

SAP Connected Health Platform and SAP Medical Research Insights
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Getting Started Guide for SAP Connected Health Platform and SAP Medical Research Insights

Cloud Appliance Library - Trial Version



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1 Solution Information

The pre-assembled trial system for SAP Connected Health platform and SAP Medical Research Insights is delivered through a software appliance format, which is specifically optimized for Cloud deployment. This appliance contains the following:

- Pre-installed HANA system
- Required software components for SAP Connected Health platform and SAP Medical Research Insights
- An active system and application configurations for the trial purpose

This guide provides the information about the generic prerequisites required to explore the platform capabilities available in the SAP Connected Health platform and SAP Medical Research Insights cloud environment. This cloud instance is fully configured for trial purpose and has an active system with pre-installed SAP SDI Data Provisioning Server and Data Provisioning agent for data integration activities.

This document is intended for system administrators and technical consultants, responsible for system setup and preparation including troubleshooting. Administrators and consultants are expected to have sound knowledge of SAP Best Practices. This document does not provide a general overview and explanation of SAP Best Practices.

Related Information

[Product Name \[page 3\]](#)

[Licenses \[page 5\]](#)

[Security Aspects \[page 6\]](#)

[Solution Provisioning in SAP Cloud Appliance Library \[page 7\]](#)

1.1 Product Name

This trial product comprises both SAP Connected Health platform and SAP Medical Research Insights. Although SAP Connected Health platform appears as the product name both on the SAP Cloud Appliance Library and in this guide, several applications within this trial version use the previous name of the product, SAP Foundation for Health.

For this trial version, these two name variations should be treated as synonyms.

Material Numbers

Table 1:

Number	Description
51050700	SAP Medical Research Insights 2.0
51050701	SAP Foundation for Health 1.0
51050838	SAP HANA, Platform Edition 1.0 SPS 11 Rev 112
51049942	HANA EIM SERVICES 1.0

Database Server Details

Table 2:

Name	Value	Description
SID	HDB	System ID of the SAP system
Instance Number	00	Instance number of the central instance of the SAP System
DB Type	HDB	Type of the database
Username	SYSTEM	These are the standard users which you can use to access the database server
Password	Tour1234	The initial password of the master system. Note that for solution provisioning in SAP Cloud Appliance Library the password is reset with the one provided when you create an instance.

OS Users and Groups

Table 3:

User	Password	Description
hdbadm	Tour1234	SAP HANA system administrator
dpagent	Tour1234	SAP IM DP Agent administrator

User	Password	Description
root	<none>	The default OS Administrator user for Linux SUSE.

1.2 Licenses

Free Trial License Agreement

This solution can be used for trial purposes within the configured free period. Note that you are not allowed to install license keys under the Free Trial License Agreement.

SAP Product License Agreement:

To use the instances created from this solution under your own SAP Product License Agreements, you have to unlock the solution in SAP Cloud Appliance Library. The prerequisites are that you own the required SAP Product licenses and that you purchase the SAP Cloud Appliance Library subscription package. For more information, see [Unlocking Solutions](#).

License Keys Installation

After you create the solution instance in SAP Cloud Appliance Library, the SAP system generates a temporary license key that is sufficient for the exploration purpose. Note that valid license is required to use the solution instance after the expiration of the pre-installed temporary license. For this solution you have to request and install the following license keys:

Table 4:

SID	Product	Version	DB	OS	Comment
HDB	SAP HANA, platform edition	1.0	n/a	Linux	Recommended quantity is minimum 64 GB Main Memory

SID	Product	Version	DB	OS	Comment
n/a	SAP Connected Health platform	1.0	n/a	Linux	Recommended quantity is minimum 64 GB Main Memory
n/a	SAP Medical Research Insights	2.0	n/a	Linux	Recommended quantity is minimum 64 GB Main Memory

For more information about how to request and install product license keys, see this [SCN](#) blog.

1.3 Security Aspects

Please note that creating your instances in the public zone of your cloud computing platform is convenient but less secure. Ensure that only port 22 (SSH) is opened when working with Linux-based solutions and port 3389 (RDP) when working with Windows based solutions. In addition, we also recommend that you limit the access to your instances by defining a specific IP range in the Access Points settings, using CIDR notation -https://en.wikipedia.org/wiki/Classless_Inter-Domain_Routing. The more complex but secure alternative is to set up a virtual private cloud (VPC) with VPN access, which is described in this tutorial on SCN -<http://scn.sap.com/docs/DOC-57869>.

The list below describes the ports opened for the security group formed by the server components of your solution instance:

To access back-end servers on the operating system (OS) level, use the following information:

Table 5:

Protocol	Port	Description
SSH	22	Used for SSH connection to Linux-based servers
RDP	3389	Used for RDP connection to Windows based servers

You must change the initial user passwords provided by SAP when you log onto the system for the first time.

Note that when using HANA based appliances, HANA systems are not installed individually but cloned from a template system. As a consequence of this cloning process, the existing root keys are cloned. For more information, see [SAP Note 2134846 - HANA encryption key handling during system cloning](#).

Security Vulnerabilities

For information about known security vulnerabilities, see the [SAP Cloud Appliance Library Public Wiki](#).

1.4 Solution Provisioning in SAP Cloud Appliance Library

If you have a user in SAP Cloud Appliance Library, you need to meet the following prerequisites before starting to use the SAP Cloud Appliance library:

Cloud Provider Configurations

You have a valid account in one of the cloud providers supported by SAP Cloud Appliance Library. If you already have an active cloud provider account, you can proceed directly with the next section. Otherwise, navigate to the cloud provider home page and sign up.

For more information about the supported cloud providers, click the link to the FAQ page: <http://scn.sap.com/docs/DOC-33673>.

Navigate to SAP Cloud Appliance Library

Open the SAP Cloud Appliance Library in your Web browser using the following link: <https://cal.sap.com>.

For more information about how to use solutions in SAP Cloud Appliance Library, see the official documentation of SAP Cloud Appliance Library (choose ► [Support](#) ► [Documentation](#) ► link and choose (expand all) button to see all documents in the structure). You can also use the context help in SAP Cloud Appliance Library by choosing the [Help](#) panel from the right side.

2 Before You Start

Related Information

[Users \[page 8\]](#)

[Ontology Content \[page 8\]](#)

[Setting Up Document Processing \[page 12\]](#)

2.1 Users

For this trial version, you can log on as the following users:

Table 6:

User	Password	Description
Administrator	Tour1234	This user has access to all standard scenarios and is intended to be the primary user for the trial version.
MIMIC	Tour1234	This user is required for integrating and using the optional MIMIC clinical data.
TA_USER	Tour1234	This user is required for integrating unstructured documents and to analyze extracted content in the patient analytics application.

If you want to learn more about user management, see the *SAP Connected Health Platform Administration Guide* at http://help.sap.com/platform_health101.

2.2 Ontology Content

Related Information

[Ontology Content Providers \[page 9\]](#)

[Integrating Content from Ontology Content Providers \[page 11\]](#)

2.2.1 Ontology Content Providers

SAP Connected Health relies on ontology content from a number of providers.

Table 7:

Content Provider	Use of Content in SAP Connected Health	Web Page
National Cancer Institute Metathesaurus (NCIm)	Biomedical concepts, including their relationships NCIm is derived from the Unified Medical Language System (UMLS).	http://ncimeta.nci.nih.gov/ ➔
Value Set Authority Center	Vocabulary value sets issued by the Value Set Authority Center (VSAC). i Note These value sets are not used by any application provided with the standard version of SAP Connected Health.	https://vsac.nlm.nih.gov/ ➔
Centers for Medicare & Medicaid Services	General equivalence mappings to translate ICD9CM codes into ICD10CM codes	http://www.cms.gov
RxNorm	Provides normalized names for clinical drugs and maps its names to many of the common drug vocabularies	http://rxnav.nlm.nih.gov/ ➔
LOINC (Logical Observations Identifiers, Names, Codes)	LOINC, produced by the Regenstrief Institute, is a database and standard for laboratory test orders and results. It applies universal code names and identifiers to medical terminology related to electronic health records.	https://loinc.org/
SAP Vocabularies	Additional reference information, including mapping and classifications of content provided by other content providers.	This vocabulary content is provided with the plug-in <i>Vocabulary ID Mappings for Ontology Services</i> .

Content Provider	Use of Content in SAP Connected Health	Web Page
National Center for Biotechnology Information (NCBI) Gene	<p>This extension provides the system with content from The National Center for Biotechnology Information (NCBI). This includes symbols and synonyms as well as description and designations of the genes. Also it provides taxonomy ID, type of gene, chromosome and corresponding map location for the genes. Moreover, it includes relations between a gene with a ID from NCBI vocabulary to other vocabularies which are existing in the system.</p> <p>This content is used to extract entities during text analysis.</p>	http://www.ncbi.nlm.nih.gov/gene ➡

Note

To integrate ontology content from these providers, the content must be available as CSV files.

Provider Ranking

If two or more providers are providing terms for identical codes, the system identifies the winning term as the term coming from whichever provider was integrated into the system first.

