**Sequences of epigenetic regulators in *L*. *boulardi*:**

***DNA methyltransferases***

1. **DNMA methyltransferase 1**

**>scaffold00067|GENSCAN\_predicted\_peptide\_1|1116\_aa**

MASKIRKCDYCNQNRTEIKNYPGHPENAVEEYITLTNPELCLFNGDENNLIEYDQWPQQKITKFSVYDEKGHLCQFDTGLIEKNVKLFFSGYVKPIYNDDPSIENGFPTKDLGPINEWFISGFEGGETALIGFNTEFAEYILMEPAEIYNSFMTPIMEKINTSKSVIEYLLDEIDPSFEDLLDKFDAELLIKHSQFICEQVFSFDTSAEIDDTMLITKSCMRSLINLSGVNLENPNSHLRRTEAKCDKIIVNQLIKKRQKNKKLLTNATTTPLVRDTFETFFHGKKLNNFELDRENGENIFTIFNKDAKWIGESIGEDNERVFYEKAILGDDVIQIKDCVLIEVNSSAQVARIFYMFEDKAGNKLIHANWYWRAADTILGETADEFELFYSERCDNIAFNTISHKVDVISNDSDEKFFCNKRYLENSARFEDPITKNFNFCQACLEFTSKKYKNIPRVFEKNGEEFERVLYGLIKFKNENFRINTGVYLKPGSFKFKNEKTKNEKQKDISKNINEDIYPEYYRKVKIIDSIPEPFDIGVITSIFGSRAKIVPPGEIWIRVRKLYRPENTCMNKESIRKLDLNLVYWSEEEIVVPFFNVVVGKCYLAFEGNFKKELLTEGSDRFYFSKTYYPEEKLFGDVSKSAKEFLQFGNNYPKVRKLATLDVFAGCGGLSEGLKQSGVSEVKWAIENDKSASVAYGLNNSNVKIFNDDCNYLLSQIMKGIFENEEGIKLPRKGEVEILCGGPPCQGFSGMNRFNSREYSFFKNSLVATYLSYCDYYRPRFFIMENVRSFVSFKKNMVLKLTLRCLTRMGYQCTFGILQAGNYGVPQTRRRLFIIAAATGEILPNFPEPRHCFSKRGCQLTSLVDNKKYLTNCEWMESAPLRMVNVRDAISDLPIINNGSNLDAMDYETFAETDYQRKLRGNQTILKDHICKLMAPLVQARIELIPKNGSDWRDLPNIIVELSDGTWSKKLEYTYHDEKAGRSSTGALRGVCSCCLGKKCDISDKQYNTLIPWCLPHTGNRHNHWAGLYGRLEWDGFFFTTITNPEPIGKQGRVLHPEQNRVISVRECARSQGFSDNYLFYGNIVDKYRQVGNAVPPPVAAAIGLEIRKCLGLRN

1. **Methyltransferase 2**

**>evm.model.scaffold00357.25 EVMevm.TU.scaffold00357.25 scaffold00357:218458-219761(-)**

MRVLELYSGIGGMHYAFNESNVEGDVIVSIDVNTVANEVYRHNFQKTTKNISRNIQSLNINEIRKFNIDTILMSPPCQPFTRVGLKKDSLDKRSESLLHILKLIPQIETLMYIIVENVKGFESSNTRNELVKCLEMKFNYKELLLSPCQFGVPNSRQRYYLLAKRNDLNFCFKDSSIINCLPDNILKILPQSRHRLLAIKDGCLNSTNCYKLRHIVDEIVEEKYLISEKILQKYSSIFDIRNNNSHGSCCFTKAYGHYVEGTGSIFCPYSDEIINENFQKLKNYREVPLEELKLLIDLKLRYFTPKEVSRLMCFPEDFSFPNSITNKQRYRLLGNSINVHVVSQLIFLLNHENANS

***Polycomb group of proteins***

1. **Polycomb**

**>scaffold00228|GENSCAN\_predicted\_peptide|426\_aa**

MERLEYNTWEPEENILDVRLIELYEESQKGTDIVTRRPRRRDTRYNEQVLANLVVEEEPGGDERVGEDSQDESTGSTSAVPRLNPVAPDEDTLHSSLDGHESSIPPELSASAFSVDSESSNSSADIPLLPRKEPAGTKRKAEVLSKESGKIGVTITTSSPSSGSTSPPPGKLPRLLPIKGNATSPTYNNHKLNGRRPSSSSVKSTTPEEPSPAMPTTPAAEDKKRPEADVPHGPSPSLPRTPQTPLSTQIETTVETTTSTSSSSSSSSTTTTSTTTTTATTTTIAASTATTTTKTRHDHRSQEKLSNGPLITTDTNGHKSPSPTDSYTNNNRLPTMVNGHHNNNNNNTNNNNNASQNQVKANSEFVTSDLYIPLTSPGTDYWHSRNPVADQVFITDVTVNLKTVTIRECKTEKGFFRERDPKSDVL

1. **Polyhomeotic**

**>evm.model.scaffold00090.35**

MTDVKQIEIXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVVPTQVQVQPQVAAIMPQQQQGGTTITTMAAHPQAVQVIQQPIQSQAYHLQQLYNTQGAPLIMPGNLALHPAGINPSSIQVITAGKPFPSATQLTPHMLTTASNPGQAGGHPGTGGTKVQGFLTGYLPVPTSTAGSGQTVVFGHHGVLGSPXXXXXXXXXXXXXXXXXXXXXXYTACAPGTPSGGRGGGMQFAPWQFAPQVAWTGLQSPTTLLTAGPNQIFIRGPTQQDMFIQNPQPIQAHNALAAQQQIQGMQQITTASGKPRVMEIQQQPQQQGKPSSSGQRPLSILPSSLQGLQAANIRPASSVSTQTVHGVQTTTGKGGGGAGKGRGKPVVRTSPGPNAAIAATKTDAANQTKSNVHHATMIMQQQPVVSNSGVNKILITANTSVATSAQPPGSPMSTGDKQNFGPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPKPMMSGMALQQQQHHQQQTNVVLGGERPIMPVVSMSGVGVATTLQMNQVPQSPMTTVQQLQLPQTINPAMMTNHLVNGTTQVHTMPMVTQSVXXXXXXXXXXXXXXXXXXXDITTSQIVVTALDRNQQTDTNIQTINIPISNEDPLKSTPKKNDILQTEEAPTPMDTSDIDQNKMIMKEELENATGKLDDKLSNNPLAGLASAVNSITNGITGSEESTAPISLPMNVNSKQTPLKAMVKPQVLTHVIEGFVIQEASEPFAINRTNLNGSLSQDSISNRNSEKDGYEEPPRKKANYTNDENMDNNHINKCEACGKQMDEQTGKLRKDKRFCSSICAKSCKKRDRDAGEKQWTEMEIDAKNNEMEAQKKSGEDKSLTTSTTPNIDDSLPKINPVKWTVNEVCDFIRNLPGCADYAEDFAIQEIDGQALMLLKEDHLMSAMSIKLGPALKIVAKIDSMRIDSMSSTSPVSSNNI\*

1. **Posterior sex combs**

**>evm.model.scaffold01161.3**

MERRIKLKTLNSHITCKICRGYLIDATTVTECLHTFCKSCLVKHLEEKHTCPTCQIVIHQSHPLQYISFDRTMQDIVYKLVPDLQENEIKREREFYRARGLSCPKDILPNAGEMEEEKSSADTHAESDYHRADEQVNVCLECMNASLKTLRRRFIRCSAQATITHLKKFIAKKVLNGIEKYRDIDILCNDELLGKDHTLKFVYVTRWRFRDPPLRIRTQAVKFLEGVVLIQTYPDPDSPKKPDDFSLEDVPLTLKIARRRKLEEEANHVMDLLIKFHGSPHVSSVNLMTCMGSLALVAKTRPQFMSNVIQALQHLQHDLPPTLSDSQVTSVQKQLKLTLLGLLKHPASVEFAQSIAKQLTQLGAKEQEIIKAYPKPEDIRRMKKRLQENAANSAAKRAKLDPPIIPVEELEPVPLPVPPPKMPDLVELSESFIAERLSVEIASDLVMDSMAWVPDTMTKIFQREYQPTATTDIIIQRQTIAKLLATQIKQAIVKKNKKDSKDEDAVMEDLIKNPTITVAXXXXXXXXXXXXXXXXXAKASLEAHEKSLAKARSRLKALKFSEVTKPLSRNVKENMLLMAVHRILNAEKVAVLGGVSEVRAKILTTVAATFNPDIRRLVLQYITDDVRSRLDLALGWLYEEYALLQGFQRRTTLCSKPQEAPHQPYNSLFCTLVHAINAVPGRDRDLLLSRIYLEAPSITDDAIEALKMVSLEENRGLAPLNLLKELSIRRPTKHFNFLNVILCHTGHESNTIRETAINLVVELHGRPELKVMIGEYAMLYLGFLRLQSPPEIVFGIDRGRPNLSEKWTESTTKACLGLYLALLPEQQILIHELARVYTSMGADVKRIVLRLVESPVRLLGMASPQLLALVENCPKGAETLVTRIIHILTEKAAPSTELVQRVRELYQTRVSDVRFLIPVLNGLTKTEVIAALPKLIKLNPIVVKEVFNRLLGTHNNESGVPHTSPVTPAELLIALHTIDPAKAELKTVIKATSLCFAEKQVYSQEIVALVIRELVEITPLPTLLMRTVIQSLSLYPRLSGFIMNILQRLIIKQVWKYPKVWEGFVKCCERTQPQSFAVILQLTHVQLADALKMSPGLKKPLLAHIDAFTENQKSHIPVLKMDAIRGTVREDFSRGNPHDNFDIAPPGDFPIEEKMETDPSEPAPPGLD\*

1. **Suppressor of zeste 2**

**>evm.model.scaffold00367.12**

MTGMSKRTYLREVNPYLICPLCRGYLIDATTVVECLHSFCRSCILKHLRSKAQCPSCLHLLNKAKPNIKADKALQDIVYKLVPGLYHKEMRKRREFYKKHPEHADSATPEQRGEDVSGRLIFVPEDAISLSLEYLPPGADPLALILSTNDADTIQSNTNNTQSNNKNEDAITHDCSRRYLQCPALVTIAHLKKFLALKYSVDVTRYCIEICHRRAPLPEHWTLMDVAYIYAWKRNAPLRFFYRIMQEEQRLEAPINDRPSTPGVGASLSAVDNGNNKNESDENQVQMEKEESLKVNKVSKKNDQIKNQLTVTNSTNTSVKVDKKLPSSPISKESAKAVKVXXXXXXXXXXXXXXXIDDETKQIKSPIKILKNSEGRYEVLRTSNNQTTPESSRTVGNVNEKKTPSPEFSVVSIGDGPNSNGVKITLKQCSPGSGLSSSKPKIVSNVLMRNGQTEKILKSHEKNRQKADLIEKQEKHKRKVTFIDKIENKVKDINEEIDRNKKITEQSDKKEFLHGFRLTAKQPWNDDKNSNKTVKIIDNTIIKSPEKQENKKNNQNDSNTIYSIKNKNTEXXXXXXXXXXXXLKTETSKRFLNGIVKDLDTNESKIDVYAFPSEPPTLPAGAVKRKCPPGLPIFEMGRKRPHLQGQIRKKTNPTPVKIAKKQQDNVYSKRVAIKDNTQSNIIPIKPPXXXXXXXXXAISDNTRNLLDGCGLNIPASLSXXXXXXXXXXXXXXXXXXXXXXTDVNNLKDNQTILSGKVNPSITLNDRSVDPRVLKALKTGQIRMPVASSRQKMKQQPILERSQPVKRKKDDILDLSGTRKLDIHPLRIPQPVSKFKSKSPILPTASSHQVVTLTGGQKYYRAPPGSLTPAVHRVSDYPQTPPSRGPVYAPSCFSHNSNNRNTTTTTNNNISSVFPSLQSLYALSQAPNLQQFQMDNRLRLPQQPESTTSNGPNKSHLAAQCAPLKPARSSFASLAVPIVKQSPPLRPITFTNTQTTELTKIKTKEDNIQNSSLTKETQEKIEKLKQSSPITSNSKQEAASTSSCIDSNSQEAASPRVSSTVSPSPPPNPVINNSINSSHTDEVSSGSISSNKSEVIVTSTKSPESPXXXXXXXXXXXXSXXXXXXXXXXXXXXXXXXIDDQAPSSKDEKIKEISKDSVTTEKEIISEEKNDKVGDTXXXXXXXXXXXXXXXXXXXXXXXVDVKQMTSEVFQKRLLAAFPSNEWANNPIAAKHLGNLLKSLTSMQTDDQGEKKNQSKETKEIITTKCVKDILPKTNVEVTD\*

