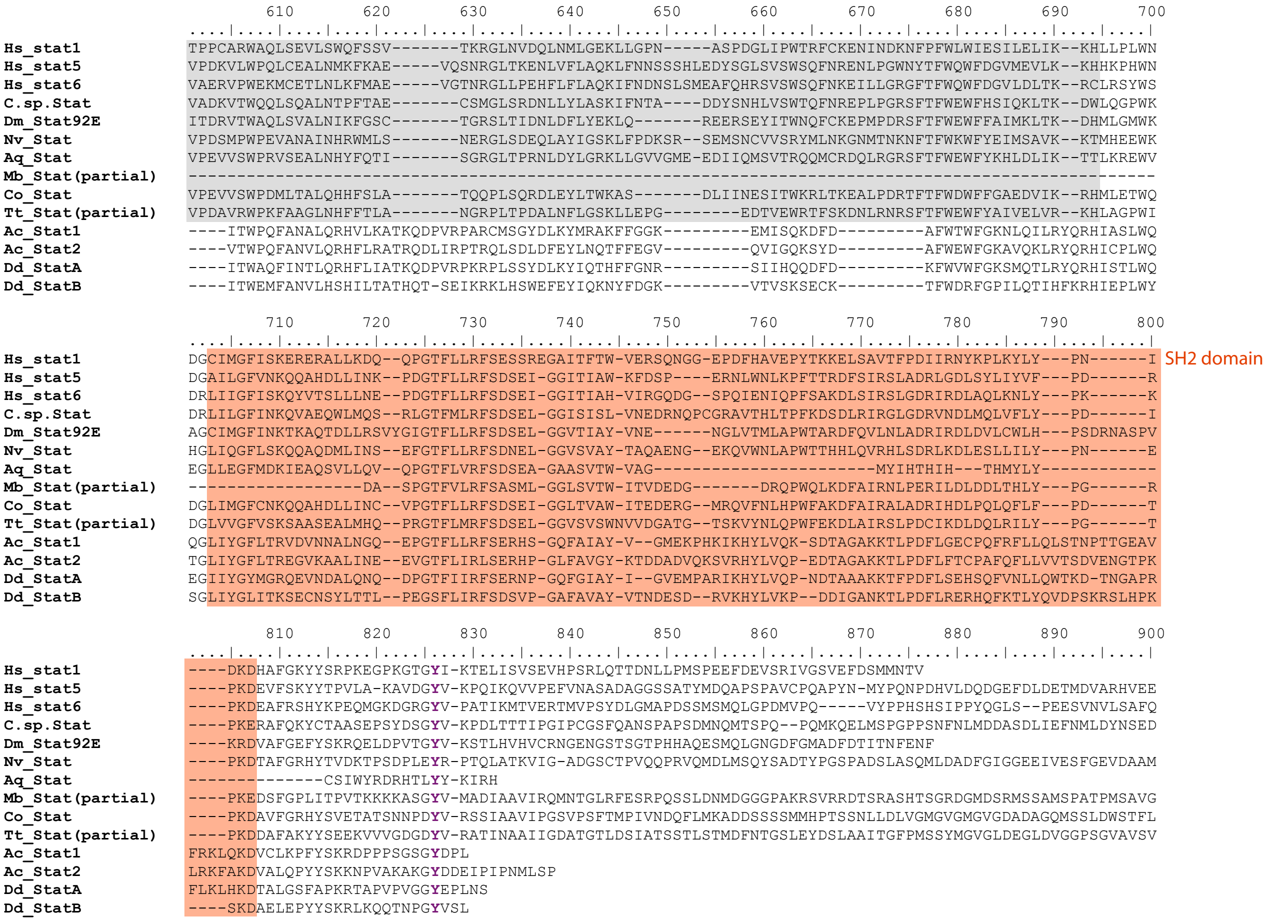
SUPPLEMENTARY MATERIAL 2

```
                           310       320       330       340       350       360       370       380       390       400
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            KIIELLNVTELTQNALINDELVEWKRRQQSACI-GGP-PNACLDQLQNW----------FTIVAESLQQVRQQLKKLEELEQKYTYEHDPITK-NKQVLW
Hs_stat5            KHQKTLQLLRKQQTIILDDELIQWKRRQQLAGN-GGP-PEGSLDVLQSW----------CEKLAEIIWQNRQQIRRAEHLCQQLPIPGPVEE--MLAEVN
Hs_stat6            LLQETTGELEAAKALVLK-RIQIWKRQQQLAGN-GAP-FEESLAPLQER----------CESLVDIYSQLQQEVGAA---------GGELEPK-TRASLT
C.sp.Stat           KFKENCNNLRALQSHILDDQLIFWKRQQQLAGN-GAP-FEASLETLQQW----------CEKLAELVWRNYQQLGQMNQLFTHLPIDLPPEQKDVLPFLT
Dm_Stat92E          TMRRSFMYYESLHEMVIH-ELKNWRHQQAQAGN-GAPFNEGSLDDIQRC----------FEMLESFIAHMLAAVKEL--MRVRLVTEEP-----ELTHLL
Nv_Stat             NLDKHLHHLYKISASLGV-EIDQWKEKQQKALS-GWP-QPQVLEPLQNL----------CEPLAELLWRLYQHCKKVDEMFKPALQKSQEELN-RMQNLI
Aq_Stat             RFLECLEEVGRTHHLVVAVELNNWKQSQRLFNHEDDP-NRNELNSLQHW----------FESLAELLWRLRQLGKQLLITQSRAATPILQQND-QFHTIT
Mb_Stat(partial)
Co_Stat             QLQANMGDIAELQLTVLPDALQAWQRAQRLESD-----DADQLDSVQAT----------CEMIAEALWRSREQTRALLLLQTQLPFDRKSYHQ-------
Tt_Stat(partial)    AHVGAITHSEQVLSILLA-KLKQWKAVQRKQTM-DESFLNDVLNHMQLQ----------FESLADVYWNIRHQLRQHEVQREQLDCGDENESA-VFDQLS
Ac_Stat1            QHKEQLDKMRHVQRQLMHPEMSVYKQVDVEQKHLKQK-LEEELQYLHKINRTYVLEPQDLHKYTFLRQELELQLQQLELFMR------------ELQLLL
Ac_Stat2            QQKDQLEKIRQFQKQLMMPQKEGYDVLLQQHAQLKNQ-IAEELRTLQALFQQVILPPAEIHKLIYLLQDLKLQQIQLELFQQ------------ELQRLT
Dd_StatA            EQEQTLVQMIHEQSLLLNNSLAPLKSLSQKQITLSGQ-MNTEMSALDATKKGMILEPTDLAKLFALKQDLQIQFKQLSLLHN------------EIQSIL
Dd_StatB            RAKEN-------QIQVINNNVQLAIDLQNIYTSMKKD-IDEENNELKNLLTIRILEPYDLRKIRECLEGLKSHLRIVDVLYN------------ELKYVL

                           410       420       430       440       450       460       470       480       490       500
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            DRTFSLFQQLIQSSFVVERQPCMPTHPQRPLVLKTGVQFTVKL--------RLLVKLQELNYNLKVKVLFDKDVNERNTVKGFRKF-NILGTHTKVMNME STAT_DNA_binding
Hs_stat5            ATITDIISALVTSTFIIEKQP--------PQVLKTQTKFAATV--------RLLVGGK-LNVHMNPPQVKATIISEQQAKSLLKNE-GEILNNCCVMEYH
Hs_stat6            GRLDEVLRTLVTSCFLVEKQP--------PQVLKTQTKFQAGV--------RFLLGLRFLGAPAKPPLVRADMVTEKQARELS----GEIINNTVPLENS
C.sp.Stat           ESIYKLLETLITSTFVIEKQP--------TQVLKKDSRFTATA--------RSLIGSR-LNLHMTLPQVTATIVSEEQARAILNNDKGNILNNKGTMEYH
Dm_Stat92E          EQVQNAQKNLVCSAFIVDKQP--------PQVMKTNTRFAASV--------RWLIGSQ-LGIHNNPPTVECIIMSEIQSQRFVTRNTGEIQNASSTMEYQ
Nv_Stat             KSSKTLLSIFLNKCFVIEKHA--------PQILKIGTKFCATL--------RHLIGGK-LNAHVHPPEVECFIVPEKFLQKNKDKIVSTILNYKKAMEYS
Aq_Stat             QHVTKYLQELISESFVLEKQP--------PQVIKTSNRFSATIRFIGDICNRLLVGSK-LQLHLNVPEVVGSIISEKQAKALLSDPSGEIVNHQKAMEYN
Mb_Stat(partial)    LAYMDVLGRLLSSALVVISQP--------PSVLKTQTKFTTTC--------AFLISDA-LALFLDPPTVTVSVINESQAIDVNERNQGGLQNNQKVLGSA
Co_Stat             --PVQQSGSHTPFVFVVETQP--------PQALKTQSKFSAQV--------RLLVGRT-LNLHMSPPEVLTTIISEAQAKQVAQQPAGDILNCRKAMECH
Tt_Stat(partial)    TQLHAQLETLLRASFVIVEQP--------PQVMKTSTKFSSAA--------RILVGGK-LNMHLSPPEVNLQLVNEPQATALVNDDEGDLLNGKQMMAYS
Ac_Stat1            Q----PPAPRCIAALAILRQP------FPMVITKSKELSEQN-----LQVQLFTGSA-VDITNYGSVRASMIIDSHQVK--GEDVEKALGACLQSLDP--
Ac_Stat2            LAPHHPHLARPVCALVIVEQP------LPMVVTKGKQLEDDP-----VVVQLLTGAN-VEIHSFSKVKVAMICDNQQVKTNSSSSSKAIENDTQTMDG--
Dd_StatA            N--PQHSAPKPNVALVLKSQP------FPVVISKGKQLGENQ-----LVVLVLTGAR-SNFHINGPVKATMICDSHPTN--KNNPTTPLEMDSQPIYP--
Dd_StatB            N----RKKPECCAALIITQQP------YSQVIFRGGKGMGEI-----FKVQMIFGV--LQPDNISPVYATINKSESNPNSTTKKEKPTLENAEASLNT--

                           510       520       530       540       550       560       570       580       590       600
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            ESTNGSLAAEFRHLQLKEQKN-AGTRTNEGPLIVTEELHSLSFETQLCQP--GL--VIDLETTSLPVVVISNVSQLPSGWASILWYNMLVAEPRNLSFFL
Hs_stat5            QAT-GTLSAHFRNMSLKRIKR-ADRRGAE---SVTEEKFTVLFESQFSVGSNEL--VFQVKTLSLPVVVIVHGSQDHNATATVLWDNAFAEPGR--VPFA
Hs_stat6            IPG-NCCSALFKNLLLKKIKR-CERKGTE---SVTEEKCAVLFSASFTLGPGKL--PIQLQALSLPLVVIVHGNQDNNAKATILWDNAFSEMDR--VPFV
C.sp.Stat           QAS-GQLSITFRNLVLKTIRR-AEKKGNE---TVTEEKFSILFQTVLTINS-DL--VYDAWTLSLPVVVIVHGNQNCNAQATILWDNQFADGGR--LPFQ
Dm_Stat92E          QNN-HVFSASFRNMQLKKIKR-AEKKGTE---SVMDEKFALFFYTTTTVN--DF--QIRVWTLSLPVVVIVHGNQEPQSWATITWDNAFAEIVR--DPFM
Nv_Stat             QRY-NSFSVEFKNLNLTKTDR-EGGKKDE---TVCEKKRSLLFYTELTIGQDRF----PLLATSFPCVVTVHGNQSPDAEATILWDNAFAEKGR--VPFV
Aq_Stat             SQT-GVLQCNFNYMQLRRIKRNSDRKSTE---IVMEEKFTILFRSKFTIPGDELDILAAAVCQSLPVVVIVHVTQQPAAEATIFWDNSFAEPNR--EPFV
Mb_Stat(partial)    SAD-GVLQAAFKTLSLKKIRR-SDKGESD---VAMDLRFVFFLTHPVTPSLRIK--VLNLHKLSAPIVVVVHGNQLPSAEATIMWDRAFALPAR------
Co_Stat             QPS-GALRVIFKNLSLKKIKR-GSNK-DE---TVTDEKFALLFQSTFSVGGGEL--LVAVRTLSLPCVVIVHNNQQHSAEATILWDNSFATMDR--APFE
Tt_Stat(partial)    EST-RTLQATFKNLSLKKIRR-HSAR-KE---VVTEEKLALIFVTSVQLG--DL--TYNLWTMSVPVVVIVHNNQLVRATATVFWDNSFGKTDR--ALWE
Ac_Stat1            ----VTHIAQFPLKFNMGTR---------------KSSVTIKFSMQLQVGHGENAIATVESEMSRHFVVITNEIQWQGSAGSLLKRDAFDGQLE------
Ac_Stat2            ----VRRIAKFYLKFLTGTR---------------KNPVRLRFGIQLQINQNGAAQVTVESNSSRPFIVITNECQWEESEGILLKKDAFGEQGE------
