NGS, microarray and bioinformatics services for research and industry

iMir: An innovative and complete pipeline for smallRNA-Seq data analysis

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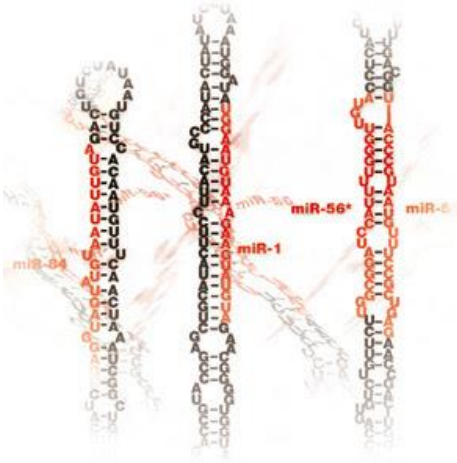
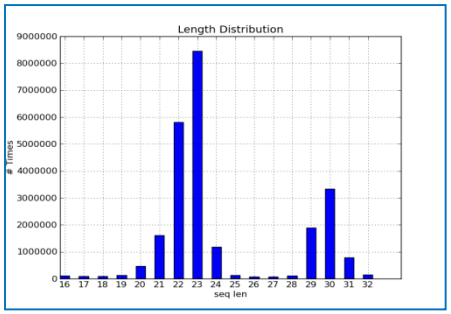
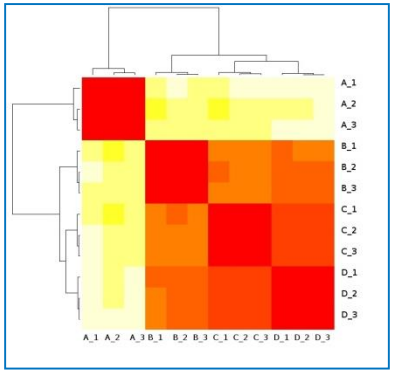
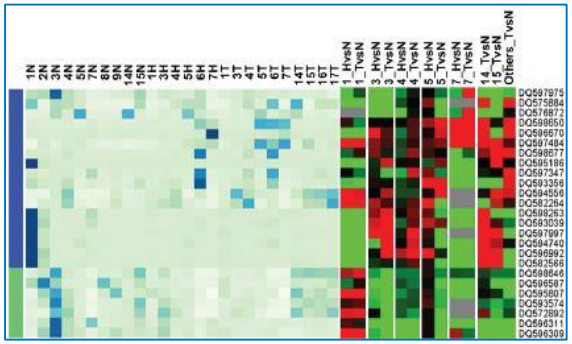
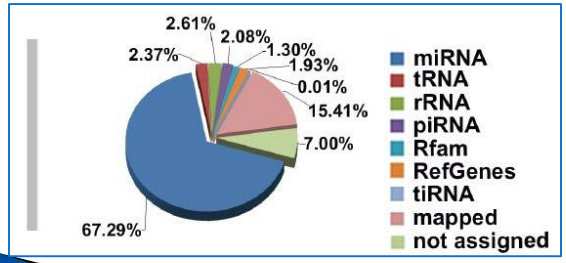
smallRNA-Seq