You can adjust the ranking by executing the following procedures:

- "SAP_HPH"."sap.hc.hph.ots.services.lib::SetWinningTermProvider"(vocabulary_id, provider_name)**
 For the specified vocabulary, this procedure sets the rank of the specified provider to 1 and lowers the rank of all others.
- "SAP_HPH"."sap.hc.hph.ots.services.lib::SetWinningVocabularyProvider"(provider_name)**
 If an external vocabulary ID refers to multiple internal vocabulary IDs based on different providers, for example ICD refers to both `ots.ICD.ICD9CM` and `ots.ICD.ICD10CM`, this procedure ensures the specified provider always wins.

2.2.2 Integrating Content from Ontology Content Providers

Import and transform ontologies from external sources by using the [Data Integration Cockpit](#).

Prerequisites

- You have the required licenses for the ontology sources you want to use.

Context

To ensure that clinical data created in different external systems using different coding systems is correctly interpreted and harmonized, SAP Connected Health supports the integration of ontology content from external providers. To integrate this content into the platform, you must import it into the system and then transform and optimize it.

Note

Based on the volume and complexity of the data, the import and transformation of ontology content can take up to several hours. Please plan accordingly.

Procedure

1. Download ontology content directly from the relevant content providers and save the files to the appropriate folder.

You save the files under `/hana/shared/ffh-data/` in the following folders:

- ncim
- valuesets
- cmsgems
- rxnorm
- vocabularies

Note

For the vocabularies content, the required file is provided with the plug-in [Vocabulary ID Mappings for Ontology Services](#) in the repository package `► sap ► hc ► hph ► plugins ► ots ► vocabularies ► data ►`.

2. Go to the SAP Fiori launchpad for SAP Connected Health.
3. Open the [Data Integration Cockpit](#) app.
4. Import the required vocabularies content provided by SAP.
 - a. Select the [Import](#) data integration extension for vocabularies.

- b. Choose [Run Profile](#).
 - c. To monitor the status of the data integration run, choose the [Monitor](#) view to see the start time, duration, and status for each applied profile.
 - d. To monitor any impacts on the related tables in the clinical data warehouse, use the [Clinical Data Warehouse Cockpit](#) app.
5. After the profile run is complete, select the [Transform](#) data integration extension for vocabularies, and choose [Run Profile](#).
 6. Repeat steps 4-5 for any ontology content providers you want to support.

Note

If you want to use CMS GEMs ontology content, you must first integrate NCIIm ontology content.

As a prerequisite to set up document processing task, you must generate dictionaries using python script in the folder `/hana/shared/ffh-py/createMedDict.py`.

Sample Code

```
python CALDocProcessing.py
```

2.3 Setting Up Document Processing

Related Information

[Integrating Unstructured Documents \[page 12\]](#)

2.3.1 Integrating Unstructured Documents

Import and transform unstructured clinical documents, such as a doctor's note, from external sources by using the [Data Integration Cockpit](#).

Prerequisites

- You have downloaded ontology content directly from the relevant content providers and save the files to the appropriate folder.
- You have imported and integrated ontology content using data integration profile runs using the [Data Integration Cockpit](#).

- You have generated dictionaries using python script in the folder `/hana/shared/ffh-py/` `createMedDict.py`.
- You have activated the [SAP Connected Health Platform Medical Text Processing Plug-In](#) and configured the [Document Type](#) by choosing the type `customer.documents`.

Context

To use unstructured documents in patient-related applications, data integration extensions are used to import the documents into SAP HANA to then generate document indexes and extract metadata that can be used in the patient-related applications.

Procedure

1. Save the unstructured clinical documents to the appropriate folder.
You save the files under `/hana/shared/ffh-data/blob` folder.
2. Go to the SAP Fiori launchpad for SAP Foundation for Health.
3. Open the [Data Integration Cockpit](#) app.
4. Select the data integration staging extension and choose [Run Profile](#).
5. Go to `/hana/shared/ffh-py/CALDocProcessing.py` and run the python script to assign documents to the specific patient.

Run the python script using "hdbadm" user credentials.

Sample Code

```
python CALDocProcessing.py
```

6. Select the data integration document processing extension and choose [Run Profile](#).

To view the documents related to a patient, use the [Patient Search](#) application, search for the specific patient, and go to the [Related Documents](#) view. To analyze the content in the documents, see [Analyzing Content Extracted from Documents \[page 42\]](#).

3 Guided Tours

Related Information

[Analyzing Clinical Data \[page 14\]](#)

[Analyzing Genomic Data \[page 30\]](#)

[Analyzing Content Extracted from Documents \[page 42\]](#)

3.1 Analyzing Clinical Data

Follow this step-by-step guide to get an introduction to how you can use SAP Connected Health to analyze clinical data.

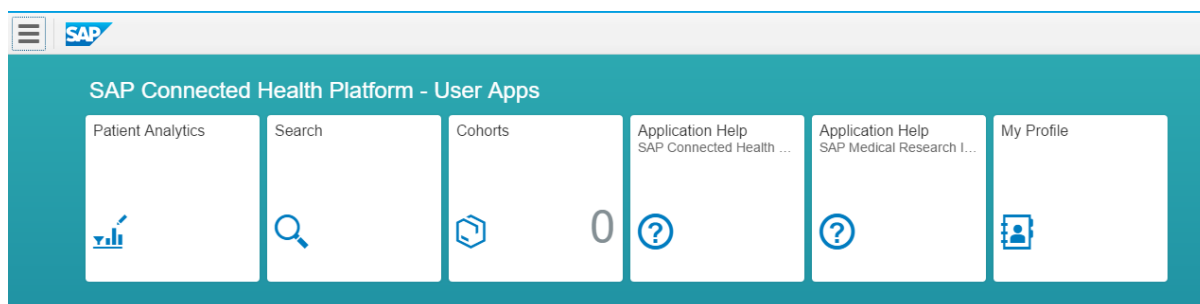
Context

Let's assume you are a physician and cancer researcher. You're considering initiating a new clinical study about special dependencies in lung cancer. Therefore, you would like to investigate particular aspects of lung cancer and create a new patient cohort.

The initial screen presents the SAP Fiori launchpad, where you can start your analysis. From the launchpad, you can also access existing patient cohorts, search for patients, and create personalized tiles. You can also get application help and change your profile.

Procedure

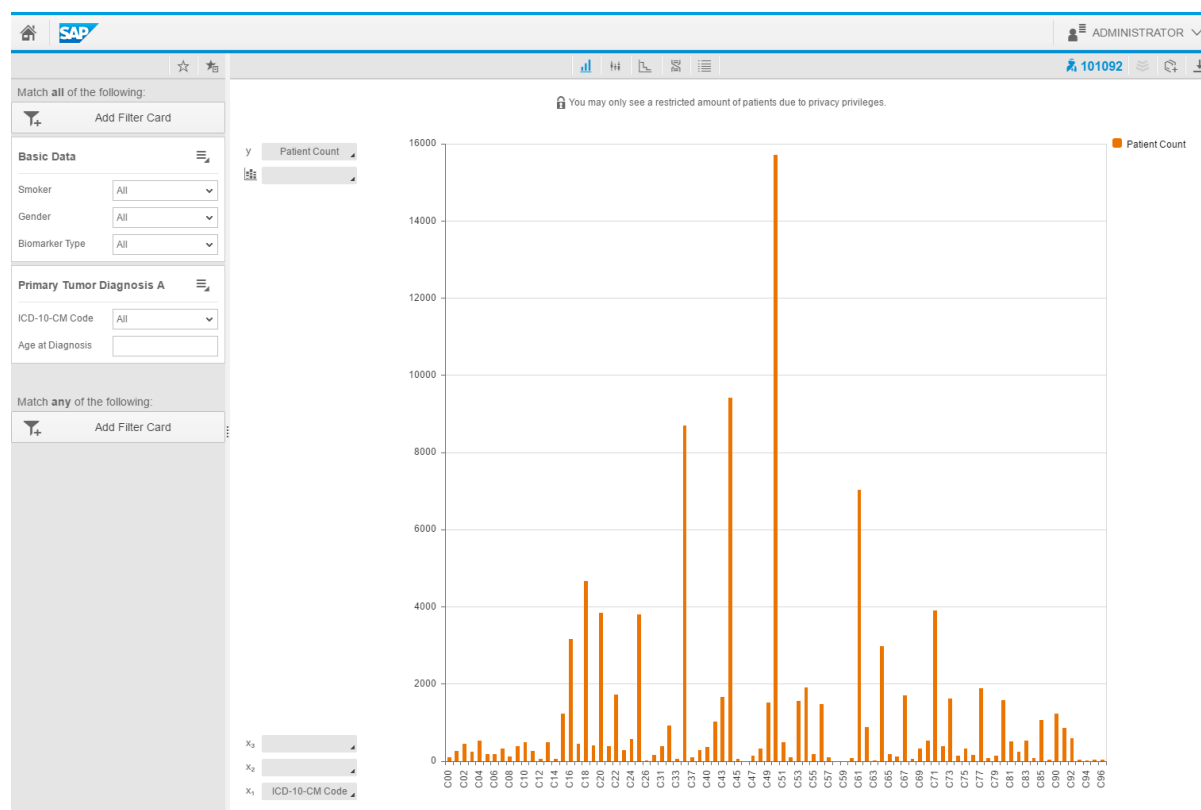
1. Open the SAP Fiori launchpad.



