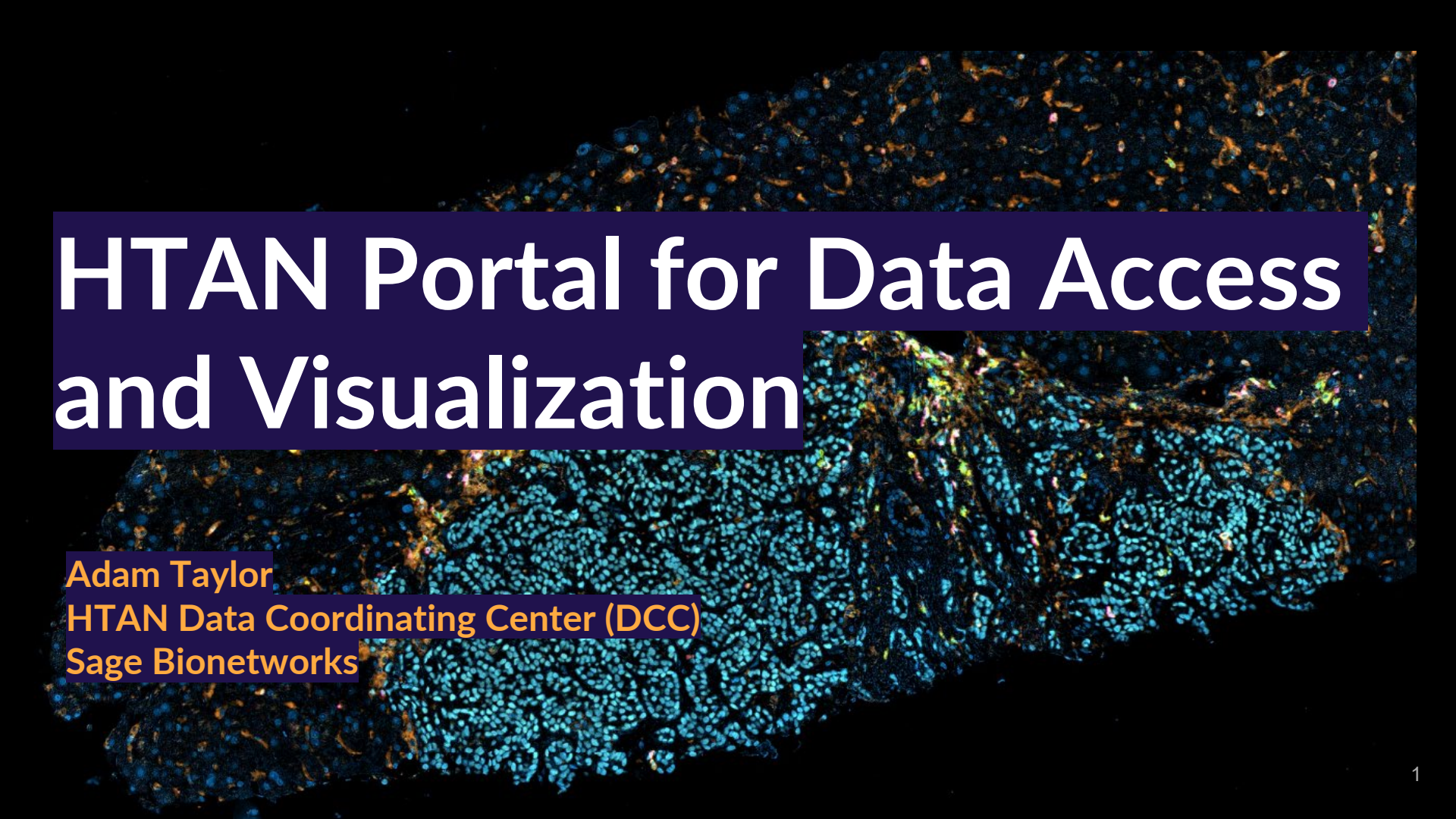


A microscopic image of tissue, likely a histological section, showing a dense population of cells. The cells are stained with a blue dye, possibly hematoxylin, which highlights the nuclei. There are also some orange or brownish structures, possibly representing cytoplasm or extracellular matrix. The overall appearance is that of a complex, interconnected network of cells.

HTAN Portal for Data Access and Visualization

Adam Taylor
HTAN Data Coordinating Center (DCC)
Sage Bionetworks

**Introduction to
HTAN DCC**

**Data Access and
Visualization**

1

2

3

**Data Standards and
Data Integration**

- 1 Develop **data standards** and enable **data integration**.
- 2 Enable **data sharing** and **data visualization** of all HTAN data.

Data Coordinating Center (DCC)



Alex



Dar'ya



Adam



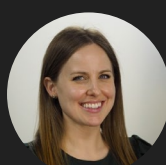
Ethan



Milen



Rochelle



Ashley



Niki



Vésteinn



Bill



Dave



Ino

Four partner institutions

- Dana-Farber Cancer Institute
- Sage Bionetworks
- Institute for Systems Biology
- Memorial Sloan-Kettering Cancer Center

