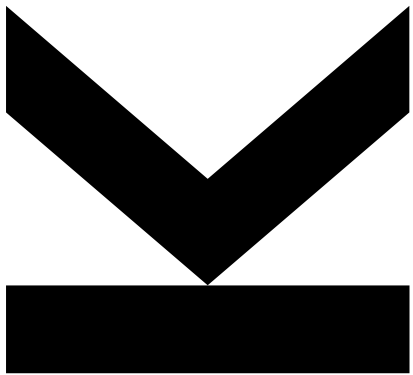


# Coral

## Web-based Visual Analysis Tool for Creating and Characterizing Cohorts



Patrick Adelberger, Klaus Eckelt, Markus J. Bauer,  
Marc Streit, Christian Haslinger, and Thomas Zichner



 <https://jku-vds-lab.at/biovis22-adelberger>

 [patrick.adelberger@jku.at](mailto:patrick.adelberger@jku.at)

# Team



Patrick Adelberger



Klaus Eckelt



Marc Streit



Thomas Zichner



Markus Bauer



Christian Haslinger

# Motivation

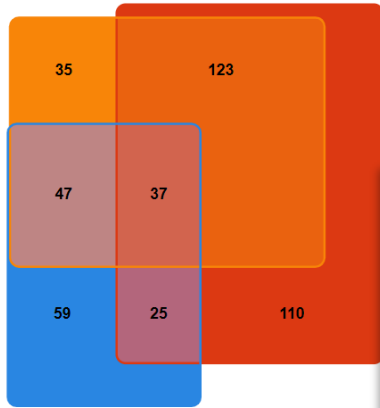
Lung Adenocarcinoma (TCGA, PanCancer Atlas)

Groups: (drag to reorder) (A) KRAS\_mut (168) (B) MUC16\_mut (242) (C) TP53\_mut (295) Select all | Deselect all

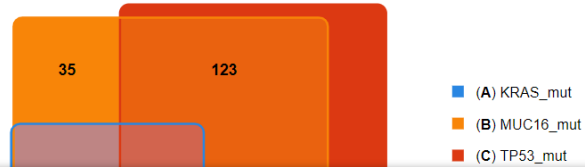
Overlap Survival Clinical Genomic Alterations mRNA Protein Microbiome Signature

- ❗ Samples (232) that overlap in the selected groups are excluded from sample-level analysis in other tabs.
- ❗ Patients (232) that overlap in the selected groups are excluded from patient-level analysis in other tabs.

Samples overlap



Patients overlap



Create Group From Selected Diagram Areas

Lung Adenocarcinoma (TCGA, PanCancer Atlas)

Groups: (drag to reorder) (A) KRAS\_mut (168) (B) MUC16\_mut (242) (C) TP53\_mut (295) Select all | Deselect all

Overlap Survival Clinical Genomic Alterations mRNA Protein Microbiome Signature

Interpret all results with caution, as they can be confounded by many different variables that are not controlled for in these analyses. Consider consulting a statistician.

❗ Samples (232) that overlap in the selected groups are excluded from sample-level analysis below.

❗ Patients (232) that overlap in the selected groups are excluded from patient-level analysis below.

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
1p Status	Sample	Chi-squared Test	1.513e-6	1.241e-4
7p Status	Sample	Chi-squared Test	5.788e-5	2.373e-3
5p Status	Sample	Chi-squared Test	1.128e-4	2.461e-3
17p Status	Sample	Chi-squared Test	1.201e-4	2.461e-3
6q Status	Sample	Chi-squared Test	3.659e-4	6.000e-3
19q Status	Sample	Chi-squared Test	5.793e-4	6.892e-3
Aneuploidy Score	Sample	Kruskal Wallis Test	5.883e-4	6.892e-3
Ragnum Hypoxia Score	Patient	Kruskal Wallis Test	1.182e-3	0.0121
9p Status	Sample	Chi-squared Test	2.913e-3	0.0248
Buffa Hypoxia Score	Patient	Kruskal Wallis Test	3.197e-3	0.0248
Winter Hypoxia Score	Patient	Kruskal Wallis Test	3.333e-3	0.0248
7q Status	Sample	Chi-squared Test	4.298e-3	0.0294
18q Status	Sample	Chi-squared Test	4.968e-3	0.0313
11p Status	Sample	Chi-squared Test	8.598e-3	0.0492
8p Status	Sample	Chi-squared Test	9.007e-3	0.0492
10p Status	Sample	Chi-squared Test	0.0166	0.0849
3q Status	Sample	Chi-squared Test	0.0203	0.0975
Mutation Count	Sample	Kruskal Wallis Test	0.0214	0.0975
11q Status	Sample	Chi-squared Test	0.0248	0.107
10q Status	Sample	Chi-squared Test	0.0308	0.126

Plot Type: 100% stacked bar chart

Legend: Gained (blue), Lost (red), Not Called (yellow)

Lung Adenocarcinoma (TCGA, PanCancer Atlas)

Groups: (drag to reorder) (A) KRAS\_mut (168) (B) MUC16\_mut (242) (C) TP53\_mut (295) Select all | Deselect all

Overlap Survival Clinical Genomic Alterations mRNA Protein Microbiome Signature

Alteration Types

- Mutations
  - Missense
  - Inframe
  - Inframe Insertion
  - Inframe Deletion
  - Truncating
  - Nonsense
  - Frameshift
  - Frameshift Insertion
  - Frameshift Deletion
  - Nonstart
  - Nonstop
  - Splice
  - Other
- Structural Variants / Fusions
- Copy Number Alterations
- Amplification
- Deletion

Genes with highest frequency in any group

Survival

Interpret all results with caution, as they can be confounded by many different variables that are not controlled for in these analyses. Consider consulting a statistician.

❗ Patients (232) that overlap in the selected groups are excluded from patient-level analysis below.

Min # Patients: 10 Columns: 1

Gene	Survival Type	Number of Patients	p-Value	q-Value
KRAS	Progression Free	183	0.606	0.925
MUC16	Disease Free	115	0.894	0.925
TP53	Disease-specific	171	0.919	0.925
EGFR	Overall	183	0.925	0.925
COL5A3				
MCP2L				
EBF1				
ARHGAP35				
DCAF8L1				
ASTN2				
MTOR				
KIF4B				

Overall patient survival status.

Gene	Number of Cases, Total	Number of Events	Median Months Overall (95% CI)
(A) KRAS_mut	54	20	88.14 (29.46 - NA)
(B) MUC16_mut	30	12	41.36 (30.31 - NA)
(C) TP53_mut	99	34	49.28 (38.37 - NA)

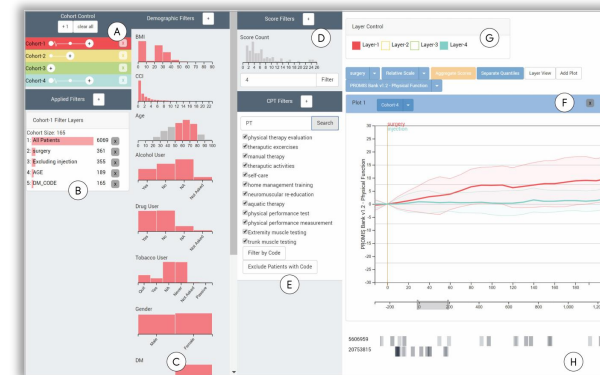
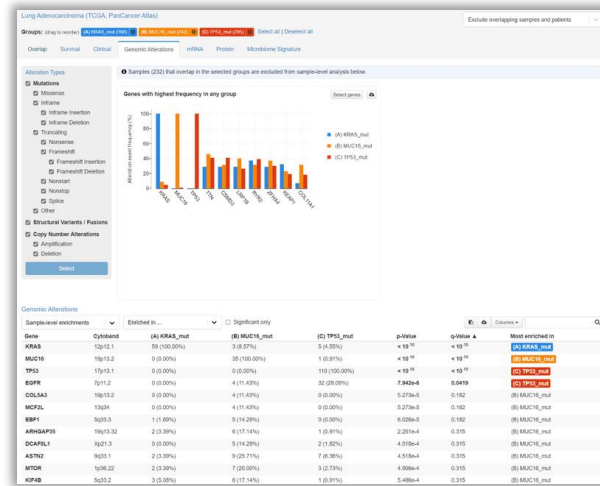
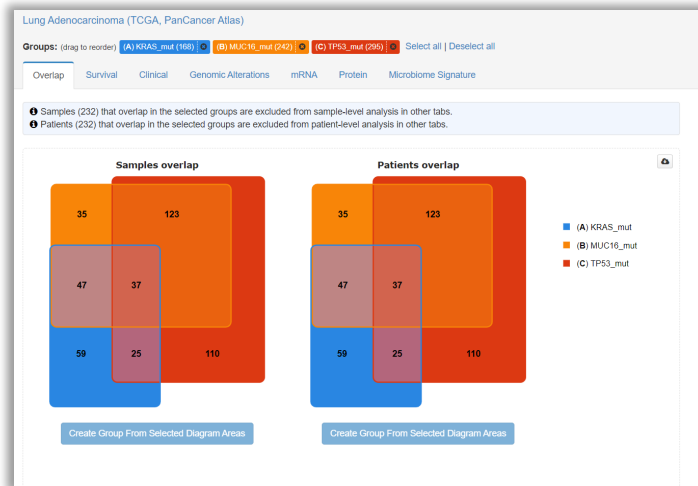
# Motivation

The image displays a comprehensive clinical data analysis workflow. It includes:

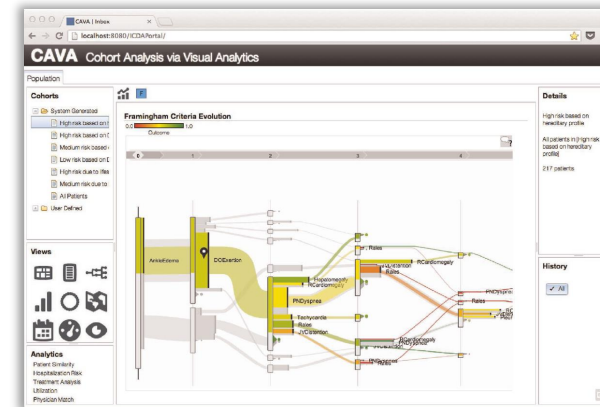
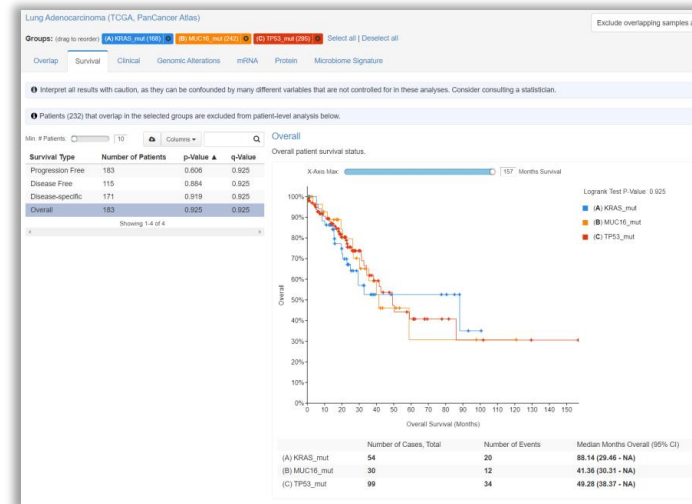
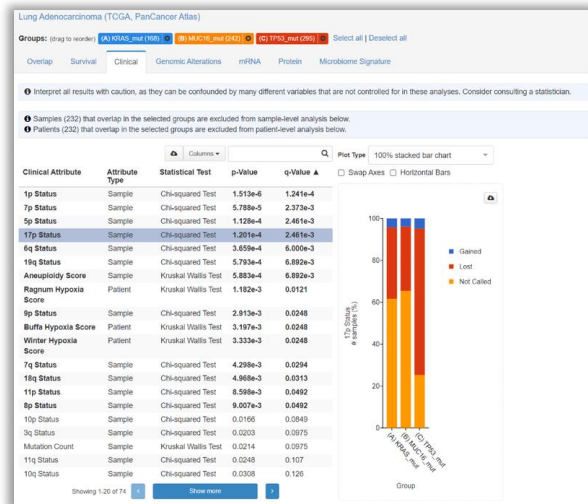
- Cohort Control:** A panel for defining cohorts (Cohort-1 to Cohort-4) with various filters and a 'Create Group From' button.
- Demographic Filters:** Histograms for BMI, CCI, Age, Alcohol User, Drug User, Tobacco User, and Gender.
- Score Filters:** A 'Score Count' histogram and a 'CPT Filters' search box.
- Layer Control:** A 'Layer View' section with 'Layer1' through 'Layer4' and a 'Plot 1' window showing a line graph of 'Physical Function' over time.
- CAVA Cohort Analysis via Visual Analytics:** A flowchart titled 'Framingham Criteria Evolution' showing transitions between risk states (e.g., Ankle Edema, DCExercise, PVDyspnea, etc.) and associated rates.
- Statistical Table:** A table listing clinical attributes (e.g., 1p Status, 7p Status, 17p Status) with their respective statistical tests, p-values, and q-values.
- Heatmap:** A large heatmap showing data for multiple patients across various clinical attributes.