1. **Enhancer of zeste**

**>evm.model.scaffold00377.21**

MSKKPVPSEWRKRIKSEYMRLRLMKRYKRADEVKISWNQNRKLLKDFLNEKNKEWTDGSAMWFALQDIPPQSLSKKKAVTSCFDENETQSLNIKIINAVTPIPTAYTWAPIKQNFMVEDETVLHNIPYMGDEILDKGDTFIEELIKNYDGKVHGNGESNFMDDSIFLDLVNALLIYEKDDKVVDEQKKEKDKENKRSENDHKNSSKDLSSFPSMQIFNAIASVFTDKGKPSELKAKYIELTQRNNPNALPPECTPNMDGIHAKSVPREQTMNSFHTLFCRRCFKYDCYLHRIEFHQEPNLKKRRESDLRRFTEPCGANCYMHLEGVKEKLAAQVIEIKEEDVKTKKPRKVRKQLSVDSGNEDSDESNDSKQSSRSSSQDFKLNVNRNSKSDKLTDEGRQLVNFSPFSLNLDDKCDKSTKDVVWTGSEQSFFRALHKVFPGNPCALAQIILTKNCTEVYEFAQKEAADIPSEESSEDLTPPRKKKKKHRLWSVHCRKIQLKKDSVANHVHNYSPCSHSGRPCDKSCPCIKDQNFCEKFCACSSDCQNRFPGCRCKAQCNTKQCPCYLAVRECDPDLCQACSSDQYDVAKISCKNVSVQRGLHKHLLLAPSDVAGWGIFLKESVAKNEFISEYCGEIISQDEADRRGKVYDKYMCSFLFNLNSEFVVDATRKGNKIKFANHSINPNCYAKVMMVNGDHRIGIFAKRAIQPGEELFFDYRYGPTEQLRFVGIEREMEFI\*

1. **Extra sexcombs**

**>evm.model.scaffold00004.44**

MKKLSTKSLAYTSSQEESENDSDETECSIGSNSTAGTHRSDTPTRSARYKRKGRRRSKTGKTKVSNDKTLYKYCSSYKEDHGQPLFGVQFNHNLKEGEPMIFATVGSNRVSIYECPEESGIRLRQCYADPDPEENFYTCAWTYDDSGKPLLAVAGSRGVIRIISPATMTCVKHYIGHGHAINELKVHPRDPNILLSASKDHALRLWNIKSDVCIAIFGGVEGHRDEVLSADFDMKGQRIISCGMDHALKLWSLEKADMQEAIKQSYFCNPSRNGRPFDSVLQHFPDFTTRDVHRNYVDCVKWFGDFILSKSCENCIVCWKPGRLEDSHLRNNETSATVLHRFEFKECDIWFIRFSMDFWQRTIALGNQVGRTYVWDLEVEEPGQARCCSLQHPRCTAPIRQTSLSRDGTVLLCVCDDATIWRWNRDT\*

1. **Suppressor of zeste 12**

**>evm.model.scaffold00071.21**

MPPKKREKDLEGQKAPRMDMVQADHELFLQAFEKPTQIYRFLRTRNQISPVFLYRNLSYMRQRMSRTHKSRRGFRINSILDKLVIKNEQQQIPGIRGYMTLTFLGFYDKKLEVPQDPVKVETLLLKICHKKRKDVSSPITQDYVGSREVPINPSENQPPPKAPTISIPNESFSSNNGHLAKTYMLLLRVYCTSNNGCLMHNCDLDEPAQKRRKTATGAIKTGGEEIKLYGSELVVYDKHNRCLLTDGDYELGLQEVQTNVRSSPKKHNSWETIPDIKDCSPFDVFTRGPTLKFRLSWTMEPSNGFVDRPVAVNPLPNGDNKENRPGNNCPTXXXXXXXXXXXXXLALPAPSPLTPAKIPVTNEKIDASNISLQIVYQFLYNNNSRQQTEACEDLHCPWCSLDCGKLYSLLKHLKLCHSRFTFTYVPIPQGARIDVAINECYDGSYAGSPHELISQPSGVAFSRTGPTRRTSVTNILVCRPKRTKPSLSEFLELDENEFESQRSYITGHNRLYHHTVTCLPIYPKEMDIDSEGENDPKWLQTKTMMMIDEFTDVNEGEKELMKMWNLHVMKHGYVGDCQIPLACQMFLETKGKELLMKNLYRNFVLHMCSLFDFGLISPVILYQVIQKLQEMMKEGGENGDVRKILQKSHEQQVERWVTTGVYAPTDNIKTNSTCAXXXXXXXXXXXXXXRKTTLPLGSPPNSQAGKSSIHNNATKHASMMGASTNKSLNLNSTIQNSLNKNGNSYTNQNGVSKNITSNTNKVTASSGTSNSVQNENSQNKQSTEPPTRRKSTDGTASMRRKSMANDNSSTNEYHRRKLILDAIQEHEIDHPYHQIPREHQIVHQCPRNLREHQIIIRVIKFQGNIKLFISVLEI\*

1. **Scm-related gene containing four mbt domains**

**>evm.model.scaffold00273.10**

MDMQAPNVYAATIPGIPELGMVWMGDMMVHGEPTHELMLDPRHAESPFFPHGSHSFDELRXXXXXXXXXXXMQPTTMVRYLPQQYHGECSEPDEAMEAVDVQEMHHCYPLFQEYDPQTESNEMTEYMTLEDYMTEEDREQVVNNAATQTQDNRNRKIKPIKHPGLVLKTPIAYQPHTDLNFIPIRKDGIAVCEKCGAIGVKHAFYTKERRFCSRACARSSEHTAPAADSTYSPSHPIENQIIVTPPSPEASKPEEEVITKEIEVEKKEPEKKDKEVIKSEPVMPEDLPVRRKRTAEMEGSYDWTPQLIEHGFCAAPVSCFKHAPISEIWDDITVGMKVEVENTDCDEVCEAFPDSFWVATVLRISGYRALLRYEGFGHNAEKDFWVSLCSNDIHPVGWCATIGKPLIPPNTIANKYKDWKDFLKRRLTGARTLPTDFYNKVNDSMKSRFRCGLQLEVVDKNRISQVKVATIQKILGKRLHVRYYDSPPDDNGFWCHEDSPLIHPVGWSRKIGQTLDAYPDYLERMSKKQYSEDDATEDIFIVPKNHTIPGFKFQEGMKLEAIDPLNLSAICAATVMRVLRKEFIMIRIDSYDEDASGADWFCYHSCSPCIFPIGFCAQHGLPLTPPKGYDPTTFTWDSYLTETNTIPAPIHLFNPEVPQHGFIEGMRLEAADLMDPRLVCVATITRVIGRLLRVHFDGWEDEYDQWLDCQSPDIYPVGWCDLVDHKLEGPRVINKTTSPTVKSPRGLKRKSKRKMKRNGKLHCGRQFLPRHSERINPTRERDRDRERERERDRERKQELELEPAQGIKIERDHELESLPEQASREPEPAEEPAGPDQTLPSPSSCQGQALSEIQSNLQVVPPSRDRNVTLCVN

1. **Pleiohomeotic**

**>evm.model.scaffold00183.17**

MASADINMASSDIIAEVEIQPDIQEVEIETIPVEIPCETVETTIEGDDGQPMIALQPLPEPGREEIILQTQEEIVGGDPLSVYDQIPVPDNDIYVESSPGPSKKVTKKPRKQGNTRFRAPDHAIFGDMASETKTRKWEQKQVQIKTLEGEFSVTMWASGTDDDEGSNPEPDPDYTEYMSGKNSTKFNHSGSSVSDGMPGLDLSDPKQLAEFARPGHKLKIRKQQMMDGVERTIACPHKGCTKMFRDNSAMRKHLHTHGPRVHVCAECGKAFVESSKLKRHQLVHTGEKPFQCTFEGCGKRFSLDFNLRTHVRIHTGDRPYVCPFDGCSKKFAQSTNLKSHILTHAKAKSRNAIGRQVQQIQLQQPQFVQVEVADVDNQQFIVYAD\*

1. **Jumonji, AT rich interactive domain 2**

**>evm.model.scaffold00083.37**

MVLSRNDKRKRKEGDLVDLMDPLSDSPKRTKIHAQRKFAQGAATFYSPSTTPVKEKEKEKSKPAAINELISHKRPNTEDFLTFLCFRGTSILPSSLNFFNVCAKKDKGDLKSIKASKASPSSSSKPRPTDSSKSDPSQKATKSKNNVSVKKEFPNGLKNTIKFKTKTSTVQALKRKYQEQRLAKQRIKNKIKTSYVIRTRSNSEKNVEKSLNKLSSRKFVTKPEKSKRHGLRSGGLIEQVCNPKIIPKNKRSIKPQKKGFGKNKNNSKDDYLDSDSGSNDEELKLAQNNKKIGKSVPKKICTRKTELRRVTRSFVETKSTQNLSRRPTRKTKEAAAVYMEILGRKLVSPDLENDDDISLDSFPELPNSRRILKEEFEIKEKVKQNAKSAAKEKEIKVENTVSSKRIDKLRTVKTVLKSKRIVKVHKYCELETDEESEISCDSEKSGKTRPMTRRSLNKTNKPANRSLRSSSRNLSVKVQVESCEVRKYIGKKEVKKEKIVLKRKREQIDEKNVDKKEETPKDEETKDIETLKNKKEGNLKSDIDNKKNDGEEEIKKLKKVEDKEKEIKIETDELKQEIKNSEKDIKEESDEETLCSLLSKIKRKRESDDELSKPIKILKEVKDSKMSDDEESFRGFTKKAISKVLDTCQSHVNSNLLVTESIESKSVQVSSISPLESTKDLDKSQNQENPTIIPFEKLIVIEPNETLEKDDVEKQDQNTNKPNNEIKIIDMPSTTTVGRKERVNMSAEQIEKWLTESSIAKEENKVELDTTYNYENTTEKPKVSHHLSISSKIQHLVRPVNVTLAKLHDKSKAQKIVLNTQTSPIKPSSSLIXXXXXXXXXXXXXXXXXXXXXXXXXSPIVDDDIVSKSDQNSPDDTPSSEKKCQDKKILPQPRKLFLPKVKERKVTTPSANAFSPENESSVYAFESDTETPISTPFRRKSKPPSPSNKIQDSNKDCTEKNDVQSPEIDNKVAEKKEELNSTKINTNDLKGFPNLANIQVLSLDKLTTNWSNVNCSASIAVQVNLDDQNQKTQNPDDDNSQQKSTEISTQTEGSNDNDDDNDGQLFYIPLQAVTRNGSNLVQGQQLIQGVAVKLGTEGPTGPNQRVLLKAKLVTKPTLTVARVPPVGTVQPTARAPPIASTSSAENPIASTSSLISNSQILPINKDSQSTSTTIGTEKIAKITKVPRERKMSVESAKFGKRFQGKSKQKIVEVCTPINTTTFPGTKDPNEEARLVEAPTFHPSEKDFQDPLEYIDKIRPIAEKFGICRVIPPPNFKPECKVSDDMRFTAYNQYVHRMLHRWGPNVKEMMAIRKYLATQSITLNHPPWIGGMEVDLPHLYQTVQSLGGLKEVIEKKKWQKVADGMKIPRSAQDRVTKLDDIYCKYLLPYDTLSQGERDKLFEEVELEWANREAKAMLRLESQSXXXXXXXXXXSSEEIEECIVKGRNMPLNAFYRIARNTQRMWFADNQRSLNEIEGASASEVEAAFWKHVTERKRHVCVHAASIDSSGRGFGFSVAKNSPFARHPWNLKVLTNNAGSVLRALGPLMGVTVPTLHVGMLFSACCWYRDPHGLPWIEYLHTGGKKIWYGIPDEHNNNFRNALAKMVPRYCKNKTIWLPSDTAMVPPELLVKNGVPLCQTVQEPGQFIVVFPKAFTSSICTGYVVSESVYFAQSPWLEAAEQVFKDIQDSCEPSIFSLEKLLFSIINDSRSHIEVLKQILPTVKRVCEREIDFRRQLKGLGLTNTEKLPTPESCKRGKSKKVKEEDGDFECETCRSNLFVSLVNNSQDDSMYCLPHAIQLLTRKKQIMKNCVLMITYSEDELDDLIHKLEDRIEAKSKKNYSFKQNK\*

