SUPPLEMENTAL DATA

Supplemental Method

Transient expression in Arabidopsis protoplasts and immunoprecipitation

The coding sequences of *SINAT5DN* and the *MtSINA* genes were cloned into a pRT104-derived vector (Töpfer et al., 1989) as N-terminal fusion with 3x HA and 3x MYC epitopes, respectively. Protoplasts from Arabidopsis ecotype Columbia were prepared as described (Dangl et al., 1987) and cotransfected with the polyethylene glycol-mediated method (Kiegerl et al., 2000). Proteins were obtained with extraction buffer (25 mM Tris-HCl, pH 7.6, 10 mM $MgCl_2$, 15 mM EGTA, 15 mM NaCl, 15 mM $pNO_2PhenylPO_4$, 15 mM β-glycerophosphate, 1 mM dithiothreitol, 1 mM NaF, 0.1 mM Na_3VO_3, 0.5 mM phenylmethylsulfonylfluoride, 10 µg/ml leupeptin and aprotinine, 0.1% Tween, and 10% glycerol); total protein concentration was determined with the Protein Assay kit (Bio-Rad, Hercules, CA). For immunoprecipitation, 300 µg protein extract was incubated with rat monoclonal anti-HA antibody 3F10 (Roche Diagnostics, Brussels, Belgium) and 25 µl of protein G Sepharose 4 Fast Flow beads (GE-Healthcare, Little Chalfont, UK) for 2 h at 4°C. Immune complexes were washed 3 times in 500 µl extraction buffer and protein complexes coupled to the anti-HA Protein G beads were dissolved in Tris-glycine-SDS sample buffer (Novex, San Diego, CA) supplemented with 100 mM β-mercaptoethanol, boiled for 5 min at 95°C, and loaded on SDS-PAGE gels according to Laemmli (1970). Proteins were transferred electrophoretically onto an Immobilon-p polyvinylidene difluoride membrane (Millipore, Bedford, MA). After blocking at 4°C in 5% skimmed milk in 100 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 0.1% Tween-20, the efficiency of the immunoprecipitation was verified with the monoclonal 12CA5 anti-HA mouse antibody (Roche Diagnostics). MYC-tagged proteins were detected with the monoclonal 9E10 anti-cMYC mouse antibody (Roche Diagnostics). The secondary anti-mouse-IgG antibody coupled to horseradish peroxidase was detected with a chemiluminescence detection kit according to the manufacturer's instructions (Perkin-Elmer Life Sciences, Boston, MA).

Literature cited

Dangl JL, Hauffe KD, Lipphardt S, Hahlbrock K, Scheel D (1987) Parsley protoplasts retain differential responsiveness to u.v. light and fungal elicitor. EMBO J **6:** 2551-2556

Kiegerl S, Cardinale F, Siligan C, Gross A, Baudouin E, Liwosz A, Eklöf S, Till S, Bögre L, Hirt H, Meskiene I (2000) SIMKK, a mitogen-activated protein kinase (MAPK) kinase, is a specific activator of the salt stress-induced MAPK, SIMK. Plant Cell **12:** 2247-2258

Laemmli UK (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. Nature **227:** 680-685

Töpfer R, Gronenborn B, Schell J, Steinbiss H-H (1989) Uptake and transient expression of chimeric genes in seed-derived embryos. Plant Cell **1:** 133-139

Table S1. Overview of primers used for amplifying ORFs, RT-PCR and qRT-PCR analyses

Gene, use, amplicon length (bp)	Forward primer	Reverse primer
SINAT5(product length 600 bp)	AAGCGTTTACGAGCTCCTTG	CCCACTGCCTCCAACTTCTA
MtSINA1, ORF, 999	ATGGATTTGGATAGTATTGAGTGT	TCAGCTGCAAAGATTTGGTATA
MtSINA2, ORF, 969	ATGATCAACCATTCATATCTCAGATCT	CTAGCTACACATGTTGGGTGTG
MtSINA3, ORF, 912	ATGACATCTAGTAATCCTTTCTTTGATGA	TCACTGCTCTTTCCAAATCCTT
MtSINA4, ORF, 972	ATGGAGTTGGATAGCATTGAGTGT	TCAGCTACATAGATTAGGTATGCAC
MtSINA5, ORF, 927	ATGGATTCAGATAGTACTGTTTCTTCATT	CTAGCTACACAAGTTGGGTATGCA
MtSINA6, ORF, 912	ATGGCATTGAGTAATCCACTCTTT	TCATTGTTCTTTCCAAATCCTACCA
MtSINA1, qRT-PCR	AGGGTACACCACGGAGTATTCG	AGTTCCTTCCTATCACCACCAGAG
MtSINA2, qRT-PCR	AGCATATCCAACAACAATCGTGAC	AACGGTTTTCATGATTTCAGCAAC
MtSINA3, qRT-PCR	CAGTCTTGAAGGAGGTGGTAATGG	GCGGTGGCTTCCCTAATGC
MtSINA4, qRT-PCR	TTTGGTGAGAGTTGATGGAGTTGG	TGACACTGGTGAATAGGAGGGTAC
MtSINA5, qRT-PCR	GTCTTCTTTCATCATTTTCAAACATACCC	ATCAATGAAGAAACAGTACTATCTGAATCC
MtSINA6, qRT-PCR	TGAAAACTCAAAACCCACCAAAACC	CCCAGCGGCCCTGAAGC
Translation elongation factor 1α (*MtELF1α*), RT-PCR	TTGGACATGTCGACTCTGGA	GCCTGGGAGGTTCCAGTAA
Translation elongation factor 1α (*MtELF1α*), qRT-PCR	ACTGTGCAGTAGTACTTGGTG	AAGCTAGGAGGTATTGACAAG

Supplemental Fig. S1. Alignment of SINA protein sequences of *M. truncatula*, Arabidopsis, rice, poplar and Siah1. The RING finger motif and the SINA domain are marked by asterisks and dollar signs, respectively.

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OsSINA5     1  ------MDMDSVECLSLPDS-SMDVDDVDGGGSVHHHHHHHHALPPHLPAGVAVGVGPGGRAFPKANVAGVGGGGAAGAP  73
OsSINA1     1  ------MDVDSVECLSLPDS-SSSSGAGAGGGGG--------------GGGGGGVGAMDAADDVGLALHAHGALLAAAA   58
OsSINA3     1  ------MDMASIECVSYSDSMDDDDDDGVGVGGVSH------------LPRPILVKPSSAAAAVNVVVVSAGSGGGAGG   61
PtSINA8     1  -------------------------------------------------------------------------------   1
SINAT5      1  -----METDSIDSVIDD-----DEIHQK-------------------------------------HQFSSTKSQGG-    29
AtSINA4     1  ------METDSMECVSSTG----NEIHQNG-------------------------------------NGHQSYQFSSTKTHGGA   37
PtSINA7     1  -----MDFDNIECVSSSDGLDEDEIHHHNLQHHHL------------------------HQFASPKPHNVNNNSNG   47
PtSINA9     1  --------------VN-----------------------------------------------NNHNNG    8
MtSINA1     1  ------MDLDSIECVSSSDGMDEDEIQHRILHPHHQ------------------------QHHHHSEFSSLKPRSGG   47
MtSINA4     1  ------MELDSIECVSSSDGMDEDEIHS-------------------------------------HHHHHSEFSSTKARNGG   39
AtSINA3     1  ------MDLDSMDCTSTMDVTDDEEIHQDR-------------------------------------HSYASVSKHHHTN   37
PtSINA3     1  -------------------------------------------------------------------------------   1
MtSINA2     1  MINHSYLRFHCDICLKMETGGVDSSILS-------------------------------------LTMMEEAEHHHH   40
MtSINA5     1  ---------------MDS---DSTVSS-------------------------------------LIMMDEDLHP-H   20
OsSINA6     1  -----MASVTYLDD---AHSEVIDPPKN-------------------------------------EEMLDVTELVDD   32
OsSINA4     1  -----MASVTYIDD---SGSEVIDPPK-------------------------------------TEVLDVTELAGD   31
PtSINA2     1  ------MT-------IRNKPEVIDPPQN-------------------------------------KDMTDIVECVNS   27
PtSINA4     1  ------MASSNLFFDDIRNKPEVIDPPQN-------------------------------------EDLTDIGESVND   35
MtSINA3     1  ------MTSSNPFFDDIRSRP-GVDPPQT-------------------------------------EESTEIPELVND   34
MtSINA6     1  ------MALSNPLFDDIRSNI-DVDPPQK-------------------------------------EESTDVGILVND   34
AtSINA2     1  ------MAPGGSALKEVMESNSTGMDYE-------------------------------------VKTAKVEVNNNK   34
AtSINA1     1  -----MAPGGSALKEALESNSTGVDYE-------------------------------------VKMAKVEANS-K   33
PtSINA6     1  -----MAPGGSAFKEVLEFHSTVADCD-------------------------------------VANSKSENNI-T   33
PtSINA10    1  ------MAPGGSAFKEVLEL---VAECD-------------------------------------IATSKSENNI-A   33
PtSINA1     1  -------------------------------------------------------------------------------MATSAAELRGS   11
PtSINA5     1  -----MAPGGIINKEEIESRIAYLDHDTG-------------------------------------HPATSNAELRGS   36
OsSINA2     1  -----MAPGSSIVTDIPESDCVSDGLS-------------------------------------EALTGIRLDGDS   34
Siah1       1  -------------------------------------------------------------------------------MSRQTATALPTGT   13

