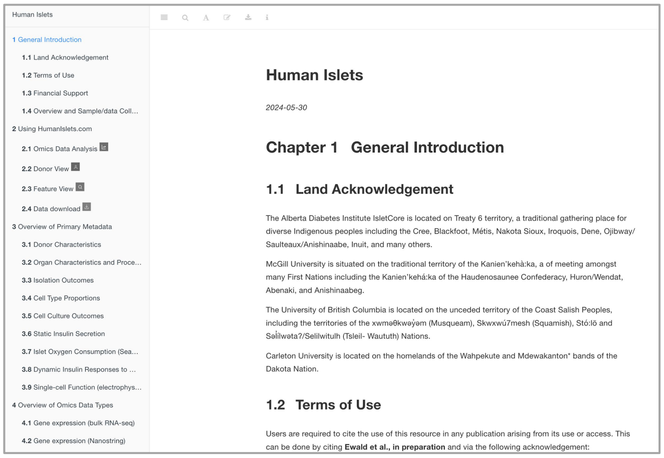
HumanIslets
Web-Tool



Human Islets

2024-05-30

Chapter 1 General Introduction

1.1 Land Acknowledgement

The Alberta Diabetes Institute IsletCore is located on Treaty 6 territory, a traditional gathering place for diverse Indigenous peoples including the Cree, Blackfoot, Métis, Nakota Sioux, Iroquois, Dene, Ojibway/Saulteaux/Anishinaabe, Inuit, and many others.

McGill University is situated on the traditional territory of the Kanien'kehà:ka, a of meeting amongst many First Nations including the Kanien'kehá:ka of the Haudenosaunee Confederacy, Huron/Wendat, Abenaki, and Anishinaabeg.

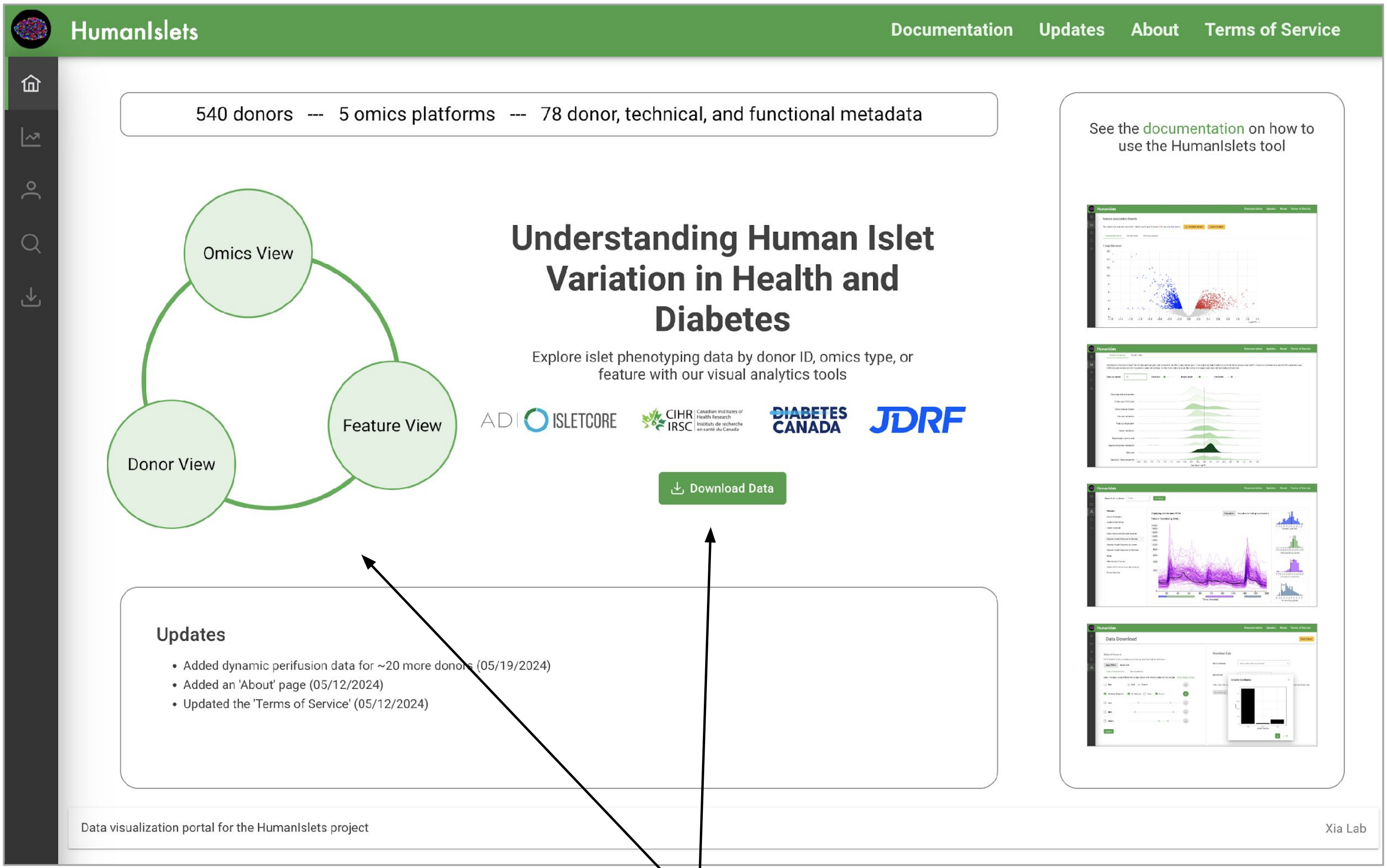
The University of British Columbia is located on the unceded territory of the Coast Salish Peoples, including the territories of the xwməθkwəy̓əm (Musqueam), Skwxwú7mesh (Squamish), Stó:lō and Səl̓ílwətaʔ/Selilwitulh (Tsleil- Waututh) Nations.

Carleton University is located on the homelands of the Wahpekute and Mdewakanton* bands of the Dakota Nation.

1.2 Terms of Use

Users are required to cite the use of this resource in any publication arising from its use or access. This can be done by citing **Ewald et al., in preparation** and via the following acknowledgement:

Access extensive documentation, recent tool updates, information on the HumanIslets team and tool roadmap, and Terms of Service here:



540 donors --- 5 omics platforms --- 78 donor, technical, and functional metadata

See the documentation on how to use the HumanIslets tool

Understanding Human Islet Variation in Health and Diabetes

Explore islet phenotyping data by donor ID, omics type, or feature with our visual analytics tools

Updates

- Added dynamic perifusion data for ~20 more donors (05/19/2024)
- Added an 'About' page (05/12/2024)
- Updated the 'Terms of Service' (05/12/2024)

Data visualization portal for the HumanIslets project

Xia Lab

The HumanIslets database can be explored from three complementary views, each accessible from the home page:

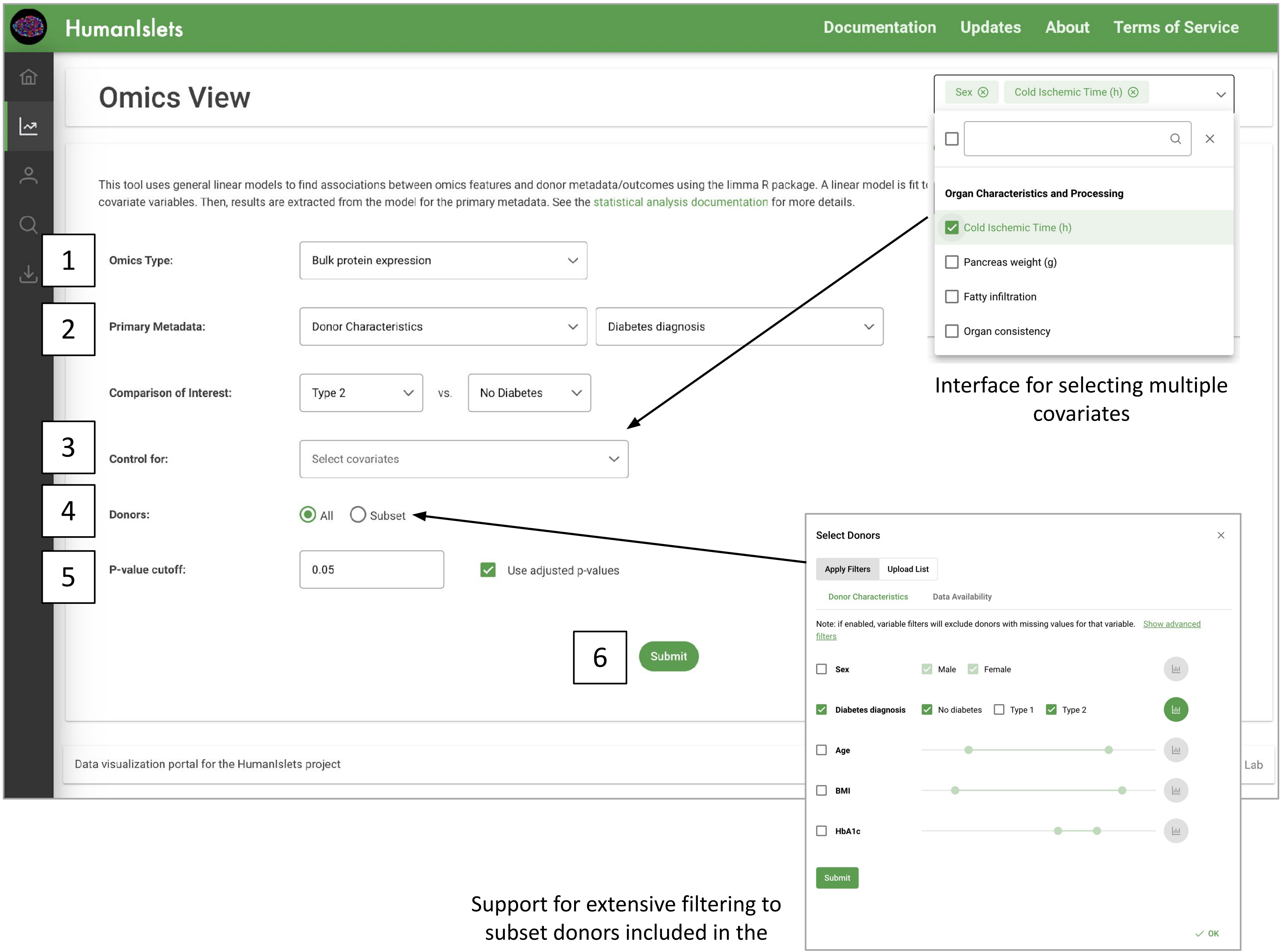
1. Omics view: compute gene-level and pathway-level associations between an omics dataset and a metadata variable of interest.
2. Feature view: query all metadata-omics associations that involve a feature of interest, sorted by statistical significance.
3. Donor view: view all metadata and functional outcomes for a specific donor, compared to the distribution of values from other donors.