Aaron Lisman

Onur Sumer

Xiang Li

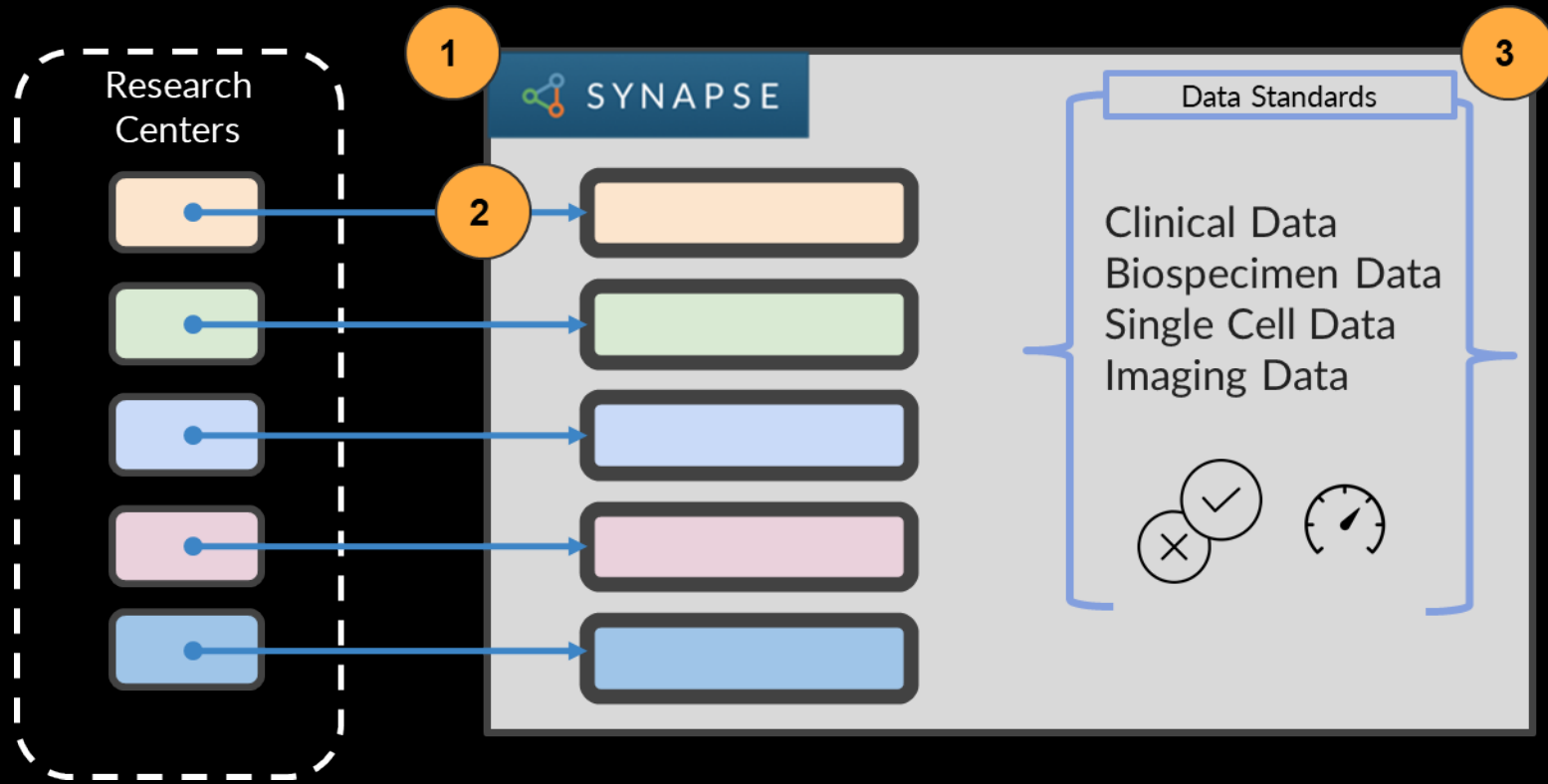
Subhi Nandakumar

Tiarah Thomas

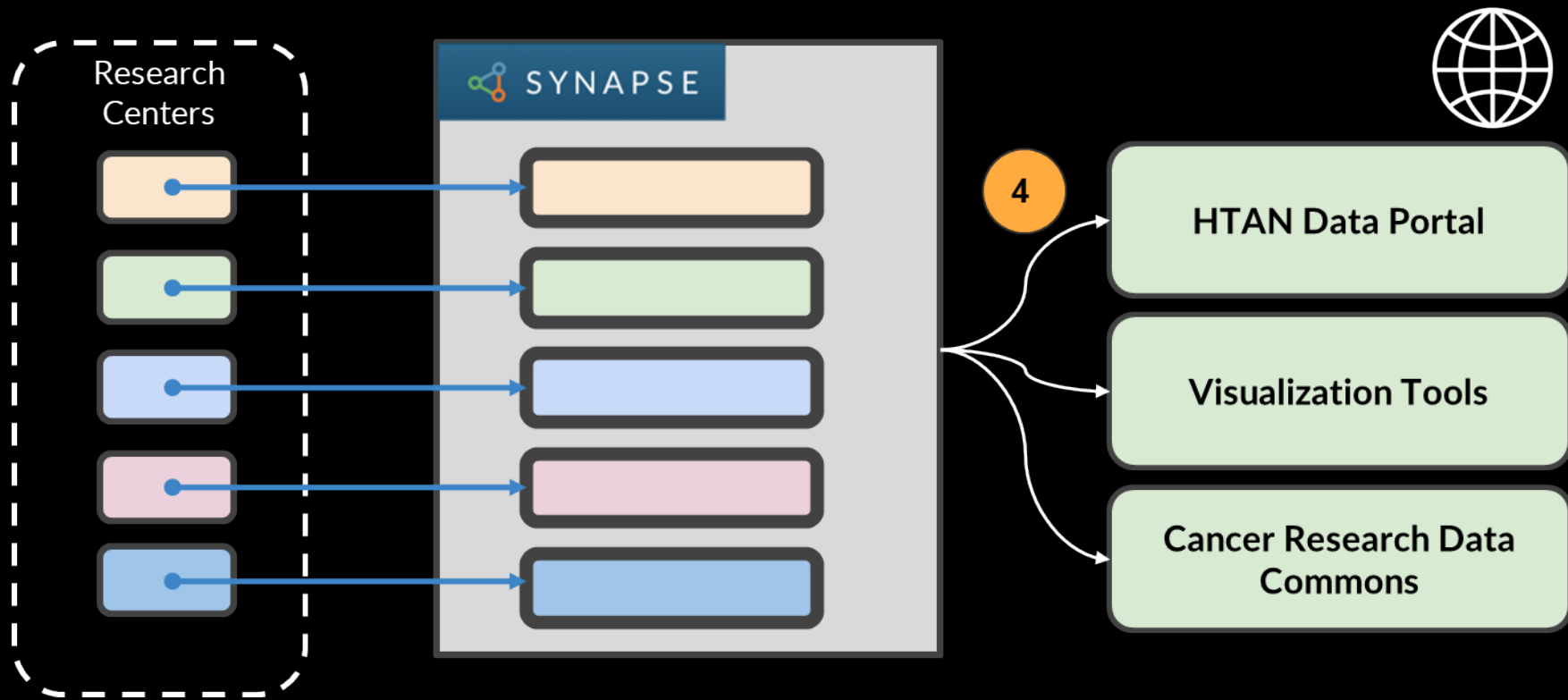
Lisa Pasquale

Bill Clifford

HTAN Data Coordinating Center (DCC)



