Master's Project

Identification of lincRNA as predictive biomarkers in locally advanced breast cancer mexican patients by transcriptome analysis

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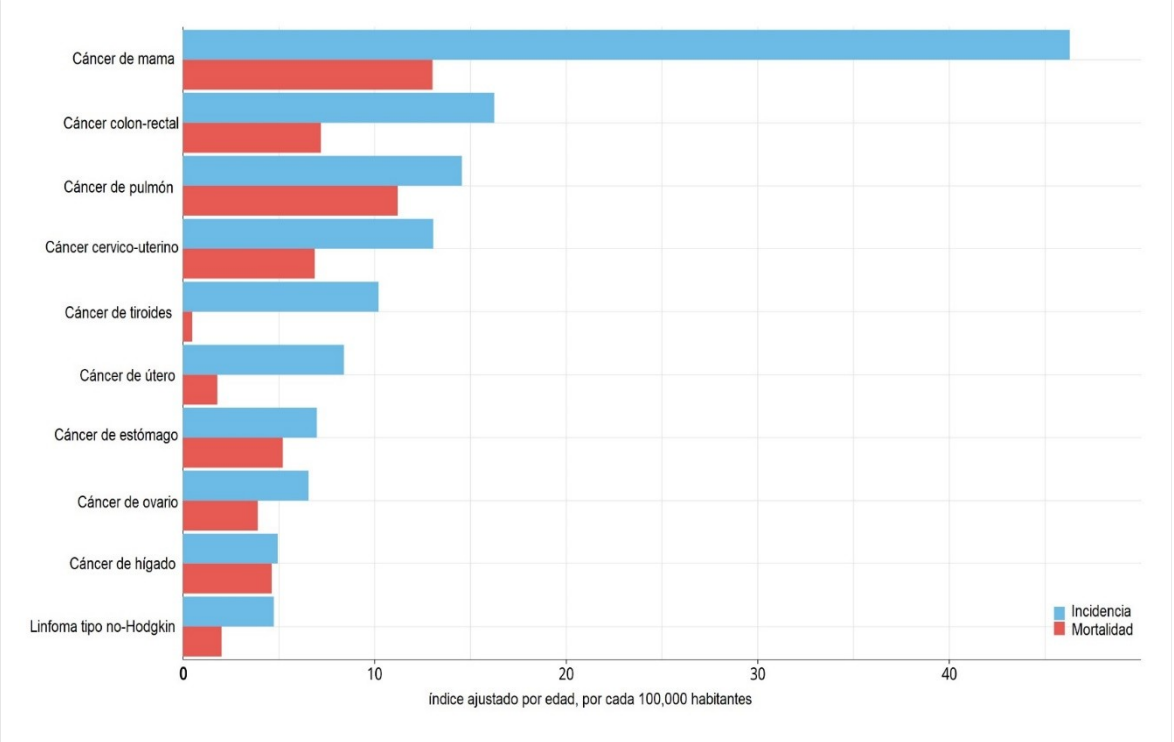
Breast cancer is health problem in Mexico

- Principal malignant neoplasia in women (Worldwide)



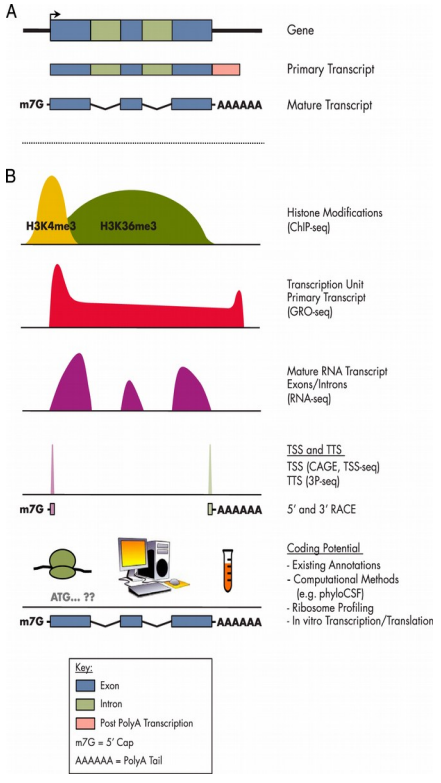
Genetic signatures improve diagnosis in breast cancer

- Gene set analysis for prognosis diagnosis and treatment improvement, but not predictive.

