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(54) Title: METHODS AND SYSTEMS FOR DETECTING CANCER VIA NUCLEIC ACID METHYLATION ANALYSIS

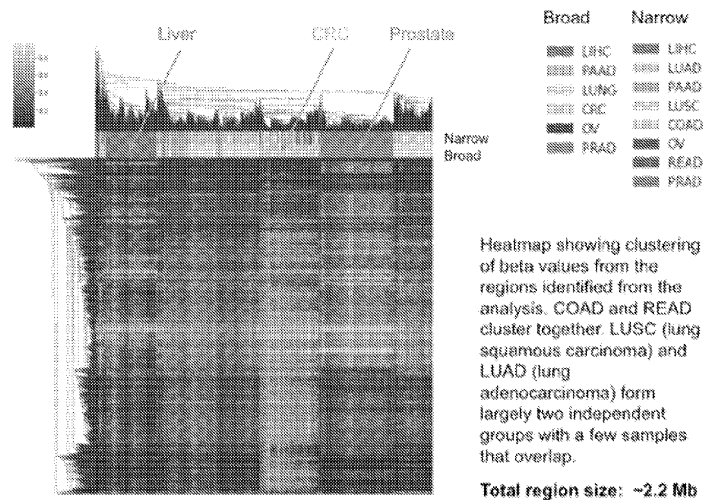


FIG. 2

(57) Abstract: The present disclosure provides methods and systems for screening or detecting a tumor or following disease progression that may be applied to cell-free nucleic acids, such as cell-free DNA. The method may use detection of methylation signals within a single sequencing read in identified genomic regions as input features to train a machine learning model and generate a classifier useful for stratifying populations of individuals. The method may comprise extracting DNA from a cell-free sample obtained from a subject, converting the DNA for methylation sequencing, generating sequencing reads, detecting proliferative cell disorder-associated signals in the sequencing information, and training a machine learning model to provide a discriminator capable of distinguishing groups in a subject population such as healthy, cancer, or distinguishing disease subtype or stage. The method may be used for, e.g., predicting, prognosticating, and/or monitoring response to treatment, tumor load, relapse, or cancer development.

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