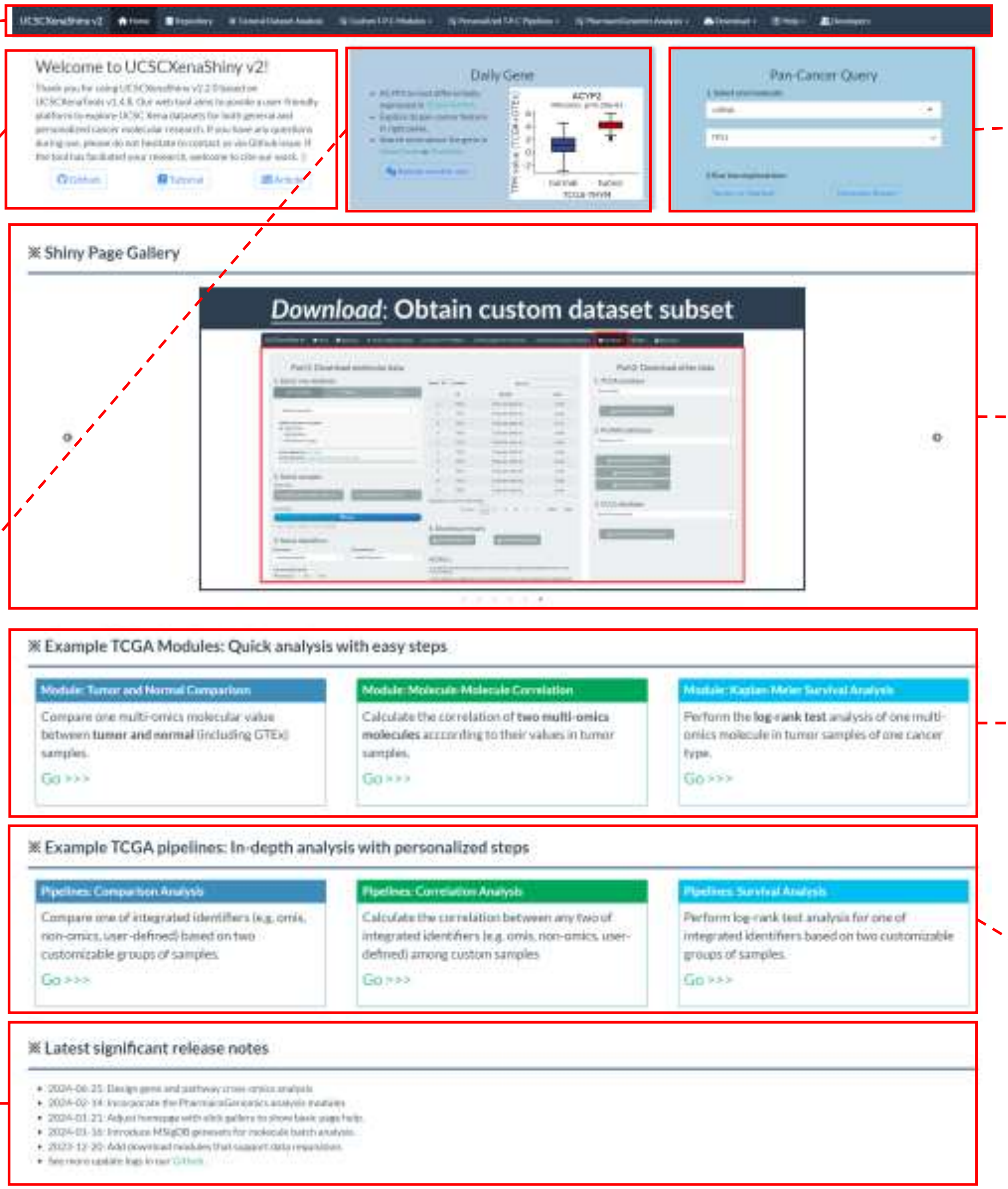


※ Example TCGA Modules: Quick analysis with easy steps

**Module: Tumor and Normal Comparison**
Compare one multi-omics molecular value between **tumor and normal** (including GTEx) samples.
Go >>>

**Module: Molecule-Molecule Correlation**
Calculate the correlation of **two multi-omics molecules** according to their values in tumor samples.
Go >>>

**Module: Kaplan-Meier Survival Analysis**
Perform the **log-rank test** analysis of one multi-omics molecule in tumor samples of one cancer type.
Go >>>

※ Example TCGA pipelines: In-depth analysis with personalized steps

**Pipelines: Comparison Analysis**
Compare one of integrated identifiers (e.g. omis, non-omics, user-defined) based on two customizable groups of samples.
Go >>>

**Pipelines: Correlation Analysis**
Calculate the correlation between any two of integrated identifiers (e.g. omis, non-omics, user-defined) among custom samples.
Go >>>

**Pipelines: Survival Analysis**
Perform log-rank test analysis for one of integrated identifiers based on two customizable groups of samples.
Go >>>

※ Latest significant release notes

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.