Dd_StatA            ----ATLTAHFPLKFLAGTR---------------KCSVNLKFGVNIRDLDNV---TTVESDASNPFVVITNECQWEGSAGVLLKKDAFDGQLE------
Dd_StatB            ----QTWEAEFKNIKVNVSTR--------------MTPSSLKFVATYKEKTSGKTVKDVESVPGSPIIVITNESQWAEAAGKLLIADAFAHRDE------


                            10        20        30        40        50        60        70        80        90       100
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1                      MS-------QWYELQQLDSKFLEQVHQLYDDSFP----MEIRQYLAQWLEKQDWEHAAN-----DVSFATIRFHDLLSQLDDQYSRFSLE STAT_interacting
Hs_stat5                      MA-------GWIQAQQLQGDALRQMQVLYGQHFP----IEVRHYLAQWIESQPWD-AIDLDNPQDRAQATQLLEGLVQELQKKAEHQVGE
Hs_stat6                      MS-------LWGLVSKMPPEKVQRLYV----DFP----QHLRHLLGDWLESQPWEFLVGSD-AFCCNLASALLSDTVQHLQASVGEQGEG
C.sp.Stat                     MA-------LWASVQQLKGEAMSTVQSVYGSHFP----IEVRHFFAQWMEQQPWN-EVDEDNSEHEQRAIGLRDMLIQLMEEKATELSTI
Dm_Stat92E                    MS-------LWKRISS-HVDCEQRMAAYYEEKGM----LELRLCLAPWIEDRIMSEQITPNTTDQLERVALKFN---EDLQQKLLSTRTA
Nv_Stat                       MG-------LLDEIQKLPLDCQAEIMTSLQNHFPDSIELEAYTYLLVWAEIQPWDLAKDVDIPEHVALAERLLAITIEQLQGLEKQFQES
Aq_Stat                       MA-------LWDKSQRLQGPLLEQMKQLYGPRFP----IEVRHYLATWIEAQMWS-DIDPDIPAHEPNARRLFEAMLIALQELIATYSAN
Mb_Stat(partial)
Co_Stat                       MAEAAATPTRWSSISTHP-----EATAIYGRDFP----LELRHYFAQWIEDQPWA-TMDPDNPEHYESIKDRVQTLGEMLHAKISQLAAS
Tt_Stat(partial)
Ac_Stat1            MA---SSPLSYHQQQHQQHGMVTMHSSDYANLDSLTTSSEGLEMMIGDGRGNGGGDNNYETWFGDHDDGASLLEQLGDGLAEVKVEVEGLTPPTMPTIFE
Ac_Stat2            MH--------------------------------------------------------------------------------------------------
Dd_StatA            MS---SAEFSMDDFEDTFDSNATISTKDLFEGSDRLPLNQSINTTIQNLYLPNGG-------FAIGDQSQQQYYQAMPPLNQSDQFNLGRSNNLTPRTNQ
Dd_StatB            MSQREWTTASTSDLMSNLLNNHNSNNSNNNNNNNNNNNNNNNNNNDNNNNNNNNNNNNNNNNNNSNNQPLLRNASTNIFFGDDWTKQNTVGLLLDPLNRG

                           110       120       130       140       150       160       170       180       190       200
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            ----NNFLLQHNIRKSKRNLQDNFQEDPIQMSMIIYSCLKEERKILENAQRFNQA----------------------QSGNIQSTVMLDKQKELDSK-VR STAT_alpa/coiled-coil
Hs_stat5            ----DGFLLKIKLGHYATQLQKTYDRCPLELVRCIRHILYNEQRLVREANNCS------------------------SPAGILVDAMSQKHLQINQT-FE
Hs_stat6            ST----------ILQHISTLESIYQRDPLKLVATFRQILQGEKKAVMEQ-------------------------------------------------FR
C.sp.Stat           ---EDMFLTRLKLQETTQQFKIMYGNHPMNLVRVVKNCLATETRMIQQTEQQS-----------------------------GDKQGANMHASIMQQ-FE
Dm_Stat92E          SDQALKFR----VVELCALIQRI---SAVELYTHLRSGLQKELQLVTEKSVAATAGQSMPLNPYNMNNTPMVTGYMVDPSDLLAVSNSCNPPVVQGIGIH
Nv_Stat             PGNFQGMMTVPKIKEIYTKLQVTHRSEPTKFCKAFGAIDYYLKAVVKQFINRLLNGDSSTMD---------------QGCDMDTEQAPDNFTLIQRE-LH
Aq_Stat             ------FITKTQLEALFAHMKGEYIQRPLELVRVVQMCLVTEAELVRKQEEFE------------------------KSNNRLTPSSNSNASQIQQL-IQ
Mb_Stat(partial)
Co_Stat             -GSEDKFLLQ--MRLQTIAADATFDENPTVLVRILKTCMERELIVWAAA------------------------------------------HKAQAT-LH
Tt_Stat(partial)                     VALEAKYASDPLELVRVILYVLGHEREILETGGTKTKFAMHSSSF---------------SSTSYGMDVSKLNDASLNAE-IQ
Ac_Stat1            IEG-SAMKKRKHEPSPMMAGAYMHAPSPASSSSSSSSAMSSPLSSSFQHSSS------------------------------------------------
Ac_Stat2            --------------------AMLGVPSPGGQQALSPPSTAAAFSSPHQHHHQ------------------------------------------------
Dd_StatA            LQQLQQQQQQQQQPQQQQQQQTYGTQSPIHMSQTPSSPLSSPLPSPTPFSRQQSYNNNNSNNTSSSQNYNNNNININNNNNNNNTNNNNNNNNGNNSN--
Dd_StatB            TSFSNLLKSPTILGDTQQSQQPQSQHTMQQLFANDPTYQQHQQEQEQQHQMMGNTTSPKSFNPYVGLSQPMIVTNTGNFNTTTTTTTTSNNNNNNNNNKN

                           210       220       230       240       250       260       270       280       290       300
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            NV---KDKVMCI---EHEIKSLEDLQDEYDFKCKT---------LQNREHETNGVAKSD--------QKQEQLLLKKMYLMLDNK---------RKEVVH
Hs_stat5            EL---RLVTQDT---ENELKKLQQTQEYFIIQYQES------LRIQAQFAQLAQL-SPQERLSRETALQQKQVSLE-AWLQREAQTLQQY----RVELAE
Hs_stat6            HLPMPFHWKQEELKFKTGLRRLQHRVGEIHL-------------LREALQKG---------------AEAGQVSLH-SLIETPANGTGPS-----EALAM
C.sp.Stat           FL---FGKTQET---ENELRQSQHKQESFVIQYQES------FRIEAQLNQLTKVEGPIEAKQR---LQQEKEAIA-AKLSGAARELLFD----RVSLLQ
Dm_Stat92E          NV-------QNTGIASPALGMVTPKVELYEVQHQ----------IMQSLNEFGNCANALKLL-----AQNYSYMLN-STSSPNAEAAYRSLIDEKAAIVL
Nv_Stat             QA---DVQYQEN---NKIMKTIEQAKEQFTILFEEKKTEMDLLELQKQEVMESSM-SEKDKEKNVLELSQKTLALQ-TELSNKGRQLTVEM---RLNMVQ
Aq_Stat             NI---MSRTEGM---ETMYRTLTAKHESFQIHYQEG------CRLEVMLHQGGGF--PPDQLGK---YRERKQLID-QIVAKDAEEMKRT----IDDLGQ
Mb_Stat(partial)
Co_Stat             HL---VGDTQHV---DNELKRLQQMQEYFVIQYQEF------CQLQAVLQRSPRSDAARGQIEL---VKRRKQEVG-TTLSTEANNIIAL----MQSLNR
Tt_Stat(partial)    KL---QEHTAET---EAALAQLLQDQEYLVIWHQDW------DELNARAQAASGAQAKA--------LAAECHTLRGNIMQAQRGAFCGT----RREILE
Ac_Stat1            -----SADPPRLYAQPMPAPRPSAH-------------------AFEAGAPTLQSTAAATAMALFPQTSSSSGLPQQLPMVNPAHQQLLQ----VHQLQQ
Ac_Stat2            -----QLQQQQQQQQQQLLLQQQQQ-------------------LQQQQQHFASQTAHMQAQLQV------------PSTLEGCQQVLEE----IYSYKQ Dyct_STAT_coil
Dd_StatA            -----NNNNNNNNNTNNNNNNNQQQ-------------------QQQQQQQQQQQQQQQQQQQQQG------------NPNLSPQPILDT----IYKLLS