There is also a data download tool.

Omics View

The main steps to computing results on this page:

1. Select an omics type of interest (ie. proteomics)
2. Select a metadata or functional outcome of interest. These are grouped into 9 categories. Categorical variables automatically prompt the selection of two specific classes to compare.
3. Select any covariates that you would like to adjust for. The tool supports the inclusion of donor metadata (ie. Age, Sex) or technical variables (ie. cold ischemic time, cell culture, etc).
4. Optionally choose to do the analysis for a subset of donors.
5. Choose a p-value cut-off to determine statistical significance.
6. Click ‘Submit’!



This tool uses general linear models to find associations between omics features and donor metadata/outcomes using the limma R package. A linear model is fit t
covariate variables. Then, results are extracted from the model for the primary metadata. See the statistical analysis documentation for more details.

1 **Omics Type:** Bulk protein expression

2 **Primary Metadata:** Donor Characteristics | Diabetes diagnosis

Comparison of Interest: Type 2 vs. No Diabetes

3 **Control for:** Select covariates

4 **Donors:** ● All ○ Subset

5 **P-value cutoff:** 0.05 ☑ Use adjusted p-values

6

Sex ⊗ Cold Ischemic Time (h) ⊗

Organ Characteristics and Processing

☑ Cold Ischemic Time (h)
☐ Pancreas weight (g)
☐ Fatty infiltration
☐ Organ consistency

Interface for selecting multiple covariates

Select Donors

Apply Filters | Upload List

Donor Characteristics | Data Availability

Note: if enabled, variable filters will exclude donors with missing values for that variable. Show advanced filters

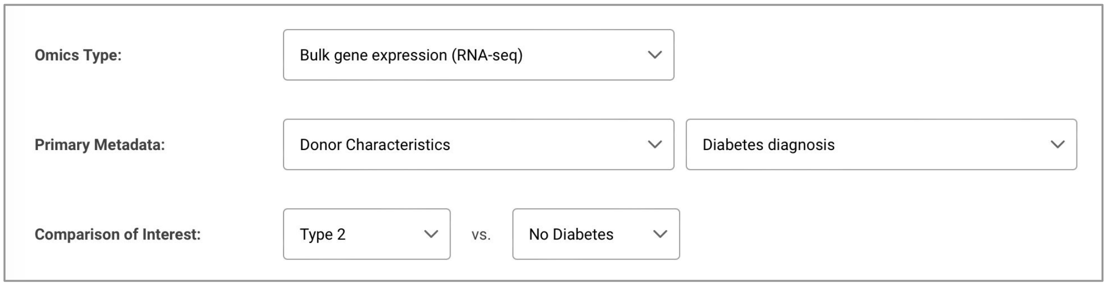
☐ **Sex** ☑ Male ☑ Female
☑ **Diabetes diagnosis** ☑ No diabetes ☐ Type 1 ☑ Type 2
☐ **Age**
☐ **BMI**
☐ **HbA1c**

Submit

✓ OK

Support for extensive filtering to subset donors included in the analysis

Controlling for technical covariates can have a big impact on the statistical analysis. We find that culture time and non-endocrine tissue proportion are the most influential variables. Here is an example of controlling for culture time in bulk RNA-seq analysis:



Omics Type: Bulk gene expression (RNA-seq)

Primary Metadata: Donor Characteristics — Diabetes diagnosis

Comparison of Interest: Type 2 vs. No Diabetes

1

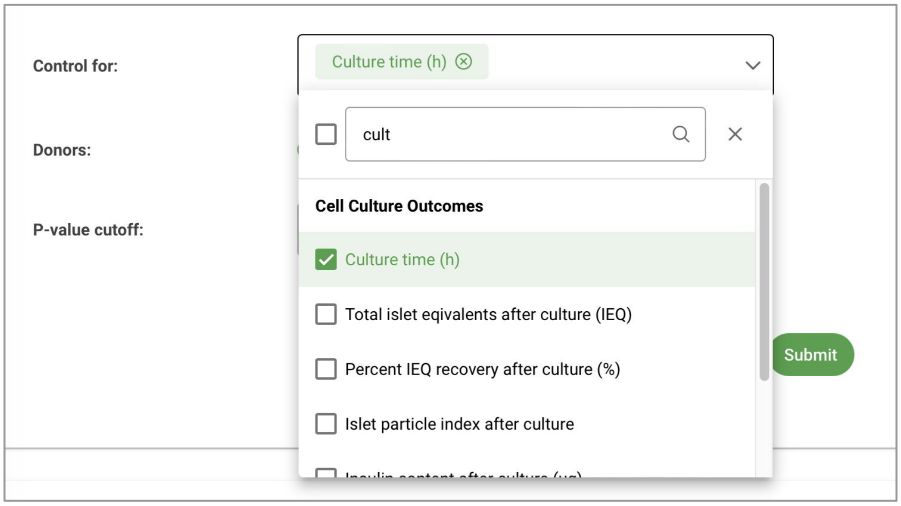
Select ‘Bulk gene expression (RNA-seq)’ and ‘Diabetes diagnosis’ (‘Type 2’ vs. ‘No Diabetes’) for the omics type and metadata of interest.

2

Select ‘Culture time (h)’ as a covariate in the ‘Control for:’ input.

3

Click ‘Submit’



Control for: Culture time (h) ⊗

Donors:

P-value cutoff:

☐ cult

Cell Culture Outcomes

☑ Culture time (h)

☐ Total islet eqivalents after culture (IEQ)

☐ Percent IEQ recovery after culture (%)

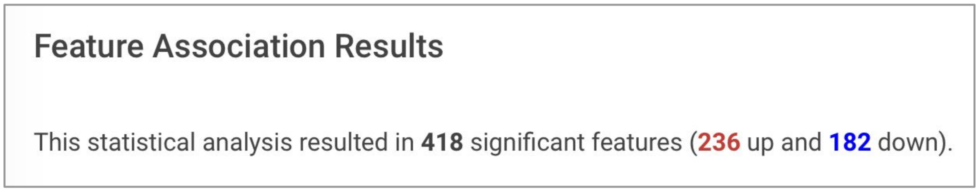
☐ Islet particle index after culture

Feature Association Results

This statistical analysis resulted in **542** significant features (**282** up and **260** down).

There are 542 mRNAs with significantly different expression values in ‘Type 2 versus No Diabetes’ in the bulk RNA-seq data, when controlling for culture time.

If we do not control for culture time, we only detect 418 mRNAs as significantly different between Type 2 and No Diabetes.

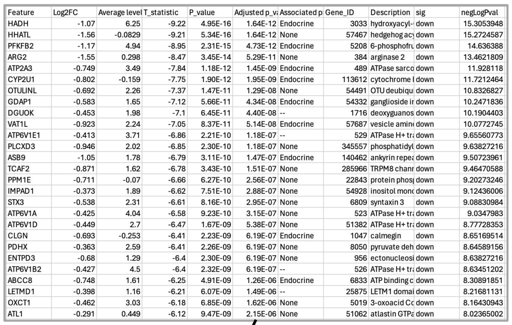


Feature Association Results

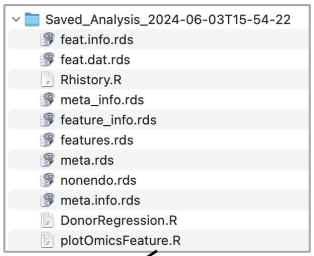
This statistical analysis resulted in **418** significant features (**236** up and **182** down).

The results can be explored in three different ways. Here is an introduction to the 'Graphical Summary'.

Download date and time-stamped results tables and copies of the input data and R scripts used for the analysis for locally reproducible results.



