

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.

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

Shiny Page Gallery



Custom TCGA modules with specific functions



General TCGA pipelines with personalized operations



Latest significant release notes

- 2024-03-21: Incorporates the PanCancerGenomics analysis modules
- 2024-03-21: Adjusts the page layout to display basic page header
- 2024-03-21: Introduces MSADE parameters for module de-batch analysis
- 2023-12-20: Add download module for first support data visualization
- See more update logs in our GitHub

Pan-Cancer Query

1. Select one molecule:

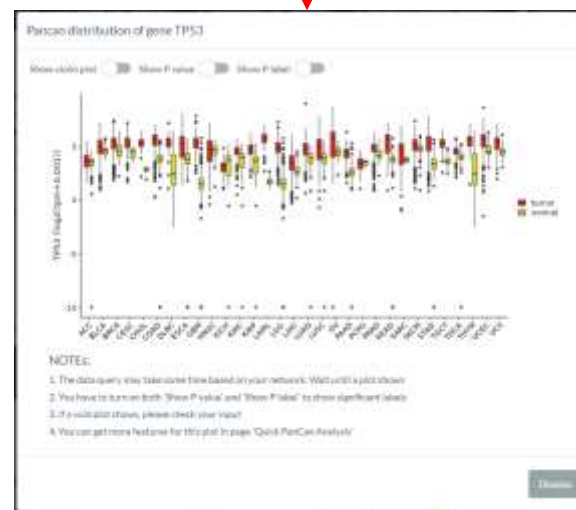
mRNA

TP53

2. Run two explorations:

Tumor vs. Normal

Generate Report



4.1 Molecular comparison between tumor and normal.

Generate an analysis report for mRNA TP53

1. Run the analysis: [Go!](#)

2. Knit the report: [Download](#)

3. Obtain analyzed result: [Download](#)

NOTES:

- 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.
- It will take about **10 seconds** for the generation of organized report in html format.
- Final, the analyzed result under the report can be directly downloaded in zip format.

4.2 Multi-faceted analysis HTML report for one molecule.

① Navigation Bar

③ Filter datasets by data hubs.

④ Filter datasets of one cohort.

⑤ Filter datasets by data types.

UCSCXenaShiny v2

Home Repository General Dataset Analysis Custom T-P-C Modules Personalized T-P-C Pipelines PharmacoGenomics Analysis Download Help Developers

How to use repository

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:

Showing 1 to 10 of 594 entries

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_fpkms.tsv	gdcHub	GDC TCGA Bladder Cancer (BLCA)	430	gene expression RNAseq	HTSeq - FPKM	log2(fpkm+1)
TCGA-BLCA.htseq_fpkms-uc.tsv	gdcHub	GDC TCGA Bladder Cancer (BLCA)	430	gene expression RNAseq	HTSeq - FPKM-UQ	log2(fpkm-uc+1)
TCGA-BLCA.masked_cn.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_snvs.tsv	gdcHub	GDC TCGA Bladder Cancer (BLCA)	411	somatic mutation (SNPs and small INDELS)	MuSE Variant Aggregation and Masking	

Showing 1 to 10 of 594 entries

Previous 1 2 3 4 5 ... 54 Next

Show Metadata Request Data Analyze Data

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_fpkim.tsv	gdcHub	GDC TCGA Esophageal Cancer (ESCA)	173	gene expression RNAseq	HTSeq - FPKM	log2(fpkim+1)
TCGA-ESCA.htseq_fpkim-uq.tsv	gdcHub	GDC TCGA Esophageal Cancer (ESCA)	173	gene expression RNAseq	HTSeq - FPKM-UQ	log2(fpkim-uq+1)
TCGA-ESCA.masked_cn.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_snvs.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

TIP: Multiple datasets can be selected.

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

Detail information...

Metadata	dataset
1 cohort	GDC TCGA Esophageal Cancer (ESCA)
2 url	https://docs.gdc.cancer.gov/Data/Release/Tables/Data_Release_Notes/Data-release-100 https://api.gdc.cancer.gov/data/
3 probeMap	genesdev22.annotGdtrngene.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 vials/positions/analyses/replicates 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

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	https://gdc.xenahubs.net/download/TCGA-ESCA.htseq_counts.tsv.gz	https://xenabrowser.net/TCGA-ESCA.htseq_counts.tsv5h

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' interface. At the top is a navigation bar with links: 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's a section for 'Pre-selected Datasets for Analysis' with an 'Upload your data?' button and a 'How to use' link. The main area features a tabbed interface with 'Scatter-Correlation', 'Matrix-Correlation', 'Group-Comparison', 'Survival-Analysis', and 'Dimension-Reduction'. The 'Scatter-Correlation' tab is active, showing a scatter plot of KRAS vs TP53 with a regression line. The plot includes the correlation coefficient $R = 0.16$ and p-value $p = 0.041$. Below the plot is a table of data entries. To the left of the plot is the 'Analysis Controls' panel, and to the right is the 'Sample Filters' panel.

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.

Sample Filters

Select phenotype dataset: NONE

Height:

Width:

Choose plot format: ☒ png ☐ pdf

Scatter Plot Data

$R = 0.16$, $p = 0.041$

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

TIP: Filter samples based on phenotype.