2. Start the analysis by clicking *Patient Analytics*.

On the left hand side, filter cards for basic patient data and the primary tumor diagnosis are displayed. This is the mechanism used to build the cohort, or set of criteria to filter out unrelated patients.

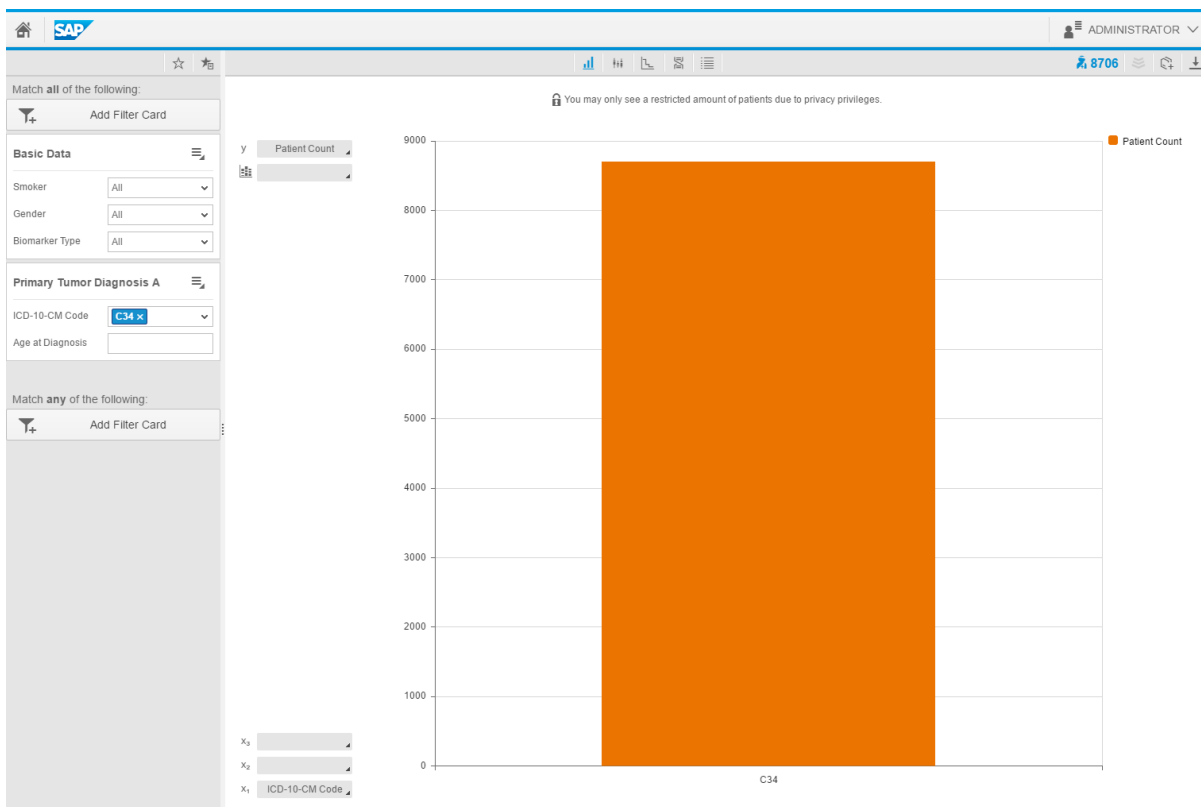
When the application is loaded, a chart is displayed that shows the number of patients per diagnosis (ICD-10-CM Code). The number at the top right corresponds to the amount of patients that are being aggregated for the current view.



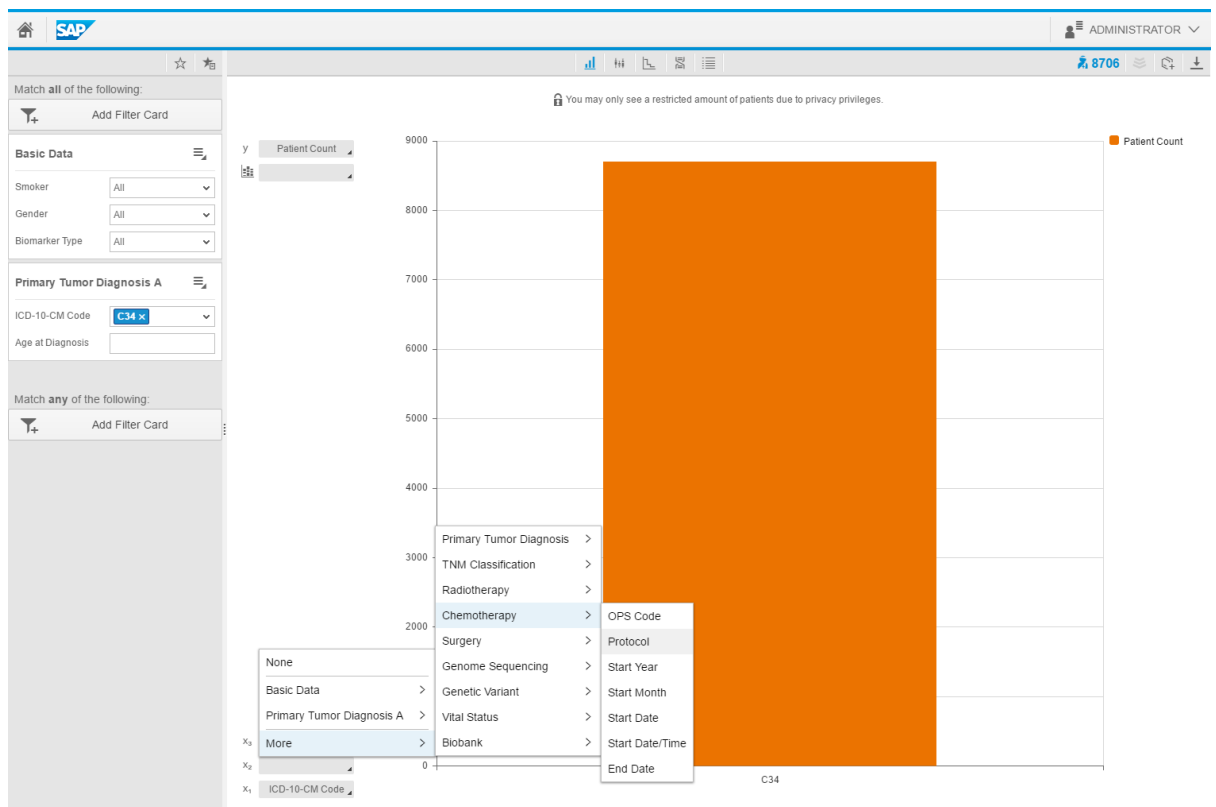
3. Search for an ICD code.

- In the *Primary Tumor Diagnosis* filter card in the *Match all of the following* area, enter descriptive terms, such as **lung**.
- Select the entry C34.

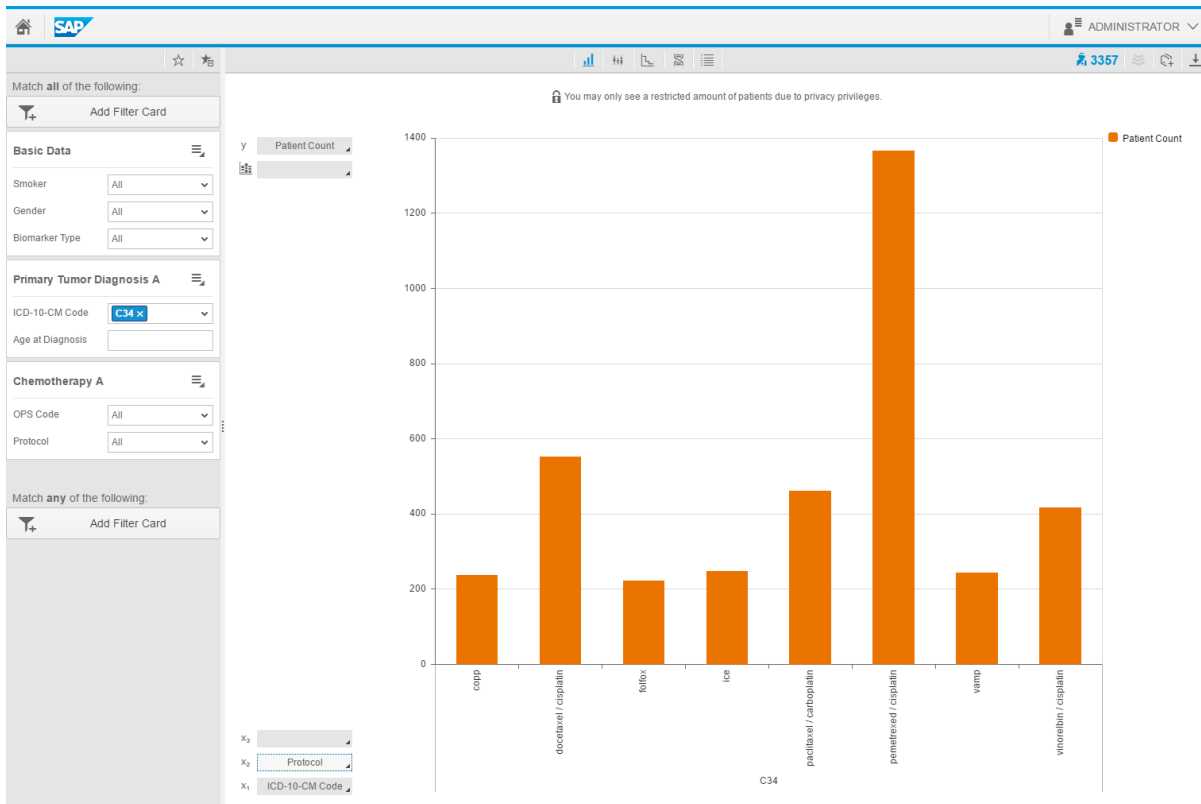
The chart now only shows a column for patients with lung cancer.




