



Taiwan View User Guide



What is this platform for?

<https://taiwanview.twbiobank.org.tw>



TAIWAN VIEW

Navigation bar

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Functional modules

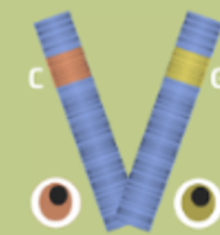
Variants: Query specific genes/variants and view their frequency or related information in the cohort.

Methylation: Uses the MethylationEPIC array to measure DNA methylation levels in blood; ~850,000 CpG sites.

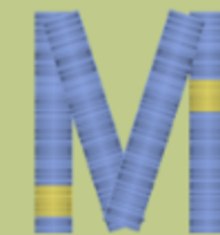
HLA: Uses next-generation sequencing (NGS) to determine the frequency distribution of typings for 9 genes in the HLA region.

PheWeb: GWAS results linking genotypes with questionnaires, physical measurements, and lab test values; >200 phenotypes in total.

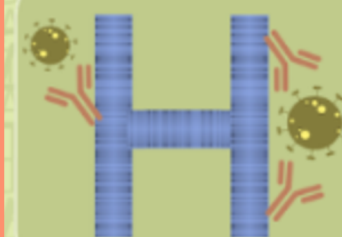
Metabolites: Blood metabolomics data covering >40 metabolites and 110 lipids, plus urine measurements of 11 plasticizers and melamine-related metabolites.



Variants



Methylation

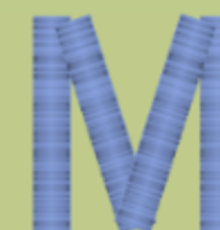


HLA



PheWeb

ABOUT
US



Metabolites

VARIANTS

Query a specific gene or variant and view its frequency and related information in the cohort.

Dropdown menu

The same variant may have different frequencies across datasets (due to differences in sample size, platform, and imputation). Please select the dataset first and keep it consistent for querying.

VARIANT SEARCH

DATABASE

TWB1 array (GRCh37)

SEARCH BY:

Region

* Please enter the range of chromosome to search for.

Chr1

From

1

To

249210707

* Click the Link to See Examples of Results for Different "Search by" Methods:

Region: [chr12: 111766887-1118117532](#)

ID: [rs671](#)

Gene: [ALDH2](#)

SEARCH

1. **ID:** Variant ID (e.g., rs671)
2. **Region:** Retrieve all variants within a chromosomal interval. "From" and "To" are genomic coordinates; confirm whether the selected dataset uses GRCh37 or GRCh38.
3. **Gene:** Variants mapped to/associated with the gene

VARIANTS

Example: rs671



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VARIANT

View and modify the current search criteria here.

IDrs671SEARCH

DATABASETWB1 and TWB2 imputed combined (...)

Narrow/Filter the query scope

CLINICAL SIGNIFICANCE

☐ PATHOGENIC☐ LIKELY PATHOGENIC☐ DRUG RESPONSE

VARIANT CONSEQUENCE

☐ PREDICTED LOSS-OF-FUNCTION☐ MISSENSE / INFRAME INDEL☐ SYNONYMOUS☐ OTHER

Clinical significance information is obtained from ClinVar, a public database of clinically relevant variants, which classifies variant–disease/phenotype relationships based on published evidence and submitter-provided information.

Variant consequence describes the predicted impact of the variant on the gene or protein.

Search results

1

CHR	POS	ID	GENE	REF	INDIVIDUALS	FREQ	CLINICAL SIGNIFICANCE	VARIANT CONSEQUENCE
CHR12	111803962	rs671	ALDH2 MIR6761	G	118908	G: 0.7169 A: 0.2831	protective risk_factor pathogenic drug_response	missense_variant downstream_gene_variant

Reference allele

Allele frequency for each allele

View detailed variant information (next page).

VARIANTS

Variant details

Cross-Population Frequency Comparison

- **Number of Samples:** Number of samples effectively included in calculations for this database.
- **Allele Count:** Total number of ALT alleles observed across all samples.
- **Allele Frequency:** ALT allele frequency (ALT count / (2 × Number of Samples)).
- **Allele Count of Homozygotes:** Number of ALT/ALT individuals.
- **Allele Count of Heterozygotes:** Number of REF/ALT individuals.

Page 5

Example:
rs671

rs671		DATABASE	
Position: chr12 - 111803962 Alleles (REF/ALT): G/A Allele Number: 237816 Allele Count of Homozygotes: 19196		Number of Samples: 118908 Allele Count: 67337 Allele Frequency: 0.2831 Allele Count of Heterozygotes: 48141	
POPULATION FREQUENCIES IN GNOMAD V3.1.2		TWB1 and TWB2 imputed combi... dbSNP Ensembl	
POPULATIONS	DESCRIPTION	GENOMES	ALLELE FREQUENCY
AFR	African/African American	20,744	0.0002
AMI	Amish	456	0.0000
AMR	Latino/Admixed American	7,647	0.0009
ASJ	Ashkenazi Jewish	1,736	0.0000
EAS	East Asian	2,604	0.2247
FIN	European (Finnish)	5,316	0.0001
NFE	European (non-Finnish)	34,029	0.0000
MID	Middle Eastern	158	0.0000
SAS	South Asian	2,419	0.0008
OTH	Other	1,047	0.0053
VARIANT EFFECT PREDICTOR			
This variant missense_variant Gene: ENSG00000111275 SYMBOL: ALDH2 Transcript: ENST00000261733 HGVS: ENST00000261733.7:c.1510G>A HGVS: ENSP00000261733.2:p.Glu504Lys PolyPhen: possibly_damaging(0.874) SIFT: deleterious(0)		This variant downstream_gene_variant Gene: ENSG00000274697 SYMBOL: MIR6761 Transcript: ENST00000617899	
QUALITY METRICS			
TWBv1 Array Imputed: No TWBv2 Array Imputed: No Excess Heterozygosity Test: 0.83		TWBv1 Array Info Score: 1.00 TWBv2 Array Info Score: 1.00 HWE Test: 0.353065	

- **External links:** dbSNP / Ensembl

- **GENOMES:** gnomAD sample count for the population
- **ALLELE FREQUENCY:** ALT allele frequency for the population

- **Imputed (Yes/No):** Indicates whether the genotype was imputed rather than directly measured.
- **Info score (imputation quality):** A reliability metric for imputation; values closer to 1 indicate higher imputation quality.
- **Excess heterozygosity test:** QC check for unusually high heterozygosity; useful for QC/anomaly detection.

