

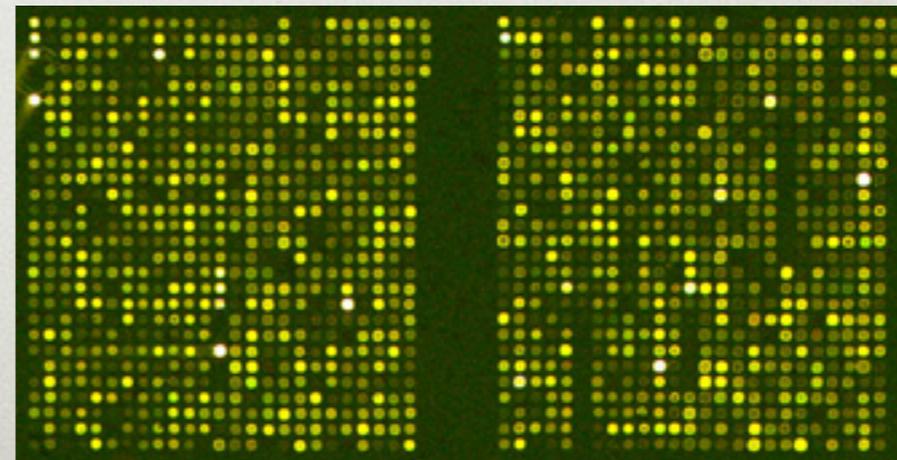
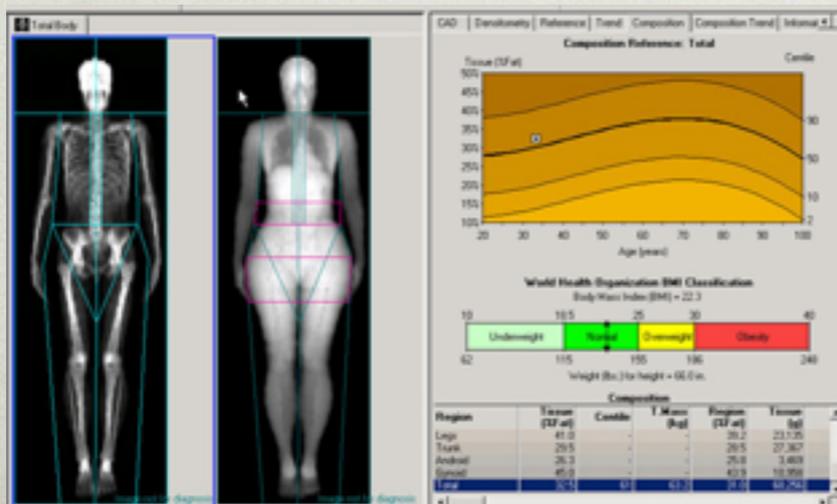
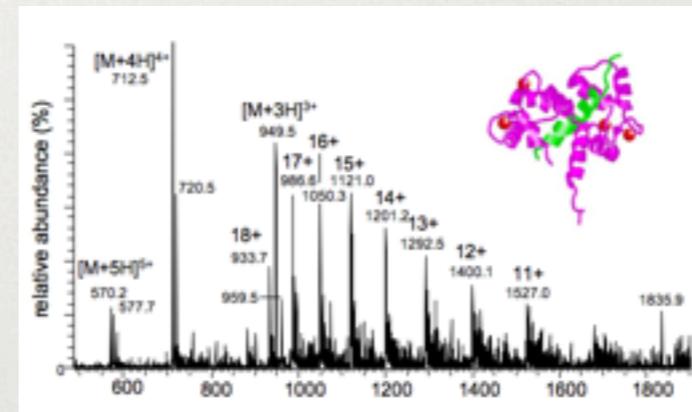
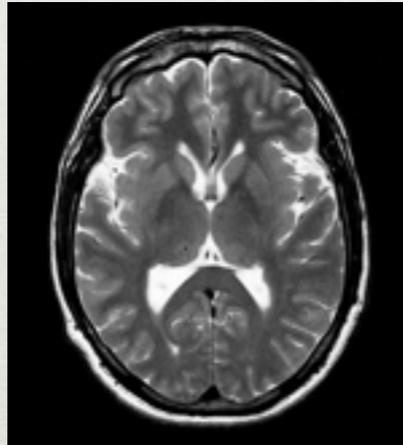
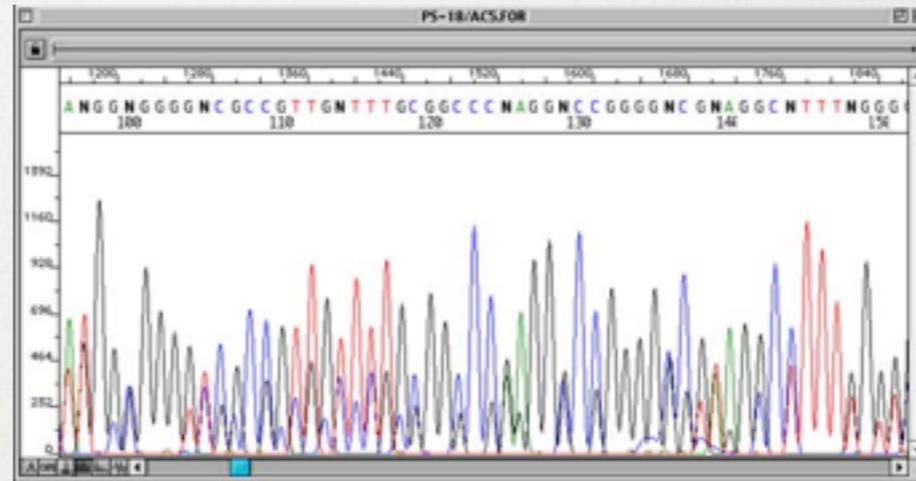
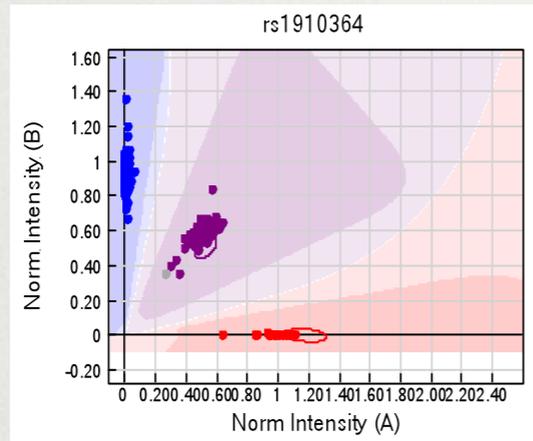
ANALYSIS OF OMICS DATA