1. **Polycomblike**

**>evm.model.scaffold00073.5**

MSEPEECPAAPDSTTKEQRIGFSHGEDVFLQLKDGKYYLGTVVEVDVARDKCLVKFLDNTSSWSSVKELTKVSTTESDVMCVLCKKSQPKTDNDIIVCDKCGRGYHQLCHQPQVIKEETPSEAHWVCKRCIDSQPRHGEPKNSMVKANIRKVCSGRDQPPPPPEDMTKLPYDPNMLSWDSNHRVNAEQIYCYCGLNGEWYTQMLQCARCKQWFHEKCVSCLTYPLYSGDRFYVFVCSMCNYGKEFVRRLEIKWVDLVHLMLYNLTVYNAKKYYDLDTVIVPYANDNWNTLQLPPRIRDVSQQIRRDSILEILISNRNRFKCGREIKKRTTIWGLRVRLPPPCPVVYLPDTGIIDDSVLRRCWGGNRRLQYLPPTTGPVLMPESTKPLIEIKQENLEISVNPTDVLRGAIYQNSETGQSSDTNLPNQSTEALRERYSGGGFVKKSFPFPKLSLQRRRRLMALGSSRERMLRKQKKREKENSESNIKLQCVREARYKKARKLLKNAIAKSKSRNCDASDLPPTPPTSVSGPPTPPATTSGISEMMVPNSVELLNQLPPSTPADTSGDETSSRGTLDSFIPPPKDFEGKNNPFRNLSELLGTPCTINQGNSNISLTFNQCPITLPLPLTPVISQPPLMRPAKRQLSEKDIIIDRNGQVKRRRQHRRGRPPQQQQTASKTAAIIPARNSDVKNEFVRNLRSSFNGSSSSHQIGNCVDYALNGRRLRQRQNIDKLPPPSSDPQIQKNKGNNLVVSGGGGVSSVPTSPKYSPVKQNAPDISIDDLKSSVNIYFGAANRIAAGEKFFIKAKRIGPNGQSQFLIEWEGPNT\*

1. **Lysine (K)-specific demethylase 2**

**>evm.model.scaffold01564.2**

MADEPVPAPKRRQLRERTKKLYTDDWAIGDEDIEGRRTFQLDEKIECERYNLSNFTGLFREMTGHELNVAYLQKHGLGIPLLFRDKAGLGLRVPSANFTINDVRTCVGSKRILDVMDVNTQKNEDMTMKEWQKYYEDQNKGRLLNVISLEFSHTKLENYVQSPTLVRQVDWVDVIWPRHLKEAQVEATNLLEDMMYPKVQKYCLMSVKGCYTDFHVDFGGTSVWYHILRGGKIFWLIPPTEKNLSLYQEWVLSGKQSDVFFGDMVERCGRVSLKAGMTLFIPTGWIHAVYTPQDSLVFGGNFLHSFGIDKQLKVAQVEEHTKVPQKFRYPFFTEMLWYVLEKYVHVLLGRSHLDIPESXXXXXXXXXXXXXXXLTPYELHGLKSIVMYLHSLPSTKKNVPDLIRDPVALIHDVRCLVEQHRHDNPEAAVTGIPVLPPPPPMTIAERERLKATKKTLTKIQRQQIIIEKQDSKSACARRRRTRCKKCEACTRQDCQECVYCQDMVKFGGTGRAKQTCLMRQCLRPMLPVTAACKICNLDGWGQQPSPLMGKPIPMTPSGLSECQVCFDIVHPQCVGVDPLSISFNEDLPNSWECLNCCEKGRNLDGKRQGKVRARKLSVSSAASSVPTTDSERATTPSKRSRPDPTETWADREPAEGEQRTALRTQLASQLTGSSSKSLKRPSVVVRPMPLPPIHRPNHDSSGQFYVYNKIAILSIFRYLPIKDLVNCALVCRAWSRYTIDPCLWRRLDLSHVQLTPAHLTGITRRQPERLTLNWTNVTKRQLAWLLSRLPQLRSLSLQGCTWSGVCALRTCACPPLTSLDLSHVSGLNDSSLREVLSPPTDSRPGLIDKTSRLKYLRNLSLAGCDITDVALRYVSQHLPHLENLDLSSCGRVTDAGVAQLAAPPAQTMNHLISLNLSNCKLLTETTLDHLLRCNALKRLDLRHTTQVSTQSVIKFAAKSIHNLHVTDVKLVEEKKGKNETRGT\*

1. **Additional sex combs**

**>evm.model.scaffold00060.26**

MEADIDVVKGDGGGETGPGCSGYSSMVHSKKVIKHALRQQAKRRRKNTTIAAGNSRTLPRIVVKPLPPPPPNDPPSPVNNIPHINSVVEEPAATMREVLASLPGFSLKSGRRRSTKRLSAAAQLEAGLVDLESPASILASTSLRALLNRHTFQGLPPLYQRKLAQLLPSVDRQDAAISGLNNEFFARACLEWRKRLAEGEFTPENQQRLKMEAERDKNKLDPWKLKHFEPIWGEKREPKLRSGFHCTEPRSVGAVTRSSLRLRPEMNVDQVIPENTRCLTTVTEEKMEENICVPETIVDVPDNVPSAQDIQQNLPEYNVTVQILEDENLESVNVNINPDEIIKNSVQEPTEQDEIVSTEIHHEVPVIEQVCPENQEVAPSLEMRHKGHELRQKNHEVRLRQEVRQKNQELKQKNELRQKNQEIKPVNQEIEEQIEETEEISQDDEILHSIEISQNCEISQNEEIPQTIELQVQDENIQIHEEIPDWDKMQNINPNPNEEIECLSDEISQTSEELSQTSEEQPIHQFNKEQFSQLTAEQIYQLECENNSTSPQDLMADESEMIINQEIQNEIHHETNQELHHDINQEIHHEMHQDIHHEINQEMHREINQEIHHEINQEIHHEINQEIHHEINQEIHHEINQEILHEMNSEIHHEMHREIPHEIHQEIHHEMNHEIQHDMNPEIHHEMHQEIHHEMHHEMNHKIQHEMHQEIHHEIQHEVEHEVQQQMHHEIQQELRNDMQTELQVEMQADMQNEIQSDIQTDMQGSNENCTDPESQLPEGMEIDIETLQRIHELEVRGEMREAYEEISGCPEEIIYPILEGMEIGSTGEEEAETSVISGPVEDVQEVEHLTVGNEDEALREANNYVCSEMLECSWAVDPNVGTVSNPNARAQEEIQVSLPLVTSLDGSVAANITVTTHDECGDTSTTTDSTNPSQFITSEAHTESINCIQLPVVQSTPFQSETLAIGTPVTNCLMKNIPTQSSPIIAFPQLQSIRFVQTSFHSGHGAPQNLNTTNAIPTQIQHNQQQQQVSIVRPHEEIVQIGTQNNVIHNNLQNGVQQNPTQDNLQNAVTVQHQNHGTNAIVIQHQTPIAAQSRQIVATLXXXXXXXXXXXXXXXXYPVVTVGSRPSRSAQGGQRSRASNKEQGGRARSSTKEPPGAVNLERSYQICQAVIQSSPNRDQLKAHLKPPPSLLARGDGAFTTTKSGGRTITTVKAQKSQQLNSHNKQTKGQAVMLRHVFTTARQTAPAEVTESNAVTQINSNGNGGLGQYILVQRTGVGDSAPRASSAPPLPPQIAGMGVGVHLVRGRPASAGEGSHQAVTLKARGALDGRGGGGAEPGAPGVIMGGDPPPPWECNMRGAMVICRQCGAFCHDDCIGPQRICATCLIR\*

1. **Sex comb on midleg**

**>evm.model.scaffold01242.10**

MMSATPNKIRGPGRPPKLKPCCTWCGETKQPLKYVLPTQHGNKEFCSQICLSEYRKGYVSERGACVHCDNVIRGTPVKLNPDGPYFCSNFCCNKHQKKDGQIDTKKNNNEQRATAASPVPSTILGNNNAXXXXXXXXXXXXXXXXXXXXXQSYKSGINITQSPSTSSGNFQFETYQTFDWEQYLKETNSTAAPAECFKQHEIPPINEFKMGMKLEALDPRNLTSTCIATVVGVLGPRLRLRLDGSDNKNDFWRIVDSNEIHPIGHCEKLGGMLQPPLGFRMNASSWPTFLLKTLNGAEMAPAKIFKREPRTPRTNMFKVGHKLEAIDKKNPQLICTATVGAVKDDRIHITFDGWRGAFDYWCEYDSRDMFPAGWCFKSGHPLQPPKQKSTGQNRFKSRTSNVLPVMAVSGSGSSAESAVTLISPTSSRAPPQLATEPDTSSANSRLSTENVTLYVNHTCSCGPYFDPRKVKAMPGQFGTGPISNVAREIFQAFLMAALNPRQMLNLLKRGEGEFITLTLESKPTTVRIPVFVEIEDFYTYIRRQLEELCVCEYLLSKRKESCNKCIINAQAVRNNDESNSSLEKRRWSADNQQNSMITISSTATSQQKQDHSQIIGIPTTQSVSSVTPSPPKQPRKSLPEFEAATSTTQSEVPVAKYSSTEPSEWTIEDVIQFIAVTDAALGQHADLFRKHEIDGKALLLLNSDMMMKYMGLKLGPALKICNLVNRIKGRRHLIL\*

