

Figure S4

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ct-h10R1      V-IIFFAFVLLLSGALAYCLALQLYVRRRKKLPSVLLFKKPSPFIFISQRSPETQDTIH
ct-zCRFB7     IGVIGVGVITL-----FMLFVCF FLRRPGKMPAVLKLAVNGWL-----PMNVGQTEVE
               :*..*:*   :*:::** **:*:* :  :   *  *  :.

ct-h10R1      PLDEEAF-----KVSPELKNLD-----LHGSTDDSGFG-----STKPSLQTEEPQ
ct-zCRFB7     SVTQKGWLLNSNKIAEKTAFDEI EELSEDEKERRESTDSGVSIGQQDSIKNRPQREEDS
               .: :.:*  *:: : * :*      : *****.  * *  * * .

ct-h10R1      FLLPDPHPQADRTLGNR---EPPVL--GDSCSSGSSNSTDSGICLQEPSPSPSTGTWEQ
ct-zCRFB7     GCGLTGTEDSLSSGRRSLEE LPF LDGGGSSSVEGTREDSGLGIQTQDISDKPKPM---
               . . . . : * *  * * * * * . . . . .  ***: : *  . : * . . *

ct-h10R1      QVGSNSRGQDSDGLVQNSE GRA GDTQGGGALGHHSPPEPEVPGVEEDPAAVAFQGYLR-
ct-zCRFB7     -----HDDLLEIVVIGDGYR SQSPSAEA-----ETETTIQCDEDANMVSRTNGYRS
               :*  ::*  .:*  .: . . . *  . * . : : * . * : . *

ct-h10R1      -QTRCAEEKATKTGCLEESPLTDGLPKFGRCLVDEAGLHPPALAKGYLKQDPLEMTLA
ct-zCRFB7     GQVTCLCSDSETCMWCKTRKHLTD CDSFSHKQTVNDND-----RSSYLKKSPLETVNM
               * . * . . . .   : . .  *** . . . : : * :   . . *** . *** .

ct-h10R1      SS GAPTGWQNPTEEWSLLALSSC SDLGISDWSFAHDLAPLGCVAAPGLLGSFNSDLVT
ct-zCRFB7     FGLDDLSCHSKTEESSLF-----ITCPLLLKEPYKLD--T
               . . . . : * * * * * :   : : * *  . : : * *

ct-h10R1      LPLISSLQSSE----
ct-zCRFB7     LPL--TLGDVELTFT
               *** : * . *

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Figure S4: Two DSG motifs similar to those found in human IL-10R1 can be identified in the zebrafish ortholog of IL-10R1. Alignment of the cytoplasmic tail of hIL-10R1 (ct-h10R1) and zebrafish CRFB7 (ct-zCRFB7) is done using the online MAFFT program [1]. The alignment is shown in ClustalW format. The '*'s denote identical amino acid residues; ':'s denote conserved amino acid substitutions and '.'s denote semi-conserved amino acid substitutions. The two conserved DSG motifs were highlighted in yellow and blue, respectively.

1. Katoh, K., K. Misawa, K. Kuma, and T. Miyata. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research* 30: 3059-3066.