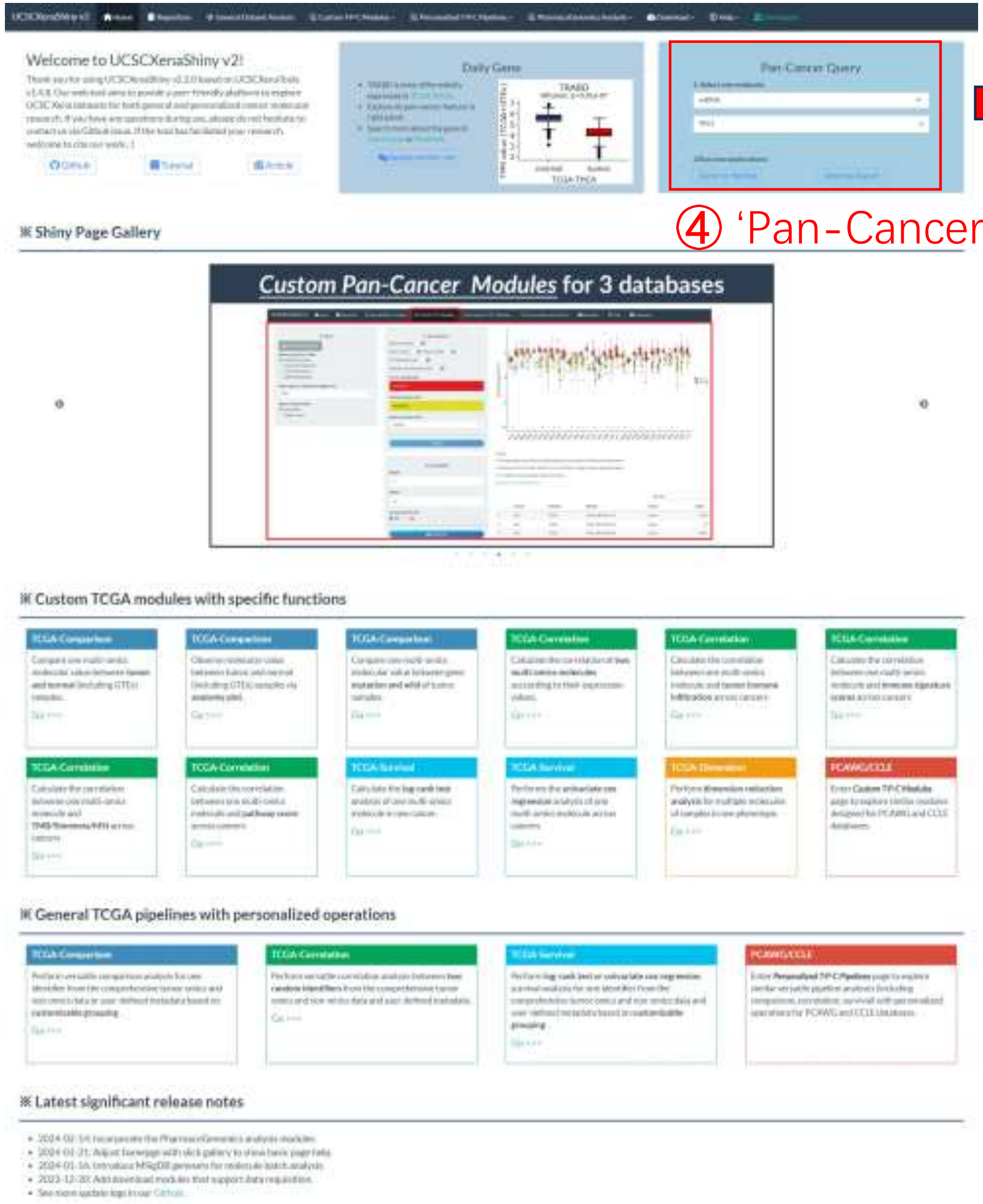
④ 'Pan-Cancer Query' Panel: Select one omics molecule to explore its pan-cancer feature. See more details in next page.

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

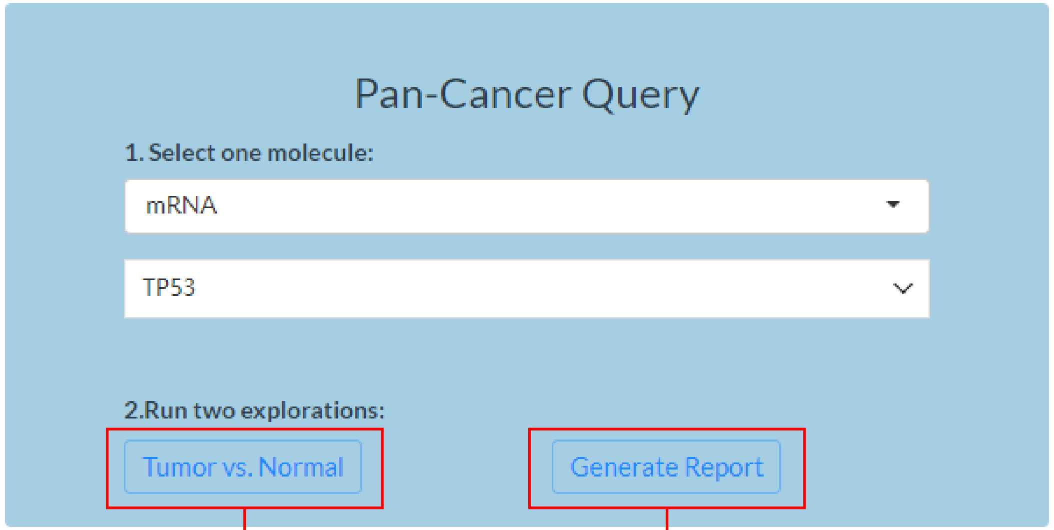
⑥ The shortcuts for custom TCGA modules in 'Custom T•P•C Modules' tab panel.

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

⑧ The release notes of recent main update.



④ ‘Pan-Cancer Query’ Panel



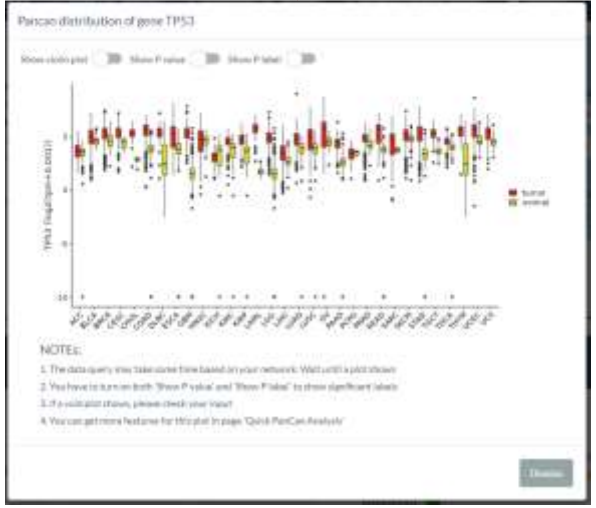
## Pan-Cancer Query

1. Select one molecule:

mRNA

TP53

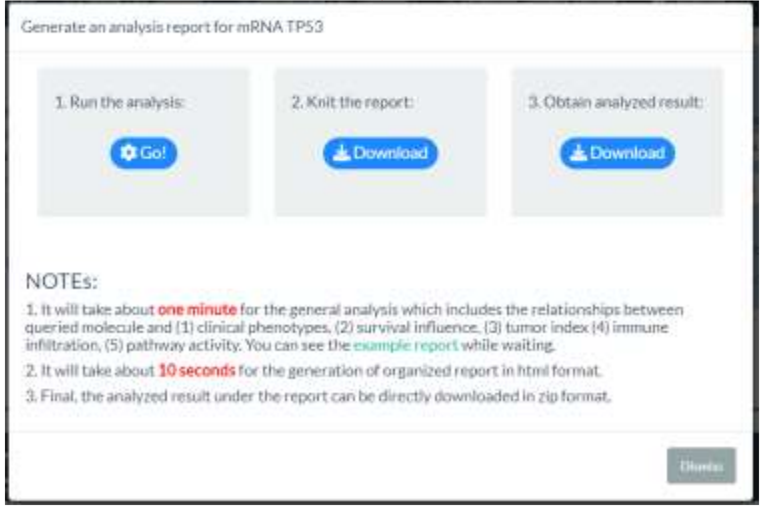
2.Run two explorations:



Pancan distribution of gene TP53

NOTEs:

1. The data query may take some time based on your network. Wait until a plot shown
2. You have to turn on both 'Show P value' and 'Show P label' to show significant labels
3. If a void plot shown, please check your input
4. You can get more features for this plot in page 'Quick PanCan Analysis'



Generate an analysis report for mRNA TP53

1. Run the analysis:
2. Knit the report:
3. Obtain analyzed result:

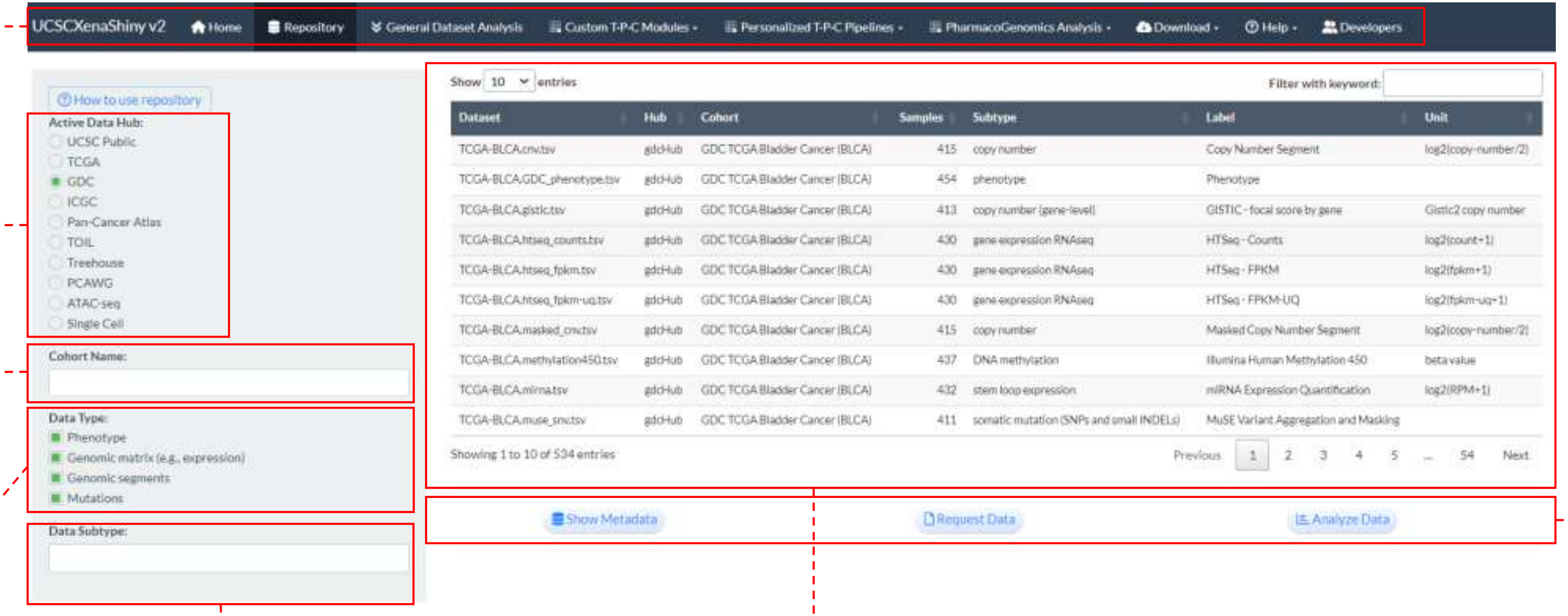
NOTEs:

1. It will take about one minute for the general analysis which includes the relationships between queried molecule and (1) clinical phenotypes, (2) survival influence, (3) tumor index (4) immune infiltration, (5) pathway activity. You can see the example report while waiting.
2. It will take about 10 seconds for the generation of organized report in html format.
3. Final, the analyzed result under the report can be directly downloaded in zip format.

**4.1** Molecular comparison between tumor and normal.

**4.2** Multi-faceted analysis HTML report for one molecule.

① Navigation Bar



Active Data Hub:
○ UCSC Public
○ TCGA
● GDC
○ ICGC
○ Pan-Cancer Atlas
○ TOIL
○ Treehouse
○ PCAWG
○ ATAC-seq
○ Single Cell

Cohort Name:

Data Type:
☑ Phenotype
☑ Genomic matrix (e.g., expression)
☑ Genomic segments
☑ Mutations

Data Subtype:

Show 10 entries

Filter with keyword:

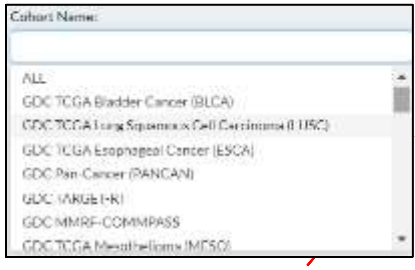
| Dataset | Hub | Cohort | Samples | Subtype | Label | Unit |
|---|---|---|---|---|---|---|
| TCGA-BLCA.cnv.tsv | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 415 | copy number | Copy Number Segment | log2(copy-number/2) |
| TCGA-BLCA.GDC_phenotype.tsv | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 454 | phenotype | 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) | 430 | gene expression RNAseq | HTSeq - Counts | log2(count+1) |
| TCGA-BLCA.htseq_fpkm.tsv | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 430 | gene expression RNAseq | HTSeq - FPKM | log2(fpkm+1) |
| TCGA-BLCA.htseq_fpkm-uq.tsv | gdcHub | GDC TCGA Bladder Cancer (BLCA) | 430 | gene expression RNAseq | HTSeq - FPKM-UQ | log2(fpkm-uq+1) |
| TCGA-BLCA.masked_cnv.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 534 entries

Previous 1 2 3 4 5 … 54 Next

③ Filter datasets by data hubs.

