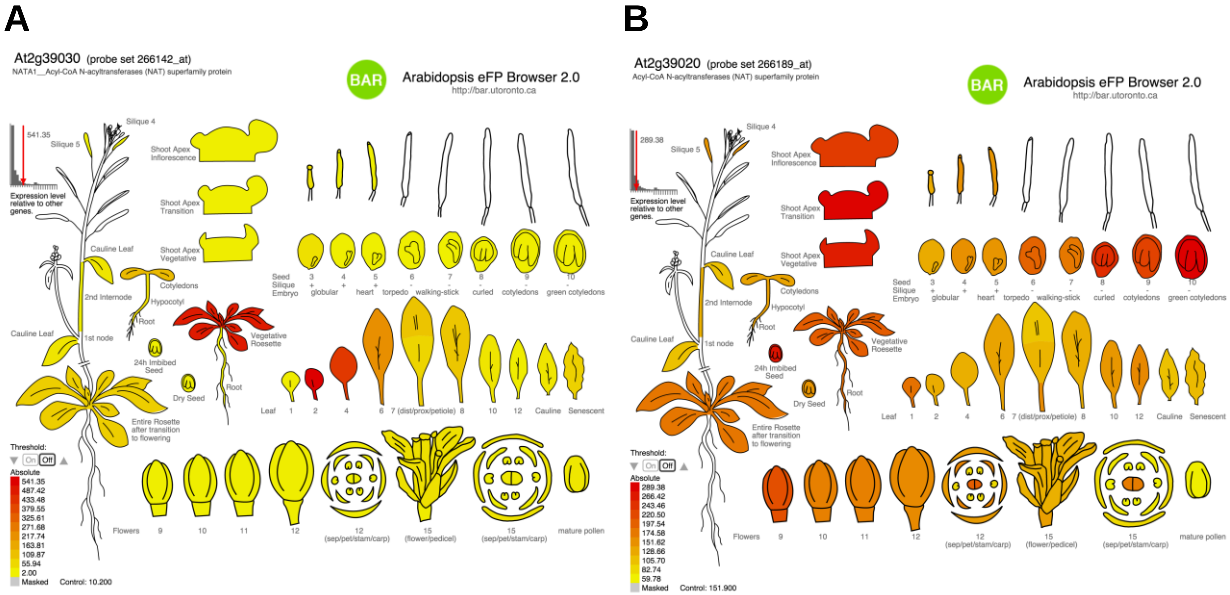
Supplemental Table 1. Primers used for cloning and PCR amplification in this study

