exploring biomarkers for early & dual asthmatic response

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problem: extract and comprehend features

given biometrics for **2 classes of subjects** (early & late asthmatic responders):

- feature extraction: are there biometric **features that discriminate** between these two classes
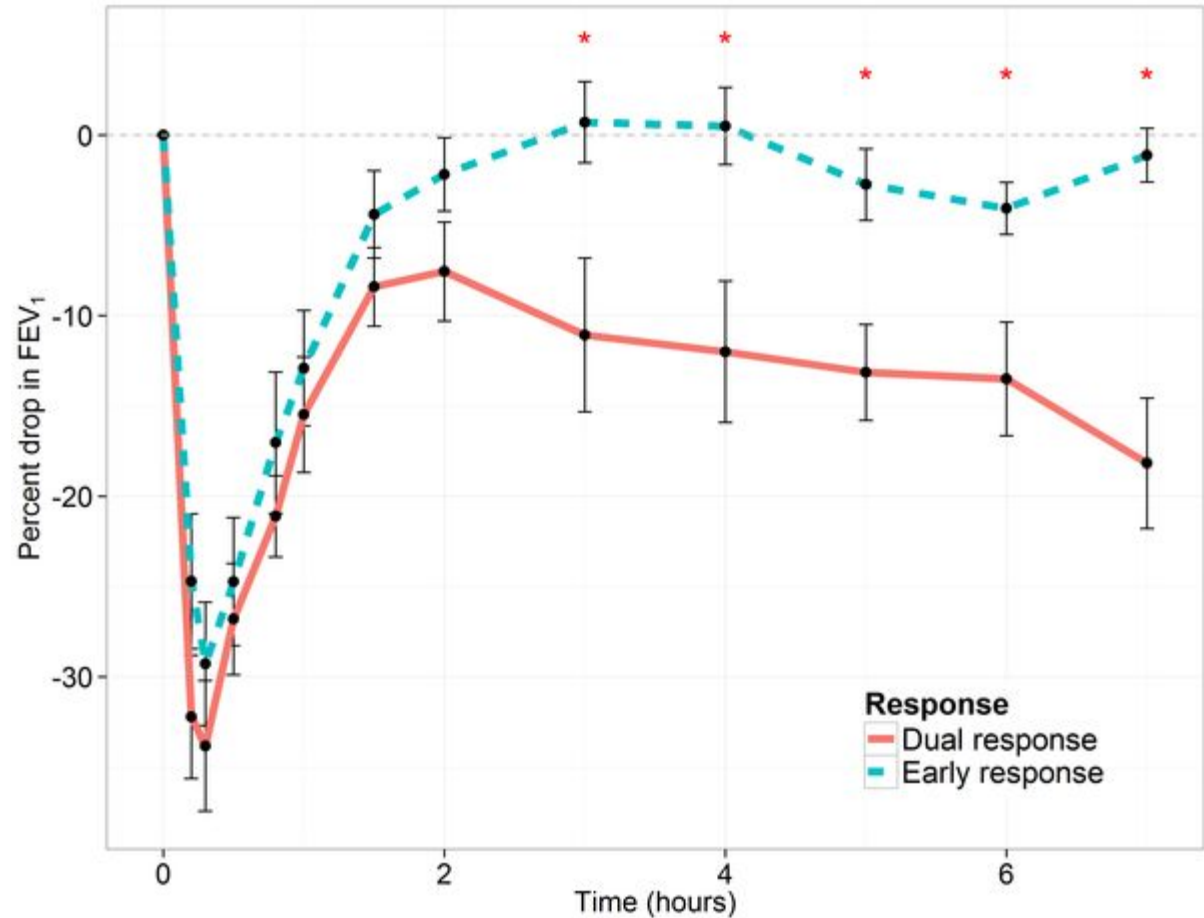- feature comprehension: are these **associations between** these discriminatory biometric features

data (n x m)

n = 36;

19 early responders (ER)