***Trithorax group of proteins***

1. **Trithorax**

**>evm.model.scaffold00063.33**

MGRSKFPGKPPKTVTRKRIKVLAWPEATQSDSITVAENIYYGLSLFNETFGDNEKEHPPFHGFSSKEAKLSASYIKTQQQDGKNSAKDSYENLPCSSSIDEDIVKNTKTSSSVKENHKIDVQENKDPIKNEKIETTSSAIVDKSDEKPSSPSTRANKSGKVEKFSNFIKTPVLKSVNNILDRHHRTRQLRNSTAKRLLQKAKSNNSNARGTPVQSTTDKSINVRKFVLPIRSAHSSRVIKPNKRFIEELEEKSTNEHSENDAKQTKKAKKGKEDENSLLKSNEKESRTKLKKLINQNSQSTGKYNEKSIAQTTSRQKINKLNSNDQHLASQYQKXXXXXXXXXGIPAKVLPNDTTNIPNSESSRIQTRSGALNNASTSQNPSQKVPENHEISMPTEETIESNNSLKNSKNSHDTNDISMNCKTDTDHFDSESSLSESGSEHGNNSEDEQSEWTGTKLSGGKVILRKARLKLDNKTLGGTEGPFSMANVQCVSNGSPNTGLTGTVKCGVCGAVRFYRFVKQARKFGIYSCESCRKFISKMIKRQACAKSTNNTLTCLQCHKGDGLCLVPPVVRSQQWNLMRCVYKARCPACWLKMCLKCYNIPAVLRTGLNAMLPPLMRDPLTISLPLCLDDNDLQNQKLIGCNMGWPNEDCLEKNLFKSAMNWNNMEIGQKSNYHSGGAGSLGGFLTKKTDKFDYPASVSPIKKRKKENRIKVRKKMKNPSVTPTTFNKSPTAVSTRQRVELKGPRVKHVCRSASVALGQPIATFPSPDCKDDVEVNKITPKAQKEGEKSDKKEEVTREKESHKSNQEGLICNINSIPQLQPKRGKNQNNLAVNFSVERSLPKQIVETLHTVSIDFWEQYDPAQVGAKGFALIGSELFHIPAICFLCGSAGREPLIHCQCCCEPYHIFCLEPSEWNACIQPNWCCPRCTVCQTCQLRSGTKLSCIRCRQSFHYSCFPKSGVSARLYSPDRPYVCQSCIKCKSCGSEGVNVYVGNLPLCSMCFKLRQRGNYCPLCQRCYNENDFDTKMMECNECSCWVHAHCEGLSDERYQILSYLPDTIEFTCRQCSSNPNSIWRNAIEAELKTGFIAVVKALSKNRKTCAALQWSPRKECLCRPLTTIRKLDFDEKFESTNKNGTINEDIDDSMTDKLTSESNCNFKGELNRFNFDLDEQPIDVPRRGLRRLRQKIHTKDCSGKMKNHSEINSKEITDQENSSDCNCSEQQIITRPSPTLLSVKQKVNGNEYGSLAQFHCDMEHVINRIGAPDLLEAYHNILKEIFPWFDTLSSSLEINLFSTPSKENQNGFDSPGMKLDNSILDAWKEEILRSPKSVTAKTGNVYSNINVEDARSCSLCKGLGDGQELKEGRLLYCGQNEWVHSNCALWSNEVFEEIDGSLQNVHSTISRGRLIRCSECGKKGASIGCCSRNCNNTFHYSCARNMNMLFNDDKTVFCSLHADDCSSKKIQNENDFCLKRPVYVELDRKKKKFAEPDKVKVMIGSLTVDCLGTISPEFSDGIEKIIPSGYKCSRLYWSTVNPLKIVRYYIRTYVQVYVPEVSTDLENNVTIDHSKEQQIEEELRIQKMEFLAVKQTLDALIDTVCNKEVDENLAEQNNTDLLPPELKEAIFEDLPHDLLDGISMQDIFPKMSIEDFLVMDLKNDAFSTELLKDEMLPTEVEELKLSENKASKTDSILDSNSQSDSWLEAKNSDLMDDIFDPKNQKQGKEIRRSKSEATGNVIVNGQRCQRSCSLTWSCKLDSTYNPTMKRRKVPRNSNSVKSNDAIMEQQDDRKSMFHDLRIPDSIMVTVGRTSTSNIISESVRELKYCVDDSSSINCRLLPSKDETKDHKNLLWHSRQQPRIVQVDGPADASSASECSSPEYNLEERILPNCPSMPQLDGANDDTSQDNKLEAKETKIQSDDAKDILKSRLQRIFEFSEIESRKKLTEQEISKNAFSLKIPQLDGADDISSDDECINPQINHEINQSIPEVITEELGDQPVKCKRCQCTYRTLDSYNRHLTNCDIMTTSDSDSETMDNKLASPDSTFSMSPQFASMSPSEGHTLLSEYPDMQVTSPLEASVPSPHPNMQIEPIAQAIITPQMHTHATVETVHQTVLTSNDMIVQTQYTRTTTTLPNSSVVPSENGVHITEIPSSDSNDLNPMNPSTETITNFSPPIPTQPSVKAPKVKSPRAPKPRTKSVRAPVVRNSGQSSIRCQAMQNNPQMIQLQQSQRQAATAPTVILQQVAPQSLMSAYVETLQQQSGQNLQYIAAIGGQHEAAFKPQFIATNQLVPGSYIQTTPDNLLALQNGGISVLPSVQLAQPQPTVLGTIIQQQPSAIQCGVISSEQLVLSSTPTLEMFTDSTGSMFVSSQPMYYGLETIVSNTVMSSSQFVAGTVPQVLASSYQTTTQVFQASKLMEPIVDVQAVSAMPNVPTVQAVQGVPGMAGSYVVVNQPASLTDTISTPQLSVSTNPEPNYTPVACTNLSSTITPTQSIESVRTSVGPILESSVRPIHNLETASSIRPILDGSIQNFETSIVDINNSLKQMPTIPRVAVRPNPMNPSENDPWKITEPILANEQPINNSIRPYFDSKHVSQNTSMIKSSISSKIPPLHNHCTHRNIVNKCNDVNSVHSNYSSSLTNNNSNCNNLTLNNSPVISNPSAQNKIMTFNTRPMNRVLPMQAVTPKLESIKQNQKSDIVEEPTKPEIKSIETEKIDLPPKEISPIIKPEIKLKINNLEMIVDATGENFKLLEEFEENDKQIFKENFRENLKENNIISLKENVKKNINENIKETFTENIKESLKENVKEFANDTLIXXXXXXXXXXXXXXXTRETIKEIKDNVRESIKEIKEYVRENIKEMKGTIKEIAKVNMKEIAKENIRENIKENLKIKENIKREKDNVKEKKDKNESMKENLKNKSDIEPKEKSPSSLKIVLQKQLQDGSYKITHNLTTTNQKKSIPQPQNQLQLLPIKTFTLKTNALSEKTVSTNNNLNFVKIKSPPIAVKKPRLASKNAVKNSKXXXXXXXXIVQQKKKLTVPSLMYEIKSQDGFTHTASSMSEVWETVFQAVQNARKAHNLPPLPHNPLTENLGLENNATVYLVEQLPGVNRCTKYKPKFHNLTPPKPGEGDGDLLTECVNGAARAEPFKERKVHDVFSWLASRHRQQPKLIAITENESRRAASTNLPMAMRFRILKETSKESVGVYHSHIHGRGLFCLRDIEAGEMVIEYAGEVIRASLTDKREKYYDSKNIGCYMFKIDDHLVVDATMKGNAARFINHSCEPNCYSRVVDILGKKHILIFALRRIVQGEELTYDYKFPFEDIKIPCTCGSRRCRKYLN\*

1. **Nejire**

**>evm.model.scaffold00117.15**

MADHLVDGPPNKRTKLADPFQGPSDSSVGMAPLMMHHAYTNYGGGGSGNIQQMQGLXXXXXXXXXXXXXXWNNHTTQKRNYMTNTDMFDLENELPEDLLSSGSWGSTTESAKPPATGPGPGQQNGALDNELRQHVQQQQLSHHLIQQQGNKNMVANSLVMAAGSLGSKSPNMQSPPNVSVSKGVVDPQMVVSLGNLPSSIASSLANNQISIANSMGGLQSSMSMSGNNPTMSMPGAMNSGLVMTSSATGNNNMSGMAGGGLIVANSLNKQPLNTVSMMSSNAQGIHHPGGPHGVAQMQNGPALMNPRAVVMQQQQHMVGAARGQSPHQQVHQVNIVGQGPRMQTPPNMANMGQMGASSPYGYNSPGNGPGPNVNVGTNNPVGVVAPQQRGVGTNMAGMQVNRFGGPGGPIGSTNVVGGQEGGMAQQAQPPAPSPAQPQSGAPSGGQPGPQQATQGQMPSGQPQGATQSTADPEKRKLIQQQLVLLLHAHKCQRRESQSNGEAWQCSLPHCKMMKNVLNHMTNCHAGKSCAVPHCSSSRQIINHWRYCTKADCPVCLPLKQADKNRHQNSVAVTVPQPTTQPNPSPSDMRRAYDALGIQCPTTTPNLLPGQTVNRGGVRLAGPPLQAPGTMADVRMAQLQTQTGPGQSVIGTGQQVVAPNVSLPLSKDPTAVSAAANQSTPTTGXXXXXXXXXXXXNIQQQTVSMQQLFGLNDSGQPGILADNRLSNVQLPPGLQAGQVTATPVQGTKEWHQSVTPDLRNHLVHKLVQAIFPTPDPQAMLDKRMHNLVAYARKVEGDMYEMANSRSEYYHLLAEKIYKIQKELEEKRQKRKXXXXXXXXXXXXXXXXGGSGAGLRPCAPPGVAANVQARPVGTVPPNLRSHSPSMGQLGISNIGMQHNRMQFPXXXXXXXXXXXXXXXXXXXXXXXXXMLVGPSGPSPNGQSASNPNMVSNPGLSPFGQPQMSQANLTTTTSSVTTSQFPTTNGTAGLPNSSPVQNQHQFSDIRVRLAQAQAQAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTANQTVNSSSMPQAPSPFSGMQQSNQNQQFQNSLSMSASTPGDSGIAASTPQTLAPSASSGPSPGPAPLTNGPQSTTSTPNTPSVPSLMTPNQNVSSANQTPPHSAATPSPVGLASLGKGMTSQERAALNAPRSSSMSSQMAAITAALDRDNSPSPPTNNNKGKLDSIKEENIKMEIKQEEGAENHRGGDGGKGGSNSEMSSIKTEIKTEPMDETSDEMTVKEEPTGTIKDEPVTPMSSQDTATSDIKPIVPEPIQPTGTSSDKKRLCLFKPDELRQALMPTLEKLYRQDPESLPFRQPVDPQALQIPDYFDIVKKPMDLSTIKRKLDTGQYSDPWEYVDDVWMMFDNAWLYNRKASRVYKYCTKLSEVFEQEIDLVMQALGYCCGRKYTFNPQVLCCYGKQLCTIPRDAKYYSYQNSLKAYGLVSDRYTFCQKCFNDIPGDTVTLGDDPTQPQTAIKKEQFQEMKNDHLESEPFVYCTDCGRKVHQICVLHMENIWPLGFTCDNCLKKKGQKRKDNKFNAKRLPVTKLGTYIETRVNNFLKKKEAGAGEVAIRVVASSDKVVEVKPGMRNRFVDNGDMPGEFPYRAKALFAFEEVDGTDVCFFGMHVQEYGSECTPPNTRRVYIAYLDSVHFFRPRQFRTAVYHEILLGYLDYAKQLGYTMAHIWACPPSEGDDYIFHCHPQEQKIPKPKRLQEWYKKMLDKGIVERIVLDYKDILKQAMEDKLSSAAELPYFEGDFWPNVLEESIKELDQEEEEKRKEAEAAEAAAAAANILSMSEDSETGPDGKKKGQKKAKKSNKSKANQRKNSKKSNTPQTGNNLSAKIFATMEKHKEVFFVIRLHSAQSAASLSSIQDPDLVINCDLMDGRDAFLTMARERHYEFSSLRRAKFSSMSMLYELHNQGQDKFVYTCNNCKSHVETRYHCTVCDDFDLCISCKEKDGHPHHMEKLGLDLDDGSSPADAKQANPQEARKLSIQRCIQSLVHACQCRDANCRLPSCQKMKRVVTHTKVCKRKTNGGCPICKQLVALCCYHAKHCQEAKCLVPFCSNIKHKLKXXXXXXXXXTAQLLRRRVAVMNTRPTGQMGAVQSAQQSSNTNMTTGVAIKPGMSPTNLPSPHQPGVGLKPGAQAPSAHVLQVVKQVQEEAARQQAPHVSYGKVSPXXXXXXXXXXXXXXQGGNVMPPPXXXXXXXXXXXXXXGTHLISMDQWTPRYQPNTVMQQNPGLRQQSSQQLMXXXXXXXXXQGQTGMGLAGQMPRQTGVLGGPLSQVGPGGTSTMHNRAYQQLMATLKSPNTPEQQNQILHILKNNPSLMATFIRQRQQQTGQHAGGVGPLGPSXXXXXXXGLQHMLSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFTQPPAPPYGQQRPIRPPLMNYGGFNEQGYGQPGLKPTPPPVPSPQGVMGPPGISVQQQLMQSVRSPPPIRSPQPNPSPRPVPSPRNQPVPSPRSGPVPSPHHHPPHGTPTHSPAHELGGPSEMMLPSGHPPNMPHHSSPAPPPTSGTDSSEMPQMTPQDQLTKFVERL\*

