SUPPLEMENTARY DATA

	FP	5'-TGTGTCTTCCTGAGAACTACCAG-3'
naa10-1	RP	5'-GCTGAGTTAAAGGTCACTGATTG-3'
	LB	5;-AACGTCCGCAATGTGTTATTAAG-3'
	FP	5'-CCTTCTACACTATTGTGGACATTG-3'
naa15-1	RP	5'-CACCTGATAGCTCTGATTGCTGC-3'
	LB	5'-GCTTCCTATTATATCTTCCCAAATTACCAATACA-3'
	FP	5'-CATTCCTCGTTTGCTTGTTTGTAG-3'
naa15-3	RP	5'-CGACTGATTATCATTAACGTAGAGAAC-3'
	LB	5'-GAAATGGATAAATAGCCTTGCTTCC-3'
Naa10-Myc,	XbaI-FP	5'-GCTCTAGAATGGTTTGCATCAGGCGAG-3'
Naa10-GFP	RP-KpnI	5'-GGGGTACCTCATTTGGAAACTGCTTTACCATC-3'
Naa10-AD,	EcoRI-FP	5'-GGAATTCATGGTTTGCATCAGGCGAGC-3'
Naa10-BD	RP-SmaI	5'-TCCCCCGGGTCATTTGGAAACTGCTTTACCATCTAC-3'
Naa15-AD,	EcoRI-FP	5'-GGAATTCATGGGGGGCTTCGCTTCCTCC-3'
Naa15-BD	RP-SmaI	5'-TCCCCCGGGTCAGGTTGCAACTGAGAGGCTC-3'
	BamHI-Naa15	5'-CGGGATCCATGGGGGGCTTCGCTTCCTCC-3'
	Naa15-SmaI	5'-TCCCCCGGGGGGTTGCAACTGAGAGGCTCTTG-3'
pNaa15::Naa15-Flag,	SmaI-Flag	5'-TCCCCCGGGCTGCAGGAATTCGATATCAAGC-3'
Naa15-YFP	Flag-SacI	5'-CGAGCTCTTAAATTCGAGCTCTGTCGACTG-3'
	HindIII-pNaa15	5'-CCCAAGCTT TTCTTATTGCACTGCTTC-3'
	pNaa15-BamHI	5'-CGGGATCC TTTATTGCGCTACTGAGAGAGCTC-3'

Supplemental Table S1. The primers used in this study.



Supplemental Figure S1. Naa10 is evolutionarily conserved among eukaryotes.

(A) Amino acid sequence alignment of Naa10 orthologs from multiple taxa. The accessions of the Naa10 homologs are: *Homo sapiens*, NP_003482; *Mus musculus*, BAB27052; *Drosophila melanogaster*, NP_648378; *Caenorhabditis elegans*, NP_501392; *Oryza sativa japonica*, NP_001054011; *Arabidopsis thaliana*,

NP_196882; Schizosaccharomyces pombe, NP_594309; Saccharomyces cerevisiae,

NP_011877; and Neurospora crassaOR74A, XP_011394752.

(B) The phylogenetic tree of the Naa10 homologs was constructed using the maximum-likelihood method with MEGA 6.

