

① Navigation Bar

② The brief introduction of UCSCXenaShiny v2 and three external links to other pages.

③ 'Daily Gene' Panel: Sample a random gene everyday to query the most related cancer type.

⑧ The release notes of recent main update.

The screenshot shows the UCSCXenaShiny v2 web application interface. At the top is a navigation bar with links for Home, Repository, General Analysis, T•P•C Modules, T•P•C Pipelines, Download, and Help. Below the navigation bar is a 'Welcome to UCSCXenaShiny v2!' message with a brief introduction and three external links (GitHub, Tutorial, About). To the right of the welcome message are three panels: 'Daily Gene' (showing a bar chart for ACY12), 'Pan-Cancer Query' (with a dropdown menu), and 'Download: Obtain custom dataset subset' (a dynamic gallery slide showing a screenshot of the download interface). Below these are two sections for TCGA modules and pipelines, each with three shortcuts. The 'Example TCGA Modules' section includes 'Tumor and Normal Comparison', 'Molecule-Molecule Correlation', and 'Kaplan-Meier Survival Analysis'. The 'Example TCGA pipelines' section includes 'Comparison Analysis', 'Correlation Analysis', and 'Survival Analysis'. At the bottom is a 'Latest significant release notes' section with a list of updates.

④ 'Pan-Cancer Query' Panel: Select one omics molecule to explore its pan-cancer feature. See more details in next page.

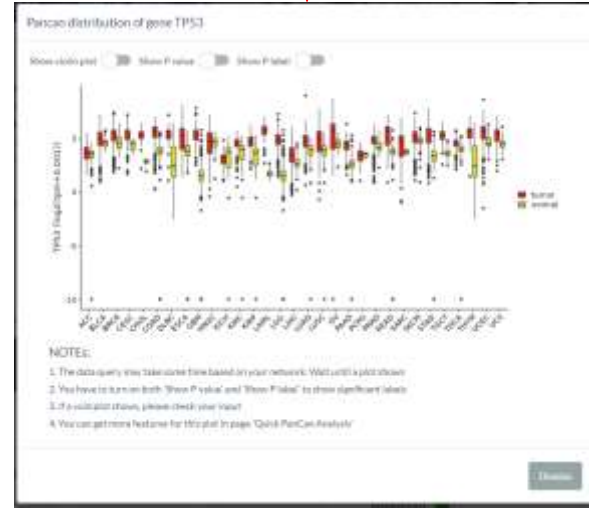
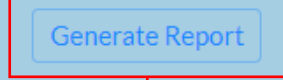
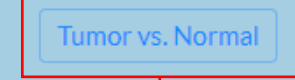
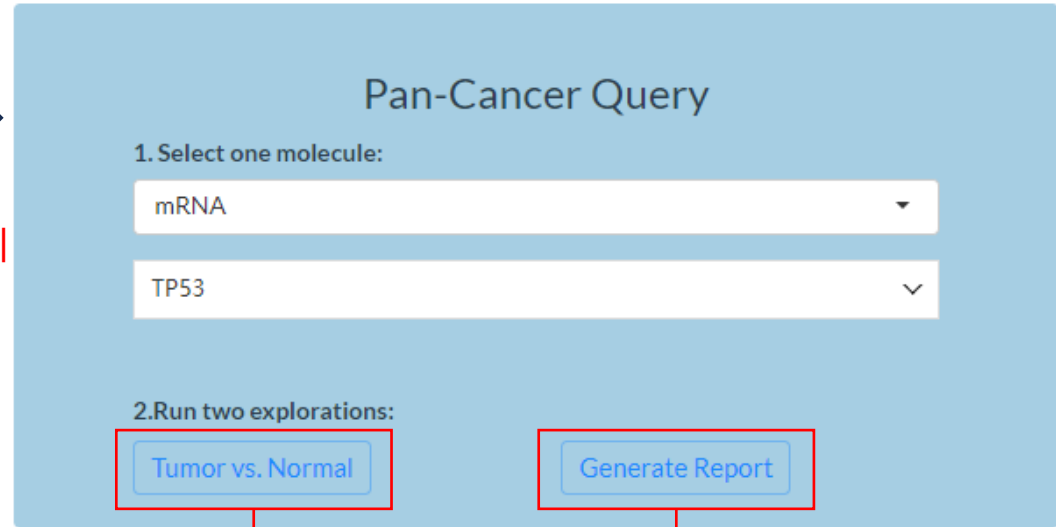
⑤ Dynamic gallery slide to display main function of each tab panel.

