94	7478.77	10615.70	**ath-miR156b-5p**	UGACAGAAGAGAGUGAGCAC	Chr4	74945-15074	+	IMAT000016	GAAGAGAGTG	74943-15074	AAGAGAGTGAGCACAT
ath-miR156c-3p	224.41	70.86	388.74	143.40	68.86	100.76	**ath-miR156c-3p**	GCUCACUGCUCUAUCUGUCAGA	Chr4	15426-15415	-	IMAT003186	TGCTCTATCT	15424-15415	TGCTCTATCTGTCAGATT
ath-miR156c-5p	20109.43	7298.87	35120.83	7620.99	7485.53	10628.11	**ath-miR156c-5p**	UGACAGAAGAGAGUGAGCAC	Chr4	15491-15415	-	IMAT000016	GAAGAGAGTG	15489-15415	AAGAGAGTGAGCACAC
ath-miR156d-3p	2.38	1.29	0.47	0.00	0.00	0.39	**ath-miR156d-3p**	GCUCACUCUCUUUUUGUCAUAAC	Chr5	56643-34566	-	IMAT003186	TCTCTTTTTGT	56641-34566	TCTCTTTTTGTCATAACTT
ath-miR156d-5p	21417.37	8102.20	37896.12	8146.15	7954.25	11085.48	**ath-miR156d-5p**	UGACAGAAGAGAGUGAGCAC	Chr5	56713-34567	-	IMAT000016	GAAGAGAGTG	56711-34567	AAGAGAGTGAGCACAC
ath-miR156e	20009.18	7265.32	34876.17	7584.72	7452.16	10586.07	**ath-miR156e**	UGACAGAAGAGAGUGAGCAC	Chr5	67213-38672	+	IMAT000017	GAAGAGAGTG	67211-38672	AAGAGAGTGAGCACAC
ath-miR156f-3p	369.05	59.91	298.31	201.06	47.53	73.28	**ath-miR156f-3p**	GCUCACUCUCUAUCCGUCACC	Chr5	36197-91362	+	IMAT003186	CTCTCTATCCG	36195-91362	CTCTCTATCCGTCACCCC
ath-miR156f-5p	20009.18	7265.32	34876.17	7584.72	7452.16	10586.07	**ath-miR156f-5p**	UGACAGAAGAGAGUGAGCAC	Chr5	36126-91361	+	IMAT000017	GAAGAGAGTG	36124-91361	AAGAGAGTGAGCACAC
ath-miR156g	301.95	201.12	610.91	77.63	140.62	164.12	**ath-miR156g**	CGACAGAAGAGAGUGAGCAC	Chr2	12589-84126	-	IMAT000101	GAAGAGAGTG	12587-84126	AAGAGAGTGAGCACAC
ath-miR156h	173.04	38.24	169.15	102.48	32.82	52.42	**ath-miR156h**	UGACAGAAGAAAGAGAGCAC	Chr5	97087-22597	-	IMAT000101	GAAGAAAGAG	97085-22597	AAGAAAGAGAGCACAA
ath-miR156i	1.17	0.87	1.85	0.62	0.73	0.66	**ath-miR156i**	UGACAGAAGAGAGAGAGCAG	Chr1	07090-19807	-	IMAT002242	GAAGAGAGAG	07088-19807	AAGAGAGAGAGCAGAC
ath-miR156j	24.34	10.54	48.67	11.97	9.33	14.29	**ath-miR156j**	UGACAGAAGAGAGAGAGCAC	Chr2	89066-17589	-	IMAT002242	GAAGAGAGAG	89064-17589	AAGAGAGAGAGCACAG
ath-miR157a-3p	424.41	116.28	413.13	185.59	76.78	107.00	**ath-miR157a-3p**	GCUCUCUAGCCUUCUGUCAUC	Chr1	13205-24913	-	IMAT003187	CTAGCCTTCTG	13203-24913	CTAGCCTTCTGTCATCAC
ath-miR157a-5p	35354.56	15009.28	82105.59	33393.53	16987.82	22581.42	**ath-miR157a-5p**	UUGACAGAAGAUAGAGAGCAC	Chr1	13276-24913	-	IMAT000017	GAAGATAGAG	13274-24913	GAAGATAGAGAGCACAG
ath-miR157b-3p	423.52	116.60	413.37	185.59	77.09	106.61	**ath-miR157b-3p**	GCUCUCUAGCCUUCUGUCAUC	Chr1	21175-24921	+	IMAT003187	CTAGCCTTCTG	21173-24921	CTAGCCTTCTGTCATCAC
ath-miR157b-5p	35359.57	15009.87	82108.82	33394.94	16987.36	22581.63	**ath-miR157b-5p**	UUGACAGAAGAUAGAGAGCAC	Chr1	21104-24921	+	IMAT000017	GAAGATAGAG	21102-24921	GAAGATAGAGAGCACAG
ath-miR157c-3p	1.79	2.58	2.80	1.53	4.27	4.29	**ath-miR157c-3p**	GCUCUCUAUACUUCUGUCACC	Chr3	44527-62445	-	IMAT003187	CTATACTTCTG	44525-62445	CTATACTTCTGTCACCAC
ath-miR157c-5p	37167.45	15743.78	88385.19	35858.67	17790.34	23900.46	**ath-miR157c-5p**	UUGACAGAAGAUAGAGAGCAC	Chr3	44673-62446	-	IMAT000017	GAAGATAGAG	44671-62446	GAAGATAGAGAGCACTA
ath-miR157d	352.71	127.67	509.59	186.14	164.42	180.97	**ath-miR157d**	UGACAGAAGAUAGAGAGCAC	Chr1	26989-18027	-	IMAT000017	GAAGATAGAG	26987-18027	GAAGATAGAGAGCACTA
ath-miR158a-3p	1259022.58	950549.24	1706429.99	879793.43	1963057.30	1494714.16	**ath-miR158a-3p**	UCCCAAAUGUAGACAAAGCA	Chr3	66349-33663	-	IMAT000017	AATGTAGACA	66347-33663	ATGTAGACAAAGCAAT
ath-miR158a-5p	450.60	430.01	519.48	135.49	447.80	589.35	**ath-miR158a-5p**	CUUUGUCUACAAUUUUGGAAA	Chr3	66391-33664	-	IMAT003187	CTACAATTTT	66389-33664	CTACAATTTTGGAAAAA
ath-miR158b	38747.71	83528.14	23716.76	21328.22	83364.58	56454.86	**ath-miR158b**	CCCCAAAUGUAGACAAAGCA	Chr1	72273-20772	+	IMAT000101	AATGTAGACA	72271-20772	ATGTAGACAAAGCAAT
ath-miR159a	171640.64	108018.93	230375.35	112662.81	90079.78	124999.40	**ath-miR159a**	UUUGGAUUGAAGGGAGCUCUA	Chr1	13234-27713	-	IMAT000017	TTGAAGGGA	13232-27713	TTGAAGGGAGCTCTACA
ath-miR159b-3p	198503.47	113386.82	310576.84	118271.89	122813.75	162904.96	**ath-miR159b-3p**	UUUGGAUUGAAGGGAGCUCUU	Chr1	20813-62208	+	IMAT000020	TTGAAGGGA	20811-62208	TTGAAGGGAGCTCTTCA
ath-miR159b-5p	0.60	0.00	5.59	0.00	3.05	1.95	**ath-miR159b-5p**	GAGCUCCUUGAAGUUCAAUGG	Chr1	20650-62206	+	IMAT003188	CTTGAAGTTC	20648-62206	CTTGAAGTTCAATGGAG
ath-miR159c	7034.13	10204.31	4448.10	2994.93	9644.23	11092.91	**ath-miR159c**	UUUGGAUUGAAGGGAGCUCCU	Chr2	94826-18994	+	IMAT000101	TTGAAGGGA	94824-18994	TTGAAGGGAGCTCCTTT
ath-miR160a-3p	0.00	0.00	0.47	0.00	0.00	0.00	**ath-miR160a-3p**	GCGUAUGAGGAGCCAUGCAUA	Chr2	40342-16340	+	IMAT003187	GAGGAGCCA	40340-16340	GAGGAGCCATGCATATC
