

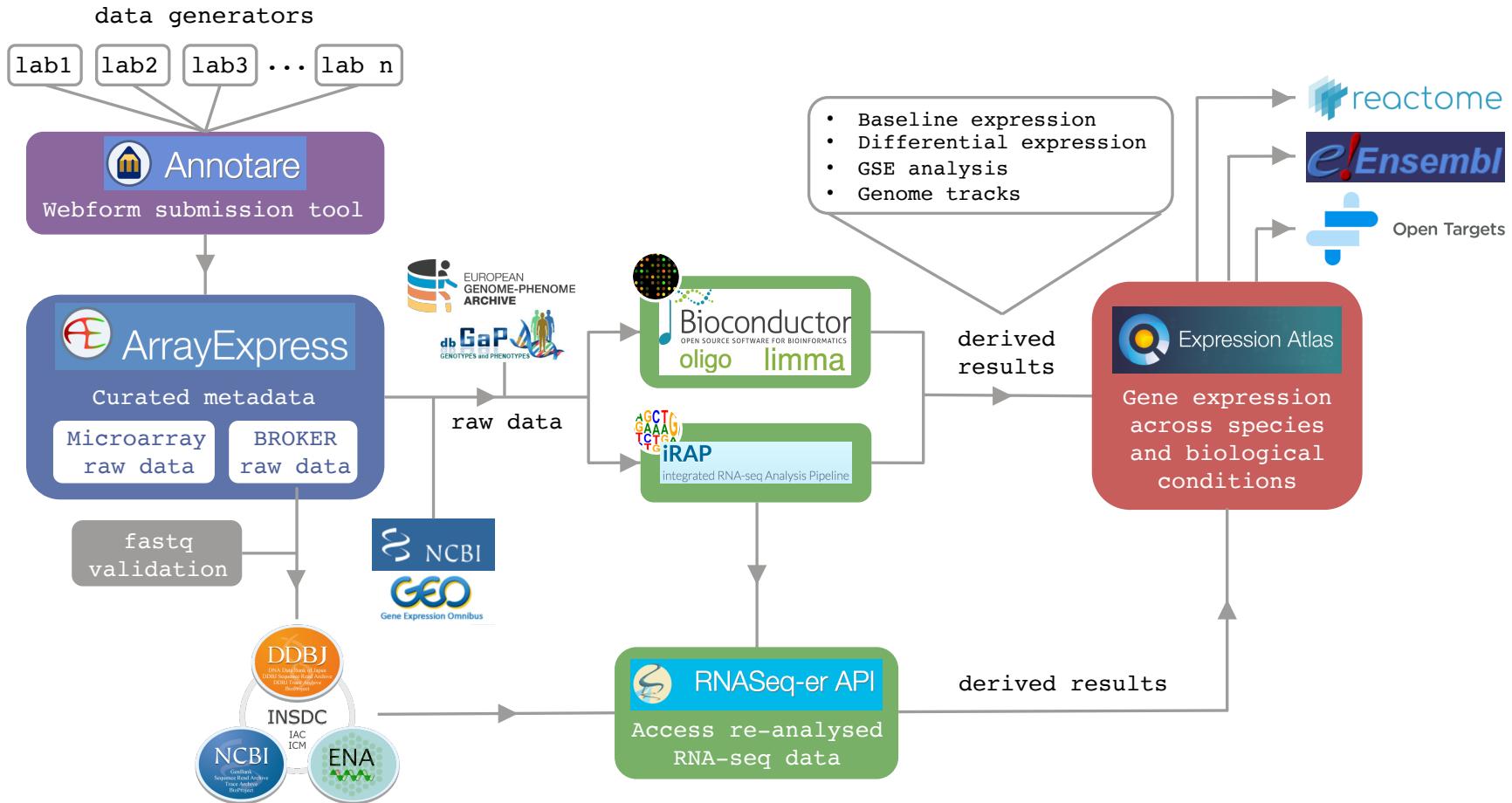
EMBL-EBI Bioinformatics resources for exploring functional genomics data

Expression Atlas: gene expression results across species and conditions

Laura Huerta, PhD
Senior Scientific Curator
lauhuema@ebi.ac.uk
10 November 2017



Functional genomics resources at EMBL-EBI





What is Expression Atlas?

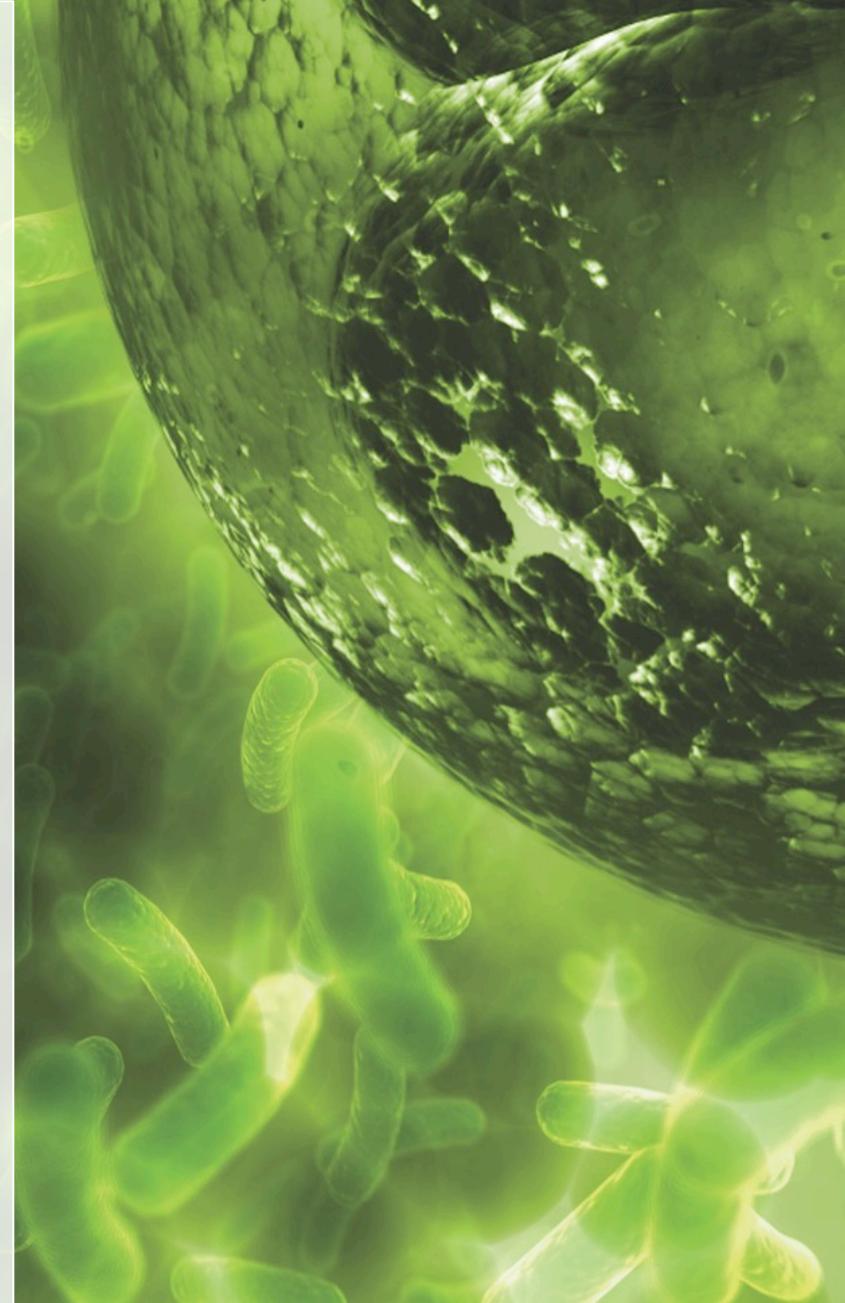


Reference resource for gene/protein expression
across species and biological conditions

www.ebi.ac.uk/gxa/home

OUR MISSION

To provide to the scientific community **freely available** information on the **abundance and localisation of RNA** (and proteins) across species and biological conditions





What is Expression Atlas?

Big Data



Generate and publish gene expression data



ENA



Gene Expression Omnibus

Big Analysis



Big Results



Where is my favourite gene expressed?

How its expression changes in a disease?



How ‘big’ is Expression Atlas data analysis?



<https://commonfund.nih.gov/gtex>

Genetic effects on gene expression across human tissues

GTEX Consortium, Lead analysts:, Laboratory, Data Analysis & Coordinating Center (LDACC);, NIH program management:, Biospecimen collection:, Pathology:, eQTL manuscript working group:, Alexis Battle, Christopher D. Brown, Barbara E. Engelhardt & Stephen B. Montgomery

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

Nature 550, 204–213 (12 October 2017) | doi:10.1038/nature24277

Received 08 September 2016 | Accepted 15 September 2017 | Published online 11 October 2017

doi:10.1038/nature24267

doi:10.1038/nature24265

doi:10.1038/nature24041



How ‘big’ is Expression Atlas data analysis?