YURII AULCHENKO

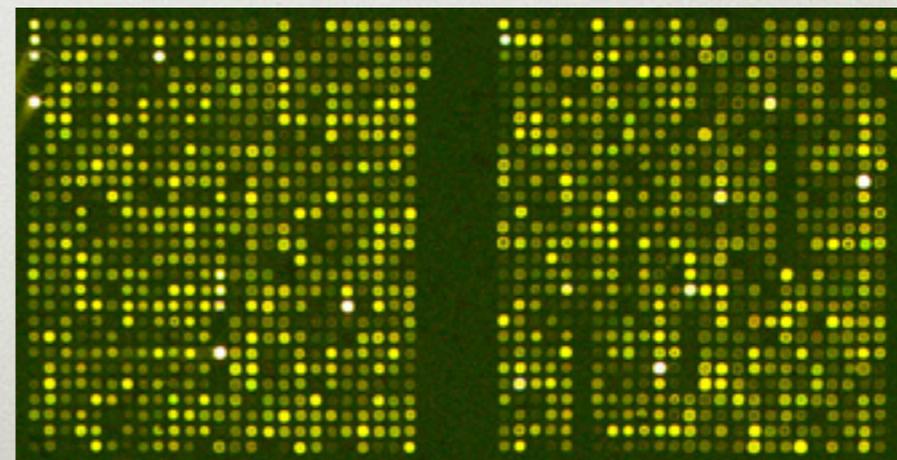
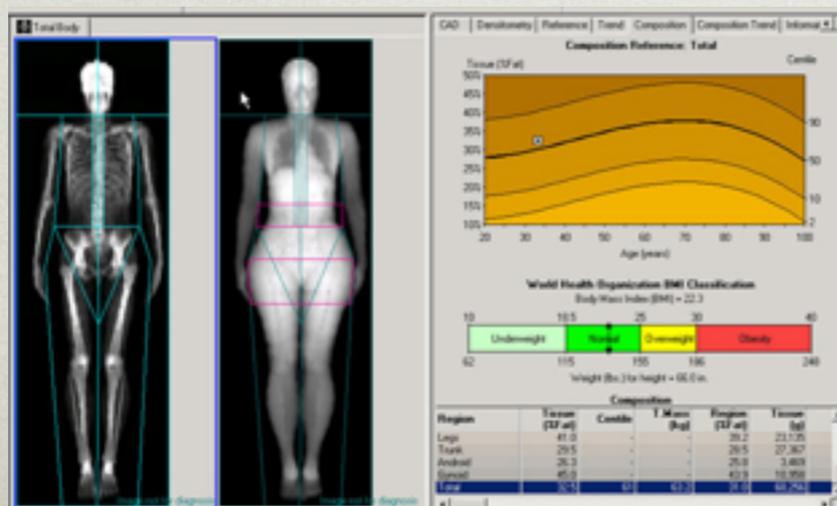
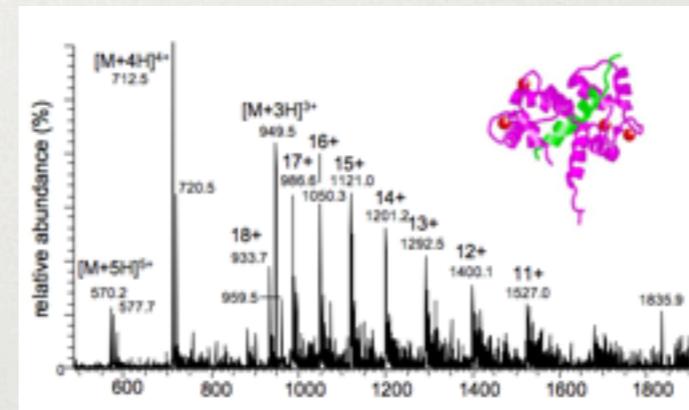
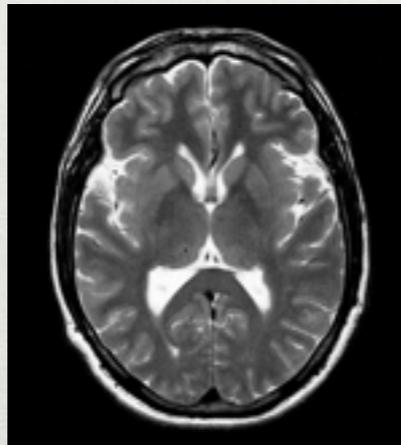
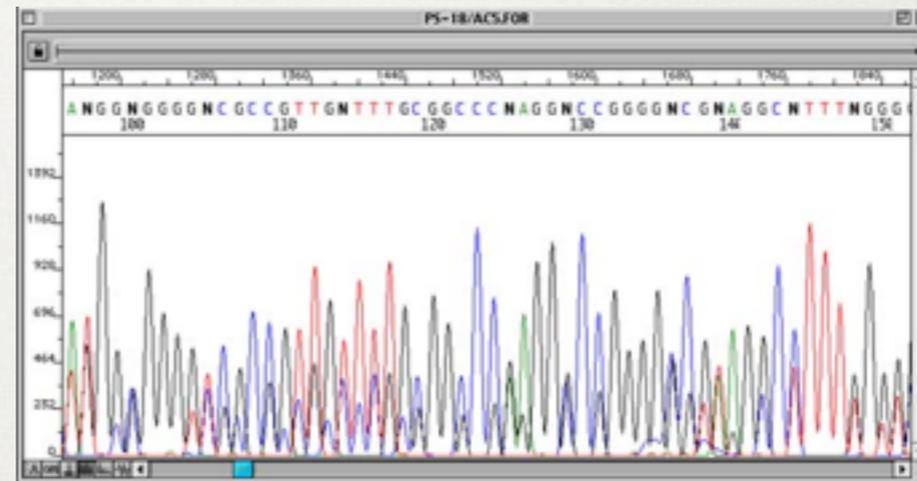
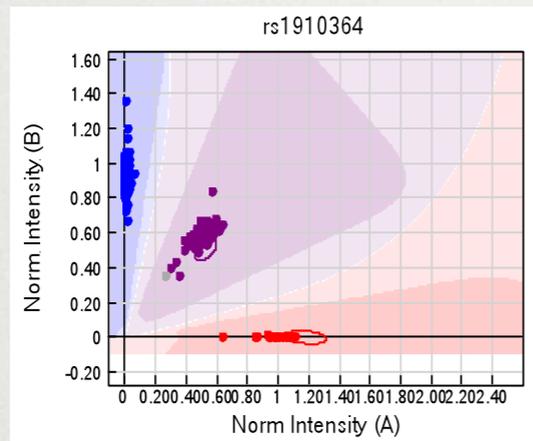
INDEPENDENT RESEARCHER & CONSULTANT

