SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1. Certain npcRNA genes are present within highly dense genomic environments. Distances of five npcRNA genes relative to neighbouring genes (as annotated in TAIR) are indicated. Positions of ATG and STOP codons are indicated for the latter. In some cases, 5' and 3'UTRs are lacking from TAIR annotations. The At3g19960 gene encoding a myosin-like protein is located 23 nt upstream of the npcRNA 43 gene. Arrowheads indicate the position of the Myos-43-Fw (5'-GATGTTCTTGAGACAACCTCGT-3') and Myos-43-Rev (5'-GATGAAGATATTACTCCTCGATCAAT-3') primers (size of primers are not on scale) that failed to amplify a PCR product in all tissues analyzed.

Supplemental Figure 2. Secondary RNA structures proposed for npcRNA fragments having statistically significant Z-scores (see Table 2). Arrows indicate the 5' end and the direction of transcription.

Supplemental Figure 3. Other npcRNAs broadly expressed in different *A. thaliana* tissues.

A, npcRNAs with comparable levels in the different plant tissues analysed. Total RNA from roots, rosettes, stems, cauline leaves, inflorescences and cell suspensions was assayed by semi-quantitative RT-PCR. **B,** npcRNAs difficult to detect in most tissues, due to low transcript levels or low amplification efficiency of primer pairs. **C**, Two RT-PCR products were obtained for npcRNA 62. Cloning and sequencing of these two PCR products allowed us to position a 98 nt intron in the 3' region of the corresponding gene. The star indicates the PCR product corresponding to the spliced RNA. +/-: RT-PCR performed with or without reverse transcriptase. Control PCRs performed on water (w) or genomic DNA (gDNA) are shown.

Supplemental Figure 4. Abundance of npcRNA 78 splicing variants in different plant tissues. RT-PCR detection of different npcRNA 78/*MIR162a* transcripts in roots, rosettes, stems, cauline leaves, inflorescences and cell suspensions, as well as in phosphate starved or cytokinin-treated roots. RT-PCR was performed using npcRNA 78 specific primers located in exons 2 and 4 (78E2F/78E4R).

Supplemental Table I. npcRNA primer pairs used in RT-PCR experiments.

npcRNA primer pairs
2-Fw TGGCTTCTAGGATTGTTGA 2-Rev AGAGATTGAAGTAATCCACCC
4-Fw ATGGTTGAGTACTGACCGGG 4-Rev TGTGGGTACACCATCTTTTT
14d3 AAGACATAAGCCGGCGAGTA 14d5 CAGAGGCGAGTTCTTTCACC
15f3 AAGCTTTCCGACATCACCAC 15f5 TTGATTCGTTTTGCAACCAG
21-Fw TATTCCCTCGGTGGATAAAGGT 21-Rev AAGAGAACCCACACACCAAT
26-Fw ATCCGACTTTGGTTCAGGTGT 26-Rev CAAAATTCAGCCCTTCAAAACC
29-Fw AGTTCTTTATGCCTTTCTCGGGTC 29-Rev GAAGCCTCTGCCTACAAAGGG
30-Fw CATCTAATTGCCATAATCGG 30-Rev GATAAGCTTAAGACGTGTCAG
33d3 ACATCGCATCACATCACACA 33d5 AACCAAACTCATCCTTCACTTCA
34d3 ACAGCGGTGCCACCTATTAC 34d5 CCTCTTGATCCGGTCATGTT
40-Fw TATACATGGTTGCTGTAGAGAGACA 40-Rev GCGATAACACAAATCGTATGTTCAG
41-Fw TAAGGAAAACATAACCTCCG 41-Rev AGAAAGAGATGGGGTCTTACA
43-Fw GCTATCTATCTTTCGGATTGGA 43-Rev GACACGTGTAGAAGACGTATATTG
48a3 TTACTTCCAGTCACCGGCAT 48a5 GTTCATTGCAAAAGGCGAT
52_Fw GATTTTCTTGTGTCGCTTATCATGG 52_Rev GAGTAATCACAAGTTTTTCCGGC
58d3 TGATGTCTGGGAAATTGGTG 58-Rev AAGGCTCATGTATCAAAACCGAGAT
60-Fw TCCCGTAGGCTCCAACCTTT 60-Rev AAAAGTGTCGACCACAAGCAG
62d3 TGTGCTGACTTGGGAACACT 62d5 GCCCTTCTGACCACCAACTA
72d3 AACCGGGATATACCACGTCA 72d5 TCGGATTTATGTTGGGGGTA
75e3 CACAGCTTAACCCACCCAAT 75e5 AGAGGTGGATCGTGGATCAG
78E5F GTGAAATCAATTGCAGTCTCCT 78E5R CAAGGCATGGCAGAGTTTACA
79_Fw TTAGCTGGAAATGGTTGTC 79_Rev GGAAAATGCTTGATTGTGTG
82d5 AATTTTCGCCATTTTGTTGC 82e3 CAGTTGAACGCACATCGACT
83-Fw AAGGCTTTGTTTCTGATGAAGG 83-Rev AGAGGTACCCACCATTGTAATTCTA
111-Fw AATAACAGGTAACAGAGGAGG 111-Rev CTGTTATCCACCGGAGTAG