METHYLATION

Uses the MethylationEPIC array to measure DNA methylation levels in blood across ~850,000 CpG sites.

Dropdown menu



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METHYLATION SEARCH

SEARCH BY:

CpG ID ▼

cg05575921

CpG ID: The probe identifier on the methylation array corresponding to a measured CpG site; each cgID maps to one measured genomic location.

SEARCH 

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METHYLATION

Example: cg05575921

Shows the query target

Narrow/Filter
the query scope

Search results



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METHYLATION

CPG ID

cg05575921

SEARCH

GENE REGION

☐ TSS1500☐ TSS200☐ 5' UTR☐ 1ST EXON☐ GENE BODY☐ 3' UTR

CPG REGION

☐ CPG ISLAND☐ N SHORE☐ S SHORE☐ N SHELF☐ S SHELF

1

CHR	POS	CPGID	GENE	GENE REGION	CPG REGION	MEAN	MEDIAN	SD
CHR5	373378	cg05575921	AHRR	Body	N_Shore	0.859	0.874	0.056

Gene region: Location of the CpG site relative to gene structure.

- TSS200/TSS1500: 200 bp / 1500 bp upstream of the transcription start site (often related to promoter regulation).
- 5'UTR / 1st Exon / Gene body / 3'UTR: Different functional regions of the gene.

CpG region: Position relative to CpG islands.

- CpG island: CpG-dense region, often in regulatory regions.
- Shore (N/S): ~0–2 kb from the CpG island.
- Shelf (N/S): ~2–4 kb from the CpG island.

Methylation (beta value) summary: 0 ≈ unmethylated; 1 ≈ fully methylated.

HLA

Query aggregated statistics for HLA alleles, including sample counts and frequency distributions.

Select a dataset and expand.



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HLA

> NGS-based HLA allele

> TWB1 array imputed HLA allele

> TWB2 array imputed HLA allele

- **NGS-based HLA:** Typing inferred from sequencing data (higher resolution, smaller sample size).
- **Array-imputed HLA:** HLA alleles imputed from array data using reference models (larger sample size).

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- > TWB1 array imputed HLA allele
- ▼ TWB2 array imputed HLA allele
 - > A - 95828 (1.000)
 - ▼ B - 85106 (1.000)
 - > B*07 - 665 (0.004)
 - > B*08 - 402 (0.002)
 - > B*13 - 14113 (0.083)
 - > B*14 - 34 (0.000)
 - ▼ B*15 - 18189 (0.107)
 - [B*15:01 - 6028 \(0.035\)](#)
 - [B*15:27 - 662 \(0.004\)](#)
 - [B*15:25 - 1174 \(0.007\)](#)
 - [B*15:19 - 222 \(0.001\)](#)
 - [B*15:18 - 1139 \(0.007\)](#)
 - [B*15:17 - 36 \(0.000\)](#)
 - [B*15:13 - 1 \(0.000\)](#)
 - [B*15:11 - 1040 \(0.006\)](#)
 - [B*15:03 - 1 \(0.000\)](#)
 - [B*15:02 - 7856 \(0.046\)](#)
 - [B*15:32 - 30 \(0.000\)](#)

Sample Size and Frequency

- HLA allele nomenclature includes the locus (A/B/C/DRB1...) and fields; more fields indicate higher resolution.
- Values are shown as counts, with frequencies provided in parentheses.



TAIWAN VIEW

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PHEWEB

Navigation bar

[Phenotypes](#)
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[Random](#)
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Enter keywords (e.g., phenotype, variant, gene).

Browse GWAS results using SAIGE

Allele coding and effect size

For each SNP (single-nucleotide polymorphism) two alleles are reported with two alleles REF (reference allele) and ALT (alternative allele). So for example, at this SNP [rs671](#) the REF allele is G and the ALT allele is A. The browser also provides effect sizes and standard errors for each SNP tested against each phenotype. In all studies, the effect allele is the ALT allele. The SNP effect sizes refer to the change in phenotype (quantitative traits) or log-odds (binary traits) corresponding to possession of an additional copy of the ALT allele.

Download

Due to national regulations, a formal application for the individual-level datasets to the Taiwan Biobank has to be submitted and approved prior to obtaining GWAS summary statistics. For relevant information, kindly refer to our [website](#).

Acknowledgements

This browser was based on [PheWeb](#)

Other resources

[TPMI PheWeb](#)

The Taiwan Precision Medicine Initiative (TPMI) is a genomic research program designed to advance precision healthcare in Taiwan. With over 500,000 Taiwanese residents already enrolled, TPMI maintains the most comprehensive dataset of genotypes and electronic medical records for Han Chinese populations.

Other Asian PheWeb Resources

PHEWEB

Navigation: Phenotypes

PheWeb

Phenotypes

Top Hits

Random

About

All Phenotypes

Category

Phenotype

#Samples

GCA0.01

#Loci<5e-8

Top variant in pheno

P-value

Nearest Gene(s)

Metabolic test	Ratio of total cholesterol to HDL cholesterol	139,379	1.75	113	16:56,959,249 G / A (rs12149545)	≤1e-320	CETP
Life style	Have ever drunk alcohol for at least 6 months	12,686 + 131,962	1.05	3	12:112,136,812 C / T (rs12231737)	≤1e-320	TRAFD1
Liver-related test	Gamma glutamyl transferase	144,095	1.73	132	22:24,596,299 T / C (rs5751901)	≤1e-320	AP000356.5, GGT1
Hematological test	Hemoglobin	144,696	1.52	61	16:377,772 C / A (rs375498857)	≤1e-320	PGAP6
Metabolic test	Glycated hemoglobin	143,546	1.64	102	17:82,842,942 G / A (rs12942471)	≤1e-320	TBCD
Metabolic test	High-density lipoprotein cholesterol	139,478	1.88	142	16:56,965,416 C / T (rs11508026)	≤1e-320	CETP
Metabolic test	Low-density lipoprotein cholesterol	139,443	1.44	75	19:44,901,174 T / C (rs741780)	≤1e-320	TOMM40
Metabolic test	Ratio of LDL cholesterol to HDL cholesterol	139,440	1.63	98	19:44,905,579 T / G (rs405509)	≤1e-320	APOE
Hematological test	Red blood cell count	144,723	1.92	114	16:377,772 C / A (rs375498857)	≤1e-320	PGAP6
Liver-related test	Serum glutamic oxaloacetic transaminase	144,166	1.47	58	6:29,947,794 C / A (rs9260251)	≤1e-320	HLA-A
Metabolic test	Triglycerides	138,898	1.81	90	11:116,741,017 C / G (rs9326246)	≤1e-320	BUD13
Liver-related test	Total bilirubin	144,361	1.33	32	2:233,741,916 T / C (rs34352510)	≤1e-320	UGT1A10, UGT1A3, UGT1A4, UGT1A5, UGT1A6, UGT1A7, UGT1A8, UGT1A9
Metabolic test	Total cholesterol	139,432	1.68	104	19:44,913,574 T / G (rs390082)	≤1e-320	APOC1
Kidney-related test	Uric acid	144,728	1.77	100	4:10,004,273 C / T (rs751092)	≤1e-320	SLC2A9
Metabolic test	Very low-density lipoprotein cholesterol	138,898	1.81	90	11:116,741,017 C / G (rs9326246)	≤1e-320	BUD13