Dd_StatB            EIPTYSGQVSNEYEQPTKFQRISTYNEESLNDRLRGDNTGSINFLQAETSKLRSRQSSQDDLERNRSFQMTHYDTGCVPISTDYYNSLLTRYNNRPEFFE
```



```
                            610       620       630       640       650       660       670       680       690       700
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            TPPCARWAQLSEVLSWQFSSV-------TKRGLNVDQLNMLGEKLLGPN-----ASPDGLIPWTRFCKENINDKNFPFWLWIESILELIK--KHLLPLWN
Hs_stat5            VPDKVLWPQLCEALNMKFKAE-----VQSNRGLTKENLVFLAQKLFNNSSSHLEDYSGLSVSWSQFNRENLPGWNYTFWQWFDGVMEVLK--KHHKPHWN
Hs_stat6            VAERVPWEKMCETLNLKFMAE-----VGTNRGLLPEHFLFLAQKIFNDNSLSMEAFQHRSVSWSQFNKEILLGRGFTFWQWFDGVLDLTK--RCLRSYWS
C.sp.Stat           VADKVTWQQLSQALNTPFTAE-------CSMGLSRDNLLYLASKIFNTA----DDYSNHLVSWTQFNREPLPGRSFTFWEWFHSIQKLTK--DWLQGPWK
Dm_Stat92E          ITDRVTWAQLSVALNIKFGSC-------TGRSLTIDNLDFLYEKLQ-------REERSEYITWNQFCKEPMPDRSFTFWEWFFAIMKLTK--DHMLGMWK
Nv_Stat             VPDSMPWPEVANAINHRWMLS-------NERGLSDEQLAYIGSKLFPDKSR--SEMSNCVVSRYMLNKGNMTNKNFTFWKWFYEIMSAVK--KTMHEEWK
Aq_Stat             VPEVVSWPRVSEALNHYFQTI-------SGRGLTPRNLDYLGRKLLGVVGME-EDIIQMSVTRQQMCRDQLRGRSFTFWEWFYKHLDLIK--TTLKREWV
Mb_Stat(partial)    ----------------------------------------------------------------------------------------------------
Co_Stat             VPEVVSWPDMLTALQHHFSLA-------TQQPLSQRDLEYLTWKAS-------DLIINESITWKRLTKEALPDRTFTFWDWFFGAEDVIK--RHMLETWQ
Tt_Stat(partial)    VPDAVRWPKFAAGLNHFFTLA-------NGRPLTPDALNFLGSKLLEPG--------EDTVEWRTFSKDNLRNRSFTFWEWFYAIVELVR--KHLAGPWI
Ac_Stat1            ----ITWPQFANALQRHVLKATKQDPVRPARCMSGYDLKYMRAKFFGGK---------EMISQKDFD---------AFWTWFGKNLQILRYQRHIASLWQ
Ac_Stat2            ----VTWPQFANVLQRHFLRATRQDLIRPTRQLSDLDFEYLNQTFFEGV---------QVIGQKSYD---------AFWEWFGKAVQKLRYQRHICPLWQ
Dd_StatA            ----ITWAQFINTLQRHFLIATKQDPVRPKRPLSSYDLKYIQTHFFGNR---------SIIHQQDFD---------KFWVWFGKSMQTLRYQRHISTLWQ
Dd_StatB            ----ITWEMFANVLHSHILTATHQT-SEIKRKLHSWEFEYIQKNYFDGK---------VTVSKSECK---------TFWDRFGPILQTIHFKRHIEPLWY

                            710       720       730       740       750       760       770       780       790       800
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            DGCIMGFISKERERALLKDQ--QPGTFLLRFSESSREGAITFTW-VERSQNGG-EPDFHAVEPYTKKELSAVTFPDIIRNYKPLKYLY---PN------I
Hs_stat5            DGAILGFVNKQQAHDLLINK--PDGTFLLRFSDSEI-GGITIAW-KFDSP----ERNLWNLKPFTTRDFSIRSLADRLGDLSYLIYVF---PD------R
Hs_stat6            DRLIIGFISKQYVTSLLLNE--PDGTFLLRFSDSEI-GGITIAH-VIRGQDG--SPQIENIQPFSAKDLSIRSLGDRIRDLAQLKNLY---PK------K
C.sp.Stat           DRLILGFINKQVAEQWLMQS--RLGTFMLRFSDSEL-GGISISL-VNEDRNQPCGRAVTHLTPFKDSDLRIRGLGDRVNDLMQLVFLY---PD------I
Dm_Stat92E          AGCIMGFINKTKAQTDLLRSVYGIGTFLLRFSDSEL-GGVTIAY-VNE------NGLVTMLAPWTARDFQVLNLADRIRDLDVLCWLH---PSDRNASPV
Nv_Stat             HGLIQGFLSKQQAQDMLINS--EFGTFLLRFSDNEL-GGVSVAY-TAQAENG--EKQVWNLAPWTTHHLQVRHLSDRLKDLESLLILY---PN------E
Aq_Stat             EGLLEGFMDKIEAQSVLLQV--QPGTFLVRFSDSEA-GAASVTW-VAG-----------------------MYIHTHIH---THMYLY------------
Mb_Stat(partial)    ------------------DA--SPGTFVLRFSASML-GGLSVTW-ITVDEDG-------DRQPWQLKDFAIRNLPERILDLDDLTHLY---PG------R
Co_Stat             DGLIMGFCNKQQAHDLLINC--VPGTFLLRFSDSEI-GGLTVAW-ITEDERG--MRQVFNLHPWFAKDFAIRALADRIHDLPQLQFLF---PD------T
Tt_Stat(partial)    DGLVVGFVSKSAASEALMHQ--PRGTFLMRFSDSEL-GGVSVSWNVVDGATG--TSKVYNLQPWFEKDLAIRSLPDCIKDLDQLRILY---PG------T
Ac_Stat1            QGLIYGFLTRVDVNNALNGQ--EPGTFLLRFSERHS-GQFAIAY-V--GMEKPHKIKHYLVQK-SDTAGAKKTLPDFLGECPQFRFLLQLSTNPTTGEAV
Ac_Stat2            TGLIYGFLTREGVKAALINE--EVGTFLIRLSERHP-GLFAVGY-KTDDADVQKSVRHYLVQP-EDTAGAKKTLPDFLFTCPAFQFLLVVTSDVENGTPK
Dd_StatA            EGIIYGYMGRQEVNDALQNQ--DPGTFIIRFSERNP-GQFGIAY-I--GVEMPARIKHYLVQP-NDTAAAKKTFPDFLSEHSQFVNLLQWTKD-TNGAPR
Dd_StatB            SGLIYGLITKSECNSYLTTL--PEGSFLIRFSDSVP-GAFAVAY-VTNDESD--RVKHYLVKP--DDIGANKTLPDFLRERHQFKTLYQVDPSKRSLHPK

                            810       820       830       840       850       860       870       880       890       900
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Hs_stat1            ----DKDHAFGKYYSRPKEGPKGTGYI-KTELISVSEVHPSRLQTTDNLLPMSPEEFDEVSRIVGSVEFDSMMNTV
Hs_stat5            ----PKDEVFSKYYTPVLA-KAVDGYV-KPQIKQVVPEFVNASADAGGSSATYMDQAPSPAVCPQAPYN-MYPQNPDHVLDQDGEFDLDETMDVARHVEE
Hs_stat6            ----PKDEAFRSHYKPEQMGKDGRGYV-PATIKMTVERTMVPSYDLGMAPDSSMSMQLGPDMVPQ-----VYPPHSHSIPPYQGLS--PEESVNVLSAFQ
C.sp.Stat           ----PKERAFQKYCTAASEPSYDSGYV-KPDLTTTIPGIPCGSFQANSPAPSDMNQMTSPQ--PQMKQELMSPGPPSNFNLMDDASDLIEFNMLDYNSED
Dm_Stat92E          ----KRDVAFGEFYSKRQELDPVTGYV-KSTLHVHVCRNGENGSTSGTPHHAQESMQLGNGDFGMADFDTITNFENF
Nv_Stat             ----PKDTAFGRHYTVDKTPSDPLEYR-PTQLATKVIG-ADGSCTPVQQPRVQMDLMSQYSADTYPGSPADSLASQMLDADFGIGGEEIVESFGEVDAAM
Aq_Stat             --------------CSIWYRDRHTLYY-KIRH
Mb_Stat(partial)    ----PKEDSFGPLITPVTKKKKASGYV-MADIAAVIRQMNTGLRFESRPQSSLDNMDGGGPAKRSVRRDTSRASHTSGRDGMDSRMSSAMSPATPMSAVG
Co_Stat             ----PKDAVFGRHYSVETATSNNPDYV-RSSIAAVIPGSVPSFTMPIVNDQFLMKADDSSSSMMHPTSSNLLDLVGMGVGMGVGDADAGQMSSLDWSTFL
Tt_Stat(partial)    ----PKDDAFAKYYSEEKVVVGDGDYV-RATINAAIIGDATGTLDSIATSSTLSTMDFNTGSLEYDSLAAITGFPMSSYMGVGLDEGLDVGGPSGVAVSV
Ac_Stat1            FRKLQKDVCLKPFYSKRDPPPSGSGYDPL
Ac_Stat2            LRKFAKDVALQPYYSKKNPVAKAKGYDDEIPIPNMLSP
Dd_StatA            FLKLHKDTALGSFAPKRTAPVPVGGYEPLNS
Dd_StatB            ----SKDAELEPYYSKRLKQQTNPGYVSL
```

