S2 Fig. (Satou-Kobayashi et al.)

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Xl_Zbtb11.S     MSSEESYLAILRYLTNEREPYAPGTEGNAKRKIRKAAACYVVRAGTLYYQRKLRDKEGFT 60
Xl_Zbtb11.L     MSSEESYLAILRYLTNEREPYAPGTEGNAKRKIRKAAACYVVREGTLYYQRKLRDKEGFT 60
Xt_Zbtb11       MSNEESYLAILRYLTNEREPYAPGTEGNAKRKIRKAAACYVVRAGTLYYQRKLRDKEGFT 60
Hs_Zbtb11       MSSEESYRAILRYLTNEREPYAPGTEGNVKRKIRKAAACYVVRGGTLYYQRRQRHRKTFA 60
Mm_Zbtb11       MSSEESYRAILRYLTNEREPYAPGTEGNVKRKIRKAAACYVVRGGTLYYQRRQRHRKTFA 60
Dr_Zbtb11       MSSEESYLAIQRYLTDEREPYAPGTHGNTKRKIRKAAACYIVRNGILYYQRRQKGLDEFT 60
                **.**** ** ****:*********.**.***********:** * *****: :  . *:
Xl_Zbtb11.S     ELEVVLQLERRKRLIEAAHVGTGGEHLTRHQTWHVLSQSYWWRGILKHMKDYIKDCSKCQ 120
Xl_Zbtb11.L     ELEVVLQPERRKGLIEAAHINTGGEHLTRHQTWHVLSQSYWWRGILKHMKDYIKDCSKCQ 120
Xt_Zbtb11       ELEVVLQPERRKGLIEAAHIGTGGEHLTRHQTWHVLSQTYWWRGILKHMKDYIKDCSKCQ 120
Hs_Zbtb11       ELEVVLQPERRRDLIEAAHLGPGGTHHTRHQTWHYLSKTYWWRGILKQVKDYIKQCSKCQ 120
Mm_Zbtb11       ELEVVLQPERRQGLIEAAHLGPGGTHHTRHQTWHDLSKTYWWRGILKQVKDYIKQCSKCQ 120
Dr_Zbtb11       ELEVVLTADRRKELITEAHITSGGEHLNQQQTWEIISQKYWWRGVLKQVKDCIKECIHCQ 120
                ******  :**: **  **: .** * .::***. :*:.*****:**::** **:* :**
Xl_Zbtb11.S     ERTDRSRPSNDASEMLEEPGLDVRS--DTNETDDESSNPASNTSHTPKPSRKKPTTKHEL 178
Xl_Zbtb11.L     ERTDRSRSTNDASEMLEELGLDARS--DTNETDDESSNPASNTSHTPKTSRKKPTAKHEL 178
Xt_Zbtb11       ERTDRSRSTNDASEMLEELGLDVRS--DTNETDDESSNPASNTYQTPKPARKKPTAKHEL 178
Hs_Zbtb11       EKLDRSRPISDVSEMLEELGLDLESGEESNESEDDLSNFTSSPTTASKPAKKKPVSKHEL 180
Mm_Zbtb11       EKLDRSRPISDASEMLEELGLDLDSGEESNESEDDLSNFTSPPSTASKSSKKKPVSKHEL 180
Dr_Zbtb11       TKQEKGR--NNTEDAPKQTARQVRQKISSACASEEEDD---EIHEDLEEEQSTTVDKHEL 175
                 : ::.*  .:..:  :: . :  .  .:  :.:: .:          :  :.... ****
Xl_Zbtb11.S     VFVDSKGIVKQASSKHGQTILDQLNQQRLNNQFCDVTLLIEGQEFKAHKAVLAASSEYFR 238
Xl_Zbtb11.L     VFVDSKGIVKQTSSKHGQTILNQLNQQRLNNQFCDVTLLIEGQEFKAHKAVLAASSEYFT 238
Xt_Zbtb11       VFVDSKGIVKQSSSKHGQTILDQLNQQRLNNQFCDVTLLIEGQEFKAHKAVLAASSEYFR 238
Hs_Zbtb11       VFVDTKGVVKRSSPKHCQAVLKQLNEQRLSNQFCDVTLLIEGEEYKAHKSVLSANSEYFR 240
Mm_Zbtb11       VFVDTKGVVKRSSPKHCQAVLKQLNEQRLSNQFCDVTLLIEGEEYKAHKSVLSANSEYFR 240
Dr_Zbtb11       VFVDSKGIVKQFLQKHGQTMLDKLNLQRMNNEFCDITLIIEGEEYRAHKAVLASCSDYFY 235
