

A. *nmat2* (At5g46920) full cDNA sequence:

5' ...**agaagaggaagaagtcgaag**ctgttccatcaatcgctccgaa**ATGCGTAGAAGCTTCTCTGTTTGGGTCCTTACAAATGGCTAAAACCTTCTTCTACATATACCAACGT**
TTACTGCTTCGTCACAAATCCTCCTCTCATTTCTAACCCTAACCAACGGCTCTGCGATTTTCCGATATCTATCTTACTTCGCACCTCAACAACGAAGACAACAACAACAGC
ACCAGATCCAGATGATCCAGCGAATCTATTGAAAGAAGATGGAGTATCTCTCTGTTCTCAGATGTGGCTTGAGAATTTCAAAGAACCTGACAAAACCGCTACTAATTTAAC
CTCGTATCTTCGTAGATTCGAGTTATGGGTATTAGCTTATCAGAAAAGTTTGTGTGATGAATTAGGTGCTTATGTTCCCTCGTAGCTCTATTCAAAGATCAGCTTTAGAGAA
TTTGTTAGCTTTTAAGAACTCTGTTCTCGATGATCGGTTTAAATGGGGTTCTCGGTTGGATTCTATATTAATCTCCTAGAGATAAGACCGATTACGAGTCGTTGTCGAA
GAGGAAGATTAAAGCGATTTTGACTACTACGCAGCCTACTCCGTTTCAGGATAGGATAGTTTCAGGAGGTTTGTGTGATGATTTTGAACCGATATACGAATCTCGGTTTTTC
GCAAAAATCGTTTTCGTTTTCGGCCCCGGGAGGACCGCGCATACGGTGTGAGAGTGATTTCGGAGGAATTCGCGGGTTATTTGTGGTATGTTAAGGGTGATTTGAGTGTGT
GTTGGATGGAATGAAAGTTGGTTTGTGATTAGTTCTTTGATGAGAGATGTTAGAGATAAGAAAGTGATTGATTGATCAAATCTGCGCTTGTTACACCTGTTGTAACGAG
TAAAGTTGAAGATGGTGAGAAGAAGAAGACTAAGAAGAGAAAATATCAGAAAAAACGGGTTTGGCTGAGGATGAGCCCCAAGCCTGATCCTTATTGGTTAGAGACGTTCTT
TGGTTTTGCTCCTGAGGAAGCTGGGAAGTCTCCGCAGTGGGGACATTGCGGGATTCTTAGTCCTCTTTGGTTAATGTATGTCTTGACGAGCTTGATCGTTGGATGGAAC
GAAAGTGAAAGACTTTTACCCTCCTTCGAAAAGCGATGTTATATGGAATAACCTGAAGGAGAAGCGGATCAAGGAAACACTTCTTGGCCGGAATTTGTTCCACGAGTGG
TCCTGACAAAACGAGGAAAATGGATTACGTTAGATATGGAGGTCATATCTTGATTGGTGTCCGTGGACCTCGAGCTGATGCTGCAACGTTAAGGAAGAGCTTATTGAGTT
TGTTGATCAGAAGTATATGCTTAGACTCGACAATGAGAATCTACCCATTGAACATATAACAAAAGGTATAATGTTCTTGATCATGTTTTGTGTGCGCGAGTTGTTTATCC
GACTCTGAGGTATACTGCGACCGGTGGGAAGATTATAAGCGAAAAAGGCGTGGGAACGCTTTTATCCGTTACAGCGAGTTTGAAGCAATGCATCAACAGTTTCGAAAGCT
GTTATTTATAAAAGGAGATCGTGATCCGGATCCACAGCCTTGTTTTAGAAATGTTCCACGCAACTCAAGCTCATACGAATAATCAGATGAATAAGTTTTTGACTACGATTGC
TGAGTGGTATCGGTTTGCAGATAACAGAAAGAAAATTGTGAATTTCTGTTCTTATATTATCCGTGGTCACTTGCTAAGCTTTATGCTGCAAAGTATAAACTTAGATCAAG
AGCAAAAGTGTATAAGTTCGCTAATCGGAATCTGAGCCTTCCGTTGTGTCAGAAAGAGTCCAGTCACCAGAATATCAGAATCTCTTAAGAATGGGCTCTGCTGAATCGGT
TGATGGACTTGTTTATACAAGAATGTCTTAGTTCCAGAACTGATTACTCGCCTTCCCGGGTAATTGGAGGCCGAGCAGCAGAGAAGTTTCTGATCGAGTACTTAACACT
CGATGAACCGAAAACCTTAGAAGAGCAAAAGAGATTTATTAGAGAGAAAGGGCTCGTTTCGCCTCAGGATTACACATCGATGTTGGTTTGGAAGTATAAGAGAAATGCTAT
TCCAATGGATCAAGTTTCAATTCTAAAGGATCAACCTTCTTGTGTTGGGATCATCAAGTACCTACAACCGCGACAATGATGATCAGAAGAATAAAGAAGAAGATGAAGATAG
TGAAGATGGG**C**TTTCGCATTGCACGCATGTAAGaaaccagaaaactgtttgacttttactcttatatcaagcttgataaatttgatgcatattagccattcccatccg
tttgtttcggctattgtatgcaaacacc**aaatttattagcattggtattttc**...3'

nMAT2 (At5g46920) protein sequence:

Predicted targeting site

MRRSFSVLGPYKWLKPSSTYTNVYCFVTNPLISPNNGSAIFRYSYFAPQRRQQQAPDPDDPANLLKEDGVSLCSQMWLENFKEPKDTATNLTSYLRRF**ELWVLAYQ**
KVCCDELGAYVPRSSIORSALENLLALRNSVLDDREFKWSRLDFYIKSPRDKTDYESLSKRRIKAILTTTQPTPFQDRIVQEVLLMILEPIYESRFSQKSFAFRPGRTAHT
VLRVIRRNFAGYLWYVKGDLSVVLDMGMKVGFVISSLMRDVRDKKVIDLIKLSALVTPVVTSKVEDGEKKKTKRKYQKKRVLAEDEPKPDYPWLETFFGFAPEEAGKSPQWG
Fingers-palm region
HCGILSPLLNVNCLDELDRWMETKVKDFYRPSKSDVIWNPEGEADQGNTSWPEFVPTSGPDKTRKMDYVRYGGHILIGVRGPRADAATLRKELIEFVDQKYMLRLDNENL
Thumb (X) domain
PIEHITKGIMFLDHVLCRRVVYPTLRYTATGGKIISEKVG**TLLSVTASLKQCIKQFRKLFLIKGDRDPDPOPCFRMFHATOAHNTNOMNKFLLTTIAEWYRFADNRKKIVN**
FCSYIIIRGSLAKLYAAKYKLRSRAKVYKFANRNLSLPLLOKKGOSPEYONLLRMGLAESVDGLVYTRMSLVPETDYSPPFGNWRPEHEKFLIEYLTLDPEKTLLEEQKRFIR
EKGLVSPQDYTSMVLWNKYRNAIPMDQVSILKDQPFLLGSSSTYNRDNDDQKNKEEDEDSEDGLRIARM

B. *pmh2* (At3g22330; full cDNA sequence)

5'...ggaactaaaaccccttgaccttctttcttcatctctctaaatccctaattctccaaattttggggttttacattttccttatcaagagaacacctgaatctgaaaATG
ATCACTACAGTGCTACGACGATCTCTCCTTGATGCGTCGAAGAGGAATCTCTCCGCTTCGTTGACCTCAATCAATACTGTTCTGTTTCACAACCTGGCCCCAGCCGCCACT
AGAGTCTCCGACCTAGCCTTAATTGGATCTTCCGATGTCAAAGCTGGGTTTCCGTTTGGTGTGAAGCGAAAGGAATTCATTTTCAATCTGGGCCGTTGGATTTTAGAGCT
TCGATGGTTTCTCAAGCTGGATTTGCGATCTCTGAGAGTAGCGAGAGAGGGTTGGTGATTTCGGAGAGTGTTGGTGGTGATGGGCTTGCATATCTGAGCTTGGGATATCT
CCGGAGATTGTTAAAGCTTTGAGTAGTAAGGGTATTGAGAAACTCTTTCCTATTGAGAAAGCTGTGCTGGAGCCAGCGATGGAGGGTCGAGATATGATTGGTCGTGCTAGG
ACTGGAACGGGAAAGACACTTGCTTTTGGGATTCTATCATTGACAAAATCATCAATACAACGCTAAACATGGACGAGGGAGGAATCCGCTTTGTTGGTTTGGCACC
ACAAGAGAGCTTGCTCGCCAGGTTGAGAAGGAGTTAGGGAGTCTGCTCCGAGCTTGGATACATTTGTCCTTATGGAGGTACACCGATTGGACAGCAAATGAGGCAGCTT
GACTATGGTGTGATGTGGCGGTTGGAACCTCAGGTCGTGTCATTGATCTGATGAAGAGAGAGCTTTGAATCTATCGGAAGTTCAGTTTGTGGTTCTGGATGAAGCTGAT
CAGATGCTTCAAGTTGGATTTGCTGAGGATGTTGAAAATAATTGGAAAAGTTGCCTGAGAAACGTCAGAGTATGATGTTTCTGCAACAATGCCGAGTTGGATCAGATCT
CTCACTAAGAAGTACCTGAATAATCCTTTGACAGTTGATCTTGTGGAGATTCTGATCAGAACTAGCAGATGGAATTACGACATATTCTATCATAGCAGATTCTTATGGA
AGAGCATCCATTATTGGTCTCTTTGTAACGGAGCATGCCAAAGGAGGAAAAATGCATTGTTTTACACAAACAAAACGAGATGCTGATCGCCTTTCATATGCATTGGCTAGA
AGCTTCAAATGTGAAGCTTTACACGGTGATATATCCAGAGTCAGAGGGAAGAACGCTTGCTGGTTTCCGAGATGGGCATTTCATATTTCTGTGCGACTGATGTTGCT
GCCCGTGGACTTGATGTACCTAATGTCGATTTGATCATTCACTATGAGCTTCTCTAATAACACGGAGACATTTGTCCATCGAACCGGGCGAACGGGTCCGGCTGGAAGAAA
GGAAAGTGCTATTCTGATCTACAGTCAAGATCAATCCAGGCTGTAAAAATAATTGAGAGAGAAGTTGGGAGCCGATTCACTGAGCTCCCTAGCATTGCTGTGGAACGTGGA
AGCGCAAGCATGTTTGAAGGAATAGGTCTCGATCCGGTGGTCTCTTTGGAGGAGGCATGAGGGATCGTGGTTCAAGCTTTGGTGGTCGTTCAGGCGGTGGTGGTTATGGT
GGCAGCAGTGGTGGTTATGGTGGTGGCGTTTCAGGCGGATCAAGCAACCGTTATTCTGGTGATTCTGACCGTCTGGTTTGGGAGCTTCGGTATGCGTTCTCCTGAGGGA
TATGGTTCGGATCGTTTCATCTCAGTCAGGTGGAAGGAGCAGCTTTGGTGGTGGTGGTTCAGGCGGATCATCAAACAATCGTTCTCTGGTTTCCGGGACTTTGGCTCTGAC
CGTTCTTCTCAGTCAGGCGGAAGGAGCAGCTTTGGTGGGTTTGGATCAAATGATGGGAAAAGATCTTACTGA^{gagaagtggttttggagccgagccggcaataattgggtt}
gacctagaggaggaggaggttcggtgactcgagtagattagttactacgcgagatcgaaggagtcgaagttatatataataatctgtagctatgtaaacacaacatatac
tttcgaagttatggttatcatcatcttcatatgaggtgattatcttctt^{tttgcataatttggttggtttatatt}...3'

