



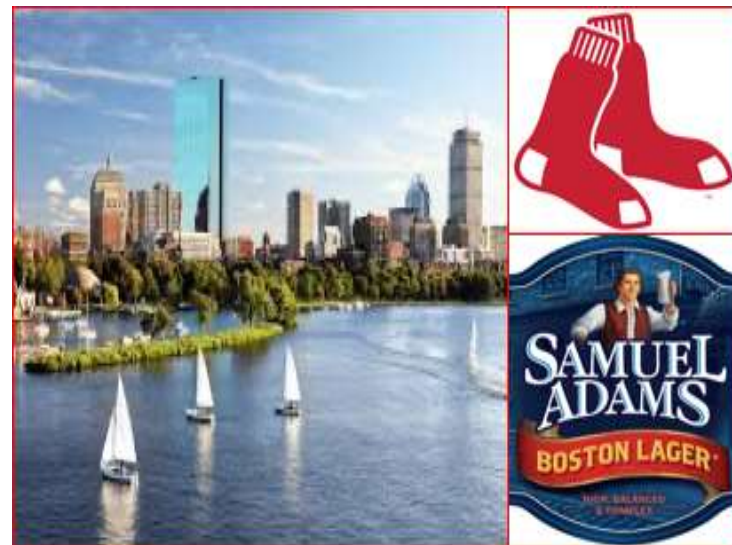
The Challenges of Meta-Analysing Metabolomics Data; Experiences from the Consortium Of METabolomics Studies (COMETS)

Rachel Kelly PhD
Channing Division of Network Medicine
BWH, HMS

Thursday 23rd April 2020
CEDAR MRC Epidemiology Seminar



Imperial College London



CHANNING DIVISION OF NETWORK MEDICINE

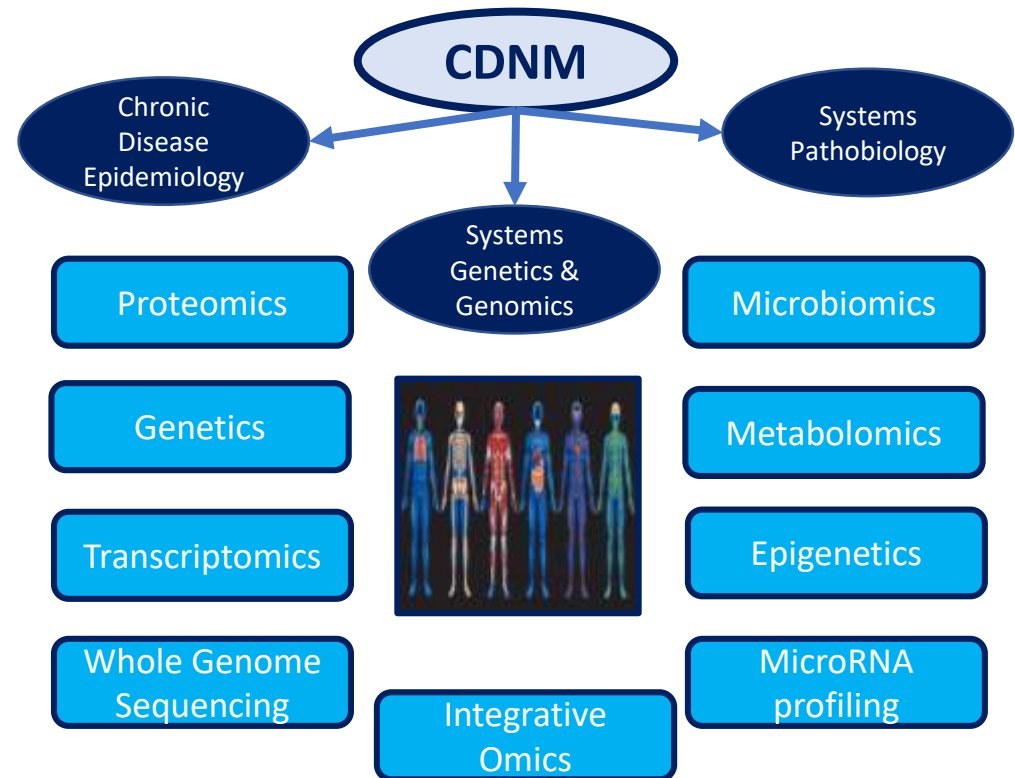


Edwin Silverman
Division Chief



Our mission is to

- (i) use an **integrated, network-based, systems biology-driven approach** to define the etiology of complex diseases;
- (ii) reclassify complex diseases based on **systems pathobiological mechanisms**;
- (iii) to develop new treatments and preventive strategies based on these new disease classifications using **systems pharmacology approaches**



<https://www.brighamandwomens.org/research/departments/channing-division-of-network-medicine>

CHANNING DIVISION OF NETWORK MEDICINE

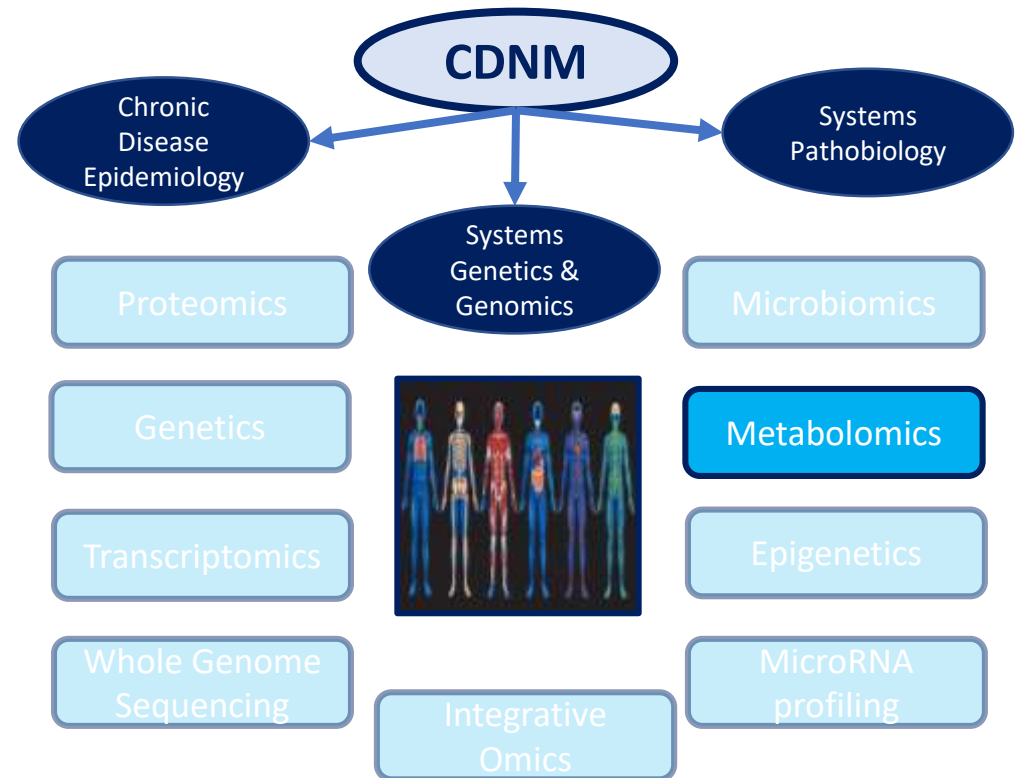


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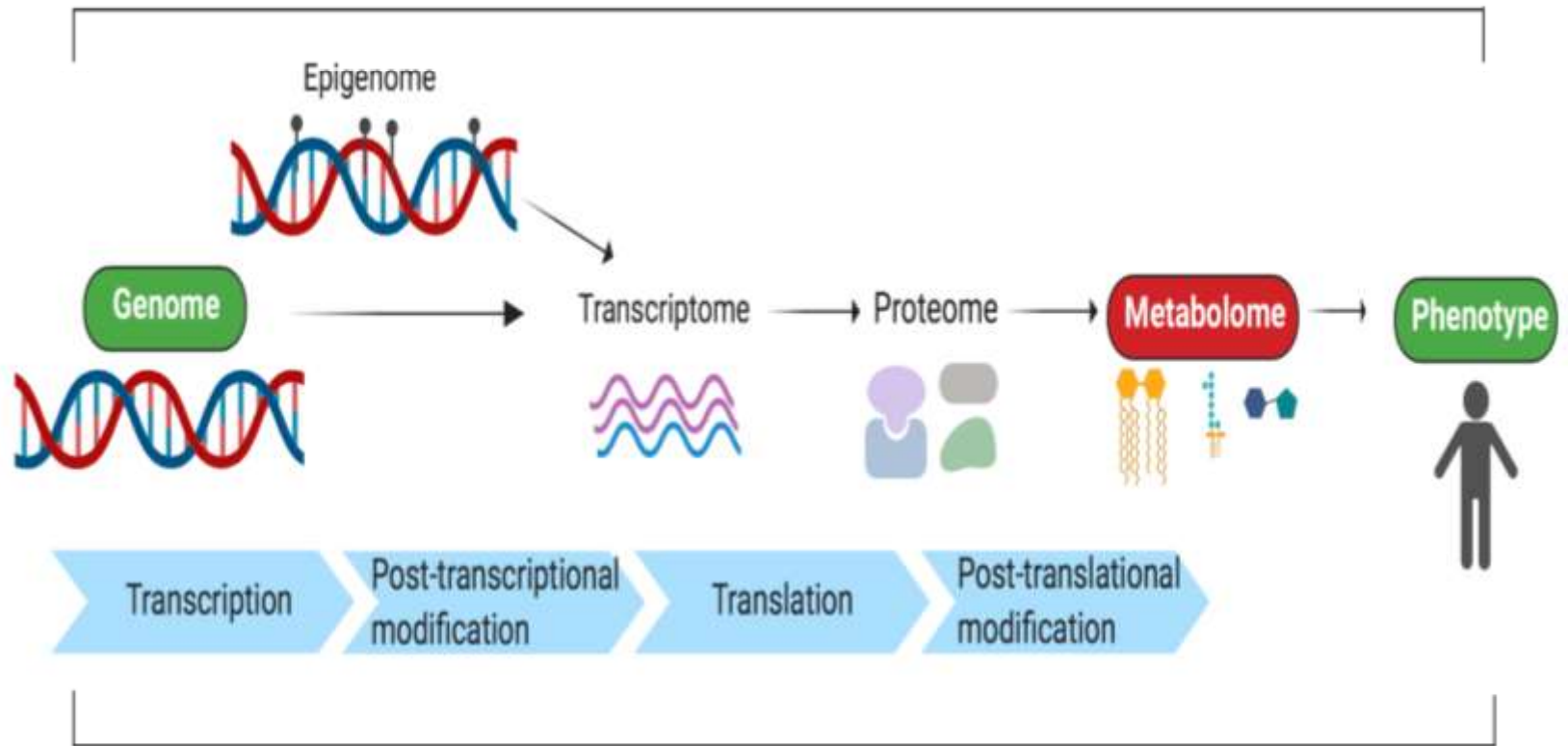


<https://www.brighamandwomens.org/research/departments/channing-division-of-network-medicine>

Metabolomics

The Central Biological Dogma

Environment; Diet; Air pollution; Geography;
Demographics



Microbiome

Metabolism of
Complex Carbohydrates

Biodegradation of
Xenobiotics

Metabolism of
Complex Lipids

Nucleotide
Metabolism

Metabolic Networks

Complete set of metabolic and physical processes determining physiological & biochemical properties of a cell

- *chemical reactions of metabolism*
 - *metabolic pathways*
 - *regulatory interactions*

Metabolism of
Amino Acids

Energy
Metabolism

Metabolism of
Cofactors and Vitamins

Biosynthesis of
Secondary Metabolites

Metabolism of
Complex Carbohydrates

Biodegradation of
Xenobiotics

Metabolism of
Complex Lipids

Nucleotide
Metabolism

Metabolomics

GLOBAL PROFILING OF ALL THE
SMALL MOLECULES
(*<900 daltons*) IN A BIOLOGICAL
SYSTEM

*Captures metabolic and physical
processes determining physiological and
biochemical properties of a cell*