1. **SET domain binding factor**

**>evm.model.scaffold00153.21**

MLSVTTPTQLHEYTEMSRLADYFIVVGYHHEKERGGISSGIILQRFPEKDWPDTPFIEGIEWFCQPQGWALSTERQEPRFYVAILTDIDANRHYCACMCFNETVSITPSKPVDEEEDPVDGVNRALVKAIPAVSHHSIMYAPKCLVLVSRLDYIETFRNCLGIIYTDYVENLGIPLETLVGNILGCIQVPPAGGPQLDVIVADLDGGSLMVPDGVSLSLLPEPLLSQTQDALSMVLQPELACADYAFPPLATRAPHPPMLDKELRAVFMRTFAQLLQGYRSCLTLIRIHPKPVITFHKAAFLGERGLTDCDFTTRILDCMFFTSFIAERGPPWRPCDVWDELYSNFSDHLKQESQDQRLILTHIQELAQQLYTNENPNPQPYVQKILKPPEGAFARIHQPMLPRINPENVQAIIDEGLAKSNLKVRLSSLRPIQPRIVPMGPHISITHDTRHLVSNSARRLEVLRNCINCIFENKISDARKTFPAVLRALKSKAARLALCMELSQHVVGNKAMLEHQQFDLVVRLMNCALQDDSSMDEHGVAAALLPLATAFCRKLCTGVIQFAYTCIQEHAVWQSLQFWEDAFYLDVQKDIKRLYLPGENTPPRQINESILSPISPRENKDFPFRERGYRVQEPSALEIAAEQMRIWSSINGDKQKELIASEESTMYSQAIHYANRMVYLLVPLDISTKTHRQDHVYDDERASNSITNSVASDSGDAESGFEEADPGETGASVIRMVSRFVDRVCTEGGVSTEHVRCLHQMVPGVVHMHIETLEAVHRESKRLPPIQKPKILTPNMLPGEEVVMDGLRVYLLPDGREEGSAGLPKTPPLLPAEGAIFLTNYRIVFKGIPCDPFACEQLVVRSFPVTSLTKEKRVSVQHLAHLDQYIQEGLQLRSCTFQLIKLAFDEEVTPENIETLRKLVQKARNPPHIFHHFAFNGQVLVTPTTHHKGKEKNATLKGFAKKTLLKTARKAGFKPKQSSKRQKYVLPNMNLTNSNKYMTSPGRMSLPMTENNDMSHDDDLSVDEFEIPGIIPAQPLTDAKTLERLSERSYVRDWYRLGLCSSRPQNNRRNEPFRLTSANCAYMLCRSYPALLLVPTAVTDDSIRRFCRLYRHNRIPVVTWRHPRTKALLIRGAGYHGKGVMGMLKAHPTSAGNLKATSSESTSSLEQEKYIMALVAATPLSILRQGSAWGMSDSSLSIDSLLLAAEDNRNNATPEQSRRNNHFNKAMGNLGSSGGKGPKNFGRWGSLKDKRHSSQASLSSVNQRGTIRHSADSDSGTECVHTFQRAALYVLGEKSYMKGVKAESAAPKTDFIPVEFYDVRHTKAAFKKLMKACVPSSPSIEPDQSFYKLIESSEWLHQLQSLMQLAGAVIDLMDVQGSSVAVCLEDGWDTTATVCSIAQVCLDPHYRTIDGFRTLIEKEWLGFGHRFGHRSNLATNSQTTNFTPTFLQFLDIVHQIQKQFPLAFEFNEYYLKFLAYHSVSCRFRTFLLDCEFDRVECGITAVEDKRGSLTSHHKGVDTGSDDETVYPGGRLAGTNMGCNLGQSIFDYIEKQHARSPLFYNFLYTPNSEHPILRPVSHLPNLDIWNYYLEEELAHGPAYDLEILQQDSQQEEEAEAADGIVKSNRKVVIQGYNSVSSMVPDQFTHLLEEIHKLETELGHLPQKWKVLWDKLELPNTDSLARHASFSTALVRHHGRLIHKRSTLELLLRGKLAGGTATGNESSVYAHPHRFERLDSATPTHCDACSGVLWGPVKAGLRCVDCGHVCHDKCADAVPKNCTKYKAVADNLQSHTLTRSGGDNGSVNSSVTTMQTTSQQYYDQFSSNVAENRTHEGYLYKRGALLKGWKQRWFVLDSIKHQLRYYDAMEDSHCKGYIDLAEVVSVTPAAPMQGPPKKTDDKSFFDLRTNRRTYNFCAGDATTAQEWIEKVQACLQ\*

1. **SET domain containing 1**

**>evm.model.scaffold00195.15**

MLIVIKLILIKFDFNKQIGFQVIAHNPPVNQLYTGPGYPGALAHPHYPHPVSDMYGWPRPAHYPYPYGAPYLPNSYQPPNNSFQGGIHNNTQGTNYFPSLQSRLQAMTNFNTYKDNPQGPTINGVLNKVVNELKQILKKDFNKKMVENTAFKLFEEWWDEKKMETNEKSQTTFEENNVTNNVINKEENHKPEGLSSLIEQATPLGFNYDGFGLGIRASMPKMPSFRRKIKPPSPVPQDEDSRLSDRLGTELIESDSDLDLPAVQKTKRPLESLPSXXXXXXXXXAGSSSDDTSSSESSSENSDDEEEEFTYDPRPLASASENTEILMELAIQRSLDCATPPGRQTPLPDLIIPTQDNELPEMCNDASPLSSPTYXXXXXXDETKEENEMKTIDDNNSEMKIIIERQKTPEINADNKKTENLWLNQEPRDIERMESSAAEALMTLAGQDNIIRHKSPGPIEANIIRSLEILSNKYINDVPILQESEKIEMFSEIPTTDSEEESLEIRRLRFQAEANLRLNGENYPDGDSGLRPLVFAEHSYSLLPAKPVVEEKSTIIENDVTPILPTTIKAKPAKLDKRKEKAEKRKNNKILKLHIQNHEREKENIIEMENRKNIYEIPKLPQPEVTYKERDLMSEMSILYQFLTRGIDAEDVEYLRRSYEALLADDAQGYWLNDTHWVDHPPTDVPSPAKRRKRDDLRLHATGCARTEGYYKVDIREKLKHKHHYAQSIQRSNDVEESGGPYAGGDGIANGPKANSKTLTGKMQALSREARSNQRRLLTAFGIDTDSDLLKFNQLKFRKKQLKFAKSGIHDWGLFAMEPIAADEMVIEYVGQMVRPVVADLRESQYEATGIGSSYLFRIDLDTIIDATKCGNLARFINHSCNVSIIFFTLSGIYF\*

1. **CXXC finger protein 1**

**>evm.model.scaffold00707.9**

MMSDKQNGLSREEIAKQFMLPERKSKIATLLKQDGQEYCICRSSDSSRFMIGCDACEEWYHGDCINITEKEAKYIKQFFCVRCKEEDPTLVTQYKPKRSEREDRKHRKHREKEKERAYRHEPIDWDAPVVKKSSKRCGECTGCLRTENCGKCDACRHLKKFGPSVRLKLRCVQKTCRISIEPLKLKSSSKSSKPSRKRRRDSSNERIEHLEPPIHCFGPACMKQSRLGSKYCSDECGMKLATNRIYQVLPQRLQEWAMTPCIAEQNNRRALENVRKQQNDVRRILHELDKRHMELDQIVERAKHSTIDPKMEIDENDDTEMSMYCITCGHEINSRTAIKHMEKCFNKYESQESFGSSFKTRIEGQVMFCDFYNPVNGTYCKRLRVLCPEHCKDPKISDTEICGCPLVSNVFNLTGEFCRAPKKSCVKHHVWEKLRRAEIDMERVRQWLKIDELVEQERQIRSNMASRAGVLALMLHSTFNHELMEQMTQEQNINQMEAMEEEYRRGYGMQNERSE\*

1. **Absent, small or homeotic discs 1**

**>evm.model.scaffold00061.18**

MSGDSGWNAVIHHPSELELQTWNWDENDGEPERELPSTVDMDAIKGGSWNPATGPNGNDSIDSEDDSESDDDSSGGTEGSCSYSDSNTESDDESSGEEEDDTESNSDCTSKHSEQTFSIRETNFEQGALKLKIAMKATKKEDKDNSKCDRSRRNLSRRTKTPSRVAKASGDSTDDSDSSANPVPQFSQPQLQSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXINQEDLAAILPDEDHEDAPFDGFEDSESGRLVSKAIERMSLGADSDSGENTDQIPVPVYSSTLLQQFVEKTALLSEPRKRRNKLVKKLNESEYACVSNVSPDSGIQSVDNSPLHLAISPVSPQAPTSQSPVQVASKPAVNVDRVLYPPKRKPGRPAKLVSTQPRGPGRPKLKPEIAAKIEKLEKNSNESQEKISIDPSCAKQTVQCKTLTNSLSESRDSSFNKKSKNKKSSPKNEPDEAKSKLAESEKVLPTRKKCLSKSNLEKQTKDTEQLNERLEKSKEQREKNKELREKSKEQRDKSSERTEIIKEQTEKSNERREKLKEQREISKEQKEKNKERKEKSKEQKEETNEPKEKNNEQRDKNKEKCNEQREKVKEQKEISKEQREKSREKINEHTEKIHKSEKNNERKEKNVEQRDKSIEQKEKNDKRLRRDKHISRKETAELPSEKQEKVILNRIPSEEKLPNNNKKSTKENRLDPTTSKKQIPVKKPVASISRRVLKENKSNKKTSANLETNVAVQTVISLPVTIPLQTEKLDFGRKYQKPETKNQSAHHHKHRHHKHCRKLVVPPKNPVRVDPFIVQELENLIEEFSKSCTLGRNNITSSSNHSELPQIFRVKKITKKRKGSEINSNDDQKLIKRRLKKEKMPSNVDSKSSTNSNSNSSSNEQRLPLKKRHYHVSSPHSSQSSAGSCNETITNSTESHIEEAIEATITRYGGDXXXXXXXXXXXVPVTPKKRHRDTEEPLPEKINTELNDTTPQIVTTSELNPRRKKKIVKDLRVTVTKLAPDTQIENKNSCEKGIKSTGEKAGKVEKAITEKIVKPEIAKPNLEVKIESVKKTETPTTIDKGVNLNLSTTNSNLKTGPTIVLKKKARRRKAINRTGFPTLKKKKKKKIVVEPMVKEVEIIPTIEETEVKIIDSVDDIQSEESLTKEIVSNQDTKTFEIVDPPPIREFSRHCFLDDDSCPTTMSLSKESSLECDGSRPCDKLCPVKFEKVQDSRIYDENATLEESLERYNMSQRVAVLNEENLRKLERSNSRETVKHELSCNNNYSHKRRRGSASPCNLTIRNLKRLKNAGYDTESDAMPSSDLASDDHDFGKQGNSIRGKRKQPRWKKRYLPAGLFSDYFKEDEPRKITNSDSGKNKMIYDPAEHPHGLLPPPYHCGKFLRQRKIPFQLPYDLWWLHTHSRLPGRDLVPSWNYRKIRSNVYYDVKPTTLYESQSCECKPESGCGDECINRMVFSECSPQFCPCGEKCKNQKIQKHDWSPGLQRFMTEAKGWGVRTQKSIKSGEFILEYIGEVVSEREFKSRMATRYANDTHHYCLHLDGGLVIDGHRMGGDGRFVNHSCEPNCEMQKWSVNGLPRMALFASRNIDAGEELTYDYNFALFNPSEGQQCRCGSDGCRGVIGGKSQRVPRSVAIVPALIDSTERKSVGRPRKNIRKSNIVQSTNSKGLCKSRRIGESSCITTPLIKPMSHQQRCFAQEHHCFLLRNFEKVKRQKLQINQVPQPGKIKAIGNVQSTKEKNGTDAKSTSDAFLSQLTALTNTNARTVRTRRLAQAQDDPEVHKTAKLAKVLKDLYSVVATAKDETDKLLCTPFMTLPPKRKLSEYYDKIQDPIDLTMIDQGIGSGHYKTAEQFDQDLIKLFDNNVRFFGRTSEIGIAAARLRKLYLGTKADFVYAITEATGLPPSQGFLPPQGSTAGEEDVIRCICGLHRDEGLMIQCERCLVWQHCDCVKADTSADSYLCERCQPRTVDLEIPLEGEEEEEGKKHYITLLRGDLQLRQGDTVYVLRDTPEKHTYKTIQNPDYEQMDIFRIERLWKNTKGERFVFGHHYLRPHETYHEPTRKFFENEVVCAPLYEAVPCDLVAARCWVLDPSTFCKGRPVGSSPEHTYVCEHRVDRAARLFTKVARSRHQVCTKPYAFETFPERIKHYRTYLPHSLDGITGGKLLKDKKKNGCQEVENNGQKAETREVNRNNKDQPPTSRQSTTKTRRRSGDNLTVPTIIVSYAQREEQRKRLNGILMNLLQRMPNKKDPLDLSFLLERNRRNRKRPGGLNP\*