YURII [DOT] AULCHENKO [AT] GMAIL [DOT] COM

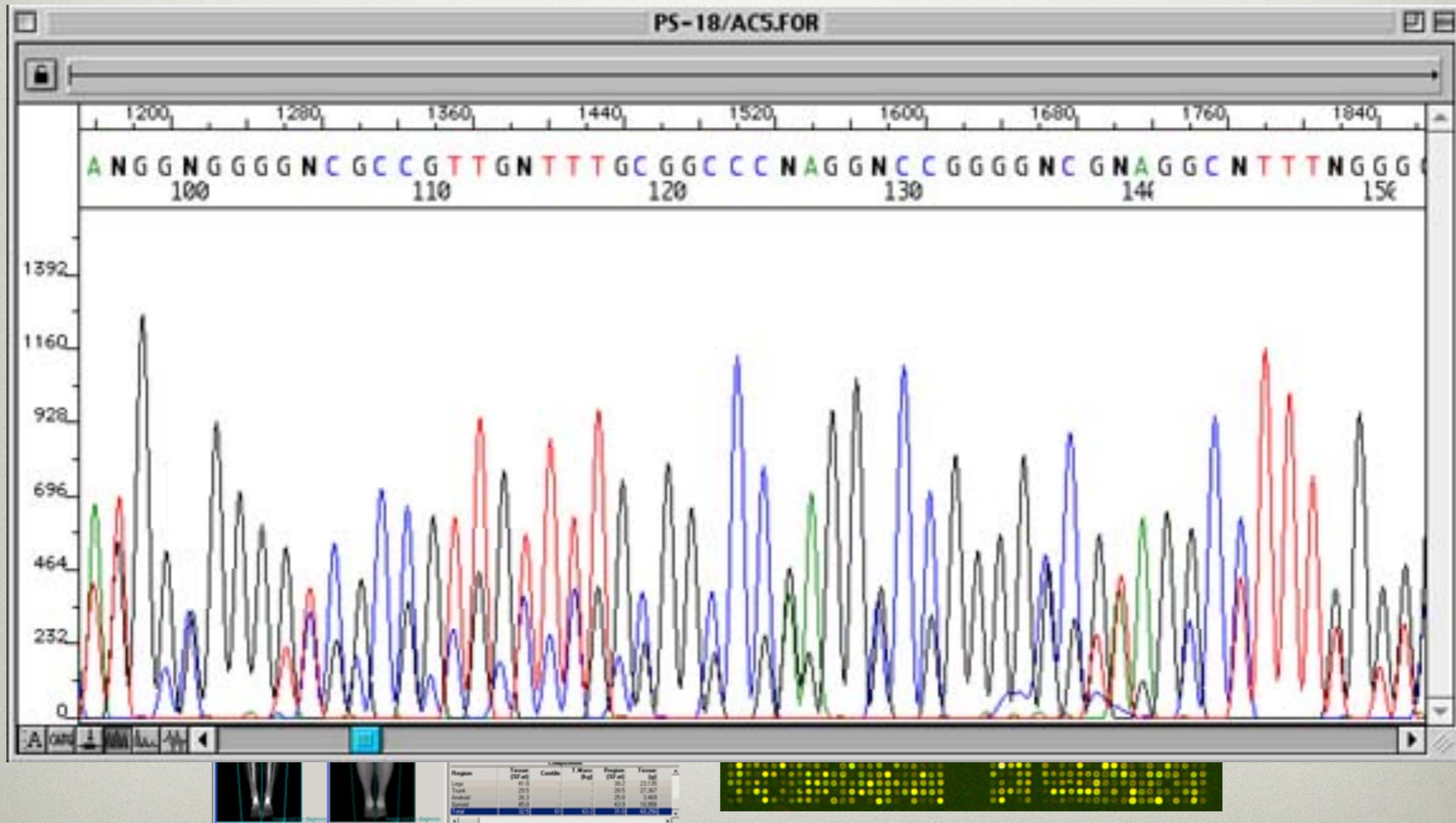
OMICS DATA



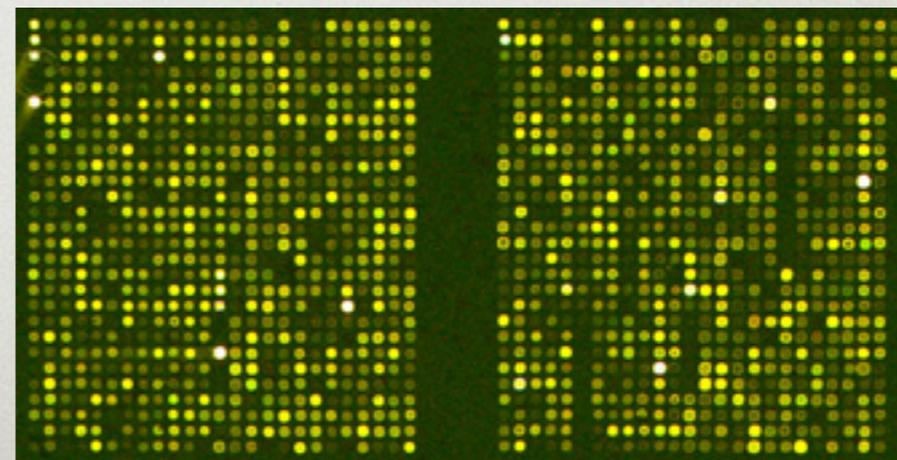
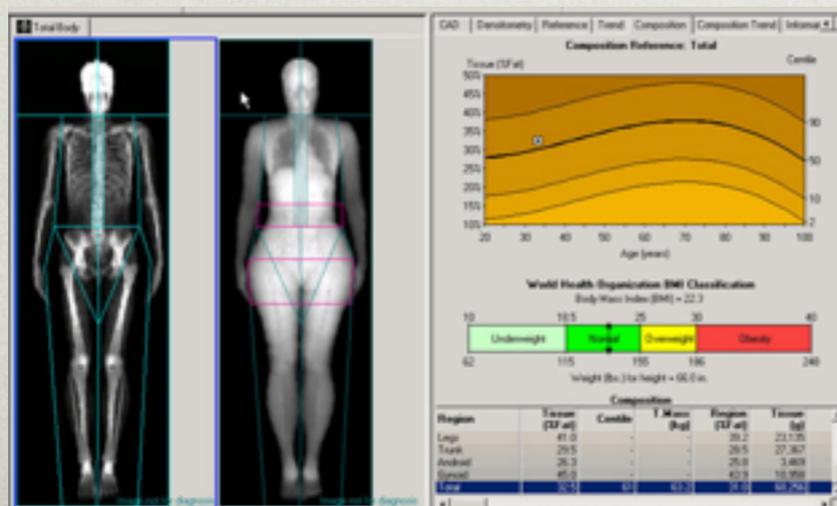
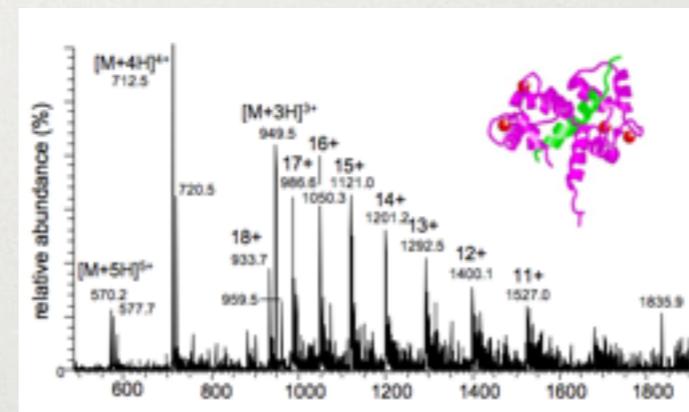
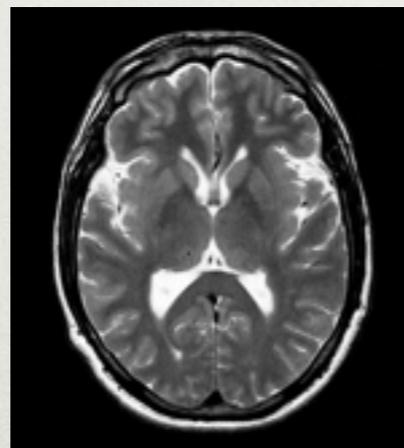
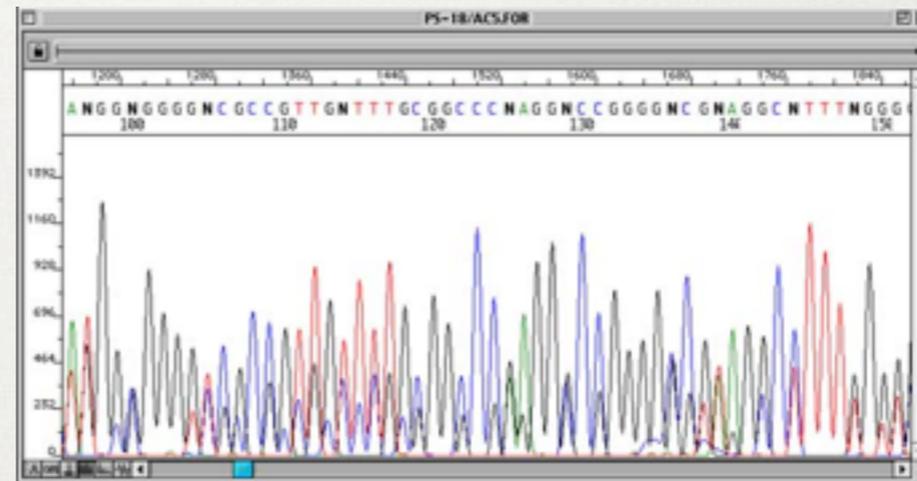
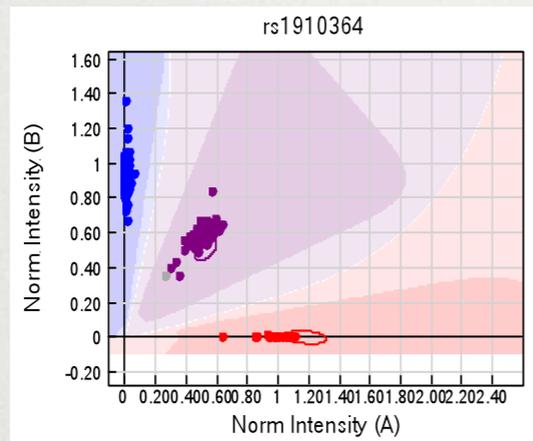
