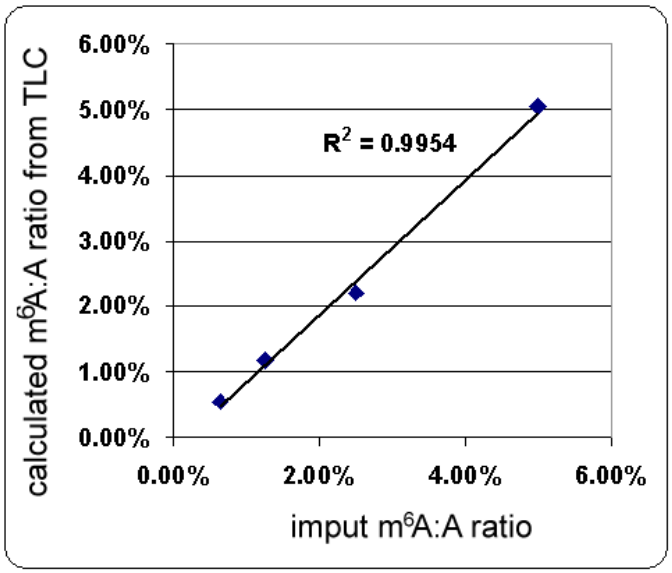
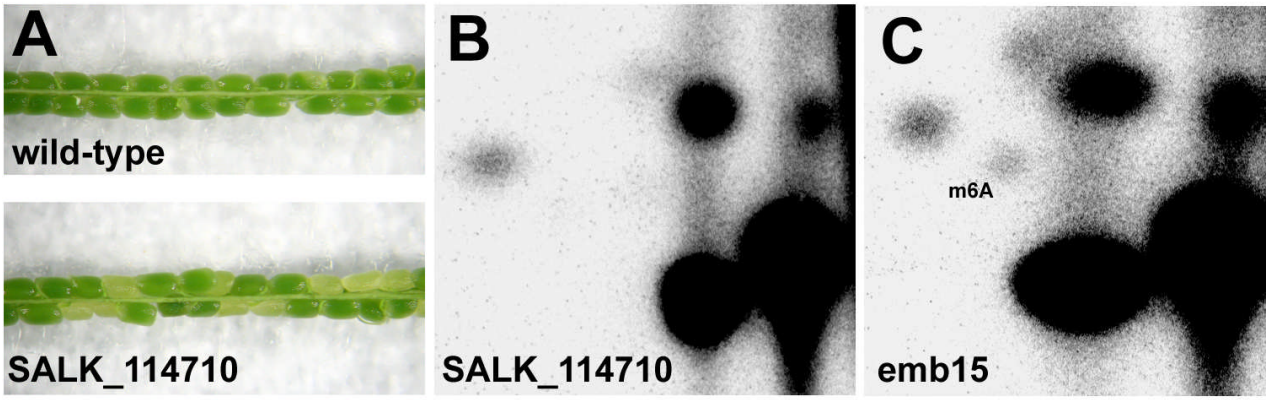
Supplemental Data. Zhong *et al*. (2008). MTA is an *Arabidopsis* mRNA adenosine methylase and interacts with a homolog of a sex-specific splicing factor



mA RNA	normal RNA	TLC result
5 ug	100 ug	5.0%
2.5 ug	100 ug	2.2%
1.25 ug	100 ug	1.2%
0.625 ug	100 ug	0.5%

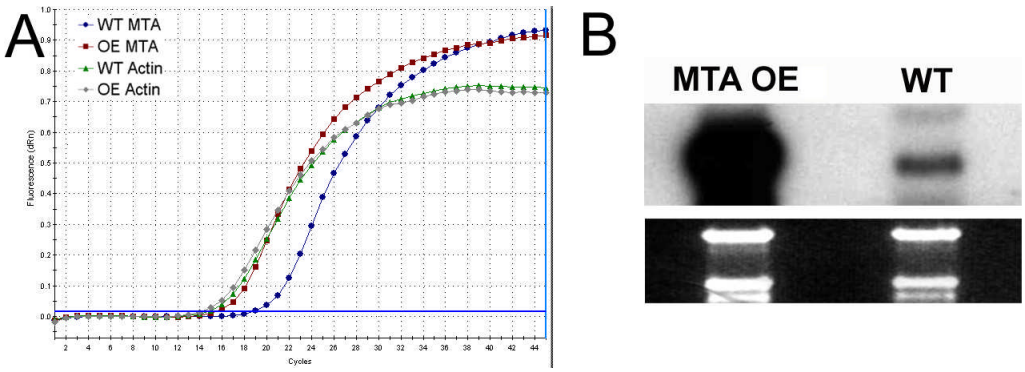
Supplemental Figure 1: TLC detection of m^{6}A in synthetic RNA.

In vitro transcribed methylated and non-methylated RNA was mixed and subjected to TLC analysis. The m^{6}A:A values obtained by phosphorimaging were plotted against the actual ratio of methylated and non-methylated RNA, showing the TLC detection method is linear over the physiological range.