OsSINA5    74  AAGGAVAGGGGPGGGPPATS-VHELLECPVCTNSMFPPIHQCQNGHTLCSTCKARVHNRCPTCRQELGDIRCLALEKVAE  152
OsSINA1    59  AARAAACSKGGGGGGAAAGSGVHELLECPVCTNSMYPPIHQCQNGHTLCSTCKARVHNRCPTCRQELGDIRCLALEKVAE  138
OsSINA3    62  GGGGVGVVAGAP-AVPPATS-VHELLECPVCTNSMYPPIHQCQNGHTLCSTCKSRVHNRCPTCRQELGDIRCLALEKVAE  139
PtSINA8     1  --------------------VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVHNRCPTCRQELGDIRCLALEKVAE   59
SINAT5     29  -ATVVIS---------PATS-VYELLECPVCTNSMYPPIHQCHNGHTLCSTCKSRVHNRCPTCRQELGDIRCLALEKVAE   98
AtSINA4    38  AAAAVVTNIVGPTATAPATS-VYELLECPVCTYSMYPPIHQCHNGHTLCSTCKVRVHNRCPTCRQELGDIRCLALEKVAE  116
PtSINA7    47  -IANVVG---GPTVIAPATS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVQNRCPTCRQELGDIRCLALEKVAE  122
PtSINA9     8  -NTIVVG---GPTAIAPATS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVQNRCPTCRQELGDIRCLALEKVAE   83
MtSINA1    48  NNNHGVI---GSTAIAPATS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVHNRCPTCRQELGDIRCLALEKVAE  123
MtSINA4    40  ANINNIL---GPTAIAPATS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVHNRCPTCRQELGDIRCLALEKVAE  115
AtSINA3    38  NNTTNVN-AAASGLLPTTTS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKARVHNRCPTCRQELGDIRCLALEKVAE  115
PtSINA3     1  --------------------VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVQNRCPTCRQELGDIRCLALEKVAE   59
MtSINA2    41  QFSS--ISKLLNN-APTTTS-VHDLLECPVCTNSMYPPIHQCHNGHTLCSNCKTRVHNRCPTCRQELGDIRCLALEKIAE  116
MtSINA5    21  QFSSSTTSKLHSNGTPTSTS-VHELLECPVCTNSMYPPIHQCHNGHTLCSTCKTRVHNRCPTCRQELGDIRCLALEKIAE   99
OsSINA6    33  HTQHSPK------PNAMVSGNVRELLECPVCLNAMYPPIHQCSNGHTLCSGCKPRVHNRCPTCRHELGNIRCLALEKVAA  106
OsSINA4    32  PVPHSPK------PNVVVSSSVRELLECPVCLSAMYPPIHQCSNGHTLCSGCKPRVHNRCPTCRHELGNIRCLALEKVAA  105
PtSINA2    28  PAKTALK------PNVTVSSSVHELLECPVCLNAMYPPIHQCSNGHTLCSSCKPRVHGRCPICRHELGNIRCLALEKVAA  101
PtSINA4    36  PAQTALK------PNVTVSSSVRELLECPVCLNAMYPPIHQCSNGHTLCSGCKPRVQNRCPTCRHELGNIRCLALEKVAA  109
MtSINA3    35  PIQTVVK------PNGTVSSSVRELLECPVCLNAMYPPIHQCSNGHTLCSGCKPRVHDRCPTCRHELGNIRCLALEKVAA  108
MtSINA6    35  PAQTALK------PTGTVLSSVRELLECPVCLNAMYPPIHQCSNGHTICSDCKPRVHNRCPTCRHELGNIRCLALEKVAA  108
AtSINA2    35  PTKPGSA--GIGKYGIHSNNGVYELLECPVCTNLMYPPIHQCPNGHTLCSNCKLRVQNTCPTCRYELGNIRCLALEKVAE  112
AtSINA1    34  PTKSGSG--SIGKF--HSSNGVYELLECPVCTNLMYPPIHQCPNGHTLCSSCKLRVQNTCPTCRYELGNIRCLALEKVAE  109
PtSINA6    34  PTKGTVV--LGGKHGVYSNNGVHELLECPVCTNLMYPPIHQCPNGHTLCSNCKLRVHNCCPTCRYDLGNIRCLALEKVAE  111
PtSINA10   31  PTKGTVV--LSGKHGVYSNNGVHELLECPVCTNLMYPPIHQCPNGHTLCSACKLRVHNCCPTCRYDLGNIRCLALEKVAE  108
PtSINA1    12  HFRKAATP-NTGNLGKQSTSNMQDLLDCPVCFTMMYPPIFQCPNGHTLCSQCRARVKNSCPICRGELGNIRCLALEKIAE   90
PtSINA5    37  PFRKAATP-STGNPGKQSTSNMQDLLDCPVCFTIMYPPIHQCPNGHTLCSHCRARVKNSCPICRGELGNIRCLALEKIAE  115
OsSINA2    35  TCKPWSTS--LVTVELSSLTGLNDLLECPVCTNSMRPPILQCPNGHTICSNCKHRVENHCPTCRQELGNIRCLALEKVAE  112
Siah1      14  SKCPPSQRVPALTGTTASNNDLASLFECPVCFDYVLPPILQCQSGHLVCSNCRPKLT-CCPTCRGPLGSIRNLAMEKVAN   92
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OsSINA5    153  SLELPCKYCSLGCPEIFPYYSKLKHEAQCSFRPYNCPYAGSECAVAGDIPFLVAHLRDDHKVDMHSGCTFNHRYVKSNPR  232
OsSINA1    139  SLELPCKYCSLGCPEIFPYYSKLKHEAQCMFRPYNCPYAGSECAVVGDIPYLVAHLRDDHKVDMHSGCTFNHRYVKSNPR  218
OsSINA3    140  SLELPCKYYSLGCPEIFPYYSKLKHESQCNFRPYNCPYAGSECSVVGDIPFLVAHLRDDHKVDMHSGCTFNHRYVKSNPR  219
PtSINA8     60  SLELPCKYMSLGCPEIFPYYSKLKHENLCNFRPYNCPYAGSECVIVGDIPFLVTHLRDDHKVDMHSGCTFNHRYVKSNPR  139
SINAT5      99  SLELPCKYYNLGCLGIFPYYSKLKHESQCNFRPYSCPYAGSECAAVGDITFLVAHLRDDHKVDMHTGCTFNHRYVKSNPR  178
AtSINA4    117  SLELPCKFYNLGCPEIFPYYSKLKHESLCNFRPYSCPYAGSECGIVGDIPFLVAHLRDDHKVDMHACSTFNHRYVKSNPR  196
PtSINA7    123  SLELPCKYYNLGCPEIFPYYSKLKHEAICNFRPYNCPYAGSECSVVGDIPFLVAHLRDDHKVDMHIGCTFNHRYVKSNPR  202
PtSINA9     84  SLEFPCKFYNLGCPEIFPYYSKLKHEAICNFRPYNCPYAGSECSVVGDIPFLVTHLRDDHKVDMHTGCTFNHRYVKSNPR  163
MtSINA1    124  SLELPCKYYSLGCPEIFPYYSKLKHETICNFRPYTCPYAGSECAGDINFLVAHLRDDHKVDMHTGCTFNHRYVKSNPR  203
MtSINA4    116  SLELPCKYYSLGCPEIFPYYSKLKHETECNFRPYSCPYAGSECSTVGDISFLVAHLRDDHKVDMHTGCTFNHRYVKSNPR  195
AtSINA3    116  SLELPCKHMSLGCPEIFPYYSKLKHETVCNFRPYSCPYAGSECSVTGDIPFLVAHLRDDHKVDMHSGCTFNHRYVKSNPR  195
PtSINA3     60  SLELPCKYMSLGCPEIFPYYSKLKHETLCNFRPYSCPYAGSECAIVGDIPFLVAHLRDDHKVDMHSGCTFNHRYVKSNPR  139
MtSINA2    117  SLEFPCRYISLGCSEIFPYFSKLKHESICTFRPYNCPYAGSDCSVVGNIPYLVAHLRDDHGVDMHSGCTFNHRYVKSNPT  196
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MtSINA5     100 SLELPCRYTSVGCPEIFPYYSKLKHESICNFRPYNCPYAGSDCSVVGDISQLVAHLRDDHRVDMHSGCTFNHRYVKSNPM 179
OsSINA6     107 SLELPCKYQNFGCLGIYPYYCKLKHESQCYYRPYTCPYAGSECTVAGDIQYLVSHLKDDHKVDMHNGSTFNHRYVKSNPH 186
OsSINA4     106 SLELPCKYQNFGCVGIYPYYCKLKHESQCQYRPYSCPYAGSECTVAGDIPYLVNHLKDDHKVDMHNGCTFNHRYVKSNPH 185
PtSINA2     102 SLELPCIYRSFGCIGIYPYHSKSKHESQCVFRPYSCPYSGSECTAIGDIPYLVAHLKDDHKVDMHNGSTFNHRYVKSNPH 181
PtSINA4     110 SLELPCKYQSFGCIGIYPYYSKLKHESQCVFRPYNCPYAGSECTVIGDIPYLVAHLKDDHKVDMHNGSTFNHRYVKSNPH 189
MtSINA3     109 SLELPCKYQGFGCIGIYPYYSKLKHESQCVYRPYNCPYAGSECAVVGDVQFLVDHLKDDHKVDMHSGCTFNHRYVKSNPQ 188
MtSINA6     109 SFALPCKFKDFGCIGIYPYYNKPEHESQCSYRPYNCPYAGSECSVVGDINYLVTHLKEDHKVDMHNGSTFNHRYVKSNPQ 188
AtSINA2     113 SLEVPCRYQNLGCHDIFPYYSKLKHEQHCRFRPYTCPYAGSECSVTGDIPTLVVHLKDDHKVDMHDGCTFNHRYVKSNPH 192
AtSINA1     110 SLEVPCRYQNLGCQDIFPYYSKLKHEQHCRFSYSCPYAGSECSVTGDIPTLVDHLKDDHKVDMHDGCTFNHRYVKSNPH 189
PtSINA6     112 SLELPCKFQSLGCLDIFPYYSKLKHEQHCRFRPYSCPYAGSECSVTGDIPALVSHLKDDHKVDMHDGCTFNHRYVKSNPH 191
PtSINA10    109 SLELPCKYQSLGCLDVFPYYSKLKHEQHCRFRPYSCPYAGSECSVTGDIPALAAHLKDDHKVDMHDGCTFNHRYVKSNPH 188
PtSINA1      91 SIELPCMYQSAGCGDIFPYYSKPKHEENCKYRPYNCPYAGAECSVTGDISLLIKHLKNDHKVDMHDGCTFNHRYVKSDAG 170
PtSINA5     116 SIELPCKYQSMGCCDIFPYYSKPKHEKNCKYRPYNCPYAGAECSVTGDIPLLVKHLRNEHKVDMHDGCTFNHRYVKSDPR 195
OsSINA2     113 SLQLPCKYQSLGCAEIHPYQNKLKHEELCRFRPYSCPYAGSECLIAGDVPMLVSHLINDHKVDLHEGCTFNHRYVKSNPY 192
Siah1        93 SVLFPCKYASSGCEITLPHTEKADHEELCFFRPYSCPCPGASCKWQGSLDAVMPHLMHQHKSITTLQG--EDIVFLATDI 170
                $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$