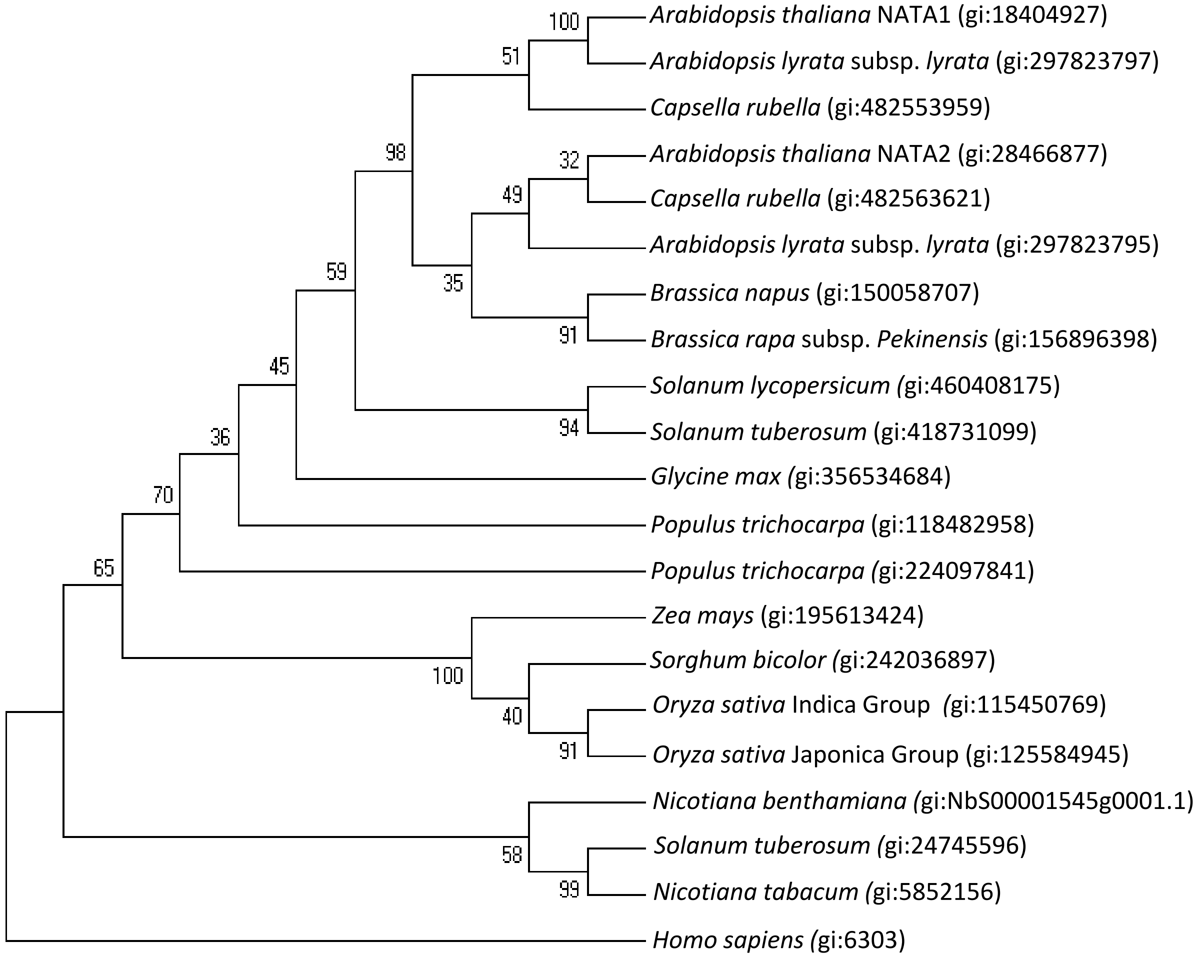
Target Gene		Primer sequence
NATA1 (At2g39030)	forward	GGG GAC AAG TTT GTA CAA AAA AGC AGG CTT CAT GGC GCC TCC AAC CGC AGC ACC A
	reverse	GGG GAC CAC TTT GTA CAA GAA AGC TGG GTC CTA GAT GTT TAG CTT GTC AAT AGC TTG AAG
NATA2 (At2g39020)	forward	GGG GAC AAG TTT GTA CAA AAA AGC AGG CTT CAT GGC AGC CGC CGC ACC G
	reverse	GGG GAC CAC TTT GTA CAA GAA AGC TGG GTC CTA GAT GTT GAC CTG ATC AAA AGC TTC
GFP (from pMDC83)	forward	GGGG ACA AGT TTG TAC AAA AAA GCA GGC TAA ATG AGT AAA GGA GAA GAA CTT TT
	reverse	GGG GAC CAC TTT GTA CAA GAA AGC TGG GTT TAG TGG TGG TGG TGG TG
NATA1 promoter region	forward	TAA GCT AAA GAA TTA AAG TAG TAA
(for ecotype analysis)	reverse	GAA GAT TAG GGT TTC GAG AAT CC

