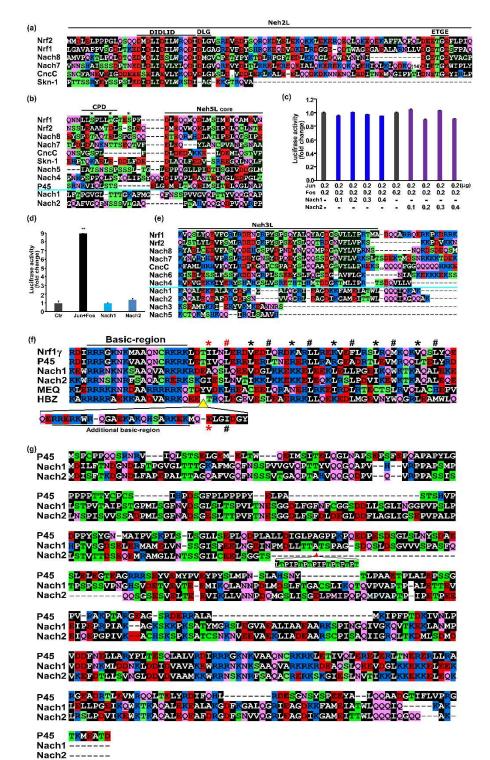


Figure S1. Identity of original homologues of BATF, Jun and C/EBP subfamilies. The multiple sequences alignments of BRLZ domains were analyzed by the DNAMAN8.0 software: (a) MEQ from *Gallid herpesvirus 2* is homologous with human BATF family. (b) Another viral protein (with a GenBank No. YP_007003813) from *Cyprinid herpesvirus 1* is conserved with human Jun family, including Fos, ATF2 and others. (c) A bacterial homologous protein (with a GenBank accession No. WP_062270874) from *Endozoicomonas arenosclerae* is classified into human C/EBP family.



- 8

9 Figure S2. Detailed schematic representation of structural domains of Nach/CNC-bZIP proteins. 10 Bioinformatic analysis by the DNAMAN8.0 software was subject to multiple sequence alignments of 11 different structural domains of: (a) the Neh2L domain, (b) the Neh5L domain, (c) Neh3L domain. 12 (d,e) Nach1 and Nach2 have no effects on basal expression of AP-1-driven reporter gene and its 13 regulation by Fos and Jun. Related methods and data calculations were referenced to determination 14 of ARE-driven luciferase reporter activity as described in the legend of main Fig. 5. (f) Shows specific 15 sequence alignments of the BRLZ domains of HBZ from Human T-Cell Leukemia Virus Type 1, MEQ 16 from *Gallid herpesvirus* 2, bacterial Nach1/2 with human Nrf1γ. The symbols * and # represent the "a" 17 and "d" positions in heptad repeats of LZ region, respectively. (g) Shows an additional alignment of 18 the full length Nach1/2 proteins with human NF-E2 P45.

- Figures S3–S13. Distinct characteristics of BRLZ domains within different bZIP subfamilies.
 Those distinct characteristics of BRLZ domain were analyzed by using three different softwares
- 21 DNAMAN8.0, MEME and Web-logo with default parameters.