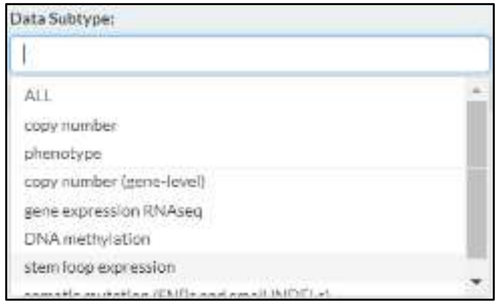
④ Filter datasets of one cohort.


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 TARGET-RT
GDC MMRF-COMMPASS
GDC TCGA Mesothelioma (MESO)

⑤ Filter datasets by data types.

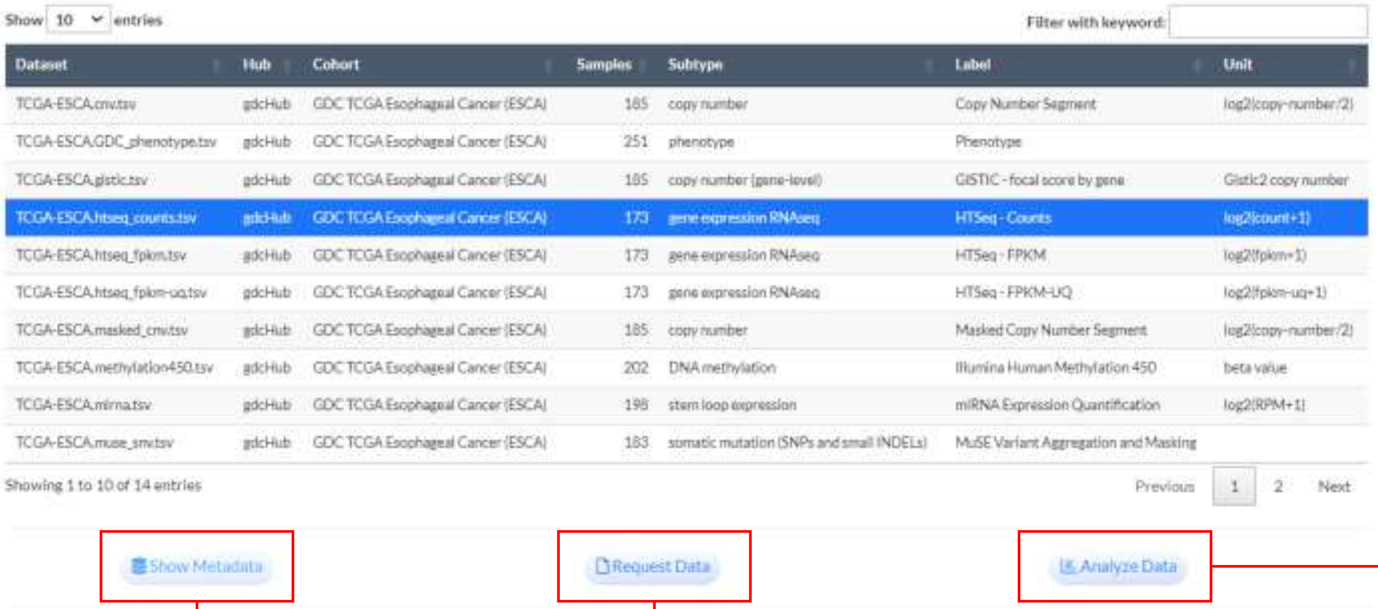
⑥ Filter datasets by data types.


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.

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



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_snv.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

**TIP**: Multiple datasets can be selected.

Detail information...

| | Metadata | dataset1 |
|---|---|---|
| 1 | cohort | GDC TCGA Esophageal Cancer (ESCA) |
| 2 | url | https://docs.gdc.cancer.gov/Data/Release_Notes/Data_Release_Notes/#data-release-180, https://api.gdc.cancer.gov/data/ |
| 3 | probeMap | gencode.v22.annotation.gene.probeMap |
| 4 | dataSubType | gene expression RNAseq |
| 5 | label | HTSeq - Counts |
| 6 | name | TCGA-ESCA.htseq_counts.tsv |
| 7 | dataproducer | Genomic Data Commons |
| 8 | wrangling_procedure | Data from the same sample but from different vials/portions/analytes/aliquotes is averaged; data from different samples is combined into genomicMatrix; all data is then log2(x+1) transformed. |
| 9 | type | genomicMatrix |
| 10 | wrangler | Xena GDC ETL script |

Submitted datasets:

| | hosts | datasets | url | browse |
|---|---|---|---|---|
| 1 | https://gdc.xenahubs.net | TCGA-ESCA.htseq_counts.tsv | https://gdc.xenahubs.net/download/TCGA-ESCA.htseq_counts.tsv.gz | https://xenabrowser.net/c<br>ESCA.htseq_counts.tsv&h |