Supplemental Table 2. Primers used for quantitative RT-PCR

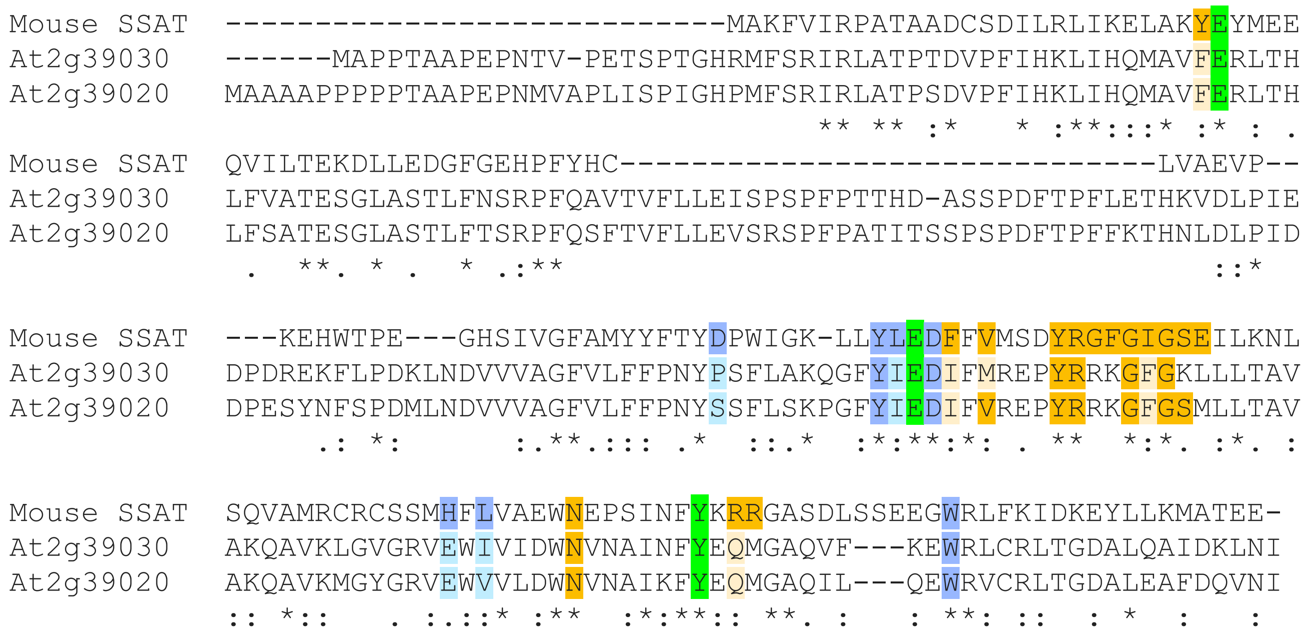
Target Gene		**Primer sequence**
EF1-α (At5g60390)	forward	TGAGCACGCTCTTCTTGCTTTCA
	reverse	GGTGGTGGCATCCATCTTGTTACA
PR1 (At2g14610)	forward	TGATCCTCGTGGGAATTATGT
	reverse	TGCATGATCACATCATTACTTCAT
PR2 (At3g57260)	forward	AGCTTCCTTCTTCAACCACACAGC
	reverse	TGGCAAGGTATCGCCTAGCATC
PR3 (At3G54420)	forward	TCTAGCTTGAACGGTGGCTGTG
	reverse	CGTGCCATTAACGGTGCTTTGG
PR4 (At3G04720)	forward	TCCAAATCCAAGCCTCCGTTGC
	reverse	GCGGCAAGTGTTTAAGGGTGAAG
PR5 (At1G75040)	forward	AGCAATGCCGCTTGTGATGAAC
	reverse	ATCACCCACAGCACAGAGACAC
PR6 (At2G38900)	forward	ATACATGTCTAGCCGGCGGTTG
	reverse	TTGCTACCGCGTTAGGGTTTGG
PAO1 (At5g13700)	forward	GCTCTAACATTCTGGTGGTGACG
	reverse	CCCAAACATGTCCCTGAGAACAC
PAO2 (At2g43020)	forward	AGATTGTAGGATGCGAGTC
	reverse	TTAGACGATATAAGAAGAGG
PAO3 (At3g59050)	forward	ACAAACCTCACGACCTCTATG
	reverse	TCAAGCACACGCATCCTG
PAO4 (At1g65840)	forward	GGGAACAGTGACATTCTCGAAAC
	reverse	AATTGGAACCCTGCTTCTGTCTG
PAO5 (At4g29720)	forward	GATGACCTAGACGCAATG
	reverse	ATGAGTTGTGGAGTAATGG
NATA1 (At2g39030)	forward	AGCAGATGGGTGCGCAGGTT
	reverse	TCGCTCGATGGGTCTCATGCA
SPDS1 (AT1G23820)	forward	GAAGAGGATAACGGCGGC
	reverse	CAGAGAACCACCCAGGAATAACAG
SPDS2 (AT1G70310)	forward	TGATTTGCCCGTGAAGAGACC
	reverse	GAGAACCATCCAGGAATAATAGAGG
SPMS (AT5G53120)	forward	GTTGTTGGTGGAGGTGATGGTG
	reverse	GGATTTACGGAGGAACTCAGCAG