1. **Brahma**

**>evm.model.scaffold00162.12**

MASPSPQSSPMPPPQAPSPMGPPQQSPSPSNPQGSPMGPPQHHPQSPTQGYQPPPPPPGGPSMPQSQQSGPPQQNYPPHPQQMPPNMGPQGQGXXXXXXXXXXXXGPMGPGGQMGPGCPINSQMGPGGPQNTQMGQGGPGSQQGPMGPNQMGPNGPQGGHHMVPGAPGQNPPGQMGPGGPPGHQYSGGMGPGSQQGPMGPGQMGHSGPQGVPHMVQQGGPGQMGSSNQSGSPVQMGQSGPPGHQFTNLGPGSQQGPMPPGQMGPNGPQGGHHMGGPGQMGSGNQGGPGQMGPGAPPGGMGPGSQQGPMAPGQMGPNGPQGGHHMGGPGQMGSGNQGGPGQMGPGGPPAGYQFSSLGGMGSGSQGPIGPGQMGPNAPQGGHHMGGSGQMGSGNQGGPGQMGPGAPQGHQMSFPGSMGPASQQGPMGPNQMGPNGPQGMPHMVQSGPGQMGSSNQSGPPSQMGPGAPPGAPNPMPPQMGPGGGGPVGQQGAPGQMGPGGSGPIIPGGPGGQMNQNAPGQMPGAPPPGPPPGPPGSGQENLNALQKAIDSMEEKGLQEDPRYSQLIALRARQGNNMGDKQTFSSQQLQQLRMQIMAYRLLARNQPLSQQLALALQGGGPPPGIVQRPIDPSQGPTSGSQAPGANAMGPAGAPRPGSQTPXXXXXXXXXXGAKTNRVTSLAKPAGLDPLLILQERENRVAARIALRMEQLSNLPTNMPEDLRIQAQIELRMLRVLNFQRQLRSEIIACTRKDTTLETAINVKGYKRTKRQGLREARATEKLEKQQKLEAERKRRQKHQEFLSSVLQHGKDFKEFHRNNLAKMSRLNKAVLNYHANAEREQKKEQERIEKERMRRLMAEDEEGYRKLIDQKKDKRLAFLLSQTDEYICNLTEMVKQHKMEQRRKQVEEQKRRKKRKRDGEVGEDGTVEDVRVSVIELSTGRTLTGDDAPMMSQLQAFMESHPGWEVIETESXXXXXXXXXXXXXXXRKTLSNWVLEFEKWAPSVVVVSYKGSPAGRRAIQSQMRATKFNVLLTTYEYVIKDKSVLAKLQWKYMIIDEGHRMKNHHCKLTQVLNTHYLAPHRLLLTGTPLQNKLPELWALLNFLLPSIFKSCSTFEQWFNAPFATTGEKVELNEEETILIIRRLHKVLRPFLLRRLKKEVESQLPDKVEYIVKCDMSGLQKVLYKHMQSKGVLLTDGSEKGKQGKGGAKALMNTIVQLRKLCNHPFMFQAIEEKYCEHVGTQGGIVAGPDLFRASGKFELLDRILPKLKATNHRVLLFCQMTQLMTIMEDYLTWRGFKYLRLDGTTKAEDRGDLLKKFNDPGSDYFLFLLSTRAGGLGLNLQAADTVVIFDSDWNPHQDLQAQDRAHRIGQKNEVRVLRLMTVNSVEERILAAARYKLNMDEKVIQAGMFDQKSTGSERQQFLQSILHQDDADDEEENEVPDDETVNQMIARSEGEFESFQKFDLERRREEAKLGSQRKPRLLEESELPDWLVKDDDEVERWAYEEDEDRFLGRGSRQRKEVDYTFSLTDKEWMKAIXXXXXXXXXXXXXXXXXXXXXXXXXXGEEDDEPMPKKRRGVSSIHPKLKRTMKKIIAEVVDYTHGADGRLLSEPFMKLPSRRELPDYYDIIKKPLTINKLLTKIEEGKYFDLDELEKDFMQLCRNAQIYNEEASLIHEDSITLQTVFTDARRKLEIEMTISEDDKDPDDGSDGDSSVKMKIKLKQKKTEGRVGRRKKSTKKYISXXXXXXXXX\*

1. **Brahma associated protein 60kD**

**>evm.model.scaffold00608.8**

MAQRFPVPNTGSNGPPPQRYPPPSVPPNLRQYSGPNFPMQQRSSFTPPPQMTNAVSGPGGIMRANPPYSGMRQAPMPNPPGGKRSTDQRIPMSQQKPYFWNSDFSHSTSKKKKKLADKILPQKVRDLVPESQAYMDLLAFERKLDATIMRKRLDIQEALKRPMKQKRKLRIFISNTFYPAKEPGEGEEGCVASWELRVEGRLLDDSKNDPNKVKRKFSSFFKSLVIELDKDLYGPDNHLVEWHRTLTTQETDGFQVKRPGDKNVRCTILLLLDYQPLQFKLDPRLARLLGVHTQTRPVIISALWQYIKTHKLQDSHEREFINCDKYLEQIFACPRMKFAEIPSRLNPLLHPPDPIVINHVISVEGTETKQTACYDIDVEVDDTLKAQMNNFLLSTASQQEIQSLDNKIHETVDTITQLKTNREFFLSFAKDPQQFINKWIISQTRDLKTMTDVVGNPEEERRAEFYYQPWAQEAVCRYFYTKVQQKRAELEQALGIRNS\*

1. **Moira**

**>evm.model.scaffold00303.40**

MLSLGPKKDGSPNLKFFESPEILTLLDGVKQWLLKNCKKYVQTDPPTNKSLAALVVQILQFQEDNLGKNISKPQMTRIPMKCFLDFKPGGGLCHILGTAYKFKQENGWRRFDFPVGKSGSRLNLLIDMLTAAERALVQNRCLILPNVFVRSDVDKATATKVKDIVRRHQGSVVENEADATHIIYPSVDPLEEEYARPFMRRDRSVLLHWYYFPDSYDTWTNLDLPWDFPEGNFGSVNPRTIYKVSATWALDLDQYNEWMNEEDYEVDDNGQKKVHKYRLSVEDLMSQPSHPPTGTKKPKRKRSPSPPPKIGKRKSGRGPAGMQGATSATAAMKKTRGGVDEEEDLTQGMEDPPAEPRIVEVVASATNSSITGSGSTGGGNTSTNKKQDNELQPLKSGNMADLDEPSEGDKNSAHSAQDREERGSSKERGEGSKSDEPEDNVTEQTHHIVVPSYSAWFDYNSIHTIEKRALYEFFNGKNKSKTPEIYLAYRNFMIDTYRLNPTEYITSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESRPTPMGPPPTSHFHVLSDTPSGLAPVNPNPPKTPQPSAAKALLDLEKKPSTPLGAGGDEKPTPNSMTNFGLKIDQYSRKPAVLKNKQASSATRDWTEQETLLLLEGLELHKDDWNKVCEHVGSRTQDECILHFLRLPIEDPYLEEGGPEGLGPLGYQPIPFSKAGNPVMSTVAFLASVVDPRVAASAAKAAMEEFAAIKDQVPAALLDQHLRNVQASANSDGKFDPAAGLAQSGIAGTGPPEPPEDSSASSTGQSNATPSTSPHPTPEAKKEDATEKTKEVVESEQPSTTPPKKEEITENERDQSEKMDVDTKESEDETKAKVDGEESDGKEKKDKQVVKDAQLQSAAAAALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETTMEREREGLEYQRQQLITERQQFHLEQLKAAEFRARQQAHQRLAQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXA\*

1. **Osa**

**>evm.model.scaffold00089.20**

MAATQAESQQNDVNLSESVKCIQKRPQVVANSSSASGKQQLDQEPADKTATRGAAQLLNYVKRADSGFEMSQYREDIGGHTAAEVKSPREPQQNNPQDQQQQSVNDASGPGHPGNHPNHPFAPNRDYSDEYASNKSNDSFSKQHVDYPGKQTAPDYGKQMPNEPERGVHHQSEMEEHYSVSKIEPRLAHIGAGPGAFPGQPRFLSGQSISQATGPTPTLNQLLQASSPMHRFHSNYPGIGPESYQQPWPMQRPPVVPPVYPQPGQRPPQTGSPRLHPGPGGPSPTPMPYQPYSQRYSSPARPHSPYGHHQINSYAQGGHPSSIYADQRGWNQAGPPNPPPPPTNQTSPSSQSPQRALSQSPAPPPSASPQPQPSGQPQNFHSMQQRSTTPNTQGIDSGELSGQNSNDSSNGPAGPGTPNSQGMRPTPSPTGSTGSRSMSPAVAGQQNVQMPPRPSSSQSEGSGPARMSHSPMATQGGYQQPLGPSPHMHSYKMNSSGPGVVQPGPVPTGLGGINPMSSGMGYAAGGAAANQPGGYPGQGSYPPPRPHMQFPQGYPPPTNSQPPPNNQYQSARSNNMVQYPPYPHKMGFNSVSPGMPPSPGPPQVYGTGAAGSMVPPGTPGIGGIGNMGPPTSSMGPPPPSPNHVSNQPPPPQHPPAATPPLNHEGSPMPPPSTTPNSHPTPAPTPTSHSSADLSAETSNDSGITTTASERRSWLDKLVTFMEEKRTPITSCPTISKNPLDLFRLYLYVKERGGFMEVCKVTKNKTWKDIAGLLGIGASSSAAYTLRKHYTKHLLPFECHFDRGGVDPQPIINQVEAGSKKKGSKGTASVPSPGSSNSQDSFPAAGSSSTSMDGYGSYQGSYPGGAPGVPGGDYTPPPPRPPSQSSAPTPHQGMQQSNYQNTGSFQNYPQEQYIRPQGSGMSQQGEFNQPYTPRTHYPPYVPDSERFVPNRGYSGGNMPPNSAGSQDMYNRYAGNQQPTSYSTGTPPGARNSNYPSTPQGHPPNAQQPPPSCQPSSSAQSSASSTFSCPQDYYRQEQSGYGAPGGSQIYPSATAANKNMPPPPPGPQQPRRHPDFAKDQQYPQYNQQRPAYPGWPGATNQYNSGSAGARVQYPSQXXXXXXXXXXXXXXXXXVASGAPAPSGVAGIPSSQQWVGQQSTRPTAQPSIPISHPPTLWERHYSSQPSTLYPPPGSHQSQLGINPMLNQQPAPKREMTFPPDSVEAVTPLLYKRRKLTRTDVAPVEAWRVMMALRSGLLAESCWALDVLNILLFDDSSVSYFGLTHLPGLLDVLLEHFSRSLSDMFESSTSDEERYWGQTVDGPEVDLGSVVRPIDPEDRTKLLSSSNYTFLSRRGRPVKMVPRDDEIFVLDSRRSWDHQDCEVETEPWQVESNTTKYIVTCFQSETGNVPFARHLRDEKPPLLQKEVDSVDSKDEIKISESSSPPENSESHRKPEQLCGGGGDKPKDIGERKQEKKKKTKSISDVLSRIKKEPVEMNDLTRELFEKKNDSSRKECEVDSKANNNVGEHFVELPKDDEESLPNQNGLSDSTSTIDSEKREIKVEPDEEGGISSEEKEGPRLKIKDPAGTLKRRRISDYEDESYSRDEASLYLVTETQNSLAQRCVCLSTILRNLTFIPGNESEFAKNVTFLSLLGKLLLLHHEHPVRTLKTRNYDREEDADFADSCSSLQGEGEWWWNFLHHIRENVLVMSANIAGHLDLSQHPEEISRPVLDGLLHWAVCPAAHGQDPFPTVSLNSSLSPQRLALEALCKLCVTESNVDLVVATPPYSRLQRLCSVLTRLLCRSEEQCLREFSVNLLYFLSAADSGVARSIALQTPCVALLVAFIEQAESSALQVANQHGLPALRENPESMGTSLDMLRRAAGTLLNLARHPDNRTLLLQHESRMLALVMSQILDQQVAAIVARVLFQCSRSSVTS\*

