

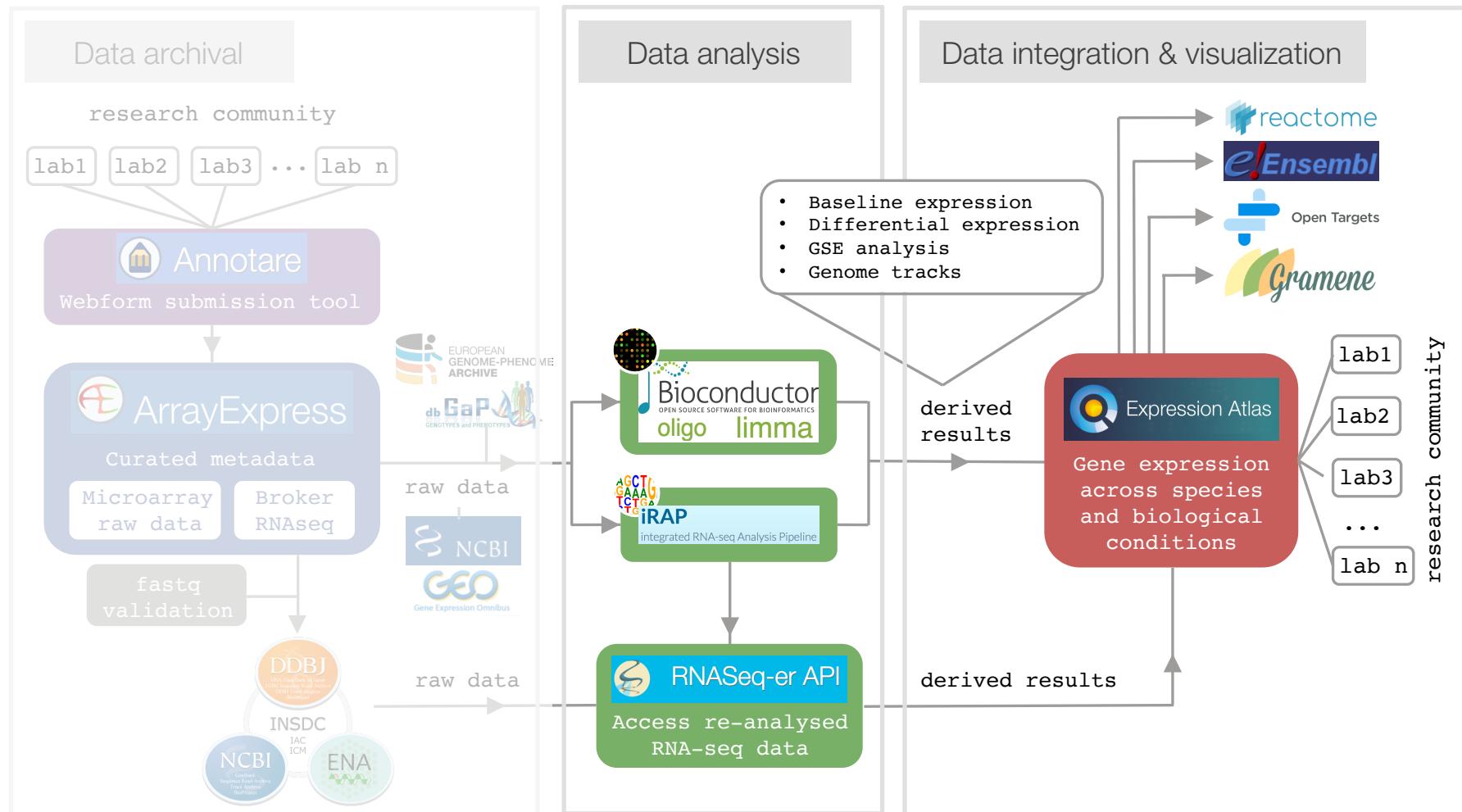
# EMBL-EBI workshop: Array Express and Expression Atlas

Expression Atlas: gene expression  
results across species and conditions

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Senior Scientific Curator  
[lauhuema@ebi.ac.uk](mailto:lauhuema@ebi.ac.uk)  
7 February 2017



# Functional genomics resources at EMBL-EBI





# What is Expression Atlas?

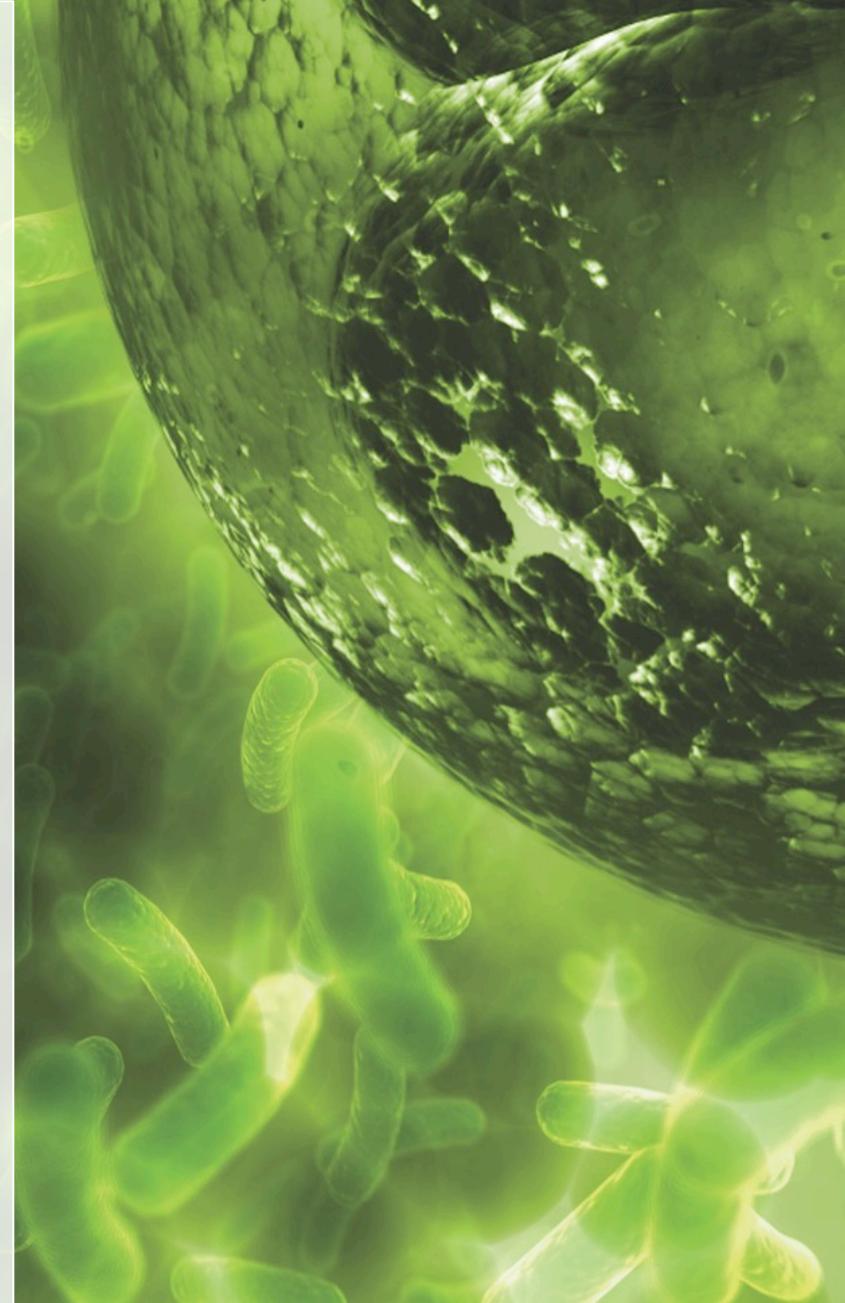


Reference resource for gene/protein expression  
across species and biological conditions

[www.ebi.ac.uk/gxa/home](http://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



