

# Using cBioPortal

exploring clinical annotation

<https://www.cbioportal.org>

# Log into cBioPortal <https://www.cbioportal.org>

- Log into the portal using a Google account for example

The screenshot displays the cBioPortal interface for selecting studies. At the top, the cBioPortal logo is on the left, and navigation links for Data Sets, Web API, R/MATLAB, Tutorials/Webinars, FAQ, News, Visualize Your Data, About, and cBioPortal Installations are on the right. Below the logo, there are buttons for Query, Quick Search Beta, and Download. A citation prompt reads "Please cite: Cerami et al., 2012 & Gao et al., 2013".

The main section is titled "Select Studies for Visualization & Analysis:" and shows "0 studies selected (0 samples)". A search bar is on the right. On the left, a list of categories and their study counts is shown:

Category	Count
PanCancer Studies	7
Pediatric Cancer Studies	13
Immunogenomic Studies	8
Cell lines	3
Adrenal Gland	3
Ampulla of Vater	1
Biliary Tract	9
Bladder/Urinary Tract	17
Bone	2
Bowel	10
Breast	18
CNS/Brain	20
Cervix	2
Esophagus/Stomach	16
Eye	5

Below this list, there are two tabs for "Quick select": "TCGA PanCancer Atlas Studies" and "Curated set of non-redundant studies". The "PanCancer Studies" section lists several studies with checkboxes and sample counts:

- MSK-IMPACT Clinical Sequencing Cohort (MSKCC, Nat Med 2017) 10945 samples
- Metastatic Solid Cancers (UMich, Nature 2017) 500 samples
- MSS Mixed Solid Tumors (Broad/Dana-Farber, Nat Genet 2018) 249 samples
- SUMMIT - Neratinib Basket Study (Multi-Institute, Nature 2018) 141 samples
- TMB and Immunotherapy (MSKCC, Nat Genet 2019) 1661 samples
- Tumors with TRK fusions (MSK, Clin Cancer Res 2020) 106 samples
- Cancer Therapy and Clonal Hematopoiesis (MSK, Nat Genet 2020) 24146 samples

The "Pediatric Cancer Studies" section lists:

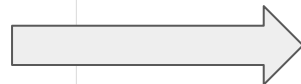
- Pediatric Preclinical Testing Consortium (CHOP, Cell Rep 2019) 261 samples
- Pediatric Acute Lymphoid Leukemia - Phase II (TARGET, 2018) 1978 samples
- Pediatric Rhabdoid Tumor (TARGET, 2018) 72 samples
- Pediatric Wilms' Tumor (TARGET, 2018) 657 samples
- Pediatric Acute Myeloid Leukemia (TARGET, 2018) 1025 samples
- Pediatric Neuroblastoma (TARGET, 2018) 1089 samples
- Pediatric Pan-Cancer (DKFZ, Nature 2017) 961 samples
- Pediatric Pan-cancer (Columbia U, Genome Med 2016) 103 samples
- Acute Lymphoblastic Leukemia (St Jude, Nat Genet 2016) 73 samples
- Acute Lymphoblastic Leukemia (St Jude, Nat Genet 2015) 93 samples
- Pediatric Ewing Sarcoma (DFCI, Cancer Discov 2014) 107 samples
- Ewing Sarcoma (Institut Curie, Cancer Discov 2014) 112 samples
- Medulloblastoma (PCGP, Nature 2012) 37 samples

At the bottom, there are buttons for "0 studies selected (0 samples)", "Query By Gene", "OR", and "Explore Selected Studies".