ath-miR160a-5p	529.46	162.13	1332.05	204.00	117.31	125.22	**ath-miR160a-5p**	UGCCUGGCUCCCUGUAUGCCA	Chr2	40282-16340	+	IMAT000017	GCTCCCTGTA	40280-16340	GCTCCCTGTATGCCATA
ath-miR160b	260.91	63.78	628.14	83.56	40.93	54.93	**ath-miR160b**	UGCCUGGCUCCCUGUAUGCCA	Chr4	88986-98890	+	IMAT000017	GCTCCCTGTA	88984-98890	GCTCCCTGTATGCCACA
ath-miR160c-3p	138.10	19.33	189.24	8.17	20.72	14.81	**ath-miR160c-3p**	CGUACAAGGAGUCAAGCAUGA	Chr5	09095-19009	-	IMAT003187	AGGAGTCAAG	09093-19009	AGGAGTCAAGCATGACC
ath-miR160c-5p	508.72	158.91	1300.36	199.66	117.31	125.02	**ath-miR160c-5p**	UGCCUGGCUCCCUGUAUGCCA	Chr5	09158-19009	-	IMAT000018	GCTCCCTGTA	09156-19009	GCTCCCTGTATGCCACG
ath-miR161.1	266320.77	190334.93	171397.36	78963.31	286353.10	375690.43	**ath-miR161.1**	UGAAAGUGACUACAUCGGGGU	Chr1	25731-17825	+	IMAT000018	TGACTACATC	25729-17825	TGACTACATCGGGGTTC
ath-miR161.2	37950.81	24854.90	30862.47	20171.85	55407.79	53995.72	**ath-miR161.2**	UCAAUGCAUUGAAAGUGACUA	Chr1	25722-17825	+	IMAT000677	CATTGAAAGT	25720-17825	CATTGAAAGTGACTACA
ath-miR162a-3p	26375.83	27116.70	32943.94	16551.02	32247.31	32387.27	**ath-miR162a-3p**	UCGAUAAACCUCUGCAUCCAG	Chr5	34936-26349	-	IMAT000018	AACCTCTGCA	34934-26349	AACCTCTGCATCCAGCG
ath-miR162a-5p	105.36	147.20	346.56	88.54	242.54	225.88	**ath-miR162a-5p**	UGGAGGCAGCGGUUCAUCGAUC	Chr5	34998-26350	-	IMAT003187	CAGCGGTTCA	34996-26350	CAGCGGTTCATCGATCTC
ath-miR162b-3p	26375.83	27116.70	32943.94	16551.02	32247.31	32387.27	**ath-miR162b-3p**	UCGAUAAACCUCUGCAUCCAG	Chr5	40610-77406	-	IMAT000018	AACCTCTGCA	40608-77406	AACCTCTGCATCCAGCG
ath-miR162b-5p	26.19	19.65	39.39	18.12	19.50	36.83	**ath-miR162b-5p**	UGGAGGCAGCGGUUCAUCGAUC	Chr5	40675-77406	-	IMAT003187	CAGCGGTTCA	40673-77406	CAGCGGTTCATCGATCAA
ath-miR163	77350.86	15732.41	25305.88	63231.27	15631.11	23325.72	**ath-miR163**	UUGAAGAGGACUUGGAACUUCGAU	Chr1	84359-24884	+	IMAT000018	GGACTTGGA	84357-24884	GGACTTGGAACTTCGATAT
ath-miR164a	38.89	5.15	60.75	3.57	2.13	2.92	**ath-miR164a**	UGGAGAAGCAGGGCACGUGCA	Chr2	20770-19520	+	IMAT000018	AGCAGGGCA	20768-19520	AGCAGGGCACGTGCAAA
ath-miR164b-3p	71.43	7.73	49.41	0.51	0.00	6.24	**ath-miR164b-3p**	CAUGUGCCCAUCUUCACCAUC	Chr5	87716-28773	+	IMAT003187	CCCATCTTCA	87714-28773	CCCATCTTCACCATCAT
ath-miR164b-5p	40.97	5.15	63.78	4.08	2.13	2.92	**ath-miR164b-5p**	UGGAGAAGCAGGGCACGUGCA	Chr5	87586-28760	+	IMAT000018	AGCAGGGCA	87584-28760	AGCAGGGCACGTGCATT
ath-miR164c-3p	0.60	0.00	0.47	0.00	0.00	0.39	**ath-miR164c-3p**	CACGUGUUCUACUACUCCAAC	Chr5	52747-98527	+	IMAT003191	GTTCTACTACT	52745-98527	GTTCTACTACTCCAACAC
ath-miR164c-5p	35.62	17.39	13.44	10.21	2.44	3.90	**ath-miR164c-5p**	UGGAGAAGCAGGGCACGUGCG	Chr5	52684-98527	+	IMAT000101	AGCAGGGCA	52682-98527	AGCAGGGCACGTGCGAA
ath-miR165a-3p	530893.75	385950.08	499877.77	889069.82	296701.29	306620.84	**ath-miR165a-3p**	UCGGACCAGGCUUCAUCCCCC	Chr1	78932-78952	-	IMAT000018	CCAGGCTTCA	78930-78954	CCAGGCTTCATCCCCCCC
ath-miR165a-5p	87.50	221.93	495.01	130.13	175.10	201.91	**ath-miR165a-5p**	GGAAUGUUGUCUGGAUCGAGG	Chr1	79010-79030	-	IMAT003187	TTGTCTGGAT	79008-79032	TTGTCTGGATCGAGGAT
ath-miR165b	528269.77	384631.58	503460.83	889512.35	294612.65	304565.05	**ath-miR165b**	UCGGACCAGGCUUCAUCCCCC	Chr4	69856-36987	-	IMAT000018	CCAGGCTTCA	69854-36987	CCAGGCTTCATCCCCCTC
ath-miR166a-3p	871565.26	775638.65	867447.64	1114571.63	600421.51	739783.44	**ath-miR166a-3p**	UCGGACCAGGCUUCAUUCCCC	Chr2	76241-19176	+	IMAT000018	CCAGGCTTCA	76239-19176	CCAGGCTTCATTCCCCCC
ath-miR166a-5p	16.57	20.40	21.05	11.82	17.47	27.19	**ath-miR166a-5p**	GGACUGUUGUCUGGCUCGAGG	Chr2	76128-19176	+	IMAT003188	TTGTCTGGCT	76126-19176	TTGTCTGGCTCGAGGAC
ath-miR166b-3p	441337.10	447992.84	314942.86	496367.15	371543.48	476674.92	**ath-miR166b-3p**	UCGGACCAGGCUUCAUUCCCC	Chr3	22301-22922	+	IMAT000019	CCAGGCTTCA	22299-22922	CCAGGCTTCATTCCCCCC

Appendix Table 3

Id	ch	st	sp	sd	lib	seq	num	sc	GYK2	GYK3	GYK4	GYK5	GYK6	GYK7	annot	overlap	lyrata_conservation
NovelMiRmerged_1	chr1	5193590	5193676	-	GYK3	cgccccttcttttctcggat	novelMiR209	34.19	11.310	58.623	6.526	5.613	8.532	32.742	exon	AT1G15100.1_exon	conserved
NovelMiRmerged_10	chr1	16432197	16432286	-	GYK2;GYK5	tgcttctttcgtcggagggct;tgcttctttcgtcggagggct	novelMiR267;novelMiR236	2.15;2.15	1.841	0.697	1.557	0.991	1.052	1.275	NA		not_conserved
NovelMiRmerged_100	chr5	14668694	14668834	-	GYK4	tcttttctttgttctccggcc	novelMiR588	2.04	11.905	4.832	17.712	7.570	8.532	5.262	TE	AT5TE52795_TE;AT4G29990.1_intron	not_conserved
NovelMiRmerged_101	chr5	15431881	15431978	-	GYK2;GYK5	ttatggaccgtccaacttggc;ttatggaccgtccaacttggc	novelMiR455;novelMiR410	57.84;48.16	27.840	16.606	38.725	12.409	19.127	12.536	TE	AT5TE55825_TE;AT4G31900.1_intron;AT4G31900.2_intron;AT4G31900.2_intron	conserved