Supplemental Figure S1. Spatial and temporal expression of (A) *NATA1* and (B) *NATA2* from Botany Array Resource (http://bar.utoronto.ca/welcome.htm).



Supplemental Figure S2. Phylogenetic tree of plant proteins with similarity to polyamine acetyltransferases. Phylogenetic tree of NATA1 protein homologs. Human (*Homo sapiens*) spermidine/spermine N^1-acetyl-transferase (SSAT) was used as an outgroup. A consensus phylogenetic tree was produced with 1000 replicates. Values at the branch points indicate bootstrap percentages.



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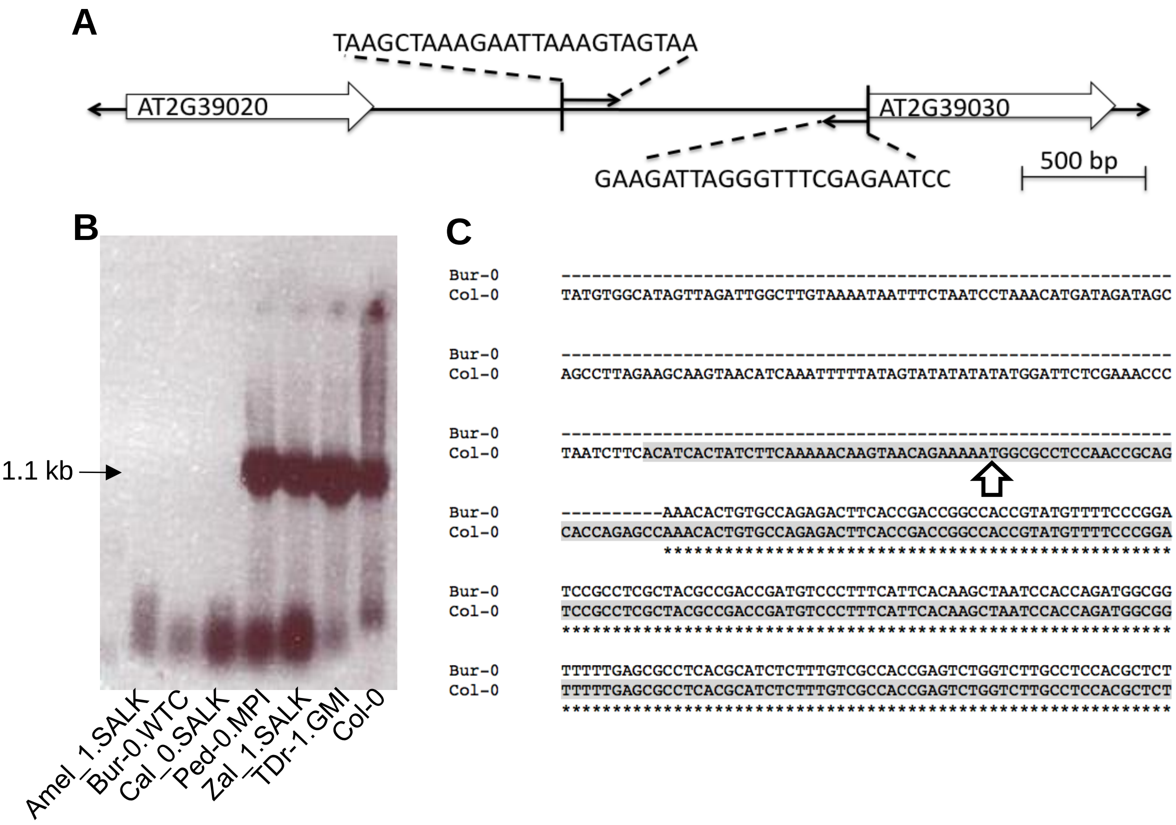
Mouse SSAT  ----------------------------MAKFVIRPATAADCSDILRLIKELAKYEYMEE
At2g39030   ------MAPPTAAPEPNTV-PETSPTGHRMFSRIRLATPTDVPFIHKLIHQMAVFERLTH
At2g39020   MAAAAPPPPPTAAPEPNMVAPLISPIGHPMFSRIRLATPSDVPFIHKLIHQMAVFERLTH
                                             ** ** :*   * :**:::* :* : .