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

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

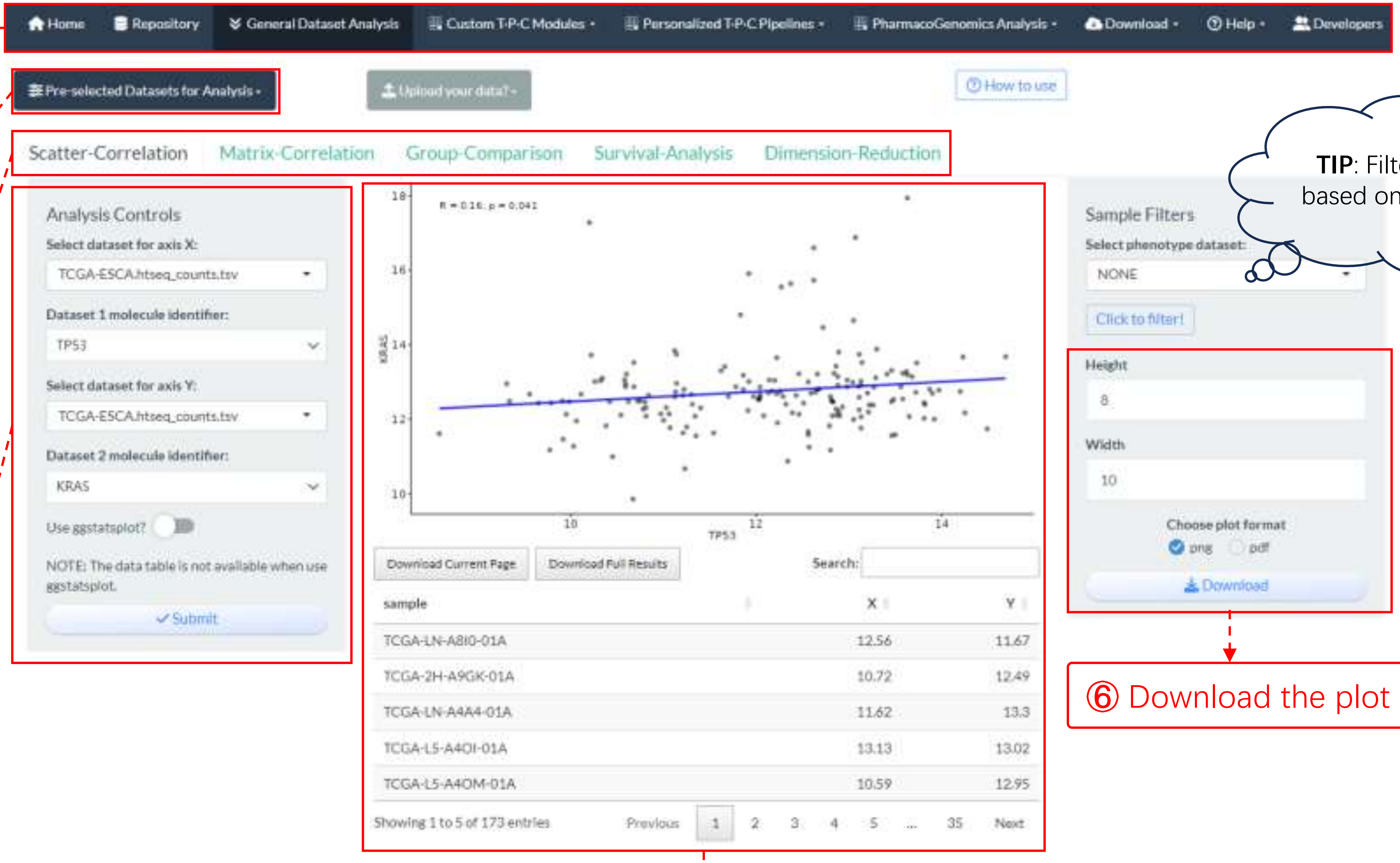
**6.3** Switch to '**General Dataset Analysis**' Panel to perform general analysis based on the selected dataset(s).

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.



Analysis Controls

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

Dataset 2 molecule identifier: KRAS

Use ggstatsplot?

NOTE: The data table is not available when use ggstatsplot.

Search:

| sample | X | Y |
|---|---|---|
| TCGA-LN-A8I0-01A | 12.56 | 11.67 |
| TCGA-2H-A9GK-01A | 10.72 | 12.49 |
| TCGA-LN-A4A4-01A | 11.62 | 13.3 |
| TCGA-L5-A4OI-01A | 13.13 | 13.02 |
| TCGA-L5-A4OM-01A | 10.59 | 12.95 |

Showing 1 to 5 of 173 entries　Previous 1 2 3 4 5 … 35 Next

Sample Filters

Select phenotype dataset: NONE

Height: 8

Width: 10

Choose plot format: ● png ○ pdf

**TIP**: Filter samples based on phenotype.

⑤ Show the analytical result and data.

⑥ Download the plot result.

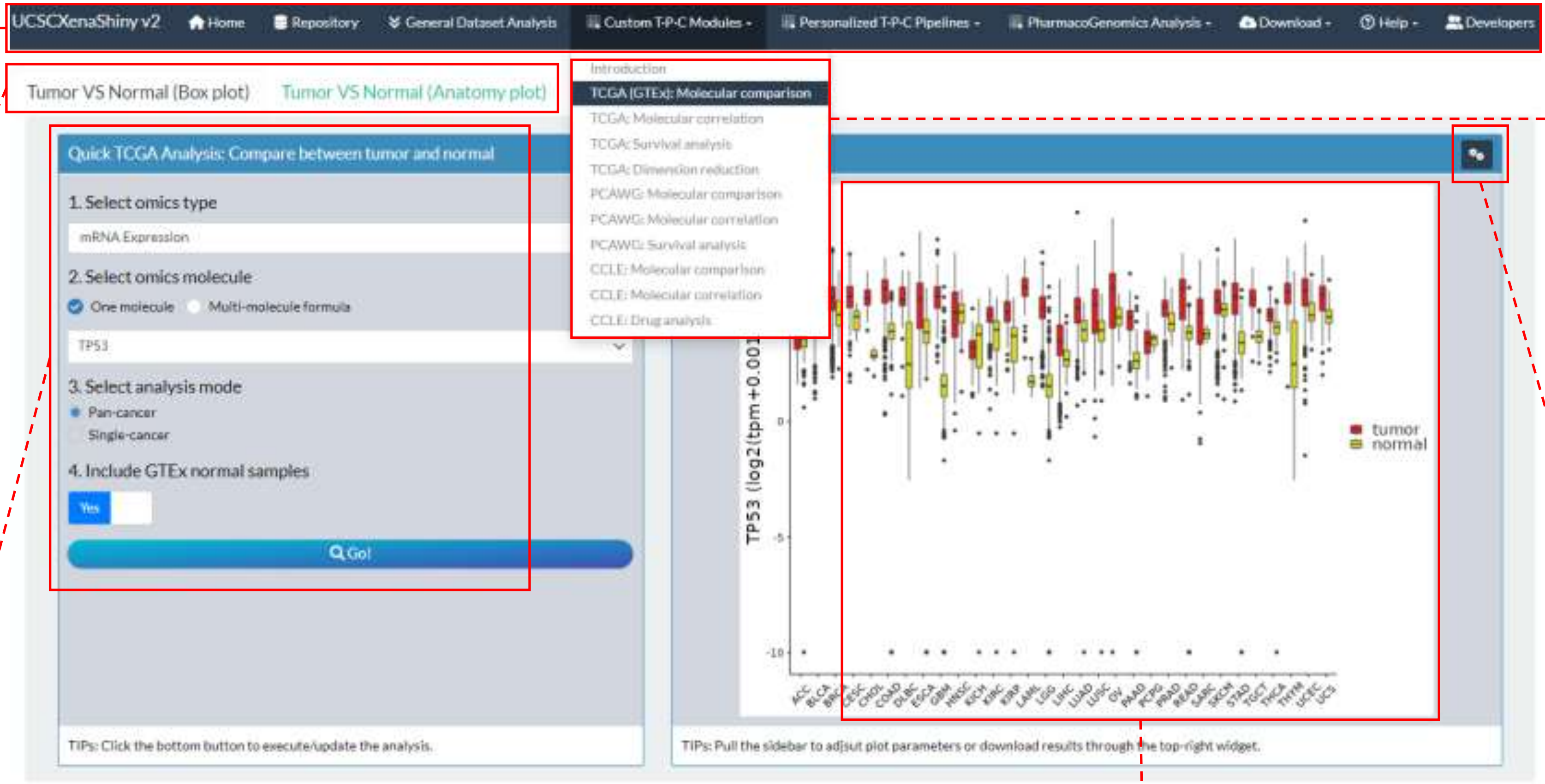
➢ Link to the tutorial book to see the detailed guide of all 5 supported analytical methods.