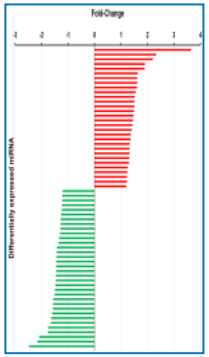


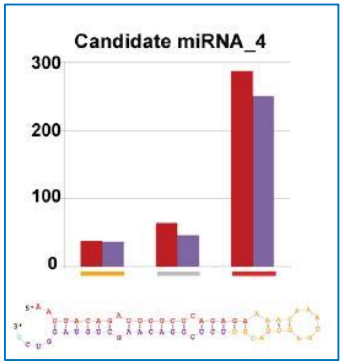




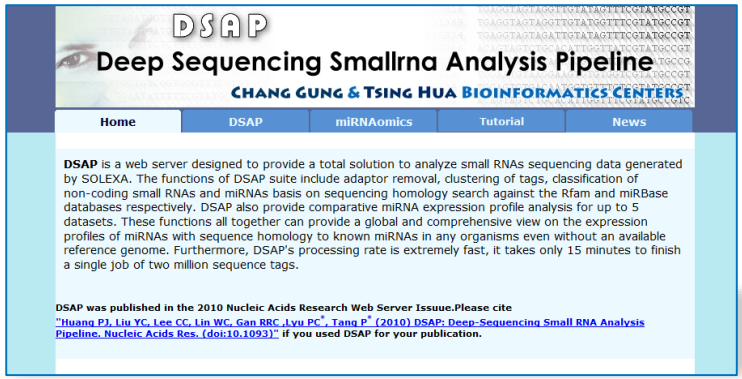


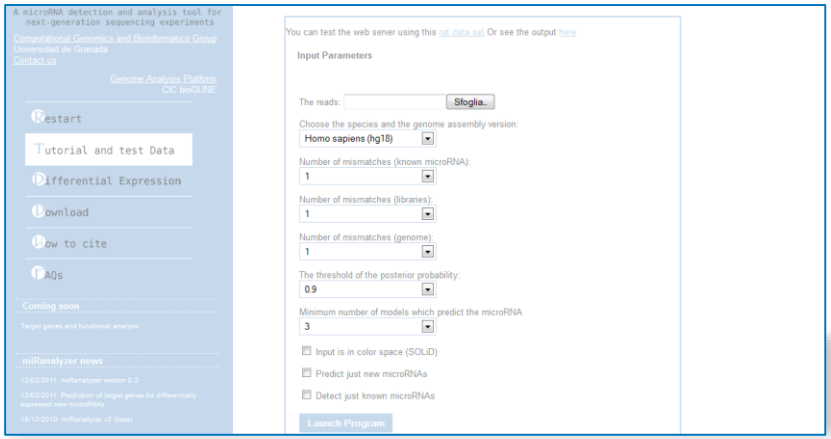






Bioinformatics Tools for sncRNA-Seq data analysis
Web-based tools





Williamson V et al., Brief Bioinform. 2013 Jan;14(1):36-45.

Bioinformatics Tools for sncRNA-Seq data analysis
Stand-alone tools

Williamson V et al., Brief Bioinform. 2013 Jan;14(1):36-45.

Modular pipeline for comprehensive analysis of sncRNA-Seq data.