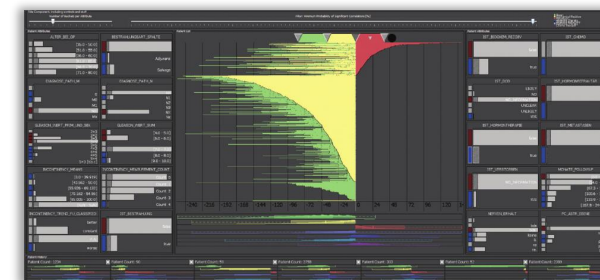
# Motivation



Rogers, Jen, et al. Composer—visual cohort analysis of patient outcomes. *Applied Clinical Informatics* 10.02 (2019): 278-285.



Zhang, Zhiyuan, David Gotz, and Adam Perer. Iterative cohort analysis and exploration. *Information Visualization* 14.4 (2015): 289-307.



Bernard, Jürgen, et al. A visual-interactive system for prostate cancer cohort analysis. *IEEE computer graphics and applications* 35.3 (2015): 44-55.

Cerami, Ethan, et al. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. *Cancer discovery* 2.5 (2012): 401-404  
 Gao, Jianjiong, et al. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. *Science signaling* 6.269 (2013): p11..

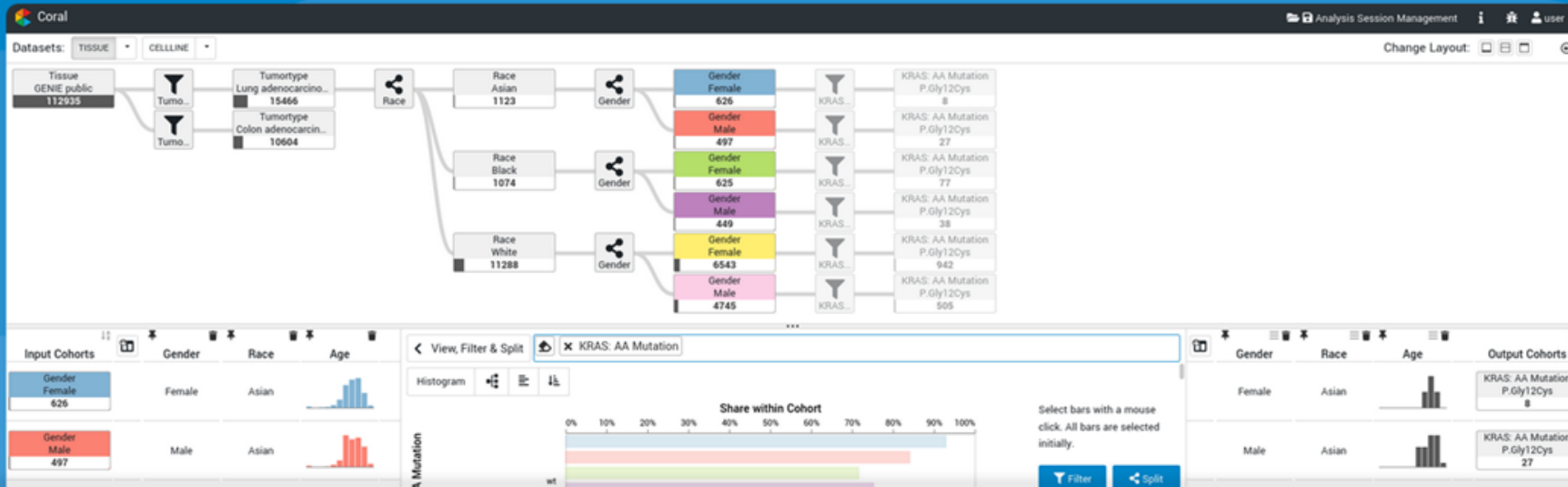


coral.jku-vds-lab.at

Coral is a cohort analysis tool to interactively create and refine patient cohorts, while visualizing their provenance in the Cohort Evolution Graph. The resulting cohorts can then be compared, characterized, and inspected down to the level of single entities.

Watch intro video

Learn more about Coral



## Getting Started

The workflow of Coral consists of two steps: creating cohorts, and characterizing them. Operations from these two categories are carried out in an iterative workflow.

### Cohort Creation

An initial cohort that contains all items of the selected dataset is created automatically. Creation operations allow users to create new sub-cohorts based on different attributes and attribute combinations. Cohorts are refined with the *Filter* operation, or divided into multiple cohorts with the *Split* operation.

### Cohort Characterization

Characterization operations give insights into the cohorts. Similarities and differences between cohorts can be checked visually with the *View* operation, and statistically with the *Compare* operation. Additional operations give access to prevalence information and the data of individual items.

Coral is a robust analysis tool to interactively create and refine patient cohorts, while visualizing their progression in the Cohort Evolution Graph. The resulting cohorts can then be compared, characterized, and inspected down to the level of single entities.

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### Getting Started

The workflow of Coral consists of two steps: creating cohorts and characterizing them. Operations from these two categories are carried out in an iterative manner.

#### Cohort Creation

In this step the user defines a set of the criteria based on which individuals from the dataset will be included in the cohort. The user can also define the cohort's name and description. The user can also define the cohort's color and the cohort's icon.

#### Cohort Characterization

In this step the user can inspect the cohort's characteristics and compare it with other cohorts. The user can also define the cohort's color and the cohort's icon. The user can also define the cohort's name and description.

