

S2 Table: Sequences of analyzed SAC components

Phallusia mammillata:

Mad1:

phmamm.CG.MTP2014.S241.g05985

MKVSVDNTDLSNTFFFMFVLVACGFEHVDVNSRQLRNTNLSGTSNTIKENTSKASDVMMRV
KMKQIEAAHASSERAHVKANIELESKFEQLTAQNKVLKDKADSLQGVNSLTTKLLDMQD
EVKQMRKDKEAEISKWENSYLHLETLKQEADSRLSEEMMMVTSQNQQQLSEHNLMLQSQNN
ILNLKCEEHYTHMDQYKRSLEASQTVLKDYQETKSKLARSEQQVNRLKQELATLQDTKTL
AKTLKEEMNRLRHIEVEFKKIHEENYLLRQNNDNFALLQEKLHVESKLRARAELOCANVP
SLEVENNMLTQRIEQLQNMVTKNEHSSLQIELSSLSQKLSTAQEEENLNLKAELSTLRNH
NIELNSSIKAIDQKLTEKSEICASLNAQLLRKRAGLLAKERDSIREILQSYDAELTMT
SHTTQLNKRIENEAASNKRLYHRIEELEDENKKLAAEEAMKNRLGIKTLESQKELKETPDS
PMVSQTMNEENSVLREKIQKYEAEERPTLIEKIEQLEAWIEQGIKGDYNPENTKVIHFAM
NPADLAHQSKQDVANLKEECIRLRQKLREAADGHEVSVVAEVESLKLAAQEEASRAELRNQ
RLKEVFTKKIQEFRQACYSLTGYRIDTLNDSQFRLVSIKAAETELCTDERERRNEVIGDG
ILNYSDBGIGEFALASPKQYSNVFKCYFSESFQSTNPGIAASSKGCKF

Mad2:

phmamm.CG.MTP2014.S64.g02288

MAAAKQLNKITLKGSAIVSEFFFFYGINNILYQRGVYPPEMFKQEKKYGLTILVSTDETL
LTYLNDNVLPQLQEWLEKGAVKRLVVVIRESETNETLERWQFEIQCESDKSENGKPKATKS
KETINSEIRAVIRQVTATVTFLPLLEPCPSFDLLFYTDKNLEVSEKWEDSSPCLIPNSEE
VKLRSFSTSVHKVDGAVSYKFSM

Bub1:

phmamm.CG.MTP2014.S849.g12351

MPLTNTGASVLTDSVYGGDNEVSEINGMFQMLTNTGASVLTDSVYGGDNEVSMPLAEP
VDKPAFEIFCDEDEDEQQMPLKFNIFKDDDKSEDSENIPTPGYVSPKRHNLSGILQPAV
GFELADPDEDSQEEEDDNIVGVEPLLTVEPAPTFLLDDVTIAAGQNLPGETNLPLNQLQDI
PCTSSNNLTNSYQANRSAMSTTNKFDDSIQINFGNRNKISAESTTYWQGSaihDVTkQDV
IEKTVNPPQEVtSEANCtEIGNQQOGVKKLSPILEASyEYEKSVQSRSLTSSETDGOAS
VAITTTGKSFihPPTINrkPLGELSAITyDPMKTSTAPTMyDMEPEFSSfMPHQGISKLQ
LHNDNDETTTSYSPMCLPVLNNTSIHPiELNPDAIMEDELCDQMSTSLQIAPPPDHsvFD
VTTFLSETNNTLTVSGRLTIVEDPWDEELLNRLLPQFAKNLHVihGKTPVARKGStLNLG
DTTYHLADMLGRGGFAKVYKATVEGKSNTIAAVKIQSPPHIWESyIVSEAKRRcNSDSFR
SSLLQIHATSVFPEASfIVSEfLSGGTLLEFVRDCAVHSRVIDDIDITfKVMKIVNSLHE
AGIihGDIKPDNFMVVSERDPCKGRLGPLAPVLKLIDFGRAIDMKAFpAGTAFKkNCGTS
GFVCSQMMDKLPWNYHIFKLDSFQQTDFHGLAGTIHVVLyNCYMTIiKQNSGEWSITKSF
PRGNRHLWSSFFKSLLNvSTPKDELpFVDSPLPNLLQlFGEAAT

