Table S1. First 30 genes with highest co-expression values with respect to IAMT1

| | Locus | Alias | Function | Supportability | Ath-m |
|---|---|---|---|---|---|
| 0 | **At5g55250** | IAMT1 | IAA carboxylmethyltransferase 1 | 1 | 0 |
| 1 | **At5g24910** | ELA1 | cytochrome P450, family 714, subfamily A, polypeptide 1 | 0 | 13 |
| 2 | **At3g22540** | DUF1677 | Protein of unknown function (DUF1677) | 2 | 15,5 |
| 3 | **At4g22460** | inhibitor | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | 2 | 17,3 |
| 4 | **At4g33790** | G7/CER6 | Jojoba acyl CoA reductase-related male sterility protein | 1 | 22,3 |
| 5 | **At5g24410** | PGL4 | 6-phosphogluconolactonase 4 | 2 | 24,4 |
| 6 | **At4g22110** | dehydrogenase | GroES-like zinc-binding dehydrogenase family protein | 2 | 27,1 |
| 7 | **At1g12550** | HPR3 | D-isomer specific 2-hydroxyacid dehydrogenase family protein | 0 | 34,6 |
| 8 | **At2g03370** | transferase | Glycosyltransferase family 61 protein | 1 | 39,7 |
| 9 | **At3g14850** | TBL41 | TRICHOME BIREFRINGENCE-LIKE 41 | 1 | 40,7 |
| 10 | **At5g15180** | Peroxidase | Peroxidase superfamily protein | 2 | 51,6 |
| 11 | **At3g62610** | MYB11/PFG2 | myb domain protein 11 | 1 | 54 |
| 12 | **At4g25830** | UPF0497 | Uncharacterised protein family (UPF0497) | 2 | 55,4 |
| 13 | **At5g07990** | TT7/CYP75B1 | Cytochrome P450 superfamily protein | 3 | 60,9 |
| 14 | **At5g51810** | GA20OX2 | gibberellin 20 oxidase 2 | 0 | 62,2 |
| 15 | **At2g43050** | PMEPCRD | Plant invertase/pectin methylesterase inhibitor superfamily | 1 | 64,7 |
| 16 | **At4g34500** | kinase | Protein kinase superfamily protein | 1 | 66,1 |
| 17 | **At5g39220** | alpha/beta-Hydrolases | alpha/beta-Hydrolases superfamily protein | 2 | 68 |
| 18 | **At4g15480** | UGT84A1 | UDP-Glycosyltransferase superfamily protein | 2 | 69,3 |
| 19 | **At3g28420** | Putative membrane lipoprotein | Putative membrane lipoprotein | 2 | 69,9 |
| 20 | **At3g18170** | transferase | Glycosyltransferase family 61 protein | 2 | 71,8 |
| 21 | **At1g25510** | protease | Eukaryotic aspartyl protease family protein | 2 | 74,8 |
| 22 | **At1g49800** | PIPL1 | PAMP-INDUCED SECRETED PEPTIDE (PIP) LIKE (PIPL) | 1 | 76,5 |
| 23 | **At4g01140** | DUF1191 | Protein of unknown function (DUF1191) | 2 | 77 |
| 24 | **At2g22620** | lyase | Rhamnogalacturonate lyase family protein | 2 | 82,2 |
| 25 | **At5g01200** | Duplicated homeodomain-like | Duplicated homeodomain-like superfamily protein | 0 | 82,5 |
| 26 | **At1g51170** | UCN | Protein kinase superfamily protein | 1 | 83,8 |
| 27 | **At1g11590** | inhibitor | Plant invertase/pectin methylesterase inhibitor superfamily | 1 | 86,5 |
| 28 | **At1g66460** | kinase | Protein kinase superfamily protein | 0 | 87,4 |
| 29 | **At5g26660** | MYB86 | myb domain protein 86 | 1 | 107,1 |
| 30 | **At5g56300** | GAMT2 | gibberellic acid methyltransferase 2 | 1 | 110,6 |

Table S2: DNA sequence of oligonucleotide primers used for genotyping.

| **Name** | **AGI number** | **Forward (5' -3')** | **Reverse (5'-3')** |
|---|---|---|---|
| SALK_072125 | AT5G55250 | TTAAAGAGAGAAGGAGAGATCCATAGAGA | CATGGCCCCACCTCTCTTAA |
| LBb1.3 |  | GTATAGTTCATCCATGCCATGTG |  |
| GUS |  | CAACGTCTGCTATCAGCGCGAAGT | TATCCGGTTCGTTGGCAATACTCC |