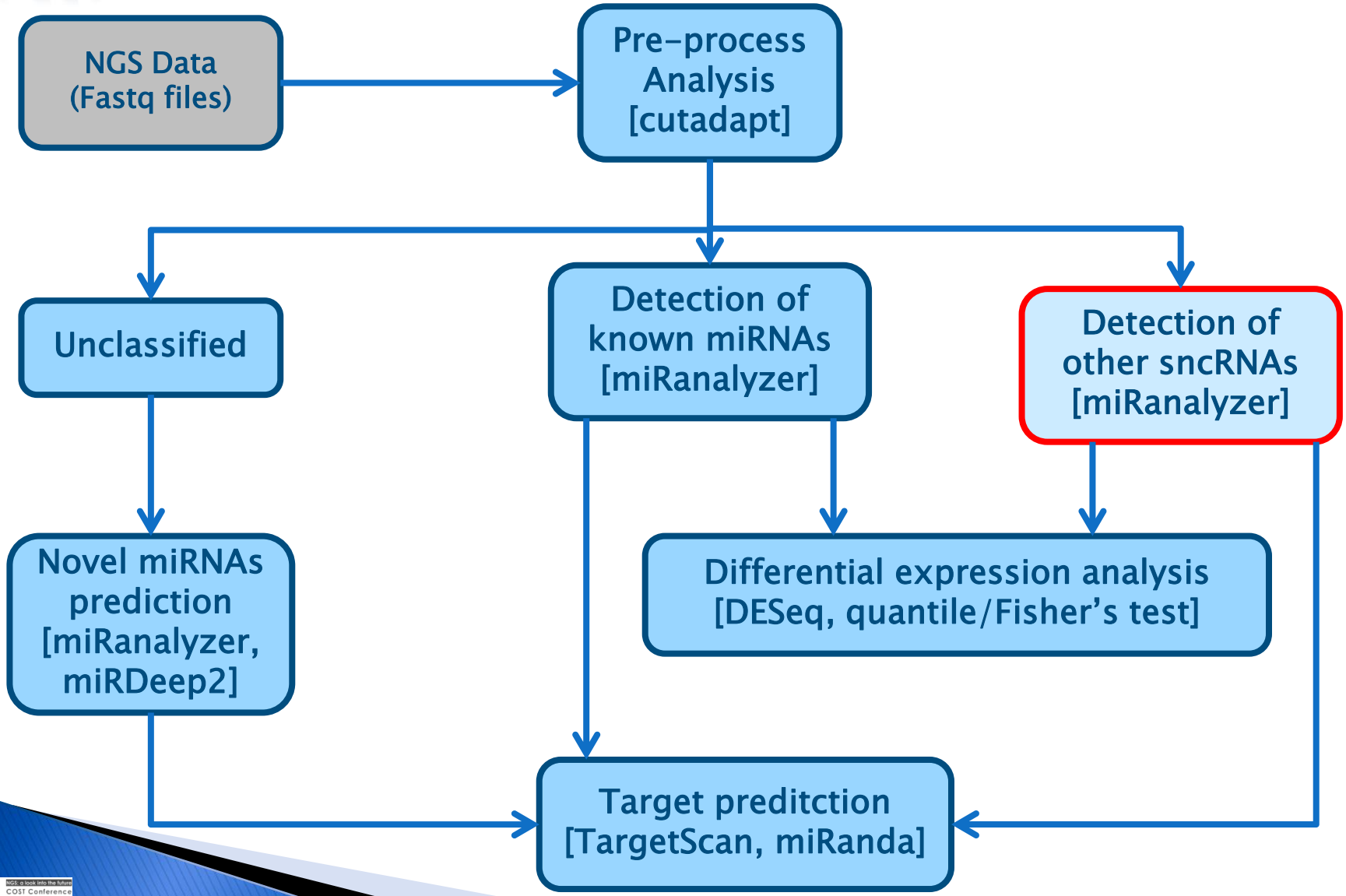
Multiple open source modules and resources linked together in automated flow

Graphical User Interface (GUI) to create projects and specify parameters

The pipeline output includes graphics and text files that are useful for a better interpretation of the results