# Log into cBioPortal <https://www.cbioportal.org>

- Select the cancer type of interest in the search box

*Make sure to select the TCGA Firehose legacy dataset!*




The screenshot shows the cBioPortal search interface. At the top, there is a navigation bar with the cBioPortal logo and links for Data Sets, Web API, R/MATLAB, Tutorials/Webinars, FAQ, News, Visualize Your Data, About, and cBioPortal Installations. Below the navigation bar, there is a search bar with the text 'Query Quick Search Beta! Download' and a search input field containing 'melanoma'. The search results are displayed in a table with columns for study name, sample size, and icons for visualization and download. The results are categorized into 'Other', 'Mixed Cancer Types', 'Skin', and 'Melanoma'. The 'Melanoma' category is expanded, showing various sub-categories like 'Acral Melanoma', 'Metastatic Melanoma', 'CUTANEOUS MELANOMA', and 'DESMOPLASTIC MELANOMA'. The 'Skin Cutaneous Melanoma (TCGA, Firehose Legacy)' study is highlighted in grey, indicating it is the selected dataset. At the bottom of the search results, there is a button for 'Query By Gene' and a button for 'Explore Selected Studies'.

Study Name	Sample Size
Uveal Melanoma (TCGA, PanCancer Atlas)	80 samples
MSS Mixed Solid Tumors (Broad/Dana-Farber, Nat Genet 2018)	249 samples
Acral Melanoma (TCGA, PanCancer Atlas)	80 samples
Metastatic Melanoma (DFCI, Nature Medicine 2019)	144 samples
Metastatic Melanoma (UCLA, Cell 2016)	38 samples
Melanoma (Broad/Dana Farber, Nature 2012)	26 samples
Melanoma (MSKCC, NEJM 2014)	64 samples
Melanomas (TCGA, Cell 2015)	359 samples
Metastatic Melanoma (DFCI, Science 2015)	110 samples
Metastatic Melanoma (MSKCC, JCO Precis Oncol 2017)	66 samples
Skin Cutaneous Melanoma (Broad, Cell 2012)	121 samples
Skin Cutaneous Melanoma (TCGA, Firehose Legacy)	479 samples
Skin Cutaneous Melanoma (TCGA, PanCancer Atlas)	448 samples
Skin Cutaneous Melanoma (Yale, Nat Genet 2012)	147 samples
Skin Cutaneous Melanoma (Broad, Cancer Discov 2014)	78 samples
Desmoplastic Melanoma (Broad Institute, Nat Genet 2015)	20 samples

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- You get an overview over all samples in the study
- Now you can define custom groups to compare!
- Click on "custom selection"

 **cBioPortal**  
FOR CANCER GENOMICS

Data Sets Web API R/MATLAB Tutorials/Webinars FAQ News Visualize Your Data About cBioPortal Installations

Logged in as [carl.m.herrmann@gmail.com](mailto:carl.m.herrmann@gmail.com)

### Skin Cutaneous Melanoma (TCGA, Firehose Legacy) [↓](#)

TCGA Skin Cutaneous Melanoma. Source data from [GDAC Firehose](#). Previously known as TCGA Provisional.

Click gene symbols below or enter here

Summary **Clinical Data** Heatmaps CN Segments

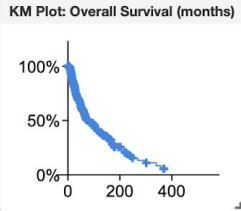
Selected: 471 patients | 480 samples

Cancer Type		
	#	Freq
<input type="checkbox"/> NA	372	77.5%
<input type="checkbox"/> Melanoma	108	22.5%

Cancer Type Detailed		
	#	Freq
<input type="checkbox"/> NA	372	77.5%
<input type="checkbox"/> Cutaneous Melanoma	73	15.2%
<input type="checkbox"/> Melanoma	29	6.0%
<input type="checkbox"/> Desmoplastic Melanoma	3	0.6%
<input type="checkbox"/> Acral Melanoma	2	0.4%
<input type="checkbox"/> Lentigo Maligna Melanoma	1	0.2%

Genomic Profile Sample Counts		
Molecular Profile	#	Freq
Methylation (HM450)	473	98.5%
mRNA expression (RNA Seq V2 R...)	472	98.3%
mRNA expression z-scores relativ...	472	98.3%
mRNA expression z-scores relativ...	472	98.3%
Mutations	368	76.7%
Putative copy-number alterations ...	367	76.5%

**KM Plot: Overall Survival (months)**



Sex

**KM Plot: Disease Free Survival (m...)** **Number of Samples Per Patient**

# Log into cBioPortal <https://www.cbioportal.org>

- Paste a list of Sample IDs in the format `skcm_tcga:TCGA-XX-XXXX-XX`
- Click on "Filter to listed samples"
- Of course replace `skcm_tcga` by the study of interest (e.g. `gbm_tcga`)

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Logged in as [carl.m.herrmann@gmail.com](#)

### Skin Cutaneous Melanoma (TCGA, Firehose Legacy)

TCGA Skin Cutaneous Melanoma. Source data from GDAC Firehose. Previously known as TCGA Provisional.