AtNaa15 M----G---A-SLPP-----KEANLFKLIVKSYETKQYKKGLKAADAILK--KFPDHGE 44 AtNaa15 0sNaa15 M----G--S--SLPA------KEANLEKVIVKSYETKOYKKGLKAADSILK--KEPEHGE 44 OsNaa15 HsNaa15 MP-----AVSLPP-----KENALFKRILRCYEHKQYRNGLKFCKQILSNPKFAEHGE 47 HsNaa15 MmNaa15 MP------AVSLPP--KENALFKR ILRCYEHKQYRNGLKFCKQ ILSNPKFAEHGE 47 MmNaa15 DmNaa15 MP----SSDPLPP--KEGALFRKLLKCYELKQYKNGLKLAKQILSNPKYMEHGE 48 DmNaa15 -CeNaa15 MPTPPGQSSSQPLPA-----KELGYFKK1VKSYEQKQYKAGLKFAQK1LTSPGFAEHGE 54 ScNaa15 MSRKR---STKPKPAAKIALKKENDQFLEALKLYEGKQYKKSLKLLDAILK--KDGSHVD 55 --QTLST------REANLFRTVIRHYEDKQYKRGLKAAEQILK---KNPRHGD 44 NcNaa15 MP----SpNaa15 M-----AKVQLSP-----KEITLFRTALKCYETKQYKKGLKAIEPLLE--RHPEHGE 45 AtNan15 TI SMKGLTI NOMDRKTEAVELVRI GVKN---DIKSHVOWHVLGLI VRSDREVREATKOVR 101 0sNaa15 TLSMKGLTLNCMDRKSEAYELVRRGLKN---DLKSHVCWHVYGLLYRSDREYREAIKCYR 101 HsNaa15 TLAMKGLTLNCLGKKEEAYELVRRGLRN---DLKSHVCWHVYGLLQRSDKKYDEATKCYR 104 MmNaa15 TLAMKGLTLNCLGKKEEAYELVRRGLRN---DLKSHVCWHVYGLLQRSDKKYDEAIKCYR 104 CeNaa15 TLAMKGLILNCMGKLQEAQDCVRRGLVS----DLRSYVCWHVFGLIQKTEKKYDEAIKAYK 111 ScNaa15 SLALKGLDLYSVGEKDDAASYVANAIRKIEGASASPICCHVLGIYMRNTKEYKESIKWFT 115 NcNaa15 TMSMKALIMNSQCKTEEAFALAKEALTV----DMKSHICWHVYGILYRQHKNFDEAIKAYK 101 SpNaa15 SLAIKGILLHSLGNTKEGYDNVRLGLRN----DVGSGVCWHIFGLISRADKDYVQAAKCYI 102 AtNaa15 NALRIDPDNLEILRDLSLLQAQMRDLSGFVETRQQLLTLKPNHRMNWIGFAVSQHLNANA 161 0sNaa15 NALRIDPDNIEILRDLSLLQAQMRDLSGFVETRQQLLTLKPNHRMNVIGFAVAHHLSSNS 161 HsNaa15 NALKWDKDNLQILRDLSLLQIQMRDLEGYRETRYQLLQLRPAQRASWIGYAIAYHLLEDY 164 MmNaa15 NALKWDKDNLQ1LRDLSLLQ1QMRDLEGYRETRYQLLQLRPAQRASW1GYA1AYHLLEDY 164 DmNaa15 NALKWEKDNLQILKDLSLLQIQMRDLEGYKETRHHLFTLRPSQHASWIGFAMSYHLLGDY 165 CeNaa15 RALMLEKDNLQILRDLSLLQIHIRDYDGYLSSKYELLQLRQTQRVSWLGYIVAHHLLKEH 171 ScNaa15 AALNNGSTNKQIYRDLATLQSQIGDFKNALVSRKKYWEAFLGYRANWTSLAVAQDVNGER 175 NcNna15 FALKLEPESQQTQRDLAVLQVQTRDYQGYYQSRFAMLKAKPHLRQNWTALATAYQLEGSL 161 SpNaa15 NAHKLEKNNSSLLRDLALLQSQLRQYKALADTRNALLQDNPGVRANWSALAVAQFLRGEY 162 AtNaa15 SKAVEILEAYEGTLEDDYPPENELIEHTEMILYKVSLLEE--S---GSFDKALEELHKKE 216 DsNaa15 SKATEVLEAYEGTLEDDYPPENERYEIISEMLLYKISLFEEC-----GMLDRALEEMQKKE 216 HsNaa15 EMAAKILEEFRKTOOTS---PDKVDYEYSELLLYONOVLREA------GLYREALEHLCTYE 217 MmNaa15 EMAAKILEEFRKTQQTS--PDKVDYEYSELLLYQNQVLREA-----GLYREALEHLCTYE 217 DuNaa15 DMANSILETFSQSQ-TSI-EAHDYRHSELLLYQNQILIE-S-N-RLQQAVDHLTKYQ 217 CeNaa15 NLALGIMAEYIKNN-T---PSGYDFEFSELILYQNLIMREA-----GLPDVALQKLEENS 222 SeNaa 15. 00A INTL SOFEKLAECK I-SDSEKYEHSECLMYKND IMYKAASDNODKLONVLKHLND IE. 234 NcNaa15 EQAENILTTYEKSMIN-V-PLKIDQEHSEALLYKNIIIAER-----GDIKRALEHLESDC 214 SpNaa15 ASAYKIVDAFESTINQGV-PVDTQEE-SEAMLFWNLVILKK--D--G-VEDAYKHLLSIE 215 AtNaa15 PKIVDKLSYKEQEVSLLSKVGRLEEANKLYRVLLSMNPDNYRYHEGLQKCLGLYSESGQY 276 0sNaa15 SKIVDKLSFKEQMACILLKLGRFEEAEKTYRSLLFMNPDNYKYFIAVQKCLGLYSENGQY 276 HsNaa15 KQICDKLAVEETKGELLLQLCRLEDAADVYRGLQERNPENWAYYKGLEKALK------ 269 MmNaa15 KQICDKLAVEETKGELLLQLCRLEDAADVYRGLQERNPENWAYYKGLEKALK 269 DmNaa15 GQ1VDKLAVRETMGDLY1KLQQQEKAVP1FESL1RRNPENVLYYEQY1AAR---CeNaa15 