17 dual responders (DR)

measurements taken before and after allergen induced asthma

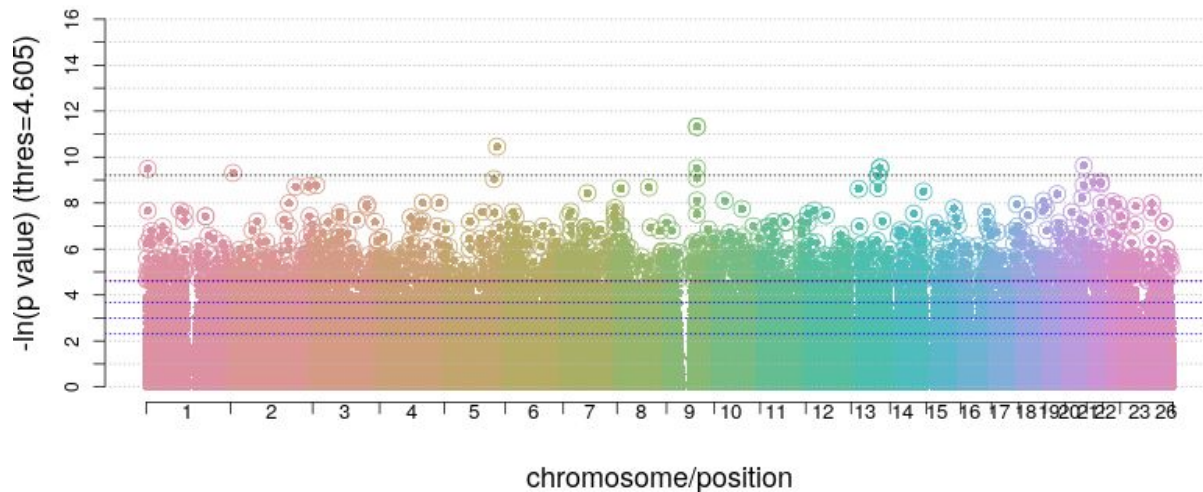# data (n x m): feature extraction

m =

- genotype
- rna seq, rna nanostring pancancer panel, rna nanostring elements panel
  - cell composition (inferred from rna)
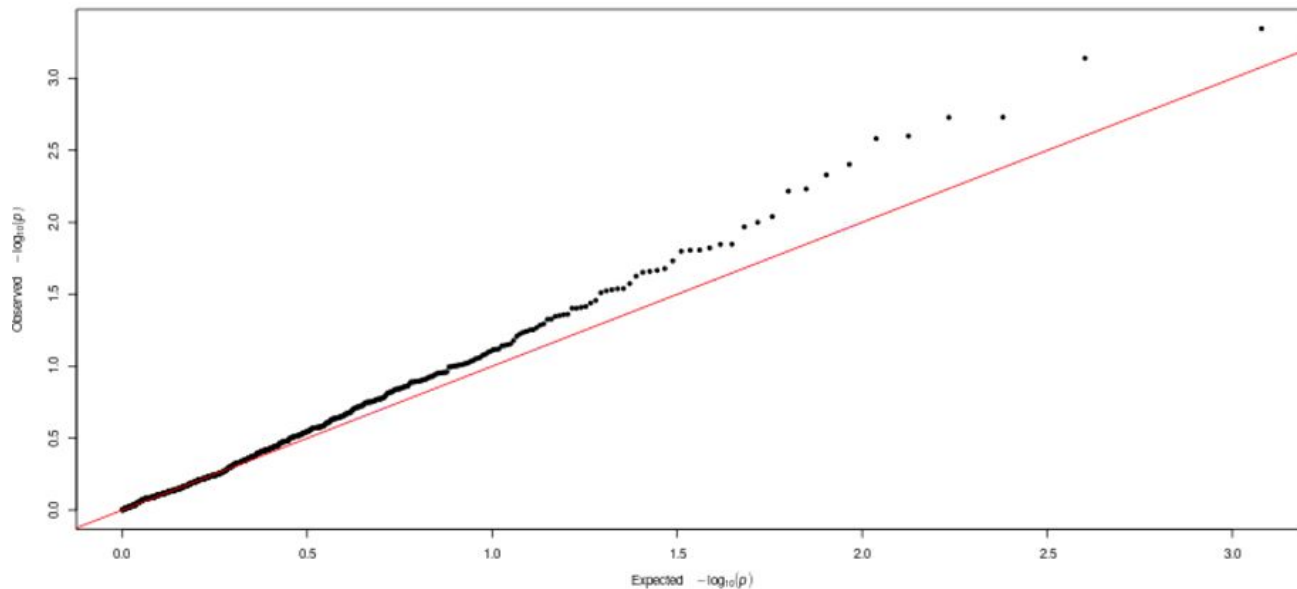- metabolomics

