Genome-wide analysis of CCHC-type zinc finger (ZCCHC) proteins in yeast, Arabidopsis, and humans

Supplementary Figures

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Air1; 1 $CX_2CX_4HX_4C$ and 3 $CX_2CX_3GHX_4C$
MSTLLSEVESIDTLPYVKDTTPTGSDSSSFNKLLAPSIEDVDANPEELRTLRGQGRYFGITDYDSNGAIMEAEPKCNNCSQRGHLKRNC
PHVICTYCGFMDDHYSQHCPKAIICTNCNANGHYKSQCPHKWKKVFCTLCNSKRHSRERCPSIWRSYLLKTKDTNQGDFDFQTVFCYNC
GNAGHFGDDCAEGRSSRVPNTDGSAFCGDNLATKFKQHYFNQLKDYKREASQRQHFDNEHEFNLLDYEYNDDAYDLPGSRTYRDKMKWK
GKVQSTRNRNSSNNRYESGNNRKKKSPFSAQNYKVTKNKRVQTHPLDFPRSSQNNRTNDYSSQFSYNRDDFPKGPKNKRGRSSSNKSQR
NGRY

Air2; 1 $CX_2CX_4HX_4C$ and 3 $CX_2CX_3GHX_4C$
MEKNTAPFVVDTAPTTPPDKLVAPSIEEVNSNPNELRALRGQGRYFGVSDDDKDAIKEAAPKCNNCSQRGHLKKDCPHIICSYCGATDD
HYSRHCPKAIQCSKCDEVGHYRSQCPHKWKKVQCTLCKSKKHSKERCPSIWRAYILVDDNEKAKPKVLPFHTIYCYNCGGKGHFGDDCK
EKRSSRVPNEDGSAFTGSNLSVELKQEYYRHMNRNSDENEDYQFSESIYDEDPLPRPSHKRHSQNDHSHSGRNKRRASNFHPPPYQKSN
VIQPTIRGETLSLNNNISKNSRYQNTKVNVSSISENMYGSRYNPSTYVDNNSISNSSNYRNYNSYQPYRSGTLGKRR

Msl5/Bbp/Sf1; 1 $CX_2CX_4HX_4C$ and 1 $CX_2CX_3GHX_4C$
MSFRRINSRYFENRKGSSMEEKKAKVPPNVNLSLWRKNTVESDVHRFNSLPSKISGALTREQIYSYQVMFRIQEITIKLRTNDFVPPSR
KNRSPSPPPVYDAQGKRTNTREQRYRKKLEDERIKLVEIALKTIPYFVPPDDYKRPTKFQDKYYIPVDQYPDVNFVGLLLGPRGRTLRK
LQEDSNCKIAIRGRGSVKEGKNASDLPPGAMNFEDPLHCLIIADSEDKIQKGIKVCQNIVIKAVTSPEGQNDLKRGQLRELAELNGTLR
EDNRPCPICGLKDHKRYDCPNRKIPNIQGIVCKICGQTGHFSRDCNSSSQRMSRFDRNATVNNSAPIQSNDVHYNSNTHPIQAPKRSRY
DNNSTEPPLKFPASSRYAPSPSPPASHISRQAQNVTPTPPPGLTSSSFSSGVPGIAPPPLQSPPESEQPKFSLPPPPGMTTVQSSIAPP
PGLSGPPGFSNNMGNDINKPTPPGLQGPPGL

Bik1; 1 $CX_2CX_3GHX_4C$
MDRYQRKIGCFIQIPNLGRGQLKYVGPVDTKAGMFAGVDLLANIGKNDGSFMGKKYFQTEYPQSGLFIQLQKVASLIEKASISQTSRRT
TMEPLSIPKNRSIVRLTNQFSPMDDPKSPTPMRSFRITSRHSGNQQSMDQEASDHHQQQEFGYDNREDRMEVDSILSSDRKANHNTTSD
WKPDNGHMNDLNSSEVTIELREAQLTIEKLQRKQLHYKRLLDDQRMVLEEVQPTFDRYEATIQEREKEIDHLKQQLELERRQQAKQKQF
FDAENEQLLAVVSQLHEEIKENEERNLSHNQPTGANEDVELLKKQLEQLRNIEDQFELHKTKWAKEREQLKMHNDSLSKEYQNLSKELF
LTKPQDSSSEEVASLTKKLEEANEKIKQLEQAQAQTAVESLPIFDPPAPVDTTAGRQQWCEHCDTMGHNTAECPHHNPDNQQFF

Gis2; 1 $CX_2CX_4HX_4C$ and 6 $CX_2CX_3GHX_4C$
MSQKACYVCGKIGHLAEDCDSERLCYNCNKPGHVQTDCTMPRTVEFKQCYNCGETGHVRSECTVQRCFNCNQTGHISRECPEPKKTSRF
SKVSCYKCGGPNHMAKDCMKEDGISGLKCYTCGQAGHMSRDCQNDRLCYNCNETGHISKDCPKA

Mpe1; 1 $CX_2CX_4HX_4C$
MSSTIFYRFKSQRNTSRILFDGTGLTVFDLKREIIQENKLGDGTDFQLKIYNPDTEEEYDDDAFVIPRSTSVIVKRSPAIKSFSVHSRL
KGNVGAAALGNATRYVTGRPRVLQKRQHTATTTANVSGTTEEERIASMFATQENQWEQTQEEMSAATPVFFKSQTNKNSAQENEGPPPP
GYMCYRCGGRDHWIKNCPTNSDPNFEGKRIRRTTGIPKKFLKSIEIDPETMTPEEMAQRKIMITDEGKFVVQVEDKQSWEDYQRKRENR
QIDGDETIWRKGHFKDLPDDLKCPLTGGLLRQPVKTSKCCNIDFSKEALENALVESDFVCPNCETRDILLDSLVPDQDKEKEVETFLKK
QEELHGSSKDGNQPETKKMKLMDPTGTAGLNNNTSLPTSVNNGGTPVPPVPLPFGIPPFPMFPMPFMPPTATITNPHQADASPKK

Slu7; 1 $CX_2CX_3GHX_4C$
MNNNSRNNENRSTINRNKRQLQQAKEKNENIHIPRYIRNQPWYYKDTPKEQEGKKPGNDDTSTAEGGEKSDYLVHHRQKAKGGALDIDN
NSEPKIGMGIKDEFKLIRPQKMSVRDSHSLSFCRNCGEAGHKEKDCMEKPRKMQKLVPDLNSQKNNGTVLVRATDDDWDSRKDRWYGYS
GKEYNELISKWERDKRNKIKGKDKSQTDETLWDTDEEIELMKLELYKDSVGSLKKDDADNSQLYRTSTRLREDKAAYLNDINSTESNYD
PKSRLYKTETLGAVDEKSKMFRRHLTGEGLKLNELNQFARSHAKEMGIRDEIEDKEKVQHVLVANPTKYEYLKKKREQEETKQPKIVSI
GDLEARKVDGTKQSEEQRNHLKDLYG

YOL029C; 1 $CX_2CX_4HX_4C$
MKPVTCCNQKNNIMPSLVPVCCSEKKIESDAKKSISKCCGDKEIYDSENRPITKEDGSWIPGSCKQCRSDPHSRNFCQSLSNKCSSSSF
SSNSALSPDLNEQQTDVNYNSIKLPEICSCKNAQMNAASDAKRYLPISYTYQKIRQHMQKNKSIQEQLNPEDSTSISSALENIASGLHV
RGQKVELQSIKDALHKMDKNVLE

Supplementary Figure 1. Yeast ZCCHC domain-containing proteins. The number of $CX_2CX_4HX_4C$ or $CX_2CX_3GHX_4C$ sequences in each protein is shown; these sequences have been highlighted. A slash separates alternative names given by different authors to the same protein.

AT5G51280 RH35; 1 CX$_2$CX$_3$GHX$_4$C

MESIMEEADSYIEYVSVAERRAIAAQKILQRKGKASELEEEADKEKLAEAKPSLLVQATQLKRDVPEVSATEQIILQEKEMMEHLSDKK
TLMSVRELAKGITYTEPLLTGWKPPLHIRKMSSKQRDLIRKQWHIIVNGDDIPPPIKNFKDMKFPRPVLDTLKEKGIVQPTPIQVQGLP
VILAGRDMIGIAFTGSGKTLVFVLPMIMIALQEEMMMPIAAGEGPIGLIVCPSRELARQTYEVVEQFVAPLVEAGYPPLRSLLCIGGID
MRSQLEVVKRGVHIVVATPGRLKDMLAKKKMSLDACRYLTLDEADRLVDLGFEDDIREVFDHFKSQRQTLLFSATMPTKIQIFARSALV
KPVTVNVGRAGAANLDVIQEVEYVKQEAKIVYLLECLQKTSPPVLIFCENKADVDDIHEYLLLKGVEAVAIHGGKDQEDREYAISSFKA
GKKDVLVATDVASKGLDFPDIQHVINYDMPAEIENYVHRIGRTGRCGKTGIATTFINKNQSETTLLDLKHLLQEAKQRIPPVLAELNDP
MEEAETIANASGVKGCAYCGGLGHRIRDCPKLEHQKSVAISNSRKDYFGSGGYRGEI

AT5G26742 RH3; 1 CX$_2$CX$_3$GHX$_4$C

MASTVGVPSLYQVPHLEISKPNSKKRSNCLSLSLDKPFFTPLSLVRRTRRIHSSSLLVPSAVATPNSVLSEEAFKSLGLSDHDEYDLDG
DNNNVEADDGEELAISKLSLPQRLEESLEKRGITHLFPIQRAVLVPALQGRDIIARAKTGTGKTLAFGIPIIKRLTEEAGDYTAFRRSG
RLPKFLVLAPTRELAKQVEKEIKESAPYLSTVCVYGGVSYTIQQSALTRGVDVVVGTPGRIIDLIEGRSLKLGEVEYLVLDEADQMLAV
GFEEAVESILENLPTKRQSMLFSATMPTWVKKLARKYLDNPLNIDLVGDQDEKLAEGIKLYAIATTSTSKRTILSDLITVYAKGGKTIV
FTQTKRDADEVSLALSNSIATEALHGDISQHQRERTLNAFRQGKFTVLVATDVASRGLDIPNVDLVIHYELPNDPETFVHRSGRTGRAG
KEGSAILMHTSSQKRTVRSLERDVGCHFEFISPPTVGDLLESSADQVVATLNGVHPDSIKFFSATAQKLYEEKGTDALAAALAHLSGFS
QPPSSRSLLSHEKGWVTLQLIRDPTNARGFLSARSVTGFLSDLYRTAADEVGKIFLIADDRIQGAVFDLPEEIAKELLEKDVPEGNSLS
MITKLPPLQDDGPSSDNYGRFSSRDRMPRGGGGSRGSRGGRGGSSRGRDSWGGDDDRGSRRSSGGGSSWSRGGSSSRGSSDDWLIGGRS
SSSSRAPSRERSFGGSCFICGKSGHRATDCPDKRGF

AT4G33370 RH43; 1 CX$_2$CX$_3$GHX$_4$C

MEVDDGYVEYVPVEERLAQMKRKVVEEPGKGMMEHLSDKKKLMSVGELARGITYTEPLSTWWKPPLHVRKMSTKQMDLIRKQWHITVNG
EDIPPPIKNFMDMKFPSPLLRMLKDKGIMHPTPIQVQGLPVVLSGRDMIGIAFTGSGKTLVFVLPMIILALQEEIMMPIAAGEGPIALV
ICPSRELAKQTYDVVEQFVASLVEDGYPRLRSLLCIGGVDMRSQLDVVKKGVHIVVATPGRLKDILAKKKMSLDACRLLTLDEADRLVD
LGFEDDIRHVFDHFKSQRQTLLFSATMPAKIQIFATSALVKPVTVNVGRAGAANLDVIQEVEYVKQEAKIVYLLECLQKTTPPVLIFCE
NKADVDDIHEYLLLKGVEAVAIHGGKDQEDRDYAISLFKAGKKDVLVATDVASKGLDFPDIQHVINYDMPGEIENYVHRIGRTGRCGKT
GIATTFINKNQSEITLLDLKHLLQEAKQRIPPVLAELNGPMEETETIANASGVKGCAYCGGLGHRILQCPKFEHQKSVAISSSRKDHFG
SDGYRGEV

AT4G36020 CSP1; 7 CX$_2$CX$_3$GHX$_4$C

MASEDQSAARSTGKVNWFNASKGYGFITPDDGSVELFVHQSSIVSEGYRSLTVGDAVEFAITQGSDGKTKAVNVTAPGGGSLKKENNSR
GNGARRGGGGSGCYNCGELGHISKDCGIGGGGGGGERRSRGGEGCYNCGDTGHFARDCTSAGNGDQRGATKGGNDGCYTCGDVGHVARD
CTQKSVGNGDQRGAVKGGNDGCYTCGDVGHFARDCTQKVAAGNVRSGGGGSGTCYSCGGVGHIARDCATKRQPSRGCYQCGGSGHLARD
CDQRGSGGGGNDNACYKCGKEGHFARECSSVA

AT4G38680 CSP2/GRP2; 2 CX$_2$CX$_3$GHX$_4$C

MSGDNGGGERRKGSVKWFDTQKGFGFITPDDGGDDLFVHQSSIRSEGFRSLAAEEAVEFEVEIDNNNRPKAIDVSGPDGAPVQGNSGGG
SSGGRGGFGGGRGGGRGSGGGYGGGGGGYGGRGGGGRGGSDCYKCGEPGHMARDCSEGGGGYGGGGGGYGGGGGYGGGGGGYGGGGRGG
GGGGGSCYSCGESGHFARDCTSGGR

AT2G17870 CSP3/GRP2B; 7 CX$_2$CX$_3$GHX$_4$C

MAMEDQSAARSIGKVSWFSDGKGYGFITPDDGGEELFVHQSSIVSDGFRSLTLGESVEYEIALGSDGKTKAIEVTAPGGGSLNKKENSS
RGSGGNCFNCGEVGHMAKDCDGGSGGKSFGGGGGRRSGGEGECYMCGDVGHFARDCRQSGGGNSGGGGGGGRPCYSCGEVGHLAKDCRG
GSGGNRYGGGGGRGSGGDGCYMCGGVGHFARDCRQNGGGNVGGGGSTCYTCGGVGHIAKVCTSKIPSGGGGGGRACYECGGTGHLARDC
DRRGSGSSGGGGGSNKCFICGKEGHFARECTSVA

AT2G21060 CSP4/GRP2b; 2 CX$_2$CX$_3$GHX$_4$C

MSGGGDVNMSGGDRRKGTVKWFDTQKGFGFITPSDGGDDLFVHQSSIRSEGFRSLAAEESVEFDVEVDNSGRPKAIEVSGPDGAPVQGN
SGGGGSSGGRGGFGGGGRGGGRGGGSYGGGYGGRGSGGRGGGGGDNSCFKCGEPGHMARECSQGGGGYSGGGGGGRYGSGGGGGGGGG
GLSCYSCGESGHFARDCTSGGAR

AT5G45400 RPA1C; 1 CX$_2$CX$_4$HX$_4$C

MAVSLTEGVVMKMLNGEVTSETDMMPVLQVTELKLIQSKLHQNQESSNRYKFLLSDGTDLAAGMLNTSLNSLVNQGTIQLGSVIRLTHY
ICNLIQTRRIVVIMQLEVIVEKCNIIGNPKEPGHSSINPQRGGVNTQSNGGSEQQQARRSDVNGGRYGVSANSPQPQVVHNSSDAGRYC
VSANSPQPQVVHSSSDAGRYGVSANSPQRQVVHNSPDAGRYGQPQVSQRYGTGSGYPETSPSTRPYVSSNAGYGGSRQDQPRAPTATTA
YSRPVQSAYQPQQPPMYVNRGPVARNEAPPRINPIAALNPYQGRWTIKVRVTSKADLRRFNNPRGEGKLFSFDLLDADGGEIRVTCFND
AVDQFFDKIVVGNVYLISRGNLKPAQKNFNHLPNDYEIHLDSASTIQPCEDDGTIPRYHFHFRNIGDIENMENNSTTDVIGIVSSISPT
VAIMRKNLTEVQKRSLQLKDMSGRSVEVTMWGNFCNAEGQKLQNLCDSGVFPVLALKAGRIGEFNGKQVSTIGASQFFIEPDFPEAREL
RQWYEREGRNAHFTSISREFSGVGRQEVRKVIAQIKDEKLGTSEKPDWITVCATISFMKVENFCYTACPIMNGDRPCSKKVTNNGDGTW
RCEKCDKCVDECDYRYILQIQLQDHTDLTWATAFQEAGEEIMGMSAKDLYYVKYENQDEEKFEDIIRSVAFTKYIFKLKIKEETYSDEQ
RVKATVVKAEKLNYSSNTRFMLEAIDKLKIGDANSLPIKAESSNYRSDAFNSGVGTSGTRDTASVDARREFGLPAANQVGQYGNQYSSD
ARSLGGFTSCNVCRSNSHVSANCPTLMSEPQGQYMGGTNAGGGMPRQHVGSY

AT4G19130 RPA1E; 1 CX$_2$CX$_3$GHX$_4$C

MEVSLTAGAIGKIMNGEVTTEADMIPVLQVTDLKQIMAQQDPTRERFRMVLSDGTYLHQGMLGTDLNNLVKEGTLQPGSIVRLTRFVGD

VIKGRRIVIVPQLEVLKQISDIIGHPVPGGKHNDQRGADSGIKFNTTEQQGSGIRQVNNIEPGRSNAAISPQVGGTGSSVPASTTPSTR
AYSNPSSGNGVTRQDYARDPPTSYPHQPQPPPPMYANRGPVARNEAPPKIIPVNALSPYSGRWTIKARVTNKAALKQYSNPRGEGKVFN
FDLLDADGGEIRVTCFNAVADQFYDQIVVGNLYLISRGSLRPAQKNFNHLRNDYEIMLDNASTIKQCYEEDAAIPRHQFHFRTIGDIES
MENNCIVDVIGIVSSISPTVTITRKNGTATPKRSLQLKDMSGRSVEVTMWGDFCNAEGQRLQSLCDSGVFPVLAVKAGRISEFNGKTVS
TIGSSQLFIDPDFVEAEKLKNWFEREGKSVPCISLSREFSGSGKVDVRKTISQIKDEKLGTSEKPDWITVSATILYLKFDNFCYTACPI
MNGDRPCSKKVTDNGDGTWRCEKCDKSVDECDYRYILQLQIQDHTDLTCVTAFQEAGEEIMGISAKDLYYVKNEHKDEEKFEDIIRKVA
FTKYNFKLKVKEETFSDEQRVKATVVKVDKLNYSADTRTMLGAMDKLRTRDANSLPINPEGSDYNADVVNTGIGSSGTRDPSSVQRRDF
GLHAHQSGQSGNHYSGGGATTSCNVCGNSGHVSAKCPGATKPQEQGQYMGGSYRGTTGSYGGGLPRQHVGSY