# Datasets



<https://www.aacr.org/professionals/research/aacr-project-genie/>



<https://cancergenome.nih.gov>




<https://portals.broadinstitute.org/ccle>



# Use Case with GENIE Dataset

The NEW ENGLAND JOURNAL of MEDICINE

CORRESPONDENCE

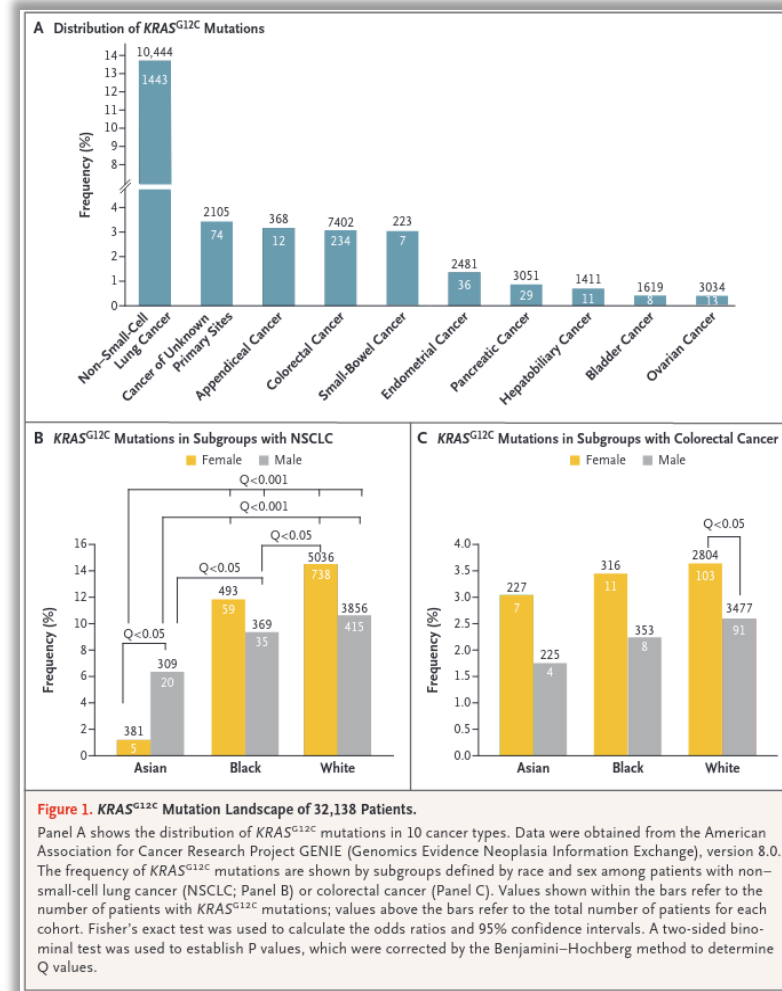


## Distribution of KRAS<sup>G12C</sup> Somatic Mutations across Race, Sex, and Cancer Type

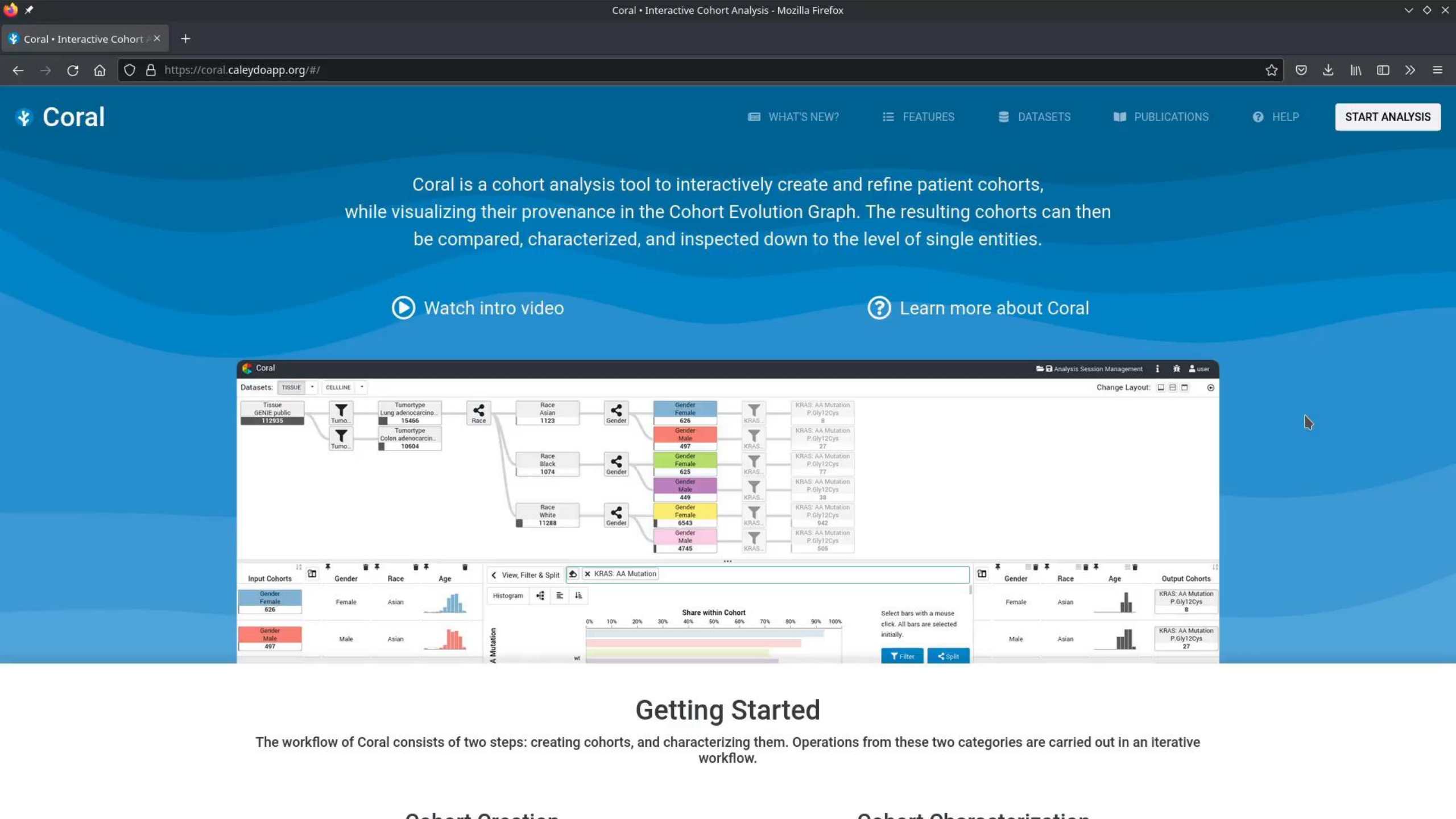
**TO THE EDITOR:** Hong et al. (Sept. 24 issue)<sup>1</sup> present results of an early-phase clinical trial of sotorasib, which showed promising clinical benefit. Patients had non-small-cell lung cancer (NSCLC; 46%) or colorectal cancer (33%), and White patients constituted 76% of the cohort. As drugs are being developed for the previously “undruggable” KRAS<sup>G12C</sup> mutation, it is imperative to study the distribution of this mutation across sex, race,<sup>2</sup> and all cancers.

We extracted data from the registry of the American Association for Cancer Research Project Genomics Evidence Neoplasia Information Exchange (GENIE), version 8.0<sup>3</sup> (see the Methods section in Supplementary Appendix 1). We studied the distribution of KRAS<sup>G12C</sup> mutations in 32,138 patients with cancer across race (Asian, Black, and White) and sex and in 10 cancer types (Table S1.1 in Supplementary Appendix 2). A total of 2045 patients (6.4%) were Asian, 2355 (7.3%) were Black, and 27,738 (86.3%) were White. KRAS<sup>G12C</sup> mutations were compared according to race and sex, and P values were correlated with colorectal cancer and those with NSCLC, female patients harbored significantly more KRAS<sup>G12C</sup> mutations than male patients (Table S1.3 in Supplementary Appendix 2).

Among patients with NSCLC, White and Black patient groups were enriched for KRAS<sup>G12C</sup> mutations more than Asians (White patients, 1153 of 8892 [13%]; Black patients, 94 of 862 [10.9%]; and Asian patients, 25 of 690 [3.6%]) (P<0.001). It is striking that there were differences by sex within the same ethnic groups of patients with NSCLC. KRAS<sup>G12C</sup> mutations occurred more often in White female patients than in White male patients with NSCLC (odds ratio, 1.4; 95% confidence interval [CI], 1.3 to 1.6; Q<0.001) and more often in Asian male patients than in Asian female patients (odds ratio, 5.2; 95% CI, 1.9 to 17.9; Q=0.01) (Fig. 1B, and Tables S1.4 and S1.5 in Supplementary Appendix 2). Among patients with colorectal cancer, White female patients were enriched for KRAS<sup>G12C</sup> mutations more than White male patients (odds ratio, 1.4; 95% CI, 1.1 to 1.9; Q=0.04) (Fig. 1C).



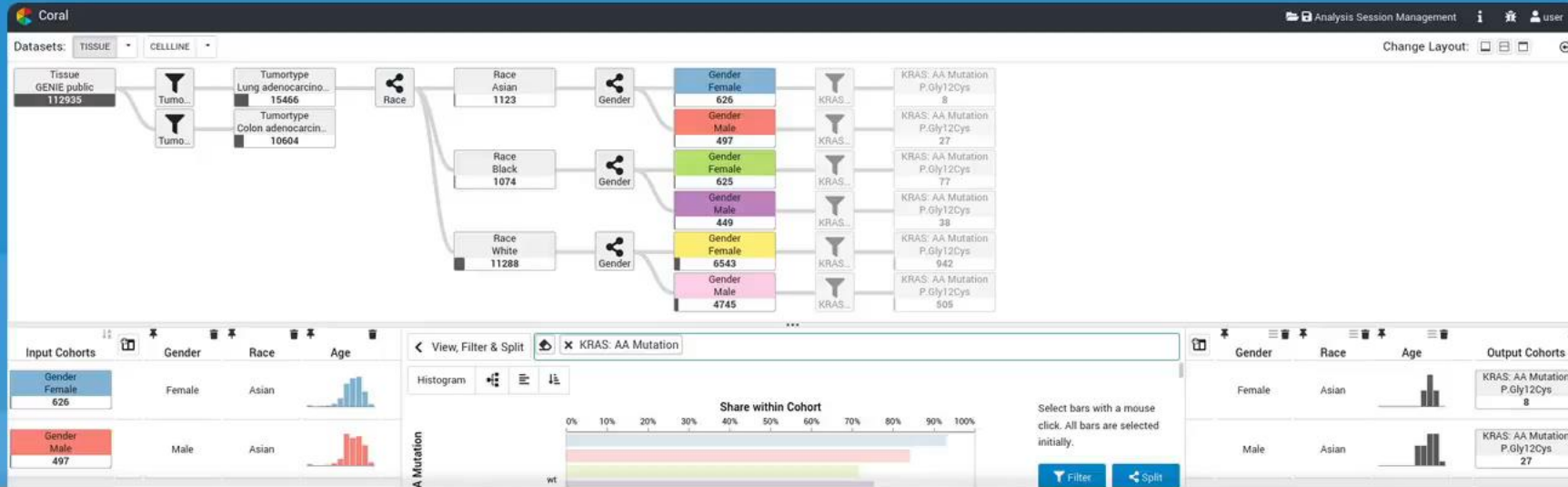
Nassar, Amin H., et al. Distribution of KRAS G12C somatic mutations across race, sex, and cancer type. *New England Journal of Medicine* 384.2 (2021): 185-187.



Coral is a cohort analysis tool to interactively create and refine patient cohorts, while visualizing their provenance in the Cohort Evolution Graph. The resulting cohorts can then be compared, characterized, and inspected down to the level of single entities.

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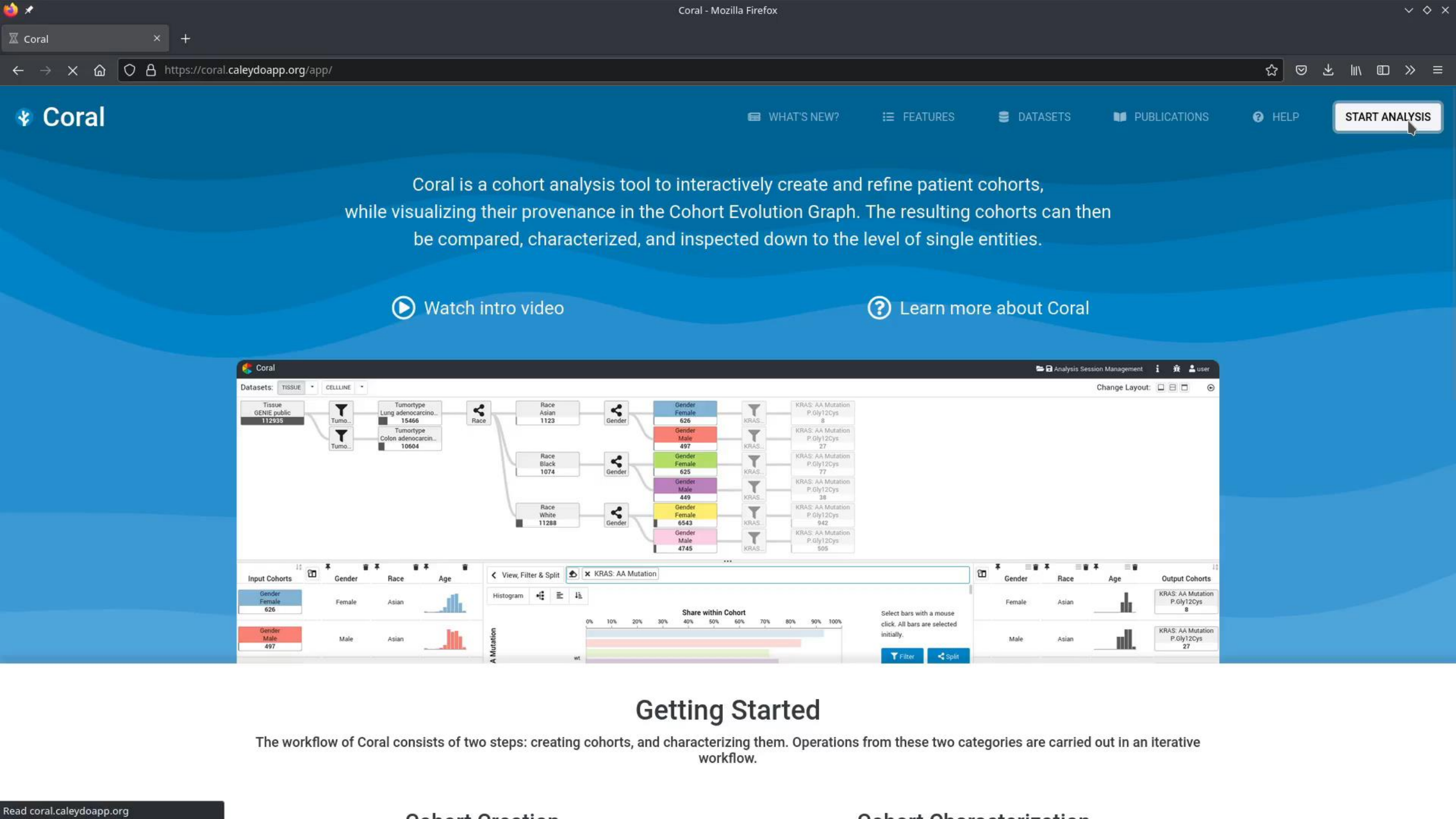


## Getting Started

The workflow of Coral consists of two steps: creating cohorts, and characterizing them. Operations from these two categories are carried out in an iterative workflow.

Cohort Creation

Cohort Characterization



Coral is a cohort analysis tool to interactively create and refine patient cohorts, while visualizing their provenance in the Cohort Evolution Graph. The resulting cohorts can then be compared, characterized, and inspected down to the level of single entities.

[Watch intro video](#)

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## Getting Started

The workflow of Coral consists of two steps: creating cohorts, and characterizing them. Operations from these two categories are carried out in an iterative workflow.