Feature	Log2FC	Average level	T_statistic	P_value	Adjusted p_va	Associated p	Gene_ID	Description	sig	negLogPval
HADH	-1.07	6.25	-9.22	4.95E-16	1.64E-12	Endocrine	3033	hydroxyacyl-	down	15.3053948
HHATL	-1.56	-0.0829	-9.21	5.34E-16	1.64E-12	None	57467	hedgehog acy	down	15.2724587
PFKFB2	-1.17	4.94	-8.95	2.31E-15	4.73E-12	Endocrine	5208	6-phosphofru	down	14.636388
ARG2	-1.55	0.298	-8.47	3.45E-14	5.29E-11	None	384	arginase 2	down	13.4621809
ATP2A3	-0.749	3.49	-7.84	1.18E-12	1.45E-09	Endocrine	489	ATPase sarco	down	11.928118
CYP2U1	-0.802	-0.159	-7.75	1.90E-12	1.95E-09	Endocrine	113612	cytochrome I	down	11.7212464
OTULINL	-0.692	2.26	-7.37	1.47E-11	1.29E-08	None	54491	OTU deubiqui	down	10.8326827
GDAP1	-0.583	1.65	-7.12	5.66E-11	4.34E-08	Endocrine	54332	ganglioside ir	down	10.2471836
DGUOK	-0.453	1.98	-7.1	6.45E-11	4.40E-08	--	1716	deoxyguanos	down	10.1904403
VAT1L	-0.923	2.24	-7.05	8.37E-11	5.14E-08	Endocrine	57687	vesicle amin	down	10.0772745
ATP6V1E1	-0.413	3.71	-6.86	2.21E-10	1.18E-07	--	529	ATPase H+ tra	down	9.65560773
PLCXD3	-0.946	2.02	-6.85	2.30E-10	1.18E-07	None	345557	phosphatidyl	down	9.63827216
ASB9	-1.05	1.78	-6.79	3.11E-10	1.47E-07	Endocrine	140462	ankyrin repea	down	9.50723961
TCAF2	-0.871	1.62	-6.78	3.43E-10	1.51E-07	None	285966	TRPM8 chanr	down	9.46470588
PPM1E	-0.711	-0.07	-6.66	6.27E-10	2.56E-07	None	22843	protein phos	down	9.20273246
IMPAD1	-0.373	1.89	-6.62	7.51E-10	2.88E-07	None	54928	inositol mon	down	9.12436006
STX3	-0.538	2.31	-6.61	8.16E-10	2.95E-07	None	6809	syntaxin 3	down	9.08830984
ATP6V1A	-0.425	4.04	-6.58	9.23E-10	3.15E-07	None	523	ATPase H+ tra	down	9.0347983
ATP6V1D	-0.449	2.7	-6.47	1.67E-09	5.38E-07	None	51382	ATPase H+ tra	down	8.77728353
CLGN	-0.693	-0.253	-6.41	2.23E-09	6.19E-07	Endocrine	1047	calmegin	down	8.65169514
PDHX	-0.363	2.59	-6.41	2.26E-09	6.19E-07	None	8050	pyruvate deh	down	8.64589156
ENTPD3	-0.68	1.29	-6.4	2.30E-09	6.19E-07	None	956	ectonucleosi	down	8.63827216
ATP6V1B2	-0.427	4.5	-6.4	2.32E-09	6.19E-07	--	526	ATPase H+ tra	down	8.63451202
ABCC8	-0.748	1.61	-6.25	4.91E-09	1.26E-06	Endocrine	6833	ATP binding c	down	8.30891851
LETMD1	-0.398	1.16	-6.21	6.07E-09	1.49E-06	--	25875	LETM1 domai	down	8.21681131
OXCT1	-0.462	3.03	-6.18	6.85E-09	1.62E-06	None	5019	3-oxoacid Co	down	8.16430943
ATL1	-0.291	0.449	-6.12	9.47E-09	2.15E-06	None	51062	atlastin GTPa	down	8.02365002



Saved_Analysis_2024-06-03T15-54-22
- feat.info.rds
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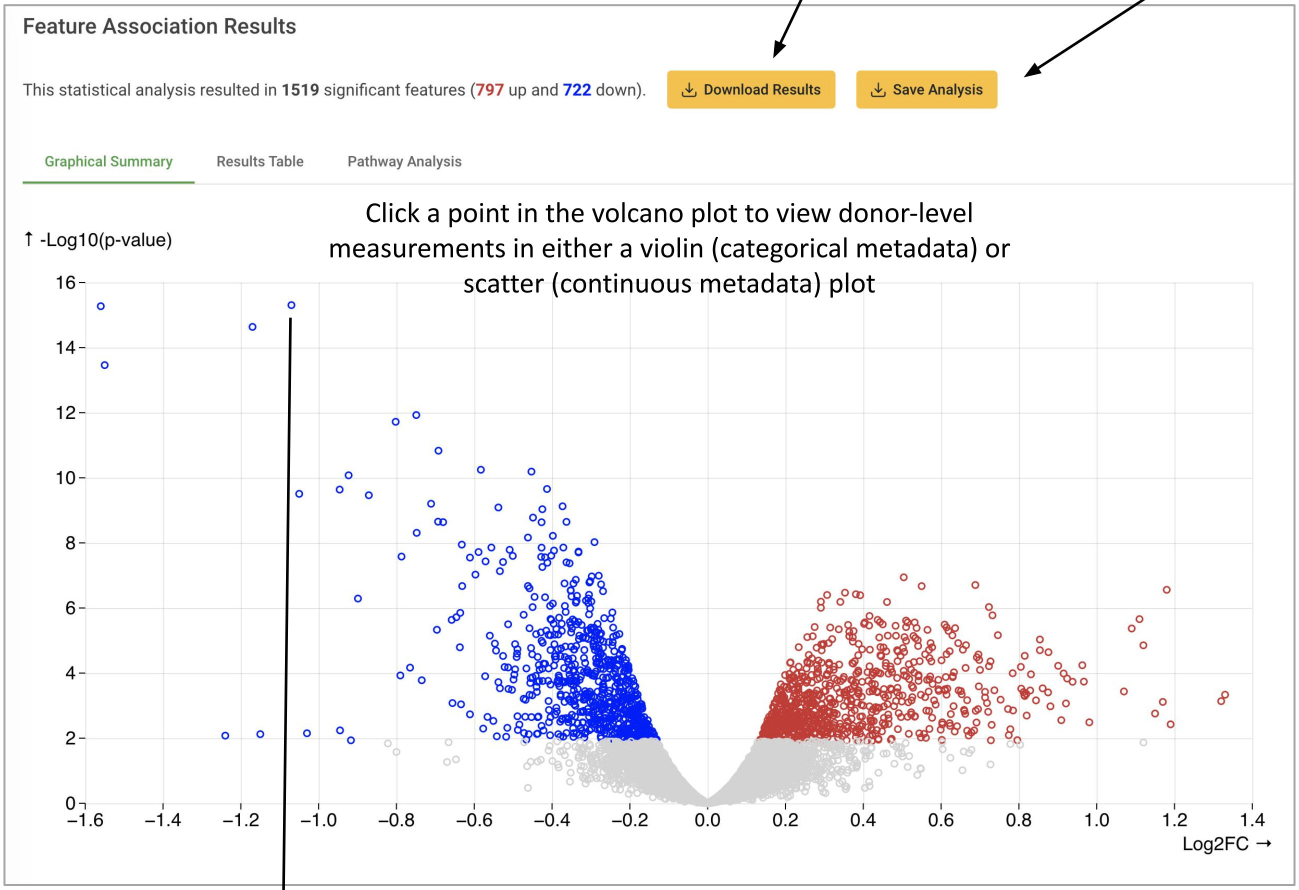
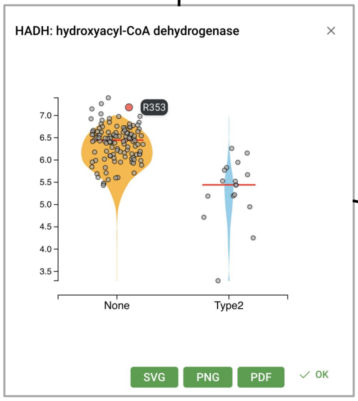
- meta_info.rds
- feature_info.rds
- features.rds
- meta.rds
- nonendo.rds
- meta.info.rds
- DonorRegression.R
- plotOmicsFeature.R



Feature Association Results

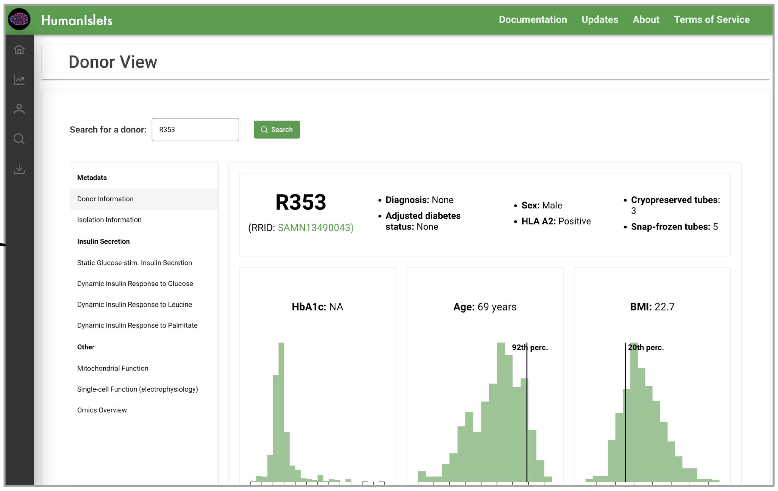
This statistical analysis resulted in **1519** significant features (797 up and 722 down).