① Navigation Bar

② Select one type of modules.

③ Select one specific module.

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



1. Select omics type: mRNA Expression

2. Select omics molecule: ● One molecule ○ Multi-molecule formula

TP53

3. Select analysis mode: ● Pan-cancer ○ Single-cancer

4. Include GTEx normal samples: Yes

TIPs: Click the bottom button to execute/update the analysis.

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

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

⑤ Show the analytical result plot.

➢ Link to the tutorial book to see the detailed guide of all supported custom TPC modules.

Quick TCGA Analysis: Compare between tumor and normal

1. Select omics type: mRNA Expression

2. Select omics molecule: ● One molecule ○ Multi-molecule formula

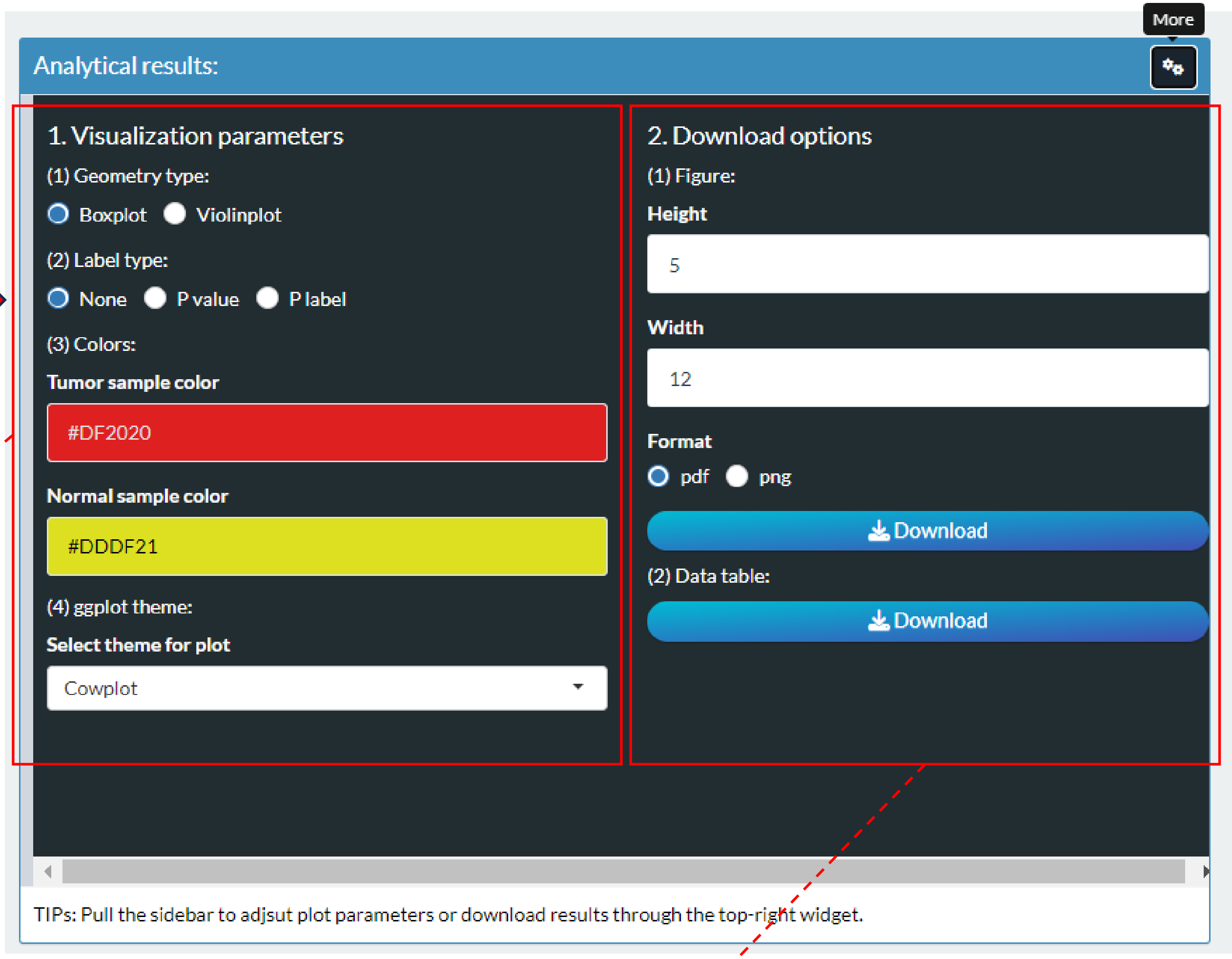
TP53

3. Select analysis mode: ● Pan-cancer ○ Single-cancer

4. Include GTEx normal samples: Yes

TIPs: Click the bottom button to execute/update the analysis.

