Table S4. Potential target genes for individual plant miRNAs.

Target gene of plant miRNAs: TOR

MIRNA	Position in target gene	Structure of binding site	minimum of free energy
ath-miR156a-5p	1687	U UGA UACA A-- GUGC UCAUUUUCU UCUG |||| |||:|:||| |||| CACG AGUGAGAGA AGAC - --- ---- AGU	-22
ath-miR160a-5p	6109	C U C AGUUAUA U A G UGGC GUAC GGGA G CCGGG CA |||| :||| |||| | ||:|| || ACCG UAUG CCCU C GGUCC GU - - U ------- - - -	-27.5
ath-miR162a-3p	3678	G AUG UA A U CUGGA GC AGA GUUUGUCGA ||||| || ||| ||||:|||| GACCU CG UCU CAAAUAGCU - A-- -- C -	-26.4
osa-miR166g-3p	5448	A UAU AUUG A GAGG AUGAAGCU UCGA |||| |||||||: :||| CUCC UACUUCGG GGCU - U-- ACCA -	-25
ath-miR167a-5p	3738	A G UCUU A--- AGAUCAUGUU GGC GC ||||||||:| ||| || UCUAGUACGA CCG CG A - U--- AAGU	-26.4
ath-miR168a-5p	1547	A -- UGGACU A- UCCUGG UGCACCA GC |||||: ||||||| || AGGGCU ACGUGGU CG A GG U----- CU	-26.6

<table>
<tr><td>ath-miR172c</td><td>5164</td><td>G UA GAA U A
CUGCAGC CA CA GAUUCU
||||||| || || ||||||
GACGUCG GU GU CUAAGA
- UA A-- U -</td><td>-24.3</td></tr>
<tr><td>ath-miR390a-5p</td><td>5148</td><td>U AUUA G C A
GUGCUAUCUU U CUG AGCU
|:||||||:: | ||| ||||
CGCGAUAGGG A GAC UCGA
C ---- G - A</td><td>-26.4</td></tr>
<tr><td>ath-miR824-5p</td><td>6380</td><td>U A A - AUA A
UCC CU UC CACAA GUGGUUUA
||| || || ||||| :||||:||
AGG GA AG GUGUU UACCAGAU
- - - A --- -</td><td>-23.6</td></tr>
</table>

Target gene of plant miRNAs: IRS

<table>
<tr><th>MIRNA</th><th>Position in target gene</th><th>Structure of binding site</th><th>minimum of free energy</th></tr>
<tr><td>ath-miR156a-5p</td><td>1765</td><td>A G CCGAUGA C
UG UCAUUUUC UCUGUCG
|| |||:|:|| ||||||:
AC AGUGAGAG AGACAGU
C G A------ -</td><td>-23</td></tr>
<tr><td>ath-miR157a-5p</td><td>4706</td><td>C GCG CCGUACG - C-
GUGCUC C UAUCU CUGUU
|||||| | ||||| ||||:
CACGAG G AUAGA GACAG
- A-- ------- A UU</td><td>-21.3</td></tr>
<tr><td>ath-miR158a-3p</td><td>860</td><td>G GG GGA --- U
GCU UG CUGC UGGGA
||| || ||:| |||||
CGA AC GAUG ACCCU
A A- A-- UAA -</td><td>-20.3</td></tr>
<tr><td>ath-miR160a-5p</td><td>859</td><td>G - GU CU A-
GGC UG GGGA GCUGGG</td><td>-27.9</td></tr>
</table>