- Find out whether these patients had a chemotherapy treatment by adding the chemotherapy protocol attribute to the chart. To do so, click the gray button labeled X_2 in the lower left corner of the graphic and select the entry [More](#) [Chemotherapy](#) [Protocol](#).

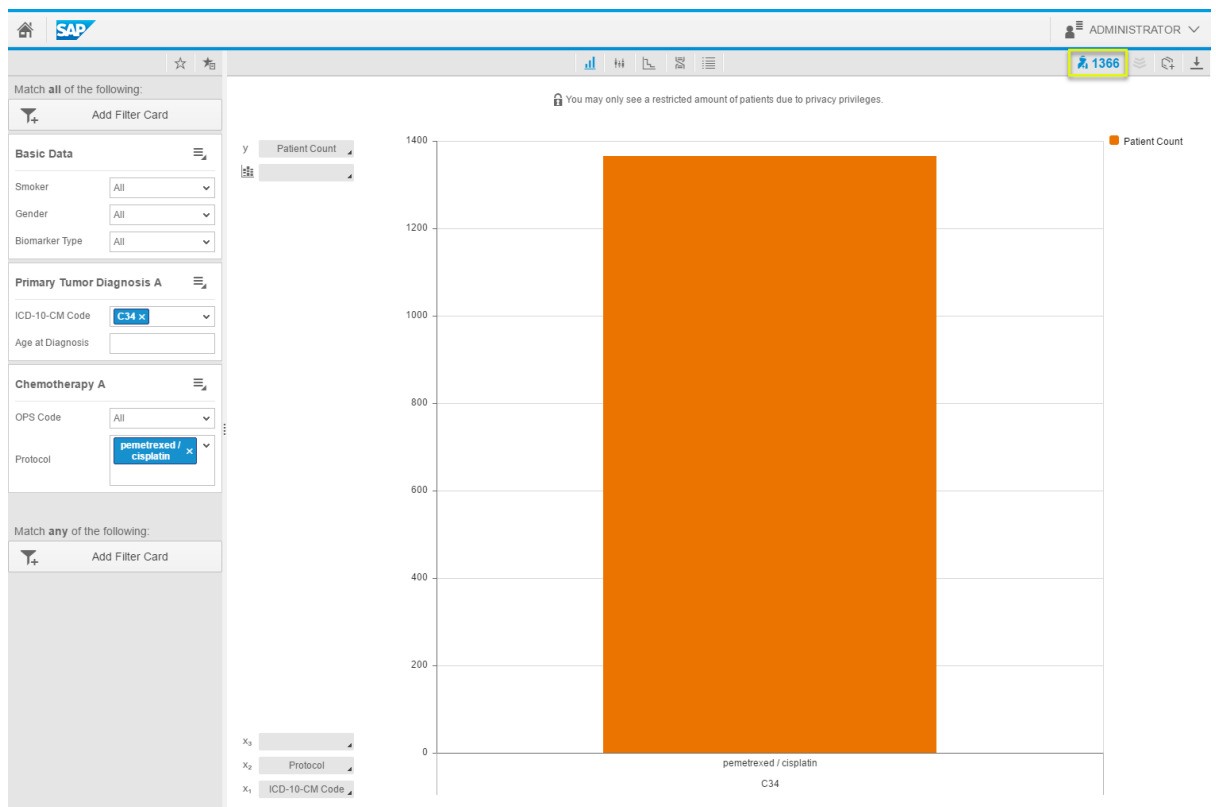


The chart now shows the number of patients per chemotherapy regimen / drug combination. Note that by adding the X_2 level on the X-axis automatically a new filter card, *Chemotherapy A*, is displayed on the left-hand side of the screen.



5. Restrict the patients to only those who received the pemetrexed / cisplatin drug in the chemotherapy. To do so, click the corresponding column in the chart and click the  icon.

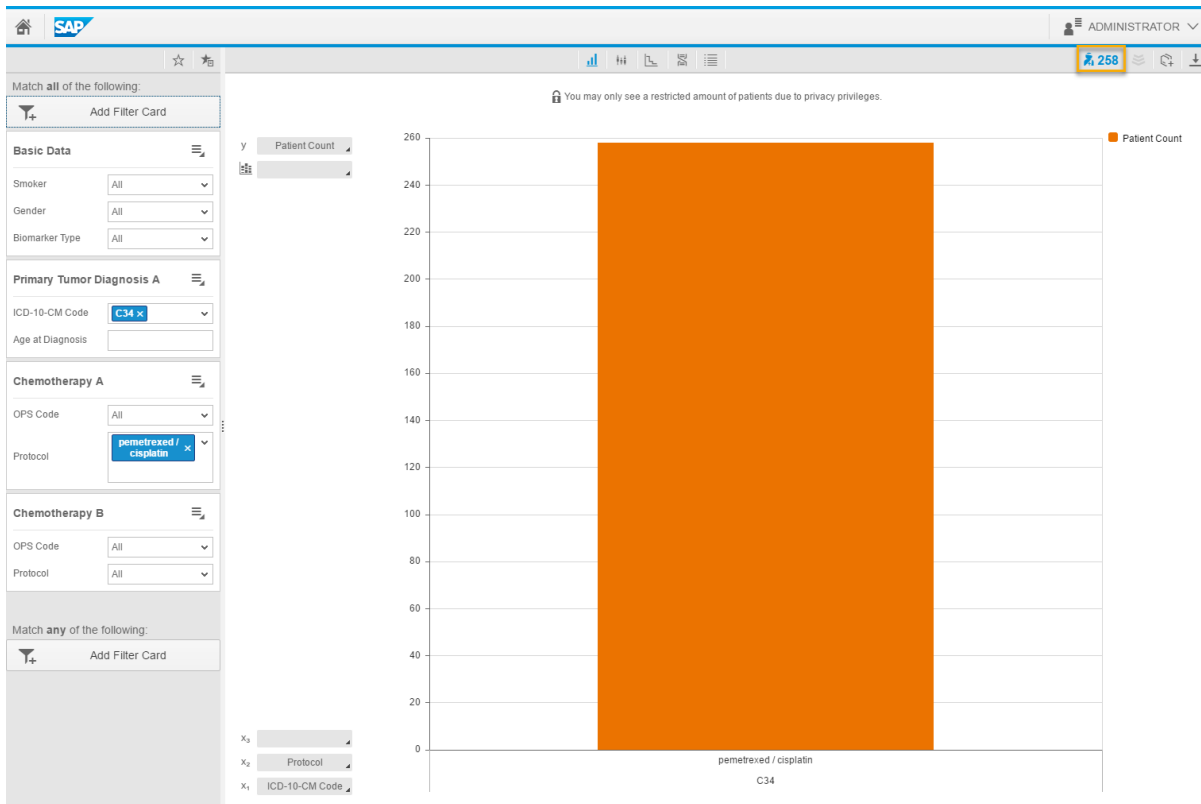
The graph displays a single bar chart that shows all lung cancer patients who received a chemotherapy with pemetrexed/cisplatin.



