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(57) Abstract: Provided are methods of labeling and analyzing features along at least one macro molecule such as a linear biopolymer, including methods of mapping the distribution and frequency of specific sequence motifs or the chemical or proteomic modification state of such sequence motifs along individual unfolded nucleic acid molecules. The present invention also provides methods of identifying signature patterns of sequence or epigenetic variations along such labeled macro molecules for direct massive parallel single molecule level analysis. The present invention also provides systems suitable for high throughput analysis of such labeled macro molecules.