CNC-bZIP	
Hs-Bach1_NP_001177	CSAREQECEVKLPFNAQRIISLSRNDFQSLLKMHKLTPEQLDCIHDI
Gg-Bach1_XP_416696	CSAREQECEVKLPFNAQRIISLSRNDFQSFLKMHKLTPEQLDCIHDI
Gg-Bach1_XP_416696 Mm-Bach1_NP_031546 Ac-Bach1_XP_003219110 X1-Bach1a_XP_018101443 X1-Bach1b_XP_018104014	CSAREQDCEVKLPFNAQRIISLSRNDFQSLLKMHKLTPEQLDCIHDI
Ac-Bach1_XP_003219110	CSAREQECEIKLPMNPQKIISLSRNDFQSFLKMHKLTPEELDCIHDI
X1-Bach1a_XP_018101443	ESCSVQECETKLPFNAQKIISLSRYDFQALVKKHSISAEQLDCIHDI
na baonab ne baoabita	CSAKELECEEKLPFKAQKIISLSRYDFQALIKRHSLTAEQLDCIHDI
Hs-Bach2_NP_068585	CPVQDRGQEVKLPFPVDQITDLPRNDFQMMIKMHKLTSEQLEFIHDV
Mm-Bach2_NP_001103131	CPVQDRGQEVKLPFPVDQITDLPRNDFQMMIKMHKLTSEQLEFIHDI
Ac-Bach2_XP_016852773 Gg-Bach2_XP_016852773 X1-Bach22_XP_015140173 X1-Bach2a_XP_015140173 X1-Bach2b_XP_018118876 X1-Bach2b_XP_018120920	CFVQDRGHEVKLPFPVDQITDLFRNDFQMMVKMHKITSEQLEFIHDV
Gg-Bach2_XP_015140173	CFVQDRGHEVKLFFFVDQITDLFRNDFQMMIKMHKLTSEQLEFIHDV
C X1-Bach2a_XP_018118876	CPVQDRGHEVKLPFPVDQITDLPRNDFQMMIKMHKLSSEQLEFIHDV
	CFVQDSGQEVKLPFPVDQITDLFRNDFQMMVKMHKLSSEQLEFIHDV
Dr-Bach2b_XP_005160605	CHVREQGPEVKLPFPVDQITNLPRNDFQMMVKMHKLTSEQLEFIHDV
Dr-Bach2a_XP_685315	FATKERTQEVKLPFSVDQITELFRNDFQLMIKMHKLSSDQLDFIHDM
Dr-Bach1b_AHX22538	SYSSERVREMALPLSVDQIVCLSRNDFQQMLKQQSLSREQLDAVHDI
Hs-Nrf3_NP_004280	SRDEQRAKALHIPFSVDEIVGMPVDSFNSMLSRYYITDLQVSLIRDI
Mm-Nrf3_NP_035033	SRDEQRAKALHIPFSVDEIVRMFVDSFNSMLSRYYLTDLQVSLIRDI
X1-Nrf3_XP_018122887	SRDERRAKSLRIPFSVDEIVSMPVEMFNNMLSKHCITESQVTVIRDI
X1-Nrf3L_XP_018124724	SRDERRAKSLRIPFSVDEIVSMPVEMFNNMLSKHCITESQVTVIRDI
Ac-Nrf3_XP_003222201	SHDEYCVKALRIPFAINDIVTLPVDSFNSMLSKYCITDNQLSLIRDI
Hs-Nrf1_NM_003204.2	SRDEHRARAMKIPFTNDKIINLFVEEFNELLSKYÇLSEAQLSLIRDI
Mm-Nrf1_NM_008686.3	SRDEHRARAMKIPFTNDKIINLFVEEFNELLSKYQLSEAQLSLIRDI
Gg-Nrf1_NM_001030756	SRDEHRARAMKIPFTNDKIINLFVEEFNELLSKYÇLSEAQLSLIRDI
Ac-Nrf1_XM_016994618	SRDEHRARAMKIPF SNEKIINLFVEEFNELLSKYQLSEAQLSLIRDI
Z X1-Nrf1L2_NP_001080013	GRDEQRAKAMKIPFTNDKIINLFVEEFNDLLAKYQLSEAQLCLIRDI
X1-Nrf1L1_XP_018090244 Dr-Nrf1b_NP_001265771	GRDECRARAMKIPFSNDKIINLFVEEFNDLLAKYCISEACICLIRDI
Dr-Nrfla JX867114	SRDERRARAMDIPFSNEKIINLPVEEFNELLAKHHINEDQLSLIRDI SRDEKRARLMNIPFSNERIINLTVDEFNRLLEKYHISEAQSHANQNT
Hs-Nrf2 NP 006155	TRDELRAKALHIPFPVEKIINLFVVDFNEMSKECFNEACIALIRDI
Mm-Nrf2 NP 035032	TRDELRAKALHIFFFVERINLEVVDFNEMSKEQFNEAQIALIRI TRDELRAKALHIFFFVERINLEVDDFNEMSKEQFNEAQIALIRI
Ac-Nrf2 XP 003226813	TRDELRAKALGIPFPVERINLEVDDFNEMMSREGFTEAGVTLIRDI
Gg-Nrf2 NP 990448	TRDECRAKALQIFFFVERINLFVDDFNEMMSKEQFFEAQUALIRDI
Dr-Nrf2b NP 001244112	SRDEQRAKALQIPFTVDMIINLFVDDFNEMMSKHCINEACLALVRDI
Z X1-Nrf2L NP 001079522	TRDECRAKVLNLPFTVEKIVNLPVDSFNEIMSKYCFNEACLALIRDI
*Dr-Nrf3 NP 998396	SRDEHRVQALGLEFSAFQIVNMEVENFLELLDRQNLSGSDVTLLRDV
Dr-Nrf2a NF 878309	CRDEORACALSLPLSVHDIIHLFVEAFNEAISTCKLNHACHTLIRDI
X1-Nrf25 NP 001086307	TRDTQRAKVLNIPFSVDKIVNLFVDSFNEMMSKYCFNEAGLALIRDI
Hs-P45 NP 006154	SRDERRALAMKIPFPTDKIVNLFVDDFNELLARYPLTESCLALVRDI
Mm-p45_NP_032711	SRDERRALAMKIPFFTDKIVNLFVDDFNELLAQYPLTESQLALVRDI
X1-p45 XP 018103033	SRDERRAAAMNIPFPTERIVNLFVEDFNELLSRYTLTDTCLALVRDI
Dr-P45 NP 778208	SRDERRALALKIPFSLEKIVNLFVDDFNELLTQFTLTDAQLALVRDI
Ac-P45 XP 003216776	SRDERRALAMKIPFPVEKIINLFVDDFNELVSRFFLSEFQLALIRDI
Dm-CncC NP 732833	TRDEKRARSLNIFISVFDIINLFMDEFNERLSKYDLSENQLSLIRDI
Nv-Nach6 AOP32002	LASKADADSLDIGVSEEKIVEMSVAEFTTFLEKLSDAQAKYVRDV
Ta-Nach3 XP 002116568	IFGVPTNSMLVLEVPERELVDMEVNEFLAMIERLPSDVAALARDV
Sp-Nach8 NF 001123278	NRDEKRAKALKLEVCLEKIINLEVDSENDLVKKYELTDEQMQLVRDI
Sp-Nach8_NP_001123278 * Ob-Nach7_XP_014784776	SRDHKRLQELKVPLSMNQIINSSVEEFNDLVRKYPLPEPQLRLIRDI
Z Aq-Nach5 XP 003385261	SLASPDIPQSFNGISKLEIIDMFYFEFKKLLDGGTFSERDKEEVKAI
Aq-Nach4 XP 011402550	MSSHNRRGGASKFITRDKLVIMFVEDFNSLLDEALLSEIEVAFMKEW
Es-Nach2_WP_062268396	RKSPINGQIVGKQVTKEKLANMFVDDFNKMLDDNKLDDIDVAVAKEW
En-Nach1_WP_034835593	RSCPISAQIIGRQLTKDMLSDMDVKEFDTLLSVNGLDDVDVAAMKKW
*Ce-Skn-1_NP_741404	SKDEQLASDNELPVSAFQISEMSLSELQQVLKNESISEYQRQLIRKI
Dr-Bach1a_NP_001035403	MTRRAFLQMLKREQLTPEQLEYVQDV

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Figure S3. Alignment of the CNC domains from those identified Nach/CNC-bZIP subfamily proteins. The blue and red asterisks represent not gregarious bZIPs in zebrafish and some CNC members with high homology beyond vertebrates, respectively. The light blue and pink backgrounds are 50% to 75% and 75% to 100% homology level.

