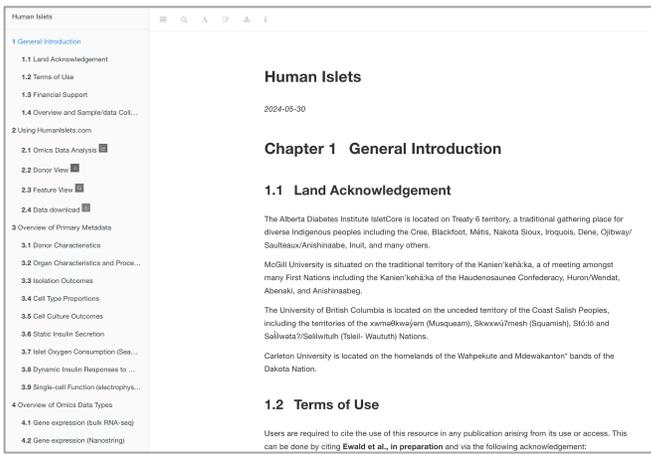


# HumanIslets Web-Tool



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

- 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.

# Omic 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'!

The screenshot shows the 'Omics View' interface for Humanslets. The main form includes the following fields:

- 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 (selected), Subset
- 5 P-value cutoff:** 0.05, Use adjusted p-values (checked)
- 6 Submit** button

Two pop-up windows are shown:

- Interface for selecting multiple covariates:** A window titled 'Organ Characteristics and Processing' with a search bar and a list of checkboxes. 'Cold Ischemic Time (h)' is checked, while 'Pancreas weight (g)', 'Fatty infiltration', and 'Organ consistency' are unchecked.
- Support for extensive filtering to subset donors included in the analysis:** A window titled 'Select Donors' with 'Apply Filters' and 'Upload List' tabs. It shows filters for 'Sex' (Male, Female), 'Diabetes diagnosis' (No diabetes, Type 1, Type 2), 'Age', 'BMI', and 'HbA1c' with sliders. The 'Diabetes diagnosis' filter is active, showing 'No diabetes' and 'Type 2' selected.

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:  cult 🔍 ×

P-value cutoff:

Cell Culture Outcomes

- Culture time (h)
- Total islet equivalents after culture (IEQ)
- Percent IEQ recovery after culture (%)
- Islet particle index after culture
- Insulin content after culture (µg)