⑥ The shortcuts for custom TCGA modules in 'Custom T•P•C Modules' tab panel.

⑦ The shortcuts for personalized TCGA pipelines in 'Personalized T•P•C Pipelines' tab panel.



④ 'Pan-Cancer Query' Panel



4.1 Molecular comparison between tumor and normal.

4.2 Multi-faceted analysis HTML report for one molecule.

① Navigation Bar



③ Filter datasets by data hubs.

How to use repository

Active Data Hub:

- UCSC Public
- TCGA
- GDC
- ICGC
- Pan-Cancer Atlas
- TOIL
- Treehouse
- PCAWG
- ATAC-seq
- Single Cell

④ Filter datasets of one cohort.

Cohort Name:

Data Type:

- Phenotype
- Genomic matrix (e.g., expression)
- Genomic segments
- Mutations

Data Subtype:

Cohort Name:

- ALL
- GDC TCGA Bladder Cancer (BLCA)
- GDC TCGA Lung Squamous Cell Carcinoma (LUSC)
- GDC TCGA Esophageal Cancer (ESCA)
- GDC Pan-Cancer (PANCAN)
- GDC (KAGE1-K)
- GDC MMRF-COMPASS
- GDC TCGA Mesothelioma (MESO)

⑤ Filter datasets by data types.

⑥ Filter datasets by data types.

Data Subtype:

- ALL
- copy number
- phenotype
- copy number (gene-level)
- gene expression RNAseq
- DNA methylation
- stem loop expression
- somatic mutation (SNPs and small INDELS)

② The data frame to display all eligible UCSC Xena datasets.

Show 10 entries Filter with keyword:

| Dataset                       | Hub    | Cohort                         | Samples | Subtype                                  | Label                                | Unit                |
|-------------------------------|--------|--------------------------------|---------|--|--------------------------------------|---------------------|
| TCGA-BLCA.onc.tsv             | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 415     | copy number                              | Copy Number Segment                  | log2(copy-number/2) |
| TCGA-BLCA.GDC_phenotype.tsv   | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 454     | phenotype                                | Phenotype                            |                     |
| TCGA-BLCA.gistic.tsv          | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 413     | copy number (gene-level)                 | GISTIC - focal score by gene         | Gistic2 copy number |
| TCGA-BLCA.htseq_counts.tsv    | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 400     | gene expression RNAseq                   | HTSeq - Counts                       | log2(count+1)       |
| TCGA-BLCA.htseq_fpkm.tsv      | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 400     | gene expression RNAseq                   | HTSeq - FPKM                         | log2(fpkm+1)        |
| TCGA-BLCA.htseq_fpkm-uniq.tsv | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 400     | gene expression RNAseq                   | HTSeq - FPKM-UQ                      | log2(fpkm-uniq+1)   |
| TCGA-BLCA.masked_onc.tsv      | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 415     | copy number                              | Masked Copy Number Segment           | log2(copy-number/2) |
| TCGA-BLCA.methylation450.tsv  | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 437     | DNA methylation                          | Illumina Human Methylation 450       | beta value          |
| TCGA-BLCA.mirna.tsv           | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 432     | stem loop expression                     | miRNA Expression Quantification      | log2(RPM+1)         |
| TCGA-BLCA.muse_snv.tsv        | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 411     | somatic mutation (SNPs and small INDELS) | MUSE Variant Aggregation and Masking |                     |

Showing 1 to 10 of 504 entries

Previous 1 2 3 4 5 ... 54 Next

⑦ Three operations for selected datasets. See more details in next page.

