

osa_Os12g0515400	MATSTSAATAPITCHHLGLRIRPLRLPSLRPIRSPSPSISLSRPTPLTPS	50
nta_107785134	MASIALTSAVNLRRLRPTPSQKSHLFSPQSLQSTQISKKTSPSFTLSFKNPILNLEKSLNLGKRS	63
zma_542560	MASSTPASPLTCHHLGSGVGRPLRPLSLISLRRSSSSSKPTSLSHSLPSKHSLAPPPAASASSRRGLTPVPASASAFAA	80
gmx_100793559	KASVALTTTALPLSLRIRRNNTTTLKPNRHASISIKPNLHASISSFPNFSLK.....KPHL	55
ath_A15g12860	KASIALSGSCSLAFPIKSRSLSLRPPSSSINLTPIRSIDSRFSILKSLPL.....VSLRRRS	59
sly_101250955	MASIALTSAVNLRRLRPTPSQKPRISITQSLHFTQTSLKSTNLGKSLNLGGK.....RLNLEK	57
consensus		
osa_Os12g0515400	PPRHRFALHASASAAPAPPPSOPPKPVLOGAAIKPIVAVITGCGVLTWVPEEDACVARNAWQLLSIFLATIVGIITQPIPL	130
nta_107785134	NLDKPRSVIILKASASTTPSAIVPPQQFVQGAALKPIITASTATGIIILWFTEPAPACVIRNAWQLLIATFLATIVGIITQPIPL	143
zma_542560	PAPDPVPVPAPPAPAFAPAPAPPPKKPALQGAALKPIITASTATGVLILWLPPEACVIRNAWQLLIATFLATIVGIITQPIPL	160
gmx_100793559	ISTRKPSAITVRASPASITPAPAPVQVQGAALKPIITASTATGVLILWFSPEVACVIRNAWQLLIATFLATIVGIITQPIPL	135
ath_A15g12860	STIVKASSTIVASASSSPTPIVPPAPVQVQGAALKPIITASTATGIIILWFVPEECVIRNAWQLLIATFLATIVGIITQPIPL	139
sly_101250955	SRFVIVKASASASASSSPAIVPQQQPFVQGAALKPIITASTATGVLILWFTEPAPACVIRNAWQLLIATFLATIVGIITQPIPL	137
consensus	qgaakpl a i t g w p p g v nawql l i f l t i v g i i t q p i p l	
osa_Os12g0515400	GAVALILGLCAVLTITLDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGSRVAYAFVSFSGSSSILGLGYALVFEALLA	210
nta_107785134	GAVALILGLCAVLTITLDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGNRIAYQVSIIFGSSSILGLGYALVFEALLA	223
zma_542560	GAVALILGLCAVLSRLTDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGSRVAYAFVAFSGSSSILGLGYALVFEALLA	240
gmx_100793559	GAVAILGLGVSLTITLDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGNRVAYQFKIFGSSSILGLGYALVFEALLA	215
ath_A15g12860	GAVALILGLCAVLTITLDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGNRVAYQFVRIFGSSSILGLGYALVFEALLA	219
sly_101250955	GAVALILGLCAVLTITLDFAFAFSAFGDP IPWLIATAIAFFFAFGFIKTGLGNRIAYQFKIFGSSSILGLGYALVFEALLA	217
consensus	gava qlq vl tl faaafs fqpdpwllalaffa qfiktqlq r ay fv fq sslqlay lvf ealla	
osa_Os12g0515400	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	290
nta_107785134	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	303
zma_542560	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	320
gmx_100793559	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	295
ath_A15g12860	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	299
sly_101250955	PAIPSVSARAGGIFIPLVKSLICVACGSNACDGTBRLGSLWMLTFCQTSVVISSEMFITAMAANPLSANITLSTINQIIGW	297
consensus	paipsvsaraggiflplvk lc acgs gdtg lg wmltfcqtsv s mfltamaanpl a l i igw	
osa_Os12g0515400	TLAAKPAIVPGILSTIVLVLILYLYTPPEVKASPDAPRIAKERLEKMGPMSSKEETILAGTILITVGLWIFCGMLNVDAYS	370
nta_107785134	MDAAKPAIVPGIVSLIVLVLILYLYTPPTVSSPDAPRIAKERLEKMGPMSSKNEITLITVGLWIFCGMLNVDAYS	383