Submit

## 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

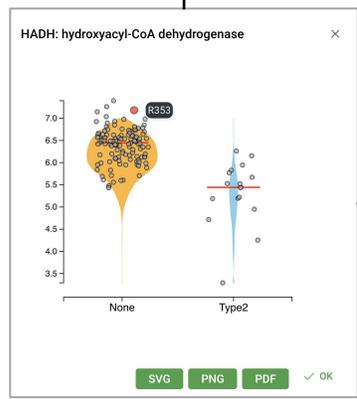
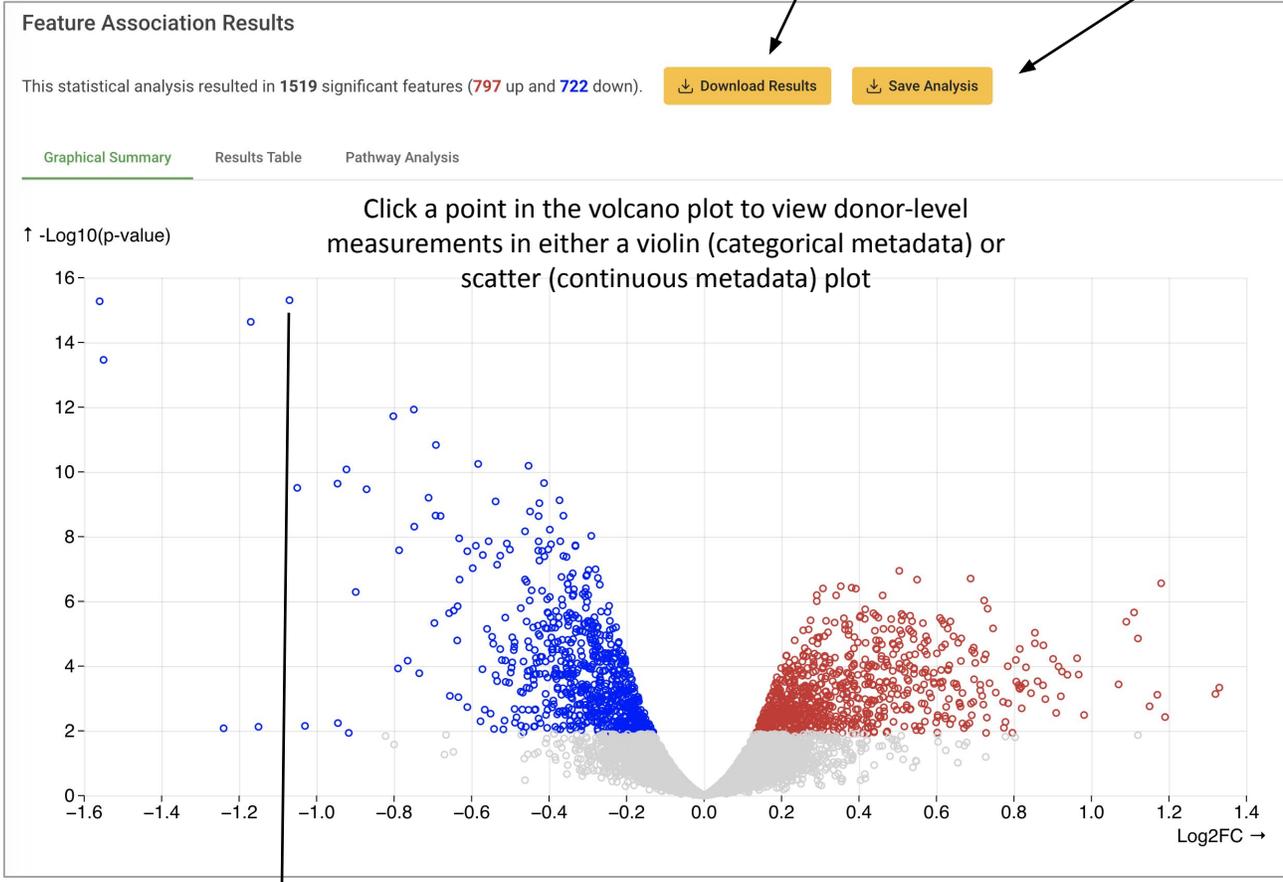
This statistical analysis resulted in **418** significant features (**236** up and **182** down).