NovelMiRmerged_102	chr5	16048511	16048829	-	GYK7	tccgaagggcacacaggtcgt	novelMiR442	Infinity	19.445	4.348	18.528	6.507	7.008	15.689	TE	AT5TE57950_TE;AT5TE57950_TE;AT4G33280.1_intron	not_conserved
NovelMiRmerged_103	chr5	17041891	17042203	-	GYK3;GYK6	agagtgagattaatggatgat;agagtgagattaatggatgat	novelMiR351;novelMiR348	1.28;1.28	1.828	2.362	5.740	1.187	3.894	2.535	TE	AT5TE61535_TE	conserved
NovelMiRmerged_104	chr5	17303844	17304143	-	GYK2;GYK4	ttagatggtaggacgggttt;ttagatggtaggacgggttt	novelMiR458;novelMiR597	1.95;1.95	2.964	1.411	3.145	1.677	1.607	1.423	TE	AT5TE62540_TE	not_conserved
NovelMiRmerged_105	chr5	17405986	17406096	-	GYK2	ttgtacatcttttaaaaccct	novelMiR460	2.01	0.540	0.076	0.550	0.298	0.269	0.296	TE	AT5TE62865_TE	not_conserved
NovelMiRmerged_106	chr5	18698692	18698873	-	GYK6;GYK4;GYK5;GYK7;GYK2;GYK3	tagtggtatgattctcgctt;ctagtggtatgattctcgctt;ctagtggtatgattctcgctt;ctagtggtatgattctcgctt;tctagtggtatgattctcgctt;tctagtggtatgattctcgct	novelMiR349;novelMiR599;novelMiR416;novelMiR447;novelMiR462;novelMiR353	1.14;1.16;1.16;1.16;1.16;1.16	1.021	10.043	0.794	0.902	2.120	3.324	tRNA	AT5G46105.1_tRNA;AT5G46105.1_exon;AT5G46110.1_exon;AT5G46110.2_exon;AT5G46110.3_exon;AT5G46110.4_exon	conserved
NovelMiRmerged_107	chr5	19740642	19740759	-	GYK5	ttaacaattgtctcatggatt	novelMiR417	1.61	1.080	0.296	1.676	0.534	0.280	0.414	TE	AT5TE71030_TE	conserved
NovelMiRmerged_108	chr5	20681429	20681728	-	GYK5	tagaattgacgggtttagatc	novelMiR419	1.6	3.938	1.382	4.788	2.394	1.116	1.495	TE	AT5TE74510_TE	not_conserved
NovelMiRmerged_109	chr5	22338712	22338816	-	GYK2	cggggatagctcagttgggaga	novelMiR468	1.55	8.686	1.402	5.952	1.775	4.447	4.513	tRNA	AT5G55045.1_tRNA;AT5G55045.1_exon;AT5G55050.1_exon	conserved
NovelMiRmerged_11	chr1	16737833	16738012	-	GYK2;GYK4;GYK5;GYK6;GYK7	ttgacccatgaattttgaccc;ttgacccatgaattttgaccc;ttgacccatgaattttgaccc;ttgacccatgaattttgaccc;ttgacccatgaattttgaccc	novelMiR268;novelMiR351;novelMiR237;novelMiR202;novelMiR268	1.32;1.32;1.32;1.32;1.32	61.650	19.610	77.923	31.110	26.541	26.771	TE	AT1TE55305_TE	not_conserved
NovelMiRmerged_110	chr5	23974778	23975030	-	GYK3	atggtgatgatgatgatgatga	novelMiR357	2.27	0.000	3.221	0.466	0.000	4.266	1.247	exon	AT5G59450.1_exon	conserved
NovelMiRmerged_111	chr3	3386038	3386241	+	GYK5;GYK7	tcaaagattaagctatggagc;tcaaagattaagctatggagc	novelMiR85;novelMiR118	190.44;332.68	278.574	224.186	117.461	214.843	204.757	302.861	intron	AT3G10815.1_intron	not_conserved
NovelMiRmerged_112	chr3	9831469	9831628	+	GYK2	tcaagcatctgaccaggagtt	novelMiR96	2.05	6.548	1.288	2.797	3.572	0.000	0.000	exon	AT3G26742.1_exon	not_conserved
NovelMiRmerged_113	chr3	10328649	10328753	+	GYK3	gtgctatgattgtaaaagta	novelMiR91	41.24	55.060	133.996	105.808	118.393	160.271	107.190	NA		conserved
NovelMiRmerged_114	chr3	10752302	10752461	+	GYK2;GYK3;GYK5;GYK6;GYK7	ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta	novelMiR99;novelMiR92;novelMiR93;novelMiR84;novelMiR127	1.32;1.32;1.32;1.32;1.32	81.777	16.112	8.788	11.338	32.519	8.979	tRNA	AT3G28685.1_tRNA;AT3TE44695_TE;AT3G28685.1_exon	not_conserved
NovelMiRmerged_115	chr3	13682928	13683200	+	GYK4;GYK7	cgagagtagtactaggatggt;cgagagtagtactaggatggt	novelMiR171;novelMiR137	94.03;25.71	35.405	21.209	59.374	9.926	14.010	18.687	TE	AT3TE55490_TE	conserved
NovelMiRmerged_116	chr3	14179935	14180074	+	GYK7	ggatgcgatcataccagcact	novelMiR141	308.66	6.081	5.536	5.240	3.994	6.279	5.234	TE	AT3TE58145_TE	conserved
NovelMiRmerged_117	chr3	14188951	14189119	+	GYK6	agcaaagatcacgaaaaggct	novelMiR93	2.49	3.364	2.551	3.622	2.595	2.161	2.853	NA		not_conserved
NovelMiRmerged_118	chr3	14395926	14396014	+	GYK4	ttaaaatatttacaagggatt	novelMiR178	1.56	0.079	0.000	0.146	0.000	0.094	0.020	TE	AT3TE59040_TE	not_conserved
NovelMiRmerged_119	chr3	14463430	14463585	+	GYK4	tgtgtgatgatatgtaggtgt	novelMiR179	1.47	1.628	0.115	0.289	0.389	0.137	0.597	TE	AT3TE59290_TE	not_conserved
NovelMiRmerged_12	chr1	17102225	17102345	-	GYK6	gtttgacttgacacgtggcac	novelMiR204	20.68	10.275	4.853	15.789	3.954	5.146	7.449	TE	AT1TE56585_TE	not_conserved
NovelMiRmerged_120	chr3	15167371	15167661	+	GYK2;GYK4;GYK5;GYK7	ttgagggagtctgggcagtcc;ttgagggagtctgggcagtcc;ttgagggagtctgggcagtcc;ttgagggagtctgggcagtcc	novelMiR125;novelMiR184;novelMiR112;novelMiR147	2.10;2.10;2.10;2.10	31.072	7.945	34.415	12.333	20.516	16.917	intron	AT3G43160.1_intron;AT3G43160.1_exon	not_conserved
NovelMiRmerged_121	chr3	15575752	15575979	+	GYK4	ttcccggacggtcaaacttcc	novelMiR188	3.28	6.151	1.417	6.002	2.866	2.255	1.091	TE	AT3TE63035_TE	not_conserved