Bub3:

phmamm.CG.MTP2014.S36.g01423

MSNEFKLNECPKDGISSVKFSPSTAQFLLASSWDVSVRLYDITENTCRFRYDHKAPVLDC
CFSDSVHAWSGALDGSLLMYDFNMGRESLAGMHNAAIRcVEYcSETNVIATGGWDETVKL
WDP RNKSSIGSYSQPGKVYTMSVCGHRLIVGTSGKSVVVWDLRNMGYVEQRRESSLKYQT
RCIRSFpNKQGFVLSSIEGRVAVEYLDPSAEEQKKKYAFKCHRIKEDGIERIFSVHTIAF
HNRYNTFATGGADGFVNMWDGFNKKRLCQFHRFPAPVSSVAFSDDGSVLAVAASPLYSSD
LEPNRDVEDAI FIRHVTDaETPKK

Mps1:

phmamm.CG.MTP2014.S420.g08523

MFKENECVAESDKENTNTLNVTGKVTSNLKEVGDDEPKWNQILQDCLKLDNTLHKKRMLK
QFFLQAKKNIDPAVHRRSETYARILAQEALFISLSSRQDAGVAFRFATDTCRPVFFIHVA
FAQYEVDSEGRLEKAKKILELGKMLPDSKEISDAIKRLKSNETNLGLKNDPMFNSSVLRD
NTNSMSTPKVAKYDFGDSIMKIFPTSKHSLTDTCIKSPIRPAHIKRELEALDFPESPRSS
VTKPSFFGITTPSPRSLFSVTKSLANRHALQTKQEHLTTSVQKPMMTSKTNGQRSGPVN
KPRRIPCALQPENDQKHKSEYPMVFPLASEVGATPTDNRIEKVFPTQPVSQVSASPTRPT
FPPPIRQPQPNLAAHAIKTDEIASWMNNVQVLRIRHHKSYIVLKMIGEGSSKVFVFDVA
AKQIKAVKHVSLKNCDAAVKKGFLDEVKFLQLRNNPNIVHLYTYELTGDDLYLVMECGS
TDLSKSLKRNNGRLEPEYVWYFWKKMLAALNTVHQHGI IHLDLKPANFLIVKGTLLKIDF
GIANSIQSDVTSVFKDTMVGTLNYMAPEAIVDMSSGGDNDLKFKISPRADVWSLGCILY
LMMYGRTPFQHINHQIRKLSAITNPNTRIEFPQYGDKRLVQIVQSCLMRDAKRRPTVEQL
IKHS

Ciona intestinalis:

Mad1: XP_002126990.1 (Gene model: KH2012:KH.C9.233)

MEQRFALGMPDNTKVMRIMGEFHFMSAAKENSMMQSSHISAIPFSLPSDDDHKQSTALQV
SNVLSKVKLKQLESNHSSEKLLIQRVTNLESKIKELEMEKQILHERCSKYQVQVTDLTQOS
IDLSDKVKDLEQTKHEEILKWEESAMEIQRLKQONEQKFAMQTQMLNERINDLMSQKLTMEK
EEQLFEINQAELCSQVEQYKSQAQAAAYQLQAKYDEKTNQVLQAEHTIHELKMRLENVQEAEN
MAHILKQDMNRLRQLEIDVSHLSRENSNLKLNQENCALLKEQLIAANTKLQRLEEKNEIPK
IVAENEALKEKLNKTQNTANVDDNVSLQNHSSFNAKLEKEIETLKEQLATSKRSLEDR
KNAAEYEIKFTEQTEAISLKAQLIRLKKRASLFAYERDSIRSLLOQTYDAELTMTSHTTQLN
KRLDNMTSVNKKLHDRIVELELESQRHVEDTLRHKLQVKQMLGGSLSGQKQEEISSVL
EEKSNEVLALKEKITSFETERNLMEKIANLEAWIEQRNLNGDYNPDKTKVLHFTMNPADLA
HQQSKRDITELKEQNAKLQLKLRQLEEGHEVSMSEIEFSKEAKTKLNAAELKNQRLKEVFSK
KIQEFRQVCYSLMGFQVVCSSDGKFKLLSMYADSETDCLEFEVKSSGEIELLETEYTKTLTD
LISLHLHHQNSIPMFLSALTVNLFQQTMMAD