Cohort Creation

Cohort Characterization

Coral - Mozilla Firefox

Coral

https://coral.caleydoapp.org/app/#clue\_graph=coral29&clue\_state=3

biovis Analysis Session Management

Datasets: TISSUE CELLLINE New Session Change Layout:

Tissue GENIE public 112935

Input Cohorts

Tissue GENIE public 112935

Output Cohorts

### Continue by Choosing an Operation

For more details about the operations, move your mouse over the respective button.

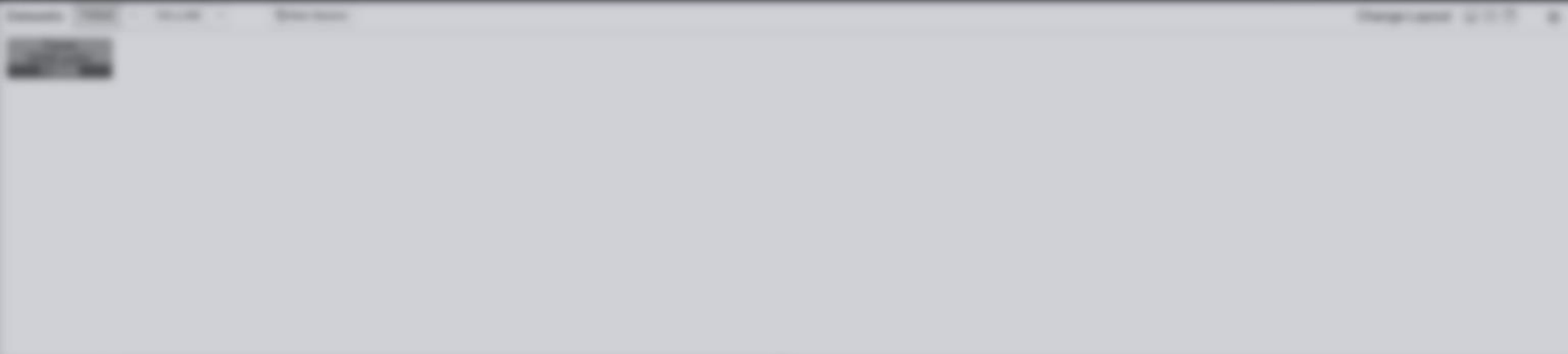
#### Create Cohorts (with output)

View Filter & Split

#### Characterize Cohorts (without output)

Prevalence Inspect Items Compare

Clear



**Continue by Choosing an Operation**  
To view results about the operation, click one of the operations below.

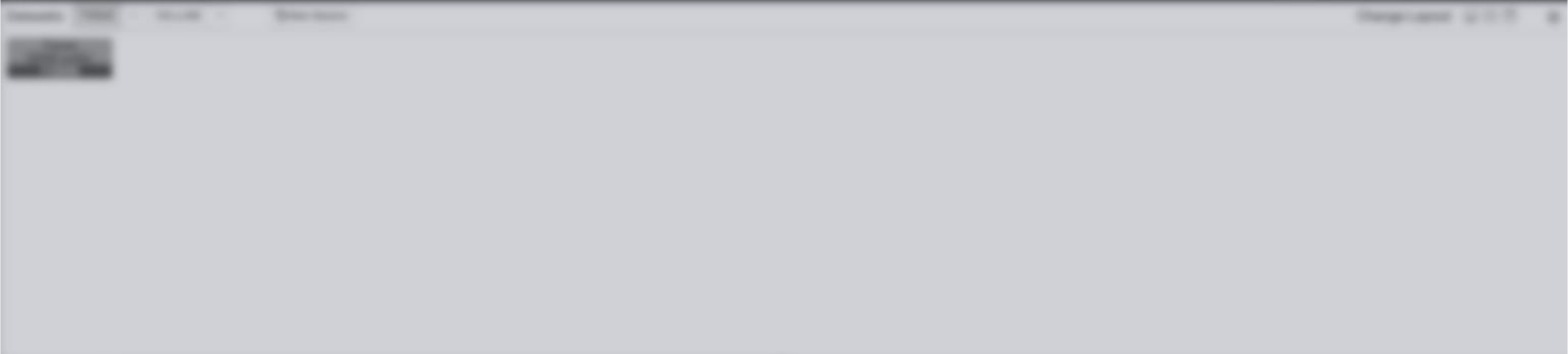
**Create Cohorts** view icon

 **View**  **Filter**

**Characterize Cohorts** view icon




 **Compare**  **Export Data**  **Global**








**Continue by Choosing an Operation**  
To view details about the operations, click on the icon in the right-hand column.

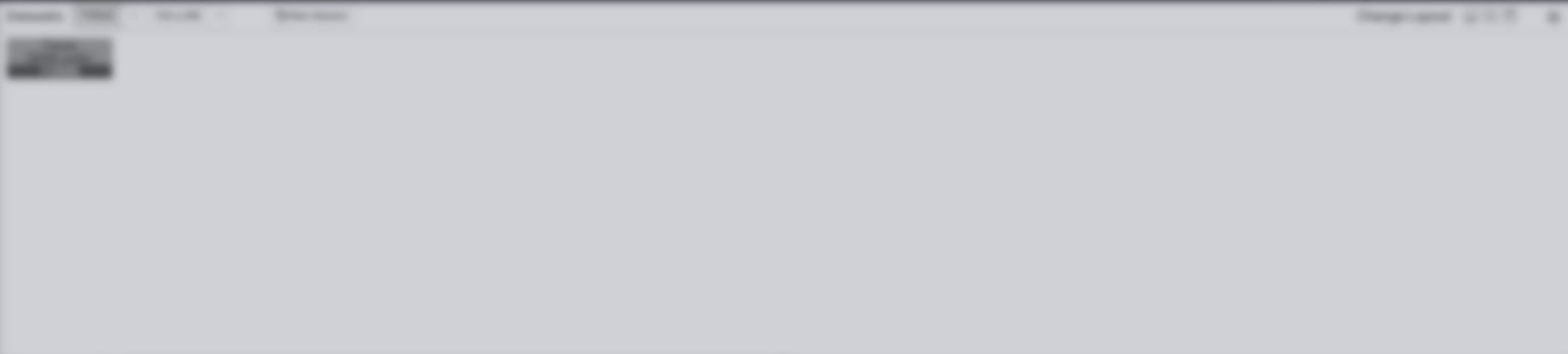
**Create Cohorts** view icon

-   

**Characterize Cohorts** view icon

-   

Bottom navigation bar with a home icon.



**Continue by Choosing an Operation**  
To view results about the operation, click one of the operation icons.

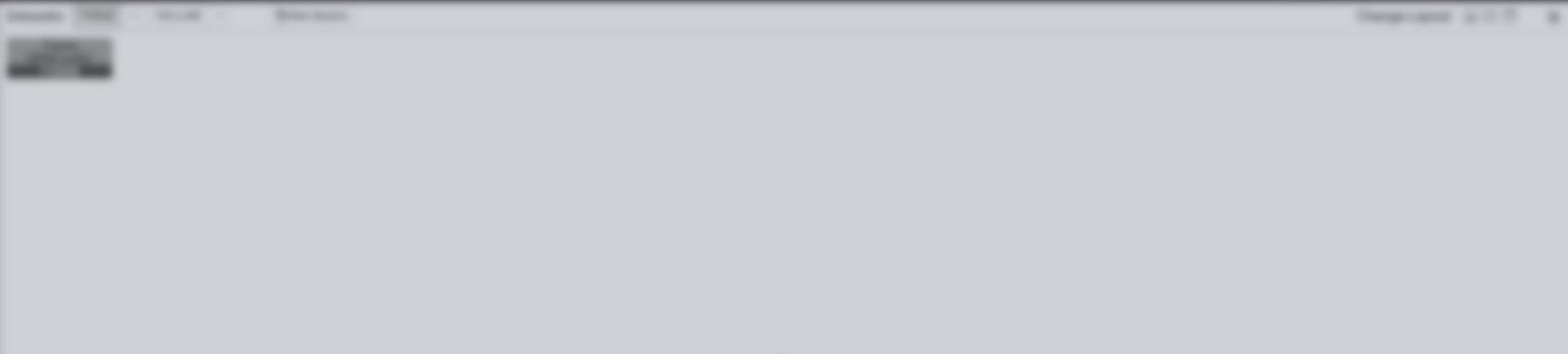
**Create Cohorts** view icon

**Characterize Cohorts** view icon



  

Prevalence






**Continue by Choosing an Operation**  
To view details about the operations, click any icon in the operation table.

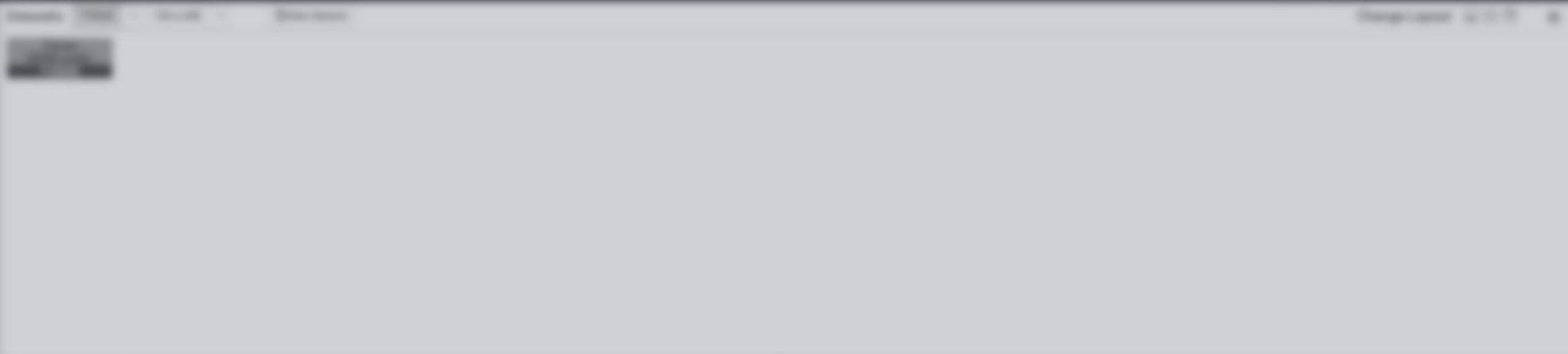
**Create Cohorts**

**Characterize Cohorts**



  

**Inspect Items**






**Continue by Choosing an Operation**  
To view results about the operation, click one of the icons below.

**Create Cohorts** Learn more

**Characterize Cohorts** Learn more

**Compare**

Coral - Mozilla Firefox

Coral

https://coral.caleydoapp.org/app/#clue\_graph=coral29&clue\_state=3

biovis Analysis Session Management

Datasets: TISSUE CELLLINE New Session Change Layout:

Tissue GENIE public 112935

Input Cohorts

Tissue GENIE public 112935

Output Cohorts

### Continue by Choosing an Operation

For more details about the operations, move your mouse over the respective button.