Figure S8. Alignment of Stat proteins. Taxa include Hs (*Homo sapiens*), Dm (*Drosophila melanogaster*), C.sp (*Capitella sp.*), Nv (*Nematostella vectensis*), Aq (*Amphimedon queenslandica*), Mb (*Monosiga brevicollis*), Co (*Capsaspora owczarzaki*), Tt (*Thecamonas trahens*), Ac (*Acanthamoeba castellanii*) and Dd (*Dictyostelium discoideum*). Different Pfam domains are shown with different colours. Key DNA binding aminoacids are highlighted in blue, nuclear importing aminoacid signals in orange, and phosphorylated regulative Tyr residue in purple. Non-conservative aminoacidic changes are depicted in red.

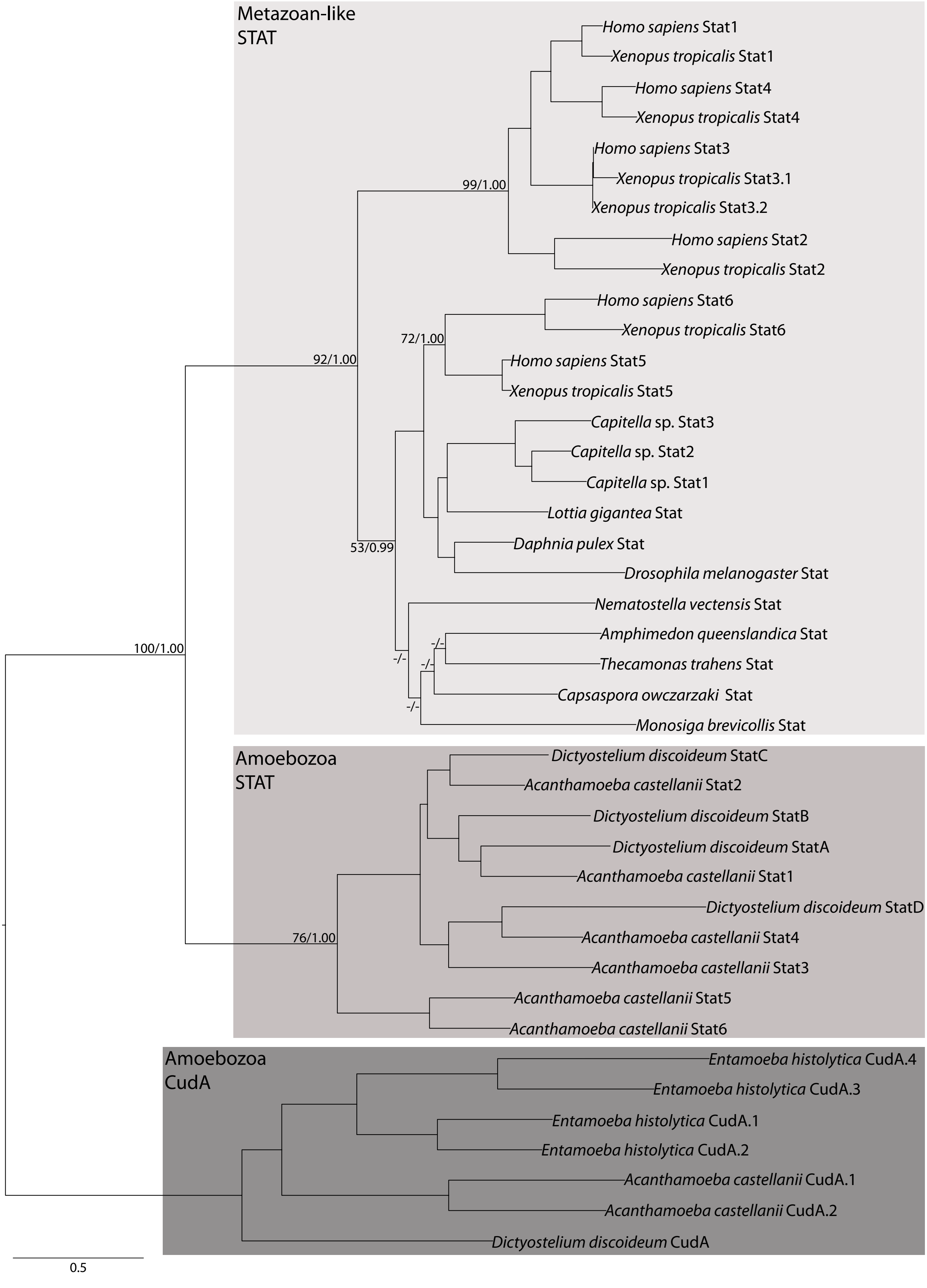


Figure S9. Maximum likelihood tree of Stat proteins. The tree is rooted using amoebozoan CudA proteins, which are distantly related to Stat proteins. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Dashes (-) indicate no statistical support. Both values are shown on key branches.