Mad2: XP_002131760.1 (Gene model: KH2012:KH.C14.279)

MASNKQLNKITLKGSAIVSEFFFYGINNIIYQRGVYPPEMFKQEKKYGLTILTTDPNLLT
YLNENVLPQLTEWIEQGVVKKRLVVVIRECETNETLERWQFEIECQSDGKENSNPKSKDISVI
NSEIRAVIRQITATVTFPLLEVPSCFDLLFYTNHDLVAPEHWEDSSACLINNSEVVKLRSF
STSVHKVDGAVSYKFSM

Bub1: XP_026692557.1 (Gene model: KH2012:KH.C11.241)

MSNEITWEVCKENVQPLRHGRNVSYLNASLQTSDEISHSLMKQKKMLEEEILTDGNLHDPID
PWDYFKWSQQHFPEGKEDLKNFLQKYIVKFNQSDRYRNDPRYVNAWLMSQIHDDAPTTFA
YMKSKSIGINCASFYIMWAELEKSGNIKKAHSIYELGEENDAEPTELLSKMRNAFQLRAAR
SISTKLNENEDDKNKSELDSTRRQRQALGSLDGRGKHKVLGTTRIGNTTAGVVRSQPRTSFKE
NRSSTKFKIFSEDENNEQHCVGNFASMPNNQINSKENTTAPSVWKGAEVQLNRNKTTTAISS
SNKPFTICQDQVPSQEQATPLASRKLKSKSVEVILTERKWKKHEESDFHRAIREQHGDADHN
VVRMYPVEKVYSAVGEFQPEEILAACWLKQREEEQKRLQRQLEEQKQIVESERREIEAQ
RAYDDKVNQLKHREQQLRNLLQLFKDKEMQIEDKVEMVKEEQEMTIALHKVCSQLQHMQQKN
NIVEVATSSQAIQGGKSLEDEVMECKPSSPTVCTKEAMGEIFGMFQKPLNTDVNVTKHEPS
MMQSQSFSIYCDDEMCKDTPVKFDIYEDASDNSENIPTEYKQAPKREGLSGILQPAVGFKL
EEDDFDDGKDEDERLFDVYPLCDDNQSLYLDRTVARAPMEKTTKNTEFPESFLNTLSH
NPPSLQSTMHVNTNEIGDDFNNPHFSAESTTRWGGGATTATTTEEGVVKLSPILEATNEYEKS
MSTKYQSGLVSLIPSMHRTNVSTAATEKFKFGAIGLEDDITYPEQSRLVDSVIDESQAIDY

DFKDLCELMSTSLCKTTIDLMPDGIGDLSKPSLGLNIIPDPWNDQLLQGLIPSTLEGVIVA
SESKVFRKGSVDVRIGNETYHLVKEIGKGAFKAYKATMVSQDEVAVKVQSPAYKWEIHMLQE
VRRRLEAKGHDVCKDYMTIMTAAVFQNSSCVVTQYLPSTLLDFLNTNKNNTVDRENIALQI
FHLVHSLHAIGVIHGDKPDNLIANVSNRGPAPTLRLIDFGRAIDLSSLPNTAFTDNCGT
SGFVCSQMKTNPWNYHIDFNGVAGTLHVLLHSAYMKTMLNNKQEWVTTKKLPRWCDEKWSS
AFHDLNFPPTNDWCPSLQDSPLPHLIQLFDA