Show Metadata

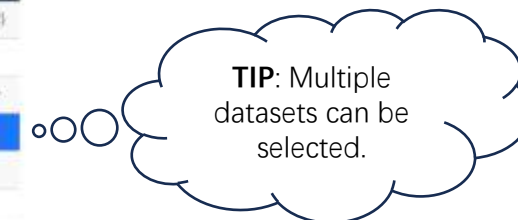
Request Data

Analyze Data

Show 10 entries Filter with keyword:

| Dataset                      | Hub    | Cohort                            | Samples | Subtype                                  | Label                                | Unit                |
|------------------------------|--------|-----------------------------------|---------|--|--------------------------------------|---------------------|
| TCGA-ESCA.cnv.tsv            | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 185     | copy number                              | Copy Number Segment                  | log2(copy-number/2) |
| TCGA-ESCA.GDC_phenotype.tsv  | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 251     | phenotype                                | Phenotype                            |                     |
| TCGA-ESCA.gistic.tsv         | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 185     | copy number (gene-level)                 | GISTIC - focal score by gene         | Gistic2 copy number |
| TCGA-ESCA.htseq_counts.tsv   | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 173     | gene expression RNAseq                   | HTSeq - Counts                       | log2(count+1)       |
| TCGA-ESCA.htseq_fpkm.tsv     | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 173     | gene expression RNAseq                   | HTSeq - FPKM                         | log2(fpkm+1)        |
| TCGA-ESCA.htseq_fpkm-uq.tsv  | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 173     | gene expression RNAseq                   | HTSeq - FPKM-UQ                      | log2(fpkm-uq+1)     |
| TCGA-ESCA.masked.cnv.tsv     | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 185     | copy number                              | Masked Copy Number Segment           | log2(copy-number/2) |
| TCGA-ESCA.methylation450.tsv | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 202     | DNA methylation                          | Illumina Human Methylation 450       | beta value          |
| TCGA-ESCA.mirna.tsv          | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 198     | stem loop expression                     | miRNA Expression Quantification      | log2(RPM+1)         |
| TCGA-ESCA.muse_smts.tsv      | gdchub | GDC TCGA Esophageal Cancer (ESCA) | 183     | somatic mutation (SNPs and small INDELS) | MuSE Variant Aggregation and Masking |                     |

Showing 1 to 10 of 14 entries Previous 1 2 Next

[Show Metadata](#)[Request Data](#)[Analyze Data](#)

Detail information...

| Metadata               | dataset  |
|------------------------|--|
| 1 cohort               | GDC TCGA Esophageal Cancer (ESCA)  |
| 2 url                  | <a href="https://docs.gdc.cancer.gov/Data/Release_Schemas/Data_Release_Notes/Data-release-100">https://docs.gdc.cancer.gov/Data/Release_Schemas/Data_Release_Notes/Data-release-100</a><br><a href="https://api.gdc.cancer.gov/data/">https://api.gdc.cancer.gov/data/</a> |
| 3 probeMap             | genes.csv22.annoGDF1.gene.probeMap   |
| 4 dataSubType          | gene expression RNAseq   |
| 5 label                | HTSeq - Counts   |
| 6 name                 | TCGA-ESCA.htseq_counts.tsv   |
| 7 dataProducer         | Genomic Data Commons   |
| 8 sequencing_procedure | Data from the same sample but from different vial/positions/analyses/ aliquotes is averaged; data from different samples is combined into geneXclMatrix; all data is then log2(x+1) transformed.   |
| 9 type                 | genomicMatrix  |
| 10 wrangler            | Xena GDC ETL script  |

[Download](#)

**6.1** Show the metadata information of selected dataset(s).

Submitted datasets:

| hosts                      | datasets                   | url   | browse  |
|----------------------------|----------------------------|---|---|
| 1 https://gdc.xenahubs.net | TCGA-ESCA.htseq_counts.tsv | <a href="https://gdc.xenahubs.net/download/TCGA-ESCA.htseq_counts.tsv.gz">https://gdc.xenahubs.net/download/TCGA-ESCA.htseq_counts.tsv.gz</a> | <a href="https://xenabrowser.net/track/TCGA-ESCA.htseq_counts.tsv5/h">https://xenabrowser.net/track/TCGA-ESCA.htseq_counts.tsv5/h</a> |

[Download data directly](#)
[Batch download in terminal](#)
[Copy R download code](#)

[Dismiss](#)

**6.2** Provide different ways to download the selected dataset(s).

**6.3** Switch to 'General Dataset Analysis' Panel to perform general analysis based on the selected dataset(s).



① Navigation Bar

② Confirm that whether to select the appropriate dataset(s).