iMir
Integrated pipeline for HT miRNA-Seq data analysis

Workflow scheme



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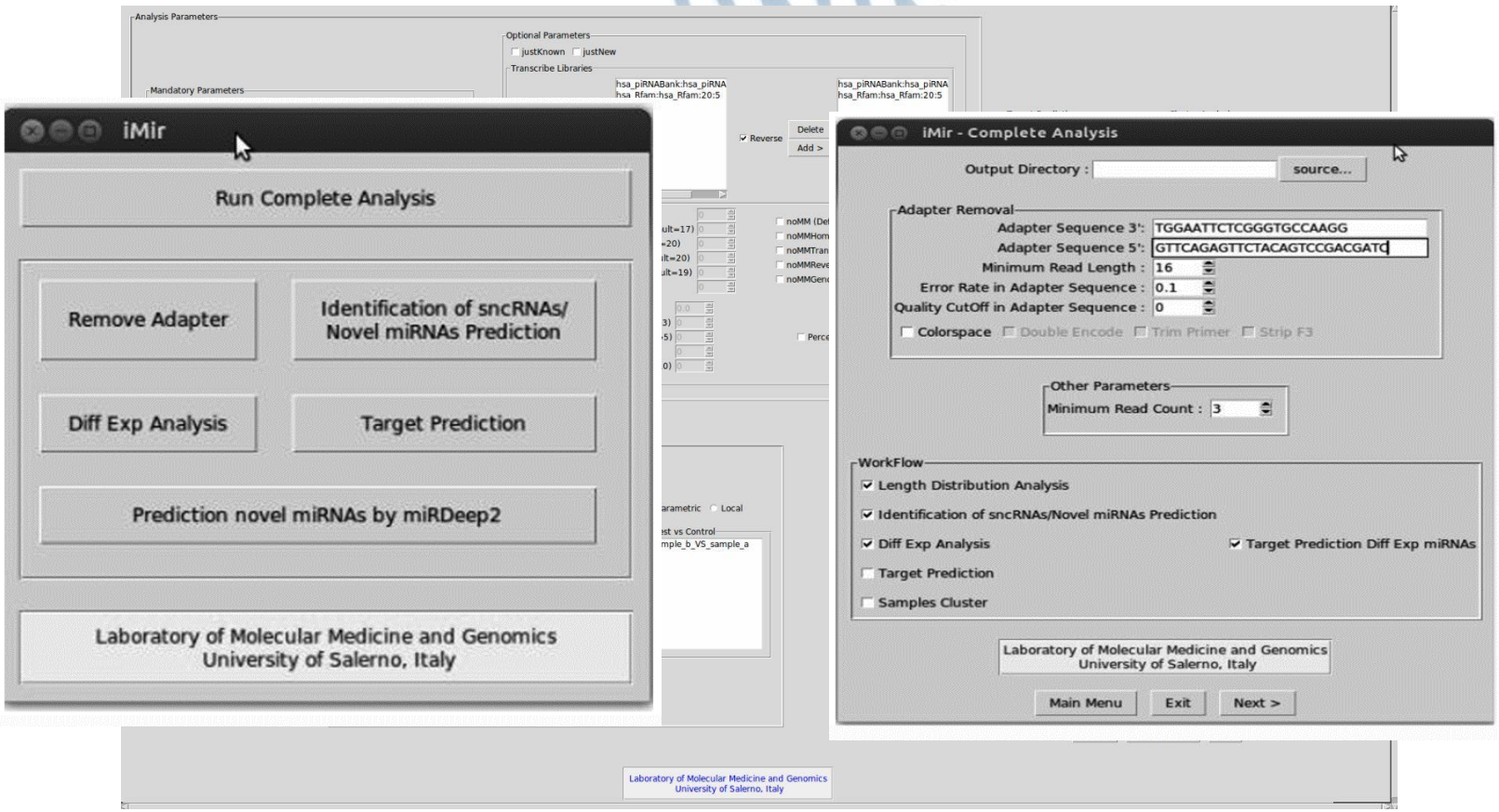
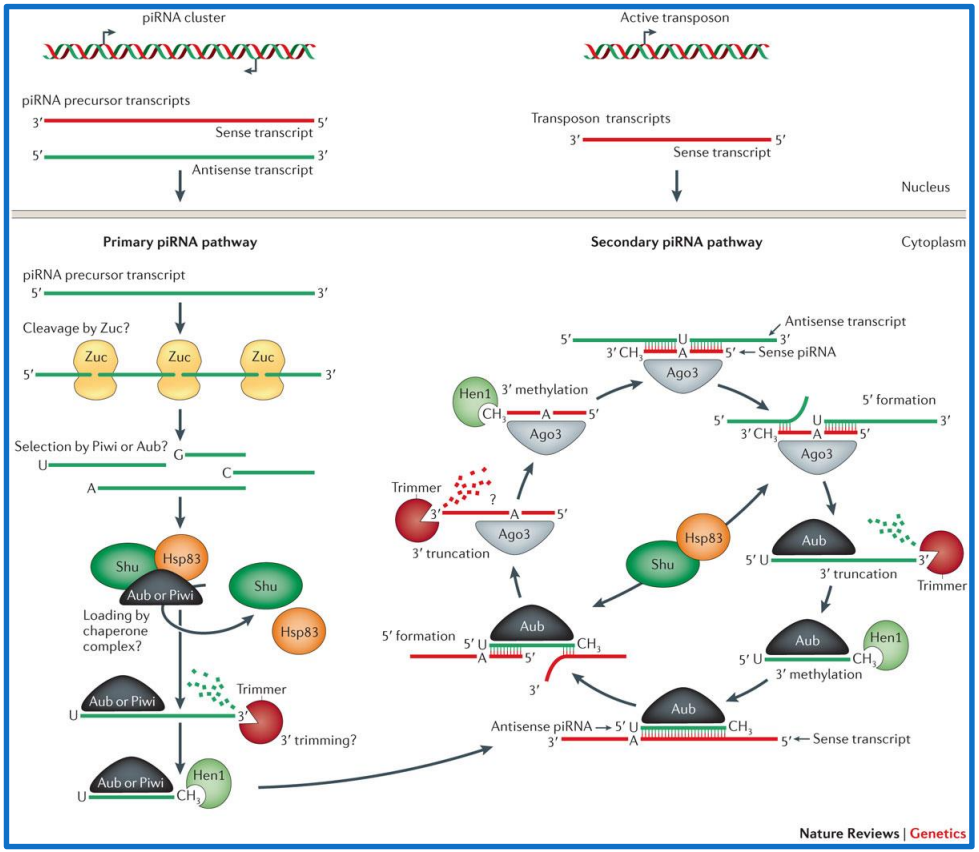
Integrated pipeline for HT miRNA-Seq data analysis