<table>
<tr><td></td><td></td><td>||| || |||| ||::||
CCG AU CCCU CGGUCC
A   U GU   --   GU</td><td></td></tr>
<tr><td>ath-miR162a-3p</td><td>1380</td><td>A   A   U   GAAAAUG   A
UGGAUG UGG GGU   UGUUGG
|||||| ::| ||| |:|:|:
ACCUAC GUC CCA   AUAGCU
G   -   U   A------   -</td><td>-22.9</td></tr>
<tr><td>ath-miR166a-3p</td><td>2497</td><td>C U   -   AGAA A A-
GG GGAA GAAGC   GG CC
|| |||| ||||| || ||
CC CCUU CUUCG   CC GG
- -   A   GA-- A CU</td><td>-23.5</td></tr>
<tr><td>osa-miR166g-3p</td><td>1589</td><td>-U   UC-   U   - A-
GGA   GAG CCUGG CC
||| :|| ||||| ||
CCU   UUC GGACC GG
CU   UAC   -   A CU</td><td>-23.6</td></tr>
<tr><td>ath-miR167a-5p</td><td>841</td><td>-C   U   ACCGG   G--
GGUCG UGCUGGU   GGCU
|:||: ||||||:   :|||
CUAGU ACGACCG   UCGA
AU   -   -----   AGU</td><td>-25.9</td></tr>
<tr><td>ath-miR168a-5p</td><td>1881</td><td>C   -   GAGACGAU UG   G
UUCC ACCUG   U CAAGCGA
|:|| ||||| | |||||||
AGGG UGGAC   G GUUCGCU
A   C   -------- UG   -</td><td>-27.9</td></tr>
<tr><td>ath-miR172a</td><td>1340</td><td>-C GU   GU CAC   G
G GCGU UC   GGAUUCU
| ||:| || :||||||
C CGUA AG   UCUAAGA
UA GU   GU U--   -</td><td>-23.7</td></tr>
<tr><td>ath-miR172c</td><td>1340</td><td>-C GU   GU CAC   G
G GCGU UC   GGAUUCU
| ||:| || :||||||
C CGUA AG   UCUAAGA</td><td>-23.7</td></tr>
</table>

<table>
<tr><td></td><td></td><td>GA GU   GU U--   -</td><td></td></tr>
<tr><td>ath-miR390a-5p</td><td>2905</td><td>-C   -   U   CC   A-
CGC AUC CCUCC GAGC
||| ||| ||||| ||||
GCG UAG GGAGG CUCG
CC   A   -   A-   AA</td><td>-27</td></tr>
<tr><td>ath-miR397a</td><td>1132</td><td>G   GUUUU   A-   G
AUCA   ACGCUGUGC AAUGG
|||| ||||||::| ||||:
UAGU   UGCGACGUG UUACU
G   -----   AG   -</td><td>-23.6</td></tr>
<tr><td>osa-miR528-5p</td><td>1337</td><td>U   GG   ACGGA   G
UCC UGCGUGUUCC   UUCU
||| |||:||::|| |||:
AGG ACGUACGGGG   AAGG
G   AG   -----   U</td><td>-26.5</td></tr>
<tr><td>ath-miR824-5p</td><td>1747</td><td>A   GCAUAA   -   A-
UCCUUC   UCACA AUGGUC
:||||| ||||| ||||||
GGGAAG   AGUGU UACCAG
A   ------   U   AU</td><td>-25.8</td></tr>
<tr><td>ath-miR827</td><td>3725</td><td>---A   AUA   -   A--
UGU   UGAUGG CAUC
||| |||||| ||||
ACA   ACUACC GUAG
UCAA   ---   A   AUU</td><td>-20.3</td></tr>
<tr><td>ath-miR845a</td><td>842</td><td>G   UUGC   C   G
GUCG   UGGUA CGGGGCUG
:||: ||||| |:|:||:|
UAGU   ACCAU GUCUCGGC
G   UA--   A   -</td><td>-26.1</td></tr>
</table>

Target gene of plant miRNAs: EGFR

MIRNA	Position in target gene	Structure of binding site	minimum of free energy

ath-miR156a-5p	4761	-A - GA G- GUUCGCUC CUU CUGU |:||:||| ||| |||| CGAGUGAG GAA GACA CA A -- GU	-23
ath-miR157a-5p	4426	---A GAUUU C UCUCUGUCUUC UCAA |||||:||||| |||| AGAGAUAGAAG AGUU CACG AC--- -	-23.5
ath-miR158a-3p	2209	G UGGAAAC AAGGUG U UGCUUU GUUUACA UUUGGG |||||| ||:|||| |||||| ACGAAA CAGAUGU AAACCC - ------- ------ U	-21.5
ath-miR160a-5p	194	A - U AG C GGC UGC GGGGAG GGGC ||| |:| :||||| :||| CCG AUG UCCCUC UCCG A U - GG U	-30.8
ath-miR162a-3p	2897	U U-- ACGCCGA G UGGAUGC GG GUCGA ||||||| || :|||| ACCUACG CC UAGCU G UCU AAA---- -	-22.8
ath-miR166a-3p	201	U A GG AGAACU A A GGGGAG G GCCUG GUC GA |||||: | ||||| ||| || CCCCUU C CGGAC CAG CU - A UU ------ G -	-30.2
osa-miR166g-3p	201	U A GG AGAACU A A GGGGAG G GCCUG GUC GA |:|||: | ||||| ||| || CUCCUU C CGGAC CAG CU - A UU ------ G -	-27.2
ath-miR167a-5p	253	---C G GGGCAGGU G UCA UGCUGGCA GCUUCG	-27.3