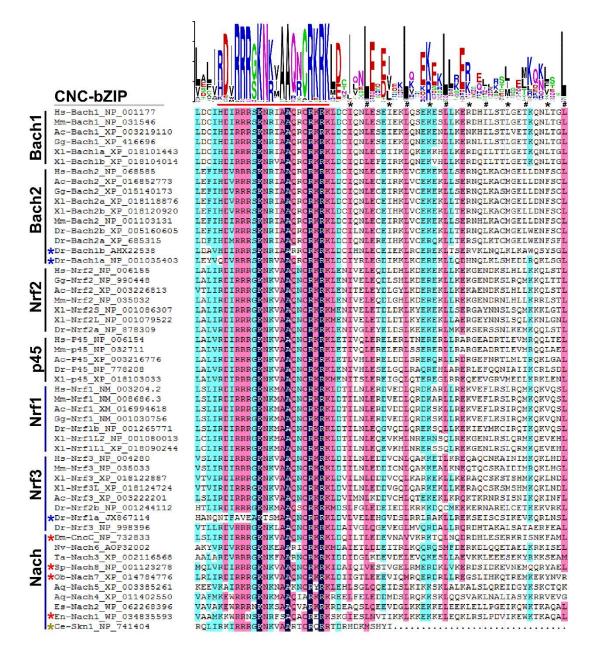


Figure S4. Alignment of the BRLZ domains from those identified Nach/CNC-bZIP subfamily proteins. The blue and red asterisks represent not gregarious bZIPs in zebrafish and some CNC members with high homology beyond vertebrates, respectively. The black symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.

CB BATF,CHOP

ATF4

ATF ATF2,ATF3.