Click gene symbols below or enter here

Summary Clinical Data Heatmaps CN Segments

Selected: 471 patients | 480 samples

Cancer Type		
	#	Freq
NA	372	77.5%
Melanoma	108	22.5%

Cancer Type Detailed		
	#	Freq
NA	372	77.5%
Cutaneous Melanoma	73	15.2%
Melanoma	29	6.0%
Desmoplastic Melanoma	3	0.6%
Acral Melanoma	2	0.4%
Lentigo Maligna Melanoma	1	0.2%

Search...

KM Plot: Disease Free Survival (m...)

Number of Samples Per Patient

100%

Molecular

By sample ID  By patient ID

currently selected currently unselected Data Format

- skcm\_tcga:TCGA-D3-A3ML-06
- skcm\_tcga:TCGA-D3-A51E-06
- skcm\_tcga:TCGA-D3-A51T-06
- skcm\_tcga:TCGA-EB-A3XB-01
- skcm\_tcga:TCGA-EB-A41A-01

Submitting will clear current filters.

Overall Survival (months)

Sex

# Log into cBioPortal <https://www.cbioportal.org>

- Now click on Groups, and define a group from the filtered samples, and give it a name!
- Repeat the procedure to select a second set of IDs to create a second group

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### Skin Cutaneous Melanoma (TCGA, Firehose Legacy)

TCGA Skin Cutaneous Melanoma. Source data from GDAC Firehose. Previously known as TCGA Provisional.

Custom Selection : 16 samples Clear All Filters

Summary Clinical Data Heatmaps CN Segments

Selected: 16 patients | 16 samples

Cancer Type		
	#	Freq
NA	10	62.5%
Melanoma	6	37.5%

Cancer Type Detailed		
	#	Freq
NA	10	62.5%
Melanoma	3	18.8%
Cutaneous Melanoma	2	12.5%
Desmoplastic Melanoma	1	6.3%

Genomic Profile Sam		
	#	Freq
Molecular Profile		
mRNA expression (RNA Seq V2 R...		
mRNA expression z-scores relativ...		
Methylation (HM450)		
mRNA expression z-scores relativ...		
Protein expression (RPPA)		

Select all (0) Deselect all Search..

Group comparison allows you to create custom groups and compare their clinical and genomic features. Use the button below to create groups based on selections.

Create new group from selected samples (16)

# Log into cBioPortal <https://www.cbioportal.org>

- You now have 2 groups of samples, which you can compare
- Click in the compare button

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**Skin Cutaneous Melanoma (TCGA, Firehose Legacy)** [Download](#)

TCGA Skin Cutaneous Melanoma. Source data from [GDAC Firehose](#). Previously known as TCGA Provisional.

Custom Selection : 12 samples [Clear All Filters](#)

Summary Clinical Data Heatmaps CN Segments

Selected: 12 patients | 12 samples

Select all (2) Deselect all Search..

high (16 samples/patients)

low (12 samples/patients)

Compare Filter Share

Create new group from selected samples (12)

Cancer Type		
	#	Freq
NA	9	75.0%
Melanoma	3	25.0%

Cancer Type Detailed		
	#	Freq
NA	9	75.0%
Cutaneous Melanoma	2	16.7%
Melanoma	1	8.3%

Genomic Profile Sam

**Molecular Profile**

mRNA expression (RNA Seq V2 R...)

mRNA expression z-scores relativ...

Methylation (HM450)

Mutations

mRNA expression z-scores relativ...

Protein expression (RPPA)

Protein expression z-score (RPPA)

# Log into cBioPortal <https://www.cbioportal.org>

- You can compare the clinical annotations and survivals of the 2 groups!