THIVDKVAYMETRANLLMDLEOPKOAENVWRALIERNPDSLEYYDMLEKCMGI------ 275 ScNaa15 PCVFDKFGLLERKATIYMKLGQLKDASIVYRTLIKRNPDNFKYYKLLEVSLGI------ 287 NcNaa15 KNCLDRLAVMEMRARYLGQLNRKEEAAKAWRALLDRNPEHPEYYKGLIEALEI-DE----SpNaa15 KKVLDRVAFLETRAEYELYLSKMEEAKSTIYLLLDRNPDNHQYYYNLQRAYGYEDASGK- 274 AtNaa15 SSDQ1EKLNALYQSLSEQYTRSSAVKR1PLDFLQD-ENFKEAVAKY1KPLLTKGVPSLFS 335 0sNaa15 STDDVDRLCELYSSLKEEYGWSSAVKRIPLDFLEG-EKFQEAADNYVRPLLTKGVPSLFS 335 HsNaa15 PANMLERLK-IYEEAWTKYPRGLVPRRLPLNFLSG-EKFKECLDKFLRMNFSKGCPPVFN 327 MmNaa15 PANMLERLK-IYEEAWTKYPRGLVPRRLPLNFLSG-EKFKECLDRFLRMNFSKGCPPVFN 327 DmNaa15 VTDSSAVVS-IYRVF0E0YPRALCPRRLPLNIANG-DEFRVVTDEYLRRGLRKGIPPLFV 327 CeNaa15 KDSPKAQL-AMLDGLAEKFKRAAAPRRLALYLVEG-EELRRRLHEWMIPMLRKGAPSLFA 333 ScNaa15 QGDNKLKK-ALYGKLEQFYPRCEPPKFIPLTFLQDKEELSKKLREYVLPQLKRGVPATFS 346 NcNaa15 K-DEAA-LKATYDEYAAKYPRSDAAKRLPLNFLTG-DSFKAAAKSYLTNMLDRGVPSVFA 326 SpNaa15 VLDSAEWLN-LYSQLAKRYPKSECPTRLPLEKLEG-DEFLTHVDLYLRKKLKRG1PSVFV 332 AtNaa15 DLSSLYDHPRKP---DILEQLVVEMKHSIGTTGSFPGSDV-K-----EPPSTLLWTLFFLAQ 388 0sNaa15 DLSPLYEQPGK---ANILEELFLKLERS IRTSGCFPGSSHT-----EPPSTLLWTLFLISQ 388 HsNna15 TLRSLYKDKEK--VAIIEELVVGYETSLKSCRLFNPNDDGKE---EPPTTLLWVQYYLAQ 382 MmNaa15 TLRSLYRDKEK-VAIVEELVVGYETSLKSCRLENPNDDGKE----EPPTTLLWVOYYLAO 382 DmNaa15 NVRTLHQIPER---AAVIEELALQYFENLTRSGHFSREDADAGIPVEPASALVWTALFLAQ 385 CoNaa15 SLVPLYKYPQK---QAVIESLITEYVKKMDDEGYGNVSLDGKDQECEPPTTALWLYVLASH 391 ScNaa15 NVKPLYQRRKSKVSPLLEKIVLDYLSGLDPT--------Q--DPIPFI-WTNYYLSQ 392 NcNaa15 NLKHLYSEVAKK--EAILALAEEYLKEHKGSEQANGDSS-K----GVGAAL----YFLAQ 375 SpNaa15 DVKSLYKDTKK---CKVVEDLVSKYASSLSTTNKFSEDDDNSQI--EIPTTLL#TYYFLAQ 388 SpNaa15 AtNaa15 HYDR--RGQYDVALCKIDEAIAHTPTVIDLYSVKSRIMKHAGDLTAAAALADEARGMDLA 446 0sNaa15 HYDR--RGQYDIALDKIDEAISHTPTVIDLYSIKGKILQHAGNFSAAAALADEARSMDLA 446 HsNaa15 HYDK-I-GQPSIALEYINTAIESTPTLIELFLVKAKIYKHAGNIKEAARWMDEAQALDTA 440 MmNaa15 HYDK-I-GQPSIALEYINTAIESTPTLIELFLVKAKIYKHAGNIKEAARWMDEAQALDTA 440 DuNaa15 HYDY-M-RDTDRALEYINVAIDHTPTLIELLITKGRIFKHAGDPVEAYYWLEEAQSMDTA 443 CeNaa15 HFDR--CGMTQLALNYIERAIQHTPTVVENYMLKARIYKHAGDYDEAARWMEEAQSLDTA 449 ScNaa15 HFLF-LK-DFPKAQEYIDAALDHTPTLVEFYILKARILKHLGLMDTAAGILEEGRQLDLQ 450 NcNaa15 HYNYHLSRDLAKAMEYVEQAIELDPKNVDFHMTKARIFKHQGDTAKASETMDRARSLDTK 435 NcNaa15 SpNaa15 HFD-HV-GELEKAEKYVDLAIDHTPTLVELFMTKARISKHKGELQTAMEIMDHARKLDLQ 446 SpNaa15 AtNaa15 DRYINSECVKRMLQADQVPLAEKTAVLFTKEGD----QLNNLHDMQCMWYDLASGDSYFRQ 503 0sNaa15 DRYLNSECVMOMLQADQVGLAEKTAVLFTKDGD---QHNNLHDMQCMWYELASGESYYRQ 503 HsNaa15 DRFINSKCAKYMLKANLIKEAEEMCSKFTREGT-SAVENLNEMQCMWFQTECAQAYKAM 498 MmNaa15 DRFINSKCAKYMLKANLIKEAEEMCSKFTREGT-SAVENLNEMQCMWFQTECAQAYKAM 498 DmNaa15 DRYINSKCAKYMLRANMYQEAEEICAKFTREG-V-SAMDNLNEMQCMWFQTECALAYQRM 501 CeNaa15 DRYINGKCGKYLLRAKRSDEANKMLAKFTREGE--NAASHLTDMOCMWYELESGRAFRSV 507 ScNaa15 DRFINCKTVKYFLRANNIDKAVEVASLFTKNDDSVNGIKDLHLVEASVFIVEOAEAYYRL 510 cNaa15 DRYINSKAAKYQLRNNENEKALETMGLFTRAETVGGPLADLTDMQCMVFLTEDGEAVQR- 494 aa15 DRFINGKCAKYMLRNDENELAAKTVSLFTRNEAVGGAVGDLADMQCLWYMLEDGKSFARQ 506 R 100 Hom Mus Drosophila melanogaster