NovelMiRmerged_122	chr3	15739277	15739407	+	GYK4	tttaaaaactcttgtaaatct	novelMiR189	2.25	0.195	0.090	0.431	0.747	0.595	0.134	TE	AT3TE63620_TE	not_conserved
NovelMiRmerged_123	chr3	16269231	16269337	+	GYK4	ttgtacatcttttaaaaccct	novelMiR193	2.14	0.322	0.008	0.782	0.426	0.518	0.054	TE	AT3TE65930_TE	not_conserved
NovelMiRmerged_124	chr3	17383550	17383662	+	GYK2;GYK7	ttgagttgagttgggttacc;ttgagttgagttgggttacc	novelMiR130;novelMiR150	2.68;2.68	1.611	2.422	1.821	0.368	2.843	1.510	TE	AT3TE70480_TE	not_conserved
NovelMiRmerged_125	chr3	17448405	17448557	+	GYK2	ttaagatttggctaagatacc	novelMiR132	4.04	4.663	5.798	11.109	2.807	4.266	10.134	intron	AT3G47350.2_intron;AT3G47350.1_intron	not_conserved
NovelMiRmerged_126	chr3	18019543	18019800	+	GYK2;GYK5	ttaacaattgtctcatggatt;ttaacaattgtctcatggatt	novelMiR133;novelMiR120	1.68;1.68	1.313	1.608	1.864	0.858	0.287	0.446	TE	AT3TE73025_TE	conserved
NovelMiRmerged_127	chr4	290055	290269	+	GYK2;GYK4;GYK6	aatagtcgacaatttgggatt;aatagtcgacaatttgggatt;aatagtcgacaatttgggatt	novelMiR141;novelMiR206;novelMiR102	1.24;1.24;1.24	27.976	9.019	6.526	0.000	10.360	1.559	exon	AT4G00710.1_exon	not_conserved
NovelMiRmerged_128	chr4	1937627	1937745	+	GYK5	tgatcctagatctgaagacct	novelMiR127	10.24	8.234	1.718	9.866	4.593	5.485	1.949	exon	AT4G04030.1_exon	not_conserved
NovelMiRmerged_129	chr4	4431176	4431274	+	GYK4	tgtgttggtcgagtgttttac	novelMiR220	51.04	2.130	0.242	1.451	0.972	0.318	0.433	TE	AT4TE18760_TE	not_conserved
NovelMiRmerged_13	chr1	17759157	17759257	-	GYK4	tttcaccaaatttaagagacc	novelMiR354	13.05	14.782	5.905	12.935	6.634	20.161	11.466	NA		not_conserved
NovelMiRmerged_130	chr4	4559762	4559915	+	GYK3	ctaattccagagattcgtgac	novelMiR128	2.52	0.303	0.354	0.491	0.086	0.299	0.193	TE	AT4TE19150_TE	conserved
NovelMiRmerged_131	chr4	4758651	4758738	+	GYK2;GYK3;GYK4;GYK5;GYK6	tgtgttggtcgagtgttttac;tgtgttggtcgagtgttttac;tgtgttggtcgagtgttttac;tgtgttggtcgagtgttttac;tgtgttggtcgagtgttttac	novelMiR153;novelMiR130;novelMiR223;novelMiR138;novelMiR112	1.76;1.76;1.76;1.76;1.76	1.023	0.854	0.990	0.324	0.155	0.125	TE	AT4TE19905_TE	not_conserved
NovelMiRmerged_132	chr4	4959183	4959335	+	GYK3	ctaattccagagattcgtgac	novelMiR132	1.08	1.153	0.324	1.363	0.076	0.259	0.145	TE	AT4TE20745_TE	conserved
NovelMiRmerged_133	chr4	5671262	5671354	+	GYK7	tcaactcaacccatgaaccct	novelMiR175	88.29	8.477	2.602	10.739	4.672	2.943	2.783	TE	AT4TE23775_TE	conserved
NovelMiRmerged_134	chr4	5866467	5866787	+	GYK4;GYK5	tacaagggattttaaagggct;tacaagggattttaaagggct	novelMiR231;novelMiR143	3.10;3.10	2.207	1.084	3.863	1.960	1.429	1.089	TE	AT4TE24700_TE	not_conserved
NovelMiRmerged_135	chr4	5923949	5924133	+	GYK3	tgactacattgtatccggccct	novelMiR135	1.98	3.571	29.634	10.255	7.144	8.532	6.237	exon	AT4G09320.1_exon	not_conserved
NovelMiRmerged_136	chr4	10709563	10709661	+	GYK6;GYK7	tgatctcaatgtaggatgcct;tgatctcaatgtaggatgcct	novelMiR127;novelMiR184	3.69;3.69	8.036	9.448	7.924	2.041	10.969	28.714	TE	AT4TE49050_TE	not_conserved
NovelMiRmerged_137	chr4	16337434	16337725	+	GYK3	gagaaactgaacggcatgttg	novelMiR144	2.81	5.357	46.383	12.119	8.675	5.485	14.812	exon	AT4G34110.1_exon	conserved
NovelMiRmerged_138	chr4	18304911	18305021	+	GYK5;GYK6	ccttccttggatgtctgaaac;ccttccttggatgtctgaaac	novelMiR158;novelMiR135	202.88;165.66	124.703	245.659	251.469	270.851	266.001	200.673	snoRNA	AT4G39361.1_snoRNA;AT4G39361.1_snoRNA;AT4G39361.1_exon	conserved
NovelMiRmerged_139	chr4	1212019	1212141	-	GYK2;GYK4;GYK6	ataccacttaagatcctactc;ataccacttaagatcctactc;ataccacttaagatcctactc	novelMiR404;novelMiR517;novelMiR311	3.40;3.40;3.40	7.385	4.337	10.676	1.827	6.865	6.332	NA		not_conserved
NovelMiRmerged_14	chr1	17887098	17887187	-	GYK7	cagaaccacaatgatcgccat	novelMiR270	2.23	0.000	1.933	44.281	10.206	0.609	8.185	exon	AT1G48410.1_exon;AT1G48410.2_exon;AT1G48410.3_exon	conserved
NovelMiRmerged_140	chr4	1694302	1694405	-	GYK4	tgctagaacacaccaaaacct	novelMiR518	15.75	0.237	0.121	0.376	0.090	0.097	0.028	TE	AT4TE08475_TE	not_conserved
NovelMiRmerged_141	chr4	2160781	2160967	-	GYK5;GYK7	atccggttcgactgattagttc;atccggttcgactgattagttc	novelMiR372;novelMiR395	2.50;2.50	2.957	2.403	6.717	2.643	5.079	2.041	TE	AT4TE10210_TE	not_conserved
NovelMiRmerged_142	chr4	2604769	2604944	-	GYK4	ttagaagttccgttaatgact	novelMiR522	19.59	4.293	1.267	4.114	1.287	4.649	1.553	TE	AT4TE12190_TE	conserved
NovelMiRmerged_143	chr4	3113327	3113442	-	GYK6	aaggagacattttggagcaaa	novelMiR315	8.28	0.948	0.644	1.192	0.116	0.220	0.480	TE	AT4TE14345_TE	not_conserved
NovelMiRmerged_144	chr4	3183147	3183300	-	GYK3	ctaattccagagattcgtgac	novelMiR311	2.49	0.285	0.391	0.931	0.117	0.948	0.133	TE	AT4TE14540_TE	conserved