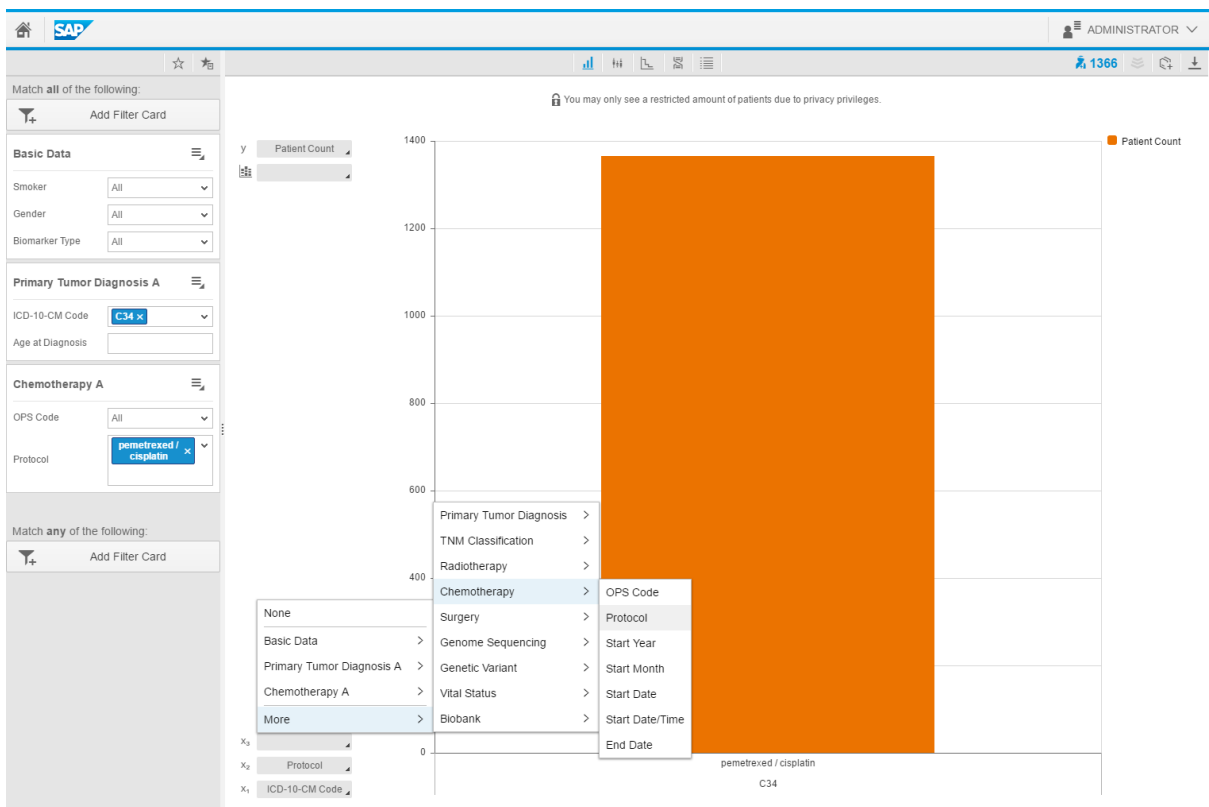
6. As you want to consider patients with various chemotherapies, add another chemotherapy filter card and require the subset to be again classified according to the new treatment. To do so, add a second chemotherapy filter card using the [Add Filter Card](#) button in the [Match all of the following](#) area at the upper left side of the screen and select [Chemotherapy](#).

The data model of the application enables you to add an arbitrary number of clinical events in a patient's history to further refine the patient cohort. The chart will adjust automatically to show patients with the different cases.

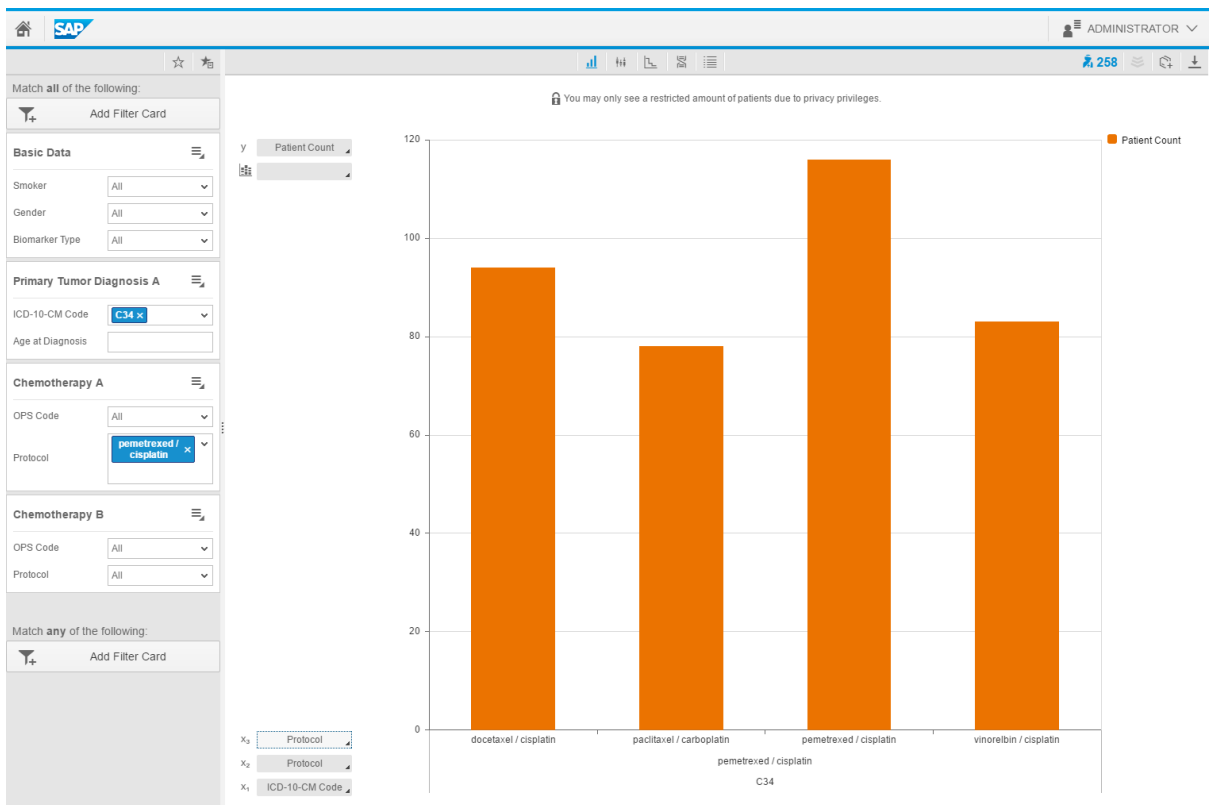
The new filter card is displayed and the number of patients reduces further.



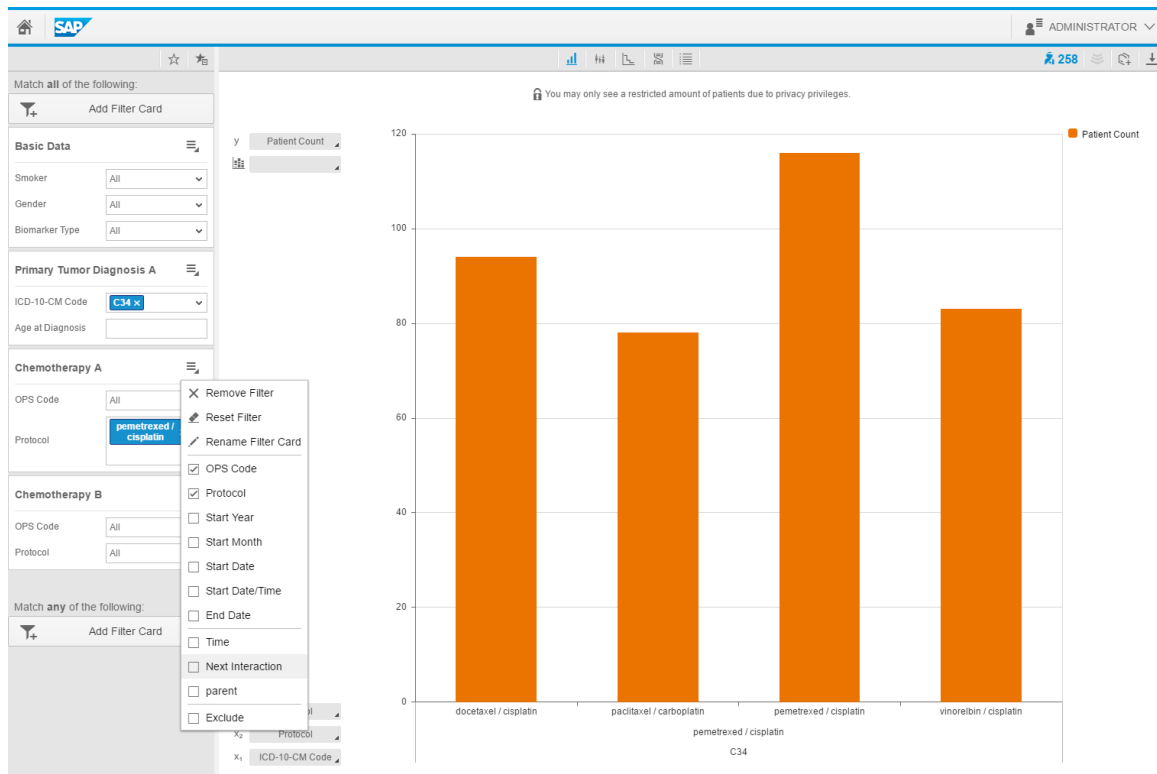
7. You want to consider only patients who had two treatments and you want to know which second therapies they received. To find out, add the protocol attribute of the *Chemotherapy B* to the chart by clicking the gray button labeled X₃ in the lower left.



