```
TCF4-K   MVTLVQHSFSNSAHSLDVYSITFLVDWHLCGQRNNTMFSKRLEKIAQVPLLFPFIFIILTNYSKMEGAVESQPSFFKTSQDIVTCTWVENCYSSFSRRPLEMESHSVIQTGVQWHHLSSLQPP
TCF4-J   MVTLVQHSFSNSAHSLDVYSITFLVDWHLCGQRNNTMFSKRLEKIAQVPLLFPFIFIILTNYSKMEGAVESQPSFFKTSQDIVTCTWVENCYSSFSRRPLEQMFCKHQSKNIISWTGMVAHTC
TCF4-L                                                                                                            MESHSVIQTGVQWHHLSSLQPP

                                  AD1
                                  _____________________________________________________________________________________________
TCF4-K   PPRFKLSSCLSLLSTRDRRLCDFAKMHHQQRMAALGTDKELSDLLDFSAMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-J   NPSTLGGQG----------LCDFAKMHHQQRMAALGTDKELSDLLDFSAMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-L   PPRFKLSSCLSLLSTRDRRLCDFAKMHHQQRMAALGTDKELSDLLDFSAMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-B                            MHHQQRMAALGTDKELSDLLDFSAMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-E                              MQRAKTELFRLQIVTDDLRKNEMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-M                        MRASKGSEGCQHAVTSQLVTGAGGDQTEMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-O                                    MLEREGVKERVRMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-P                                     MEMDIATFMAKMFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-C                                                    MFSPPVSSGKNGPTSLASGHFTGSNVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-N                                                         MLKMFFRISQVAGSSWYSKDVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-F                                                                    MEEDSRDVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-R                                                                     MSIFENVEDRSSSGSWGNGGHPSPSRNYGDGTPYDHMTSRDLGSHDNLSPPFVNS
TCF4-Q                                                                                                               MTSRDLGSHDNLSPPFVNS
TCF4-G                                                                                                      MKDIFFQFIIARVRKCYSLSCLHTLPVV

                                     1                               NLS                         2
                                                                     ______________________
TCF4     RIQSKTERGSYSSYGRESNLQGCHQ{[Q]SLLGGDMDMGNPGTLSPTKPGSQYYQYSSNNPRRRPLHSSAMEVQTKKVRKVPPGLPSS}VYAPSASTADYNRDSPGYPSSKPATSTFPSSFFMQDGH
TCF4-G   PTLRKTERGSYSSYGRESNLQGCHQ{[Q]SLLGGDMDMGNPGTLSPTKPGSQYYQYSSNNPRRRPLHSSAMEVQTKKVRKVPPGLPSS}VYAPSASTADYNRDSPGYPSSKPATSTFPSSFFMQDGH
TCF4-D                                      MDMGNPGTLSPTKPGSQYYQYSSNNPRRRPLHSSAMEVQTKKVRKVPPGLPSS}VYAPSASTADYNRDSPGYPSSKPATSTFPSSFFMQDGH
TCF4-A                                                                            MYCAYTIPGMGGNSLMYYYNGKAVYAPSASTADYNRDSPGYPSSKPATSTFPSSFFMQDGH
TCF4-H                                                                            MKFKQCRCSDTGLCCLDHEGKAEVYAPSASTADYNRDSPGYPSSKPATSTFPSSFFMQDGH
TCF4-I                                                                                                                                   MQDGH

                                                                                                                            AD2
                                                                                                                            ________
TCF4     HSSDPWSSSSGMNQPGYAGMLGNSSHIPQSSSYCSLHPHERLSYPSHSSADINSSLPPMSTFHRSGTNHYSTSSCTPPANGTDSIMANRGSGAAGSSQTGDALGKALASIYSPDHTNNSFSSN

                       3
         ________________________________________________________________
TCF4     PSTPVGSPPSLS[A]GTAVWSRNGGQASSSPNYEGPLHSLQSRIEDRLERLDDAIHVLRNHAVGPSTAMPGGHGDMHGIIGPSHNGAMGGLGSGYGTGLLSANRHSLMVGTHREDGVALRGSHSL

                                                                                            4                 bHLH
                                                                                                              ________________________
TCF4     LPNQVPVPQLPVQSATSPDLNPPQDPYRGMPPGLQGQSVSSGSSEIKSDDEGDENLQDTKSSEDKKLDDDKKDIKSIT[RSRS]SNNDDEDLTPEQKAEREKERRMANNARERLRVRDINEAFKE

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TCF4     LGRMVQLHLKSDKPQTKLLILHQAVAVILSLEQQVRERNLNPKAACLKRREEEKVSSEPPPLSLAGPHPGMGDASNHMGQM
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Supporting Figure S1. Alignment of TCF4 isoforms. Amino acids different from the consensus are in blue, localization of functional domains is indicated with lines above the sequence. Amino acid(s) in parentheses are absent from (1) isoforms coded by transcripts spliced at acceptor II of exon 8, (2) Δ isoforms coded by transcripts without exons 8-9, (3) isoforms coded by transcripts spliced at acceptor II of exon 15, (4) – isoforms (as opposed to + isoforms) coded by transcripts spliced at donor I of exon 18. AD, activation domain; NLS, nuclear localization signal; bHLH, basic helix-loop-helix domain.