PMH2 (At3g22330) full protein sequence

Predicted targeting site

MITTVLRRSLLDASKRNLSASLTSIINTVLFHNLAPAATRVSDALIGSSDVKAGFFPGVEAKGIHFQSGPLDFRASMVSQAGFAISESSERRVGDSESVGGDGLAISELGI
SPEIVKALSSKIEKLFPIQKAVLEPAMEGRDMIGRARTGCTGKTLAFGIPIIDKIIKYNAKHGRGRNPLCLVLAPTRELARQVEKEFRESAPSLDITICLYGGTPIGQQMRQ
LDYGVDVAVGTPGRVIDLMKRGALNLSEVQFVVLDEADQMLQVGFADVEIILEKLPEKRQSMFSAITMPSWIRSLTKKYLNNPLTVDLVGDSQKLADGITYSIADSY
GRASIIGPLVTEHAKGGKCIIVFTQTKRDADRLSYALARSFKCEALHGDISQSQRERTLAGFRDGHFNILVATDVAARGLDVNPVDLIIHYELPNNTETFEVHRTGRTGRAGK
KGSAILIYSQDQSRVAKIIEREVGSRFTLPSIAVERGSASMFEIGIGSRSGGSFGGGMRRDGRSSFGGRSGGGYGGSSGGYGGGRSGGSSNRYSGDSRSGFSFGMRSP
GYGSDRSSQSGGRSSFGGGRSGGSSNRRSSGFGDFGSDRSSQSGGRSSFGGFSNDGKRSY

Figure S2. The topology of nMAT2 and PMH2.

The cDNA sequences of nMAT2 (A) and PMH2 (B) were obtained by RT-PCR with specific oligonucleotides (underlined and marked in red letters). The PCR products were cloned into the pGEM-T vector system II (Promega) and sequenced (The Center for Genomic Technologies at the Hebrew University of Jerusalem). The resulting sequencing data is illustrated on the corresponding sequences of nMAT2 and PMH2. Capital blue letters indicate the coding regions, while black lower-case letters represent 5' and 3' UTR regions. The insertion sites of T-DNAs in *nm2* (SALK-line 064659) and *pmh2* (SAIL-line 628C06) genes are indicated by red arrows. The deduced amino acid sequences of nMAT2 and PMH2 are given below each cDNA sequence. Arrows represent conserved domains in nMAT2 and PMH2 as predicted by the SMART (Letunic *et al.* 2012) and Conserved Domain Database (CDD) (Marchler-Bauer *et al.* 2003) servers. These include the N-termini mitochondrial targeting signals (marked in blue) and the fingers-palm (amino acids 104 - 461) and thumb (X) domains (amino acids 486 - 625) of nMAT2 and the two conserved motifs typical to DEAD-box RNA helicases (amino acids 124 - 326 and 364 - 443). The consensus ATP binding site (amino acids 148 - 154) is underlined.