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:
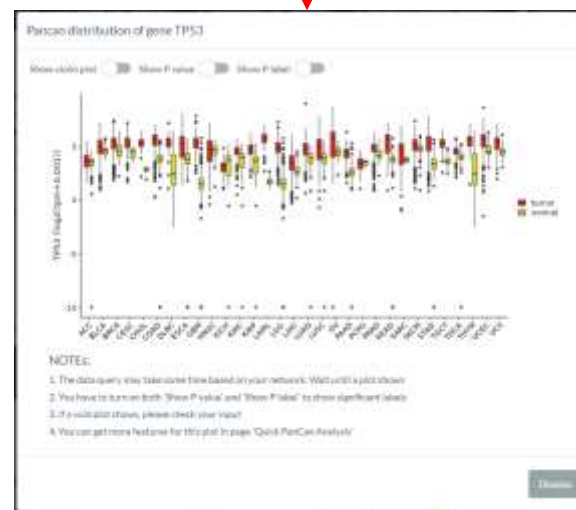
mRNA

TP53

2. Run two explorations:

Tumor vs. Normal   Generate Report

4.1 Molecular comparison between tumor and normal.

4.2 Multi-faceted analysis HTML report for one molecule.

① Navigation Bar

UCSCXenaShiny v2　🏠 Home　📋 Repository　✤ General Dataset Analysis　📋 Custom T·P·C Modules ▾　📋 Personalized T·P·C Pipelines ▾　📋 PharmacoGenomics Analysis ▾　☁ Download ▾　⑦ Help ▾　👥 Developers

③ Filter datasets by data hubs.

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:

⑤ Filter datasets by data types.

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)

⑥ Filter datasets by data types.

Data Subtype:

ALL
copy number
phenotype
copy number (gene-level)
gene expression RNAseq
DNA methylation
stem loop expression

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

📋 Show Metadata　　　　📄 Request Data　　　　📊 Analyze Data

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

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

TIP: Multiple datasets can be selected.

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

🏠 Home   📚 Repository   ⚓ General Dataset Analysis   📊 Custom T·P·C Modules ▾   📊 Personalized T·P·C Pipelines ▾   📊 PharmacoGenomics Analysis ▾   ☁ Download ▾   ⑦ Help ▾   👥 Developers

≣ Pre-selected Datasets for Analysis ▾   ⬆ Upload your data? ▾   ⑦ How to use

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

Scatter-Correlation   Matrix-Correlation   Group-Comparison   Survival-Analysis   Dimension-Reduction

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.

✓ Submit

③ Select one of analytical methods.

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

R = 0.16, p = 0.041

TIP: Filter samples based on phenotype.

Sample Filters

Select phenotype dataset:

NONE ▾

Click to filter!

Height

8

Width

10

Choose plot format

⚫ png   ⚪ pdf

⬇ Download

⑥ Download the plot result.

Download Current Page   Download Full Results   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

⑤ Show the analytical result and data.

➢ 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.

⑤ Show the analytical result plot.

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

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

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.

② Select one type of pipelines.

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

⑤ Fetch the analytical data through S2 step.

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
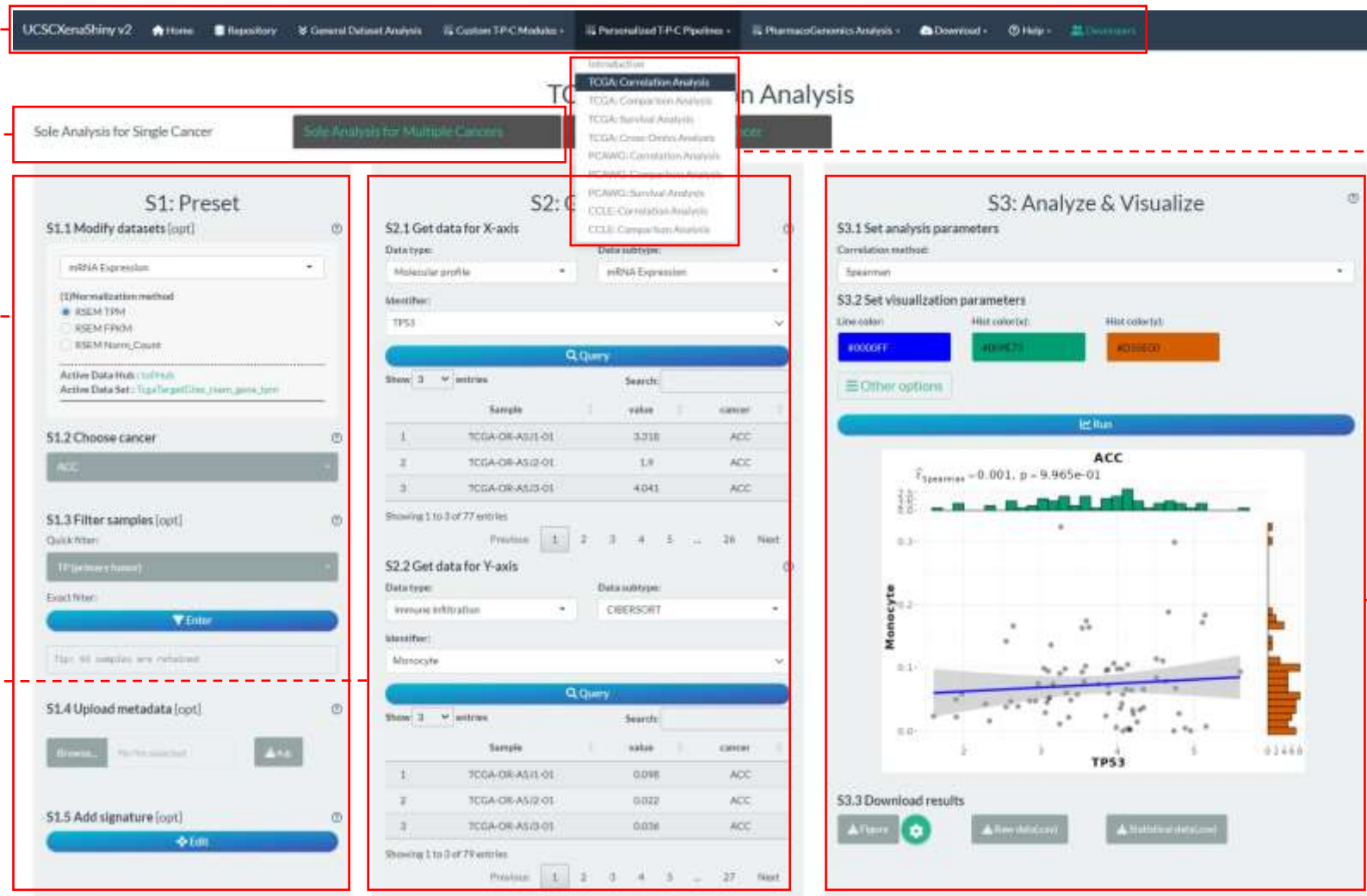
③ Download molecular data of TPC samples

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

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

① Navigation Bar

UCSCXenaShiny v2   🏠 Home   🖥 Repository   ⌄ General Dataset Analysis   ▦ Custom T·P·C Modules ▾   ▦ Personalized T·P·C Pipelines ▾   ▦ PharmacoGenomics Analysis ▾   ☁ Download ▾   ⑦ Help ▾   👥 Developers

Help menu:
- Quick Guide
- Tutorial Book
- **TPC ID Query**
- Citation
- UCSCXenaShiny v1

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

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

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