AT5G63920 TOP3A; 1 $CX_2CX_4HX_4C$ and 1 $CX_2CX_3GHX_4C$

MSRRGGGPVTVLNVAEKPSVAKSVAGILSRGTFRTREGRSRYNKIFEFDYAINGQPCRMLMTSVIGHLMELEFADRYRKWHSCDPADLY
QAPVMKHVPEDKKDIKKTLEEEARKSDWLVLWLDCDREGENIAFEVVDVCRAVKHNLFIRRAHFSALIDRDIHEAVQNLRDPNQLFAEA
VDARQEIDLRIGASFTRFQTMLLRDRFAIDSTGEERSRVISYGPCQFPTLGFIVERYWEIQAHEPEEFWTINCSHQSEEGLATFNWMRG
HLFDYASAVILYEMCVEEPTATVMNVPHPRERFKYPPYPLNTIELEKRASRYFRLSSEHTMKVAEELYQAGFISYPRTETDSFSSRTDL
RAMVEEQTRHPAWGSYAQRLLEPEGGLWRNPANGGHDDKAHPPIHPTKFSSGESNWSRDHLNVYELVVRHYLACVSQPAVAAETTVEID
IAGERFSASGRAILAKNYLEVYRFESWGGSVIPVYEKGQQFIPTTLTLDAAVTRPPPLLCEADLLSCMDKAGIGTDATMHDHIKKLLDR
GYATKDANTRFSPTNLGEALVMGYDDMGYELWKPNLRALMEHDMNEVSVGRKTKAEVLETCLQQMKACFLDARVKKSKLLEAMTIFFER
SNNTDESESQTAGEVVRRCNLCNESDMALRKNRDGNFMVGCMNYPQCRNAVWLPGPTLEASVTTNVCQSCGPGPVYKILFKFRQIGIPP
GFDVNHLGCVGGCDDILKQLIDICGTGSRSQARRTPGTAPSNNIQGSNTRQSNVCIHCQQRGHASTNCPSRVPASRNSRPTATNPRNDE
STVSCNTCGSQCVLRTANTEANRGRQFFSCPTQGCSFFAWEDSINNSSGNATTGSNSGGSGRRGSRGRGRGGRGGQSSGGRRGSGTSFV
SATGEPVSGIRCFSCGDPSHFANACPNRNNSNGNYF

AT5G47390 KUA1; 1 $CX_2CX_3GHX_4C$

MTRRCSHCNHNGHNSRTCPNRGVKLFGVRLTEGSIRKSASMGNLSHYTGSGSGGHGTGSNTPGSPGDVPDHVAGDGYASEDFVAGSSSS
RERKKGTPWTEEEHRMFLLGLQKLGKGDWRGISRNYVTTRTPTQVASHAQKYFIRQSNVSRRKRRSSLFDMVPDEVGDIPMDLQEPEED
NIPVETEMQGADSIHQTLAPSSLHAPSILEIEECESMDSTNSTTGEPTATAAAASSSSRLEETTQLQSQLQPQPQLPGSFPILYPTYFS
PYYPFPFPIWPAGYVPEPPKKEETHEILRPTAVHSKAPINVDELLGMSKLSLAESNKHGESDQSLSLKLGGGSSSRQSAFHPNPSSDSS
DIKSVIHAL

AT5G61620 MYB_related-type transcription factor; 1 $CX_2CX_3GHX_4C$

MVKETVTVAKTCSHCGHNGHNARTCLNGVNKASVKLFGVNISSDPIRPPEVTALRKSLSLGNLDALLANDESNGSGDPIAAVDDTGYHS
DGQIHSKKGKTAHEKKKGKPWTEEEHRNFLIGLNKLGKGDWRGIAKSFVSTRTPTQVASHAQKYFIRLNVNDKRKRRASLFDISLEDQK
EKERNSQDASTKTPPKQPITGIQQPVVQGHTQTEISNRFQNLSMEYMPIYQPIPPYYNFPPIMYHPNYPMYYANPQVPVRFVHPSGIPV
PRHIPIGLPLSQPSEASNMTNKDGLDLHIGLPPQATGASDLTGHGVIHVK

AT1G70000 putative MYB_related-type transcription factor; 1 $CX_2CX_3GHX_4C$

MSRSCSQCGNNGHNSRTCPTDITTTGDNNDKGGGEKAIMLFGVRVTEASSSCFRKSVSMNNLSQFDQTPDPNPTDDGGYASDDVVHASG
RNRERKRGTPWTEEEHRLFLTGLHKVGKGDWRGISRNFVKTRTPTQVASHAQKYFLRRTNQNRRRRRSSLFDITPDSFIGSSKEENQLQ
TPLELIRPVPIPIPIPPSRKMADLNLNKKKTPATTEMFPLSLNLQRPSSSTSSSSNEQKARGSRASSGFEAMSSNGDSIMGVA

AT5G56840 putative MYB_related-type transcription factor; 1 $CX_2CX_3GHX_4C$

MGRRCSHCGNVGHNSRTCSSYQTRVVTSSSPPPPPPPSILAAAIKKSFSMDCLPACSSSSSSFAGYLSDGLAHKTPDRKKGVPWTAEEH
RTFLIGLEKLGKGDWRGISRNFVVTKSPTQVASHAQKYFLRQTTTLHHKRRRTSLFDMVSAGNVEENSTTKRICNDHIGSSSKVVWKQG
LLNPRLGYPDPKVSVSGSGNSGGLDLELKLASIQSPESNIRPISVT

AT2G28910 CXIP4; 1 $CX_2CX_3GHX_4C$

MPATAGRVRMPANNRVHSSAALQTHGIWQSAIGYDPYAPTSKEEPKTTQQKTEDPENSYASFQGLLALARITGSNNDEARGSCKKCGRV
GHLTFQCRNFLSTKEDKEKDPGAIEAAVLSGLEKIRRGVGKGEVEEVSSEEEEESESSDSDVDSEMERIIAERFGKKKGGSSVKKTSSV
RKKKKRVSDESDSDSDSGDRKRRRRSMKKRSSHKRRSLSESEDEEEGRSKRRKERRGRKRDEDDSDESEDEDDRRVKRKSRKEKRRRRS
RRNHSDDSDSESSEDDRRQKRRNKVAASSDSEANVSGDDVSRVGRGSSKRSEKKSRKRHHRKERE

AT5G58760 DDB2; 1 $CX_2CX_3GHX_4C$

MSSTRSRRKRDPEIVIARDTDSELSSSEEEEEEEDNYPFSESEEEDEAVKNGGKIELEKNKAKGKAPITVKLIKKVCKVCKQPGHEAGF
KGATYIDCPMKPCFLCKMPGHTTMSCPHRVVTDHGILPTSHRNTKNPIDFVFKRQLQPRIPPIKPKYVIPDQVHCAVIRYHSRRVTCLE
FHPTKNNILLSGDKKGQIGVWDFGKVYEKNVYGNIHSVQVNNMRFSPTNDDMVYSASSDGTIGYTDLETGTSSTLLNLNPDGWQGANSW
KMLYGMDINSEKGVVLAADNFGFLHMIDHRTNNSTGEPILIHKQGSKVCGLDCNPVQPELLLSCGNDHFARIWDMRKLQPKASLHDLAH
KRVVNSAYFSPSSGTKILTTCQDNRIRIWDSIFGNLDLPSREIVHSNDFNRHLTPFKAEWDPKDTSESLIVIGRYISENYNGTALHPID
FIDASNGQLVAEVMDPNITTITPVNKLHPRDDVLASGSSRSLFIWRPQDNTEMVEEKKDKKIIICYGDSKKKGKKQKRGSDDEDDEDDI
FSSKGKNIKVNKYQAKTTKKTKT

AT5G38600 proline-rich spliceosome-associated (PSP) family protein; 1 $CX_2CX_4HX_4C$

METEDVLDIPASSNFGSEVKKNSLESGNGSPEANSLVGNDENVKGNLDLDLTEENLRIVGGQESGEILTEQVSDVFNASVESVAVDEKL
GIQKETLVHSTTLDVSSKAGVKRPRTSYDEQQPTVHVTYKHLTRASKQKLESLLQKWSEWEAENTSLAQDQEQLFESGEETCFPAIRVG
LQKTSSVSFWIDNQTGHKPLEDFVLVESSTTPLYDRKFAIGLNSADGSRNVEGGLEIIDDDPPRCFNCGGYSHSLRECPRPFDRSAVNS
ARKLQKSKRNQNSSGPRLPSRYYQKTQTGKYDGLKPGTLDAETRQLLNLGELDPPPWLNRMREIGYPPGYLAPEDDHLSGITIFGEEVE

TREEIESEDGEILEKANHPPEPQMKKTVEFPGINAPFPENADEWLWEAAPSHRNSSRSGRWQQQKTSRGHDYRDDGPLGVEPSSYPPRY
GSRYDYGYGSNEYGSRSRSPGIDRSLSERSKRDYSSYDADFRERDRDRDRNRDRDRDRDWDRDRDRDCDRDRDRDDRDWSYRLSSRR

AT5G43630 TZP; 1 $CX_2CX_3GHX_4C$ and 1 $CX_2CX_4HX_4C$

MGDGDEQSKELGGVSSSSRRCSSGTAGAANAEARMKFAAVDAITELVWSPSNGLSLRCADISFTGKAKLLSPNFFDIGLTNMAIHSNST
SIEDQEDHVDVELRNRDQVNQAMIGGSVEDMKPEMVEDKVETNDDIKNEEAGCSKRSSDSPKAMEGETRDLLVNEQLRMESAGSQEEGD
KAHNRVDRLESMDENNLATLAVVACEGKGDYLPEGEAGPSGSYRRREKAKGKEKALSDENFGGDGEDEDEESFGSVESCNSAGLLSRGK
KRPGFEEQLIFGSKRLKTLNQECLGSTSKLKQDSSFMNWISNMTKGIWKGNEEDNSPFVALTTTSNANGHGQVNAIVDQQQLSPCCVKE
NSGCRNTGFQSFFQSIYCPKKQSQDVVDMDFPNDVNAAPLQELPWIPEHCDISKGDDLSSSGNEIGPVAEPNISSGKVVFNQTSKTQSS
ENKREDKEPNISLMSLSKSKPNEEPKTCGEADGKVSPCLTNRNSGLKSLWISRFSSKGSFPQKKASETAKEANASASDAAKTRDSRKML
ADKNVIRPSISSVDGPDKPDTVLPIVSSMRIESSEAMASLFARRLEAMKSIMPSGSLAENAEEEQRDLICFYCGKKGHCLRDCLEVTDT
ELRDLVQNISVRNGREEASSLCIRCFQLSHWAATCPNAPLYGSGAEGRAMKNALASTSGMKLPISGFTDVPRAVFDAVQVLRLSRTDVL
KWINTKKSVSGLEGFFLRLRLGKWEEGLGGTGYYVARIDGDTEGQSSRRHSEKSLISVKVKGVTCLVESQFISNQDFLEEELKAWWQSA
GKSARTSGYDGIPSAEELSRKIQQRKMLGF

AT5G51300 SF1; 2 $CX_2CX_3GHX_4C$

MESVEMNNPNSQTLDQPPPSSNGDTAPLALDHMNPQNSESVALNGSSTPIPDTNGSSAKPELLRPLLSENGVSKTLSGNDKDQSGGEEE
TTSRRKRRSRWDPPPSESINNPSAEGGTDSGTGTRKRKSRWADDEPRTQIQLPDFMKDFTGGIEFDPEIQALNSRLLEISRMLQSGMPL
DDRPEGQRSPSPEPVYDNMGIRINTREYRARERLNRERQEIIAQIIKKNPAFKPPADYRPPKLHKKLFIPMKEFPGYNFIGLIIGPRGN
TQKRMERETGAKIVIRGKGSVKEGRHQQKKDLKYDPSENEDLHVLVEAETQEALEAAAGMVEKLLQPVDEVLNEHKRQQLRELATLNGT
IRDEEFCRLCGEPGHRQYACPSRTNTFKSDVLCKICGDGGHPTIDCPVKGTTGKKMDDEYQNFLAELGGTVPESSLKQSATLALGPGSS
GSNPPWANNAGNGASAHPGLGSTPTKPPSKEYDETNLYIGFLPPMLEDDGLINLFSSFGEIVMAKVIKDRVTGLSKGYGFVKYADVQMA
NTAVQAMNGYRFEGRTLAVRIAGKSPPPIAPPGPPAPQPPTQGYPPSNQPPGAYPSQQYATGGYSTAPVPWGPPVPSYSPYALPPPPPG
SYHPVHGQHMPPYGMQYPPPPPHVTQAPPPGTTQNPSSSEPQQSFPPGVQADSGAATSSIPPNVYGSSVTAMPGQPPYMSYPSYYNAVP
PPTPPAPASSTDHSQNMGNMPWANNPSVSTPDHSQGLVNAPWAPNPPMPPTVGYSQSMGNVPWAPKPPVQPPAENPSSVGESEYEKFMA
EMK

AT1G23860 RSZ21; 1 $CX_2CX_3GHX_4C$

MTRVYVGNLDPRVTERELEDEFKAFGVLRNVWVARRPPGYAFLEFDDERDALDAISALDRKNGWRVELSHKDKGGRGGGGGRRGGIEDS
KCYECGELGHFARECRRGRGSVRRRSPSPRRRRSPDYGYARRSISPRGRRSPPRRRSVTPPRRGRSYSRSPPYRGSRRDSPRRRDSPYG
RRSPYANGV

AT4G31580 RSZ22; 1 $CX_2CX_3GHX_4C$

MSRVYVGNLDPRVTERELEDEFRAFGVVRSVWVARRPPGYAFLDFEDPRDARDAIRALDGKNGWRVEQSHNRGERGGGGRGGDRGGGGG
GRGGRGGSDLKCYECGETGHFARECRNRGGTGRRRSKSRSRTPPRYRRSPSYGRRSYSPRARSPPPPRRRSPSPPPARGRSYSRSPPPY
RAREEVPYANGNGLKERRRSRS

AT2G24590 RSZ22A; 1 $CX_2CX_3GHX_4C$

MSRVYVGNLDPRVTERELEDEFRSFGVIRSVWVARRPPGYAFLDFEDSRDARDAIREVDGKNGWRVEQSHNRGGGGGRGGGRGGGDGGR
GRGGSDLKCYECGESGHFARECRSRGGSGGRRRSRSRSRSPPRYRKSPTYGGRRSYSPRARSPPPPRRRSPSPRGRNYSRSPPPYRARD
EVPYANGNGLKDVRRSRS

AT3G53500 RSZ32; 2 $CX_2CX_3GHX_4C$

MPRYDDRYGNTRLYVGRLSSRTRTRDLERLFSRYGRVRDVDMKRDYAFVEFSDPRDADDARYYLDGRDFDGSRITVEASRGAPRGSRDN
GSRGPPPGSGRCFNCGVDGHWARDCTAGDWKNKCYRCGERGHIERNCKNSPSPKKARQGGSYSRSPVKSRSPRRRRSPSRSRSYSRGRS
YSRSRSPVRREKSVEDRSRSPKAMERSVSPKGRDQSLSPDRKVIDASPKRGSDYDGSPKENGNGRNSASPIVGGGESPVGLNGQDRSPI
DDEAELSRPSPKGSESP

AT2G37340 RSZ33; 2 $CX_2CX_3GHX_4C$

MPRYDDRYGNTRLYVGRLSSRTRTRDLERLFSRYGRVRDVDMKRDYAFVEFGDPRDADDARHYLDGRDFDGSRITVEFSRGAPRGSRDF
DSRGPPPGAGRCFNCGVDGHWARDCTAGDWKNKCYRCGERGHIERNCKNSPKKLRRSGSYSRSPVRSRSPRRRRSPSRSLSRSRSYSRS
RSPVRRRERSVEERSRSPKRMDDSLSPRARDRSPVLDDEGSPKIIDGSPPPSPKLQKEVGSDRDGGSPQDNGRNSVVSPVVGAGGDSSK
EDRSPVDDDYEPNRTSPRGSESP

AT1G60650 RZ-1B/RBGB1; 1 $CX_2CX_3GHX_4C$

MKDRENDGNLESRIFVGGLSWDVTERQLESTFDRYGKITECQIMVGRDTGRPRGFGFITFTDRRGADDAIKHMHGRELGNKVISVNKAE
PKVGGEDVDQLKKGGGYSSRGKGTEDECFKCRRPGHWARDCPSTGDDRERFRVPLAMRSRIGDIDGHRDRYGDRDLEREREREREFDRY
MDGRRDRDGGRYSYRDRFDSGDKYEPRDHYPFERYAPPGDRFVSDRYGMPEHHLENEYRGRERSYDRDRYARDTSDRYGDMGPIRDEGR
PYRSRPGPYDRPSRPGGRPSSYERW

AT5G04280 RZ-1C/RBGB3; 1 $CX_2CX_3GHX_4C$

MAAKEGSRIFVGGLSPEVTDRDLERAFSRFGDILDCQIMLERDTGRSRGFGFITFADRRAMDESIREMHGRDFGDRVISVNRAEPKLGR
DDGESHGSRGGRDSGYSIAGKGSFGGGGGGGGRVGEDECFKCGRVGHWARDCPSAGGGRGGPVGGFSSRASAYGGSDGRVDRYADRDRY
VDRERYIDDRYDGAARYGARDRFDSREAYIPRDRYASDRYAAPADRFAGGDRYSRGSDRYPPGSYDKARSFERDIAPSAGSDRYGGGRA
GGPIRGGGEEGRGFRSRAGAPYERPSRSGGGGAYPSSSTFDRY

AT3G10400 U11/U12-31K; 1 CX$_2$CX$_3$GHX$_4$C

MKKRKIHHSDDEEDDTFYYRYSSVAAPPPSNPKHQPSSSAKSSAPGGGSGGLAPSKSTLYVSNLDFSLTNSDIHTLFSTFGKVARVTVL
KDRHTRQSRGVAFVLYVSREDAAKAARSMDAKILNGRKLTVSIAADNGRASEFIKKRVYKDKSR**CYECGDEGHLSYEC**PKNQLGPRERP
PPPKKRGRRKEEEGEAEEISWSAAAPSLAVAEEEFEEENWASVVDNEAGERLRKREAEEEEERRMKRKEKKVSYFSDESDDED