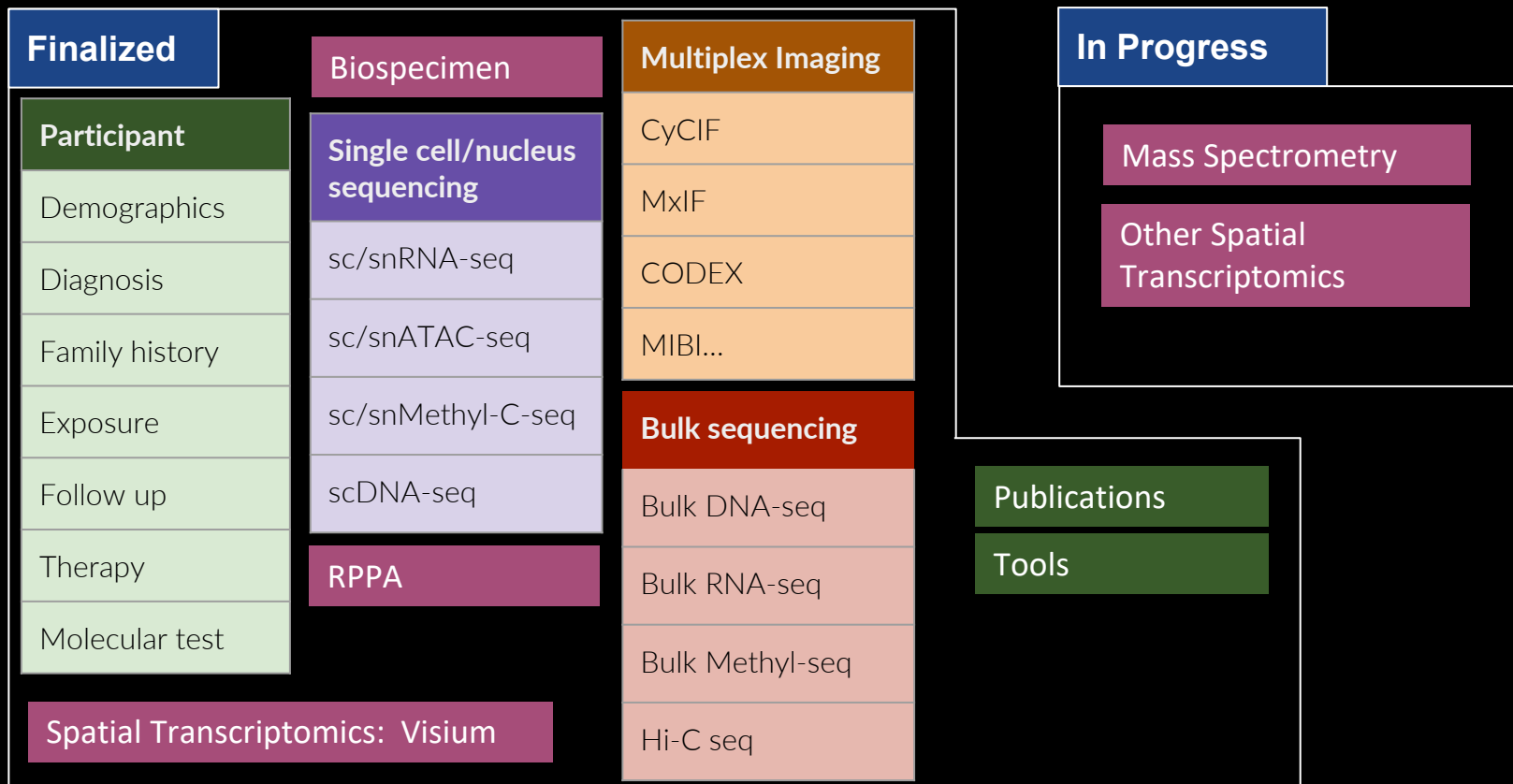
HTAN Data Integration



HTAN Data Distribution

Data Standards and Integration

02



HTAN Standards

Full details at:
<https://humantumoratlas.org>

Single Cell RNA-Seq

1

Metadata attributes harmonized with Human Cell Atlas metadata.

2

Level 1: Unaligned
sequenced reads

FASTQs or unaligned BAMs.

Level 2: Aligned
sequence reads

Aligned BAMs

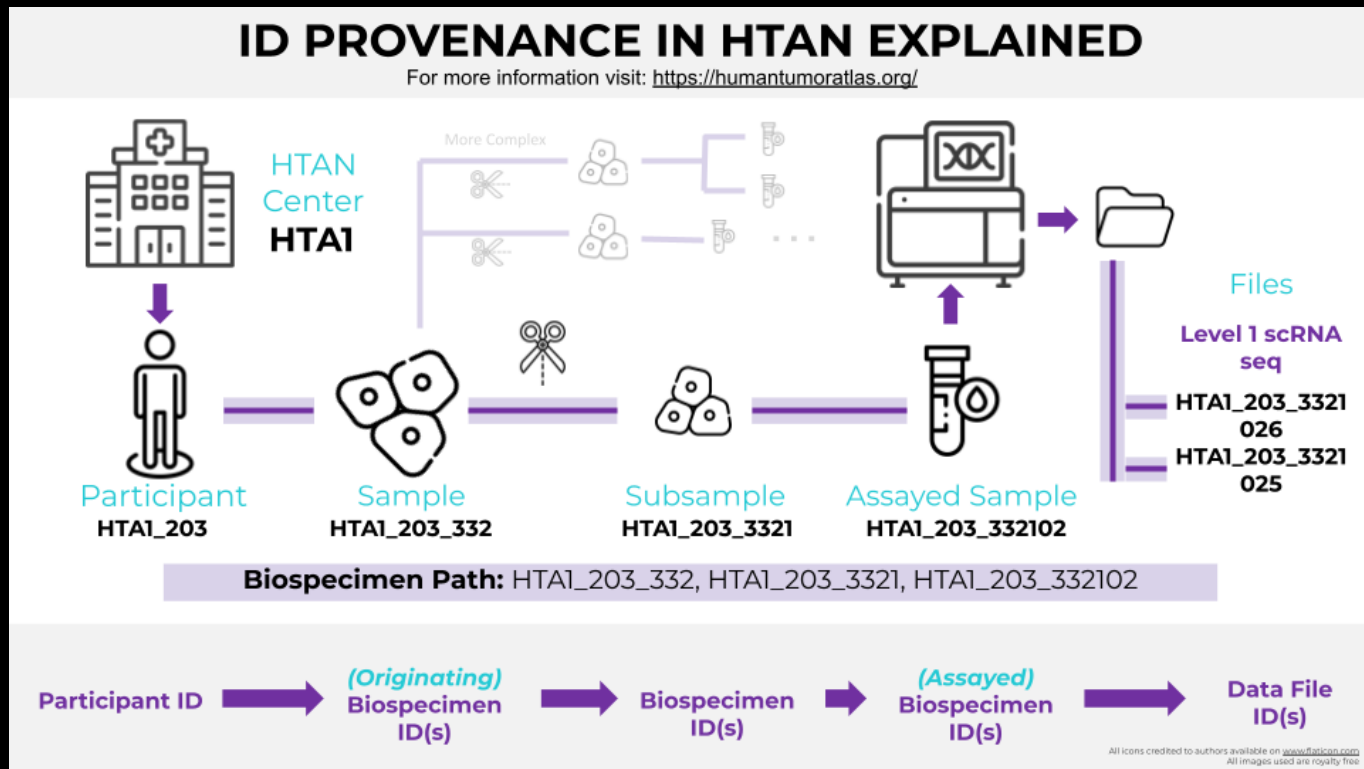
Level 3: Gene
expression values

MTX and CSV file format. Genes are specified with Ensembl IDs (GENCODE v. 34)

Level 4: Cell type
assignments

Anndata and CSV file format. Can be used to assign cell type annotations, tSNE coordinates, etc.

ID Provenance



More info on <https://docs.humantumoratlas.org>

Data Access and Visualization

03

1

HTAN Portal

2

Visualization
Tools

3



SYNAPSE

4



NATIONAL CANCER INSTITUTE
Cancer Research Data Commons

5



Google BigQuery

Five Modes of Data Access

Data	Data Access	Status
De-identified clinical and biospecimen data, and assay metadata	Open	Available via the HTAN Portal, Synapse and Google BigQuery.
Level 1-2 Sequencing Data	Access Controlled	Available via Cancer Data Service (CDS) and Cancer Genomics Cloud (Seven Bridges/Velsera).
Level 3-4 Data	Open	Available via the HTAN Portal, Synapse, CellxGene, and BigQuery.
Image Browsing	Open	Available via the HTAN Portal and Synapse.
Image Processing	Open	Available via the Cancer Data Service (CDS) and Cancer Genomics Cloud (Seven Bridges/Velsera)

We currently do data releases every 2-3 months.