#### Create Cohorts (with output)

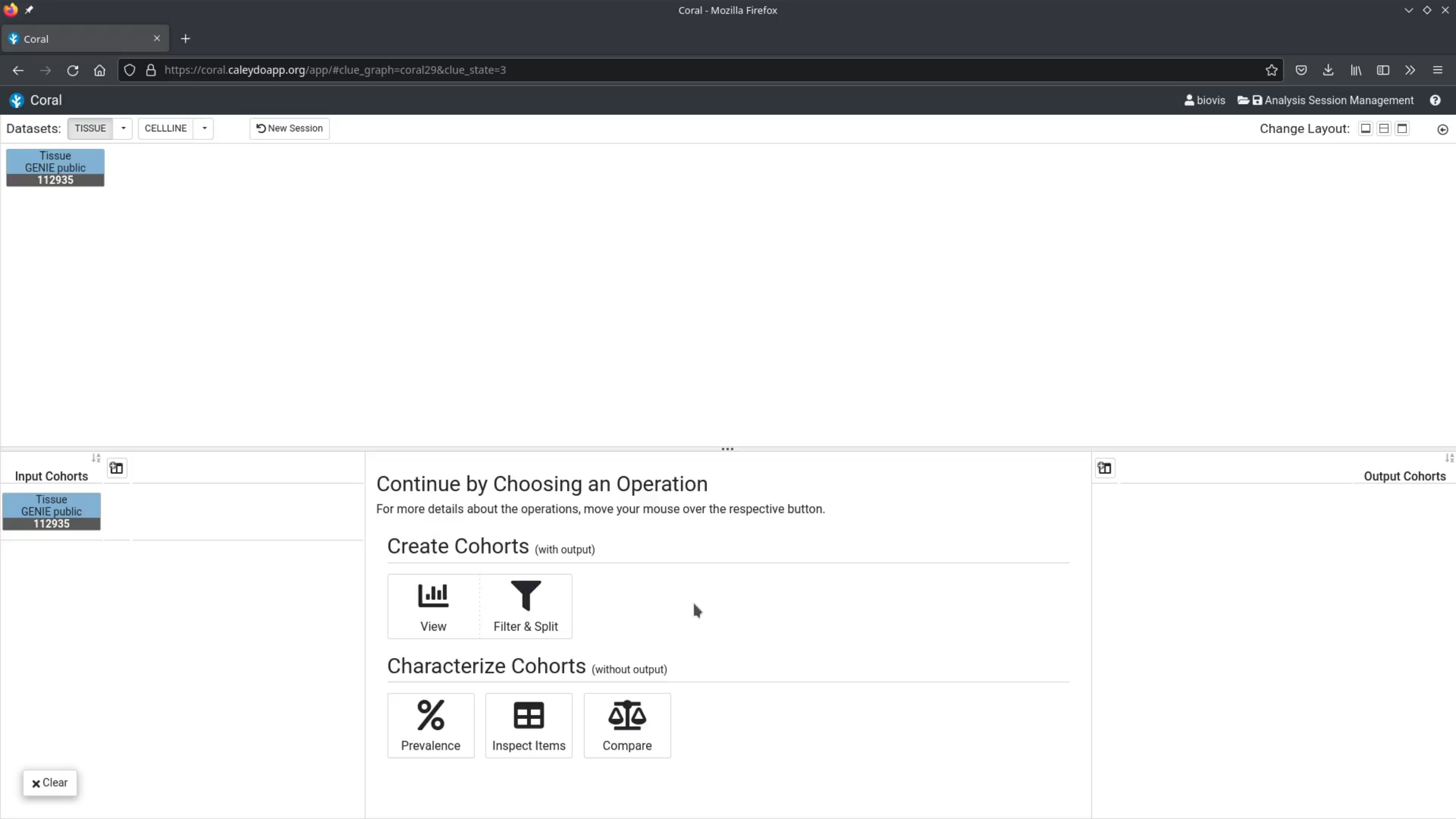
View Filter & Split

#### Characterize Cohorts (without output)

Prevalence Inspect Items Compare

Clear





Tissue  
GENIE public  
112935

Input Cohorts

Tissue  
GENIE public  
112935

Clear

Continue by Choosing an Operation

For more details about the operations, move your mouse over the respective button.

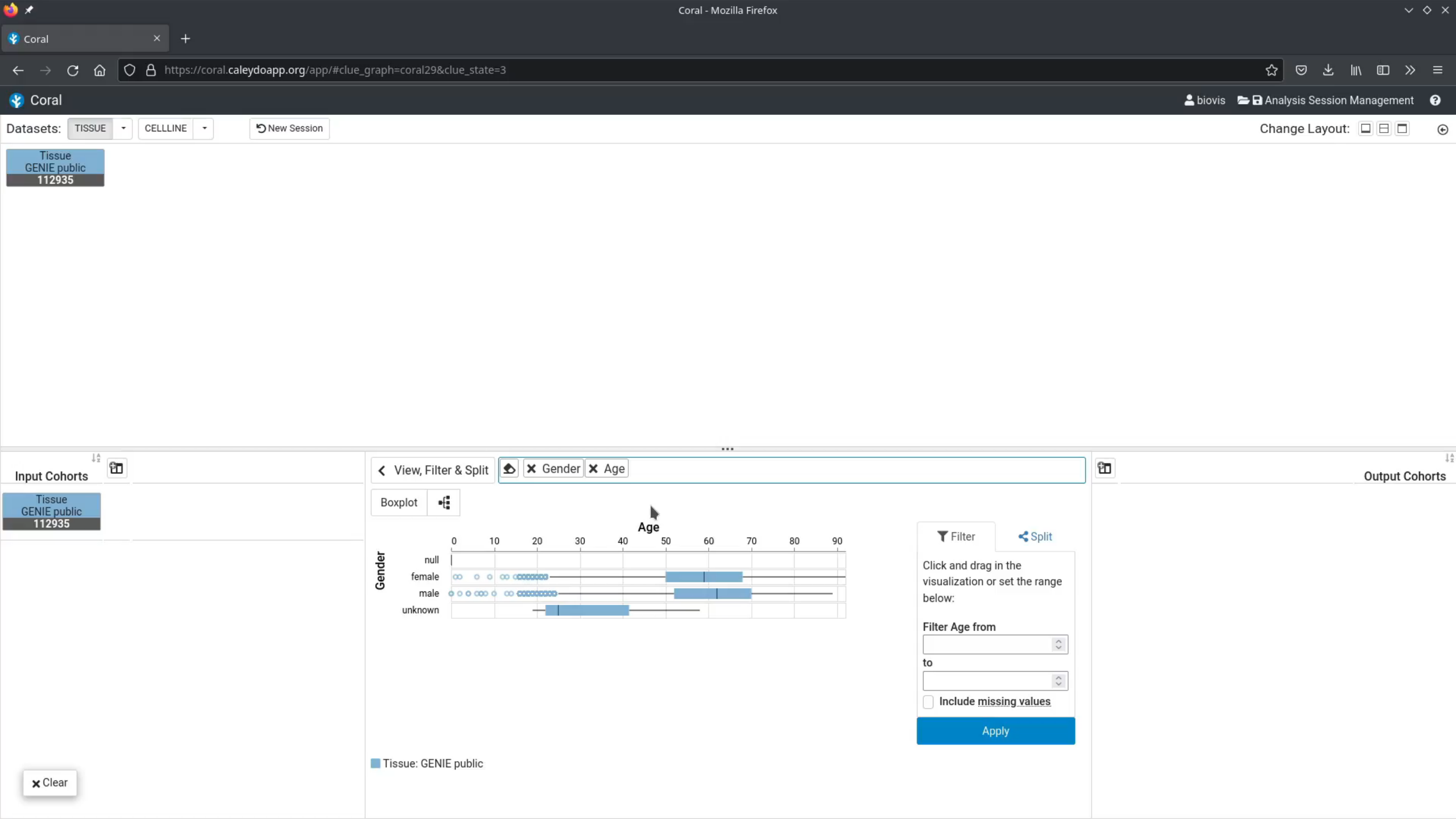
Create Cohorts (with output)

View Filter & Split

Characterize Cohorts (without output)

Prevalence Inspect Items Compare

Output Cohorts



Datasets: TISSUE CELLLINE New Session

Change Layout: [Icons]



**Input Cohorts**

Tissue GENIE public 112935

View, Filter & Split **Tumortype**

colorectal adenocarcinoma	[Bar]
acute myeloid leukemia	[Bar]
bladder urothelial carcino...	[Bar]
glioblastoma multiforme	[Bar]
rectum adenocarcinoma	[Bar]
invasive breast carcinoma	[Bar]
melanoma	[Bar]
cutaneous melanoma	[Bar]
uterine endometrioid carci...	[Bar]
lung squamous cell carcin...	[Bar]
glioblastoma	[Bar]
breast invasive lobular car...	[Bar]
gastrointestinal stromal tu...	[Bar]
unknown	[Bar]
esophageal adenocarcino...	[Bar]
non-small cell lung cancer	[Bar]
myelodysplastic syndromes	[Bar]
papillary thyroid cancer	[Bar]
adenocarcinoma, nos	[Bar]
cancer of unknown primary	[Bar]
renal clear cell carcinoma	[Bar]

Select bars with a mouse click. All bars are selected initially.