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

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

Feature	Log2FC	Average level	T_statistic	P_value	Adjusted_p_val	Associated p	Gene_ID	Description	sig	negLogPval
HADH	-1.07	6.25	-9.22	4.95E-16	1.64E-12	Endocrine	3033	hydroxycyl-down		15.3052948
HHA1L	-1.56	-0.0029	-9.21	5.34E-16	1.64E-12	None	57467	hedgehog-act-down		15.2724597
PFKFB2	-1.17	4.94	-8.95	2.31E-15	4.73E-12	Endocrine	5206	6-phosphofru-down		14.636388
ARG2	-1.55	0.298	-8.47	3.45E-14	6.29E-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		11.926118
CYP2D1	-0.802	-0.199	-7.75	1.90E-12	1.96E-09	Endocrine	113612	cytochrome down		11.7212464
OTLAINL	-0.692	2.26	-7.37	1.47E-11	1.29E-08	None	54491	OTU deubiqu-down		10.8326827
GDAP1	-0.583	1.65	-7.12	5.66E-11	4.34E-08	Endocrine	54332	ganglioside II-down		10.2471836
DGUCOK	-0.453	1.98	-7.1	8.45E-11	4.40E-08		1716	deoxyguanos-down		10.1694403
VAT1L	-0.823	2.24	-7.05	8.37E-11	5.14E-08	Endocrine	57687	vesicle amin-down		10.0772745
ATP9V1E1	-0.413	3.71	-6.86	2.21E-10	1.18E-07	...	529	ATPase H+ tr-down		9.65560773
PLCAD3	-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 regul-down		9.50729661
TCAF2	-0.871	1.62	-6.78	3.43E-10	1.51E-07	None	285968	TRPM8 chan-down		9.46470588
PKMT1E	-0.711	-0.07	-6.66	6.27E-10	2.96E-07	None	22843	protein phosph-down		9.32027046
MPH01	-0.373	1.89	-6.62	7.61E-10	2.86E-07	None	54908	protoporph-down		9.13480086
STX3	-0.538	2.31	-6.61	8.16E-10	2.95E-07	None	6809	syntaxin 3-down		9.08830984
ATP9V1A	-0.425	4.04	-6.58	8.23E-10	3.15E-07	None	523	ATPase H+ tr-down		9.0347983
ATP9V1D	-0.449	2.7	-6.47	1.67E-09	5.38E-07	None	51382	ATPase H+ tr-down		8.77228353
CLGN	-0.683	-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 dehydro-down		8.64489196
ENTPD3	-0.58	1.29	-6.4	2.35E-09	6.19E-07	None	859	ectonucleotid-down		8.63827216
ATP9V1B2	-0.427	4.5	-6.4	2.32E-09	6.19E-07	...	526	ATPase H+ tr-down		8.63451202
ABCC8	-0.748	1.61	-6.25	4.91E-09	1.26E-06	Endocrine	6833	ATP binding-down		8.30891851
LETM1	-0.388	1.16	-6.21	6.07E-09	1.49E-06	...	26875	LETM1 domain-down		8.21681131
CWC11	-0.462	3.03	-6.19	6.86E-09	1.62E-06	None	5919	3-methylcroton-down		8.16400443
ATL1	-0.281	0.449	-6.12	9.47E-09	2.15E-06	None	51082	antistatin GTP-down		8.02385002

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  - feature\_info.rds
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  - meta.rds
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  - meta.info.rds
  - DonorRegression.R
  - plotOmicsFeature.R



Humanislets | Donor View

Search for a donor: R353

Metadata

Donor Information: R353 (RRID: SAMN13490043)

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

Insulin Secretion

Static Glucose-stim: Insulin Secretion

Dynamic Insulin Response to Glucose

Dynamic Insulin Response to Leucine

Dynamic Insulin Response to Palmitate

Other

Mitochondrial Function

Single-cell Function (electrophysiology)

Omics Overview

HBA1c: NA | Age: 69 years | BMI: 22.7

92th perc. | 26th perc.

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

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.

HumanIslets Documentation Updates About Terms of Service

Feature View

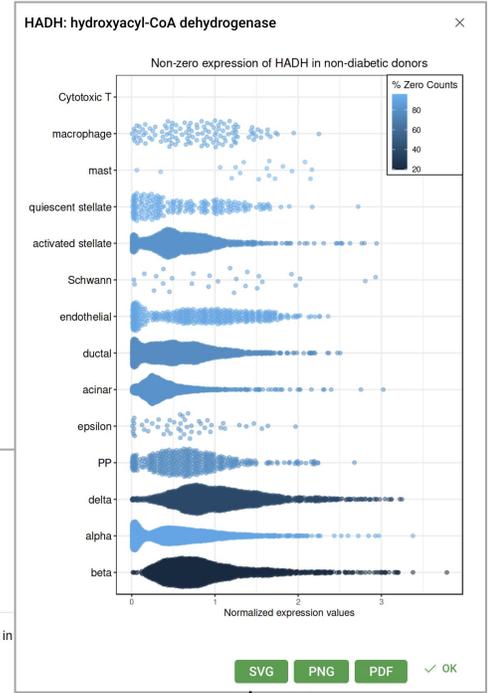
We computed all omics feature - metadata associations across five different omics types and more than 100 metadata variables. Sex, age, BMI, and culture time were included as covariates in all analyses, unless one of these variables was the primary metadata variable. Search either a gene/protein symbol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

Search a gene or metadata variable...