Click a point in the volcano plot to view donor-level measurements in either a violin (categorical metadata) or scatter (continuous metadata) plot



HADH: hydroxyacyl-CoA dehydrogenase

Feature-level plots are interactive. Hovering over a point reveals the donor ID and clicking navigates to the donor-view page for that donor.



Donor View

Search for a donor: R353

R353

(RRID: SAMN13490043)

- **Diagnosis:** None
- **Adjusted diabetes status:** None
- **Sex:** Male
- **HLA A2:** Positive
- **Cryopreserved tubes:** 3
- **Snap-frozen tubes:** 5

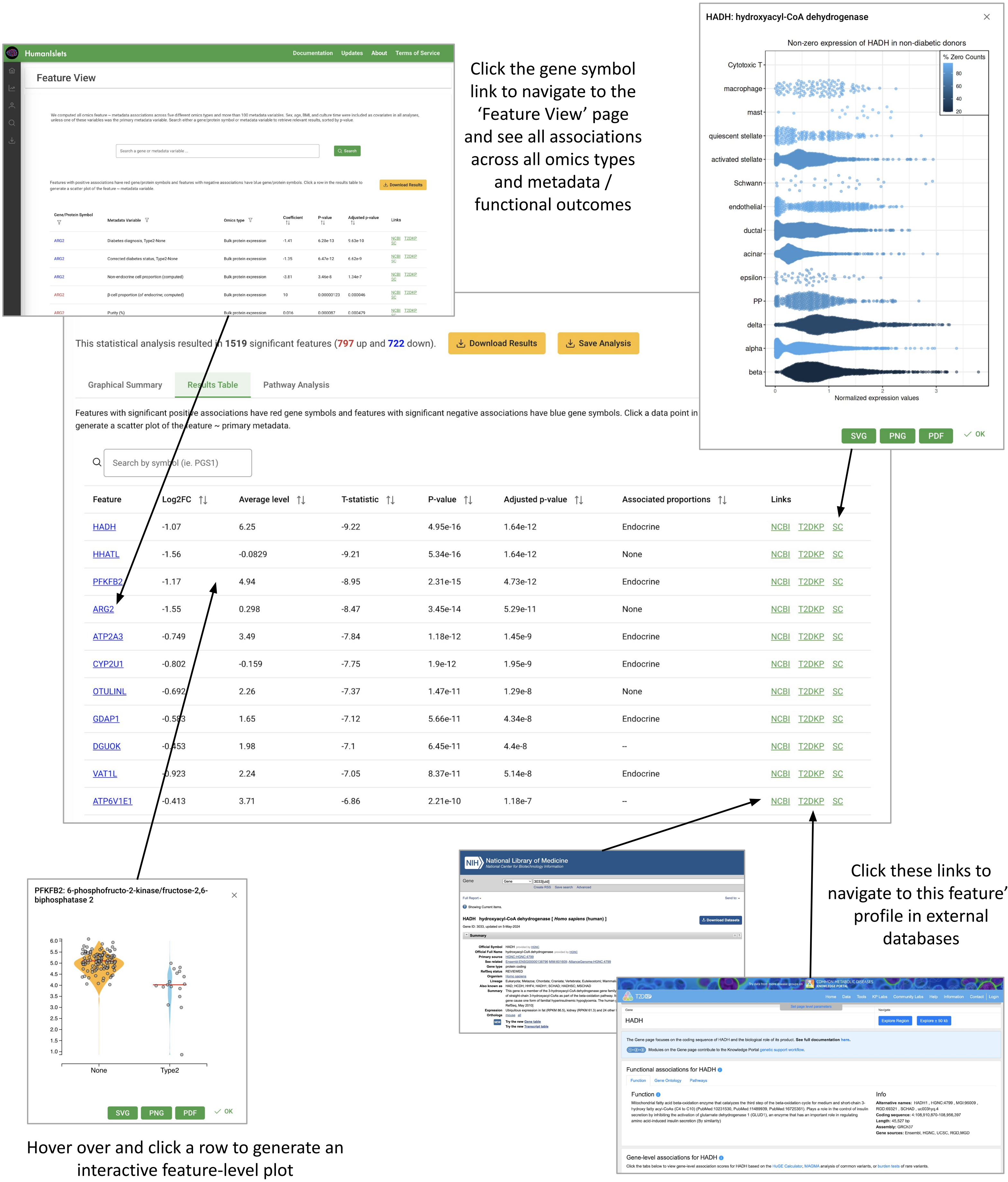
HbA1c: NA

Age: 69 years

BMI: 22.7

The results table is interactive, with many links that generate more detailed plots or navigate to other tool pages/external databases.

Click ‘SC’ to view this feature’s gene expression across cell type in our single-cell database comprised of data from 7 publicly available single-cell RNA-seq islet datasets.



Click the gene symbol link to navigate to the ‘Feature View’ page and see all associations across all omics types and metadata / functional outcomes

Feature View

We computed all omics feature ~ metadata associations across five different omics types and more than 100 metadata variables. Sex, age, BMI, and culture time were included as covariates in all analyses, unless one of these variables was the primary metadata variable. Search either a gene/protein symbol or metadata variable to retrieve relevant results, sorted by p-value.

Features with positive associations have red gene/protein symbols and features with negative associations have blue gene/protein symbols. Click a row in the results table to generate a scatter plot of the feature ~ metadata variable.

Gene/Protein Symbol	Metadata Variable	Omics type	Coefficient	P-value	Adjusted p-value	Links
ARG2	Diabetes diagnosis, Type2-None	Bulk protein expression	-1.41	6.28e-13	9.63e-10	NCBI T2DKP SC
ARG2	Corrected diabetes status, Type2-None	Bulk protein expression	-1.35	6.47e-12	6.62e-9	NCBI T2DKP SC
ARG2	Non-endocrine cell proportion (computed)	Bulk protein expression	-3.81	3.46e-8	1.34e-7	NCBI T2DKP SC
ARG2	β-cell proportion (of endocrine; computed)	Bulk protein expression	10	0.00000123	0.000046	NCBI T2DKP SC
ARG2	Purity (%)	Bulk protein expression	0.016	0.000087	0.000479	NCBI T2DKP

HADH: hydroxyacyl-CoA dehydrogenase

This statistical analysis resulted in **1519** significant features (797 up and 722 down).

Features with significant positive associations have red gene symbols and features with significant negative associations have blue gene symbols. Click a data point in generate a scatter plot of the feature ~ primary metadata.

Feature	Log2FC	Average level	T-statistic	P-value	Adjusted p-value	Associated proportions	Links
HADH	-1.07	6.25	-9.22	4.95e-16	1.64e-12	Endocrine	NCBI T2DKP SC
HHATL	-1.56	-0.0829	-9.21	5.34e-16	1.64e-12	None	NCBI T2DKP SC
PFKFB2	-1.17	4.94	-8.95	2.31e-15	4.73e-12	Endocrine	NCBI T2DKP SC
ARG2	-1.55	0.298	-8.47	3.45e-14	5.29e-11	None	NCBI T2DKP SC
ATP2A3	-0.749	3.49	-7.84	1.18e-12	1.45e-9	Endocrine	NCBI T2DKP SC
CYP2U1	-0.802	-0.159	-7.75	1.9e-12	1.95e-9	Endocrine	NCBI T2DKP SC
OTULINL	-0.692	2.26	-7.37	1.47e-11	1.29e-8	None	NCBI T2DKP SC
GDAP1	-0.583	1.65	-7.12	5.66e-11	4.34e-8	Endocrine	NCBI T2DKP SC
DGUOK	-0.453	1.98	-7.1	6.45e-11	4.4e-8	--	NCBI T2DKP SC
VAT1L	-0.923	2.24	-7.05	8.37e-11	5.14e-8	Endocrine	NCBI T2DKP SC
ATP6V1E1	-0.413	3.71	-6.86	2.21e-10	1.18e-7	--	NCBI T2DKP SC

PFKFB2: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2

Showing Current items.

HADH hydroxyacyl-CoA dehydrogenase [*Homo sapiens* (human)]

Gene ID: 3033, updated on 5-May-2024

Summary

Official Symbol HADH provided by HGNC
Official Full Name hydroxyacyl-CoA dehydrogenase provided by HGNC
Primary source HGNC:HGNC:4799
See related Ensembl:ENSG00000138796 MIM:601609; AllianceGenome:HGNC:4799
Gene type protein coding
RefSeq status REVIEWED
Organism Homo sapiens
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammali
Also known as HAD; HCDH; HHF4; HADH1; SCHAD; HADHSC; MSCHAD
Summary This gene is a member of the 3-hydroxyacyl-CoA dehydrogenase gene family of straight-chain 3-hydroxyacyl-CoAs as part of the beta-oxidation pathway. Its gene cause one form of familial hyperinsulinemic hypoglycemia. The human RefSeq, May 2010]
Expression Ubiquitous expression in fat (RPKM 86.5), kidney (RPKM 61.3) and 24 other
Orthologs mouse all

NEW **Try the new** Gene table
Try the new Transcript table

HADH

The Gene page focuses on the coding sequence of HADH and the biological role of its product. **See full documentation here.**

①–②–③ Modules on the Gene page contribute to the Knowledge Portal genetic support workflow.

