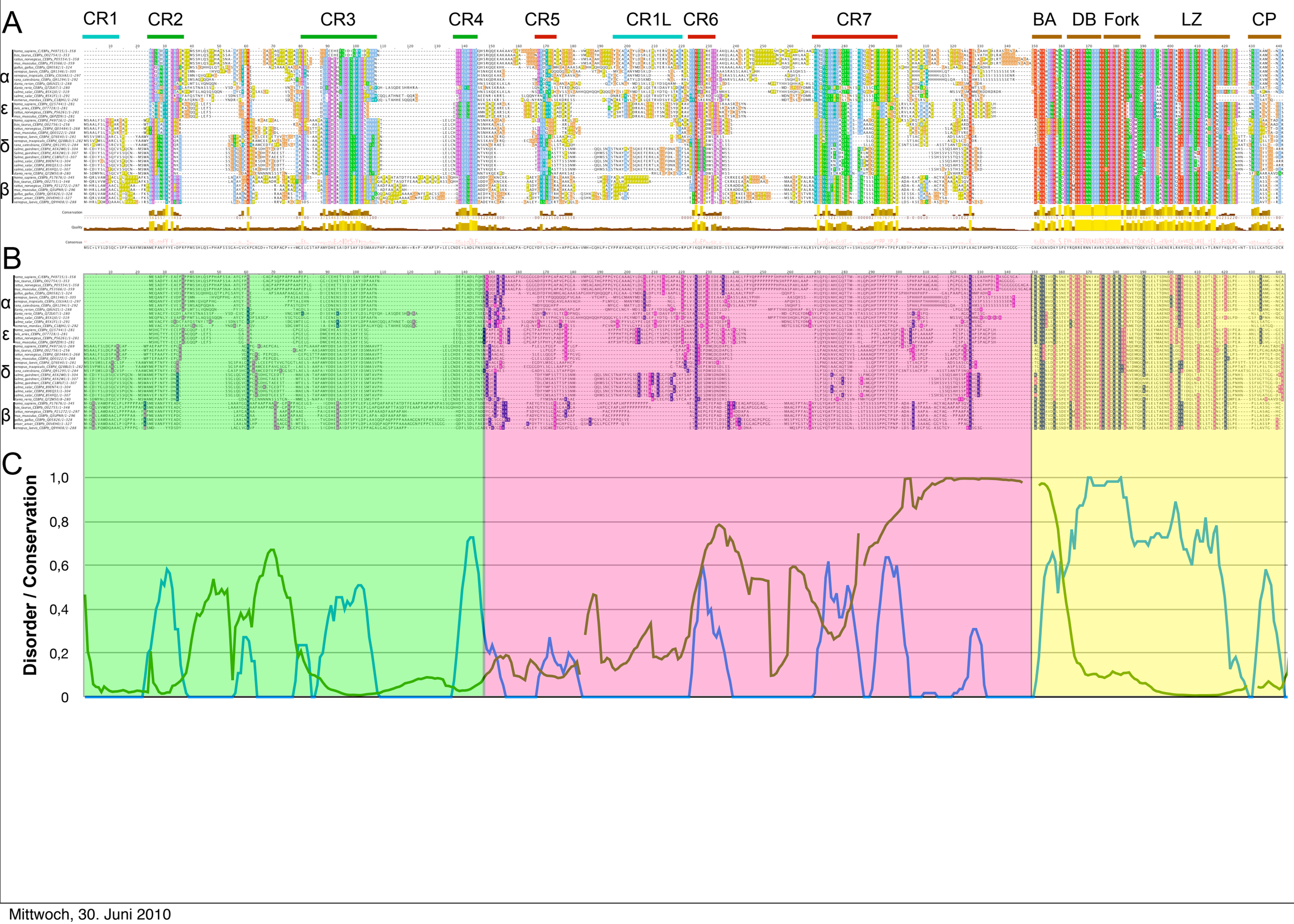
A
CR1
CR2
CR3
CR4
CR5
CR1L
CR6
CR7
BA
DB
Fork
LZ
CP
α
ε
δ
β
Conservation
Quality
Consensus
B
C
Disorder / Conservation
1,0
0,8
0,6
0,4
0,2
0

Supplementary Figure 1: Alignment of C/EBPα,β,δ,ε from vertebrates.

A. C/EBPα,ε,δ,β from various species as indicated on the left. C/EBP alignments in Jalview were manually curated and coloring indicates conservation of amino acid residues. Conserved regions (CR) are indicated on the top. CR1 (turquoise) is contained in C/EBPβ and C/EBPδ and a functionally similar region (CR1 like; CR1L) has been identified in C/EBPα. The bZip region consists of a pre-bZip basic/acidic (BA) region, the DNA binding region (DB), a fork region (Fork), the leucine zipper (LZ) and a post-bZip C-terminal peptide (CP). Underneath: Conservation, quality lines, and consensus, according to Jalview (http://www.jalview.org/) (magnification of Figure to 400% recommended).
B. Same alignment as shown in A with arginine and lysine residues highlighted in magenta and blue, respectively. Transactivation domain (green shading) regulatory domain (red shading) and bZip domain (yellow shading), as determined in C/EBPβ, are indicated in accordance to Figure 1 and 2.
C. Conservation and disorder profile for the Multiple Alignment. The normalized relative conservation values derived from the alignment were smoothed for clarity using a window of size 5 (-2..+2; blue line). Disorder predictions (probabilities, ranging from 0 to 1) for human C/EBPα,β,δ,ε were obtained from DisoPred (http://bioinf.cs.ucl.ac.uk/disopred/) and the average was plotted (green line). Gaps in the disorder profile result from alignment positions. Although generally conservation and disorder show opposing trends, there are several conserved positions inside disordered regions important for C/EBP function.