

Supplemental Figure 2

HS zeb2	1	-----MKQPIMADGPRCKRRK-----	16
DR zeb2a	1	-----MKQEIMAEGRCKRRK-----	16
DR zeb2b	1	MHWCVWGIGGPMGLSGAPVVTIRASFADWKTEHLNEQLRLGCPGGSTSHLDSPALIFIPSE	60
HS zeb2	17	--QANPRRK-----MVNYDMVDTGSETDEEDKLHIAEDDGIANPLDQETSPASV	65
DR zeb2a	17	--QANPRRK-----WLSYENVVDAGSGSDDERLLGSE-----GEGSPAGV	56
DR zeb2b	61	DLSPFPRLTPSWALAEFYDMLDFENVVETGSETEEEDRLLVSEEDALLN--GAGSPASL	117
HS zeb2	66	PNHE----SSPHVSCALLFR-EEEEEIREGGVEHPW-NNEILQASVDGFEEKEDYDTM	120
DR zeb2a	57	PSLE----ASPRVAHALLSCRGDENEESQDGAGAHVWRHGELN----GSEERKAEYNSM	107
DR zeb2b	118	VNHESEARPSFTLSHTLLRKTVDEDDMKDSGLENVWHENDLLNASIDGTDELKADYDTM	177
HS zeb2	121	GPEATIQTAINNGTVKMANCTSDFEYFAKRKLEERDGHAVSIEEYLQRSDTAIIYPEAP	180
DR zeb2a	108	SPDISLHG-IGNGTVKGIDASSELESFFAKRKLDGEGHAASIAEYLQ--DTVIIYPEDP	164
DR zeb2b	178	GTDVSLIEP-IGNGTVKSVMCDTDFEDFFGKRKLVDTESHVVSIAEYLQRGDTAIIYPEAP	236
HS zeb2	181	EELSR--LGTPEANGQEEN--DLPPGTPDFAQALLTCPYCDRGYKRLTSLKEHIKYRHEK	236
DR zeb2a	165	EEGTR--LGTPEANGQDENENDLALRTPDFAQALLTCPYCDRGYKRLTSLKEHIKYRHEK	222
DR zeb2b	237	EELSRSLATPEATGHEEN--DLPPGTPDFAQALLTCPYCDRGYKRLTSLKEHIKYRHEK	294
HS zeb2	237	NEENFSCPLCSYTFAYRTQLERHMT HKPGTDQHQLTQGAGNRKFKCTECGKAFKYKHH	296
DR zeb2a	223	NDESFPCPLCSDTFAYRTQLERHMT HKPARDQFQLLNEGAGNRKFKCTECGKAFKYKHH	282
DR zeb2b	295	NEENFACPLCSYTFAYRTQLERHMT HKPGRDQHQILNQSGNRKFKCTECGKAFKYKHH	354
HS zeb2	297	LKEHLRIHSGEKPYECPNCKKRFSHSGSYSSHISSKKCIGLISVNGRMRN--NIKTGSSP	354
DR zeb2a	283	LKEHLRIHSGEKPYEQSNCKKRFSHSGSYSSHISSKKCIGLISINGRVRHGVNKNKFGSSP	342
DR zeb2b	355	LKEHLRIHSGEKPYECPNCKKRFSHSGSYSSHISSKKCIGLIAINGRVRN--NLKTGSSP	412
HS zeb2	355	NSVSSSPTNSAITQLRNKLENGKPLSMSEQTGLLKIKTEPLDFNDYKVLMAATHG-FSGTS	413
DR zeb2a	343	NSAASSFGSPALAAQLRHKL ENGRSMSLQDFSAHTDIKSEFMDFNEYRLMIASQGEYGASG	402
DR zeb2b	413	TSASSSPTNNAISQLRHKL ENGKPLGLQDQSNHLNLIKSEPLDFNDYKLMMAASHG-YATGS	471
HS zeb2	414	PFMNGGLGATSPLGVHPSAQSPMOHLGVGMEAPLLGFPTMNSNLSEVQKVLQIVDNTVSR	473
DR zeb2a	403	AFLNGGRGGSPFGMHSSQNPLQHLGIGSDSHPLGYTGFINNMSVQKVLQIVDNTVCR	462
DR zeb2b	472	PFLNGVRGGSPLGIHNSQSPLQHLGMGIEGQMLGYPSLGNNLSEVQKVLQIVDNTVCR	530

HS zeb2 474 QKMDCKAEEISKLGKGYHMKQPCSQFEEQ--GVTSPIPFVGLPVVSHNGATKSIIDYTL 531
 DR zeb2a 463 QKMDGNPEEISKLRAY-MKELGSGMEEQ---NRVLAQQQSFLGVGHNSPTKTIIDYTL 517
 DR zeb2b 531 QKMDCKPEEISKLKAY-MKELGSHIEEQKQGLNSGGGQGTLPINHNGATKSIIDYTL 589

HS zeb2 532 KVNEAKACLQSLTTDSRRQISNIKKEKLRITLIDLVTDDKMIENHNISTPFSCQFCKESFF 591
 DR zeb2a 518 KVNEAKACLQSLTEDSKRRLLMDIKKERPSHAMDLLSEDKALERDQYAPFSCQYCKETFS 577
 DR zeb2b 590 KVNEAKACLQSLTTDSKRQISNIKKEKANHMLDLGMEEKAHENNLMTFSCQYCKETFP 649

HS zeb2 592 GPIPLQHHERYLCKMNEEIKAVLQPHENIVFNKAGVFVDNKALLSSVLSEKGMTSPINP 651
 DR zeb2a 578 GPIPLQHHERYLCKMNEEIKAVLKPNQDTVFTGRRGLFGSEQCAGVISSSLERNATSPVNP 637
 DR zeb2b 650 GPIPLQHHERYLCKMNEEIKAVLQPAQNALTNKFGFLSEKHGLLHPSIIPKSLNGPISE 709