#Samples: Number of samples analyzed for the phenotype. If shown as cases + controls, it is a binary phenotype with case/control counts; if a single number, it is typically a continuous trait (e.g., glucose).

#Loci < 5e-8: Number of independent loci reaching genome-wide significance.

GCA (genomic control lambda): Used to assess overall inflation of test statistics.

242 phenotypes

A catalog of the PheWeb database, showing for each phenotype which SNP is most strongly associated.

PHEWEB

Navigation: Top Hits

PHEWEB

PheWeb Search for a variant, gene, or phenotype

Phenotypes **Top Hits** Random About

Top Hits

This page shows only the peaks with a p-value $< 10^{-6}$. Variants are hidden if any variant within 500kb in the same phenotype has a smaller p-value. Only the top 2000 variants of each phenotype are considered. This table is limited to the top 1000 hits, but the download button includes all hits.

Search... "TCF7L2", "rs1861867", etc. 1000 hits

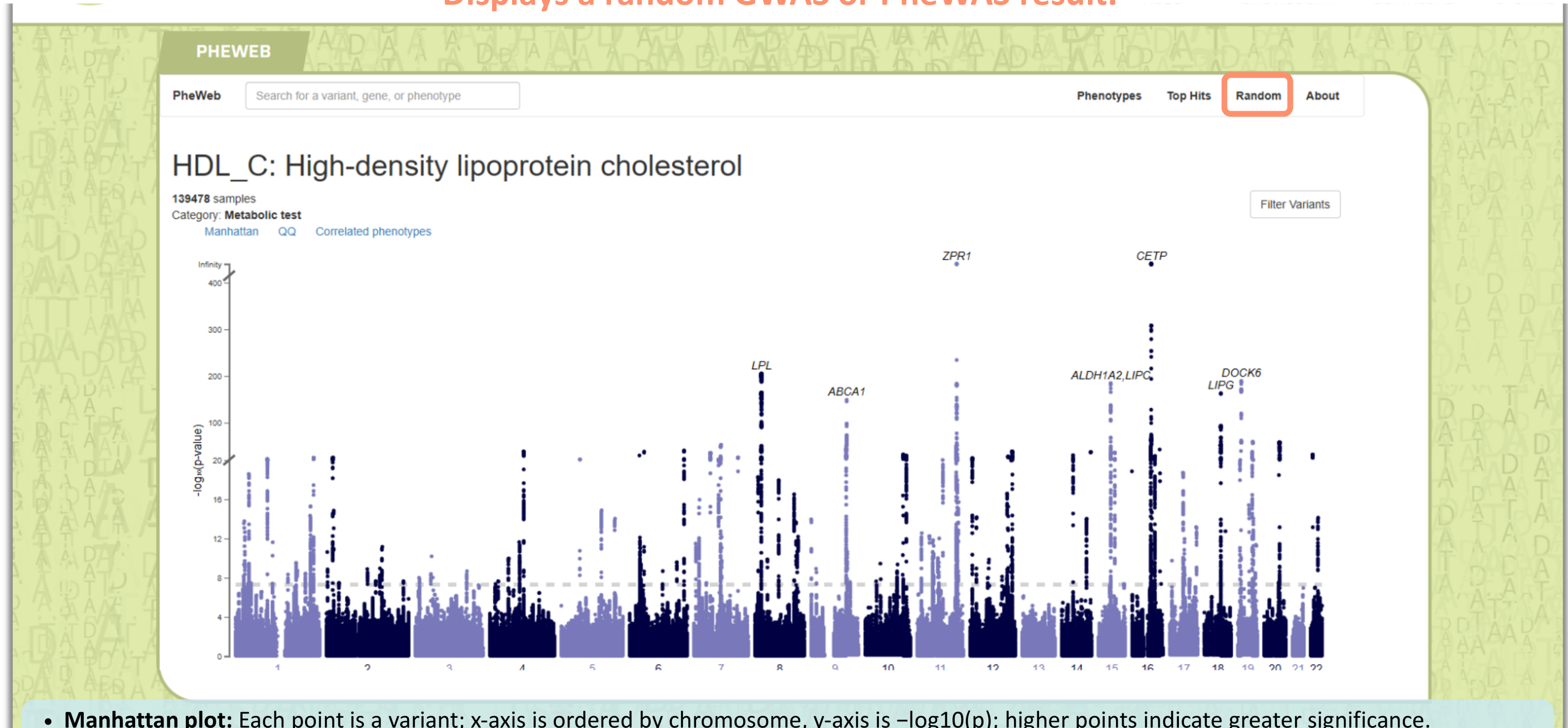
Category	Phenotype	Top variant in locus	P-value	MAF	Nearest Gene(s)
Metabolic test	Ratio of total cholesterol to HDL cholesterol	11:116,715,567 T / C (rs7350481)	$\leq 1e-320$	0.24	<i>BUD13</i>
Metabolic test	Ratio of total cholesterol to HDL cholesterol	16:56,956,804 C / A (rs247617)	$\leq 1e-320$	0.16	<i>CETP</i>
Metabolic test	Ratio of total cholesterol to HDL cholesterol	19:44,912,383 G / A (rs445925)	$\leq 1e-320$	0.084	<i>APOC1</i>
Life style	Have ever drunk alcohol for at least 6 months	12:111,672,685 T / C (rs3782886)	$\leq 1e-320$	0.29	<i>BRAP</i>
Liver-related test	Gamma glutamyl transferase	22:24,593,402 T / TG (rs145673095)	$\leq 1e-320$	0.11	<i>AP000356.5</i>
Hematological test	Hemoglobin	16:377,772 C / A (rs375498857)	$\leq 1e-320$	0.016	<i>PGAP6</i>
Metabolic test	Glycated hemoglobin	17:82,726,104 C / T (rs9895455)	$\leq 1e-320$	0.48	<i>FN3KRP</i>
Metabolic test	High-density lipoprotein cholesterol	11:116,779,090 G / A (rs75198898)	$\leq 1e-320$	0.068	<i>ZPR1</i>
Metabolic test	High-density lipoprotein cholesterol	16:56,954,132 C / T (rs173539)	$\leq 1e-320$	0.22	<i>CETP</i>
Metabolic test	Low-density lipoprotein cholesterol	19:44,893,642 T / C (rs157584)	$\leq 1e-320$	0.32	<i>TOMM40</i>
Metabolic test	Ratio of LDL cholesterol to HDL cholesterol	16:56,956,804 C / A (rs247617)	$\leq 1e-320$	0.16	<i>CETP</i>
Metabolic test	Ratio of LDL cholesterol to HDL cholesterol	19:44,893,642 T / C (rs157584)	$\leq 1e-320$	0.32	<i>TOMM40</i>
Hematological test	Red blood cell count	16:377,772 C / A (rs375498857)	$\leq 1e-320$	0.016	<i>PGAP6</i>
Hematological test	Red blood cell count	11:4,999,362 C / T (rs147341630)	$\leq 1e-320$	0.0055	<i>OR51L1</i>
Liver-related test	Serum glutamic oxaloacetic transaminase	6:29,947,794 C / A (rs9260251)	$\leq 1e-320$	0.023	<i>HLA-A</i>