EBI infrastructure

## 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



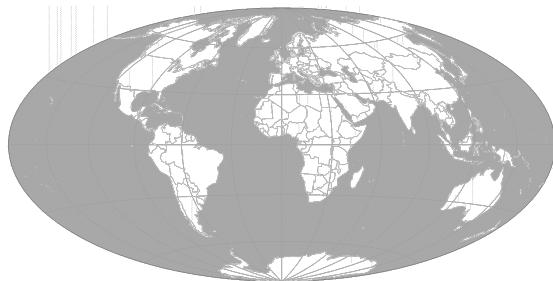
DMDD

Deciphering the Mechanisms  
of Developmental Disorders



Mouse models

# Expression Atlas contains thousands of selected and curated datasets



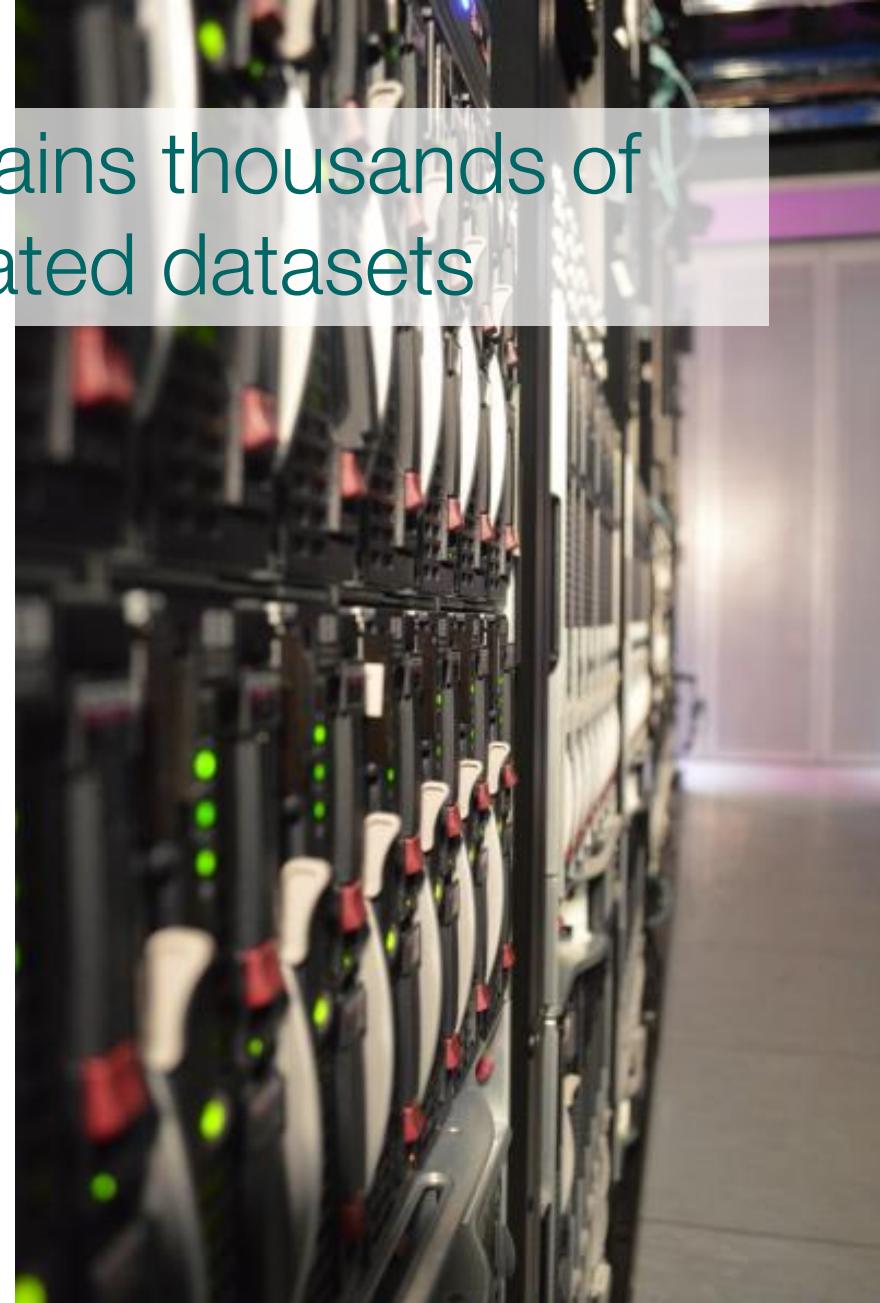
> 3,100 datasets



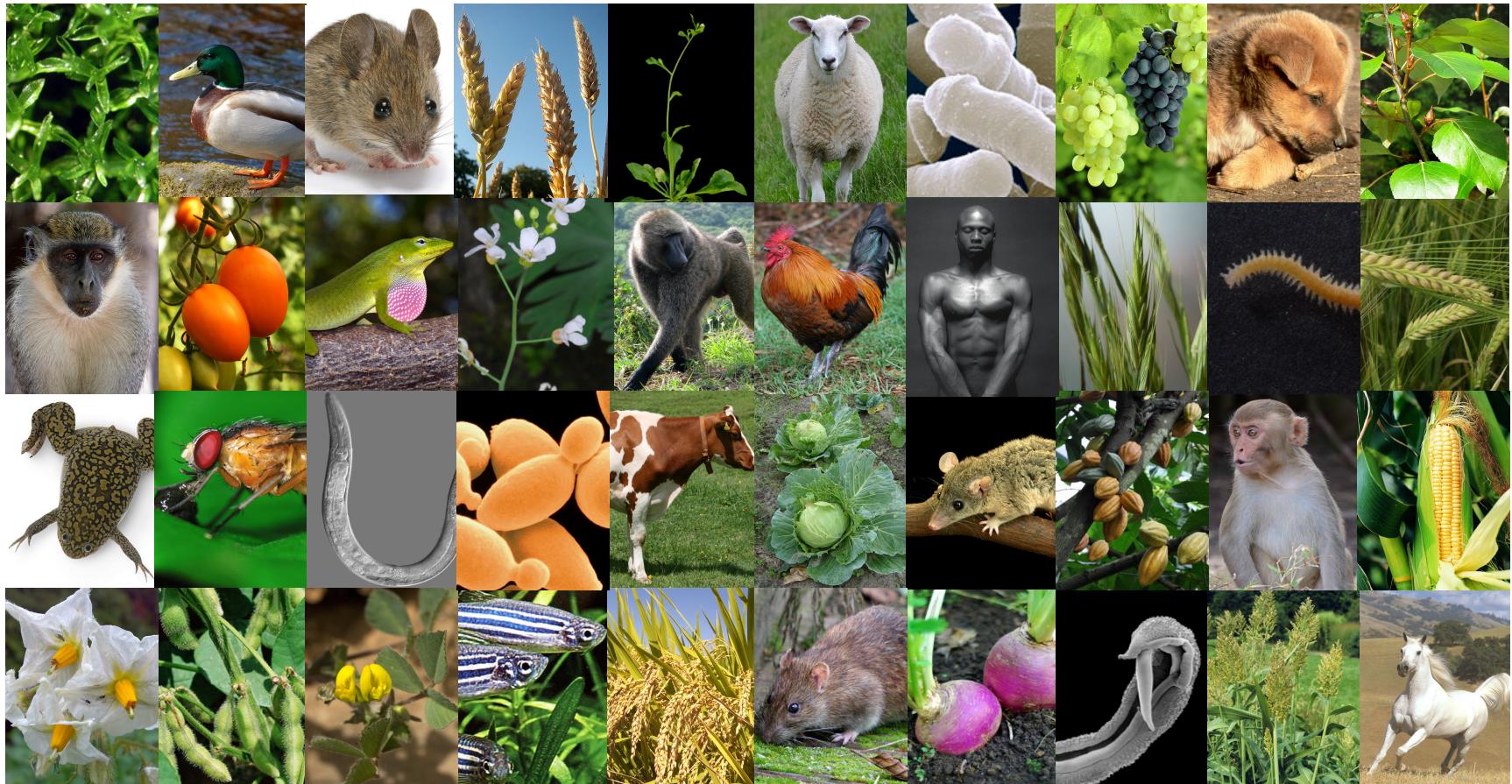
> 550 RNA-sequencing data



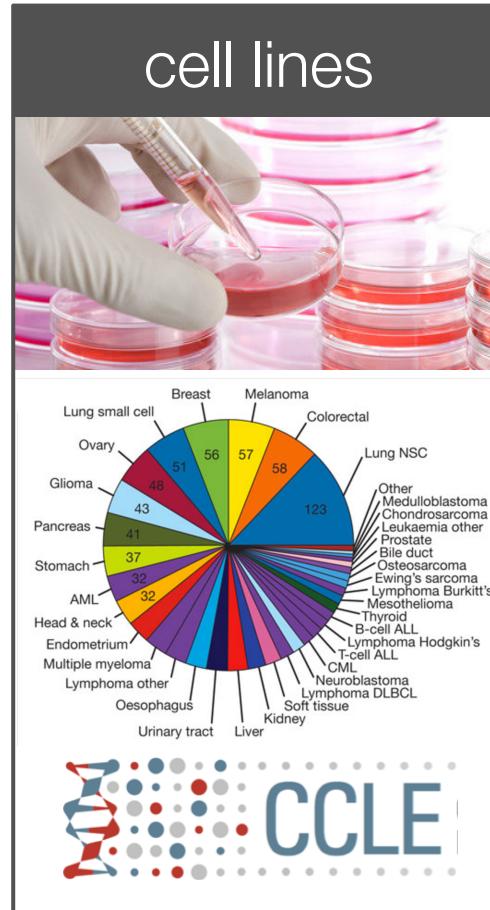
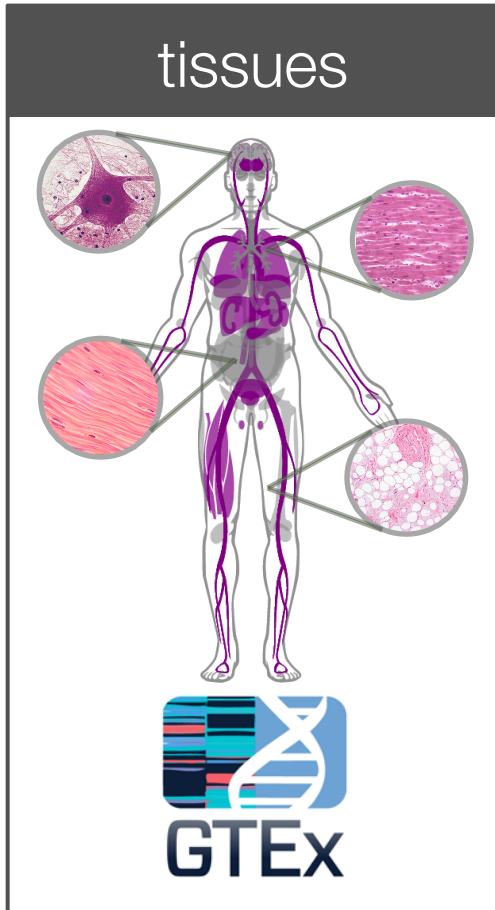
> 2,550 microarray data



... across more than 40 species ...