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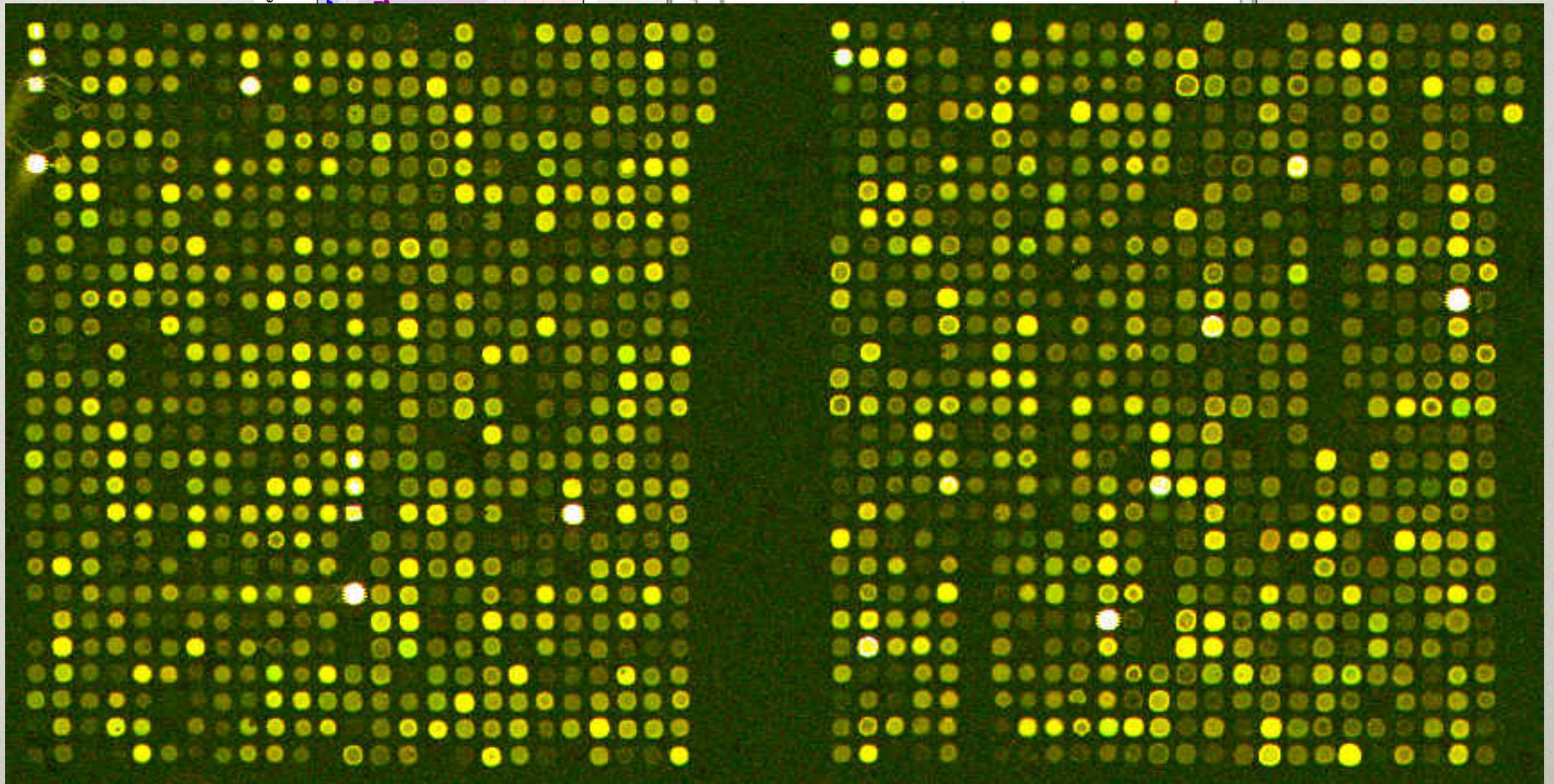
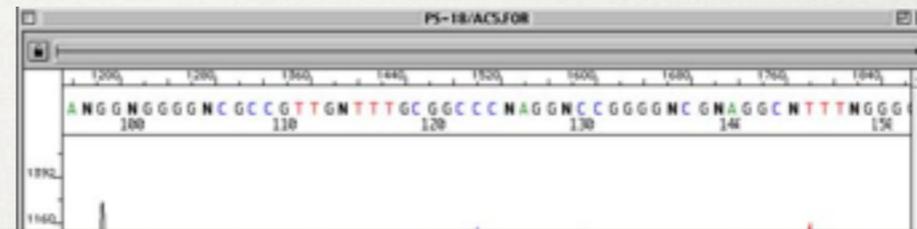
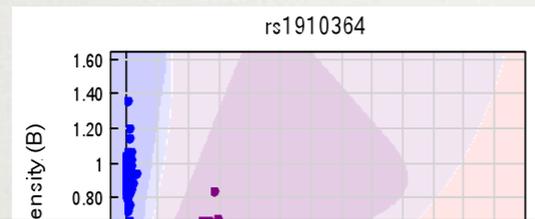
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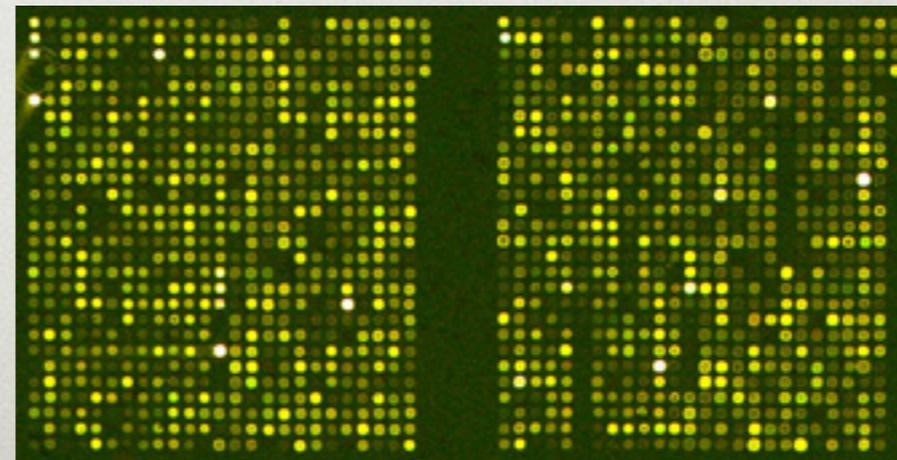
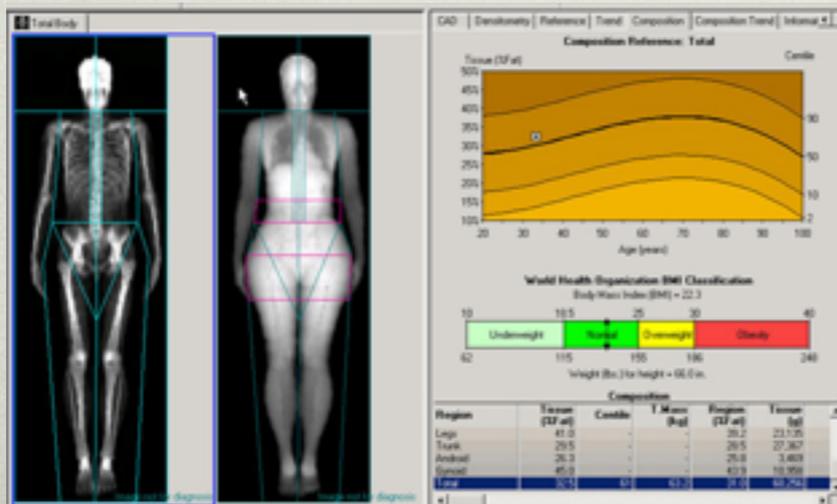
