

MEAL “2”: story of a software package

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Problem 1

- ▶ Different methods to analyze methylation data
- ▶ Not easy to run all in the same dataset
 - Different packages
 - Different input and output objects
 - Different parameters names
 - Different visualization of results

Solution 1

- ▶ Develop **MEAL** package
- ▶ Includes wrappers to methylation data analyses
 - ▶ limma, DiffVar, bumphunter, blockFinder, DMRcate, RDA
 - Same input object (GenomicRatioSet – minfi package)
 - Common parameter names
 - Run several methods with one function
- ▶ Includes commonly used plots
 - Violin plot, Manhattan, QQplot...
- ▶ Uses single class to encapsulate all type of results
 - ResultSet – MultiDataSet package

ResultSet

- ▶ Stores data required to make plots and produce results
 - Analysis results
 - Feature data
- ▶ Unique methods to get results and plots
- ▶ Can store results from different methods
- ▶ New plot with different layers of information

Joint work with Carles Hernandez-Ferrer

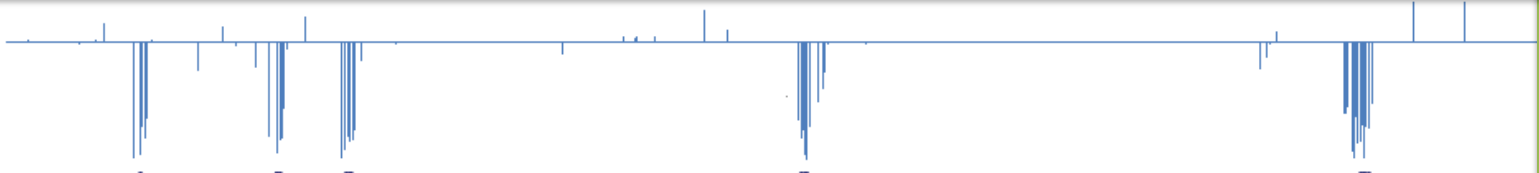
Chromosome X



Annotation



Region Results



Different Mean Results



Different Mean Results



Different Variance Results



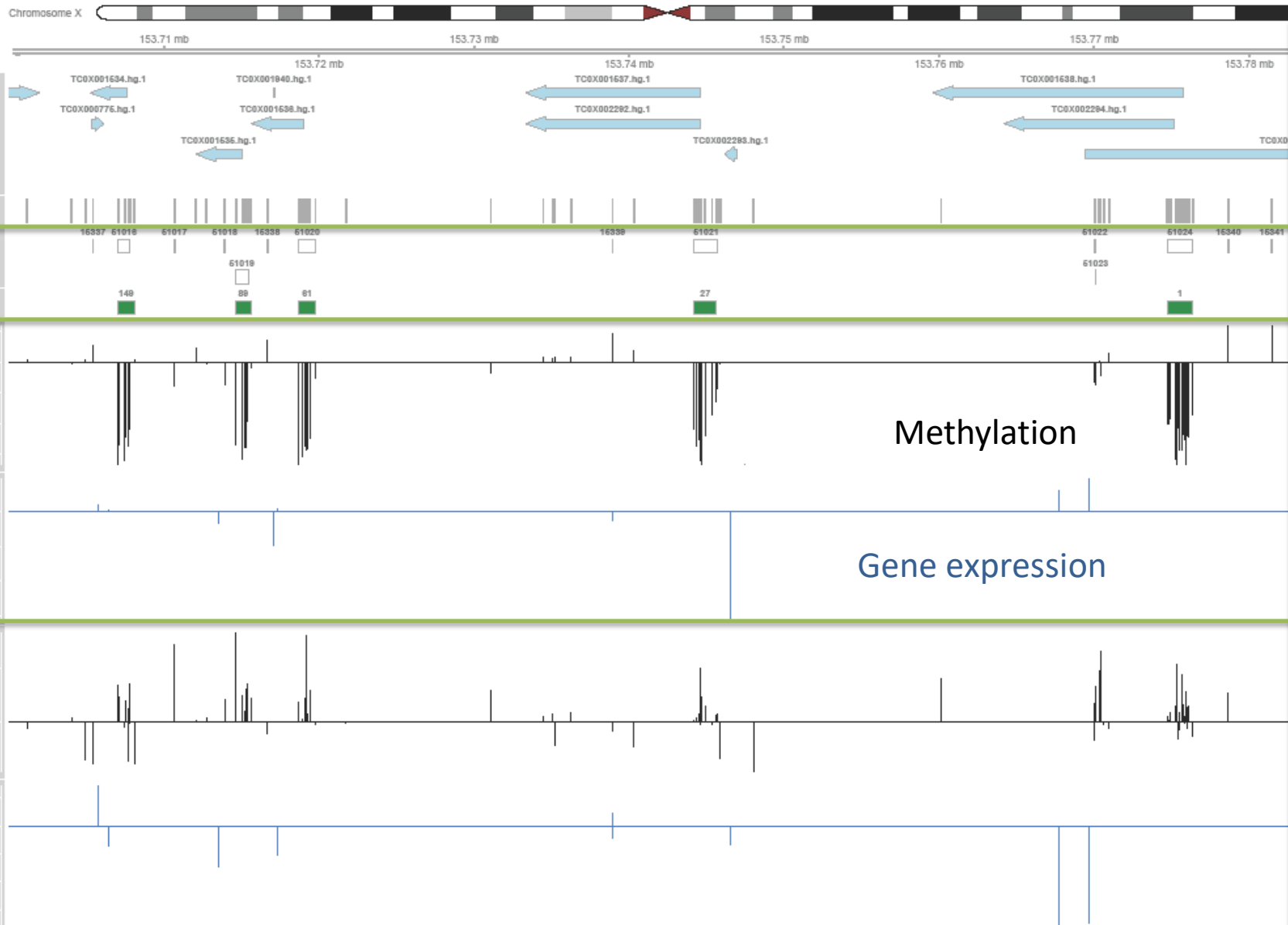
Different Variance Results

Problem 2

- ▶ Changes in methylation can produce changes in gene expression
- ▶ Some methods in **MEAL** are common for gene expression and methylation data
 - Limma, DiffVar and RDA
- ▶ Co-analysis of expression and methylation

Solution 2

- ▶ Adapt **MEAL** wrappers to also accept expression data
 - Accept ExpressionSet and SummarizedExperiment
- ▶ Add plot to simultaneously show **methylation and expression** analysis results



Annotation

Region Results

Methylation
 Different Mean Results

Gene expression
 Different Variance Results

Take-home message

- ▶ **MEAL** is a package that eases performing methylation and gene expression data analyses
 - Homogenizes input and output
 - Includes plots to easy visualize results
 - Includes a new plot to simultaneously visualize gene expression and methylation results

True story

1. Encapsulates functions to run methylation analysis
 2. Implement classes to manage methylation data and results
 3. Encapsulate functionality in a package (**MEAL**)
 4. Add new functionalities 1
 5. Add new functionalities 2
 6. ...
-
- ▶ **Problem:** design of original package was not prepared for new functionalities
 - ▶ MEAL “2”?
 - major changes to original package
 - remove of original functions and substitution of classes

Questions

- ▶ New package or new version?
- ▶ If new version:
 - New main version or new subversion?
 - Deprecate old names functions?
 - Maintain compatibility with old result classes?

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- ▶ Carles Hernandez-Ferrer

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