                ****:**:**:   ** *::*.:** **:.*:***:**:***:*::***:**:: *:**
Xl_Zbtb11.S     ELFIEKGAVSSHEAFVDLSGFCKSSFLPLLEFAYTSELIFDFCSMAEISMLARHLFMNEV 298
Xl_Zbtb11.L     ELFIEKGAVTSHEAVVDLSGFCKSSFLPLLEFAYTSELVFDFCSMAEISMLARHLFMNEV 298
Xt_Zbtb11       ELFIEKGAVSSHEAFVDLSGFCKSSFLPLLEFAYTSELVFDFCSMAEISMLARHLFMNEV 298
Hs_Zbtb11       DLFIEKGAVSSHEAVVDLSGFCKASFLPLLEFAYTSVLSFDFCSMADVAILARHLFMSEV 300
Mm_Zbtb11       DLFIEKGAVSSHEAVVDLSGFCKASFLPLLEFAYTSVLSFDFCSMADVAVLARHLFMSEV 300
Dr_Zbtb11       ELFVEKGAVSSHEAVVDLSGFSKASFLPLLDFAYTSNLTFNFCVMAEVATLARHLLMAEV 295
                :**:*****:****.******.*:******:***** * *:** **::: *****:* **
Xl_Zbtb11.S     LEICESVHRQMETNQINLCQKVDVVSENSLLDASVVKLQAVGNNAPPLLAEVINSQKTSL 358
Xl_Zbtb11.L     LEICESVHRQMETNQINLCQKVDVVSESSCLDGRVVELQTVGINAPPLLAEVITSQKTSL 358
Xt_Zbtb11       LEICESVHKQMETNQINLCQKVDVVSENGLLDGRVVKLQAVGNNAPQLLAEVINSQKTSL 358
Hs_Zbtb11       LEICESVHKLMEEKQLTVYKKGEVQT--------------------------VASTQDLR 334
Mm_Zbtb11       LEICESVHKLMEEKQLTVYKKGEVQT--------------------------VASTQDLA 334
Dr_Zbtb11       LQICESVHKKVEEQKLMVYQRGDIHT------------------VLPNQPASTQPITPTA 337
                *:******: :* ::: : :: :: :                            .
Xl_Zbtb11.S     SNNENLECETVATETVTNSTDVAVSQLSEVPTVQLVTGPEVHISSLTGTAAIYLSDVSSE 418
Xl_Zbtb11.L     VNNKNVACEPVATETVTNSTDGVLSQLSEEPTVHLVTSPEVPISSLTGMTAIYLSDMSSE 418
Xt_Zbtb11       VNNENVECEAAATETVTNSTDGAISQSSEESTVQLVTSPEIPISSLTGTTAIYLSDVSSE 418
Hs_Zbtb11       VQNGGTAPPVASSEGTTTS---LPTELGDCEIVLLVNG-ELPEAEQNGEV---------- 380
Mm_Zbtb11       AHNGTTTPPGTRNEATTT----LSGELGHCEIVLLVNG-ELPEAEQNGEP---------- 379
Dr_Zbtb11       AETYVVTMQSDGTAEAGQSLAVITSEIGTAESLALLAGATVDGETMTVVTHSGQAGSAES 397
                 ..          .  .          : .    : *: .  :     .
Xl_Zbtb11.S     LQPAVIIPAVIDASNVQ-HQQILGDAPEDSTPADHMESQQPTGDNNIDASDKVQSVMFTT 477
Xl_Zbtb11.L     LQTAVIIPAVKDISNVHEHQQILSDTQEDSTPAEHSESPQSTGNGNMDASDKVQPVTLAT 478
Xt_Zbtb11       LQPAVIIPAVIDVSNVQEHQQILGDTPEDSTTAEHPESQQSTAGSNMDVPDEVLSVTCTT 478
Hs_Zbtb11       ------------------------GRQPEPQVSSEAESALSSVGCIADSHPEMESVDLIT 416
Mm_Zbtb11       ------------------------EQQPAPQASPEAEASVSPVEGIPEPHPEMGTASLAK 415
Dr_Zbtb11       LAMVAHS----------------GQAEEGETMTLVTHSGQAGSGESLAVVQACWSVEEPQ 441
                                                :   .:  .             ..
