

Table S3 The 6mA quantification data in *P. sojae* and *P. infestans* using UPLC-ESI-MS/MS by three replicates.

Sample	Rep1(p.p.m)	Rep2(p.p.m)	Rep3(p.p.m)	average	STDEV	% <i>P. sojae</i> WT
<i>P. sojae</i>	337.58406	454.60349	448.41423	413.53393	65.84	100
<i>P. infestans</i>	550.23693	648.71949	308.99527	502.65056	174.78	121.5504

Table S5 A brief summarize of the mutations of each *psdamt1*, *psdamt2*, *psdamt3* mutant.

Mutant	Mode of destruction	Sequence change
<i>psdamt1</i> -T21	Frame shift	-139bp(homozygote)
<i>psdamt1</i> -T50	Frame shift	-1bp(homozygote)
<i>psdamt1</i> -T115	Frame shift	-5bp/-1bp
<i>psdamt2</i> -T10	HDR mediated replacement	RFP replace(homozygote)
<i>psdamt2</i> -T18	HDR mediated replacement	RFP replace(homozygote)
<i>psdamt2</i> -T52	Frame shift	-1bp(homozygote)
<i>psdamt3</i> -T3	Frame shift	-373bp(homozygote)
<i>psdamt3</i> -T9	Frame shift	-374bp(homozygote)
<i>psdamt3</i> -T16	Frame shift	Insertion, +1bp(homozygote)

Table S6 6mA quantification data in *P. sojae* DAMT mutants using UPLC-ESI-MS/MS by three replicates.

Sample	Rep1(p.p.m)	Rep2(p.p.m)	Rep3(p.p.m)	Average	STDEV	% <i>P. sojae</i> WT
<i>psdamt1</i> -T21	10.84669	49.71185	40.20488	33.58781	20.25	8.122%
<i>psdamt2</i> -T52	19.38118	26.94702	25.27419	23.86746	3.97	5.771%
<i>psdamt3</i> -T9	62.84280	31.04520	42.37782	45.42194	16.11	10.983%

Table S7 Total normalized read counts at different TE categories

	DNA elements	LTR elements	all TE
WT	38508.67	66927.42	117867.3
<i>psdamt3</i>	56305.21	58578.37	122564.7