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	Bulk protein expression	-1.41	4.29e-13	1.62e-10	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
ARG2	Corrected diabetes status_Type2	Bulk protein expression	-1.35	6.47e-12	4.62e-9	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
ARG2	Non-endocrine cell proportion (computed)	Bulk protein expression	-3.81	3.46e-8	1.34e-7	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
ARG2	β cell proportion (of endocrine; computed)	Bulk protein expression	10	0.00000123	0.000046	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
ARG2	Purity (%)	Bulk protein expression	0.016	0.000087	0.000479	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>

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



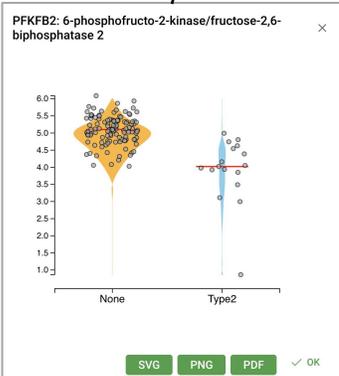
This statistical analysis resulted in 1519 significant features (797 up and 722 down).

Graphical Summary **Results Table** Pathway Analysis

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.

Search by symbol (ie. PGS1)

Feature	Log2FC	Average level	T-statistic	P-value	Adjusted p-value	Associated proportions	Links
<a href="#">HADH</a>	-1.07	6.25	-9.22	4.95e-16	1.64e-12	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">HHATL</a>	-1.56	-0.0829	-9.21	5.34e-16	1.64e-12	None	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">PFKFB2</a>	-1.17	4.94	-8.95	2.31e-15	4.73e-12	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">ARG2</a>	-1.55	0.298	-8.47	3.45e-14	5.29e-11	None	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">ATP2A3</a>	-0.749	3.49	-7.84	1.18e-12	1.45e-9	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">CYP2U1</a>	-0.802	-0.159	-7.75	1.9e-12	1.95e-9	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">OTULINL</a>	-0.692	2.26	-7.37	1.47e-11	1.29e-8	None	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">GDAP1</a>	-0.593	1.65	-7.12	5.66e-11	4.34e-8	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">DGUOK</a>	-0.453	1.98	-7.1	6.45e-11	4.4e-8	--	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">VAT1L</a>	-0.923	2.24	-7.05	8.37e-11	5.14e-8	Endocrine	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
<a href="#">ATP6V1E1</a>	-0.413	3.71	-6.86	2.21e-10	1.18e-7	--	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>



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

National Library of Medicine  
National Center for Biotechnology Information

Gene:

Full Report:

Showing Current Items

**HADH** hydroxyacyl-CoA dehydrogenase [ Homo sapiens (human) ]  
Gene ID: 3051, updated on 14-Feb-2004

Summary

Official Symbol: HADH, provided by HUGO  
Official Full Name: hydroxyacyl-CoA dehydrogenase, provided by HUGO  
Primary Name: HADH  
Gene Type: protein-coding  
RefSeq Status: REVIEWED  
MIM: 103490  
OMIM: 103490  
Aliases: HAD, HADH, HADH1, HADH2, HADH3, HADH4, HADH5, HADH6, HADH7, HADH8, HADH9, HADH10, HADH11, HADH12, HADH13, HADH14, HADH15, HADH16, HADH17, HADH18, HADH19, HADH20, HADH21, HADH22, HADH23, HADH24, HADH25, HADH26, HADH27, HADH28, HADH29, HADH30, HADH31, HADH32, HADH33, HADH34, HADH35, HADH36, HADH37, HADH38, HADH39, HADH40, HADH41, HADH42, HADH43, HADH44, HADH45, HADH46, HADH47, HADH48, HADH49, HADH50, HADH51, HADH52, HADH53, HADH54, HADH55, HADH56, HADH57, HADH58, HADH59, HADH60, HADH61, HADH62, HADH63, HADH64, HADH65, HADH66, HADH67, HADH68, HADH69, HADH70, HADH71, HADH72, HADH73, HADH74, HADH75, HADH76, HADH77, HADH78, HADH79, HADH80, HADH81, HADH82, HADH83, HADH84, HADH85, HADH86, HADH87, HADH88, HADH89, HADH90, HADH91, HADH92, HADH93, HADH94, HADH95, HADH96, HADH97, HADH98, HADH99, HADH100, HADH101, HADH102, HADH103, HADH104, HADH105, HADH106, HADH107, HADH108, HADH109, HADH110, HADH111, HADH112, HADH113, HADH114, HADH115, HADH116, HADH117, HADH118, HADH119, HADH120, HADH121, 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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).

[Download Results](#)

[Save Analysis](#)

Graphical Summary   Results Table   **Pathway Analysis**

### 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:

Library:

[Submit](#)

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.

[Download Results](#)

[Save Analysis](#)

Graphical Summary   Results Table

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

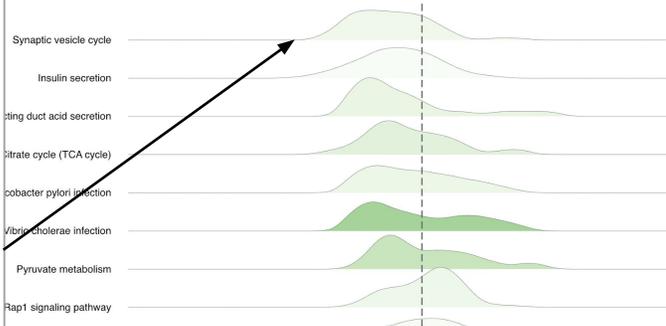
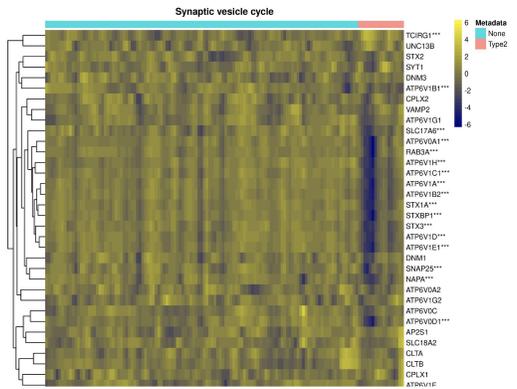
Resolution

Density height

Row height

### 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.



Full results table shows statistics and IDs for all gene sets

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

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.

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## 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.

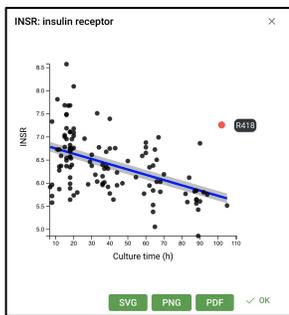
Insulin

Search

- 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

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	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Purity (%)	Bulk gene expression (Nanosttring)	-0.0148	3.61e-9	4.44e-7	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Culture time (h)	Bulk gene expression (RNA-seq)	-0.0111	2.04e-7	0.00000159	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Purity (%)	Bulk protein expression	-0.00713	7.15e-7	0.00000817	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Trapped (%)	Bulk gene expression (Nanosttring)	0.0151	0.0000051	0.000157	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Purity (%)	Bulk gene expression (RNA-seq)	-0.0152	0.00000558	0.00031	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Trapped (%)	Bulk gene expression (RNA-seq)	0.0224	0.0000659	0.0026	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Culture time before experiment (days)	Bulk gene expression (RNA-seq)	-0.268	0.00013	0.00381	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Non-endocrine cell proportion (computed)	Bulk gene expression (RNA-seq)	2.36	0.000116	0.00506	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Diabetes diagnosis, Type2-None	Bulk gene expression (RNA-seq)	0.652	0.0000349	0.00516	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Diabetes diagnosis, Type2-None	Bulk protein expression	0.238	0.00163	0.0106	<a href="#">NCBI</a> <a href="#">T2DKP</a> <a href="#">SC</a>
INSR	Corrected diabetes status, Type2-None	Bulk gene expression (Nanosttring)	0.416			<a href="#">T2DKP</a> <a href="#">SC</a>