Xl_Zbtb11.S     SEKKLCAEEPQPKDVSLKEITNSNTNGDPQISVAVAEESSASVIDLETTCAEDVVIGNTD 537
Xl_Zbtb11.L     SENKLPADDPQPKDVCLKEFAYSSTNGDPQISVSVAEEPSISVIDLETTCAEDVVIGNTD 538
Xt_Zbtb11       TEEKLPADDPQPKDVSMKELINSSTNGDPQVSVPVAEESSISVIDLETTCAEDVVIGNTD 538
Hs_Zbtb11       KNN-------QTE---------LETSNNRENNTVSNIHPKLSKENVISSSPEDSGMGNDI 460
Mm_Zbtb11       ESN-------QPE---------SAVT--REDGIVASVHPKISKENVTNASQEDSDTGNDT 457
Dr_Zbtb11       VGDTPVVQSMQTG-AFLISVDPGKTGASEIVHLAAAAPPAVQDEPQASKPIHQTEPPAAA 500
                  .       *.            .             .  .     .   .:
                                        Venus-BTB construct --->|
Xl_Zbtb11.S     PEP-----KVKIGEDPKRKRGRPHKSP--EDIENSSKKTRQILQSGEKCTYKGK--LRDC 588
Xl_Zbtb11.L     PEQ-----EFKS-EVPKRKRGRPRKSP--EDVEKSSKETKETLPSDDKCKYKGK--LRDC 588
Xt_Zbtb11       PDP-----EAKIGEVPKRKRGRPRKSP--EDVEKSCKETRETLPSGGKCTYKGK--LRDC 589
Hs_Zbtb11       SAE-----DICAEDIPKHRQ-KVDQPL--KDQENLVASTAKTDFGPDDDTYRSR--LRQR 510
Mm_Zbtb11       SPE-----DIGAKDCPDHSQ-SPGQPS--KDEDTLTEATEKTDSGPDDDTYRSR--LRQR 507
Dr_Zbtb11       PQPSPAPLKRRPGRPPKVKQQEPPPPLPSEDEPMEMEGVEDDEKQEDECIDPNKRYLRKR 560
                .       .      *.  :     .   :*       . .      .    .:  **.
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S2 Fig. (Satou-Kobayashi et al.)

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Xl_Zbtb11.S      LVGKGGYIRLHQGQG----------------KTLKKR-------KTNP-----KSAVQQA 620
Xl_Zbtb11.L      LVGTGGYIKLHKGQG----------------KPLKKR-------KTNP-----KSAVQQA 620
Xt_Zbtb11        LVGKGGYIMLHRGQE----------------KALKKR-------KANP-----KSAVQQA 621
Hs_Zbtb11        SVNEGAYIRLHKGME----------------KKLQKR-------KAVP-----KSAVQQV 542
Mm_Zbtb11        SVNEGGYIRLHKGME----------------KKLQKR-------KAIS-----KSAVQQV 539
Dr_Zbtb11        SVREGGYVRLHMGLETEEEEKITSPPAKIPQKGLAKRGRPVQSAKKNPETEFSETNLEAA 620
                  *  *.*: ** *                  * * **       *  .     :: :: .
                   |---> Venus-Znf construct
Xl_Zbtb11.S      AMKLLQRGKKKR--LVAPKKQIAE------------AQFKCDDCGLMFERRYALIMHSVK 666
Xl_Zbtb11.L      AMKLLQRGKKKR--LVAPKKQTAE------------AQFKCNDCGMMFQRRYALLMHSVK 666
Xt_Zbtb11        AMKLLQRGKKKR--LMVPKKQIAE------------AQFKCNDCGMMFQRRYALIMHSVK 667
Hs_Zbtb11        AQKLVQRGKKMKQPKRDAKENTEE------------ASHKCGECGMVFQRRYALIMHKLK 590
Mm_Zbtb11        AQKLVQRGKKMKQPKRDAKESTEE------------TAHKCGECGMVFPRRYAFIMHTLK 587
Dr_Zbtb11        PNAIVTSAKEPEPVIVEQPETVEEGALPGDPEGAVEGEHACNECGMVFQRRYTLIMHALK 680
                 .  ::  .*: .       :   *               . *.:**::* ***:::** :*
Xl_Zbtb11.S      HEKSKEFKCPLCTKEFQYRASLRAHLIRHSKTGK---SEVNVVETEG-----DTVKGGTK 718
Xl_Zbtb11.L      HEKSKEFKCPLCTKEFQYSASLRAHLIRHSKTGK---AEVNVVETET-----DTVKGGTK 718