Most recent release on Mar 19, 2025. See <https://humantumoratlas.org/data-updates>

14

Atlases

2,147

Cases

9,286

Biospecimens

Data Releases

Search all filters

Atlas

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Disease

Demographics

Treatment

Assay

File

Data Access

Viewer

Atlases

Cases

Biospecimens

Files

Plots *Beta!*

Summary: 14 Atlases 21 Organs 59 Cancer Types 2147 Cases 9237 Biospecimens 30 Assays 201181 Files

Download Metadata

Columns (12/16)

Search



☐	Atlas Name	Atlas Description	Publications
☐	BU	The Lung Pre-Cancer Atlas	
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)	
☐	SRRS	Standardized Repository of Reference Specimens	
☐	CHOP	Center for Pediatric Tumor Cell Atlas	
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer	
☐	Duke	Breast Pre-Cancer Atlas	
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin	
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis	
☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers	
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis	
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens	
☐	TNP SARDANA	Compare imaging methods across centers	
☐	Vanderbilt	Colon Molecular Atlas Project	
☐	WUSTL	Washington University Human Tumor Atlas Research Center	

Metadata	Cases	Biospecimens				
	183	1651		1		
	201		127			
		200		1	3	
		308				
	767	1229	1023			
	116	722	659			11
	127	293	58	12	11	3
	21	300	149	1		1
	39	271				
	51	1571	1293			
	2	80	276			
	156	362	123	3	4	1
	276	1021	150			

List of all
atlases

1

Search all filters

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Atlases Cases Biospecimens Files Plots *Beta!*

Summary: 14 Atlases 21 Organs 59 Cancer Types 2147 Cases 9237 Biospecimens 30 Assays 20181 Files

Download Metadata

Columns (12/16)

Search



Filter data

☐	Atlas Name	Publications	Metadata	Cases	Biospecimens						
☐	BU	The Lung Pre-Cancer Atlas			183	1651				1	
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)			201	1105			127		
☐	SRRS	Standardized Repository of Reference Specimens			16	157					
☐	CHOP	Center for Pediatric Tumor Cell Atlas			69	200				1	3
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer			123	308					
☐	Duke	Breast Pre-Cancer Atlas			767	1229			1023		
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin			116	722			659		11
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis			127	293			58	12	11
☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers			21	300			149	1	
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis			39	271					
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens			51	1571			1293		
☐	TNP SARDANA	Compare imaging methods across centers			2	80			276		
☐	Vanderbilt	Colon Molecular Atlas Project			156	362			123	3	4
☐	WUSTL	Washington University Human Tumor Atlas Research Center			276	1021			150		

Search all filters

Atlas

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Atlases Cases Biospecimens Files Plots Beta!

☐	Atlas Name	Atlas Description	Publication
☐	BU	The Lung Pre-Cancer Atlas	
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)	
☐	SRRS	Standardized Repository	
☐	CHOP	Center for Pediatric Tumor	
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer	
☐	Duke	Breast Pre-Cancer Atlas	
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin	
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis	
☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers	
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis	
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens	
☐	TNP SARDANA	Compare imaging methods across centers	
☐	Vanderbilt	Colon Molecular Atlas Project	
☐	WUSTL	Washington University Human Tumor Atlas Research Center	

Filter by Assay

Assay:

Files

☐	10X Visium	2945
☐	10X Xenium ISS	1
☐	Accessory Manifest	5
☐	Bulk DNA	8900
☐	Bulk Methylation-seq	131
☐	Bulk RNA-seq	4854
☐	CODEX	2791
☐	CyCIF	5139
☐	Electron Microscopy	93000
☐	ExSEQ	21156
☐	H&E	2149
☐	Hi-C-seq	102
☐	IMC	79
☐	Imaging	3000
☐	LC-MS/MS	493
☐	LC-MS3	479
☐	MERFISH	18626
☐	MIBI	816
☐	Mass Spectrometry	57
☐	MxIF	6467
☐	NanoString GeoMX DSP	252
☐	RPPA	78
☐	RareCyte Orion	150
☐	SABER	6
☐	Shotgun MS (lipidomics)	214
☐	Slide-seq	383
☐	Slide-seq V2	34
☐	mIHC	753
☐	scATAC-seq	4224
☐	scRNA-seq	23897

21 Organs 59 Cancer Types 2147 Cases 9237 Biospecimens 30 Assays 201181 Files

Columns (12/16)

Search



Biospecimens



1651		1		
1105	127			
157				
200		1	3	
308				
1229	1023			
722	659			11
293	58	12	11	3
300	149	1		1
271				
1571	1293			
80	276			
362	123	3	4	1
1021	150			

Search all filters

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Atlases Cases Biospecimens Files Plots Beta

☐	Atlas Name	Atlas Description	Publications	Files	Assays	Biospecimens	Cases
☐	BU	The Lung Pre-Cancer Atlas					
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)					
☐	SRRS	Standardized Repository					
☐	CHOP	Center for Pediatric Tumor					
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer					
☐	Duke	Breast Pre-Cancer Atlas			767	1229	1023
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin			116	722	659 11
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☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers			21	300	149 1 1
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis			39	271	
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens			51	1571	1293
☐	TNP SARDANA	Compare imaging methods across centers			2	80	276
☐	Vanderbilt	Colon Molecular Atlas Project			156	362	123 3 4 1
☐	WUSTL	Washington University Human Tumor Atlas Research Center			276	1021	150

Filter by Level

Level:

Files

☐	Auxiliary	507
☐	Level 1	92340
☐	Level 2	71340
☐	Level 3	11342
☐	Level 4	4382
☐	Unknown	21270

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AtlasesCasesBiospecimensFilesPlotsBeta

☐	Atlas Name	Atlas Description	Publications
☐	BU	The Lung Pre-Cancer Atlas	
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)	
☐	SRRS	Standardized Repository of Refer	
☐	CHOP	Center for Pediatric Tumor Cell Atlas	
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer	
☐	Duke	Breast Pre-Cancer Atlas	
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin	
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis	
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☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens	
☐	TNP SARDANA	Compare imaging methods across centers	
☐	Vanderbilt	Colon Molecular Atlas Project	
☐	WUSTL	Washington University Human Tumor Atlas Research Center	

Filter by Access

Data Access:

Files

☐ CDS/SB-CGC (dbGaP)

☐ CDS/SB-CGC (Open Access)

☐ Synapse (Open Access)

☐ Coming Soon

35859

24272

130527

10539

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Disease ▾



Demographics ▾



Treatment ▾



Assay ▾



File ▾



Data Access ▾



Assay (scRNA-seq OR CODEX)

AND

Level (Level 3 OR Level 4)

AND

File Format hdf5

✕ Clear all filters

Atlases

Cases

Biospecimens

Files

Plots Beta!