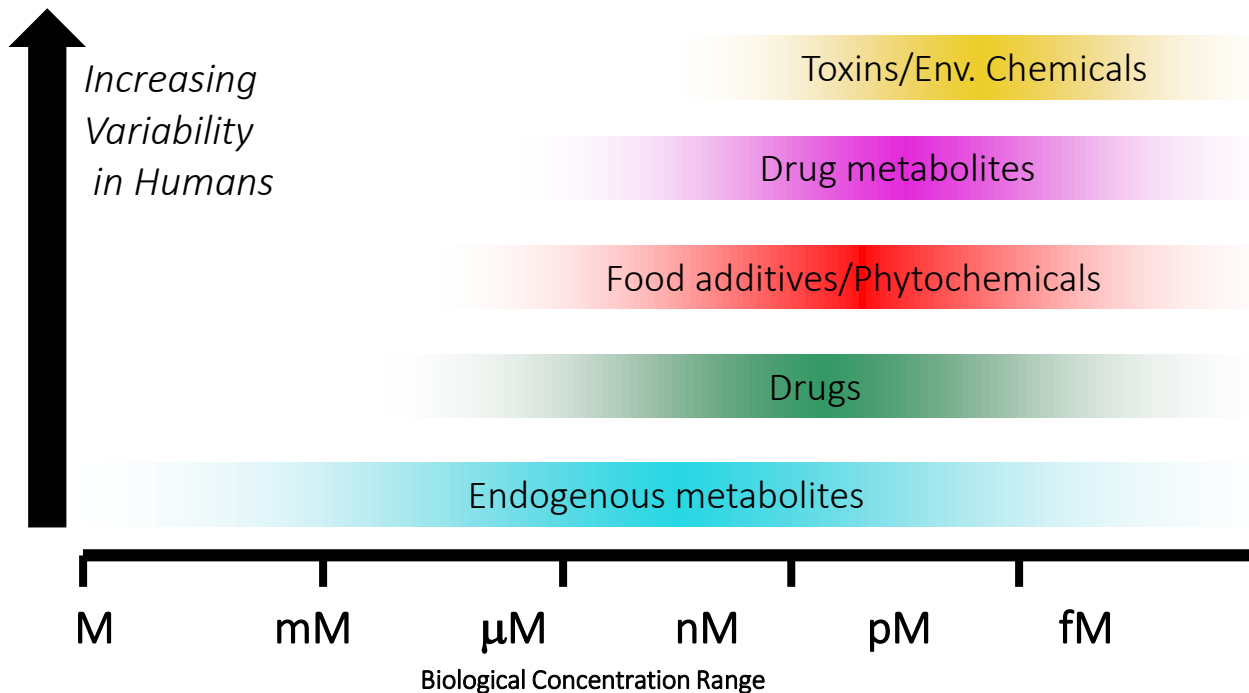
Metabolism of
Amino Acids

Energy
Metabolism

Metabolism of
Cofactors and Vitamins

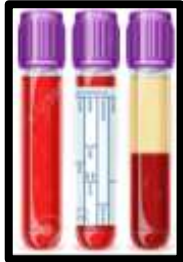
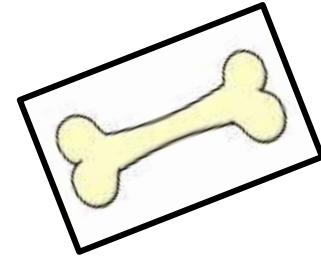
Biosynthesis of
Secondary Metabolites

The Human Metabolomes



Courtesy of bioinformatics.ca

The Human Metabolomes



*Increasing
Variability
in Humans*

Toxins/Env. Chemicals

Drug metabolites

Food additives/Phytochemicals

Drugs

Endogenous metabolites

M mM μ M nM pM fM

Biological Concentration Range



Courtesy of bioinformatics.ca



Metabolomic Profiling Platforms

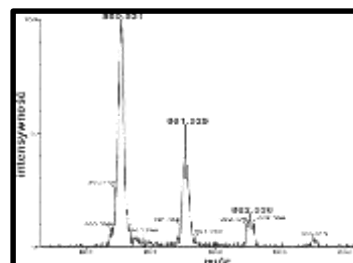
Nuclear Magnetic Resonance

- Most commonly H^1 or C^{13}
- Spectra based on the chemical shift induced by strong magnetic field
- Quantitative
- Highly reproducible
- Provides structural information



Mass spectrometry

- Ionization followed by assessment of mass-to-charge ratio
- More Sensitive
- Can measure more metabolites



Metabolomic Profiling Data: *Targeted versus Untargeted*



Untargeted

- Comprehensive 'Global' analysis of all measurable analytes in a biological sample
- Includes metabolites of unknown identity
- *Relative* abundance

Targeted

- Measurement of defined groups of chemically characterized and biochemically annotated metabolites
- Fewer Metabolites
- *Absolute* quantification



What can the Metabolome tell us?

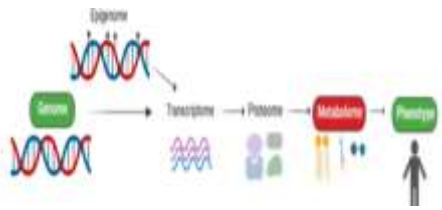


“Instantaneous Snapshot of the Physiological Status of a Biological System”

PAST

Environment

Preceding “omes”



FUTURE

Pre/Early Stage Pathogenesis



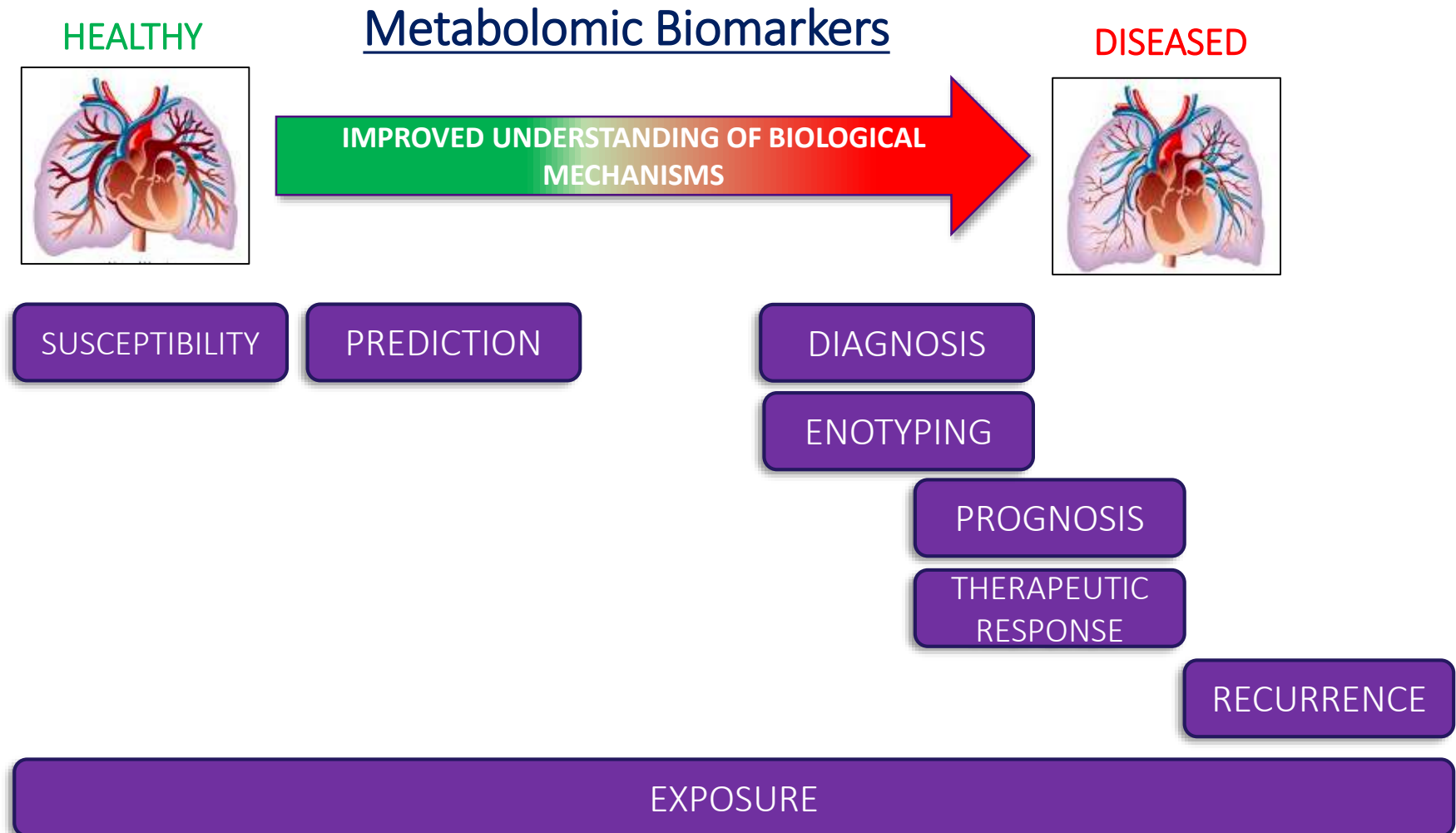
PRESENT

Environment

Phenotype

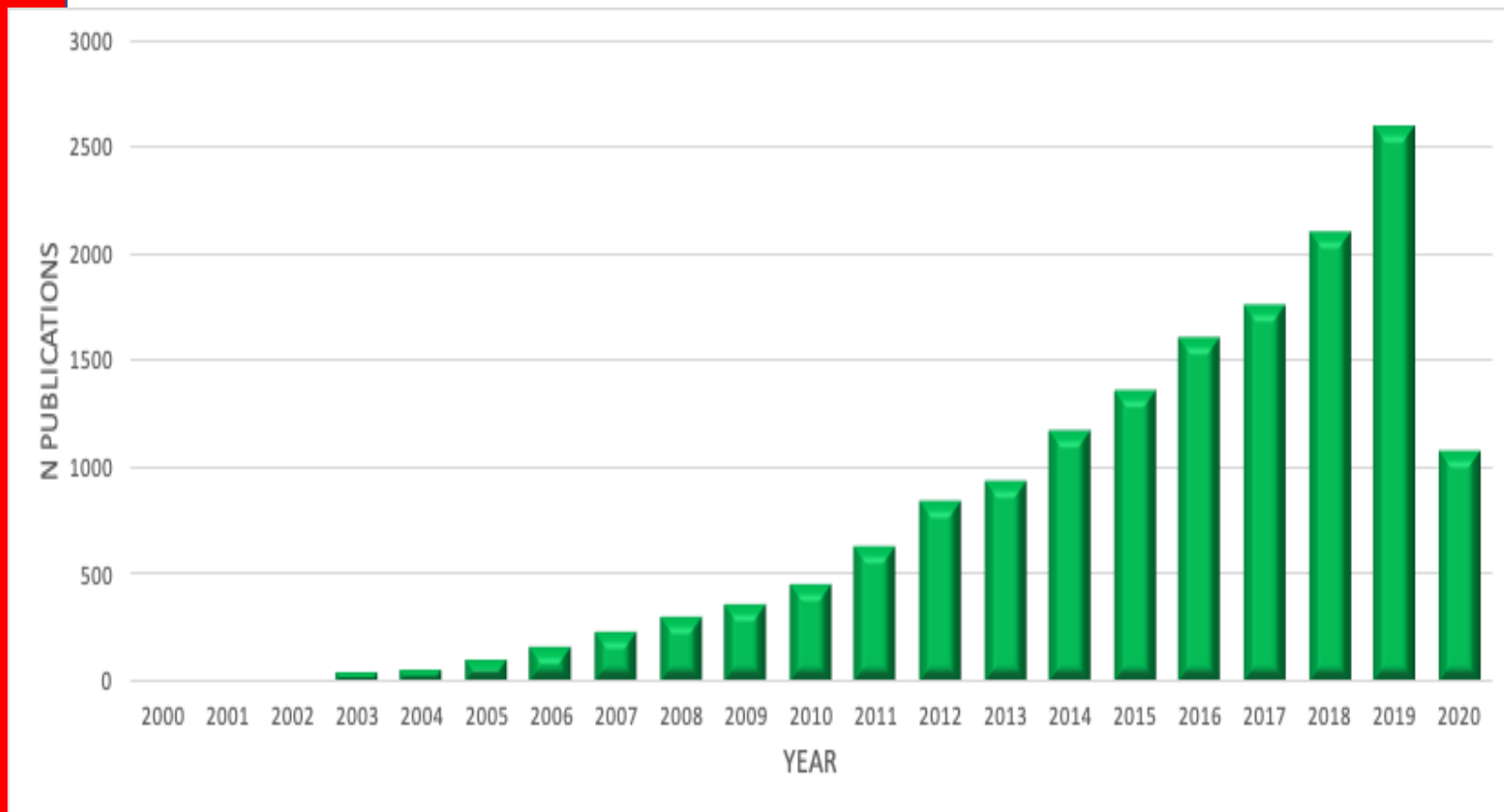


What can the Metabolome do for us?