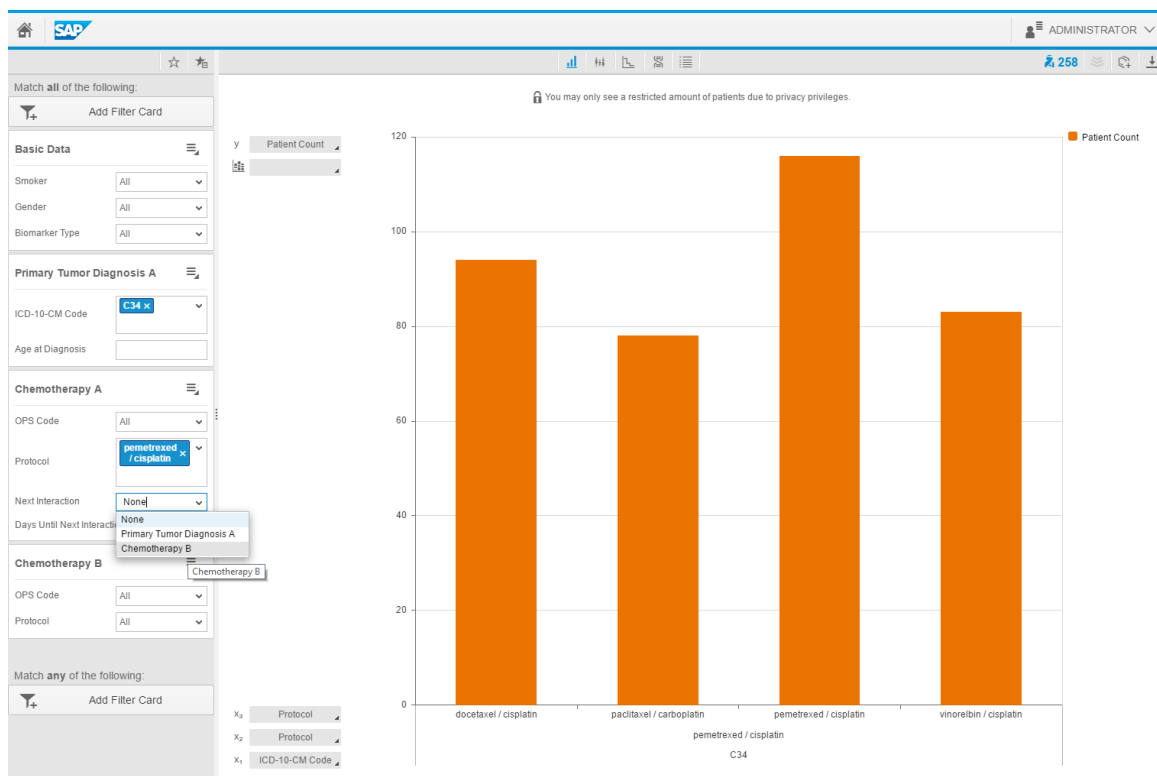
Four bars showing four different second chemotherapies appear on the screen.



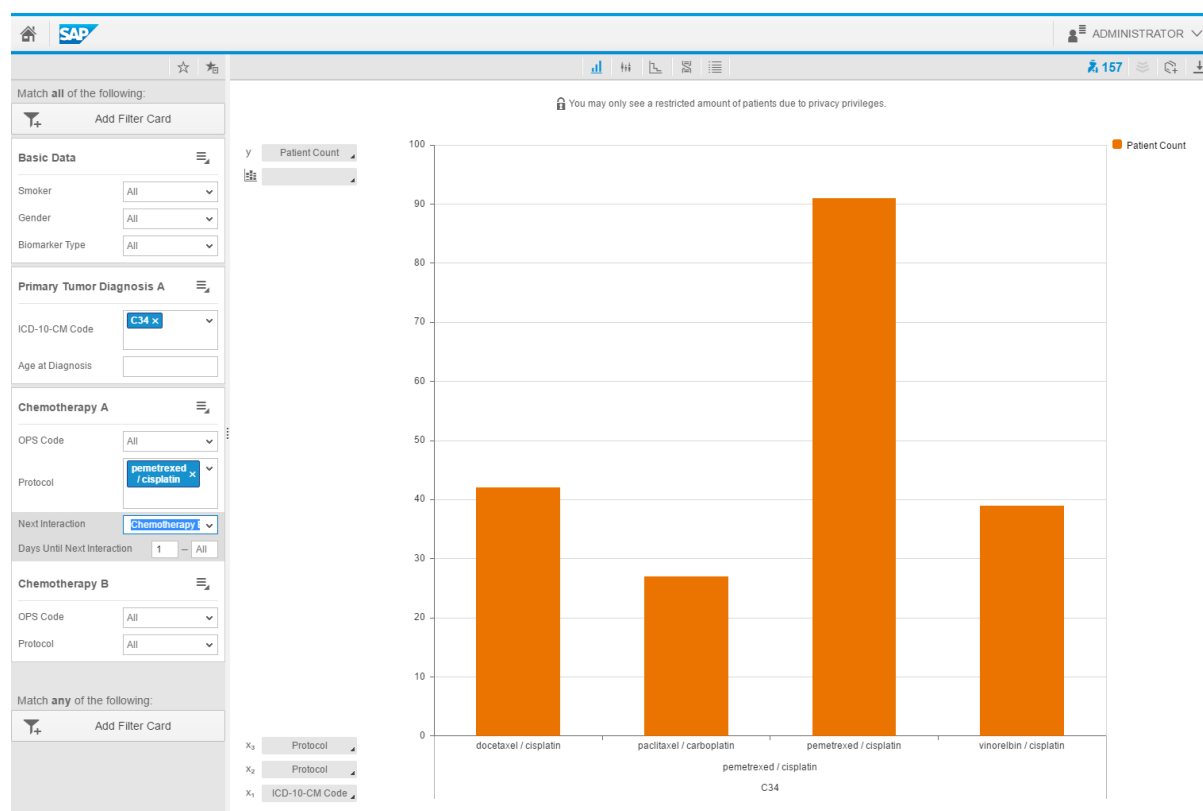
8. Add a time constraint to show only patients who had an additional chemotherapy after their pemetrexed / cisplatin therapy.
 - a. Open the menu of the filter card *Chemotherapy A* and choose *Time* and *Next Interaction*.




- b. Set the *Next Interaction* filter option to *Chemotherapy B*.

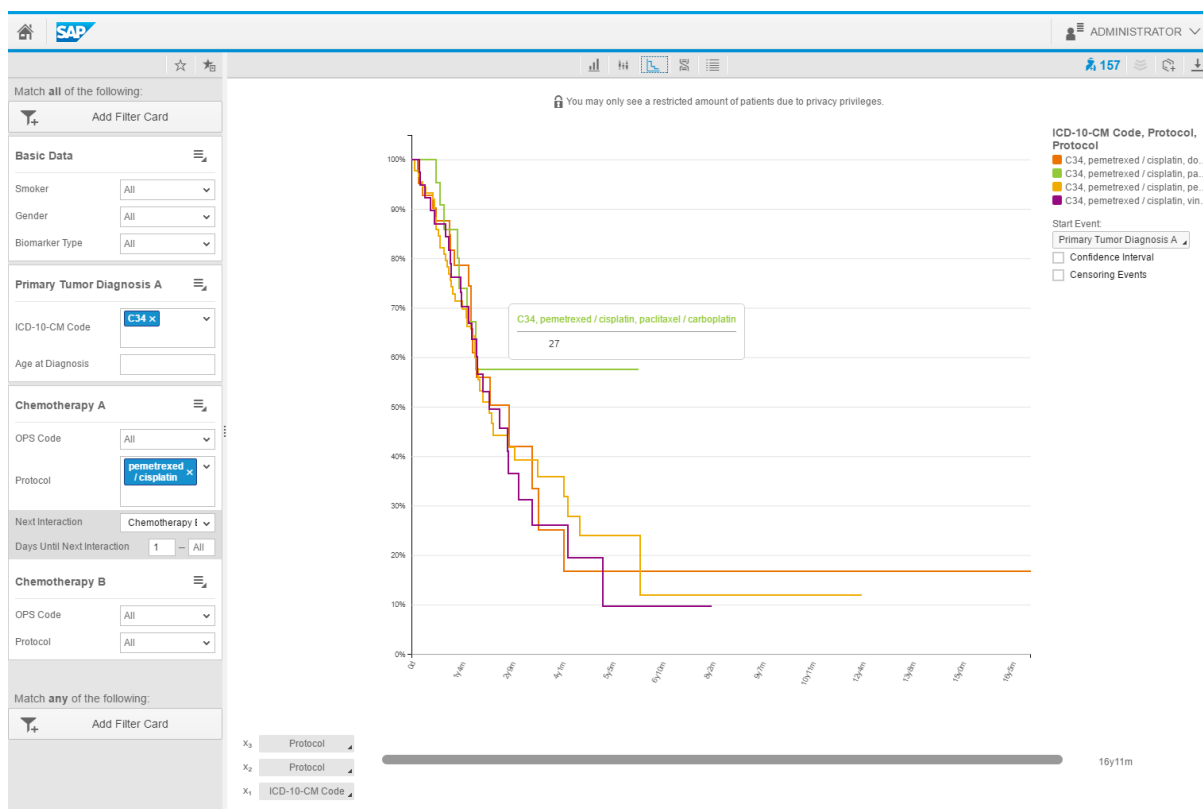


Note that the patient numbers become smaller as the chart now only displays patients that had an additional chemotherapy after their initial pemetrexed / cisplatin therapy.