AT3G55340 PHIP1; 2 CX$_2$CX$_3$GHX$_4$C

MVLSNKKLKQRIRQDLAESLSVSVSETNPQSQSLKLLLDSSSHKPRLSKREKRRNCETFAREDDEIRENEVGNGGSSEKTDTKIKKKRK
RDDAVEVDELEGDEGTKEEQKPQKKKNKKKKKKRKVNKTPKKAEEGNVEEKVKVEEIEVNTDNKEEDGVVPNKLYVGGIPYQSTEDEIR
SYFRSCGVIIKVDCKMRPEDGAFSGIAFITFDTEDGAKRALAFDRAAMGDRYLTIQQYVKTTTPSIPRRKTSSGFAPEMVDGYNRVYIG
NLAWDTTERDIRKLFSDCVINSVRLGKNKETGEFKGYAHVDFKDSVSVAIALKLDQQVICGRPVKICCALKDRPATDHTPGETNNAGSY
NMEDTYAAADPVPALAGRSEVDDGNYFATTVSSSKVKRRV**CYECGEKGHLSTAC**PIKLQKADDQANSKLGQETVDGRPAMQSYGLPKNS
GDSYYMNETYASTNETYNGGYSASAVGTGKVKRRN**CYECGEKGHLSTAC**PIKLQNTSHTNSTLDHQTVEAGPTQVTSYSLQKKTRDTEN
NGGSFMDESYATVPISIDVTNGANDASLTSAVSTGKIKKRNCYECGEKGHLSSACPNKLQKQG

AT1G53720 CYP59; 1 CX$_2$CX$_4$HX$_4$C

MSVLIVTSLGDIVIDLHSDKCPLTCKNFLKLCKIKYYNGCLFHTVQKDFTAQTGDPTGTGAGGDSIYKFLYGEQARFYKDEIHLDLKHS
KTGTVAMASGGENLNASQFYFTLRDDLDYLDGKHTVFGQIAEGFDTLTRINEAYVDPKNRPYKNIRIKHTHILDDPFDDPPQLAEMMPD
ASPEGKPKEEVKDDVRLEDDWVPMDEELGAQELEEVIREKAAHSSAVVLESIGDIPEAEVKPPDNVLFVCKLNPVTEDEDLHTIFSRFG
TVVSADVIRDFKTGDSLCYAFIEFENKESCEQAYFKMDNALIDDRRIHVDFSQSVSKLWSQFRQKDSQKGKGNG**CFKCGSTDHIAKDC**V
GGPSSKFIVKDQNRQHGGGEGYEMVFEGDVHETPKHNSHERERSEKIQRRSPHGNGEGKRQHRDERDDGRRQHDREDARELERKHRERK
ERESREDEDRRRRRRREESRDKESRRERDEDDHRSHRDYKERRRERDDRHGREARHERRDR

AT5G49930 EMB1441; 1 CX$_2$CX$_3$GHX$_4$C

MVKVRMNTADVAAEVKCLKRLIGMRCSNVYDISPKTYMFKLLNSSGITESGESEKVLLLMESGVRLHTTAYVRDKSNTPSGFTLKLRKH
IRTRRLEDVRQLGYDRIIVFQFGLGANAHYVILELYAQGNIILTDSEYMIMTLLRSHRDDNKGFAIMSRHRYPIEICRVFERTTVSKLQ
ESLTAFVLKDHDAKQIEPKEQNGGKKGGKSNDSTGAKQYTLKNILGDALGYGPQLSEHIILDAGLVPTTKLSEDKKLDDNEIQLLVQAV
IVFEDWLEDIINGQKVPEGYILMQKQILANDTTSESGGVKKMYDEFCSILLNQFKSRVYEKFETFDAALDEFYSKIESQRSEQQQKAKE
DSASLKLNKIRQDQENRVQILKKEVNHCVNMAELIEYNLEDVDAAILAVRVALAKGMGWDDLARMVKEEKKLGNPVAGVIDRLYLEKNC
MTLLLCNNLDEMDDDEKTVPVEKVEVDLSLSAHGNARRWYEMKKKQETKQEKTVSAHEKAFRAAEKKTRHQLSQEKVVATISHMRKVHW
FEKFNWFISSENYLVISGRDAQQNEMIVKRYMSKGDLYVHAELHGASSTVIKNHKPEQNVPPLTLNQAGCFTVCHSQAWDSKIVTSAWW
VYPHQVTKTAPTGEYLTVGSFMIRGKKNFLPPHPLIMGFGLLFRLDESSLGAHLNERRVRGEEEGMNDVVMETHAPDEHSDTESENEAV
NEVVSASGEVDLQESSTALSQDTSSLDMSSSGITEENVASATSQLEDLLDRTLGLGAATVAGKKDTIETSKDDMEEKMKQEEKNAVVRD
KPYMSKAERRKLKMGQSGNTAADGNTGQEKQQRKEKDVSSLSQATKSIPDNKPAGEKVSRGQRGKLKKMKEKYADQDEDERKIRMALLA
SSGKPQKTDVESQNAKTAVTEVKKPSEETDDAVKI**CYRCKKVGHLARDC**HGKETSDMDKVVMEEDDIHEVGDEEKEKLIDVDYLTGNPL
PTDILLYAVPVCGPYNALQSYKYRVKAIPGSMKKGKAAKTAMNLFTHMSEASVREKELMKACTDPELMAALVGNVKITAAGLTQLKQKQ
KKGKKSGKQQHS

AT5G47430 PQT3L; 1 CX$_2$CX$_3$GHX$_4$C

MAIYYKFKSARDYDTIAMDGPFISVGILKDKIFETKHLGTGKDLDIVVSNAQTNEEYLDEAMLIPKNTSVLIRRVPGRPRITVITTQEP
RIQNKVEDVQAETTNFPVADPSAAEFPEDEYDEFGTDLYSIPDTQDAQHIIPRPHLATADDKVDEESKIQALIDTPALDWQQRQGQDTF
GAGRGYGRGMPGRMNGRGFGMERKTPPPGYV**CHRCNIPGHFIQHC**PTNGDPNYDVKRVKPPTGIPKSMLMATPDGSYSLPSGAVAVLKP
NEDAFEKEMEGLPSTTRSVGELPPELKCPLCKEVMKDAALTSKCCYKSFCDKCIRDHIISKSMCVCGRSDVLADDLLPNKTLRDTINRI
LEAGNDSTENVGSVGHIPDLESARCPPPKALSPTTSVASKGEKKPVLSNNNDASTLKAPMEVAEITSAPRASAEVNVEKPVDACESTQG
SVIVKEATVSKLNTQAPKEEMQQQVAAGEPGKKKKKKPRVPGNDMQWNPVPDLAGPDYMMQMGPGPQYFNGMQPGFNGVQPGFNGVQPG
FNGFHPGFNGFGGPFPGAMPPFMGYGLNPMDMGFGGGMNMMHPDPFMAQGFGFPNIPPPHRDLAEMGNRMNLQRAMMGRDEAEARNAEM
LRKRENERRPEGGKMFRDGENSRMMMNNGTSASASSINPNKSRQAPPPPIHDYDRRRRPEKRLSPEHPPTRKNISPSRDSKRKSERYPD
ERDRQRDRERSRHQDVDREHDRTRDRRDEDRSRDHRHHRGETERSQHHHRKRSEPPSSEPPVPATKAEIENNLKSSVFARISFPEEETS
SGKRRKVPSSSSTSVTDPSASASAAAAVGTSVHRHSSRKEIEVADYESSDEDRHFKRKPSRYARSPPVVVSDVSEDKLRYSKRGKGERS
RA

AT4G17410 PQT3; 1 CX$_2$CX$_4$HX$_4$C

MAIYYKFKSARDYDTISMDGPFITVGLLKEKIYETKHLGSGKDLDIVISNAQTNEEYLDEAMLIPKNTSVLIRRVPGRPRIRIITREEP
RVEDKVENVQADMNNVITADASPVEDEFDEFGNDLYSIPDAPAVHSNNLCHDSAPADDEETKLKALIDTPALDWHQQGADSFGPGRGYG
RGMAGRMGGRGFGMERTTPPPGYV**CHRCNVSGHFIQHC**STNGNPNFDVKRVKPPTGIPKSMLMATPNGSYSLPSGAVAVLKPNEDAFEK
EMEGLTSTTRSVGEFPPELKCPLCKEVMRDAALASKCCLKSYCDKCIRDHIIAKSMCVCGATHVLADDLLPNKTLRDTINRILESGNSS
AENAGSMCQVQDMESVRCPPPKALSPTTSAASGGEKKPAPSNNNETSTLKPSIEIAEITSAWASAEIVKVEKPVDASANIQGSSNGKEA
AVSQLNTQPPKEEMPQQVASGEQGKRKKKKPRMSGTDLAGPDYMMPMGPGPGNQYFNGFQPGFNGVQHGFNGVQPGFNGFHHGFNGFPG
PFPGAMPPFVGYGFGGVIHPDPFAAQGFGFPNIPPPYRDLAEMGNRMNLQHPIMGREEFEAKKTEMKRKRENEIRRSEGGNVVRDSEKS
RIMNNSAVTSSPVKPKSRQGPPPPISSDYDRRRRSDRSSPERQSSRRFTSPPRSSSRKSERDRHHDLDSEHDRRRDRPRETDRKHRKRS
EKSSSDPTVEIDDNNKSNVFTRISFPEESSGKQRKTSKSSPAPPESSVAPVSSGRRHHSRREREMVEYDSSDDEDRHFKRKPSRYKRSP
SVAPSDAGDEHFRHSKRSKGERARA

AT3G45950 Pre-mRNA splicing Prp18-interacting factor; 1 CX$_2$CX$_4$HX$_4$C

MATASVAFKSRKDHRKQKELEEARKAGLAPAEVDEGGKEINLHIPKYLTIPPLYAKSEKPSLKHQKNWKTKPVSTTSYYDRGAKTYQAE
KYRKGA**CQNCGAMTHDVKTC**MERPRKVGAKYTDKNIAPDEKIESLEFDYDGKRDRWNGYDPSSYCHVRDRHEAKENAREKYLNEQQLIA
KLEEKNIDGEEEDLRVDEAKIDESMQVDFAKVKKRVRTTDGGSKGTVRNLRIREDPAKYLLNLDVNSAYYDPKSRSMREDPLPYTDPNE

KFCLRDNQYRNSGQAIEFKQQNMYSCEAFDKGQDIHMQAAPSQAELCYKRVKIAKEKLNSQRKDAIIAKYGDAAAKDDIPMELLLGQSK
LIKTSQANGIKLVPNVFVNLCFLVFVFIS

AT1G65660 SMP1/SLU7A; 1 CX$_2$CX$_4$HX$_4$C
MATASVAFKSREDHRKQIELEEARKAGLAPAEVDEDGKEINPHIPQYMSSAPWYLNSEKPSLKHQRKWKSDPNYTKSWYDRGAKIFQAE
KYRKGACQNCGAMTHTAKACMDRPRKIGAKYTNMNIAPDEKIESFELDYDGKRDRWNGYDPSTYHRVIDLYEAKEDARKKYLKEQQLKK
LEEKNNNEKGDDANSDGEEDEDDLRVDEAKVDESRQMDFAKVEKRVRTTGGGSTGTVRNLRIREDTAKYLLNLDVNSAHYDPKTRSMRE
DPLPDADPNDKFYLGDNQYRNSGQALEFKQLNIHSWEAFDKGQDMHMQAAPSQAELLYKSFQVAKEKLKSQTKDTIMDKYGNAATEDEI
PMELLLGQSERQVEYDRAGRIIKGQEVILPKSKYEEDVHANNHTSVWGSYWKDHQWGYKCCQQIIRNSYCTGSAGIEAAEAALDLMKAN
IARKEATEESPKKVEEKRMASWGTDIPEDLELNEEALANALKKEDLSRREEKDERKRKYNVKYNNDVTPEEMEAYRMKRVHHEDPMKDF
L

AT4G37120 SMP2/SLU7B; 1 CX$_2$CX$_4$HX$_4$C
MATASVAFKSREDHRKKLELEEARKAGLAPAEVDEDGKEINPHIPEYMSKAPWYLKSEQPSLKHQKNWKIEPEPKKIWYDRGKKIYQAE
QYRKGACINCGAMTHSSKACMDRPRKIGAKYTNMNIAADEKIESFELDYDGKRDRWNGYDTSTYRHVVDRYDAKEEARKKYLKEQQLKK
LEEKNNNENGDDATSDGEEDLDDLRVDEAKVDESRQMDFAKVEKRVRTTGGGSTGTVRNLRIREDTAKYLLNLDVNSAHYDPKTRSMRE
DPLPDADPNEKFYLGDNQYRNSGQALEFKQINIHSCEAFDKGHDMHMQAAPSQAELLYKNFKVAKEKLKTQTKDTIMEKYGNAATEGEI
PMELLLGQSERQIEYDRAGRIMKGQEVIIPKSKYEEDVHANNHTSVWGSWWKDHQWGYKCCQQTIRNSYCTGSAGIEAAEASIDLMKAN
IARKEASKESPKKVEEKKMATWGTDIPEDLELNEEALANALKKEDLSRREEKDERKRKYNVNYTNDVTSEEMEAYRMKRVHHEDPMRNF
PG

AT5G42540 XRN2; 1 CX$_2$CX$_3$GHX$_4$C
MGVPSFYRWLIQRYPLTIQEVIEEEPLEVNGGGVTIPIDSSKPNPNGYEYDNLYLDMNGIIHPCFHPEDKPSPTTFTEVFQCMFDYIDR
LFVMVRPRKLLFMAIDGVAPRAKMNQQRARRFRAAKDAAEAAAEEEQLREEFEREGKKLPPKVDSQVFDSNVITPGTEFMATLSFALRY
YIHVRLNSDPGWKNIKVILSDANVPGEGEHKIMSYIRCNKNHPGYNPNTHHCLYGLDADLIMLSLATHEIHFSILREVVFFPGEEGKCF
LCGQEGHRAADCEGKIKRKTGEMLDNTEADVVVKKPYEFVNIWILREYLEHDMQIPGAKKNLDRLIDDFIFICFFVGNDFLPHMPTLEI
REGAIELLMSVYKNKFRSAKKYLTDSSKLNLRNVERFIKAVGMYENQIFQKRAQVQQRQSERFRRDKARDKARDNARDNAQASRQFSGK
LVQLDSLDEVSDSLHSSPSRKYLRLSLDDNIGVANVETENSLKAEELDNEEDLKFKLKKLLRDKGDGFRSGNGEQDKVKLNKVGWRERY
YEEKFAAKSVEEMEQIRRDVVLKYTEGLCWIMHYYYHGVCSWNWFYPYHYAPFASDLKGLEKLDIKFELGSPFKPFNQLLAVLPSASAH
ALPECYRSLMTNPDSPIADFYPADFEIDMNGKRYSWQGISKLPFVEEKRLLEAAAQVEKSLTNEEIRRNSALFDMLFVVASHPLGELIR
SLNSRTNNLSNEERATIIEKIDPGLSDGMNGYIASCGGDSQPSCFCSTVEGMEDVLTNQVICAIYKLPEDIRGSEITHQIPRLAIPKKT
ISLVDLKSGGLLWHEDGDKRRAPPKVIKIKRYNPEGSISGGRLGKASHRLVLQTINAQPDYMNINSEPALCPNTVFQNERVPKKIPTFK
DNGIQWISPPPSQITPKKMNSPQRQKAWKKDETPQSREKSKKLKSSLKVNPLKMKKTKSPQREFTREKKKENITPQRKLTKAQRQVKHI
RMMEEAKMIKQRKKEKYLRKKAKYAQGAPPKTA

AT1G75660 XRN3; 1 CX$_2$CX$_3$GHX$_4$C
MGVPSFYRWLAEKYPLLVADVIEEEPVEIEGIKIPVDTSKPNPNNLEYDNLYLDMNGIIHPCFHPEDRPSPTTFEEVFQCMFDYIDRLF
VMVRPRKLLYMAIDGVAPRAKMNQQRSRRFRSAKDASDAAAEEERLREEFEREGRRLPPKVDSQVFDSNVITPGTEFMGVLSIALQYYV
HLRLNHDVGWKNIKVILSDANVPGEGEHKIMSYIRLQRNLPGFDPNTRHCLYGLDADLIMLGLATHEVHFSILREVVYTPGQQERCFLC
GQMGHFASNCEGKPKKRAGESDEKGDGNDFVKKPYQFLHIWVLREYLELEMRIPNPPFEIDLERIVDDFIFICFFVGNDFLPHMPTLEI
REGAINLLMAVYKKEFRSFDGYLTDGCKPNLKRVEQFIQAVGSFEDKIFQKRAMQHQRQAERVKRDKAGKATKRMDDEAPTVQPDLVPV
ARFSGSRLASAPTPSPFQSNDGRSAPHQKVRRLSPGSSVGAAIVDVENSLESDERENKEELKTKLKELIREKSDAFNSDTTEEDKVKLG
QPGWRERYYEEKFSVVTPEEMERVRKDVVLKYTEGLCWVMHYYMEGVCSWQWFYPYHYAPFASDLKDLGEMDIKFELGTPFKPFNQLLG
VFPAASSHALPERYRTLMTDPNSPIIDFYPTDFEVDMNGKRFSWQGIAKLPFIDERRLLEAVSEVEFTLTDEEKRRNSRMCDMLFIATS
HRLAELVFSLDNHCRQLSARERVDFKVKIKPKLSDGMNGYLTPCSGETHPPVFRSPMEGMEDILTNQVICCIYRLPDAHEHITRPPPGV
IFPKKTVDIGDLKPPPALWHEDNGRRPMHNNHGMHNNHGMHNNQGRQNPPGSVSGRHLGNAAHRLVSNSLQMGTDRYQTPTDVPAPGYG
YNPPQYVPPIPYQHGGYMAPPGAQGYAQPAPYQNRGGYQPRGPSGRFPSEPYQSQSREGQHASRGGGYSGNHQNQHQQQQWHGQGGSEQ
NNPRGYNGQHHHQQGGDHDRRGRGRGSHHHHDQGGNPRHRY