**Filter** **Split**

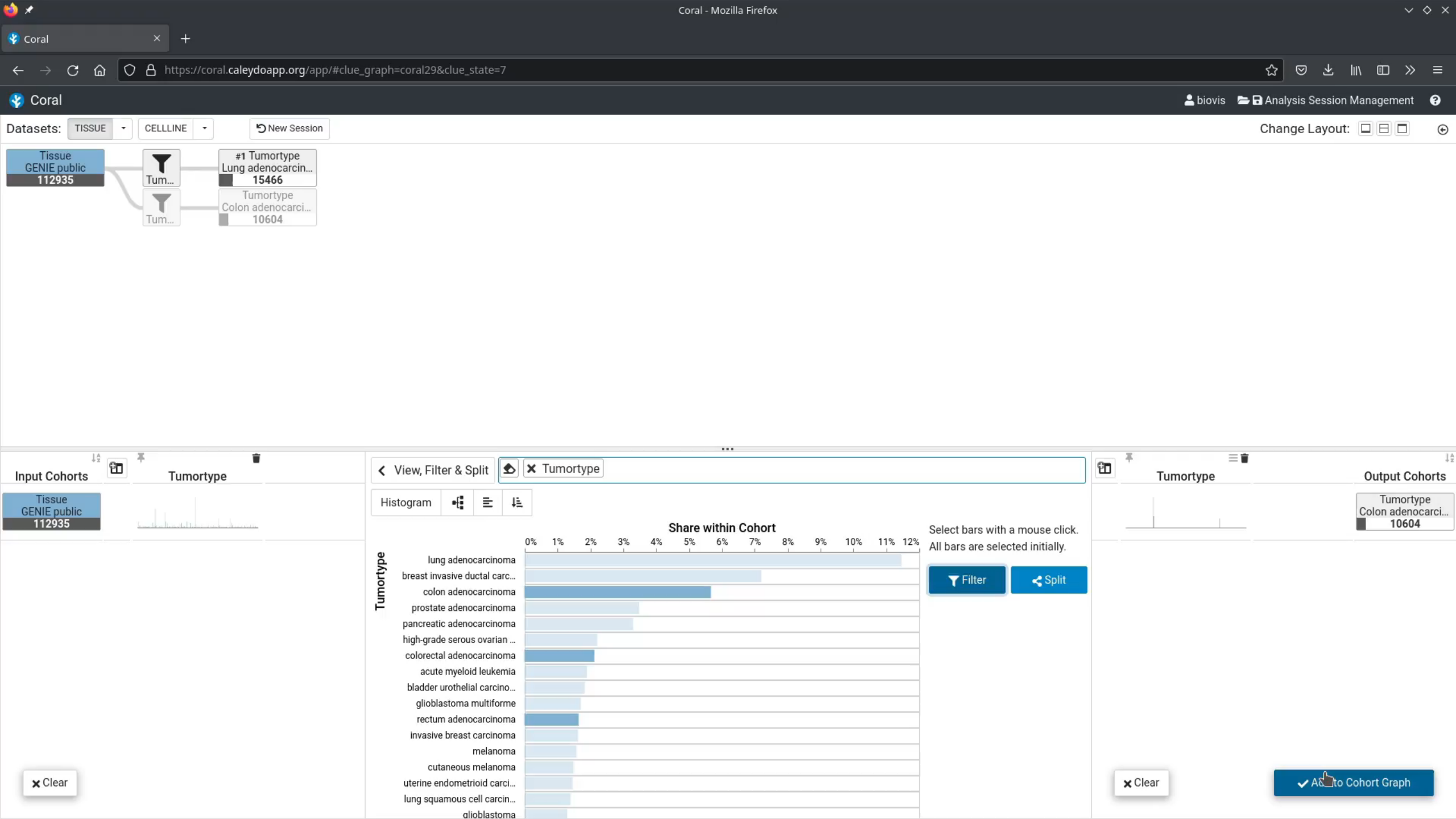
**Output Cohorts**

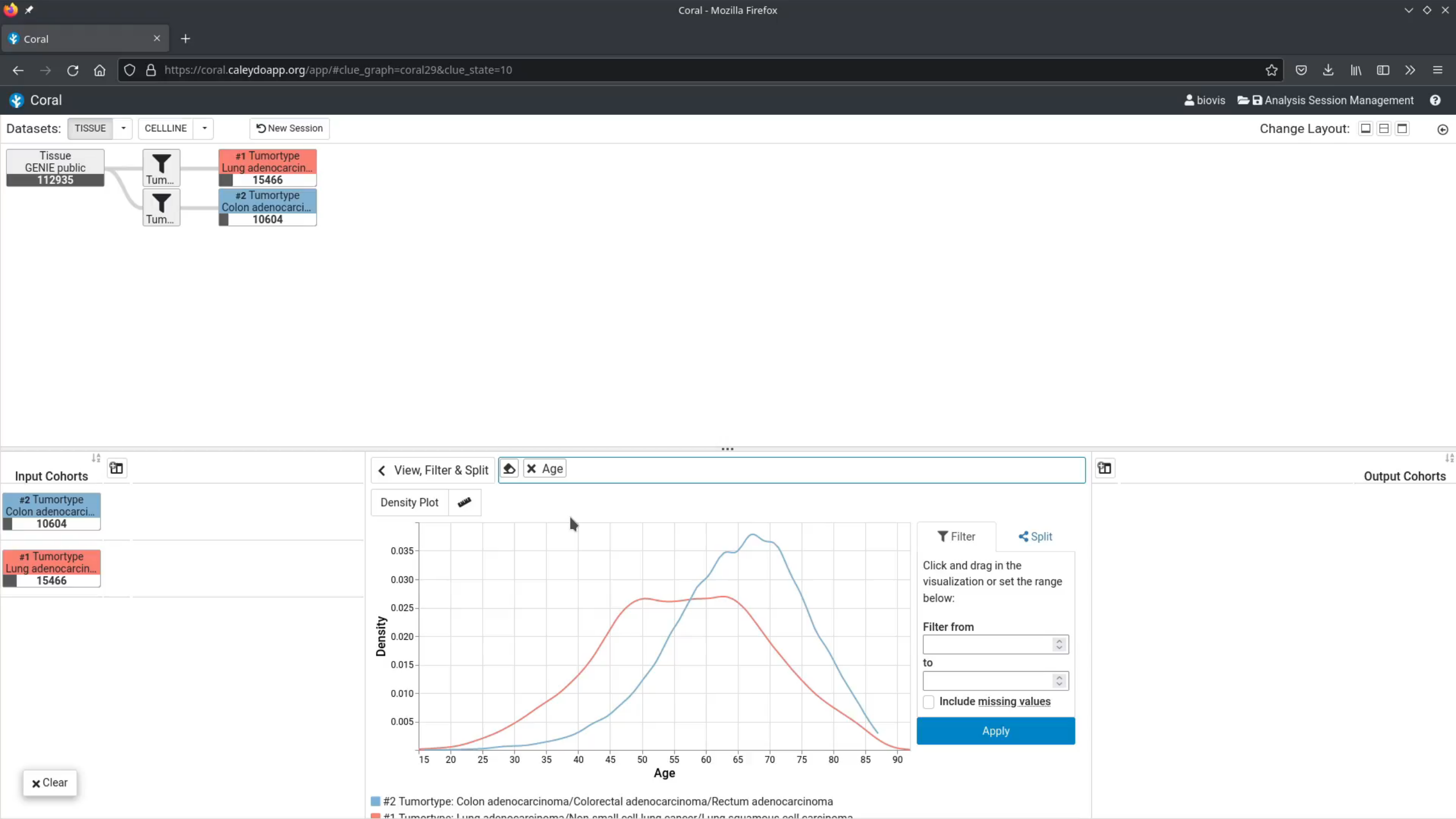
Tumortype Lung adenocarcin... 15466

Clear

Clear

Add to Cohort Graph







Coral - Mozilla Firefox

Coral

https://coral.caleydoapp.org/app/#clue\_graph=coral29&clue\_state=10

biovis Analysis Session Management

Datasets: TISSUE CELLLINE New Session

Change Layout: [Icons]

Tissue GENIE public 112935

Tum... #1 Tumortype Lung adenocarcin... 15466

Tum... #2 Tumortype Colon adenocarci... 10604

Input Cohorts

#2 Tumortype Colon adenocarci... 10604

#1 Tumortype Lung adenocarcin... 15466

Clear

Compare [X] Age [X] Gender

### Difference of Cohorts

Click a value in the table for details.

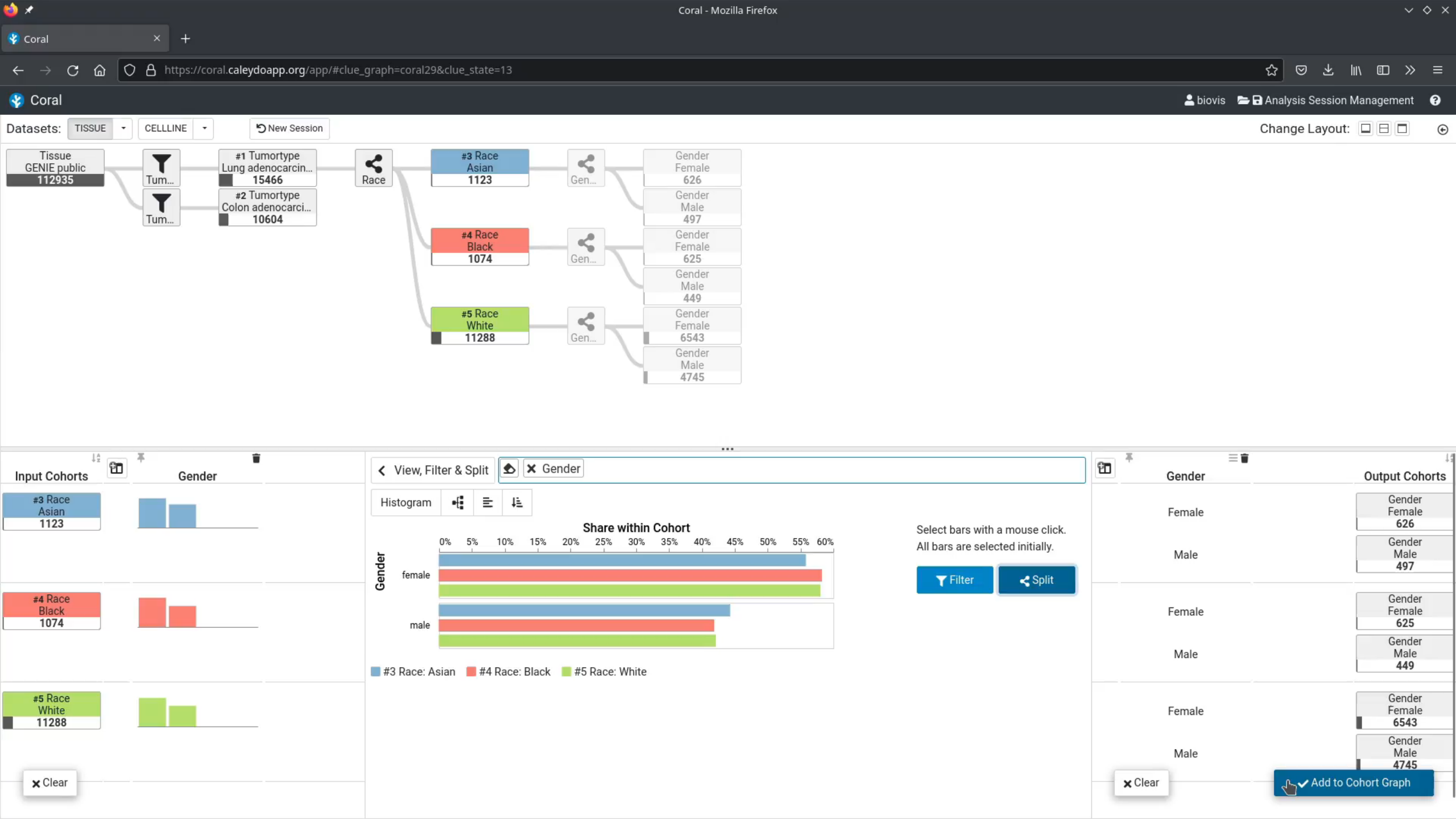
	#2 Tumortype: Colo...	#1 Tumortype: Lun...
Age	.000	.000
Gender	.000	.000

**Data Column:** Gender / **Comparing** #2 Tumortype: Colon adenocarcinoma/Colorectal adenocarcinoma/Rectum adenocarcinoma [10604] vs. #1 Tumortype: Lung adenocarcinoma/Non-small cell lung cancer/Lung squamous cell carcinoma [15466]

**Chi-Square Test:** 0.122, p-Value: 0.000e+0

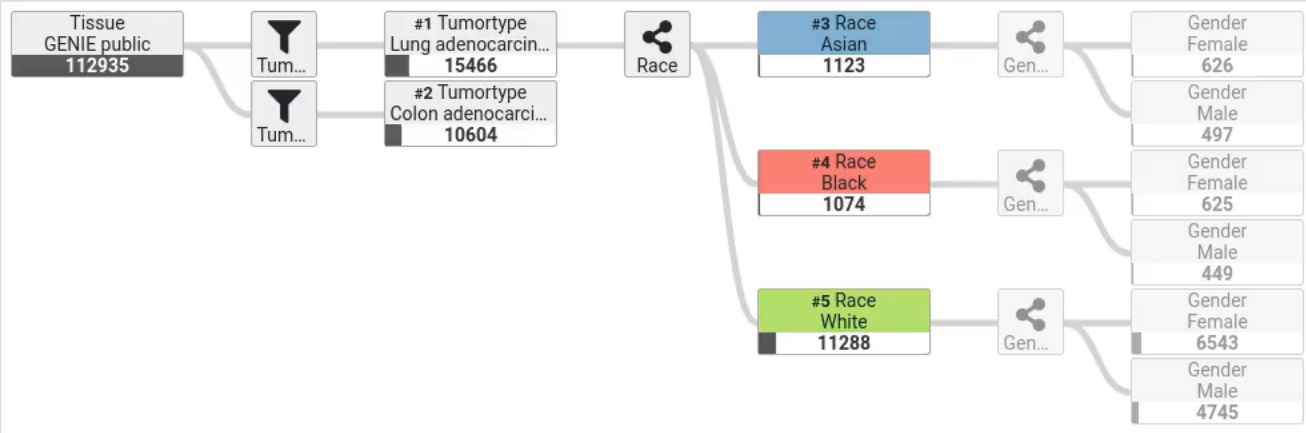
**Description:** The Chi-Square test compares the distribution of categories in two sets.