LncRNA are important regulators in cell processes

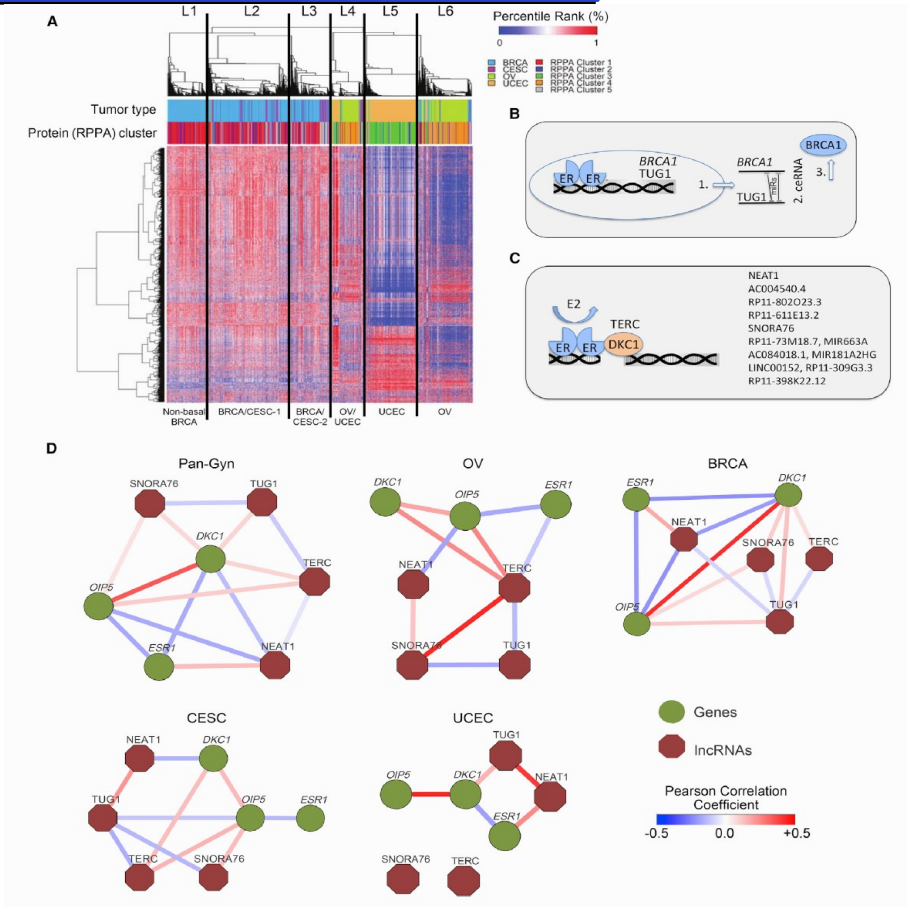
- Transcripts > 200 bp

  with non coding potential
- Regulatory functions
- Genomic position Classification
  - LincRNA
    - Intergenic regions



