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TilingScan: an application for the identification of differentially expressed DNA regions in Tiling Microarray data

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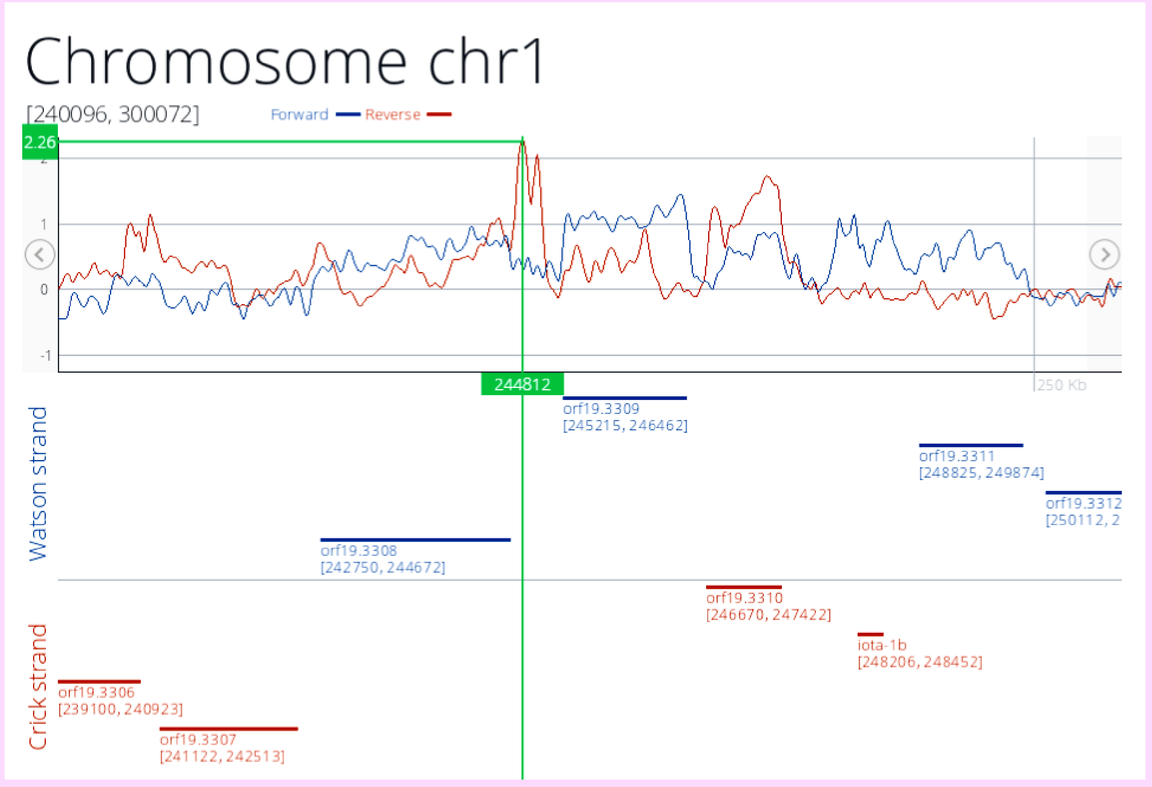
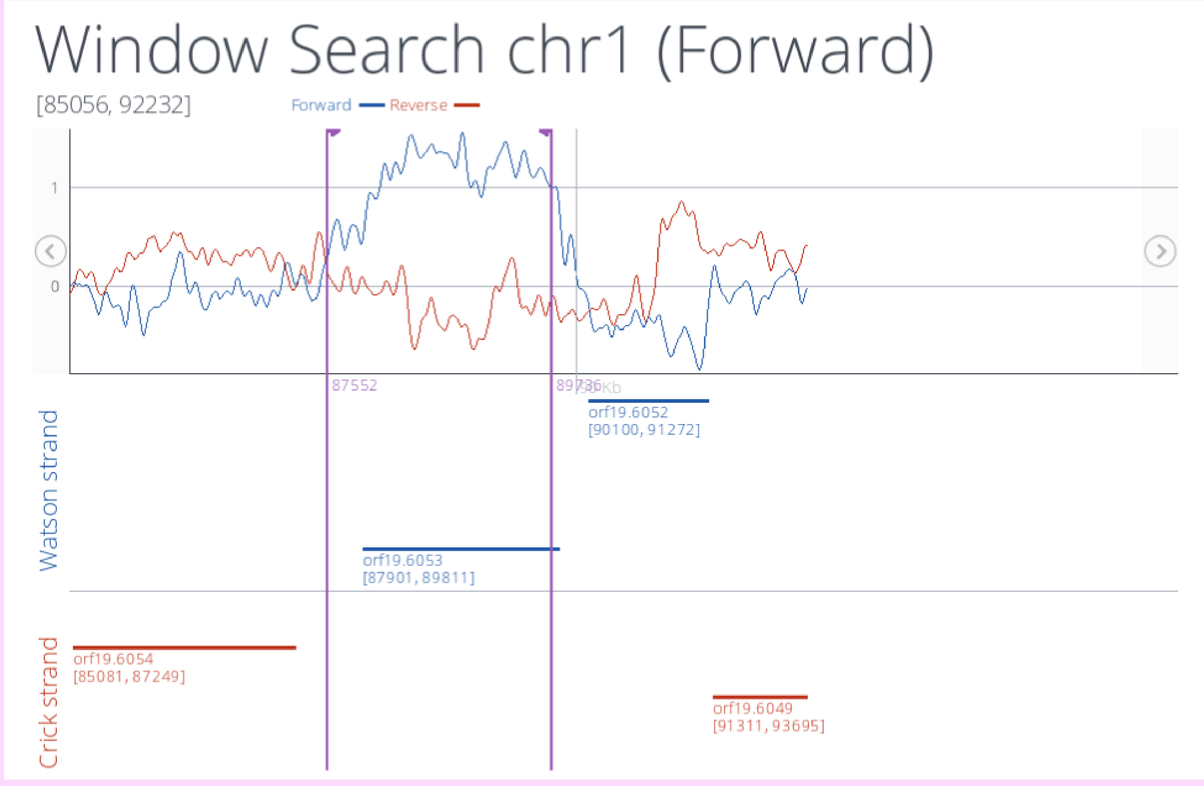
INTRODUCTION