Summarizes the most significant peaks for each phenotype in a table, allowing rapid scanning of key signals across the database.

PHEWEB

Navigation: Random

Displays a random GWAS or PheWAS result.



- **Manhattan plot:** Each point is a variant; x-axis is ordered by chromosome, y-axis is $-\log_{10}(p)$; higher points indicate greater significance.
- **Dashed line:** Typically indicates the significance threshold (e.g., 5×10^{-8}).
- **Peak:** A region in which multiple highly correlated variants show significant associations; often requires fine-mapping and/or functional follow-up.

PHEWEB

Navigation: About

PHEWEB

PhWeb Search for a variant, gene, or phenotype

Phenotypes Top Hits Random **About**

About This PheWeb

Results displayed in this PheWeb include genome-wide associations from 145,490 participants in Taiwan Biobank. All individuals were genotyped on the Axiom Genome-Wide TWB Array or Axiom Genome-Wide TWB2.0 Array. The genotype data were then imputed using a merged reference panel consisting of East Asian population from 1000 Genomes phase 3 (n=504) and whole-genome sequencing data from Taiwan Biobank (n=1,451) by [IMPUTE2](#) software.

Associations were conducted using [SAIGE](#) software with adjustment for age, sex, BMI, genotyping array, and top 5 principal components (The height, weight, and BMI phenotypes were adjusted for age, sex, genotyping array, and top 5 principal components). We processed a set of 242 phenotypes including 111 quantitative traits as well as 131 binary traits with at least 100 cases. Genetic correlations were estimated across phenotypes with heritability z score > 2 by [LDSC](#) using East Asian LD scores from 1000 Genomes Project phase 3.

All positions are on GRCh38.