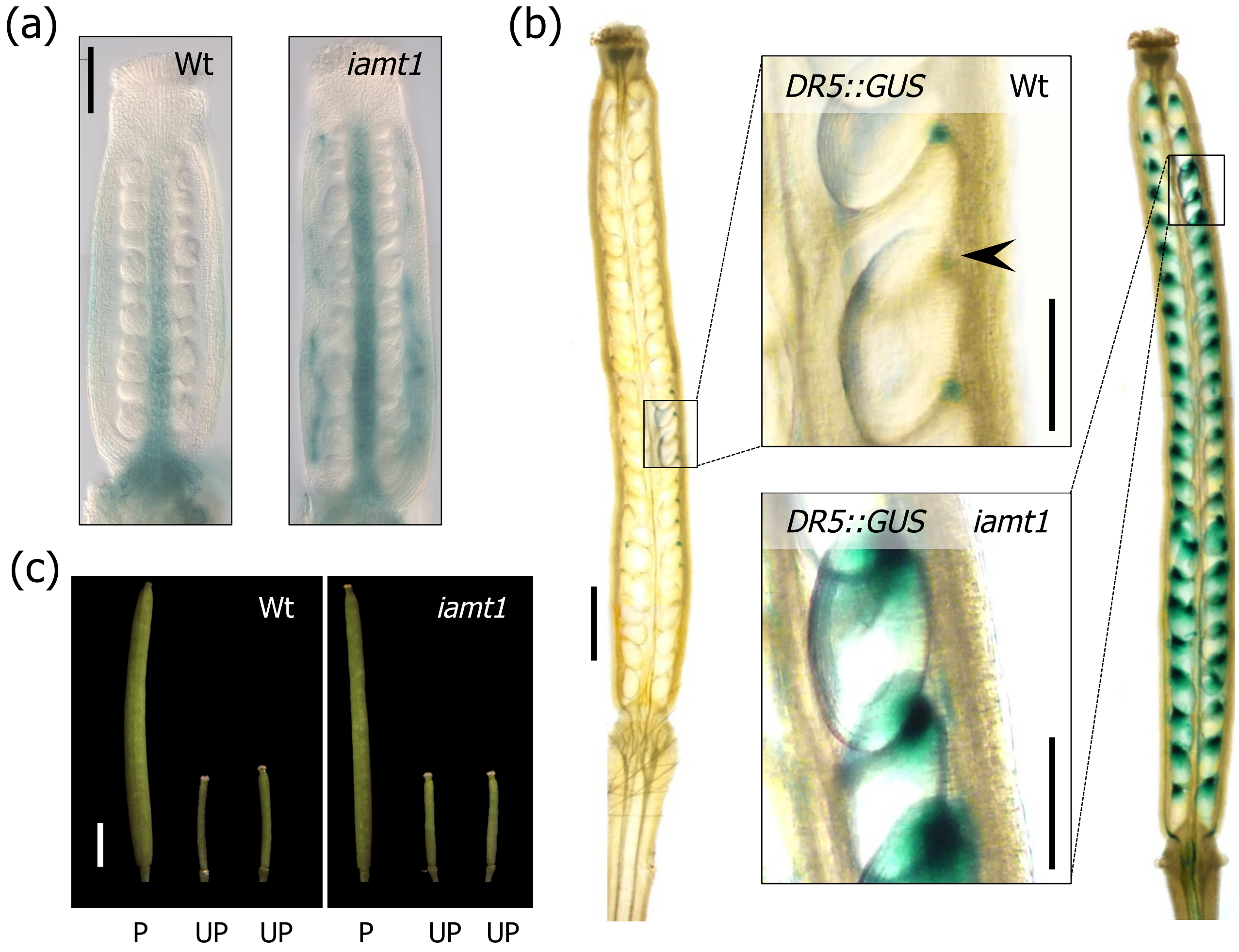


**Figure S1.** (a) Increased levels of *DR5::GUS* expression in preanthesis ovaries. Bar length = 100 µm. (b) Localized increase in auxin activity in the funiculi of *iamt1* mutant fruits, shown by *DR5::GUS* staining. Bar length = 500 µm (full fruit), 200 µm (close up). (c) The *iamt1* mutant is not parthenocarpic. Bar length = 2mm. P, pollinated; UP, unpollinated.

