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Cover An illustration of putative transcriptional regulatory regions (pTRRs) that are conserved in different clades (primates, placental mammals, or all vertebrates). The figure shows a plethora of signals from ENCODE experiments, including transcription (Affy RNA HeLa), protein–DNA interactions (UCD E2F1, UCD C-Myc, UT Myc HeLa, UT Myc st-Fb, UT E2F4 Fb, RFBR Clusters), chromatin interactions and accessibility (FAIRE Signal, HeLa DNase I), and evolutionary constraint (Moderate Constraint, Weak Constraint), for a portion of ENCODE region ENm012 located on human chromosome 7. The phylogenetic tree shows the species used for the ENCODE sequence comparisons. In the background, is a collection of tracks from the UCSC Genome Browser for a portion of ENCODE region ENm005 located on human chromosome 21. (Cover illustration by George Asimenos, with concept and design contributions from Aarron Willingham, Darryl Leja, Ross Hardison, James Taylor, Elliott Margulies, Philipp Kapranov, and Thomas Gingeras. All species pictures (except human) were originally drawn by Juan Montoya-Burgos. [For details and related work, see Margulies et al., pp. 760–774; King et al., pp. 775–786; Denoeud et al., pp. 746–759; Zhang et al., pp. 787–797; Jin et al., pp. 807–817; Giresi et al., pp. 877–885; Bhinge et al., pp. 910–916; and Thurman et al., pp. 917–927.]