Xt_Zbtb11        HEKSKEFKCPLCTKEFQYRASLRAHLIRHSKTGK---AEVNVVETEA-----DTAKGGTK 719
Hs_Zbtb11        HERARDYKCPLCKKQFQYSASLRAHLIRHTRKDAPSSSSSNSTSNEASGT--SSEKGRTK 648
Mm_Zbtb11        HERARDYKCPLCKKQFQYSASLRAHLIRHTRKEAPTSSSSNSTSTEASGG--SSEKGRTK 645
Dr_Zbtb11        HEKARIFKCSICNKEFQYAASLRAHLARHKHQKSQRASLTRAMATEDSQGSDDQARFRTR 740
                 **::: :**.:*.*:*** ******* **.:       :  .    .*       .  :  *:
Xl_Zbtb11.S      RQFICGICGRTLPKLYSLRIHMLKHTGVKPHACEICGKAFTHKHGLKMHQALHESHKQFK 778
Xl_Zbtb11.L      RQFICGICGRTLPKLYSLRIHMLKHTGVKPHACEICGKAFTHRHGLKMHQALHEAHKQFK 778
Xt_Zbtb11        RQFICGICGRTLPKLYSLRIHMLKHTGVKPHACEVCGKTFTHKHGLKMHQALHESHKQFK 779
Hs_Zbtb11        REFICSICGRTLPKLYSLRIHMLKHTGVKPHACQVCGKTFIYKHGLKLHQSLHQSQKQFQ 708
Mm_Zbtb11        REFICSICGRTLPKLYSLRIHMLKHTGVKPHACQVCGKTFIYKHGLKLHQSLHQSQKQFQ 705
Dr_Zbtb11        REFVCDICGKTMPKLYSLRIHMLNHTGVRPHSCKVCGKSFATKHSLKMHRALHDSLKRFH 800
                 *:*:*.***:*:************:****:**:*::***:*  :*.**:*::**:: *:*:
Xl_Zbtb11.S      CDMCDKSFVTNRSLQEHVSTHTGESKYLCSVCGKPFHRASGLSKHLKKHKPKVETRGYHC 838
Xl_Zbtb11.L      CHMCDKSFVTNRSLQEHVSTHTGESKYLCSVCGKAFHRASGLSKHLKKHKPKVETRGYHC 838
Xt_Zbtb11        CDMCEKSFVTNRSLQEHVSTHTGESKYLCSVCGKAFHRASGLSKHLKKHKPKVETRGYHC 839
Hs_Zbtb11        CELCVKSFVTKRSLQEHMSIHTGESKYLCSVCGKSFHRGSGLSKHFKKHQPKPEVRGYHC 768
Mm_Zbtb11        CELCVKSFVTKRSLQEHMSIHTGESKYFCSICGKSFHRGSGLSKHLKKHQPKPEVRGYHC 765
Dr_Zbtb11        CTVCEKSFVTKRSLEEHTSIHTGESKYLCTTCGASFHRASGLSKHLKKHQPKPEVRSFHC 860
                 * :* *****:***:** * *******:*: ** .***.******:***:** *.*.:**
Xl_Zbtb11.S      TQCEKSFFELRDLQQHMNKHLGVKPFECEYCGKSYSWKKDWYSHVKSHSVKEPYRCSVCG 898
Xl_Zbtb11.L      TQCEKSFFELRDLQQHMNKHLGVKPFECEFCGKSYSWKKDWYSHVKSHSVTEPYRCSVCG 898
Xt_Zbtb11        TQCEKSFFELRDLQQHMNKHLGVKPFECEFCGKCYSWKKDWYSHVKSHSVTEPYRCSVCG 899
Hs_Zbtb11        TQCEKSFFEARDLRQHMNKHLGVKPFQCQFCDKCYSWKKDWYSHVKSHSVTEPYRCNICG 828
Mm_Zbtb11        TQCEKSFFEARDLRQHMNKHLGVKPFQCQFCDKCYSWKKDWYSHVKSHSVTEPYRCNICG 825
Dr_Zbtb11        SHCDKSFFEAKDLQQHMNKHLGLKPFQCQVCGKCYSWKKDWYSHVKSHSVAEPFRCNVCG 920
                 ::*:***** :**:********:***:*: *.*.**************** **:**.:**
Xl_Zbtb11.S      KEFYEKALYRRHVNKATHGKKGRTKLNFEKTCEHCGKVFTQFREYRRHVNNHEGVKPFEC 958
Xl_Zbtb11.L      KEFYEKALYRRHVNKATHGKKGRTKLNFEKACEHCGKIFTQFREYRRHVNNHEGVKPFEC 958
Xt_Zbtb11        KEFYEKALYRRHVNKATHGKKGRTKLNFEKACEHCGKIFTQFREYRRHVNNHEGVKPFEC 959
Hs_Zbtb11        KEFYEKALFRRHVKKATHGKKGRAKQNLERVCEKCGRKFTQLREYRRHMNNHEGVKPFEC 888
Mm_Zbtb11        KEFYEKALFRRHVKKATHGKKGRAKQNLERVCDQCGRKFTQLREYRRHMNNHEGVKPFEC 885
Dr_Zbtb11        KEFFEKALFRRHVKKATHGKKGRVKQNLERECEHCGRKFTQLREYRRHMNNHQGVKPFEC 980