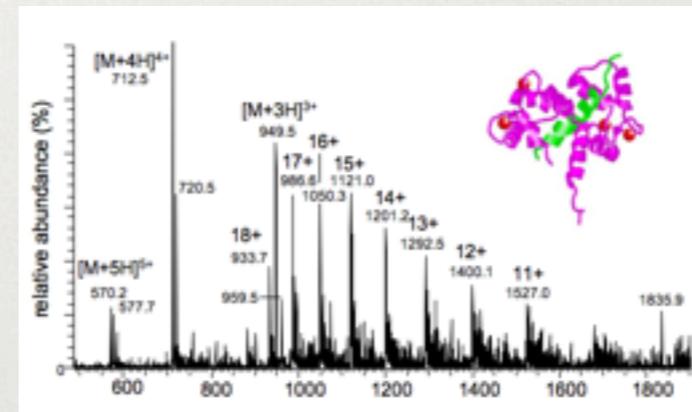
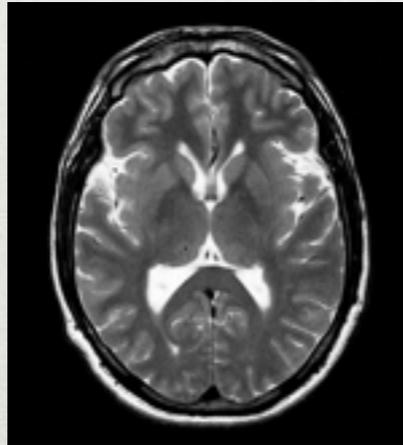
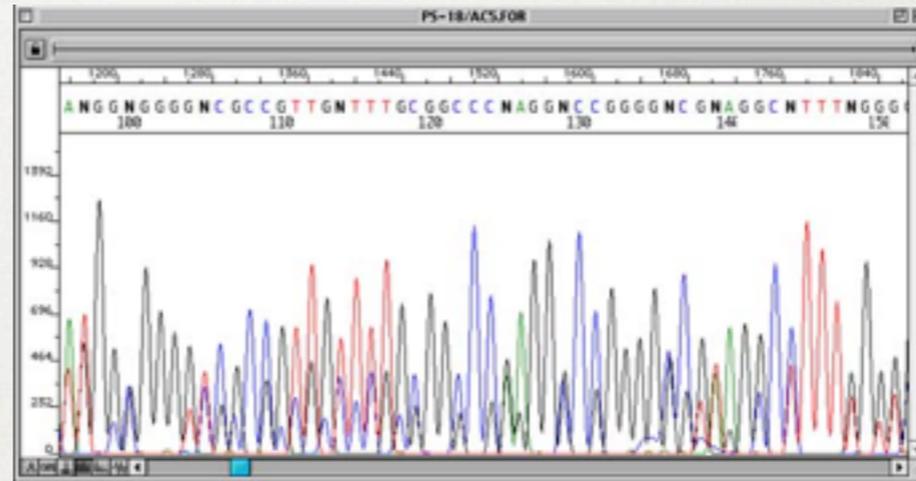
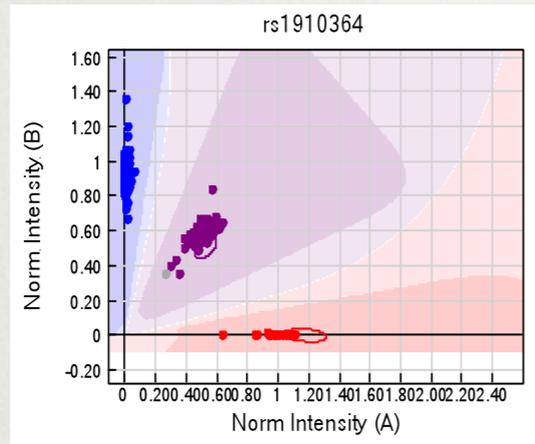
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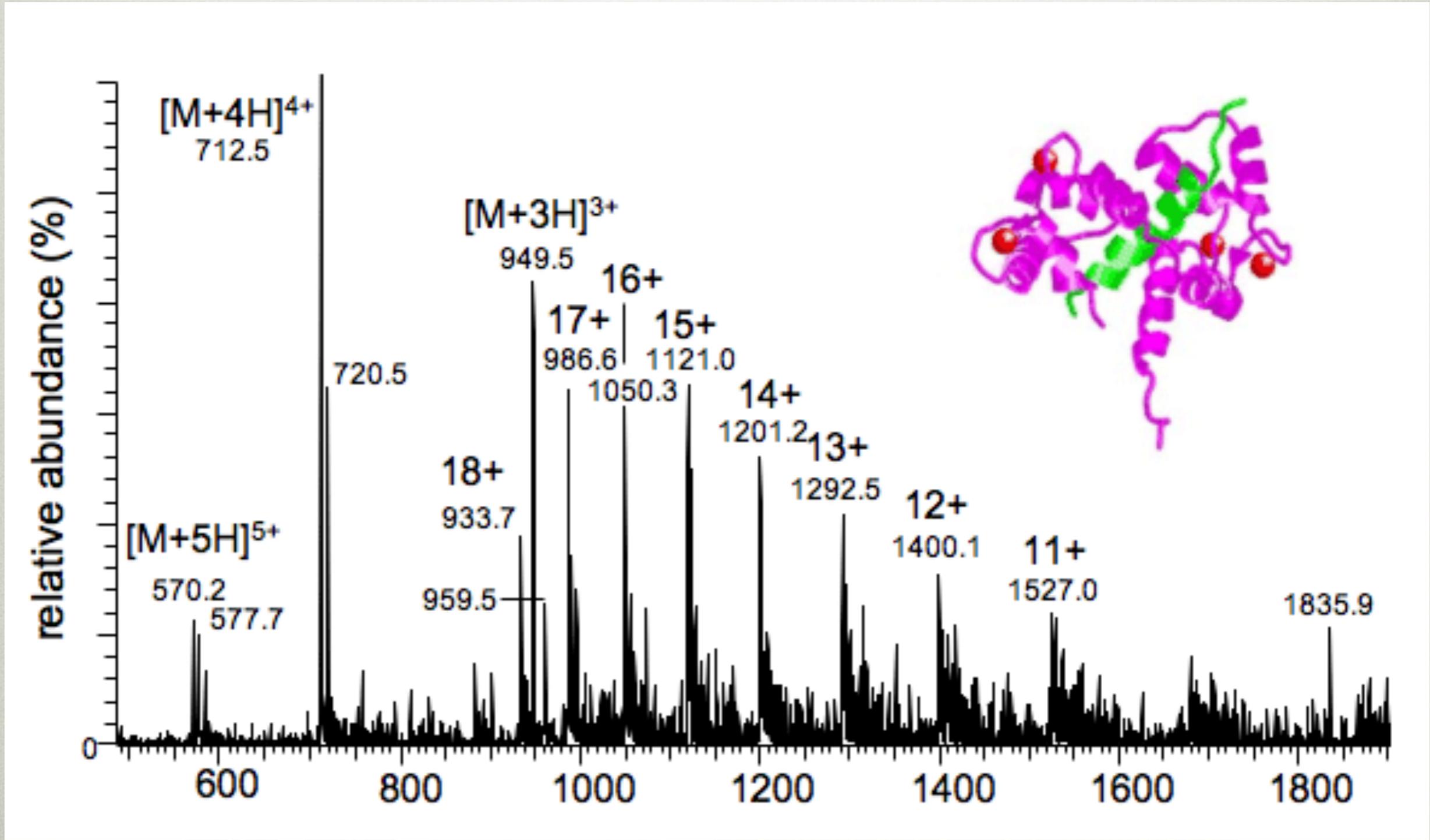
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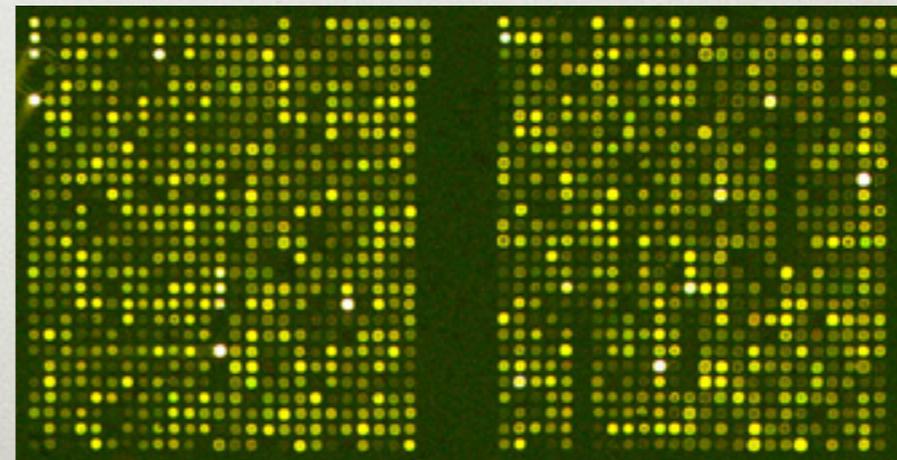
