



Figure 25. An extended gene concept. An average mammalian gene spans a region of ~50 kb and consists of several alternative promoters (P₁, P₂, P₅), 7–8 exons, and 6–7 introns. Genome-wide RNA sequencing (RNA-seq) indicates that many “classic genes” are embedded within larger regions of transcriptional activity. In addition to the gene locus giving rise to the primary RNA transcript (mRNA), the “extended gene” concept integrates these neighboring regions (spanning >300 kb) that produce ncRNAs (e.g., eRNAs, miRNAs, lncRNAs). Several of these ncRNAs have been described to modulate the expression of the primary RNA transcript by either the recruitment of stimulating (mediator) or repressive protein complexes (Polycomb).