METHODS AND SYSTEMS FOR ANALYZING NUCLEIC ACID MOLECULES

ABSTRACT

The disclosure provides methods for processing nucleic acid populations containing different forms (e.g., RNA and DNA, single-stranded or double-stranded) and/or extents of modification (e.g., cytosine methylation, association with proteins). These methods accommodate multiple forms and/or modifications of nucleic acid in a sample, such that sequence information can be obtained for multiple forms. The methods also preserve the identity of multiple forms or modified states through processing and analysis, such that analysis of sequence can be combined with epigenetic analysis.

Fig. 1