OsSINA5     233 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDENEARNYTYSLEVGGNGRKMVWEGTPRSIRDSHRKV 311
OsSINA1     219 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDENEARNYSYSLEVGANGRKMVWEGTPRSVRDSHRKV 297
OsSINA3     220 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGVAPVYMAFLRFMGDENDARNYSYSLEVGANGRKMIWEGTPRSIRDSHRKV 298
PtSINA8     140 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDETEARNYSYSLEVGGNGRKLIWEGMPRSIRDSHRKV 218
SINAT5      179 EVENATWMLTVFQCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDEDDARNYTYSLEVGGSGRKQTWEGTPRSVRDSHRKV 257
AtSINA4     197 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMGPVYMAFLRFMGDEEDARSYSYSLEVGGSGRKLTWEGTPRSIRDSHRKV 275
PtSINA7     203 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDEAEARNYSYSLEVGGNGRKLIWEGTPRSVRDSHRKV 281
PtSINA9     164 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDETEARNYTYSLEVGGHGRKLTWEGTPQSVRDSHRKV 242
MtSINA1     204 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDENEARNYTYSLEVGANGRKLIWEGTPRSIRDSHRKV 282
MtSINA4     196 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDENDARNYSYSLEVGANGRKLIWEGTPRSVRDSHRKV 274
AtSINA3     196 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDETEARNYNYSLEVGGYGRKLIWEGTPRSIRDSHRKV 274
PtSINA3     140 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDEAEARNYSYSLEVGGNGRKLIWEGTPRSIRDSHRKV 218
MtSINA2     197 EVENATWMLTVFHCFGQYFCLHFEAFQ-LETSPVYMAFLRFMGDRDAKNYSYSLEVGGNGRKLTFEGSPRSIRDSHKKV 275
MtSINA5     180 EVENATWMLTVFHCFGQYFCLHFEAFQ-LGMAPVYMAFLRFMGDERDARSYSYSLEVGGSGRKLIYEGSPRSIRDSHKKV 258
OsSINA6     187 EVENATWMLTVFSCFGQYFCLHFEAFQ-LGMAPVYIAFLRFMGDDAEAKNYSYSLEVGGSGRKMTWQGVPRSIRDSHRKV 265
OsSINA4     186 EVENATWMLTVFSCFGQYFCLHFEAFQ-LGMAPVYIAFLRFMGDDLEAKNYSYSLEVGGTGRKMIWQGVPRSIRDSHRKV 264
PtSINA2     182 EVENATWMLTVFSCFGQYFCLHFEAFH-LGMSPVYIAFLRFMGDDNEAKNHSYSLQVCGSGRKMTWQGVPRSIRDSHRKV 260
PtSINA4     190 EVENATWMLTVFSCFGQYFCLHFEAFQ-LGMAPVYIAFLRFMGDDNEAKNYSYSLEVGGNGRKMIWQGVPRSIRDSHRKV 268
MtSINA3     189 EVENATWMLTVFSCFGQYFCLHFEAFQ-LGMAPVYIAFLRFMGDDDQAKNYTYSLEVGGNGRKMTWQGVPRSIRESHRKV 267
MtSINA6     189 DVENATWMLTVFSCFGKYFCLHFETFQ-LGMAPVYIAFLRFMGEDSEAKNYSYSLEVGGNGRKMVWQGVPRSIRESHSKI 267
AtSINA2     193 EVENATWMLTVNCFGRQFCLHFEAFQ-LGMAPVYMAFLRFMGDENEAKKFSYSLEVGAHGRKLTWQGIPRSIRDSHRKV 271
AtSINA1     190 EVENATWMLTVNCFGRQFCLHFEAFQ-LGMAPVYMAFLRFMGDENEAKKFSYSLEVGAHSRKLTWQGIPRSIRDSHRKV 268
PtSINA6     192 EVENATWMLTVNCFGRQFCLHFEAFQ-LGMAPVYMAFLRFMGDDNEAKKFSYSLEVGGNGRKLVWQGIPRSIRDSHRKV 270
PtSINA10    189 EVENATWMLTVNCFGRQFCLHFEAFQ-LGMAPVYMAFLRFMGDDNEAKKFSYSLEVGGNGRKLVWQGIPRSIRDSHRKV 267
PtSINA1     171 EIDNATWMLTVNCFGRQFCLHFETFF-IGMSPVYMAFLRFMGTEDEAREFSYSIEVGGNGRKLTWQGVPRSIRDSHOKV 249
PtSINA5     196 EIDNATWMLTVFSCFGRQFCLHFETFH-LGMSPVYMAFLRFMGTEDEAREFSYSLEVGGNGRKLTWQGIPRSIRDSHKKV 274
OsSINA2     193 EVENATWMLTVFKCFGQHFCLHFEAFL-LGMAPVYMAFLRFMGDESEARNFCYSLEVGGNGRKLTWQGIPRSIRDSHKKV 271
Siah1       171 NLPGAVDWVMMQSCFGFHEMLVLEKQEKYDGHQQFFAIVQLIGTRKQAENFAYRLELNGHRRRLTWEATPRSIHEGIATA 250
               $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$