<table>
<tr><td></td><td></td><td>||| |||||||| |||||:
AGU ACGACCGU   CGAAGU
AUCU   -   --------   -</td><td></td></tr>
<tr><td>ath-miR168a-5p</td><td>2968</td><td>A   GAUAUCU   U   AG   U
UCCUGGCC   UGC AUCA GGCGA
|||:|:|| ||| |:|| :||||
AGGGCUGG   ACG UGGU UCGCU
A   -------   -   --   -</td><td>-29.9</td></tr>
<tr><td>ath-miR172a</td><td>2020</td><td>U   C   U UAU   G
UGCGG CAUCAUCA G   UUCU
|||:| |||||||| | ||||
ACGUC GUAGUAGU C   AAGA
U   -   U U--   -</td><td>-26.2</td></tr>
<tr><td>ath-miR172c</td><td>2020</td><td>U   C   U UAU   G
UGCGG CAUCAUCA G   UUCU
|||:| |||||||| | ||||
ACGUC GUAGUAGU C   AAGA
G   -   U U--   -</td><td>-26.4</td></tr>
<tr><td>ath-miR390a-5p</td><td>270</td><td>A   UCGGG   AA   GCGG   G-
GGUGCU   CCC UCC   GAGU
||:||| ||| ||| |||:
CCGCGA   GGG AGG   CUCG
-       UA---   --   A---   AA</td><td>-27.9</td></tr>
<tr><td>ath-miR397a</td><td>5603</td><td>A   G AUU   C--
CAUCGA GC   UGUAUUCGA
||||:| || ||:|:||:|
GUAGUU CG   ACGUGAGUU
-       G ---   ACU</td><td>-23.5</td></tr>
<tr><td>ath-miR403-3p</td><td>3263</td><td>G   GUUGAG AUG   C   A--
GAGUU   GU   GCG GAAUC
||||| || ||| |||||
CUCAA   CA   CGC CUUAG
G   A----- ---   A   AUU</td><td>-20.2</td></tr>
<tr><td>osa-miR528-5p</td><td>3144</td><td>-C   - AGUA   G
UUUCUGCAU CC   CUUCCG
::||||||| || |||||:
GGAGACGUA GG   GAAGGU</td><td>-27.5</td></tr>
</table>

<table>
<tr><td></td><td></td><td>GA C G--- -</td><td></td></tr>
<tr><td>ath-miR824-5p</td><td>2118</td><td>C G C C G-
CCCUUC C CAA UGG C
|||||| | ||| ||| |
GGGAAG G GUU ACC G
A A U U A AU</td><td>-20.8</td></tr>
<tr><td>ath-miR845a</td><td>2492</td><td>---A ACA UU A
AAUUGGUGU CAGA GCC
|||||||:| |||| |||
UUAACCAUA GUCU CGG
GUAG --- -- C</td><td>-23.2</td></tr>
</table>