... e.g. GTEx dataset



550 donors
53 tissues

19,000 paired
RNA-sequencing libraries

22 years
of processing time in a
single machine

78 terabytes
of EMBL-EBI storage capacity



Large-scale RNA-seq experiments

Access gene expression results of large-scale datasets



Basic research



Key cell line
models



Genentech

Cancer research



Proteomics



Zebrafish development



Prenatal human brain



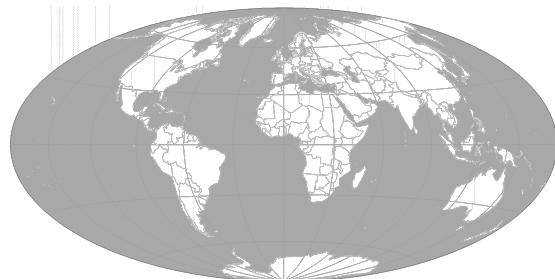
DMDD

Deciphering the Mechanisms
of Developmental Disorders



Mouse models

Expression Atlas contains thousands of selected and curated datasets



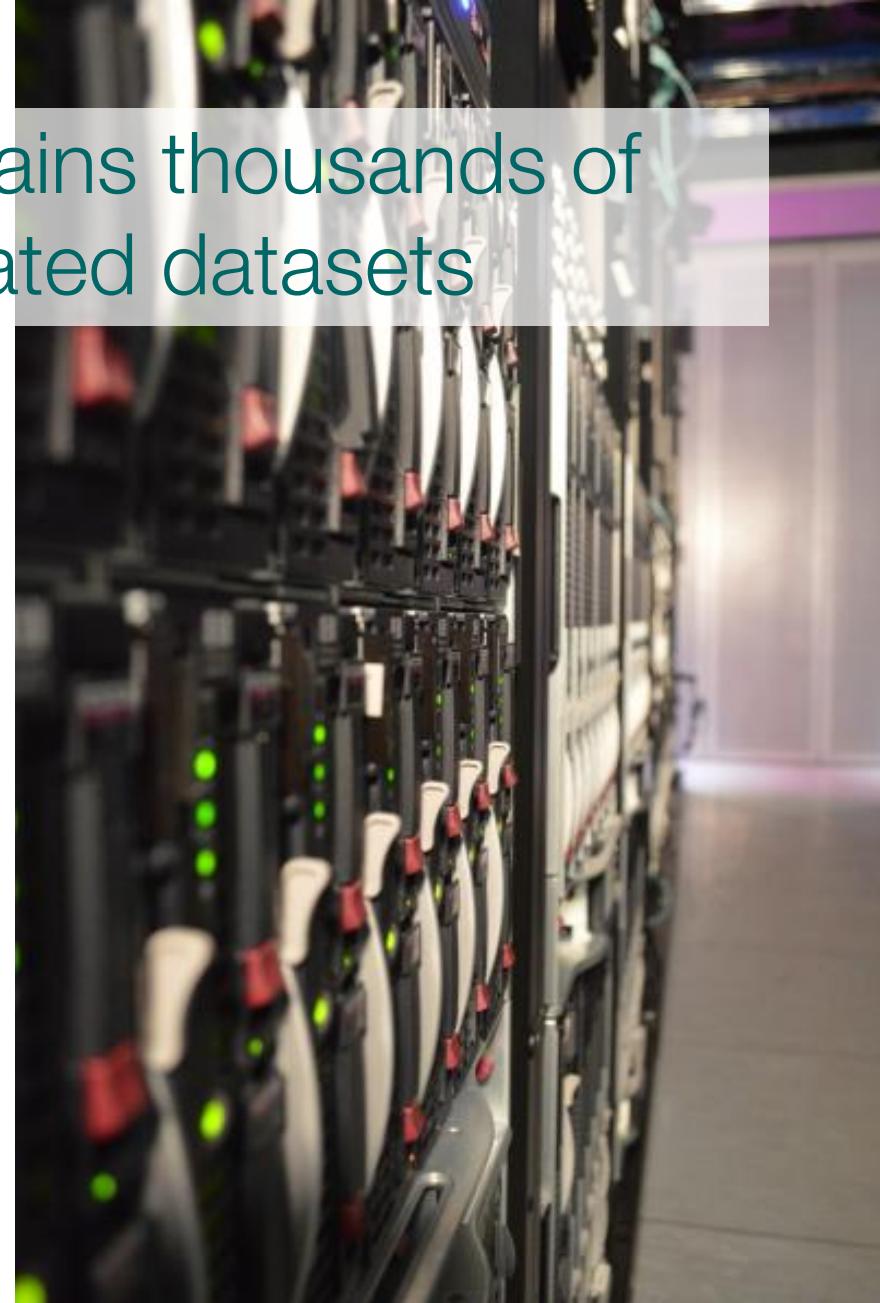
> 3,000 datasets



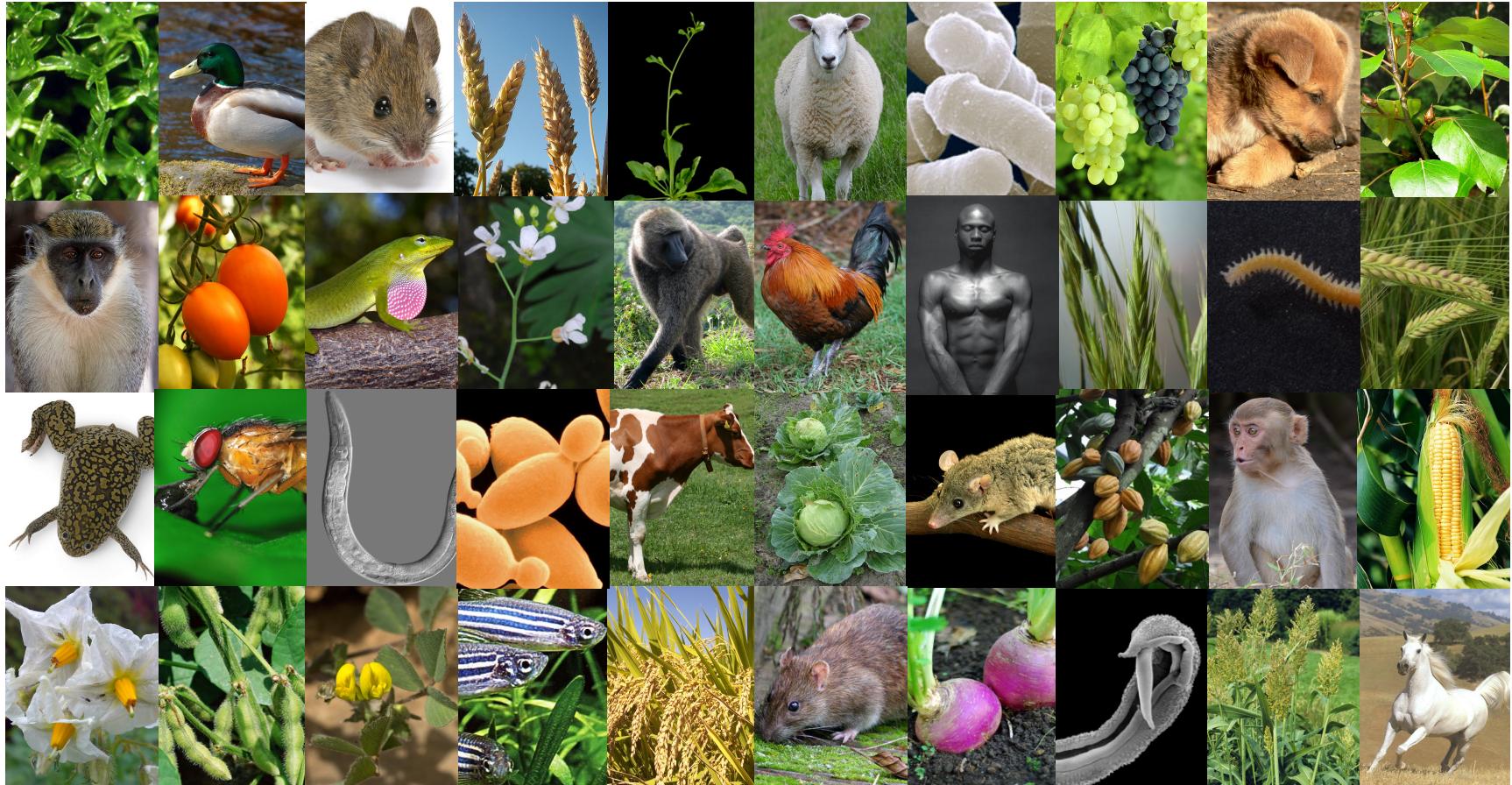
> 500 RNA-sequencing data



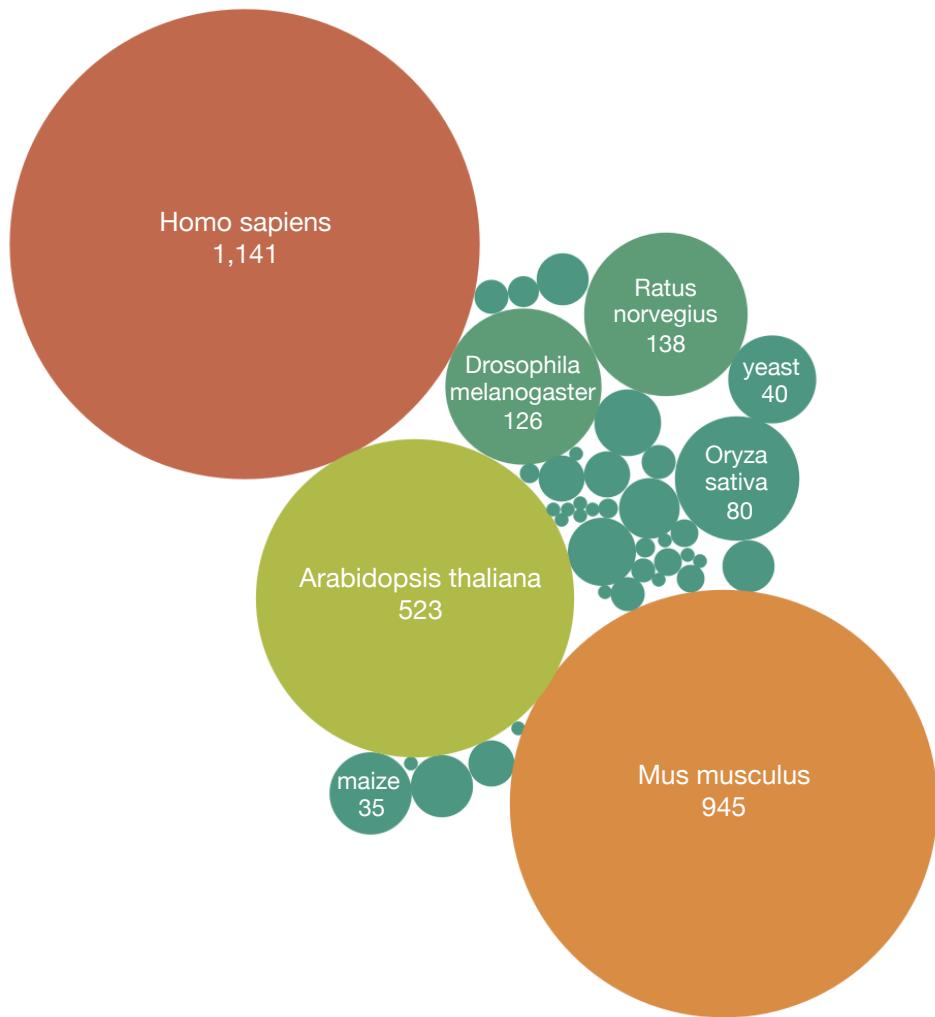
> 2,500 microarray data



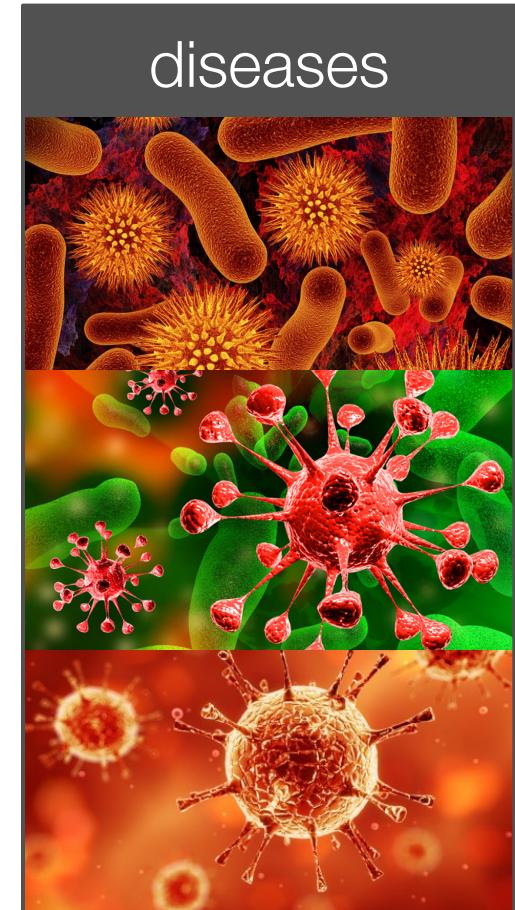
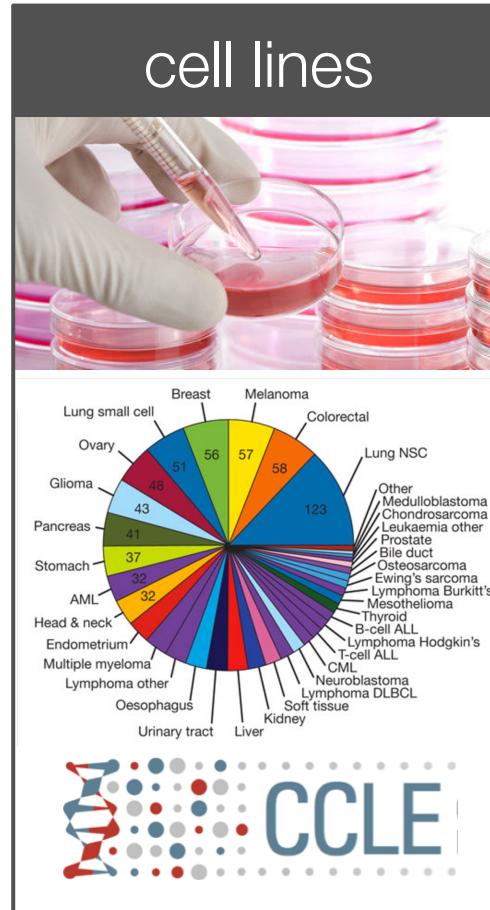
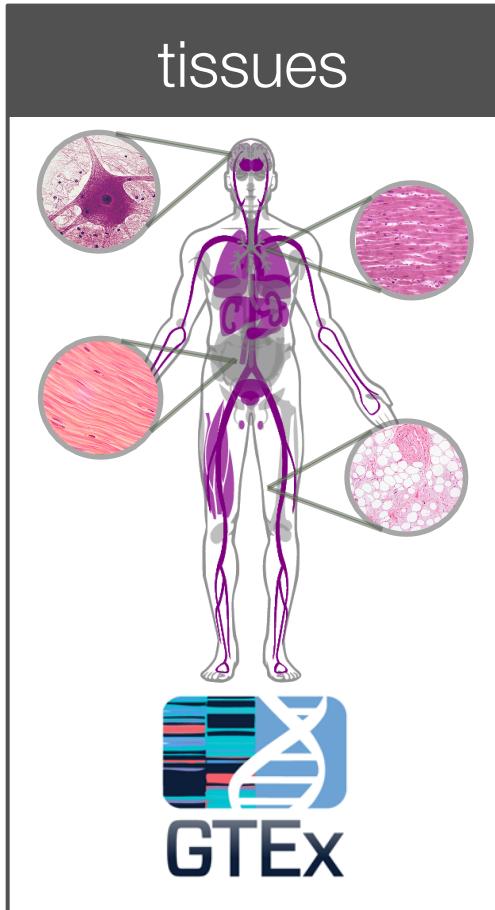
... across more than 40 species ...



... across more than 40 species ...



... under different biological conditions ...



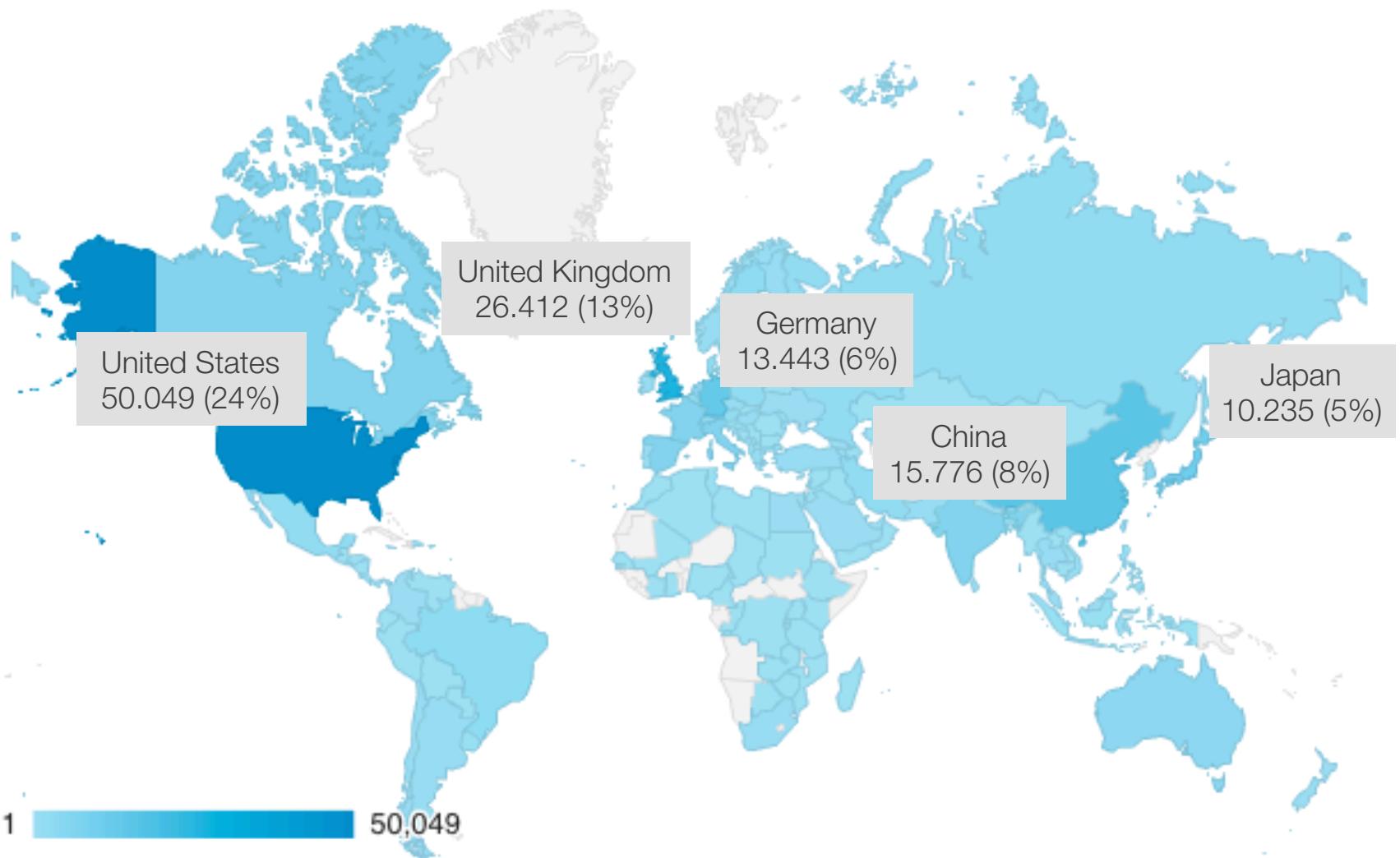
... to help scientists find answers ...

In which conditions
is my favourite gene
expressed?

What genes are
differentially expressed in
a particular condition?

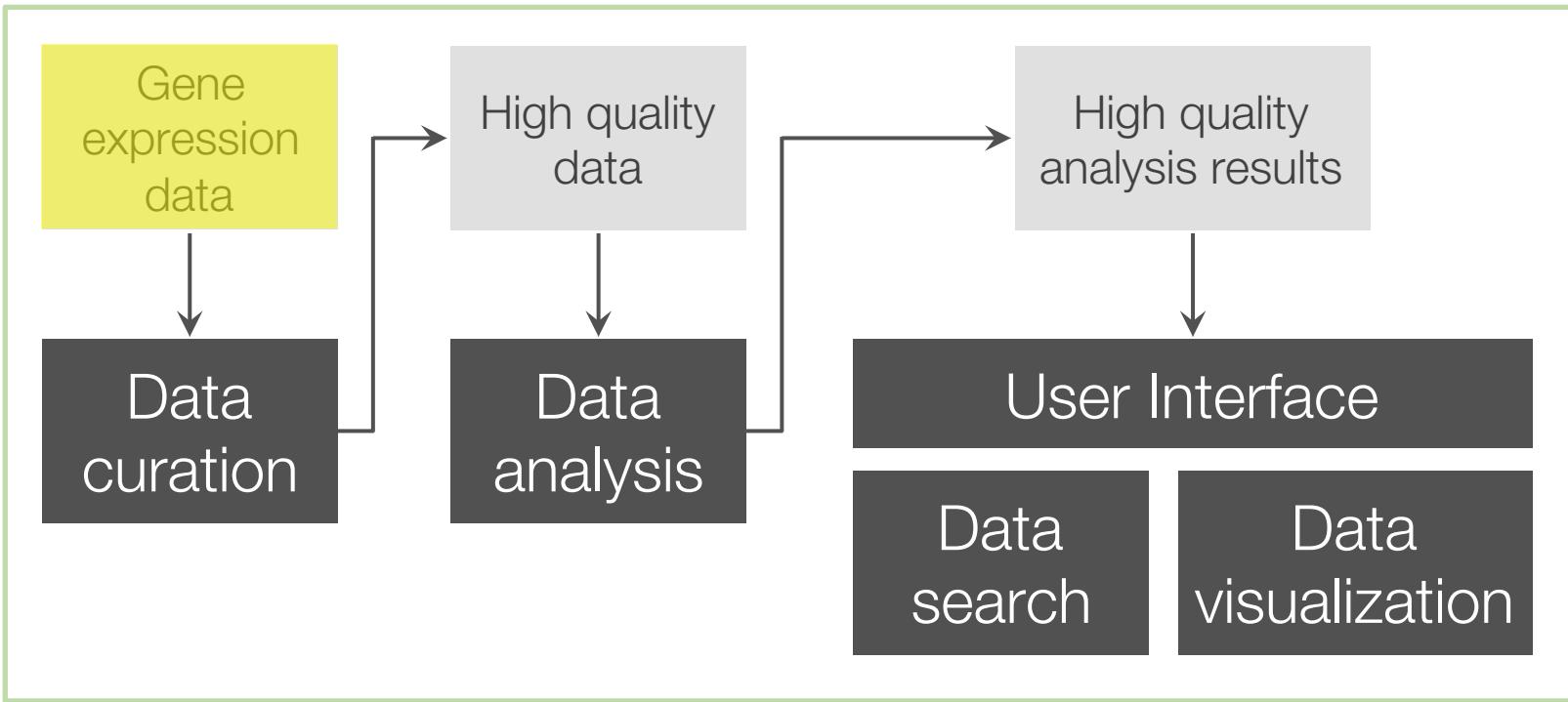
What genes are
expressed in a
particular condition?

... all across the world ...





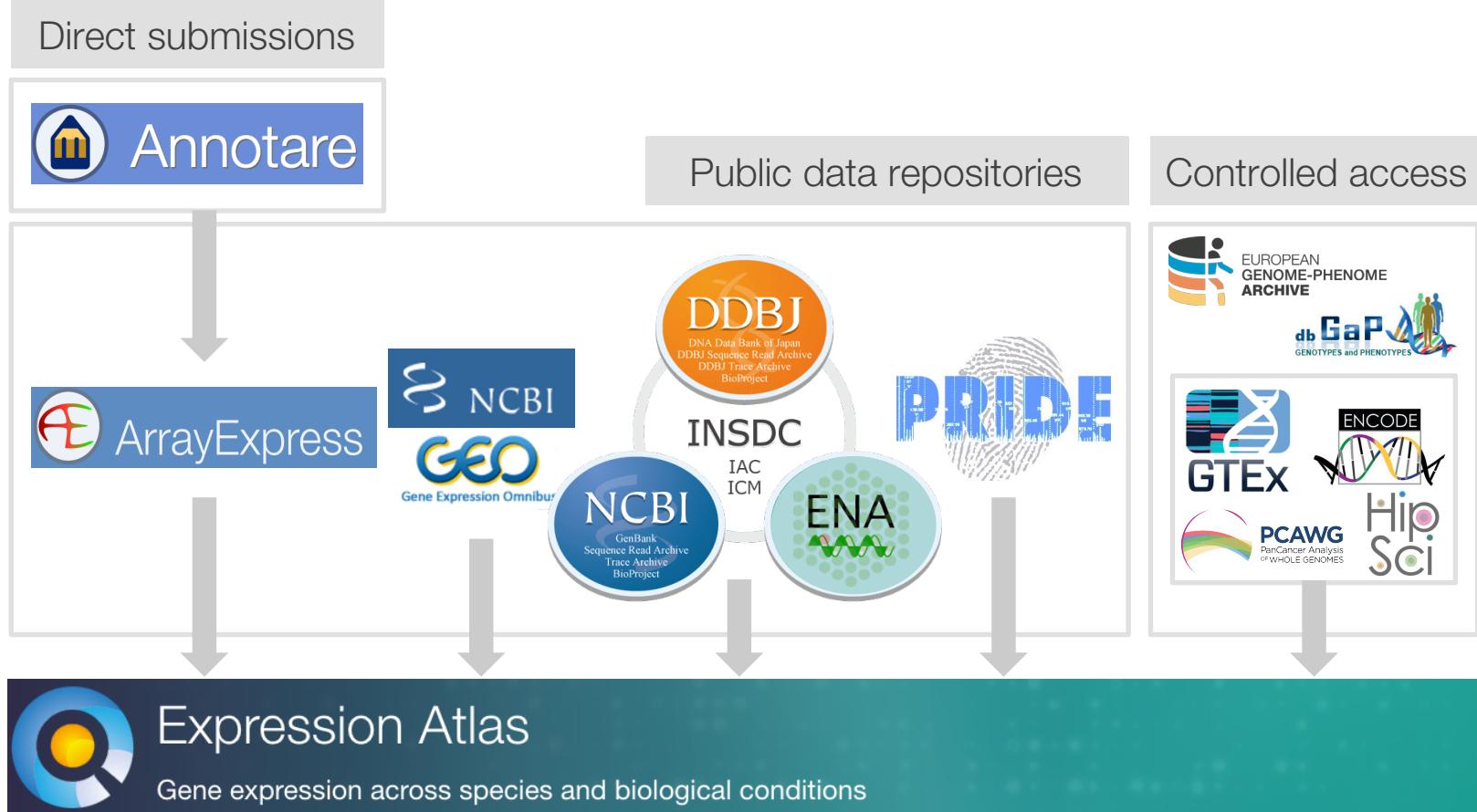
How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy

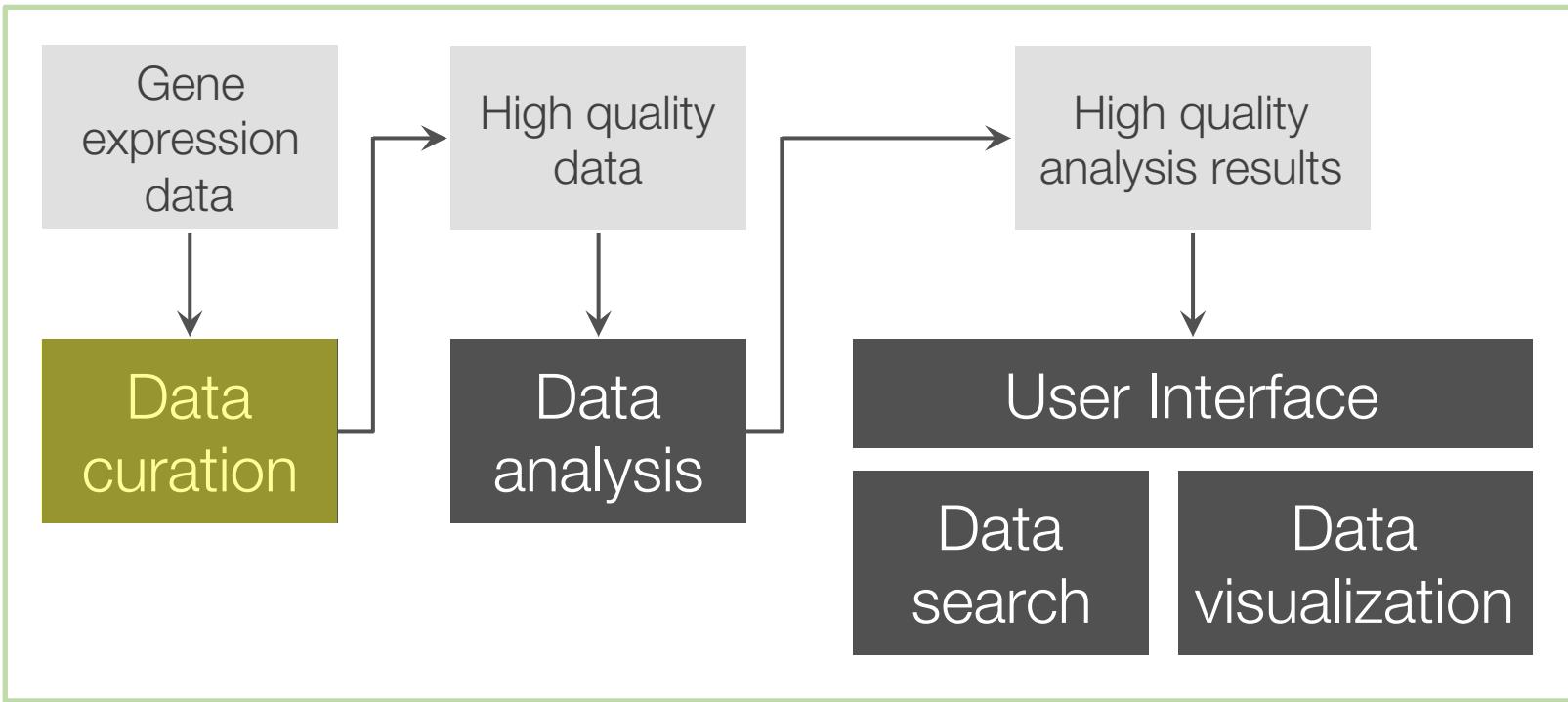


Where does expression data come from?