AT1G54490 XRN4; 1 CX$_2$CX$_4$HX$_4$C
MGVPAFYRWLADRYPKSISDVVEEEPTDGGRGDLIPVDITRPNPNGFEFDNLYLDMNGIIHPCFHPEGKPAPATYDDVFKSMFEYIDHL
FTLVRPRKILYLAIDGVAPRAKMNQQRSRRFRAAKDAAEAEAEEERLRKDFEMEGQILSAKEKAETCDSNVITPGTPFMAILSVALQYY
IQSRLNHNPGWRYVKVILSDSNVPGEGEHKIMSYIRLQRNLPGFDPNTRHCLYGLDADLIMLSLATHEVHFSILREVITYPGQQEKCFV
CGQTGHFASDCPGKSGSNNAAADIPIHKKKYQFLNIWVLREYLQYELAIPDPPFMINFERIIDDFVFLCFFVGNDFLPHMPTLEIREGA
INLLMHVYRKEFTAMGGYLTDSGEVLLDRVEHFIQAVAVNEDKIFQKRTRIKQSMDNNEEMKQRSRRDPSEVPPEPIDDKIKLGEPGYK
ERYYAEKFSTTNPEETEQIKQDMVLKYVEGLCWVCRYYYQGVCSWQWFYPYHYAPFASDLKNLPDLEITFFIGEPFKPFDQLMGTLPAA
SSNALPGEYRKLMTDPSSPILKFYPADFELDMNGKRFAWQGIAKLPFIEEKLLLAATRKLEETLTVEEQQRNSVMLDLLYVHPAHPLGQ
RILQYYHFYQHMPPHECLPWMIDPNSSQGMNGFLWFSERNGFQTRVDSPVNGLPCIEQNRALNVTYLCPAKHSHISEPPRGAIIPDKIL
TSVDIKPFPPLWHEDNSNRRRQARDRPQVVGAIAGPSLGEAAHRLIKNTLNMKSSTGAASGLIDPNGYYRNVPGNYSYGGVNRPRAPGP
SPYRKAYDDDSSYYYGKYNNSTQGTFNNGPRYPYPSNGSQDYNRNYNSKIVAEQHNRGGLGAGMSGLSIEDNGRSKQLYSSYTEAANAN
LNPLPSPPTQWIGTQPGGNFVGGYYRDGVGYSETNGKSVKKVIYQAKTQPSHRGANL

AT1G54930 protein of unknown function; 1 CX$_2$CX$_4$HX$_4$C
MSSGDCFHCHQPGHWAKNCPLKTTTKPTAAAAPSPPDIHCPCNAGPCNTVTSKTEKNPNRRFYTCPSCGYFKWCDQGLGDCGFFKWEDG
ESLLHETELDSDGNVKRNRLGVVVELELNPASSSESNTLGNRIVDTLPVNPVTVGKESIPVFAGFNDQGSVSNSIVPSFDLITLYDDAV
RLETKEPVLPSVAPKHLDTQVETLCGNALEAVESSSQNTSDLVLNANNKPEHIHQRAATSGETEASYSGSSSMMVLIEQYKSEKLYLES

ISMKHVEALTAYTGSYKQLESLRDRAHSLKKQLLEVEKQVKLCEAETSEFAASVQEVSGEMAKSQKKMVEIAGKVAKEVRVDKQRD

AT1G67210 proline-rich spliceosome-associated (PSP) family protein; 1 $CX_2CX_4HX_4C$

MAASSGSGLEAEEGEISIDMEEDMDLTEDDFRNVSGQFSGQASIVEVGDAVDVRVETVKVDVSSKSGVKRARTISLEQQPSVHVTYKHLTRDSKQKLESLLQQWSEWEAEQNSLSEDQEQVLEAGDETYFPALRVGLQKTSSVSFWFDYQTGHSSSKKSVPVESSTTPLYNRGFTIGLDSGSNNVEGGLEIIDDPPRCFNCGAYSHSIRECPRPFDRSAVSNARRQHKRKRNQTPGSRLPSRYYQSLQRGKYDGLKPGSLDAETRKLLGLKELDPPPWLNRMREIGYPPGYFAVEEDDDDHSRITIFGEEETKEEEEVKTEEGEILEKASPQEPRKIMTVGFPGINAPIPENADSWLWEQRNSNTGHTNYHNHLRPQYEMGPLGIQLSSSFPPMHGIRYDHRFGL

AT1G75560 protein of unknown function; 8 $CX_2CX_3GHX_4C$

MSSMSRSRSRSRSRSRSRDRFRSRSPRDRRMRSERVSYHDAPSRREREPRRAFSQGNLCNNCKRPGHFARDCSNVSVCNNCGLPGHIAAECTAESRCWNCREPGHVASNCSNEGICHSCGKSGHRARDCSNSDSRAGDLRLCNNCFKQGHLAADCTNDKACKNCRTSGHIARDCRNDPVCNICSISGHVARHCPKGDSNYSDRGSRVRDGGMQRGGLSRMSRDREGVSAMIICHNCGGRGHRAYECPSARVADRGFRRY

AT2G06904 protein of unknown function; 1 $CX_2CX_3GHX_4C$

MPLKRSRGRESVEEEGRSLDLPSRRYDLRERVRGIAAMPERIIREDVQIRDGMMIDSDCEDDFVITGVRTVEQKLASEGHEIVMVHDYVSVSSKSSASPSFALSLYSPISYESDPKEDQDPPISPYVPEAVDHSPDSPFALLWEGTSPILRFEADMRADAIPTFDGGFTSGIKILFCFICGEDGHYPQDCQFYTQYIPWPLLVSTVESMSIMRLPVC

AT2G12880 putative CCHC-type zinc finger protein; 2 $CX_2CX_3GHX_4C$

MAPKFTLNQERDNDRERTRASYNNDRRRNDYDPRACYKCGKLGHFARSCHVVTQPTTAYITCYFCSEEGHRSNGCPNKRTDQVNPKGHCYWCGNQDHRFNLIIWRSRCLFRLMKPKYAF

AT2G15180 putative CCHC-type zinc finger protein; 1 $CX_2CX_3GHX_4C$

METIIYSSSDEEDSYGCSQDSYYNETRFVESWHDDGYSSSSDFEEEPDGGAPEPEPPDRYSSHATPPSYSKPWISWNPIPKTNFYPTFYPTRKVIYKLFVHNGSKTYGPEFFLFSGLGYLQWESNMNYYFEFHSTAQEDKLSIALGQLKGSALWWWDQDEYNRWYERRAPIRTWERLKWNMCAKYSPQSLSPAHVVQQKQKPTFLPQMQATTQGKCTFQTKHVELTCYRCKQEGHIAKICPTRETTTKVGLEQQELLKAKEKQEIVSSPKGKNEQAETCQTDLNNSMNVITHLSSAKSIAKVSGTKENITDQGEASTMEKVFTEESKNQGGPTLDEITVNKDESVNDTIQIKGEPSDAQQFPKTQCNLLNPYTLQWTNLTYLCVGKKVLRTKPLEEGGDDVRMGADVPADALVDRLLAGFFDGLSDGLPEVLHVSNQLVRTKESYPFLPFCASQSHIWKLGDPLRHPEPFTLNP

AT3G02820 putative SWI3-like component of replication fork protection complex; 1 $CX_2CX_3GHX_4C$

MESAPTGCFKCGRPGHWSRDCPSSAPVAGNNSVSSSSAPSQIPNNEFQRSSSKSGTSIAPAPKVTKTRVQRPKLTPELLLSEDGLGYVLRYFPKSFKYRGRGKEVSDLGNLIRLYSEWHTHLLPYYSFDHFVHKVQQVASTKRVKNCINELRERVASGVDPNKLYEKQEENTVPSDDQDMDQPSHDEENIPSKSVDADTNADAFEDSMLNEIFDNASKLPSDEQNMDKSSELTEEQRARMEANRLKAMEKAQNISEEQRVRMEANRLKALERAKARLQPNQD

AT3G42860 putative CCHC-type zinc finger protein; 4 $CX_2CX_3GHX_4C$

MKKITIPVESLDEEDDFLLQLAAIEAEAAAKRPRVSSIPEGPYMAALKGSKSDQWQQSPLNPASKSRSVAVTTGGFQRSDGGGGVAGEQDFPEKSCPCGVGICLILTSNTPKNPGRKFYKCPNREENGGCGFFQWCDAVQSSGTSTTTSNSYGNGNDTKFPDHQCPCGAGLCRVLTAKTGENVGRQFYRCPVFEGSCGFFKWCNDNVVSSPTSYSVTKNSNFGDSDTRGYQNAKTGTPCYKCGKEGHWARDCTVQSDTGPVKSTSAAGDCFKCGKPGHWSRDCTAQSGNPKYEPGQMKSSSSSGECYKCGKQGHWSRDCTGQSSNQQFQSGQAKSTSSTGDCYKCGKAGHWSRDCTSPAQTTNTPGKRQRQY

AT3G43490 putative CCHC-type zinc finger protein; 2 $CX_2CX_4HX_4C$

MPPKRKDINFLFDDGEDTVAIIDDEANEDLRLKILEKAFSRRNVDNKLDSDLSFDPGVVSTVMVNGGKSEEVKNSKSNKKMKRNKLEAANEIVTHCVERQDEDNMVEDVVRGEEEDGETTSNSVMTKLLRGARYFDPLDAGWVTCYSCGEKDHITVSCPTLTNCRKSCFICASLEHGARQCTKVWDIDANLGIHQDKTQRFKGKLCGSGDDDEVTDLMLNPQHRGLENMIQGLFLARIRDYTKPKWFDSTNYLELARTMI

AT3G43590 putative CCHC-type zinc finger protein; 6 $CX_2CX_3GHX_4C$ and 1 $CX_2CX_4HX_4C$

MPRQNKDEKFVFDDGEDEDREDPVAITEVDNGEEEDDDEANEDLSLKILEKALSRRDVGNKLDSDLSSDSGVVSTVMVNGVKSKVKKSESSKKMKRNKLEADHEIPIVWNDQDEEKVVEEIVKGEGEDDEVERSDEPKTEETASNLVLKKLLRGARYFDPPDAGWVSCYSCGEQGHTSFNCPTPTKRRKPCFICGSLEHGAKQCSKGHDCYICKKTGHRAKDCPDKYKNGSKGAVCLRCGDFGHDMILCKYEYSKEDLKDVQCYICKSFGHLCCVEPGNSLSWAVSCYRCGQLGHSGLACGRHYEESNENDSATPERLFNSREASECYRCGEEGHFARECPNSSSISTSHGRESQTLCYRCNGSGHFARECPNSSQVSKRDRETSTTSHKSRKKNKENSEHDSTPHESNGKTKKKKKKKTHKEEQPQTSPRKRKHRGGWITEEPEEESFQRGKMRRPKSPITPSGYNRSPSTHIGHNYRSPKFNSGGHYPGSQSSRHHSGPSPSRWQPSHQHHHHHQHLHHHHQNHSYEPAPPRHGRANRYSEFAGNYERW

AT3G62330 putative CCHC-type zinc finger protein; 1 $CX_2CX_3GHX_4C$

MESTRSDPELDDDFSEIYKEYTGPASAVTNNNIQDKDKPVKQRSEERCDEEEEQLPDPNSVPTDFTSREAKVWEAKSKATERNWKKRKEEEMICKICGESGHFTQGCPSTLGANRKSQEFFERVPARDNNVRVLFTEKVMESIERETSCKIKLDEKFIIVSGKDRLILRKGVDAVHKVKEDGEMKSSSVSHRSRSRSPRRTSVGPSRARNSEPQRQQLPSHGSSSFPERSGRQDKFVDNRFREETRVRENQRNVPRGSPQAYGSDRARSRSTHSKSPGRPRYSGWDKPYDRQKPEVSGYRSERWDQERMGGSSDIQVSHQFERPPFPQTLEELELEYTRDALELEKKRDKEEDEENNKHRETIRELRESYMKKLAGLRGMNAKQWDDFLQLDAQRRQQQARQQNSGLSYGNYRQFPPYAEFDDGYSSNPPPYGGNNMPMDSKGRYPNHGDNYSSRHQDNNYGGFQRQRREEYGKAYNRY

AT4G00980 protein of unknown function; 1 $CX_2CX_3GHX_4C$

MENSLLDSGETMEIVATQKIEETVKSILSESDMDQMTEFKLRLDASAKLGIDLSGTNHKKLVRDVLEVFLLSTPGEALVPETVAPAKNETVSVAAASVGGEDERFICKLSEKQNATVQRYRGQPFLSIGSQEHGKAFRGAHLSTNQWSVIKKNFAAIEDGIKQCQSKLKSEAARNGDTSEAVDKDSSHGFSVIKISRFDGKSYLYWASQMELFLKQLKLTYVLSEPCPSIGSSQGPETNPREITRADATGKKWLRDDYLCYTHLMNSLSDHLYRRYSQKFKHAKELWDELKWVYQCDESKSKRSQVRKYIEFRMVEERPILEQVQVFNKIADSIVSAGMFLDEAFHVSTIISKFPPSWRGFCTRLMEEEYLPVWMLMERVKAEEELLRNGAKGVTYRPATGSSQMERTPSLGTTHRGSQSVGWKRKEPERDERVIIV**CDNCGRKGHLAKHC**WGSKSDERASGKSNRINSSVAAPVESETQATTNNDRG

AT4G05360 putative Rad21/Rec8-like protein; 1 $CX_2CX_4HX_4C$ and 1 $CX_2CX_3GHX_4C$

MGKIKDQKGKEHDHSQCRRYVLQSYLLRTEHISPNSTRNINMITQDDSLCLLSISIYTLNSSHASLWLFTRSEEESADFGESEDPSKTVRKRKKLSSSKLGFRRLDNQSKKDQLFNEPLFTGFSNVLLSVFKKDCVAKSYFAAPKEPASVPVSSPTREAETEINSASPVTQSTVPDSTNQESTVQRSSGQQTEHFQGVALKFVLPGLNILEYMLSPPPRSSPFRTNGFTIHPETWETGSYRTQPSTSNNTEELHFLEEGVNTPVRSPVTQDSGGFSGRTRALAQHLKERYSGYLSLNKILEGKTRKIAARMFYETLGEVPEIVQKIIQEVRQSLKSRLMEILRLPFKKRFSWNERNRALHEFKVDGNKEVLYKSSKGKR**CFECKGFRHMCSEC**ANLMKEKEKKFIMSDSEIDSDDGEELKNLVAFTTFESSIASASASGPTSASATGSTSASATGPATGSDNDQSDDDDLSISDEEFAENYKALYEHCVKVVEENSVLTKEKLKLEAKVVKTLKFAAEKEEEASQLEETQKNLRMLNNGTKKLGHILSIGKTDKCGLGFKGNPSKSDPVFVYGGKITSASGTVKETATVAEIASDTRTDSRTDTETTSGTRKVQKLQSEPRRVFRPV**CHHCGVVGHIRPRC**FRLLREKNRLMNAYDVRFHGPKCYHYGVQGHIKRNCFRFIRECSHEGLRRNKVWVRKDDFHGSGGENDDVFGDVVLELELMSSQHSQKGGDLKM

AT5G20220 putative CCHC-type zinc finger protein; 4 $CX_2CX_3GHX_4C$

MRKKKTRFQFLLNPNSKFVFFPRAISSSSSSSSDNNNDGSVSSSRQNNRQMGYDPSEELFGVDFKPRFISGDSREPRSWFGPNGQYIRELPCPTCRGRGYTSCSNCGIERSRLDCPQCKGKGIMTCLRCLGDCVIWEESIDERPWEKARSSSPFRVKEDDEVDNLEIKFSKRRKSKRIYQSPTPEVGQKISRSLKSLNAKTGLFSKRMKIIHRDPVLHAQRVAAIKKAKGTPAARKHASESMKAFFSNPVNREQRSLSMKGTKFY**CKNCGQEGHRRHYC**PELGTNADRKFR**CRGCGGKGHNRRTC**PKSKSIVTKGISTRYHK**CGICGERGHNSRTC**RKPTGVNPSCSGENSGEDGVGKITYA**CGFCKKMGHNVRTC**PSKQVSDSDSCLEQEGS

AT4G06479 protein of unknown function; 1 $CX_2CX_4HX_4C$ and 1 $CX_2CX_3GHX_4C$

MAKDSESTESDISIESDPSEYLESTEDANNHDGPLSSEEANHVEWMITEDGELFAVPTENAIEQQTNDSLNNMLSQFYVPSTDKEGSFGGPNLGTIGGHGLELEEADGAFGAMNEYGADDEYDMLMLMGNNVEDENGAIENEIENELEHVSLSVINISLDSSHAILMIPNSSKADSCWEDEMFKGDEPSEDEENGRWDKMLLEQELNHESLMNHLRLDEERSKGKLVDKAGENEKWKGKRAVEMNMESEKAKDQRIVGVNLHPVGIGYGINSKVKPGIQATARKSVGKKLATPAKRP**CEICSHTDHPTEEC**LYPPQTIPYTDDYAK**CYYCEGMGHMSMYC**LYIAPNAGEGSLRGVGPLMTTTTEEKCLNE

AT4G06526 protein of unknown function; 1 $CX_2CX_4HX_4C$ and 1 $CX_2CX_3GHX_4C$

MSSTKGSNIVSPLHGLNVPNLENFVLPSSIDDENVDNHDGMLSSEEANHVEWMITEDGELYAVPTENATEEQACDSLNNILSRFYVPSTDEEGSFSVPNMGTIGEHGLELEEVNGDMFDVPLIQANGAFGAMNKYGDDDEYDMLMLMGNDEEDESGVIENEIENELEQAIDKLIAYKADSCWEGEMFKGNEPSEDEGNGRLDEEKSKGKLVDKAEENERWKGKRAAEMGMESEKAKDQRIVGVNPLPLGMEYGINTKVKPRIQATARKSVGKKLATPAKRP**CEICSHTDHPTKEC**LYPPHTMPYMDDCAK**CSCCGGVGHMSMYC**PYVAPNASEGSSRGVRPLMTTVAEEKCLNEGMPSFLWVRRFKTFVKMMGEFIEVGNDQSQLTAYAQTLPKLQRAKMSMNGHEWAKMGKVGRAAAKFALPAAELTWVGHLTRGALRLNRSLWGGGVTPVATCRQALLSGWLYEKFHLVEVGPETPVACGHDICSDMWQQAGIVDCGLGDSPET

AT1G48095 protein of unknown function; 1 $CX_2CX_4HX_4C$

MSDFENIVLPSSCDSQVTAWPVLELDFNQDTSTYVAFIRVKIRLVFTDRLRFFRRVRFESREGAMIGFEYEKLRRI**CTNCCRITHHVNNC**PFLNAPVIHDDEVEVLDVPVWEEGAASNTITDQTHMTSSDSSDISSASLISQPLPPASLASHEPHLVAGSEASRLVNPRPIPQNHFSSSSSDFKGKGKAKMEIGECSKRKKDKQVVDDALRNVRQCRKDQGIRIMILQINLDIELASFVRTAGAVASHKMMKLLTPFSTVVLRRSKYSILDDLEGYITSGVYTYKVTISTKLKICFSLYFHLF