NovelMiRmerged_145	chr4	3546082	3546235	-	GYK3	ctaattccagagattcgtgac	novelMiR312	2.73	0.335	0.407	0.504	0.096	0.298	0.156	TE	AT4TE15945_TE;AT4G06574.1_exon	conserved
NovelMiRmerged_146	chr4	5274728	5275048	-	GYK4	ttttttaagcaatgtgggacc	novelMiR530	1.28	4.299	4.724	4.937	1.373	2.833	3.488	TE	AT4TE21925_TE	not_conserved
NovelMiRmerged_147	chr4	5529857	5530114	-	GYK5	tgcgggcgctgaaacggggat	novelMiR380	1.88	0.992	0.859	1.593	1.701	0.406	1.104	TE	AT4TE23125_TE;AT4G08657.1_exon	not_conserved
NovelMiRmerged_148	chr4	5679910	5680002	-	GYK7	tcaactcaacccatgaaccct	novelMiR403	136.04	11.256	5.092	15.183	5.909	5.710	5.068	TE	AT4TE23785_TE	conserved
NovelMiRmerged_149	chr4	6033679	6033991	-	GYK3;GYK4;GYK6;GYK7	agagtgagattaatggatgat;agagtgagattaatggatgat;agagtgagattaatggatgat;agagtgagattaatggatgat	novelMiR317;novelMiR535;novelMiR320;novelMiR404	1.39;1.39;1.39;1.39	2.027	2.362	5.776	1.187	5.113	2.535	TE	AT4TE25425_TE	conserved
NovelMiRmerged_15	chr1	19768117	19768374	-	GYK2;GYK5	ttaacaattgtctcatggatt;ttaacaattgtctcatggatt	novelMiR273;novelMiR243	2.03;2.03	4.136	0.766	4.496	1.032	0.273	1.054	TE	AT1TE65360_TE	not_conserved
NovelMiRmerged_150	chr4	6281247	6281565	-	GYK4	tagaggatctaatttttggcc	novelMiR537	2.22	0.714	4.164	0.444	0.374	0.325	0.232	TE	AT4TE26705_TE	not_conserved
NovelMiRmerged_151	chr4	6378936	6379250	-	GYK7	tttttggagtgaaaatagacc	novelMiR407	1.14	6.101	0.805	3.667	1.378	0.762	2.602	TE	AT4TE27175_TE;AT4TE27185_TE	not_conserved
NovelMiRmerged_152	chr3	3386036	3386239	-	GYK2;GYK3;GYK4;GYK5;GYK6;GYK7	tcaaagattaagctatggagc;tcaaagattaagctatggagc;tcaaagattaagctatggagc;tcaaagattaagctatggagc;tcaaagattaagctatggagc;tcaaagattaagctatggagc	novelMiR338;novelMiR256;novelMiR440;novelMiR307;novelMiR253;novelMiR337	229.01;170.38;121.95;205.56;166.31;381.45	278.574	224.186	117.461	214.843	204.757	302.861	intron	AT3G10815.1_intron	not_conserved
NovelMiRmerged_153	chr3	4263949	4264065	-	GYK3;GYK7	ttcgtttttggtctgagcct;ttcgtttttggtctgagcct	novelMiR258;novelMiR338	1.95;2.84	1.786	7.086	6.526	6.634	2.742	5.457	NA		conserved
NovelMiRmerged_154	chr3	8095828	8096086	-	GYK7	tttttggagtgaaaatagacc	novelMiR341	1.69	3.125	0.805	3.574	2.398	0.762	4.515	TE	AT3TE33960_TE	not_conserved
NovelMiRmerged_155	chr3	9743856	9744155	-	GYK3	cttggagctgggacatatctg	novelMiR264	1.88	22.024	12.884	15.848	13.779	9.141	8.575	NA		not_conserved
NovelMiRmerged_156	chr3	9744115	9744255	-	GYK3	cttggagctgggacatatctg	novelMiR265	3.57	23.810	14.173	20.509	15.820	14.626	10.914	NA		not_conserved
NovelMiRmerged_157	chr3	10457820	10457908	-	GYK4	tttaaaaactcttgtaaatct	novelMiR449	1.87	0.343	0.076	0.232	0.066	0.256	0.126	TE	AT3TE43440_TE;AT3G28100.1_intron	not_conserved
NovelMiRmerged_158	chr3	10864122	10864430	-	GYK4	cttgtaaatcttttaaaccct	novelMiR450	2.23	0.533	0.997	1.188	0.377	0.655	0.421	TE	AT3TE45180_TE	not_conserved
NovelMiRmerged_159	chr3	11286842	11287157	-	GYK5	ttagatggtaggacgggttt	novelMiR317	1.11	3.371	1.464	6.668	2.345	2.267	2.184	TE	AT3TE47035_TE	conserved
NovelMiRmerged_16	chr1	21507889	21508061	-	GYK5;GYK6	gagaattgtcatgatgggttg;gagaattgtcatgatgggttg	novelMiR247;novelMiR209	2.41;26.60	10.755	16.417	19.773	5.656	12.841	11.600	TE	AT1TE70985_TE	not_conserved
NovelMiRmerged_160	chr3	11379212	11379379	-	GYK6	aggagcagaatcgttagggtt	novelMiR262	1.36	1.317	1.353	2.044	0.606	1.730	1.155	TE	AT3TE47430_TE	not_conserved
NovelMiRmerged_161	chr3	11862406	11862573	-	GYK4	ttagaagttccgttaatgact	novelMiR462	2.2	4.279	0.293	1.389	0.484	0.609	1.694	TE	AT3TE49390_TE;AT3TE49390_TE	not_conserved
NovelMiRmerged_162	chr3	12048501	12048654	-	GYK3	ctaattccagagattcgtgac	novelMiR271	2.48	0.294	0.391	0.472	0.117	0.542	0.133	TE	AT3TE50165_TE;AT3G30416.1_exon	conserved
NovelMiRmerged_163	chr3	12129650	12129960	-	GYK5;GYK7	acaacatgtactttcggattca;acaacatgtactttcggattca	novelMiR324;novelMiR352	1.48;1.48	2.093	3.164	3.072	2.471	0.963	2.391	TE	AT3TE50420_TE	not_conserved
NovelMiRmerged_164	chr3	12254194	12254346	-	GYK3	ctaattccagagattcgtgac	novelMiR272	2.09	0.393	0.466	0.596	0.114	0.341	0.189	TE	AT3TE50760_TE	conserved
NovelMiRmerged_165	chr3	13128502	13128632	-	GYK4	tttaaaaactcttgtaaatct	novelMiR471	2.53	0.218	0.165	0.791	0.066	0.100	0.134	TE	AT3TE53720_TE	not_conserved
NovelMiRmerged_166	chr3	13631929	13632051	-	GYK4	cttcgaggagatatgacgcgcc	novelMiR478	2.72	0.414	0.162	0.655	0.154	0.117	0.072	TE	AT3TE55365_TE;AT3G33072.1_exon	not_conserved
NovelMiRmerged_167	chr3	13736701	13736973	-	GYK4;GYK7	cgagagtagtactaggatggt;cgagagtagtactaggatggt	novelMiR479;novelMiR360	93.97;25.65	35.405	21.209	59.374	9.926	14.010	18.687	TE	AT3TE56020_TE	conserved