How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy

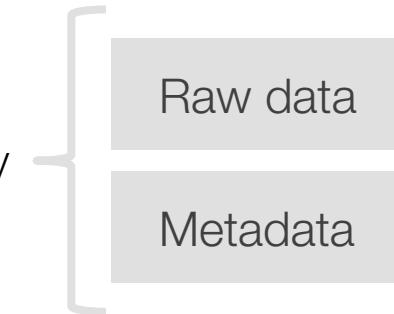


Expression Atlas – data curation

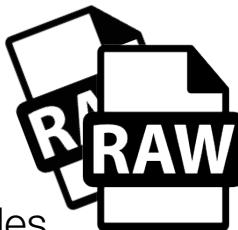
Biocuration



Translation and integration of information relevant to biology into a database or resource



Raw data



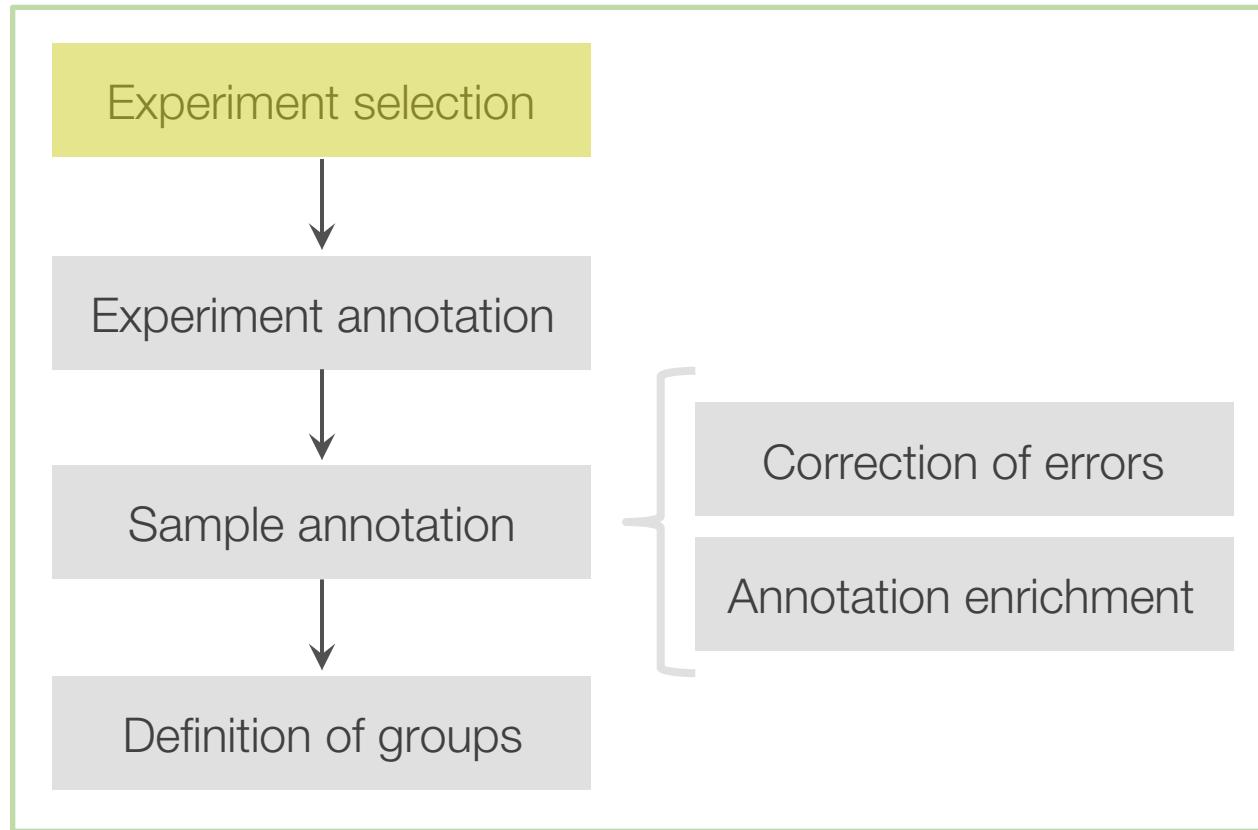
- unprocessed data files
- **Microarray:** files from the scanner (e.g. Affymetrix CEL files, Agilent feature extraction *txt* files, Illumina *idat* files)
- **Sequencing:** raw sequence read files (e.g. FASTQ files)

Metadata

- Experiment description
- Experiment title
- Sample annotation
- Protocols
- Publication details (if any)
- Author contact details



Expression Atlas – data curation





Expression Atlas – data curation

Experiment selection

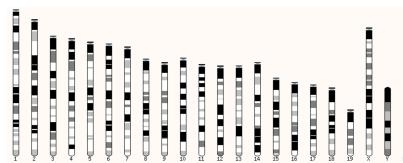


Raw data



Experiment type

www.ensembl.org



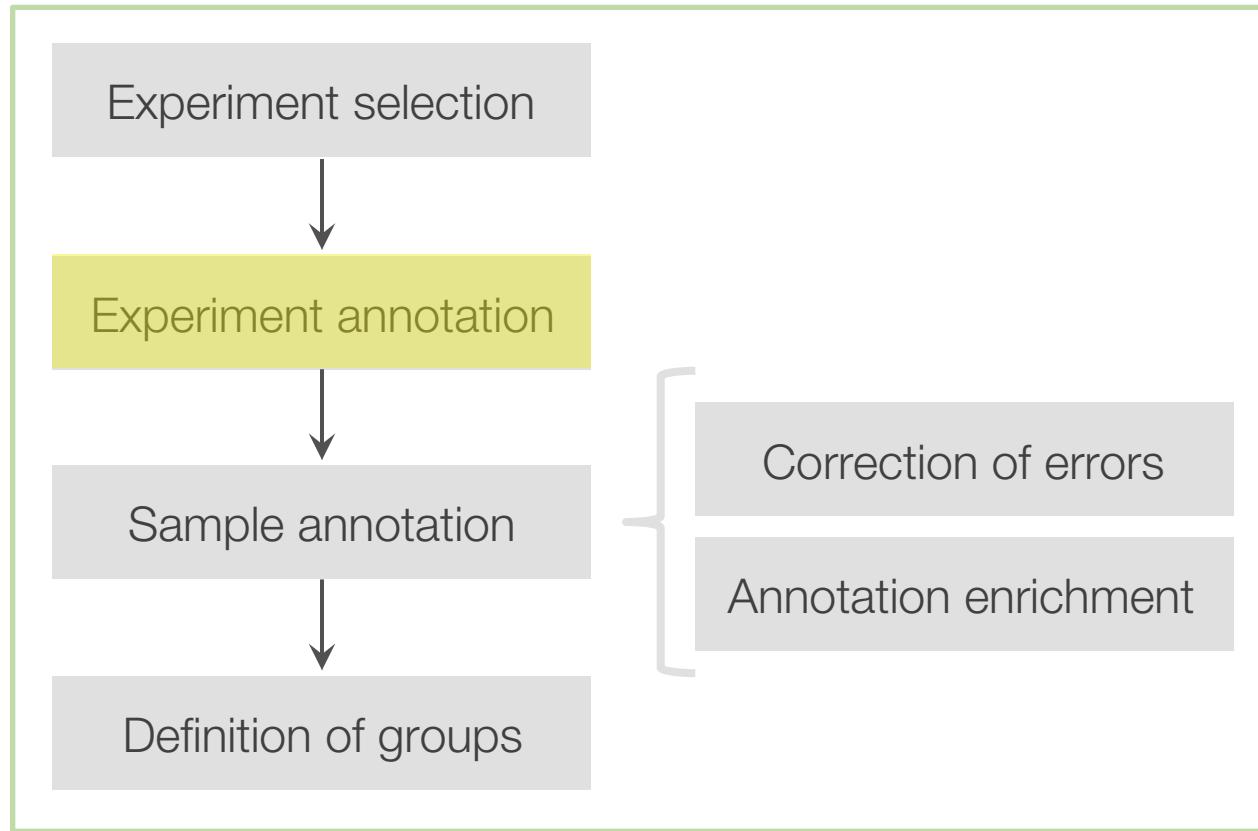
Reference genome



Biological replicates



Expression Atlas – data curation





Expression Atlas – data curation

Experiment annotation



Clear experiment intent

<title> "rice transcriptome project" →

"Transcription profiling by high throughput sequencing of rice oscerk1 mutants treated with two fungus-secreted substances"

Informative title



Protocol
description



Europe PMC

□ Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans.
(PMID:25954001 PMID:PMC4547484)

Abstract · Citations · BioEntities · Related Articles · External Links

GTEx Consortium
+ Collaborators (139)

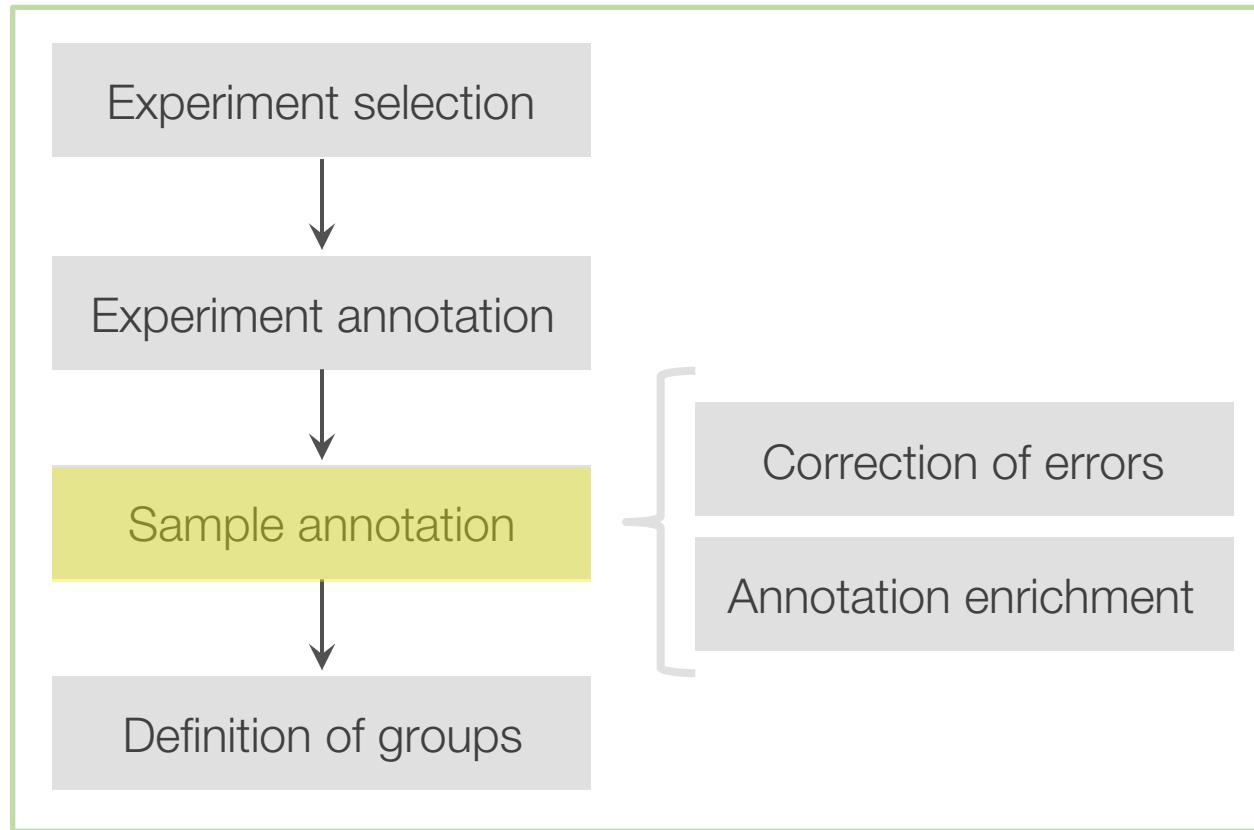
Science (New York, N.Y.) [07 May 2015, 348(6235):648-660]

Type: Research Support, Non-U.S. Gov't, research-article, journal Article, Research Support, N.I.H., Extramural
DOI: 10.1126/science.1262110

