

S2 Table: Sequences of analyzed SAC components

Phallusia mammillata:

Mad1:

phmamm.CG.MTP2014.S241.g05985

MKVSVDNTDLSNTFFFMFVLVACGFEHVDVNSRQLRNTNLSGTSNTIKENTSKASDVMMRV
KMKQIEAAHASSERAHVKANIELESKFELTAQNKVLKDKADSLQGVNSLTTKLLDMQD
EVKQMRKDKEAEISKWENSYLHLETCLKQEADSRLSEEMMMVTSQNQQQLSEHNLMLQSQNN
ILNLKCEEHYTHMDQYKRSLEASQTVLKDYQETKSKLARSEQQVNRLKQELATLQDTKTL
AKTLKEEMNRLRHIEVEFKKIHEENYLLRQNNDNFALLQEKLSVESKLARAELQCANVP
SLEVENNMLTQRIEQLQNMSTKNEHSSLOIELSSLSQKLSTAQEEENLNLKAELESTLRNH
NIELNSSIKAIDQKLTEKSEICASLNAQLLRRLKRAGLLAKERDSIREILQSYDAELTMT
SHTTQLNKRINEEAASNKRLYHRIEELEDENKKLAEEMKNRLGIKTLESQKELKETPDS
PMVSQTMNEENSVLREKIQKYEAERPTLIEKIEQLEAWIEQGKIKGDYNPENTKVIHFAM
NPADLAHQSKQDVANLKEECIRLRQKLREAADGHEVSVAEVESLKLAEQEEASRAELRNQ
RLKEVFTKKIQEFQACYSLTGYRIDTLNDSQFRLVSIKAAETELCTDERERRNEVIGDG
ILNYSBGIGEFALASPKQYSNVFKCYFSESFQSTNPGIAASSKGCKF

Mad2:

phmamm.CG.MTP2014.S64.g02288

MAAAKQLNKITLKGSAIVSEFFFFYGINNILYQRGVYPPEMFKQEKKYGLTILVSTDETL
LTYLNDNVLPQLQEWLEKGAVKRLVVVIRESETNETLERWQFEIQCESDKSENGKPKATKS
KETINSEIRAVIRQVTATVTFLPLLEPCPSFDLLFYTDKNLEVSEKWEDSSPCLIPNSEE
VKLRFSFSTSVHKVDGAVSYKFSM

Bub1:

phmamm.CG.MTP2014.S849.g12351

MPLTNTGASVLTDVYGGDNEVSEINGMFQMPLTNTGASVLTDVYGGDNEVSMMPLAEP
VDKPAFEIFCDEDEDEQQMPLKFNIFKDDDKSEDSENIPTGYVSPPKRHNLSGILQPAV
GFELADPDEDSQEEEDDNIVGVEPLLTVEPAPTFLDDVTIAAGQNLPGETNLPLNQLQDI
PCTSSNNLTNSYQANRSAMSTTNKFDDSIQINFGNRNKISAESTTYWQGSaihDVTQKDV
IEKTVNPPQEVTEANCTEIGNQQQGVKKLSPILEASYEYKSVQSRSLTSSETDGOAS
VAITTTGKSFIHPPTINRKPLGELSAITYDPMKTSTAPTMYDMEPEFSSFMPHQGISKLQ
LHNDNDETTTSYSPMCLPVLNNTSIHPIELNPDAIMEDELCDQMSTSLQIAPPPDHVSFD
VTTFLSETNNTLTVSGRLTIVEDPWDEELLNRLPPQFAKNLHVHIGKTPVARKGSTLNLG
DTTYHLADMLGRGGFAKVYKATVEGKSNTIAAVKIQSPPHIWESYIVSEAKRRCNDSFR
SSLLQIHATSVFPEASFIVSEFLSGGTLLEFVRDCAVHSRVIDDIDITFKVMKIVNSLHE
AGIIHGDIKPDNFMVVSERDPCKGRLGPLAPVLKLIDFGRAIDMKAFPAFTAFAKKNCGTS
GFVCSQMMDKLPWNYHIFKLDSFQQTDFHGLAGTIHVVLNLCYMTIIKQNSGEWSITKSF
PRGNRHLWSSFFKSLNVTSPKDELFPVDSPLNLLQLFGAAT

