

OsAM1	--NDAEMMAPALAAHLQDSPMRPOVSRYYSKRR--GSSHSRNGKDIANHDESKNQSPGLPLSRQSLSSATHYHTGAFYEIDHEKLPKKSPT	90
AM1	MDVETVQAGPALAAHLQDASPKPOVKYYFKKTSSSHSRNGKDIYNHDSITQ--RSPLSRQSLTFDAIPYHAGAFYEIDHDLPPKSP	91
SW1	-----MVKRNPIRETTAGTISSPSPITN-----VAIAHIRAGSYVEIDASILQKRSPE	50
OsAM1	HLKSRIVVYVSGYTSIDVTVSPFSLILLRSEFSSERSCTG-----PFDERFVMSNHAARILRRVREBELAGDMHODSFWLTK	172
AM1	HLKSRIVVYVSEGNIDITVRFPSLQLLRSEFSSYAPGTC-----PFDERFVMSNHAARILRRVREBELAGDMHODSFWLTK	172
SW1	NLKSRIVVYVSKTASDVSLRYPSMFSRSHRDYRMRNRNPKMKRSGGGLLEVFDESHVMASELGDLIYRRIIPHELSMNRN-SWGFVWSS	142
OsAM1	RCYDFEASS--RHVITPSPPPAT--QAKPAPSSCLLDTLKCDGAGWVRRRVYVGRHHASAEASASLDGYNTEVSYVEEQORLRLR	262
AM1	RLYDFEAPQOVESITCLPFPAPPPATLGLTDECLITLTKCDGAGWGMRRRVYVGRHREAPKE--ASVDGYDTESSVREVOCP----	258
SW1	S-----SRNKFERRFVSCRAYNRLCRASPEGKCSSELKSGGMIKGRRLVQVQSRHIDPRNKEGEESRVKDEIYKEEEMK-----	225
OsAM1	LRLRQRREOENKSTNGKKREAESSMDKSAARKKAKTYKSPKVEK---RRVVEAKDGDPRGKDRWSAERYAAERLLIMRSHCA	352
AM1	-----PATQEVKRSERNCKKREAEASSKNNNGDEGRNKKVQGASKKSKAKKRTVESKDGDERHSGDRWSAERYAAEKLLIMRSDA	346
SW1	-----EEDDDGNEIGGTQEAKEITNGNRRLIESSTERAQKAVYDOKETQIVVYRKSERKFDKWSVERVKLAERNMLKVMKEKNA	313
OsAM1	CFCNVMRQALREARKHIGDTGLLDHLLKHMAGRVECSAARFRRRHNADGAMEYWLEPAELAEVRRLAGVSDPYWPPPGWKKGDDNSATA	445
AM1	RFCNVMRQVLRREARKHIGDTGLLDHLLKHMAGRVECSVHRRRRHNADGAMEYWLEPAELAEVRKQAGVSDPYWPPPGWKKGDDNSLWV	439
SW1	VFCNSILRPELRSEARKHIGDTGLLDHLLKHMAGKVAPEGQRRFRMRKHADGAMEYWLESSDITHRKQAGVSDPYWPPPGWKLGDNP---S	403
OsAM1	GDILVKKVEELAEVGVKREIEQLSNLVQLEKETKSEAESKSSRKEKYQLWKANEKLEKQVLSMKDMYEHLVQKKGKLRKREVSLRDR	538
AM1	GDILVKKROVEELAEVNGVKRMEQLLCKDDGDFGAEPRDYSSLKEKYQRAWRANEKLEKQVLCMKDMCENVVMNSELKREVSATREK	527
SW1	QDFVTCAGIIRDIEELASLKRLLKRLAS-----KKEEEELVIMTTPNSCVTSQNDNLTPAKELIYALIKKRYIEEQLIIGET	483
OsAM1	YKLVLEKNDKLEEQMASLSSSELSLKEQLLPRNGDNIMRRERVEVTLGKQEGLVGEPHYDGDRISSQADAVVYVVEPKTARKSSFR	631
AM1	YEHVADKNDKLEEQVYLSLSSFLFSDLVVA-----LKLRLAPSEA-----VPRTALFVASGE---MTGVVIGSEDAERSSFRV	603
SW1	LKRVEMDMGAKKTVDENYPKKPDSTIFELLESPFQTLLEGELK-----VNGNQITESPKNREKGRKHDOQERSPLSLISNIGFR	568
OsAM1	CKPQCFNVMRHMASGTSVAISCEGSSCFVNSGFEQ-LFRSSSCPSGPGGLPSSRAAEVYVWSP-LDEHYVARGGNIPFANSTNAFA	722
AM1	CKPQCFNLPMSASC--MTIGRASSTCFADATEGPGIIPRSTSPSP--GLPSSRGEVYVAASGLDEHYVFGAHSSTPSSASTNDAAK	692
SW1	CRFVEMDMGAPALAAAIDNASSP-----SHRQVYVSPFPVRELAAKRPLGLT	618
OsAM1	AKLPPPEPTSELCTRALT-----LAFVPAIHNHSGLLRHHDSSEFSSAPCG--ARKMVTLEFGCRGISVVGTELALATPSYC	803
AM1	LQNS-LPSFRSPLCPQLRDTVTAAASLFSQKRLMHFSGLIRRDVDFSSSSGACGSGLLEKRVLEFALAGSISAVGTELALATPSYC	780
SW1	FPFPIIEEAPKNLFNV-----	635

Supplementary information, Figure S4 Alignment of rice OsAM1 with SWITCH1 of *Arabidopsis* and AMEIOTIC1 of maize.

Black boxes indicate identical amino acids, and gray boxes indicate similar amino acids. The red box indicates the position of the amino acid substitution in the *Osam1-1* allele.