data (n x m): feature extraction

m =

- genotype: each position in the genome is either a common (0) or rare (2) allele e.g. (AA is a common allele, AT, and TT exhibit the uncommone allele)
    - GWAS (genome wide association study) (1552/261958 SNPs with p value < .01)

data (n x m): feature extraction

m =

- rna seq, rna nanostring pancancer panel, rna nanostring elements panel: abundance of rna in the blood (reflects expression volumes of certain genes)
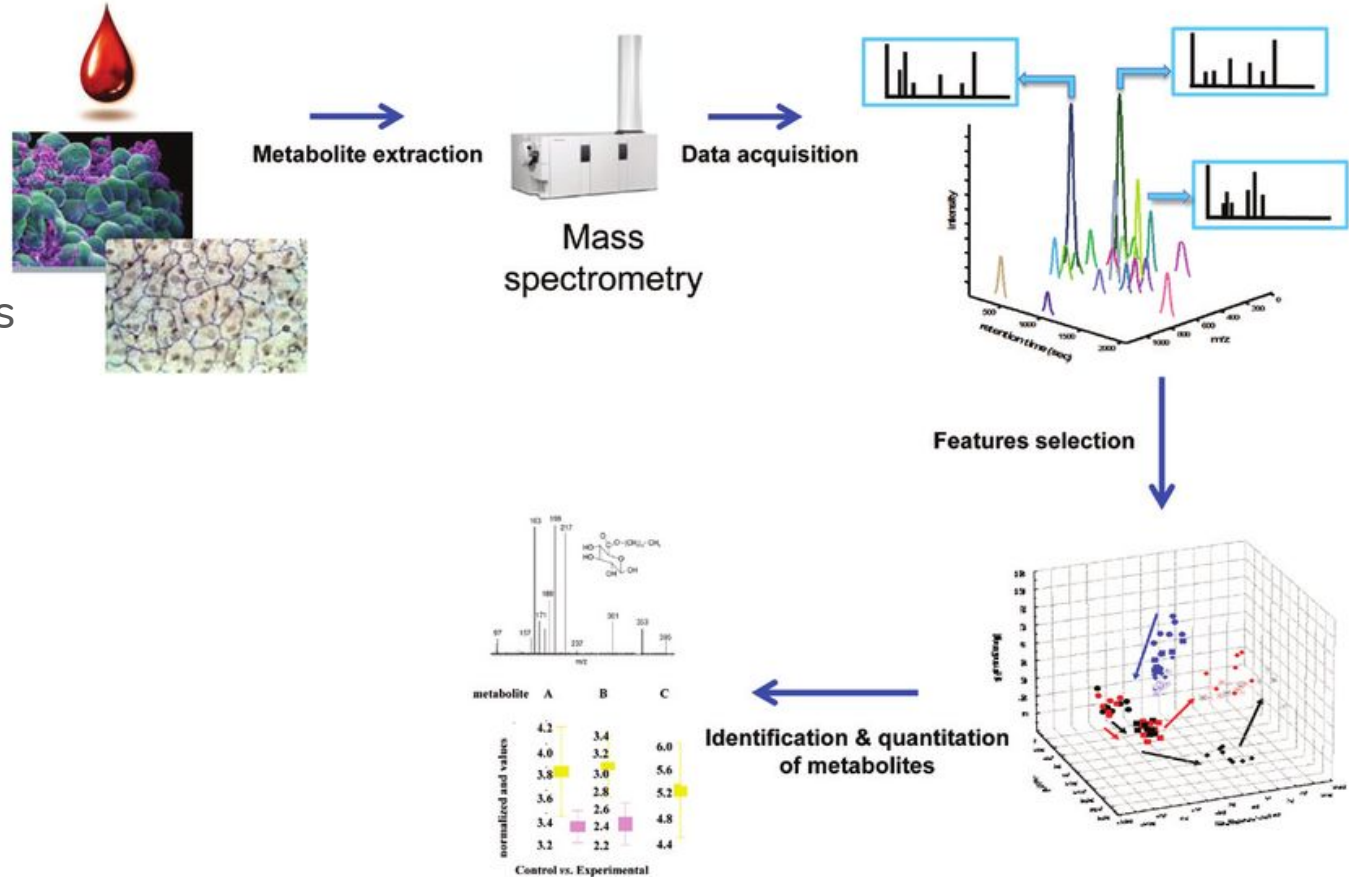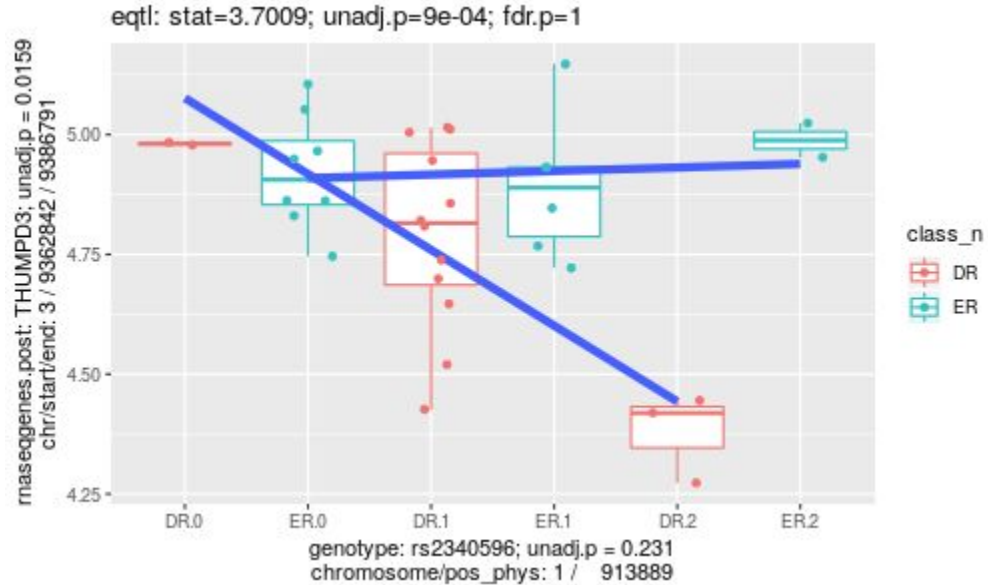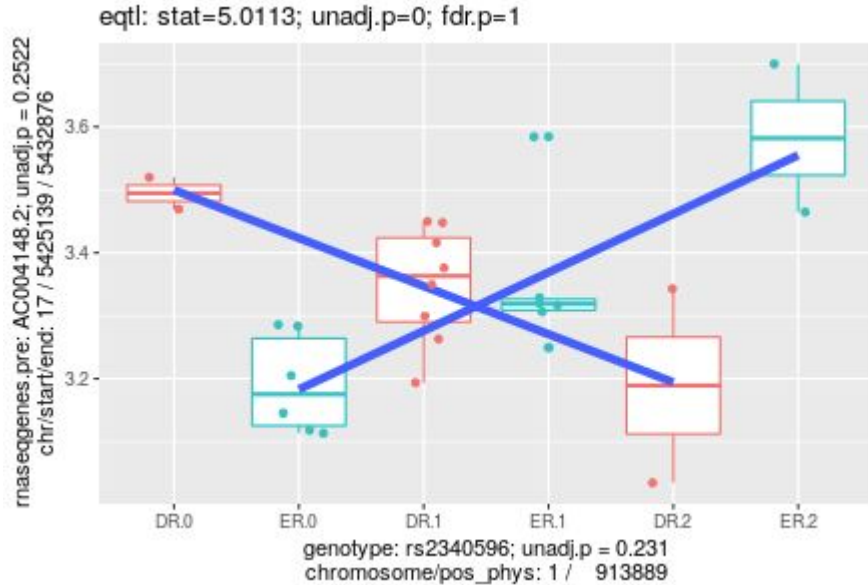
data (n x m): feature extraction

m =

● metabolomics

measured using mass spectrometry

min p value 0.047

data (n × m): feature comprehension

eQTL (expression quantitative trait loci)

data (n x m): feature comprehension (annecdotes)

Bcl11b gene:

- related to group 2 innate lymphoid cell development
- suppresses Th1 while limiting Th2 cell differentiation

TNFSF4 and FAM167A-BLK gene:

- includes asthma associated SNPS

mental illness and inflammation type SNPs were also enriched

thank you!