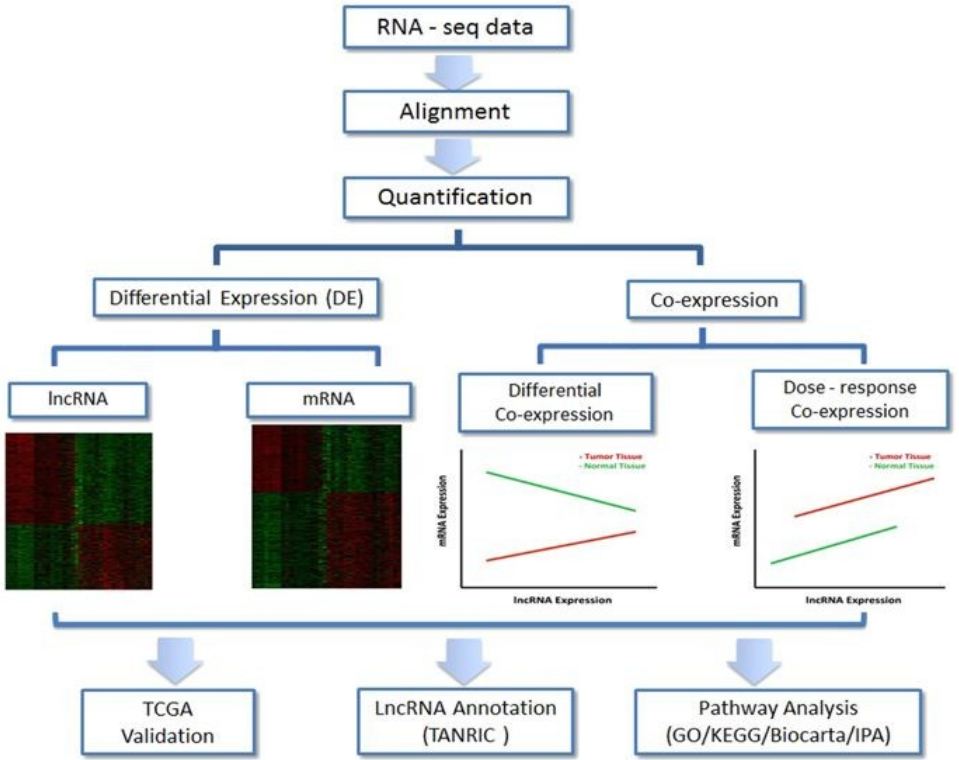
LincRNA are disregulated in breast cancer

- Particular expression profiles



RNA-Seq improves lincRNA identification in breast cancer

- Transcriptome analysis
- Only annotation.
  - The vast majority of lincRNA are not caracterized



