The utility of REDCap and Cbioportal in collecting and analyzing oncological patient's clinical data

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REDCap as a research enabler, 4-Jun-2023

Thank you

Sharett institute of Oncology staff; Tamar Hamburger

Pathology department staff;

Hadas - Onco-genetic clinic staff;

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Yuval Dor Group

Ittai Ben-Porath

Amir Eden

Rotem Karni

Ben Berman

Nir Fridman

Efrat Shema

Tommy Kaplan

What kind of data do we want for our research?

- Demographic (Age, Sex, Martial statues, number of children, address)
- Oncological Diagnosis
- Medical history
- Treatment (Surgical, Radiotherapy, Medical)
- Molecular findings (pathogenic variations,
- Immunohistochemistry, somatic variations, expression data)
- Research data

Statues

- Machar – The work environment of the Hadassah Medical center. Contains electronic medical records spanning 40 years. Some fields are tabulated but most of the information is in free text. One person at a time one patient at a time.

- TriNetX – An interface allowing anonymized data interrogation for some fields. One person at a time.

Aim

A graphical interphase that automatically captures data from the Machar and research, allows entry of new fields, multiple users can work simultaneously, easy to use.

cBioportal

- https://www.cbioportal.org/

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

The cBioPortal for Cancer Genomics provides **visualization**, **analysis** and **download** of large-scale cancer genomics data sets.
Please adhere to the TCGA publication guidelines when using TCGA data in your publications.

Please cite Gao et al. *Sci. Signal.* 2013 & Cerami et al. *Cancer Discov.* 2012 when publishing results based on cBioPortal.

Query	Download

Please cite: Cerami et al., 2012 & Gao et al., 2013

Select Studies for Visualization & Analysis:

0 studies selected (0 samples)   Search...

☐ **Select all listed studies (4)**

Bowel   `1`

Bowel

Colorectal Adenocarcinoma

☐ Metastatic Colorectal Cancer (Hadassah Medical Center, 2017-2021)   119 samples ⓘ 📖 🥧

Lung   `1`

Lung

☐ hadassah_elcap   1279 samples ⓘ 📖 🥧

Other   `2`

Other   SELECT ALL

Cancer of Unknown Primary

→ MIXED CANCER TYPES

☐ GENIE BPC NSCLC v2.0-public   2004 samples ⓘ 📖 🥧

☐ Hadassah FoundationOneCDx   566 samples ⓘ 📖 🥧

0 studies selected (0 samples)   Query By Gene   OR   🥧 Explore Selected Studies

Click gene symbols below or enter here | Query

Summary | Clinical Data | CN Segments

Selected: 117 patients | 119 samples

Custom Selection ▾ | Charts ▾ | Groups

Sex

51 | 66

Age at Diagnosis

OS_STATUS

51 | 66

KM Plot: OS_ Survival (months)

METASTASECTOMY_STATUS

51 | 66

METASTATIC_ORGANS_AT_DIAGNOSIS
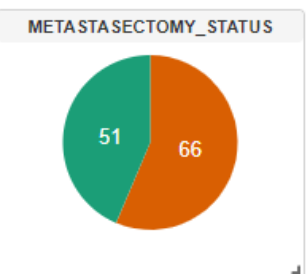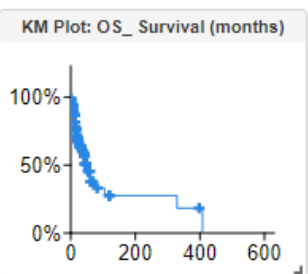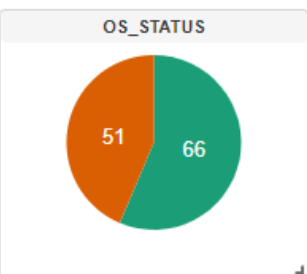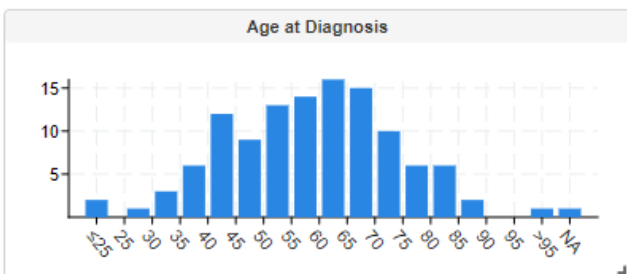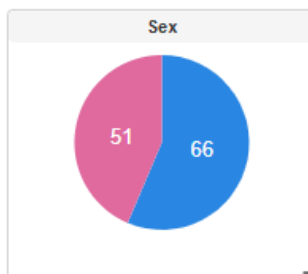
	#	Freq ▾
■ (C22) LIVER AND INTRAHEPA...	☐ 56	47.9%
■ (C48) RETROPERITONEUM A...	☐ 11	9.4%
■ (C34) BRONCHUS AND LUNG	☐ 8	6.8%
■ (C76) OTHER AND ILL-DEFIN...	☐ 5	4.3%
■ (C77) LYMPH NODES	☐ 4	3.4%
■ (C34) BRONCHUS AND LUNG,...	☐ 3	2.6%
■ (C56) OVARY	☐ 3	2.6%
■ (C48) RETROPERITONEUM A...	☐ 2	1.7%
■ (C71) BRAIN	☐ 2	1.7%
■ (C77) LYMPH NODES, (C22) LI...	☐ 2	1.7%
■ NA	☐ 2	1.7%

Search...

Treatment by Patient

Treatment	# ▾
Folfox	☐ 82
Bevacizumab	☐ 67
Folfiri	☐ 65
Simplified_De_Gramont	☐ 38
Cetuximab	☐ 36
Xelox	☐ 26
Capecitabine	☐ 16
Nivolumab	☐ 9
Irinotecan	☐ 8
Pembrolizumab	☐ 6
Panitumumab	☐ 6

Search...