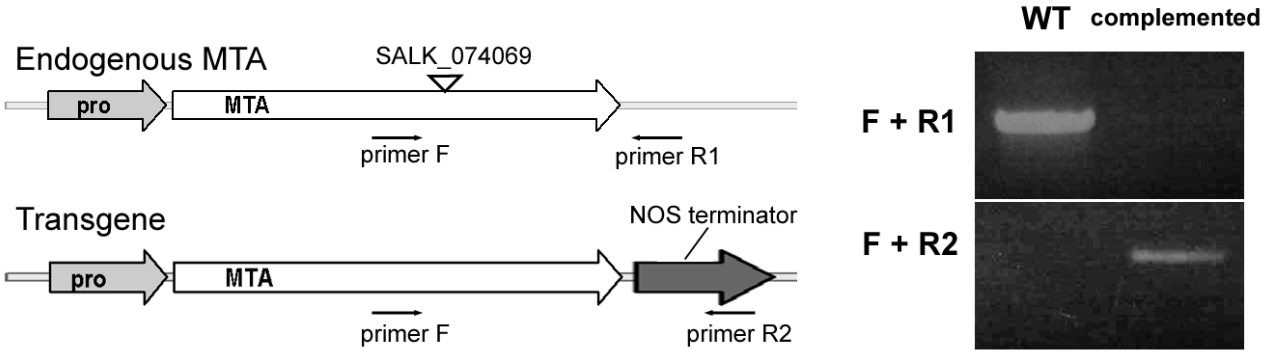
Supplemental Figure 2: Embryo lethality and absence of m^{6}A in MTA SALK_114710.

(A) Representative silique from a plant hemizygous for the SALK_114710 insertion (bottom) and from a wild type control (top). **(B)** TLC analysis of mRNA from embryo defective seeds of SALK_114710 show m^{6}A to be absent. **(C)** TLC analysis showed the presence of m^{6}A in the emb15 control white seeds.



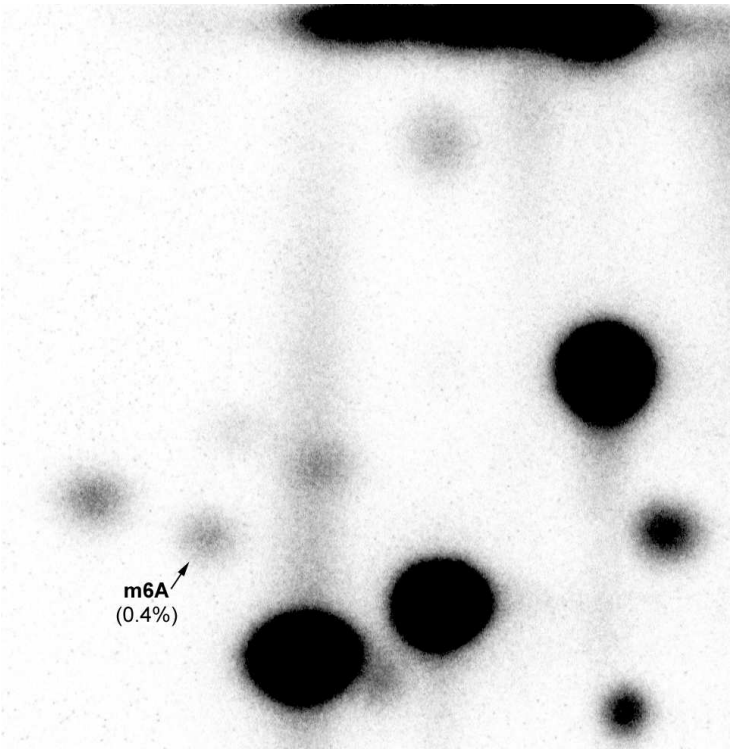
Supplemental Figure 3: Amplification plots for qRTPCR and northern analysis.

(A) Reverse transcription was carried out using SuperScriptII (Invitrogen) and oilgo dT(25) on wild-type (WT) and the transgenic *MTA* over-expression plants (OE). Real-time PCR was carried out using the MX3005P qPCR machine and the Brilliant SYBR Green qPCR master mix (Stratagene). The fluorescence threshold for log phase measurements was determined by the MAXpro software. **(B)** Northern blot assay confirms that the transgenic plant (OE) accumulates higher level of *MTA* when compared to wild-type (WT). RNA was extracted from 2-week-old seedlings.



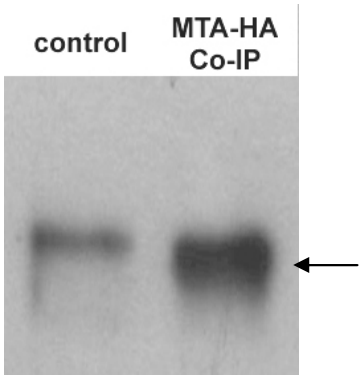
Supplemental Figure 4: Complementation of SALK_074069 with the endogenous promoter-driven construct.

The MTA transgene driven by its own 1.5k promoter was cloned into binary vector pGWB13 (Nakagawa *et al.*, 2007). This construct was used to transform the hemizygous SALK_074069 mutant. Complemented plants homozygous for the SALK T-DNA insertion were identified by PCR using primer F: 5'-ACTTGCAAATACGTGCATTA-3' and Primer R1: 5'-GCTGAGACATTTGGCTTTGT-3'; these primers give a PCR product of 0.9 kb from wild type plants but do not give a product when the SALK T-DNA insertion is present. The presence of the MTA transgene was confirmed in these plants by PCR amplification of a 1.2 kb band using Primer F and Primer R2: 5'-CTCTAAGCGCTGCACTGAGC-3'.



Supplemental Figure 5: mRNA from control white seeds of the embryo defective mutant SALK_072168 contains wild type levels of m^6A.

The SALK_072168 T-DNA disrupts a gene encoding a vitamin B6 biosynthetic enzyme, At5G60546, and results in seed arrest at the globular stage. TLC analysis of this control tissue shows that it contains wild-type levels of m^6A.



Supplemental Figure 6: Co-immuno-precipitation of MTA-HA and FIP37.

Native protein from transgenic *Arabidopsis* plants expressing MTA-HA was extracted and immuno-precipitated using the anti-HA antibody. An immuno-blot was carried out using the anti-FIP37 antibody (Vespa *et al.*, 2004). A 48 kDa band corresponding to FIP37 was detected (arrowed).