piRNAs biogenesis

- **The recent discovery of major class of sncRNAs initially identified in the germline of a variety of species, called PIWI-interacting RNA (piRNA), raised questions concerning their biogenesis and functions.**
- **piRNAs are frequently encoded by genes clustered in intergenic regions of the genome and have defined characteristics:**
  - **an average length of 24-35 nt,**
  - **a strong preference for uracil at the 5'-end and 2'-O-methylation of the 3' base,**
  - **high sequence diversity.**
- **They are generated by an intricate pathway conserved in evolution, comprising primary processing and amplification loops ('ping-pong' cycles) and are known to be involved in germline development, silencing of selfish DNA elements and maintenance of germline DNA integrity.**
- **Recent evidences suggest that the Piwi/piRNA pathway may be functionally active also in somatic tissues, but this possibility has not yet been fully explored.**



HEPATOLOGY
Official Journal of the American Association for the Study of Liver Diseases

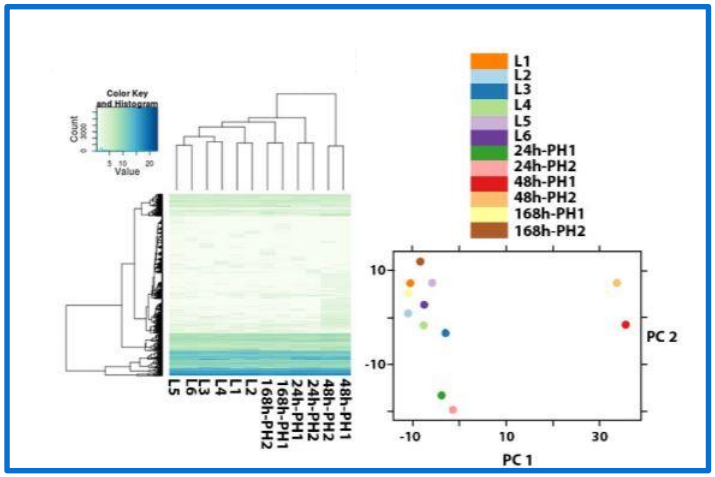
RAPID COMMUNICATION

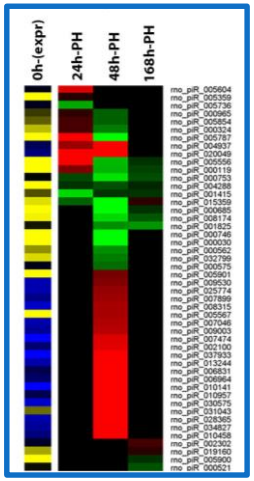
Timed Regulation of P-Element-Induced Wimpy Testis–Interacting RNA Expression During Rat Liver Regeneration