AT5G13920 protein of unknown function; contains GRF-type zinc-binding domain; 1 $CX_2CX_3GHX_4C$

MLNGTMQTGD**CFRCRQAGHWINDC**PLKSYTDDPPPAIQCPCGGGFCEIKVANTRENPGRKFYKCPTAQNCCFFKWCDKVTDEDIKFRPAFTIPICSCGAGPCRRVKDVSGRAYLICCIKKGFGACGFFKWEDVEMIPSCDVMDEIDFWVEADQILSDVESSLQARGGVIPEIANQMASEKECQASVSGIEDDCVVECQDSVSAEDDSTLENLDSISMSVSDVHSTALNQGISLFDPVTSEPEEPWKKTQNGDQPTNSALSKLSVDEAMSDLIRDTVSSGSVVIHGRTNHEQPEIDGAEWSFPCLQNLIDQYNSEKLQLESISGKHVQMLSEFMASYRRLRLLHEKTSHLRKTLLETEKEMVCCEAETLKFGASCREVAGEMAESQKRMQETADKLGKEVEVFKQNEFVGLKRRRT

AT5G34870 protein of unknown function; 1 $CX_2CX_3GHX_4C$

MSSSKGSNTVSLLHSVNVPNLENSAPSSSTDDESLFVAMNDQFMAEDSDSTESDTSIESDPSDVWKLFAVPTENATEEQVNDSLNNMLTQFYVPSTDEEGSFGVPNLGTIGEHGLKLEELNADLFDVPVIHANGAFGAMNEYGANDEYEMLMLMGNNKEDENEAIENELEHAIDQLIAECAQDFGLIGEKGGGNGNDGGDSSSDSFESLTLEPKSPSVINISSDSSQPIVMMLNPSKPESCWEIEMFKGDEPSEEEGRGRWDPMLLEQELNHEYLMNRLKLDEERSKEKMAQRIVGVNLHPLRIGYGINSKVKPRIRATARKSVRRKLPTPAKRPWEICGYIDHPTEQCLHPPQAMPYMVDCAK**CYSCGGVGHVSMYC**PYLAPNAGEGSSRDALVFMGKGETSHERRHEGDSKTFVKMSEEFVGDRMRKSCLNAWPIDRMCPESTKPAKGKDGQEWARMGKDGKSWACRGRNFPCRVQNRHVWTPHLRCLAAQVTNLGAKVGLVLEPKLAESWSRS

AT5G36240 putative CCHC-type zinc finger protein; 4 $CX_2CX_3GX_4C$

MIKLPNPISRVCDPLIMPRHNDDEAEV**CLRCGGFGHDMTLC**KYEYSHEDLKNIKCYVCNSLGHLCCIEPGHTQSWTVS**CYRCGQLGHTGLAC**GRHYDDSVSPS**CFICGREGHFEHQC**HNSFSVCFPEDSSEDECQGPDSSSVRFQENTREEEEGHFEHQCPDSSSVCFQEISREEGFISLNSSSKSTSKGRETRRL**CYECKGKGHIARDC**PNSSQVVSISLSTFCALSSSVLSFLSCYYSRINFLCFFQDKYGI

AT5G49400 zinc knuckle (CCHC-type) family protein; 1 CX$_2$CX$_3$GHX$_4$C
MSNSKDEKSQDAADRIKAATLTAAKGLSRTQAERAAAAAARNVNAYGQKEEGPSRWQEKRELKRQMYLMSTEKAVRLGERKDKTMSASA
VGSSASAASQCQKCFQAGHWTYECKNERVYISRPSRTQQLKNPKLRTKPSVDDLDGSDDDDEEERPDATNGKAEVEKRSKKSKRKHRSK
SDSESDSEASVFETDSDGSSGESSSEYSSSSDSEDERRRRKAKKSKKKQKQRKERRRRYSSSSSESSESESASDSDSDEDRSRRKKKS
KRHSNKRR

AT5G52380 CCHC-type zinc finger protein; 3 CX$_2$CX$_3$GHX$_4$C and 2 CX$_2$CX$_4$HX$_4$C
MVNQRRRLAQKRYKEANPELFPKAEPTPPKDPNKKKKKKSLFKKKKPGSSTDRPQRTGSSTRHPLRVPGMKPGEGCFICHSKTHIAKLC
PEKSEWERNKICLQCRRRGHSLKNCPEKNNESSEKKLCYNCGDTGHSLSHCPYPMEDGGTKFASCFICKGQGHISKNCPENKHGIYPMG
GCCKVCGSVAHLVKDCPDKFNQESAQPKKTSRFDATPRGKLTKFSGDDLEDDFTEEPKSSKKINTSDDSAQNSVEVKKKKQGPKIVNFV
G

AT2G01050 protein of unknown function; 1 CX$_2$CX$_3$GHX$_4$C
MLDVGEKGRPPGDPPDKLESWATKVKGSAGGGILKPEDVIDDEFVRERVGLEFPDGEDEEPVITIGEEVLEAMNGLWKKCMIVKVLGSQ
IPISVLNRKLRELWKPSGVMTVMDLPRQFFMIRFELEEEYMAALTGGPWRVLGNYLLVQDWSSRFDPLRDDIVTTPVWVRLSNIPYNYY
HRCLLMEIARGLGRPLKVDMNTINFDKGRFARVCIEVNLAKPLKGTVLINGDRYFVAYEGLSKICSSCGIYGHLVHSCPRNVVVKVSAG
AETVTDRAVVPVGMEGDDGFTVVQRTARRPAAPVQKMVFAVGASGGRSKQRLRELPKNQGVDLANRFGGLDGNGDLPDLREVAITEGPN
KENEYHGRNVGKVMGVPLVKEARGSTQMEKGKGGSKGGFKWKRNGGMKALEPIGPKQKHGAANKPARGLIFGPTKDANSVPVGEDLLSN
GKRLRVEQRDVGRPGGVYSSAMGSHAHEASFDLDSSSTLSQRFQREDLMSEIAVVSHEGSEVGNSSEGMA

AT5G36228 protein of unknown function; 1 CX$_2$CX$_4$HX$_4$C
MSDELWNAIQHMDLGREEPELYIPYHAYVGALASNRLSLLGRILNPQTQSVERAILELPYQWGLGTQVHGRILDDRCFQVRFRSEIDLL
NGLRRAPWVFNEWFIALQRWEDFPTEDFLTFIDVWVHIRGIPLPYVSERTVEIIASTLGEVVAMDFNEETTSQITFIRVKVRMDFTEPL
RFFRRVRFASRERAMIGFEYEKLQRVCTNCCRVNHQVSHCPYVVHQEEMDNEPDVLVSPERYDDEDSLNQEDHGRHSQSSVISSFSSLT
PISLNAPPVVNWNDNMIGNIPHRFPSTSVSSSHTVSDGYLAASEWRPKDQVSYEVGESSKRKKGKQVLEVPERSIRQRRMGSGIRFYPV
NGENP

AT2G07760 protein of unknown function; 1 CX$_2$CX$_3$GHX$_4$C
MNSVSVLTQGKETEVGPKVVVVDSSNVNSVPDPRWPYLTRWTQNSPSPSPSVISPSISLVKPLTIGSSPKIARSSSLDFVNLTSSLDST
LPVTVEPPIEHVVSITSLSYSAEVSLPTSALPPIVSATLDESIAPVKLVSPTLKGAWAKQLKFTSSSASQQDVGGAPMQSHLEATKEDN
VRFPWAAKMDPAARNLYRATSPEFMEDGIPKRGLWHVDDCLMFVAPWSTVNTFDLPEISTIPVWVTLKNIPNRLYSILGISHIASGLGA
PMATYKPRLDPSLMSEANILVEVELSKAFPPRIAAVDKKGNISMVNVEYAWIPAKCGKCGQLGHKASRCMKPHLAHEKVTEIVSEEIIT
PAIVSLASATNLVSPITLQTKTPIDVPITNSKIQIDTVFDIEAGPIQDKDNCTGVADCFTNVEAEVVTEETCTVESVFEIAGTKDKFSR
LGSSFPDGDSLHSDEDSIVSVESDSGSELMELMTPSGQRLLRERPVKPSIKAKEIQASSTTRGRGNRGRGNRGRGNRGRGNRGRG

AT3G24070 protein of unknown function; 1 CX$_2$CX$_4$HX$_4$C
MWLKIRGIPIQYLCDGTVREIASSMGEVMEVELDDGMVDLSSVRARVNVCVDTRLCFKKVARFDSGEVKIVSFRYEDIGMSKARFKFCF
NCGDMNHLARNCLIPWVDVPDPYERSLSPPPHESNSDGSAEGNCGDGGTSSGTLELLELVDAVQDFPVGDGEQLELAGVVQDLPVGDGE
QQQQGLDGVEEANATQVDSEMVGISSEGSKRKFDAVEQGDENPEKRLRGITDATEGGSTDATQGGSTDATEEGLGVSLKPLQGE

AT3G31430 protein of unknown function; 1 CX$_2$CX$_4$HX$_4$C
MATDKAICRRLLYYLFVTPLVTVYREFAGKVVCFFTAHSLVVISTVESTIHRDATSSASGNVLLKFRFTIPESTNLISLKPPNHFPLRF
YQPLSQMADNLRRAVQDINLGVDDIPFALPEDIVNHAVAENRFILFGRPVMPRRQNLRSIVASMPRIWGQSGLVHGRIMEGRQFHFIFT
LEESLETVLRRGPWAFNDWMILLQRWEPQIPLFPFIPFWVQIRGIPFQFLNRGVVEHIGRALGQVLDTDFNVEVVARMDFARVLLHWDI
THPLRFQRHFQFTAGVNTLLRFRYERLRGFCEVCGMLTHDFGACLIQNGGEEQADDDDDDEEHPQTYHN

AT3G42140 protein of unknown function; 1 CX$_2$CX$_4$HX$_4$C
MADNLQRQMQEIALGVQEEAINLLIELCDEALRKPNLASLQNRCPKNVDEEVVGRILEIHKIEFLFQSEESMFSILRRGPWSFNDWMCV
IQRWTKLHSDAEFKRIPFWIQIRGIPLRFLTARIITSIGERMGLFLETNLGRDVSVLKFQYEKLKNFCTTCGMLSHDASECPTSGNQGP
HADDDDDDDDNDANEDHPDVPGDNPDQVHGPMNQQHPEESTEDEHQNAPKRGKLKPLLQRLTMEVPWCVATCARPMPQKILNTAWLKDR
EGNHKF

AT5G32613 protein of unknown function; 1 CX$_2$CX$_3$GHX$_4$C
MPKKKKSVRPSWPPIPSKFFRVLAVSSAPGSSVSSVPDSVLSCVGADASSTLVEMNRVRPSSPKVLGSMLELCQDIVPLTSFDLVEVLD
KSVKLPEARISSEIAVPVSENSSIGTVELEQGCEITSATAPELEISSSVPVDTLINSSFDRITNPSPTSSKGPLWMTPSTFLEDGTPMV
VAPASVLLKTAEMSLWEHYGSSVLEDGGVDFHSFSKYSPMGESPLEPQELQTAQTWAILKNVPPQLYSLEGISVIASGIGEPLHTEKSR
LGPVNIGRTKVKVVTNLGTPLPDSIVVRDVQGNTARVAVTYPRPPPKCLNCGRYGHLLSRCSKPLMKKLPFKKDLPSGSKEVQILVISL
PTSQEAQRGIMLESSIEDQKTTTTQAKSKCRRSRSKKRSASLPSASIGPLEIQKGVKEGKSDRLAAVAKPKWIVKADVKRPGTASQPTL
SSPTIIDASCEL

AT2G17920 Nucleic acid binding/zinc ion binding protein; 1 CX$_2$CX$_4$HX$_4$C
MADELWDEIQNLELRQEGPSLFIPNEAYIMVAGRNRLSIIARPLNPRVQNLQAIITALPRAWGLTAHVHGRIIDDTYVQFLFQSEMDLL
SVQRREPWLFNNWFVASQRWQPAPALNFVTTIDLWVQMRGIPFLYVSEETALEIAQEIGAIISLDFHDTTSTQIAYIRVRVRVGITDSL
RFFQRITFESGESALIRFQYERLRRICSNCFRFTHNRNYCPYRPRVQILDRERAALHDSVLRSSNNSQSQMTESSFPAPLTPPPRVPAP
PLNHQELAAATPYFPSKNCSFPALHSSYYSKWYWQTSSFP

AT3G21000 Gag-Pol-related retrotransposon family protein; 1 $CX_2CX_4HX_4C$
MATANIRDGVVSDQFDYEIWAPITKSTLIEQGLWDVVVNGVPQDPSKNPELAATIQPEELSKWRDFVVKDAKALQILQSSLTDSVFRKT
LSASSAKDVWDLLRKGNEQATIRRLEQVTIRRLEKQLEDLKMVDKESGSSYLDKALEILERLGRAKLEKSDYEICKNVFTTLSGSFDGL
DSMLEELIDVHKMTSKSLVEYFYYRVHESSTEEAIFGLLKDLRLKSKSEKWCGLCYKNNHNQEDCKFRIHTDKEEKEDEIVVDYRLETV
PNLGAKTYDDDIWIIHKMAPINMTPYVKYFTTLDRTFKATVGTVDGTVLLVEGKGDVKIRMKEGKKKTIRNVIFVPGLNRNVLSFGKMV
SKRYSISTGMQGECIVCDRGENKLGDAMWMTDETEMALRLKVIEGKLTY

AT5G18636 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MADELWDEIQNLELGQEDPALFIPHEAYVMVEASNNLSLIARPLNPRVQNLNSVVVALPRSWGLTTQVHGRVLDATYVQFVFANEIDLM
MVQRREPWLFNNWFVAATRWQVAPAHNLVTTIDLWVQIRGIPLPYVSEETVLEIAQDLGEIISLDFHEATSPQIAFIRVRVRFGITDRL
RFFQRIIFDSGETATIRFQYERLRRLCSSCFRFTHNRAYCPYRQRSLSIARERALFCDSVQRSSMNSQSQMTESSFPVPMTPPPRVDPP
PMNHSEFVAAYPHLATATNVNYRFTGDSSTSRQDLSSGSNNILPRRTTHFTDHRRCFEAGQSSRQNENREPRRPTERMLPPSHFDHVQR
SGGILKPPKKR

AT5G25200 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MADELWDEIQNLELGQEDPALFIPHEAYVMVEASNNLSLIARPLNPRVQNLNSVVVALPRSWGLTTQVHGRVLDATYVQFLFANEIDLM
MVQRREPWLFNNWFVAATRWQVAPAHNLVTTIDLWVQIRGIPLPYVSEETVLEIAQDLGEIISLDFHEATSPQIAFIRVRVRFGITDRL
RFFQRIIFDSGETATIRFQYERLRRLCSSCFRFTHNRAYCPYRQRPLSIARERALFCDSVQRSSMNSQSQMTESSFPVPMTPPPRVDPP
PMNHSEFVAAYPHLATATNVNYRFTGDSSTSRQDLSSGSNNILPRRTTHFTDHRRCFETGQSSRQNENREPRRPTERMLPPSHFDHVQR
AGGILKPPKKR

AT2G13450 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MADELWDELQHLELGREDPALFIPHEAYAIVESRNRLSLIARPLNPRSQNLHAVISALPRAWGLTNRVHGRVLNDTFVQFIFQSEIDLL
SVLRREPWLYNNWFVTAQRWEVNLTFHLLTSIELWVQMRGIPLLYVCEETALEIAHELGEIITLDFHDSTTTQIAYIRVRIRFGITDRL
RFFLRIIFDSGETALISFQYERLRRICSSCFRMTHHRNSCLYRQIESLHRVTNTTAQRNVREEVFMRDENLRSSMNSQSQMSESSFPTP
IDPPPRIPHPPLNPDELVAAYYPHTRATSLPNFAGPLPQVPLRRNVDERDSNIQPFSGPAFAAHSPRLVEVGESSRQGENTQNVHTVEK
GDSSKRKNMGGPKFKDDARKSNEDEHMNGGILKPPKKR

AT2G16676 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MRGIPLLYVCEATVTEIALGLGQIISLDFHDATTTQIAFIRVRIRFEITDRIRFFQRITFDSGETALIRFQYERLRRICSSCFRLTHHR
NYCPYRQPEPRSIIRGPTNNLTRSRREGVCTRDEYHRSSLNSQSQMSENAFPAPIEPPPRVAAPPLNPDEFRAAYFPEGRAGSLPNIGT
LNLNPPSRRQEASRNSNVQPFTGPAFGANVPRVVEVGECS

AT2G41590 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MSDELWNEIQNLELGQEDPALFIPHEAYVMVEATNRLSMIARPLNPRVQNLNSVVVALPRTWGLTNQVHGRILDATYVQFLFQNEIDLM
MVQRKEPWLFNNWFVAATRWEVAPAHNFVTTIDLWVQIRGIPLPYVSEETVMEIAQDLGEVLMLDYHDTTSIQIAYIRVRVRFGITDRL
RFFQRIVFDSGETATIRFQYERLRRICSSCFRFTHNRAYCPYRPRPLSIARERALFRDSVHRSSMNSQSQMTDSSFPIPQTPPPRISHP
PLNHDEFVAAYPHLDSGRNDHIRCEGESSNFRQDLSSASNSITPRREPQYLTDRRHFEPGQSSRRHDVRDLRRGSERIGNLNQQNYVQR
SGGILKPPKKR

AT3G47920 Ta11-like non-LTR retrotransposon;1 $CX_2CX_4HX_4C$
MLDATYVQFLFQNEVDLLSVQRRELWLFNNWFVANHRWEPAPVLNFVTTIDLWVQMRGIPLLYVCEETALEIAHEIGEIITLDFHDATM
TQIAYIRVRVRIGITDRLRFFQRITFDSGETALIRFQYERLRRICSSCFRVTHHRNYCPYRPRLPNYGRERAVFHDERLRSSMNSQSQM
TESSFPAPVLPPPRIVTPPLNHGEFLAAHPNFPAPREGLNHQGRGTYYQGLCQGQQVSTDSNITPSVGTALSTGSRRVFEVGQSSRGVE
TRETRKRQEEKGTHDEQDKAHMKGGILNPPKKR

AT4G02000 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MTSLTIDLLSVLRREPWLYNNWFVTTHRWEVNLTFHLLTSIELWVQMRGIPLLYVCEETALEIAHELGKILTLDFHDSTTTQIAYIRVR
IRFGITDRLRFFQRIIFDFGEAALISFQYERLRRICSSCFRMTHHRNSCPYRQIEPLHRVTNSTAQRNVREEVFMRDENLRSSMNSQSQ
MSESSFPTPIDPPPRIPHPPLNPDELVAAYYPHTRATSLPNFAGPLPQVPLRKNVDERDSNIQPFSGPAFAAHSPRLVEVGESSRQGEN
TQNVHTVEKGDSSKRKNMGGPRFKDDARKSNEDEHMNGGILKPPKKR

AT2G02103 Ta11-like non-LTR retrotransposon; 1 $CX_2CX_4HX_4C$
MADELWDEIQNLELGQEDPALFIPHEAYVMVEASNNLSLIARPLNPRVQNLNSVVVALPRSWGLTTQVHGRILDATYVQFLFANEIDLL
MVQRREPWLFNNWFVAATRWQVAPAHNLVTTIDLWVQIRGIPLPYVSEETVMEIAHDLGEIISLDFHEATSPQIAFIRVRVRFGITDRL
RFFQRVIFDSGETATIRFQYERLRRLCSSCFRFTHNRAYCPYRQRPLSIARERALFCDSVQRSSMNSQSQMTESSFPVPLTPPPRVDPP
PVNHAEFTAAYPHLATATNENHRDVGESSTSRQDMSSGSNNFLARRTTHFTDHRRCFEGGQASRQNENREPRRPTERMRSPTHFDHVQR
SGGILKPPKKTLNHSIVFCHFLGKIAGLEASQLQDEEACLVGYGFWL

Supplementary Figure 2. Arabidopsis ZCCHC domain-containing proteins. The number of $CX_2CX_4HX_4C$ or $CX_2CX_3GHX_4C$ sequences in each protein is shown; these sequences have been highlighted. The Arabidopsis Genome Initiative (AGI) gene identifier (ATNGNNNNN) is shown, together with the TAIR10 annotation or protein name. A slash separates alternative names given by different authors to the same protein.