Bub3:

phmamm.CG.MTP2014.S36.g01423

MSNEFKLNECPKDGISSVKFSPSTAQFLLASSWDVSVRLYDITENTCRFRYDHKAPVLDC
CFSDSVHAWSGALDGSLLMYDFNMGRESLAGMHNAIRCVEYCSETNVIATGGWDETVKL
WDPRNKSSIGSYSQPGKVYTMSVCGHRLIVGTSGKSVVWDLRNMGYVEQRRESSLKYQT
RCIRSFPPNKQGFVLSSIEGRVAVEYLDPSAEQKKKYAFKCHRIKEDGIERIFSVHTIAF
HNRYNTFATGGADGFVNMWDGFNKKRLCQFHRFPAPVSSVAFSDDGSVLAVAASPLYSSD
LEPNRDVEDAIFIRHVTDAETPKK

Mps1:

phmamm.CG.MTP2014.S420.g08523

MFKENECVAESDKENTNTLNVTGKVTSNLKEVGDDPEKWNQILQDCLKLDNTLHKKRMLK
QFFLQAKKNIDPAVHRRSETYARILAEALFISLSSRQDAGVAFRFATDTCRPVPFIHVA
FAQYEVDSEGRLEKAKKILELGKMVLPSKEISDAIKRLKSNETNLGLKNDPMFNSSVLRD
NTNSMSTPKVAKYDFGDSIMKIFPTSKHSLTDTCIKSPIRPAHIKRELEALDFPESPRSS
VTKPSFFGITTPSPRSLFSVTKSLANRHALQTKQEHLTTSVQKPMMTSKTNGQRSGPVN
KPRRIPCALQPENDQKHKSEYPMVFPLASEVGATPTDNRIEKVFPTQPVSQVSASPTRPT
FPPPIRQPQPNLAAHAIKTDEIASWMNNVQVLRHHKSYIVLKMIGEGSSKVFVFDVA
AKQIKAVKHVSLKNCDAVKKGFLDEVKFLEQLRNNPNIVHLYTYELTGDDLYLVMECGS
TDLSKSLKRNNRLEPEYVWYFWKKMLAALNTVHQHGIHLDLKPANFLIVKGTCLKLIDF
GIANSIQSDVTSVFKDTMVGTLNYMAPEAIVDMSSGGDGNLDFKISPRADVWSLGCILY
LMMYGRTPFQHINHQIRKLSAITNPNTRIEFPQYGDKRLVQIVQSCLMRDAKRRPTVEQL
IKHS

Ciona intestinalis:

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

MEQRFALGMPDNTKVMRIMGEFHDMSAAKENSMMQSSHISAIPFSLPSDDDHKQSTALQV
SNVLSKVKLKQLESNHSSEKLLIQRVTNLESKIKELEMEKQILHERCSKYQVQVTDLTQQS
IDLSDKVKDLEQTKHEEILKWEESAMEIQRLKQQNEQKFAMQTQMLNERINDLMSQKLTMEK
EEQLFEINQAE LCSQVEQYKSQAQAAAYQLQAKYDEKTNQVLQAEHTIHELKMRLENVQEAEN
MAHILKQDMNRLRQLEIDVSHLSRENSNLKLNQENCALLKEQLIAANTKLQRLKEKCNEIPK
IVAENEALKEKLNKTQNTATTANVDDNVSLQNHSFNKLEKEIETLKEQLATSKSRSLDR
KNAAEYEIKFTEQTEAISLKAQLIRLKKRASLFAYERDSIRSLQTYDAELTMTSHTTQLN
KRLDNMTSVNKKLHDRIVELELESQRHVEDTLRHKLQVKQMLGGSLSGQKQEESSISSL
EEKSNEVLALKEKITSFETERTNLMEKIANLEAWIEQRNLNGDYNPDKTKVLHFTMNPADLA
HQQSKRDITELKEQNAKLQLKLRQLEEGHEVSMSEIEFSKEAKTKLNAAELKNQRLKEVFSK
KIQEFRQVCYSLMGFQVVCSSDGKFKLLSMYADSETDCLEFEVKSSGEIELLETEYTKTLTD
LISLHLHHQNSIPMFLSALTVNLFQQQTMMAD

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

MASNKQLNKITLKGSAIVSEFFFYGINNIIYQRGVYPPEMFKQEKKYGLTILTTTDPNLLT
YLNENVLPQLTEWIEQGVVKRLVVVIRECETNETLERWQFEIECQSDGKENSNPKSKDISVI
NSEIRAVIRQITATVTFLPLLEVPCSFDLLFYTNHDLVAPEHWEDSSACLINNSEVVKLSF
STSVHKVDGAVSYKFSM