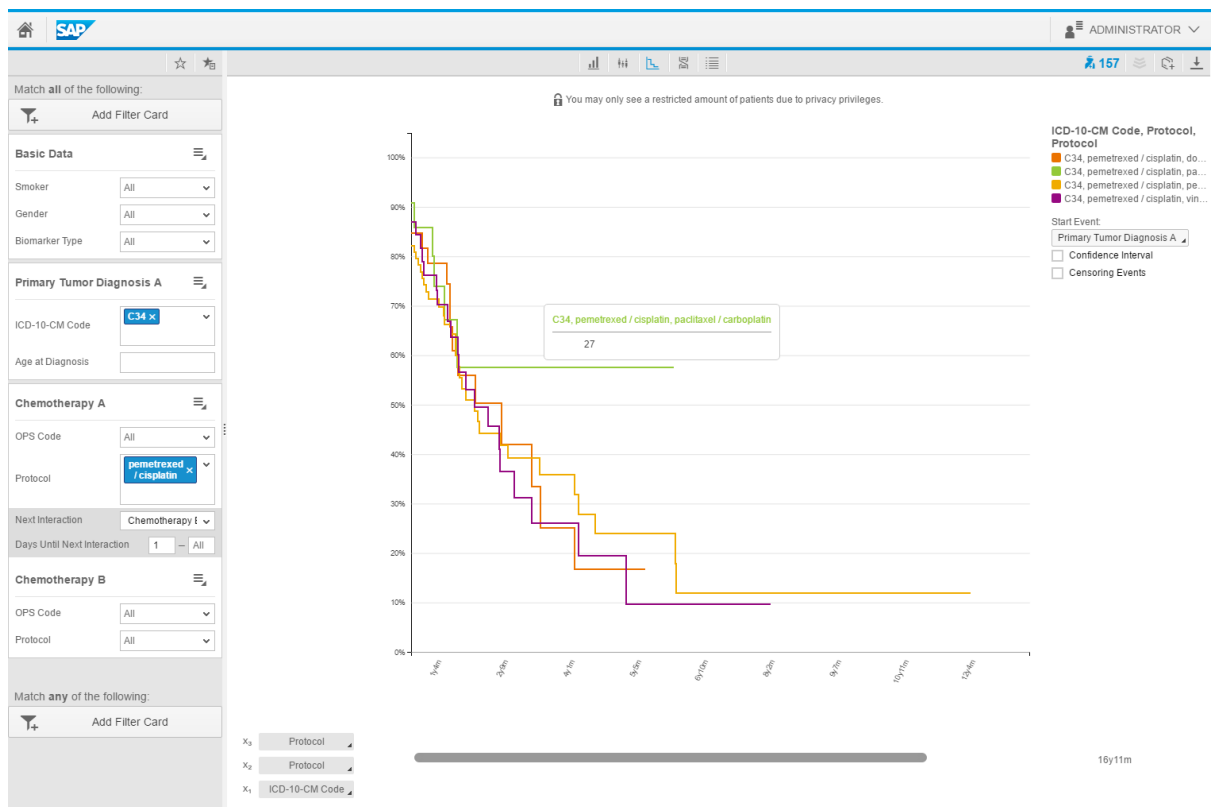
- As you want to prove your hypothesis using the statistical life expectations of this patient cohort, have a look at the Kaplan-Meier chart. To do so, switch to the Kaplan-Meier visualization by clicking  icon.



The Kaplan-Meier chart shows how long the patients with the combination of chemotherapies lived after the primary tumor diagnosis was made.



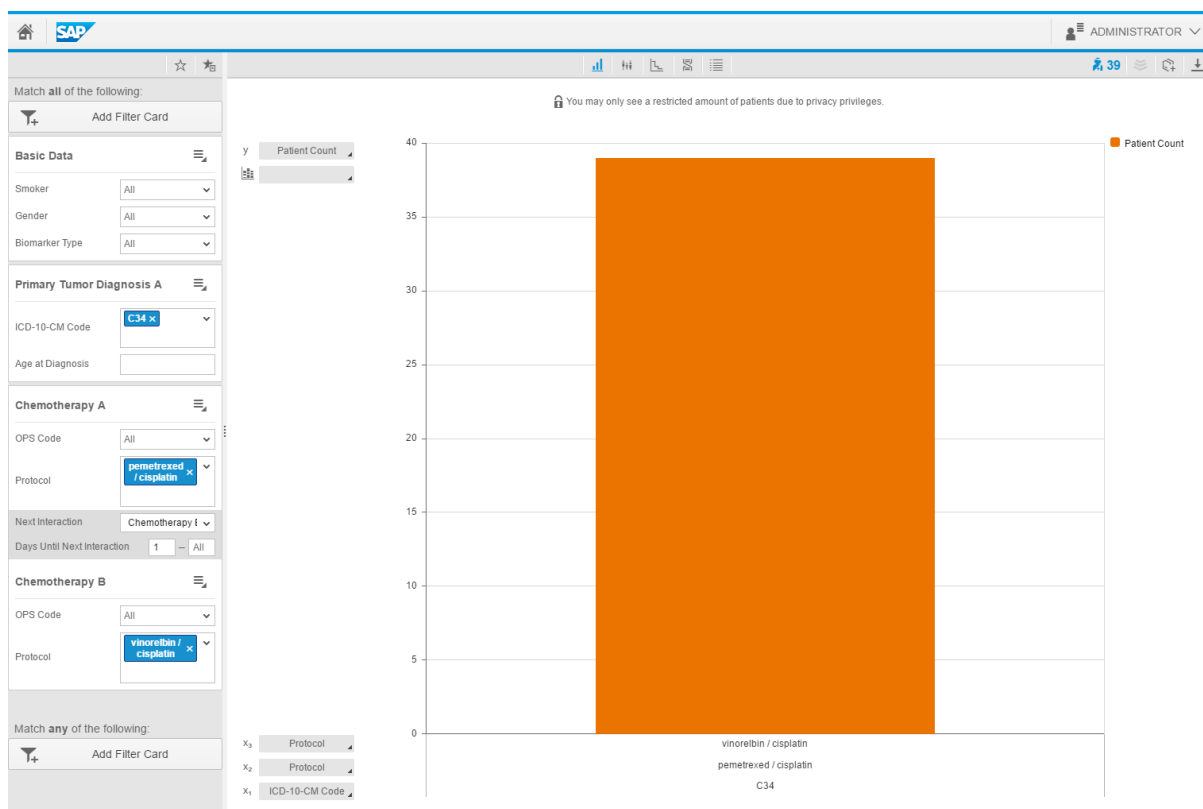
10. If this overview may not be detailed enough, click anywhere on the Kaplan-Meier chart and click again to zoom or use the mouse-wheel to zoom in and out.

Now it looks like the patients who received pemetrexed/cisplatin as first chemotherapy and vinorelbine/ cisplatin as second chemotherapy (purple line) have a lower survival rate.



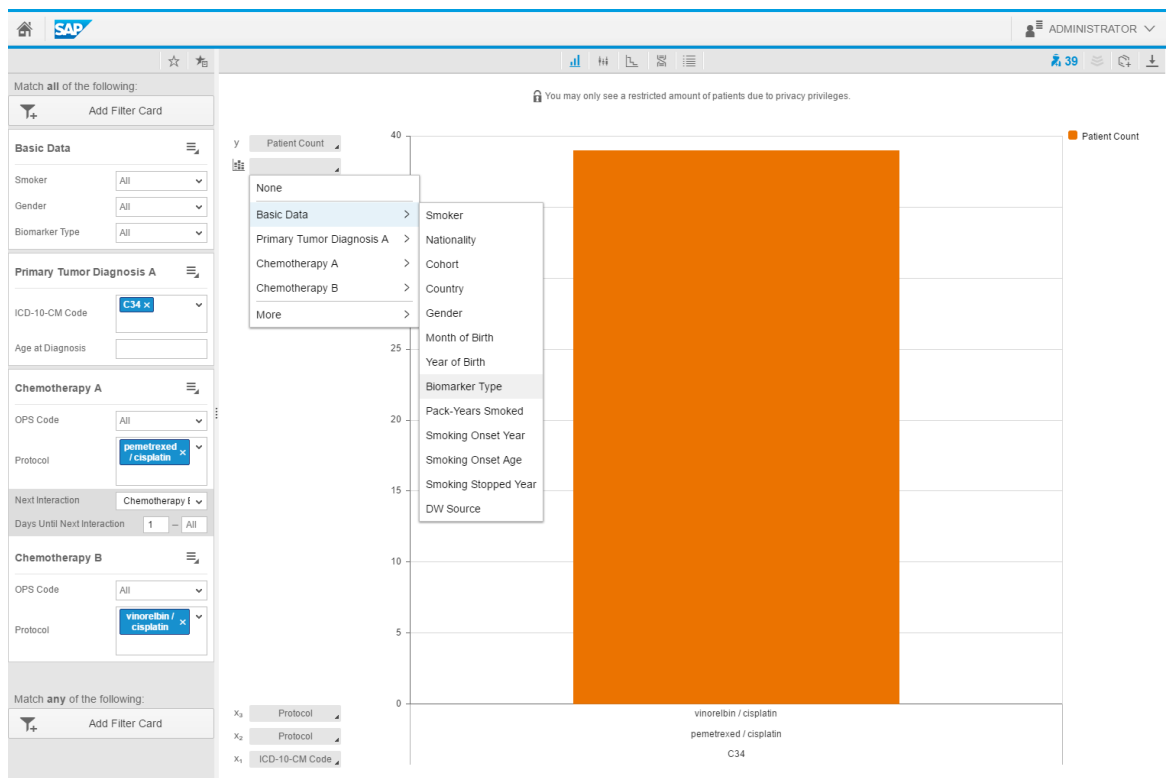
11. As patients who received this combination of chemotherapies have a lower survival rate, let's investigate further.
 - a. Click the  and return to the bar chart screen.
 - b. Select the patients in last bar chart on the screen who had vinorelbine/cisplatin as second chemotherapy and click the  icon.