Mouse SSAT  QVILTEKDLLEDGFGEHPFYHC------------------------------LVAEVP--
At2g39030   LFVATESGLASTLFNSRPFQAVTVFLLEISPSPFPTTHD-ASSPDFTPFLETHKVDLPIE
At2g39020   LFSATESGLASTLFTSRPFQSFTVFLLEVSRSPFPATITSSPSPDFTPFFKTHNLDLPID
             .  **. * .  * .:**                                    ::*

Mouse SSAT  ---KEHWTPE---GHSIVGFAMYYFTYDPWIGK-LLYLEDFFVMSDYRGFGIGSEILKNL
At2g39030   DPDREKFLPDKLNDVVVAGFVLFFPNYPSFLAKQGFYIEDIFMREPYRRKGFGKLLLTAV
At2g39020   DPESYNFSPDMLNDVVVAGFVLFFPNYSSFLSKPGFYIEDIFVREPYRRKGFGSMLLTAV
                 .: *:      :.**.::: .*  ::.*  :*:**:*: . **  *:*. :*. :

Mouse SSAT  SQVAMRCRCSSMHFLVAEWNEPSINFYKRRGASDLSSEEGWRLFKIDKEYLLKMATEE-
At2g39030   AKQAVKLGVGRVEWIVIDWNVNAINFYEQMGAQVF---KEWRLCRLTGDALQAIDKLNI
At2g39020   AKQAVKMGYGRVEWVVLDWNVNAIKFYEQMGAQIL---QEWRVCRLTGDALEAFDQVNI
            :: *::   . :.::* :**  :*:**:: **. :   : **: ::  : *  :   :
```

Supplemental Figure S3. Active site amino acid sequence alignment of Arabidopsis NATA1 and NATA2 with mouse spermidine/spermine acetyltransferase (SSAT; GI:6677849). Orange: CoA binding region, blue: spermine binding residues, and green: proposed catalytic site. Sequences were aligned with Clustal Omega (http://www.clustal.org/omega/).