Summary:

4 Atlases

5 Organs

5 Cancer Types

229 Cases

346 Biospecimens

1 Assay

42 Files

Download 2 selected files

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Columns (10/31) ▾

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Filename

3

Atlas Name

Level

Organ

Diagnosis

Data Access

Metadata

View



VUMC_ABNOR...PI_V2.h5ad

HTAN
Vanderbilt

62
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

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[CellxGene](#) [BigQuery](#)



VUMC_HTAN...PI_V2.h5ad

HTAN
Vanderbilt

117
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

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VUMC_HTAN...PI_V2.h5ad

HTAN
Vanderbilt

59
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

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[CellxGene](#) [BigQuery](#)



VUMC_HTAN...PI_V2.h5ad

HTAN
Vanderbilt

195
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

[View Metadata](#)



VUMC_HTAN...xgene.h5ad

HTAN
Vanderbilt

62
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

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VUMC_HTAN...PI_V2.h5ad

HTAN
Vanderbilt

79
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

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VUMC_HTAN...xgene.h5ad

HTAN
Vanderbilt

59
Biospecimens

scRNA-seq

Level 4

Not Reported

Not Reported

Synapse

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Atlas ▾

Assay (scRNA-seq OR CODEX) AND Level (Le

Atlases

Cases

Biospecimens

Files

Plots

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Filename

Atlas
Name

Biospe



VUMC
_V2.h5

55
Biospe



VUMC
V2.h5

62
Biospe



VUMC
V2.h5ad

117
Biospe



VUMC_HTAN_...PI_
V2.h5ad

HTAN
Vanderbilt

59
Biospe



VUMC_HTAN_...PI_
V2.h5ad

HTAN
Vanderbilt

195
Biospe



VUMC_HTAN_...xge
ne.h5ad

HTAN
Vanderbilt

62
Biospe



VUMC_HTAN_...PI_
V2.h5ad

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79
Biospe



VUMC_HTAN_...xge
ne.h5ad

HTAN
Vanderbilt

59
Biospe

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Instructions

Download Selected Files

Your selection include files that are:

- Available through Synapse

Follow the instructions below on how to access data from each of these sources. Further details are available in the [HTAN Manual](#).

Files available in Synapse

The files listed below are available through [Synapse](#).

-  VUMC_HTAN_DIS_EPI_V2.h5ad ([syn27056097](#))
-  VUMC_ABNORMALS_EPI_V2.h5ad ([syn27056096](#))

You can use the [Synapse CLI](#) command below to download the selected files.

```
synapse get syn27056097
synapse get syn27056096
```

You'll need to [register](#) for a Synapse account to be able to use the [client](#). More information can be found in the [Synapse documentation](#). Files can also be downloaded manually through the Synapse web interface by clicking on the file name.

Close

Assay ▾

File ▾

Data Access ▾

Cancer Types

229 Cases

346 Biospecimens

1 Assay

42 Files

Search



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Data
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Metadata

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Synapse

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Atlases

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Cases

Biospecimens

Files

Plots Beta!

Summary: 14 Atlases 21 Organs 59 Cancer Types 2147 Cases 9253 Biospecimens 30 Assays 201197 Files

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Columns (8/11) ▾

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Title

Single-cell analyses define a core of cell state and composition changes in the malignant transformation of colorectal cancer
Transition to invasive breast cancer associated with progressive changes in the structure and composition of tumor stroma
Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer

Duke University

Memorial Sloan Kettering Cancer Center

4

Browse data
per publication

Authors

Becker WR, Nevins SA,
Chen DC, Chiu R, et al.

Risom T, Glass DR,
Averbukh I, Liu CC, et al.

Chan JM, Quintanal-
Villalonga A, Gao VR, Xie
Y, et al.

Journal

Nature Genetics

Cell

Cancer Cell

Publication Date

2022 Jul

2022 Jan

2021 Nov

PubMed

[35726067](#) 

[35063072](#) 

[34653364](#) 

Participants

21

63

50

Biospecimens

169

72

57

Rows per page: 50 ▾

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⏪

⏩

⏴

⏵

HTAN: Search for a publication

HTAN
HUMAN TUMOR ATLAS NETWORK

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AtlasesPublicationsCasesBiospecimensFilesPlots BetaSummary: 14 Atlases21 Organs59 Cancer Types2147 Cases9253 Biospecimens30 Assays201197 Files

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Title	Atlas	Authors	Journal	Publication Date	Participants	Biospecimens
Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer	Stanford University	Becker WR, Nevins SA, Chen DC, Chiu R, et al.	Nature Genetics	2022 Jul		169
Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma	Duke University	Risom T, Glass DR, Averbukh I, Liu CC, et al.	Cell	2022 Jan		72
Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer	Memorial Sloan Kettering Cancer Center	Chan JM, Quintanal-Villalonga A, Gao VR, Xie Y, et al.	Cancer Cell	2021 Nov	34653364	57

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Files

Plots **Beta!**

Summary: 14 Atlases 21 Organs 59 Cancer Types 2147 Cases 9253 Biospecimens 30 Assays 201197 Files

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Title	Atlas	Authors	Journal	Publication Date	PubMed	Participants	Biospecimens
Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer	Stanford University	Becker WR, Nevins SA, Chen DC, Chiu R, et al.	Nature Genetics	2022 Jul			169
Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma	Duke University	Risom T, Glass DR, Averbukh I, Liu CC, et al.	Cell				72
Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer	Memorial Sloan Kettering Cancer Center	Chan JM, Quintanal-Villalonga A, Gao VR, Xie Y, et al.	Cancer Cell	2021 Nov	34653364 	50	57

Go to publication page

Rows per page: 50 ▾

1-3 of 3

Publication



Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer

Authors: Chan JM, Quintanal-Villalonga Á, Gao VR, Xie Y, Allaj V, Chaudhary O, Masilionis I, Egger J, Chow A, Walle T, Mattar M, Yarlagadda DVK, Wang JL, Uddin F, Offin M, Ci de Stanchina E, Bhanot UK, Lai WV, Bott MJ, Jones DR, Ruiz A, Baine MK, Li Y, Rekhtman N, Poirier JT, Nawy T, Sen T, Mazutis L, Hollmann TJ, Pe'er D, Rudin CM

Journal: Cancer Cell Pubmed: [34653364](#) DOI: [10.1016/j.ccell.2021.09.008](#)

Atlas: [Memorial Sloan Kettering Cancer Center](#)

Overview

Participants 50

Biospecimens 57

scRNA-seq 886

Tools 1

Supporting Links

Abstract

Small cell lung cancer (SCLC) is an aggressive malignancy that includes subtypes defined by differential expression of ASCL1, NEUROD1, and POU2F3 (SCLC-A, -N, and -P, respectively). To define and their associated microenvironments across subtypes, we sequenced 155,098 transcriptomes from 21 human biospecimens, including 54,523 SCLC transcriptomes. We observe greater tumor diversity in SCLC compared to lung adenocarcinoma, driven by canonical, intermediate, and admixed subtypes. We discover a PLCG2-high SCLC phenotype with stem-like, pro-metastatic features. SCLC exhibits greater immune sequestration and less immune infiltration than lung adenocarcinoma, and SCLC-N shows less immune infiltration. We identify an immunosuppressive monocyte/macrophage population in SCLC tumors that is particularly associated with the recurrent, PLCG2-high subpopulation.