Publication details

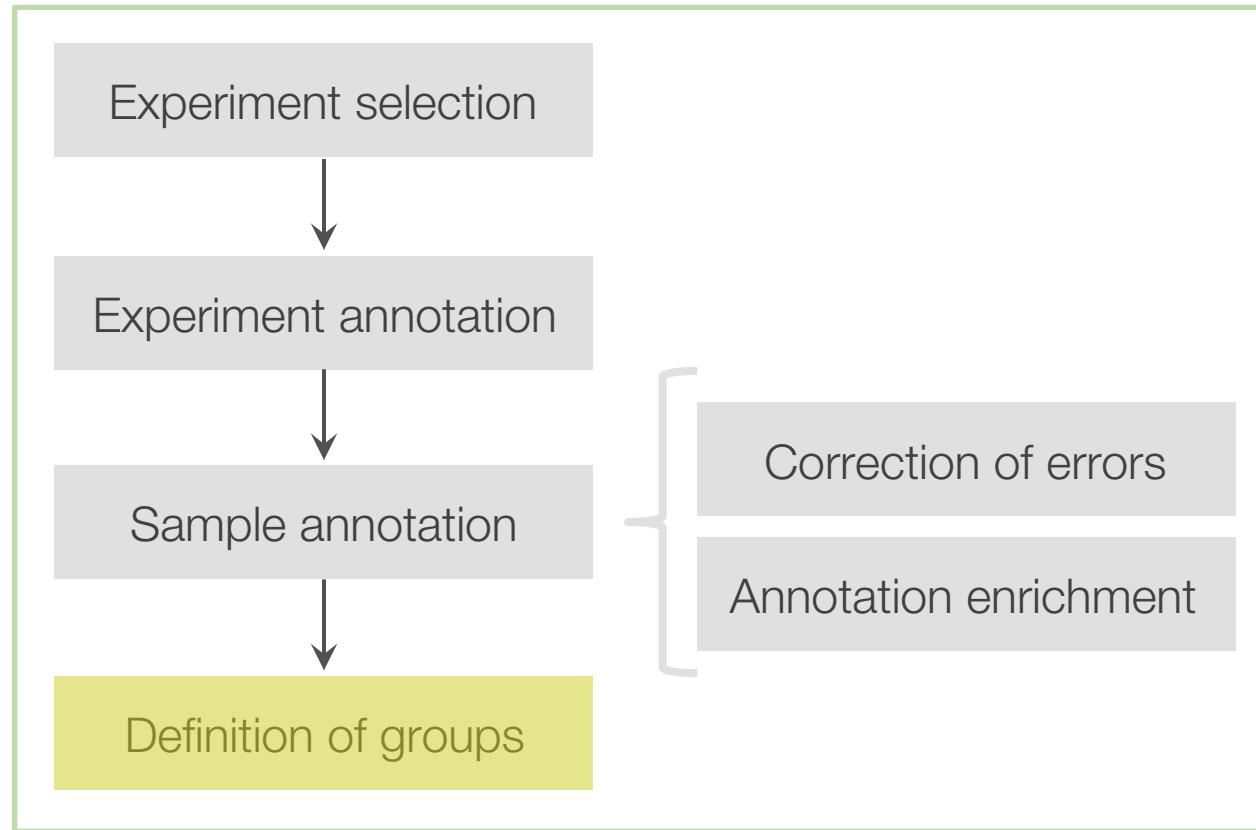


Expression Atlas – data curation



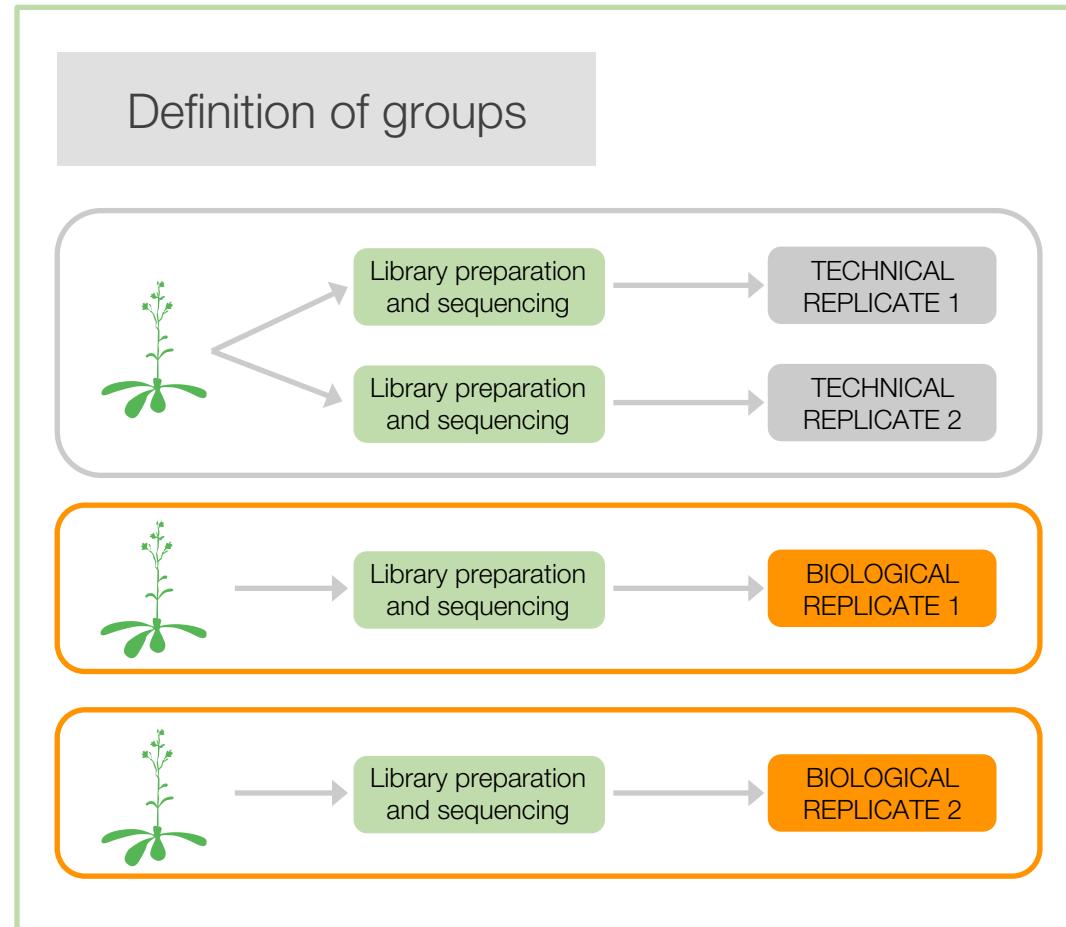


Expression Atlas – data curation



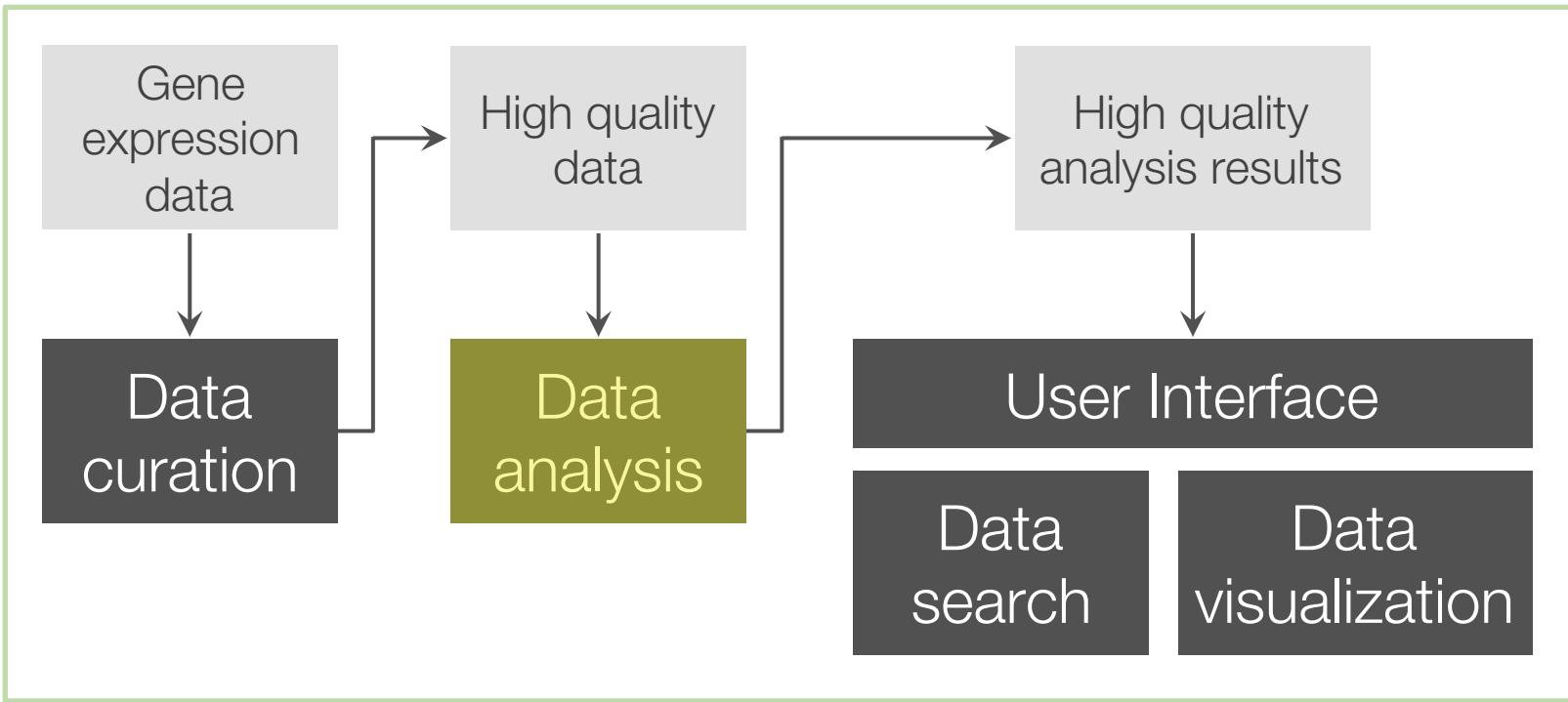


Expression Atlas – data curation



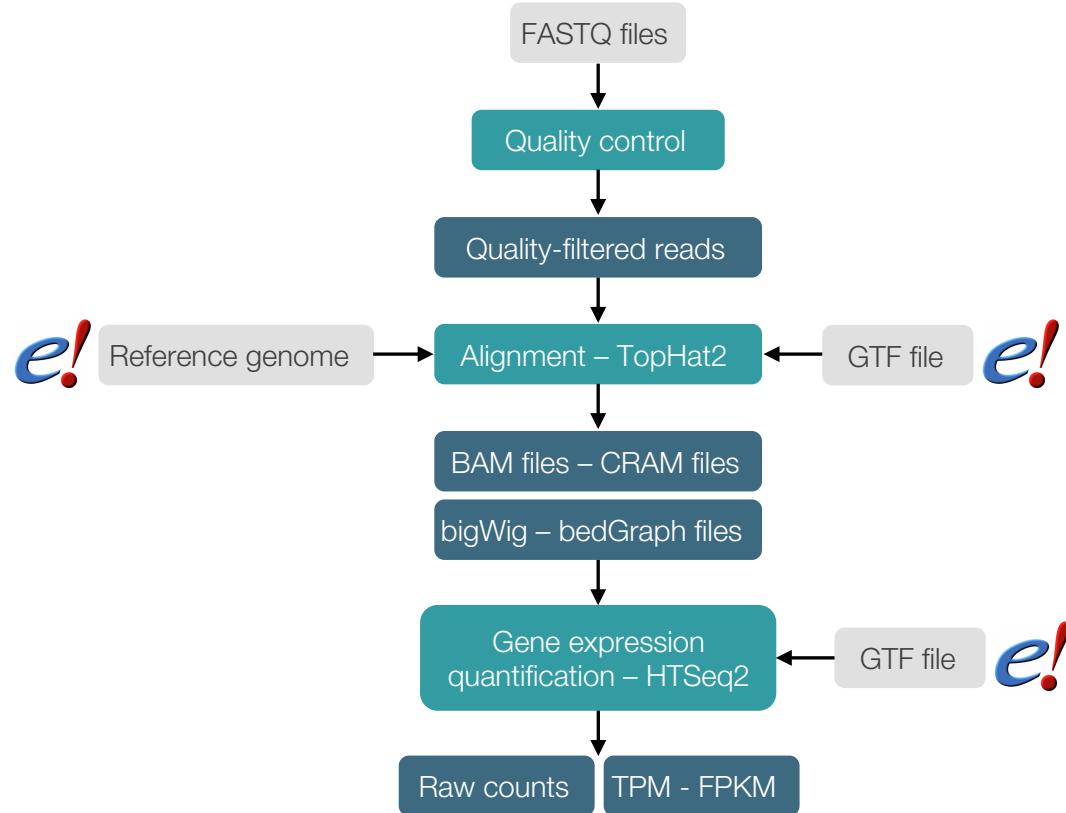


How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy

RNA-seq data analysis



<https://github.com/nunofonseca/irap/>

RNA-seq data analysis

Pages

[New Page](#)

1 News	Last updated on Jan 20
2 How to install and update iRAP	Last updated on May 11
3 How to run iRAP	Last updated on Jan 31
4 Output files and directory structure	Last updated on Mar 23
5 Tools supported	Last updated on Dec 14, 2016
6 Virtual Machines	Last updated on Feb 16, 2016
7 Quick Example	Last updated on Dec 20, 2016
8 Configuration file	Last updated on Aug 21
9 Gene set analysis in iRAP	Last updated on Mar 19, 2015
FAQ	Last updated on Jun 3, 2016
GSE	Last updated on Feb 16, 2016
iRAP single library	Last updated on Dec 20, 2016
LSF	Last updated on Feb 16, 2016

<https://github.com/nunofonseca/irap/wiki>



RNA-seq data analysis

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Functional genomics (II):
Common technologies and
data analysis methods

[Introduction](#)[Real-time PCR](#)[Microarrays](#)[Next Generation Sequencing \(NGS\)](#)[RNA sequencing](#)[Biological interpretation of gene expression data](#)[Genotyping, epigenetic and DNA/RNA-protein interaction methods](#)[Summary](#)[Quiz: Check your learning](#)[Your feedback](#)[Learn more](#)[References](#)[Contributors](#)

Functional genomics (II): Common technologies and data analysis methods

This is the second part of our functional genomics course. This course will introduce you to common technologies in functional genomics studies, including microarrays and next generation sequencing (NGS), with a special focus on RNA-seq. We will look at important considerations when designing your experiments, data analysis methods, and discuss when to use one technology over another.

We recommend that you look at [Functional genomics \(I\): Introduction and designing experiments](#) before starting this course.

About this course

Author(s): Laura Huerta, Melissa Burke

Gene Expression

Beginner

2 hours

[Start the course](#)

Learning objectives:

- Evaluate different functional genomics technologies and know when to use them
- List some of the considerations when designing your own functional genomics experiments using these technologies
- Describe the steps involved in data analysis of microarray and RNA-seq experiments

<https://www.ebi.ac.uk/training/online>



RNA-seq data analysis

Functional genomics (II):
Common technologies and
data analysis methods

Introduction
Real-time PCR
▪ Microarrays
Next Generation Sequencing (NGS)
▪ RNA sequencing
Advantages of RNA-seq over hybridisation-based approaches
Applications of RNA-seq
▪ Performing a RNA-seq experiment
▪ Design considerations
Number of replicates
Laboratory performance
▪ Data analysis
Quality control
Read mapping or alignment
Quantification
Differential gene expression analysis
▪ Biological interpretation of gene expression data
▪ Genotyping, epigenetic and DNA/RNA-protein interaction methods
Summary
Quiz: Check your learning
Your feedback
Learn more
References
Contributors



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International license

Performing a RNA-seq experiment

There is no common pipeline for all the different types of RNA-seq. Both the experimental design and the analysis procedures will be different depending on the organism being studied and the research goals. As the primary objective of many biological studies is a comparison of gene expression between samples, we outline a possible workflow for detecting differential expression using RNA-seq (Figure 7).

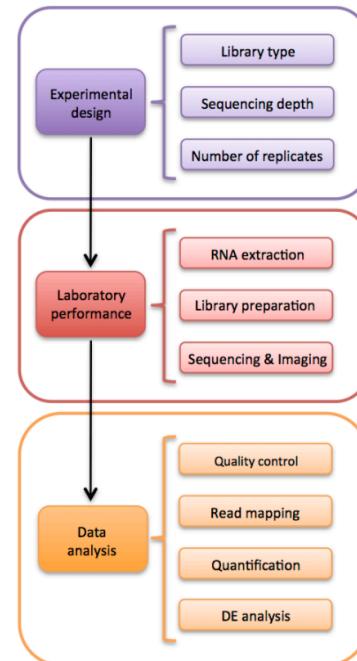


Figure 7 Overview of a RNA-seq experiment for detecting differential expression (DE).

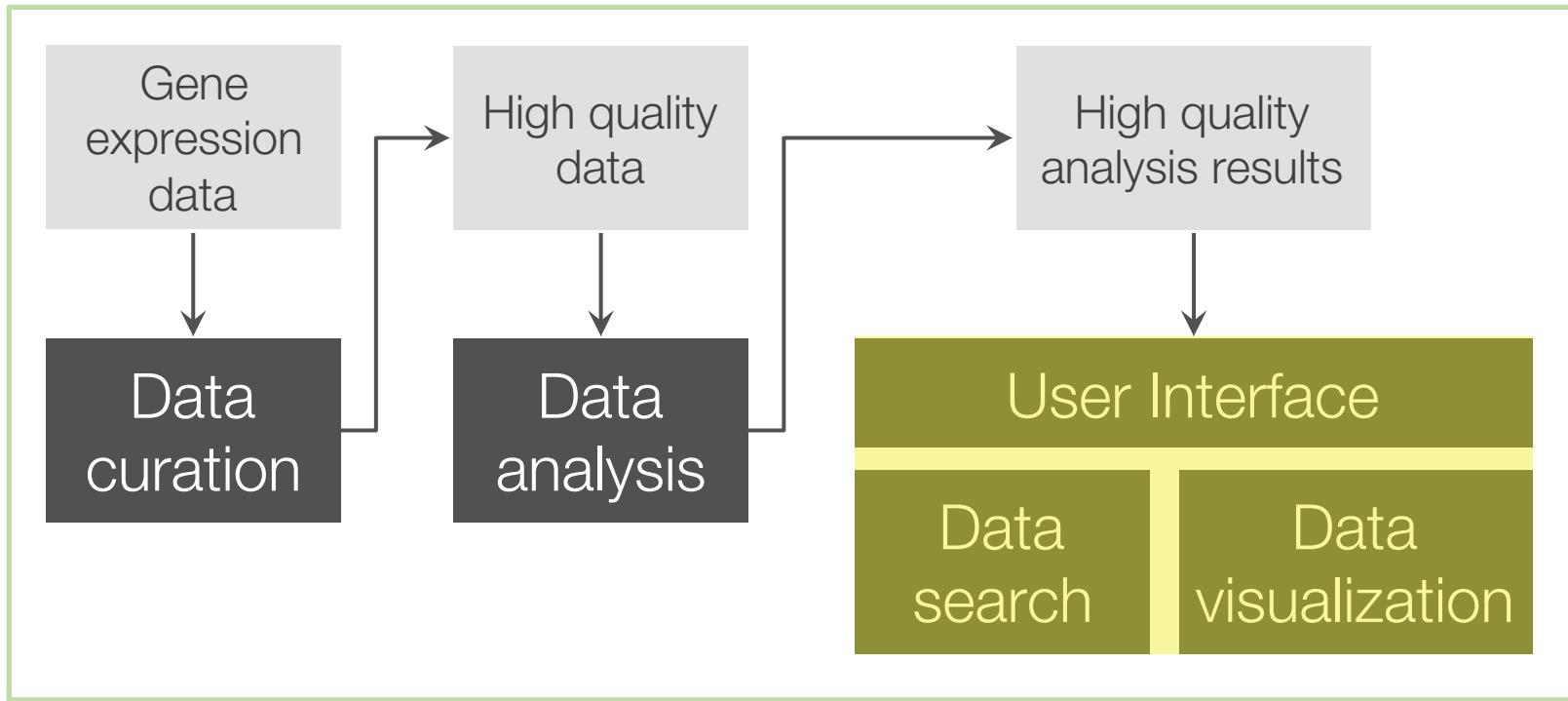
« Applications of RNA-seq

Next: Design considerations »

<https://www.ebi.ac.uk/training/online>



How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy



Let's try Expression Atlas

Expression Atlas

Gene expression across species and biological conditions

Home | Download | Release notes | FAQ | Help | Licence | About

Exploring gene expression results across species under different biological conditions

Expression Atlas is an open science resource that gives users a powerful way to find information about gene and protein expression across species and biological conditions such as different tissues, cell types, developmental stages and diseases among others. Expression Atlas aims to help answering questions such as 'where is a certain gene expressed?' or 'how its expression changes in a disease?'.

[Read more about Expression Atlas](#)

Search Gene set enrichment

Gene / Gene properties
CFHR2 [x](#)
Examples: REG1B, zinc finger
[Search](#) [Clear](#)

Organism
Homo sapiens [▼](#)

Biological conditions
Enter condition query...
Examples: lung, leaf, valproic acid, cancer

wwwdev.ebi.ac.uk/gxa/home



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In which conditions is my favourite gene expressed?

Organism

- ✓ Homo sapiens
- Mus musculus
- Arabidopsis thaliana
- Rattus norvegicus
- Drosophila melanogaster
- Zea mays

Any

- Anas platyrhynchos
- Anolis carolinensis
- Anopheles gambiae
- Arabidopsis lyrata
- Arabidopsis thaliana
- Aspergillus fumigatus
- Bos taurus
- Brachypodium distachyon
- Brassica oleracea
- Brassica rapa
- Caenorhabditis elegans

Biological conditions

Enter condition query...

Examples: lung, leaf, valproic acid, cancer

Discover and interpret gene expression analysis results quickly and easy



Baseline expression results

Baseline expression

Differential expression

Show anatomograms

Filter your results

Homo sapiens

Organism part

Cell line

Danio rerio

Developmental stage

Mus musculus

Organism part

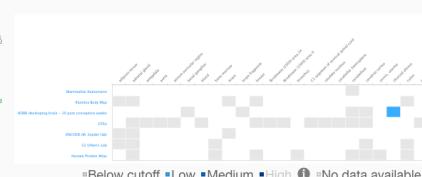
Cell type

Developmental stage

Homo sapiens — Organism part



Showing 7 of 7 experiments found:



All or
which

Expression levels are
visualised using heatmaps

Danio rerio — Developmental stage

Showing 1 of 1 experiment found:

Experiment: 18 White et al
Experimental condition: larval day 5
Expression level: 26 FPKM

By experiment type Filters Download table content

Mus musculus — Organism part



Showing 23 of 23 experiments found:



Below cutoff

Low

Medium

High



No data available



Baseline expression results

Results for CFHR2

Baseline expression Differential expression

Show anatomograms

Organism part

Filter your results

Homo sapiens

Organism part

Cell line

Danio rerio

Developmental stage

Mus musculus

Organism part

Cell type

Developmental stage

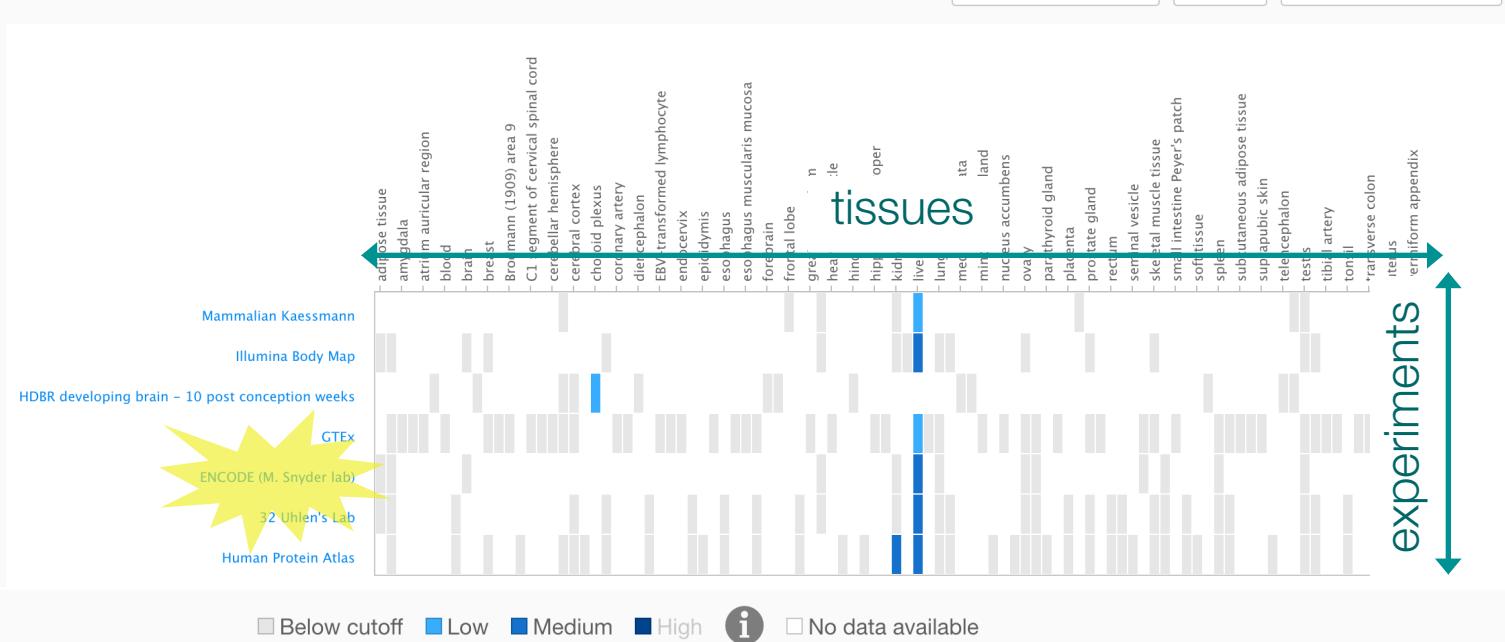
HEATMAP: For each species, *CFHR2* gene expression values for the selected condition (columns) in all experiments (rows) in which *CFHR2* gene is expressed