Metabolomics
is a Rapidly
Growing Field

Number of Metabolomics Related Publications Per Year Since 2000



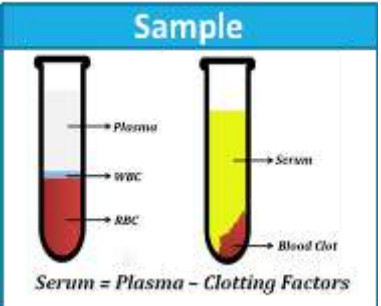
PUBMED SEARCH TERMS: (metabolom*[title] OR (Metabolite profil*[title]) OR (metabolite signature[title]))
SEARCH DATE: 22/4/2020

Metabolomics Can be Noisy

Biological Heterogeneity

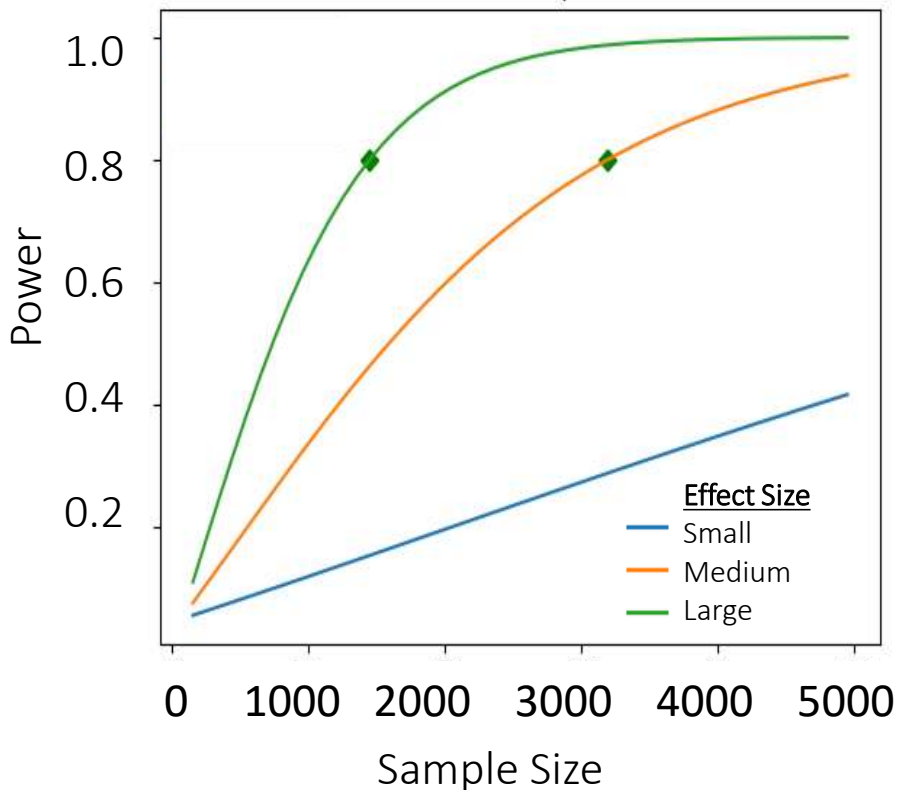


Technical Heterogeneity



Obtaining the Strongest Metabolomic Findings

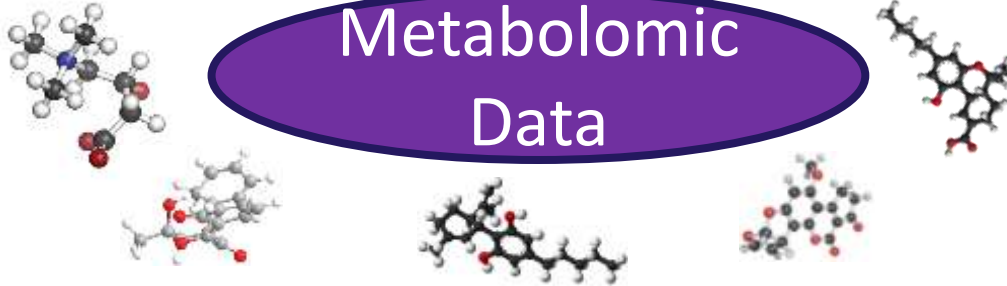
Power vs. Sample Size



- Many existing metabolomic cohorts have limited sample sizes
- Meta-analyses provide:
 - More power to detect an effect
 - More precise and accurate effect estimates
 - More generalizable findings

Meta-Analyzing Metabolomic data Can be Complex

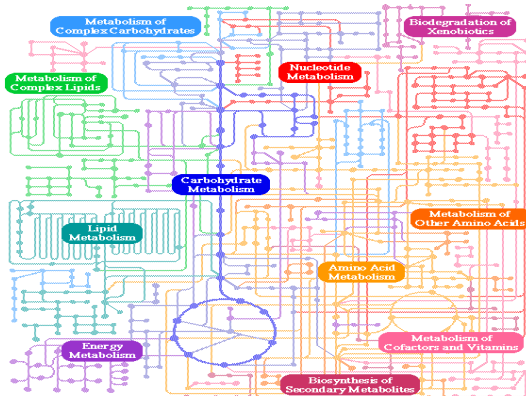
Metabolomic Data



Incomplete Coverage of the Metabolome

Inconsistent Nomenclature

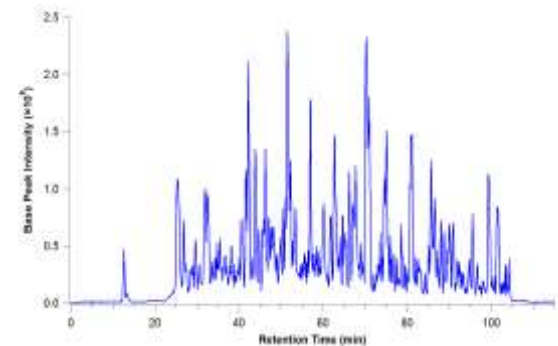
Relative Nature of Measurement



(2S)-2-amino-3-(1H-indol-3-yl)Propanoic acid
 (2S)-2-amino-3-(1H-indol-3-yl)Propanoate
 (S)- α -amino-1H-Indole-3-propanoate
 (S)- α -amino-1H-Indole-3-propanoic acid
 (S)- α -amino- β -(3-Indolyl)-propionic acid
 (S)-Tryptophan
 1H-Indole-3-alanine
 L-(-)-Tryptophan
 L- β -3-Indolylalanine
 L- β -3-indolylalanine



Plus 71 other synonyms...



The Consortium of METabolomic Studies (COMETS)



COnsortium of METabolomics Studies

- *Extramural-intramural partnership promoting collaboration among prospective metabolomic epidemiology studies*
- **Mission and Objectives**
- Provide framework to foster international collaborations among studies sharing common objectives;
- Provide forum for the discussion, development & pursuit of new research
- Advance knowledge of the metabolome
- **Membership Eligibility**
- Prospective cohort, 100+ participants with blood metabolomics
- Phenotype follow-up
- MS or NMR



Krista Zanetti:
COMETS Program Officer



Jessica Lasky-Su
COMETS Chair

<https://epi.grants.cancer.gov/comets/>



COMETS Analytics

<http://www.comets-analytics.org>



“a freely-accessible cloud-based, self-serviced analytic platform developed for consortium-based metabolomics analyses”

Built-in Metabolite Harmonization: continually updating master list of metabolites with multiple levels of information

Yu et al. *AJE*, (2019) 188; 6
Methods paper in Development (Temprosa et al.)

Steven C. Moore



Marinella Temprosa



Ewy Mathé



Analysis Pipeline

Meta-Analyses

Centralized analyses of aggregated cohort data

Cohort-Specific Analyses

Conduct patient level analyses for data exploration, and approved, manuscript proposals



Metabolite Harmonization

Create mapping of metabolites across cohorts and platforms

Data Preparation

Facilitate creation of common input file

Data Integrity

Identify possible data problems prior to analyses

Metabolite Harmonization: All available metabolite information



COMETS Analytics maintains a dynamic continually updating master list of metabolites with multiple levels of information on every metabolite submitted for analysis, including:

- *Chemical Id (HMDB, KEGG, CHEBI, etc.)*
- *Platform assigned super pathways*
- *m/z and retention time*
- *Metabolite classification via metabolomics work bench and metabolon*

