

Erratum 1.

The following text replaces section 4.4 on page 62

4.4. *COHI* promoter region (unpublished)

The CpGProD program (Ponger and Mouchiroud, 2001), designed to predict promoters associated with CpG islands, was used in the prediction of a potential transcription regulating region 5'-upstream of the *COHI* coding sequence. In humans a GC-rich promoter region was observed to start 1,310 nucleotides upstream from the *COHI* translation start codon, covering 1,498 nucleotides downstream. The strength of the prediction was moderate with a start-p value of 0.31. It is known that 50%-60% of human genes display a CpG island over the transcription start site (Ponger and Mouchiroud, 2001). In the corresponding mouse and rat genome sequences, good start-p values of 0.57 and 0.53 for the GC-rich promoter region was predicted starting 1162 and 1179 nucleotides upstream from the putative *COHI* translation start codon.

Three conserved putative transcription factor (TF) binding sites (ELK1, ETS1P54, and NRF2) in human, mouse and rat were observed with the MATCH program (<http://www.gene-regulation.com/pub/programs.html#match>). These overlap in the genomic region upstream of the *COHI* translation start codon (Figure 9). *ELK1* (Rao et al., 1989) belongs to the *ETS* gene family (Watson et al., 1988), of which the ETS1 family comprises proteins encoding nuclear phosphoproteins (Li et al., 2000). The ETS proteins are transcription factors that interact with purine rich promoter/enhancer region sequences of genes (Karim et al., 1990). Characteristically, proteins regulated by ETS transcription factors do not possess typical transcription regulating "TATA" or "GAAT" elements (Mavrothalassitis et al., 1990; Jorcyk et al., 1991), which holds true also for the *COHI* gene promoter region. In general, ETS proteins are associated with processes of cell growth control, embryological development and hematopoietic differentiation (Hromas and Klemsz, 1994; Seth et al., 1992; Crepieux et al., 1994).

Erratum 2.

Chapter 2.1 on page 49, line 20, the correct sentence is: The translation start codon resides in the second exon and the full-length transcript predicts a 4,022 amino acid protein.