-GRALKKFLAVEKHYADISE 525

-GRALKNFLAVEKHYADMTE 525

-GEALKKCHEIERHFIEITD 520 -GEALKKCHEIERHFIEITD 520

729

CDI

-GDL---

-NKF-

NKF





Supplemental Figure S2. Naa15 is evolutionarily conserved among eukaryotes.

(A) Amino acid sequence alignment of Naa10 orthologs from multiple taxa. The accessions of the Naa10 homologs are: *Homo sapiens*, NP_476516; *Mus musculus*, NP_444319; *Drosophila melanogaster*, NP_573384; *Caenorhabditis elegans*,

NP_497180.3; Oryza sativa japonica, NP_001043582; Arabidopsis thaliana,

NP_001185448; *Schizosaccharomyces pombe*, NP_588160; *Saccharomyces cerevisiae*, AJU80945; and *Neurospora crassaOR74A*, XP_962452.

(B) The phylogenetic tree of the Naa15 homologs was constructed using the maximum-likelihood method with MEGA 6.



Supplemental Figure S3. Subcellular localization of Naa10 and Naa15 in *N. benthamiana* and root of transgenic *Arabidopsis*.

The *Naa10* and *Naa15* CDSs were fused to GFP and YFP, respectively, driven by the 35S promoter, and cloned into pCambia1300. Naa10-GFP or Naa15-YFP was expressed in *N. benthamiana* leaf epidermal cells (top panel and bottom panel, respectively), *p35S::Naa10-GFP* was transformed into *Arabidopsis* (middle panel). The subcellular localization of Naa10-GFP or Naa15-YFP was observed by confocal laser scanning microscopy..



Supplemental Figure S4. No physical interaction was detected between Naa10

and Naa15 in a yeast two-hybrid assay.

(A) There was no physical interaction between Naa10 and Naa15 in yeast. Positive control: pGADT7-T/pGBKT7-53; negative control: pGADT7-T/pGBKT7-Lam. The interaction between Naa10 and Naa15 was assessed by growth on SD/-His/-Leu/-Trp and SD/-Ade/-His/-Leu/-Trp media.

(B) Both Naa10 and Naa15 were expressed in yeast. HA-specific antibodies were used to detect the proteins expressed as a fusion to an HA epitope tag from pGADT7. c-Myc-specific antibodies were used to detect the proteins expressed as a fusion with the c-Myc epitope tag from pGBKT7. AH109 cells without plasmid transformation were used as a negative control.