Bub3: XP_002129118.1 (Gene model: KH2012:KH.C5.394)

MANEFKLNCPDGISSVKFSPSTSQFLLASSWDMVRLYDVTENSQRFKYEHKSPVLDCCF
SDSVHWSGGLDGSMYDLNTGRETIVGRHNNSIRCVEYCSDTNVVVTGSWDQTIKLWDP
SHNNIGSYSQPGKVFTMSVCGDHIIVGTCGKSVVWDLRNMGYVEQRRESSLKYQTRCIKSF
PNKQGYVLSIEGRVAVEYLDPSVEVQKKKYAFKCHRIKENGIEHIYSVHAI AFHQRYSTFA
TGGADGYVMWDGFNKKRLCQFHLPAAVSSLAFSNDGSMMLAVASSPLYGAELSPSSNGEDA
IYIRHVTD AETKPKTSSGLA

Mps1: XP_002124942.1 (Gene model: KH2012:KH.L149.3)

MASQFTTEGLGDNPKWFSMLQSCNLQNGEKNLLKQIFVTANRSLTAEKHKTS E IYAKI
LAEAAAFVGSTNVNKGRNMFKHAVYVCR TIPIIHLTYAQFEVRNGHFDKALHILEFGKMVTG
CKLLFEQAI SKLENGYVKFNSTLSMDLNQATPLKNI TNTECNEKVTECQKRSYTD TALKTPP
SYRFRALDTKY YDIKTPSPMLKMSPTNTFPNRFTFNMP TSIKSSVTNFTPTPASATKT TG
LTKGPQ RVLRLSKSLENADNDKEHDIGTHQTPYSLKHHPLVSNVEPQIPDSPKPPVIIDPS
PINPPTPIIPLKKEIFPYP SKQTPQPKLTPNPPKNLGT LNPEIRQNPSKSTPMKTD TSNLNH
NSMPPPKFPFPQ RVPCKPAEPQNGLHTWFNPNSAICVNNKH YLVIRELGE GGS SKVLQVFC
AETKAILALKKVSLKDCDESTKNEFTNEIEFLKLRNNPHIVHLYDFELTPDFIHLVMECGS
TDLAKLLHSHKTQNSRLEVYEI IYFWKMLLAVQTIHKHGV IHRDLK PANFLLVKGNLKLID
FGISNAINADATSVIKETQCGTLNYMAPEAILDMSGGYNP DSPKFKI SPMA DVWSLGCILYS
MLYGCTPFQHIKHQLLKLNAITNDQHRIEFPFKDENFVKIVQKCLKRNPKHRPTVDQLLQF
S

Branchiostoma lanceolatum:

Mad1:

>lcl|BL00512_evm0

MMGDFNSYLAEGRRQKSNS SLLFDMGDTTAGKGD LTMQLD TTRDDSTVQWDRPETAKRNRVR
RLEQTQAI EKEGELLWTRSKVAKLETAITQLTTEKKRDKIEFEKGQETFRM QYERDLEQVND
LRHKLEFLVKEEKQAKEELAEERK KLTTIKTQMEKRIMVLQREKLCVQAE LDELREASRSQI
SNLRNQVKRLEAELEMSDSELAE AQQQVQH HQQAQARLEQVQQLQEDRIRAVTAEHKVKEL
ELQLNQVQESAAMAKLMSTRLSRYEQLEKENK LLEQNKFYRETS ENNQLLKEKLLSLETKY
GRAEHSNLELIKEVEDLRGRLKQWEGIDPSGGQIPRSPAEIAKWIAELQRKEVLLTEKTGQL
TSSARDSEAGQKAATGRLREVESQLFAATEKTNQADLIKKLQRRLLLVTKDRDSIRNILVS
YESEVTRASSDDAMLQRLQDSEEA AQRYQRHMASLEEEMQRVNAQASEERIKAHKLEVELSQ
MKTQTPAPANTISSQEV TMLRKKVEDLEKDRQKLLEEKEILEARVEQRHLQGNYP TTKTKV
VHFGLNPTALRRQRHQEELEKLREECEKLRQRLRAAEEGGADVTASILLTPSSKEMEDLKK
QLTTAETKNTRLKEVFQQKIHEFRQACYMLLGYKVDVVKDNNYKLM SMYAERQEDCLMFQMV
PGGELQ LLETEFSNSQAVMMLVDLHLKTQHSIPAFLSAL TLDLFSQQTIA