Genomic technologies allow laboratories to produce large-scale data sets, either through the use of next-generation sequencing or microarray platforms. To explore these data sets and obtain maximum value from the data, researchers view their results alongside all the known features of a given reference genome. To study transcriptional changes that occur under a given condition, researchers search for regions of the genome that are differentially expressed between different experimental conditions. In order to identify these regions several algorithms have been developed over the years, along with some bioinformatic platforms that enable their use. However, currently available applications for comparative microarray analysis exclusively focus on changes in gene expression within known transcribed regions of predicted protein-coding genes, the changes that occur in non-predictable genetic elements, such as non-coding RNAs.

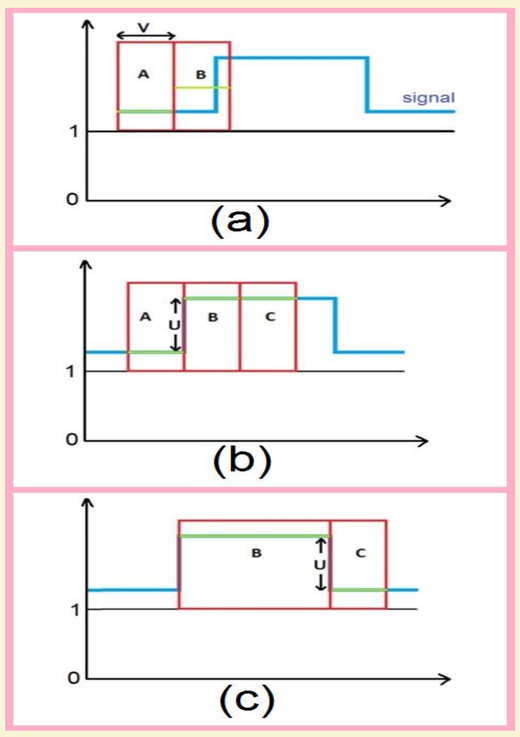
WEB APPLICATION: http://tilingscan.uv.es/

We present a web application for the visualization of strand-specific tiling microarray or next-generation sequencing data that allows customized detection of differentially expressed regions all along the genome in an unspecific manner, that allows identification of all RNA sequences, predictable or not.





DESCRIPTION OF THE SEARCH ALGORITHM



a) At the beginning of the data set, two windows are defined, “A” and “B”, both of the selected size “V”.

b) For each window, the average intensity value (fold-change) of the probes contained within them is calculated. These two windows will slide along the data set, until the difference between the average value of A and the average value of B surpasses the fold-change threshold “U”.

c) When this happens, the start point of a region will be defined from the first point of B. To determine the end point of the region of change, a new window (C), of fixed size = V will be created adjacent to the end of B. The comparison between B and C will be repeated in the same way, extending window B until the difference between B and C is equal to the selected threshold (U). This will determine the length of the detected region.

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