Functional associations for HADH

Function

Mitochondrial fatty acid beta-oxidation enzyme that catalyzes the third step of the beta-oxidation cycle for medium and short-chain 3-hydroxy fatty acyl-CoAs (C4 to C10) (PubMed:10231530, PubMed:11489939, PubMed:16725361). Plays a role in the control of insulin secretion by inhibiting the activation of glutamate dehydrogenase 1 (GLUD1), an enzyme that has an important role in regulating amino acid-induced insulin secretion (By similarity)

Info

Alternative names: HADH1 , HGNC:4799 , MGI:96009 , RGD:69321 , SCHAD , uc003hyq.4
Coding sequence: 4:108,910,870-108,956,397
Length: 45,527 bp
Assembly: GRCh37
Gene sources: Ensembl, HGNC, UCSC, RGD,MGD

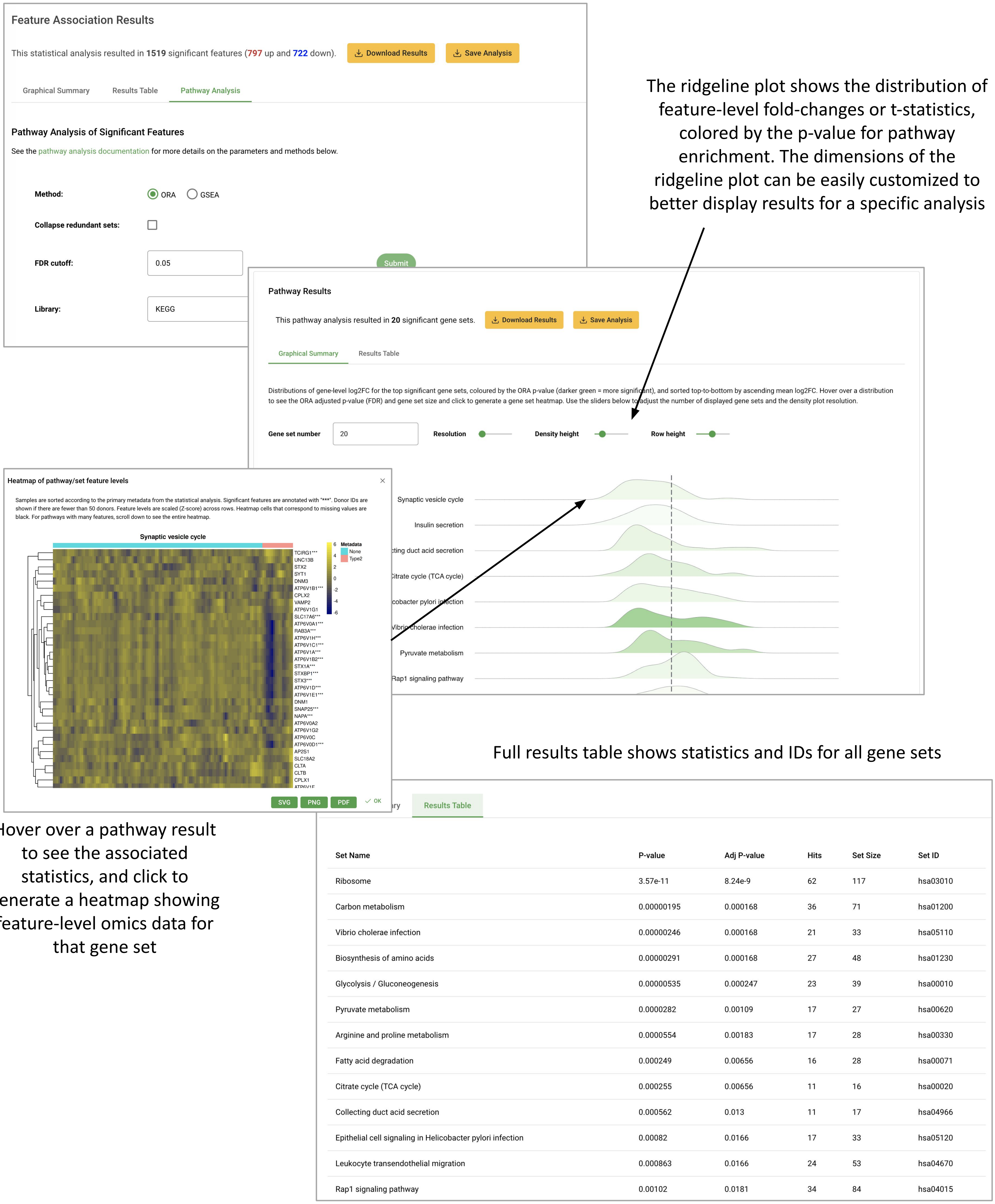
Gene-level associations for HADH

Click the tabs below to view gene-level association scores for HADH based on the HuGE Calculator, MAGMA analysis of common variants, or burden tests of rare variants.

Click these links to navigate to this feature’s profile in external databases

Hover over and click a row to generate an interactive feature-level plot

The pathway analysis tab supports pathway/gene set analysis of the associations results using two different method (ORA and GSEA) for 8 different gene set libraries.



Feature Association Results

This statistical analysis resulted in **1519** significant features (797 up and 722 down).

Pathway Analysis of Significant Features

See the pathway analysis documentation for more details on the parameters and methods below.

Method: ● ORA ○ GSEA

Collapse redundant sets: ☐

FDR cutoff: 0.05

Library: KEGG

The ridgeline plot shows the distribution of feature-level fold-changes or t-statistics, colored by the p-value for pathway enrichment. The dimensions of the ridgeline plot can be easily customized to better display results for a specific analysis

Pathway Results

This pathway analysis resulted in **20** significant gene sets.

Distributions of gene-level log2FC for the top significant gene sets, coloured by the ORA p-value (darker green = more significant), and sorted top-to-bottom by ascending mean log2FC. Hover over a distribution to see the ORA adjusted p-value (FDR) and gene set size and click to generate a gene set heatmap. Use the sliders below to adjust the number of displayed gene sets and the density plot resolution.

Gene set number 20

Heatmap of pathway/set feature levels

Samples are sorted according to the primary metadata from the statistical analysis. Significant features are annotated with "***". Donor IDs are shown if there are fewer than 50 donors. Feature levels are scaled (Z-score) across rows. Heatmap cells that correspond to missing values are black. For pathways with many features, scroll down to see the entire heatmap.

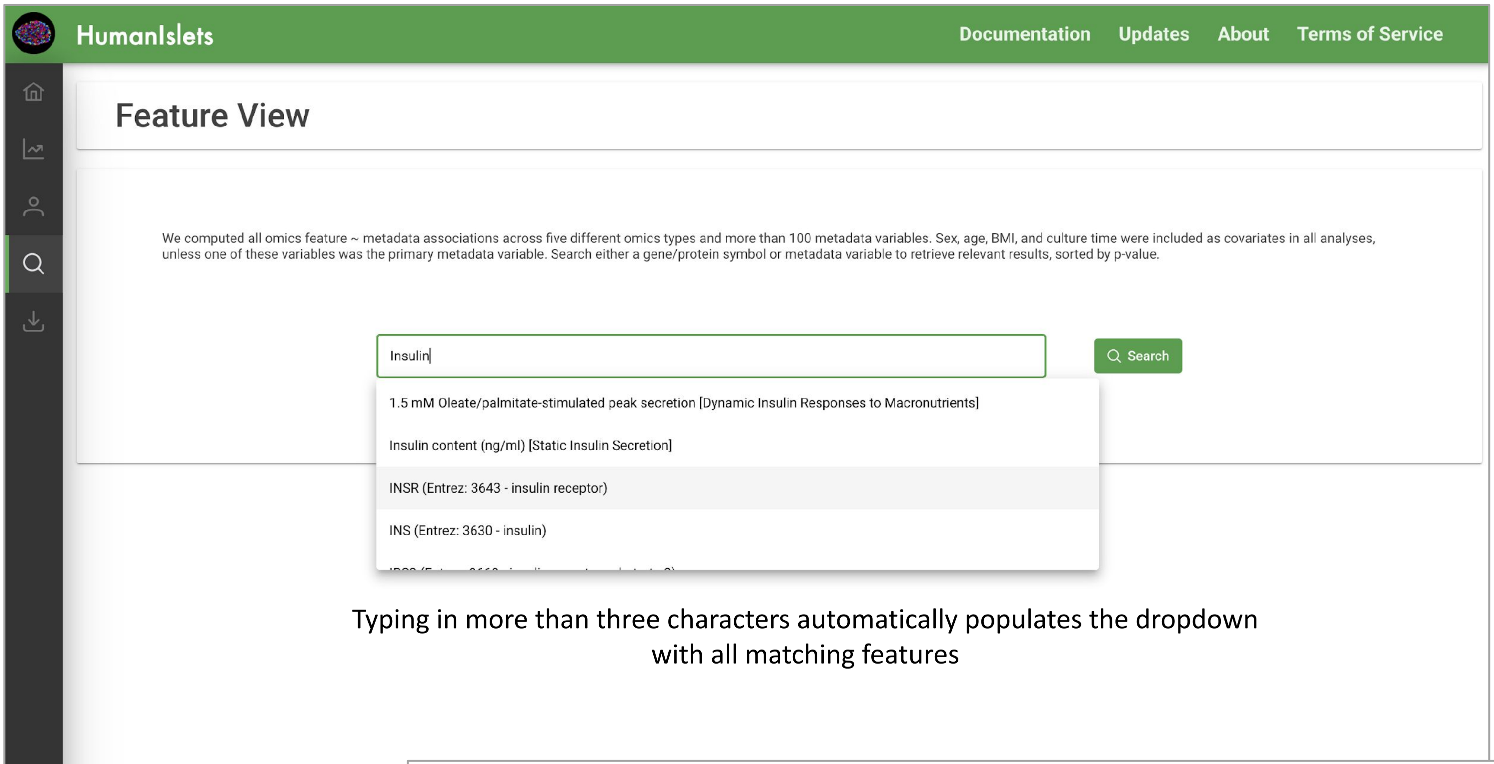
Hover over a pathway result to see the associated statistics, and click to generate a heatmap showing feature-level omics data for that gene set