Mad2:

>lcl|BL13880_evm0

MAGVLQAAKNSITLKGSAEIVAEFFSYGINSILYQ RGIYPPETFSRVQKYVTGHDRQRAEDV
LKQYWL LDKTVEKLVVVVTSIDTQEVLERWQFDIECDKMTDDSKPREKSQKEINDEIKAVI

RQITASVTFLPLLEENCSDLLIYTDKDLQVPETWEESGPHFIAKSEEVRLRSFSTSIHKVD
AMVCYKNAD

Bub1:

>lcl|BL16332_cuf4
MDPTENSWELSKENVQPLRQGRKIANLTAALQPVNGHDGGLTRVQHEKQAFEELRMYSGDD
PFSVWDRYIKWTEQNYPKGGKDGSLSTLLERCLLFFKDDKRYSDHRYLQAWIKFAGMTNQF
VDIYSFLHDQAIGAQVALFWEAWAELEQEGDTKKADAVYMEGIQKQAQPVDLLVRKQKEFQ
ARVTRATLEGGVVQSADVSGTEAQRVTLGGLRGHGKKHQAPVNRGTGAATKVYSSGLGVKPCA
PPQVGQAFSVFSEDNPQDQVIPTPTGEWTNPPLPRVTSRENTHKPGKWTEAKVSQKAVPAIP
FKAVSMNASSEFSIHVEEGAAQPQPTPQKPIEMGTQVLSARKPEKSLNPLRNMYPPEFEDP
NKIPKYCKKFVYTGLEEFQFEELRAARHVEMEKKRKMEEMRRQEEQRREMEKQHQLMLAQO
RQQLQOMQQTFOEQQLALQOERKOMMEQCRQOQLRERAEEMERLLVDRMRDTTLESAQLPGAA
PDGEPQDMPDASHAAQDSHIMPDSHAMQNSHVMQDSHAAQNSHTLKGSHVVQDSHIMLDSRQT
MQDSHIMQDSHAAQENDPSTAAGLTESHREHTVTKHLNFEESLASGLQPSVVSAMAEIEDYK
TDVEMVEPTPVKTAPQADTGLRSGQFLLSSATPASTGKMVTSREQLVKTNPNTSTCSGPTP
STTPGRRPITDPSPTINTKAAMMELGFFRDDIGFGAVGGSDGFEDMFAAGPSGGTASSGLS
FSAPQAQTDFKGFITIFDESKDTGLEDRMDKDNIVLEDQENPPGGYQTGAKRRGLGVLPQ
SQGIPVEEIKEVDDLGIPEFADDNPDMTFASTGNQSSFCMARMASPTFNRTGPELPELPA
SSIRPVHNSTRKALGMLIISTEDLAEAGGSGAGRVSAAESTEETFDMTVGNRPAAALSPIME
NSSEEKQVSTDHGSTDSAPSLSVAMQSTSCADPSSESEAVATLNSPAEDEVFVTDVNPFD
EVSLLAKVRGSLTSHQEQEEDGHMPQIKPGVAINLGTELYHIDKLVGSGAFAKIYQASM
LDADDLTDLEGERKVTLLKVVQPGCPWEFYINSQVHERVNRQLQDPMDIKPSLMSIDAMHVFSD
GSVLVNEQHSCGSLLDIINLYRTAGKKMSEVMVVFYTLILEYIVEQLHRCHIIHADLKPDNF
LIRDGFEDKTECLFSGELRGLKLIDFGISLDMELFPNNTTFRARSNTSAFQCIEMQTGKPWS
YQADLYAIVSTVHCMLFGEYMKAYYEGGRWKITQTPRTHDPVWRRFFDTFLNIPSCDELPS
LSYWISEFHQCWEEKKTFDKEKWAQYTMFEKH