① Navigation Bar

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: More

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

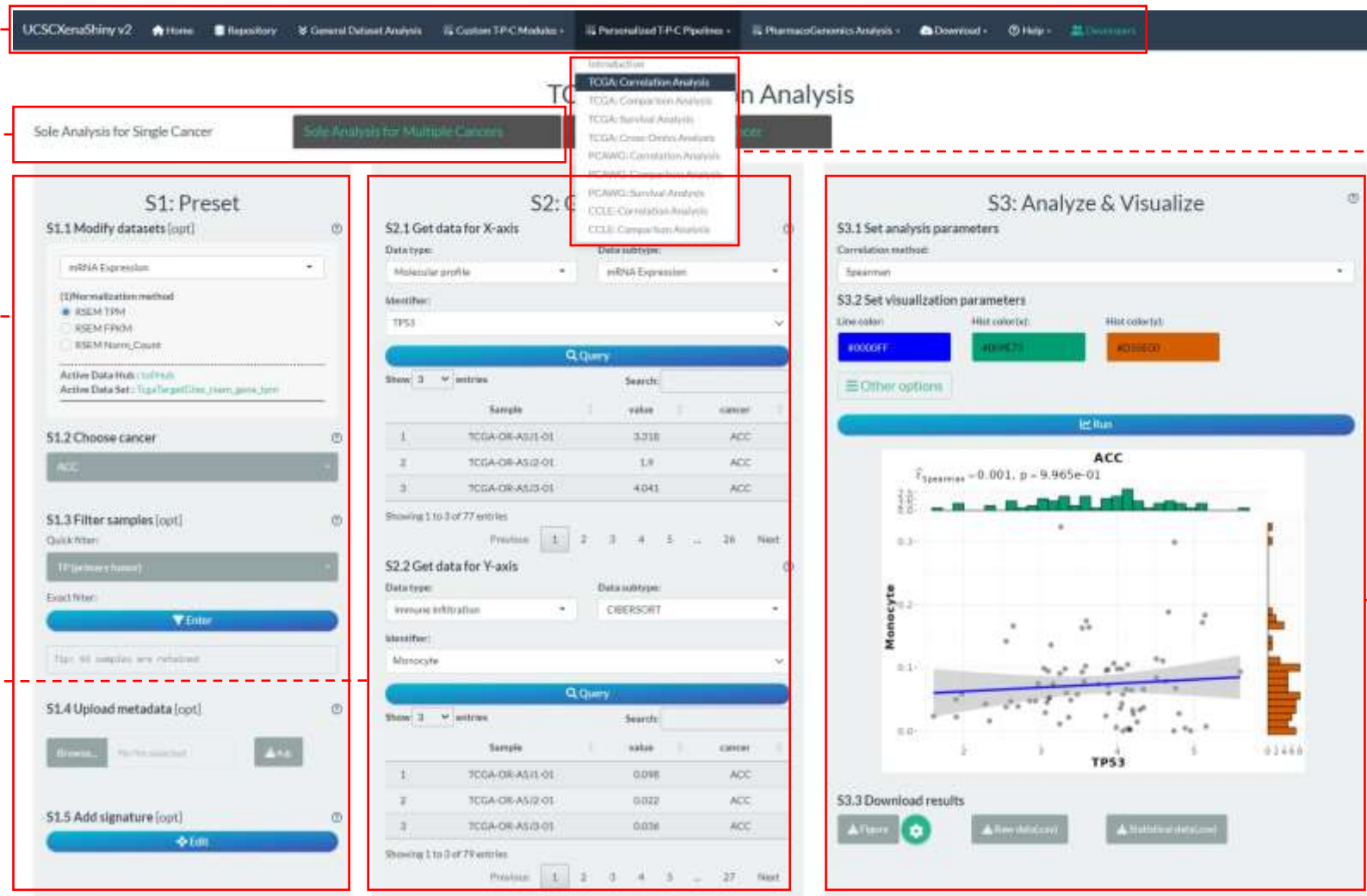
③ Select one specific mode of pipelines.

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

② Select one type of pipelines.

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

⑤ Fetch the analytical data through S2 step.



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.

The screenshot displays the UCSCXenaShiny v2 web application interface. The top navigation bar includes links for Home, Repository, General Dataset Analysis, Custom TPC Modules, Personalized TPC Pipelines, Pharmacogenomics Analysis, Download, Help, and Download. The main content area is divided into two parts: 'Part1: Download molecular data' and 'Part2: Download other data'.

Part1: Download molecular data

1. Select one database: TCGA (TOR), PCAWG, CCLE. The TCGA (TOR) database is selected.

2. Select samples: Quick filter: ACC, BRCA, BRCA, COAD, COAD, COA. The filter is set to 'ALL TAME, TAME, TB, TME, TET, TH'.

3. Select identifiers: Data type: Molecular profile. Data subtype: mRNA Expression. Choose multi-ids by: Selective. The multi-ids list contains 'TP53'.

4. Download results: Download table (csv), Download table (json).

Part2: Download other data

1. TCGA database: Inquire infiltration. Download CHRNA1001 Load, Download CHRNA1001 AJIS1 Load, Download TPC Load, Download MTC2001011 Load, Download CHRNA1001 Load, Download TAME Load.

2. PCAWG database: Basic Phenotype data. Download Basic Phenotype Load.

3. CCLE database: Basic Phenotype data. Download Basic Phenotype Load.

Table of results (Part1):

id	Sample	value
1	TP53	TCGA-02-0047-01
2	TP53	TCGA-02-0055-01
3	TP53	TCGA-02-2489-01
4	TP53	TCGA-02-2485-01
5	TP53	TCGA-04-1331-01
6	TP53	TCGA-04-1332-01
7	TP53	TCGA-04-1337-01
8	TP53	TCGA-04-1338-01
9	TP53	TCGA-04-1341-01
10	TP53	TCGA-04-1343-01

NOTES:

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

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

Search:

	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

Previous

1

2

3

4

5

...

6,050

Next

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