Showing 7 of 7 experiments found:

By experiment type ▾

Filters

Download table content





Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues
RNA-Seq mRNA baseline
Organism: *Homo sapiens*
Raw Data Provider: The Human Protein Atlas

Results Experiment Design Supplementary Information Download

Genes



Showing 50 of 34,068 genes found:

Expression level in FPKM

0 3.659

PRM2
MHN2
THP1
PRK27
ANHBD7
FLC2
CAUS14
F2
C10orf68
TUBA1C
SMCP
F9
RODIL2
CYP1A2
ULP1
KRT77
SLC10A1
LCZ28
HAO1
FATE1
CTD-212N2N3.1
PCK2
SERPINA11
GDF1
AKAP4
SPATA8
PRB2
SLC10A1
ERVH48-1
SERPINA12
TSHR
SLC12A1
LCZ1C
S100G
LCZ1A
C16orf82
SP93
MBL2
C10orf62
UBR4N1
LCZ6A
HHLB
ACTL7A
TH
HMGB4
DDX4
C10orf12
ACVR2C
SLC34A1
PRK17

Specific checked

Most specific

Expression value

0.5

See distribution

Data units

TPM
 FPKM

Organism parts

Select

Selected: 32 / 32

HEATMAP: top 50 genes (rows)
most specifically expressed
across all tissues (columns)

Genes expressed only
in one tissue first
Within that, genes with
highest expression first



Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues
RNA-Seq mRNA baseline
Organism: Homo sapiens
Raw Data Provider: The Human Protein Atlas

Results Experiment Design Supplementary Information Download

Genes

Specific unchecked

Most specific

Expression value

0.5

See distribution

Data units

TPM

FPKM

Organism parts

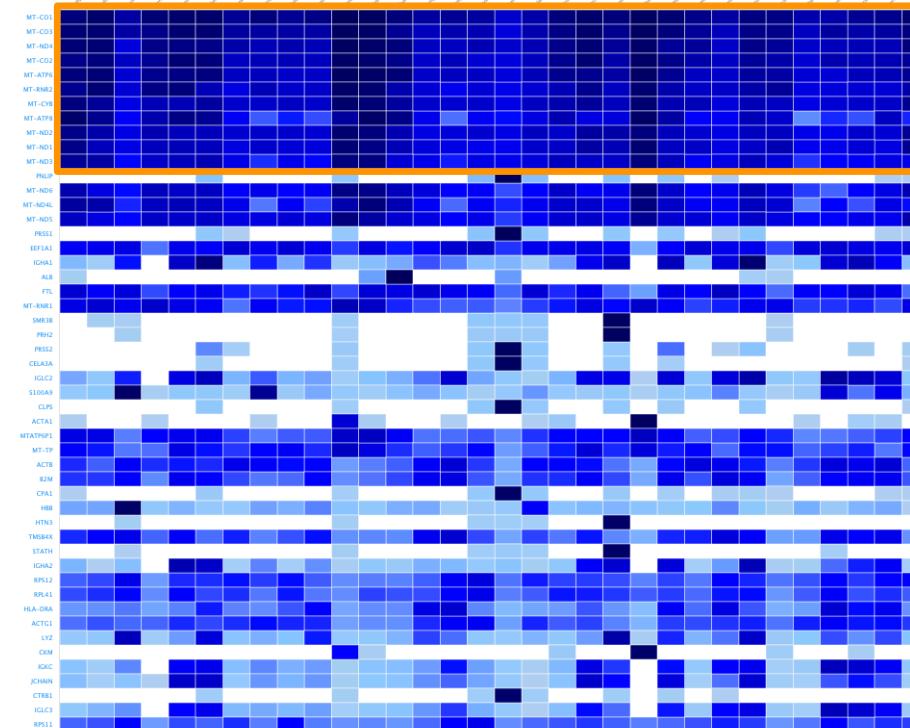
Select

Selected: 32 / 32



Showing 50 of 34,068 genes found:

Expression level in FPKM
0 95.074



HEATMAP: top 50 genes (rows)
most highly expressed across all
tissues studied (columns)

Genes with highest
expression first



Baseline experiment page

General information

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues

RNA-Seq mRNA baseline

Organism: *Homo sapiens*

Raw Data Provider: The Human Protein Atlas

Results

Experiment Design

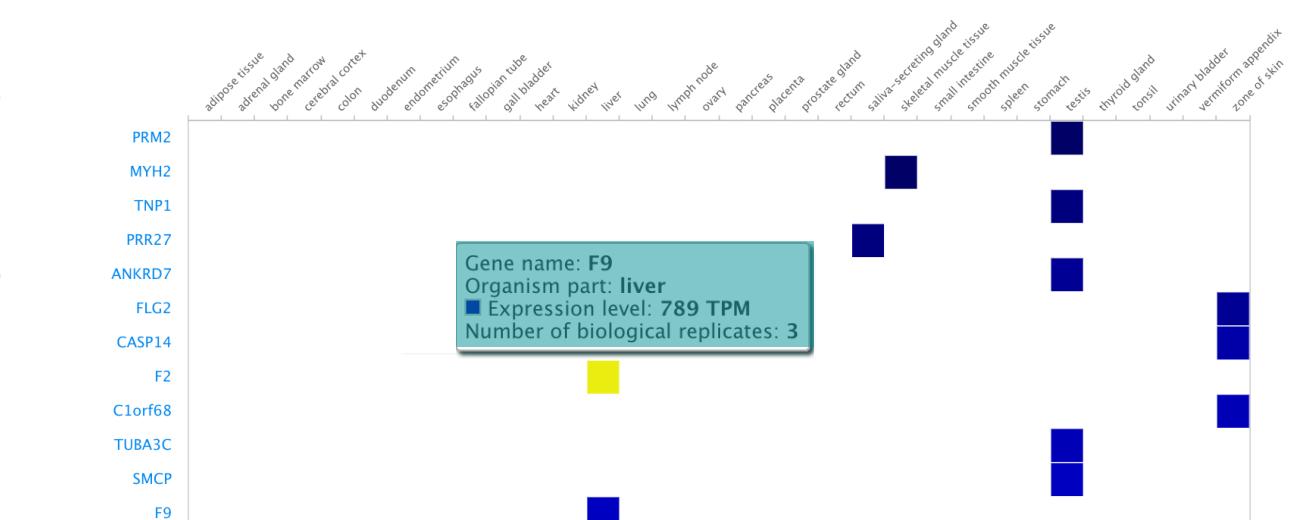
Supplementary Information

Downloads

Genes expressed above 0.5 TPM

Showing 50 of 41,210 genes found:

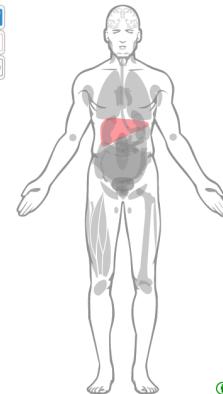
Expression level in TPM
0 1,112



Download displayed results

[Download table content](#)

Genes



①

Apply

Clear

Most specific

Expression value

0.5

[See distribution](#)

Data units

TPM

FPKM

Organism parts

[Select](#)

Selected: 32 / 32



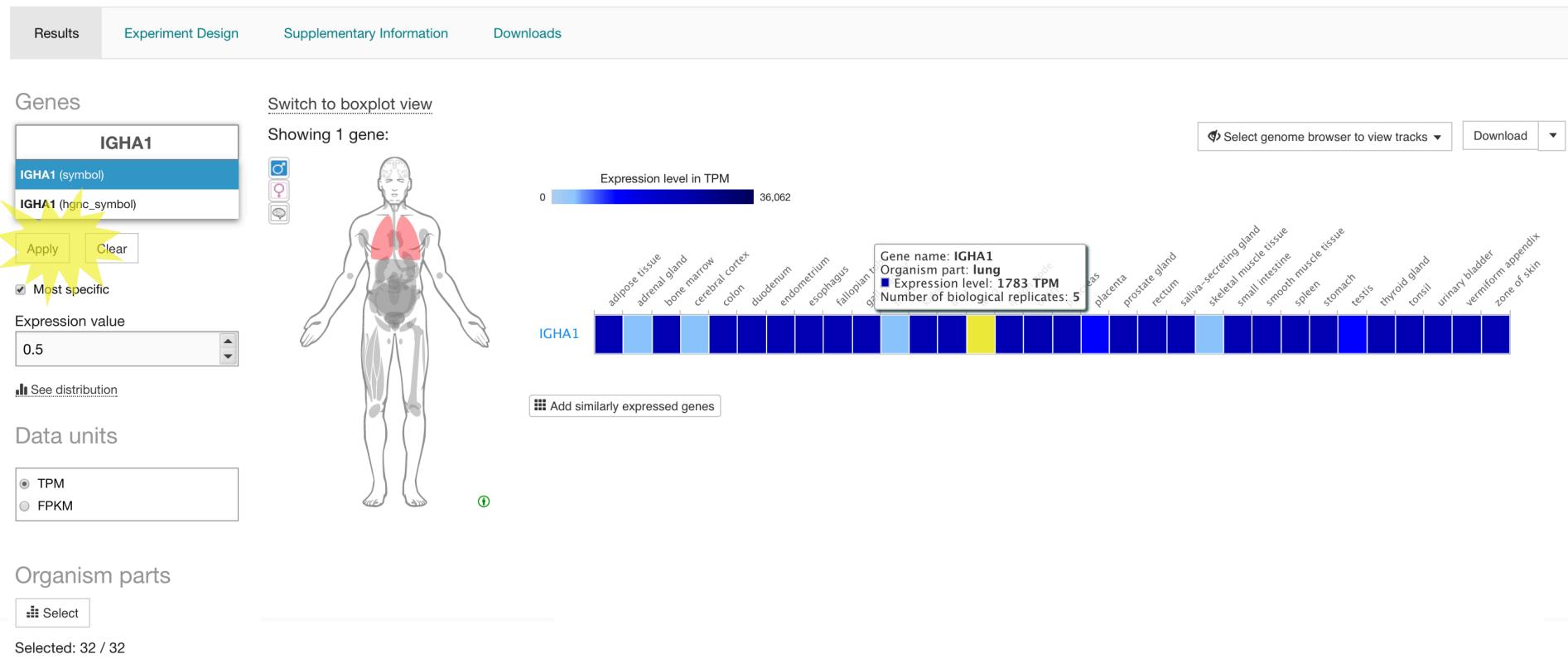
Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues

RNA-Seq mRNA baseline

Organism: *Homo sapiens*

Raw Data Provider: The Human Protein Atlas





Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues

RNA-Seq mRNA baseline

Organism: *Homo sapiens*

Raw Data Provider: The Human Protein Atlas



Genes

IGHA1

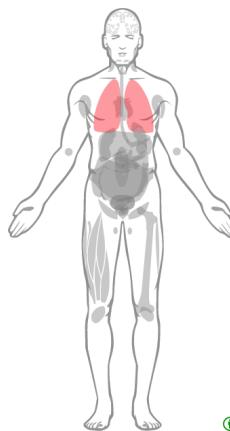
IGHA1 (symbol)

IGHA1 (hgnc_symbol)

Apply

Switch to boxplot view

Showing 1 gene:



Most specific

Expression value

0.5

See distribution

Data units

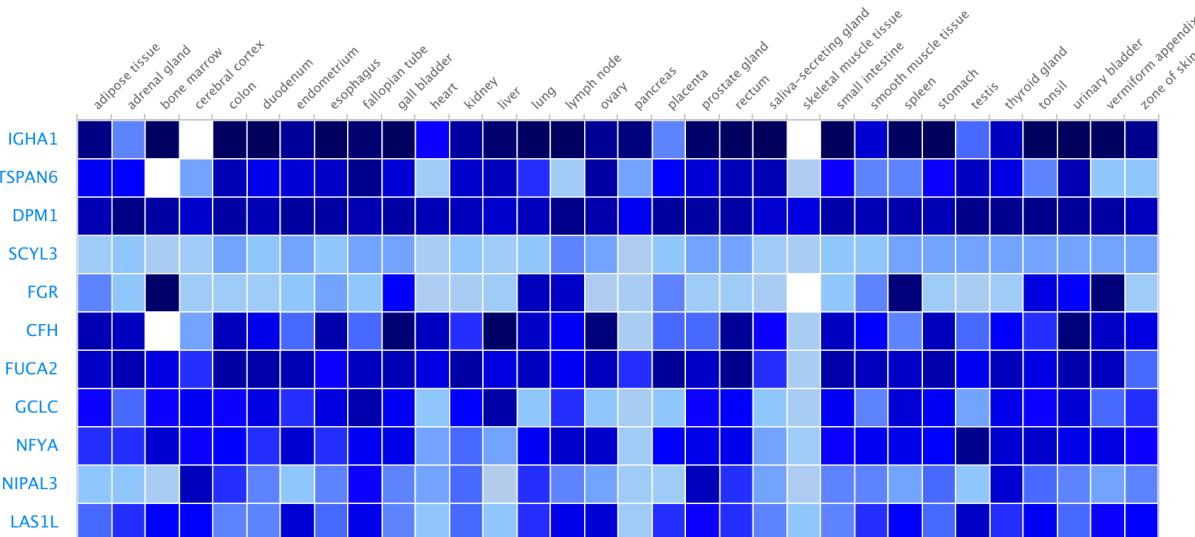
TPM

FPKM

Organism parts

Select

Selected: 32 / 32



Display genes with similar expression to IGH A1:

off 10 49



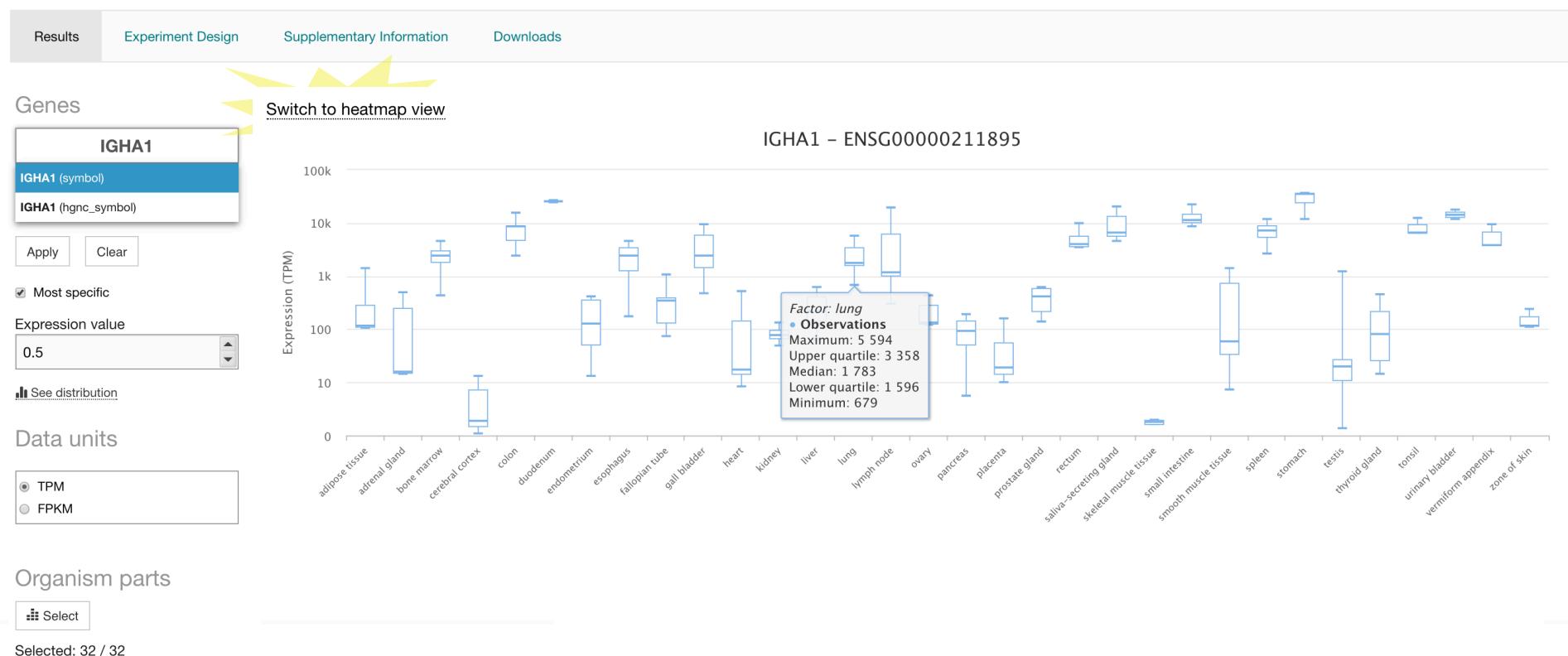
Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues

RNA-Seq mRNA baseline

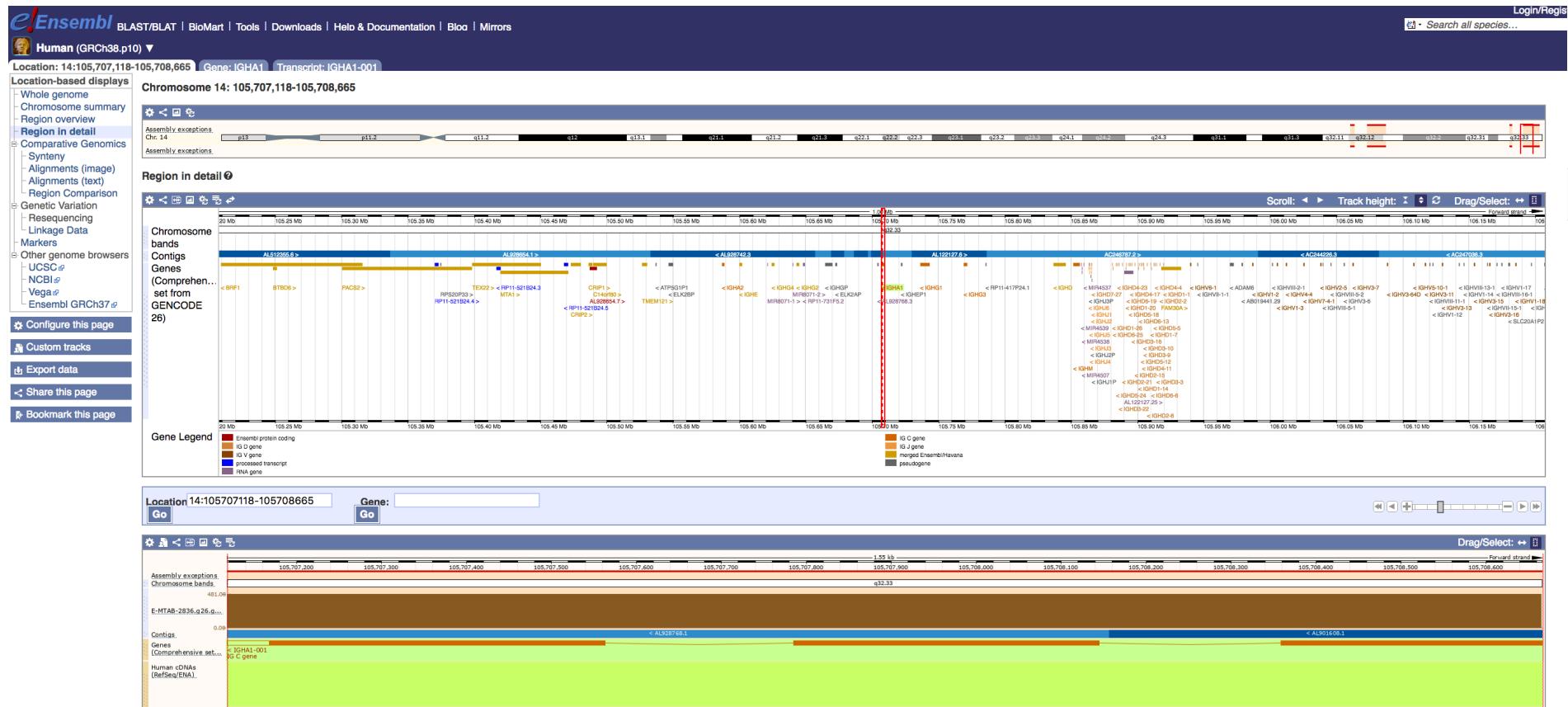
Organism: *Homo sapiens*

Raw Data Provider: The Human Protein Atlas





Baseline experiment page





Baseline experiment page

RNA-seq of coding RNA from tissue samples of 122 human individuals representing 32 different tissues

RNA-Seq mRNA baseline

Organism: *Homo sapiens*

Raw Data Provider: The Human Protein Atlas

Results

Experiment Design

Supplementary Information

Downloads

Expression values across all genes (TPM)

Expression values across all genes (FPKM)

Summary of the expression results for this experiment ready to view in R

- Heatmap of aggregated expression data

Experiment Design (tsv)



Let's try Expression Atlas

Baseline expression

Hands-on activity

Look up expression of *TNNI3* gene in
normal human tissues



In pairs



Let's try Expression Atlas

Expression Atlas

Gene expression across species and biological conditions

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- Anopheles gambiae
- Arabidopsis lyrata
- Arabidopsis thaliana
- Aspergillus fumigatus
- Bos taurus
- Brachypodium distachyon
- Brassica oleracea
- Brassica rapa
- Caenorhabditis elegans

Biological conditions

Enter condition query...