E4BP4

C/EBP,PAR.E

Fos

B(ATF1

CRIC

CNC, Mat

JN,OASIS,ATF6,XBP

	Human vs Unclassified bZIP	
	Sc-Yap5_NP_012283 Sc-Yap7 KZV07854	ENDEELQKKKRQNRDAQRAYRERKNNK.LQVLEETIESLSKVVKNYETKLNRLQNELQAKESENHAL NGVDSVEKRRQNRDAQRAYRERKTTR.IQVLEEKVEMLHNIVDDWQRKYKLLESEFSDTKENLQKS
5	Sc-Cin5_NP_014671	GKPLRNTKRAAQNRSAQKAFRQRREKY.IKNLEEKSKLEDGIMKENSELKKMIESIKSKLKE.
Ē	Sc-Yap6_EGA87413	GKTLRNTRRAAQNRTAQKAFRQRKEKY.IKNLEQKSKIFDDLAENNNFKSLNDSLRNDNNIL
Ę,	Sc-Yap1_NP_013707 Sc-Yap3 NP_011854	LDPETKQKRTAQNRAAQRAFRERKERK.MKELEKKVQSLESIQQQNEVEATFLRDQLITLVNELKKY VPDDSKAKKKAQNRAAQKAFRERKEAR.MKELQDKLLESERNRQSLLKEIEELRKANTEINAENRLL
'n	*Hs-CHOF_P35638	EEDQGRTRKRKQSGHSFARAGKQRMKEKEQENERKVAQLAEENERLKQEIERLTREVEATRRALIDR
	Dd-HY5L1_XP_641680	ERHQKRQRRLVKNREAAQLFRQRQKAY.IQDLEKKVSDLTGINSEFRARVELLNSENKLIREQLLYL
	Sc-Met28p_EWG90397 #Hs-BATF AAC50314	ELDKIKQERRRNTEASQRFRIRKKQKNFENMN.KLQNLNTQINKIRDRIEQINKENEFWKAKISDI SDDVRRVQRREKNRIAAQKSRQRQTQK.ADTLHLESEDLEKQNAALRKEIKQLTEELKYFTSVINSH
.	*Gh2-MEQ_YP_001033993	EEKQKLERRRKRNRDAARRRRRKQTDY.VDKLHEACEELQRANEHLRKEIRDLRTECTSLRVQLACH
Ā	*Hs-ATF2_CAA33886	DPDEKRRKFLERNRAAASRCRQKRKVW.VÇSLEKKAEDLSSINGÇLQSEVTLLRNEVAQIKQILLAH
	★Hs-ATF3_AAA20506 ★Hs-ATF4_CAG30270	EEDERKKRRRERNKIAAAKCRNKKKEK.TECLQKESEKLESVNAELKAQIEELKNEKQHLIYMINLH EKIDKKLKKMEQNKTAATRYRQKKRAE.QEALTGECKELEKKNEALKERADSLAKEIQYIKDLIEEV
AI F3	Mb-bZIP-TF1_XP_001743420	DDDDHAGSISNPNKSAADRYRKKKREE.FERIQHDTEAMKAENLEIKTRISKIRNEAEFIANMIQSA
Y	Ce-bZIP-TF2_NP_500318	DETKLLSRKRQQNKVAAARYRDKQKAK.WQDILDQLEAEEDRNQRIKLQAGHLEKEVAEMRQAFLAK
4	Co-ATF2L2_XP_004364450 Co-ATF4L1_XP_004343869	DDESNKNKLRERNKTAAAKSRLKKKQR.EHQLQQRARHMVERNGDLKTAMAKMETEVQALREKMAAA LDEEEKIEKRRNKIAAARCRDKKREK.QSILDERTERMREENINLKQKVAQLEMEVSYLKNLVLAA
	Ob-ATF4L1 KOF68678	DEELKKEKRRECNRRAAARCRNKKKWE.ERLSCANLFEEKKCIMLKSIVRKLTDMKCNMEKLLSNV
	HS-CEBPa CAA72289	KNSNEYRVRRERNNIAVRKSRCKAKQR.NVETQQKVLELTSCNCRLRKRVEQLSRELDILRGIFRQL
	Mb-bZIP-TF5_XP_001743794 Sc-GCN4 NP 010907	EDSNNYRIKRIRNNEAVRRCRIKKKQE.MEEKAMRLELLEHKVSDLENCNRKLSELIVEQQKEIQRL ESSDPAALKRARNTEAARRSRARKLQR.MKQLEDKVEELLSKNYHLENEVARLKKLVGER
ì	*Co-bZIP-TF1 XP 004363551	ETLADYLDKRKKNNDAVKKCRARKRMA.VVATEEECQRLSGENASLRDRVGSLEAEVAYLKNLLISA
Ť	*Co-ATF4L2_XP_004349044	DLPQRKLSRRERNNIAVRRCRDKNREK.SLAAKSQCETVAQENANLRVRIHSLEQEVSYLKSMLLSQ
¥	*Aq-ATF7L_XP_011402548 *Ce-bZIP-TF1 NP 502961	SKLAKKAERKEKNNAASKVSRAKRKQK.MKSIFEREKELESENARIKLQVEEMTKEAEKLKKQLILR QKDEAYLDRRRRNNEAARKSRESRKKV.DQDNSVRVTYLERENQCLRVYVQQLQLQNESMRQHLLLQ
ŗ,	*Hs-DBP AAA81374	CKDEKYWSRRYKNNEAAKRSRDARRIK.ENCISVRAAFLEKENALIRCEVVAVRCEISHYRAVISRY
ų	Sp-HLFL1-BRLZ1_XP_003724320	TKDARYWVKRIKNNISAKRSREKRRMA.DNVMESKVSKLAQENEDIRSELANIKRIVQDNIIKDTKQ
	Ob-HP8-BRLZ1_XP_014769996 Hr-HP8L_XP_009021353	RKDÇCYWEKRRKNNEAARRSREKRRIH.DMALEKRIVELSRESCILRIÇIYAVKKRYGIPREEPIIL KKDKEYWMKRQKNNAAAKKSREKRRIN.DVVLINQIVQLINENKRLKVELQAIKQRFGISISSPY
	*Hs-E4BP4 AAA93067	KKDAMYWEKRRKNNEAAKRSREKRRLN.DIVLENKLIALGEENATLKAELLSLKLKFGLISSTAYAQ
	Hs-cFos_CAA24756	EEEEKRRIRRERNKMAAAKCRNRRREL.TDTIQAETDQLEDEKSAIQTEIANLLKEKEKLEFILAAH