Gender	#2 Tumortype: Colon adenocarcinoma/Colorectal adenocarcinoma/Rectum adenocarcinoma [10604]	#1 Tumortype: Lung adenocarcinoma/Non-small cell lung cancer/Lung squamous cell carcinoma [15466]
female	~45%	~55%
male	~55%	~40%
unknown	~0%	~0%



Datasets: TISSUE CELLLINE New Session

Change Layout: [Icons]

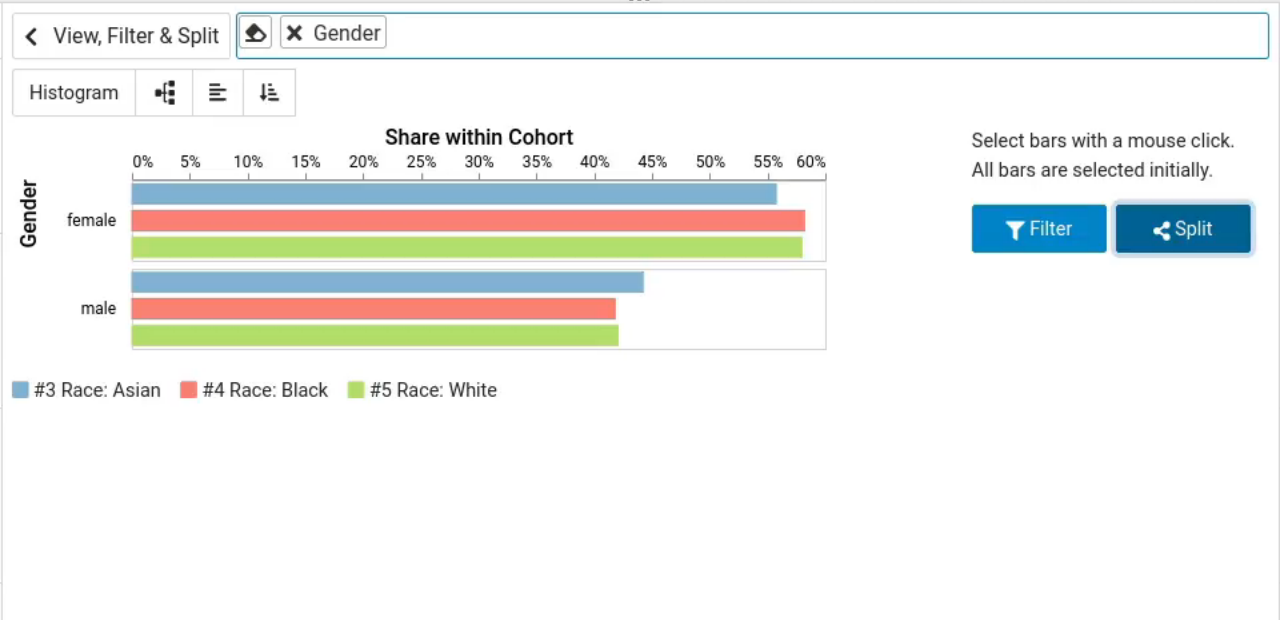


**Input Cohorts**

Cohort	Count
#3 Race Asian	1123
#4 Race Black	1074
#5 Race White	11288

Gender

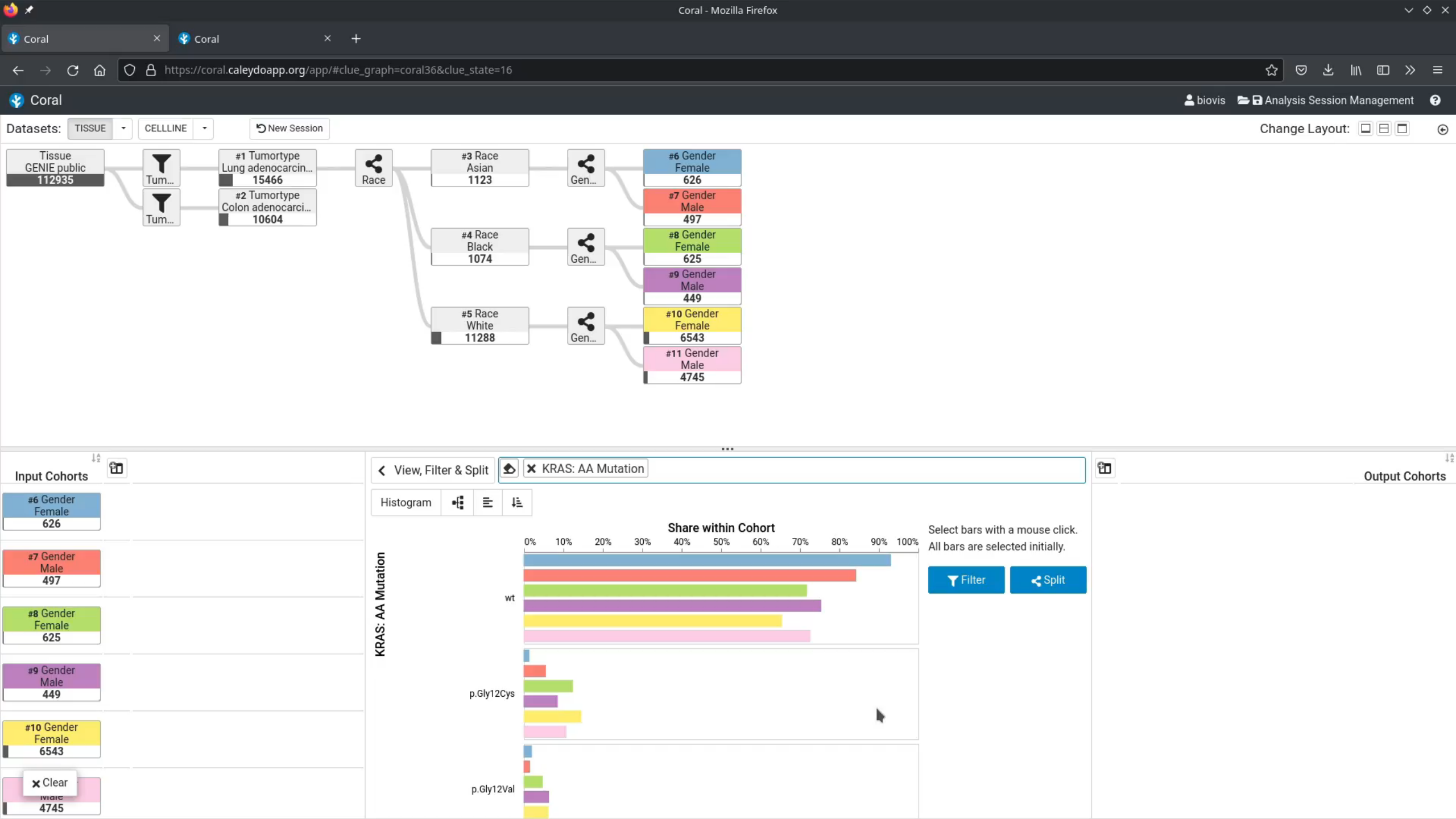
Clear

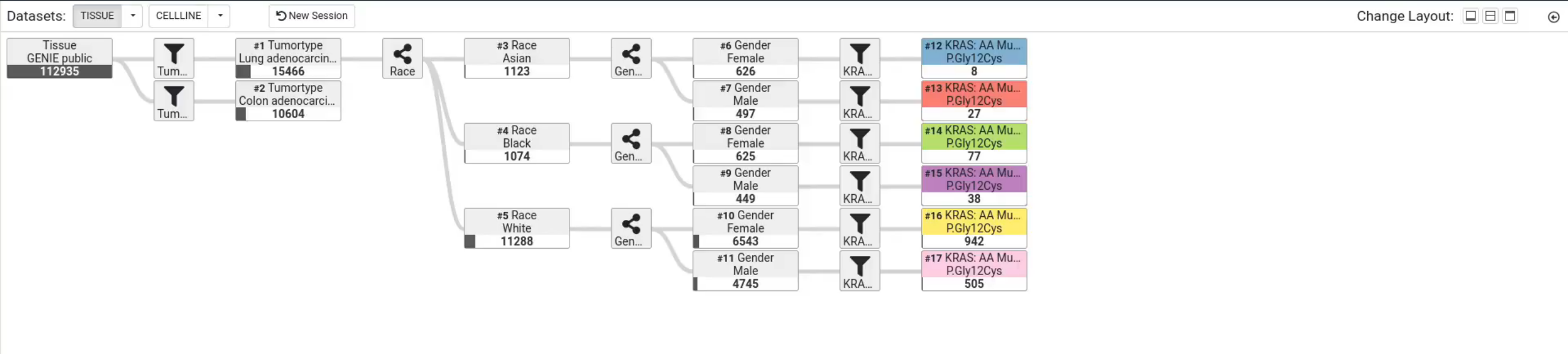


**Output Cohorts**

Female	Gender Female 626
Male	Gender Male 497
Female	Gender Female 625
Male	Gender Male 449
Female	Gender Female 6543
Male	Gender Male 4745

Clear Add to Cohort Graph





Input Cohorts

#12 KRAS: AA Mu... P.Gly12Cys 8
#13 KRAS: AA Mu... P.Gly12Cys 27
#14 KRAS: AA Mu... P.Gly12Cys 77
#15 KRAS: AA Mu... P.Gly12Cys 38
#16 KRAS: AA Mu... P.Gly12Cys 942
#17 KRAS: AA Mu... P.Gly12Cys 505

Prevalence

Filter out the missing values from the reference cohorts.

Tissue: GENIE public

Reference, defined by

- Tumortype: Lung adenocarcinoma/Non-small c...  Race: Asian  Gender: Female  KRAS: AA Mutation: P.Gly12Cys
- #12 KRAS: AA Mutation: P...  Tumortype: Lung adenocarcinoma/Non-small c...  Race: Asian  Gender: Female  KRAS: AA Mutation: P.Gly12Cys

1% ± < 1% 8 | 100% 626

---

Tissue: GENIE public

Reference, defined by

- Tumortype: Lung adenocarcinoma/Non-small c...  Race: Asian  Gender: Male  KRAS: AA Mutation: P.Gly12Cys
- #13 KRAS: AA Mutation: P...  Tumortype: Lung adenocarcinoma/Non-small c...  Race: Asian  Gender: Male  KRAS: AA Mutation: P.Gly12Cys