Examples: lung, leaf, valproic acid, cancer

Discover and interpret gene expression analysis results quickly and easy



Differential expression results

Results for CFHR2 (symbol)



Filter your results

Experimental variables

- Growth condition
- Time
- Genotype
- Treatment
- Cell type
- Diet
- Disease
- Sampling time
- Infect
- Phenotype

Log ₂ -fold	Species	Gene	Comparison	Experimental variables	Experiment name
Adjusted p-value	Log ₂ -fold change				
1.575 × 10 ⁻¹⁷	6.5		'lung carcinoma' vs 'normal' in 'CD11b-CD11c- epithelial cell'	cell type, disease	Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq
		CFH	Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq 'lung carcinoma' vs 'normal' in 'lung cell'		
		CFH	Property Test value (N=3) Reference value (N=3)		
			cell type lung cell lung cell		
			disease lung carcinoma normal		
			organism Mus musculus Mus musculus		
			organism part lung lung		
		CFHR2	'pancreatic adenocarcinoma' vs 'normal'	block, disease	RNA-seq of blood platelets from six tumor types and healthy donors
		CFHR2	'non-small cell lung carcinoma' vs 'normal'	block, disease	RNA-seq of blood platelets from six tumor types and healthy donors
		CFHR2	'hepatobiliary carcinoma' vs 'normal'	block, disease	RNA-seq of blood platelets from six tumor types and healthy donors
		Cfhr2	'lung carcinoma' vs 'normal' in 'lung cell'	cell type, disease	Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq

All organisms and all conditions in which *CFHR2* gene is differentially expressed



Differential experiment page

General information

Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq

RNA-Seq mRNA differential

Organism: *Mus musculus*

Reference(s): 25704820 (Filter by genes in paper)

Results

Plots

Experiment Design

Supplementary Information

Downloads

Differentially expressed genes

Showing 50 of 7,557 genes found:



Genes

Download displayed results

Most specific

Criteria to select DE genes

Log₂-fold change

Adjusted p-value

Comparisons

Selected: 3 / 3





Differential experiment page

Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq

RNA-Seq mRNA differential

Organism: *Mus musculus*

Reference(s): 25704820 (Filter by genes in paper)

Results

Plots

Experiment Design

Supplementary Information

Downloads

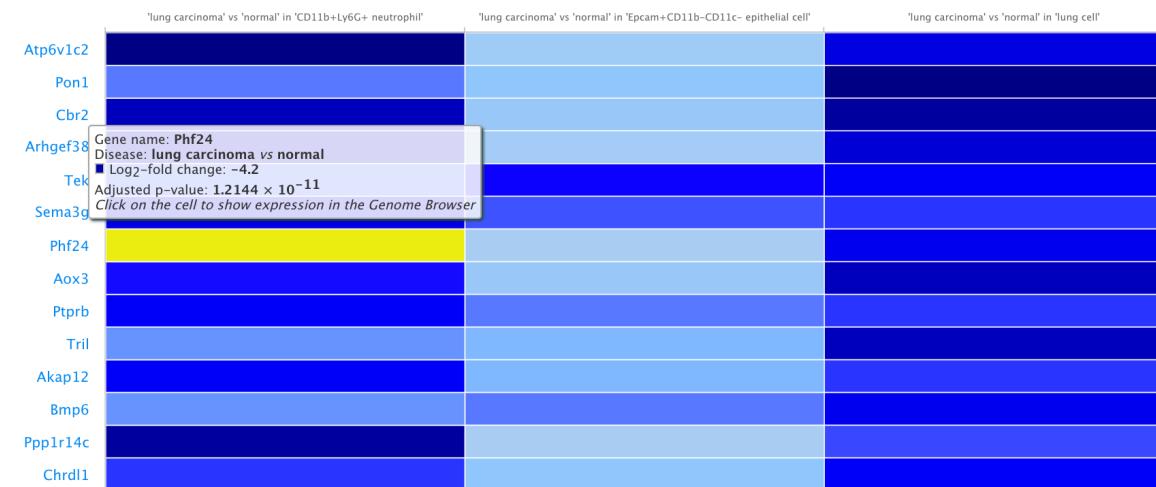
Genes

Showing 50 of 3,792 genes found:

[Download table content](#)

Log₂-fold change

-5.5 0



Specific unchecked

Most specific

Up- or downregulated
 Upregulated only
 Downregulated only

Log₂-fold change

1.0

Adjusted p-value

0.05

Comparisons

Select

Selected: 3 / 3



Differential experiment page

Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq

RNA-Seq mRNA differential

Organism: *Mus musculus*

Reference(s): 25704820 (Filter by genes in paper)

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'lung carcinoma' vs 'normal' in 'CD11b+Ly6G+ neutrophil'

GO terms enrichment analysis

Interpro domains enrichment analysis

Reactome pathways enrichment analysis

MA plot for the contrast across all genes

'lung carcinoma' vs 'normal' in 'Epcam+CD11b-CD11c- epithelial cell'

GO terms enrichment analysis

Interpro domains enrichment analysis

Reactome pathways enrichment analysis

MA plot for the contrast across all genes

'lung carcinoma' vs 'normal' in 'lung cell'

GO terms enrichment analysis

Interpro domains enrichment analysis

Reactome pathways enrichment analysis

MA plot for the contrast across all genes



piano

Platform for integrative analysis of omics data

Bioconductor version: Release (3.5)

Piano performs gene set analysis using various statistical methods, from different gene level statistics and a wide range of gene-set collections. Furthermore, the Piano package contains functions for combining the results of multiple runs of gene set analyses.

Author: Leif Varemo <piano.rpkg@gmail.com> and Intawat Nookae piano.rpkg@gmail.com

Maintainer: Leif Varemo <piano.rpkg@gmail.com>

Citation (from within R, enter `citation("piano")`):

Varemo L, Nielsen J and Nookae I (2013). "Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods." *Nucleic Acids Research*, **41**(8), pp. 4378-4391. doi: [10.1093/nar/gkt111](https://doi.org/10.1093/nar/gkt111).



Differential experiment page

Transcriptome analysis of isolated stromal cells and tumor

RNA-Seq mRNA differential

Organism: *Mus musculus*

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Results Plots Experiment Design Supplementary Information Downloads

'lung carcinoma' vs 'normal' in 'CD11b+Ly6G+ neutrophil'

GSE GO terms enrichment analysis

GSE Interpro domains enrichment analysis

GSE Reactome pathways enrichment analysis

MA MA plot for the contrast across all genes

'lung carcinoma' vs 'normal' in 'Epcam+CD11b-CD11c- epithelial cell'

GSE GO terms enrichment analysis

GSE Interpro domains enrichment analysis

GSE Reactome pathways enrichment analysis

MA MA plot for the contrast across all genes

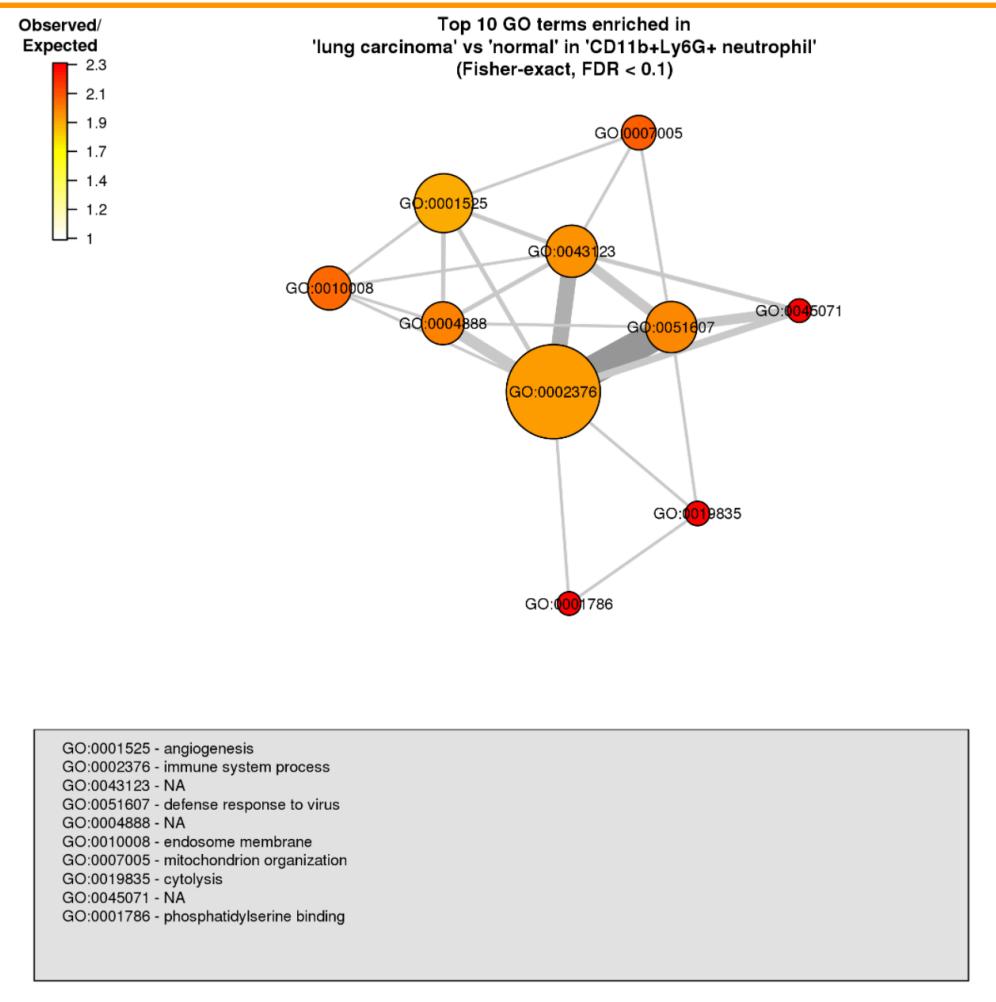
'lung carcinoma' vs 'normal' in 'lung cell'

GSE GO terms enrichment analysis

GSE Interpro domains enrichment analysis

GSE Reactome pathways enrichment analysis

MA MA plot for the contrast across all genes





More information about *CFHR2* gene

Login/Register

e!Ensembl BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors

Human (GRCh38.p10) ▾

Location: 1:196,943,772-196,959,226

Gene-based displays

- Summary
- Splice variants
- Transcript comparison
- Gene alleles

- Sequence
 - Secondary Structure

- Comparative Genomics
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Ensembl protein families

- Ontologies
 - GO: Cellular component
 - GO: Molecular function
 - GO: Biological process

- Phenotypes

- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants

- Gene expression
- Regulation
- External references
- Supporting evidence

Gene: CFHR2 ENSG00000080910

Description complement factor H related 2 [Source:HGNC Symbol;Acc:[HGNC:4890](#)]

Synonyms FHR2, HFL3, CFHL2

Location [Chromosome 1: 196,943,772-196,959,226](#) forward strand.
GRCh38:CM000663.2

About this gene This gene has 6 transcripts ([splice variants](#)), [16 orthologues](#), [11 paralogues](#), is a member of [1 Ensembl protein family](#) and is associated with [3 phenotypes](#).

Transcripts [Hide transcript table](#)

Show/hide columns (1 hidden)

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
CFHR2-001	ENST00000367415.6	1059	270aa	Protein coding	CCDS30959	P36980	NM_005666 NP_005657	TSL:1 GENCODE basic APPRIS P2
CFHR2-005	ENST00000476712.6	1020	254aa	Protein coding	-	V9GYE7	-	TSL:3 GENCODE basic APPRIS ALT2
CFHR2-006	ENST00000496448.5	811	No protein	Processed transcript	-	-	-	TSL:2
CFHR2-002	ENST00000473386.1	599	No protein	Processed transcript	-	-	NM_001312672	TSL:1
CFHR2-004	ENST00000489703.1	424	No protein	Processed transcript	-	-	-	TSL:3
CFHR2-003	ENST00000485647.1	376	No protein	Processed transcript	-	-	-	TSL:5



Let's try Expression Atlas

Differential expression

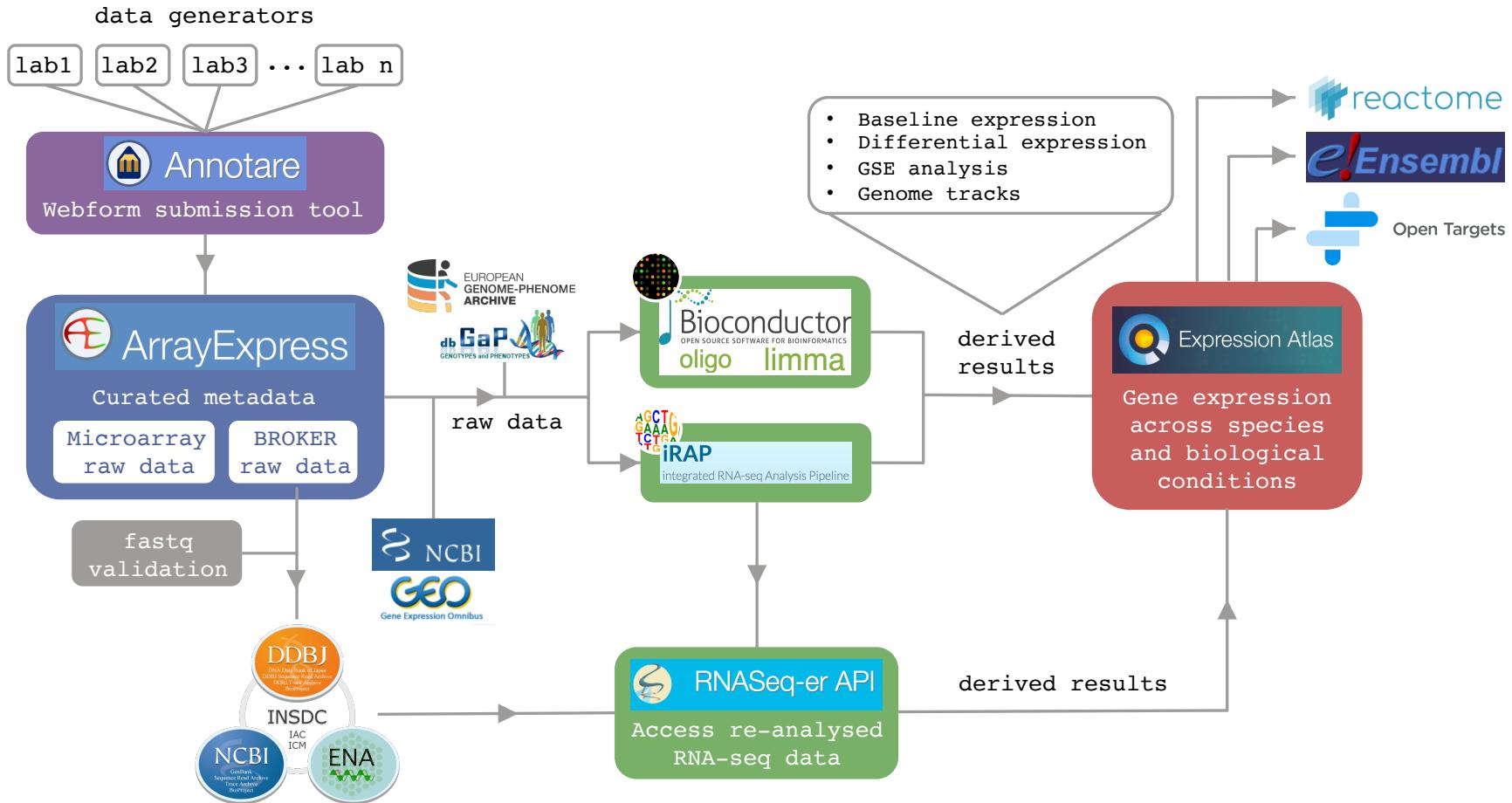
Hands-on activity

Find differentially expressed genes in patients with hepatocellular carcinoma



In pairs

Functional genomics resources at EMBL-EBI





RNASeq-er API



RNASeq-er API

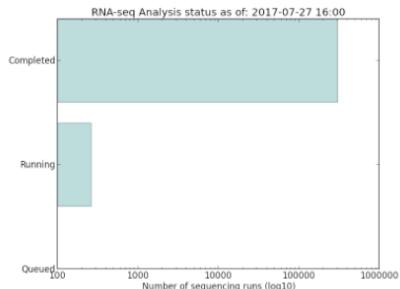
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[Feedback](#)

Welcome to RNASeq-er API - a gateway to systematically updated analysis of public RNA-Seq data

The RNASeq-er REST API provides easy access to the results of the systematically updated and continually growing analysis of public RNA-seq data in [European Nucleotide Archive \(ENA\)](#). The analysis of each sequencing run is performed by the EMBL-EBI's Gene Expression Team using the [iRAP pipeline](#).