CNA Genes (2 profiled samples)

▼ Gene	Cytoband	CNA	#	Freq ▾
TIAF1	17q11.2	AMP	☐ 1	50.0%
NEUROD2	17q12	AMP	☐ 1	50.0%
EFCAB5	17q11.2	AMP	☐ 1	50.0%
CRYBA1	17q11.2	AMP	☐ 1	50.0%
PNMT	17q12	AMP	☐ 1	50.0%
ARL5C	17q12	AMP	☐ 1	50.0%
NUFIP2	17q11.2	AMP	☐ 1	50.0%
MED1	17q12	AMP	☐ 1	50.0%
TP53I13	17q11.2	AMP	☐ 1	50.0%
ANKRD13B	17q11.2	AMP	☐ 1	50.0%
PREX1	20q13.13	AMP	☐ 1	50.0%

Search...

Mutated Genes (116 profiled samples)

▼ Gene	# Mut	#	Freq ▾
TP53	63	☐ 61	52.6%
KRAS	53	☐ 53	45.7%
SMAD4	25	☐ 24	20.7%
PIK3CA	11	☐ 11	9.5%
BRAF	9	☐ 9	7.8%
APC	10	☐ 8	6.9%

Grade

64 | 29

HER2

60 | 56

NTRK1_2_3

109

MMR

93

| X-Axis Max: | 408 | Months Survival |

Logrank Test P-Value: 7.158e-6

■ (A) FALSE
■ (B) TRUE

OS_
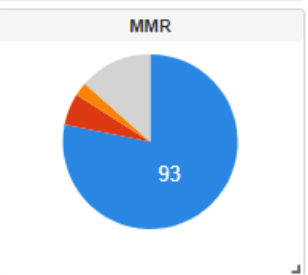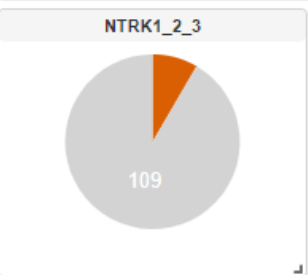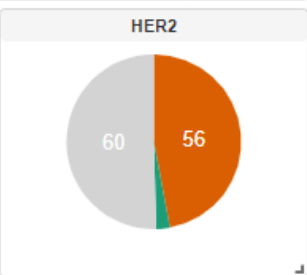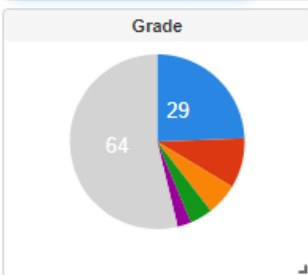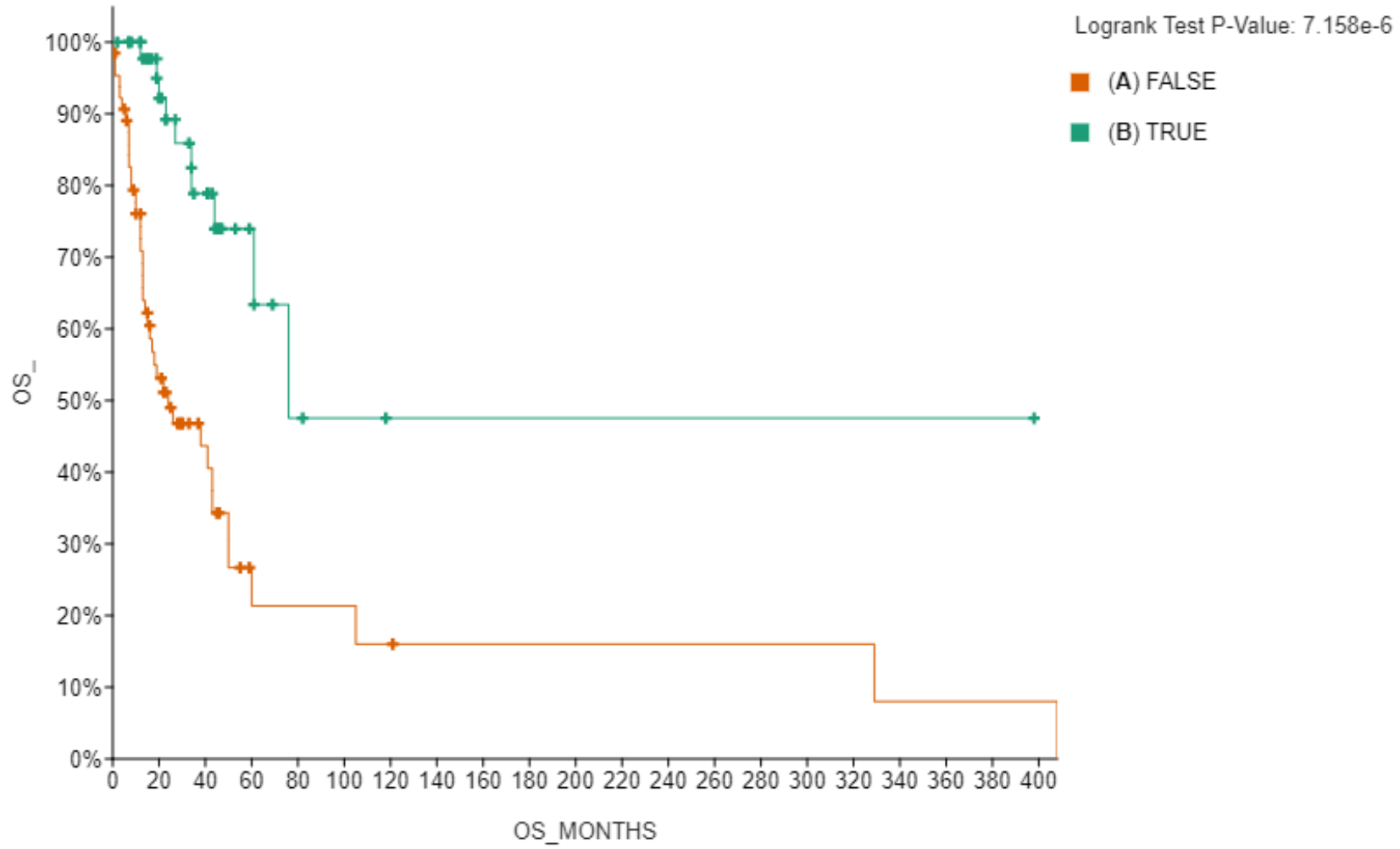
OS_MONTHS

	Number of Cases, Total	Number of Events	Median Months OS_ (95% CI)
(A) FALSE	65	41	24.00 (15.00 - 50.00)
(B) TRUE	51	10	76.00 (61.00 - NA)

Groups from **METASTASECTOMY_STATUS**

Groups: (drag to reorder) (A) FALSE (67/66) (B) TRUE (52/51) Select all | Deselect all

Overlap   Survival   Clinical   Genomic Alterations

ℹ 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.