zma_542560	TLAAKPAIVPGILSTIVLVLILYLYTPPEVKASPDAPRIAKERLEKMGPMSSKEETILAGTILITVGLWIFCGMLNVDAYS	400
gmx_100793559	TLAAKPAIVPGILSTIVLVLILYLYTPPTVSSPDAPRIAKERLEKMGPMSSKNEITLITVGLWIFCGMLNVDAYS	375
ath_A15g12860	TLAAKPAIVPGIVSLIVLVLILYLYTPPTVSSPDAPRIAKERLEKMGPMSSKNEITLITVGLWIFCGMLNVDAYS	379
sly_101250955	MDAAKPAIVPGIVSLIVLVLILYLYTPPTVSSPDAPRIAKERLEKMGPMSSKNEITLITVGLWIFCGMLNVDAYS	377
consensus	wakaaivpgl sl vp ly iypv k spdap la e l kmgpm e im tl ltvglw fg l dav	
osa_Os12g0515400	FAILGLSVLILISGVVWKECIQEAFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	450
nta_107785134	FAILGLSVLILITGVVWKECIQEAFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	463
zma_542560	FAILGLAVLILISGVVWKECIAESFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	480
gmx_100793559	FAILGLSVLILITGVVWKECIAESFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	455
ath_A15g12860	FAILGLSVLILITGVVWKECIAESFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	459
sly_101250955	FAILGLSVLILITGVVWKECIAESFAWDITITWFAALIAAGYLNRYGLISWFSQTVVKEVGGIGLSWQISFGILVLLIFY	457
consensus	aaigl vl qvvtwkecl e vawdtltwfaaliamagylnk gli wfs tvvk vgglg swqlsfg l v l l y f y	
osa_Os12g0515400	SHYFFASGFAHIGAMFTAFLSVSSALGTPPLIAFVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	530
nta_107785134	SHYFFASGFAHIGAMFTAFLSVASALGTPPYLCAVLVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	543
zma_542560	SHYFFASGFAHIGAMFTAFLSVASALGTPSLFAFVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	560
gmx_100793559	SHYFFASGFAHIGAMFTAFLSVATLGTPTPFCAIVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	535
ath_A15g12860	THYFFASGFAHIGAMFTAFLSVSTALGTPPYFAFVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	539
sly_101250955	SHYFFASGFAHIGAMFTAFLSVASALGTPPYLCAVLVLSFLSNMGGITHYGIGSAPVFYGCANYVPIAQQWGYGFPVLSIVN	537
consensus	hyffasgaaahigamftafslv algt p a vl flsn m g g t h y g i g s a p f g a y v p l a q w g y g f s v n	
osa_Os12g0515400	IIWLGLGCGGWAKMIGLW	548
nta_107785134	IIWLGLGCGGWAKMIGLW	561
zma_542560	IIWLGLGCGGWAKMIGLW	578
gmx_100793559	IIWLGLGCGGWAKMIGLW	553
ath_A15g12860	IIWLGLGCGGWAKMIGLW	557
sly_101250955	IIWLGLGCGGWAKMIGLW	555
consensus	iwl g g w w k g l w	

Supplementary information, Figure S6 Amino acid sequence alignments of SOM787.

Amino acid sequence alignments of SOM787 in *Arabidopsis thaliana* (ath), *Zea mays* (zma), *Solanum lycopersicum* (sly), *Nicotiana tabacum* (nta), *Glycine max* (gmx), and *Oryza sativa* (osa). The red line indicates the dicarboxylate transporter domain. Dark blue and cyan shading indicate 100% and > 50% conserved amino acid residues, respectively. The red, blue and green triangles indicate the mutation sites of *som787*, *som812* and *som2073*, respectively.