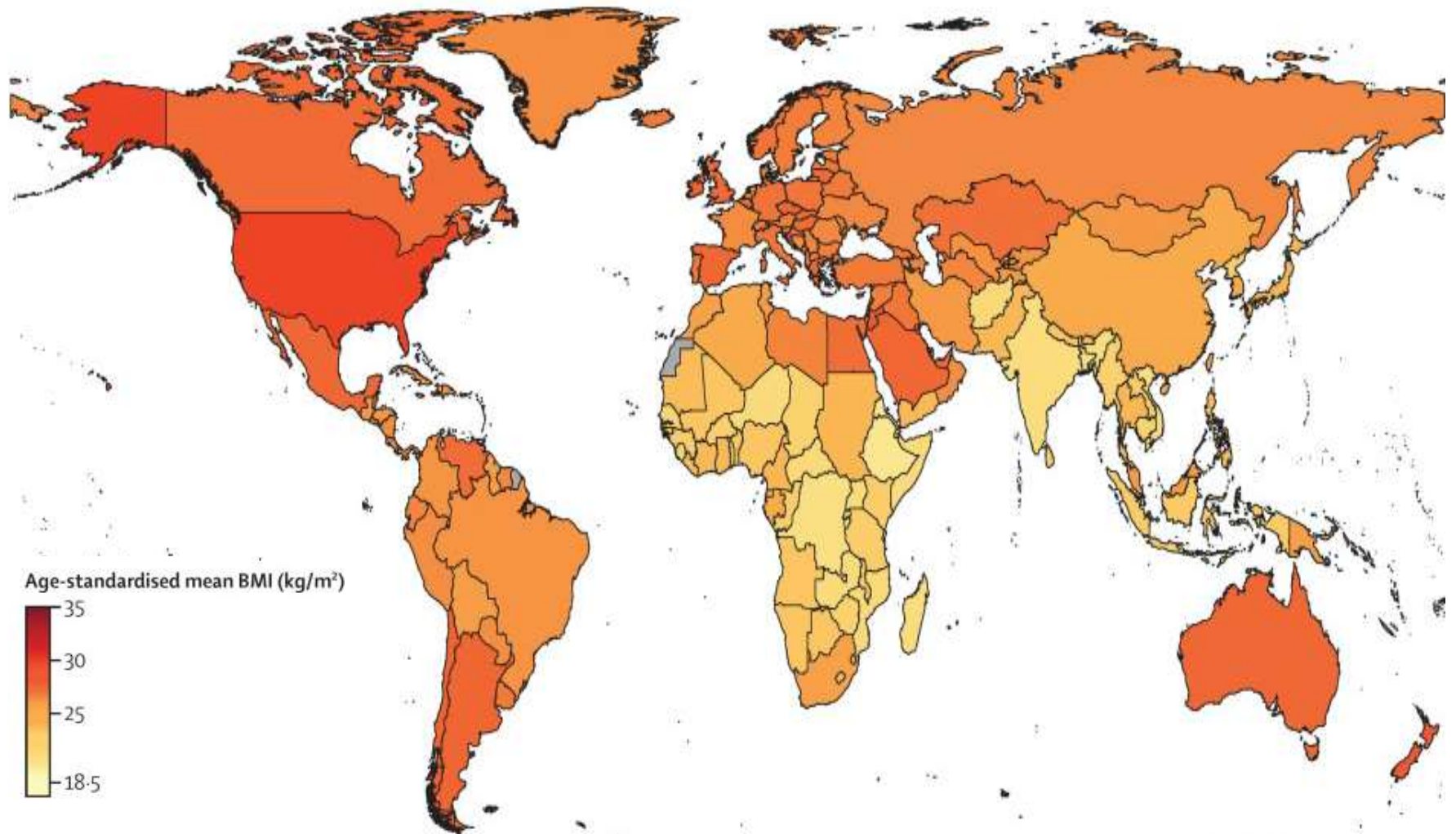
Automatic and manual curation



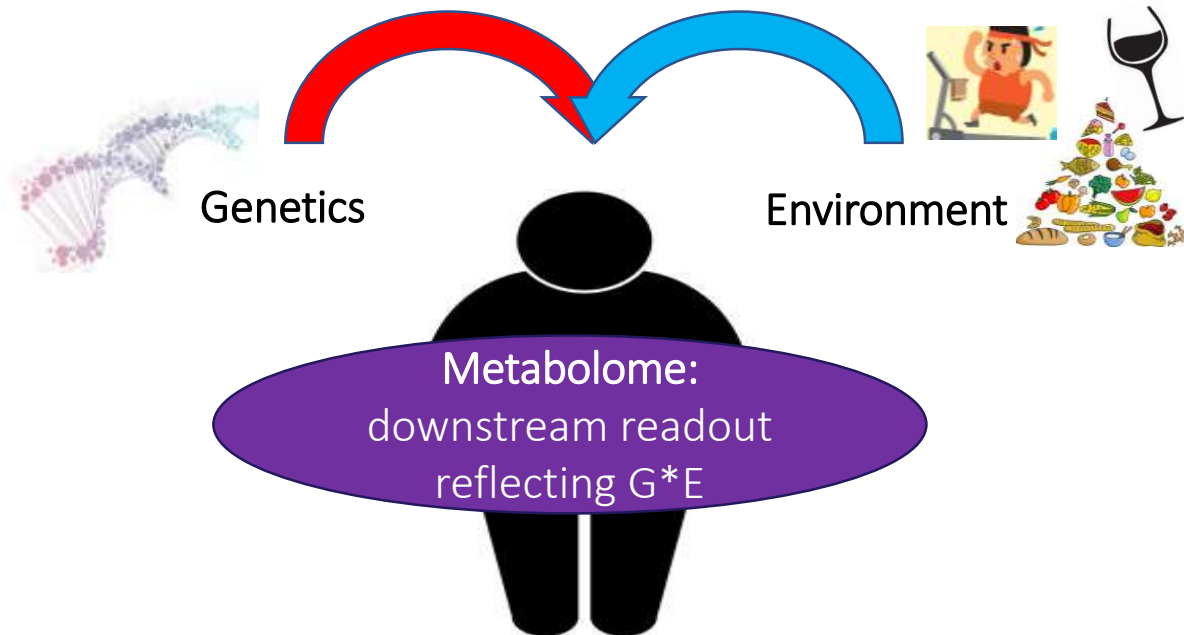
	A	B	C	D	E	F	G	H	I	J	K	L
	metabid	metabolite _name	SUPER_ PATHWAY	SUB_PATHWAY	COMP _ID	PLATFORM	PUBCHEM	HMDB_ID	KEGG ID	chEBI ID	m/z	rt
1	ACETOACETATE	acetoacetate	Lipid	Ketone Bodies	33963	GC/MS	96	HMDB00060	NA	NA	NA	NA
2	ACETYLCARNITINE	acetylcarnitine	Lipid	Fatty Acid Metabolism(Acyl Carnitine)	32198	LC/MS Pos	1	HMDB00201	NA	NA	NA	NA
3	ACISOGA	acisoga	Amino Acid	Polyamine Metabolism	43258	LC/MS Pos	129397	NA	NA	NA	NA	NA
4	ADENINE	adenine	Nucleotide	Purine Metabolism, Adenine containing	554	LC/MS Pos	190	HMDB00034	NA	NA	NA	NA

The Metabolome of BMI: A COMETS Meta-analysis

Age Standardized Mean BMI in Men by Country in 2014



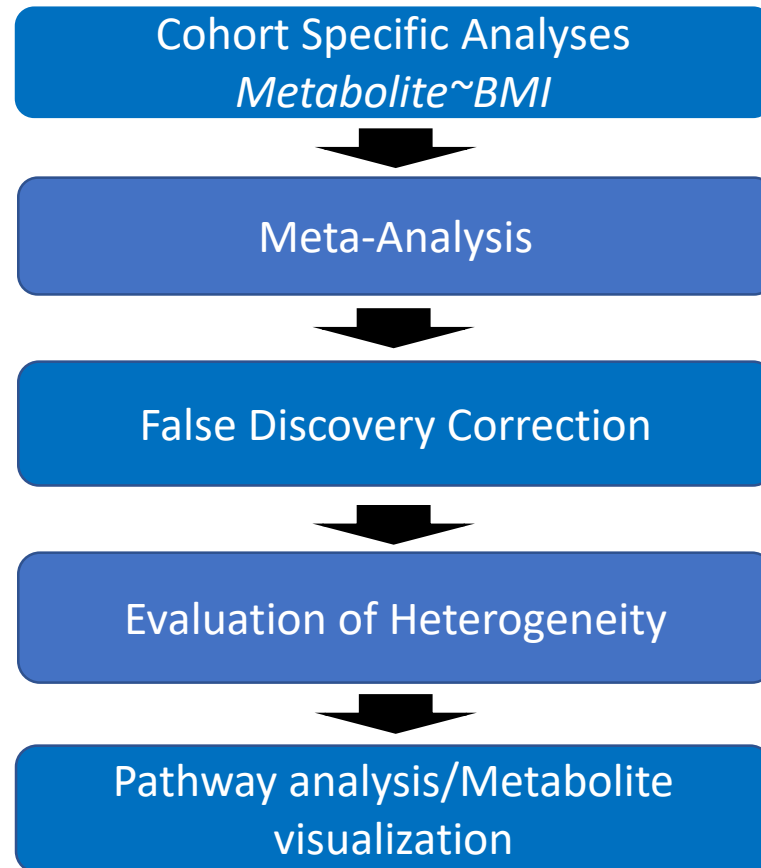
BMI is perfectly suited to Metabolomic Exploration



COMETS Proposal: The BMI of Obesity

- *Aim 1:* To evaluate relationships between blood metabolite concentrations and BMI across multiple cohorts utilizing a meta-analysis approach within the **COMETS** consortium
- *Aim 2:* To evaluate heterogeneity of associations by participant characteristics and by study characteristics

Methods



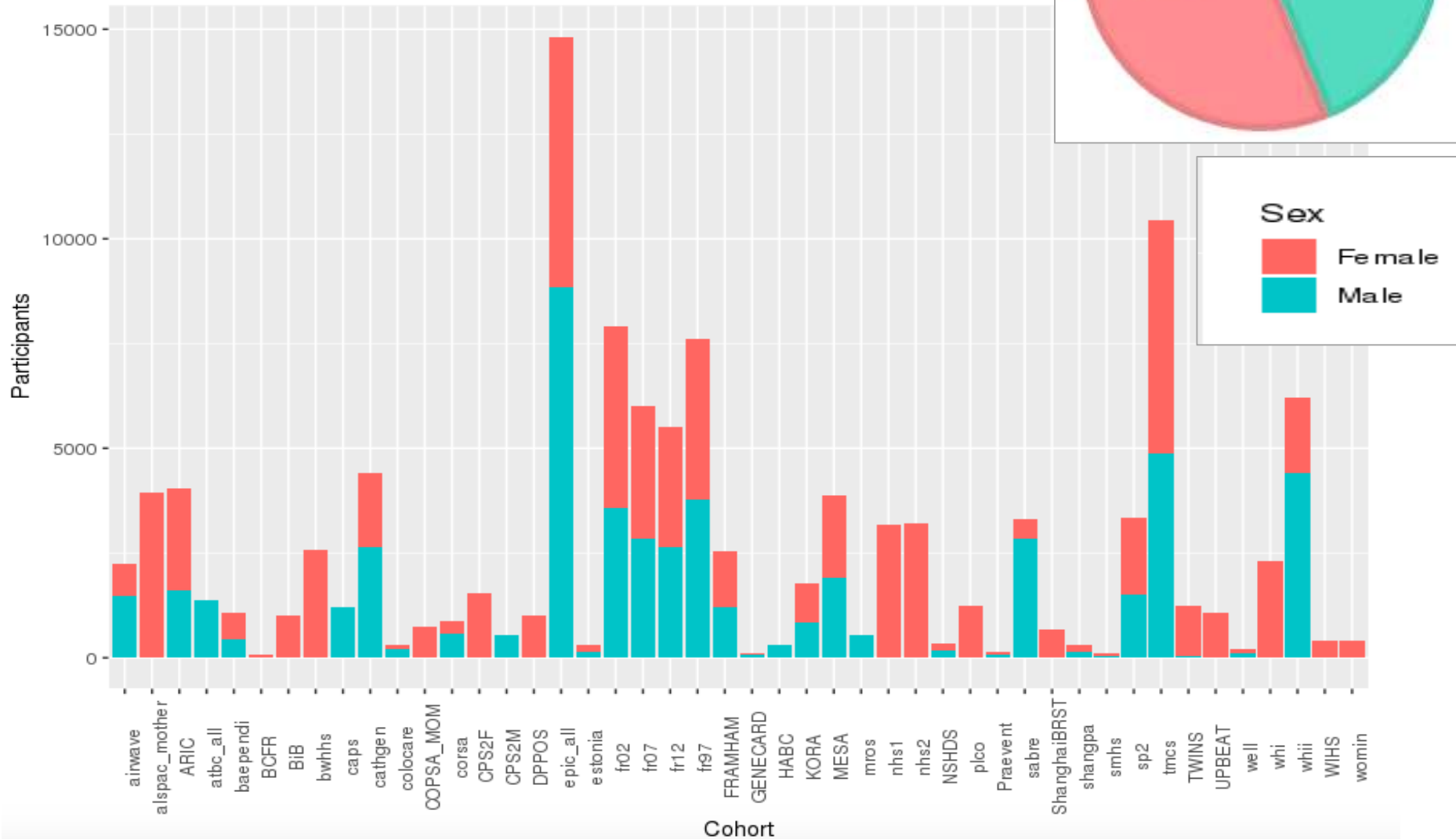
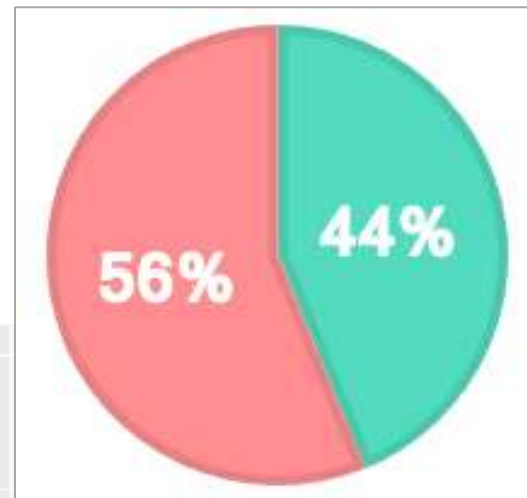
Investigated Models