113d3 CAACAAAGCAAAGCGTTGAA 113d5 CAAGAGTGAAGCGTCCATGA
131d3 GGTGCTGAAGACACGTGAGA 131d5 CTTTGTCTACGGCGAGGTTC
149-Fw GATTCTGGACATTTTCTGCT 149-Rev AGCCAAGTGAACAGACCCA
150b3 GCCTACAACGATTGTGCAGCAAGA 150b5 GATGACTTATCGGCATGTGTTACAGTT
155d3 AATCTCACCCATAGCTAAAACAAA 155d5 ACAATGGCCATCGAAAAGAG
156b3 CTGAATAAAGCTACAAAGGGC 156b5 GTTTTCCGACGACGTTCTATGA
157-Fw GACGGCGGCTAGGGTTTG 157-Rev TTTCCTCACTACCTTTGTCAATCTC
311-Fw ACAGAGGAACCTCAGTTTGG 311-Rev TCAAGATCCACTATACCACC
325-Fw TGGGAGATTCAATATCGTTG 325-Rev GCATGGCTTCTATAATTACC
326b3 CAAAACATTTACAAAGCCCAAACCC 326b5 CCTCACCGTCAACAAATGTA
351_Fw TAGATGTAATCGGTGGTGGAGTC 351_Rev ACCTATCCACGCGTCAGG
370-Fw AGTCACGCTTTTCTTTTCGGCTT 370-Rev GCCTTTGTCACCCTCGCC
375f3 TTCGAATCCGGACTCACTTC 375f5 GGCACTTCCAAAGAGCTGAC
415f3 AGTCACCAACCGACTCATCC 415f5 TGGTTCGGATGGTTAGATCC
431-Fw ACAAATTAGTGCCTGAGGCCG 431-Rev AAGAACGTCTCTGCTTTGACAG
PLS-Fw GGAGACAGGAAAGGGACGG PLS-Rev CATCCTAGACAAGACACTGACATAG
DVL20-Fw TCTTTCTCCGTCTTCTCACATTTC DVL20-Rev CCATGTGGCTACACTTCGC
RPL41-Fw TCCATAGGACGTGTCTCAAAA RPL41- Rev CCAGAACTGCATCTAGTGG

Supplemental Table II. Other primer pairs used in RT-PCR experiments.

RNA	**Primer pairs**
β-TUBULIN4	beta-tub_4_Fw 5'-GCTTACGAATCCGAGGGTGCC-3' beta-tub_4_Rev 5'-GTCCAGTGTCTGTGATATTGCACC-3'
ACTIN2	actin2-Fw 5'-GCACCCTGTTCTTCTTACCG-3' actin2-Rev 5'-AACCCTCGTAGATTGGCACA-3'
DICER-LIKE1	DCL-cleav-F 5'-GAGTTCGCGATTCTTTTTGG-3' DCL-cleav-R 5'-CCCTTGAAAGCAAGAGATGC-3'
miRNA precursor primers	
RNA	**Primer pairs**
npcRNA 78/ pri-miR162a	The primers used for pri-miR162a amplification using semi-quantitative RT-PCR are the same as those mentioned in Materials and Methods as 78E2F and 78E4R. Real-time RT-PCR was performed using 78E5F and 78E5R (see Supplementary Table I).
pri-miR162b	pri-miR162b-F1[a] 5'-TGCATCTATCCACCTCTCTCTG-3' pri-miR162b-R1[b] 5'-CGAATCCATTGTCCTGCTTC-3' (for qRT-PCR) or pri-miR162b-R2[c] 5'-TTGGATTCAGTGGCTCAACA-3'
pri-miR172b	pri-miR172b-Fw 5'-CGGATTAGGGCGTTAATTACAATG-3' pri-miR172b-Rev 5'-GGTCTCTGGACGAACTATTCTGTA-3'

[a] F1 primer position: 3 nucleotides upstream of the 5' end of the *MIR162b* primary transcript mapped by Xie et al. (2005) using 5'RACE (see GenBank accession DQ063621 for the sequence of the 467 nucleotide long primary transcript described by these authors).

[b]R1 primer position: 147 nucleotides upstream of the 3' end of the primary transcript mapped using 3'RACE by Xie et al. (2005).

[c]R2 primer position: 258 nucleotides downstream of the 3' end of the primary transcript mapped using 3'RACE by Xie et al. (2005).