OsSINA5     312 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQTNPD---GACIPNLCS- 361
OsSINA1     298 RDSHDGLIIQRNMALFFSGGDRKELKLRITGRIWKEQQTPD---GACIPNLCS- 347
OsSINA3     299 RDSHDGLIIQRNMALFFSGGPRKELKLRVTGRIWKEQQNPDS--GACIPNLFS- 349
PtSINA8     219 RDSHDGLVIQRNMALFFSGGDRKELKLRVTGRIWKEQQNPEG--GACIPNLCS- 269
SINAT5      258 RDSHDGLIIQKNMALFFSGGDKELKLRVTGRIWKEQQNPDS--GVCITSMCSS 309
AtSINA4     276 RDSNDGLIIQRNMALFFSGGDRKELKLRVTGKIWKEQHSPDS--GLSIPNLSSS 327
PtSINA7     282 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQQSPET--GVCIPNLCS- 332
PtSINA9     243 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQQNPET--GVCIPNLCS- 293
MtSINA1     283 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQQNPDG--GVCIPNLCS- 333
MtSINA4     275 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQ-NQDA--AVCIPNLCS- 324
AtSINA3     275 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQQQSGEGGGACIPNLS-- 326
PtSINA3     219 RDSHDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQQNPE--GGACIPNLCS- 269
MtSINA2     276 KDSHDGLIIYRNMALFFSGGDRKELKLRVTGRIWKEQQNSE-----CTPNMCS- 323
MtSINA5     259 RDSHDGLIIYRNMALFFSGGDRKELKLRVTGRIWKEQQNPEG--GVCIPNLCS- 309
OsSINA6     266 RDSYDGLIIQRNMALFFSGGDKELKLRVTGRIWKEQ-----------------  302
OsSINA4     265 RDSYDGLIIQRNMALFFSGGERKELKLRVTGRIWKEQ-----------------  301
PtSINA2     261 RDSFDGLVIQRNMALLFSGGDRKELKLRVTGRIWKEQ-----------------  297
PtSINA4     269 RDSFDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQ-----------------  305
MtSINA3     268 RDSFDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQ-----------------  304
MtSINA6     268 RDSFDGLIIQRNMALFFSGGDRKELKLRVTGRIWKEQ-----------------  304
AtSINA2     272 RDSQDGLIIPRNLALYFSGGDRQELKLRVTGRIWKEE-----------------  308
AtSINA1     269 RDSQDGLIIPRNLALYFSGSDKEELKLRVTGRIWKEE-----------------  305
PtSINA6     271 RDSQDGLIIQRNLALYFSGGDRQELKLRVTGRVWKEE-----------------  307
PtSINA10    268 RDSQDGLIIQRNLALYFSGGDRQELKLRVTGRVWKEE-----------------  304
PtSINA1     250 RDSQDGLIIQRNLALFFSGGDRKVSGRIWKEQ-----------------  286
PtSINA5     275 RDSQDGLIIQRNLALFFSGGERQELKLKVSGRIWKEQ-----------------  311
OsSINA2     272 RDSFDGLIIHRNMALFFSGGNRQELKLRVTGRIWKEQ-----------------  308
Siah1       251 IMNSDCLVFDTSIAQLFAENGNLGINVTISMC--------------------  282
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Supplemental Fig. S2. Nucleotide sequence alignment (690 bp assembled conserved regions) used to design the phylogenetic tree shown in Fig. 1B.

```
OsSINA5    AGCGTGGAGCTGCTCGAGTGCCCCGTCTGCAACATGTTCCCGCCCATCCA  [50]
OsSINA1    AGCGTGGAGCTGCTCGAGTGCCCCGTCTGCAACATGTACCCGCCGATCCA  [50]
OsSINA3    AGCGTCGAGCTGCTCGAGTGCCCCGTCTGCAACATGTACCCGCCCATCCA  [50]
PtSINA8    ---GTTGAGCTCCTTGAATGCCCTGTTTGTAATATGTACCCTCCTATTCA  [47]
PtSINA3    ---GTTGAGCTCCTTGAATGCCCTGTTTGTAATATGTACCCTCCTATTCA  [47]
PtSINA7    AGTGTTGAGCTCCTAGAATGTCCTGTTTGTAATATGTACCCACCAATTCA  [50]
PtSINA9    AGTGTTGAGCTGCTAGAATGTCCTGTTTGTAATATGTACCCACCAATCCA  [50]
MtSINA1    AGTGTTGAGTTGTTGGAATGTCCTGTTTGTAATATGTATCCTCCAATTCA  [50]
MtSINA4    AGTGTTGAATTGCTTGAATGTCCTGTTTGTAATATGTACCCTCCTATTCA  [50]
AtSINA3    AGTGTTGAGCTTCTCGAATGTCCTGTCTGCAATATGTACCCTCCCATTCA  [50]
MtSINA2    AGTGTCGATCTTCTTGAATGTCCGGTTTGCAATATGTACCCTCCAATCCA  [50]
MtSINA5    AGTGTTGAGCTTCTTGAATGTCCTGTTTGTAATATGTACCCTCCAATTCA  [50]
SINAT5     AGCGTTGAGCTCCTTGAATGCCCTGTCTGCAATATGTACCCACCAATCCA  [50]
AtSINA4    AGCGTGGAGCTTCTGGAGTGCCCTGTCTGTTATATGTATCCTCCTATCCA  [50]
OsSINA6    GGCGTGGAGCTACTGGAATGCCCTGTGTGTAATATGTATCCTCCAATTCA  [50]
OsSINA4    AGCGTGGAACTGCTTGAATGTCCAGTCTGCAGCATGTATCCTCCCATTCA  [50]
PtSINA2    AGCGTTGAATTATTGGAGTGTCCCGTGTGCAATATGTATCCTCCAATTCA  [50]
PtSINA4    AGCGTTGAATTACTGGAGTGTCCTGTGTGCAATATGTATCCTCCAATTCA  [50]
MtSINA3    AGCGTTGAGCTTTTAGAGTGCCCTGTGTGCAATATGTACCCTCCAATCCA  [50]
MtSINA6    AGCGTTGAGCTTCTAGAGTGTCCTGTATGCAATATGTACCCTCCAATCCA  [50]
AtSINA2    AATGTTGAGCTTCTTGAATGTCCCGTCTGTAATATGTACCCTCCAATTCA  [50]
AtSINA1    AATGTTGAGCTCCTTGAATGTCCGGTTTGTAATATGTATCCTCCAATTCA  [50]
PtSINA6    AATGTGGAGCTCCTTGAGTGTCCTGTCTGTAATATGTACCCTCCAATTCA  [50]
PtSINA10   AATGTCGAACTCCTTGAGTGTCCTGTCTGTAATATGTATCCTCCAATTCA  [50]
PtSINA1    AGTATGGACCTTCTTGACTGTCCTGTTTGCACTATGTACCCTCCAATTTT  [50]
PtSINA5    AGTATGGACCTTCTTGATTGTCCTGTTTGTACCATGTATCCTCCAATTTT  [50]
OsSINA2    ACGTTGGATTTGCTCGAGTGTCCAGTCTGCAACATGCGCCCACCTATACT  [50]
Siah1      AATTTGAGTCTTTTTGAGTGTCCAGTCTGCGACGTGTTACCGCCCATTCT  [50]


OsSINA5    CCAGTGCAATGGACACACTTTATGTTCATGCAAGAGAGTCAACCGGTGCC  [100]
OsSINA1    CCAGTGCAATGGACACACTCTGTGTTCCTGCAAAAGGGTGAACCGTTGCC  [100]
OsSINA3    CCAGTGCAATGGTCATACTCTGTGTTCATGCAAACGTGTGAACCGCTGCC  [100]
PtSINA8    TCAGTGCAATGGCCATACACTCTGTTCATGTAAACGAGTAAATCGGTGTC  [97]
PtSINA3    TCAGTGCAATGGCCACACACTCTGTTCATGTAAACGAGTAAATCGGTGCC  [97]
PtSINA7    TCAGTGTAATGGGCACACGCTATGTTCCTGTAAAAGGGTAAATCGCTGCC  [100]
PtSINA9    TCAGTGTAATGGGCACACGCTATGTTCCTGTAAAAGGGTAAATCGCTGCC  [100]
MtSINA1    TCAGTGCAACGGTCACACATTGTGTTCCTGTAAAAGGGTGAATCGATGTC  [100]
MtSINA4    CCAGTGTAATGGCCACACACTATGTTCCTGCAAACGAGTGAACCGATGTC  [100]
AtSINA3    TCAGTGTAATGGACATACGTTGTGTTCATGTAAAAGGGTTAACCGCTGCC  [100]
MtSINA2    TCAGTGTAATGGACATACCCTTTGTTCATGTAAGAGGGTAAACAGATGTC  [100]
MtSINA5    TCAGTGTAATGGGCATACCCTATGTTCATGTAAGAGGGTAAACAGGTGCC  [100]
SINAT5     TCAGTGTAATGGACATACTTTATGTTCATGTAAAAGAGTGAATCGGTGTC  [100]
AtSINA4    TCAGTGTAATGGACATACATTGTGCTCGTGTAAAAGGGTTAACAGGTGTC  [100]
OsSINA6    TCAGTGCAATGGTCATACTCTATGTTCCTGCAAGAGGGTTAACCGCTGCC  [100]
OsSINA4    TCAGTGCAATGGTCATACATTGTGCTCTTGCAAAAGGGTTAATCGCTGTC  [100]
PtSINA2    TCAGTGTAATGGTCACACATTATGTTCCTGCAAGAGAGTTGGCCGATGCC  [100]
PtSINA4    CCAGTGTAATGGCCACACATTATGTTCTTGCAAGAGGGTTAACCGATGCC  [100]
MtSINA3    CCAGTGCAATGGTCACACTCTATGCTCTTGCAAAAGAGTCGACCGGTGCC  [100]
MtSINA6    TCAGTGTAATGGTCACACTATATGCTCATGCAAAAGAGTAAACCGGTGCC  [100]
AtSINA2    TCAGTGTAATGGCCACACATTATGTTCATGCAAAAGAGTGAACACATGCC  [100]
AtSINA1    TCAGTGCAACGGCCACACATTGTGTTCATGCAAAAGAGTGAACACATGCC  [100]
PtSINA6    CCAGTGCAATGGACACACTTTATGTTCGTGCAAGAGAGTAAACTGTTGCC  [100]
PtSINA10   CCAGTGCAATGGACACACTCTATGTTCATGCAAGAGAGTAAACTGTTGCC  [100]
PtSINA1    CCAGTGTAATGGCCACACTCTATGCTCATGCAGGAGAGTAAACTCTTGCC  [100]
PtSINA5    CCAGTGTAATGGCCACACTCTATGTTCATGCAGGAGAGTGAACTCTTGCC  [100]
OsSINA2    GCAGTGCAATGGTCACACAATATGCTCTTGCAAGAGGGTGAATCATTGCC  [100]
Siah1      TCAATGTAGTGGCCATCTTGTTTGTAGCTGTCGCAAGCTC---TGTTGTC  [97]
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OsSINA5     CTACCTGCAGACAAGAGCTCGGTGATATTAGGTGCTTGGCACTGGAGAAA      [150]
OsSINA1     CTACATGCAGACAAGAGCTTGGTGATATCAGGTGTTTGGCCCTGGAGAAA      [150]