☁ Columns ▾ [🔍]   ☐ Swap Axes ☐ Log Scale

Clinical Attribute	Attribute Type	Statistical Test	p-Value	q-Value
METASTASECTOMY_STATUS	Patient	Chi-squared Test	$< 10^{-10}$	$< 10^{-10}$
PRIMARY_RESECTION_STATUS	Patient	Chi-squared Test	**7.752e-5**	**5.943e-4**
Grade	Sample	Chi-squared Test	**8.893e-3**	**0.0409**
PRIMARY_TUMOR_LOCATION	Patient	Chi-squared Test	**0.0123**	**0.0471**
Age at Diagnosis	Patient	Wilcoxon Test	**0.0145**	**0.0475**
MMR	Sample	Chi-squared Test	0.0484	0.139
Gene Panel	Sample	Chi-squared Test	0.151	0.387
Sample Type	Sample	Chi-squared Test	0.283	0.650
Fraction Genome Altered	Sample	Wilcoxon Test	0.317	0.663
TMB	Sample	Wilcoxon Test	0.384	0.688
PRIMARY_RESECTION_DAYS_FROM_DIAGNOSIS	Patient	Chi-squared Test	0.389	0.688
Anatomical Site	Sample	Chi-squared Test	0.541	0.718
METASTATIC_ORGANS_AT_DIAGNOSIS	Patient	Chi-squared Test	0.546	0.718
PRIMARY_TUMOR_SITE	Patient	Chi-squared Test	0.571	0.718
Specimen Type	Sample	Chi-squared Test	0.584	0.718
SAMPLE_CLASS	Sample	Chi-squared Test	0.591	0.718
Number of Samples Per Patient	Patient	Chi-squared Test	0.593	0.718
Cancer Type	Sample	Chi-squared Test	0.652	0.750
Sex	Patient	Chi-squared Test	0.784	0.832
Mutation Count	Sample	Wilcoxon Test	0.796	0.832
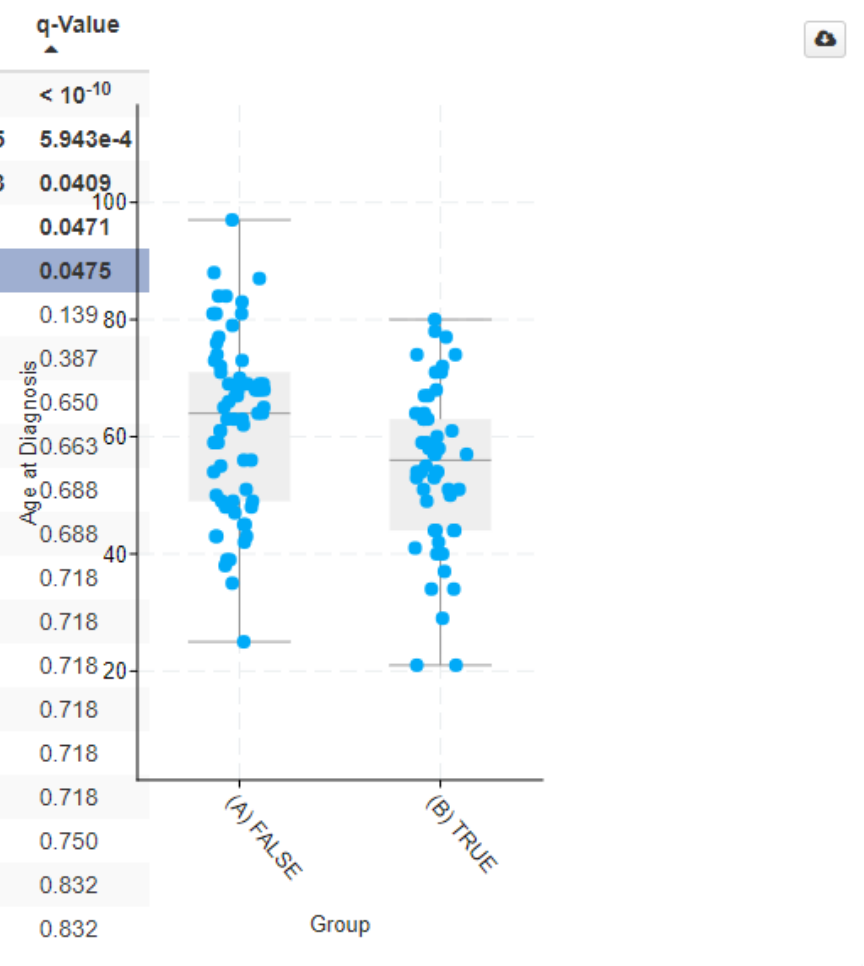
Showing 1-20 of 21   ‹   **Show more**   ›

Overlap   Survival   Clinical   **Genomic Alterations**

Alteration Types

- ☑ **Mutations**
  - ☑ Missense
  - ☑ Inframe
    - ☑ Inframe Insertion
    - ☑ Inframe Deletion
  - ☑ Truncating
    - ☑ Nonsense
    - ☑ Frameshift
      - ☑ Frameshift Insertion
      - ☑ Frameshift Deletion
    - ☑ Nonstart
    - ☑ Nonstop
    - ☑ Splice
  - ☑ Other
- ☑ **Copy Number Alterations**
  - ☑ Amplification
  - ☑ Deletion