Data Availability

Files	CDS/SB-CGC (dbGaP )	Synapse (Open Access )
scRNA-seq Level 1	356	0
scRNA-seq Level 2	52	0
scRNA-seq Level 3	0	208
scRNA-seq Level 4	0	270

Find all data associated with a publication

HTAN

EXPLORE

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MANUAL

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ABOUT HTAN

SUBMIT DATA

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Viewer

Atlases

Cases

Biospecimens

Files

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Summary:

14 Atlases

21 Organs

59 Cancer Types

2147 Cases

9237 Biospecimens

30 Assays

20181 Files

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	Atlas Name	Atlas Description	Publications	Metadata	Cases	Biospecimens						
☐	BU	The Lung Pre-Cancer Atlas			183	16				1		
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)			201						127	
☐	SRRS	Standardized Repository of Reference Specimens										
☐	CHOP	Center for Pediatric Tumor Cell Atlas								1	3	
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer										
☐	Duke	Breast Pre-Cancer Atlas			767		1229				1023	
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin			116		722				659	11
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis			127		293			58	12	11
☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers			21		300			149	1	
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis			39		271					
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens			51		1571				1293	
☐	TNP SARDANA	Compare imaging methods across centers			2		80				276	
☐	Vanderbilt	Colon Molecular Atlas Project			156		362			123	3	4
☐	WUSTL	Washington University Human Tumor Atlas Research Center			276		1021				150	

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find data files ...
1 SELECT * FROM `isb-cgc-bq.HTAN.id\_provenance\_current`
2 where HTAN_Participant_ID in (
3 SELECT HTAN_Participant_ID FROM `isb-cgc-bq.HTAN.clinical\_tier1\_demographics\_current`
4 where Race like '%lack`
5]
RUNSHARESCHEDULESAVE QUERYThis query will process 89.95

Query results
SAVE RESULTSEXPLORE DATA
JOB INFORMATIONRESULTSCHARTJSONEXECUTION DETAILSEXECUTION GRAPH
RowHTAN_Parent_Data_File_IDHTAN_Originating_Biospecimen_IDHTAN_Participant_IDBiospecimen_Path
1NoneHTA3_50307_1000681HTA3_50307HTA3_50307_1000681,HTA3_5...
2NoneHTA3_50307_1000681HTA3_50307HTA3_50307_1000681,HTA3_5...
3NoneHTA3_50307_1000682HTA3_50307HTA3_50307_1000682,HTA3_5...
WUSTLWashington University Human Tumor Atlas Research Center

Metadata

18316127
201
69
123
767
11672265911
1272935812113
2130014911
39271
5115711293
280276
156362123341
2761021150

6
For more complex metadata queries use Google BigQuery

Search all filters

Atlas

Organ

Disease

Demographics

Treatment

Assay

File

Data Access

Viewer

Atlases Cases Biospecimens Files Plots **Beta!**

Summary: 14 Atlases 21 Organs 59 Cancer Types 2147 Cases 9237 Biospecimens 30 Assays 20181 Files

Download Metadata

Columns (12/16)

Search

☐	Atlas Name	Atlas Description	Publications	Metadata	Cases	Biospecimens
☐	BU	The Lung Pre-Cancer Atlas			183	1651
☐	HTAPP	Human Tumor Atlas Pilot Project (HTAPP)			201	1105
☐	SRRS	Standardized Repository of Reference Specimens				
☐	CHOP	Center for Pediatric Tumor Cell Atlas				
☐	DFCI	The Cellular Geography of Therapeutic Resistance in Cancer			123	308
☐	Duke	Breast Pre-Cancer Atlas			767	1229
☐	HMS	Pre-Cancer Atlases of Cutaneous and Hematologic Origin			116	722
☐	MSK	Transition to Metastatic State: Lung Cancer, Pancreatic Cancer and Brain Metastasis			127	293
☐	OHSU	Omic and Multidimensional Spatial Atlas of Metastatic Breast Cancers			21	300
☐	Stanford	Multi-omic Characterization of Transformation of Familial Adenomatous Polyposis			39	271
☐	TNP TMA	Generate spatially resolved cell type/state census from tissue microarray breast FFPE specimens			51	1571
☐	TNP SARDANA	Compare imaging methods across centers			2	80
☐	Vanderbilt	Colon Molecular Atlas Project			156	362
☐	WUSTL	Washington University Human Tumor Atlas Research Center			276	1021

7

Visualize & Query data

		1			
127					
		1	3		
1023					
659				11	
58		12	11	3	
149	1				1
1293					
276					
123		3	4		1
150					



https://data.humantumoratas.org/

The HTAN Data Portal is in the alpha release phase. Only level 3 and 4 data can be downloaded. Feedback is welcome!

HTAN

EXPLORE DATA STANDARDS DATA TRANSFER ANALYSIS TOOLS HTAN MAIN SITE

Search all filters Atlas Organ Disease Type Demographics Assay Type File Type

Assay: t-CyCIF Clear all filters

Atlases Cases Biospecimens Files

Summary: 1 Atlas 6 Organs 2 Cancer Types 16 Cases 0 Biospecimens 1 Assay 16 Files

Columns (9/55) Search

Filename	Atlas Name	Biospecimen	Assay	Level	Organ	Diagnosis	Details	View
☐ CRC02.ome.tif	HTAN HMS	HTA7_926_2	t-CyCIF	Level 2	Rectum NOS	Rectum NOS	View Details	
☐ CRC03.ome.tif	HTAN HMS	HTA7_927_2	t-CyCIF	Level 2	Sigmoid colon	Sigmoid colon	View Details	
☐ CRC04.ome.tif	HTAN HMS	HTA7_932_2	t-CyCIF	Level 2	Sigmoid colon	Sigmoid	View Details	
☐ CRC05.ome.tif	HTAN HMS	HTA7_934_2	t-CyCIF	Level 2	Rectosigmoid junction	Rectosigmoid junction	View Details	

<https://borysgham.github.io/HTA-CRCATLAS-Minervaviz004-overview.html>

Visualizing multiplex
imaging data via MINERVA:
https://docs.humantumoratas.org/data_visualization/minerva/

Minerva Visualization (collab with Sorger Group)



APPLICATION

Collections
Datasets
Gene Expression
Cell Guide
Differential Expression
NEW

CENSUS
API
Models

Filters

Assay
Cell Type
Consortia
Human Tumor Atlas Networ...
Development Stage
Disease
Organism
Publication
Publication Date
Self-Reported Ethnicity
Sex
Suspension Type
Tissue