AIR1/ZCCHC7; 4 CX$_2$CX$_3$GHX$_4$C
MMFGGYETIEAYEDDLYRDESSSELSVDSEVEFQLYSQIHYAQDLDDVIREEEHEEKNSGNSESSSSKPNQKKLIVLSDSEVIQLSDGS
EVITLSDEDSIYRCKGKNVRVQAQENAHGLSSSLQSNELVDKKCKSDIEKPKSEERSGVIREVMIIEVSSSEEEESTISEGDNVESWML
LGCEVDDKDDDILLNLVGCENSVTEGEDGINWSISDKDIEAQIANNRTPGRWTQRYYSANKNIICRNCDKRGHLSKNCPLPRKVRRCFL
CSRRGHLLYSCPAPLCEYCPVPKMLDHSCLFRHSWDKQCDRCHMLGHYTDACTEIWRQYHLTTKPGPPKKPKTPSRPSALAYCYHCAQK
GHYGHECPEREVYDPSPVSPFICYYDDKYEIQEREKRLKQKIKVLKKNGVIPEPSKLPYIKAANENPHHDIRKGRASWKSNRWPQENKE
TQKEMKNKNRNWEKHRKADRHREVDEDFPRGPKTYSSPGSFKTQKPSKPFHRSSHYHTSREDKSPKEGKRGKQKKKERCWEDDDNDNLF
LIKQRKKKS

AIR2/ZCCHC8; 1 CX$_2$CX$_4$HX$_4$C
MAAEVYFGDLELFEPFDHPEESIPKPVHTRFKDDDGDEEDENGVGDAELRERLRQCEETIEQLRAENQELKRKLNILTRPSGILVNDTK
LDGPILQILFMNNAISKQYHQEIEEFVSNLVKRFEEQQKNDVEKTSFNLLPQPSSIVLEEDHKVEESCAIKNNKEAFSVVGSVLYFTNF
CLDKLGQPLLNENPQLSEGWEIPKYHQVFSHIVSLEGQEIQVKAKRPKPHCFNCGSEEHQMKDCPMPRNAARISEKRKEYMDACGEANN
QNFQQRYHAEEVEERFGRFKPGVISEELQDALGVTDKSLPPFIYRMRQLGYPPGWLKEAELENSGLALYDGKDGTDGETEVGEIQQNKS
VTYDLSKLVNYPGFNISTPRGIPDEWRIFGSIPMQACQQKDVFANYLTSNFQAPGVKSGNKRSSSHSSPGSPKKQKNESNSAGSPADME
LDSDMEVPHGSQSSESFQFQPPLPPDTPPLPRGTPPPVFTPPLPKGTPPLTPSDSPQTRTASGAVDEDALTLEELEEQQRRIWAALEQA
ESVNSDSDVPVDTPLTGNSVASSPCPNELDLPVPEGKTSEKQTLDEPEVPEIFTKKSEAGHASSPDSEVTSLCQKEKAELAPVNTEGAL
LDNGSVVPNCDISNGGSQKLFPADTSPSTATKIHSPIPDMSKFATGITPFEFENMAESTGMYLRIRSLLKNSPRNQQKNKKASE

CLIP1/CLIP-170; 1 CX$_2$CX$_3$GHX$_4$C
MSMLKPSGLKAPTKILKPGSTALKTPTAVVAPVEKTISSEKASSTPSSETQEEFVDDFRVGERVWVNGNKPGFIQFLGETQFAPGQWAG
IVLDEPIGKNDGSVAGVRYFQCEPLKGIFTRPSKLTRKVQAEDEANGLQTTPASRATSPLCTSTASMVSSSPSTPSNIPQKPSQPAAKE
PSATPPISNLTKTASESISNLSEAGSIKKGERELKIGDRVLVGGTKAGVVRFLGETDFAKGEWCGVELDEPLGKNDGAVAGTRYFQCQP
KYGLFAPVHKVTKIGFPSTTPAKAKANAVRRVMATTSASLKRSPSASSLSSMSSVASSVSSRPSRTGLLTETSSRYARKISGTTALQEA
LKEKQQHIEQLLAERDLERAEVAKATSHVGEIEQELALARDGHDQHVLELEAKMDQLRTMVEAADREKVELLNQLEEEKRKVEDLQFRV
EEESITKGDLEQKSQISEDPENTQTKLEHARIKELEQSLLFEKTKADKLQRELEDTRVATVSEKSRIMELEKDLALRVQEVAELRRRLE
SNKPAGDVDMSLSLLQEISSLQEKLEVTRTDHQREITSLKEHFGAREETHQKEIKALYTATEKLSKENESLKSKLEHANKENSDVIALW
KSKLETAIASHQQAMEELKVSFSKGLGTETAEFAELKTQIEKMRLDYQHEIENLQNQQDSERAAHAKEMEALRAKLMKVIKEKENSLEA
IRSKLDKAEDQHLVEMEDTLNKLQEAEIKVKELEVLQAKCNEQTKVIDNFTSQLKATEEKLLDLDALRKASSEGKSEMKKLRQQLEAAE
KQIKHLEIEKNAESSKASSITRELQGRELKLTNLQENLSEVSQVKETLEKELQILKEKFAEASEEAVSVQRSMQETVNKLHQKEEQFNM
LSSDLEKLRENLADMEAKFREKDEREEQLIKAKEKLENDIAEIMKMSGDNSSQLTKMNDELRLKERDVEELQLKLTKANENASFLQKSI
EDMTVKAEQSQQEAAKKHEEEKKELERKLSDLEKKMETSHNQCQELKARYERATSETKTKHEEILQNLQKTLLDTEDKLKGAREENSGL
LQELEELRKQADKAKAAQTAEDAMQIMEQMTKEKTETLASLEDTKQTNAKLQNELDTLKENNLKNVEELNKSKELLTVENQKMEEFRKE
IETLKQAAAQKSQQLSALQEENVKLAEELGRSRDEVTSHQKLEEERSVLNNQLLEMKKRESKFIKDADEEKASLQKSISITSALLTEKD
AELEKLRNEVTVLRGENASAKSLHSVVQTLESDKVKLELKVKNLELQLKENKRQLSSSSGNTDTQADEDERAQESQIDFLNSVIVDLQR
KNQDLKMKVEMMSEAALNGNGDDLNNYDSDDQEKQSKKKPRLFCDICDCFDLHDTEDCPTQAQMSEDPPHSTHHGSRGEERPYCEICEM
FGHWATNCNDDETF

CNBP/ZCCHC22/ZNF9; 7 CX$_2$CX$_3$GHX$_4$C
MSSNECFKCGRSGHWARECPTGGGRGRGMRSRGRGGFTSDRGFQFVSSSLPDICYRCGESGHLAKDCDLQEDACYNCGRGGHIAKDCKE
PKREREQCCYNCGKPGHLARDCDHADEQKCYSCGEFGHIQKDCTKVKCYRCGETGHVAINCSKTSEVNCYRCGESGHLARECTIEATA

CPSF4; 1 CX$_2$CX$_3$GHX$_4$C
MQEIIASVDHIKFDLEIAVEQQLGAQPLPFPGMDKSGAAVCEFFLKAACGKGGMCPFRHISGEKTVVCKHWLRGLCKKGDQCEFLHEYD
MTKMPECYFYSKFGECSNKECPFLHIDPESKIKDCPWYDRGFCKHGPLCRHRHTRRVICVNYLVGFCPEGPSCKFMHPRFELPMGTTEQ
PPLPQQTQPPAKQSNNPPLQRSSSLIQLTSQNSSPNQQRTPQVIGVMQSQNSSAGNRGPRPLEQVTCYKCGEKGHYANRCTKGHLAFLS
GQ

DDX41; 1 CX$_2$CX$_3$GHX$_4$C
MEESEPERKRARTDEVPAGGSRSEAEDEDDEDYVPYVPLRQRRQLLLQKLLQRRRKGAAEEEQQDSGSEPRGDEDDIPLGPQSNVSLLD
QHQHLKEKAEARKESAKEKQLKEEEKILESVAEGRALMSVKEMAKGITYDDPIKTSWTPPRYVLSMSEERHERVRKKYHILVEGDGIPP
PIKSFKEMKFPAAILRGLKKKGIHHPTPIQIQGIPTILSGRDMIGIAFTGSGKTLVFTLPVIMFCLEQEKRLPFSKREGPYGLIICPSR
ELARQTHGILEYYCRLLQEDSSPLLRCALCIGGMSVKEQMETIRHGVHMMVATPGRLMDLLQKKMVSLDICRYLALDEADRMIDMGFEG
DIRTIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPVTINVGRAGAASLDVIQEVEYVKEEAKMVYLLECLQKTPPPVLIFAEKKADV
DAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFREGKKDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGRSGNTGIATT
FINKACDESVLMDLKALLLEAKQKVPPVLQVLHCGDESMLDIGGERGCAFCGGLGHRITDCPKLEAMQTKQVSNIGRKDYLAHSSMDF

LIN28A/ZCCHC1/CSDD1; 2 CX$_2$CX$_4$HX$_4$C
MGSVSNQQFAGGCAKAAEEAPEEAPEDAARAADEPQLLHGAGICKWFNVRMGFGFLSMTARAGVALDPPVDVFVHQSKLHMEGFRSLKE
GEAVEFTFKKSAKGLESIRVTGPGGVFCIGSERRPKGKSMQKRRSKGDRCYNCGGLDHHAKECKLPPQPKKCHFCQSISHMVASCPLKA
QQGPSAQGKPTYFREEEEEIHSPTLLPEAQN

LIN28B/CSDD2; 2 CX$_2$CX$_4$HX$_4$C
MAEGGASKGGGEEPGKLPEPAEEESQVLRGTGHCKWFNVRMGFGFISMINREGSPLDIPVDVFVHQSKLFMEGFRSLKEGEPVEFTFKK
SSKGLESIRVTGPGGSPCLGSERRPKGKTLQKRKPKGDRCYNCGGLDHHAKECSLPPQPKKCHYCQSIMHMVANCPHKNVAQPPASSQG
RQEAESQPCTSTLPREVGGGHGCTSPPFPQEARAEISERSGRSPQEASSTKSSIAPEEQSKKGPSVQKRKKT

pNO40/ZCCHC17; 1 CX$_2$CX$_3$GHX$_4$C

MNSGRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRTHMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKV
VNQGTGKDLDPNNVIIEQEERRRRSFQDYTGQKITLEAVLNTTCKKCGCKGHFAKDCFMQPGGTKYSLIPDEEEEKEEAKSAEFEKPDP
TRNPSRKRKKEKKKKKHRDRKSSDSDSSDSESDTGKRARHTSKDSKAAKKKKKKKKHKKKHKE

RBBP6; 1 CX$_2$CX$_3$GHX$_4$C

MSCVHYKFSSKLNYDTVTFDGLHISLCDLKKQIMGREKLKAADCDLQITNAQTKEEYTDDNALIPKNSSVIVRRIPIGGVKSTSKTYVI
SRTEPAMATTKAIDDSSASISLAQLTKTANLAEANASEEDKIKAMMSQSGHEYDPINYMKKPLGPPPPSYTCFRCGKPGHYIKNCPTNG
DKNFESGPRIKKSTGIPRSFMMEVKDPNMKGAMLTNTGKYAIPTIDAEAYAIGKKEKPPFLPEEPSSSSEEDDPIPDELLCLICKDIMT
DAVVIPCCGNSYCDECIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNETGYTKRLRKQLPPPPPPIPPPRPLIQRNLQP
LMRSPISRQQDPLMIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDITATVSISVHSEKSDGPFRDSDNKILPAAALASE
HSKGTSSIAITALMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGGRPGWEHSNKLGYLVSPPQQIRRGERSCYRSINR
GRHHSERSQRTQGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPPGQPPPAGYSVPPPGFPPAPANLSTPWVSSGVQTA
HSNTIPTTQAPPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQKERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRS
RSYSRSFSRSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYRRYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYRE
VPPPYDMKAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAQPRPSANRENFSPERFLPLNIRNSPFTRGRREDYVGGQSHR
SRNIGSNYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRRKGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPS
RDDATPVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAVSKKENIVKPAKGPQEKVDGERERSPRSEPPIKKAKEETPK
TDNTKSSSSSQKDEKITGTPRKAHSKSAKEHQETKPVKEEKVKKDYSKDVKSEKLTTKEEKAKKPNEKNKPLDNKGEKRKRKTEEKGVD
KDFESSSMKISKLEVTEIVKPSPKRKMEPDTEKMDRTPEKDKISLSAPAKKIKLNRETGKKIGSTENISNTKEPSEKLESTSSKVKQEK
VKGKVRRKVTGTEGSSSTLVDYTSTSSTGGSPVRKSEEKTDTKRTVIKTMEEYNNDNTAPAEDVIIMIQVPQSKWDKDDFESEEEDVKS
TQPISSVGKPASVIKNVSTKPSNIVKYPEKESEPSEKIQKFTKDVSHEIIQHEVKSSKNSASSEKGKTKDRDYSVLEKENPEKRKNSTQ
PEKESNLDRLNEQGNFKSLSQSSKEARTSDKHDSTRASSNKDFTPNRDKKTDYDTREYSSSKRRDEKNELTRRKDSPSRNKDSASGQKN
KPREERDLPKKGTGDSKKSNSSPSRDRKPHDHKATYDTKRPNEETKSVDKNPCKDREKHVLEARNNKESSGNKLLYILNPPETQVEKEQ
ITGQIDKSTVKPKPQLSHSSRLSSDLTRETDEAAFEPDYNESDSESNVSVKEEESSGNISKDLKDKIVEKAKESLDTAAVVQVGISRNQ
SHSSPSVSPSRSHSPSGSQTRSHSSSASSAESQDSKKKKKKKEKKKHKKHKKHKKHKKHAGTEVELEKSQKHKHKKKKSKKNKDKEKEK
EKDDQKVKSVTV

RBM4B/LARK/ZCCHC15; 1 CX$_2$CX$_3$GHX$_4$C

MVKLFIGNLPREATEQEIRSLFEQYGKVLECDIIKNYGFVHIEDKTAAEDAIRNLHHYKLHGVNINVEASKNKSKASTKLHVGNISPTC
TNQELRAKFEEYGPVIECDIVKDYAFVHMERAEDAVEAIRGLDNTEFQGKRMHVQLSTSRLRTAPGMGDQSGCYRCGKEGHWSKECPVD
RTGRVADFTEQYNEQYGAVRTPYTMGYGESMYYNDAYGALDYYKRYRVRSYEAVAAAAAASAYNYAEQTMSHLPQVQSTTVTSHLNSTS
VDPYDRHLLPNSGAAATSAAMAAAAATTSSYYGRDRSPLRRAAAMLPTVGEGYGYGPESELSQASAATRNSLYDMARYEREQYVDRARY
SAF

RBM4A/LARK/ZCCHC21; 1 CX$_2$CX$_3$GHX$_4$C

MVKLFIGNLPREATEQEIRSLFEQYGKVLECDIIKNYGFVHIEDKTAAEDAIRNLHHYKLHGVNINVEASKNKSKTSTKLHVGNISPTC
TNKELRAKFEEYGPVIECDIVKDYAFVHMERAEDAVEAIRGLDNTEFQGKRMHVQLSTSRLRTAPGMGDQSGCYRCGKEGHWSKECPID
RSGRVADLTEQYNEQYGAVRTPYTMSYGDSLYYNNAYGALDAYYKRCRAARSYEAVAAAAASVYNYAEQTLSQLPQVQNTAMASHLTST
SLDPYDRHLLPTSGAAATAAAAAAAAAAVTAASTSYYGRDRSPLRRATAPVPTVGEGYGYGHESELSQASAAARNSLYDMARYEREQYA
DRARYSAF

ZCCHC4; 1 CX$_2$CX$_4$HX$_4$C

MAASRNGFEAVEAEGSAGCRGSSGMEVVLPLDPAVPAPLCPHGPTLLFVKVTQGKEETRRFYACSACRDRKDCNFFQWEDEKLSGARLA
AREAHNRRCQPPLSRTQCVERYLKFIELPLTQRKFCQTCQQLLLPDDWGQHSEHQVLGNVSITQLRRPSQLLYPLENKKTNAQYLFADR
SCQFLVDLLSALGFRRVLCVGTPRLHELIKLTASGDKKSNIKSLLLDIDFRYSQFYMEDSFCHYNMFNHHFFDGKTALEVCRAFLQEDK
GEGIIMVTDPPFGGLVEPLAITFKKLIAMWKEGQSQDDSHKELPIFWIFPYFFESRICQFFPSFQMLDYQVDYDNHALYKHGKTGRKQS
PVRIFTNIPPNKIILPTEEGYRFCSPCQRYVSLENQHCELCNSCTSKDGRKWNHCFLCKKCVKPSWIHCSICNHCAVPDHSCEGPKHGC
FICGELDHKRSTCPNIATSKRANKAVRKQKQRKSNKMKMETTKGQSMNHTSATRRKKRRERAHQYLGS