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

MSNEITWEVCKENVQPLRHGRNVSYLNASLQTSDEISHSLMKQKKMLEEEILTGNLHDPID
PWDYFKWSQQHFPEGKEDLKNFLQKYIVKFQNSDRYRNDPRYVNAWLTSQIHDDAPTTF
YMKSKSIGINCASFYIMWAELEKSGNIKKAHSIYELGEENDAEPTELLSKMRNAFQLRAAR
SISTKLNENEDDNKSELDSRRQRQALGSLDGRGKHKVLGTTRIGNTTAGVVRSPRTSFKE
NRSSTKFKIFSEDENNEQHCVGNFASMPNNQINSKENTTAPSVWKGAEVQLNRNKTSTAIS
SNKPFTICQDQDVPSQEQATPLASRKLSKSVEVILTERKWKKEESDFHRAIREQHGDADHN
VVRMYPVEKVYSAVGEFQPEEILAACWLKKQREEEQKRLQRLQLEEQRKQIVESERREIEAQ
RAYDDKVNQLKHREQQRLNLLQLFKDKEMQIEDKVEMVKEEQEMTIALHKVCSQLQHMQQKN
NIVEVATSSQAIQGGKSLEDEVMECKPSSPTVCTKEAMGEIFGMFQKPLNTDVNVTKHEPS
MMQQSQFSIYCDAMKDKTPVKFDIYEDASDNSENIPTPEYKQAPKREGLSGILQPAVGFKL
EEDDFDDDGKDEDERLFDVYPLCDDNQSLYLDDRTVARAPMEKTTKNTEFPESFLNTLSH
NPPSLQSTMHVNTNEIGDDFNNPHFSAESTTRWGGGATTATTTEEGVVKLSPILEATNEYEKS
MSTKYQSGLVSLIPSMHRTNVSTAATEKFKFGAIGLEDDITIPEQSRVDSVIDESQAIDY

DFKDLCELMSTSLCKTTIDLMPDGIGDLSKPSLGLNIIPDPWNDQLLQGLIPSTLEGVIVA
SESKVFRKGSVDVRIGNETYHLVKEIGKGAFAYKATMVSGDEVAVKVQSPAYKWEIHMLQE
VRRRLEAKGHDVCKDYMTIMTAAVFQNSSCVVTQYLPSTLDFLNTNKNNTVDRENIALQI
FHLVHSLHAIGVIGHGDVVKPDNLIANVSNRGPAPTLRLIDFGRAIDLSSLPPNTAFTDNCGT
SGFVCSQMKTNPWNYHIDFNGVAGTLHVLHLSAYMKTMLNNKQEWVTTKKLPRWCDEKWSS
AFHDLNLFPTPTNDWCPSLQDSPLPHLIQLFDA

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

MANEFKLNNCPTDGISSVKFSPSTSQFLLASSWDMSVRLYDVTENSQRFKYEHKSPVLDCCF
SDSVHWSWGGLDGSMYDLNTGRETIVGRHNSIRCVEYCSDTNVVVTGSWDQTIKLWDPR
SHNNIGSYSQPGKVFTMSVCGDHIIVGTCGKSVVWDLRNMGYVEQRRESSLKYQTRCIKSF
PNKQGYVLSSIEGRVAVEYLDPSVEVQKKKYAFKCHRIKENGIEHIYSVHAI AFHQRYSTFA
TGGADGYVNMWDGFNKKRLCQFHLFPAAVSSSLAFSNDGSMLAVASSPLYGAELSPSSNGEDA
IYIRHVTD AETKPKTSSGLA

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

MASQFTTEGLGDNPDKWFMSLQSCNLQNGEEKNNLLKQIFVTANRSLTAEKHKTSEIYAKI
LAEEAAFGVSTNVNKGKRMFKHAVYVCRTIPIIHLTYAQFEVRNGHFDKALHILEFGKMVTG
CKLLFEQAISKLENGYVKFNSTLSMDLNQATPLKNITNTECNEKVTECQKRSYTD TALKTPP
SYRFRALDTKYDYDIKTPSPMLKMSPTNTFPNRFTFNMPTSISKSSVTNFTPTPASATKTG
LTKGPQVRVLRSLKSSLENADNDKEHDIGTHQTPYSLKHHPLVSNVEPQIPDSPKPPVIIDPS
PINPPTPIIPLKKEIFPYPKQTPQPKLTPNPPKNLGTNLNPEIRQNPSKSTPMKTDTSNLNH
NSMPPPKFPQVRVPCSKPAEPQNGLHTWFNPNSAICVNNKHVLYVIRELGEGGSSKVLQVFC
AETKAILALKKVSLKDCDESTKNEFTNEIEFLLKLRRNPHIVHLYDFELTPDFIHLVMECGS
TDLAKLLHSHKTQNSRLEVYEIIYFWKKMLLAVQTIHKHGVHRDLK PANFLLVKGNLKLID
FGISNAINADATSVIKETQCGTLNYMAPEAILDMSGGYNPDSPKFKISPMADVWSLGCILYS
MLYGCTPFQHIKHQLLKLNAITNDQHRIEFPPFKDENFVKIVQKCLKRNPKHRPTVDQLLQF
S