Bub3:

>lcl|BL20329_cuf2
ICQSYNYCPTYLHATNMPTVAETPNEFKLNCCPTDGISAVKFSPTSSQLLLVSSWDCSVRLY
DVSGNNLRNKYTHSSAVLDCCFFDPVHPYSGGLDQMLKTCDLNLSQETVVGNHDAAIRCVEY
CPEVNVVITGSDQTVKLWDPRTPCNAGSFSQPGKVYTMAVTGDRDIVGTAGRRVLVWDLRN
MGYVQQRRESSLKYQTRCIRAFPNKQGYVLSSEIGRVAVEYLDPSPEIQKKYAFKCHRIKE
DGIKIIYPVNAIAFHSLHNTFATGGSDGFVNIWDGFHKKRLCQFHRYPTSIAFLAFSHDGSV
LAIASSMYEELDVEHPEDAIYIRNVTDQETPKP

Mps1:

>lcl|BL08039_evm0
MVEKSDRQIMSRLKSLQSRLOSISYRDEKDDTNNTGNLTGTGTYNLTDHTSWIDRISAAGNK
PSDWLEFLTQAQGRTSFSSPQARYTYLLTVYDKALHHPVELCRRDESYAKILIQLAHIKGD
HNEEDGQTGFKFARVNAKTFVHVAQAQFELSRGREEKAQSILQKGLDVGAEPTEMLNTAL
IRLGNKEKLLMEDKENVWVICYPDSVQPSFSAAKPKGPALTKQPPQNQTTPVDPSPSLVSM
STIVFQKQGGCRNDSGGSSSLDENDTLPLLWGHREKPPQLSRSTWSATKLPGRELHTPQSQT
QRVVTSHTEGPNANKRQPARVPLRVKRSSLPKLREMSTEDVNDDSDDTDCFLGVKPLKNIS
PPTGMDTLAARAKPPLPFTGRKVSPESENTNTNDSKAFKGLSLCKFSKSSLLSHTTPRGQ
MLSKETSPTENTASSKPTEPLRETSKAPLVSNPGHHSTHKNPITDSARKAQSISPTSTVVSF
PERQPPCAKVPSASDTADAATVAFNSMQVPGAQASHMHIPPVSSNLPPGNKTIEHLPSQHAH
QAPKMLDSLKSVVPEVRSNSLHTVGISHEVSGGQGSVQLGTRSGPATGPTVVPKNSQMPTPN
IVNQNTMPGFFTPSASLPGAQQHVQPHSQHFQOVAPPPQPFATPRMPCAPTERSDVICVK
GKPFRIISIIGKGGSSKVYQVYDEKGVYALKLVNLEEGDETTVQGYINEITHLSNLQHSR
VIKLYDFEVTDERIVLVMEKGSVDLATFLRNKKKQQGSIAADDVLWFYWRHMLEAVDTIHRQG

IVHSDLKPANFLFVDGDLKLIDFGIANAIQSDKTSVIKDQQVGTLYMSPETIREYNPAQYR
DGNSKKLFKINCRSDVWSLGCILYYMVYGKTPFQHIPNHFAKLQAIVDPNYEIQFPPIKNHL
LLDMLKKCLIRDPYNRPSTADLLAHPYLNSERSGAKEQPCPAAPALPMTADQIQQLLTQLS
QAQSMSPNSISTVSKGLAAQLQSGQAPDL SAVLKKRQGPSQDKENLPPQHLLRKGPGCTLQH
ALPRPPSEHTLGRP