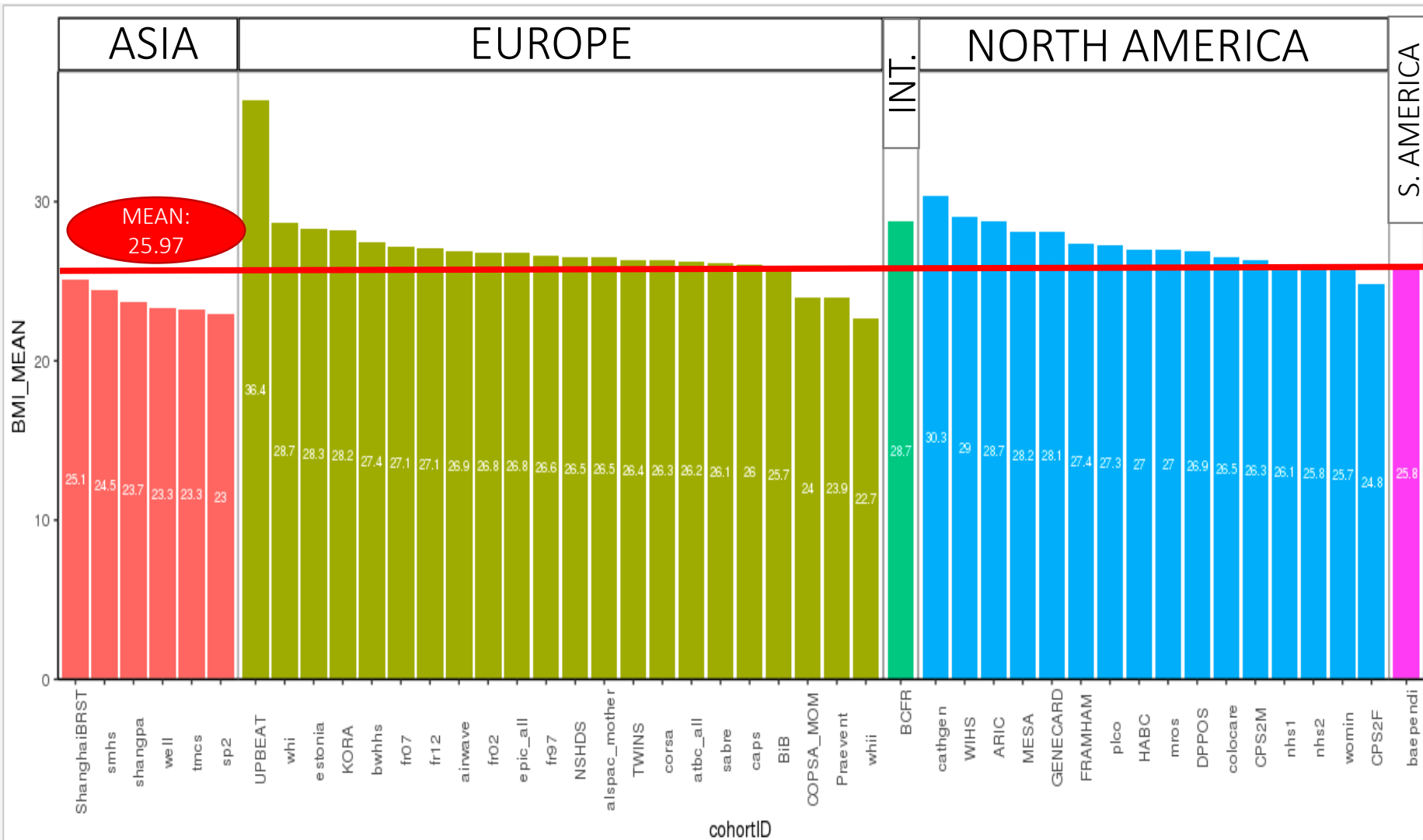
	A	B	C	D	E	F
1	MODEL	OUTCOMES	EXPOSURE	ADJUSTMENT	STRATIFICATION	WHERE
2	BMI.1.0 Basic adjustment	All metabolites	bmi	age female race_grp nested_case		bmi>=1
3	BMI.1.1 Multivariable adjusted	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted nested_case		bmi>=1
4	BMI.1.2 Multivariable and diabetes	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted prev_diabetes nested_case		bmi>=1
5	BMI.2.0 Gender stratified	All metabolites	bmi	age race_grp educ_grp smk_grp alc_grp fasted nested_case	female	bmi>=1
6	BMI.2.1 Gender stratified diabetes	All metabolites	bmi	age race_grp educ_grp smk_grp alc_grp fasted prev_diabetes nested_case	female	bmi>=1
7	BMI.3.0 Race stratified	All metabolites	bmi	age female educ_grp smk_grp alc_grp fasted nested_case	race_grp	bmi>=1
8	BMI.3.1 Race stratified diabetes	All metabolites	bmi	age female educ_grp smk_grp alc_grp fasted prev_diabetes nested_case	race_grp	bmi>=1
9	BMI.4.0 Fasted stratified	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp nested_case	fasted	bmi>=1
10	BMI.4.1 Fasted stratified diabetes	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp prev_diabetes nested_case	fasted	bmi>=1
11	BMI.5.0 Diabetes stratified	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted nested_case	prev_diabetes	bmi>=1
12	BMI.6.0 nested_case stratified	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted	nested_case	bmi>=1
13	BMI.7.0 Age stratified	All metabolites	bmi	female race_grp educ_grp smk_grp alc_grp fasted nested_case	age_grp	bmi>=1
14	BMI.7.1 Age stratified diabetes	All metabolites	bmi	female race_grp educ_grp smk_grp alc_grp fasted prev_diabetes nested_case	age_grp	bmi>=1
15	BMI.7.2 Age stratified age-adj	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted nested_case	age_grp	bmi>=1
16	BMI.7.3 Age stratified age-adj diabetes	All metabolites	bmi	age female race_grp educ_grp smk_grp alc_grp fasted prev_diabetes nested_case	age_grp	bmi>=1
17						
18						

Pre-specified Models in
the User Input File

126,423 Participants from 46 Cohorts



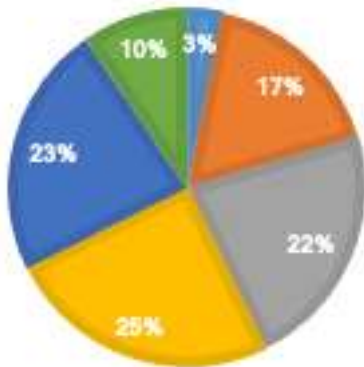
Participant Mean BMI



Participant Characteristics

AGE (YRS)