```
Bur-0      ------------------------------------------------------------
Col-0      TATGTGGCATAGTTAGATTGGCTTGTAAAATAATTTCTAATCCTAAACATGATAGATAGC

Bur-0      ------------------------------------------------------------
Col-0      AGCCTTAGAAGCAAGTAACATCAAATTTTTATAGTATATATATATGGATTCTCGAAACCC

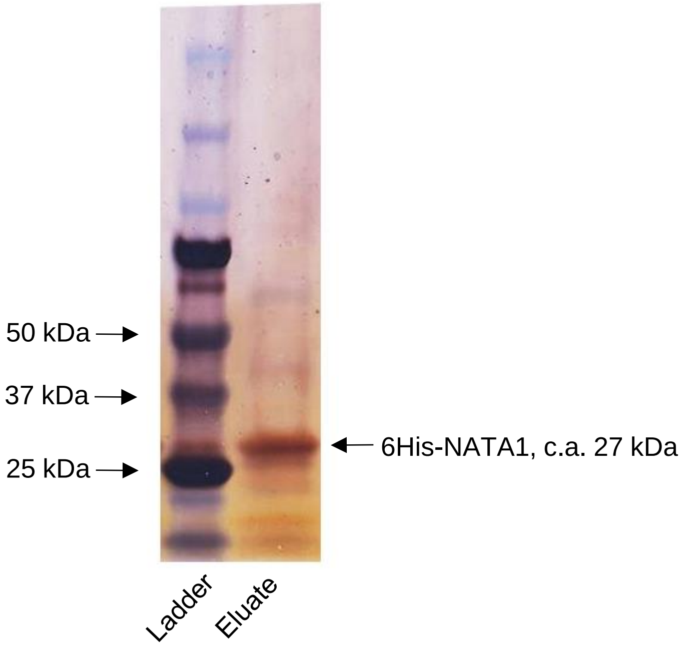
Bur-0      ------------------------------------------------------------
Col-0      TAATCTTCACATCACTATCTTCAAAAACAAGTAACAGAAAAATGGCGCCTCCAACCGCAG

Bur-0      ----------AAACACTGTGCCAGAGACTTCACCGACCGGCCACCGTATGTTTTCCCGGA
Col-0      CACCAGAGCCAAACACTGTGCCAGAGACTTCACCGACCGGCCACCGTATGTTTTCCCGGA
                     **************************************************

Bur-0      TCCGCCTCGCTACGCCGACCGATGTCCCTTTCATTCACAAGCTAATCCACCAGATGGCGG
Col-0      TCCGCCTCGCTACGCCGACCGATGTCCCTTTCATTCACAAGCTAATCCACCAGATGGCGG
           ************************************************************