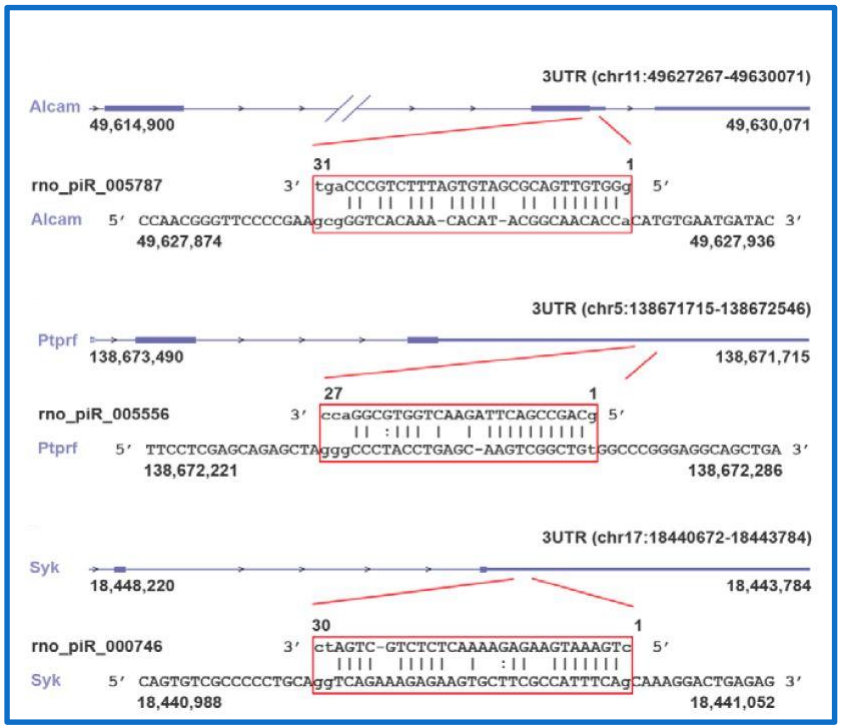
Francesca Rizzo,[1*] Adnan Hashim,[1*] Giovanna Marchese,[1] Maria Ravo,[1] Roberta Tarallo,[1] Giovanni Nassa,[1] Giorgio Giurato,[1] Antonio Rinaldi,[1] Angela Cordella,[2] Marcello Persico,[3] Pia Sulas,[4] Andrea Perra,[4] Giovanna M. Ledda-Columbano,[4] Amedeo Columbano,[4] and Alessandro Weisz[1]

•We investigated piRNAs expression in rat liver and its response to the stimuli exerted by regenerative proliferation of this organ.

• RNA sequencing before, during and after the wave of cell proliferation that follows partial hepatectomy identified ~1400 mammalian germline piRNAs expressed, including 72 showing timed changes in expression 24-48 hours post-PH.







Rizzo et al., Hepatology. 2014 Sep;60(3):798-806.

www.impactjournals.com/oncotarget/ Oncotarget, Vol. 5, No. 20

RNA sequencing identifies specific PIWI-interacting small non-coding RNA expression patterns in breast cancer

Adnan Hashim[1,*], Francesca Rizzo[1,*], Giovanna Marchese[1], Maria Ravo[1], Roberta Tarallo[1], Giovanni Nassa[1], Giorgio Giurato[1], Gianluca Santamaria[1], Angela Cordella[2], Concita Cantarella[3] and Alessandro Weisz[1,4]