Target gene of plant miRNAs: PDK1

<table>
<tr><th>MIRNA</th><th>Position in target gene</th><th>Structure of binding site</th><th>minimum of free energy</th></tr>
<tr><td>ath-miR156a-5p</td><td>4978</td><td>-C C CUC C U
GU CACUCUCU UCU GUCG
|: |||||||| ||| |||:
CG GUGAGAGA AGA CAGU
CA A --- - -</td><td>-25</td></tr>
<tr><td>ath-miR157a-5p</td><td>5143</td><td>-A A GACGCG U A
GC UCUU GUC UUCUGUCGA
|| |||: :|| |||||||:|
CG AGAG UAG AAGACAGUU
CA - A----- - -</td><td>-24.2</td></tr>
<tr><td>ath-miR160a-5p</td><td>4947</td><td>G AAA C G U
GGCG ACGGGG GC CAGGC
|||: ||:||| || |||||
CCGU UGUCCC CG GUCCG
A A-- U - U</td><td>-33</td></tr>
<tr><td>ath-miR162a-3p</td><td>1617</td><td>C GUC CUUAGG G
CUGGA CGGAG GUCGA
||||| |:||| :||||
GACCU GUCUC UAGCU
- AC CAAA-- -</td><td>-23.2</td></tr>
</table>

ath-miR166a-3p	4798	G GG GG AA UU U GGGGG G G UGGU GG ||||: | | |||| |: CCCCU C C ACCA CU - UA UU GG GG -	-29.9

osa-miR166g-3p	4798	G GG GG AA UU U
		  GGGGG G G UGGU GG
		  |:||: | | |||| |:
		 CUCCU C C ACCA CU
		- UA UU GG GG -
			-26.9

ath-miR167a-5p	240	-C - GAG G U GAUCG GC GG AGCUUC ||||: || || |||||| CUAGU CG CC UCGAAG AU A A-- G U	-26.8

ath-miR168a-5p	896	G G CCCCCUU CUCCAGG G
		   UC CCGGCCUGC CCG AGCGA
		   || |||:||||| ||: |||||
		  AG GGCUGGACG GGU UCGCU
		A - U------ ------- -
			-31.3

ath-miR172a	1857	-C A CG G
		  GCA UGUC CGGGAUUC
		  ||| ::|| |::|||||
		  CGU GUAG GUUCUAAG
		UA C UA A
			-23.5

ath-miR172c	1857	-C A CG G
		  GCA UGUC CGGGAUUC
		  ||| ::|| |::|||||
		  CGU GUAG GUUCUAAG
		GA C UA A
			-23.5

ath-miR390a-5p	993	U AG G CAGUC G
		   GGCG AUCCCUC U GGCU
		   |||| ||||||| | :|||
		 CCGC UAGGGAG A UCGA
		- GA G C---- A
			-27.3

ath-miR397a	1010	A U G G-- GUCGGC GCU GUGCUCGA	-24.6

<table>
<tr><th></th><th></th><th></th><th></th></tr>
<tr><td></td><td></td><td>:||::| ||| |::|||||
UAGUUG CGA CGUGAGUU
G   - -   ACU</td><td></td></tr>
<tr><td>ath-miR403-3p</td><td>2568</td><td>A   GAAAAAUA   U   U
CGAG   GCGUG AUCUGG
|||| ||||| ||||::
GCUC   CGCAC UAGAUU
-   AAACA---   U   -</td><td>-21.6</td></tr>
<tr><td>osa-miR528-5p</td><td>899</td><td>-G GGC   C--   C
CC CUGC CCCCUUCCG
|| |||| ||||||||:
GG GACG GGGGAAGGU
GA A--   UAC   -</td><td>-29.2</td></tr>
<tr><td>ath-miR824-5p</td><td>1701</td><td>A   GAGGGA   UUGG   G G
UCCC   UUCGCA   AAUGGU UA
|||| :||:|| |||||| ||
AGGG   GAGUGU   UUACCA AU
-   AA----   ----   G -</td><td>-23.7</td></tr>
<tr><td>ath-miR845a</td><td>1005</td><td>U   CGGCUGC   C -   A
CGUCAGU   UGGUG UC GAGCC
|:|||:| ||||: || |||||
GUAGUUA   ACCAU AG CUCGG
-   -------   - U   C</td><td>-25.2</td></tr>
</table>

Target gene of plant miRNAs: MKP3

<table>
<tr><th>MIRNA</th><th>Position in target gene</th><th>Structure of binding site</th><th>minimum of free energy</th></tr>
<tr><td>ath-miR156a-5p</td><td>186</td><td>-A   UACU   C G   C
GCUC   GCUCUCU C UGUU
|||| :|||||| | |||:
CGAG   UGAGAGA G ACAG
CA   ----   A -   U</td><td>-22.9</td></tr>
<tr><td>ath-miR157a-5p</td><td>193</td><td>C   CC G   G G G
UGCUCUCU GU UUC GU GA
|||||||| :| ||| || :|
ACGAGAGA UA AAG CA UU</td><td>-24.3</td></tr>
</table>