S	*Nv-bZIP-TF1_XP_001628839 *Co-bZIP-TF3_XP_004349462	EEEEKRRIRRERNKQAANRCRKRKRCK.IEMLERTAQEIDDSNKALEIDIANMRTELIEIMSVIRSH GSIDKRSIKRIRNREAAARCRNRRRQL.IDELSIQVAELVAEKIIMAATIARLEAELAITRGN
Ľ	Sc-ATF2L2_Sko1p_AJT01605	EQERKRKEFLERNRVAASKFRKRKKEY.IKKIENDLQFYESEYDDIIQVIGKLCGIIFSSSSNSQFN
	Sc-HAC1_NP_116622	EKEQRRIERILRNRRAAHQSREKKRLH.LQYLERKCSLLENLLNSVNLEKLADHEDALTCSHDAFVA
	Sp-cFos_XP_003726998 #Hs-ATF1_AAH29619	EEEVRRRLQKERNRDAASKCRSKKRNA.VGHLVEEAQQLETENMKLREEMKALESERSQLQFLLDMH DPQLKREIRLMKNREAARECRRKKEY.VKCLENRVAVLENQNKTLIEELKTLKDLYSNKSV
	*Hr-ATF4L1_XP_009024663	HDSLRKNRRREQNRIAARKCREKKRVQ.VDSILKGYADILKENKKLKQETQVLKLVVNNLQNVLTSH
Ξ	Co-bZIF-TF6_KJE89372	NDTDFNQRRREKNREAAQACRIKKKVY.VNSMQGSVDSVAETNNHLNLQLSMVQQNTLRIHGFSQQL
Ř	★Co-XBP1L_XP_004347974 ★Hs-Nrf1 NM 003204.2	ISDLKMQRRRVKNREAAQVCRKKKKSF.VVDLEGNMSVLQREQDNLRENLRTAEATFQQAKTATATK LSLIRDIRRRGKNKMAAQNCRKRKLDT.ILNLERDVEDLQRDKARLLREKVEFLRSLRQMKQKVQSL
Ÿ	*Hs-Bach1 NP 001177	LDCIHDIRRRSKNRIAAQRCRKRKLDC.IQNLESEIEKLQSEKESLLKERDHILSTLGETKQNLTGL
<u>ن</u>	Es-Nach2_WP_062268396	VAVAKEWRRRNKNKSAAQVARKRKRDE.AQSIQEEVDGLKKEKKELEEKLELLPGEIKQWKTKAQAL
Ĕ,	En-Nach1_WP_034835593 *Co-bZIP-TF5_XP_004343898	VAAMKKWRRNSKNRFSAÇACRERKSKG.IESLNVTIKKLKKEKKELEQKLRSLPDVIKEWKTKAQAL IRDLKDLRRKMKNRNAAARCRQRKRKE.IGVIRDRMSGLHVEVAFLRQENAILKSFLRTAGISLPDS
SN CE	Hs-cMaf_AAC27037	VIRLKÇKRRTLKNRGYAÇSCRFKRVÇÇ.RHVLESEKNQLLÇÇVDHLKQEISRLVRERDAYKEKYEKL
	*Hr-bZIP-TF1_XP_009009099	VQELKKKRRQLKNRNYAKTCRHKKITK.NVSLEEEVKMLRQERIHYVNEISKYKEEIKLLKMKLEIT
	Mb-bZIP-TF3 XP 001744453 Vb-bZIP-TF2 CEM00542	VADVKAKRRRIKNRISARICSNKKREK.CSELEDTNRDLIAKIRQVAQENKTIKSETNRIKEANTAL SHIDKKEQQRIRNRISAQQSRDRKKE.FEGISIQVDTITTENADIRRENVAIRAENTAIAAHRDQI
	*Co-bZIP-TF2_XP_004347848	PEMDKKLQRLIKNREAASQSRKRKKDQ.FDTLERDLNTIKTHNAALRSQVVALEQENAVLKADNERL
_	VD-bZIP-TF3_CEM20300	EEEERMSQCKLRNRLSAQAHRDRCKRL.MRDLCERVERLSAENCHLHRENSELKCDNARLIRDVACL
'n	★Hs-XBP1U_NP_005071 ★Hs-ATF6 BAA34722	SPEEKALRRKIKNRVAAQTARDRKKAR.MSELEQQVVDLEEENQKILLENQLIREKTHGIVVENQEL IAVLRRQQRMIKNRESACQSRKKKKEY.MIGLEARIKAALSENEQIKKENGTIKRQIDEVVSENQRL
à	₩VD-bZIP-TF1_CEL94591	VDEIKKQRKRDQNRASAVRSRAKKKEY.YTSLEHEVEALRHEATSIRAENQLLKQQLSFLQSLVQPN
R	Dd-bZIP-TF1_XP_642532	EEAKKKKIRQMQNRQSAAQYRERKKEY.LEKLETIVDNLESDRNQLLQQTKQLGMLQNENYLKINQL
Ś,	₩Mb-bZIP-TF2_XP_001742296 ₩Hs-OASIS BAC01278	EIKEKKERRMIKNRESASISRKRKKEY.IETLEHQIHDAQQQIGRAQHQIQQLQNDNHVIREQIANY EKALKRVRRKIKNKISAQESRRKKEY.VECLEKKVETETSENNELWKKVETLENANRTIIQQIQKI
Š	*Hr-bZIF-TF2_XF_009020232	EKNLKKIRRKIKNKISAÇESRRKKKEY.LESLEKKVEÇITÇENSGLKKKVNVLENNNRNLIAELÇKL
'n,	Mb-bZIP-TF4_XP_001750907	SRELKRMRRKVKNKLSAKDSRRRKKEY.VTQLEEENAQLRARLVTLHDQSMARQSMPATTSSSSSTT
5	Dd-HY5L2_XP_638790 *Dd-bZIP-TF2_XP_644283	EKVKKRQVRLLKNRQSAALSRSRKKEY.IANLESKAQELTHSTQELHVQYNKISSTTFETKSRLEFL EKELKKQRRLVKNREYASQSRSRRKIY.VENIETKLQKTNQDCASIKSQLNSVKEENKALKKQLYSL
	Co-bZIF-TF4_XP_004363356	SSDESKVAKLEKNRQSARDCRKRKKQY.IGNLEAKVEFLTEENARLARQLAEFLATSTKLVPSINQP
	Hs-cJun_AAA59197	QERIKAERKEMEREIAA SKORKEKLER, IARLEEKVKTLKAQNSELASTANMLREQVAQLKQKVMNH
	KOb-bZIP-TF1_XP_014790770	FSRNLQMIRRKKNRLAAQKCREKKKER.IRILEEEIKSLIKENYSLKQANYELGEKLSEQQKKLEEA