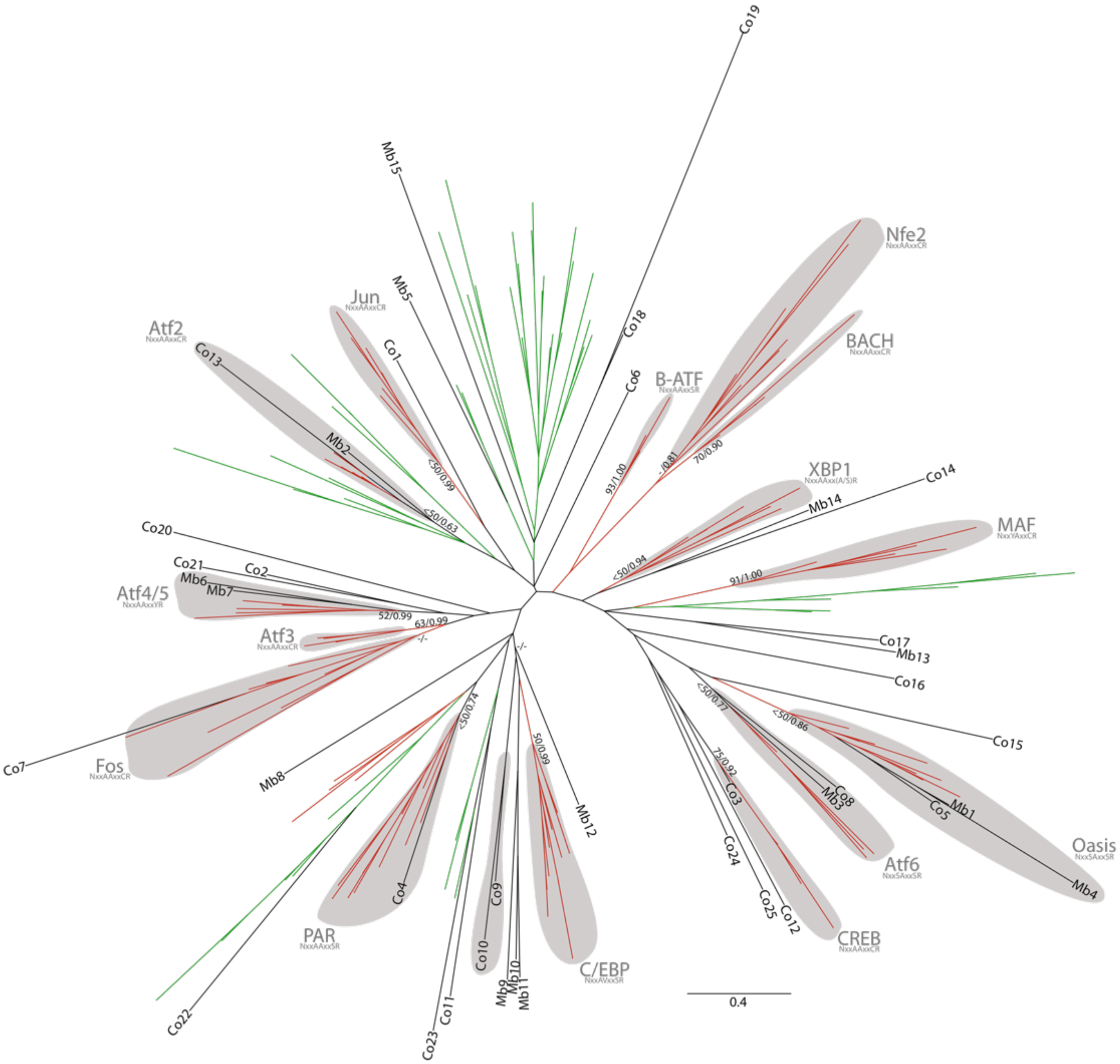


Figure S10. Maximum likelihood tree of bZIP genes including all *Capsaspora* homologs and some fungi. The tree is rooted using the midpoint-rooted tree option. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches. Co (*Capsaspora owczarzaki*), Mb (*Monosiga brevicollis*). Metazoan branches depicted in red and fungal branches in green. For each family, the signature sequence for DNA recognition is indicated and only proteins with this conserved motif are included in the family (Fujii et al. 2000).

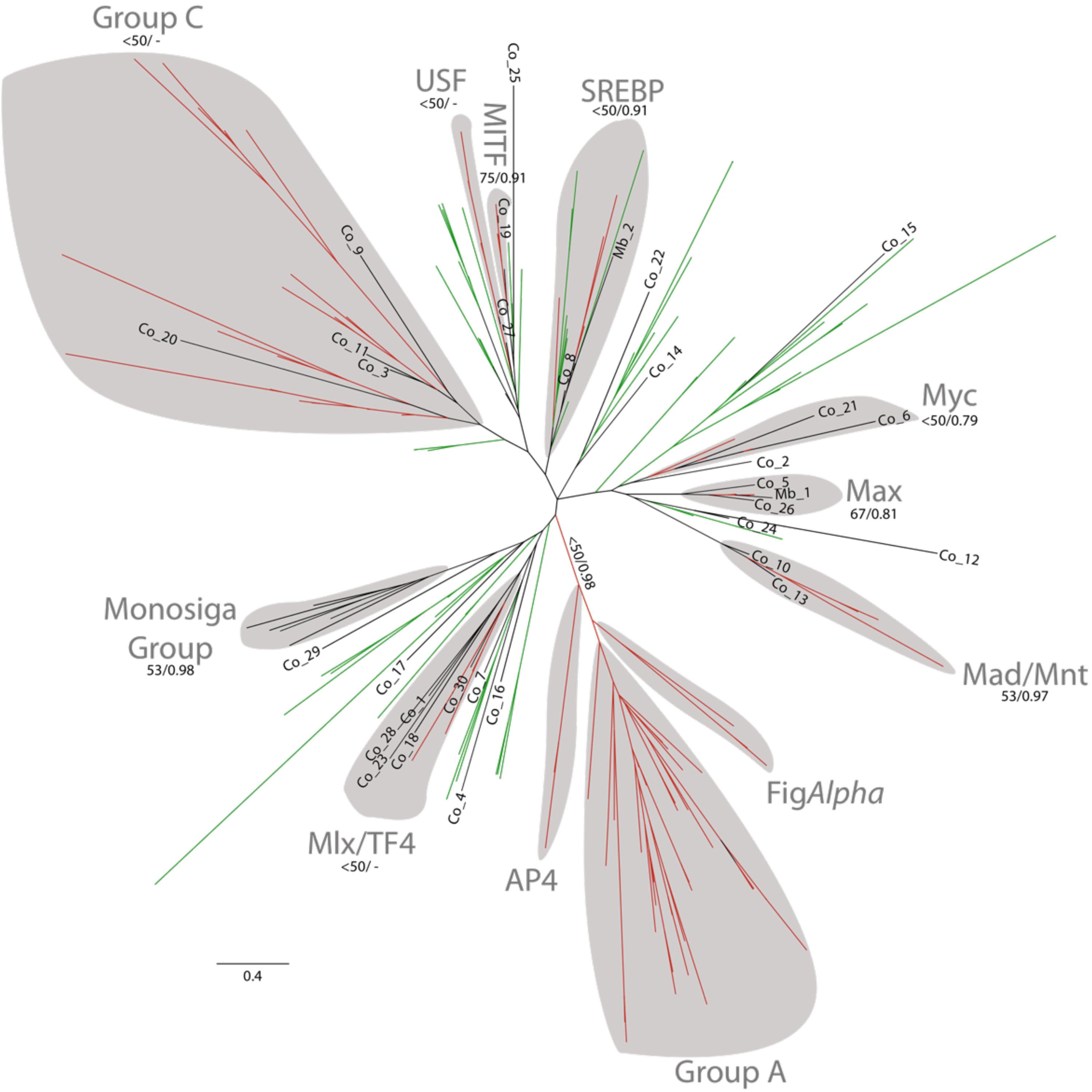


Figure S11. Maximum likelihood tree of bHLH domains including all *Capsaspora* homologs and some fungi. The tree is rooted using the midpoint-rooted tree option. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches. Mb (*Monosiga brevicollis*), Co (*Capsaspora owczarzaki*). Metazoan branches depicted in red and fungal branches in green.

