Supplementary Table. 1 Alignment of Notch1 homologs between Human and Zebrafish by Clustal Omega

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CLUSTAL O(1.2.4) multiple sequence alignment


Human   MPPLLAPLLCL-ALLPALAARGPRCSQPGETCLNGGKCEAA-NGTEACVCGGAFVGPRCQ   58
Zebra   MNRFLVKLTLTTAASLATVAQGQRC----SEYCQNGGICEYKPSGEASCRCPADFVGAQCQ   57
        *  : *. *  *   *.:* *:    *.*   .    *     *  :.* . *** :*:

Human   DPNPCLSTPCKNAGTCHVVDRRGVADYACSCALGFSGPLCLTPLDNACLTNPCRNGGTCD  118
Zebra   FPNPCNPSPCRNGGVCRPQMOGNEVGVKCDCVLGFSDRLCLTPVNHACMNSPCRNGGTCS  117
        .****  :*:*:*:.*    :  .  .  *.*.***  ****:.:.**:.*.*******.

Human   LLTLTEYKCRCPPGWSGKSCQQADPCASNPCANGGQCLPFEASYICHCPPSFHGPTCRQD  178
Zebra   LLTLDTFTCRCQPGWSGKTCQLADPCASNPCANGGQCSAFESHYICTCPPNFHGQTCRQD  177
        ****  : *** ******:** ************** .:*.: **.***.*** *****

Human   VNECGQKPGLCRHGGTCHNEVGSYRCVCRATHTGPNCERPYVPCSPSPCQNGGTCRPTGD  238
Zebra   VNECAVSPSPCRNGGTCINEVGSYLCRCPPEYTGPHCQRLYQPCLPSPCRSGGTCVQTSD  237
        ****   *. **.***  ***** * *  * *.**:*:* * * **  **:.****  *.*

Human   VTHECACLPGFTGQNCEENIDDCPGNNCKNGGACVDGVNTYNCRCPPEWTGQYCTEDVDE  296
Zebra   TTHTCSCLPGFTGQTCEHNVDDCTQHACENGGPCIDGINTYNCHCDKHWTGQYCTEDVDE  297
        .**.* ********.**:*:***   .*:***.* *.*:*****:*  .***********

Human   CQLMPNACQNGGTCHNTHGGYNCVCVNGWTGEDCSENIDDCASAACFHGATCHDRVASFY  358
Zebra   CELSPNACQNGGTCHNTIGGFHCVCVNGWTGDDCSENIDDCASAACSHGATCHDRVASFF  357
        *:* *************:**::*********:***************.***********:

Human   CECPHGRTGLLCHLNDACISNPCNEGSNCDTNPVNGKAICTCPSGYTGPACSQDVDECSL  418
Zebra   CECPHGRTGLLCHLDDACISNPCQKGSNCDTNPVSGKAICTCPPGYTGSACNQDIDECSL  417
        **************:********::*********.*********.****.**.**:****

Human   GANPCEHAGKCINTLGSFECQCLQGYTGPRCEIDVNECVSNPCQNDATCLDQIGEFQCIC  478
Zebra   GANPCEHGGRCLNTKGSFQCKCLQGYEGPRCEMDVNECKSNPCQNDATCLDQIGGFHCIC  477
        *******.*:* .** ::*:****** *****:*****.**************** *:***

Human   MPGYEGVHCEVNTDECASSPCLHNGRCLDKINEFQCECPTGFTGHLCQYDVDECASTPCK  538
Zebra   MPGYEGVFCQINSDDCASQPCL-NGKCIDKINSFHCECPKGFSGSLCQVDVDECASTPCK  536
        *******.*::*.*:***.***.*:* ****.*:****.**:*.****.***********

Human   NGAKCLDGPNTYTCVCTEGYTGTHCEVDIDECDPDPCHYGSCKDGVATFTCLCRPGYTGH  598
Zebra   NGAKCTDGPNKYTCECTPGFSGIHCELDINECASSPCHYGVCRDGVASFTCDCRPGYTGR  596
        ***** ****.*** ** *::* ***:**:**.. ***** *:****:***.*******:

Human   HCETNINECSSQPCRHGGTCQDRDNAYLCFCLKGTTGPNCEINLDDCASSPCDSGTCLDK  658
Zebra   LCETNINECLSQPCRNGGTCQDRENAYICTCPKGTTGVNCEINIDDCRKPCDYGKCIDK   656
        ******** *****:*******:***:* * *****.****** ***   **.*.* *:*