# ... under different biological conditions ...



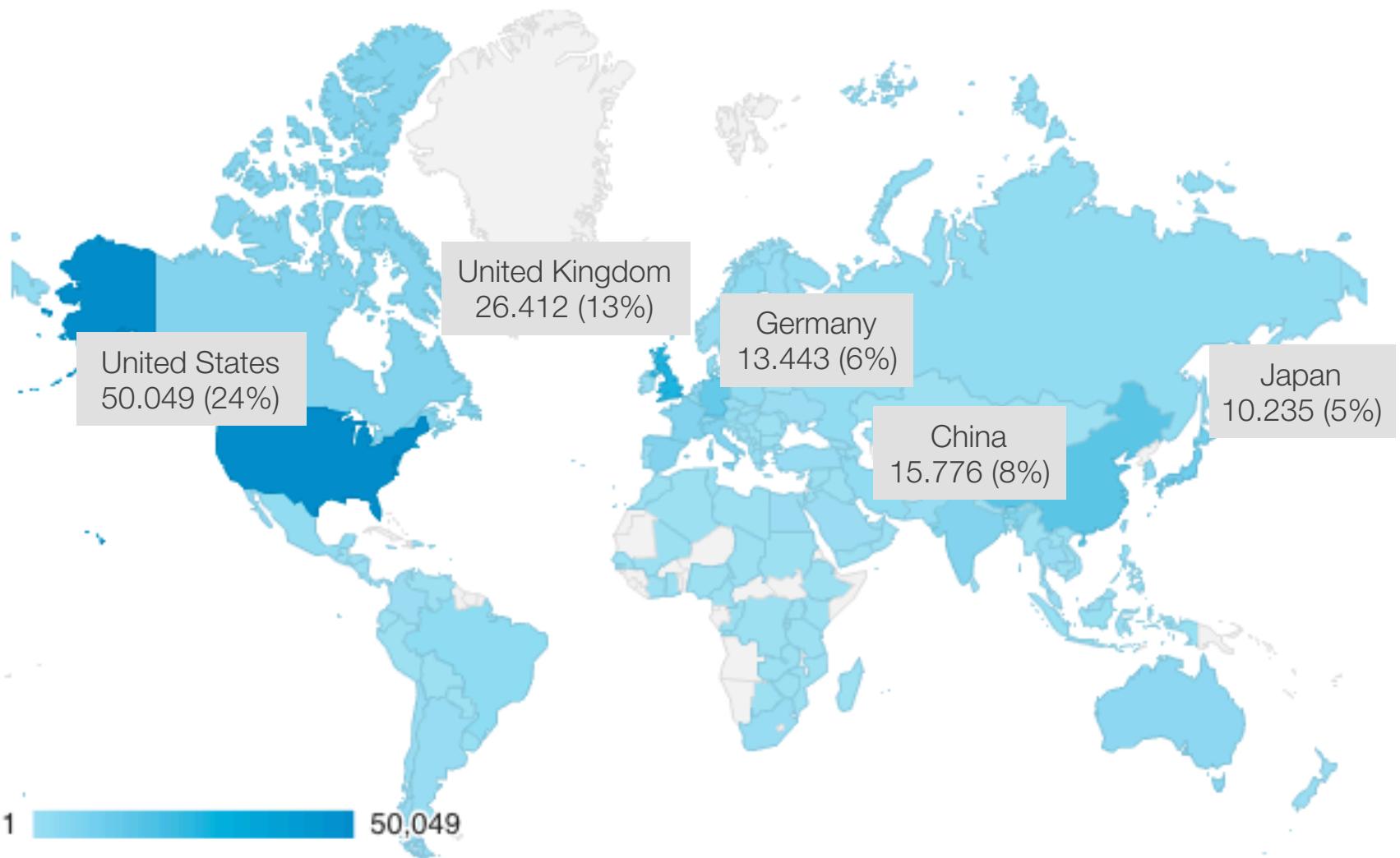
# ... to help scientists find answers ...

In which conditions  
is my favourite gene  
expressed?

What genes are  
differentially expressed in  
a particular condition?

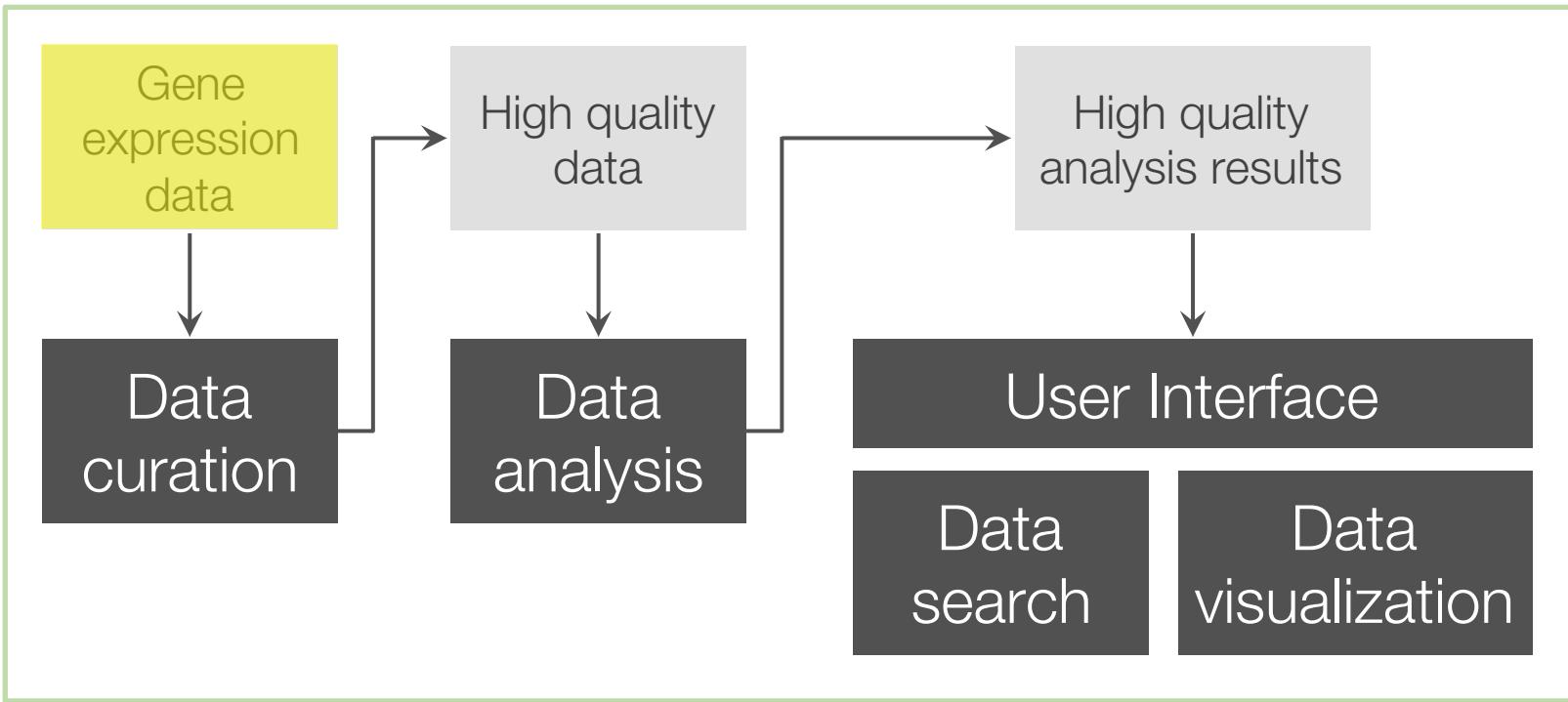
What genes are  
expressed in a  
particular condition?

... all across the world ...





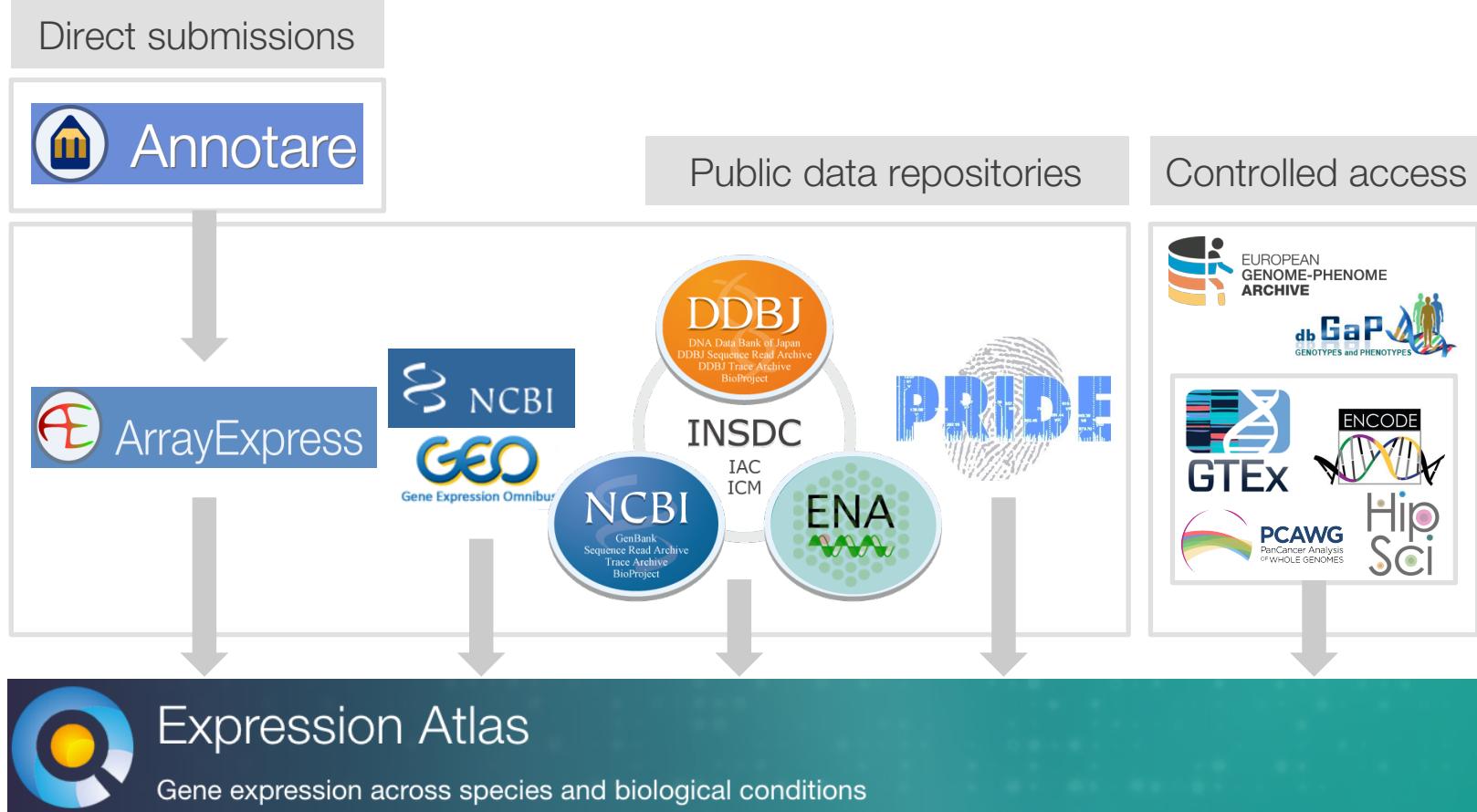
# How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy

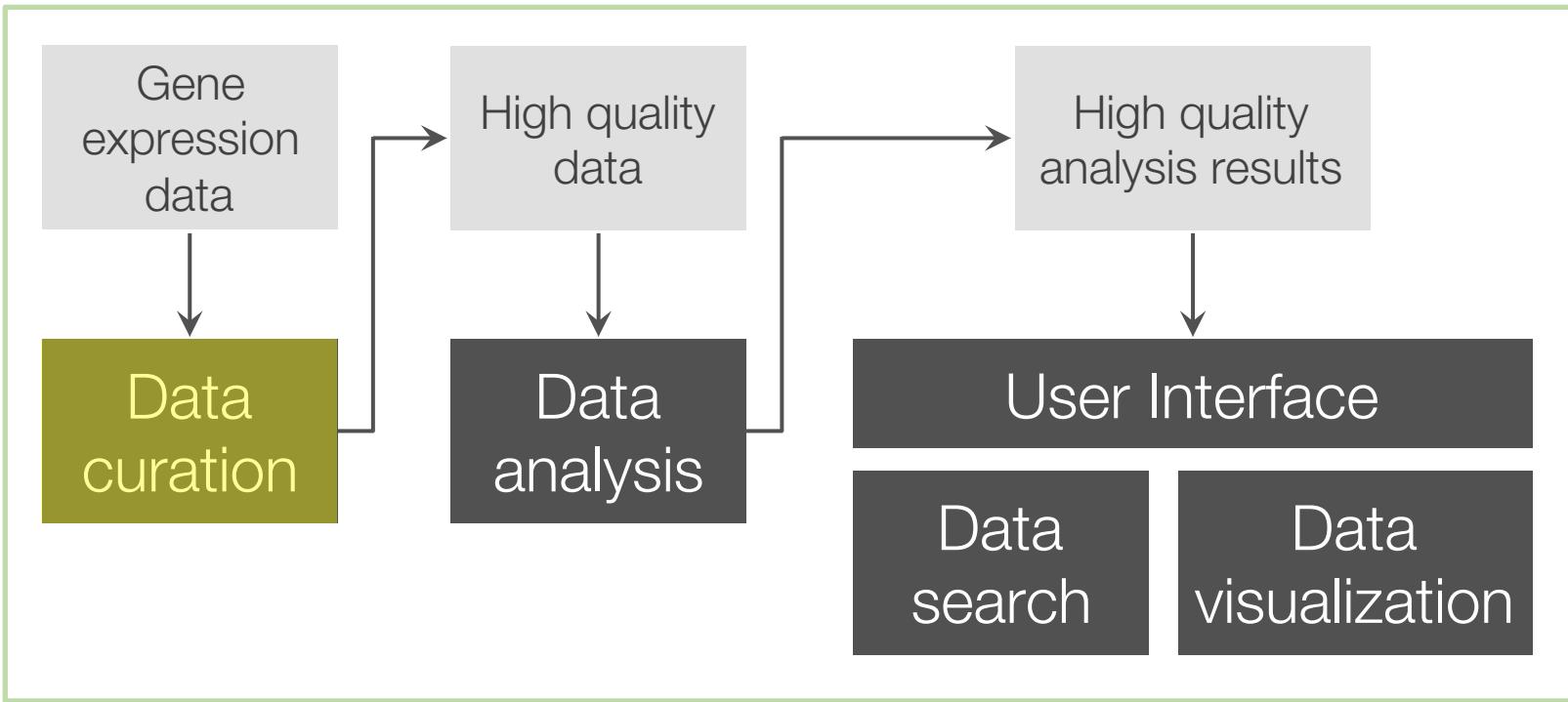


# Where does expression data come from?





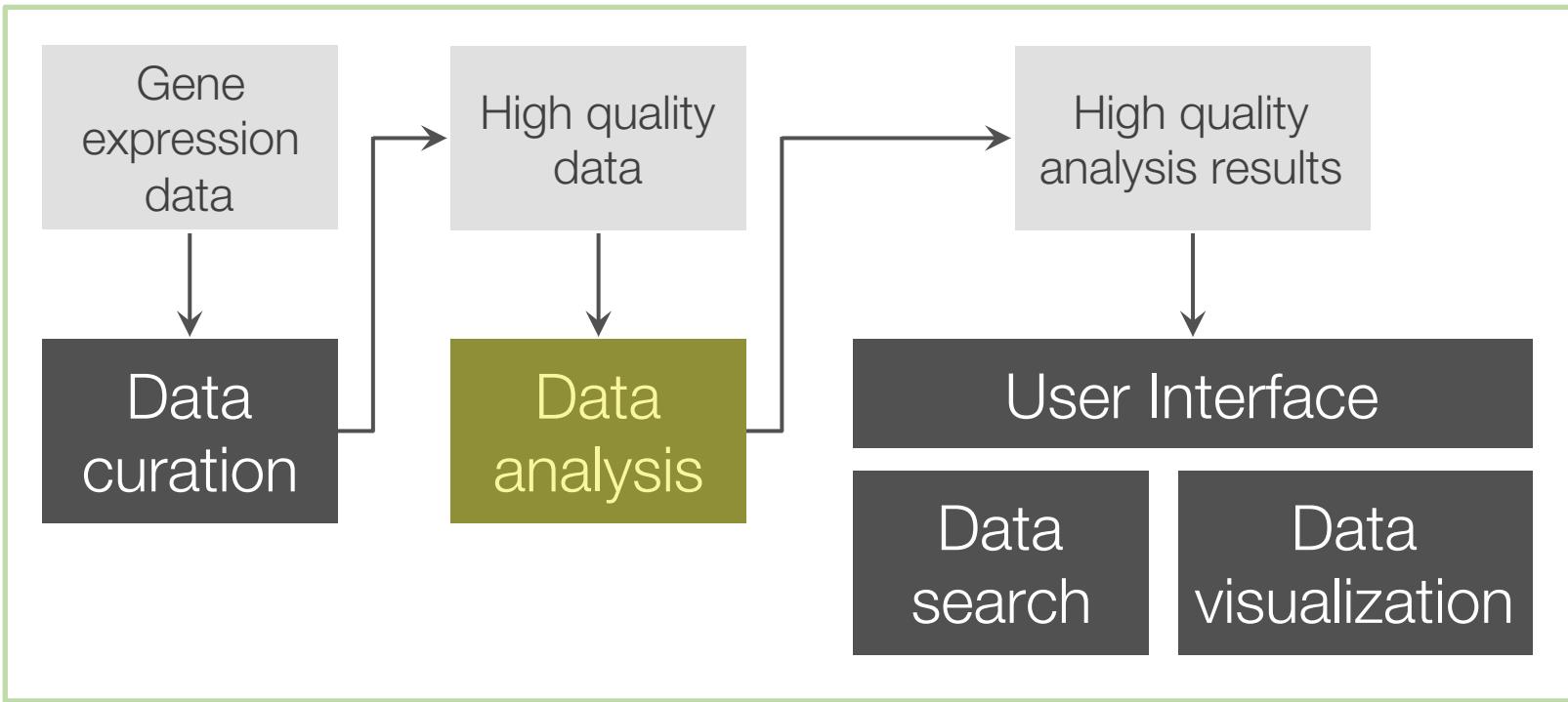
# How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy



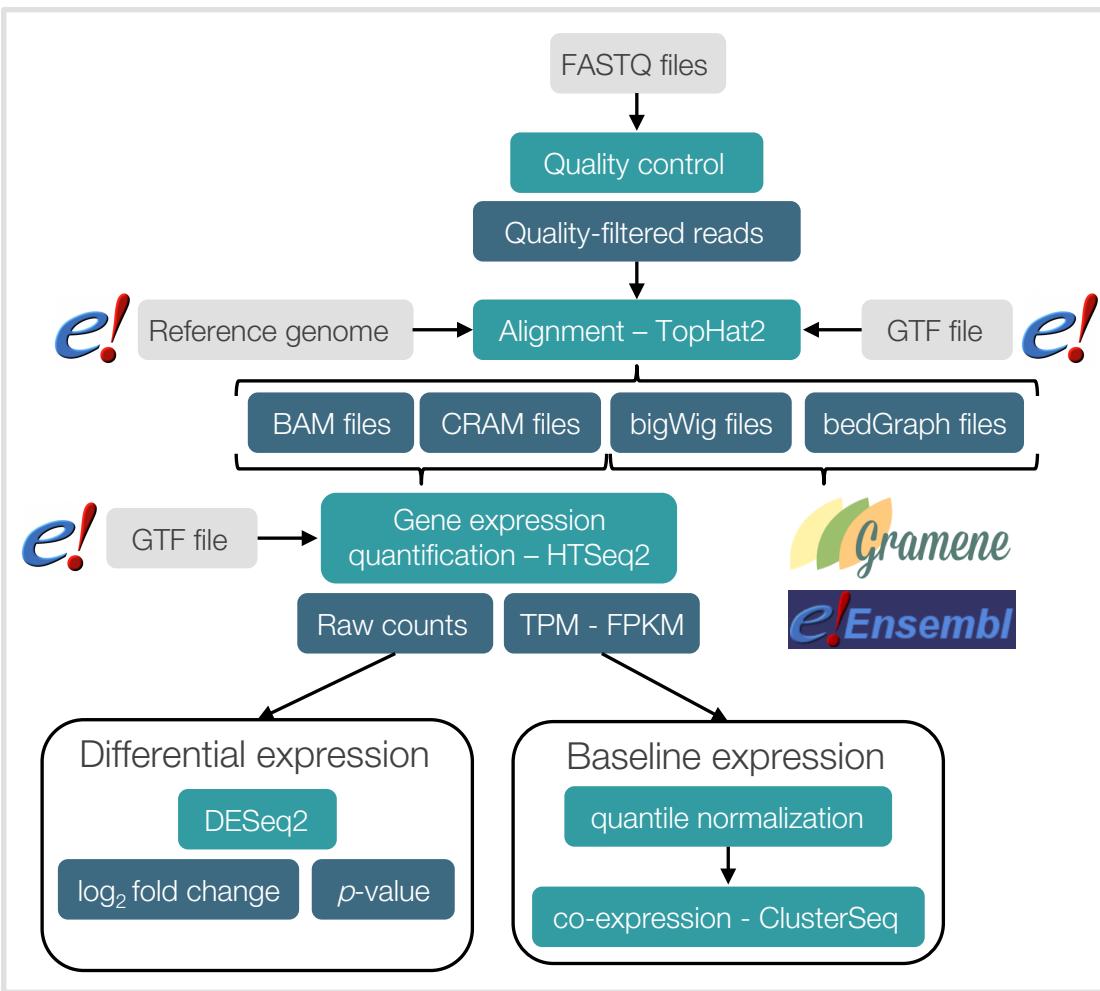
# How does Expression Atlas do it?