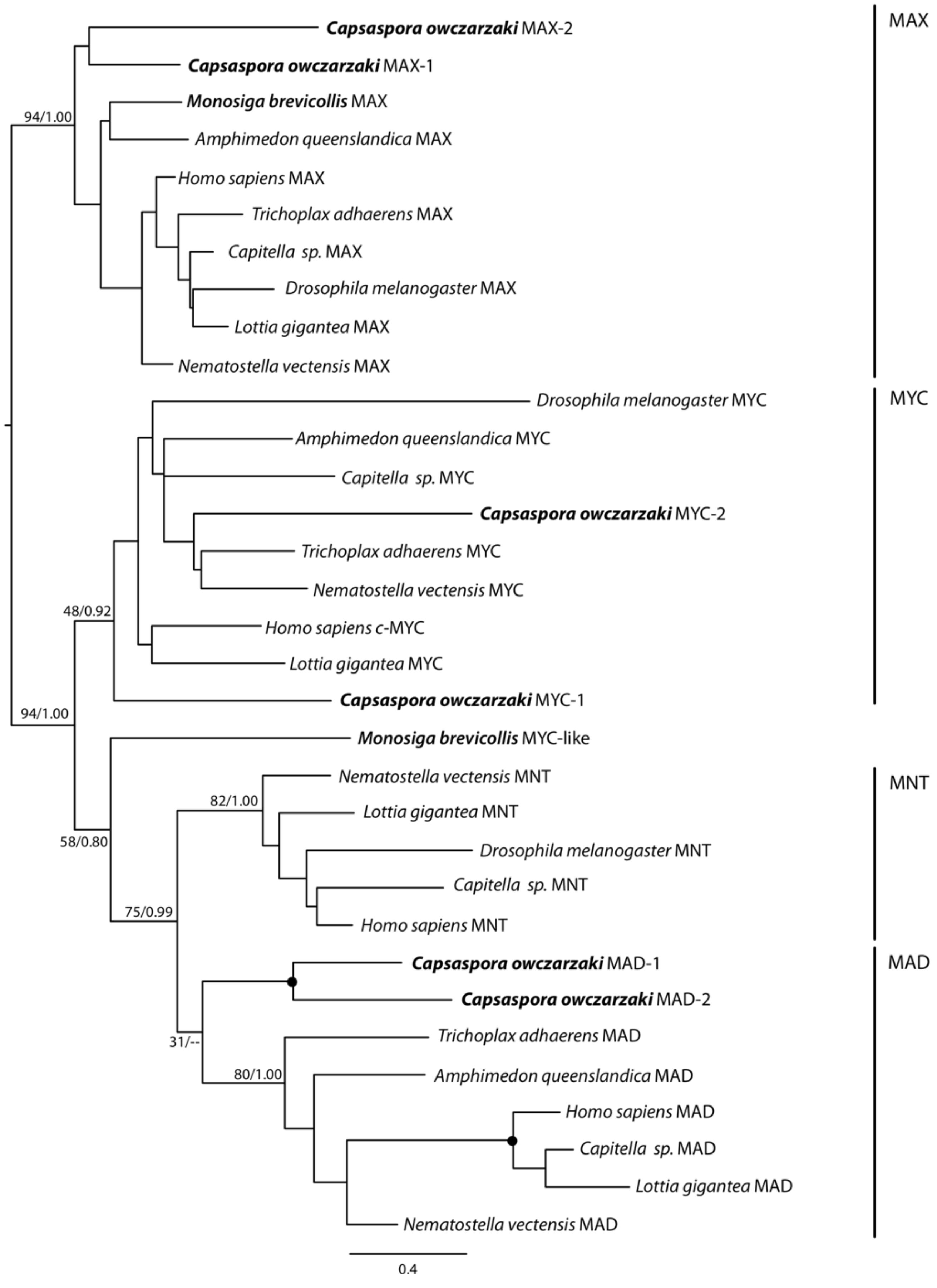


Figure S12. Maximum likelihood tree from the bHLH domain plus the LZ of Myc, Max, Mad and Mnt proteins. The tree is rooted using the midpoint-rooted tree option. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches. A black dot indicates BV > 90% and BPP > 0.95.

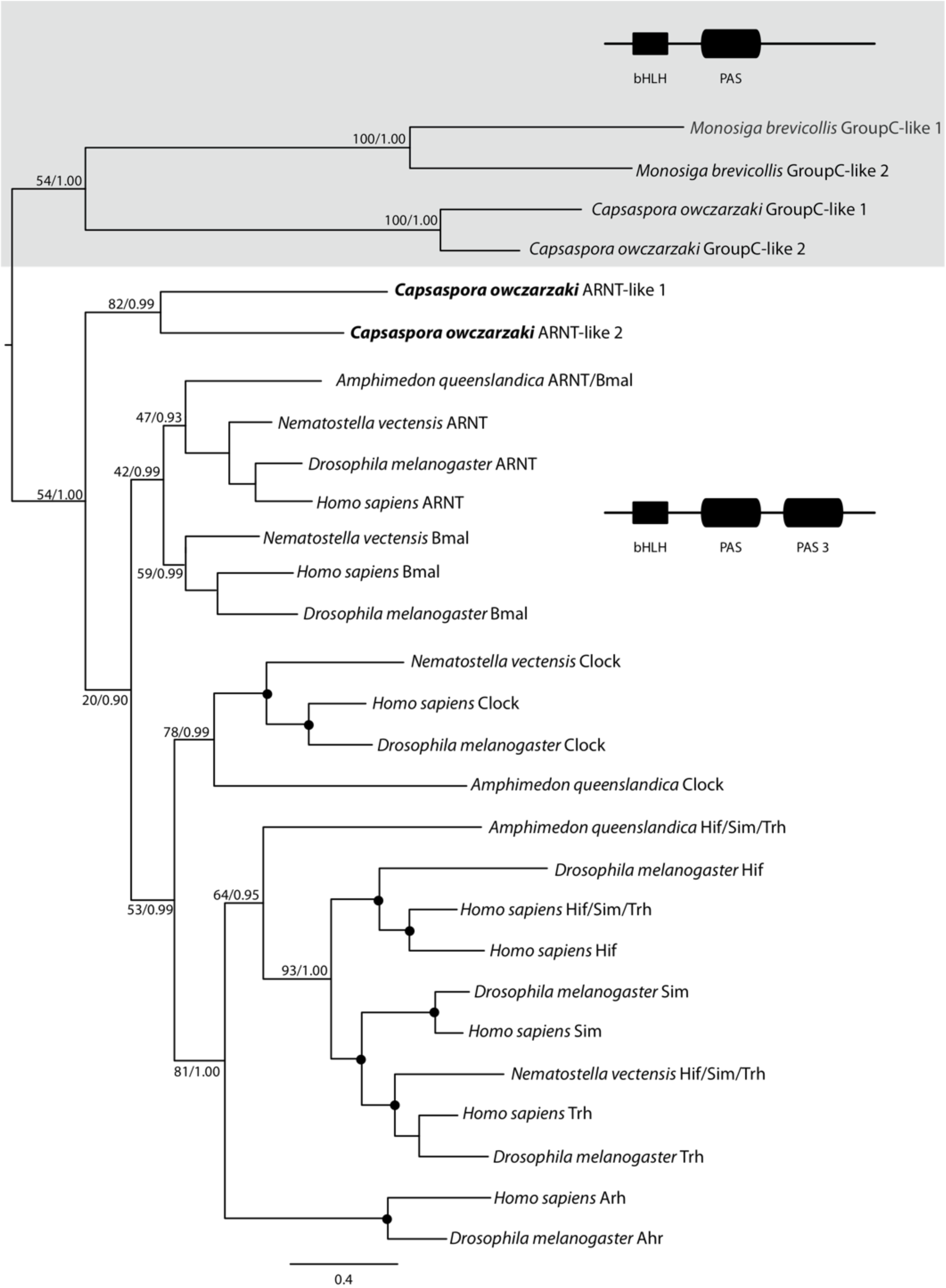
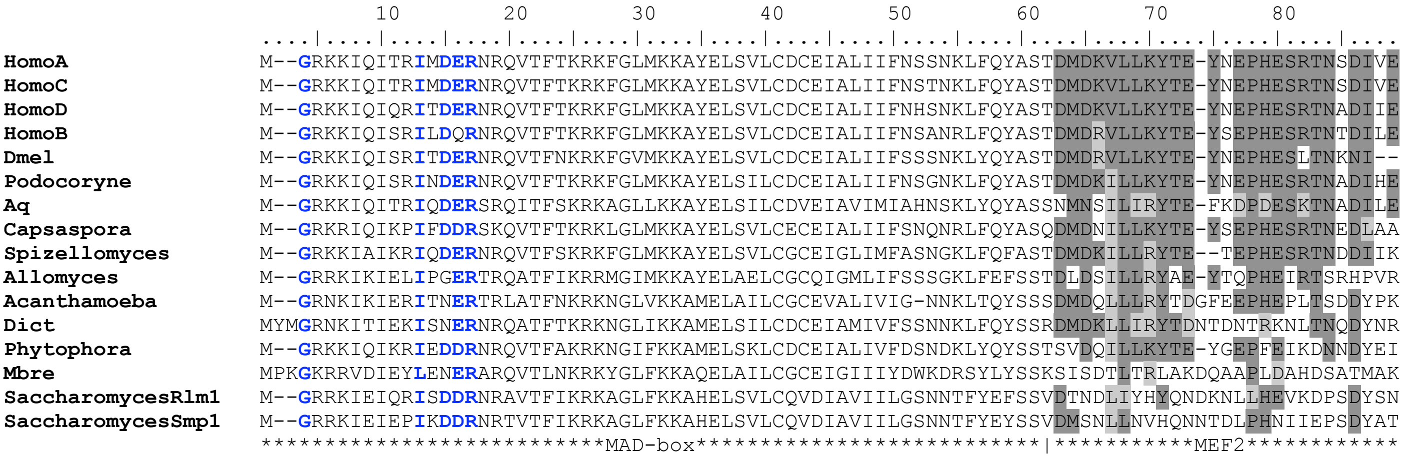