0-20 20-40 40-50 50-60 60-70 >70



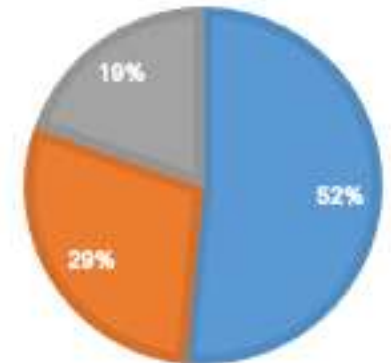
RACE

Black Hispanic White Asian Other



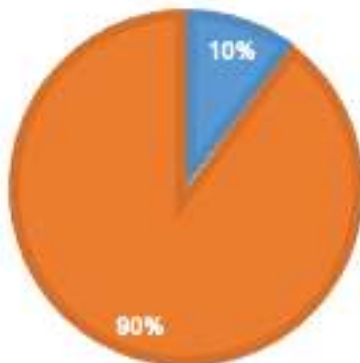
SMOKING STATUS

never former current



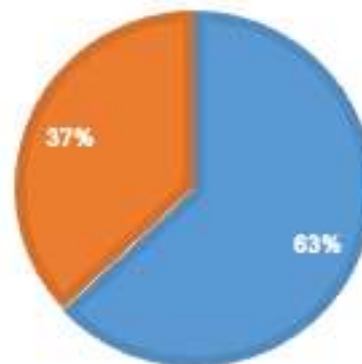
DIABETES STATUS

Yes No



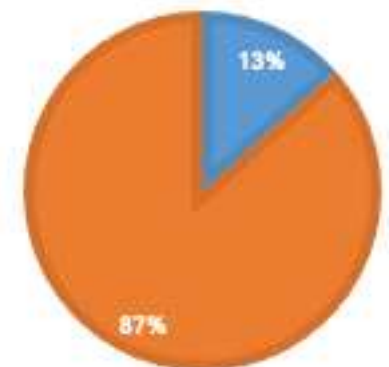
FASTING STATUS

Yes No

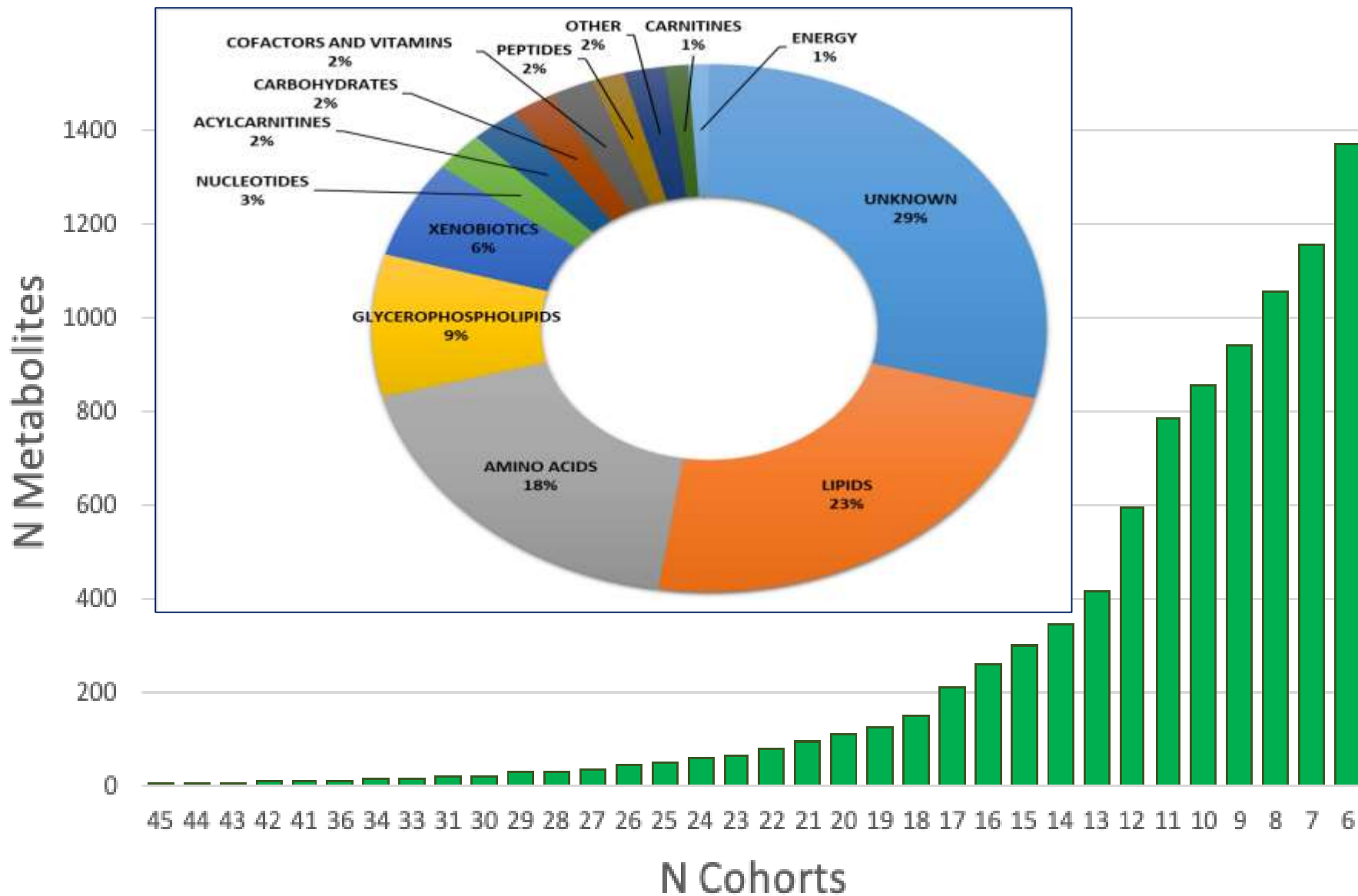


NESTED CASE STATUS

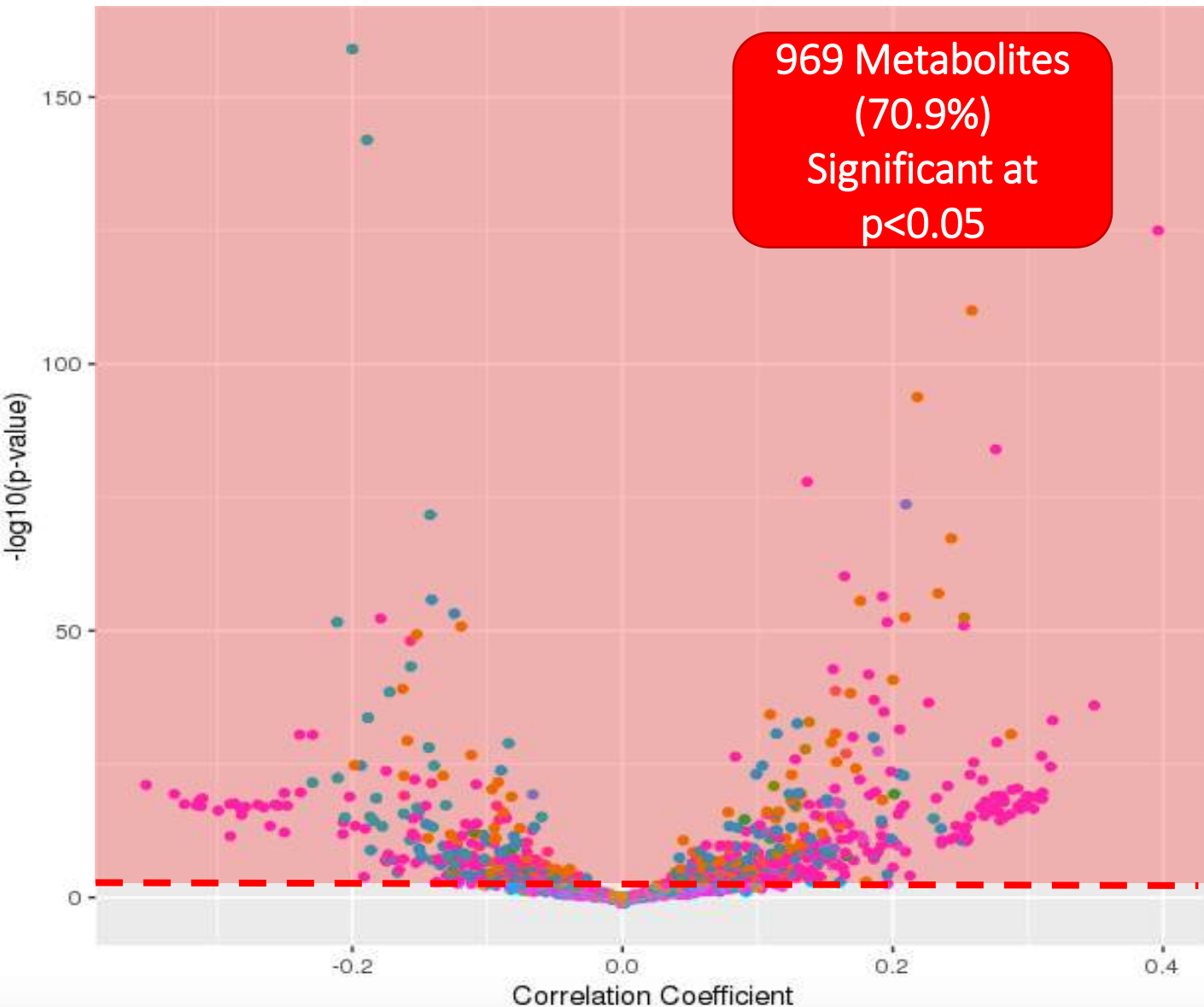
Yes No



1367 Harmonized Metabolites



BMI~Metabolite Correlations



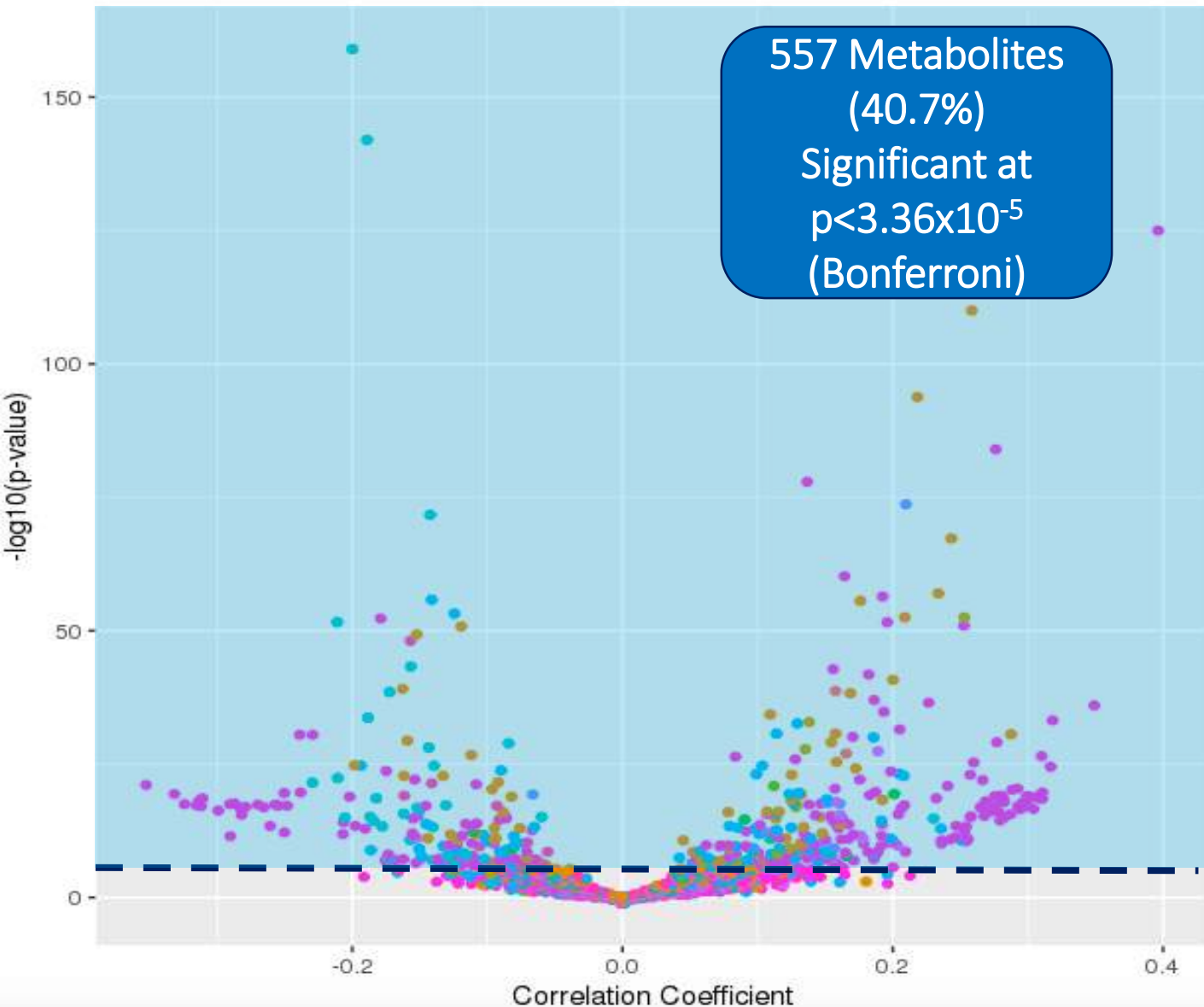
1.2 Multivariable Adjusted Model

SuperPathway

- ACYLCARNITINES
- AMINO ACIDS
- CARBOHYDRATES
- CARNITINES
- COFACTORS AND VITAMINS
- ENERGY METABOLITES
- GLYCEROPHOSPHOLIPIDS
- LIPIDS
- NUCLEOTIDES
- PEPTIDES
- UNKNOWN
- XENOBIOTICS

Adj for; age, gender, race, educational level, smoking status, alcohol consumption, fasting status, nested case-control status

BMI~Metabolite Correlations



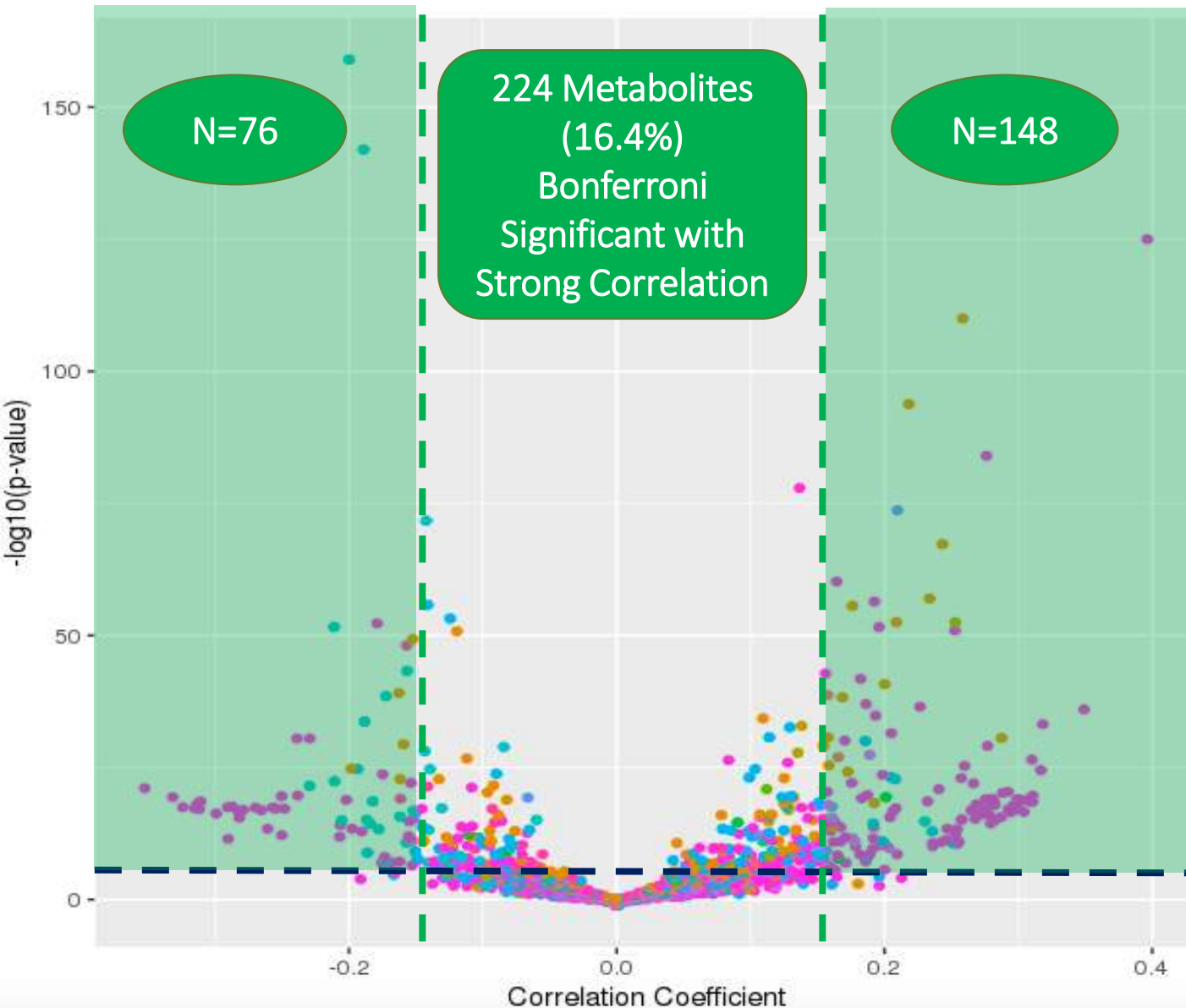
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*Adj for; age, gender, race,
educational level, smoking
status, alcohol
consumption, fasting
status, nested case-control
status*

BMI ~ Metabolite Correlations



1.2 Multivariable Adjusted Model



Adj for; age, gender, race, educational level, smoking status, alcohol consumption, fasting status, nested case-control status