③ Select one of analytical methods.

④ Set the analytical parameters and, then submit the analysis.

⑤ Show the analytical result and data.

⑥ Download the plot result.

The screenshot displays the 'General Dataset Analysis' web application interface. At the top is a navigation bar with links for Home, Repository, General Dataset Analysis, Custom T·P·C Modules, Personalized T·P·C Pipelines, PharmacoGenomics Analysis, Download, Help, and Developers. Below the navigation bar, there are buttons for 'Pre-selected Datasets for Analysis', 'Upload your data?', and 'How to use'. The main content area is divided into several sections:

- Analysis Controls:** A panel on the left with dropdown menus for 'Select dataset for axis X:' (TCGA-ESCA.htseq\_counts.tsv), 'Dataset 1 molecule identifier:' (TP53), 'Select dataset for axis Y:' (TCGA-ESCA.htseq\_counts.tsv), and 'Dataset 2 molecule identifier:' (KRAS). It also has a 'Use ggstatsplot?' toggle and a 'Submit' button. A note states: 'NOTE: The data table is not available when use ggstatsplot.'
- Scatter Plot:** A central plot showing a positive correlation between TP53 (X-axis) and KRAS (Y-axis). The plot includes a blue regression line and the statistics  $R = 0.16, p = 0.041$ . Below the plot are buttons for 'Download Current Page' and 'Download Full Results', and a search bar.
- Sample Filters:** A panel on the right with a 'Select phenotype dataset:' dropdown (set to NONE) and a 'Click to filter!' button. Below it are input fields for 'Height' (8) and 'Width' (10), a 'Choose plot format' section with radio buttons for 'png' (selected) and 'pdf', and a 'Download' button.
- Data Table:** A table below the plot showing sample data. The table has columns for 'sample', 'X', and 'Y'. The data rows are:

| sample           | X     | Y     |
|------------------|-------|-------|
| TCGA-LN-A210-01A | 12.56 | 11.67 |
| TCGA-2H-A9GK-01A | 10.72 | 12.49 |
| TCGA-LN-A4A4-01A | 11.62 | 13.3  |
| TCGA-L5-A40I-01A | 13.13 | 13.02 |
| TCGA-L5-A40M-01A | 10.59 | 12.95 |

TIP: Filter samples based on phenotype.

① Navigation Bar

The screenshot displays the UCSCXenaShirry v2 web interface. At the top is a navigation bar with links for Home, Repository, General Dataset Analysis, Custom T-P-C Modules, Personalized T-P-C Pipelines, PharmacoGenomics Analysis, Download, Help, and Developers. Below the navigation bar, there are two tabs: "Tumor VS Normal (Box plot)" and "Tumor VS Normal (Anatomy plot)". The "Tumor VS Normal (Box plot)" tab is active, showing a configuration panel on the left and a box plot on the right. The configuration panel includes: 1. Select omics type: mRNA Expression; 2. Select omics molecule: TP53; 3. Select analysis mode: Pan-cancer; 4. Include GTEx normal samples: Yes. A "Go" button is at the bottom of the configuration panel. The box plot shows TP53 expression levels (log2(tpm + 0.001)) across various cancer types, comparing tumor (red) and normal (yellow) samples. A legend indicates "tumor" in red and "normal" in yellow. A top-right widget allows for adjusting plot parameters and downloading results. A dashed red line connects this widget to a callout box on the right. A "TIPs" section at the bottom of the plot area reads: "TIPs: Pull the sidebar to adjust plot parameters or download results through the top-right widget."

③ Select one specific module.

④ Set the analytical parameters and, then submit the analysis.

② Select one type of modules.

⑥ Adjust plot parameters and download results. See more details in next page.

⑤ Show the analytical result plot.