Figure S13. Maximum likelihood tree from the bHLH domain plus the PAS domain of Group C proteins. The tree is rooted using the Group-C-like proteins as the outgroup. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches. A black dot indicates BV > 90% and BPP > 0.95. Domain architectures from Pfam of the Group-C-like and Group C proteins are shown.



```
                                   10        20        30        40        50        60        70        80
                              ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
HomoA                         M--GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTE-YNEPHESRTNSDIVE
HomoC                         M--GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSTNKLFQYASTDMDKVLLKYTE-YNEPHESRTNSDIVE
HomoD                         M--GRKKIQIQRITDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNHSNKLFQYASTDMDKVLLKYTE-YNEPHESRTNADIIE
HomoB                         M--GRKKIQISRILDQRNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSANRLFQYASTDMDRVLLKYTE-YSEPHESRTNTDILE
Dmel                          M--GRKKIQISRITDERNRQVTFNKRKFGVMKKAYELSVLCDCEIALIIFSSSNKLYQYASTDMDRVLLKYTE-YNEPHESLTNKNI--
Podocoryne                    M--GRKKIQISRINDERNRQVTFTKRKFGLMKKAYELSILCDCEIALIIFNSGNKLFQYASTDMDKILLKYTE-YNEPHESRTNADIHE
Aq                            M--GRKKIQITRIQDERSRQITFSKRKAGLLKKAYELSILCDVEIAVIMIAHNSKLYQYASSNMNSILIRYTE-FKDPDESKTNADILE
Capsaspora                    M--GRKRIQIKPIFDDRSKQVTFTKRKLGLMKKAYELSVLCECEIALIIFSNQNRLFQYASQDMDNILLKYTE-YSEPHESRTNEDLAA
Spizellomyces                 M--GRKKIAIKRIQDERNRQVTFSKRKFGLMKKAYELSVLCGCEIGLIMFASNGKLFQFASTDMDKILLRYTE--TEPHESRTNDDIIK
Allomyces                     M--GRRKIKIELIPGERTRQATFIKRRMGIMKKAYELAELCGCQIGMLIFSSSGKLFEFSSTDLDSILLRYAE-YTQPHEIRTSRHPVR
Acanthamoeba                  M--GRNKIKIERITNERTRLATFNKRKNGLVKKAMELAILCGCEVALIVIG-NNKLTQYSSSDMDQLLLRYTDGFEEPHEPLTSDDYPK
Dict                          MYMGRNKITIEKISNERNRQATFTKRKNGLIKKAMELSILCDCEIAMIVFSSNNKLFQYSSRDMDKLLIRYTDNTDNTRKNLTNQDYNR
Phytophora                    M--GRKKIQIKRIEDDRNRQVTFAKRKNGIFKKAMELSKLCDCEIALIVFDSNDKLYQYSSTSVDQILLKYTE-YGEPFEIKDNNDYEI
Mbre                          MPKGKRRVDIEYLENERARQVTLNKRKYGLFKKAQELAILCGCEIGIIIYDWKDRSYLYSSKSISDTLTRLAKDQAAPLDAHDSATMAK
SaccharomycesRlm1             M--GRRKIEIQRISDDRNRAVTFIKRKAGLFKKAHELSVLCQVDIAVIILGSNNTFYEFSSVDTNDLIYHYQNDKNLLHEVKDPSDYSN
SaccharomycesSmp1             M--GRRKIEIEPIKDDRNRTVTFIKRKAGLFKKAHELSVLCQVDIAVIILGSNNTFYEYSSVDMSNLLNVHQNNTDLPHNIIEPSDYAT
                              ***************************MAD-box***************************|***********MEF2************
```

Figure S14. Alignment of MADS-box and mef2 domain. Conserved amino acids (dark grey), conservative changes (light grey) and key DNA binding aminoacids (blue) are depicted.

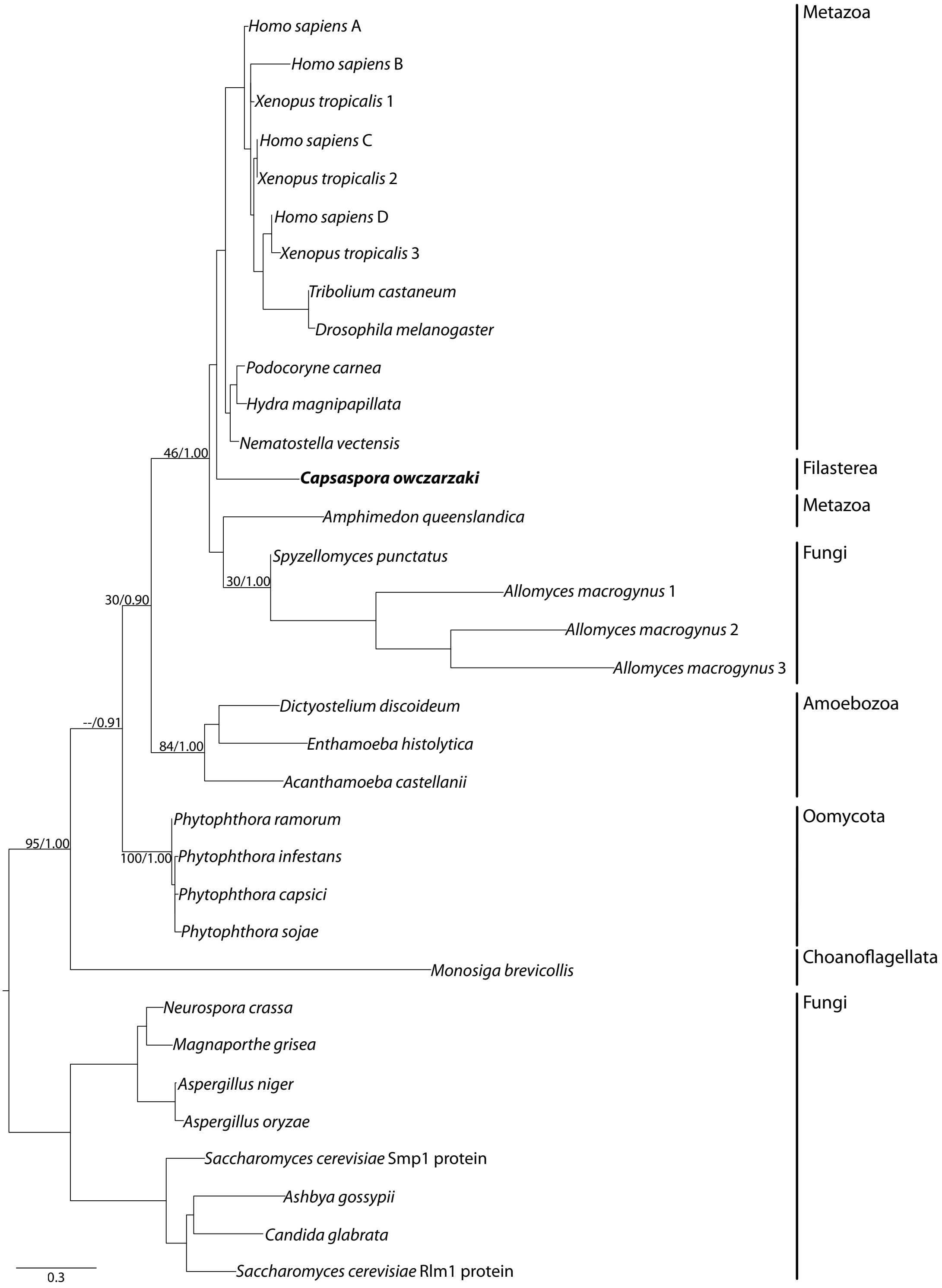


Figure S15. Maximum likelihood tree of Mef2-like genes. The tree is rooted using fungi. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches.