1. **Polybromo**

**>evm.model.scaffold00271.10**

MNKRRRTSSVASRGTEDDPDDVQPEPTKRRKKFDPSDLCQQLYDILRTHRKEDGSLLCDAFIRVPKRRQEPGYYEVVSNPIDLLKVQQKLKTDEYRDMEDLASDIHLMVNNAKAFYMRTSPEYKDATELWELCTCTKNRISEEYEDAETKGKIMLKAKKVSVKQEDAEDTSESSTNPDEESTQVYEELFSTVMTVTDPTDNNRPLHSMFQLKPSKKLYPEYYEVIDTPIDLKMIAKKIQDGAYGCIGDMERDLMLMCRNACQFNEPGSQIYKDAKLLKKIISVAARKQDGGMSAAVSKSLANAPSTRSKRGTRSGASSLIAQTAALPDEDDESDDEEEEGAENDESDNPQWQLFQTIRTAPNNQGVRMSEYFWKLPSKRLYPDYYRMIKNPISLLQIRTKIKKGGYGTVSEVAGDMNIMFENAKKYNVHTSRLYKCAVKLQKIMQEKVQELLEFDRESESESETECNQQPKLIKRASNVLTRGKYTDNIPLKKRLYALVKCVVEYVYEDGRQPMLLFMEKPSKKLYPDYYQVINEPIDMLAIEANIKAEKYQTENELIQDFKLMFSNCRQYNEEGSLIYEDANTLERILMEKVKELGPLPDVKNKSTASTPTRNVGRPKKVVSLRIQKLRTMYDTIKDYHDSKGRQLSLIFMKLPNKNEYPDYYEVIKQPMNMEKIAATLKNHGYESLEELVSDFILMFDNACKYNEPDSQIYKDALILQRLVLQTKLQLSEDEESVPDVAAAVQEILATIFTALYNHQDEEGRCYSDSMAELPEHDIVDGKKIRGLSLDLIKRRLDKGVYKRLDRFQEDVFTCLERARKLSRTDSQPFEDSVELQAFFLRTRDDVTRSGDLLHSPALNYMLIDLSTQIAELKRIKLQQEISLPAEDESCDGNDKESESNSSTGASNGDGATMSFNQEVYRAGDFVYVEPSERGMEFSVVLIERLWTNSMGEQMLYGNLFYRPSETYHIASRKFLDKELFKSDVHNAVPLVKVAGRCCVLSVKDYFRMLPEGFLEKDVYVCESRYSTKARSFKKIKNWNFDPDRLKLVAREKLIEPKRVISVYKERLEKHKEEIAELEEGEKLIEKERPNVIQFNSDDSDNTYYEQYNTCIGSVKTGDFVYVATEGGRQQIAQIDTIWSTKEGKTYMKGPWLLTPSEIPHAPTKLFYKQEMFLSTIDGTHPVVAIVGKCAVLDYGEYVCSRPTEIPEDDIFICESTYDETKNLMRKLNLDGLKKYNHSSAVTDDEIYFFRKPINPAKVSSEVAQMQSQIKPLSASGSFDMDSSPIIPKLEPDVLSMGVGLGVGVGEDSMDAGGPPSVGSMEAQPVLSNTQTPVSTKKKSTGKKLVTGYILYSSKHRTPITQNNPDSTFGEISRIVGNEWRKLPAGEKQTWEEKAIKMNEEIGQVKGNSLPISSQDHCFECCWDTCDYQFEDMTDCIDHCIAEQSGHVQTTFANLSGEENVIFQCQWRGCGRTKKSVPPFPSVQRLARHVKEVHILKSNGRIILPADRSKYIEGLNVENRYISNWDKQMSATPENTQIPEITKLPSEWLGNGVGNHGNVVNALWTLRNMMMRDVLAINKTL\*

1. **Trithorax-related**

**>evm.model.scaffold00009.9**

MKNAIREDSEVPLDIINPGDKSPRMIGPGGAVTCRRQKSLAKCRNPNVTNFIEPIEELTIVGYSEEPDVGILFEPTGHFYAHFSCAVWSSNNQNVTPELISATVIQASSRRCASCSHYGAGLSCKVGSCNRYFHLPCSAASSCFQEKTTLSLFCNIHSDQVPRLLNFDVSCMICGQMGDVSKLVMCSSCHQHYHGLCVGLRLLPGVRAGWQCSTCRVCQGCREHEDVSKVMVCERCDKAYHPGCMRPIVTSIPKFGWKCLCCRICTDCGSRTPGAGLSSRWHAQYTVCDSCYQQRNKGFSCPLCRKAYRAAAYREMVQCNGCKKFVHGTCDPDADPHTYQKRKEENPDYEYVCKNCKNQALMKRKDSLDEHGLDMSLTGSQDSLYDGDSSEYDYTGGYDESYYPMGMGKGKPFCASKIAKKRFGGGVVGRPKGMGKHGYQKRQKMNEFGRKRGPKAKMRGIFGVPGVGLQCMSDSSKEDEPGVENRLVLCSAKDKFVLTQDICVMCGAIGTDQEGCLIACAQCGQCYHPYCASVKVTKVILQKGWRCLDCTVCEGCGEKTDEGRLILCDDCDISYHIYCLEPPLDYVPQGSWKCKWCAQCQTCGSDNPGFNCSWQKNYTQCGPCASHTICLECQLPYTEGDLIIQCSQCQRWLHCSCDAIKTEDDAEKCAEVGYNCTQCRPSDEPPPHILRSLPKPQPKYPRSPPPLTRSPEHYKPSPQQYLVDGVYLSESGMNHIKSLTFEHQQTRKKRRKLPVVDKEADIMATIESVVAGGSHDNSLDDGSGKLELLDVKDEPNEVLKEGMAWTPRSGEPPPEGFSIYTTENGVTVLRRKRQRNLQKLGIGGFVVRLRXXXXXXXXXXXXXXLPEGIMSLSDDKPRRKPQRRKPKTKLSECFPSYMQEAFFGKVLMGTTKDKDLESSSDSDNEHKTNHNTGTIQLSQDELKAIQQVKAKQEKEEIKIPMELHIKREEMMDEDASDPEALGDILPISGDLLDSDLVNTIMNEPDEDLAKASEALEELDDAQGSTKDELTDILSPHFNLESMVRDTGLPNMDSKDVEEIFKGVLTDESQESQESSVFPIQPQVTPHASAPSTPLVSPSPHPGLQGSLQLARPQVSTSLPSVGQNNLNSPMSFPPPSPYHSEYSNSPQQFSPAFSEPPSPWVNPEDEGAGVNSGVPHNQRGNNPKMEADEVLGTGATISMVLYANINHPEWKTEFPAWPDRHKQIQKKWRALPAETKAPYLTQARENRAANRMKKTQQIPKDLPSTNPVTATSAPIITTKPVTTMPSAQVPPVVPMVTSQKQIGLLSSVDGDKSXXXXXXXXXXXXXXXXXXGQLAEEQERLTNRDRSTREAEQERQWKXXXXXXXXXXXXXXXXIHEQRVHAMARVHRQINEDGTPVMNQDGTTGLTTQLQVSTSQDSNQISSIASPSPGSRATFAAPPIKVTRGMAPQSPLQGMPRLPNQTCTTGMRPMGNVVRPGIPQAFPQPPSPFSPQAPQSPHDFPQSPASTQSQEHFQRFENSEAFSQGSQTPRSQIVNTPTYATSPRNDVFTQPPGTPRPVFNANNNRSTTHVYAPSRTPDPYISQPATPSPVSNYPSPRSETRSEPQSTEAFSQQPEVNRQLRDLLQRQQFSKKIETHGASWPQDGQNPGDVLPQQFEPGQIQLPQHPQLSGKSAEGTFRQPLPPGIVRPRMPQPNVLVRNPIGVSPRHVMAGKLDSTRLQGLDPRTRLLLRPPVSVGVPQQHFQSNQVLQRLPGPRAALQEHYEVIQQQRFSEPNQGQITQRIVRAGQDAISQGIRMLGAQSMIRPPVISTRVNETNVNTPEASEIPDNVTAELEELEQEREAPLGEVESVSAILGDLGEDDDELLAEMGADFNILEYADPELDNLTGGGKTNILDLDLEQVEVEPKEEKQKKDSKVEPKPEDLGGTTTAHTESNEKIVTSTVQTPTETTSAPTQTQTVQGIAPAAQTSQPSAGVIPQTHPQAAIQQLNQHLQTAAAMGRPVAPGTRLLAPDGTIGVVTSTNTVTVSYPSTFPGHPQRIAQTHMQVQQHQRLGMRVAGVQNVAGRIVSVSHMIGPRMPLPPPPPPPYPGPPPPYRGPIQEQPLLLEELLEQEKRXXXXXXXXXXXXXXXXPSGALLSDSEFERLRAEALASPPQGIATVTGGVTAIRPACAPRPPSSPGANWSPATPDPSKLVVQAARQPISTQTPPEPRIVTFNIPQLPAPPAPPENIITEQDRQVQLQYEQWLNHQNQILGQQLKFYETEVQKLRKLKKSLNSKQRQLRKSGNELTENDNAELIRITSEQGILQKHLDASRKQTRQHGMLMQEYHSKQQQRQLQPQSNESCSPMMSPSQHSSPLSSPAALVSHSPGPGSASSTMIQHSPANSIVQHSPNPPMLQHSPGNSQTNPGTMSPHNMQPSPRIGTPLSQGDESPFSPGAMPSPGICVPAATRMTSPQHRAVITGRLTTSPGAFTTDARSPQQIIGDQNIRMHGITQRFVRPPAVGEINQRPRMTLQAGIVYGQRSPLGSPQPQSQPILTQQQHQQMLHRQQMIQQQHEVVPQDNQQNITQRTLQMVQHRQQLLQQQQQQQQQQQQLLQQQRQQFLQLQQQQNQQQLQQQTLQQQNLQQQNLQQQQNLQQQTLQQQPLQQSHQLQQQLQQQQQLQQQQIQQQQQQMQQQQQHMLQKPPTSPMVNQPVSSPSPQLHQQMQQNYGQQPPSSPLARSPVVQTMGSPMIQQQLNQSSQPPSPMGSRVHNHPSTSPMLQHQLNNSHHPPPCQTPNSPMPRSPMVGGSPMQMQRRQSSGNSPAMPDRPQSVENPGTPRTPHTPHTPHGNYSQNSMNHDQQIQQQEQNTMDHSRGGGNPHNPVNPLPVPRSFGRFGYFKLGLRGGSPMWSTKPETSKGKTTEPTLSIDEKPNPPTLVHRKTSLKNSLVCADYNDFDDDSHTPPQTSPLTIEPKATTSLTDSALSSPNDKLEPIPDTTDYDDDKNVVNSEVTLSSAAQGDNDDINDIEQFGDTNLEDVICPLEADNQDEYTLNGLFAQDMVLIDSNDSLSNALINDSNQNHNLQMQILGLEPSETQPEVHLGDEDVQLHVRNKKDLHLNIVKPVETGKRLAAVTDTPESSDQEELHTILPQTQAVIPTKGGKIPDQNIRSENVNKVIEXXXXXXXXXXXXXXXKSDTKVLESILEKPKLYHEPVPRTVTNPQVSTVTIVSSRANPFTVAKSSSIHATTSVNIEKPAPKSNTTFASYTSKETSSFDNQNRGGLTMGSIVTDAKIAARLTQATLKGTYLKDSKADAPPVSLKTGIEKTIEEVSKAIKPDINPKINIPIQKMQMSTSKILIPEALKKEPVTKLIDSKAGTSREEEKKKENCVERKIEVEKTPKIETKEDRKPDSSNTTDELELELAALHNPAENIANGERNLKKEDPNPPTMENSFQGRHISPVTEDNESLVHILENDSEPVTESVVREEKPENSQQEKVKPRLEPETNNNPISLNRDNDANSFSRKNAAVQKILMEESPDEILDLLDGIISLKPEMANADKQKTNLHYQVPTPSGTLPANILQDSSADLEQGTSGTERTERTSPQTPQVVQRRESSNTQNTIPIMPTVVTVAQLQRATSSVSHHSPLSKPSDLTQNIKNGSQQLRNLLSSYQSNHSQSHVTTTTNIVTLLSPSSTSNSKSGTTATTSSISAPLSSMNVQGNRLQTTTPVITSTVHGKSDSEIISTNTQQIKETNTAVTLVSNLAKSLPSDHFLRVTVSGIQTQTSTIALHTPTNTAPRPTGISITSNAMLNAMLAGTNSAKPTMAGRANTHLTHTSNLLSSVMPSSSIQRAQNVQAILQVSSSCSSVPSRVLVNVTSAAVSSSMQCVRTIVPPMVTATTTPVNVTTSILQSTLSQAPTLLHSQLTSGDVQFKTGSLPIDSKNVEPDALPMSSTIKKEPDGLQSKLHSSENSTTRLDSDINKIGATSHRLEESQNVLLKQLLQNTACATTTLSSSSSQGPSLPLVPSLEAQLARPVPPTPSSLLPPLLNELPVSKTPPTKQVLTKETSFVSHAITTPKMQSTILKEETPKVSPLQQPVTTSSLNVQTIARSLETLAKQQVHNQHIKNLSLTIPGGIQTPPVTKTVPTPPVVSESSTTPLENVSSQSSIVSTSEVIAQVTQVQQRATTPVTVARHIVQTKPIVTTIALKAALSNSEVVSNLVQTAQQFSTPITQAVVSEAXXXXXXLVLPPKPPTPVQQTQQQSPVVSTIQPSVPQMTTHPLSRPQAQMPQSTITSHTVPLMEVKKEILDEVLPGGNSVQLNDTKDFLPAKEELVDGTIDDKNDLKKLKRRQYQQKRRQSQGKDAVMGPQKKRARKEPRLVEDYDTYIDNVMLQLRQLPGMAVLEPLLSRNYGVCPVFGSGELSKIGTAKDYNTRTGDLIGSYGNARLSGISDHYNTQPFGELDPLPPVPPVSTQRGFYDQEFPPLKFDDNDRKENMSATRDIDTPDTVVSSSSPECVIPDTLHKFPYLRVIMDDESDDDSENQNRYSPPIPLLNPVPIRAGPGSFIKEIANNDKENLGTSRIGKTSPVTAKETGNINVTVTLNSQSSDDILGVLKDLANILNCPAPTDYQIEERTTTPPSQKLGLYRTKGKDGKEGAPIDIQSILNGAAKFCRHCDVVILNTLIRKRVSEFSLMSKDDLEPADEVCFCSAECYFQFSVIYKTSNISQDKAAAIVDHLSQKTDSKFIEENLKKFQDKKFFGKQSLDRDENILRLKRLLPDYDRCKNEIDLQDGRFGKKRSVSVLDEPMINSNEPHPPVKVHKGDRYKVWSAGVLQPSVKYKKLNEREITEMLFRMGVTVSPAKAEDTRRCIFCQNQGDGAADGPARLLNFDVDKWVHLNCALWAQEVFETVNGALMQFDEALQHTLTLNCVVCEKPGASVRCYKTRCTNYYHLGCAVKDNCVFFKSKNTFCSQHASKNDKDEELTTLSVYRRVYVNRDENRQVASVMHHSEHNHLLRVGSLIFLSVGQLLPHQLANFHTPNHIYPVGYKIVRFYWSMRTLNKRCRYVCSIHDVSGKPEFRVLVQEPPQEDLELRDATPRAVWNRILEPLAQLRRDEKSVQLFQRYITGEDLFGLTEPAVVRVLESLPGIETLTDYRFKYGRNPLLELPLAINPTGSARTEARLKNQLPWKRPHTQRTGSSARQNFAPTTNVAGEATCPYSKQFVHSKSSQYKKMKQEWRNNVYLARSKIQGLGLYAARDLEKHTMVIEYIGEMIRSEVAETREKQYEARNRGIYMFRLDEDRVIDATLCGGLARYINHSCSPNCTTEIVEVDRDLRIIIFAKRRISRGEELSYDYKFDIEDDQHKIPCACGAPTCRKWMN\*