OsSINA3     CAACCTGTCGACAGGAGCTTGGTGATATTAGATGTCTAGCATTGGAGAAA      [150]
PtSINA8     CCACTTGTAGACAGGAGCTTGGTGACATTAGATGTCTAGCTTTGGAAAAA      [147]
PtSINA3     CCACTTGTAGACAGGAGCTTGGTGACATTAGATGTCTAGCATTGGAAAAA      [147]
PtSINA7     CCACATGTAGGCAGGAGCTTGGAGACATTAGATGTTTGGCCCTAGAAAAG      [150]
PtSINA9     CTACTTGCAGGCAGGAGCTCGGAGACATTAGGTGTTTAGCCCTAGAGAAG      [150]
MtSINA1     CGACCTGTAGACAAGAGCTTGGAGATATTAGGTGTCTGGCACTGGAAAAG      [150]
MtSINA4     CGACTTGTAGACAAGAGCTTGGAGATATCAGGTGTCTAGCACTGGAGAAG      [150]
AtSINA3     CAACTTGTAGACAAGAGCTCGGTGATATCCGTTGTTTGGCACTGGAAAAA      [150]
MtSINA2     CAACTTGCAGGCAAGAGCTAGGCGATATAAGGTGTTTAGCATTGGAGAAA      [150]
MtSINA5     CAACTTGCAGACAGGAACTGGGCGATATTCGGTGTTTAGCATTGGAAAAA      [150]
SINAT5      CAACGTGTAGACAAGAGCTTGGAGATATTAGATGTTTAGCTCTTGAGAAA      [150]
AtSINA4     CCACATGTAGACAAGAACTTGGAGATATTAGATGTTTAGCTCTTGAGAAA      [150]
OsSINA6     CAACTTGCAGACATGAATTGGGTAACATAAGATGCCTTGCTCTGGAAAAG      [150]
OsSINA4     CAACTTGTAGGCATGAACTGGGTAATATTAGATGTCTTGCTCTCGAGAAG      [150]
PtSINA2     CCATTTGCAGGCATGAACTTGGCAACATTAGATGTCTTGCGCTAGAGAAA      [150]
PtSINA4     CCACTTGCAGGCACGAACTCGGCAACATTAGATGTCTTGCACTAGAGAAA      [150]
MtSINA3     CTACTTGTCGGCATGAGCTCGGCAATATTAGATGTCTGGCATTGGAGAAG      [150]
MtSINA6     CTACTTGTAGGCATGAGCTGGGAAATATTAGATGTCTAGCACTGGAGAAG      [150]
AtSINA2     CTACATGTCGCTACGAGCTTGGTAACATAAGATGCTTAGCTCTTGAGAAA      [150]
AtSINA1     CTACATGCCGCTATGAGCTTGGTAACATAAGATGCTTGGCTCTTGAGAAG      [150]
PtSINA6     CTACTTGCCGCTATGATCTTGGAAATATACGCTGTTTGGCTTTGGAGAAA      [150]
PtSINA10    CTACTTGCCGCTATGATCTTGGAAATATACGGTGCTTGGCTTTGGAGAAA      [150]
PtSINA1     CAATTTGCCGAGGAGAGCTAGGAAATATAAGGTGCTTGGCTCTGGAAAAA      [150]
PtSINA5     CAATTTGCCGAGGAGAACTAGGAAATATAAGGTGCTTGGCTCTGGAGAAA      [150]
OsSINA2     CTACTTGTCGCCAAGAACTGGGTAATATCAGATGTTTGGCTCTTGAGAAG      [150]
Siah1       CAACTTGCCGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAA      [147]

OsSINA5     GTAGCAGAGTCACTCGAGCTTCCTTGCAAGTATTCTTTAGGTTGCATTTT      [200]
OsSINA1     GTAGCTGAATCGCTTGAGCTTCCCTGTAAGTACTCTTTGGGGTGCATCTT      [200]
OsSINA3     GTGGCTGAATCGCTTGAGCTACCCTGCAAATATTCACTAGGTTGTATCTT      [200]
PtSINA8     GTAGCTGAATCACTCGAGCTACCTTGCAAATACTCACTTGGATGCATTTT      [197]
PtSINA3     GTAGCTGAATCACTTGAGCTGCCTTGCAAATACTCGCTTGGATGCATTTT      [197]
PtSINA7     GTGGCTGAGTCACTAGAACTGCCTTGCAAATATAACTTGGGGTGCATATT      [200]
PtSINA9     GTGGCTGAGTCACTGGAATTTCCTTGCAAATTTAACTTGGGGTGCATATT      [200]
MtSINA1     GTTGCTGAATCACTCGAGTTACCATGCAAATACTCTCTTGGATGTATCTT      [200]
MtSINA4     GTGGCTGAATCACTTGAGTTACCGTGCAAGTACTCCCTCGGATGTATATT      [200]
AtSINA3     GTAGCCGAATCACTTGAACTACCTTGTAAACACTCACTTGGATGTATCTT      [200]
MtSINA2     ATAGCAGAATCACTTGAATTTCCTTGTAGATACTCTCTTGGTTGTATATT      [200]
MtSINA5     ATAGCAGAATCACTTGAACTTCCTTGCAGATACTCTGTTGGCTGTATATT      [200]
SINAT5      GTAGCTGAGTCGCTTGAGTTACCGTGCAAGTATAATCTTGGATGCATTTT      [200]
AtSINA4     GTAGCCGAGTCGCTTGAGCTGCCTTGCAAGTTTAATCTGGGATGTATCTT      [200]
OsSINA6     GTAGCTGCATCACTAGAGCTTCCATGCAAATATAACTTTGGGTGCATATA      [200]
OsSINA4     GTGGCTGCGTCGCTTGAACTTCCATGCAAGTACAACTTCGGGTGTATTTA      [200]
PtSINA2     GTTGCTGCATCTCTTGAACTTCCATGTATTTATAGTTTTGGGTGCATATA      [200]
PtSINA4     GTTGCTGCATCTCTTGAACTTCCATGTAAATATAGTTTTGGGTGCATATA      [200]
MtSINA3     GTGGCTGCATCACTAGAACTTCCGTGTAAATATGGTTTTGGGTGCATATA      [200]
MtSINA6     GTGGCTGCATCTTTTGCACTCCCCTGTAAATTCGATTTTGGGTGCATATA      [200]
AtSINA2     GTTGCAGAGTCTTTGGAAGTTCCATGCCGGTACAATTTGGGGTGTATTTT      [200]
AtSINA1     GTTGCGGAATCATTGGAAGTTCCATGCCGGTACAATTTAGGGTGTATTTT      [200]
PtSINA6     GTTGCAGAATCATTGGAGCTGCCCTGCAAATTCAGCTTAGGATGCATTTT      [200]
PtSINA10    GTTGCAGAATCATTGGAGCTGCCCTGCAAATACAGTTTAGGATGTGTTTT      [200]
PtSINA1     ATTGCTGAGTCAATAGAACTTCCTTGCATGTACAGTGCGGGATGTATATT      [200]
PtSINA5     ATTGCCGAGTCAATAGAACTCCCCTGCAAATACAGTATGGGATGTATATT      [200]
OsSINA2     GTGGCTGAGTCACTTCAGCTTCCATGCAAATATAGCCTAGGCTGTATTCA      [200]
Siah1       GTGGCTAATTCAGTACTTTTCCCCTGTAAATATTCTTCTGGATGTACTCT      [197]

OsSINA5     TCCATACTACAGCAAGATAAAGCATGAATGCTTTAGGCCATATAACTGCC      [250]
OsSINA1     CCCATACTACAGCAAGATAAAACATGAATGCTTTAGACCATACAATTGCC      [250]
OsSINA3     TCCGTACTACAGCAAACTCAAGCATGAATGCTTCAGGCCATACAACTGCC      [250]
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PtSINA8     TCCATACTACAGTAAACTAAAACATGAGTGCTTTAGGCCATACAACTGTC     [247]
PtSINA3     TCCATACTACAGTAAACTGAAACATGAGTGCTTTAGGCCATACAGCTGTC     [247]
PtSINA7     TCCATATTACAGCAAGCTCAAGCACGAGTGCTTCAGACCATATAATTGCC     [250]
PtSINA9     TCCATATTACAGCAAGCTCAAGCACGAGTGCTTCAGACCATATAATTGCC     [250]
MtSINA1     TCCATACTACAGCAAGCTGAAGCATGAGTGCTTTAGACCATACACTTGTC     [250]
MtSINA4     TCCATACTACAGCAAGCTTAAGCATGAGTGTTTTAGACCTTATAGTTGTC     [250]
AtSINA3     CCCTTATTACAGTAAGCTCAAACATGAGTGTTTCAGACCTTATAGCTGCC     [250]
MtSINA2     TCCATATTTTAGCAAACTCAAACATGAGTGTTTTAGACCATACAATTGCC     [250]
MtSINA5     TCCCTATTACAGCAAACTCAAACACGAGTGTTTCAGACCTTATAACTGCC     [250]
SINAT5      CCCTTATTACAGTAAACTAAAGCATGAGTGTTTTAGACCTTATAGTTGTC     [250]
AtSINA4     TCCTTACTACAGCAAACTGAAGCACGAGTGTTTCAGACCTTACAGTTGTC     [250]
OsSINA6     TCCTTATTACTGCAAGCTGAAGCATGAGTGCTACAGGCCCTATACTTGCC     [250]
OsSINA4     TCCTTACTACTGCAAGCTGAAGCATGAGTGCTATAGGCCTTATAGCTGTC     [250]
PtSINA2     CCCTTATCACAGCAAGTCAAAACATGAATGTTTTAGACCGTATAGCTGCC     [250]
PtSINA4     CCCTTATTACAGCAAGCTAAAACATGAATGTTTTAGACCATATAACTGCC     [250]
MtSINA3     CCCATATTACAGCAAGCTAAAACATGAGTGTTTTAGACCCTATAACTGTC     [250]
MtSINA6     TCCATACTACAACAAGCCAGAACATGAATGTTATAGACCCTATAACTGTC     [250]
AtSINA2     CCCTTACTACAGCAAGCTTAAGCACGAGTGCTTTAGGCCTTACACTTGCC     [250]
AtSINA1     CCCATACTACAGCAAGCTCAAGCACGAGTGCTTTCGATCCTACAGCTGTC     [250]
PtSINA6     CCCATACTACAGCAAGCTCAAGCATGAGTGTTTCCGTCCATATAGCTGTC     [250]
PtSINA10    CCCATACTACAGCAAGCTCAAGCATGAGTGTTTTCGTCCATATAGCTGCC     [250]
PtSINA1     TCCCTACTACAGCAAGCCAAAACATGAATGCTATCGTCCATACAACTGCC     [250]
PtSINA5     TCCCTACTACAGCAAGCCAAAACATGAATGCTATCGCCCATACAACTGCC     [250]
OsSINA2     TCCTTACCAAAACAAACTTAAGCATGAGTGCTTCAGGCCATATAGTTGTC     [250]
Siah1       GCCACACACAGAAAAAGCAGACCATGAATGTTTTAGGCCTTATTCCTGTC     [247]

OsSINA5     CTTATGCTGGTTCTGAATGTGGTGATATTCTTGTTCATTTGAGGGACGAC     [300]
OsSINA1     CTTATGCTGGTTCTGAGTGTGGTGATATCCTTGTTCATTTGAGGGATGAT     [300]
OsSINA3     CTTATGCTGGCTCTGAATGCGGGGATATTCTAGTTCATCTGAGGGATGAC     [300]
PtSINA8     CATATGCTGGATCAGAGTGTGGGGATATCCTTGTTCATCTGAGGGATGAT     [297]
PtSINA3     CATATGCTGGATCAGAGTGTGGGGATATCCTTGTCCATCTAAGAGATGAT     [297]
PtSINA7     CCTATGCTGGATCAGAATGCGGGGACATCCTAGTTCATCTAAGGGATGAT     [300]