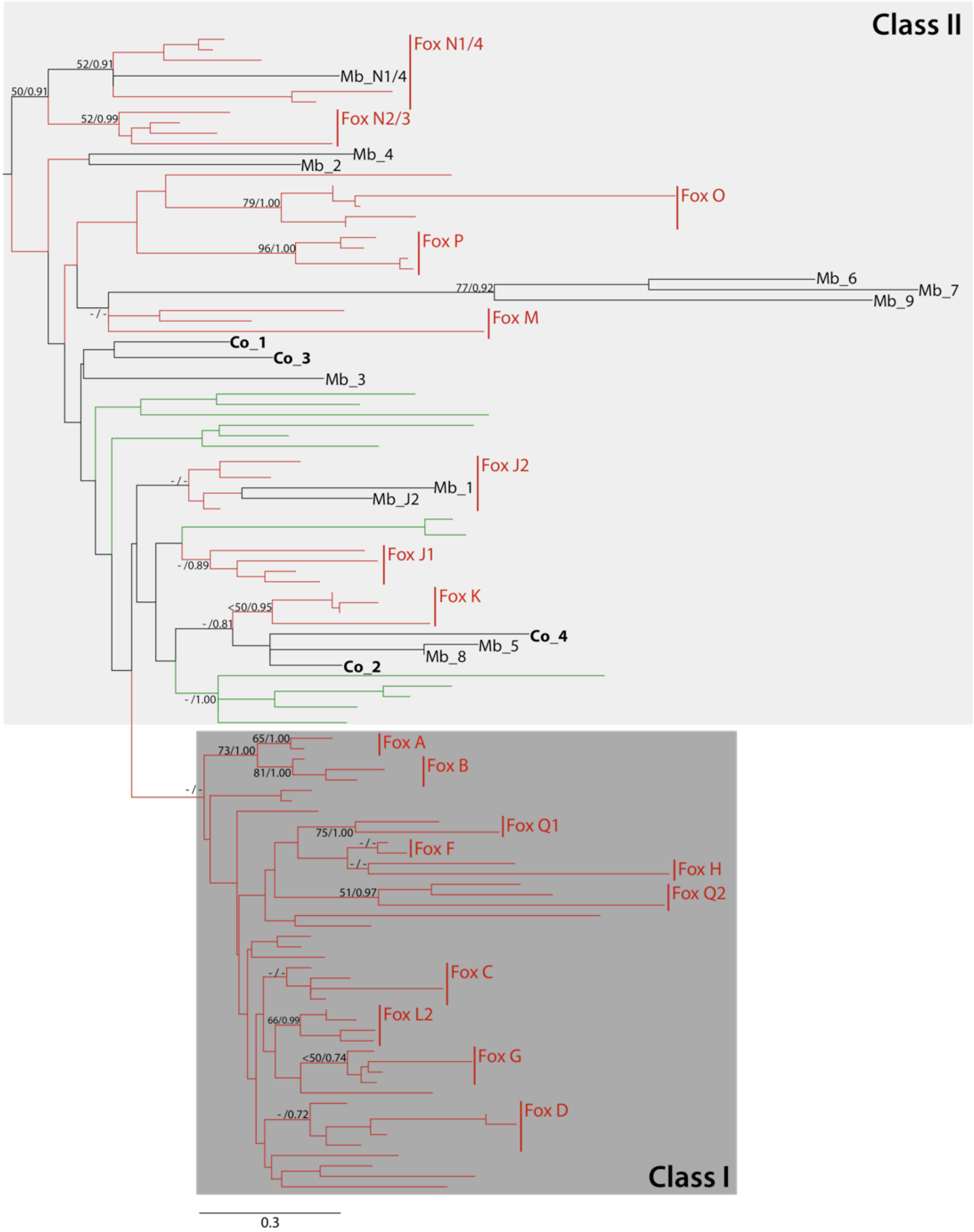


Figure S16. Maximum likehood tree of all *Capsaspora* and *Monosiga* homologs. The trees is rooted using the midpoint-rooted tree option. Statistical support was obtaind by RaxML with 100-bootstrap replicates (BV) and Bayes Posterior Probabilities (BPP). Both values are shown on key branches. Co (*Capsaspora owczarzaki*), Mb (*Monosiga brevicollis*). Metazoan branches depicted in red and fungal branches in green.

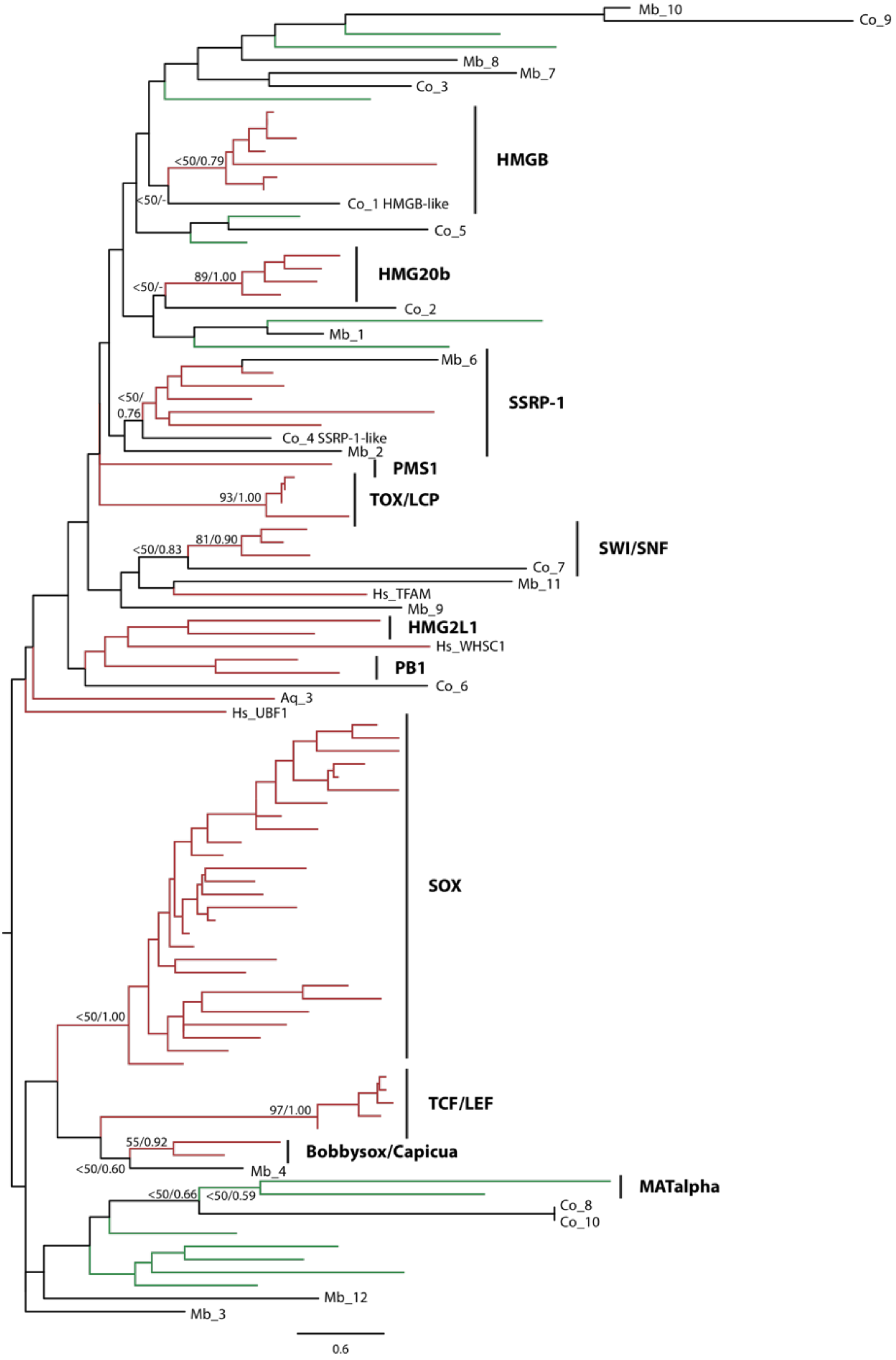


Figure S17. Maximum likelihood tree of HMGbox domains including all *Capsaspora* and *Monosiga* homologs. The tree is rooted using the midpoint-rooted tree option. Statistical support was obtained by RAxML with 100-bootstrap replicates (BV) and Bayesian Posterior Probabilities (BPP). Both values are shown on key branches. Mb (*Monosiga brevicollis*), Co (*Capsaspora owczarzaki*), Hs (*Homo sapiens*). Metazoan branches depicted in red and fungal branches in green.