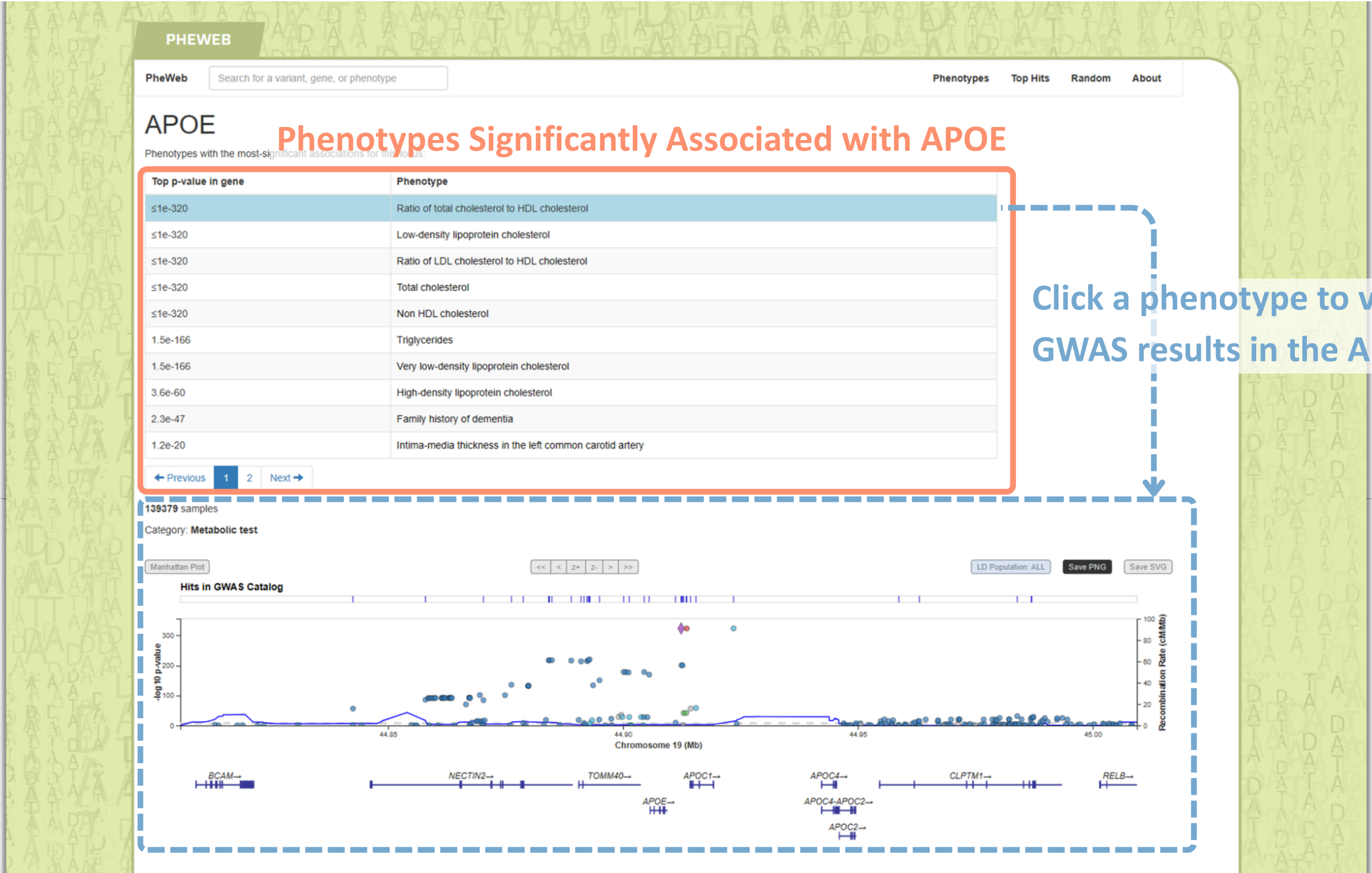
Acknowledgements

This site was built with [PheWeb](#) version 1.3.16.

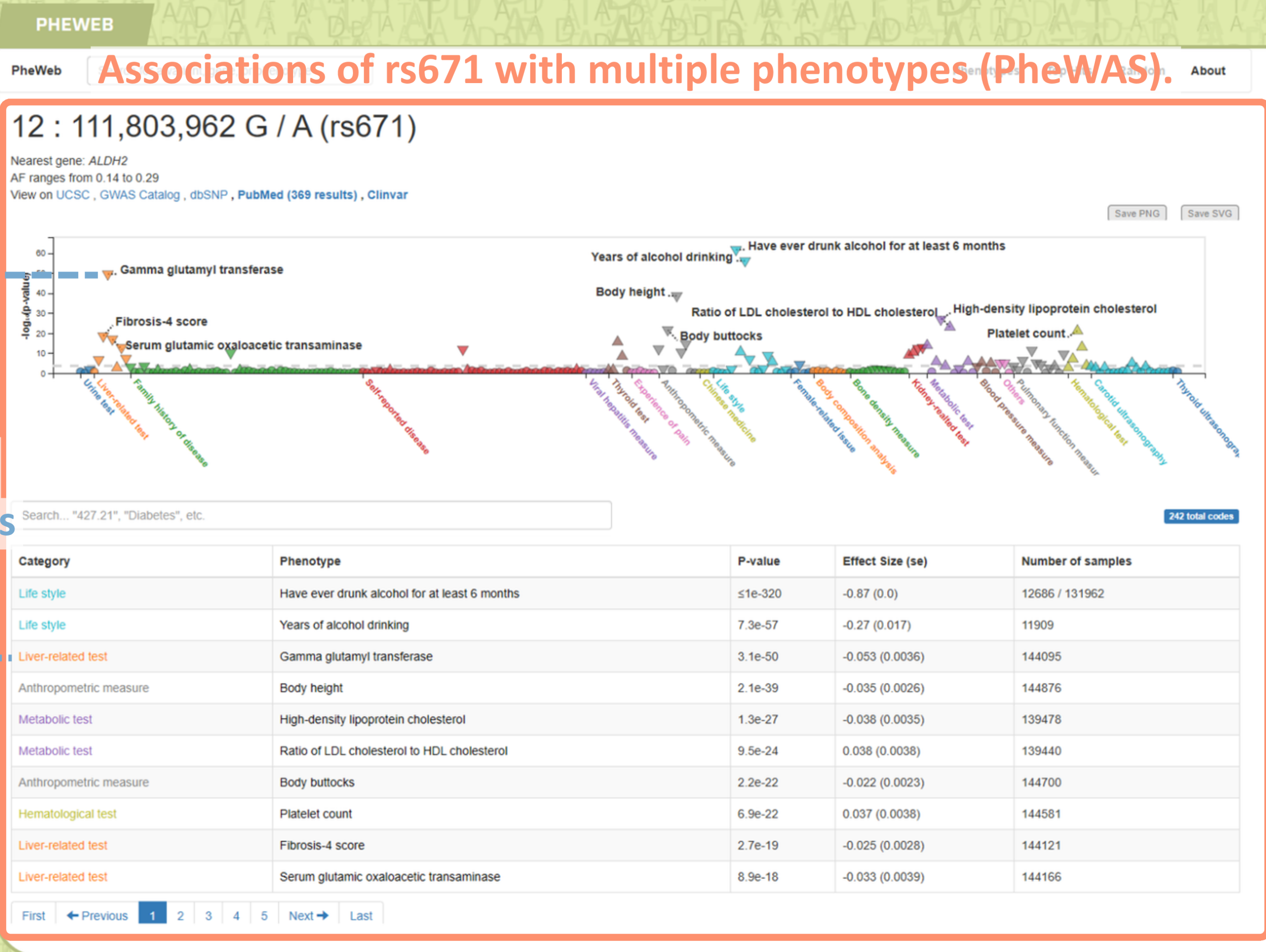
Helps users understand the platform's data foundation, analytical workflow, and methodological quality, so they can interpret the results with a clear understanding of how the data were generated.

PHEWEB

Example 1: APOE



Use a phenotype to
view its GWAS results
in more detail.