Top Metabolite Hits

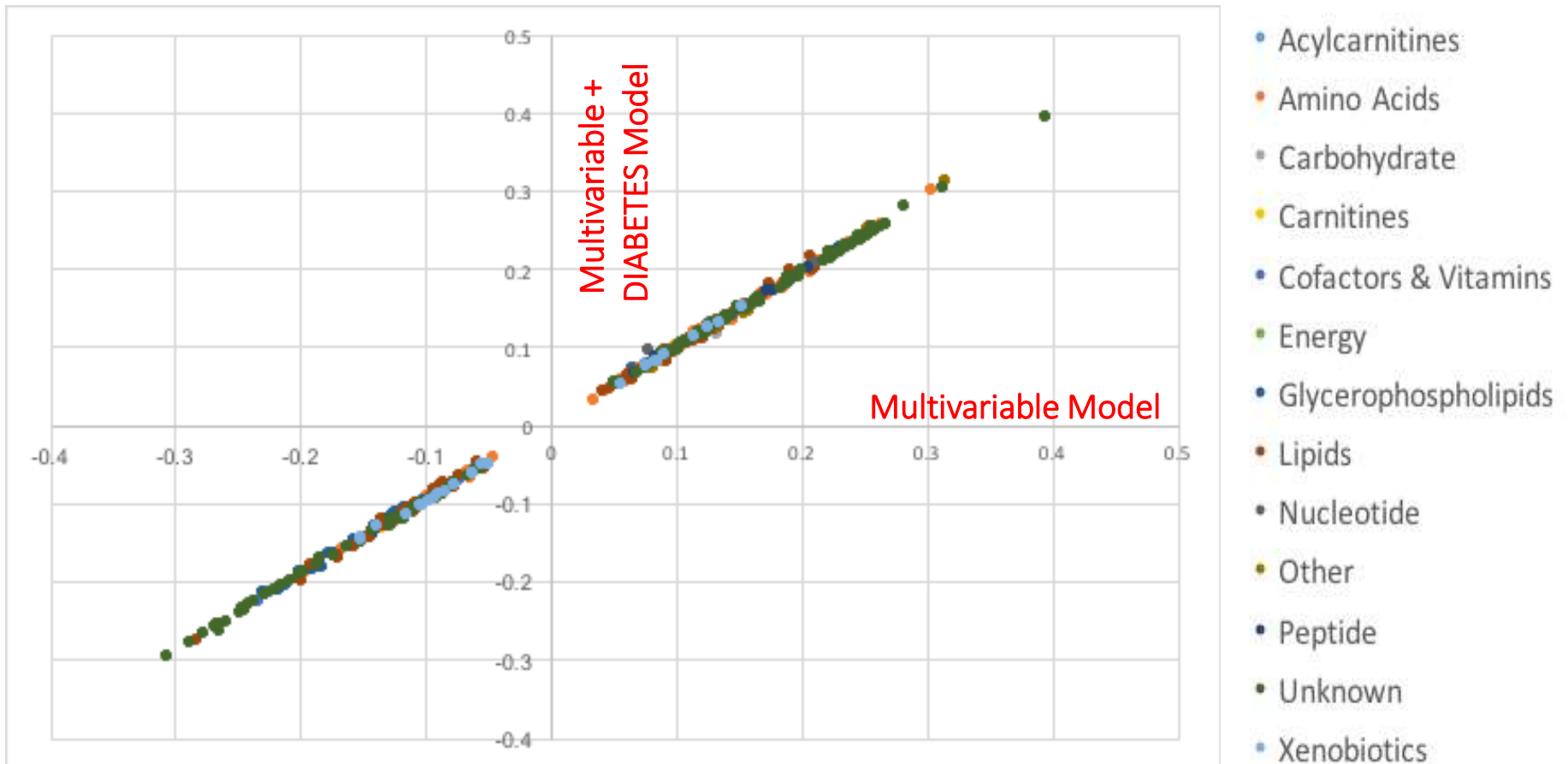


Metabolite	Superpathway	Coef. (95%CI)	P-Value
PC(o-22:0/22:6(4Z,7Z,10Z,13Z,16Z,19Z))	GLYCERO-PHOSPHOLIPIDS	-0.2 (-0.21,-0.19)	6.41E-160
PC(18:0/24:0)	GLYCERO-PHOSPHOLIPIDS	-0.19 (-0.2,-0.17)	5.90E-143
X - 11315	UNKNOWN	-0.18 (-0.2,-0.16)	4.57E-53
LysoPC(18:2(9Z,12Z))	GLYCERO-PHOSPHOLIPIDS	-0.21 (-0.24,-0.18)	2.56E-52
Guanidinosuccinic acid	AMINO ACIDS	-0.15 (-0.17,-0.13)	4.91E-50
Cinnamoylglycine	XENOBIOTICS	-0.16 (-0.18,-0.14)	8.32E-49
2-3-PROPYL2-(TRIMETHYLAMMONIO)ETHYLPHOSPHATE	GLYCERO-PHOSPHOLIPIDS	-0.16 (-0.18,-0.13)	5.50E-44
L-Asparagine	AMINO ACIDS	-0.16 (-0.19,-0.14)	7.42E-40
PC(18:1(9Z)/24:0)	GLYCERO-PHOSPHOLIPIDS	-0.17 (-0.2,-0.15)	3.20E-39
LysoPC(18:1(9Z))	GLYCERO-PHOSPHOLIPIDS	-0.19 (-0.22,-0.16)	1.85E-34

Metabolite	Superpathway	Coef. (95%CI)	P-Value
cortolone glucuronide	UNKNOWN	0.4 (0.37,0.43)	2.06E-125
L-Valine	AMINO ACIDS	0.26 (0.24,0.28)	1.39E-110
L-Tyrosine	AMINO ACIDS	0.22 (0.2,0.24)	1.76E-94
X - 17340	UNKNOWN	0.28 (0.25,0.3)	1.05E-84
N2,N2-Dimethyl guanosine	NUCLEOTIDES	0.21 (0.19,0.23)	1.83E-74
L-Isoleucine	AMINO ACIDS	0.24 (0.22,0.27)	5.57E-68
2-Hydroxy butyric acid	ALPHA HYDROXY ACIDS	0.16 (0.15,0.18)	6.64E-61
L-Leucine	AMINO ACIDS	0.23 (0.21,0.26)	1.12E-57
X - 17357	UNKNOWN	0.19 (0.17,0.22)	3.61E-57
L-Kynurenine	AMINO ACIDS	0.18 (0.15,0.2)	2.71E-56

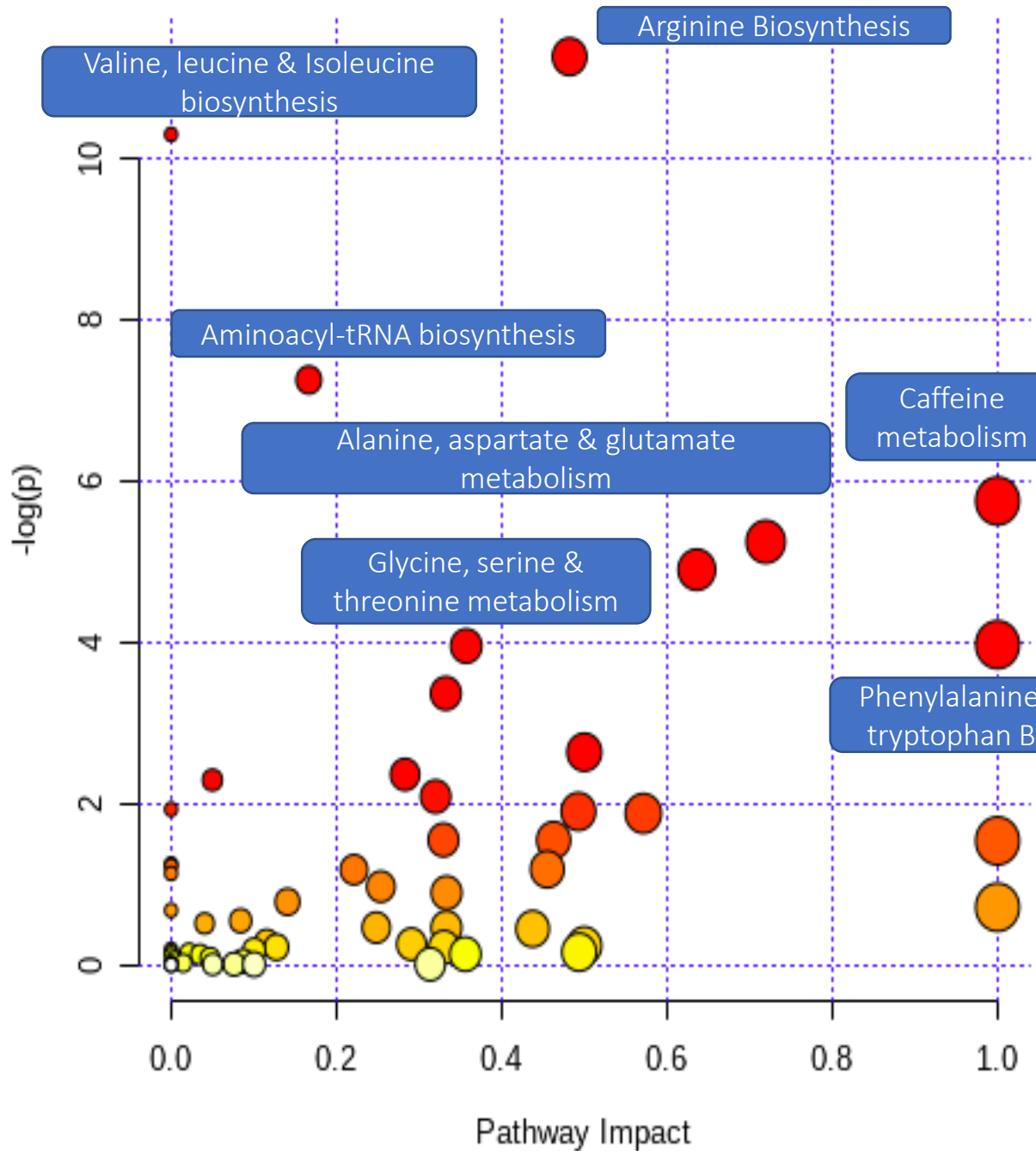
Additional Adjustment for Diabetes

Comparison of Correlation Coefficients for significant metabolites in the two models



Adj for; age, gender, race, educational level, smoking status, alcohol consumption, fasting status, nested case-control status (and Diabetes)

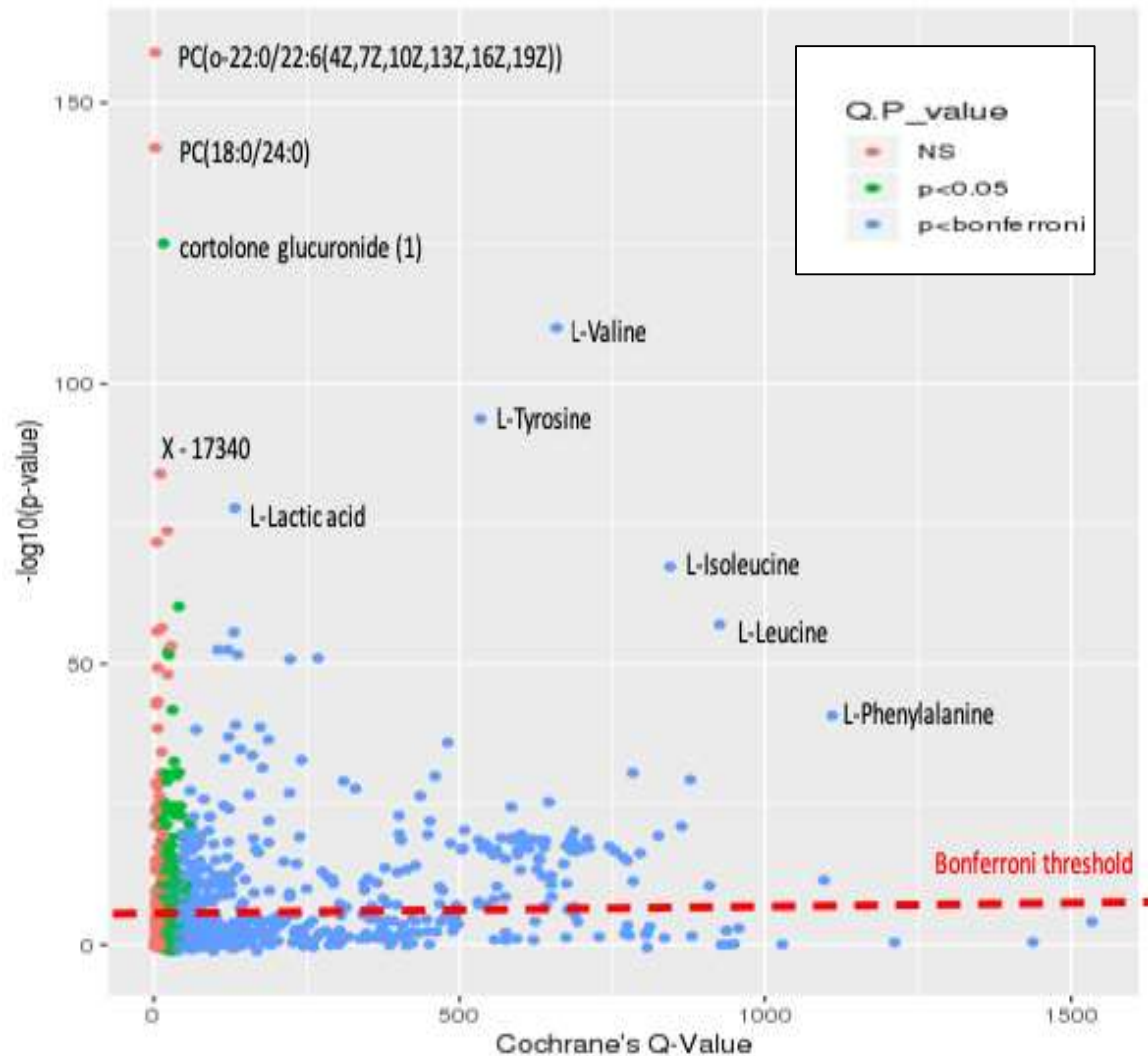
Pathway Analysis of 969 Significant Metabolites

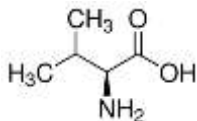


Cochrane's Q-Value

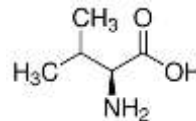
Cochrane's Q-Value versus $-\log_{10}(p\text{-value})$ for Each Metabolite

- ❖ Used to assess between Study Heterogeneity
- ❖ describes % variability in effect estimates due to heterogeneity rather than chance
- ❖ Larger Q value (& smaller Q p-value) means more likely there is heterogeneity between studies
- ❖ 460/557 Bonferroni significant metabolites, (82.6%) were 'significantly' heterogeneous
- ❖ Sensitive to large numbers