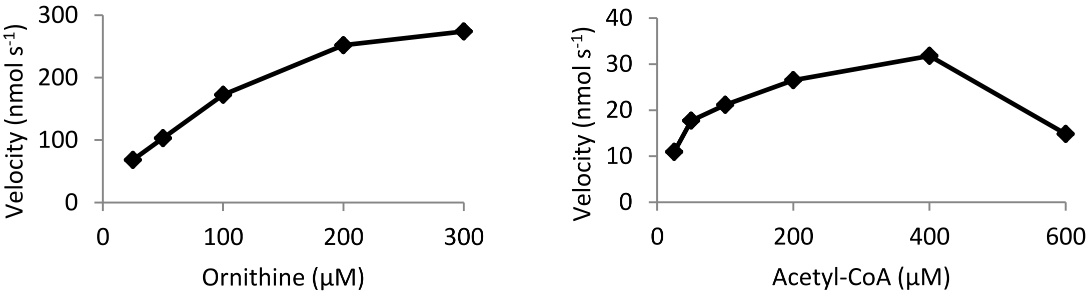
Bur-0      TTTTTGAGCGCCTCACGCATCTCTTTGTCGCCACCGAGTCTGGTCTTGCCTCCACGCTCT
Col-0      TTTTTGAGCGCCTCACGCATCTCTTTGTCGCCACCGAGTCTGGTCTTGCCTCCACGCTCT
           ************************************************************
```

Supplemental Figure S4. Arabidopsis ecotypes with natural *nata1* knockout mutations were identified through the 1001 Genomes Project (http://1001genomes.org/). (A) *NATA1* (AT2G39030) promoter regions from the Amel-1, Bur-0, Cal-0, Ped-0, Zal-1, TDr-1 and Col-0 ecotypes were amplified with the indicated primers. (B) Agarose gel showing bands corresponding to the *NATA1* promoter regions of the indicated Arabidopsis ecotypes. (C) Sequence alignment of Chr2:16305177..16305536 from Bur-0 and Col-0. The NATA1 transcript is marked in grey and the ATG translation start codon is indicated with an arrow. Sequences were aligned with Clustal Omega (http://www.clustal.org/omega/).

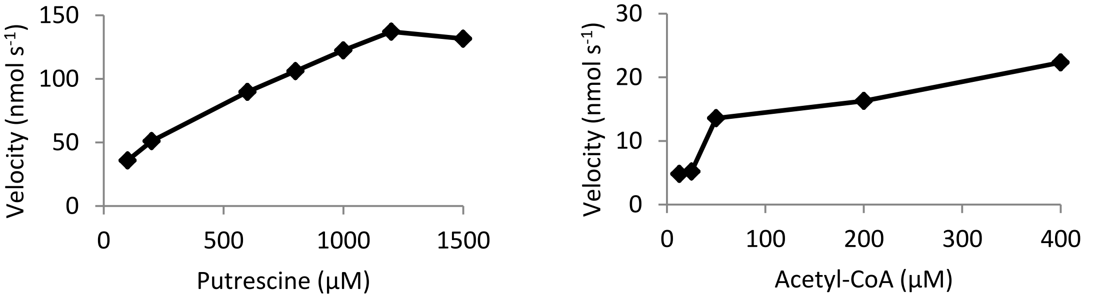