**6.1** Adjust plot parameters and resubmit the analysis to update the plot.

Analytical results:

1. Visualization parameters

(1) Geometry type:  
 Boxplot  Violinplot

(2) Label type:  
 None  P value  P label

(3) Colors:

Tumor sample color  
#DF2020

Normal sample color  
#DDDF21

(4) ggplot theme:  
Select theme for plot  
Cowplot

2. Download options

(1) Figure:  
Height: 5  
Width: 12  
Format:  pdf  png  
Download

(2) Data table:  
Download

Tips: Pull the sidebar to adjust plot parameters or download results through the top-right widget.

**6.2** Download the result plot and analytical data.

① Navigation Bar

③ Select one specific mode of pipelines.

④ Prepare the sample range and tumor data through S1 step.

⑤ Fetch the analytical data through S2 step.

② Select one type of pipelines.

⑥ Set parameters; submit analysis and download results through S3 step.

UCSCxenaShiny v2

TCGA: Correlation Analysis  
TCGA: Comparison Analysis  
TCGA: Survival Analysis  
TCGA: Cross-Domain Analysis  
TCGA: Correlation Analysis  
TCGA: Comparison Analysis  
TCGA: Survival Analysis  
TCGA: Correlation Analysis  
TCGA: Comparison Analysis

Sole Analysis for Single Cancer  
Sole Analysis for Multiple Cancers

S1: Preset

S1.1 Modify datasets [opt]

mRNA Expression

([Normalization method])  
RSEM TPM  
RSEM FPKM  
RSEM Norm\_Count

Active Data Hub: [Full Hub](#)  
Active Data Set: [TCGA: Target, Lines, Tumor, Gene, Jctns](#)

S1.2 Choose cancer

ACC

S1.3 Filter samples [opt]

Quick filter:  
TP (primary tumor)

Exact filter:  
TP: 60 samples are included

S1.4 Upload metadata [opt]

Browse... No files uploaded

S1.5 Add signature [opt]

Edit

S2: Get data for X-axis

Data type: Molecular profile  
Data subtype: mRNA Expression

Identifier: TP53

Show: 3 entries

| Sample            | value | cancer |
|-------------------|-------|--------|
| 1: TCGA-OR-AS1-01 | 3.318 | ACC    |
| 2: TCGA-OR-AS2-01 | 1.8   | ACC    |
| 3: TCGA-OR-AS3-01 | 4.041 | ACC    |

Showing 1 to 3 of 77 entries

S2: Get data for Y-axis

Data type: Immune infiltration  
Data subtype: CIBERSORT

Identifier: Monocyte

Show: 3 entries

| Sample            | value | cancer |
|-------------------|-------|--------|
| 1: TCGA-OR-AS1-01 | 0.098 | ACC    |
| 2: TCGA-OR-AS2-01 | 0.022 | ACC    |
| 3: TCGA-OR-AS3-01 | 0.038 | ACC    |

Showing 1 to 3 of 77 entries

S3: Analyze & Visualize

S3.1 Set analysis parameters  
Correlation method: Spearman

S3.2 Set visualization parameters  
Line color: #0000FF  
Hit color (x): #008000  
Hit color (y): #D2691E

Other options

Run

ACC  
Spearman = -0.001, p = 9.965e-01

Monocyte

TP53

S3.3 Download results  
Force  
New tab (copy)  
Statistical (download)



① Navigation Bar

③ Download molecular data of TPC samples

② Download raw data based on integrated TPC analysis

④ Download other meta-data of TPC samples, directly.

UCSCXenaShiny v2

Home Repository General Dataset Analysis Custom TPC Modules Personalized TPC Pipelines Pharmacogenomics Analysis Download Help

### Part1: Download molecular data

1. Select one database

TCGA (DE) PCAWG CCLE

ncRNA Expression

1) Normalization method

- RSEM TPM
- RSEM FPKM
- RSEM Name\_Count

Active Data Hub: [tshub](#)

Active Data Set: [TsgTargetGene\\_name\\_gene\\_tpc](#)

2. Select samples

Quick filter: ACC, BICA, BRCA, COAD, LIHC, LGG, ... NL, TAM, TAP, TB, TH, TITR

Exact filter:

3. Select identifiers

Data type: Molecular profile

Data subtype: ncRNA Expression

Choose multi-ids by:  Selected  All  File

TP53

Tip: 1. Genes: 145 are selected.

