small RNA-Seq

genomatix

Small RNA expression and novel microRNAs

Detecting known small RNAs

To detect known small RNAs Genomatix has developed an approach to map reads to our small RNA library without the need for prior linker removal. Usually linker removal is needed, because small RNAs are in most cases shorter than the sequenced read length. Typical microRNAs, for example, are about 21-23 bps long. The Genomatix mapper automatically detects these linkers and removes them, even without prior knowledge of the linker sequence. Our small RNA library is a comprehensive compilation from sources like mirBase, Rfam and snoRNAbase.

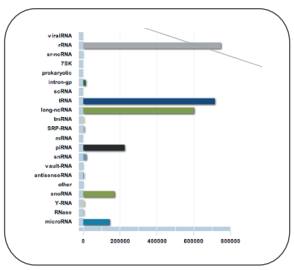
Detection of novel microRNAs

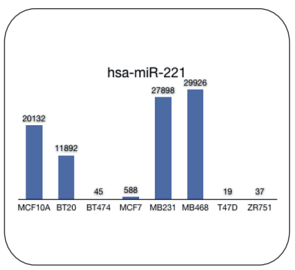
For predicting novel microRNAs we provide the package miRDeep (Friedländer et al. Nature Biotechnology 2008). The reads are mapped to the genome to obtain all unique and multiple hits. For microRNAs multiple hits are often biologically relevant, since they can occur in multiple copies in the genome. After mapping the reads, novel microRNAs are predicted using miRDeep and an extensive report is generated.

Biological insight

The role of small RNAs has been elucidated in many recent publications. These publications can help to shed light on the effect of differentially expressed small RNAs. We provide tools to extract relevant publications that allow linking microRNAs to genes, tissues or diseases. In addition, our pathway tool (GePS) can be used to generate microRNA networks, for example by interconnecting them with transcription factors.

workflow





mapping | visualization | expression | prediction | literature

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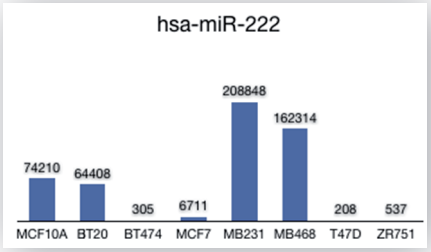
Genomatix visualization and user interface

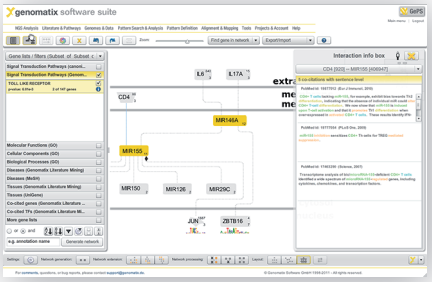
Mapping

The Genomatix mapping approach allows the user to map small RNA data either to our small RNA library or to the genome. After mapping to the small RNA library an overview of the results is provided (see left) and results can be exported for further analyses. After mapping to the genome miRDeep can be run to predict novel microRNAs.



Expression analysis

After mapping, the expression of small RNAs can be investigated under different conditions. To the left you can see the expression of hsa-miR-222 in eight different breast cancer cell lines, with very low expression in all ER+ cell lines.



Genomatix Pathway System (GePS)

GePS allows to perform enrichment analysis for microRNAs, and is capable of generating literature based networks linking microRNAs and coding genes. For each connection the PubMed ids and relevant sentences from the publications are provided.

mapping statistics small RNA

library	genome library	small RNA library
BT-20	77%	60%
BT-474	74%	66%
MCF-7	76%	74%
MCF-10A	83%	77%

Mapping statistics

Mapping statistics of four breast cancer cell lines. The reads are mapped to the genome and small RNA library. For mapping to the genome library linkers are removed dynamically before mapping each read. For mapping to the small RNA library no linker removal is required at all, since the Genomatix mapper can implicitly detect linkers.

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About us

Genomatix is one of the world's leading suppliers of technologies to analyze and interpret genomic data. As well as laying the groundwork for microarray experiments and NGS data sequencing analyses, our hardware and software solutions help answer the typical questions posed by systems biology. Our approach: combine multiple lines of evidence to perform an integrated meta-analysis.