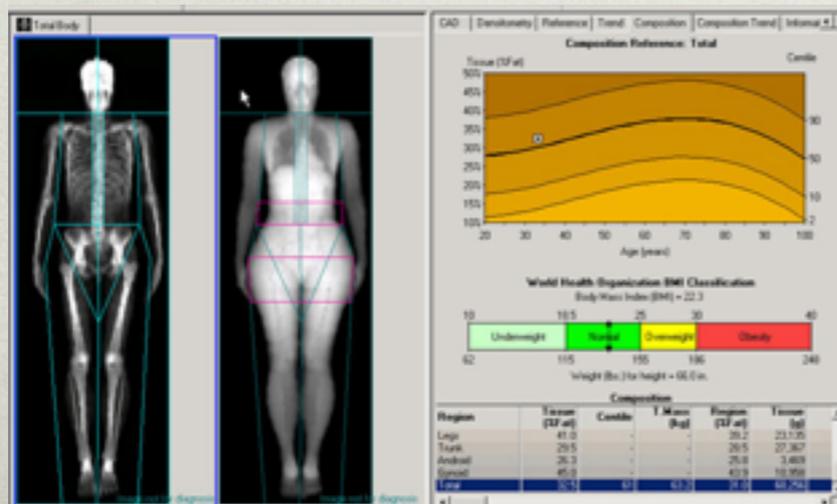
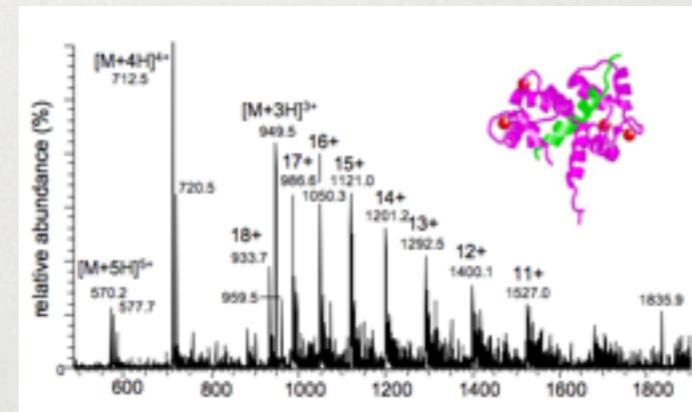
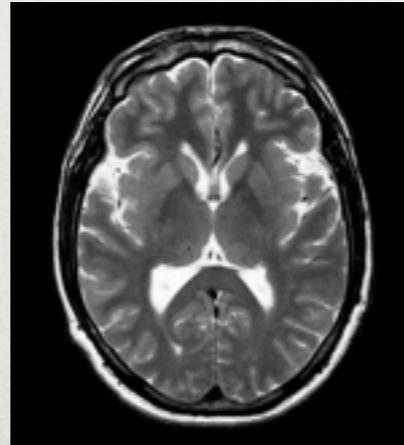
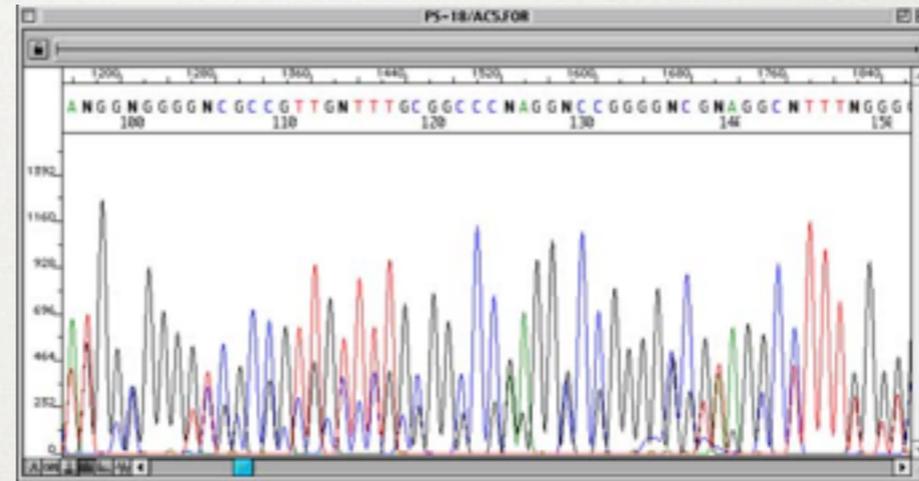
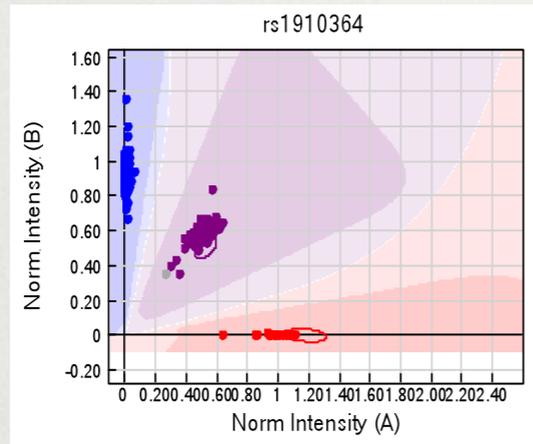
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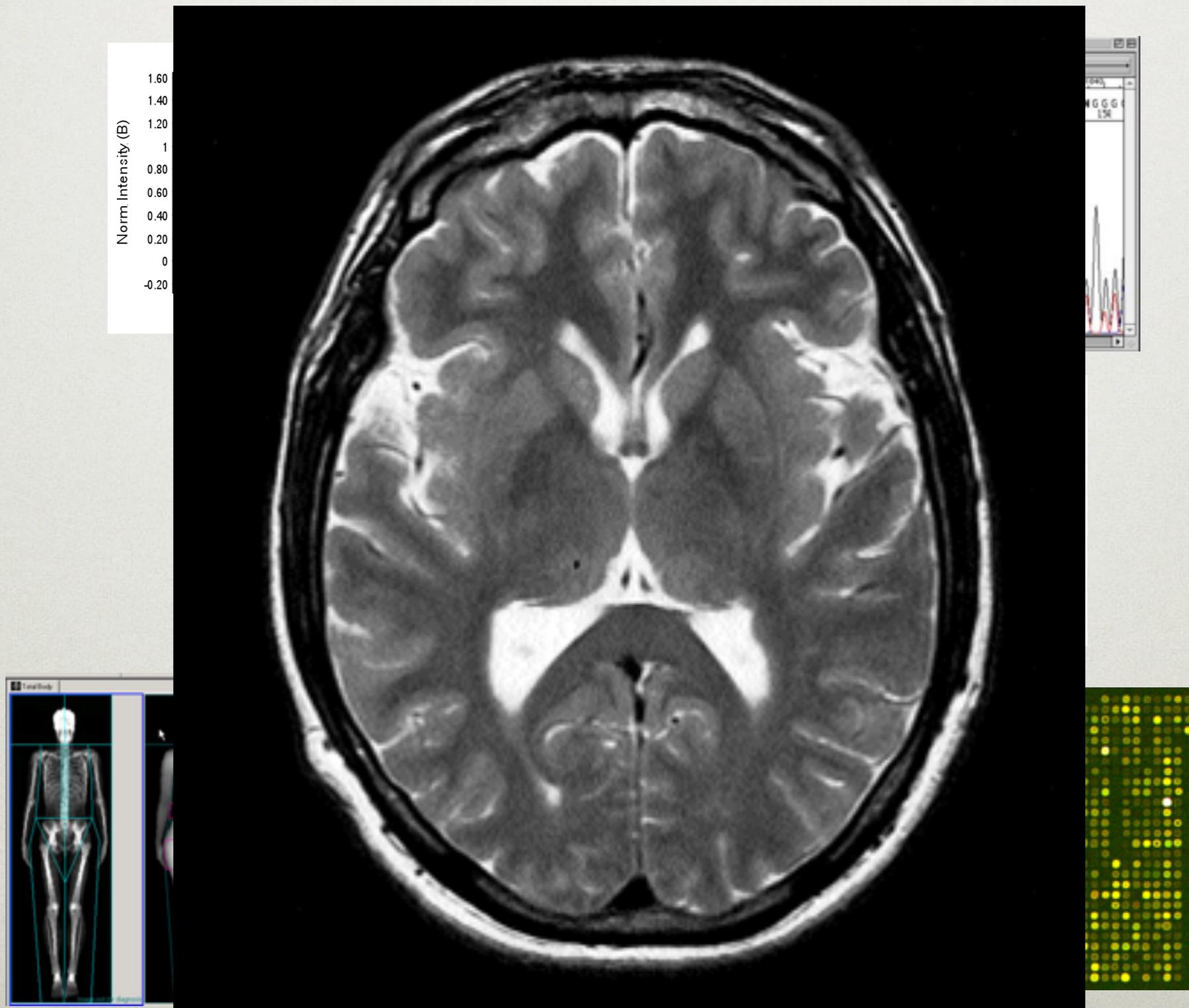
METABOLOME