Collections

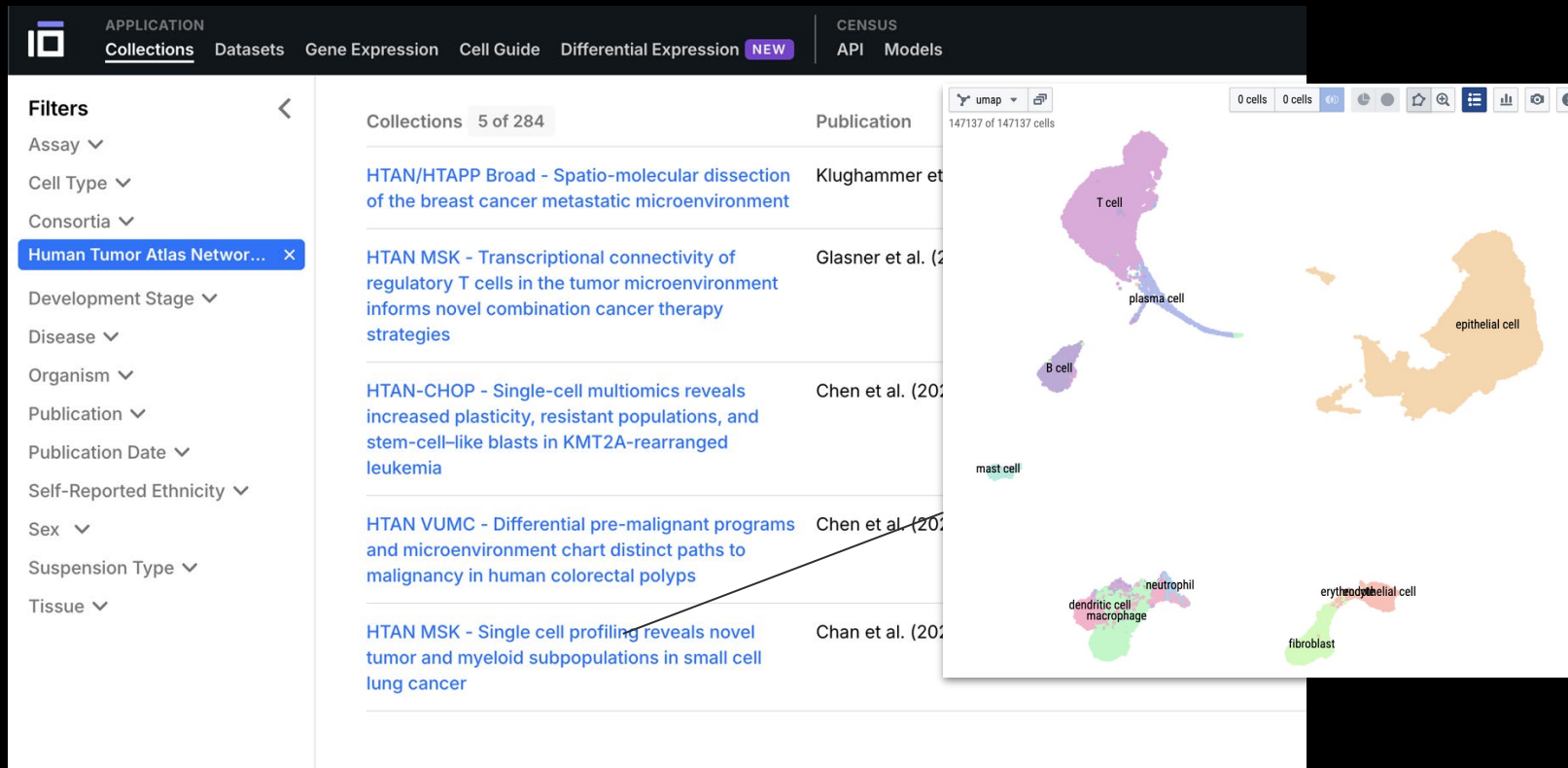
5 of 284

Publication

Tissue

HTAN/HTAPP Broad - Spatio-molecular dissection of the breast cancer metastatic microenvironment	Klughammer et al. (2024) Nat Med	9 tissues
HTAN MSK - Transcriptional connectivity of regulatory T cells in the tumor microenvironment informs novel combination cancer therapy strategies	Glasner et al. (2023) Nat Immunol	8 tissues
HTAN-CHOP - Single-cell multiomics reveals increased plasticity, resistant populations, and stem-cell-like blasts in KMT2A-rearranged leukemia	Chen et al. (2022) Blood	blood
HTAN VUMC - Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps	Chen et al. (2021) Cell	7 tissues
HTAN MSK - Single cell profiling reveals novel tumor and myeloid subpopulations in small cell lung cancer	Chan et al. (2021) Cancer Cell	8 tissues

Cell x Gene Visualization (collab with CZI)



Cell x Gene Visualization (collab with CZI) 2



Patient: HTA9_1, Female, 64 years old, Breast Cancer (Breast Invasive Ductal Carcinoma), LIVING (128 months)

Breast Cancer

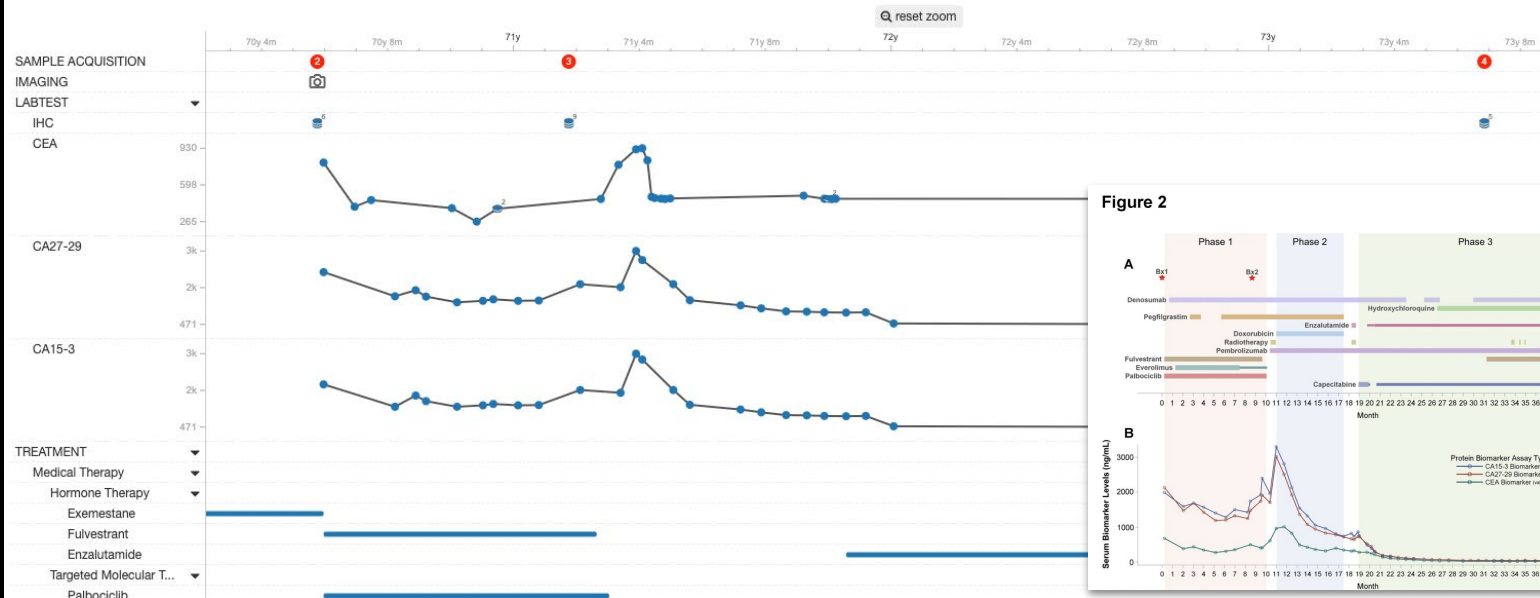
Samples: 1 HTA9_1-PR, Primary (Breast NOS) 2 HTA9_1-Bx1, Metastasis (Liver) 3 HTA9_1-Bx2, Metastasis (Liver) 4 HTA9_1-Bx3, Metastasis (Bone NOS) 5 HTA9_1-Bx4, Metastasis (Liver)