<table>
<tr><td></td><td></td><td>C   -- G   A G -</td><td></td></tr>
<tr><td>ath-miR160a-5p</td><td>47</td><td>G   C   CA   CU   AGA   C
UGGC UGCAG   GG   GGCU   AGGC
|||| |:||| || :||: ||||
ACCG AUGUC   CC   UCGG   UCCG
-     U   --   --   ---   U</td><td>-27.3</td></tr>
<tr><td>ath-miR162a-3p</td><td>1679</td><td>-----A   GACAUUUG   U
GUAGAGG   UAUUGA
|:||||| |||:||
CGUCUCC   AUAGCU
GACCUA   AA------   -</td><td>-20.6</td></tr>
<tr><td>ath-miR166a-3p</td><td>2250</td><td>A   UGC   UUCACU   -   A
GGGAG   UGG   GUCUGG CCGG
||||: ||: |:|||| |||:
CCCUU   ACU   CGGACC GGCU
C   ---   U-----   A   -</td><td>-27.1</td></tr>
<tr><td>osa-miR166g-3p</td><td>2250</td><td>A   UGC   UUCACU   -   A
GGGAG   UGG   GUCUGG CCGG
:|||: ||: |:|||| |||:
UCCUU   ACU   CGGACC GGCU
C   ---   U-----   A   -</td><td>-25.3</td></tr>
<tr><td>ath-miR167a-5p</td><td>802</td><td>G   -   AGC   GC   G
AGA CG   UGCUGGCAGU   CA
||| |: |||||||||: ||
UCU GU   ACGACCGUCG   GU
A   A   ---   AA   -</td><td>-26.9</td></tr>
<tr><td>ath-miR168a-5p</td><td>45</td><td>-G G   G   U-
U UGGCCUGCA CAGGC
: :|:|||||| ||:||
G GCUGGACGU GUUCG
AA G   G   CU</td><td>-30.5</td></tr>
<tr><td>ath-miR172a</td><td>1719</td><td>C   G -   G--
UGCAG A CAUCAGGU
||||| | |||||:|:|
ACGUC U GUAGUUCUA
U   G A   AGA</td><td>-24.1</td></tr>
</table>

ath-miR172c	1718	C G - G-- CUGCAG A CAUCAGGGU |||||| | |||||:|:| GACGUC U GUAGUUCUA - G A AGA	-25.8
ath-miR390a-5p	2641	-----G A UAU G GUCCCUCCU G GCU :|||||||| | ||| UAGGGAGGA C CGA CCGCGA - U-- A	-25.3
ath-miR397a	427	--A A CUCUGUG A UAACGC GCAU UUAGUGA :||||| |||: |:|:||| GUUGCG CGUG AGUUACU GUA A ------- -	-22.5
ath-miR403-3p	1830	C G--- GG U CGAGU GUGUGAA UAG ||||| |:||||| ||: GCUCA CGCACUU AUU - AACA AG -	-21.2
osa-miR528-5p	2645	C A- G--- U CUCCU GUAUGCU CCA ||||| |:||||: ||| GAGGA CGUACGG GGU - GA GGAA -	-24.3
ath-miR824-5p	1465	A AAGA C C- CU UCA CAGAUGGUC |: ||| ||:|||||| GG AGU GUUUACCAG A GAAG - AU	-21.2
ath-miR845a	1694	G ACUCUA U U UAUUGAUUGGUG CAGA CC :||::||||||: |||| || GUAGUUAACCAU GUCU GG - A----- C C	-21.1