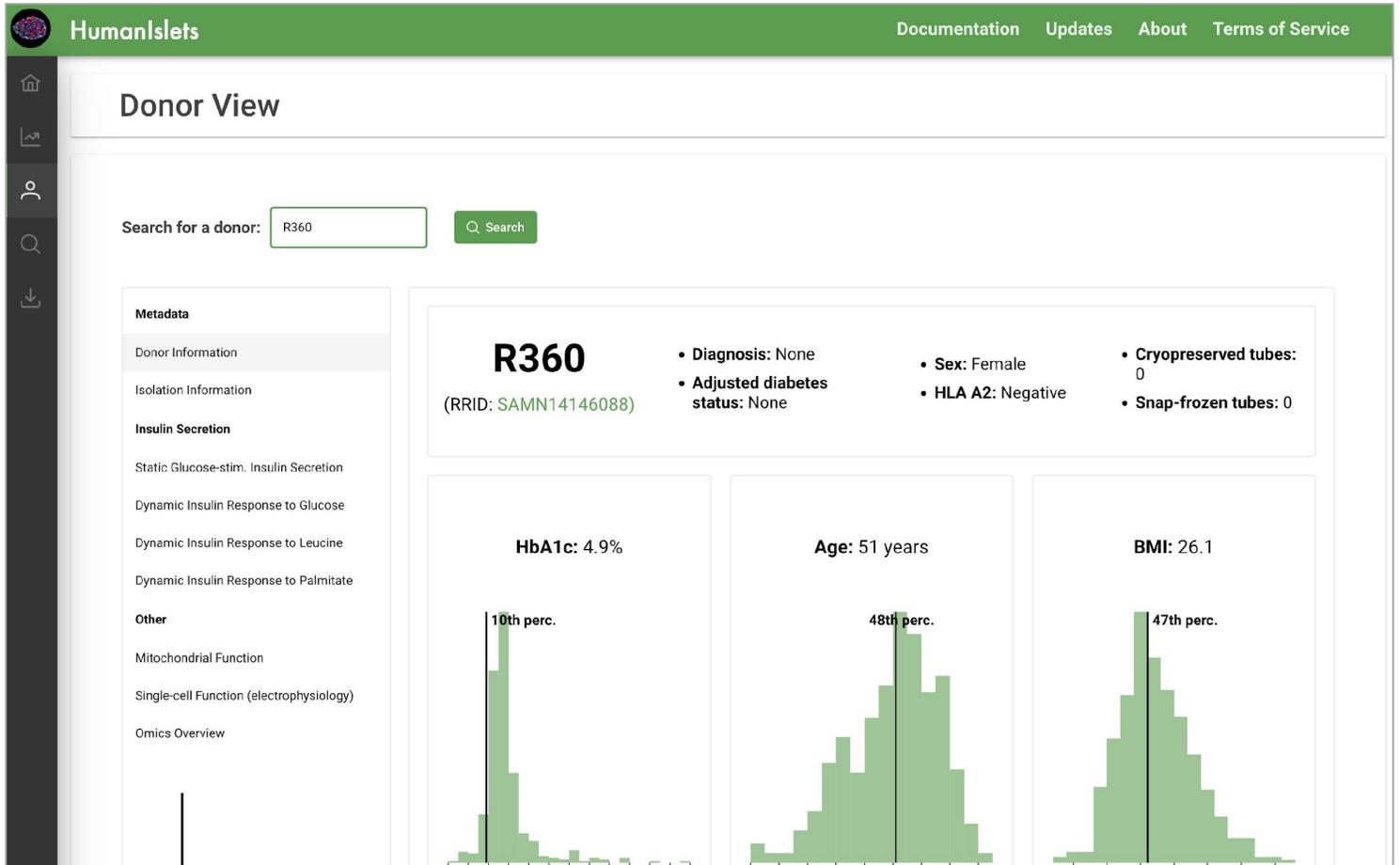


The results table shows all results for the queried feature, sorted by statistical significance. Interactive table components are the same as on the omics analysis page.

The results table enables filtering, for example by omics type