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



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

(2) Data table:

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

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

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

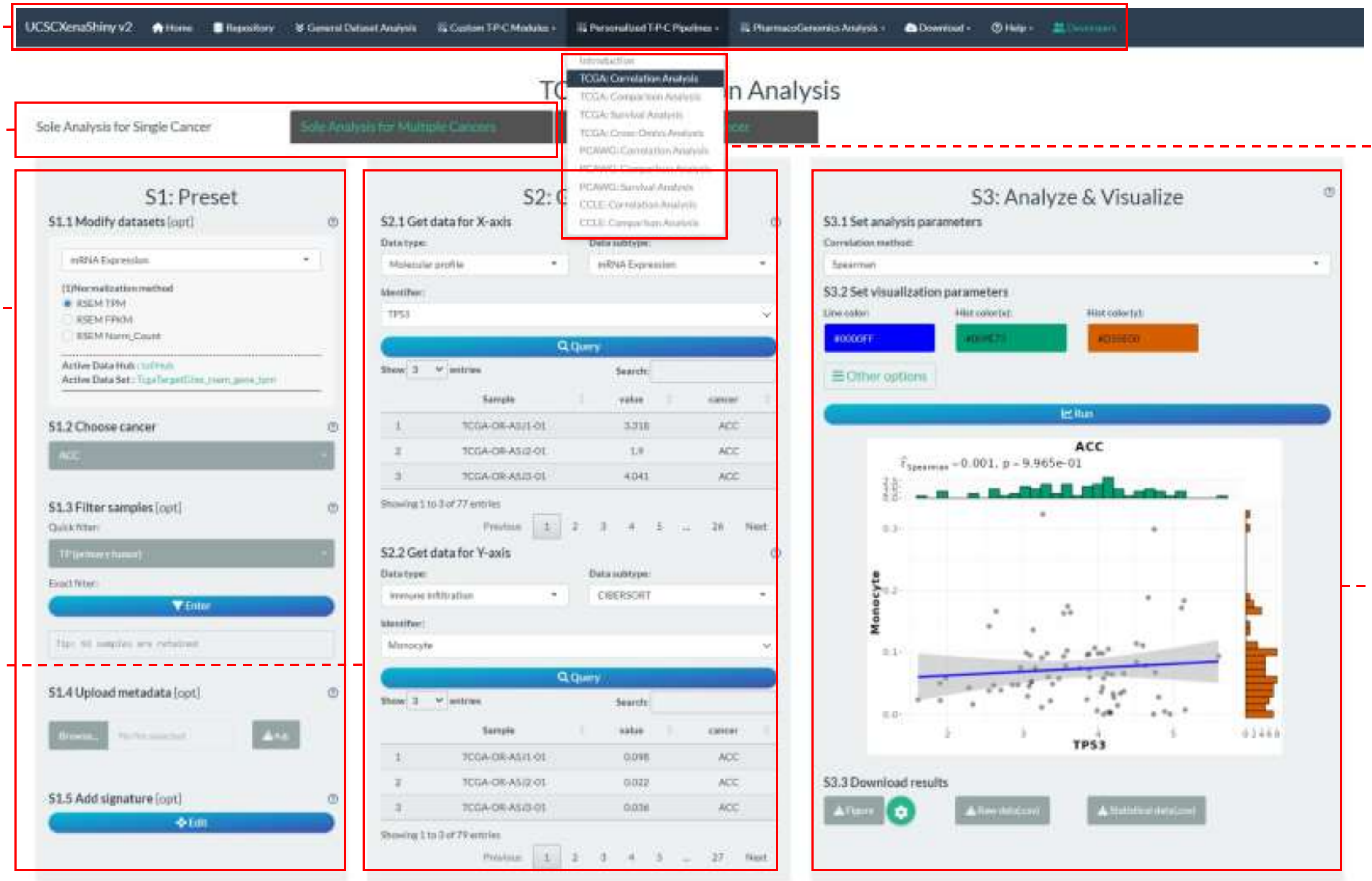
- Link to the tutorial book to see the detailed guide of all supported custom TPC modules.

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.

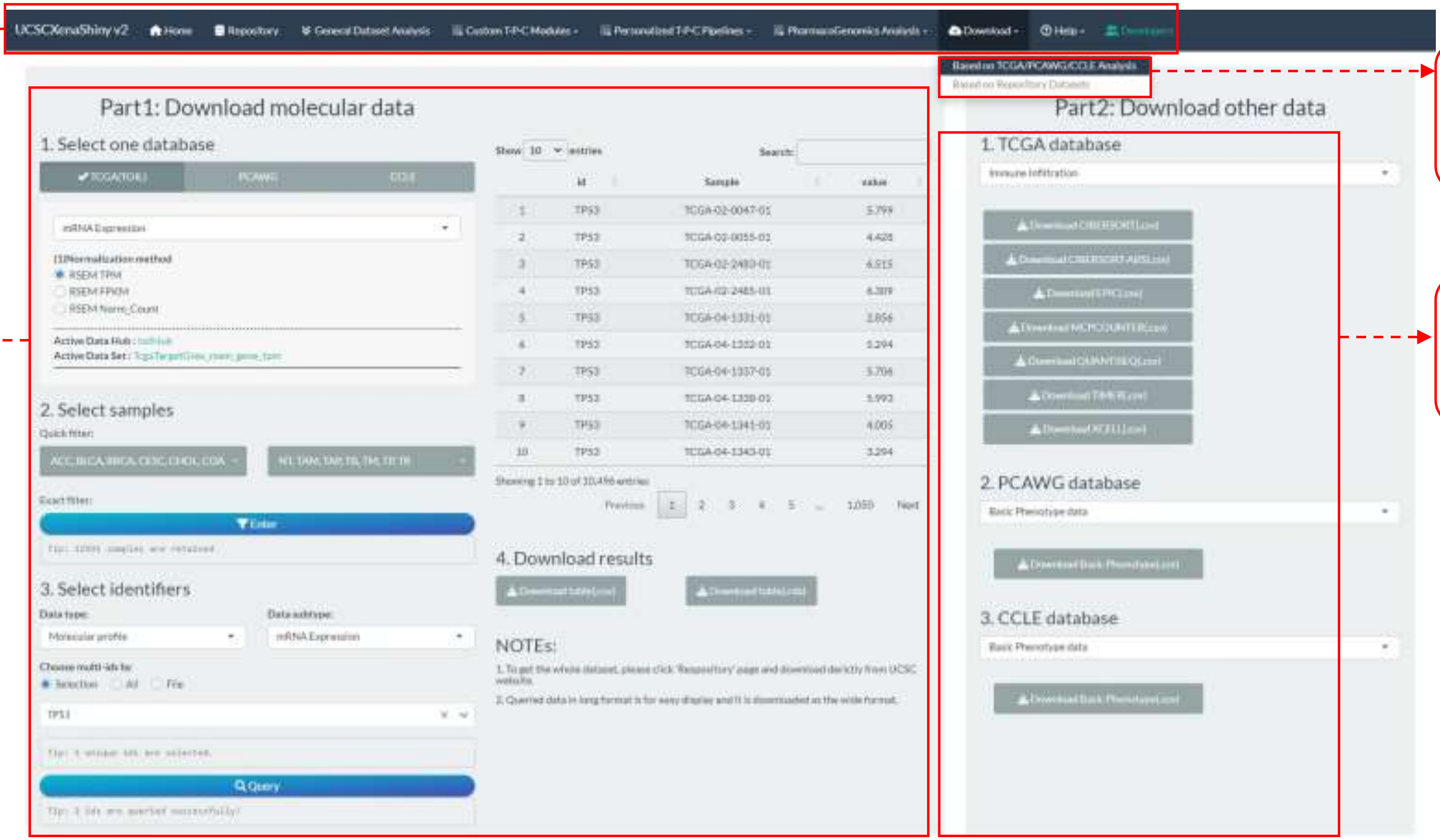
- ➢ Link to the tutorial book to see the detailed guide of all supported personalized TPC pipelines.