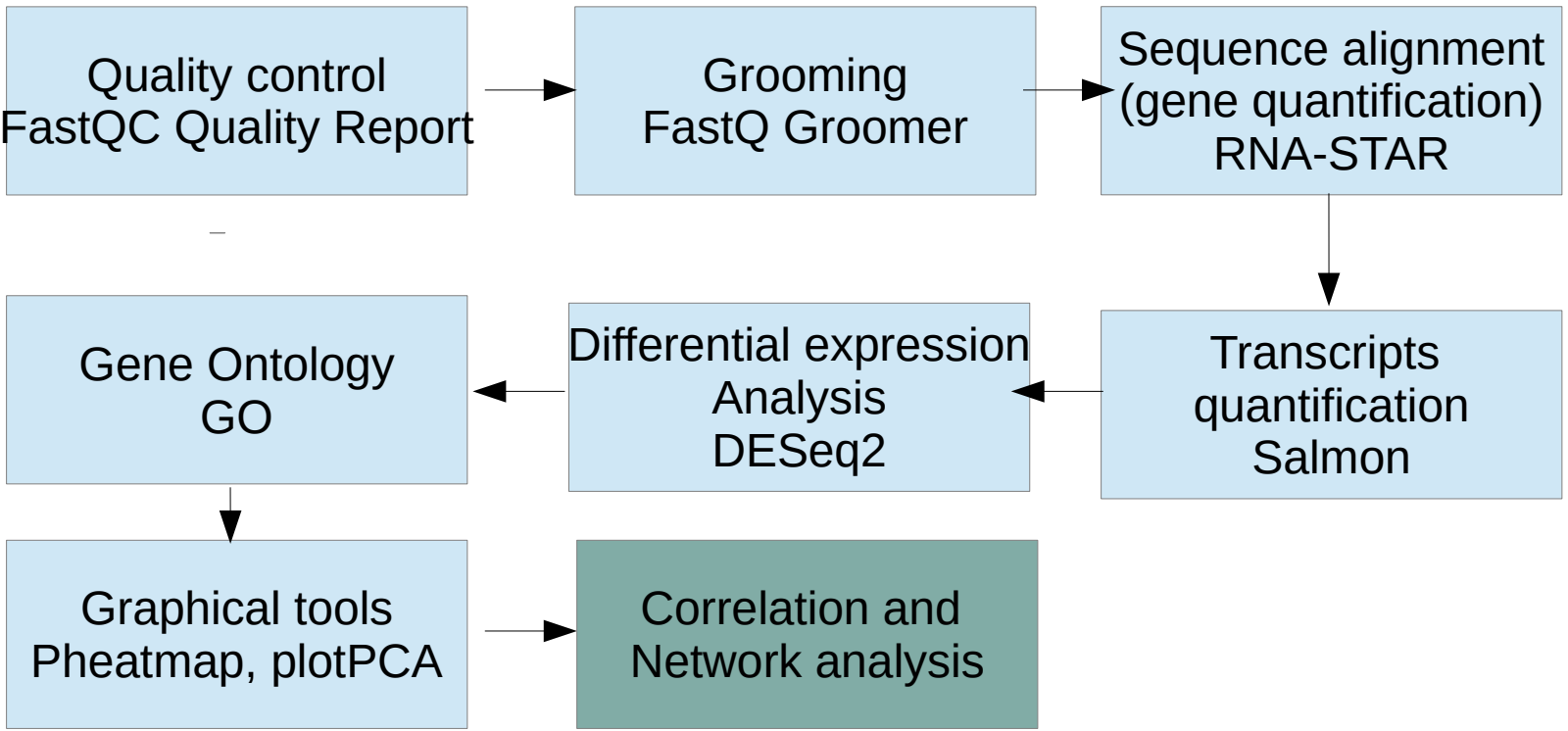
Justification

- Breast cancer is the most common cancer in mexican women, and is usually diagnosed in advanced stages. For these group of patients, neoadjuvant chemotherapy is the gold standard treatment, but only 15% present response. Thus, is necessary to improve predictive tools for the management of oncological patients. LincRNA are non coding transcripts with differential expression profiles in human tissues and pathologies, and represent potential predictive biomarkers because their expression specificity

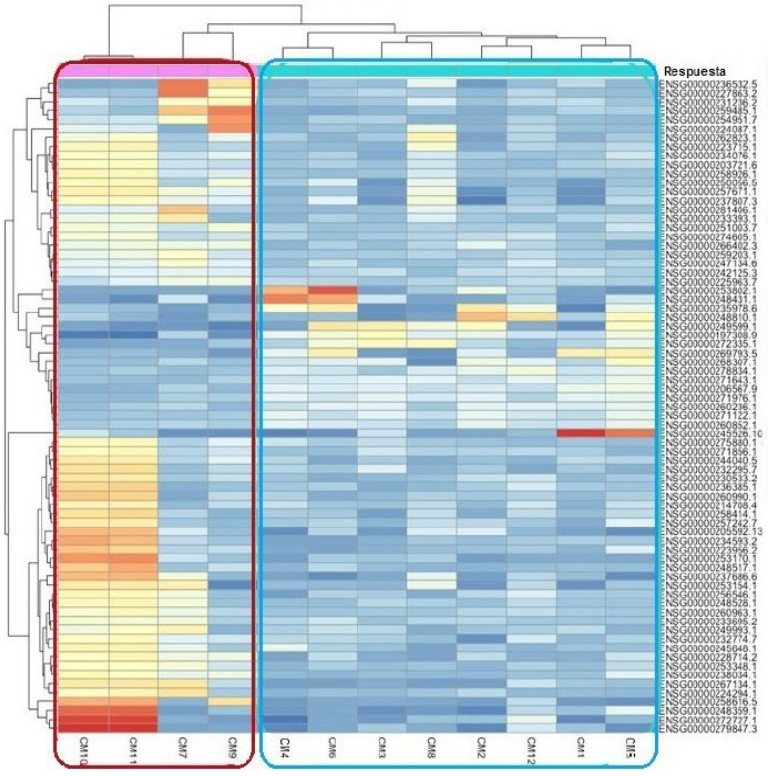
Objectives

- General
  - Identification of lincRNA with predictive value in locally advanced breast cancer mexican patients, by transcriptome analysis.
- Particular
  - To analyze RNA-Seq data from tumor biopsies by differential expression analysis in control-case study (Resistant vs. Response)
  - To identify lincRNA with differential expression profile and to obtain information from scientific literature about their functions.
  - To validate lincRNA expression in cDNA patients (experimental procedure)

