

**Table S1. Proteins identified in the co-IP assays by LC/MS-MS analysis**A. Proteins identified by co-IPs with the anti-HA antibodies from *nmat2/nMAT2-HA*

Peptides	At number	Notes
<b>Intron maturase, type II family protein (nMAT2)</b> MYPYDVPDYAYPYDVPDYAYPYDVPDYA SDVIWNNPEGEADQGNTSWPEFVPTSGPDK IVQEVLLMILEPIYESR YLSYFAPQQR NSVLDDR TAHTVLR ADAATLR GLVSPQDYTSMLVWNYK EDGVSLCSQMWLENFK FLTITAEWYR VEDGEK	At5g46920	Maturase related protein / splicing
<b>DEAD-box ATP-dependent RNA helicase 53 (PMH2/ARTH53)</b> GLDVPNVDLIIHYELPNNTETVHR SGGGYGGSSGGYGGGR GRNPLcLVLAPTR SSFGGFGSNDGKR DADRLSYALAR SGGSFGGGMGR AVLEPAMEGR FTELPsIAVER SSGFGDFGSDR ESAPSLDTicLYGGTPIGQQMR TLAGFR RSSFGGFGSNDGKRS KTLAFGIPIIDKI	At3g22330	RNA chaperon / splicing
<b>pentatricopeptide repeat-containing protein</b> INAYASLGNLQK SALTVVDDMIK VMDTALK MLLLGK	At1g26460	RNA metabolism?
<b>pentatricopeptide repeat-containing protein</b> HILANAPFAPSSVTYR LPDSTSALVGQR TMAFSSAEEAAAER VVADFGAR	At1g10270	RNA metabolism?
<b>pentatricopeptide repeat-containing protein</b> AGMFENAQK IISLYGK TNDFLK	At1g55890	RNA metabolism?
<b>pentatricopeptide repeat-containing protein (PPR36)</b> IAFSAAVENLAEK SEKDPDRILEicR AALSLLK	At1g61870	Translation or RNA metabolism?
<b>Mitochondrial 28S ribosomal protein S29-like protein</b> STHAAVNvvvr DTTLSQLTHK WLAPFMR KSYLALR FDEAALK	At1g16870	Translation
<b>Probable ribosomal protein S11 (putative mitochondrial protein, SUBA3)</b> FREQVPVSGESANNSGLSNTGR MTNYTADATAENIGR ATSGSLPDLK	At1g31817	Translation

AIIAFR		
<b>Prohibitin-1, mitochondrial (PHB1)</b> VGIIGGLGLYGATHSLYNVEGGHR SAQLIGQAIANNQAFITLR AVVAQYNASQLITQR DKVYPEGTHLMIPWFERPVIYDVR ARPYLVESTSGSR EIAQTIANANK VYPEGTHLMIPWFERPVIYDVR VLPSIINETLK SLGENYSER EFTAAIEAK QVAAQEAER	At4g28510	Mitochondria biogenesis
<b>Prohibitin-6, mitochondrial (PHB6)</b> SAQLIGQAIANNQAFITLR AVVAQYNASQLITQR VLPSIIHETLK QVAAQEAER AKPYLVESTSGSR EIAQTISR VLTRPMADQLPEVYR SLGENYR DKVYPEGTHLMIPWFERPIIYDVR	At2g20530	Mitochondria biogenesis
<b>Prohibitin-7, mitochondrial (PHB7)</b> SAQLIGQAIANNEAFITLR VLPSIINETLK QVAAQEAER VLTRPMGDR	At5g44140	Mitochondria biogenesis

B. Proteins identified by co-IPs with the anti-HA antibodies from *nmat2/empty vector control*

Peptides	At number	Notes
<b>Chaperonin CPN60</b> KANLQDLAALTGGEVITDELGMNLEK KANLQDLAALTGGEVITDELGMNLEK QVANATNDVAGDGTcATVLTR LLEQDNPD LGYDAAKGEYVDMVK TPVYTIASNAGVEGAVIVGK LLEQDNPD LGYDAAKGEYVDmVK AAVEEGILPGGGVALLYAAR SAIELSTSDYDKEK VTVSKDDTVILDGAGDKK TQKcELDDPLILIHEK MISTSEEIAQVGTISANGER IGGASEAEVGEKKDR cELDDPLILIHEK TLFNELEVVEGmKLDK RGISMAVD AVVTNLK	At3g23990	Molecular chaperon / mitochondrial import and macromolecular assembly
<b>Heat shock 70 kDa protein 10 (mtHsc70-2)</b> ELLLLDVTPLSLGIETLGGVFTR IELSSTSQTENLPFITADASGAK GVNPDEAVAMGAALQGGILR AKIELSSTSQTENLPFITADASGAK IINEPTAAALSYGMTNK SRFETLVNHLIER SQVFSTAADNQTQVGIR EKIPSEIAKEIEDAVADLR	At3g23990	Chaperone / protein folding