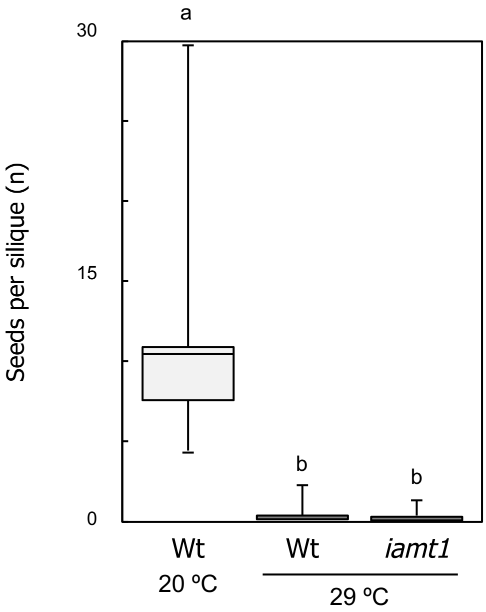
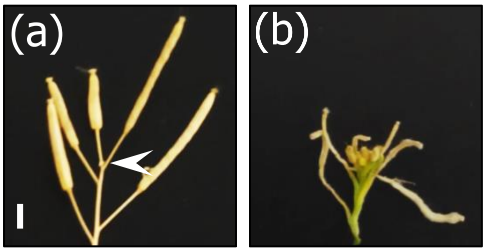


**Figure S2.** Loss of IAMT1 function in pollen does not protect from higher temperature stress. Wild-type and *iamt1* mutant plants were transferred from 20 to 29ºC for 7 days after bolting, and pollen from newly produced flowers was used to manually pollinate wild-type plants at 20ºC. As a control, wild-type pollen at 20ºC was also used. At least 12 flowers per genotype were examined. Letters indicate significant differences between groups, $p < 0.01$ (One way ANOVA, Tukey HSD Post Hoc test).



GP arrested SAM

Prematurely arrested SAM

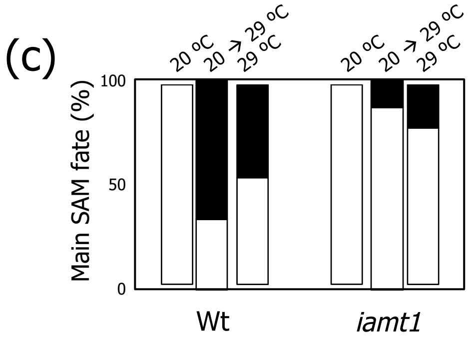


**Figure S3.** Shoot apical meristems (SAM) from *iamt1* mutants are partially resistant to temperature stress conditions. Illustration of SAM phenotypes of wild-type plants grown under standard (a) or higher (b) temperatures. (c) Quantification of SAM fate under different temperature conditions. White and black colours represent normal and prematurely arrested, respectively. "GP" stands for "Global Proliferative".