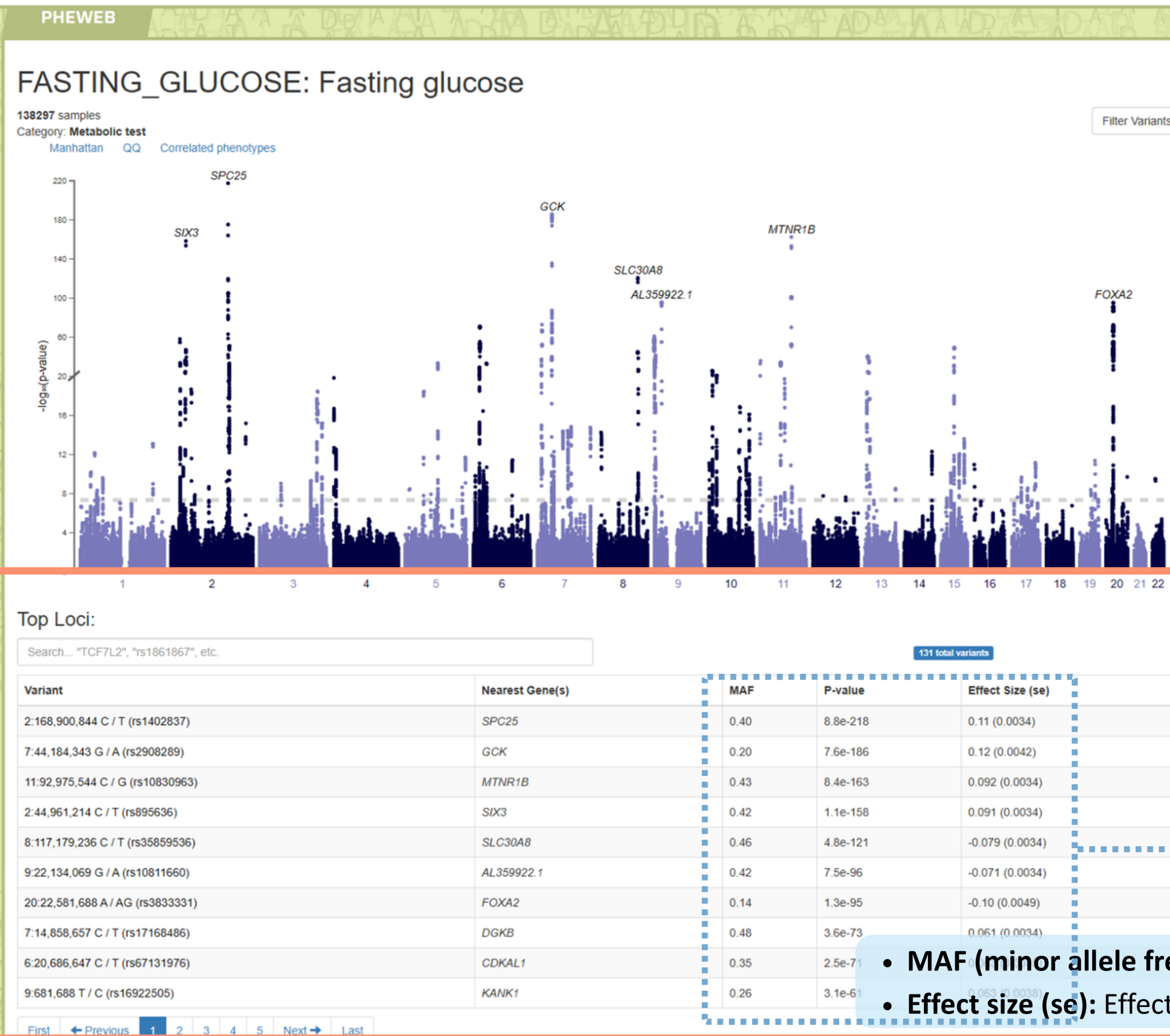


PHEWEB

Example 3: FASTING_GLUCOSE

Manhattan plot

Information on Significant Loci



- **MAF (minor allele frequency):** Frequency of the minor allele.
- **Effect size (se):** Effect estimate and standard error.

PHEWEB

9:681,688 T / C (rs16922505)

KANK1

0.26

3.1e-61

0.063 (0.0038)

First

Previous

1

2

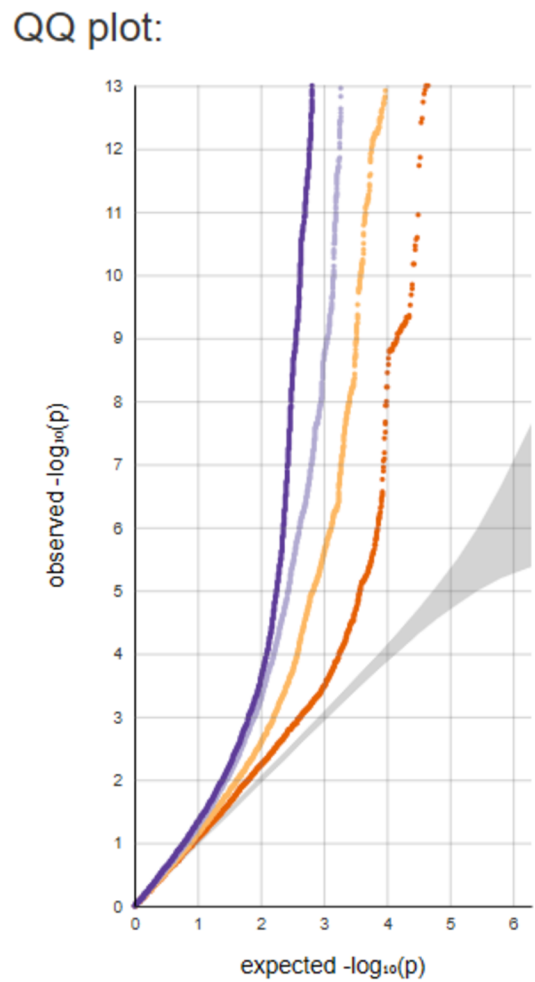
3

4

5

Next

Last



GC lambda 0.5: 1.200
GC lambda 0.1: 1.268
GC lambda 0.01: 1.559
GC lambda 0.001: 3.414
(Genomic Control lambda calculated based on the 50th percentile (median), 10th percentile, 1st percentile, and 1/10th of a percentile)

QQ plot

- **Genetic correlation (r^g):** Estimated from GWAS summary statistics; Values closer to 1 indicate shared genetic effects in the same direction, whereas values closer to -1 indicate shared effects in opposite directions.
- **LDSC (LD Score Regression):** A summary-statistics method to estimate genetic correlation and diagnose sources of test statistic inflation (In simple terms, it is a method for assessing genetic correlation and test statistic inflation.)

Phenotypes Most Genetically Correlated with Fasting Glucose

Correlated phenotypes for FASTING_GLUCOSE: Fasting glucose

Genetically correlated traits are calculated using genome-wide association summary statistics via LD Score regression (LDSC).