EAEHAQKDKER GVNPDEAVAmGAALQGGILR QAVTNPTNTVSGTKR SSGGLSEDDIQK EVDEVLLVGGMTR		
<b>Glycine dehydrogenase (decarboxylating) 2 (GLDP2)</b> DKATSNiCTAQALLANMTAMYAVYHGPEGLK VVMATDLLALTMLKPPGEFGADIVVGSQGR VVMATDLLALTmLKPPGEFGADIVVGSQGR RHNSATPDEQAQmANYcGFDNLNTLIDSTVPK VVmATDLLALTmLKPPGEFGADIVVGSQGR ESPYLTHPIFNMYHTEHELLR FSGIFDEGLTESQmIEHMSDLASK NImENPAWYTQYTPYQAEISQGR RLMDYGFHGTMSWPVPGTLMIEPTESK NIMENPAWYTQYTPYQAEISQGR FGVPMGYGGPHAAFLATSQEYKR	At2g26080	Glycine decarboxylase enzyme
<b>ATP synthase subunit alpha (AtpA)</b> EVAFAQFGSDLDAATQALLNR GmALNLENENVGIVVFGGDTAIKEGDLVKR GMALNLENENVGIVVFGGDTAIKEGDLVKR GMALNLENENVGIVVFGGDTAIKEGDLVK AILNSVKPELLQALK LTEVLKQPQYAPLPIEK VVDAMGVPIDGKGALSDHEQR GMALNLENENVGIVVFGGDTAIK ATSESETMYcVYVAIGQK GmALNLENENVGIVVFGGDTAIK DNGMHALIIYDDLK DNGmHALIIYDDLK IRNFYANFQVDEIGR GIRPAINVGLSVSR KmELDAFLKER KSVHEPMQTGLK KSVHEPmQTGLK KMELDAFLKER EAFPGDVFYLHSR NFYANFQVDEIGR	AtMg01190	Complex V / membrane ATP synthase subunit alpha

C. Proteins identified by co-IPs with the anti-SHMT antibodies from *nmat2/nMAT2-HA*

Peptides	At number	Notes
<b>Serine hydroxymethyltransferase 1 (SHMT1)</b> AVmLADmAHISGLVAANVIPSPFDYADVTTTTHK WGVNVQPLSGSPANFHVYTALLKPHER AVMLADMAHISGLVAANVIPSPFDYADVTTTTHK LDPEKWGVNVQPLSGSPANFHVYTALLKPHER EVLYDFEDKINQAVFPGLQGGPHNHTITGLAVALK ALEAFRLDPEKWGVNVQPLSGSPANFHVYTALLKPHER VLEAVHIASNKNTVPGDVSAMVPGGIR LKDFVSAMESSSTIQSEIAK LKDFVSAmESSSTIQSEIAK QLNAPLEEVDPEIADIIIEHEK ImALDLPHGGHLSHGYQTDTKK KISAVSIFSETMPYRLDESTGYIDYDQMEK GYELVSGGTDNHLVLVNLKPK GLELIPSENFTSVSVMQAVGSVMTNK INQAVFPGLQGGPHNHTITGLAVALK GLELIPSENFTSVSVMQAVGSVmTNK	At4g37930	L-serine metabolic process

IMALDLPHGGHLSHGYQTDTKK DFVSAMESSSTIQSEIAK IMALDLPHGGHLSHGYQTDTK ImALDLPHGGHLSHGYQTDTK GLELIPSENFSTSVSmQAVGSVmTNK YYGGNEYIDMAETLcQKR LDESTGYIDYDQmEK KISAVSIFFETMPYR YYGGNEYIDMAETLcQK QATTSEYKAYQEQLSNSAK YYGGNEYIDmAETLcQK YYGGNEYIDmAETLcQKR NTVPGDVSA MVPGGIR LRHEVEEFAK ISAVSIFFETmPYR NTVPGDVSAmVPGGIR LDESTGYIDYDQMEK VAEYFDKAVTIALK ISAVSIFFETMPYR KISAVSIFFETmPYR ALEAFRLDPEK VLEAVHIASNK ISAVSIFFETMPYRLDESTGYIDYDQmEK LIVAGASAYAR AYQEQLSNSAK HEVEEFAK SATLFRPK GFVEEDFAK mGTPALTSR FAQTLMER YSEGYPGAR MGTPALTSR FAQTLmER QATTSEYK EVLDFEDK QFPTIGFEK VAEYFDK GAMIFFRK AVTIALK LYDYAR ALEAFR		
<b>Serine hydroxymethyltransferase 2 (SHMT2)</b> ImALDLPHGGHLSHGYQTDTKK QLNASLDEIDPEVADIIELEK INQAVFPGLQGGPHNHTITGLAVALK IMALDLPHGGHLSHGYQTDTKK IMALDLPHGGHLSHGYQTDTK ImALDLPHGGHLSHGYQTDTK YYGGNEYIDMAETLcQKR KISAVSIFFETMPYR YYGGNEYIDMAETLcQK YYGGNEYIDmAETLcQK YYGGNEYIDmAETLcQKR LDENTGYIDYDQLEK NTVPGDVSA MVPGGIR ISAVSIFFETmPYR NTVPGDVSAmVPGGIR ISAVSIFFETMPYR GYDLVSGGTDNHLVLVNLK KISAVSIFFETmPYR LIVAGASAYAR	At5g26780	L-serine metabolic process

LREMVEEYAK VLELVHIAANK mGTPALTSR YSEGYPGAR VAEYFDLAVK MGTPALTSR ALEAFQLDPSK GFIEEDFAK EVMYDYEDR QFPTIGFEK GAMIFFRK LQSEMSK AYQDQVLR SAVLFRPK LYDYAR GAmIFFR		
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