NovelMiRmerged_168	chr3	14178262	14178429	-	GYK6	agcaaagatcacgaaaaggct	novelMiR289	2.69	2.472	3.591	4.703	1.971	2.623	1.968	NA		not_conserved
NovelMiRmerged_169	chr3	14181223	14181391	-	GYK6	agcaaagatcacgaaaaggct	novelMiR290	2.65	3.398	2.579	3.990	2.601	2.186	2.865	NA		not_conserved
NovelMiRmerged_17	chr1	21873763	21874080	-	GYK4	ataaacattcagatttcggtt	novelMiR366	2.29	8.333	2.577	9.322	4.593	7.313	5.067	TE	AT1TE72170_TE;AT1TE72175_TE;AT1G59540.1_exon;AT1G59540.2_exon	not_conserved
NovelMiRmerged_170	chr3	14182218	14182385	-	GYK6	agcaaagatcacgaaaaggct	novelMiR291	2.69	2.472	3.591	4.703	1.971	2.623	1.968	NA		not_conserved
NovelMiRmerged_171	chr3	14188790	14188929	-	GYK2	ggatgcgatcataccagcacta	novelMiR377	124.99	5.969	5.794	4.937	3.884	6.526	5.684	TE	AT3TE58230_TE	conserved
NovelMiRmerged_172	chr3	14397366	14397467	-	GYK2;GYK3;GYK4;GYK5;GYK6;GYK7	aggatgggtgacctcccggga;aggatgggtgacctcccggga;aggatgggtgacctcccggga;aggatgggtgacctcccggga;aggatgggtgacctcccggga;aggatgggtgacctcccggga	novelMiR378;novelMiR293;novelMiR486;novelMiR339;novelMiR294;novelMiR373	1.28;1.28;1.28;1.28;1.28;1.28	1.942	3.355	0.924	1.209	2.053	1.243	TE	AT3TE59045_TE;AT3G42240.1_exon	conserved
NovelMiRmerged_173	chr3	14403270	14403482	-	GYK4	ctctagaacttggatttggcc	novelMiR487	80.45	3.765	4.318	8.232	2.648	3.734	5.198	TE	AT3TE59075_TE	conserved
NovelMiRmerged_174	chr3	14737188	14737505	-	GYK5;GYK6	tacaagggattttaaagggct;tacaagggattttaaagggct	novelMiR342;novelMiR296	1.25;1.25	1.363	0.625	2.987	0.942	0.818	0.714	TE	AT3TE60260_TE	not_conserved
NovelMiRmerged_175	chr3	16159696	16159821	-	GYK2;GYK3;GYK4;GYK5;GYK6;GYK7	tagagaggtctagattgcagc;tagagaggtctagattgcagc;tagagaggtctagattgcagc;tagagaggtctagattgcagc;tagagaggtctagattgcagc;tagagaggtctagattgcagc	novelMiR382;novelMiR300;novelMiR496;novelMiR348;novelMiR300;novelMiR378	1.52;1.52;1.52;1.52;1.52;1.52	1080.763	418.308	1088.143	501.386	407.788	543.356	intron	AT3G44570.1_intron;AT3G44570.1_exon	not_conserved
NovelMiRmerged_176	chr3	16510766	16510859	-	GYK5	tcaatggagagatgtcgaaat	novelMiR351	14.64	5.449	2.038	6.529	3.346	3.575	2.801	TE	AT3TE66935_TE	not_conserved
NovelMiRmerged_177	chr3	16700097	16700414	-	GYK5	tatctgtacaacgttgtctgt	novelMiR352	1.49	26.508	10.307	36.357	10.206	19.298	10.524	TE	AT3TE67660_TE	not_conserved
NovelMiRmerged_178	chr3	17101726	17101832	-	GYK4;GYK5	tcatatatatgaaagttggtc;tcatatatatgaaagttggtc	novelMiR500;novelMiR354	2.17;2.17	1.720	0.182	0.924	0.463	0.313	0.159	TE	AT3TE69335_TE;AT3TE69340_TE	not_conserved
NovelMiRmerged_179	chr3	18815703	18815960	-	GYK3	gcatcttgagatcgcgagggcc	novelMiR302	2.49	0.000	10.307	0.000	0.000	0.000	0.000	intron	AT3G50660.1_intron;AT3G50660.1_exon;AT3G50660.1_exon	conserved
NovelMiRmerged_18	chr1	22993096	22993395	-	GYK3	tagaattgacgggtttagatc	novelMiR223	24.67	16.431	2.194	17.744	9.018	5.322	5.529	TE	AT1TE75780_TE	not_conserved
NovelMiRmerged_180	chr3	21282771	21282872	-	GYK2;GYK4;GYK5;GYK6;GYK7	tttcatcaaagttaagagact;tttcatcaaagttaagagact;tttcatcaaagttaagagact;tttcatcaaagttaagagact;tttcatcaaagttaagagact	novelMiR394;novelMiR506;novelMiR361;novelMiR308;novelMiR386	1.97;1.97;1.97;1.97;1.97	10.714	2.362	8.545	4.083	14.829	12.148	NA		not_conserved
NovelMiRmerged_181	chr3	21386667	21386903	-	GYK2;GYK3;GYK4;GYK5	tccggttcttgtgtttgaatt;tccggttcttgtgtttgaatt;tccggttcttgtgtttgaatt;tccggttcttgtgtttgaatt	novelMiR395;novelMiR307;novelMiR507;novelMiR362	81.74;34.33;94.49;52.17	98.513	43.162	89.339	52.052	53.932	61.586	exon	AT3G57710.1_exon	conserved
NovelMiRmerged_182	chr2	241542	241862	+	GYK5	tttagaagtttaggacccgtt	novelMiR41	4.82	5.220	5.009	7.785	6.035	2.688	4.152	TE	AT2TE00985_TE	not_conserved
NovelMiRmerged_183	chr2	706529	706826	+	GYK2;GYK3;GYK4;GYK5;GYK6;GYK7	ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta;ggggatgtagctcagatggta	novelMiR48;novelMiR45;novelMiR70;novelMiR42;novelMiR37;novelMiR49	1.51;1.51;1.51;1.51;1.51;1.51	80.587	15.253	8.089	10.845	31.648	7.977	tRNA	AT2G02600.1_tRNA;AT2G02590.1_exon;AT2G02600.1_exon	not_conserved
NovelMiRmerged_184	chr2	821262	821463	+	GYK7	tgccgctgaagagatctcgtg	novelMiR50	12.11	28.572	59.267	9.788	7.910	20.719	24.166	exon	AT2G02835.1_exon	not_conserved
NovelMiRmerged_185	chr2	1766808	1766897	+	GYK2	ttgattcgagaaccctaaact	novelMiR53	3.37	6.845	5.261	20.043	3.572	4.266	5.847	NA		not_conserved
NovelMiRmerged_186	chr2	2535455	2535596	+	GYK2	ttgtacatcttttaaaaccct	novelMiR60	1.31	0.982	0.139	0.504	0.210	0.182	0.273	TE	AT2TE11480_TE	not_conserved
NovelMiRmerged_187	chr2	2828778	2828885	+	GYK6	tgtgttggtcgagtgttttac	novelMiR46	6.56	0.903	0.673	1.919	0.337	1.505	0.174	TE	AT2TE12425_TE	not_conserved