PHENOME



PHENOME



PHENOME

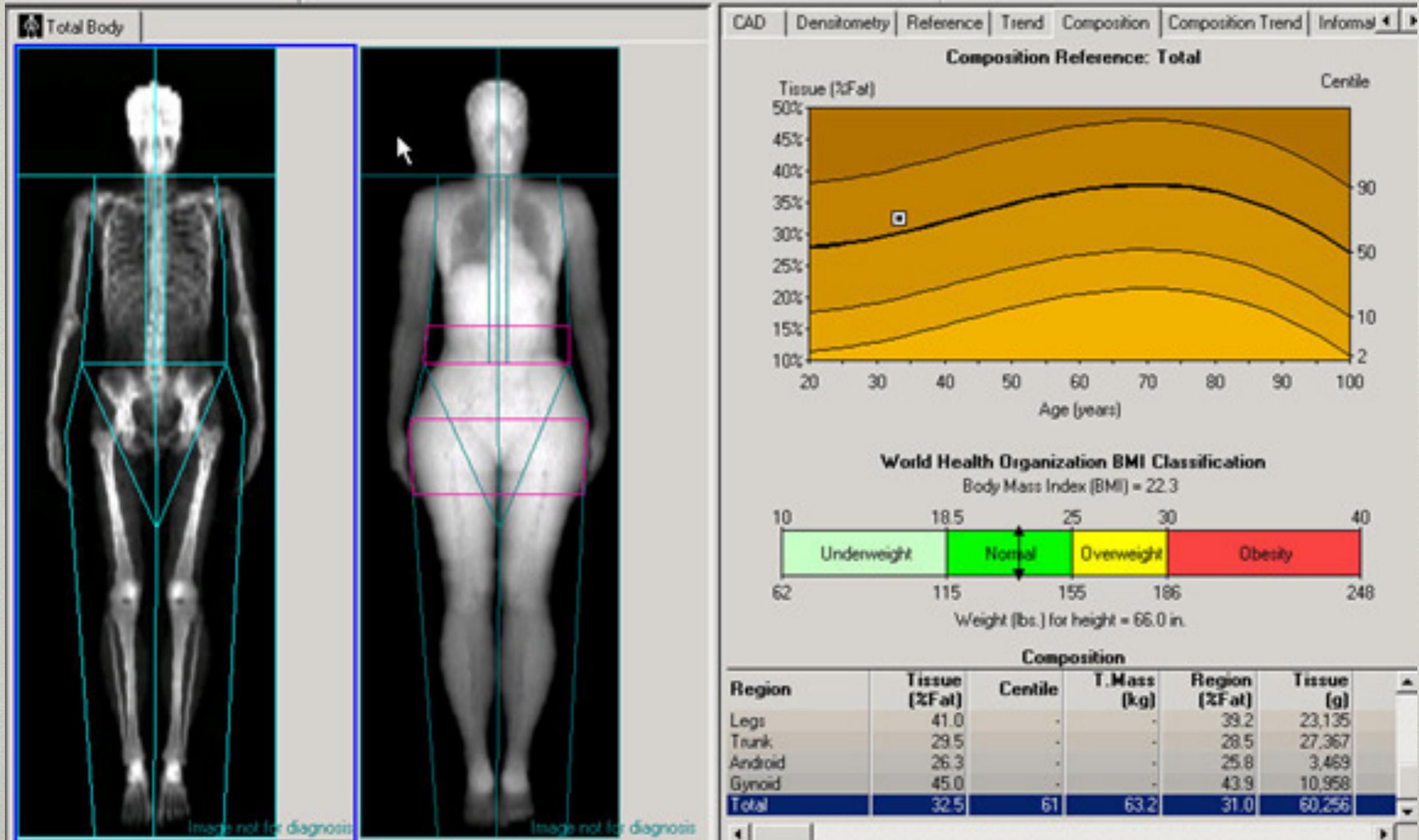
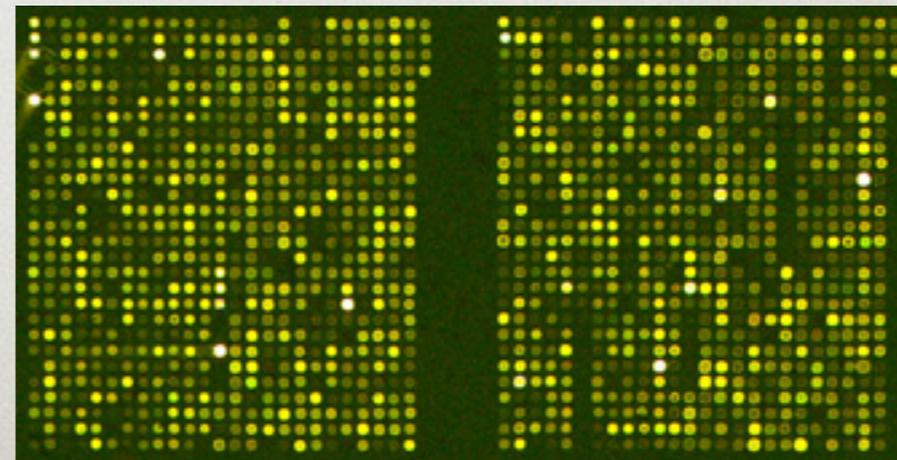
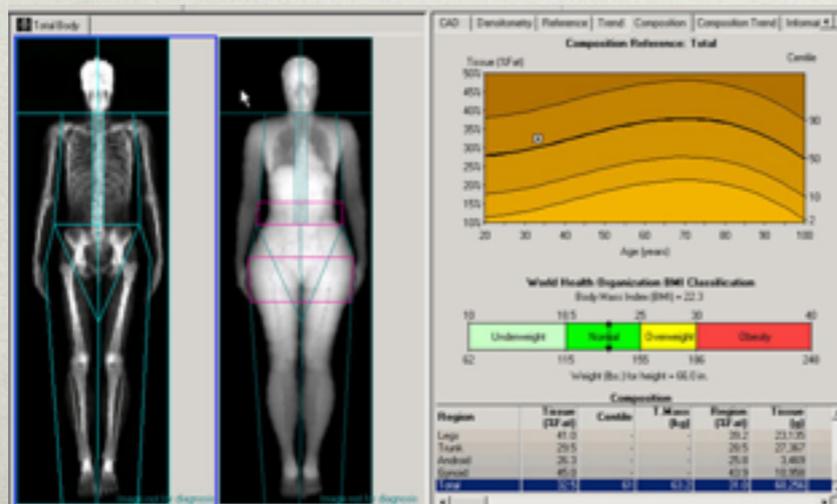
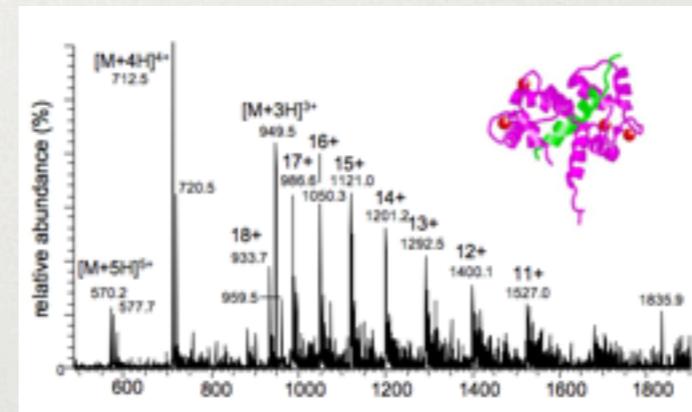
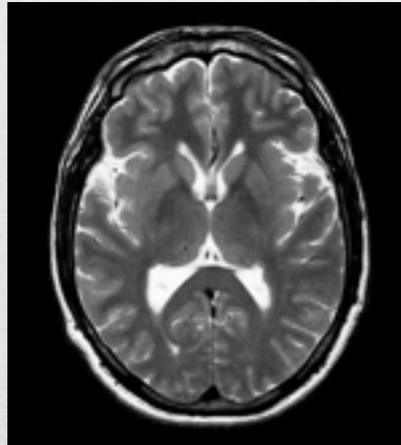
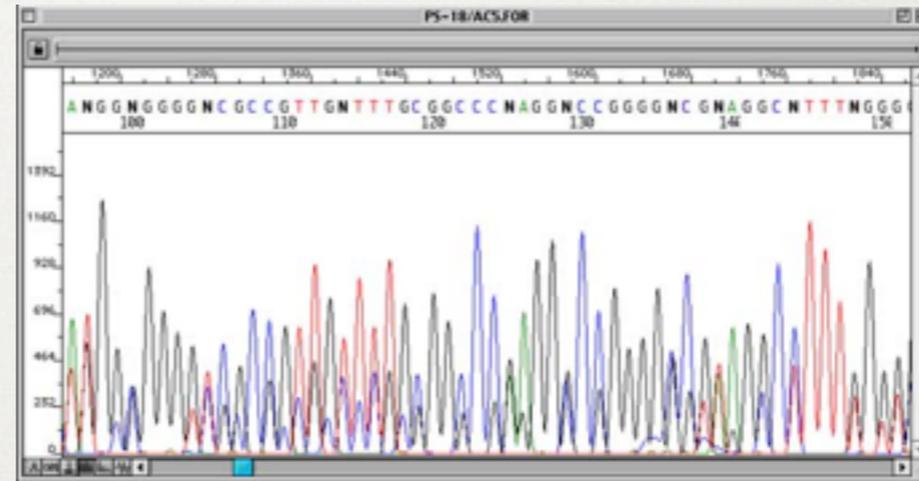
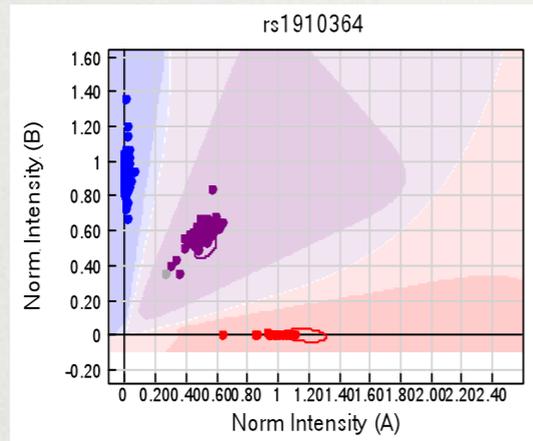