Trait	r_g	SE	Z	P-value	Method
					filter column...
HBA1C: Glycated hemoglobin	0.6096	0.054651	11.155	6.7943999999999...	LDSC
eAG: Estimated average glucose	0.6096	0.054651	11.155	6.7946999999999...	LDSC
DIABETES: Diabetes mellitus	0.6288	0.057662	10.904	1.0982e-27	LDSC
T2D: Type 2 diabetes mellitus	0.6366	0.059109	10.769	4.811e-27	LDSC
DIABETES_FH: Family history of diabetes mellitus	0.5153	0.062886	8.1935	2.537e-16	LDSC
SGOT_SGPT: Ratio of SGOT to SGPT	-0.2413	0.036674	-6.5784	4.7561e-11	LDSC
WHR: Waist-to-hip ratio	0.2127	0.037458	5.6779	1.3639e-8	LDSC
HEART_RATE: Heart rate	0.173	0.030506	5.6713	1.4168e-8	LDSC
VLIDL: Very low-density lipoprotein cholesterol	0.259	0.047768	5.4213	5.918e-8	LDSC

METABOLITES

Search metabolites by name and view summary statistics and sample counts.

- **Analysis method:** The measurement platform or technology used. (e.g., NMR = nuclear magnetic resonance; IVDr = in vitro diagnostics–grade platform).
- **Biospecimen:** Specimen type (e.g., plasma).
- **#participants at baseline/follow-up:** Effective sample size at baseline (initial visit) and follow-up.



TAIWAN VIEW

METABOLITE

Metabolites

Search metabolites

METABOLITES

ETHANOL

TRIMETHYLAMINE-N-OXIDE

2-AMINOBTYRIC ACID

ALANINE

ASPARAGINE

CREATINE

CREATININE

GLUTAMIC ACID

Click to select

ANALYSIS METHOD	BIOSPECIMEN	# OF PARTICIPANTS AT BASELINE	# OF PARTICIPANTS AT FOLLOW-UP
NMR, IVDr Platform	Plasma	323	185
NMR, IVDr Platform	Plasma	3	8
NMR, IVDr Platform	Plasma	134	174
NMR, IVDr Platform	Plasma	1,227	1,608
NMR, IVDr Platform	Plasma	108	52
NMR, IVDr Platform	Plasma	1,001	1,408
NMR, IVDr Platform	Plasma	1,226	1,607
NMR, IVDr Platform	Plasma	1,176	1,595