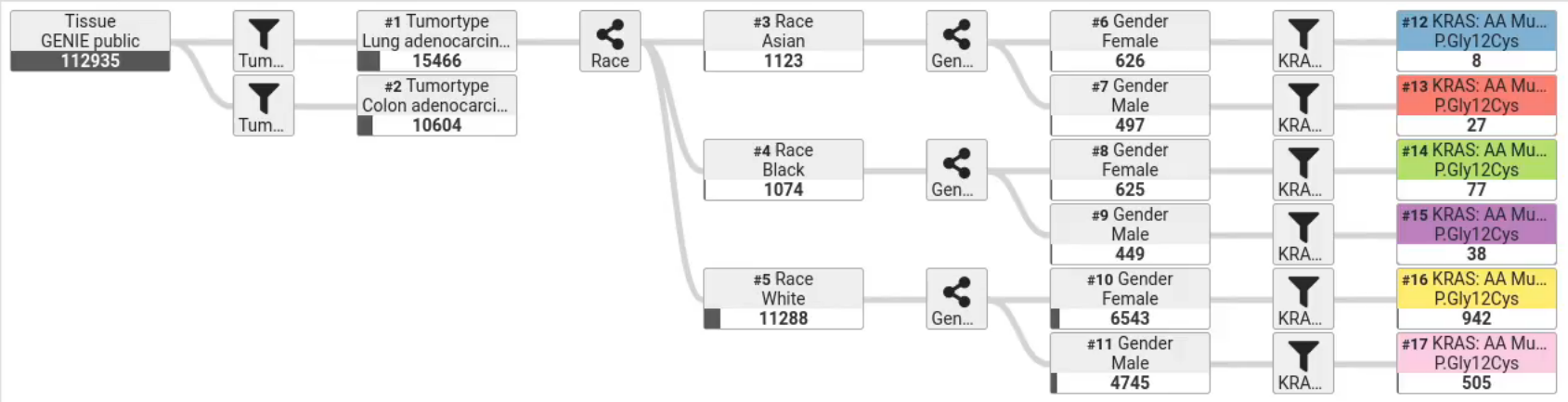
100% 2510 | 1% ± < 1% 27

---

Tissue: GENIE public

Reference, defined by

- Tumortype: Lung adenocarcinoma/Non-small c...  Race: Black  Gender: Female  KRAS: AA Mutation: P.Gly12Cys



Input Cohorts

#12 KRAS: AA Mu... P.Gly12Cys 8
#13 KRAS: AA Mu... P.Gly12Cys 27
#14 KRAS: AA Mu... P.Gly12Cys 77
#15 KRAS: AA Mu... P.Gly12Cys 38
#16 KRAS: AA Mu... P.Gly12Cys 942
#17 KRAS: AA Mu... P.Gly12Cys 505

Inspect Items

Age Gender

Aggr...	Rank	Id	Cohort	# Age	Gender
				39.00	female
				87.00	male
10		GENIE-DFCI-007663			male
11		GENIE-DFCI-090232			male
12		GENIE-DFCI-117915			male
13		GENIE-DFCI-161382			male
14		GENIE-JHU-02855-0			male
15		GENIE-MSK-P-00035			male
16		GENIE-MSK-P-00058			male
17		GENIE-MSK-P-00068			male
18		GENIE-MSK-P-00120			male
19		GENIE-MSK-P-00164			male
20		GENIE-MSK-P-00246			male
21		GENIE-MSK-P-00269			male
22		GENIE-MSK-P-00269			male
23		GENIE-MSK-P-00269			male

Export Data

Showing 1,597 of 1,597 items

Column Summaries

Id

Filter Id...

Use regular expressions

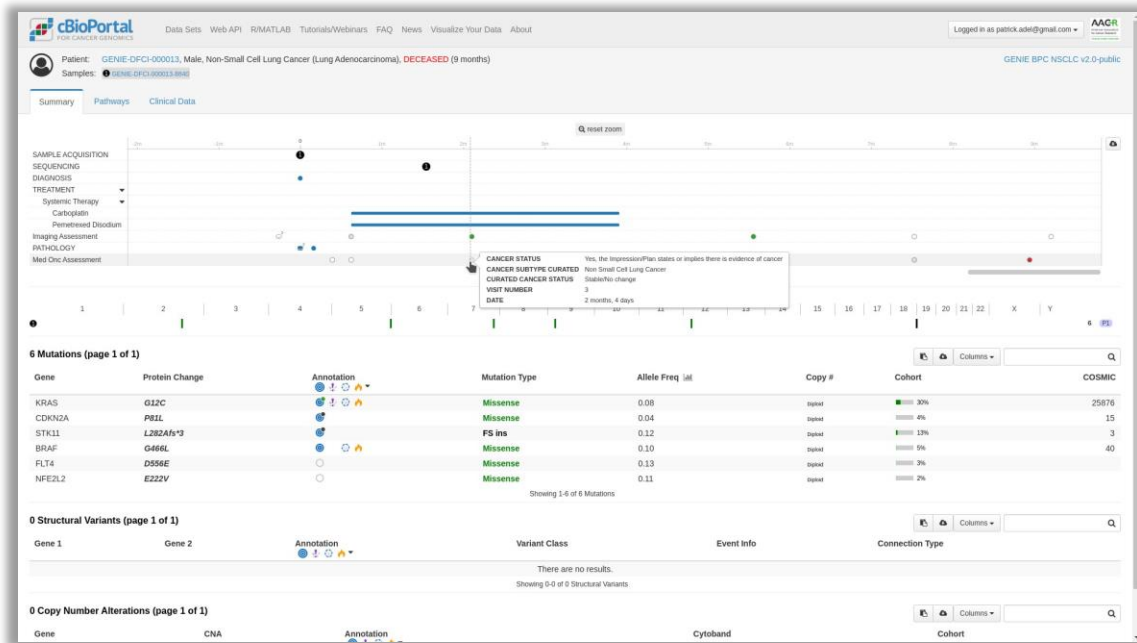
Filter rows containing missing values

Cohort

Filter 0 missing value rows



# Future Work



cBioPortal, <https://genie.cbioportal.org/>

# Future Work

The image displays two overlapping software interfaces. The background interface is cBioPortal, showing patient information for GENIE-DFCI-000113, a male with Non-Small Cell Lung Cancer (Lung Adenocarcinoma), and a list of mutations including KRAS G12C, CDKN2A P81L, and others. The foreground interface is Coral, showing a flowchart of cohort selection based on attributes like Tissue, Tumor type, Race, and Gender, leading to specific cohort IDs. Below the flowchart, there is a table of cohort differences and a heatmap visualization of gene importance across various genes like EGFR, TP53, and KRAS.

**cBioPortal Patient Data:**

- Patient: GENIE-DFCI-000113, Male, Non-Small Cell Lung Cancer (Lung Adenocarcinoma), DECEASED (9 months)
- Genotype: GENIE-BPC NSCLC v2.0-public

**6 Mutations (page 1 of 1)**

Gene	Protein Change	Annotation	Mutation Type
KRAS	G12C	Missense	Missense
CDKN2A	P81L	Missense	Missense
STK11	L282Afs*3	FS ins	FS ins
BRAF	G466L	Missense	Missense
FLT4	D556E	Missense	Missense
NFE2L2	E222V	Missense	Missense

**0 Structural Variants (page 1 of 1)**

There are no results. Showing 0 of 0 Structural Variants.

**0 Copy Number Alterations (page 1 of 1)**

Showing 0 of 0 Copy Number Alterations.

**Coral Cohort Selection:**

- #1 Tumor type: Lung adenocarcinoma (15466)
- #2 Race: Asian (1123)
- #3 Race: Black (1074)
- #4 Race: White (11288)
- #5 Gender: Female (626)
- #6 Gender: Male (497)
- #7 Gender: Female (625)
- #8 Gender: Male (449)
- #9 Gender: Female (6543)
- #10 Gender: Male (4745)

**Cohort Differences:**

Compare by Meta-Data | Compare by AA Mutated | Exclude the cohorts' defining attributes

Agg...	Rank	Gene	Δ Attribute	Category	# Importance
1	1	EGFR	0.00	1.00	111
2	2	TP53	0.00	1.00	111
3	3	KRAS	0.00	1.00	111
4	4	STK11	0.00	1.00	111
5	5	PIK3CA	0.00	1.00	111
6	6	CTNNB1	0.00	1.00	111
7	7	ATM	0.00	1.00	111
8	8	BRAF	0.00	1.00	111
9	9	ERBB2	0.00	1.00	111
10	10	CDKN2A	0.00	1.00	111
11	11	PDGFRA	0.00	1.00	111
12	12	SMAD4	0.00	1.00	111

cBioPortal, <https://genie.cbioportal.org/>

# Future Work

**6 Mutations (page 1 of 1)**

Gene	Protein Change	Annotation	Mutation Type
KRAS	G12C	Missense	Missense
CDKN2A	PEL1	Missense	Missense
STK11	L282Afs*3	FS ins	FS ins
BRAF	G466L	Missense	Missense
FLT4	D556E	Missense	Missense
NFE2L2	E222V	Missense	Missense

cBioPortal, <https://genie.cbioportal.org/>

**Input Cohorts**

#	Gender	Count
#5	Female	626
#7	Female	625
#9	Female	6543

Kaggle, <https://www.kaggle.com/datasets>

## Datasets

Explore, analyze, and share quality data. Learn more about data types, creating, and collaborating.

+ New Dataset

Search datasets

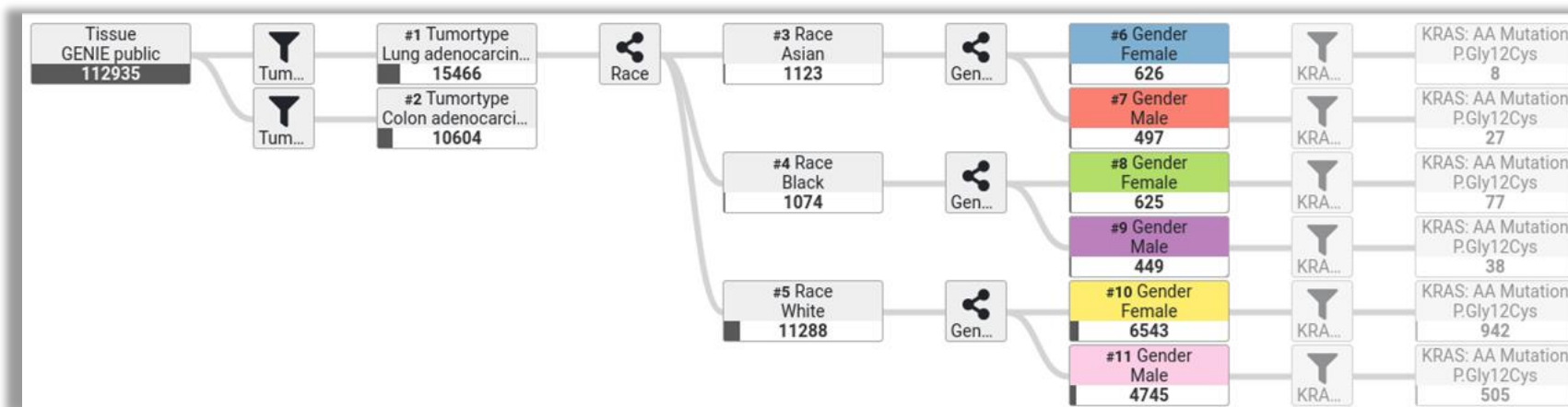
Computer Science Education Classification Computer Vision NLP Data Visualization Pre-Trained Model

### Trending Datasets



- Happy Fourth Of July 2022 (Twitter Dataset)**  
BrandofWinds - Updated 2 hours ago  
Usability 10.0 - 34 MiB  
1 File (other)
- Valve & Blizzard Games Dataset**  
Eduick-Kesuma - Updated 4 hours ago  
Usability 8.8 - 5 KiB  
2 Files (CSV)
- NIFTY-500 Stocks Dataset**  
Souhav Banerjee - Updated 17 hours ago  
Usability 10.0 - 31 KiB  
1 File (CSV)
- Cyclicistic Capstone Project**  
Shane Martin - Updated 17 hours ago  
Usability 6.5 - 53 MiB  
2 Files (CSV)

# Coral

## Web-based Visual Analysis Tool for Creating and Characterizing Cohorts



Patrick Adelberger, Klaus Eckelt, Markus J. Bauer,  
Marc Streit, Christian Haslinger, and Thomas Zichner

 <https://jku-vds-lab.at/biovis22-adelberger>  
 [patrick.adelberger@jku.at](mailto:patrick.adelberger@jku.at)