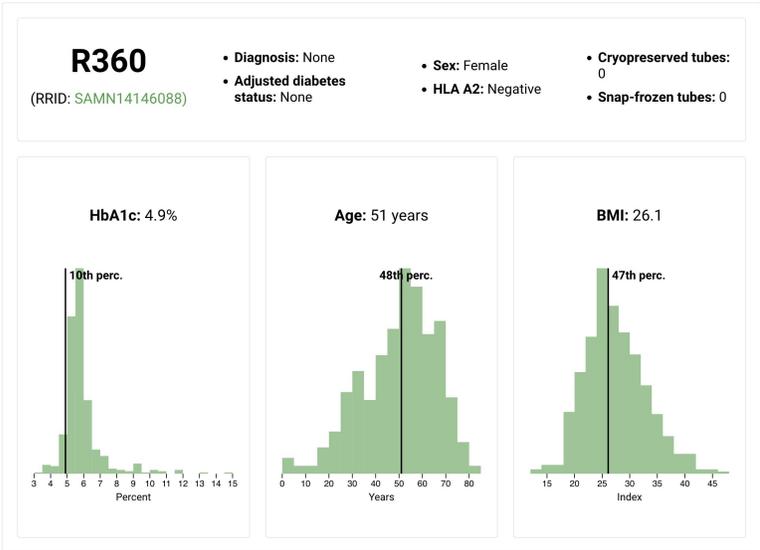
Donor View

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).



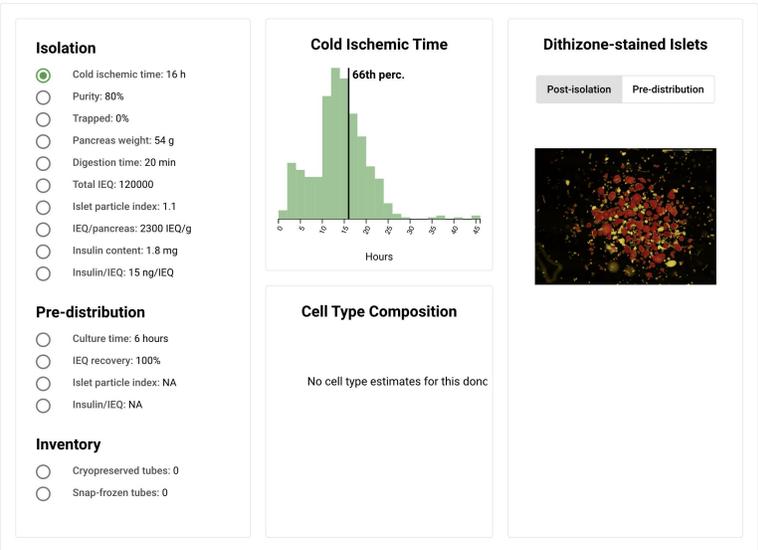
There are currently nine types of data available to view. More data will be added over time as it is collected.