Select
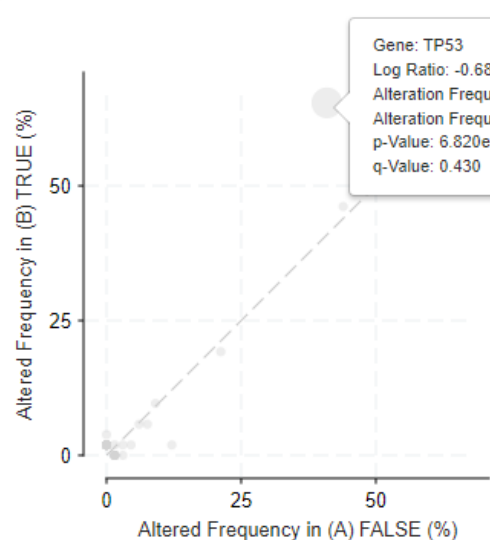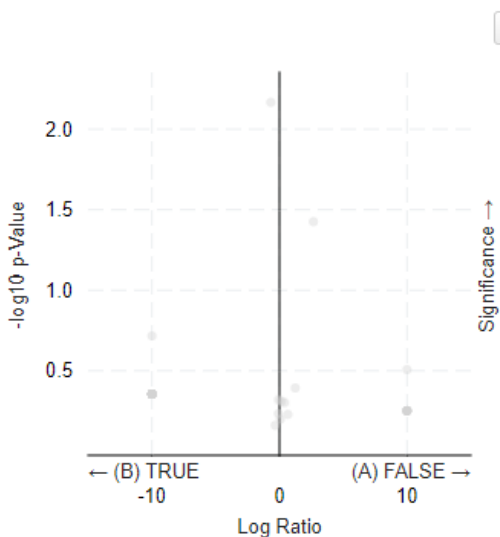
Gene: TP53
Log Ratio: -0.68
Alteration Frequency in (A) FALSE: 41%
Alteration Frequency in (B) TRUE: 65%
p-Value: 6.820e-3
q-Value: 0.430

...with highest frequency i...
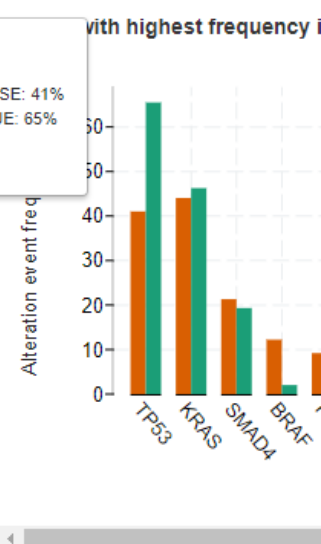
Genomic Alterations

Sample-level enrichments ▾   Enriched in ... ▾   ☐ Significant only   Columns ▾

Gene	Cytoband	(A) FALSE	(B) TRUE	Co-occurrence Pattern	Log Ratio	p-Value	q-Value ▲	Enriched in
TP53	17p13.1	27 (40.91%)	34 (65.38%)		-0.68	6.820e-3	0.430	(B) TRUE
BRAF	7q34	8 (12.12%)	1 (1.92%)		2.66	0.0375	0.591	(A) FALSE

Metastatic Colorectal Cancer (Hadassah Medical Center, 2017-2021)

Summary   Pathways   Clinical Data

🔍 drag to zoom

	0	2y		4m		8m		1y		1y 4m		1y 8m		2y	

SPECIMEN

SURGERY

TREATMENT ▾

MedicalTherapy ▾

Immunotherapy▾

Nivolumab

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Y

MUT   1
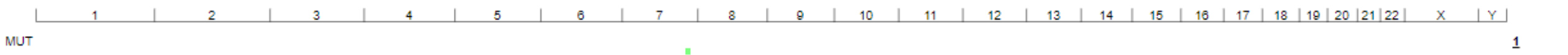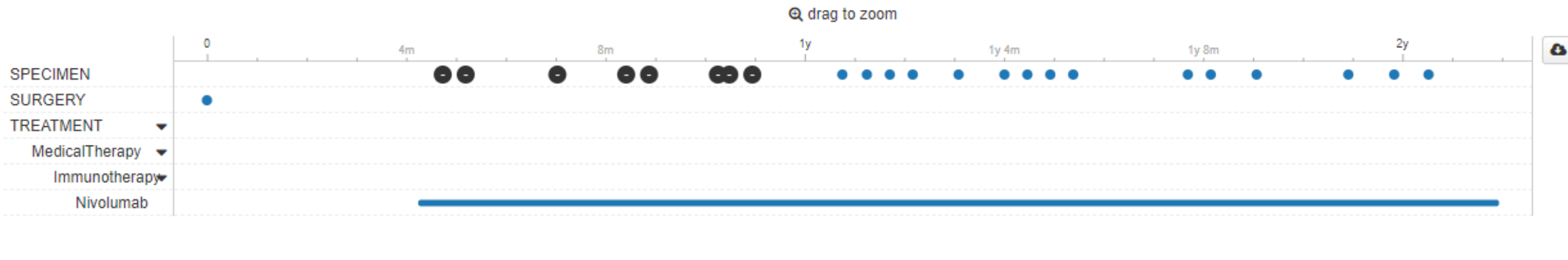
1 Mutation (page 1 of 1)

🗐 ☁ Columns ▾   🔍

Gene	Protein Change	Annotation ◎ ❄ 🔥 ▾	Mutation Type	Copy #	Cohort	COSMIC
BRAF	*V600E*	◎ ❄ 🔥	Missense		▌ 8%	23294