Full results table shows statistics and IDs for all gene sets

Set Name	P-value	Adj P-value	Hits	Set Size	Set ID
Ribosome	3.57e-11	8.24e-9	62	117	hsa03010
Carbon metabolism	0.00000195	0.000168	36	71	hsa01200
Vibrio cholerae infection	0.00000246	0.000168	21	33	hsa05110
Biosynthesis of amino acids	0.00000291	0.000168	27	48	hsa01230
Glycolysis / Gluconeogenesis	0.00000535	0.000247	23	39	hsa00010
Pyruvate metabolism	0.0000282	0.00109	17	27	hsa00620
Arginine and proline metabolism	0.0000554	0.00183	17	28	hsa00330
Fatty acid degradation	0.000249	0.00656	16	28	hsa00071
Citrate cycle (TCA cycle)	0.000255	0.00656	11	16	hsa00020
Collecting duct acid secretion	0.000562	0.013	11	17	hsa04966
Epithelial cell signaling in Helicobacter pylori infection	0.00082	0.0166	17	33	hsa05120
Leukocyte transendothelial migration	0.000863	0.0166	24	53	hsa04670
Rap1 signaling pathway	0.00102	0.0181	34	84	hsa04015

Feature View

Statistical associations between each omics type and each metadata/function outcome were computed and stored in a database (>3.8 million relationships). Age, sex, BMI, and culture time were included as covariates in the analysis. The pre-computed results can be queried by either gene symbol or by metadata/functional outcome name.



Feature View

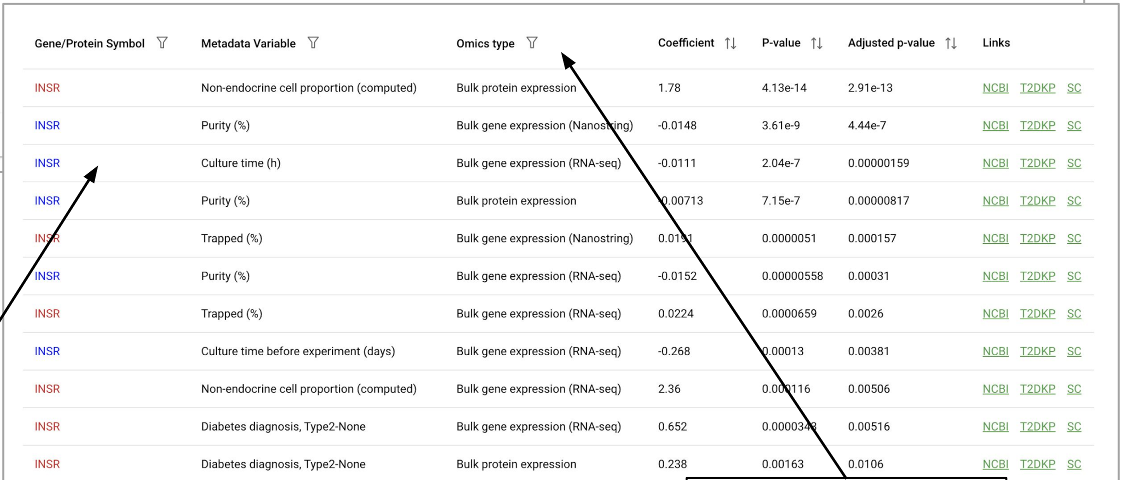
We computed all omics feature ~ metadata associations across five different omics types and more than 100 metadata variables. Sex, age, BMI, and culture time were included as covariates in all analyses, unless one of these variables was the primary metadata variable. Search either a gene/protein symbol or metadata variable to retrieve relevant results, sorted by p-value.

Insulin

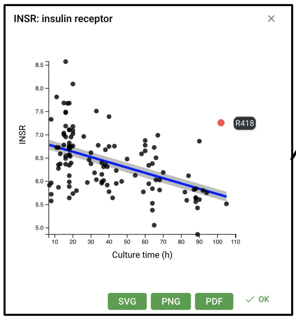
- 1.5 mM Oleate/palmitate-stimulated peak secretion [Dynamic Insulin Responses to Macronutrients]
- Insulin content (ng/ml) [Static Insulin Secretion]
- INSR (Entrez: 3643 - insulin receptor)
- INS (Entrez: 3630 - insulin)

Typing in more than three characters automatically populates the dropdown with all matching features

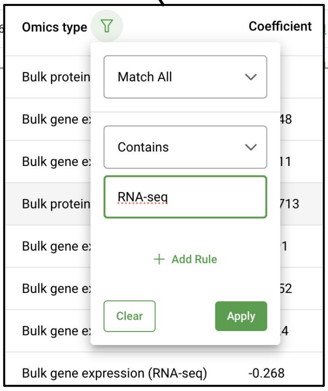
Data visualization portal for the HumanIslets project



Gene/Protein Symbol	Metadata Variable	Omics type	Coefficient	P-value	Adjusted p-value	Links
INSR	Non-endocrine cell proportion (computed)	Bulk protein expression	1.78	4.13e-14	2.91e-13	NCBI T2DKP SC
INSR	Purity (%)	Bulk gene expression (Nanostring)	-0.0148	3.61e-9	4.44e-7	NCBI T2DKP SC
INSR	Culture time (h)	Bulk gene expression (RNA-seq)	-0.0111	2.04e-7	0.00000159	NCBI T2DKP SC
INSR	Purity (%)	Bulk protein expression	-0.00713	7.15e-7	0.00000817	NCBI T2DKP SC
INSR	Trapped (%)	Bulk gene expression (Nanostring)	0.0191	0.0000051	0.000157	NCBI T2DKP SC
INSR	Purity (%)	Bulk gene expression (RNA-seq)	-0.0152	0.00000558	0.00031	NCBI T2DKP SC
INSR	Trapped (%)	Bulk gene expression (RNA-seq)	0.0224	0.0000659	0.0026	NCBI T2DKP SC
INSR	Culture time before experiment (days)	Bulk gene expression (RNA-seq)	-0.268	0.00013	0.00381	NCBI T2DKP SC
INSR	Non-endocrine cell proportion (computed)	Bulk gene expression (RNA-seq)	2.36	0.000116	0.00506	NCBI T2DKP SC
INSR	Diabetes diagnosis, Type2-None	Bulk gene expression (RNA-seq)	0.652	0.0000348	0.00516	NCBI T2DKP SC
INSR	Diabetes diagnosis, Type2-None	Bulk protein expression	0.238	0.00163	0.0106	NCBI T2DKP SC
INSR	Corrected diabetes status, Type2-None	Bulk gene expression (Nanostring)	0.416			T2DKP SC
INSR	Diabetes diagnosis, Type2-None	Bulk gene expression (Nanostring)	0.42			



The results table shows all results for the queried feature, sorted by statistical significance. Interactive table components are the same as on the omics analysis page.