1. **Utx histone demethylase**

**>evm.model.scaffold00559.1**

AVKSFQEVLWVEPGFTRACEVHIRLGLMLKVHGDFDAALKHLTLALIDATTPASFSKLEIKFHIAHLHEVQGKYRLAKDHYETLLKEKSLPSHLKADICRQLGWMYHVVDCHLLGITLPRQHKQNIAIQCLQKSIEAEPKSGQSLYLLGRCLAASGKIHEAFIAYRNSVEKSESNADTWCSIGVLYQQQNQPTDALQAYICAVQLDKSHSAAWTNLGILYESVSQPKDALACYINASRGNNNTPNCTNSLINIGGAKSSGNASMNPSLRQRINFLQNHLCQAPMPSVATTRRQLPPIDEAWNLPISAEMSSRQQQQQPAAGGPGCRYGGTPAHPPPPYPQGQGQAANVKRFKTGDDAISPCGQQRPPSFYLSPQQLQMLQCLQQNQGSLSPQQQALLAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPRGLRPGQPGYPASFTHSQPGQPGVIKNYGLPQQPQGGTVALQTGFSDSTVGYSPAATGNTQQPAGMPYKSASDPNFPPRQQTPGXXXXXXXXXXGSQGFTQISSTTSCYPEGSAANNKDLGVTDQELQALLSQKDIATTLAEDLLKHFGSDDLDEKDVVSPNIMNNGTLSSGPFSPSNLEDSNEKVMLVKDVKIEKTDDIVIQPTSTSNIVIDINKGIKQSMTVKCEATSSTNKVESVLKFESLCESQQEQEFNIEMDSKAIIELSKGQGLKGVPNCSILSDRSPPPAPPDPPSQRLTKEQLLPSTPSVYLENKKDAFSPQLQEFCLKHPIAVVRGLAAALKLDLGLFSTKTLVEANPDHGIEVRTQMQQTSDENWDQSMGRRVWGCISHRSHTTIAKYAHYQASSFQESLKEERDKSQGIHSSNLSDSDSKDSTGVVRRKKNSYGVVGRPASKMLRFGTNVDLSDERKWKIQLQELMKLPAFARVVSAGNMLSHVGHVILGMNTVQLYMKVPGSRTPGHQENNNFCSININIGPGDCEWFAVPDAYWGVICALCERNNINYLHGSWWPSLEDLYEENIPVYRFLQRPGDLVWVNAGCVHWVQAVGWCNNIAWNVGPLTARQYQLAIERYEWNKLQSFKSIVPMVHLSWNLARNIKVSDPRLFELIKNCLLRTMRQCCLILEFVKSKGVEVRFHGRGKNEASHYCGQCEIEVFNILFIREQEKRHVVHCMDCARKQAPSLEGFVCLEEYRMRDLMDVYDGFSLHTTLSAPASHSVQTTQSS\*

***Heterochromatin factors***

1. **Heterochromatin protein 1**

**>evm.model.scaffold00140.11**

MSKAKDSPVTEPETEEEFSVEKVLDRRVVKGKVEYFLKWKGYSNDENTWEPEENLDCPDLIAQFEEQRKKREAVPSGKRHEDKDKKRKSSSTPTPTQAKKKAPEEKKAEGFDRNLDPERIIGATDSSGELMFLMKWKGTDDADLVPAKEANVRCPQIVIKFYEERLTWHSPAHDEEGSTKPDPE\*

1. **Suppressor of variegation 3-9**

**>evm.model.scaffold00360.6**

MCDSKCDDSVPEGCQDVESEVEDMLERTSEDNVSIQQILQEMTNEFNRGVSPKQSVERDCSNKQELPSPENFDVILKDDVKISKAAKNVKLGKITNLVNSSGKLTKDISEKSGQELKDNLKTNECNEIKENQDAKESFKKDTNIPRIVLTFRTIDENTDSGKKTKISSCSSNLTLVPDELVNCNQIGGVSVKIETSEEYSDCIDKSDNEEGKVEKTIETINKNVDNEKNEEDINEGGQSEHLDLDQVPLVYKIDENRDADVSFSEPTADKEFENNSTFIKKQRKRRLRVASHVIEGAPSPKRSARRMCKESLKSTVLESAIARKEKSNYTEEHLQFKPIRKYNKPGRPKKILSTKEVSKQIHSKVTETDNESDNNTVEGNNSSNEINLSQENSKNWSINESSTSDLTINDSQNSCTEFDGMPKLSPILKNTDSSQTKSGNSIKNSITDDVASMSDNDKPFLKPVIGKTKRERGRPKGSLGARKIAKSDSFEDGSNETGKHQDSEEDSFPAKRTRRSMAPSPSLVEIQGSKPESTVILNETCKKSMMCLCQVRSQLYVTVSDNSTPLYCTAIDSIDNKKVGCCNEVDNNDVTMRRPSTCVPFIVLCRMHKERLFRHNCCPTCGLFCSQGKFIQCMNGHQYHRDCEIYLSKQGACPHCGCESPDYDIVISINGLRIPIYIPTRRKFSSLPSAKMTLPGKGDNTKLAGRPPSPLIQPELIKIPEPTTGSSDRPERYTIMSLYTSVKNGDLEKLVNVLTCGYNANHTFRDYANRTSLHLAAEKGQLACLHVLIQAGGQVDVMDKNQLTPLMLAACKGRADVVRYLIRIGADTTLKGVDGMTALHMAAKSGHLYVCRIILTECKVPRTLIDSVDDGGWTSLIWACEFRHTAVARFLIEQKCDPLIRDAEQNIALHWSAFSGSSEITELLLNEGCDVNAVNVHGDTPLHIAARQDQYAVSILLLARGAKIVEVNSAGETAINCCSSDGDTLAALKLNAKVNELSEHMWEKTVKILCNDISRGKETNPIQCVNGYDSEDKPTDFLYVTENCFTSNINVDRTITSLQSCRCENNCSTEKCLCGTISLRCWYDEEGKLLPEFNYADPPMLFECNPSCDCNKITCINRVVQHGTTQRFQLFRTKEKGWGLRTLKHIPKGTYVCEYVGEIISDSEADHREDDSYLFDLDNRDGETYCIDARRYGNVARFINHSCAPNLLPVRLFVEHQDLHFPRIAFFANQNIEADEELGFDYGEKFWIIKCKSFTCTCGAESCRYSKKTIQATLDNYRRRIQQEEMLITQTSLE\*