PtSINA9     CCTATGCTGGATCAGAATGCGGAGATATTCTGGTTCATCTAAGGGATGAT     [300]
MtSINA1     CTTATGCTGGATCAGAGTGCGGCGATATTCTTGTTCATTTGAGGGACGAT     [300]
MtSINA4     CTTATGCTGGATCAGAGTGTGGAGATATTCTCGTTCATTTGAGGGATGAT     [300]
AtSINA3     CTTATGCTGGATCCGAGTGTGGCGATATCTTAGTTCATCTGAGGGATGAT     [300]
MtSINA2     CTTATGCTGGATCAGACTGTGGAAATATTCTTGTTCATTTAAGGGATGAC     [300]
MtSINA5     CTTATGCCGGATCAGACTGTGGTGATATTCTTGTTCATTTAAGGGACGAC     [300]
SINAT5      CATATGCTGGCTCGGAGTGTGGTGACATTCTTGTTCATTTAAGAGATGAT     [300]
AtSINA4     CTTATGCTGGTTCGGAGTGTGGGGACATCCTTGTACATCTCAGGGATGAT     [300]
OsSINA6     CATATGCTGGATCTGAATGCGGTGACATTCTAGTACACTTGAAAGATGAT     [300]
OsSINA4     CATATGCTGGATCTGAATGCGGTGACATTTTGGTGCACTTGAAAGATGAC     [300]
PtSINA2     CATATTCTGGATCAGAATGCGGTGATATTCTGGTGCATTTGAAAGATGAT     [300]
PtSINA4     CATATGCTGGATCAGAATGCGGTGATATTCTGGTGCATTTGAAAGATGAT     [300]
MtSINA3     CATATGCTGGCTCAGAATGTGGTGATGTATTGGTGCACCTGAAAGATGAT     [300]
MtSINA6     CATATGCTGGTTCAGAATGCGGTGATATATTGGTGCATCTGAAAGAAGAT     [300]
AtSINA2     CTTATGCTGGTTCTGAGTGTGGTGATATCCTTGTCCATCTCAAAGATGAT     [300]
AtSINA1     CTTATGCTGGTTCTGAGTGTGGTGATATTCTTGTTCATCTCAAAGATGAT     [300]
PtSINA6     CTTATGCTGGGTCTGAGTGCGGTGACATCCTTGTTCATCTCAAGGATGAT     [300]
PtSINA10    CTTATGCTGGGTCTGAGTGTGGTGACATCCTTGCTCATCTCAAGGACGAT     [300]
PtSINA1     CTTATGCTGGAGCTGAATGTGGTGACATTCTCATCCATCTTAAGAATGAT     [300]
PtSINA5     CTTATGCTGGAGCTGAATGTGGTGACATCCTTGTCCATCTCAGAAACGAA     [300]
OsSINA2     CATATGCAGGTTCAGAATGCGGCGATGTTCTTGTCCATCTCATAAACGAC     [300]
Siah1       CGTGCCCTGGTGCTTCCTGTGGCTCTCTGGTAATGCATCTGATGCATCAG     [297]

OsSINA5     CACAAAGTTGATATGCACGGCTGCACATTCAACCACAGATATGTCAAATC     [350]
OsSINA1     CACAAAGTTGATATGCATGGTTGCACATTCAACCATAGATATGTCAAGTC     [350]
OsSINA3     CATAAAGTTGACATGCACGGGTGCACATTCAACCATCGCTATGTTAAGTC     [350]
PtSINA8     CACAAAGTGGACATGCATGGGTGTACTTTCAACCATCGCTATGTCAAGTC     [347]
PtSINA3     CACAAGGTGGACATGCATGGGTGTACTTTCAACCATCGCTATGTCAAGTC     [347]
PtSINA7     CACAAGGTGGACATGCACGGATGCACTTTCAACCATCGCTATGTGAAGTC     [350]
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PtSINA9    CACAAGGTGGACATGCATGGATGCACTTTCAACCATCGCTATGTGAAGTC    [350]
MtSINA1    CATAAGGTGGACATGCACGGATGCACATTCAACCATCGTTATGTGAAGTC    [350]
MtSINA4    CATAAGGTGGACATGCACGGATGCACATTCAACCATCGTTATGTGAAGTC    [350]
AtSINA3    CATAAGGTGGATATGCATGGGTGTACTTTCAACCATCGTTATGTCAAGTC    [350]
MtSINA2    CATGGGGTTGATATGCATGGATGCACTTTTAACCATCGTTATGTCAAATC    [350]
MtSINA5    CACAGAGTTGATATGCATGGATGCACTTTTAATCATCGTTATGTCAAGTC    [350]
SINAT5     CATAAAGTCGATATGCATGGATGTACGTTTAATCATCGTTATGTTAAATC    [350]
AtSINA4    CATAAAGTTGACATGCACGGTTCCACTTTTAACCACCGCTATGTCAAATC    [350]
OsSINA6    CATAAGGTTGACATGCACGGAAGCACCTTCAATCACCGTTATGTCAAATC    [350]
OsSINA4    CACAAGGTTGACATGCATGGCTGCACCTTCAACCATCGCTATGTCAAGTC    [350]
PtSINA2    CACAAAGTTGACATGCATGGCAGTACTTTCAACCACAGATATGTCAAATC    [350]
PtSINA4    CACAAAGTTGACATGCATGGCAGTACTTTCAATCACAGATATGTCAAATC    [350]
MtSINA3    CACAAAGTTGACATGCATGGCTGCACTTTTAATCATCGTTACGTCAAATC    [350]
MtSINA6    CACAAAGTGGACATGCACGGTAGCACTTTTAACCATCGTTATGTCAAATC    [350]
AtSINA2    CATAAAGTCGATATGCATGGATGCACCTTCAACCACCGTTATGTAAAGTC    [350]
AtSINA1    CATAAAGTTGACATGCATGGGTGCACTTTCAACCATCGTTATGTGAAGTC    [350]
PtSINA6    CACAAGGTTGACATGCATGGGTGTACCTTTAATCATCGTTATGTTAAGTC    [350]
PtSINA10   CACAAGGTTGATATGCATGGGTGTACCTTCAATCATCGTTATGTCAAATC    [350]
PtSINA1    CATAAGGTTGATATGCATGGATGCACCTTCAATCACAGATATGTCAAGTC    [350]
PtSINA5    CACAAAGTTGACATGCATGGATGCACCTTCAATCACAGATATGTCAAGTC    [350]
OsSINA2    CATAAGGTGGACTTGCATGGCTGCACCTTTAACCACCGTTATGTGAAGTC    [350]
Siah1      CATAAGTCCATTACAACCCAGGGA------GAGGATATAGTTTTTCTTGC    [341]

OsSINA5    TAATCCAGAGGTTGAGAATGCGACCTGGATGCTAACAGTGTTCTGTTTCG    [400]
OsSINA1    CAACCCAGAAGTCGAAAATGCCACCTGGATGCTGACGGTCTTCTGTTTCG    [400]
OsSINA3    AAACCCCGAGGTCGAAAATGCTACTTGGATGTTGACTGTCTTTTGCTTTG    [400]
PtSINA8    TAATCCTGAAGTAGAAAATGCAACATGGATGTTAACAGTTTTCTGTTTTG    [397]
PtSINA3    CAATCCTGAAGTAGAAAATGCAACATGGATGTTAACTGTTTTCTGTTTTG    [397]
PtSINA7    TAATCCCGAAGTGGAGAATGCCACTTGGATGTTGACGGTCTTCTGTTTTG    [400]
PtSINA9    TAATCCCGAAGTGGAGAATGCCACTTGGATGTTGACGGTCTTCTGTTTTG    [400]
MtSINA1    AAATCCGGAAGTAGAGAATGCTACTTGGATGCTCACTGTATTTTGTTTTG    [400]
MtSINA4    AAATCCCGAAGTAGAGAATGCAACCTGGATGCTCACAGTATTTTGTTTTG    [400]
AtSINA3    TAATCCTGAAGTCGAAAACGCCACATGGATGTTAACTGTCTTTTGCTTCG    [400]
MtSINA2    AAATCCTGAAGTAGAAAATGCTACTTGGATGCTAACGGTTTTCTGTTTTG    [400]
MtSINA5    AAATCCCGAAGTAGAAAATGCTACATGGATGTTAACAGTCTTCTGTTTTG    [400]
SINAT5     TAATCCAGAAGTAGAGAACGCTACTTGGATGCTAACGGTGTTTTGTTTTG    [400]
AtSINA4    CAATCCGGAAGTAGAGAACGCTACTTGGATGCTAACCGTATTCTGCTTTG    [400]
OsSINA6    AAATCCTGAAGTTGAGAATGCTACCTGGATGCTCACGGTTTTCTGTTTCG    [400]
OsSINA4    GAATCCTGAAGTTGAGAATGCCACCTGGATGCTTACGGTTTTCTGCTTTG    [400]
PtSINA2    AAATCCAGAAGTTGAGAACGCAACATGGATGCTGACGGTTTTTTGCTTTG    [400]
PtSINA4    AAATCCAGAAGTTGAGAATGCAACATGGATGCTGACGGTCTTTTGCTTTG    [400]
MtSINA3    AAATCCTGAAGTTGAAAATGCCACATGGATGTTAACGGTTTTTTGCTTCG    [400]
MtSINA6    AAATCCTGATGTTGAAAATGCAACATGGATGTTAACGGTTTTCTGTTTTG    [400]
AtSINA2    AAATCCAGAGGTCGAAAATGCTACATGGATGCTTACGGTGTTCTGTTTTG    [400]
AtSINA1    AAATCCGGAGGTCGAGAATGCTACATGGATGCTTACGGTCTTCTGTTTCG    [400]
PtSINA6    AAATCCAGAAGTTGAAAATGCCACATGGATGCTTACAGTTTTTTGTTTTG    [400]
PtSINA10   AAATCCAGAAGTTGAAAATGCCACATGGATGCTTACTGTATTTTGTTTTG    [400]
PtSINA1    TGATGCCGAAATCGACAATGCCACATGGATGTTAACTGTTTTTTGTTTTG    [400]
PtSINA5    TGATCCCGAAATCGACAATGCCACATGGATGTTAACTGTTTTCTGTTTCG    [400]
OsSINA2    CAACCCTGAAGTGGAAAACGCTACATGGATGCTGACGGTTTTCTGTTTTG    [400]
Siah1      TACAGACAATCTTCCTGGTGCTGTTGACTGGGTGATGATGCAGTGTTTTG    [391]

OsSINA5    GGCAGTATTTCTGCCTGCATTTCGAGGCGTTCCAGCTTGGAATGGCACCA    [450]
OsSINA1    GGCAATACTTCTGCCTGCACTTTGAGGCCTTCCAGCTTGGGATGGCACCA    [450]
OsSINA3    GGCAGTACTTCTGCTTGCATTTCGAGGCCTTCCAACTTGGAGTGGCTCCG    [450]
PtSINA8    GCCAGTATTTCTGCCTTCATTTTGAAGCTTTCCAGCTTGGGATGGCTCCT    [447]
PtSINA3    GCCAGTATTTCTGCCTCCATTTTGAAGCTTTCCAACTCGGGATGGCTCCT    [447]
PtSINA7    GTCAATACTTCTGCCTTCACTTTGAAGCTTTCCAGCTTGGCATGGCCCCT    [450]
PtSINA9    GTCAGTACTTCTGCCTTCACTTTGAAGCTTTCCAGCTTGGCATGGCCCCT    [450]
MtSINA1    GCCAATACTTCTGCCTTCACTTTGAAGCTTTCCAGCTAGGCATGGCTCCG    [450]
MtSINA4    GCCAATATTTCTGCCTTCATTTCGAAGCTTTTCAGCTTGGCATGGCCCCT    [450]
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AtSINA3     GTCAATACTTCTGTCTTCACTTTGAGGCATTCCAGCTCGGAATGGCTCCA    [450]
MtSINA2     GTCAATATTTTTGTCTCCATTTTGAAGCATTCCAGCTTGAAACGTCACCT    [450]