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

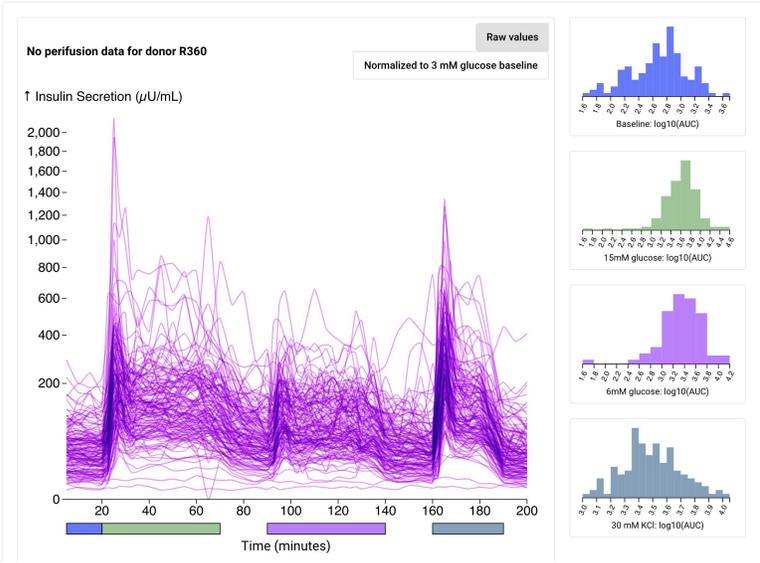


← Basic donor metadata, including availability of isolated islets for future research projects

Technical islet isolation outcomes, including images of the isolated islets →



← 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 (Nanosttring)	✓ 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

The screenshot shows the 'Data Download' interface. The 'Select Donors' section has two tabs: 'Apply Filters' and 'Upload List'. Under 'Apply Filters', there are sections for 'Donor Characteristics' (Sex, Diabetes diagnosis, Age, BMI, HbA1c) and 'Data Availability'. A 'Variable Distribution' histogram for 'Age' is shown, with a callout box explaining that clicking it generates a distribution of values to help choose a cut-off. A 'Show' link is visible next to the histogram. The 'Upload List' tab is highlighted, showing a list of donor IDs: R391, R399, R343, R200, R022, R246, R212, R329, R191, R173, R357, R272, R286, R321, R392, R395. A 'Submit' button is at the bottom of the 'Upload List' tab.

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

This screenshot shows the 'Data Availability' section of the 'Select Donors' page. It includes a note: "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." Below this is a 'Select datasets:' section with a dropdown menu. The dropdown is open, showing options for 'Mitochondrial Function' and 'Proteomics' under 'Other Outcomes', and 'Gene Expression (Nanosting)' and 'Proteomics' under 'Omics Data'. The 'Submit' button is visible at the bottom left.

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

The 'Advanced Filters' dialog box is shown, with tabs for 'Donor Information', 'Distribution Information', 'Isolation Information', and 'Inventory'. A note states: "Note: if enabled, variable filters will exclude donors with missing values for that variable." Below this are several filter options, each with a slider and a 'List' button: 'Cold ischemia time', 'Pancreas weight', 'Digestion time', '% Purity', 'Total IEQ', 'Islet particles', 'Islet particle index', and 'IEQ/Pancreas weight'. The 'OK' button is at the bottom right.

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.

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## Data Download

Reset Dataset

Select data types to download

Select Donors

Click "Submit" with

Apply Filters

Donor Character

Note: if enabled, v

advanced filters

Sex

Diabetes diagnosis  No diabetes  Type 1  Type 2

Age

BMI

HbA1c

Submit

**Other Outcomes**

Electrophysiology Outcomes

Mitochondrial Function

**Omics Data**

Gene Expression (Nanostring)

Proteomics

**Download Data**

Select datasets: Select data types to download

Data format: Comma separated values (.csv)

Note: due to its large size, download of single-cell patches is done differently. Click

Download Summary

Comma separated values (.csv)

Comma separated values (.csv)

Text file (.txt)

R object (.rds)

Excel (.xlsx)



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