Human   IDGYECACEPGYTGSMCNININDECAGNPCHNGGTCEDGINGFTCRCPEGYHDPTCLSEVN  718
Zebra   INGYECVCEPGYSGSMCNININDDCALNPCHNGGTCIDGVNSFTCLCPDGFRDATCLSQHN  716
        *:****.*****.******* **:**.*********:**:*.***.**:*::* ****. *

Human   ECNSNPCVHGACRDSLNGYKCDCDPGWSGTNCDINNNECESNPCVNGGTCKDMTSGYVCT  778
Zebra   ECSSNPCIHGSCLDQINSYRCVCEAGWMGRNCDININECLSNPCVNGGTCKDMTSGYLCT  776
        **.****:**:* *. *.*:*.*:.** * ***:*.*** *****************:**

Human   CREGFSGPNCQTNINECASNPCLNQGTCIDDVAGYKCNCLLPYTGATCEVVLAPCAPSPC  838
Zebra   CRAGFSGPNCQMNINECASNPCLNQGSCIDDVAGFKCNCMLPYTGEVCENVLAPCSPRPC  836
        ** ********.**************.********:****:*****  **.*****:* **

Human   TQYRCECPSGWTGLYCDVPSVSCEVAAQRQGVDVARLCQHGGLCVDAGNTHHCRCQAGYT 1138
Zebra   ASFTCQCASGWTGIYCDVPSVSCEVAARQQGVSVAVLCRHAGQCVDAGNTHLCRCQAGYT 1136
        :.: *:* *****.************:::**::*.:** *.. :********:********

Human   GSYCEDLVDECSPSPCQNGATCTDYLGGYSCKCVAGYHGVNCSEEIDECLSHPCQNGGTC 1198
Zebra   GSYCQEQVDECQPNPCQNGATCTDYLGGYSCECVPGYHGMNCSKEINECLSQPCQNGGTC 1196
        ****:: ****.*.*.************.**:**.****:***:**:****:.********

Human   LDLPNTYKCSCPRGTQGVHCEINVDDCNPPVDPVSRSPKCFNNGTCVDQVGGYSCTCPPG 1258
Zebra   IDLVNTYKCSCPRGTQGVHCEIDIDDCSPSVDPLTGEPRCFNGGRCVDRVGGYGCVCPAG 1256
        :** ***************:**:::* .** .  ::**:* *** : **:*.:** **.*

Human   FVGERCEGDVNECLSNPCDARGTQNCVQRVNDFHCECRAGHTGRRCESVINGCKGKPCKN 1318
Zebra   FVGERCEGDVNECLSDPCDPSGSYNCVQLINDFRCECRTGYTGKRCETVFNGCKDTPCKN 1316
        ***************.***..*:.**** :***:****:*:**:***:*:.***. .***

Human   GGTCAVASNTARGFICKCPAGFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGPF 1378
Zebra   GGTCAVASNTKHGYICKCQPGYSGSSCEYDSQSCGSLRCRNGATCVSGHLSPRCLCAPGF 1376
        **********:.*:****. *::*::**.*::******* **.**:**  ** ***.  *

Human   TGPECQFPASSPCLGGNPCYNQGTCEPTSESPFYRCLCPAKFNGLLCHILDYSFGGGAGR 1438
Zebra   SGHECQTRMDSPCLV-NPCYNGGTCQPISDAPFYRCSCPANFNGLLCHILDYSFSGGQGR 1435
        :* *** .  ****: ***** ***:* *::*****.***:*************.** **

Human   DIPPPL-IEEACELPECQEDAGNKVCSLQCNNHACGWDGGDCSLNFNDPWKNCTQSLQCW 1497
Zebra   DIAPPVEVEIRCEIAQCEGRGGNAICDTQCNNHACGWDGGDCSLNFDDPWQNCSAALQCW 1495
        **.**: :*  **: :**  .**  *. ***************::***:**: :****

Human   KYFSDGHCDSQCNSAGCLFDGFDCQRAEGQCNPLYDQYCKDHFSDGHCDQGCNSAECEWD 1557
Zebra   RYFNDGKCDEQCATAGCLYDGFDCQRLEGQCNPLYDQYCRDHYADGHCDQGCNNAECEWD 1555
        :**.**:**.**.:****:******* ************:**::*******:*:******


Human   GLDCAEHVPERLAAGTLVVVVLMPPEQLRNSSFHFLRELSRVLHTNVVFKRDAHGQQMIF 1617
Zebra   GLDCADOVPQKLAVGSLVLVVHIPPDELRNRSSSFLRELSSLLHTNVVFRRDANGEALIF 1615
        *****: **::**.*:**:**::**::***.:*:.*****  **********:**.*  :*