Showing 1-1 of 1 Mutation

Sex

261 | 287

Age at Diagnosis

OS_STATUS

257 | 292

KM Plot: OS_ Survival (months)
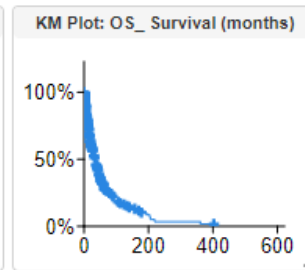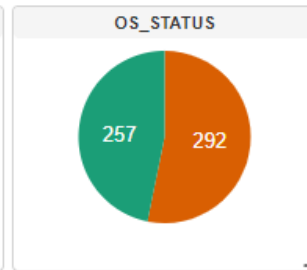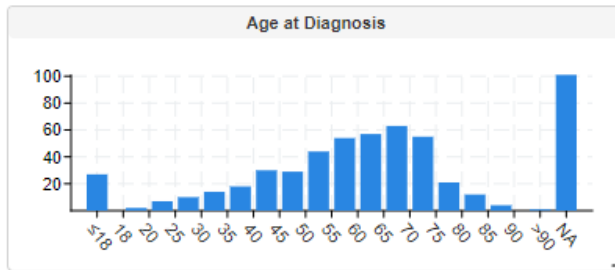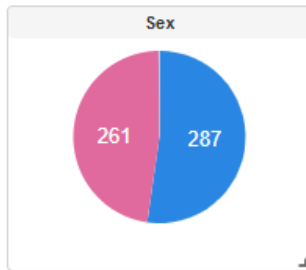
TUMOR_SITE

		#	Freq ▼
■ Lung, NOS		☐ 96	17.5%
■ Breast, NOS		☐ 61	11.1%
■ NA		☐ 45	8.2%
■ Pancreas, NOS		☐ 36	6.6%
■ Colon, NOS		☐ 31	5.6%
■ Brain, NOS		☐ 28	5.1%
■ Thyroid gland		☐ 21	3.8%
■ Stomach, NOS		☐ 16	2.9%
■ Rectum, NOS		☐ 15	2.7%
■ Extrahepatic bile duct		☐ 12	2.2%
■ Prostate gland		☐ 12	2.2%

Search...

CANCER_TYPE

		#	Freq ▼
■ Adenocarcinoma, NOS		☐ 148	27.0%
■ NA		☐ 138	25.1%
■ Infiltrating duct carcinoma, NOS		☐ 34	6.2%
■ Squamous cell carcinoma, NOS		☐ 26	4.7%
■ Glioblastoma, NOS		☐ 16	2.9%
■ Carcinoma, NOS		☐ 12	2.2%
■ Neuroendocrine carcinoma, NOS		☐ 12	2.2%
■ Papillary carcinoma, NOS		☐ 12	2.2%
■ Malignant melanoma, NOS		☐ 11	2.0%
■ Glioma, malignant		☐ 6	1.1%
■ Mucinous adenocarcinoma		☐ 6	1.1%

Search...

Mutated Genes (566 profiled samples)

▼ Gene	# Mut	#	Freq ▼
TP53	300	☐ 260	45.9%
KMT2D	122	☐ 103	18.2%
KRAS	102	☐ 99	17.5%
ATM	117	☐ 96	17.0%
MED12	99	☐ 95	16.8%
APC	122	☐ 94	16.6%
BRCA2	93	☐ 79	14.0%
TSC2	80	☐ 78	13.8%
DNMT3A	101	☐ 74	13.1%
NF1	79	☐ 68	12.0%
MAP3K1	77	☐ 67	11.8%

Search...

CNA Genes (277 profiled samples)

▼ Gene	Cytoband	CNA	#	Freq ▼
CDKN2A	9p21.3	HOMDEL	☐ 95	34.3%
CDKN2B	9p21.3	HOMDEL	☐ 85	30.7%
MTAP	9p21.3	HOMDEL	☐ 50	18.1%
MYC	8q24.21	AMP	☐ 25	9.0%
EGFR	7p11.2	AMP	☐ 21	7.6%
CCND1	11q13.3	AMP	☐ 18	6.5%
FGF19	11q13.3	AMP	☐ 15	5.4%
MDM2	12q15	AMP	☐ 14	5.1%
RB1	13q14.2	HOMDEL	☐ 13	4.7%
FGF4	11q13.3	AMP	☐ 13	4.7%
TEK	9p21.2	HOMDEL	☐ 12	4.3%

Treatment by Patient

Treatment	# ▼
Palonosetron	☐ 152
Carboplatin	☐ 143
Fluorouracil	☐ 113
Oxaliplatin	☐ 108
Leucovorine	☐ 108
Paclitaxel	☐ 104
Irinotecan	☐ 103
Gemcitabine	☐ 100
Bevacizumab	☐ 100
Cisplatin	☐ 99
Zolendronic Acid	☐ 61

Summary | Pathways | Clinical Data

🔍 drag to zoom

6 Mutations (page 1 of 1)

Samples	Gene	Protein Change	Annotation ◎ ◌ 🔥 ▾	Mutation Type	Cohort	COSMIC
❷	TP53	*M246I*	◎ 🔥	Missense	▨ 46%	92
❷	SETD2	*E2089**	◎	Nonsense	▨ 9%	
❷	SMAD4	*S154**	◎	Nonsense	▨ 6%	
❶	BRCA2	*E2220Q*	○	Missense	▨ 14%	
❷	IKZF1	*M476R*	○	Missense	▨ 1%	

REDCap

ABOUT

REDCap was created in 2004 at Vanderbilt University. It originally supported a small group of clinical researchers who needed a secure data collection tool that met HIPAA compliance standards. REDCap quickly became their go-to method for supporting both single and multi-site research studies.

REDCap's developers firmly believed that nobody could know the research as well as the researcher. So a user-friendly web-based interface was introduced to put the researchers in total control of their work. No background knowledge or technical experience was needed to use REDCap; researchers could directly manage their own projects whenever and however they wished, through any browser on any device.

Vanderbilt was now able to invest minimal institutional resources yet still safely and reliably support an increasing number of research studies in REDCap. They explored ways to disseminate the now mature software, as well as to foster broader collaboration for future development.

In 2006, the REDCap consortium officially launched. The consortium began as a handful of non-profit organizations interested in expanding REDCap's functionality through collaborative software development. Each partner site was given access to the codebase so that they could install their own REDCap system and offer it to their researchers as Vanderbilt had done for its own clinical researchers.

The consortium focused on building a strong community, with international participation right from the start. REDCap usage began to grow rapidly as organizations realized they could 1) fully customize their systems to meet their local security policies, 2) personalize features/functionality to address user needs, and 3) have direct input into the future direction of the software – all at *no cost*.