HS zeb2 652 YKDHMSVLKAYYAMNMEPNSEDELLKISIAVGLPQEFVKWFQQRK---VYQYSNSRSPSL 708
 DR zeb2a 638 YKDHMSLLNVYFSMNTTEPNSEELRKISMAVGLPQEFVKDAFVQWKAQSHHSFSRKRSPFP 697
 DR zeb2b 710 YKDHMSVLKAYFAMNMEPNSEELLKISIAVGLPQEFVKWFQQRK---VFQYTTSTRTPPL 766

HS zeb2 709 ERS-SKPLAFN-SNPPTKDSLIFRSF--VKPMDSITSPSIAELHNSVTNCDPPLRLTKP 763
 DR zeb2a 698 ERS-----GETNHMRDSAFARSF--VSLGQYGDSTAEIQAITN---GDSGHKLSRT 743
 DR zeb2b 767 DRSPVESIHPVSAHTPTKDSLGI RSPMSLVKGS DRITSPAIFELHN---NCDTPLRLSKT 823

HS zeb2 764 SHFTNIPV-----EKL DHSRNTPSPLNL SSTSSKNSHSSSYTPNSFSSEELQAEPLDL 818
 DR zeb2a 744 HQITGTRQTNEKPLDSVDHURGETPSPLNLSSSSSKHSHSSSYTPNSLTSEDAHGEPLDL 803
 DR zeb2b 824 PQYSNHKQLG----DKMDHSRNTPSPLNLSSASSKNSHTSSYTPNSFTSEDLQAEPLDL 879

HS zeb2 819 SLPKQMKEPKSIATKNTKASSISLDHNSVSSSSSENSDEPLNLTFI-KKEFS-----NS 872
 DR zeb2a 804 SLPKQVS-----KAERRAKFNGFSIEHTSNSTAREPGTEPLNLAHI-KKEFNGPNSLGN 856
 DR zeb2b 880 SLPKLMKEPKHILTVKSLRLKLSGPM DHHVATPREHADEPLNLAYLSKKEFGS---NA 936

HS zeb2 873 NNLDNKSTNPVFSMNPFSAKPLYTALPPQSAFPPTFMPPVQTSIPGLRPYPGLDQMSFL 932
 DR zeb2a 857 ENQMDKSSSPIFSINPFGGGMYSLSLPPHGAFFPPTFMSTTQASIPGLRPYPGLDPMMSFL 916
 DR zeb2b 937 NSNLDKSSSPMFGLNPF AAKPMYTSLSLPPQSAFPPTFMPPVQASLPGLRPYPSLDQISFL 996

HS zeb2 933 PHMAYTYPTGAATFADMQQRKYQRKQGFQGELL DGAQDYMSGLDDMTDSDSCLSRKKIK 992
 DR zeb2a 917 FPMAYTYAAGAA TFAEMQQRKYQRKQGFQGDLLDSAGDYLSGLEDLTDSESLARKKIK 976
 DR zeb2b 997 PHMAYTYAAGAA SFAEMQQRKYQRKFGFQSEL LDGFADYLSLDDMADPEACL SRKKIK 1056

HS zeb2	993	KTESGMYACDLCDKTFQKSSSLLRHKYEHTGKRPHQCQICKKAFKHKHHLIEHSRLHSGE	1052
DR zeb2a	977	KTESGMYACDLCDKTFQKSSSLLRHKYEHTGKRPHQCQICKKAFKHKHHLIEHSRLHSGE	1036
DR zeb2b	1057	KTESGMYACDLCDKTFQKSSSLLRHKYEHTGKRPHQCQICKKAFKHKHHLIEHSRLHSGE	1116
HS zeb2	1053	KPYQCDKCGKRF SHSGSY SQHMNHRY SYCKREA EEREAA EREAREKG - HLEPT ELLMNRA	1111
DR zeb2a	1037	KPYQCDKCGKRF SHSGSY SQHMNHRY SYCKREA EEREAA KQENHNNGGFLEPT ELLMRRA	1096
DR zeb2b	1117	KPYQCDKCGKRF SHSGSY SQHMNHRY SYCKREA EEREAA EREAREKG - HLEPT EMLLNRA	1175
HS zeb2	1112	YLQSIITPCGYSDSEE-RESMPRDGE---SEKEHEKEGEDGYGKLGRODGDDEFEFEFEFE	1166
DR zeb2a	1097	YLQGLGPLGFSDPEDCAEDITRENTILRDGTESGARETEETIYAEVTDROETGLMGEEEME	1156
DR zeb2b	1176	YLQGI GPAGYFEHPE-REFILRDALNG--SIRERLQEVFGAFVKMSRRE--HDFEFEFEDE	1230
HS zeb2	1167	SENKSMDDTDPETIRDEEET--GDHSMDDSSSEDGKMETKSDHEEDNMEDGM	1214
DR zeb2a	1157	GQRFDTTRSPDGTAKDEKSEVTGGTEDESS----EEGKRNHGGENEDAD-	1201
DR zeb2b	1231	SENK--STDGDTMRDEEEN--GEHSMDESS--KSESKSDH-EDAMEDGV	1272

Figure S2. Clustal sequence comparison of zebrafish *Zfhx1b* sequences with human. Deduced amino acid sequences are shown, with areas of homology shaded gray. Note the high degree of similarity between the isoforms in areas of homology, but that the homology between human (HS, *Homo sapiens*) zeb2 and zebrafish (DR, *Danio rerio*) zeb2b is higher than human compared to zebrafish zeb2a.