Discover and interpret gene expression analysis results quickly and easy



# RNA-seq data analysis



## Pages

[New Page](#)

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

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



# RNA-seq data analysis

## Train online

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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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Attribution-ShareAlike 4.0  
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).

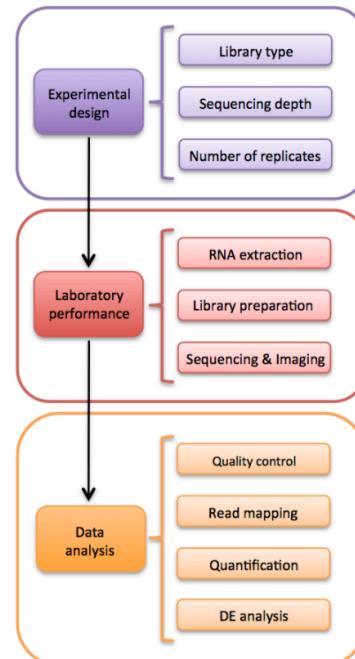


Figure 7 Overview of a RNA-seq experiment for detecting differential expression (DE).

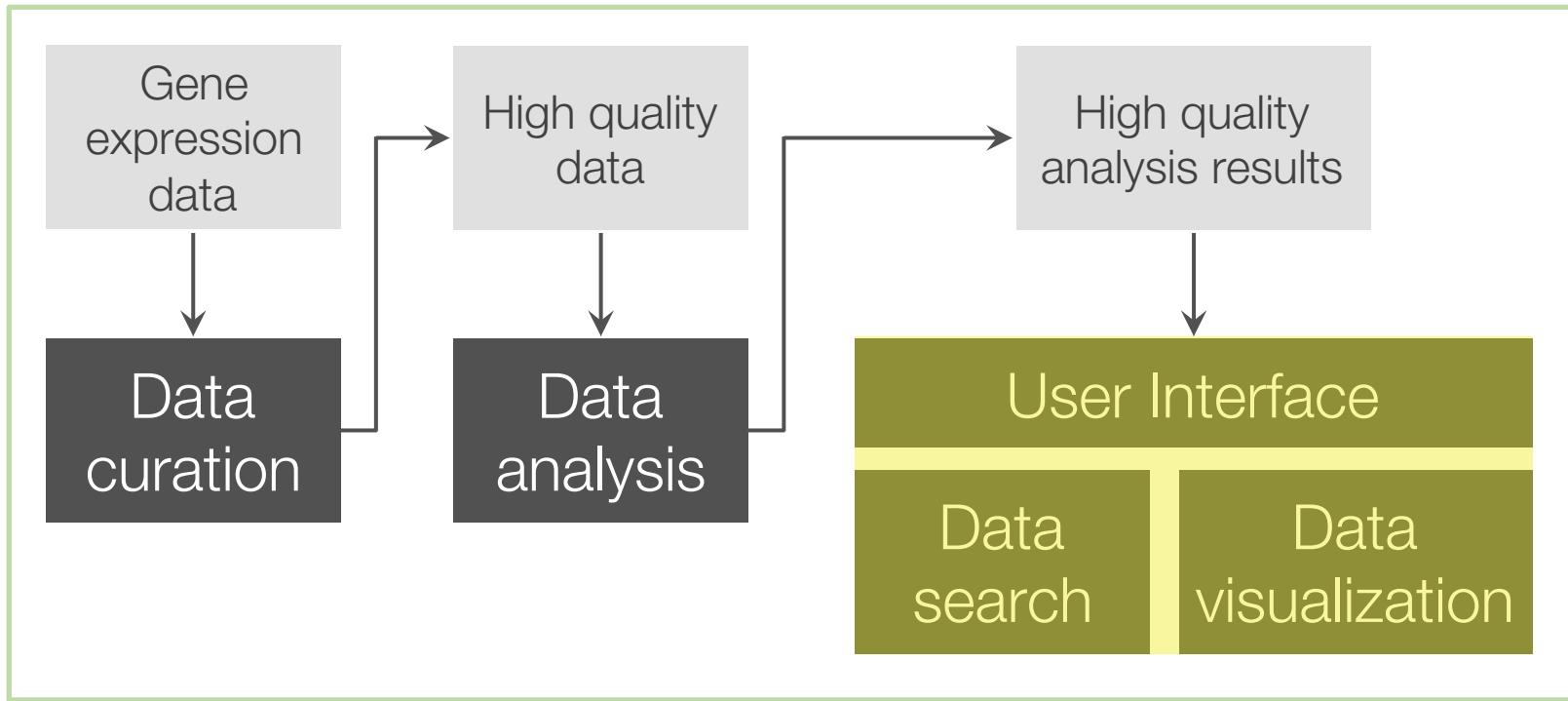
« Applications of RNA-seq

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

Search this project

Enter gene query... Examples: ASPM, Apoptosis, ENSMUSG00000021789, zinc finger

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

[www.ebi.ac.uk/gxa/home](http://www.ebi.ac.uk/gxa/home)



# Let's try Expression Atlas

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[Read more about Expression Atlas](#)

**In which conditions is my favourite gene expressed?**

Gene / Gene properties  
CFHR2 x

CFHR2	symbol
Cfhr2	symbol
cfr2	synonym
Cfr2	
cfr2	

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

Search this project

Enter gene query...  
Examples: ASPM, Apoptosis, ENSMUSG00000021789, zinc finger

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

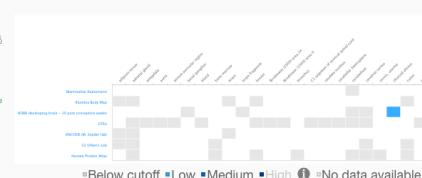
Cell type

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:

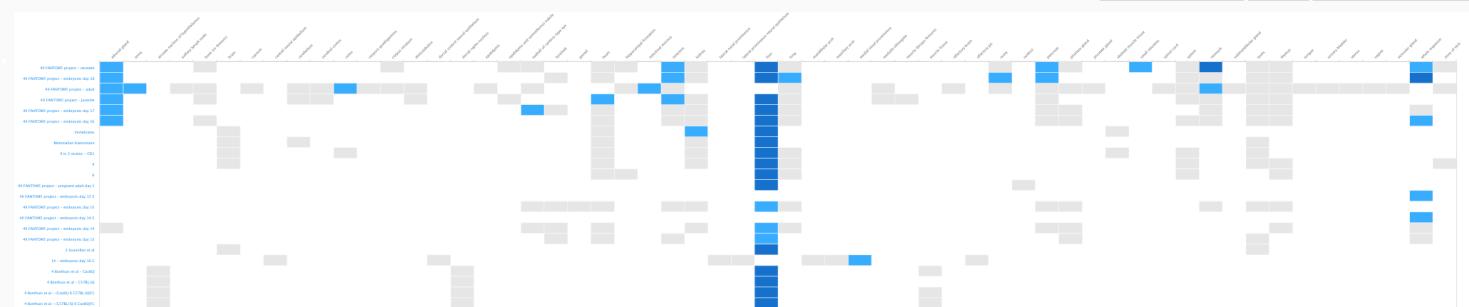
Experiment: 18 White et al  
Experimental condition: larval day 5  
Expression level: 26 FPKM