Match All

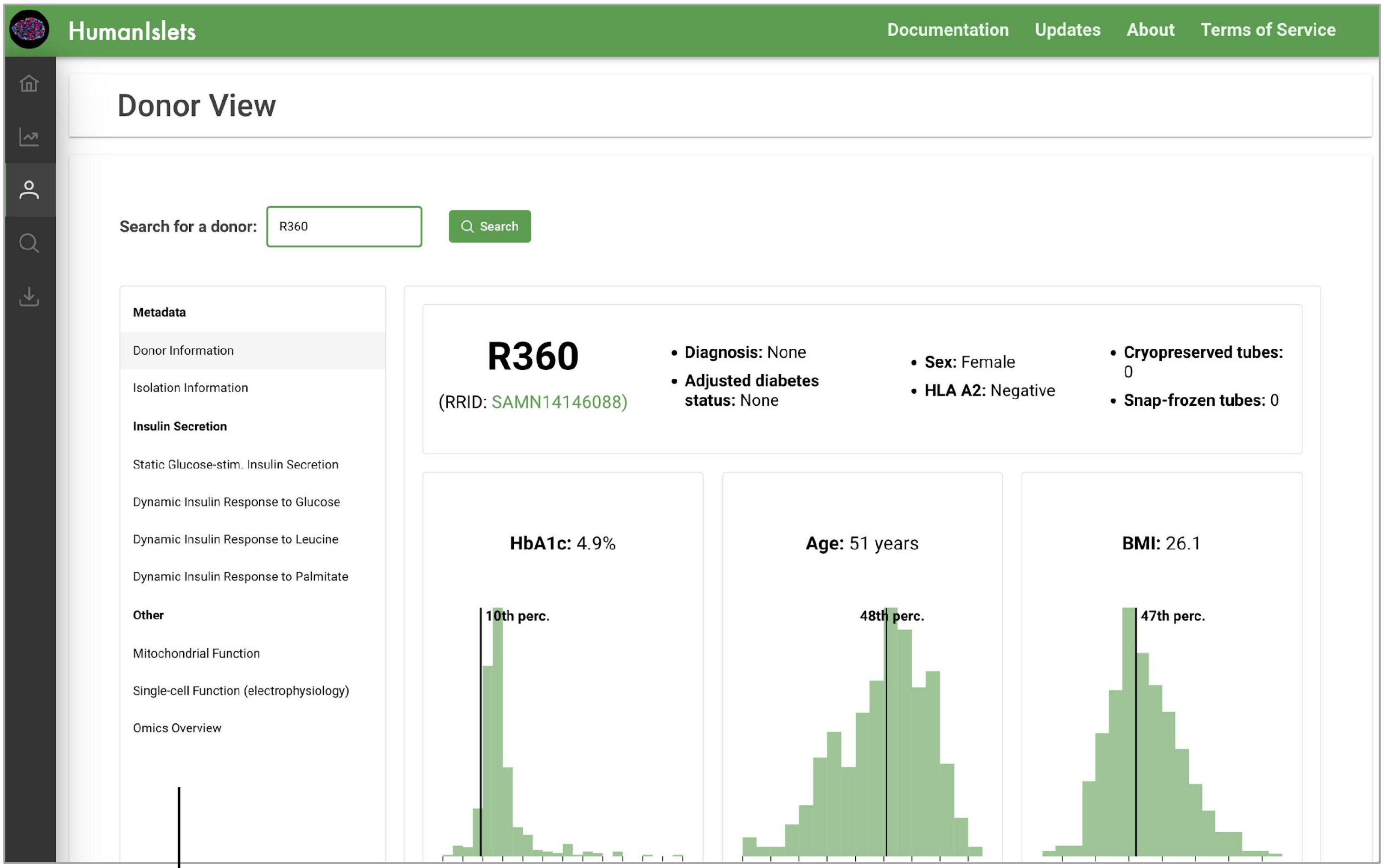
Contains

RNA-seq

The results table enables filtering, for example by omics type

Donor View

The Donor View page shows a summary of each donor's outcomes, displayed against the distribution of values from different donors across the HumanIslets database. Donors can be searched by either donor ID (ie. R360) or RRID (ie. SAMN14146088).



Donor View

Search for a donor: R360

R360

(RRID: SAMN14146088)

- **Diagnosis:** None
- **Adjusted diabetes status:** None
- **Sex:** Female
- **HLA A2:** Negative
- **Cryopreserved tubes:** 0
- **Snap-frozen tubes:** 0

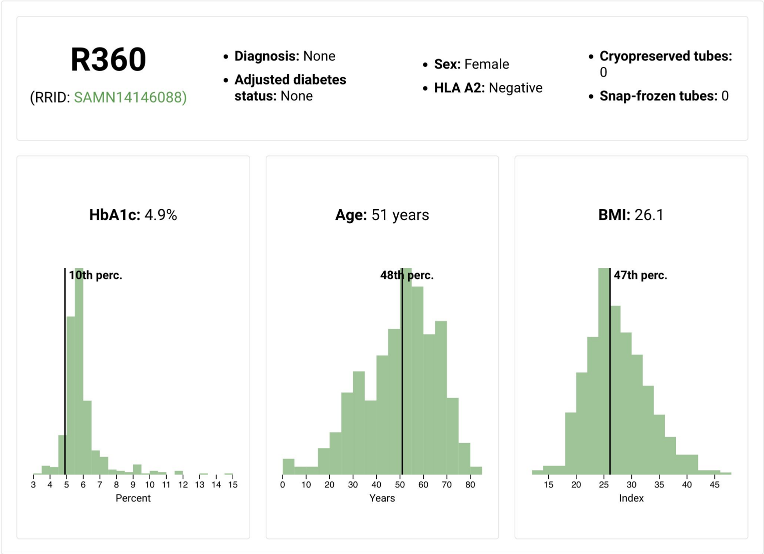
HbA1c: 4.9%

Age: 51 years

BMI: 26.1

There are currently nine types of data available to view. More data will be added over time as it is collected.

Each tab shows a summary of a different kind of dataset. For example …



R360

(RRID: SAMN14146088)

- **Diagnosis:** None
- **Adjusted diabetes status:** None
- **Sex:** Female
- **HLA A2:** Negative
- **Cryopreserved tubes:** 0
- **Snap-frozen tubes:** 0

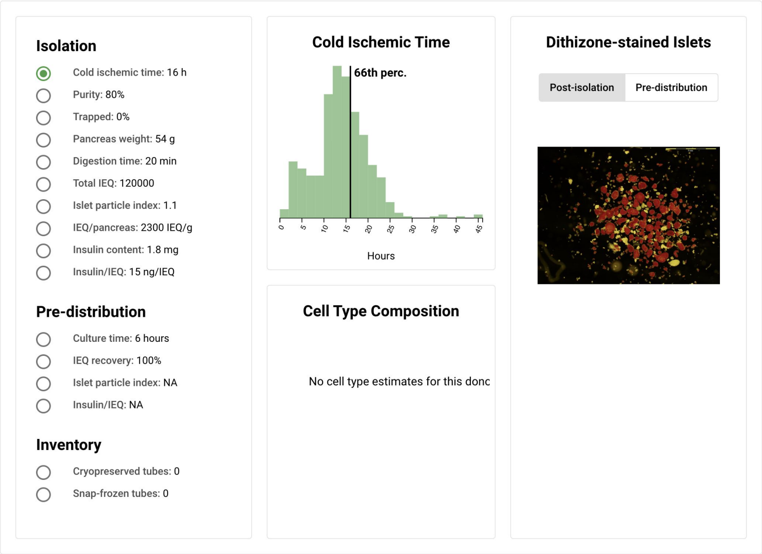
HbA1c: 4.9%

Age: 51 years

BMI: 26.1

Basic donor metadata, including availability of isolated islets for future research projects

Technical islet isolation outcomes, including images of the isolated islets



Isolation

● Cold ischemic time: 16 h
○ Purity: 80%
○ Trapped: 0%
○ Pancreas weight: 54 g
○ Digestion time: 20 min
○ Total IEQ: 120000
○ Islet particle index: 1.1
○ IEQ/pancreas: 2300 IEQ/g
○ Insulin content: 1.8 mg
○ Insulin/IEQ: 15 ng/IEQ

Pre-distribution

○ Culture time: 6 hours
○ IEQ recovery: 100%
○ Islet particle index: NA
○ Insulin/IEQ: NA

Inventory

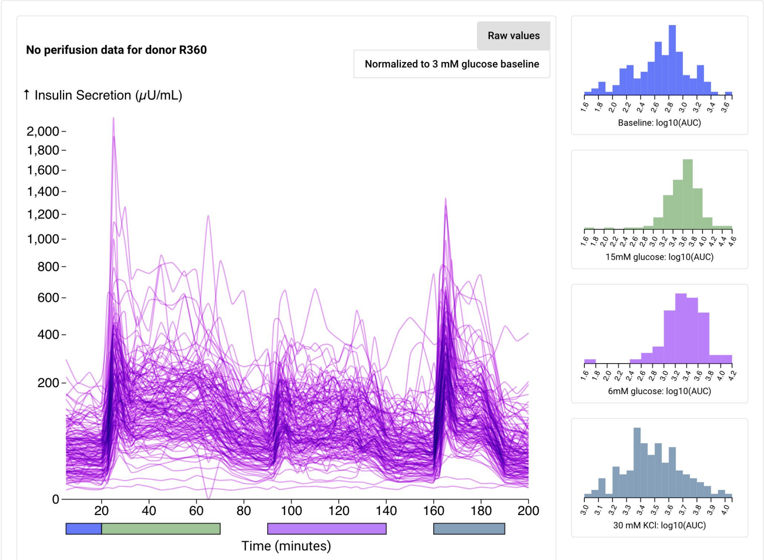
○ Cryopreserved tubes: 0
○ Snap-frozen tubes: 0

Cold Ischemic Time

Cell Type Composition

No cell type estimates for this donc

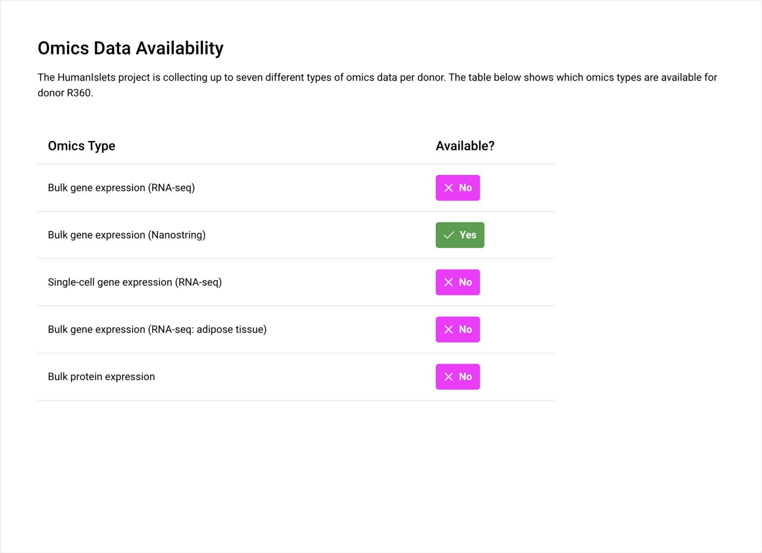
Dithizone-stained Islets



No perifusion data for donor R360

Functional outcomes such as dynamic insulin secretion in response to three different nutrients. Functional data also include static insulin secretion, oxygen consumption and single-cell electrophysiology outcomes.

