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Interrogating RNA heterogeneity

The unfolding of the instructions encoded in the genome is triggered by the transcription of DNA into RNA, and the subsequent processing of the resulting primary RNA transcripts into functional mature RNAs. RNA is thus the first phenotype of the genome, mediating all other phenotypic changes at the organism level caused by changes in the DNA sequence. While current technology is too primitive to provide accurate measurements of the RNA content of the cell, the recent development of Massively Parallel Sequencing Instruments has dramatically increased the resolution with which we can monitor cellular RNA. Using these instruments, the ENCODE project has surveyed the RNA content of multiple cell lines and subcellular compartments. The results of these surveys underscore pervasive transcription, as well as great RNA heterogeneity between and within cells. Comparison of RNA surveys with other genome wide epigenetic surveys—such as those of binding sites for Transcription Factors, or of Histone modifications—reveals a very tightly coupling between the different pathways involved in RNA processing, transcription and splicing in particular.