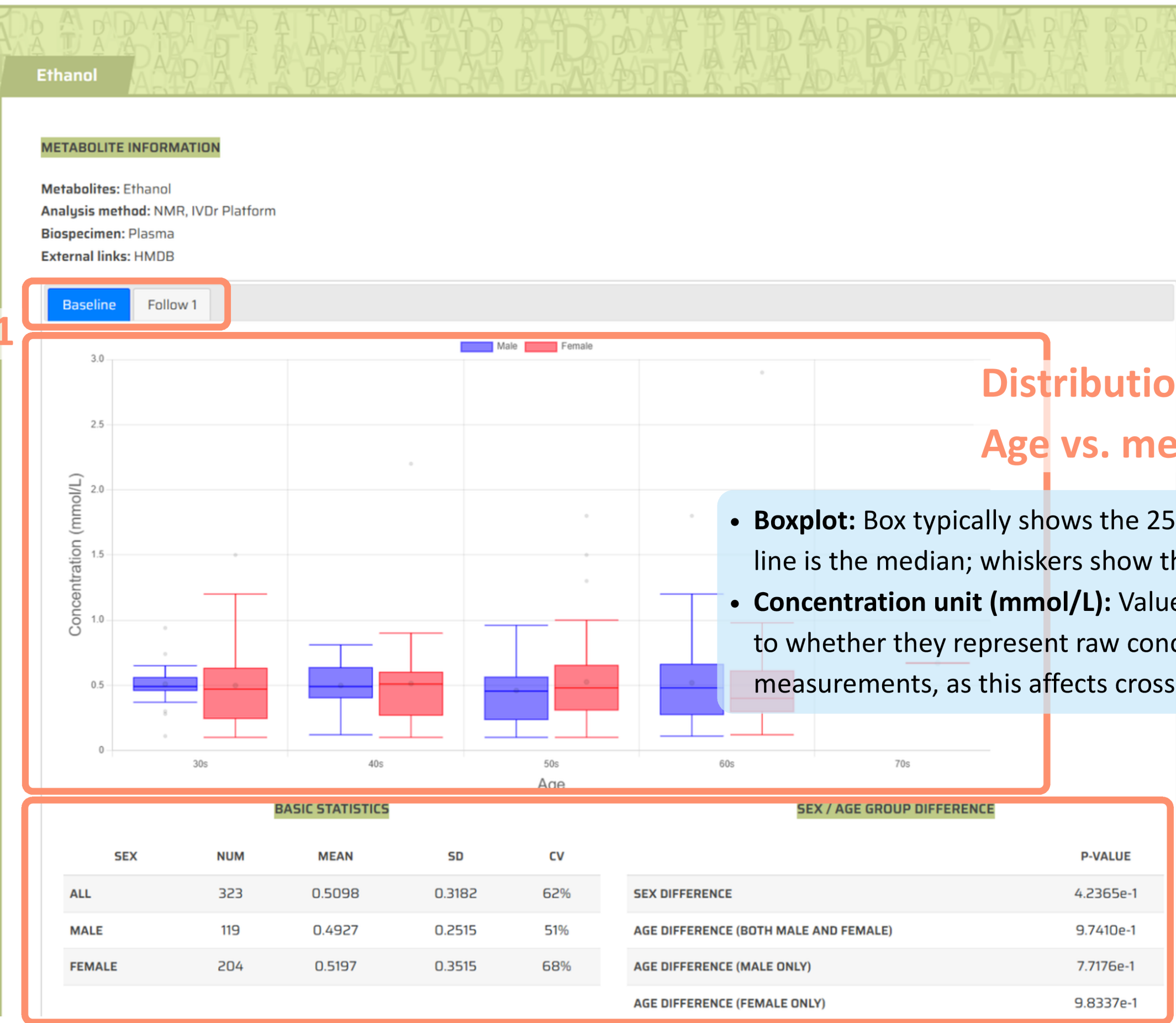
METABOLITES

Example: Ethanol

Basic information

Switch between
Baseline and Follow 1

Statistical results

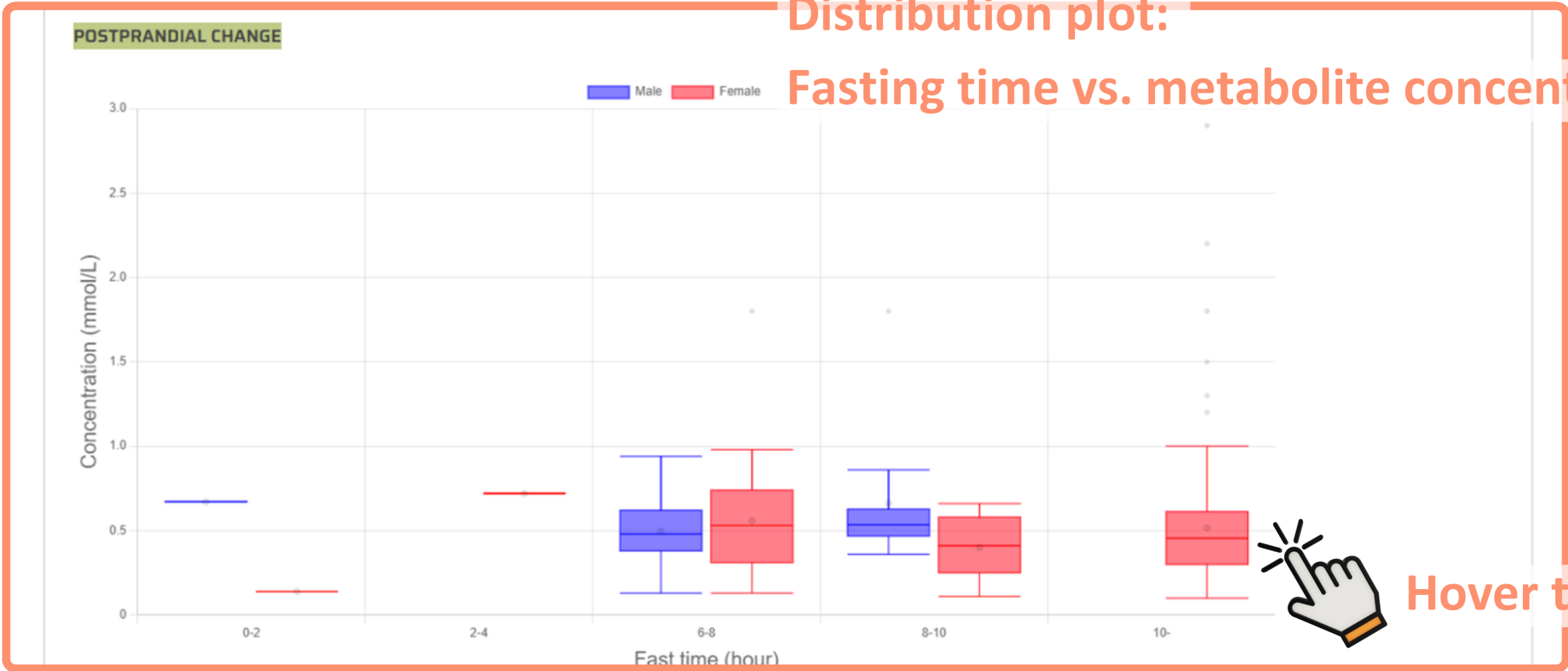


Distribution plot:
Age vs. metabolite concentration

- **Boxplot:** Box typically shows the 25th–75th percentiles (IQR); the center line is the median; whiskers show the range; points are often outliers.
- **Concentration unit (mmol/L):** Values should be interpreted with attention to whether they represent raw concentrations or transformed/normalized measurements, as this affects cross-study comparability.

METABOLITES

Example: Ethanol



CORRELATION BETWEEN OTHER METABOLITES

Correlation between ethanol and other metabolites

Switch by Sex: **ALL** Male Female

METABOLITES	SPEARMAN'S RANK CORRELATION COEFFICIENT	P-VALUE
Trimethylamine-N-oxide	0.0000e+0	0.0000e+0
Choline	0.0000e+0	0.0000e+0
D-Galactose	0.0000e+0	0.0000e+0
3-Hydroxybutyric acid	2.6077e-1	1.4228e-5
LDL Subfractions, Cholesterol, LDL-6	-1.4787e-1	7.7722e-3
LDL Subfractions, Apo-B, LDL-6	-1.4479e-1	9.1666e-3
Calculated Figures, LDL-6 Particle Number, LDL-6 Particle Number	-1.4455e-1	9.2841e-3
LDL Subfractions, Free Cholesterol, LDL-6	-1.4426e-1	9.4261e-3

- **Spearman correlation (ρ):** Measures monotonic association strength between two metabolite concentrations; ranges from −1 to 1.
- **Magnitude guide:** Values of 0.1, 0.3, and 0.5 may be interpreted as small, moderate, and large, respectively.
- **p-value:** With large sample sizes, p-values may become very small; interpretation should therefore consider effect size (ρ) and multiple-testing issues.

DOWNLOAD

How to apply

TAIWAN VIEW

ABOUT ▼ BROWSE DATA **DOWNLOAD** TUTORIAL

DOWNLOAD

Dear Users,

Greetings!

If you wish to download the "**Population Summarized Data**", please contact us via the official service email: biobankrs@gate.sinica.edu.tw.

Please write in Chinese or English and indicate your name and affiliation.

The following datasets are available upon request:

- HLA type (1,097 samples).zip
- illumina (1,492 samples) (GRCh38).zip
- methylation (2,091 samples) (GRCh37).zip
- TWB1 and TWB2 imputed combined (118,908 samples) (GRCh38).zip
- TWB1 array (24,679 samples) (GRCh37).zip
- TWB1 array imputed (24,679 samples) (GRCh38).zip
- TWB2 array (100,288 samples) (GRCh38).zip
- TWB2 array imputed (100,288 samples) (GRCh38).zip

Please note that PheWeb data is not available for download.
If you are interested in accessing the original data of PheWeb, kindly contact us at the above email address for application details.

Best regards,
Taiwan Biobank

Application steps

1. Go to the Download page and confirm which datasets are available.
2. Send an email to the official service address: biobankrs@gate.sinica.edu.tw
3. In the email, clearly state:
 - a. Name/title
 - b. Affiliation
 - c. Requested dataset name(s) (using the wording shown on the Download page)
 - d. Intended use/purpose (brief)

Available
downloadable
datasets