Branchiostoma lanceolatum:

Mad1:

>lcl|BL00512_evm0

MMGDFNSYLAEGRRQKSNSLLFDMGDTTAGKGDLTMQLD TTRDDSTVQWDRPETAKRNRVR
RLEQTQAIEKEGELLWTRSKVAKLETAITQLTTEKKRDKIEFEKGQETFRMQYERDLEQVND
LRHKLEFLVKEEKQAKEELAEERKKLTTIKTQMEKRIMVLQREKLCVQAEDELREASRSQI
SNLRNQVKRLEAELEMSDSELAEAQQQVQH HQQAQARLEQVQQLQEDRIRAVTAEHKVKEL
ELQLNQVQESAAMAKLMSTRLSRYEQLEKENKKLLEQNKFYRETSENNQLLKEKLLSLETKY
GRAEHSNLELIKEVEDLRGLKQWEGIDPSGGQIPRSPAEIAKWIAELQ RKEVLLTEKTGQL
TSSARDSEAGQKAATGRLREVESQLFAATEKTNQADLIKKLQRRLLLVTKDRDSIRNILVS
YESEVTRASSDDAMLQRLQDSEEAQRYQRHMASLEEEMQRVNAQASEERIKAHKLEVELSQ
MKTQTPAPAPNTISSQEV TMLRKKVEDLEKDRQKLLEEKEILEARVEQRHLQGNYP TTKTV
VHFGLNPTALRRQHRQEELEKLREECEKLRQRLRAAEEGGADVTASILLTPSSKEMEDLKK
QLTTAETKNTRLKEVFQQKIHEFRQACYMLLGYKVDVVKDNNYKLMSMYAERQEDCLMFQMV
PGGELQLLETEFSNSQAVMMLVDLHLKTQHSIPAFLSALTDLFSQQTIA

Mad2:

>lcl|BL13880_evm0

MAGVLQAAKNSITLKGSAEIVAEFFSYGINSILYQ RGIYPPETFSRVQKYVTGHDRQRAEDV
LKQYWL LDKTVEKLVVVVTSIDTQEVLERWQFDIECDKMTDDSKPREKSQKEINDEIKAVI

RQITASVTFLPLLEENCSDLLIYTDKDLQVPETWEESGPHFIAKSEEVRLRSFSTSIHKVD
AMVCYKNAD

Bub1:

>lcl|BL16332_cuf4

MDPTENSWELSKENVQPLRQGRKIANLTAALQPVNGHDGGLTRVQHEKQAFEAELRMYSGDD
PFSVWDRIYKWTEQNYPKGGKDGSLSTLLERCLLFFKDDKRYSDNDHRYLQAWIKFAGMTNQF
VDIYSFLHDQAIGAQVALFWEAWAELEQEGDTKKADAVYMEGIQKQAQPVDLLVRKQKEFQ
ARVTRATLEGGVVQSADVSGTEAQRVTLGGLRGHGKKHQAPVNRTGAATKVYSSGLGVKPCA
PPQVGQAFSVFSEDNPQDQVIPTPTGEWTNPPLPRVTSRENTHKPGKWTEAKVSQKAVPAIP
FKAVSMNASSEFSIHVEEGAAQPQPTPQKPIEMGTQVLSARKPEKSLNPLRNMYPPEFEDEP
NKIPKYCKKFVYTGLEEFQFEELRAARHVEMEKKRKMEEMRRQEEQRREMEKQHQLMLAQQ
RQQLQQMQQTFOEQELALQQERKQMMEQCRQQMLRERAEEMERLLVDRMRDTTLESAQLPGAA
PDGEPQDMPDSHAAQDSHIMPDSHAMQNSHVMQDSHAAQNSHTLKGSHVVQDSHIMLDSRQT
MQDSHIMQDSHAAQENDPSTAAGLTESHREHTVTKHLNFEESLASGLQPSVVSAMAEIEDYK
TDVEMVEPTPVKTAPOADTGDLRSGQFLLSSATPASTGKMVTSREQSLVKTPNTSTCSGPTP
STTPGRRPITDPSPTINTKAAMMELGEFFRDDIGFGAVGGSDFEDMFAAGPSGGTASSGLS
FSAPQAQTTFDFKGFITIFDESKDTGLEDRMDMKDNIVLEDQENNPFGGYQTGAKRRGLGVLQP
SQGIPVEEIKEVDLDGIEPFADDNPDMTFASTGNQSSFCMARMASPTFNRGTGPELPELPA
SSIRPVHNSTRKALGMLEISTTEDLAEAGGSGAGRVSAAESTEETFDMTVGNRPAAALSPIME
NSSEEKSQVSTDHGSTDAPSLSVAMQSTSCADPSSESEAVATLNSPAEDEVFVTDVNPFD
EVSLLAKVRGSLTSHQEYQEEDGHMPQIKPGVAINLGTELYHIDKLVGSGAFAKIYQASM
LDADDLTDLGERKVTLKVQQPGCPWEFYINSQVHERVNRQLQDPMDIKPSLMSIDAMHVFSD
GSVLVNEQHSCGSLLDIINLYRTAGKKMSEVMVVFYTLLEILYIVEQLHRCHIIHADLKPDNF
LIRDGFEDKTECLFSGELRGLKLIDFGISLDMELFPNNTTFRARSNTSAFQCIEMQTKPWS
YQADLYAIVSTVHCMLFGEYMKAYYEGGRWKITQTPRTHDPVWRRFFDTFLNIPSCDELPS
LSYWISEFHCWEEKKTFDKEKWAQYTMFEKH