Over the next few years, consortium sites across the world found that REDCap empowered them to take control of their work in a way they couldn't with previous data collection tools. Researchers reported that the very process of using the software actually improved research, through REDCap's fundamental features/functionality (like the Project Setup checklist and Shared Library of pre-built

DIVE DEEPER

If you represent a not-for-profit institution and you seek to join the REDCap Consortium, then visit the Join page.

Learn more about our software or sign up for a free demonstration account of REDCap.

Learn more about REDCap's story and the REDCap Consortium, a community that collectively supports REDCap activities.

If you are already at a member institution, find your group on our world map or in our list of REDCap partners.

Search ...

NEWEST FEATURE

File Repository Improvements: The File Repository page has been redesigned to make it easier to store, organize, and share the files in your projects.

📖 My Projects
💬 REDCap Messenger
✉️ Contact REDCap administrator

Project Home and Design ⊟

🏠 Project Home · ⋮≣ Project Setup
📝 Designer · 🗷 Dictionary · 📙 Codebook
⬛ Project status: **Development**

Data Collection ⊟

⊞ Record Status Dashboard
   - View data collection status of all records
📄 **Add / Edit Records**
   - Create new records or edit/view existing ones

⫘ Record ID **420**   Select other record
Data Collection Instruments:
   Patients
   Breast methylation results
   cfNANO results
   Timelines

Applications ⊟

🖥 Project Dashboards
🔔 Alerts & Notifications
🌐 Multi-Language Management
⊞ Calendar
📤 Data Exports, Reports, and Stats
📥 Data Import Tool
≠ Data Comparison Tool
📑 Logging and 📤 Email Logging
💬 Field Comment Log
📁 File Repository
👤 User Rights and 👥 DAGs
📋 Data Quality
📱 REDCap Mobile App

Reports 🔍 Search 📂 Organize ✏️ Edit ⊟

1) Sample for DNA purification
2) Pateints not excluded or haven't been

Breast Biopsy v2   PID 217

📄 Patients

ⓐ Adding new Record ID **420**.

| Record ID	420

Excluded
- ☐ previous cancer
- ☐ current cancer
- ☐ genomic feature
- ☐ medical file not in HMO
- ☐ biopsy not performed
- ☐ other
- ☐ previous antineoplastic treatment

Patient ID

Temporary ID (	
Temporary ID (	○ Yes ⦿ No reset
ID Number	[_____]
First Name	[_____]
Last Name	[_____]
Date of birth	[_____] 📅 Today D-M-Y
Date at sample collection	[_____] 📅 Today D-M-Y
Age at sample collection	[_____] View equation
PL Number:	[_____]

Save & Exit Form
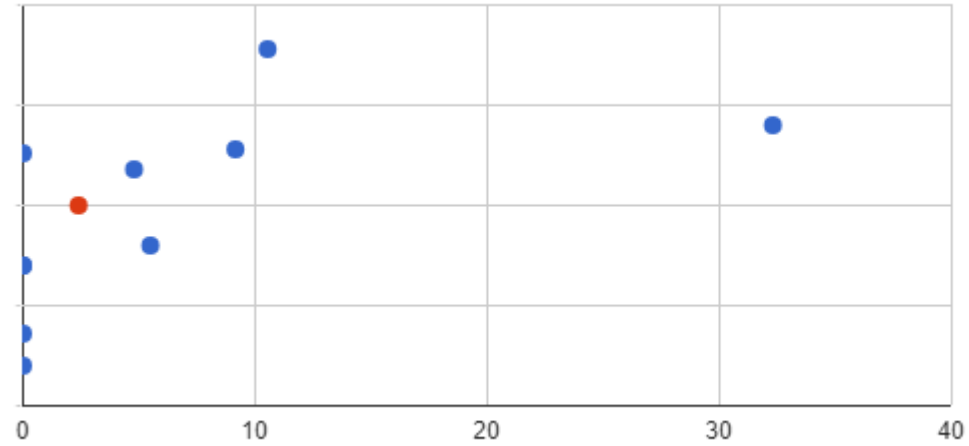**Save & Stay** ▾
– Cancel –
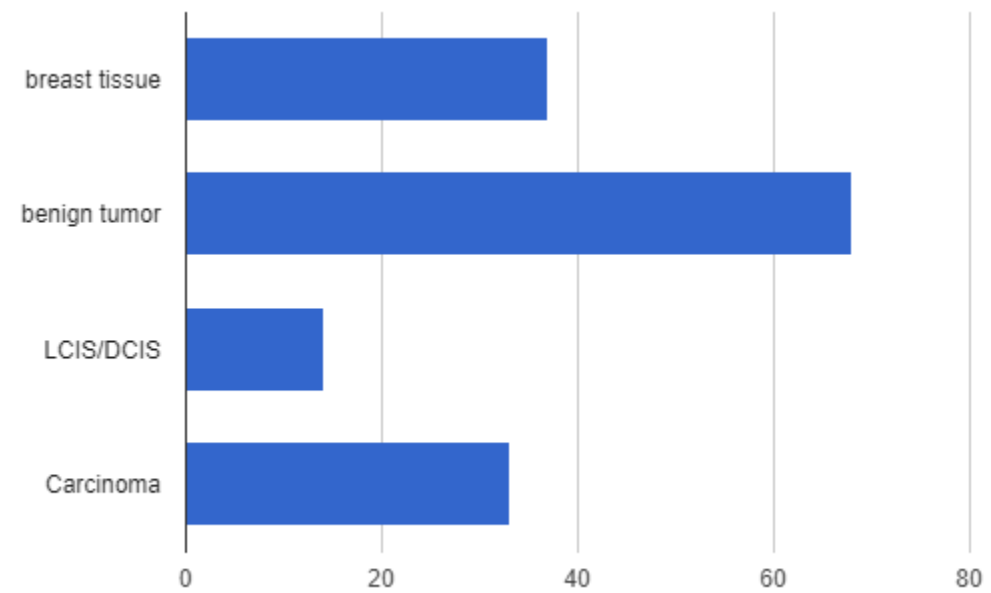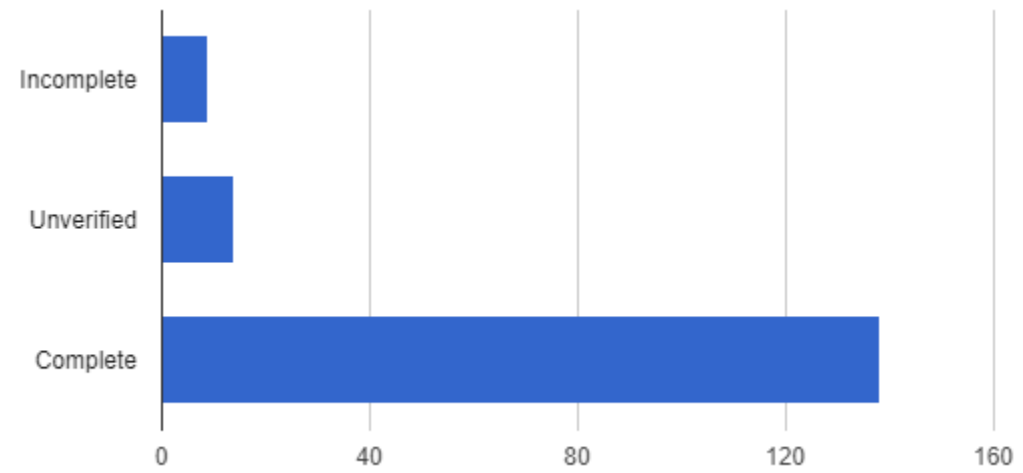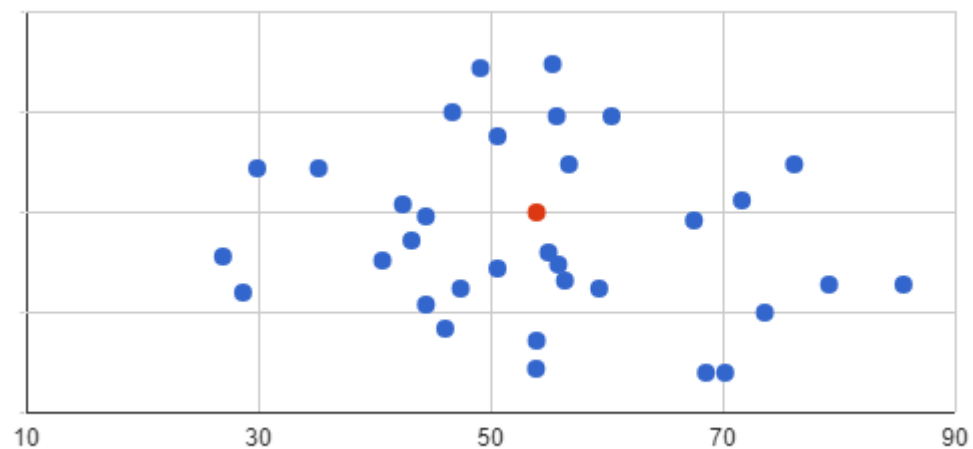
Age at sample collection *(age_at_sample_collection)*   Refresh Plot