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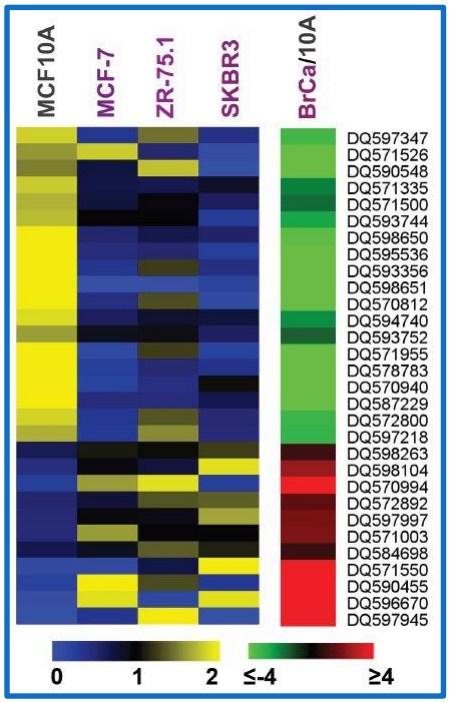
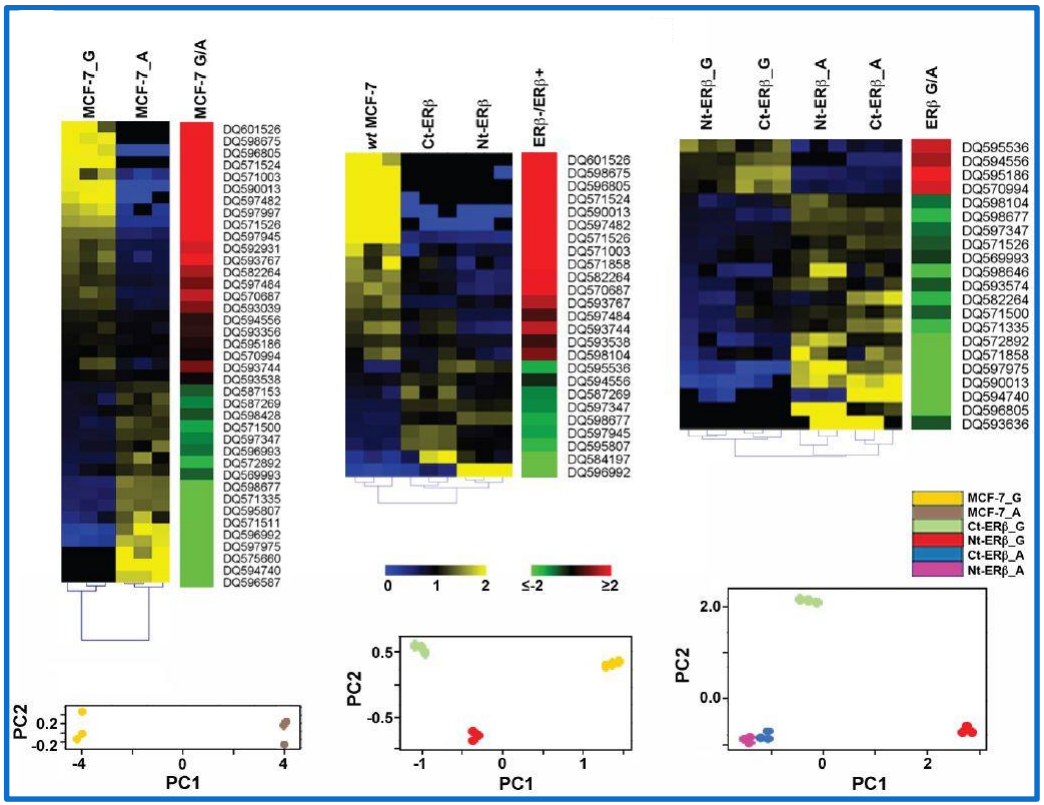
[3] Consiglio per la Ricerca e la Sperimentazione in Agricoltura, Centro di Ricerca per l'Orticoltura, Pontecagnano, SA, Italy

[4] Division of Molecular Pathology and Medical Genomics, 'SS. Giovanni di Dio e Ruggi d'Aragona' Hospital, University of Salerno, Salerno, Italy

•We found that piRNA biogenesis and effector pathway are present in human breast cancer cell lines and tumor biopsies.

• We identified > 100 BC piRNAs, including some very abundant and/or differentially expressed in mammary epithelial compared to BC cells, where these were influenced by estrogen or estrogen receptor β.