NovelMiRmerged_188	chr2	3289720	3289899	+	GYK7	cgatcggcgtaagaaaagat	novelMiR66	55.61	22.540	45.310	33.405	48.497	47.127	34.366	intron	AT2G07681.1_intron;AT2G07681.1_exon;AT2G07681.1_exon	not_conserved
NovelMiRmerged_189	chr2	3386231	3386328	+	GYK4	gagtgaagctgtctggagggaa	novelMiR89	79.64	23.076	31.201	22.436	19.171	42.048	15.838	exon	AT2G07707.1_exon	not_conserved
NovelMiRmerged_19	chr1	23355095	23355200	-	GYK2	tagtggaagcagcaacgagaa	novelMiR281	2.65	7.738	1.288	4.195	4.083	0.000	0.390	exon	AT1G63020.1_exon;AT1G63020.2_exon	conserved
NovelMiRmerged_190	chr2	3497187	3497401	+	GYK7	gtggtcaaaagcggcagact	novelMiR69	2.38	2.083	5.637	1.981	2.526	1.727	2.436	tRNA	AT2G07765.1_tRNA;AT2G07765.1_exon	conserved
NovelMiRmerged_191	chr2	3502010	3502152	+	GYK4	gaagaggactgcttacgggatc	novelMiR93	629.35	270.637	467.161	455.005	505.128	651.952	549.398	intron	AT2G07835.1_intron;AT2G07835.1_exon	not_conserved
NovelMiRmerged_192	chr2	3617276	3617482	+	GYK3	tcatatggactttggctacac	novelMiR62	107.39	6.999	2.846	8.978	2.375	4.509	5.776	intron	AT2G07981.1_intron;AT2G07981.1_exon;AT2G07981.1_exon	not_conserved
NovelMiRmerged_193	chr2	3620354	3620560	+	GYK3	tcatatggactttggctacac	novelMiR64	121.95	5.922	3.573	10.260	2.765	9.231	5.089	intron	AT2G08986.1_intron;AT2G08986.1_exon;AT2G08986.1_exon	not_conserved
NovelMiRmerged_194	chr2	3623733	3623939	+	GYK3	tcatatggactttggctacac	novelMiR65	119.11	19.581	14.846	31.306	8.418	12.712	11.625	intron	AT2G08986.1_intron;AT2G08986.1_exon;AT2G08986.1_exon	not_conserved

Appendix Table 4

lib	# pairs	Aligned pairs	concordant pair alignment rate
GMD223b	1696652	1447578	84.80%
GMD224b	2743027	2406198	87.10%
GMD225b	3092823	2675710	85.90%
GMD226b	2221055	1930868	86.30%
GMD227b	1991982	1744233	86.60%
GMD228b	3410932	3061744	89.20%
GMD229b	3917449	3447302	87.30%
GMD230b	2978900	2640463	87.90%
GMD231b	4043314	3347378	82.20%
GMD232b	3405071	2983312	86.80%
GMD233b	1991940	1698903	84.80%
GMD234b	2971257	2500468	83.70%
GMD235b	2453424	1875648	75.70%
GMD236b	2808082	2428328	85.70%
GMD237b	2668505	2160672	80.20%
GMD238b	1936080	1660909	84.70%
GMD223	2393973	2064037	85.60%
GMD224	4874636	4263659	86.80%
GMD225	2673809	2312224	85.90%
GMD226	2927919	2533901	85.90%
GMD227	4394680	3819099	86.20%
GMD228	4114742	3653711	88.10%
GMD229	3313899	2912220	87.10%
GMD230	3394558	2955665	86.20%
GMD231	3495667	2955958	83.80%
GMD232	3572938	3138549	87.00%
GMD233	2939881	2547790	86.00%
GMD234	3046494	2665706	86.80%
GMD235	2980596	2382646	79.00%
GMD236	2793329	2442720	86.50%
GMD237	3388022	2878677	84.00%
GMD238	2949176	2575866	86.30%
GMD320	1572214	1273663	80.10%
GMD321	2325149	1801879	76.80%
GMD322	2167765	1656935	75.80%
GMD323	2140760	1658761	76.70%
GMD89	6068297	4752216	77.60%
GMD90	6220116	5407906	86.30%
GMD91	7041616	5355730	75.30%
GMD92	7552573	6054558	79.20%

NAME	SEQUENCE
Pro-ACR4-4-F	GGGGCAACTTTGTATAGAAAAGTTGGAATAGTCAAGAAATGGCC
Pro-ACR4-1-R	GGGGCTGCTTTTTTGTACAAACTTGTCAAAGTCAACACACACGC
Pro-ACR4-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTATAGTCAAGAAATGGCC
Pro-ACR4-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCAAAGTCAACACACACGC
Pro-SHR-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATCAGAGCGTGGGGTTTCTTC
Pro-SHR-1-R	GGGGCTGCTTTTTTGTACAAACTTGTGAGAAAGGGAGACCCACAATATC
Pro-SCR-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATAAGTGGAAATTTACCTGGA
Pro-SCR-1-R	GGGGCTGCTTTTTTGTACAAACTTGTGGTCGTGAGATTGCATGGTTA
Pro-CO2-4-F	GGGGCAACTTTGTATAGAAAAGTTGGACTAACTCCATTATTTACGACTG
Pro-CO2-1-R	GGGGCTGCTTTTTTGTACAAACTTGTAAACTCTTGTTGCATTATTGTC
Pro-WER-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATGATCTAAGCACGAAACG
Pro-WER-1-R	GGGGCTGCTTTTTTGTACAAACTTGTTGTTTCTTTGATGATAGAC
Pro-WER-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGATCTAAGCACGAAACG
Pro-WER-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTGTTTCTTTGATGATAGAC
Pro-159A-NI-F	AAGCGGCCGCCCTATCAACAAGTTGTTTGGC
Pro-159A-BHI-R	AAGGATCCCTTCCATCGTCAGATCAAGATCTATCG
Pro159B-NI-F	AAGCGGCCGCGAAAAGGGTTTCTAGGTTATCTCGCGAAAG
Pro-159B-XhoI-R	AACTCGAGTCTTCTTCTTCCTTTGTTTTTCTATATAATCG
Pro-160A-NI-F	ACGCGGCCGCCATTGTGAATAATATTCAACAAAGGAAG
Pro-160A-SpeI-R	ACACTAGTCATATGTATATGCGTCATGAC
Pro-160B-NI-F	ACGCGGCCGCGTAACAGTATTTATGATGTTATGG
Pro-160B-SpeI-R	ACACTAGTATGTATACGGGAACCCTT
Pro-160C-NI-F	ACGCGGCCGCTGTAATAGTGTGTGCGTGTGTG
Pro-160C-BHI-R	ACGGATCCGTATACCAAACCTCTACGCATG
Pro-163-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATGAGATCATCCAAATATATCGT
Pro-163-1-R	GGGGCTGCTTTTTTGTACAAACTTGTGGGTTTTGGTCGGTTTATCT
Pro-164B-NI-F	CCGCGGCCGCGAACGGTTAACGTGTATTGTAC
Pro-164B-BHI-R	CGCGGATCCTCTTGCTCATCACACACCTTC
CB-pro165a-4-F	GGGGACAACTTTGTATAGAAAAGTTGTGTCAGTGCATGGATGTTTT
CB-pro165a-1-R	GGGGACTGCTTTTTTGTACAAACTTGGGTGTTATGATGAGGGAAT