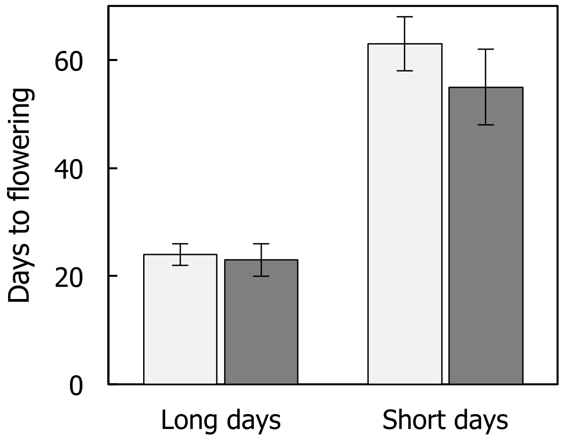


**Figure S4.** Flowering time measured in days of wild-type and *iamt1* mutant plants grown under short and long days.

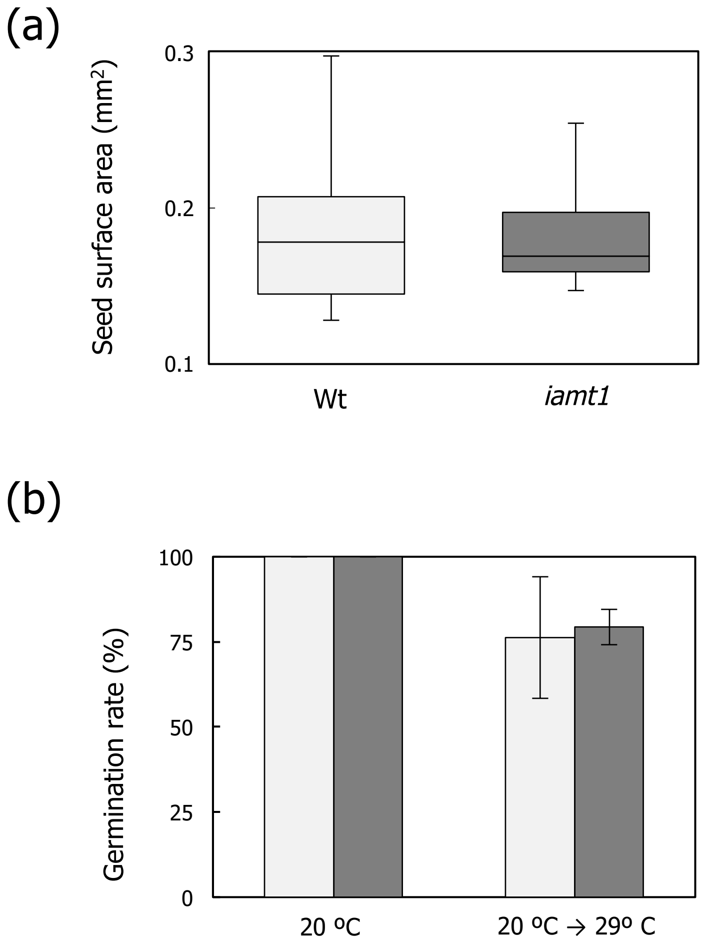


**Figure S5.** Seeds produced at 29ºC are normal. (a) Surface area of the seeds produced at 29ºC by wild-type and mutant plants (n=100). (b) Germination rate of seeds collected from wild-type and *iamt1* mutant pants growing at 20ºC or transferred to 29ºC. Germination was assessed 5 days after sowing.

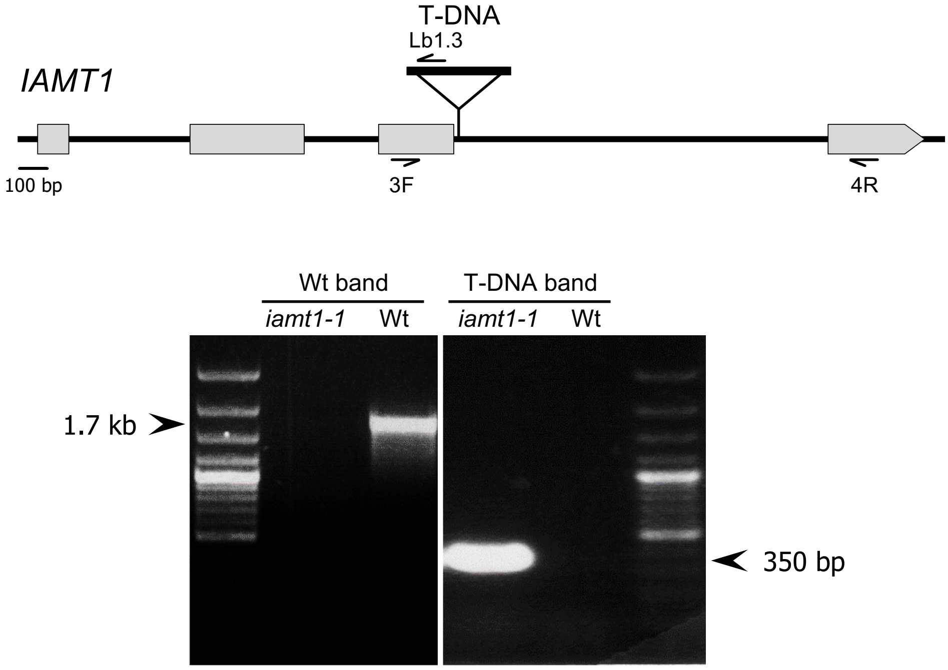


**Figure S6.** Scheme of the *IAMT1* locus indicating the position of the T-DNA insertion of *iamt1-1* and the genotyping result.