Target gene of plant miRNAs: PIK3

<table>
<tr><th>MIRNA</th><th>Position in target gene</th><th>Structure of binding site</th><th>minimum of free energy</th></tr>
<tr><td>ath-miR167a-5p</td><td>346</td><td>--U   GUA A-   A
AUCG GC GCAGCUUCA
|||: || |||||||||
UAGU CG CGUCGAAGU
AUC   A-- AC   -</td><td>-23.8</td></tr>
<tr><td>ath-miR172a</td><td>1108</td><td>C   GU   CCA   C
UGCAG UAUCAUU   GAGAUUUU
||||| :|||||:   :|||||:|
ACGUC GUAGUAG   UUCUAAGA
U   --   ---   -</td><td>-23.2</td></tr>
<tr><td>ath-miR390a-5p</td><td>4859</td><td>--A C   A   A-
GCU UUCUUCC GAGC
||| |:|:||| ||||
CGA AGGGAGG CUCG
CCG U   A   AA</td><td>-26.3</td></tr>
<tr><td>ath-miR397a</td><td>2521</td><td>U A   A UG   U-
CGU AACGC UGU UCAAU
|:| ||||| ||: |||||
GUA UUGCG ACG AGUUA
- G   - UG   CU</td><td>-22.8</td></tr>
<tr><td>osa-miR528-5p</td><td>1659</td><td>U   AG   -- A - C
CUCC CUGCA CC CCU CCA
|||| ||||| || ||| |||
GAGG GACGU GG GGA GGU
-    A-   AC - A -</td><td>-26.5</td></tr>
<tr><td>ath-miR824-5p</td><td>5498</td><td>G   AUUA   C   A---
UCUCUUC   UACA GUGG
||:|||| :||| :|||
AGGGAAG   GUGU UACC
-       A---   U   AGAU</td><td>-20.2</td></tr>
<tr><td>ath-miR845a</td><td>5244</td><td>--C G   C   G</td><td>-24.4</td></tr>
</table>

<table>
<tr><td></td><td></td><td>CAA UGGUAUUAG GUCG
||| ||||||:|| |:||
GUU ACCAUAGUC CGGC
GUA A U -</td><td></td></tr>
</table>

Target gene of plant miRNAs: PI3K

<table>
<tr><th>MIRNA</th><th>Position in target gene</th><th>Structure of binding site</th><th>minimum of free energy</th></tr>
<tr><td>ath-miR156a-5p</td><td>5375</td><td>-G GUCGGA A
GCUCAUUUUU UCUGUCA
|||||:|:|: |||||||
CGAGUGAGAG AGACAGU
CA A----- -</td><td>-27</td></tr>
<tr><td>ath-miR157a-5p</td><td>1722</td><td>-C CUAUCUC U-
GCUCUCUAUCU UCUGUC
||||||||||| ||||||
CGAGAGAUAGA AGACAG
CA ------- UU</td><td>-31.2</td></tr>
<tr><td>ath-miR158a-3p</td><td>6549</td><td>U GG AUCUG ACG A
UGUU GUC GCGU GGGA
||:| ||| :|:| ||||
ACGA CAG UGUA CCCU
- AA A---- AA- -</td><td>-20.9</td></tr>
<tr><td>ath-miR160a-5p</td><td>4738</td><td>G - UCCGU CC A
UGGCA GCGGG GGCCA GGCA
||||| :|:|| :|||| ||||
ACCGU UGUCC UCGGU CCGU
- A C---- -- -</td><td>-31</td></tr>
<tr><td>ath-miR162a-3p</td><td>3233</td><td>-A C A GC- G
G GAUG AGGGG GUCGA
| |||| ||:|| :||||
C CUAC UCUCC UAGCU
GA - G AAA -</td><td>-22.6</td></tr>
</table>

<table>
<tr><td>ath-miR166a-3p</td><td>530</td><td>A   AGAAAU   A   C   A-
   GGGAA   UGAAG CUUGG CC
   ||||| ||||| |:||| ||
 CCCUU   ACUUC GGACC GG
C   ------   -   A   CU</td><td>-27.4</td></tr>
<tr><td>osa-miR166g-3p</td><td>3368</td><td>G   ACGA   CG--   A
   GAGGAAU   GAAGCU   CCGA
   ||||||| |||||: ||||
 CUCCUUA   CUUCGG   GGCU
-        ----   ACCA   -</td><td>-26.2</td></tr>
<tr><td>ath-miR167a-5p</td><td>4729</td><td>-C   U G   GGG C
  GAUCG UG UGGCAGC   UC
  ||||: || ||||||| ||
  CUAGU AC ACCGUCG   AG
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