SF1/BBP/ZCCHC25; 1 CX$_2$CX$_3$GHX$_4$C

MATGANATPLDFPSKKRKRSRWNQDTMEQKTVIPGMPTVIPPGLTREQERAYIVQLQIEDLTRKLRTGDLGIPPNPEDRSPSPEPIYNS
EGKRLNTREFRTRKKLEEERHNLITEMVALNPDFKPPADYKPPATRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIR
GKGSVKEGKVGRKDGQMLPGEDEPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGTLREDDNRILRPWQS
SETRSITNTTVCTKCGGAGHIASDCKFQRPGDPQSAQDKARMDKEYLSLMAELGEAPVPASVGSTSGPATTPLASAPRPAAPANNPPPP
SLMSTTQSRPPWMNSGPSESRPYHGMHGGGPGGPGGGPHSFPHPLPSLTGGHGGHPMQHNPNGPPPPWMQPPPPPMNQGPHPPGHHGPP
PMGKSVPGKYACGLWGLSPASRKRYDAATTYGHDAAAAAASQWAAPTPSLWSSSPMATTAAAASATPSAQQQYGFQYPLAMAAKIPPRG
GDGPSHESEDFPRPLVTLPGRQPQQRPWWTGWFGKAA

SLU7; 1 CX$_2$CX$_4$HX$_4$C

MSATVVDAVNAAPLSGSKEMSLEEPKKMTREDWRKKKELEEQRKLGNAPAEVDEEGKDINPHIPQYISSVPWYIDPSKRPTLKHQRPQP
EKQKQFSSSGEWYKRGVKENSIITKYRKGACENCGAMTHKKKDCFERPRRVGAKFTGTNIAPDEHVQPQLMFDYDGKRDRWNGYNPEEH
MKIVEEYAKVDLAKRTLKAQKLQEELASGKLVEQANSPKHQWGEEEPNSQMEKDHNSEDEDEDKYADDIDMPGQNFDSKRRITVRNLRI
REDIAKYLRNLDPNSAYYDPKTRAMRENPYANAGKNPDEVSYAGDNFVRYTGDTISMAQTQLFAWEAYDKGSEVHLQADPTKLELLYKS
FKVKKEDFKEQQKESILEKYGGQEHLDAPPAELLLAQTEDYVEYSRHGTVIKGQERAVACSKYEEDVKIHNHTHIWGSYWKEGRWGYKC

CHSFFKYSYCTGEAGKEIVNSEECIINEITGEESVKKPQTLMELHQEKLKEEKKKKKKKKKKHRKSSSDSDDEEKKHEKLKKALNAEEA
RLLHVKETMQIDERKRPYNSMYETREPTEEEMEAYRMKRQRPDDPMASFLGQ

SREK1IP1/P18SRP; 1 CX$_2$CX$_3$GHX$_4$C

MAVPGCNKDSVRAGCKKCGYPGHLTFECRNFLRVDPKRDIVLDVSSTSSEDSDEENEELNKLQALQEKRINEEEEKKKEKSKEKIKLKK
KRKRSYSSSSTEEDTSKQKKQKYQKKEKKKEKKSKSKKGKHHKKEKKKRKKEKHSSTPNSSEFSRK

SRSF7/ZCCHC20/RMB37/9G8; 1 CX$_2$CX$_3$GHX$_4$C

SRYGRYGGETKVYVGNLGTGAGKGELERAFSYYGPLRTVWIARNPPGFAFVEFEDPRDAEDAVRGLDGKVICGSRVRVELSTGMPRRSR
FDRPPARRPFDPNDRCYECGEKGHYAYDCHRYSRRRRSRSRSRSHSRSRGRRYSRSRSRSRGRRSRSASPRRSRSISLRRSRSASLRRS
RSGSIKGSRYFQSPSRSRSRSRSISRPRSSRSKSRSPSPKRSRSPSGSPRRSASPERMD

TUT4/ ZCCHC11; 3 CX$_2$CX$_3$GHX$_4$C

MEESKTLKSENHEPKKNVICEESKAVQVIGNQTLKARNDKSVKEIENSSPNRNSSKKNKQNDICIEKTEVKSCKVNAANLPGPKDLGLV
LRDQSHCKAKKFPNSPVKAEKATISQAKSEKATSLQAKAEKSPKSPNSVKAEKASSYQMKSEKVPSSPAEAEKGPSLLLKDMRQKTELQ
QIGKKIPSSFTSVDKVNIEAVGGEKCALQNSPRSQKQQTCTDNTGDSDDSASGIEDVSDDLSKMKNDESNKENSSEMDYLENATVIDES
ALTPEQRLGLKQAEERLERDHIFRLEKRSPEYTNCRYLCKLCLIHIENIQGAHKHIKEKRHKKNILEKQEESELRSLPPPSPAHLAALS
VAVIELAKEHGITDDDLRVRQEIVEEMSKVITTFLPECSLRLYGSSLTRFALKSSDVNIDIKFPPKMNHPDLLIKVLGILKKNVLYVDV
ESDFHAKVPVVVCRDRKSGLLCRVSAGNDMACLTTDLLTALGKIEPVFIPLVLAFRYWAKLCYIDSQTDGGIPSYCFALMVMFFLQQRK
PPLLPCLLGSWIEGFDPKRMDDFQLKGIVEEKFVKWECNSSSATEKNSIAEENKAKADQPKDDTKKTETDNQSNAMKEKHGKSPLALET
PNRVSLGQLWLELLKFYTLDFALEEYVICVRIQDILTRENKNWPKRRIAIEDPFSVKRNVARSLNSQLVYEYVVERFRAAYRYFACPQT
KGGNKSTVDFKKREKGKISNKKPVKSNNMATNGCILLGETTEKINAEREQPVQCDEMDCTSQRCIIDNNNLLVNELDFADHGQDSSSLS
TSKSSEIEPKLDKKQDDLAPSETCLKKELSQCNCIDLSKSPDPDKSTGTDCRSNLETESSHQSVCTDTSATSCNCKATEDASDLNDDDN
LPTQELYYVFDKFILTSGKPPTIVCSICKKDGHSKNDCPEDFRKIDLKPLPPMTNRFREILDLVCKRCFDELSPPCSEQHNREQILIGL
EKFIQKEYDEKARLCLFGSSKNGFGFRDSDLDICMTLEGHENAEKLNCKEIIENLAKILKRHPGLRNILPITTAKVPIVKFEHRRSGLE
GDISLYNTLAQHNTRMLATYAAIDPRVQYLGYTMKVFAKRCDIGDASRGSLSSYAYILMVLYFLQQRKPPVIPVLQEIFDGKQIPQRMV
DGWNAFFFDKTEELKKRLPSLGKNTESLGELWLGLLRFYTEEFDFKEYVISIRQKKLLTTFEKQWTSKCIAIEDPFDLNHNLGAGVSRK
MTNFIMKAFINGRKLFGTPFYPLIGREAEYFFDSRVLTDGELAPNDRCCRVCGKIGHYMKDCPKRKSSLLFRLKKKDSEEEKEGNEEEK
DSRDVLDPRDLHDTRDFRDPRDLRCFICGDAGHVRRECPEVKLARQRNSSVAAAQLVRNLVNAQQVAGSAQQQGDQSIRTRQSSECSES
PSYSPQPQPFPQNSSQSAAITQPSSQPGSQPKLGPPQQGAQPPHQVQMPLYNFPQSPPAQYSPMHNMGLLPMHPLQIPAPSWPIHGPVI
HSAPGSAPSNIGLNDPSIIFAQPAARPVAIPNTSHDGHWPRTVAPNSLVNSGAVGNSEPGFRGLTPPIPWEHAPRPHFPLVPASWPYGL
HQNFMHQGNARFQPNKPFYTQDRCATRRCRERCPHPPRGNVSE

TUT7/ZCCHC6; 3 CX$_2$CX$_3$GHX$_4$C

MGDTAKPYFVKRTKDRGTMDDDDFRRGHPQQDYLIIDDHAKGHGSKMEKGLQKKKITPGNYGNTPRKGPCAVSSNPYAFKNPIYSQPAW
MNDSHKDQSKRWLSDEHTGNSDNWREFKPGPRIPVINRQRKDSFQENEDGYRWQDTRGCRTVRRLFHKDLTSLETTSEMEAGSPENKKQ
RSRPRKPRKTRNEENEQDGDLEGPVIDESVLSTKELLGLQQAEERLKRDCIDRLKRRPRNYPTAKYTCRLCDVLIESIAFAHKHIKEKR
HKKNIKEKQEEELLTTLPPPTPSQINAVGIAIDKVVQEFGLHNENLEQRLEIKRIMENVFQHKLPDCSLRLYGSSCSRLGFKNSDVNID
IQFPAIMSQPDVLLLVQECLKNSDSFIDVDADFHARVPVVVCREKQSGLLCKVSAGNENACLTTKHLTALGKLEPKLVPLVIAFRYWAK
LCSIDRPEEGGLPPYVFALMAIFFLQQRKEPLLPVYLGSWIEGFSLSKLGNFNLQDIEKDVVIWEHTDSAAGDTGITKEEAPRETPIKR
GQVSLILDVKHQPSVPVGQLWVELLRFYALEFNLADLVISIRVKELVSRELKDWPKKRIAIEDPYSVKRNVARTLNSQPVFEYILHCLR
TTYKYFALPHKITKSSLLKPLNAITCISEHSKEVINHHPDVQTKDDKLKNSVLAQGPGATSSAANTCKVQPLTLKETAESFGSPPKEEM
GNEHISVHPENSDCIQADVNSDDYKGDKVYHPETGRKNEKEKVGRKGKHLLTVDQKRGEHVVCGSTRNNESESTLDLEGFQNPTAKECE
GLATLDNKADLDGESTEGTEELEDSLNHFTHSVQGQTSEMIPSDEEEEDDEEEEEEEEEPRLTINQREDEDGMANEDELDNTYTGSGDED
ALSEEDDELGEAAKYEDVKECGKHVERALLVELNKISLKEENVCEEKNSPVDQSDFFYEFSKLIFTKGKSPTVVCSLCKREGHLKKDCP
EDFKRIQLEPLPPLTPKFLNILDQVCIQCYKDFSPTIIEDQAREHIRQNLESFIRQDFPGTKLSLFGSSKNGFGFKQSDLDVCMTINGL
ETAEGLDCVRTIEELARVLRKHSGLRNILPITTAKVPIVKFFHLRSGLEVDISLYNTLALHNTRLLSAYSAIDPRVKYLCYTMKVFTKM
CDIGDASRGSLSSYAYTLMVLYFLQQRNPPVIPVLQEIYKGEKKPEIFVDGWNIYFFDQIDELPTYWSECGKNTESVGQLWLGLLRFYT
EEFDFKEHVISIRRKSLLTTFKKQWTSKYIVIEDPFDLNHNLGAGLSRKMTNFIMKAFINGRRVFGIPVKGFPKDYPSKMEYFFDPDVL
TEGELAPNDRCCRICGKIGHFMKDCPMRRKVRRRRDQEDALNQRYPENKEKRSKEDKEIHNKYTEREVSTKEDKPIQCTPQKAKPMRAA
ADLGREKILRPPVEKWKRQDDKDLREKRCFICGREGHIKKECPQFKGSSGSLSSKYMT
QGKASAKRTQQES

XRN2; 1 CX$_2$CX$_3$GHX$_4$C

MGVPAFFRWLSRKYPSIIVNCVEEKPKECNGVKIPVDASKPNPNDVEFDNLYLDMNGIIHPCTHPEDKPAPKNEDEMMVAIFEYIDRLF
SIVRPRRLLYMAIDGVAPRAKMNQQRSRRFRASKEGMEAAVEKQRVREEILAKGGFLPPEEIKERFDSNCITPGTEFMDNLAKCLRYYI
ADRLNNDPGWKNLTVILSDASAPGEGEHKIMDYIRRQRAQPNHDPNTHHCLCGADADLIMLGLATHEPNFTIIREEFKPNKPKPCGLCN
QFGHEVKDCEGLPREKKGKHDELADSLPCAEGEFIFLRLNVLREYLERELTMASLPFTFDVERSIDDWVFMCFFVGNDFLPHLPSLEIR
ENAIDRLVNIYKNVVHKTGGYLTESGYVNLQRVQMIMLAVGEVEDSIFKKRKDDEDSFRRRQKEKRKRMKRDQPAFTPSGILTPHALGS
RNSPGSQVASNPRQAAYEMRMQNNSSPSISPNTSFTSDGSPSPLGGIKRKAEDSDSEPEPEDNVRLWEAGWKQRYYKNKFDVDAADEKF
RRKVVQSYVEGLCWVLRYYYQGCASWKWYYPFHYAPFASDFEGIADMPSDFEKGTKPFKPLEQLMGVFPAASGNFLPPSWRKLMSDPDS
SIIDFYPEDFAIDLNGKKYAWQGVALLPFVDERRLRAALEEVYPDLTPEETRRNSLGGDVLFVGKHHPLHDFILELYQTGSTEPVEVPP
ELCHGIQGKFSLDEEAILPDQIVCSPVPMLRDLTQNTVVSINFKDPQFAEDYIFKAVMLPGARKPAAVLKPSDWEKSSNGRQWKPQLGF
NRDRRPVHLDQAAFRTLGHVMPRGSGTGIYSNAAPPPVTYQGNLYRPLLRGQAQIPKLMSNMRPQDSWRGPPPLFQQQRFDRGVGAEPL
LPWNRMLQTQNAAFQPNQYQMLAGPGGYPPRRDDRGGRQGYPREGRKYPLPPPSGRYNWN

ZCRB1/ZCCHC19/(U11/U12-31K); 1 $CX_2CX_3GHX_4C$
MSGGLAPSKSTVYVSNLPFSLTNNDLYRIFSKYGKVVKVTIMKDKDTRKSKGVAFILFLDKDSAQNCTRAINNKQLFGRVIKASIAIDN
GRAAEFIRRRNYFDKSKCYECGESGHLSYACPKNMLGEREPPKKKEKKKKKKAPEPEEEIEEVEESEDEGEDPALDSLSQAIAFQQAKI
EEEQKKWKPSSGVPSTSDDSRRPRIKKSTYFSDEEELSD

ZCCHC2; 1 $CX_2CX_3GHX_4C$
MLRMKLPLKPTHPAEPPPEAEEPEADARPGAKAPSRRRRDCRPPPPPPPPAGPSRGPLPPPPPPRGLGPPVAGGAAAGAGMPGGGGGPS
AALREQERVYEWFGLVLGSAQRLEFMCGLLDLCNPLELRFLGSCLEDLARKDYHYLRDSEAKANGLSDPGPLADFREPAVRSRLIVYLA
LLGSENREAAGRLHRLLPQVDSVLKSLRAARGEGSRGGAEDERGEDGDGEQDAEKDGSGPEGGIVEPRVGGGLGSRAQEELLLLFTMAS
LHPAFSFHQRVTLREHLERLRAALRGGPEDAEVEVEPCKFAGPRAQNNSAHGDYMQNNESSLIEQAPIPQDGLTVAPHRAQREAVHIEK
IMLKGVQRKRADKYWEYTFKVNWSDLSVTTVTKTHQELQEFLLKLPKELSSETFDKTILRALNQGSLKREERRHPDLEPILRQLFSSSS
QAFLQSQKVHSFFQSISSDSLHSINNLQSSLKTSKILEHLKEDSSEASSQEEDVLQHAIIHKKHTGKSPIVNNIGTSCSPLDGLTMQYS
EQNGIVDWRKQSCTTIQHPEHCVTSADQHSAEKRSLSSINKKKGKPQTEKEKIKKTDNRLNSRINGIRLSTPQHAHGGTVKDVNLDIGS
GHDTCGETSSESYSSPSSPRHDGRESFESEEEKDRDTDSNSEDSGNPSTTRFTGYGSVNQTVTVKPPVQIASLGNENGNLLEDPLNSPK
YQHISFMPTLHCVMHNGAQKSEVVVPAPKPADGKTIGMLVPSPVAISAIRESANSTPVGILGPTACTGESEKHLELLASPLPIPSTFLP
HSSTPALHLTVQRLKLPPPQGSSESCTVNIPQQPPGSLSIASPNTAFIPIHNPGSFPGSPVATTDPITKSASQVVGLNQMVPQIEGNTG
TVPQPTNVKVVLPAAGLSAAQPPASYPLPGSPLAAGVLPSQNSSVLSTAATSPQPASAGISQAQATVPPAVPTHTPGPAPSPSPALTHS
TAQSDSTSYISAVGNTNANGTVVPPQQMGSGPCGSCGRRCSCGTNGNLQLNSYYYPNPMPGPMYRVPSFFTLPSICNGSYLNQAHQSNG
NQLPFFLPQTPYANGLVHDPVMGSQANYGMQQMAGFGRFYPVYPAPNVVANTSGSGPKKNGNVSCYNCGVSGHYAQDCKQSSMEANQQG
TYRLRYAPPLPPSNDTLDSAD

ZCCHC3; 1 $CX_2CX_4HX_4C$ and 2 $CX_2CX_3GHX_4C$
MATGGGAEEERKRGRPQLLPPARPAARGEEADGGREKMGWAQVVKNLAEKKGEFREPRPPRREEESGGGGGSAGLGGPAGLAAPDLGDF
PPAGRGDPKGRRRDPAGEAVDPRKKKGAAEAGRRKKAEAAAAAMATPARPGEAEDAAERPLQDEPAAAAAGPGKGRFLVRICFQGDEGA
CPTRDFVVGALILRSIGMDPSDIYAVIQIPGSREFDVSFRSAEKLALFLRVYEEKREQEDCWENFVVLGRSKSSLKTLFILFRNETVDV
EDIVTWLKRHCDVLAVPVKVTDRFGIWTGEYKCEIELRQGEGGVRHLPGAFFLGAERGYSWYKGQPKTCFKCGSRTHMSGSCTQDRCFR
CGEEGHLSPYCRKGIVCNLCGKRGHAFAQCPKAVHNSVAAQLTGVAGH

ZCCHC9; 2 $CX_2CX_4HX_4C$ and 2 $CX_2CX_3GHX_4C$
MTRWARVSTTYNKRPLPATSWEDMKKGSFEGTSQNLPKRKQLEANRLSLKNDAPQAKHKKNKKKKEYLNEDVNGFMEYLRQNSQMVHNG
QIIATDSEEVREEIAVALKKDSRREGRRLKRQAAKKNAMVCFHCRKPGHGIADCPAALENQDMGTGICYRCGSTEHEITKCKAKVDPAL
GEFPFAKCFVCGEMGHLSRSCPDNPKGLYADGGGCKLCGSVEHLKKDCPESQNSERMVTVGRWAKGMSADYEEILDVPKPQKPKTKIPK
VVNF