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

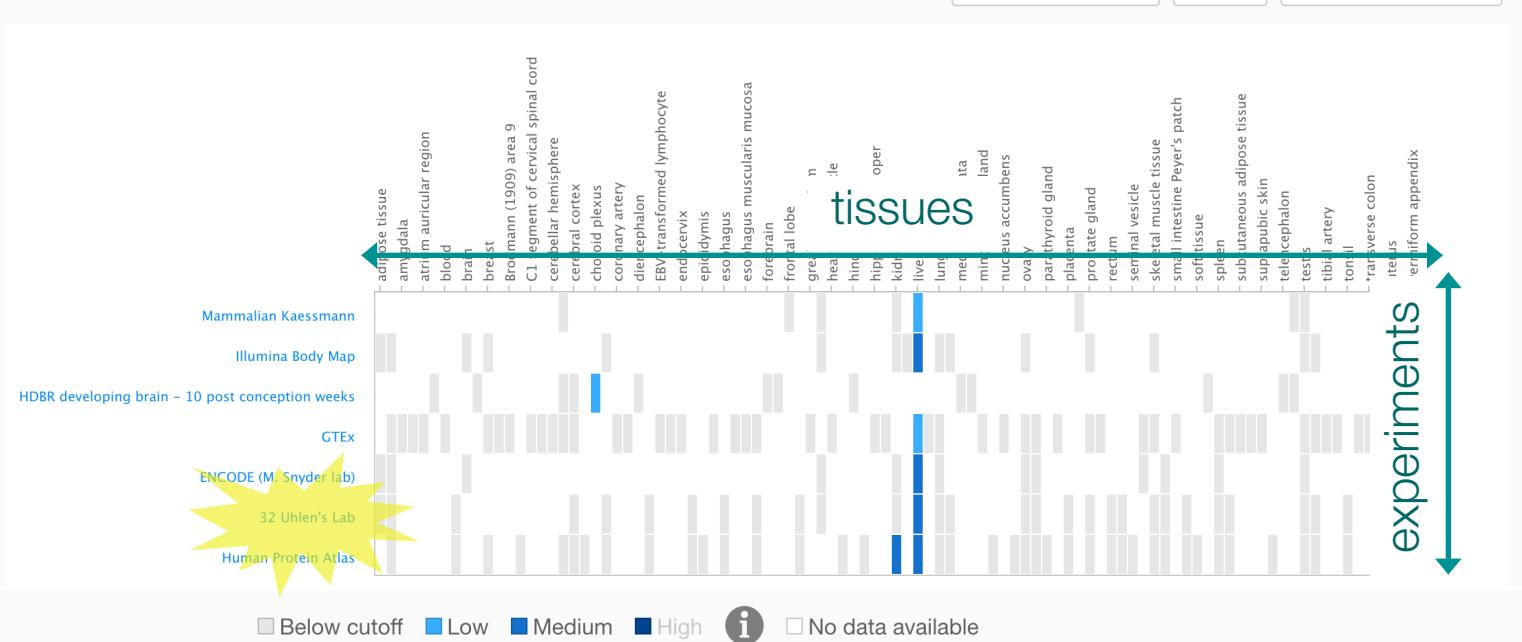
**HEATMAP:** For each species, *CFHR2* gene expression values for the selected condition (columns) in all experiments (rows) in which *CFHR2* gene is expressed

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  
UBRN1  
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

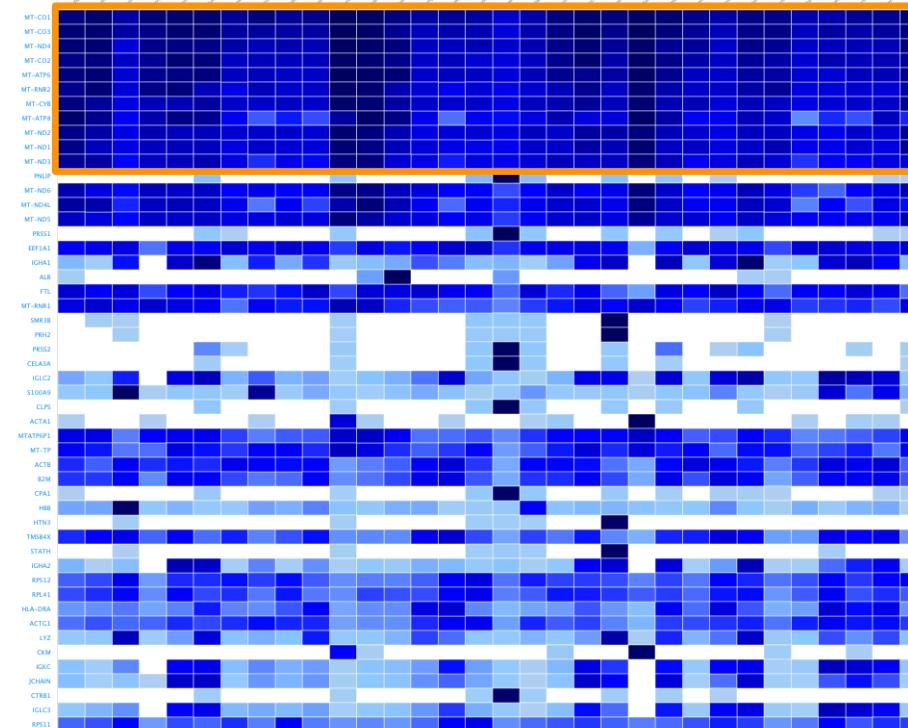
Select

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

Download results

Genes

Showing 50 of 41,210 genes found:



Genes expressed above 0.5 TPM



Select genome browser to view tracks

Download

C1orf68

TUBA3C

SMCP

BOD1L2

F9

AF305872.1

LELP1

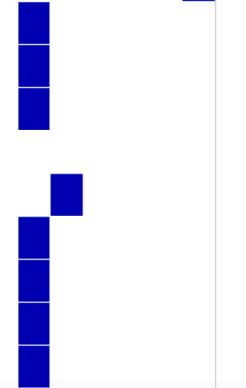
PGK2

ODF1

AKAP4

Expression level of a gene

Gene name: F9  
Organism part: liver  
Expression level: 789 TPM  
Number of biological replicates: 3



Minimum expression level

Expression level

See distribution

Switch data units

TPM

FPKM

See sample annotations

Select

Selected: 32 / 32



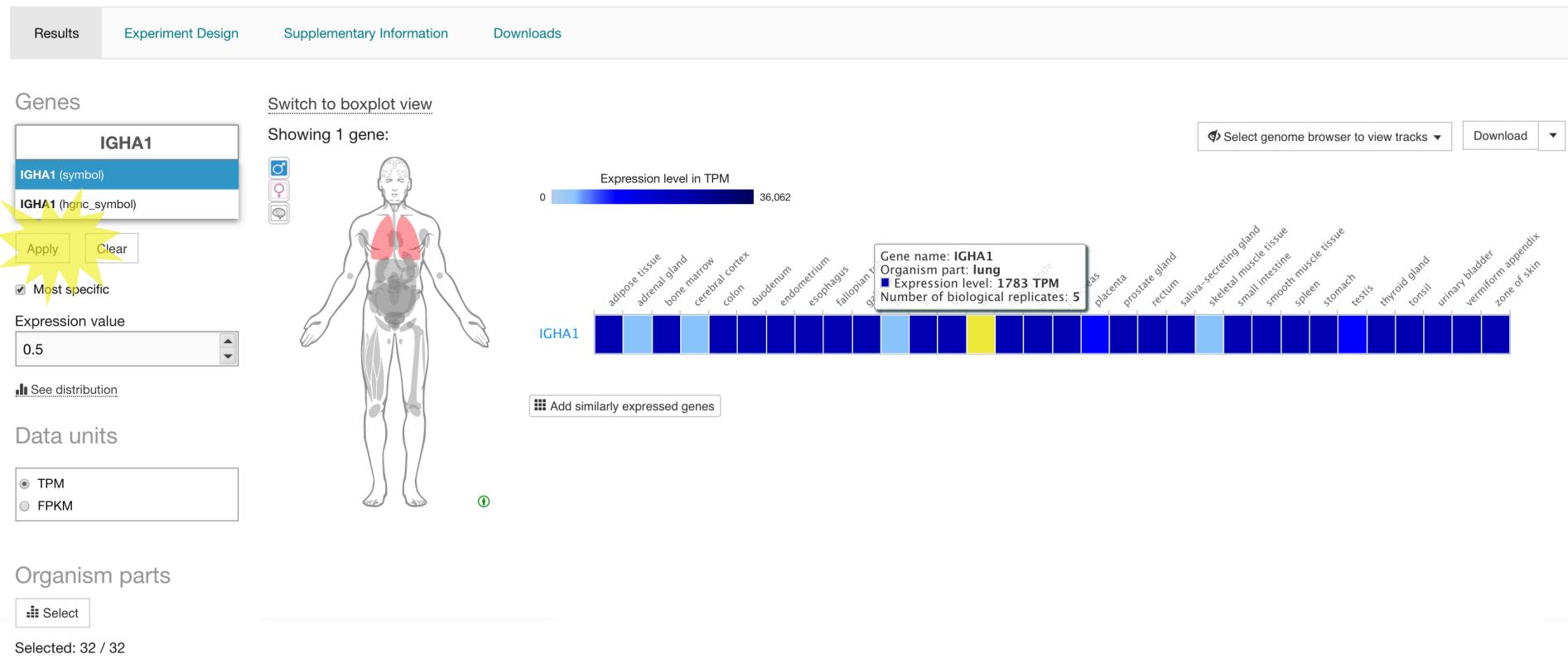
# Baseline experiment page

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)

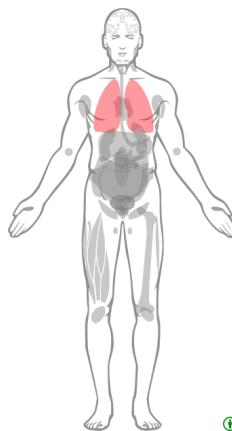
IGHA1 (hgnc\_symbol)

Apply

Clear

Switch to boxplot view

Showing 1 gene:



Most specific

Expression value

0.5

See distribution

### Data units

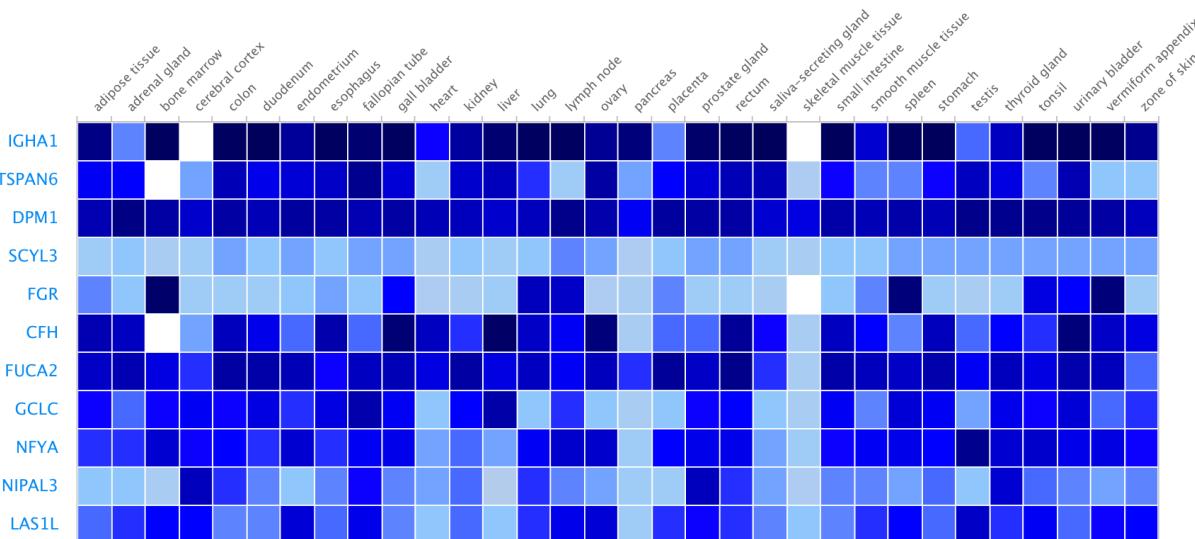
TPM

FPKM

### Organism parts

Select

Selected: 32 / 32



Display genes with similar expression to IGH A1:





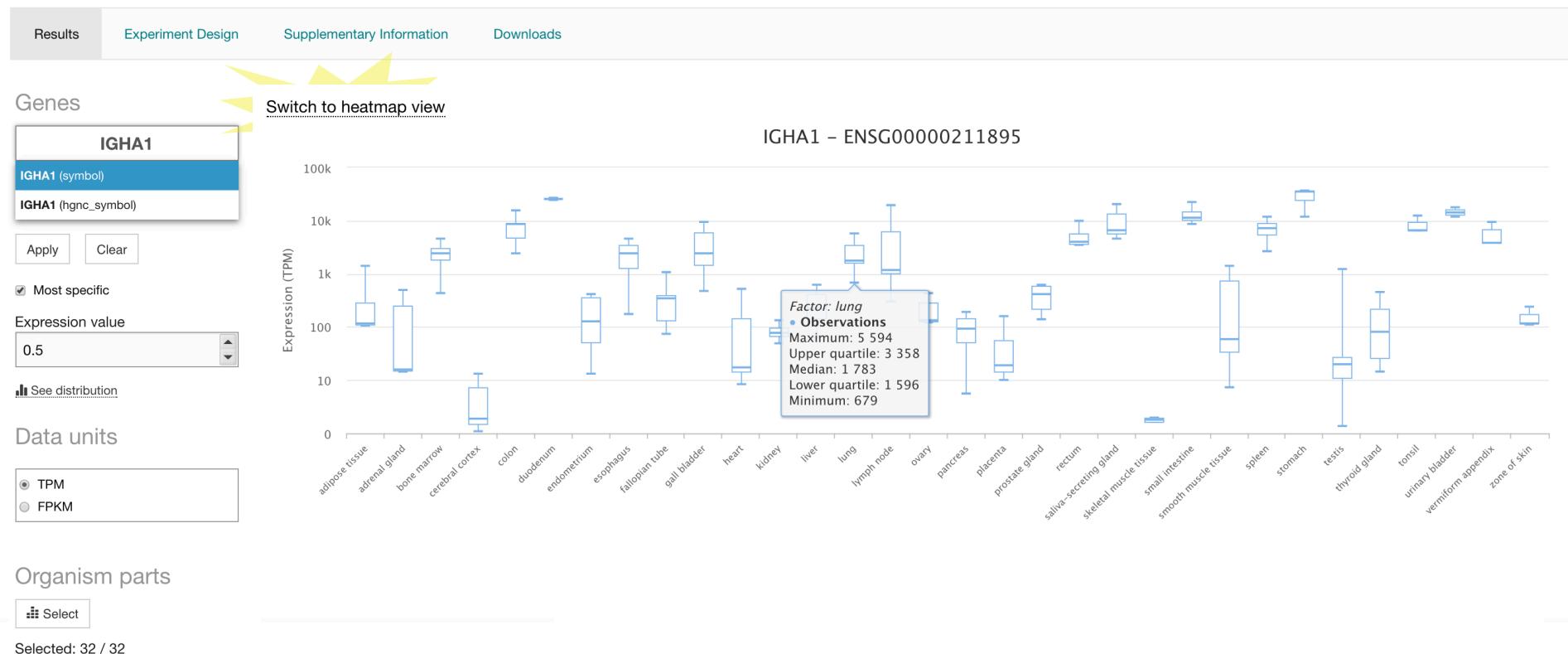
# Baseline experiment page

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



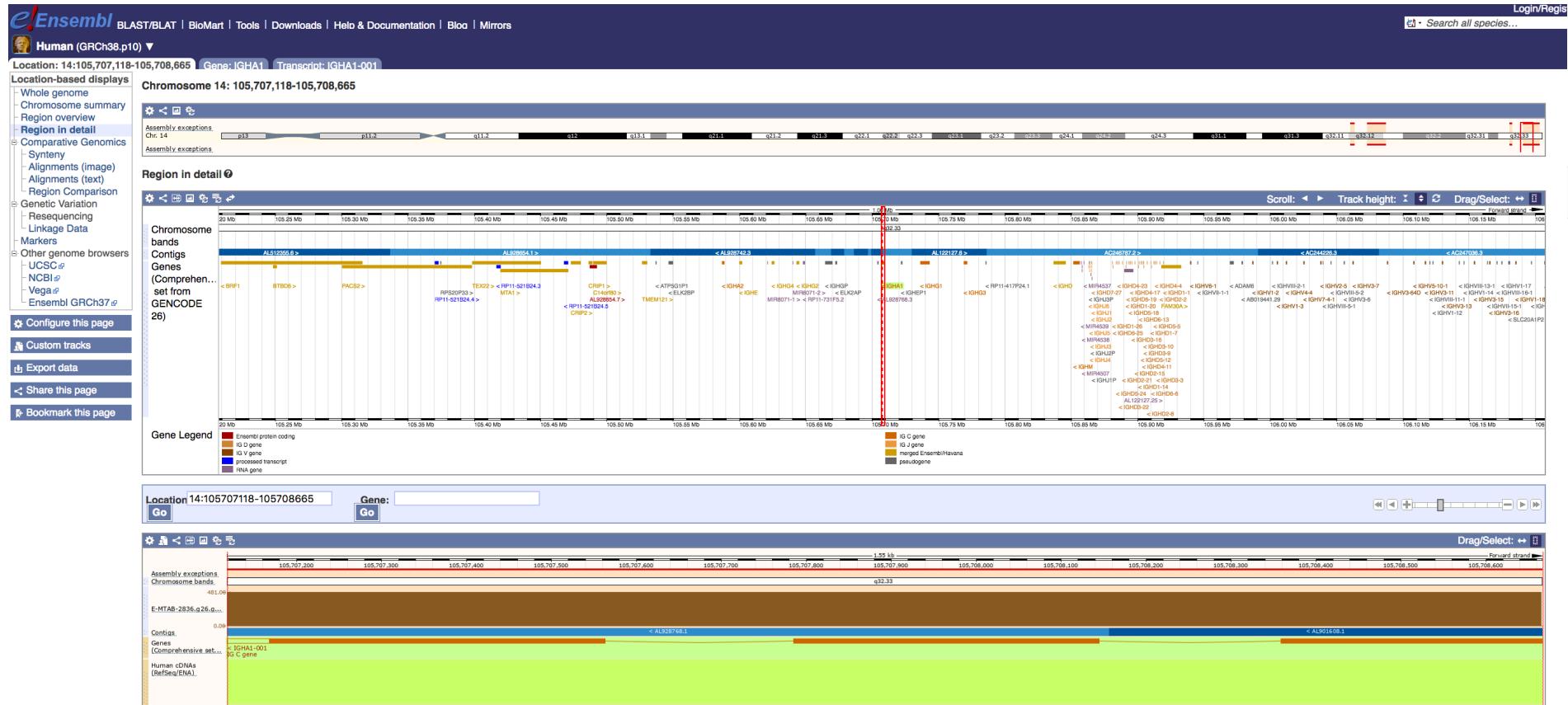
## Organism parts

Select

Selected: 32 / 32



# 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

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

Exploring gene expression results across species under different biological conditions

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[Read more about Expression Atlas](#)

In which conditions is my favourite gene differentially 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



# Differential expression results

Results for CFHR2 (symbol)

Baseline expression Differential expression



Display log<sub>2</sub>-fold change

Filter your results

Experimental variables

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

Log <sub>2</sub> -fold	Species	Gene	Comparison	Experimental variables	Experiment name	
Adjusted p-value	Log <sub>2</sub> -fold change					
1.575 × 10 <sup>-17</sup>	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		<b>Transcriptome analysis of isolated stromal cells and tumor epithelial cells in mouse lung cancer by RNA-Seq</b> 'lung carcinoma' vs 'normal' in 'lung cell'			
	CFH	Property	Test value (N=3)	Reference value (N=3)		
	CFH	cell type	lung cell	lung cell		
	CFH	disease	lung carcinoma	normal		
	CFH	organism	Mus musculus	Mus musculus		
	CFH	organism part	lung	lung		
	CFH	strain	C57BL/6	C57BL/6		
	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

Igkv14-126  
Ighv1-64  
Muc5ac  
Gm43745  
Aldh1a3  
Dio3  
Otc  
BC016579  
D930028M14Rik  
Hoxb6  
Dlk1  
Twist1

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

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

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

Gene name: BC016579  
Disease: lung carcinoma vs normal  
■ Log<sub>2</sub>-fold change: 5.4  
Adjusted p-value:  $4.5153 \times 10^{-11}$   
Click on the cell to show expression in the Genome Browser

## Criteria to select DE genes

Log<sub>2</sub>-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](#)