MtSINA5     GACAATATTTCTGTCTCCATTTTGAAGCCTTTCAACTTGGAATGGCTCCA    [450]
SINAT5      GTCAATACTTTTGTCTTCATTTTGAAGCGTTTCAGCTCGGTATGGCTCCA    [450]
AtSINA4     GGCAGTACTTCTGCCTCCATTTCGAAGCGTTCCAGCTTGGGATGGGTCCA    [450]
OsSINA6     GCCAGTACTTTTGCCTGCACTTTGAGGCATTCCAGTTGGGCATGGCACCT    [450]
OsSINA4     GCCAGTACTTCTGCCTACATTTCGAAGCATTTCAGCTGGGGATGGCACCT    [450]
PtSINA2     GTCAGTATTTTTGTCTGCATTTTGAAGCATTCCACCTCGGGATGTCCCCA    [450]
PtSINA4     GTCAGTATTTTTGTCTACATTTTGAAGCATTCCAGCTTGGGATGGCCCCG    [450]
MtSINA3     GTCAGTATTTTTGCCTGCATTTTGAAGCTTTTCAACTGGGAATGGCTCCT    [450]
MtSINA6     GTAAGTACTTTTGTCTACATTTTGAAACTTTTCAACTTGGAATGGCTCCT    [450]
AtSINA2     GGAGACAGTTCTGTTTACACTTCGAGGCGTTCCAGCTGGGAATGGCTCCA    [450]
AtSINA1     GAAGACAGTTCTGCTTACACTTTGAGGCGTTTCAGCTCGGGATGGCACCA    [450]
PtSINA6     GAAGACAGTTCTGCTTACATTTTGAGGCTTTCCAGCTGGGCATGGCACCT    [450]
PtSINA10    GAAGACAGTTCTGCTTGCATTTTGAGGCTTTCCAACTGGGCATGGCACCT    [450]
PtSINA1     GCCGACAGTTTTGCTTGCACTTTGAGACTTTTTTTATAGGAATGTCACCT    [450]
PtSINA5     GCCGACAGTTTTGCCTGCACTTTGAGACATTTCATCTAGGAATGTCACCT    [450]
OsSINA2     GACAGCACTTCTGCCTGCATTTTGAGGCATTCCTGCTGGGGATGGCACCA    [450]
Siah1       GCTTTCACTTCATGTTAGTCTTAGAGAAACAGGAATACGATGGTCACCAG    [441]


OsSINA5     GTTTATATGGCCTTCCTCCGTTTCATGGGGGATGAGGAAGCGAGGAACTA    [500]
OsSINA1     GTCTATATGGCCTTTCTCCGTTTCATGGGTGATGAAGAGGCAAGGAACTA    [500]
OsSINA3     GTTTACATGGCCTTCCTCCGTTTTATGGGCGACGAAGATGCCAGGAACTA    [500]
PtSINA8     GTTTATATGGCATTCCTCAGATTCATGGGTGATGAGGAAGCTCGGAATTA    [497]
PtSINA3     GTTTATATGGCATTCCTCAGATTCATGGGTGATGAGGAGGCCAGGAATTA    [497]
PtSINA7     GTTTATATGGCATTCCTCCGTTTCATGGGTGATGAGGAGGCTCGGAATTA    [500]
PtSINA9     GTTTATATGGCATTCCTCCGTTTCATGGGTGATGAGGAGGCTCGGAATTA    [500]
MtSINA1     GTTTACATGGCATTCCTTCGTTTCATGGGAGACGAGGAGGCTCGGAACTA    [500]
MtSINA4     GTTTACATGGCATTCCTTCGGTTTATGGGCGACGAAGATGCCCGGAACTA    [500]
AtSINA3     GTCTACATGGCGTTCCTGCGTTTCATGGGGGACGAGGAAGCTCGAAACTA    [500]
MtSINA2     GTTTACATGGCGTTTCTTCGATTCATGGGTGATGACGACGCCAAGAACTA    [500]
MtSINA5     GTTTACATGGCATTTCTCCGTTTCATGGGAGATGAAGATGCCAGGAGCTA    [500]
SINAT5      GTTTACATGGCGTTTCTGAGATTCATGGGCGATGAAGACGCACGAAACTA    [500]
AtSINA4     GTATACATGGCATTCCTGAGATTCATGGGGGACGAGGATGCACGGAGCTA    [500]
OsSINA6     GTCTACATCGCCTTCCTACGGTTCATGGGAGATGATGAAGCCAAGAACTA    [500]
OsSINA4     GTGTACATCGCCTTCCTGAGGTTCATGGGTGATGACGAAGCAAAGAACTA    [500]
PtSINA2     GTCTACATAGCATTCCTGAGGTTTATGGGCGATGACGAGGCAAAGAACCA    [500]
PtSINA4     GTCTACATAGCATTCCTACGGTTTATGGGGGATGACGAGGCAAAGAACTA    [500]
MtSINA3     GTCTACATAGCATTTTTGCGGTTTATGGGCGATGATCAGGCAAAAAACTA    [500]
MtSINA6     GTCTACATAGCCTTTTTGCGGTTCATGGGTGAAGATGAAGCAAAAAATTA    [500]
AtSINA2     GTGTACATGGCATTCCTTCGTTTTATGGGAGATGAGGAGGCGAAGAAGTT    [500]
AtSINA1     GTGTACATGGCGTTTCTAAGGTTTATGGGAGACGAGGAGGCTAAGAAGTT    [500]
PtSINA6     GTCTATATGGCCTTCTTAAGGTTTATGGGTGATGATGAAGCTAAGAAATT    [500]
PtSINA10    GTCTATATGGCTTTTCTTAAGGTTTATGGGTGATGATGAAGCAAAGAAATT    [500]
PtSINA1     GTTTACATGGCCTTCCTAAGATTCATGGGCACCGAAGAGGCAAGGGAATT    [500]
PtSINA5     GTTTACATGGCCTTCCTGAGATTCATGGGTACAGAAGAGGCAAGAGAATT    [500]
OsSINA2     GTGTACATGGCGTTCCTGAGGTTCATGGGCGAGGACGAGGCCCGGAACTT    [500]
Siah1       CAGTTCTTCGCAATCGTACAGCTGATAGGAACACGCCAAGCTGAAAATTT    [491]


OsSINA5     CACCTACAGCCTAGAGGTTGGTGGTAATGGCAGGAAGATGTGGGAAGGCC    [550]
OsSINA1     TAGCTACAGCCTTGAGGTCGGCGCAAACGGCAGGAAAATGTGGGAGGGCC    [550]
OsSINA3     TAGTTATAGCCTTGAGGTTGGCGCGAATGGCCGGAAGATGTGGGAGGGCC    [550]
PtSINA8     CAGCTACAGCCTGGAGGTTGGGGGAAATGGTCGGAAACTTTGGGAAGGCC    [547]
PtSINA3     CAGCTACAGCCTGGAGGTTGGGGGAAATGGTCGGAAACTATGGGAAGGCC    [547]
PtSINA7     TAGCTATAGCCTTGAGGTCGGAGGAAATGGCAGGAAACTTTGGGAGGGTC    [550]
PtSINA9     TACCTACAGCCTTGAGGTCGGGGGACATGGCAGGAAACTGTGGGAGGGCC    [550]
MtSINA1     TACCTATAGCCTCGAGGTTGGAGCAAATGGAAGAAAACTCTGGGAGGGTC    [550]
MtSINA4     CAGCTATAGCCTGGAAGTTGGGGCCAATGGCAGGAAACTATGGGAAGGTC    [550]
AtSINA3     CAATTACAGTTTAGAAGTGGGAGGTTATGGTCGGAAGCTGTGGGAAGGAC    [550]
MtSINA2     CAGCTACAGCTTAGAAGTGGGAGGAAATGGACGTAAACTATTTGAAGGGC    [550]
MtSINA5     CAGCTACAGTCTTGAGGTAGGAGGGAGCGGACGCAAACTATACGAGGGCC    [550]
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SINAT5      TACATACAGTTTAGAAGTTGGAGGCAGTGGGAGAAAACAGTGGGAAGGGC      [550]
AtSINA4     CAGCTACAGCTTAGAAGTGGGAGGCAGTGGGAGGAAGCTATGGGAAGGAC      [550]
OsSINA6     TAGCTACAGCCTGGAGGTCGGAGGCAGTGGTCGGAAGATGTGGCAAGGCC      [550]
OsSINA4     CAGCTACAGCCTGGAGGTAGGAGGCACTGGCCGCAAAATGTGGCAAGGGC      [550]
PtSINA2     TAGTTACAGTCTTCAAGTATGTGGAAGTGGTAGGAAGATGTGGCAAGGGC      [550]
PtSINA4     TAGTTACAGTCTTGAAGTGGGTGGTGGTGGGAGGAAGATGTGGCAAGGGC      [550]
MtSINA3     TACCTACAGTCTTGAGGTAGGTGGTAATGGGAGAAAGATGTGGCAGGGAC      [550]
MtSINA6     TAGCTACAGTCTAGAGGTAGGCGGAAATGGGAGGAAGATGTGGCAAGGAC      [550]
AtSINA2     CAGTTACAGCTTGGAAGTAGGAGCTCATGGACGGAAATTATGGCAAGGGC      [550]
AtSINA1     CAGTTACAGCTTGGAAGTTGGAGCTCACAGTCGTAAACTATGGCAAGGGC      [550]
PtSINA6     CAGTTACAGCTTAGAAGTTGGTGGGAATGGTCGTAAACTGTGGCAAGGAC      [550]
PtSINA10    CAGTTACAGCTTAGAAGTTGGTGGCAATGGCCGGAAACTGTGGCAAGGAC      [550]
PtSINA1     CAGTTATAGTATTGAAGTTGGTGGTAATGGAAGAAAGCTTTGGCAAGGAC      [550]
PtSINA5     TAGTTACAGTCTTGAAGTTGGTGGAAATGGTAGAAAGCTTTGGCAAGGAC      [550]
OsSINA2     CTGCTACAGCCTGGAGGTGGGCGGGAACGGGCGGAAGCTGTGGCAGGGCC      [550]
Siah1       TGCTTACCGACTTGAGCTAAATGGTCATAGGCGACGATTGTGGGAAGCGC      [541]

OsSINA5     CTAGGAGCATCCGCGACAGCCGGAAGGTGCGGGACAGCCATGACGGCCTC      [600]
OsSINA1     CCCGAAGTGTCCGGGACAGCCGGAAGGTGCGGGACAGCCATGATGGCCTC      [600]
OsSINA3     CCCGCAGCATAAGGGACAGCCGGAAGGTTAGGGACAGCCATGACGGCCTC      [600]
PtSINA8     CACGGAGTATAAGAGATAGCAGGAAGGTTAGGGACAGCCATGATGGACTT      [597]
PtSINA3     CACGGAGTATAAGAGATAGTAGGAAGGTTAGGGACAGCCATGATGGACTT      [597]
PtSINA7     CGCGAAGTGTCCGAGATAGCCGGAAGGTCAGGGATAGTCATGACGGTCTC      [600]
PtSINA9     CACAAAGTGTTCGAGATAGCCGGAAAGTCAGGGATAGTCATGATGGTCTC      [600]
MtSINA1     CACGGAGTATTCGTGATAGCCGTAAAGTTCGAGATAGTCACGACGGCCTC      [600]
MtSINA4     CACGAAGTGTTCGAGATAGCCGTAAAGTTCGGGATAGCCATGATGGTCTC      [600]
AtSINA3     CAAGAAGCGTAAGAGACAGCAGGAAAGTTAGAGACAGTCATGATGGACTA      [600]
MtSINA2     CAAGAAGCATTAGAGATAGTAAGAAAGTGAAGGATAGTCATGACGGCCTA      [600]
MtSINA5     CAAGGAGCATTAGAGACAGCAAGAAAGTTAGAGACAGTCATGATGGCCTC      [600]
SINAT5      CAAGAAGTGTCAGAGATAGTAGGAAAGTCAGAGACAGTCATGACGGTCTT      [600]
AtSINA4     CAAGAAGCATCAGAGATAGCAGGAAAGTAAGAGACAGCAACGACGGTCTC      [600]
OsSINA6     CCCGAAGCATCAGAGACAGTAGGAAAGTTCGGGACAGCTACGACGGCCTT      [600]
OsSINA4     CCCGGAGCATCAGAGACAGCCGGAAGGTCCGGGATAGCTATGATGGGCTT      [600]