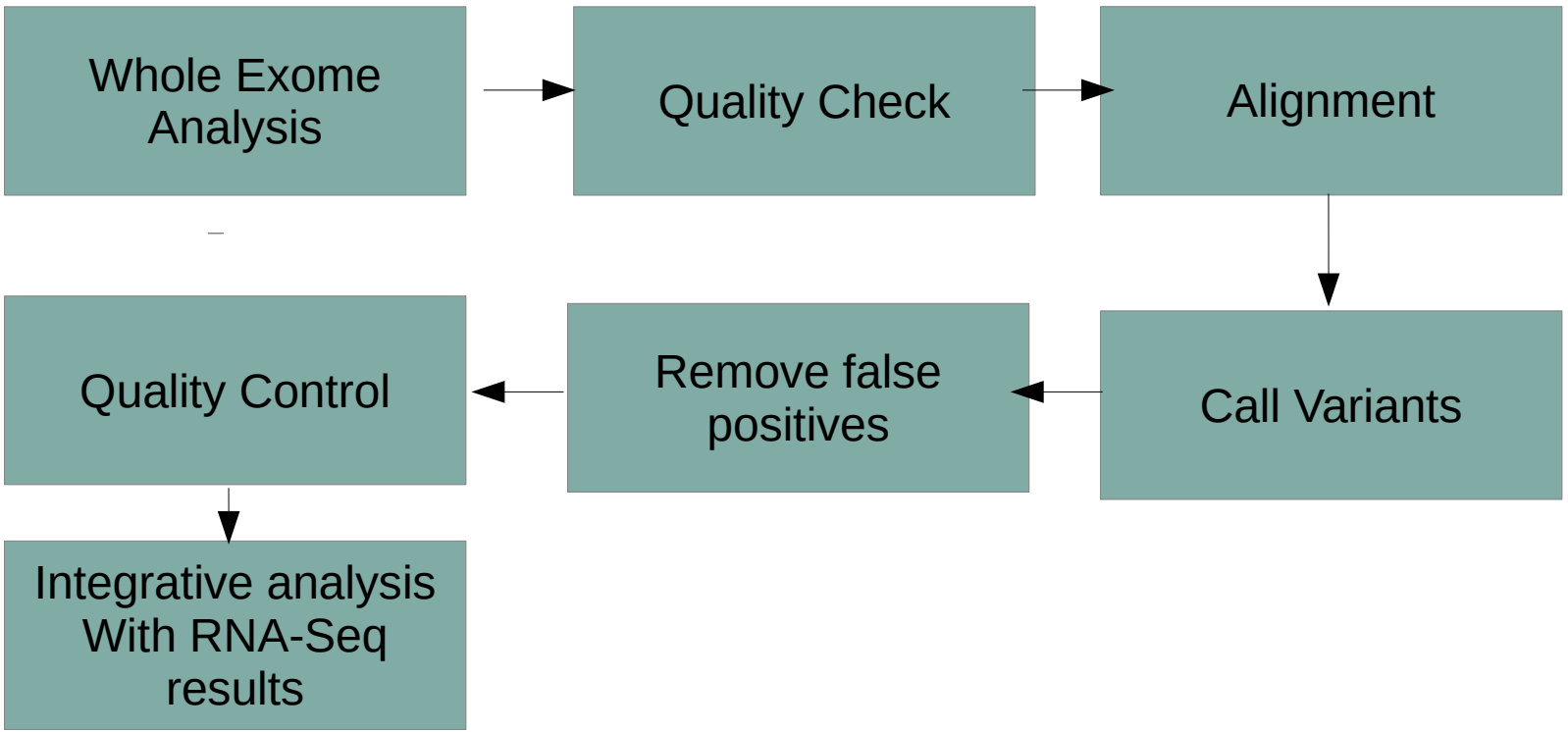
Initial Workflow



Results



Prospective Workflow



Acknowledgments