ZCCHC10; 1 $CX_2CX_3GHX_4C$
MATPMHRLIARRQAFDTELQPVKTFWILIQPSIVISEANKQHVRCQKCLEFGHWTYECTGKRKYLHRPSRTAELKKALKEKENRLLLQQ
SIGETNVERKAKKKRSKSVTSSSSSSSDSSASDSSSESEETSTSSSSEDSDTDESSSSSSSSASSTTSSSSSDSDSDSSSSSSSSTSTD
SSSDDEPPKKKKKK

ZCCHC13; 4 $CX_2CX_3GHX_4C$
MSSKDFFACGHSGHWARGCPRGGAGGRRGGGHGRGSQCGSTTLSYTCYCCGESGRNAKNCVLLGNICYNCGRSGHIAKDCKDPKRERRQ
HCYTCGRLGHLARDCDRQKEQKCYSCGKLGHIQKDCAQVKCYRCGEIGHVAINCSKARPGQLLPLRQIPTSSQGMSQ

ZCCHC14; 1 $CX_2CX_3GHX_4C$
MASNHPAFSFHQKQVLRQELTQIQSSLNGGGGHGGKGAPGPGGALPTCPACHKITPRTEAPVSSVSNSLENALHTSAHSTEESLPKRPL
GKHSKVSVEKIDLKGLSHTKNDRNVECSFEVLWSDSSITSVTKSSSEVTEFISKLCQLYPEENLEKLIPCLAGPDAFYVERNHVDLDSG
LRYLASLPSHVLKNDHVRRFLSTSSPPQQLQSPSPGNPSLSKVGTVMGVSGRPVCGVAGIPSSQSGAQHHGQHPAGSAAPLPHCSHAGS
AGSALAYRTQMDTSPAILMPSSLQTPQTQEQNGILDWLRKLRLHKYYPVFKQLSMEKFLSLTEEDLNKFESLTMGAKKKLKTQLELEKE
KSERRCLNPSAPPLVTSSGVARVPPTSHVGPVQSGRGSHAAELRVEVEQPHHQLPREGSSSEYSSSSSSPMGVQAREESSDSAEENDRR
VEIHLESSDKEKPVMLLNHFTSSSARPTAQVLPVQNEASSNPSGHHPLPPQMLSAASHITPIRMLNSVHKPERGSADMKLLSSSVHSLL
SLEERNKGSGPRSSMKVDKSFGSAMMDVLPASAPHQPVQVLSGLSESSSMSPTVSFGPRTKVVHASTLDRVLKTAQQPALVVETSTAAT
GTPSTVLHAARPPIKLLLSSSVPADSAISGQTSCPNNVQISVPPAIINPRTALYTANTKVAFSAMSSMPVGPLQGGFCANSNTASPSSH
PSTSFANMATLPSCPAPSSSPALSSVPESSFYSSSGGGGSTGNIPASNPNHHHHHHHQQPPAPPQPAPPPPGCIVCTSCGCSGSCGSSG
LTVSYANYFQHPFSGPSVFTFPFLPFSPMCSSGYVSAQQYGGGSTFPVVHAPYSSSGTPDPVLSGQSTFAVPPMQNFMAGTAGVYQTQG
LVGSSNGSSHKKSGNLSCYNCGATGHRAQDCKQPSMDFNRPGTFRLKYAPPAESLDSTD

ZCCHC24; 1 $CX_2CX_3GHX_4C$
MSLLSAIDTSAASVYQPAQLLNWVYLSLQDTHQASAFDAFRPEPTAGAAPPELAFGKGRPEQLGSPLHSSYLNSFFQLQRGEALSNSVY
KGASPYGSLNNIADGLSSLTEHFSDLTLTSEARKPSKRPPPNYLCHLCFNKGHYIKDCPQARPKGEGLTPYQGKKRCFGEYKCPKCKRK
WMSGNSWANMGQECIKCHINVYPHKQRPLEKPDGLDVSDQSKEHPQHLCEKCKVLGYYCRRVQ

PEG10; 1 $CX_2CX_3GHX_4C$
MTERRRDELSEEINNLREKVMKQSEENNNLQSQVQKLTEENTTLREQVEPTPEDEDDDIELRGAAAAAAPPPPIEEECPEDLPEKFDGN
PDMLAPFMAQCQIFMEKSTRDFSVDRVRVCFVTSMMTGRAARWASAKLERSHYLMHNYPAFMMEMKHVFEDPQRREVAKRKIRRLRQGM
GSVIDYSNAFQMIAQDLDWNEPALIDQYHEGLSDHIQEELSHLEVAKSLSALIGQCIHIERRLARAAAARKPRSPPRALVLPHIASHHQ

VDPTEPVGGARMRLTQEEKERRRKLNLCLYCGTGGHYADNCPAKASKSSPAGKLPGPAVEGPSATGPEIIRSPQDDASSPHLQVMLQIH
LPGRHTLFVRAMIDSGASGNFIDHEYVAQNGIPLRIKDWPILVEAIDGRPIASGPVVHETHDLIVDLGDHREVLSFDVTQSPFFPVVLG
VRWLSTHDPNITWSTRSIVFDSEYCRYHCRMYSPIPPSLPPPAPQPPLYYPVDGYRVYQPVRYYYVQNVYTPVDEHVYPDHRLVDPHIE
MIPGAHSIPSGHVYSLSEPEMAALRDFVARNVKDGLITPTIAPNGAQVLQVKRGWKLQVSYDCRAPNNFTIQNQYPRLSIPNLEDQAHL
ATYTEFVPQIPGYQTYPTYAAYPTYPVGFAWYPVGRDGQGRSLYVPVMITWNPHWYRQPPVPQYPPPQPPPPPPPPPPPPSYSTL

RTL3/ZCCHC5; 1 $CX_2CX_3GHX_4C$
MVEDLAASYIVLKLENEIRQAQVQWLMEENAALQAQIPELQKSQAAKEYDLLRKSSEAKEPQKLPEHMNPPAAWEAQKTPEFKEPQKPP
EPQDLLPWEPPAAWELQEAPAAPESLAPPATRESQKPPMAHEIPTVLEGQGPANTQDATIAQEPKNSEPQDPPNIEKPQEAPEYQETAA
QLEFLELPPPQEPLEPSNAQEFLELSAAQESLEGLIVVETSAASEFPQAPIGLEATDFPLQYTLTFSGDSQKLPEFLVQLYSYMRVRGH
LYPTEAALVSFVGNCFSGRAGWWFQLLLDIQSPLLEQCESFIPVLQDTFDNPENMKDANQCIHQLCQGEGHVATHFHLIAQELNWDEST
LWIQFQEGLASSIQDELSHTSPATNLSDLITQCISLEEKPDPNPLGKSSSAEGDGPESPPAENQPMQAAINCPHISEAEWVRWHKGRLC
LYCGYPGHFARDCPVKPHQALQAGNIQACQ

RTL4/ZCCHC16; 1 $CX_2CX_3GHX_4C$
MEKCTKSSSTMQVEPSFLQAENLILRLQMQHPTTENTAKRGQVMPALATTVMPVPYSLEHLTQFHGDPANCSEFLTQVTTYLTALQISN
PANDAQIKLFFDYLSQQLESCGIISGPDKSTLLKQYENLILEFQQSFGKPTKQEINPLMNAKFDKGDNSSQQDPATFHLLAQNLICNET
NQSGQFEKALADPNQDEESVTDMMDNLPDLITQCIQLDKKHSDRPELLQSETQLPLLASLIQHQALFSPTDPPPKKGPIQLREGQLPLT
PAKRARQQETQLCLYCSQSGHFTRDCLAKRSRAPATTNNTAHQ

PNMA3; 1 $CX_2CX_3GHX_4C$
MPLTLLQDWCRGEHLNTRRCMLILGIPEDCGEDEFEETLQEACRHLGRYRVIGRMFRREENAQAILLELAQDIDYALLPREIPGKGGPW
EVIVKPRNSDGEFLNRLNRFLEEERRTVSDMNRVLGSDTNCSAPRVTISPEFWTWAQTLGAAVQPLLEQMLYRELRVFSGNTISIPGAL
AFDAWLEHTTEMLQMWQVPEGEKRRRLMECLRGPALQVVSGLRASNASITVEECLAALQQVFGPVESHKIAQVKLCKAYQEAGEKVSSF
VLRLEPLLQRAVENNVVSRRNVNQTRLKRVLSGATLPDKLRDKLKLMKQRRKPPGFLALVKLLREEEEWEATLGPDRESLEGLEVAPRP
PARITGVGAVPLPASGNSFDVRPSQGYRRRRGRGQHRRGGVARAGSRGSRKRKRHTFCYSCGEDGHIRVQCINPSNLLLVKQKKQAAVE
SGNGNWAWDKSHPKSKAK

PNMA7A/ZCCHC12/SIZN1; 1 $CX_2CX_3GHX_4C$
MASIIARVGNSRRLNAPLPPWAHSMLRSLGRSLGPIMASMADRNMKLFSGRVVPAQGEETFENWLTQVNGVLPDWNMSEEEKLKRLMKT
LRGPAREVMRVLQATNPNLSVADFLRAMKLVFGESESSVTAHGKFFNTLQAQGEKASLYVIRLEVQLQNAIQAGIIAEKDANRTRLQQL
LLGGELSRDLRLRLKDFLRMYANEQERLPNFLELIRMVREEEDWDDAFIKRKRPKRSESMVERAVSPVAFQGSPPIVIGSADCNVIEID
DTLDDSDEDVILVESQDPPLPSWGAPPLRDRARPQDEVLVIDSPHNSRAQFPSTSGGSGYKNNGPGEMRRARKRKHTIRCSYCGEEGHS
KETCDNESDKAQVFENLIITLQELTHTEMERSRVAPGEYNDFSEPL

PNMA7B/ZCCHC18; 1 $CX_2CX_3GHX_4C$
MASITACVGNSRQQNAPLPPWAHSMLRSLGRSLCPLVVKMAERNMKLFSGRVVPAQGKETFENWLIQVNEVLPDWSMSEEEKLKRLMKT
LRGPAREVMRLLQAANPNLSVADFLRAMKLVFGESESSVTAHGKFFNTLQAQGEKASLYVIRLEVQLQNAIQAGILAEKDANQTRLQQL
LLGAELNRDLRFRLKHLLRMYANKQERLPNFLELIKMIREEEDWDDAFIKRKRPKRSEPIMERAASPVAFQGAQPIAISSADCNCNVIE
IDDTLDDSDEDVILVVSLYPSLTPTGAPPFRGRARPLDQVLVIDSPNNSGAQSLSTSGGSGYKNDGPGNIRRARKRKYTTRCSYCGEEG
HSKETCDNESNKAQVFENLIITLQELTHTEERSKEVPGEHSDASEPQ

Supplementary Figure 3. Human ZCCHC domain-containing proteins. The number of $CX_2CX_4HX_4C$ or $CX_2CX_3GHX_4C$ sequences in each protein is shown; these sequences have been highlighted. A slash separates alternative names given by different authors to the same protein.

Supplementary Figure 4. Amino acid frequencies in ZCCHC domains.

		Amino acid																			
	Position	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
Saccharomyces cerevisiae	1	0	0	0	0	0	0	0	4	2	1	0	0	2	2	3	1	0	4	0	1
	2	1	0	0	0	3	0	0	1	3	2	1	0	1	3	1	1	0	1	1	1
	3	0	**20**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	0	0	0	1	1	0	0	0	1	0	0	2	1	0	1	1	3	0	0	**9**
	5	0	0	0	0	0	0	1	2	2	2	0	**10**	0	0	1	0	1	1	0	0
	6	0	**20**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	7	0	0	2	0	0	**10**	0	0	1	0	0	5	0	0	0	2	0	0	0	0
	8	1	0	0	4	0	3	0	0	2	1	0	1	0	5	0	2	1	0	0	0
	9	3	0	0	0	0	0	0	1	4	0	1	1	2	0	3	0	4	1	0	0
	10	0	0	2	0	0	**15**	0	0	1	0	0	1	0	0	1	0	0	0	0	0
	11	0	0	0	0	0	0	**20**	0	0	0	0	0	0	0	0	0	0	0	0	0
	12	0	0	0	0	3	0	0	2	2	3	2	1	0	0	0	2	0	2	1	2
	13	2	0	0	1	0	2	0	1	4	0	0	0	0	1	4	4	1	0	0	0
	14	1	0	2	3	0	0	0	0	5	0	0	0	0	0	4	3	1	0	0	1
	15	0	0	**11**	3	0	0	0	0	0	0	0	2	0	2	2	0	0	0	0	0
	16	0	**20**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	17	1	0	1	0	0	0	0	0	1	0	2	1	**11**	1	0	0	2	0	0	0
	18	0	0	0	4	0	0	5	0	2	0	1	2	0	0	0	4	1	1	0	0
Homo sapiens	1	3	0	6	0	0	3	1	4	6	2	1	3	2	5	5	3	4	7	0	2
	2	2	3	0	1	1	6	2	4	8	4	0	1	1	1	10	2	4	5	0	2
	3	0	**57**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	1	0	1	2	11	1	3	0	3	3	0	1	0	1	3	4	1	0	0	**22**
	5	0	0	0	2	2	0	2	6	7	6	0	10	0	0	10	3	1	2	0	6
	6	0	**57**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	7	1	0	1	1	1	**43**	1	0	2	1	0	1	0	2	1	2	0	0	0	0
	8	2	1	1	15	0	4	0	0	11	0	2	1	0	3	7	6	1	1	0	2
	9	2	0	2	8	4	2	0	5	5	7	2	0	5	0	4	7	3	1	0	0
	10	0	0	3	3	0	**47**	0	0	0	0	1	0	0	0	0	1	2	0	0	0
	11	0	0	0	0	0	0	**57**	0	0	0	0	0	0	0	0	0	0	0	0	0
	12	1	0	0	2	4	1	2	7	2	12	3	0	0	1	2	3	0	3	5	9
	13	**20**	0	0	0	1	1	0	5	7	1	3	0	0	2	3	7	4	3	0	0
	14	4	0	2	2	1	1	1	2	**21**	0	0	2	1	2	8	2	3	1	0	4
	15	2	0	**25**	11	0	0	0	0	1	0	0	7	0	2	1	4	3	0	0	1
	16	0	**57**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	17	1	0	5	1	2	0	1	1	7	1	0	1	**26**	0	2	3	6	0	0	0
	18	5	0	3	8	1	2	2	2	9	5	3	5	0	6	2	0	2	2	0	0
Arabidopsi thaliana	1	6	0	5	6	2	21	2	4	13	6	1	9	6	0	17	10	5	5	0	3
	2	8	1	7	5	5	11	0	9	14	7	0	3	6	1	12	14	6	11	0	1
	3	0	**121**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	2	0	1	3	30	3	5	3	6	4	0	6	0	3	2	7	3	0	1	**42**
	5	0	1	0	10	2	1	6	15	16	4	2	24	0	3	14	10	4	5	0	4
	6	0	**121**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	7	1	2	0	1	4	**87**	2	0	9	0	0	4	0	1	6	4	0	0	0	0
	8	4	0	10	24	0	18	4	3	15	1	3	3	0	13	12	6	1	4	0	0
	9	3	0	3	10	4	1	0	1	9	13	7	4	14	4	6	12	9	17	0	4
	10	1	0	4	2	0	**98**	0	0	0	0	0	2	0	0	1	6	7	0	0	0
	11	0	0	0	0	0	0	**121**	0	0	0	0	0	0	0	0	0	0	0	0	0
	12	1	1	5	0	23	2	1	14	1	15	6	8	3	1	10	6	4	6	13	1
	13	**58**	1	0	3	1	2	0	6	0	5	2	0	1	1	4	23	8	6	0	0
	14	6	0	0	1	2	1	3	2	18	3	4	5	1	4	**51**	10	5	1	0	4
	15	10	0	**40**	19	0	2	6	1	1	3	0	12	0	5	3	4	9	1	0	5
	16	0	**121**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	17	2	0	3	2	1	3	3	0	5	7	4	0	**53**	1	9	10	16	1	1	0
	18	4	0	5	7	2	10	1	5	10	2	0	21	0	6	8	18	9	3	0	10
All together	1	9	0	11	6	2	24	3	12	21	9	2	12	10	7	25	14	9	16	0	6
	2	11	4	7	6	9	17	2	14	25	13	1	4	8	5	23	17	10	17	1	4
	3	0	**198**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	4	3	0	2	6	42	4	8	3	10	7	0	9	1	4	6	12	7	0	1	**73**
	5	0	1	0	12	4	1	9	23	25	12	2	44	0	3	25	13	6	8	0	10
	6	0	**198**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	7	2	2	3	2	5	**140**	3	0	12	1	0	10	0	3	7	8	0	0	0	0
	8	7	1	11	43	0	25	4	3	28	2	5	5	0	21	19	14	3	5	0	2
	9	8	0	5	18	8	3	0	7	18	20	10	5	21	4	13	19	16	19	0	4
	10	1	0	9	5	0	**160**	0	0	1	0	1	3	0	0	2	7	9	0	0	0
	11	0	0	0	0	0	0	**198**	0	0	0	0	0	0	0	0	0	0	0	0	0
	12	2	1	5	2	30	3	3	23	5	30	11	9	3	2	12	11	4	11	19	12
	13	**80**	1	0	4	2	5	0	12	11	6	5	0	1	4	11	34	13	9	0	0
	14	11	0	4	6	3	2	4	4	44	3	4	7	2	6	**63**	15	9	2	0	9
	15	12	0	76	33	0	2	6	1	2	3	0	21	0	9	6	8	12	1	0	6
	16	0	**198**	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	17	4	0	9	3	3	3	4	1	13	8	6	2	**90**	2	11	13	24	1	1	0
	18	9	0	8	19	3	12	8	7	21	7	4	28	0	12	10	22	12	6	0	10

Values indicate the number of cases in which each amino acid is present in a given position (from the first to the eightieth; 1-18 in the column headed as “Position”) within 20 ZCCCH domains from 7 yeast factors, 57 from 34 human factors, and 121 from 69 Arabidopsis factors. Numbers are also shown for all the 198 sequences from the 110 factors taken together. Transposon-derived and uncertain ZCCHC domains have been omitted from the analysis. The C and H residues that characterize the ZCCHC domain are highlighted in red, the highly conserved G at the seventh and tenth positions in green, and residues occupying positions with a frequency higher than 30% in blue.