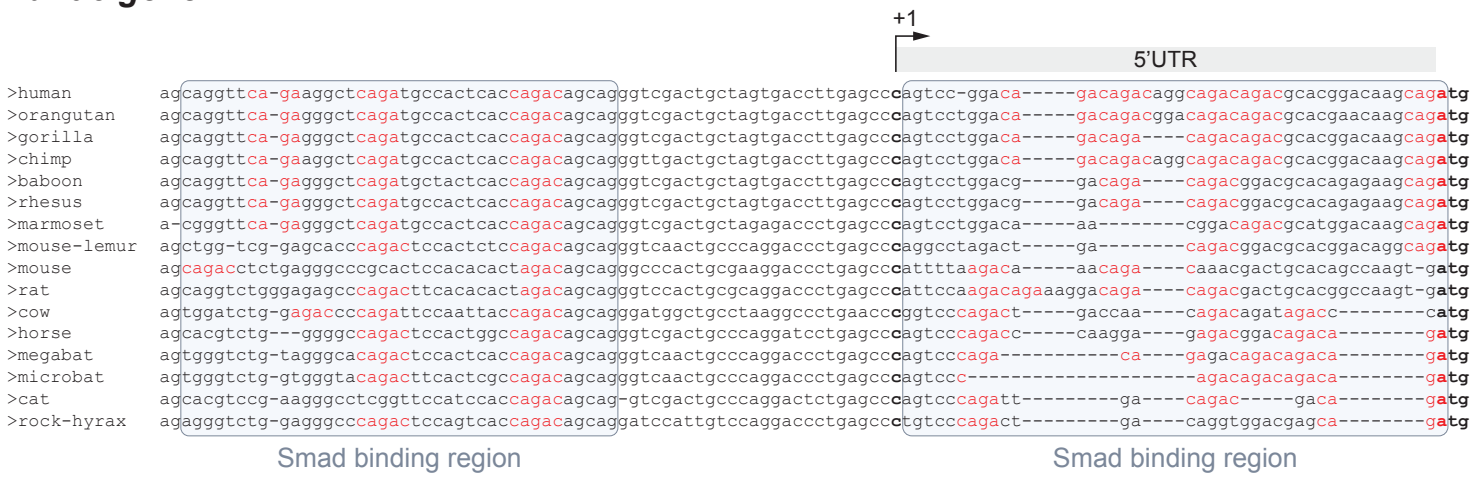
Supplemental_Fig_S4

Dand5 gene



Supplemental_Fig_S4. Distribution of putative Smad2/3 binding sites in 5' of the mammalian *Dand5* gene. Clustal alignment of the sequence surrounding the transcription start site (+1) of the mammalian *Dand5* gene. The two conserved Smad binding regions have been predicted by the Contra V3 server (http://bioit2.irc.ugent.be/contra/v3/#/step/1) (Kreft et al., 2017). The Smad3 binding sites CAGAC are highlighted in red.