PtSINA2     CTAGGAGCATTAGGGATAGCCGGAAGGTTCGTGACAGCTTTGATGGTCTT      [600]
PtSINA4     CAAGGAGCATAAGGGACAGCCGAAAGGTTCGAGACAGTTTTGATGGTCTG      [600]
MtSINA3     CTAGAAGCATTAGGGAAAGCCGCAAGGTTCGCGACAGTTTTGATGGTCTC      [600]
MtSINA6     CAAGAAGCATCAGGGAAAGTAGCAAGATCCGCGACAGTTTTGATGGTCTT      [600]
AtSINA2     CTAGAAGCATCCGTGACAGTAGGAAAGTCCGGGACAGTCAAGACGGACTC      [600]
AtSINA1     CAAGAAGCATCAGAGACAGTAGGAAAGTCCGAGATAGTCAAGACGGACTC      [600]
PtSINA6     CCAGGAGCATCCGTGACAGTAGGAAAGTCCGTGACAGCCAGGATGGGCTT      [600]
PtSINA10    CCAGGAGCATCCGTGATAGTAGGAAAGTTCGCGATAGCCAGGATGGGCTT      [600]
PtSINA1     CCAGAAGTATAAGGGATAGCCAGAAAGTTAGAGACAGCCAAGATGGACTG      [600]
PtSINA5     CGAGAAGTATCCGGGATAGCCAGAAAGTTCGAGACAGCCAAGATGGATTG      [600]
OsSINA2     CCCGGAGCATCAGGGACAGCAAGAAGGTCCGGGACAGCTTCGACGGCCTC      [600]
Siah1       CTCGATCTATTCATGAAGGAGCAACAGCCATTATGAATAGCGACTGTCTA      [591]

OsSINA5     ATCATCCAGAGGAACATGGCACTCTTCTTCTCCGGCGGTGACAGGAAGGA      [650]
OsSINA1     ATCATCCAGAGGAACATGGCGCTGTTCTTCTCGGGGGGCGACCGAAAGGA      [650]
OsSINA3     ATAATTCAGCGGAACATGGCTCTGTTCTTCTCAGGCGGAGAGAGGAAAGA      [650]
PtSINA8     GTTATACAACGTAACATGGCACTTTTCTTCTCTGGAGGAGATAGGAAGGA      [647]
PtSINA3     ATCATACAACGTAACATGGCACTTTTCTTCTCTGGAGGAGATAGGAAGGA      [647]
PtSINA7     ATAATTCAACGAAATATGGCACTTTTCTTCTCTGGTGGGGATAGGAAGGA      [650]
PtSINA9     ATTATTCAACGAAACATGGCACTTTTCTTCTCTGGTGGGGATAGGAAGGA      [650]
MtSINA1     ATAATTCAACGAAATATGGCCCTATTTTTCTCTGGTGGTGATAGGAAGGA      [650]
MtSINA4     ATCATTCAAAGAAATATGGCACTATTTTTCTCTGGTGGGGATAGGAAGGA      [650]
AtSINA3     ATTATACAAAGAACATGGCTCTCTTCTTCTCAGGTGGAGATAGGAAAGA      [650]
MtSINA2     ATCATATACCGTAACATGGCACTTTTCTTCTCAGGTGGGGATAGAAAAGA      [650]
MtSINA5     ATTATATACCGGAACATGGCACTTTTCTTCTCTGGTGGAGATAGGAAAGA      [650]
SINAT5      ATAATCCAAAAGAACATGGCACTCTTCTTTTCCGGTGGAGACAAGAAAGA      [650]
AtSINA4     ATCATCCAAAGAAACATGGCTCTCTTTTTTCTCCGGTGGAGACAGGAAAGA      [650]
OsSINA6     ATCATCCAGCGGAACATGGCCTTGTTCTTCTCCGGTGGCGACAAGAAGGA      [650]
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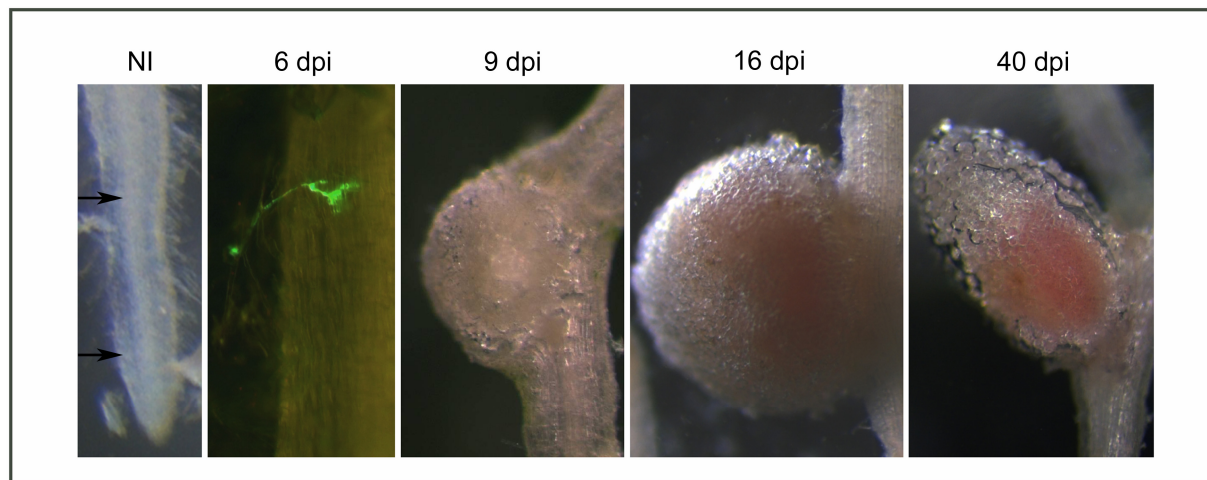
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OsSINA4     ATCATCCAACGGAACATGGCCTTGTTCTTCTCTGGTGGAGAAAGGAAGGA    [650]
PtSINA2     GTTATCCAGCGCAACATGGCCCTTTTATTCTCTGGTGGAGATCGGAAGGA    [650]
PtSINA4     ATCATTCAACGCAACATGGCCCTTTTCTTCTCTGGTGGGGATAGGAAGGA    [650]
MtSINA3     ATCATTCAGAGGAACATGGCTCTCTTCTTTTCTGGGGGTGATAGGAAGGA    [650]
MtSINA6     ATTATTCAGAGGAATATGGCGCTTTTCTTTTCAGGTGGTGACCGGAAAGA    [650]
AtSINA2     ATCATCCCAAGGAACCTCGCACTCTACTTCTCTGGAGGTGATAGGCAAGA    [650]
AtSINA1     ATAATCCCTAGAAACTTGGCTTTGTACTTCTCTGGCAGTGACAAAGAAGA    [650]
PtSINA6     ATTATTCAAAGGAATTTGGCTCTCTACTTCTCTGGTGGGGATAGGCAAGA    [650]
PtSINA10    ATTATTCAAAGGAATTTGGCTCTCTACTTCTCTGGTGGGGATAGGAAAGA    [650]
PtSINA1     ATCATTCAGAGAAACTTGGCACTTTTCTTCTCCGGAGGGGATCGGCAGGA    [650]
PtSINA5     ATCATTCAGAGAAACTTGGCACTTTTCTTTTCTGGAGGGGAACGGCAGGA    [650]
OsSINA2     ATCATCCACCGGAACATGGCCCTCTTCTTCTCCGGCGGCAACAGGCAGGA    [650]
Siah1       GTCTTTGACACCAGCATTGCACAGCTTTTTGCAGAAAATGGCAATTTAGG    [641]

OsSINA5     GCTGAAGCTGAGGGTGACCGGCCGTATCTGGAAAGAACAG    [690]
OsSINA1     GCTGAAGCTGAGGATCACCGGCCGGATCTGGAAGGAGCAG    [690]
OsSINA3     GTTGAAATTGCGGGTCACCGGCCGAATCTGGAAGGAACAG    [690]
PtSINA8     GTTAAAGCTGCGAGTTACAGGACGGATATGGAAAGAACAG    [687]
PtSINA3     GTTAAAGCTGCGAGTTACAGGACGGATATGGAAAGAACAG    [687]
PtSINA7     GCTGAAGCTTAGAGTTACCGGGAGGATATGGAAGGAACAA    [690]
PtSINA9     GCTGAAGCTAAGAGTTACCGGGAGGATATGGAAGGAACAA    [690]
MtSINA1     ACTGAAATTAAGAGTCACAGGAAGAATATGGAAAGAACAA    [690]
MtSINA4     GTTGAAACTTAGAGTCACCGGAAGAATATGGAAGGAACAG    [690]
AtSINA3     GCTGAAACTTCGAGTCACTGGAAGGATATGGAAAGAGCAA    [690]
MtSINA2     GTTGAAACTAAGAGTAACAGGAAGGATATGGAAAGAGCAG    [690]
MtSINA5     GCTGAAGTTACGAGTAACAGGAAGGATATGGAAAGAACAG    [690]
SINAT5      ACTGAAACTTAGAGTCACTGGAAGAATCTGGAAAGAGCAA    [690]
AtSINA4     GCTTAAACTTAGAGTCACTGGTAAAATCTGGAAAGAGCAA    [690]
OsSINA6     GCTCAAACTGCGTGTCACCGGAAGGATTTGGAAGGAGCAG    [690]
OsSINA4     GCTCAAATTGCGGGTCACTGGGAGAATTTGGAAGGAACAG    [690]
PtSINA2     ATTGAAGCTTCGGGTGACTGGTCGGATTTGGAAAGAACAG    [690]
PtSINA4     ATTGAAGCTTAGGGTGACTGGTCGAATTTGGAAAGAACAG    [690]
MtSINA3     ATTGAAGCTACGAGTTACCGGAAGGATTTGGAAAGAGCAG    [690]
MtSINA6     GTTGAAGCTAAGGGTTACTGGTAGGATTTGGAAAGAACAA    [690]
AtSINA2     ACTCAAGTTGAGAGTGACTGGACGAATCTGGAAAGAGGAG    [690]
AtSINA1     GCTCAAGTTGCGAGTCACTGGACGGATTTGGAAAGAAGAA    [690]
PtSINA6     GCTGAAATTGAGGGTTACTGGTCGTGTATGGAAAGAAGAA    [690]
PtSINA10    GCTGAAGTTGAGGGTTACTGGTCGTGTATGGAAAGAAGAA    [690]
PtSINA1     GTTAAAACTGAAAGTTTCAGGACGGATTTGGAAAGAACAG    [690]
PtSINA5     GTTAAAACTGAAAGTTTCTGGACGGATATGGAAAGAACAG    [690]
OsSINA2     GCTCAAGCTGCGGGTTACCGGCCGCATCTGGAAGGAGCAA    [690]
Siah1       CATCAATGTAACTATTTCCATGTGT---------------    [666]
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Supplemental Fig. S3. Stereomicroscopical images representing the different stages of nodule development that were harvested for qRT-PCR analysis.

From uninoculated roots, the zone just above the tip between the arrows, was harvested at the same time as the 6-dpi tissue. At 6 dpi, root sections were collected on which invading infection threads were seen. At 9 dpi, incipient nodule primordia were taken that were still white, a sign for premature symbiosis. At 16 dpi, round nodules were isolated that were pinkish, indicating the presence of leghemoglobin and initiation of nitrogen fixation, and at 40 dpi elongated fixing nodules were collected (see "Materials and Methods").

Supplemental Fig. S4. Co-immunoprecipitation of MtSINA1 and MtSINA3 with SINAT5DN. Immunoblots with the anti-cMYC antibody for detection of MtSINA1 and MtSINA3 proteins fused to the 3x MYC tag are shown. The upper and lower panel visualize the MYC-MtSINA proteins (33-kD fragment), present in the protein extracts before (input, 1/10 amount of the immunoprecipitated fraction) and after immunoprecipitation with the anti-HA antibody, respectively. Lanes 1 and 3 correspond to extracts from protoplasts transfected with only MtSINA3 and MtSINA1, respectively, whereas lanes 2 and 4 correspond to extracts of protoplasts cotransfected with HA-SINAT5DN (HA-SDN) and MYC-MtSINA3 and MYC-MtSINA1, respectively. Arrows mark the 33-kD band of the MtSINA proteins. The 25-kD band observed in the bottom panels corresponds to the size of the light chain of the anti-HA antibody used for immunoprecipitation. The 37-kD band in the input fraction is due to background signal in the extracts.