① Navigation Bar

② Download raw data based on integrated TPC analysis

③ Download molecular data of TPC samples

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



Show 10 entries

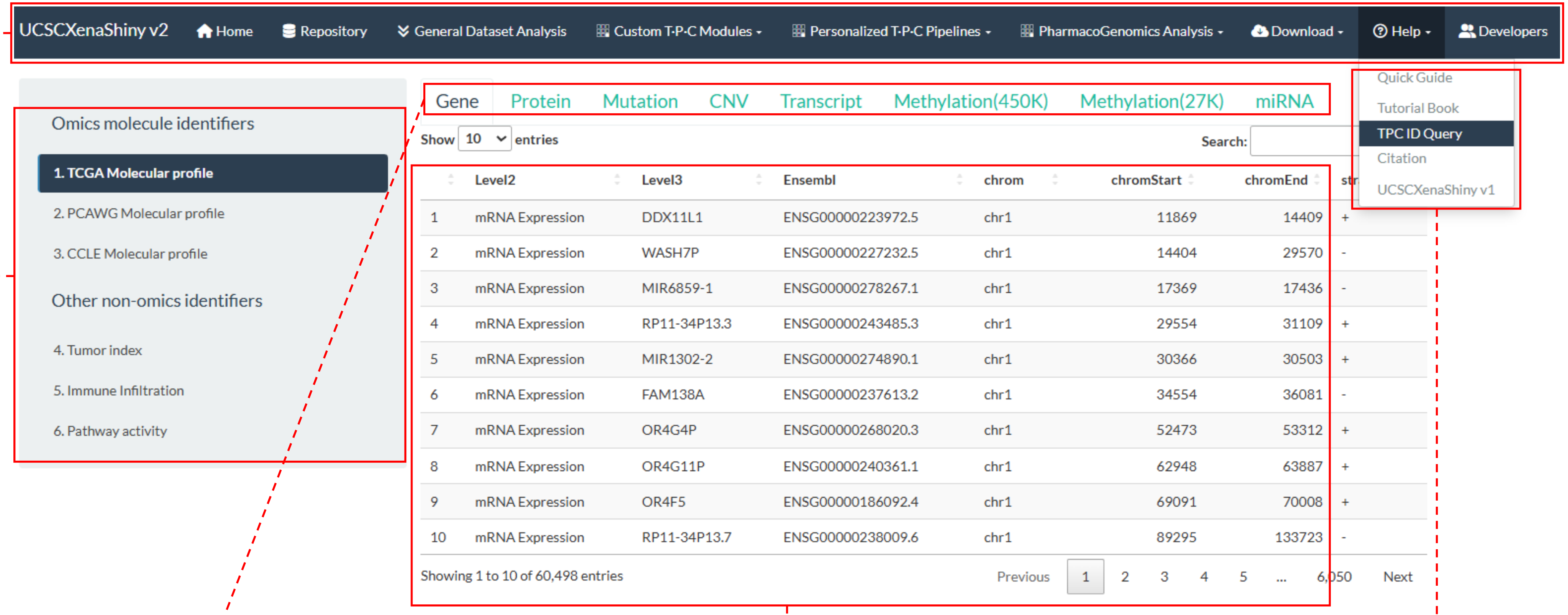
|  | id | Sample | value |
|---|---|---|---|
| 1 | TP53 | TCGA-02-0047-01 | 5.799 |
| 2 | TP53 | TCGA-02-0055-01 | 4.428 |
| 3 | TP53 | TCGA-02-2483-01 | 6.915 |
| 4 | TP53 | TCGA-02-2485-01 | 6.319 |
| 5 | TP53 | TCGA-04-1331-01 | 3.856 |
| 6 | TP53 | TCGA-04-1332-01 | 5.294 |
| 7 | TP53 | TCGA-04-1337-01 | 5.706 |
| 8 | TP53 | TCGA-04-1338-01 | 5.993 |
| 9 | TP53 | TCGA-04-1341-01 | 4.005 |
| 10 | TP53 | TCGA-04-1343-01 | 3.294 |

Showing 1 to 10 of 10,496 entries

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

- Link to the tutorial book to see another way to download molecular data based on repository datasets.

① Navigation Bar



| | 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

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

④ Select the subtype (Level 2) of identifiers.

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

② Search the integrated identifiers of TPC data