Total Count (N)	Missing*	Unique	Min	Max	Mean	StDev	Sum	Percentile						
								0.05	0.10	0.25	0.50 Median	0.75	0.90	0.95
33	0 (0.0%)	33	26.88	85.50	53.92	14.46	1779.2	29.34	36.22	44.37	53.90	60.35	73.16	77.29

Lowest values: 26.875181101140566, 28.608276236564294, 29.82664485467418, 35.116281192175975, 40.6139984622089

Highest values: 71.57447905615219, 73.55101975628064, 76.08917363121762, 79.08991971087703, 85.50198384178547

breast2(all T) *(breast2_all_t)* [Refresh Plot](#)

Total Count (N)	Missing*	Unique	Min	Max	Mean	StDev	Sum	Percentile						
								0.05	0.10	0.25	0.50 Median	0.75	0.90	0.95
10	23 (69.7%)	6	0	32.30	6.22	10.02	62.24	0	0	0	2.39	8.23	12.71	22.50

Lowest values: 0, 0, 0, 0, 0

Highest values: 4.783106393, 5.484216066, 9.148394004, 10.53340576, 32.2952744

Calculated Categorial Pathology	Ⓗ ◌	Carcinoma ▾
		This is a temporary field to be replaced by a calculator

stage	Ⓗ ◌	Stage IV ▾

Invasive pathology	Ⓗ ◌	IDC ▾

ER Ⓗ ◌
- ○ 0
- ○ 1
- ○ 2
- ● 3

reset

PR Ⓗ ◌
- ○ 0
- ○ 1
- ○ 2
- ● 3

reset

HER2 Ⓗ ◌
- ○ 0
- ○ 1
- ● 2
- ○ 3

reset

ERBB2 AMPLIFIED Ⓗ ◌
- ○ Yes
- ● No

reset

KI-67 Ⓗ ◌
- ○ 1-14%
- ● Above 15%

reset

Grade Ⓗ ◌
3 ▾

Record_id	Patient Demographic Data	Oncology Data	Tumor Properties Data	Cyto Medication Data	Procedure Data	Patients	Pathology Information From Midgam
1 (Patient_ID_Original	●	○	○	○	○	○	○
2 (Patient_ID_Original	●	● +	● +	●)) +	○	○	○
3 (Patient_ID_Original	●	● +	● +	●)) +	○	○	○
4 (Patient_ID_Original	●	○	○	○	○	○	○
5 (Patient_ID_Original	●	○	○	○	○	○	○
6 (Patient_ID_Original	●	● +	● +	●)) +	○	○	○
7 (Patient_ID_Original	●	○	○	○	○	○	○
8 (Patient_ID_Original	●	○	○	○	○	○	○
9 (Patient_ID_Original	●	●)) +	●)) +	○	○	○	○
10 (Patient_ID_Origina	●	○	○	○	○	○	○
11 (Patient_ID_Origina	●	● +	● +	○	○	○	○
12 (Patient_ID_Origina	●	○	○	●)) +	○	○	○
13 (Patient_ID_Origina	●	●)) +	●)) +	●)) +	○	○	○
14 (Patient_ID_Origina	●	●)) +	●)) +	●)) +	○	○	○
15 (Patient_ID_Origina	●	● +	● +	○	○	○	○
16 (Patient_ID_Origina	●	●)) +	●)) +	●)) +	○	○	○
17 (Patient_ID_Origina	●	○	○	○	○	○	○
18 (Patient_ID_Origina	●	○	○	●)) +	○	○	○
19 (Patient_ID_Origina	●	○	○	●)) +	○	○	○
20 (Patient_ID_Origina	●	● +	● +	○	○	○	○
21 (Patient_ID_Origina	●	●)) +	●)) +	○	○	○	○
22 (Patient_ID_Origin	●	○	○	○	○	○	○