Log<sub>2</sub>-fold change

-5.5 0



Specific unchecked

Most specific

Up- or downregulated  
 Upregulated only  
 Downregulated only

Log<sub>2</sub>-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)

Results

Plots

Experiment Design

Supplementary Information

Downloads

'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 Nookaew <piano.rpkg@gmail.com>

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

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

Varemo L, Nielsen J and Nookaew 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*

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

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

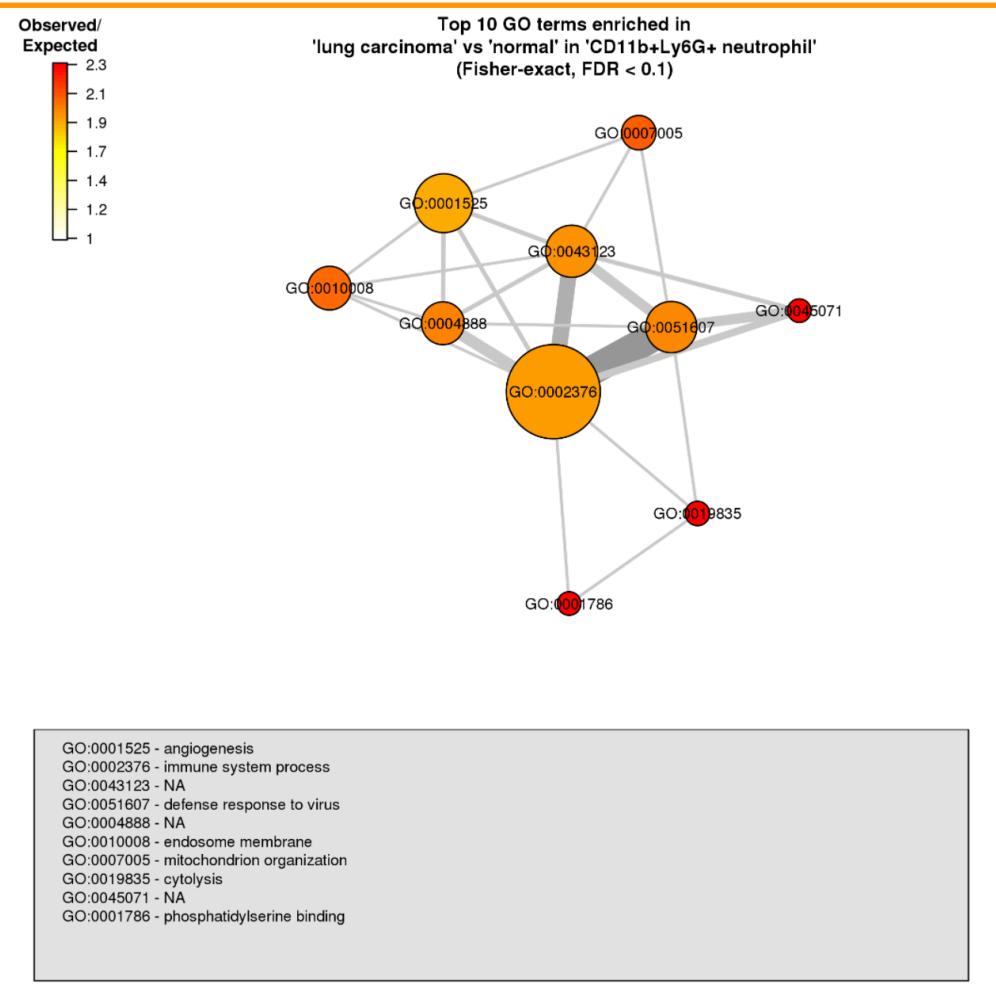
'lung carcinoma' vs 'normal' in 'lung cell'

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	<a href="#">ENST00000367415.6</a>	1059	270aa	Protein coding	<a href="#">CCDS30959</a>	<a href="#">P36980</a>	NM_005666 NP_005657	TSL:1 GENCODE basic APPRIS P2
CFHR2-005	<a href="#">ENST00000476712.6</a>	1020	254aa	Protein coding	-	<a href="#">V9GYE7</a>	-	TSL:3 GENCODE basic APPRIS ALT2
CFHR2-006	<a href="#">ENST00000496448.5</a>	811	No protein	Processed transcript	-	-	-	TSL:2
CFHR2-002	<a href="#">ENST00000473386.1</a>	599	No protein	Processed transcript	-	-	<a href="#">NM_001312672</a>	TSL:1
CFHR2-004	<a href="#">ENST00000489703.1</a>	424	No protein	Processed transcript	-	-	-	TSL:3
CFHR2-003	<a href="#">ENST00000485647.1</a>	376	No protein	Processed transcript	-	-	-	TSL:5



# Let's try Expression Atlas

Differential expression

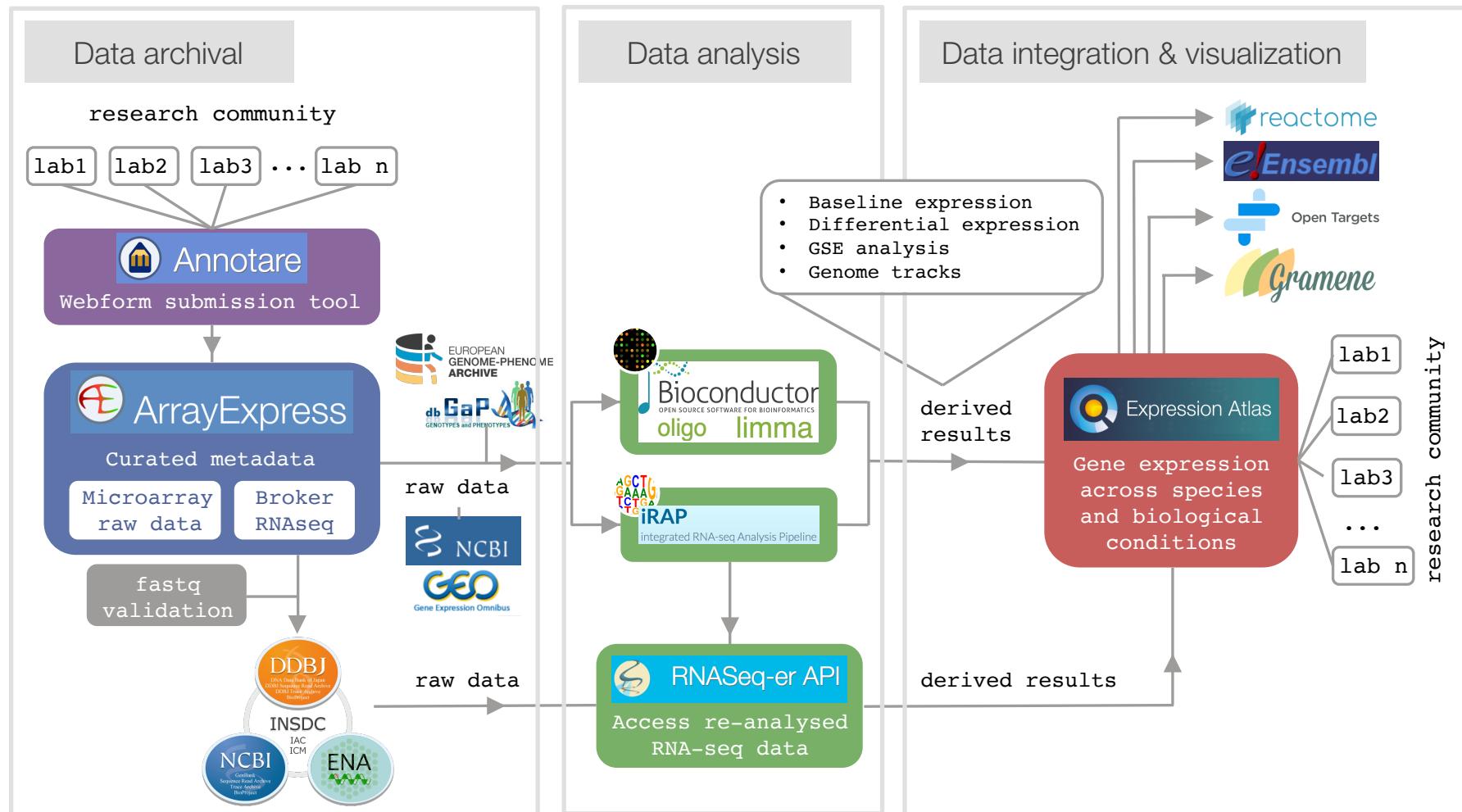
## Hands-on activity

Find differentially expressed genes in patients with hepatocellular carcinoma



In pairs

# Functional genomics resources at EMBL-EBI



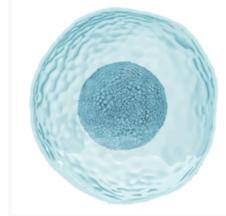


# New project on single-cell...

 Single Cell Expression Atlas

Single-cell gene expression across species

[Home](#) [Browse experiments](#) [Download](#) [Help](#) [About](#)



## 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	<a href="#">Analysis result</a>	
 06-02-2017 Single-cell RNA-sequencing resolves a CD4+ T cell fate bifurcation <i>Mus musculus</i>	752	<a href="#">Analysis result</a>	
 06-02-2017 Single-cell RNA-sequencing of <i>Platynereis dumerilii</i> larval brain cells <i>Platynereis dumerilii</i>	285	<a href="#">Analysis result</a>	

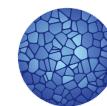
## Marker genes search

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 document 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 second 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](mailto:atlas-feedback@ebi.ac.uk)



@ExpressionAtlas

# Please fill in the survey before you go!

*<https://www.surveymonkey.co.uk/r/VFLSRSD>*



EMBL-EBI workshop: Array Express and Expression Atlas, Feb 2018

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 workshop: Array Express and Expression Atlas

Expression Atlas: gene expression  
results across species and conditions

Laura Huerta, PhD  
Senior Scientific Curator  
[lauhuema@ebi.ac.uk](mailto:lauhuema@ebi.ac.uk)  
7 February 2017