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Figure S5. Alignment of the BRLZ domains of unclassified bZIP proteins with human bZIP representatives. The blue, red and black asterisks represent not gregarious bZIPs, unnamed and representative bZIPs, respectively. The black symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The light blue and pink backgrounds are 50% to 75%, 75% to 100% homology level. The Blue lines are corresponding to the classification on the left.

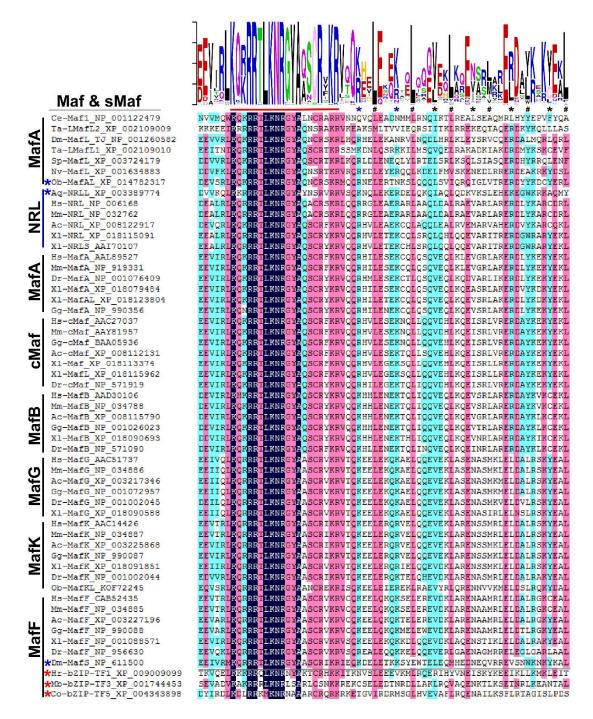


 Figure S6. Alignment of the BRLZ domains from within both Maf and sMaf subfamilies. The left blue and red asterisks represent interesting Mafs and unnamed bZIPs, respectively. The black symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively, where the blue symbols * are the first and second repeat "a" position with basic amino acids. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.

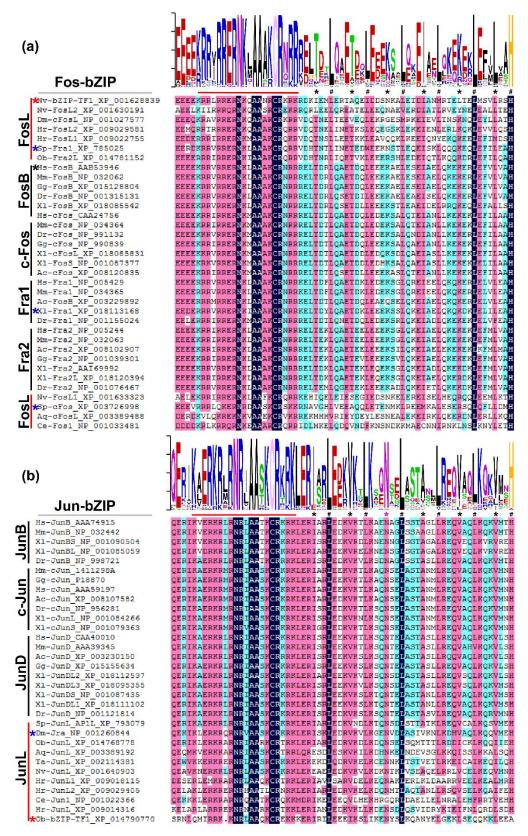




Figure S7. Alignment of the BRLZ domains from within both Fos (a) and Jun (b) subfamilies. The left
blue and red and black sterisks represent interesting bZIPs, unnamed and representative bZIPs,
respectively. The black symbols * and # represent the "a" and "d" positions in heptad repeats of LZ
region, respectively. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and
100% homology level.

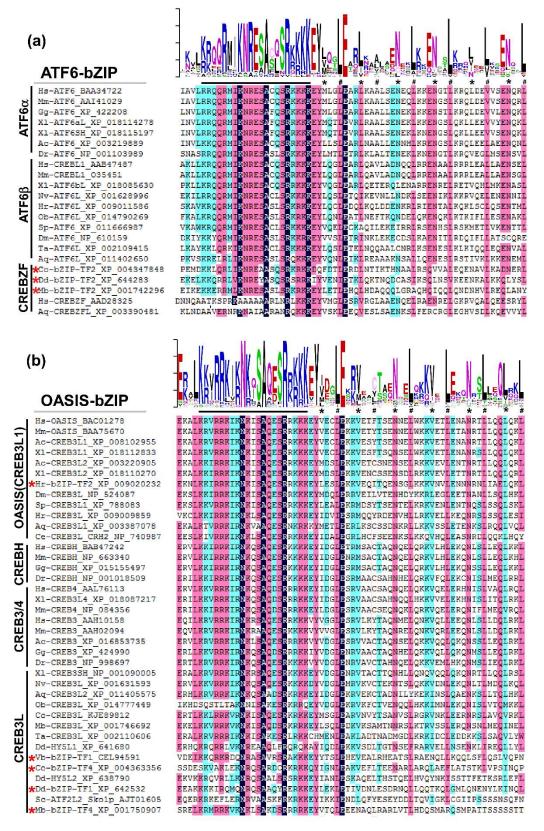




Figure S8. Alignment of the BRLZ domains from within both ATF6 (a) and OASIS (b) subfamilies. The left red asterisks represent unnamed bZIPs. The black symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.