An overview of the omics data available for this donor



Omics Data Availability

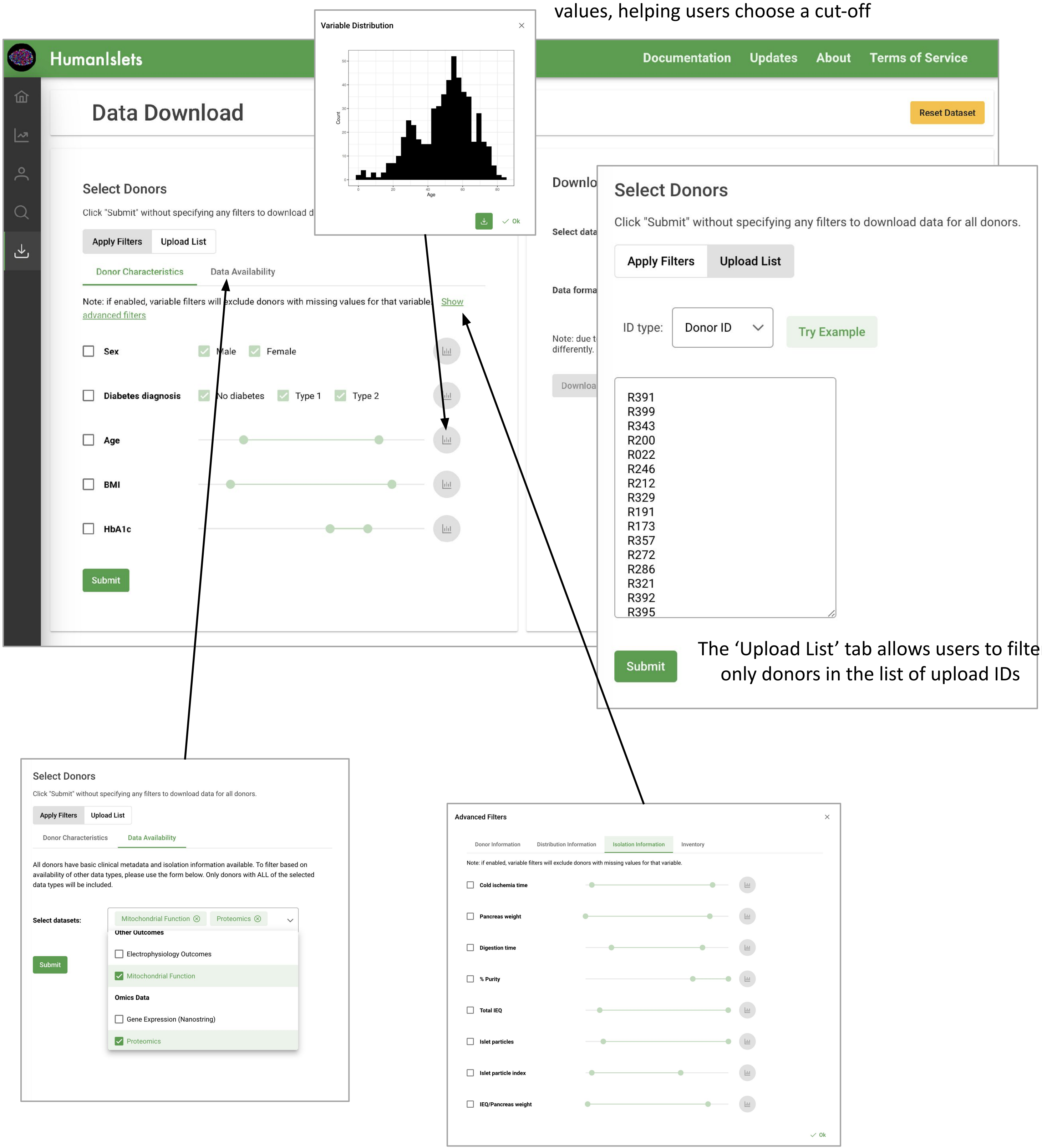
The HumanIslets project is collecting up to seven different types of omics data per donor. The table below shows which omics types are available for donor R360.

Omics Type	Available?
Bulk gene expression (RNA-seq)	✕ No
Bulk gene expression (Nanostring)	✓ Yes
Single-cell gene expression (RNA-seq)	✕ No
Bulk gene expression (RNA-seq: adipose tissue)	✕ No
Bulk protein expression	✕ No

Data Download

The data download page has two steps: 'Select Donors' and 'Download Data'. In the first step, users can filter donors by metadata, data availability, or a donor list.

Clicking this generates a distribution of the values, helping users choose a cut-off



Click "Submit" without specifying any filters to download data for all donors.

Note: if enabled, variable filters will exclude donors with missing values for that variable. Show advanced filters

R391
R399
R343
R200
R022
R246
R212
R329
R191
R173
R357
R272
R286
R321
R392
R395

The 'Upload List' tab allows users to filter only donors in the list of upload IDs

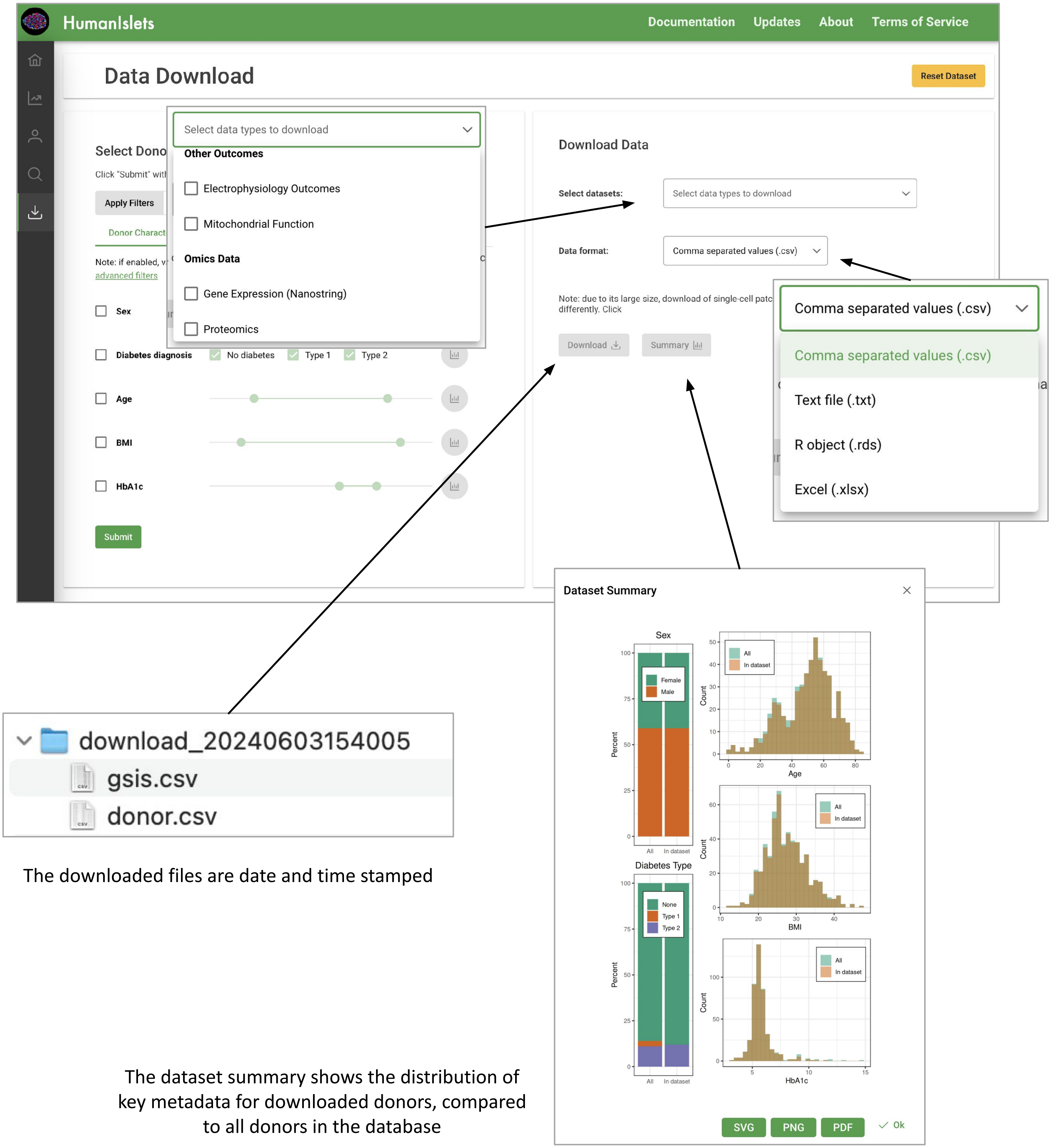
All donors have basic clinical metadata and isolation information available. To filter based on availability of other data types, please use the form below. Only donors with ALL of the selected data types will be included.

Note: if enabled, variable filters will exclude donors with missing values for that variable.

Users can filter to include only donors with specific data types available

Clicking the advanced filters link allows users to filter by many more variables

Once the donors have been selected, users can choose the data types that they'd like to download and the format that they want it in.



The downloaded files are date and time stamped

The dataset summary shows the distribution of key metadata for downloaded donors, compared to all donors in the database