- [1. Get Started](#)
- [2. What does the RNASeq-er pipeline do?](#)
- [3. How is the RNASeq-er performed?](#)
- [4. How to use the RNASeq-er API?](#)
- [5. What are the main classes of API calls?](#)
 - [5.1. Analysis results Per Run](#)
 - [5.1.1. Making per-run API calls](#)
 - [5.1.2. Results of per-run API calls](#)
 - [5.2. Analysis results Per Study](#)
 - [5.2.1. Making per-study API calls](#)
 - [5.2.2. Results of per-study API calls](#)
 - [5.3. Sample Attributes Per Run](#)
 - [5.3.1. Making sample attributes per-run API calls](#)
 - [5.3.2. Results of sample attributes per-run API calls](#)
 - [5.4. Baseline expression By Gene](#)
 - [5.4.1. Making baseline expression per-gene API calls](#)
 - [5.4.2. Results of baseline expression per-gene API calls](#)
 - [5.5. Mapping Quality Statistics For All Organisms](#)
 - [5.5.1. Retrieving the mean and standard deviation of mapping quality for all organisms](#)



<https://www.ebi.ac.uk/fg/rnaseq/>

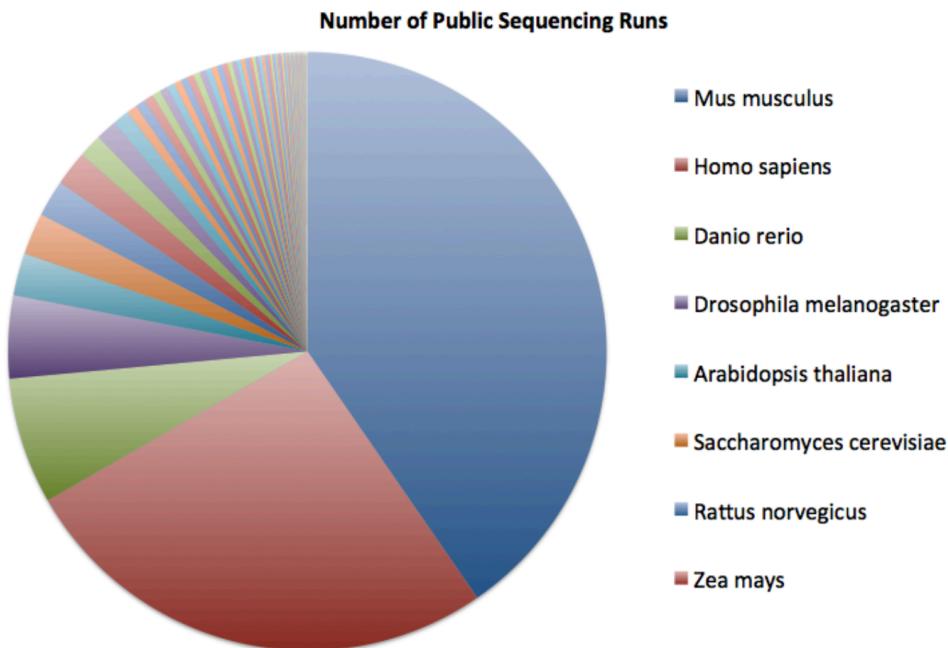


RNASeq-er API

> 270,000 analysed runs

> 15,000 studies

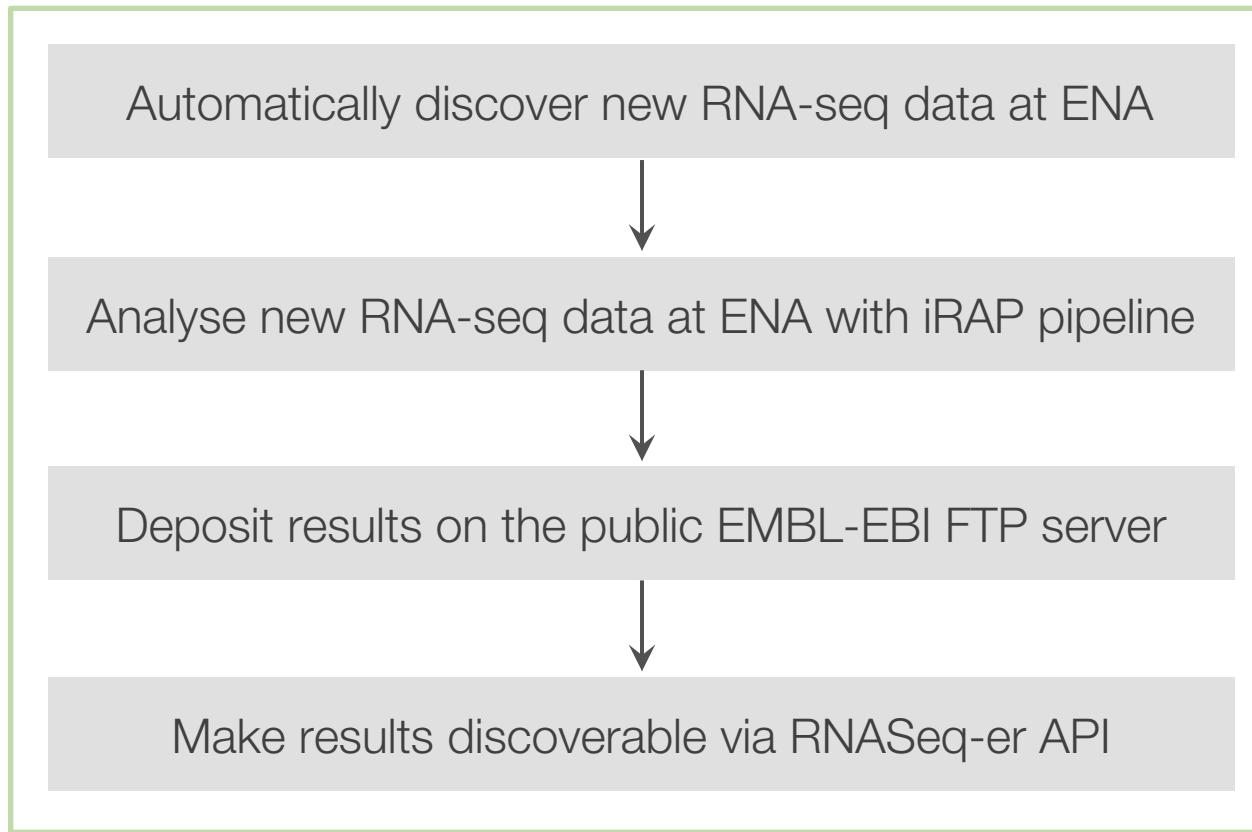
> 300 species (163 genome references)



800,000 runs not analysed from 6,500 species, not available via API (no reference genome/gene annotation available in public databases)



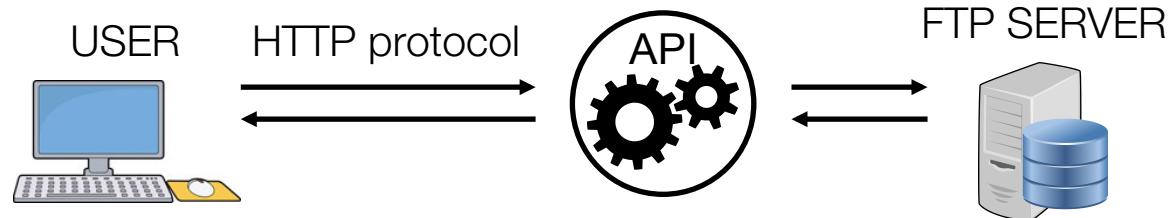
RNASeq-er API



<https://doi.org/10.1093/bioinformatics/btx143>

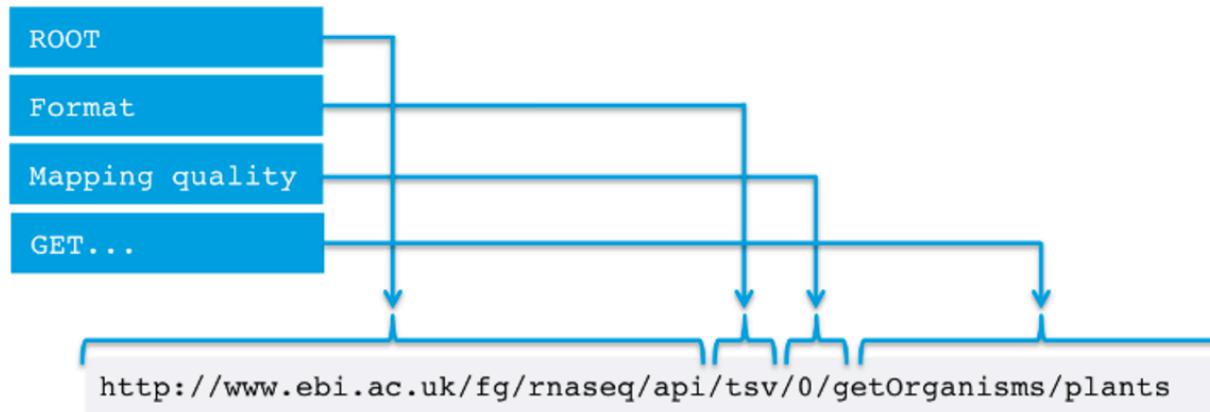


RNASeq-er API



How to built API calls?

How to built the URL?





RNASeq-er API

Accessing the results of alignments

Access alignments of RNA-seq data involving human autism samples

https://www.ebi.ac.uk/fg/rnaseq/api/tsv/0/getRunsByOrganismCondition/homo_sapiens/autism

Secure | https://www.ebi.ac.uk/fg/rnaseq/api/tsv/0/getRunsByOrganismCondition/homo_sapiens/autism

STUDY_ID	SAMPLE_IDS	BIOREP_ID	RUN_IDS	ORGANISM	REFERENCE_ORGANISM	STATUS	ASSEMBLY_USED	ENA_LAST_UPDATED	LAST_PROCESSED_DATE	CRAM_LOCATION	BEDGRAPH_LOCATION
SRP007483	SAMN00668205	SRR309133	SRR309133	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Sat Aug 22 2015 10:42:42		
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.cram				ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.bedgraph
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.bw	96			disease autism
SRP007483	SAMN00668205	SRR309134	SRR309134	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Aug 10 2015 23:07:36		
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309134/SRR309134.cram				ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309134/SRR309134.bedgraph
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309134/SRR309134.bw	96			disease autism
SRP007483	SAMN00668206	SRR309135	SRR309135	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Aug 24 2015 23:30:14		
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309135/SRR309135.cram				ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309135/SRR309135.bedgraph
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309135/SRR309135.bw	95			disease autism
SRP007483	SAMN00668206	SRR309136	SRR309136	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Jul 27 2015 07:34:38		
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309136/SRR309136.cram				ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309136/SRR309136.bedgraph
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309136/SRR309136.bw	95			disease autism
SRP007483	SAMN00668207	SRR309137	SRR309137	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Tue Aug 11 2015 22:40:15		
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309137/SRR309137.cram				ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309137/SRR309137.bedgraph
							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309137/SRR309137.bw	94			disease autism
SRP007483	SAMN00668207	SRR309138	SRR309138	homo_sapiens	homo_sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Sat Aug 15 2015 13:44:31		
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							ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309138/SRR309138.bw	95			disease autism

alignment results in EMBL-EBI FTP server



RNASeq-er API

Accessing the results of alignments

Access alignment results of all samples of a RNA-seq study

<https://www.ebi.ac.uk/fg/rnaseq/api/tsv/0/getRunsByStudy/SRP007483>

Secure | <https://www.ebi.ac.uk/fg/rnaseq/api/tsv/0/getRunsByStudy/SRP007483>

STUDY_ID	SAMPLE_IDS	BIOREP_ID	RUN_IDS	ORGANISM	REFERENCE_ORGANISM	STATUS	ASSEMBLY_USED	ENA_LAST_UPDATED	LAST_PROCESSED_DATE	CRAM_LOCATION	BEDGRAPH_LOCATION
BIGWIG LOCATION MAPPING_QUALITY											
SRP007483	SAMN00668205	SRR309133	SRR309133	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Sat Aug 22 2015 10:42:42		
										ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.cram	ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.bedgraph
										ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309133/SRR309133.bw	96
SRP007483	SAMN00668205	SRR309134	SRR309134	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Aug 10 2015 23:07:36		
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SRP007483	SAMN00668206	SRR309135	SRR309135	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Aug 24 2015 23:30:14		
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										ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309136/SRR309136.bw	95
SRP007483	SAMN00668207	SRR309137	SRR309137	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Tue Aug 11 2015 22:40:15		
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										ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309137/SRR309137.bw	94
SRP007483	SAMN00668207	SRR309138	SRR309138	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Sat Aug 15 2015 13:44:31		
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SRP007483	SAMN00668208	SRR309140	SRR309140	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Aug 24 2015 21:30:41		
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SRP007483	SAMN00668209	SRR309141	SRR309141	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Mon Jul 27 2015 00:06:37		
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SRP007483	SAMN00668209	SRR309142	SRR309142	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Sun Aug 16 2015 03:50:59		
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SRP007483	SAMN00668210	SRR309144	SRR309144	homo sapiens	homo sapiens	Complete	GRCh38	Fri Jun 19 2015 20:17:06	Fri Jul 24 2015 20:40:35		
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										ftp://ftp.ebi.ac.uk/pub/databases/arrayexpress/data/atlas/rnaseq/SRR309/SRR309144/SRR309144.bw	96



RNASeq-er API

Accessing sample metadata

<https://www.ebi.ac.uk/fg/rnaseq/api/tsv/getSampleAttributesPerRunByStudy/SRP007483>

STUDY_ID	RUN_ID	TYPE	VALUE_EFO_URL
SRP007483	SRR309133		clinical information brain region BA22 (temporal cortex) NA
SRP007483	SRR309133		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309133		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309133		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309133		clinical information brain region BA22 (temporal cortex) NA
SRP007483	SRR309134		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309134		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309134		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309134		clinical information brain region BA41 (temporal cortex) NA
SRP007483	SRR309134		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309134		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309134		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309137		clinical information brain region BA41 (temporal cortex) NA
SRP007483	SRR309137		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309137		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309137		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309138		clinical information brain region BA41 (temporal cortex) NA
SRP007483	SRR309138		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309138		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309138		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309139		clinical information brain region BA09 (frontal cortex) NA
SRP007483	SRR309139		disease autism http://www.ebi.ac.uk/efo/EFO_0003758
SRP007483	SRR309139		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309139		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309140		clinical information brain region BA09 (frontal cortex) NA
SRP007483	SRR309140		disease normal http://purl.obolibrary.org/obo/PATO_0000461
SRP007483	SRR309140		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309140		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
SRP007483	SRR309144		clinical information brain region BA41 (temporal cortex) NA
SRP007483	SRR309144		disease normal http://purl.obolibrary.org/obo/PATO_0000461
SRP007483	SRR309144		organism Homo sapiens http://purl.obolibrary.org/obo/NCBITaxon_9606
SRP007483	SRR309144		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955
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SRP007483	SRR309144		organism part brain http://purl.obolibrary.org/obo/UBERON_0000955

samples from
patients with autism

samples from
normal individuals



RNASeq-er API

Accessing gene expression quantification results

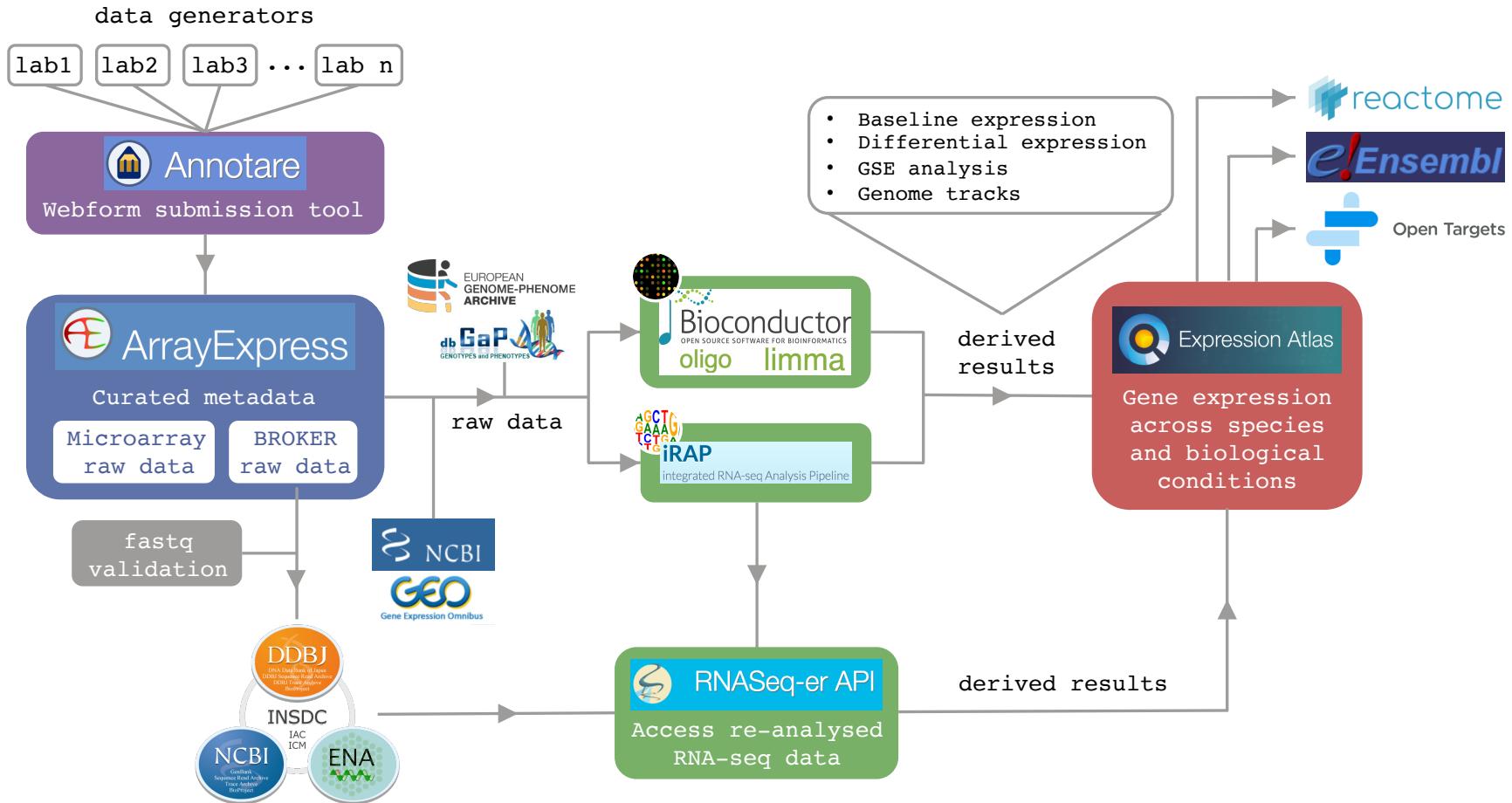
Access gene expression quantification results of a RNA-seq study