Human   PYYGREEELRKHPIKRAAEGNAAPDALLGQVKASLLPGGSEGGRRRELDPMDVRGSIVY  1677
Zebra   PYYGSEHELSKHK----RSDWTDPGQLMQRARRSLTS--FLKPRTRRELDHMEVKGSIVY 1669
        ****.*:** .**    ..: *:*.*::: *  **:.    * *:.:***:**:***

Human   LEIDNRQCVQASSQCFQSATDVAAFLGALASLGSLNIPYKIEAVQSETVEPPPPAQLHFM 1737
Zebra   LEIDNRQCFQQSDECFQSATDVAAFLGALASSGNLNVPYIIEAVTSEGG-PPKTGEMYPM 1728
        ********.* :.:************** * *.:**:**:**** **   ** . *:: *

Human   YVAAAAFVLLFFVGCGVLLSRKRRRQHGQLWFPEGFKVSEASKKKRREPLGEDSVGLKPL 1797
Zebra   FLVLLALAVLALAAVGVVVSRKRKREHGQLWFPEGFKVNEP-KKKRREPVGEDSVGLKPL 1787
        ::*.  *:.:* *   *::.*****:*:**************.   *****.*********

Human   KNASDGALMDDNQNEWGDEDLETKKFRFEEPVVLPDLDDQTDHRQWTQQHLDAADLRMSA 1857
Zebra   KNS-DSSLMDEQLSEWAEDDT-NKRFRFEGQSIL-EMSGQLDHRQWTQQHLDAADLRLNS 1844
        **: :.**:::* .* :*: .**:*:*  : :* :**.*.****************:.*

Human   MAPTPPQGEVDADCMDVNVRGPDGFTPLMIASCSGGGLETGNSEEEED-APAVISDFIYQ 1916
Zebra   MAPTPPQGQIENDCMDVNVRGPDGFTPLMIASCSGGGLENENGEAEEDPSADVITDFIYH 1904
        ********:: :.*************************.*.: .*:.**. :*:**:****:

Human   GASLHNQTDRTGETALHLAARYSRSDAAKRLLEASADANIQDNMGRTPLHAAVSADAQGV 1976
Zebra   GANLHNQTDRTGETALHLAARYARSDAAKRLLESCADANVQDNMGRTPLHAAVAADAQGV 1964
        **.*******************:**********:.****:**************:******

Human   FQILIRNRATDLQARMHDGTTPLILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAA 2036
Zebra   FQILIRNRATDLQARMHDGTTPLILATRLAVEGMVEELINCHADPNAVDDSGKSALHWAA 2024
        *************************:********:*:***.*** *****.*********

Human   AVNNVDAAVVLLKNGANKDMQNNREETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2096
Zebra   AVNNVDAAVVLLKNGANKDLQNNKEETPLFLAAREGSYETAKVLLDHLANRDIADHLDQL 2084
        *******************:***:***********************:*****:**:*:*

Human   PRDIAQERMHHDIVRLLDEYNLVRSPQLHGAPLGGTPTLSPPLCSPNGYLGSLKPG---- 2152
Zebra   PRDIAHERMHHDIVRLLEEYNLVRSPPL---------PLSPPLCCPNTYLGIKPSPGNNN 2135
        *****:***********:********.*          :*****.**.***  *.

Human   VQGKKVRKPSSKGLACGSKEAKDLKARRKKSQDGKGCLLDSSGMLSPVDSLESPHGYLSD 2212
Zebra   NTAKKTRKPGGKGVG-GKDSGKDIRTKKKKSGDGKNGGIMEVGVLSPVDSLESPHGYLSD 2194
        . .***:***..**:  .*:.*:: : ::** ***:  :::.*:**************

Human   VASPPLLPSPFQQSPSVPLNHLPGMPDTHLGIGHLNVAAKPEMAALGGGGRLAFETGPPR 2272
Zebra   VSSPPMMTSPFQQSPPISLNQLQGLADSHMGGALQGLG------------KPF-DSAPR  2240
        *:***:::*******  :**:* * ::*:: * .   :            *   .*  *

Human   LSHLPVASGTSTVLGSSSGGALNFTVGGSTSLNGQCEWLSRLQSGMVPNQYNPLRGSVAP 2332
Zebra   LSHLPVANNVG----------------GAQAGACDWLQRVQQQQQQQQQQQAGMLMP    2282
        *******..           .  *: *:  :.   : *   :.

Human   GPLSTQAPSLQHGMVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQM 2392
Zebra   --------------------TMLSATNMPQVMGYPTMQSSHLGAPSHMIAHQNMAPMQH-- 2321
                            :*:: : *.*  :*:::* : :*:  *: :  *: * :

Human   QQQNLQPANIQQQQSLQPPPPPQPHLGVSSAASGHLGRSFLSGEPSQADVQPLGPSSLA  2452
Zebra   --QNIS---------------------H--------HFL-GDLSGLDLQS-SSGHAP    2345
          **:.                                 ** *: * *:*  .:

Human   VHTILPQESPALPTSLPSSLVPPVTAAQFLTPPSQHSYSSPVDNTPSHQLQVPEHPFLTP 2512
Zebra   IQTILPQDS--------QRMAPPISSTQFLTPPSQHSYSNPMDNTPNHQ-QVPDHPFLTP 2396
        ::*****:.        :::* *:::::***********.*:****.**  ***:******

Human   SPESPDQWSSSSPHSNVSDWSEGVSSPPTSMQSQIARIPEAFK  2555
Zebra   SAGSPDQWSSSSPHSNLSDWSEGISSPPTSMQ---MNHIPEAFK 2437
        *  **************:******:********   :*:******
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Supplementary Table. 2 Alignment of YTHDF2 homologs between Human and Zebrafish by Clustal Omega

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CLUSTAL O(1.2.4) multiple sequence alignment


Human       MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARPNNAYTAMSDSYLPSYY      60
Zebrafish   MSASSLLEQRPKGQANKVQNGAVTQKDTLNDDEFEPYLNAQPRQSNAYTAMSDSYMPSYY      60
            **************.******:* *** ****:****. * * .**********:****

Human       SPSIGFSYSLGEAAWSTGGDTAMPYLTSYGQLSNGEPHFLPDAMFGQPGALGSTPFLGQH     120
Zebrafish   SPSIGFTYSLNEAAWSTGGDPPMPYLASYGQLSNGEHHFLPDAMFGQSGALGNNPFLGQH     120
            ******:***_********* ****:********* ********** ****..******

Human       GFNFFPSGIDFSAWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFA-NETLNKA     179
Zebrafish   GFNFFPSGIDFPAWGNSSSQGQSTQSSGYSSSYAYAPSTLGGAMIDGQSPFAANEPLNKA     180
            *********** **** .*************** ******:********** ** ** ****

Human       PGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNIVASNSLPPATIAPPKPASW     239
Zebrafish   VGMNSLDQGMAGLKIGAGDMA----PKVVGSGLPGGPL-SQVSAAPTMPPASMAPAKTASW     236
             ***::*****_**:*: ::* ******.: _*_: *:: *: ::**::** * ***

Human       ADIASKPAKQQPKLKTKNGIAGSSLPPPPIKHNMDIGTWDNKGPVAKAP--SQALVQNIG     297
Zebrafish   ADIASKPAKPQPKLKTKGGLGGTNLPPPPIKHNMDIGTWDNKGNMPKPAAPQQTSLPTNG     296
            ********* ******* *:_*:_********************* : * _*: : _ *

Human       QPT-QGSPQPVGQQANNSPPVAQ------ASVGQQ-TQPLPP------PPPQPAQLSVQQ     343
Zebrafish   QPPNQSSPQPG-ATAGGVPQLPLSNGQLVPPTGQLVQHPLPPGGQPGAVPPQLSQGPPVS     355
            ** *.****   *.. * :        .** :**** *** :*    .

Human       QAAQPTRWVAPRNRGSGFGHNGV-DGNGVGQSQAGSGSTPSEPHPVLEKLRSINNYNPKD     402
Zebrafish   QPSQPTRWVPPRNRANGFGDAAGGPGQSPPNSGMGGITVPAEPHPVLEKLRMVNNYNPKD     415
            * :****** ****.._***_.   *:. :* *. :.*:********** :*******

Human       FDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNKRLDAAYRSMNGKGPVYLLFSVN     462
Zebrafish   FDWNPKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNKRLDAAYRSLANKGPPYLLFSVN     475
            **** ***********************************:_.*** *******

Human       GSGHFCGVAEMKSAVDYNTCAGVWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKP     522
Zebrafish   GSGHFCGVAEMRSPVDYNTCAGVWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKP     535
            ***********:* **********************************************

Human       VTNSRDTQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQEEEESVKKERQGRGK---     579
Zebrafish   VTNSRDTQEVPLDKARQVLKIIASYKHTTSIFDDFSHYEKRQEEEESVKKVTCHGLAPSG     595
            ************:**:********************************** *

Human       -     579
Zebrafish   I     596
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