Image not for diagnosis

Image not for diagnosis

OMICS DATA



DATA ANALYSIS



Data

DATA ANALYSIS



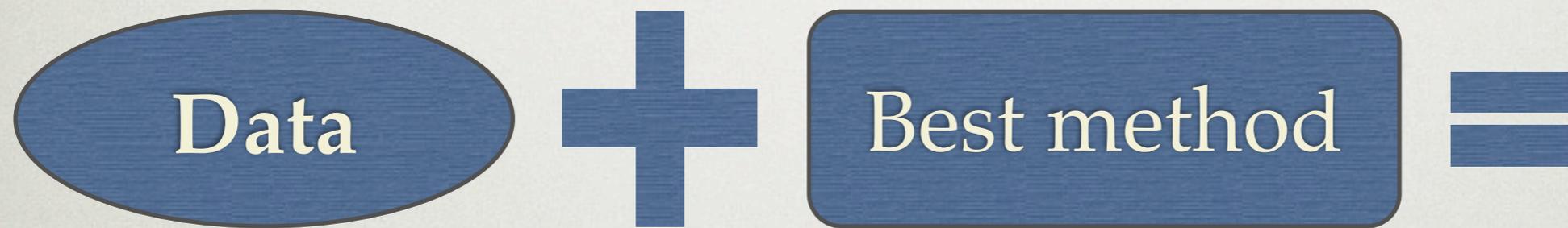
DATA ANALYSIS



DATA ANALYSIS



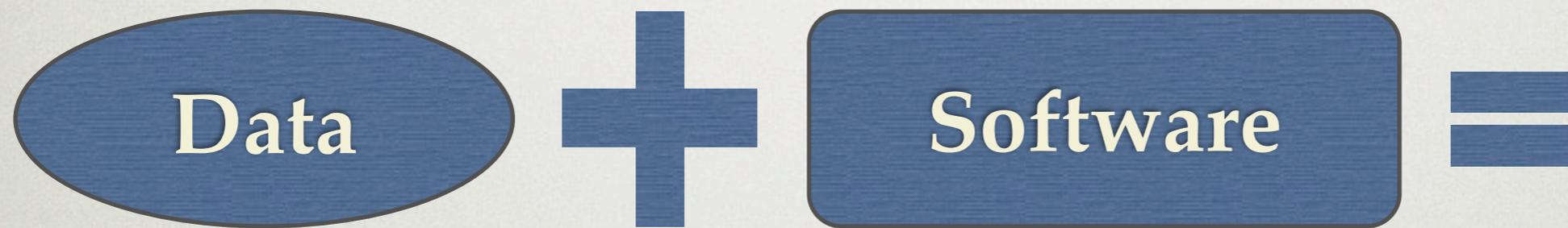
DATA ANALYSIS



DATA ANALYSIS



DATA ANALYSIS



DATA ANALYSIS



METHOD TO SOFTWARE

Method

METHOD TO SOFTWARE

Approximation

Method

METHOD TO SOFTWARE

Algorithm

Approximation

Method

METHOD TO SOFTWARE

Implementation

Algorithm

Approximation

Method

METHOD TO SOFTWARE

Software

Implementation

Algorithm

Approximation

Method

THE GENABEL PROJECT

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The mission of the **GenABEL project** is to provide a free framework for collaborative, robust, transparent, open-source based development of statistical genomics methodology. We aim to streamline methodology discussion, development, implementation, dissemination and maintenance; through the community.

The **GenABEL suite** (aka *ABEL suite) is practical result of implementation of statistical genomics methods developed in GenABEL project. The GenABEL suite is an umbrella name for a number of open-source software packages. The suite is

- Rich in functionality. Many packages containing 100+ functions related to genomic analysis [[Packages](#)]
- Efficient. Meaning you can run a genome-wide association scan on a netBook
- Flexible. Programming your custom analysis is easy
- Open, transparent, free. At present, all code is released under the GNU GPL [[GNU GPL](#)]
- Well documented. More then 200 pages of reference manuals and about 300 pages of tutorials [[Tutorials](#) | [Manuals](#)]
- Supported. By our community [[Forum](#)]
- Collaborative. The community is open for your contribution [[Contribute](#)]

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EXAMPLE PROBLEM

- Genome-wide analysis of association of “omics” data in genetically isolated population
- 2,500,000 genetic locations
- 30,000 traits
- Hence $\sim 10^{11}$ tests (in 3,000 individuals)

STATE IN 2007

- Single test takes ~5 minutes (ASReml)
- ... single GWAS takes 24 years
- ... 700k years to analyze 30k phenotypes

STATE IN 2009

- Single test takes <0.01 second (mmscore)
- ... single GWAS takes 5 hours
- ... 17 years to analyze 30k phenotypes

STATE IN 2012

- Single test takes ... (depends)
- ... single GWAS takes <1 hour
- ... few days to analyze 30k phenotypes