



**Figure 22.** The epigenomic landscape is very large. (A) The epigenomic characterization of a 700-kb chromatin region in a lymphoblastoid human cell line (GM12878). Annotated genes are indicated on *top* and signal tracks for open chromatin (blue), histone modifications (red), and CTCF/RNA Pol II (green) are shown. (B) In addition to the DNA sequence, the definition of an “epigenome” requires analysis of the chromatin structure and RNA output (*y*-axis) in a given cell type (*x*-axis) under defined differentiation and environmental conditions (gray shaded area). Thus, the analysis of epigenomes is much more complex than the description of the DNA sequence in one genome. (A, Adapted from ENCODE Project Consortium 2012; B, IHEC Steering Committee, pers. comm.)