Supplemental Figure S5. Heterologously expressed NATA1 protein was purified with Ni-NTA and visualizedd using a silver-stained protein gel. Shown is a representative gel.

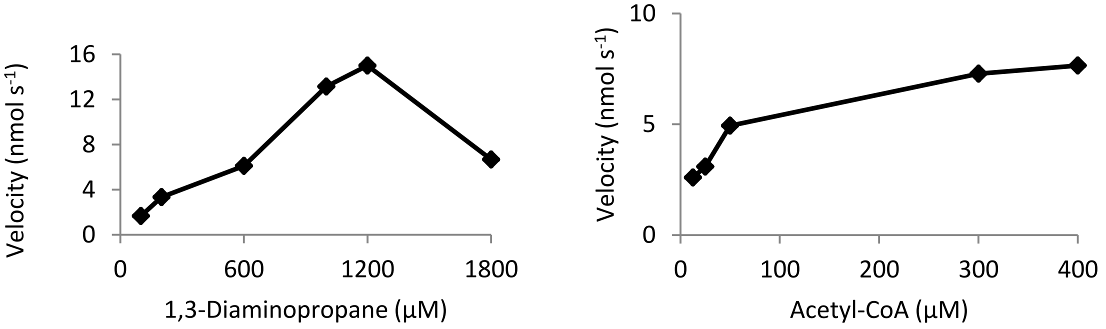
A ornithine



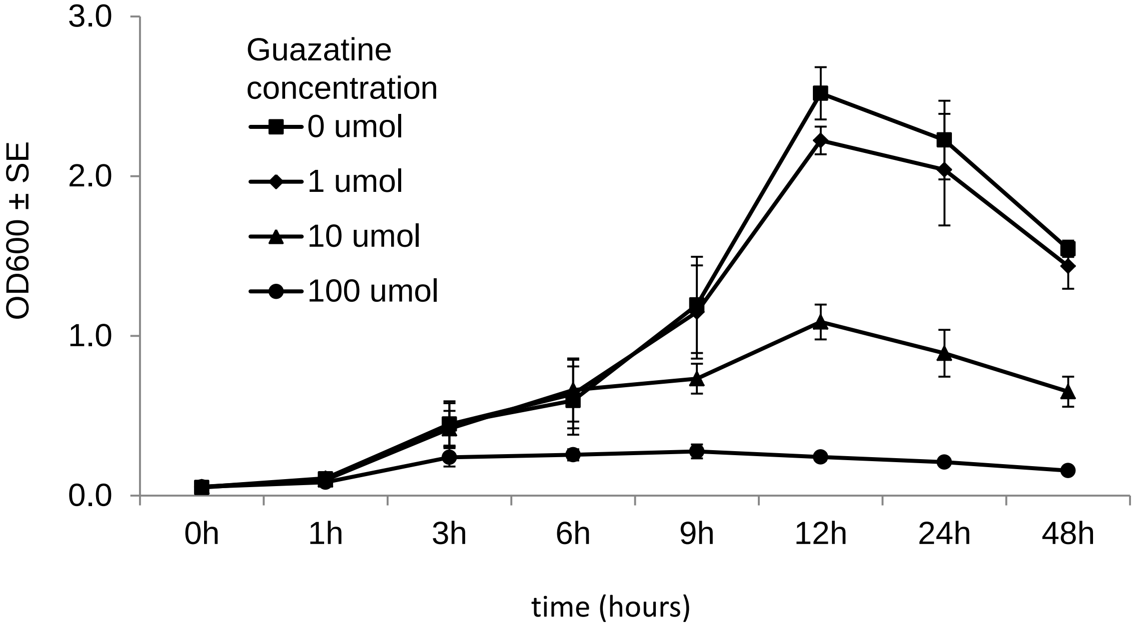
B putrescine



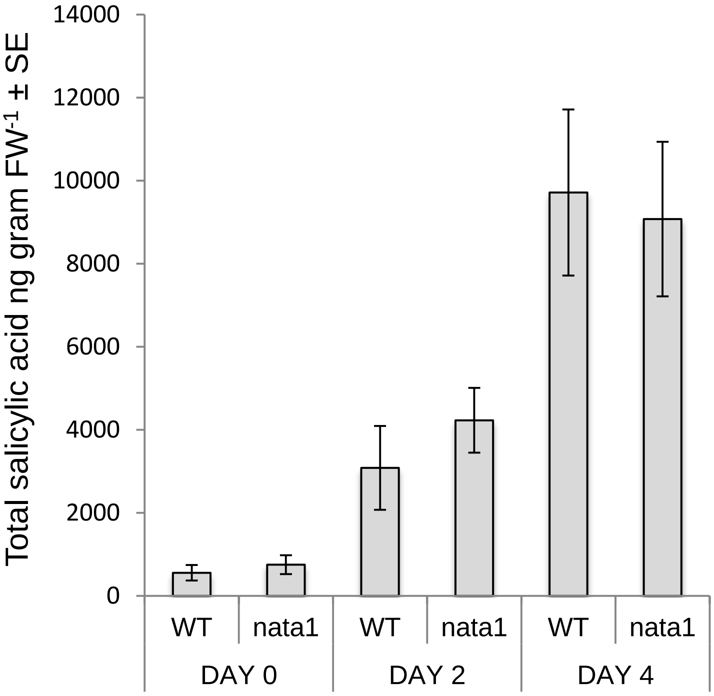
C 1,3-diaminopropane



Supplemental Figure S6. Representative Michaelis Menten curves. The kinetics of heterologously expressed NATA1 were determined by Michaelis-Menten curves for (A) ornithine, (B) putrescine and (C) 1,3-diaminopropane by changing concentration of the potential substrate and acetyl-CoA, respectively. Shown are the means of three technical replicates.



Supplemental Figure S7. Growth of *P. syringae* in LB medium supplemented with guazatine. Mean ± SE of N =4.



Supplementary Figure S8. Time course of total salicylic acid accumulation in response to *P. syringae* infection. Mean ± SE of n = 12.