Hashim et al., Oncotarget. 2014 Oct 30;5(20):9901-10

www.impactjournals.com/oncotarget/ Oncotarget, Advance Publications 2015

Small non-coding RNA deregulation in endometrial carcinogenesis

Maria Ravo[1], Angela Cordella[2], Antonio Rinaldi[1], Giuseppina Bruno[1], Elena Alexandrova[1,3], Pasquale Saggese[1], Giovanni Nassa[1], Giorgio Giurato[1], Roberta Tarallo[1], Giovanna Marchese[1,3], Francesca Rizzo[1], Claudia Stellato[1], Rossella Biancardi[4], Jacopo Troisi[4], Attilio Di Spiezio Sardo[5], Fulvio Zullo[5], Alessandro Weisz[1,6], Maurizio Guida[4]

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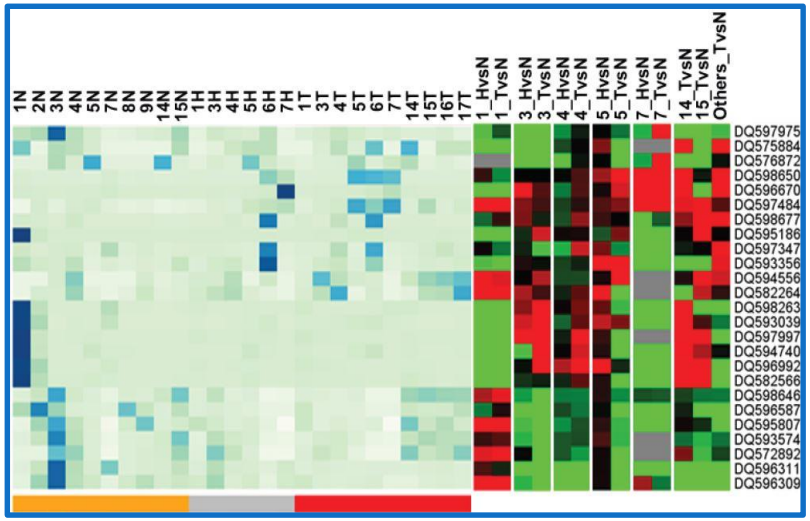
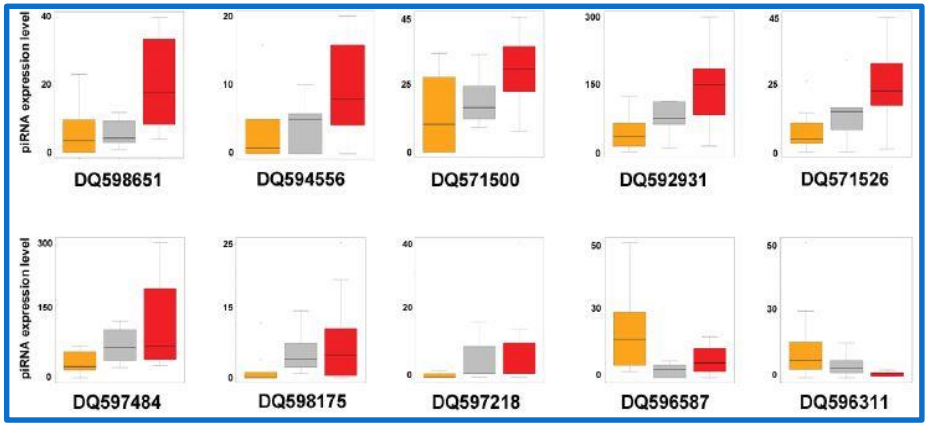
- Changes in sncRNA expression were identified by high-throughput genomic analysis of paired normal,hyperplastic and cancerous endometrial tissues,

- This led to the definition of a sncRNA signature of neoplastic trasformation.

- Considering the regulatory role of sncRNAs, this newly identified signature is likely to reflect the events leading to endometrial cancer





Normal (N)
Hyperplastic (H)
Tumoral (T)

Ravo et al., Oncotarget. 2015

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http://www.labmedmolge.unisa.it/inglese/research/imir

Acknowledgements

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Giovanna Marchese