Bub3:

>lcl|BL20329_cuf2

ICQSYNYCPTYLHATNMPTVAETPNEFKLNNCPTDGISAVKFSPTSSQLLLVSSWDCSVRLY
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CPEVNVVITGSDQTVKLWDPRTPCNAGSFSQPGKVYTMAVTGDRILVGTAGRRVLVWDLRN
MGYVQQORRESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEIQKKYAFKCHRIKE
DGIEKIYPVNAIAFHSLHNTFATGGSDFVNIWDGFHKKRLCQFHRYPTSIASLAFSHDGSV
LAIASSMYEELDVEHPEDAIYIRNVTDQETPKP

Mps1:

>lcl|BL08039_evm0

MVEKSDRQIMSRLKSLQSRLOSIYSRDEKDDTNNTGNLTGTGTYNLTDHTSWIDRISAAGNK
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HNEEDGQTGFKFARVNAKTFVHVAAAQFELSRGREEKAQSILQKGLDVGAEPTEMLNTAL
IRLGNKEKLLMEDKENVWGICYPDSVQPSFSAAKPKGPALTKQQPPQNQTTPVDPSPSLVSM
STIVFQKQGGCRNDSSGSSSLDENDTLPLLWGHREKPPQLSRSTWSATKLPGRELHTPQSQT
QRVVTSHTEGPNANKRQPARVPLRVKRSSLPLKREMSTEDVNDDSDDTDCFLGVKPLKNIS
PPTEGMDTLAARAKPPLPFTGRKVSPESTNTTNDKAFKGLSLCKFSKSSSLLSHTTPRGQ
MLSKETSPTENTASSKPTPLRETSKAPLVSNPGHHSTHKNPITDSARKAQSIPTSTVVSF
PERQPPCAKVPSASDTADAATVAFNSMQVPGAQASHMHIPPVSSNLPPGNKTIEHLPSQHAH
QAPKMLDSLKSVVPEVRSNSLHTVGISHEVSGGQGSVQLGTRSGPATGPTVVPKNSQMPTPN
IVNQNTMPGFFTPSASLPGAQQHVQQPHSQHFQQVAPPPQPFATPRMPCAPTERSDVICVK
GKPFRIISIIGKGGSSKVYQVYDEKGVYALKLVNLEEGDETTVQGYINEITHLSNLQHSR
VIKLYDFEVTDERIVLVMEKGSVDLATFLRNKKKQQGSIADDVLWFWYRHMLEAVDTIHRQG

IVHSDLKPANFLFVDGDLKLIDFGIANAIQSDKTSVIKDQQVGTLNYMSPETIREYNPAQYR
DGNSKKLFKINCRSDVWSLGCILYYMVYGKTPFQHIPNHFAKLQAIVDPNYEIQFPPIKNHL
LLDMLKKCLIRDPYNRPSTADLLAHPYLNSESSGAKEQPCPAAPALPMTADQIQQLLTQLS
QAQSMSPNSISTVSKGLAAQLQSGQAPDLSAVLKKRQGPSQDKENLPPQHLLRKGPCTLQH
ALPRPPSEHTLGRP