Tip: 2. Ids are queried successfully!

4. Download results

Download table (raw) Download table (norm)

NOTES:

- To get the whole dataset, please click 'Repository' page and download directly from UCSC website.
- Queried data in long format is for easy display and it is downloaded as the wide format.

|    | Gene | Sample          | Value |
|----|------|-----------------|-------|
| 1  | TP53 | TCGA-02-0047-01 | 5.799 |
| 2  | TP53 | TCGA-02-0055-01 | 4.420 |
| 3  | TP53 | TCGA-02-2489-01 | 6.515 |
| 4  | TP53 | TCGA-02-2485-01 | 6.309 |
| 5  | TP53 | TCGA-04-1331-01 | 3.856 |
| 6  | TP53 | TCGA-04-1332-01 | 5.294 |
| 7  | TP53 | TCGA-04-1337-01 | 5.706 |
| 8  | TP53 | TCGA-04-1328-01 | 5.992 |
| 9  | TP53 | TCGA-04-1341-01 | 4.005 |
| 10 | TP53 | TCGA-04-1343-01 | 3.294 |

### Part2: Download other data

1. TCGA database

Inquire Refinement

- Download CIBERSORT Load
- Download CIBERSORT\_ABS Load
- Download EPC Load
- Download MFC\_COUNTER Load
- Download QUANTILE\_Q Load
- Download TMRW Load
- Download XCELL Load

2. PCAWG database

Basic Phenotype data

- Download Basic Phenotype Load

3. CCLE database

Basic Phenotype data

- Download Basic Phenotype Load

① Navigation Bar

UCSCXenaShiny v2 [Home](#) [Repository](#) [General Dataset Analysis](#) [Custom T-P-C Modules](#) [Personalized T-P-C Pipelines](#) [PharmacoGenomics Analysis](#) [Download](#) [Help](#) [Developers](#)

③ Select the main type (Level 1) of identifiers.

Omics molecule identifiers

- 1. TCGA Molecular profile
- 2. PCAWG Molecular profile
- 3. CCLE Molecular profile

Other non-omics identifiers

- 4. Tumor index
- 5. Immune Infiltration
- 6. Pathway activity

④ Select the subtype (Level 2) of identifiers.

Gene Protein Mutation CNV Transcript Methylation(450K) Methylation(27K) miRNA

Show 10 entries

|    | Level2          | Level3       | Ensembl           | chrom | chromStart | chromEnd | str |
|----|-----------------|--------------|-------------------|-------|------------|----------|-----|
| 1  | mRNA Expression | DDX11L1      | ENSG00000223972.5 | chr1  | 11869      | 14409    | +   |
| 2  | mRNA Expression | WASH7P       | ENSG00000227232.5 | chr1  | 14404      | 29570    | -   |
| 3  | mRNA Expression | MIR6859-1    | ENSG00000278267.1 | chr1  | 17369      | 17436    | -   |
| 4  | mRNA Expression | RP11-34P13.3 | ENSG00000243485.3 | chr1  | 29554      | 31109    | +   |
| 5  | mRNA Expression | MIR1302-2    | ENSG00000274890.1 | chr1  | 30366      | 30503    | +   |
| 6  | mRNA Expression | FAM138A      | ENSG00000237613.2 | chr1  | 34554      | 36081    | -   |
| 7  | mRNA Expression | OR4G4P       | ENSG00000268020.3 | chr1  | 52473      | 53312    | +   |
| 8  | mRNA Expression | OR4G11P      | ENSG00000240361.1 | chr1  | 62948      | 63887    | +   |
| 9  | mRNA Expression | OR4F5        | ENSG00000186092.4 | chr1  | 69091      | 70008    | +   |
| 10 | mRNA Expression | RP11-34P13.7 | ENSG00000238009.6 | chr1  | 89295      | 133723   | -   |

Showing 1 to 10 of 60,498 entries

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⑤ Show the metadata information of corresponding identifiers (Level3).

② Search the integrated identifiers of TPC data

Quick Guide  
Tutorial Book  
TPC ID Query  
Citation  
UCSCXenaShiny v1