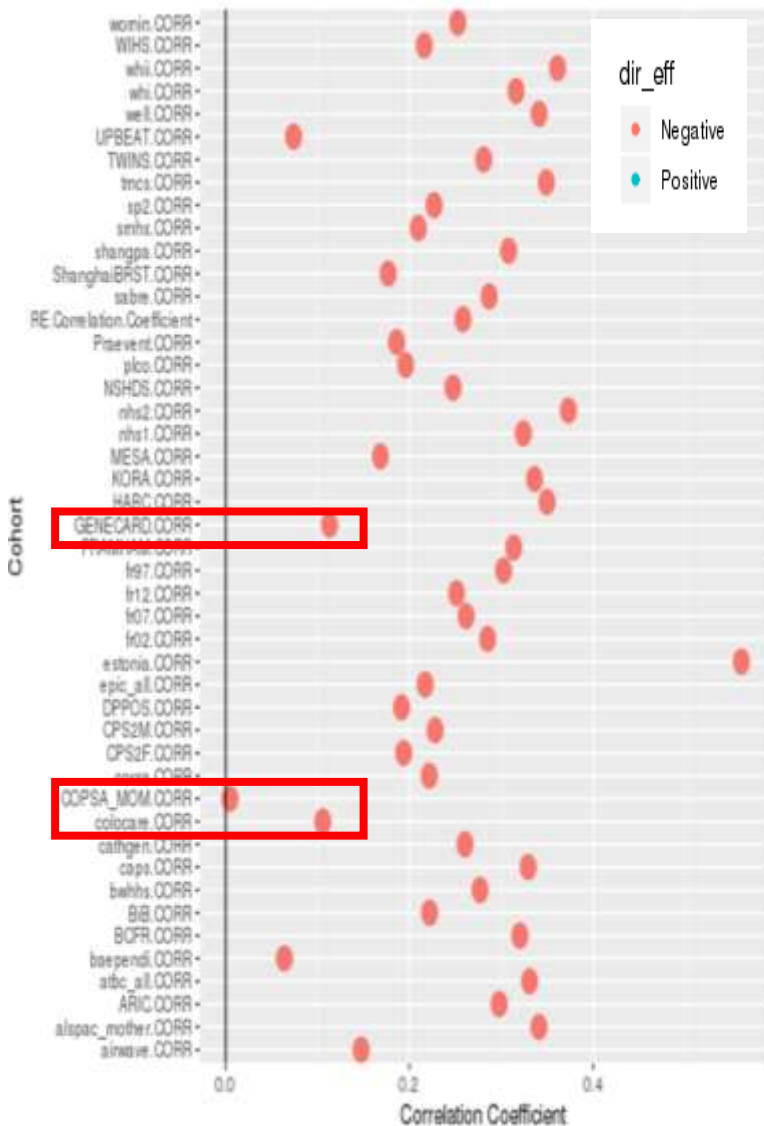




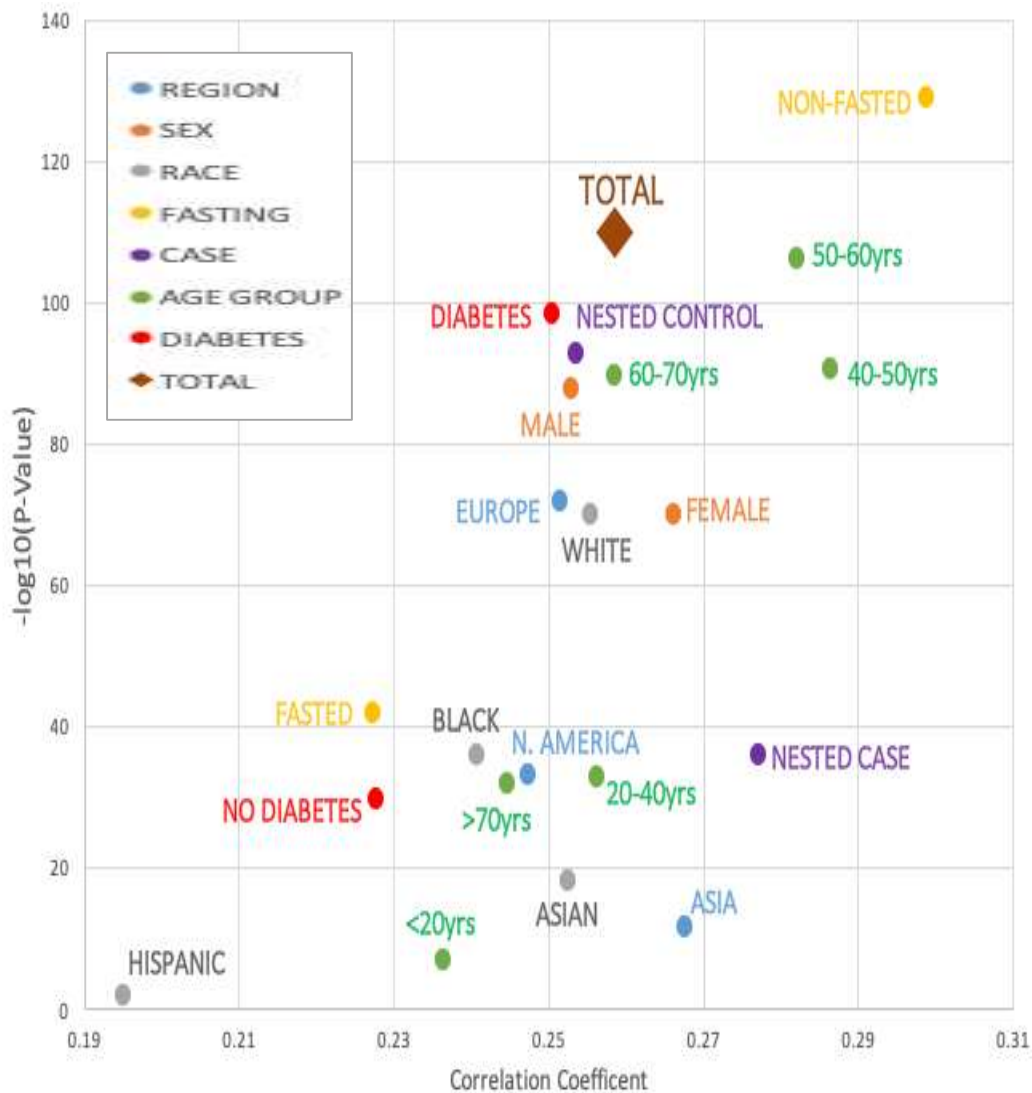
Valine



Correlation Coefficient by Cohort



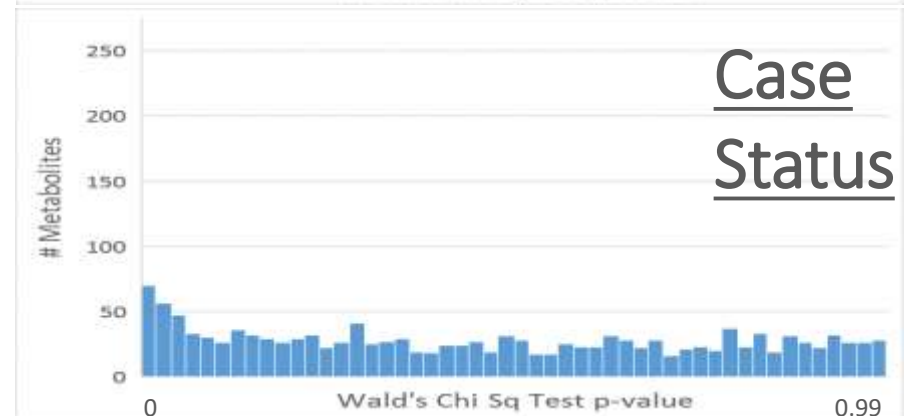
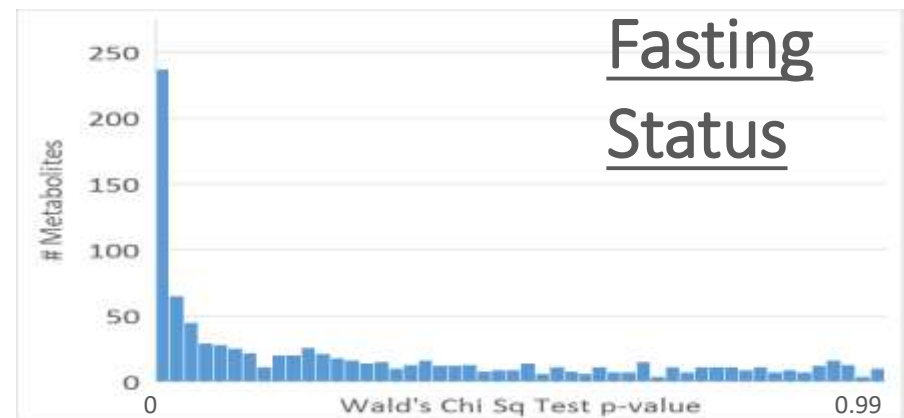
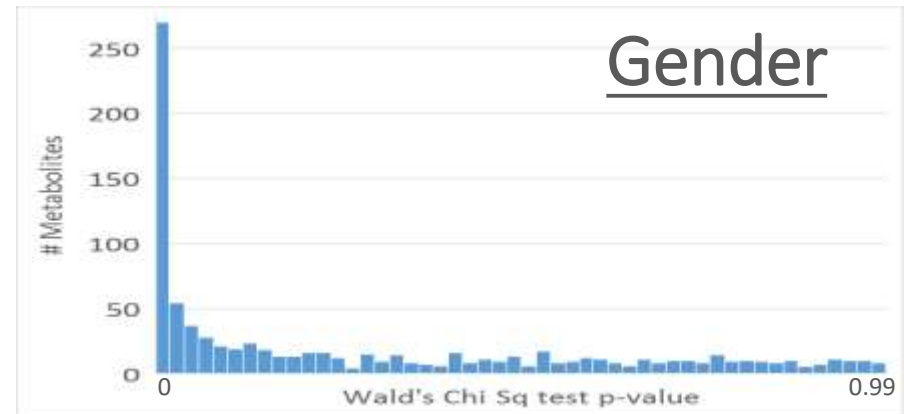
Correlation Coefficient by Strata



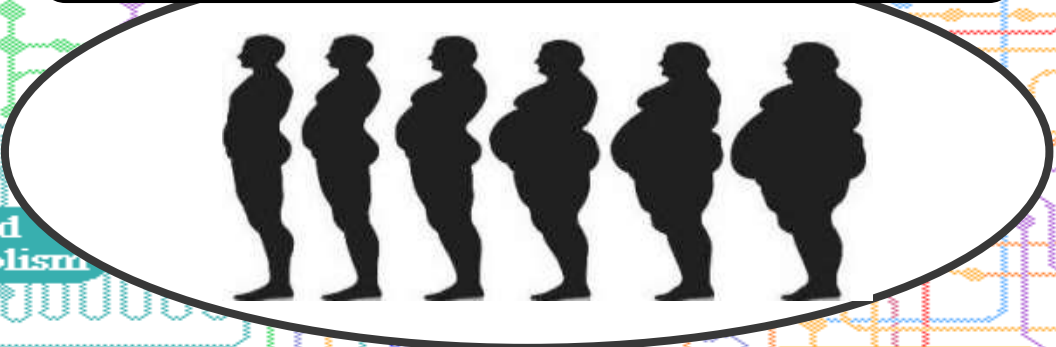
Sources of Heterogeneity

- Wald's Chi Square Test used to assess between Strata heterogeneity
- Fasting Status and Gender are the biggest sources of heterogeneity
- Case status does not appear to be a significant source of heterogeneity

N Metabolites Exhibiting Significant Heterogeneity by Strata



Metabolome of BMI



Altered
Glucose
Metabolism

Oxidative
Stress

Altered Lipid
Metabolism

Insulin
Resistance

Steatosis

Dyslipidaemia

Enhanced
Cell Growth

Low-grade
Inflammatory
State

Metabolism of
Complex Carbohydrates

Biodegradation of
Xenobiotics

Metabo
Comple

leotide
abolism

Lipid
Metabolism

Metabolism of
Other Amino Acids

Amino Acid
Metabolism

Energy
Metabolism

Metabolism of
Cofactors and Vitamins

Biosynthesis of
Secondary Metabolites

Conclusions & Future Directions

Conclusions

- ❖ It is **feasible** to perform large scale meta-analyses across multiple diverse metabolomics cohorts
 - *Different populations*
 - *Different profiling platforms*
 - *Targeted and untargeted*
 - *NMR and Mass Spec*
 - *Serum and plasma*
- ❖ We demonstrate that such meta-analyses can provide **robust and biologically informative results**
- ❖ An increased BMI is associated with increased levels of amino acids, in particular branched chain amino acids, and with decreased levels of cholesterol esters and High Density Lipoproteins

Next Steps

- ❖ Incorporate remaining studies
- ❖ Further exploration of heterogeneity
- ❖ Assessing correlation between “top hits”
- ❖ Identification of metabolite profiles/signatures in addition to individual metabolites
- ❖ Considerations of extremes of BMI
- ❖ Consideration of adiposity measures in a subset
- ❖ Pathway/Network Interpretation



- ❖ Recruitment of cohorts is ongoing
- ❖ Any participating investigator can submit a project proposal for a meta-analysis across the cohorts
- ❖ A wealth of data is waiting to be explored!



<https://epi.grants.cancer.gov/comets/>

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<https://epi.grants.cancer.gov/comets/>



<http://www.comets-analytics.org>



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