Oncology Data (5)

1	⦿	, C18.9,
2	⦿	, C19.9c,
3	⦿	, C19.9c, Grade IV
4	⦿	, C19.9c,
5	⦿	, C18.9, Grade IV

+ Add new

Tumor Properties Data (3)

1	⦿	, C19.9c
2	⦿	, C19.9c
3	⦿	, C18.9

+ Add new

Cyto Medication Data (83)

1	⦿	2013-02-24T08:52:17.510Z, FLUOROURACIL 5000MG INJ
2	⦿	2014-01-19T09:16:53.883Z, CAMPTO 1 MG
3	⦿	2013-08-11T07:57:33.620Z, CAMPTO 1 MG
4	⦿	2013-08-11T12:01:10.917Z, AVASTIN 100MG
5	⦿	2013-12-15T10:38:44.890Z, FLUOROURACIL 5000MG INJ
6	⦿	2013-02-24T08:52:17.510Z, LEUCOVORINE 500MG INJ
7	⦿	2013-05-05T07:37:12.377Z, CAMPTO 1 MG
8	⦿	2014-02-02T11:16:03.813Z, AVASTIN 100MG

Sex

3,574

Age at Diagnosis

4000
3000
2000
1000

≤10 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 >90 NA

OS_STATUS

5,551

KM Plot: OS_ Survival (months)

100%
50%
0%
0   200   400   600
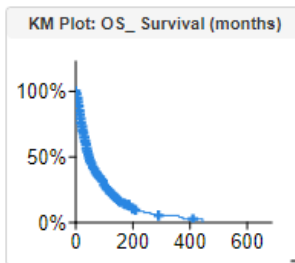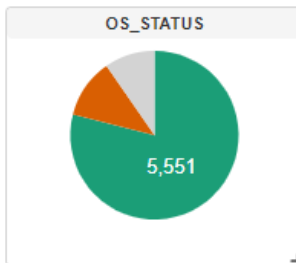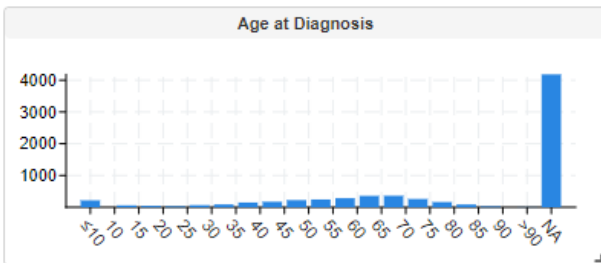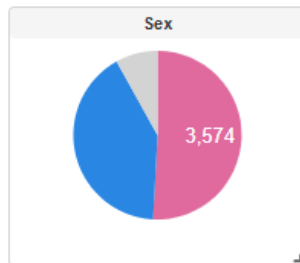
TUMOR_SITE

		#	Freq ▼
▢	NA	☐ 3,939	56.0%
■	Breast, NOS	☐ 862	12.3%
■	Colon, NOS	☐ 196	2.8%
■	Lung, NOS	☐ 179	2.5%
■	Lymph node, NOS	☐ 109	1.6%
■	Prostate gland	☐ 99	1.4%
■	Bone marrow	☐ 90	1.3%
■	Rectum, NOS	☐ 88	1.3%
■	Blood	☐ 87	1.2%
■	Skin, NOS	☐ 87	1.2%
■	Thyroid gland	☐ 80	1.1%

Search...

CANCER_TYPE

		#	Freq ▼
▢	NA	☐ 4,587	65.2%
■	Adenocarcinoma, NOS	☐ 547	7.8%
■	Infiltrating duct carcinoma, NOS	☐ 398	5.7%
■	Malignant melanoma, NOS	☐ 154	2.2%
■	Malignant lymphoma, large B-c...	☐ 72	1.0%
■	Squamous cell carcinoma, NOS	☐ 72	1.0%
■	Papillary carcinoma, NOS	☐ 64	0.9%
■	Transitional cell carcinoma, NOS	☐ 55	0.8%
■	Acute leukemia, NOS	☐ 51	0.7%
■	Intraductal carcinoma, noninfiltr...	☐ 40	0.6%
■	Hodgkin lymphoma, NOS	☐ 39	0.6%

Search...

Treatment by Patient

Treatment	# ▼
Cyclophosphamide	☐ 853
Doxorubicin	☐ 753
Mesna	☐ 486
Vincristine	☐ 479
Paclitaxel	☐ 472
Palonosetron	☐ 463
Carboplatin	☐ 461
Leucovorine	☐ 369
Rituximab	☐ 331
Etoposide	☐ 306
Cisplatin	☐ 290

Search...

Patient: ██████ Female, Adenocarcinoma, NOS, DECEASED (29 months)

Samples: ① 1186 ② plasma_2382_1 ③ plasma_2382_2 ④ plasma_2382_3 ⑤ plasma_2382_4 ⑥ serum_2382_1 ⑦ serum_2382_2 ⑧ serum_2382_3

Summary | Pathways | Clinical Data

🔍 drag to zoom

	0	4m	8m	1y	1y 4m	1y 8m	2y	2y 4

TREATMENT ▼
Medical Therapy ▼
Biologicaltherapy ▼
Cetuximab
Bevacizumab
Chemotherapy ▼
Irinotecan

Conclusion and plans

- REDCap and Cbioportal are part of routine research and entering clinical care.

- Much more work is needed to add various aspects to the platforms.

- Integration across different medical and research disiplinaries

Thank you!