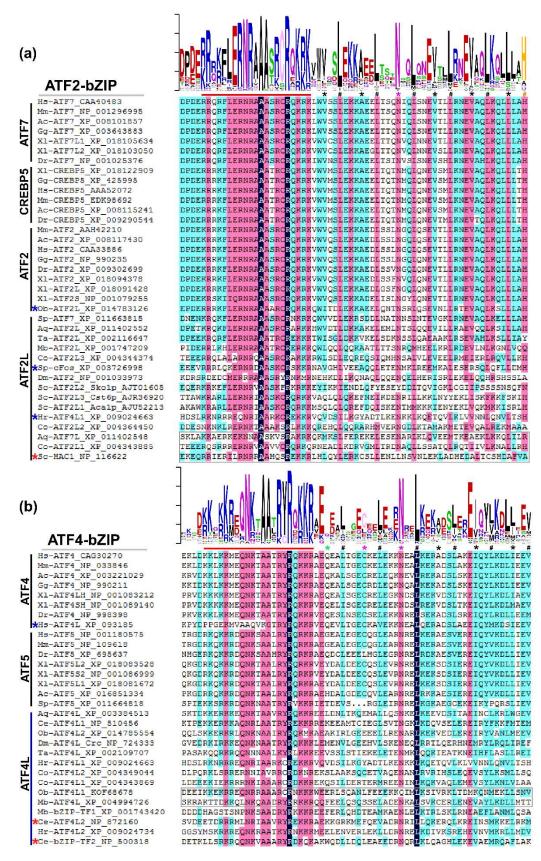
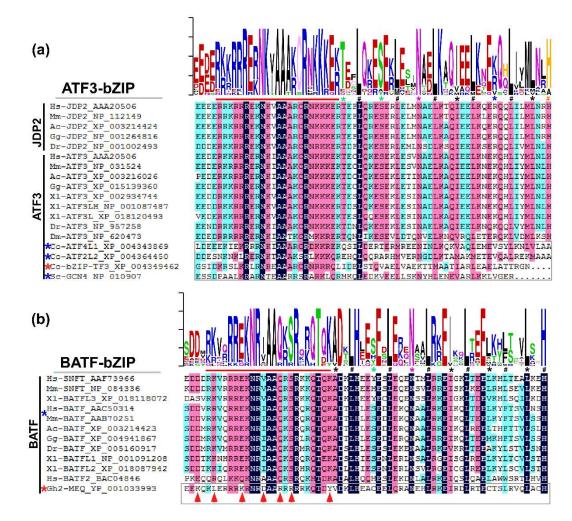


Figure S9. Alignment of the BRLZ domains from within both ATF2 (a) and ATF4 (b) subfamilies. The left blue and red asterisks represent interesting bZIPs and unnamed bZIPs, respectively. The different colors above symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.



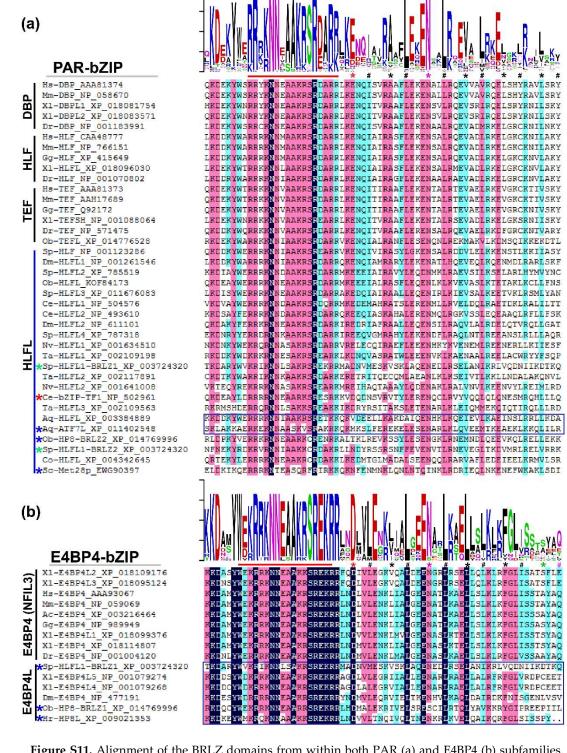


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Figure S10. Alignment of the BRLZ domains from within both ATF3 (a) and BATF (b) subfamilies. The left blue and red asterisks represent interesting bZIPs and unnamed bZIPs, respectively. The different colors above symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The red triangles represent the amino acids in Gh2-MEQ is different from others. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.



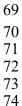


Figure S11. Alignment of the BRLZ domains from within both PAR (a) and E4BP4 (b) subfamilies. The left blue, green and red asterisks represent not gregarious, contained two BRLZ domains and unnamed bZIPs, respectively. The different colors above symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The blue boxes represent highly similar bZIPs, the red lines represent the nuclear localization signal (NLS) in the basic region. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.

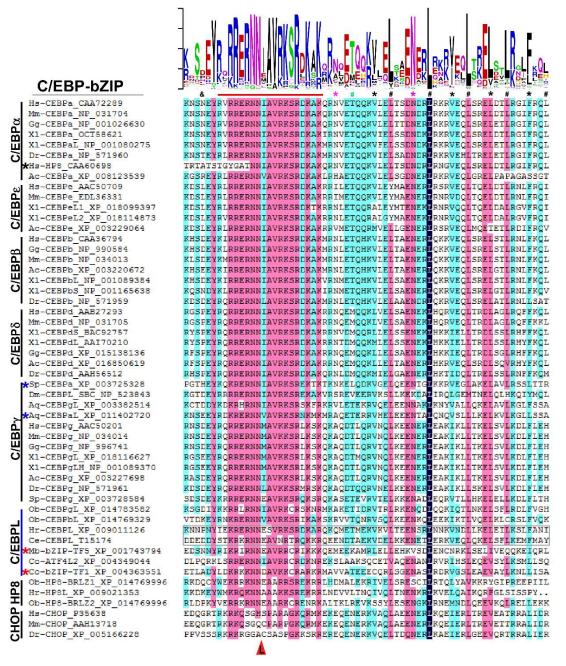


Figure S12. Alignment of the BRLZ domains from within the C/EBP subfamilies. The left blue and red and black asterisks represent interesting, unnamed and representative bZIPs, respectively. The different colors above symbols * and # represent the "a" and "d" positions in heptad repeats of LZ region, respectively. The grey boxes represent highly similar bZIPs, the red triangle represents a cumbrous leucine in Dr-CHOP. The light blue, pink and black backgrounds are 50% to 75%, 75% to 100% and 100% homology level.