Summary

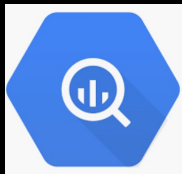
Genomic Evolution

Pathways

Clinical Data



cBioPortal Visualization



ISB-CGC Data Browsers Resources Documentation About Publications Help Sign In

BigQuery Table Search

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Find tables of interest based on category, reference genome build, data type and free-form text search.

Status: CURRENT

Name:

Program:

Category: ☐ CLINICAL BIOSPECIMEN DATA ☐ FILE METADATA ☐ PROCESSED -OMICS DATA ☐ REFERENCE DATABASE

Reference Genome: ALL

Source: HTAN-VUMC

Data Type:

Show 10 entries

Columns CSV Download Search:

Name	Program	Category	Source	Data Type	Status	Rows	Created	Example Joins	Preview	Open
HTAN HG38 SCRNAseq GENE EXPRESSION CUMULATIVE ABNORMAL EPITHELIAL	HTAN	PROCESSED - OMICS DATA	HTAN-VUMC	GENE EXPRESSION	CURRENT	62,420,820	6/23/2022			

Full ID: lib-cgc-bq.HTAN.scRNAseq_VUMC_ABNORMALS_EPI_V2_current COPY OPEN

Dataset ID: HTAN

Table ID: scRNAseq_VUMC_ABNORMALS_EPI_V2_current

Description: Data was derived in April 2022 from an 14040 file (syn21056000) submitted by the Vanderbilt HTAN Center. This data set contains raw gene expression counts from 62 patient samples. Data was generated using the 10X Genomics (see https://doi.org/10.1101/129642-020-06843-0) and was processed using a DropSeq-based pipeline (see https://doi.org/10.1016/j.xpro.2021.100450) where reads were mapped to HG38, followed by processing with scranpy and aformentioned pipeline to filter cells. Low-dimensional embeddings are derived from a regular space, generated using SCENIC. This dataset contains abnormal/tumor-specific epithelial cells derived from both the discovery (DIS) and validation (VAL) cohorts, as described in https://doi.org/10.1016/j.xpro.2021.11.031.

Schema:

Field Name	Type	Mode	Description
iObs	INTEGER	undefined	Index to cell barcodes.
iVar	INTEGER	undefined	Index to cell barcodes.
X_value	INTEGER	undefined	Expression value for a given gene and cell.
Cell_Barcode_Number	STRING	undefined	Barcodes used for each droplet that contains the cell in the sequencing process
HTAN_Parent_Data_File_ID	STRING	undefined	HTAN Data File identifier indicating the file(s) from which these files were derived
HTAN_Biospecimen_ID	STRING	undefined	HTAN ID associated with a biosample based on HTAN ID SOP (see HTAN SOP 2022)
Tissue_Subtype	STRING	undefined	TA = tubular adenoma, HP = hyperplastic polyp, TVA = tubulovillous adenoma, SSL = sessile serrated lesion, MSI-H microsatellite instability high CRC, MSS = microsatellite stable CRC
Tissue_Type	STRING	undefined	AD = conventional adenoma, SER = serrated polyp, MSI-H microsatellite instability high CRC, MSS = microsatellite stable CRC
Gene_Name	STRING	undefined	Measured gene

HTAN BigQuery Notebooks

HTAN is a National Cancer Institute (NCI)-funded Cancer MoonshotSM initiative to construct 3-dimensional atlases of the dynamic cellular, morphological, and molecular features of human cancers as they evolve from precancerous lesions to advanced disease (Cell, April 2020).

Investigating HTAN scRNA-seq with BigQuery

Title: Investigating HTAN scRNA-seq with BigQuery
Author: Dar'ya V. Poshidayeva (dpzhida@systemsbiology.org)
Created: 2022-6-28
Purpose: Explore single cell RNA seq data in HTAN.
URL: NA
Notes: NA

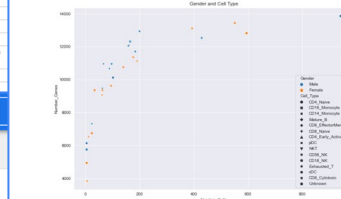
1. Introduction & Overview

HTAN is a National Cancer Institute (NCI)-funded Cancer MoonshotSM initiative to construct 3-dimensional atlases of the dynamic cellular, morphological, and molecular features of human cancers as they evolve from precancerous lesions to advanced disease (Cell April 2020)

This notebook shows examples of how HTAN single cell RNA sequencing data can be accessed and analyzed using Python.

```
[In [16]] see nextscript (library=HTAN, y="Number", color="y", y="Number", hue="Number", style="Cell_Type", cell(1:1000) "Number" and Cell Type")
```

```
[Out [16]] (Number, 1.0, "Number" and Cell Type)
```



Next, when we select a cell type to focus on, we can explore the Seurat Clusters generated for this data set. Maybe we are interested in comparing between males and females for the same cluster.

Data Query & Computational Notebooks

The HTAN Manual

- Overview >
- Data Model >
- Open Access Data >
- Access Controlled Data >
- Submitting Data >
- Additional Information >
- Frequently Asked Questions (FAQ)

The HTAN Manual

Written by the HTAN Data Coordinating Center (DCC), with contributions from Adam Taylor, Clarisse Lau, Vésteinn Thorsson, Ino de Bruijn, David Gibbs, Ethan Cerami, Alex Lash and Jen Altreuter.

About this Manual

The HTAN Manual provides an overview of Human Tumor Atlas Network (HTAN) data, including the various levels of data access. If you have any questions regarding the manual or HTAN data, please contact us:

[HTAN Help Desk](#).

The manual can be found at <https://docs.humantumoratlas.org/>.

HTAN Manual: <https://docs.humantumoratlas.org/>