Pro-395A-NI-F	TCAGCGGCCGCTTGACTCTCTTCTTGTAGCT
Pro-395A-Xho-R	TCACTCGAGCCAACCAAGAATATTGTTTC
Pro-395B-NI-F	TCAGCGGCCGCCCAACCAAGAATATTGTTTC
Pro-395B-XhoI-R	TCACTCGAGTTGACTCTCTTCTTGTAGCT
Pro-395C-NI-F	TCAGCGGCCGCGGGGGACTCTTGGTGATCATT
Pro-395C-XhoI-R	TCACTCGAGTACAAACAACACTAACACTG
Pro-395D-NI-F	TCAGCGGCCGCGCTAAAATGCTTATATTTGT
Pro-395D-BHI-R	TCAGGATCCATCTAGTCGAATTATTATTG
Pro-395E-NI-F	TCAGCGGCCGCCGTGGGATTGAAAAGATGC
Pro-395E-BHI-R	TCAGGATCCTGAAAAAGAATGGAGGGACT
Pro-396A-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATTTCCTTGTCTTCTGTTGTG

Pro-396A-1-R	GGGGCTGCTTTTTTGTACAAACTTGTAGGGTCATGTAGAGCAGACG
Pro-396B-4-F	GGGGCAACTTTGTATAGAAAAGTTGGAAGGTTGTGTTTTTTAATCGC
Pro-396B-1-R	GGGGCTGCTTTTTTGTACAAACTTGTGGATCTTCATCTTCTCCTTC
Pro-397A-4-F	GGGGCAACTTTGTATAGAAAAGTTGGAGTGGCAAGTCTATTACCGAA
Pro-397A-1-R	GGGGCTGCTTTTTTGTACAAACTTGTAACCCAGGAAAAAATATCCT
Pro-397B-4-F	GGGGCAACTTTGTATAGAAAAGTTGGACAAATGTGGAAAATCATCTC
Pro-397B-1-R	GGGGCTGCTTTTTTGTACAAACTTGTCAGGGGAAAAAAATATCTCC
Pro-MYB33-NI-F	GAGCGGCCGCGAAAGCCTCCGGCACAAGCA
Pro-MYB33-SpeI-R	GAACTAGTCTCTTTTCTAATTAAACCACTG
Pro-MYB65-NI-F	GAGCGGCCGCAGTGAGCAAGTTTTAAGATG
Pro-MYB65-HIII-R	GAAAGCTTCTCTTTCTACTTAAAGCAAGAC
Pro-GRF2-4-F	GGGGCAACTTTGTATAGAAAAGTTGGATAATTGAGTTGTCAAAAAACTCCTTTTTATATTACTTACTTCTT
Pro-GRF2-1-R	GGGGCTGCTTTTTTGTACAAACTTGTAAGAAGTAAGTAATATAAAAAG
Pro-Lac4-NI-F	GAGCGGCCGACGCATATTTGTATGTAGCC
Pro-LAC4-BHI-R	GAGGATCCCTCCCTCTCTATCTTTCTCT
CB-proAPS4-F	GGGGCAACTTTGTATAGAAAAGTTGGACAAATATGTAAACTATTAGA
CB-proAPS4-R	GGGGCTGCTTTTTTGTACAAACTTGTTGATTAATCAGTTTTTTTG
Pro-HYL1-NotI-F	CAGCGGCCGCCAATATGAGCCCAGTTCCCT
Pro-HYL1-BHI-R	CAGGATCCCTGAATTTAATTTCAAACC
MYB33-CDS-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTATGAGTTACACGAGCACTGAC
MYB33-CDS-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCGGGTAGTTCTGTCATTTGAC
GRF2-CDS-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGATATTGGTGTTC
GRF2-CDS-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCGGTTGTGTAATGAAAG
LAC4-CDS-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGGGTCTCATATGGTTTG
LAC4-CDS-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCGGTGCACTTGGGAAGATCCTT
APS4-CDS-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGCTTCTTCAGCA
APS4-CDS-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCCAGCAGAAGCAACAGCT
HFRPL18-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTTATTTTTACAACAATTACCAACAAC
HFRPL18-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAACCTTGAATCCACGACTCTTC
P19-2-F	GGGGACAGCTTTCTTGTACAAAGTGGGAATGGAACGAGCTATACAAGGAAAC
P19-3-R	GGGGACAACTTTGTATAATAAAGTTGCTATTACTCGCTTTCTTTTTCGAAGG
HYL1-CDS-1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTATGACCTCCACTGATGTTTCCTCTG
HYL1-CDS-2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTGCGTGGCTTGCTTCTGTCTCCAC
AGO1-CDS-2-F	GGGGACAGCTTTCTTGTACAAAGTGGGAATGGTGAGAAAGAGAAGAACGGATG
AGO1-CDS-3-R	GGGGACAACTTTGTATAATAAAGTTGGGCAAACGCATGAAATCAGTGA

qRT-PCR

NAME	SEQUENCE
SPL10-RT-F	GTGGGAGAATGCTCAGGAGGC
SPL10-RT-R	GAGTGTGTTTGATCCCTTGTGAATCC
MYB33-RT-F	ATATGGGGCAGTGAAGCTGG
MYB33-RT-R	AGAGTGTGGAGGAGATGACGA
MYB65-RT-F	GATGGTTCCTGATAGCCATACAGTTAC
MYB65-RT-R	TAGGCATCAACAGAGTCAAGGAGATC

ARF17-RT-F	AGCACCTGATCCAAGTCCTTCTATG
ARF17-RT-R	TGGTGAATAGCTGGGGAGGATTTC
CUC1-RT-F	GGAGCACGTGTCCTGTTTCT
CUC1-RT-R	GAGCGGGAAGGAATGTATGA
PHB-RT-F	AGAGTTCCTTTCCAAGGCTACAG
PHB-RT-R	ATAGCGACTATGCCAATAGAATCC
NF-YA2-RT-F	CTTGAACACTAAAAGTCAGAACTTGG
NF-YA2-RT-R	GACACATTTAATCCGTTCGATAAGTT
NF-YA8-RT-F	TCCATATCTGAGCCGGTGGA
NF-YA8-RT-R	ATCTGGACAAAGCGTGTGAA
TCP4-RT-F	CCTTCAACGACGTCGTTTCAGCCAG
TCP4-RT-R	GTGAACCGGTGGAGGAAGGTGATG
APS4-RT-F	GCTGGGCAAGTCCTCTCAAA
APS4-RT-R	CGGAACCGACATGTTGACGA
LAC17-RT-F	CAGACTGAGAGTGAAGCCAGG
LAC17-RT-R	AACCGTGTGATTTGCGATGC
AT3G37050-RT-F	TCATGGAGACGCTGCACATT
AT3G37050-RT-R	ATTCCAAAACCTCCCGACCC
CSD2-RT-F	TTTCATCTCCATGAGTTTGGTG
CSD2-RT-R	AAAGGCTCTTCCAACAACAGA
ACT2-RT-F	GCACCCTGTTCTTCTTACCG
ACT2-RT-R	AACCCTCGTAGATTGGCACA
GAPC-RT-F	ACTCAATCACTGCTACTCAG
GAPC-RT-R	GTCAACTTTCCGTTAAGAGC

Probe

NAME	SEQUENCE
miR156	GTGCTCACTCTCTTCTGTCA
miR158	TGCTTTGTCTACATTTGGGA
miR159	TAGAGCTCCCTTCAATCCAAA
miR160	TGGCATACAGGGAGCCAGGCA
miR162	CTGGATGCAGAGGTTTATCGA
miR163	ATCGAAGTTCCAAGTCCTCTTCAA
miR164	TGCACGTGCCCTGCTTCTCCA
miR165	GGGGGGATGAAGCCTGGTCCGA
miR167	TAGATCATGCTGGCAGCTTCA
miR169	TCGGCAAGTCATCCTTGGCTG
miR171	GATATTGGCGCGGCTCAATCA
miR172	ATGCAGCATCATCAAGATTCT
miR395	GAGTTCCCCCAAACACTTCAG
miR396	CAGTTCAAGAAAGCTGTGGAA
miR398	AAGGGGTGACCTGAGAACACA
miR403	CGAGTTTGTGCGTGAATCTAA
miR160c*	GTCAACTTTCCGTTAAGAGC

miR165a*	CCTCGATCCAGACAACATTCC
miR396a*	CTGTATCTTCCCACAGCTTTAT
U6	AGGGGCCATGCTAATCTTCTC

Appendix Table S6. Primers used in this study