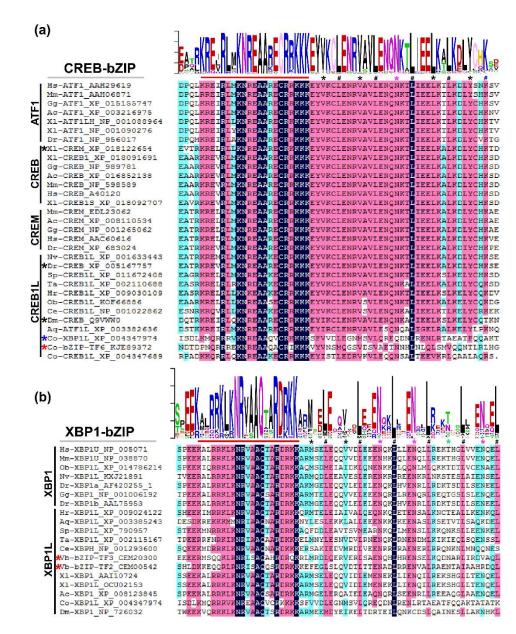
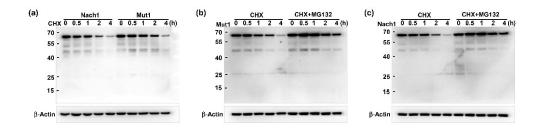


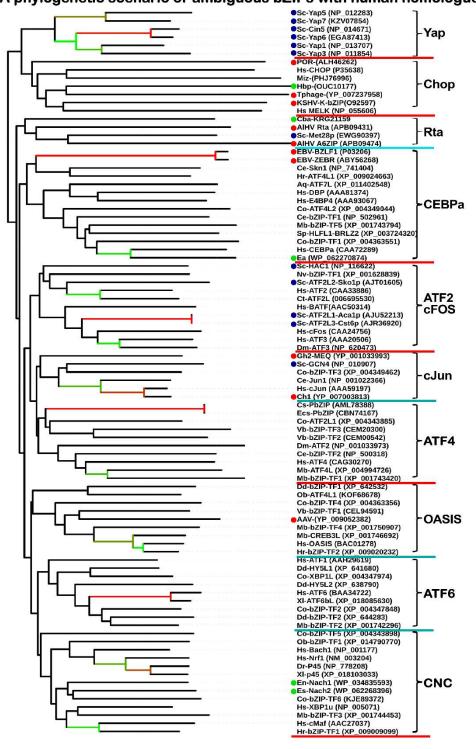
Figure S13. Alignment of the BRLZ domains from within both CREB (a) and XBP1 (b) subfamilies.
The left blue, red and black asterisks represent interesting, unnamed and representative bZIPs,
respectively. The different colors above symbols * and # represent the "a" and "d" positions in
heptad repeats of LZ region, respectively. The light blue, pink and black backgrounds are 50% to
75%, 75% to 100% and 100% homology level.



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Figure S14. The whole images of figure 5I. (**a** to **c**) Western blotting of Nach1 and its Mut1 that had been resolved by the whole PAGE gels containing 10% polyacrylamide, of which the cropped images were also shown in the main i1, i2 and i3 in Figure 5i, respectively.



A phylogenetic scenario of ambiguous bZIPs with human homologues

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Figure S15. The phylogenetic analysis of unclassified bZIP proteins with human bZIP representatives. The dots with different color are interesting bZIPs, the lines with different color are corresponding to the classification on the right.

Name	Forward (5'-3')	Reverse (5'-3')
1, The followi	ng primers used for expression plasmids	
Nach1	CGGGATCCATGGATATTTTGTTTA CAAATGATGGC	CCGCTCGAGCTTTTGCTTTCTGAATT TGCTGCTGTAGCC
Nach2	CGGGATCCATGGATATTTCGTTTACA AAGGATGGCAAT	CCGCTCGAGCCTTTGCTTGTTGCCC CTGAATCTGCT
Mut1	CCATGCTGTCAGGATTCAATGTAACT AGTCCTGTTCTTACTAATGAAAG	CTTTCATTAGTAAGAACAGGACTAGT TACATTGAATCCTGACAGCATGG
Mut2	GATTCAATGTAGACGCCGGACTAGC ACTGACTAGTCCTG	CAGGACTAGTCAGTGCTAGTCCGGC GTCTACATTGAATC
2, The followi	ng primers used for qRT-PCR analysis	
Nrf1	GGAGGAGTTCAATGAACTGCTGTC	CTCTGGACCTTCTGCTTCATCTGT
ATF1	AGGACTCATCCGACAGCATAG	TTCTGCCCCGTGTATCTTCAG
ATF2	GCACAGCCCACATCAGCTATT	GGTGCCTGGGTGATTACAGT
ATF3	GCTAACCTGACGCCCTTTGT	TTCAGTTCAGCATTCACACTTTCC
ATF4	CCCTTCACCTTCTTACAACCTC	TGCCCAGCTCTAAACTAAAGGA
СНОР	GGAAACAGAGTGGTCATTCCC	CTGCTTGAGCCGTTCATTCTC
DBP	AGCTGATCTTGCCCTATCAAGCA	TTGGCTGCCTCGTTGTTCTTGTA
JUND	TCATCATCCAGTCCAACGGG	TTCTGCTTGTGTAAATCCTCCAG
MAFF	GTGTGCCAGAAGGAGGAGCT	TTGACGATGGTGATGACGCT
NRL	GGCTCCACACCTTACAGCTC	GGCCCATCAACAGGGACTG
β -actin	CATGTACGTTGCTATCCAGGC	CTCCTTAATGTCACGCACGAT

Table S1. The primers for qRT-PCR analysis and expression plasmids.