                 ***:****:****:*********.* *:*: *::**: ***:******:***:*******
Xl_Zbtb11.S      LTCGVAWADARSLKRHVRTHTGERPYVCPVCNDGYIDARTLRKHMTKTHKDYVPGKIMLE 1018
Xl_Zbtb11.L      ITCGVAWADARSLKRHVRTHTGERPYVCPVCNEGYIDARTLRKHMTKTHKDYVPGKIMLE 1018
Xt_Zbtb11        LTCGVAWADARSLKRHVRTHTGERPYVCPVCNEGYIDARTLRKHMTKTHKDYVPGKIMLE 1019
Hs_Zbtb11        LTCGVAWADARSLKRHVRTHTGERPYVCPVCSEAYIDARTLRKHMTKFHRDYVPCKIMLE 948
Mm_Zbtb11        LTCGVAWADARSLKRHVRTHTGERPYVCPVCSEAYIDARTLRKHMTKFHRDYVPCKIMLE 945
Dr_Zbtb11        LTCGVAWADARSLKRHVRTHTGERPYVCPLCQEAHIDARTLRKHITKFHGDQLPGKIMLE 1040
                 :****************************:*.:.:*********:** * * :* *****
Xl_Zbtb11.S      KDSLQFHNQGTQVEHAVSILSAELDEPQAEIVT---EEIETVMVA------EEAMAQPPI 1069
Xl_Zbtb11.L      KDSLQFHNQGTQVEHAVSILSTELDEPQAEIVT---EEIETAVVA------EEAMVQALN 1069
Xt_Zbtb11        KDSLQFHNQGTQVEHAVSILSTDLDEPQAEIVT---EEIETVVVA------EEAMAQTPN 1070
Hs_Zbtb11        KDTLQFHNQGTQVAHAVSILTAGMQE-QESSGP---QELETVVVTGETMEALEAVAATEE 1004
Mm_Zbtb11        KDTLQFHNQGTQVEHAVSILTADMQE-QESSGP---QELETVVVTGETMEVLEAVAATEE 1001
Dr_Zbtb11        KDTLQFHNQGTQVEHAVSILSSELPPELQPPQPPATEEIETVLITEET---VEAVQAMND 1097
                 **:********** ******:: :         .   :*:**.:::       **:
Xl_Zbtb11.S      CTAVSSLSDQSIMQVVNYVLSQQQGQPITDVAEELETVEVEVGQISEVV 1118
Xl_Zbtb11.L      DTAVSSLSDQSIMQVVNYVLAQQQGQKMTDVSEELETVEVEVGQISEVV 1118
Xt_Zbtb11        STAVSSLSDQSIMQVVNYVLSQQQGQKIS--EEEIETVEVEVGQISEVV 1117
Hs_Zbtb11        YPSVSTLSDQSIMQVVNYVLAQQQGQKLSEVAEAIQTVKVEVAHISGGE 1053
Mm_Zbtb11        CPSVSTLSDQSIMQVVNYVLAQQQGQKLSEVAEAIQTVEVEVAHMPEAE 1050
Dr_Zbtb11        GAAVTTLSDQSIMQVVNYVLAQQAAVKVEEAPEIIQTMEVEVAHVAEVE 1146
                  .:*::***************:** .  :    * ::*::***.:::.
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S2 Fig. Alignment of Zbtb11 amino acid sequences between different species. Alignment of Zbtb11 amino acid sequences between *Xenopus laevis* (Xl), *Xenopus tropicalis* (Xt), *Homo sapiens* (Hs), *Mus musculus* (Mm), and *Danio rerio* (Dr). *Xenopus laevis* has two homeologs: L and S genes. Light blue boxes, the conserved regions CR1, CR2 and CR3; purple box, the integrase-like histidine-histidine-cysteine-cysteine (HHCC) motif; brown box, the BTB domain; magenta boxes, C2H2 type zinc fingers. The blue-coloured cysteine residue (C116) indicates a mutation site in the neutrophil-deficient zebrafish mutant (marsanne, mne). Red histidine residues (H729 and H880) indicate ZBTB11 mutation sites that are associated with intellectual disability. Arrows indicate the end of the Venus-BTB construct, and the beginning of the Venus-Znf construct.