<https://www.ebi.ac.uk/fg/rnaseq/api/tsv/getStudy/SRP007483>

Secure | https://www.ebi.ac.uk/fg/rnaseq/api/tsv/getStudy/SRP007483

STUDY_ID	ORGANISM	REFERENCE_ORGANISM	ASSEMBLY_USED	GTF_USED	STATUS	GENES_FPKM_COUNTS_FTP_LOCATION	GENES TPM COUNTS FTP LOCATION	GENES_RAW_COUNTS_FTP_LOCATION	EXONS_FPKM_COUNTS_FTP_LOCATION																																																																																																																																								
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<table><thead><tr><th>Gene ID</th><th>SRR309133</th><th>SRR309134</th><th>SRR309135</th><th>SRR309136</th><th>SRR309137</th><th>SRR309138</th><th>SRR309139</th></tr><tr><th>SRR309140</th><th>SRR309141</th><th>SRR309142</th><th>SRR309143</th><th>SRR309144</th><th></th><th></th><th></th></tr></thead><tbody><tr><td>ENSG000000000003</td><td>3.13</td><td>3.04</td><td>3.39</td><td>3.33</td><td>5.97</td><td>7.32</td><td>3.35</td><td>3.75</td><td>3.25</td></tr><tr><td>ENSG000000000005</td><td>0</td><td>0</td><td>0.06</td><td>0.12</td><td>0.25</td><td>0.18</td><td>0.43</td><td>0.29</td><td>0.27</td></tr><tr><td>ENSG00000000419</td><td>7.47</td><td>7.95</td><td>16.86</td><td>15.17</td><td>21.79</td><td>22.01</td><td>24.15</td><td>24.09</td><td>42.88</td></tr><tr><td>ENSG00000000457</td><td>0.67</td><td>0.73</td><td>0.55</td><td>0.48</td><td>2.7</td><td>3.24</td><td>3.2</td><td>2.15</td><td>3.97</td></tr><tr><td>ENSG00000000460</td><td>0.21</td><td>0.32</td><td>0.1</td><td>0.21</td><td>1.06</td><td>1.14</td><td>0.66</td><td>0.52</td><td>0.53</td></tr><tr><td>ENSG00000000938</td><td>0.78</td><td>0.55</td><td>1.44</td><td>1.73</td><td>8.71</td><td>9.22</td><td>3.48</td><td>3.74</td><td>2.5</td></tr><tr><td>ENSG00000000971</td><td>0.88</td><td>1.09</td><td>6.58</td><td>6.57</td><td>5.12</td><td>4.69</td><td>1.85</td><td>1.76</td><td>1.28</td></tr><tr><td>ENSG00000001036</td><td>4.93</td><td>5.5</td><td>5.5</td><td>5.31</td><td>14.87</td><td>15.48</td><td>9.32</td><td>8.59</td><td>9.99</td></tr><tr><td>ENSG00000001084</td><td>5.49</td><td>5.32</td><td>5.74</td><td>6.07</td><td>11.03</td><td>10.79</td><td>8.32</td><td>7.28</td><td>8.88</td></tr><tr><td>ENSG00000001167</td><td>5.31</td><td>5.69</td><td>6.83</td><td>7.37</td><td>11.83</td><td>12.78</td><td>8.28</td><td>8.19</td><td>8.08</td></tr><tr><td>ENSG00000001460</td><td>0.78</td><td>0.69</td><td>1.34</td><td>1.04</td><td>6.2</td><td>6.48</td><td>5.02</td><td>4.67</td><td>8.36</td></tr><tr><td>ENSG00000001461</td><td>14.64</td><td>14.75</td><td>17.54</td><td>17.8</td><td>47.25</td><td>46.31</td><td>18.4</td><td>17.97</td><td>39.94</td></tr></tbody></table>										Gene ID	SRR309133	SRR309134	SRR309135	SRR309136	SRR309137	SRR309138	SRR309139	SRR309140	SRR309141	SRR309142	SRR309143	SRR309144				ENSG000000000003	3.13	3.04	3.39	3.33	5.97	7.32	3.35	3.75	3.25	ENSG000000000005	0	0	0.06	0.12	0.25	0.18	0.43	0.29	0.27	ENSG00000000419	7.47	7.95	16.86	15.17	21.79	22.01	24.15	24.09	42.88	ENSG00000000457	0.67	0.73	0.55	0.48	2.7	3.24	3.2	2.15	3.97	ENSG00000000460	0.21	0.32	0.1	0.21	1.06	1.14	0.66	0.52	0.53	ENSG00000000938	0.78	0.55	1.44	1.73	8.71	9.22	3.48	3.74	2.5	ENSG00000000971	0.88	1.09	6.58	6.57	5.12	4.69	1.85	1.76	1.28	ENSG00000001036	4.93	5.5	5.5	5.31	14.87	15.48	9.32	8.59	9.99	ENSG00000001084	5.49	5.32	5.74	6.07	11.03	10.79	8.32	7.28	8.88	ENSG00000001167	5.31	5.69	6.83	7.37	11.83	12.78	8.28	8.19	8.08	ENSG00000001460	0.78	0.69	1.34	1.04	6.2	6.48	5.02	4.67	8.36	ENSG00000001461	14.64	14.75	17.54	17.8	47.25	46.31	18.4	17.97	39.94
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Functional genomics resources at EMBL-EBI





Expression Atlas data in other resources



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Welcome to Open Targets

For biomedical researchers who need to identify a biological target for a
of therapeutic targets based on genome-scale experiments and analysis
human diseases, and is committed to sharing its data openly with the sc

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Open Targets Platform

Find new targets for drug discovery

CYP1A2



CYP1A2

cytochrome P450 family 1 subfamily A member 2

156 diseases associated

Target

Cytochromes P450 are a group of heme-thiolate monooxygenases. In liver microsomes, this enzyme is involved in an NADPH-dependent electron transport pathway. It oxidizes a variety of structurally unrelated compounds, including steroids, fatty acids, and xenobiotics. Most active in catalyzing 2-hydrox...



Expression Atlas data in other resources

156 diseases associated with CYP1A2

[View CYP1A2 profile](#)

Filter by

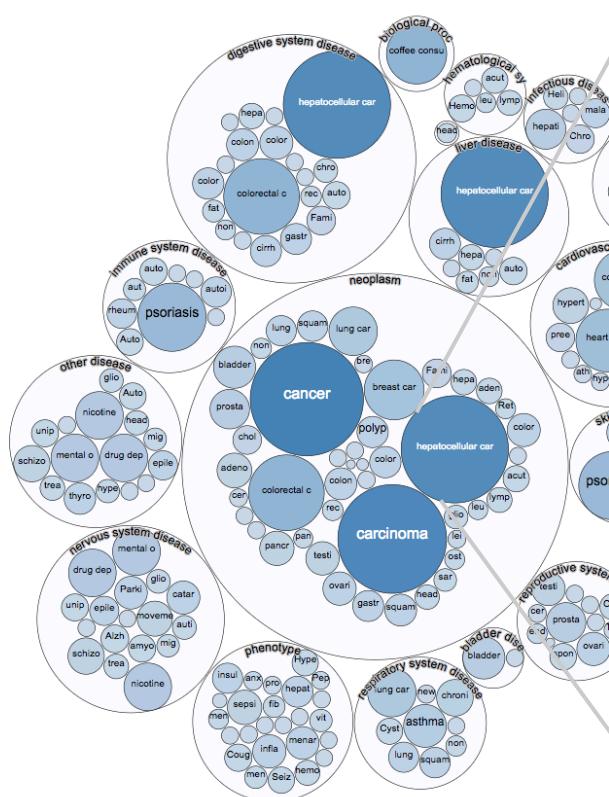
Bubbles Table Tree

Data types

- Genetic associations (4)
- Somatic mutations (0)
- Drugs (0)
- Affected pathways (0)
- RNA expression (13)
- Text mining (152)
- Animal models (0)

Therapeutic area

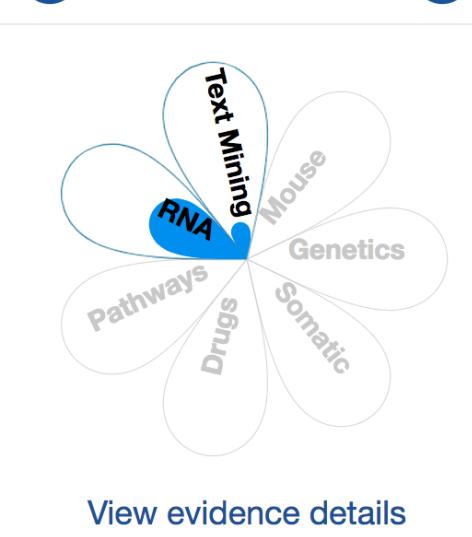
- Neoplasm (46)
- Phenotype (25)
- Digestive system disease (20)
- Nervous system disease (17)
- Endocrine system disease (16)
- Other (16)
- Metabolic disease (15)
- Cardiovascular disease (13)
- Reproductive system disease (12)
- Genetic disorder (10)
- Immune system disease (9)
- Respiratory system disease (9)
- Liver disease (8)
- Infectious disease (6)
- Hematological system disease (5)
- Skin disease (4)
- Skeletal system disease (4)
- Eye disease (3)
- Bladder disease (2)
- Head disease (1)
- Kidney disease (1)
- Biological process (1)



hepatocellular carcinoma
(Association Score: 0.57)



[Profile | Associations](#)



[View evidence details](#)

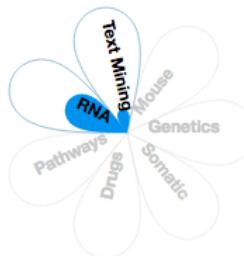
EMBL-EBI





Expression Atlas data in other resources

Evidence for CYP1A2 in hepatocellular carcinoma



CYP1A2

cytochrome P450 family 1 subfamily A member 2

Synonyms: P3-450, CP12

Cytochromes P450 are a group of heme-thiolate monooxygenases. In liver microsomes, this enzyme is involved in an NADPH-dependent electron transport pathway. It oxidizes a variety of structurally unrelated compounds.

hepatocellular carcinoma

Synonyms: Cancer, Liver, Hepatocellular Carcinomas, Liver Cancer, Adult, NEOPL HEPATIC, Hepatomas, Primary Car...

Tumors or cancer of the LIVER.. A primary malignant neoplasm of epithelial liver cells. It ranges from a well-differentiated tumor with EPITHELIAL CELLS indistinguishable from normal HEPATOCYTES to a ...

Genetic associations

Somatic mutations

Drugs

Affected pathways

RNA expression

Text mining

Animal models



Expression Atlas data in other resources

Evidence for CYP1A2 in hepatocellular carcinoma

Source: Expression Atlas

Showing 1 to 4 of 4 entries

Search:



Disease	Gene-disease evidence							Experiment overview and data	Publications
	Comparison	Activity	Tissue/cell	Evidence source	Log ₂ fold change	P-value	Percentile rank		
hepatocellular carcinoma	'liver tumor' vs 'adjacent non-tumor tissue'	decreased ↘	liver	differential gene expression evidence from RNA-seq experiment	-10.1	3.32e-63	100	Transcriptome sequencing of human hepatocellular carcinoma ↗	
hepatocellular carcinoma	'tumor' vs 'paratumoral tissue'	decreased ↘	liver	differential gene expression evidence from RNA-seq experiment	-3.3	3.67e-6	98	Transcriptomic characterization of Hepatocellular Carcinoma with CTNNB1 mutation ↗	
hepatocellular carcinoma	'minor tumor' vs 'normal' in 'IL28B rs8099917 TG/GG'	decreased ↘	liver	differential gene expression evidence from microarray experiment	-3.3	4.93e-3	99	Hepatic gene expression of HCV related Hepatocellular carcinoma and non-cancerous tissue with IL28B rs8099917 TT genotype and TG/GG genotype ↗	

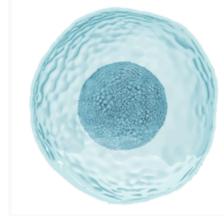


New project on single-cell...

 Single Cell Expression Atlas

Single-cell gene expression across species

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Analysing gene expression for single cells experiments

The cell is a natural unit of biology, whose type and state can vary according to external influences or to internal processes. In multicellular organisms, all cells are derived from a single zygote which, through regulated programmes of proliferation and differentiation, generates all of the diverse cell types that populate the organism. Dysregulation of these programmes in single 'renegade' cells can lead to diseases such as cancers, neurological disorders and developmental disorders.

List of single-cell experiments

Total : 3 experiments

 06-02-2017 Single-cell RNA-seq analysis of human pancreas from healthy individuals and type 2 diabetes patients <i>Homo sapiens</i>	3514	Analysis result	
 06-02-2017 Single-cell RNA-sequencing resolves a CD4+ T cell fate bifurcation <i>Mus musculus</i>	752	Analysis result	
 06-02-2017 Single-cell RNA-sequencing of <i>Platynereis dumerilii</i> larval brain cells <i>Platynereis dumerilii</i>	285	Analysis result	

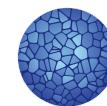
Marker genes search

Gene ID, gene name or gene feature

Species

Any

Examples: REG1B, zinc finger, lung, leaf, valproic acid, cancer



HUMAN
CELL
ATLAS



Expression Atlas: Who we are?

Robert
Petryszak
Team Leader



Irene
Papatheodorou
Co-ordinator



Data curation



Laura Huerta

Data analysis



Suhail Mohammed



Nuno Fonseca

User Interface



Alfonso Fuentes



Elisabet Barrera



Nancy George

Anja Fullgrabe



Wojtek Bazant



Haider Iqbal

Getting help and sending feedback

The screenshot shows the Expression Atlas homepage. At the top left is a blue circular logo with a yellow and white 'Q'. To its right is the text 'Expression Atlas' and 'Gene expression across species and biological conditions'. Below this is a horizontal navigation bar with six items: 'Home', 'Download', 'Release notes', 'FAQ' (which is highlighted in green), 'Help', 'Licence', and 'About' (which is also highlighted in green). The main content area has a teal background. It features a large heading 'About Expression Atlas', followed by 'What is Expression Atlas?'. Below this is a paragraph about the project's mission to provide freely available information on gene and protein expression across various biological conditions. Another paragraph explains the project's aim to answer questions like 'where is my favourite gene expressed?' and 'how its expression changes in a disease?'. A final paragraph describes the project's objective of involving data curation, analysis, and development of a web application. To the right of the text is a diagram consisting of four teal boxes labeled 'Data curation', 'Data analysis', 'Data search', and 'Data visualisation'. Below these are four smaller teal boxes: 'High quality data' (with a checkmark icon), 'High quality results' (with a bar chart icon), 'Accessible results' (with a sunburst chart icon), and '... easy to interpret' (with a grid icon). A grey arrow points from the bottom of the first column to the bottom of the fourth column.

About Expression Atlas

What is Expression Atlas?

Expression Atlas is an open science resource that gives users a powerful way to find information about gene and protein expression. Our mission is to provide the scientific community with freely available information on the abundance and localisation of RNA (and proteins) across species and biological conditions such as different tissues, cell types, developmental stages and diseases among others.

Expression Atlas aims to help answering questions such as 'where is my favourite gene expressed?' or 'how its expression changes in a disease?'

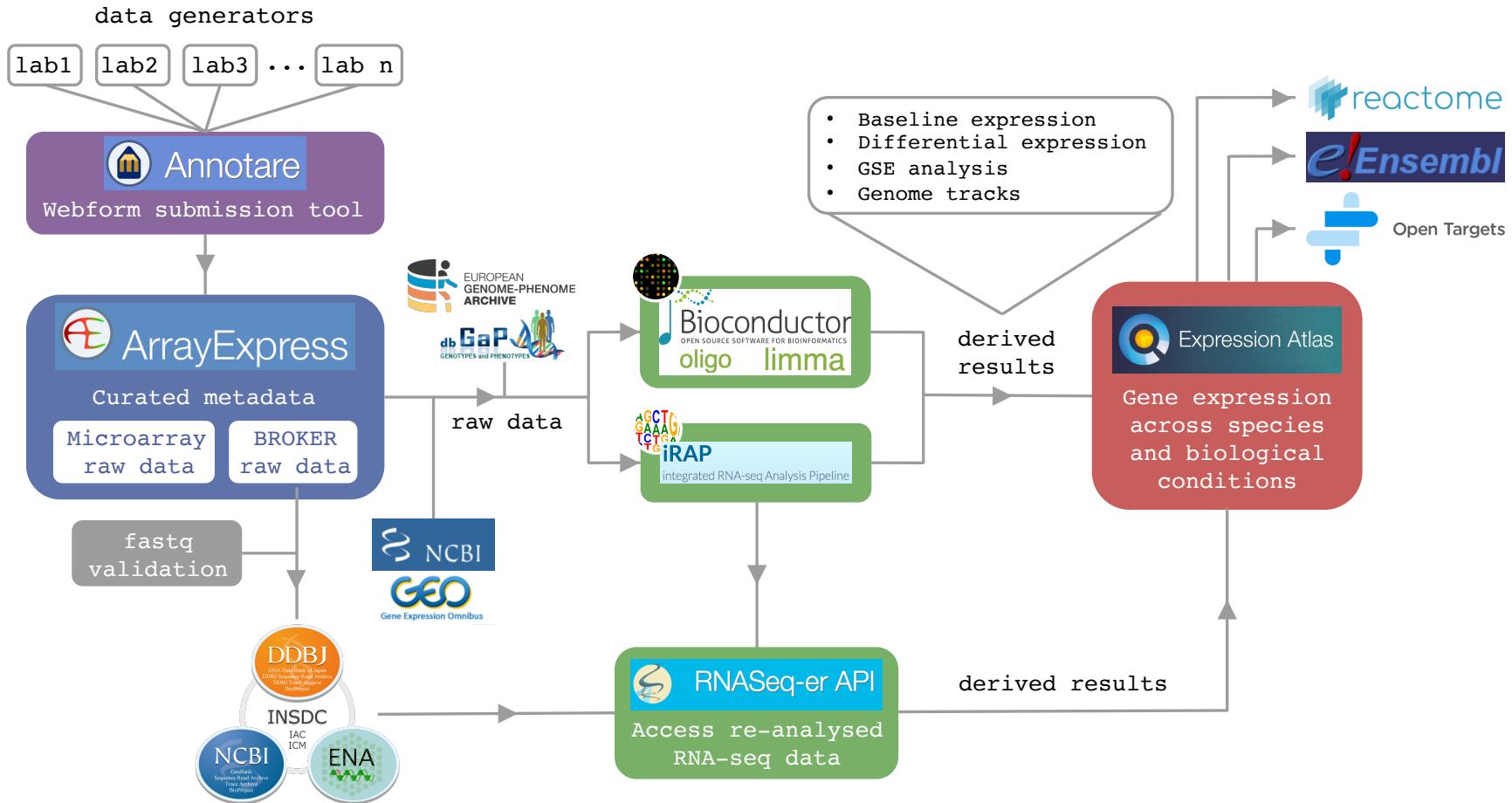
To achieve this objective, our project involves data curation, data analysis and the development of a web application to access and visualise publicly available data.

atlas-feedback@ebi.ac.uk



@ExpressionAtlas

Functional genomics resources at EMBL-EBI



Please fill in the survey before you go!

<https://www.surveymonkey.co.uk/r/PV25ZHB>

EMBL-EBI



EMBL-EBI Bioinformatics resources for exploring functional genomics data, DKFZ, Heidelberg, Nov 2017

Workshop Evaluation Form

EMBL-EBI collects feedback from every course and workshop we run. The survey is a way for you to inform us about the workshop you have participated in, what you enjoyed, what you found useful and how we can make improvements. This information is also used to inform the development of new courses and workshops.

Next >>

EMBL-EBI Bioinformatics resources for exploring functional genomics data

Expression Atlas: gene expression results across species and conditions

Laura Huerta, PhD
Senior Scientific Curator
lauhuema@ebi.ac.uk
10 November 2017