Now you can see that only 39 patients had vinorelbine/cisplatin as second chemotherapy.

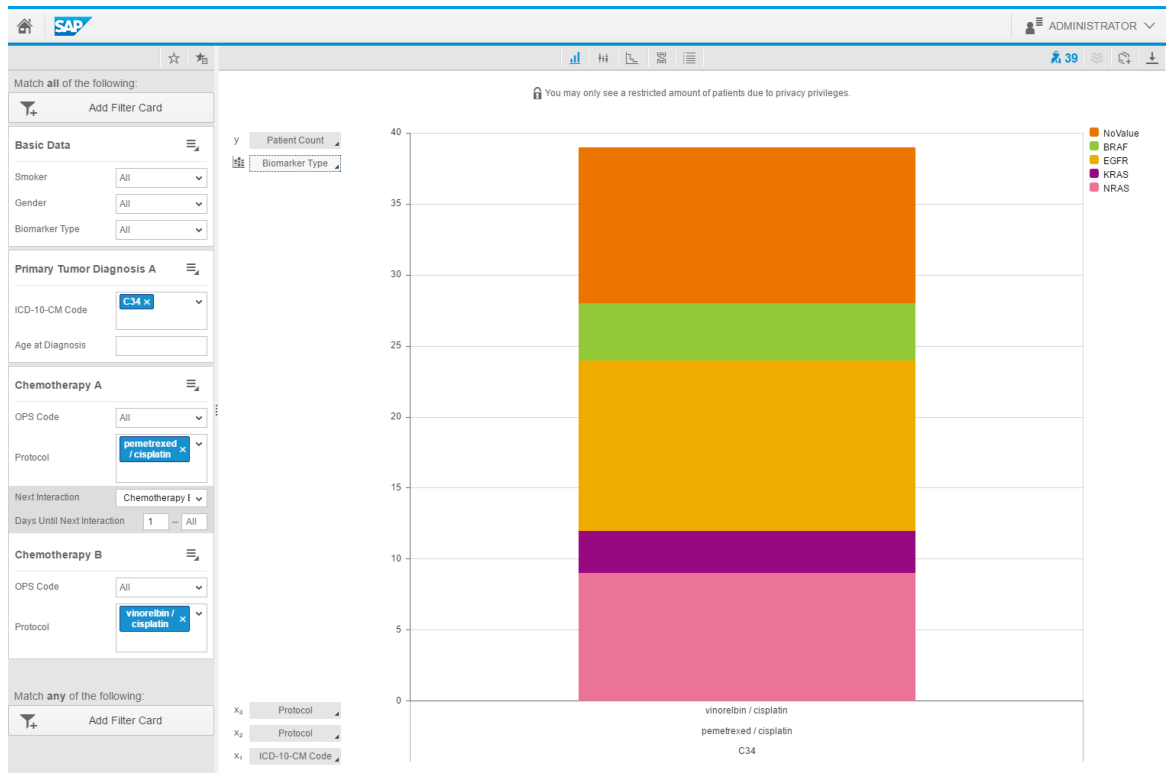



12. As mutations that lead to over expression of EGFR are associated with lung cancer, try to find biomarkers present in those specific group of patients. In addition, find out how many patients in your cohort are suffering from lung cancer even though they are non-smokers.

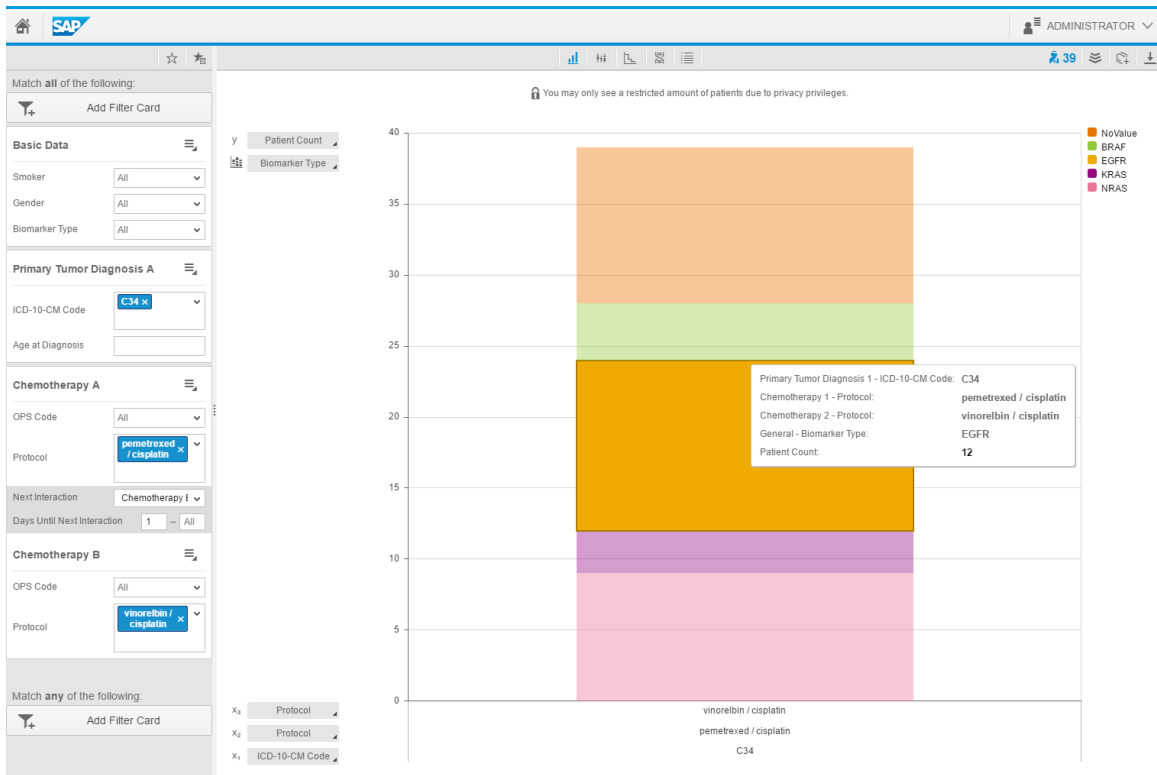
- a. For the stacked bar chart value, select **Basic Data** **Biomarker Type**.



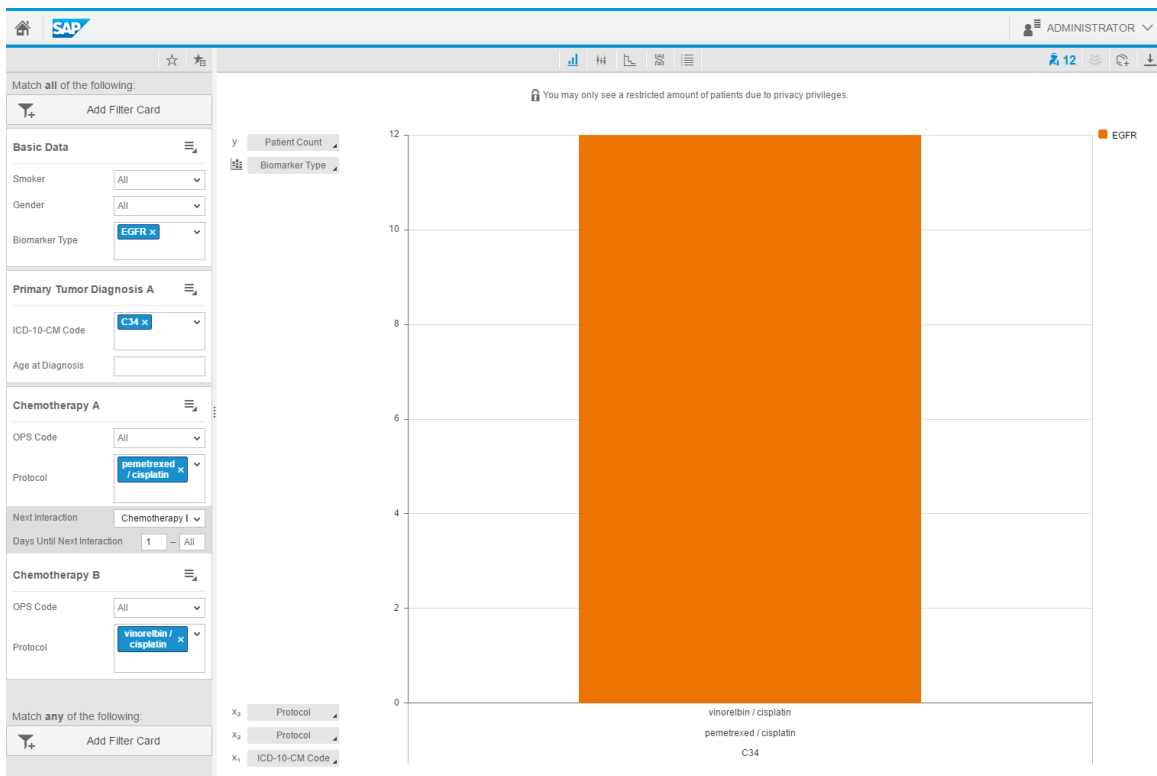
The biomarkers are displayed on a stacked bar chart.



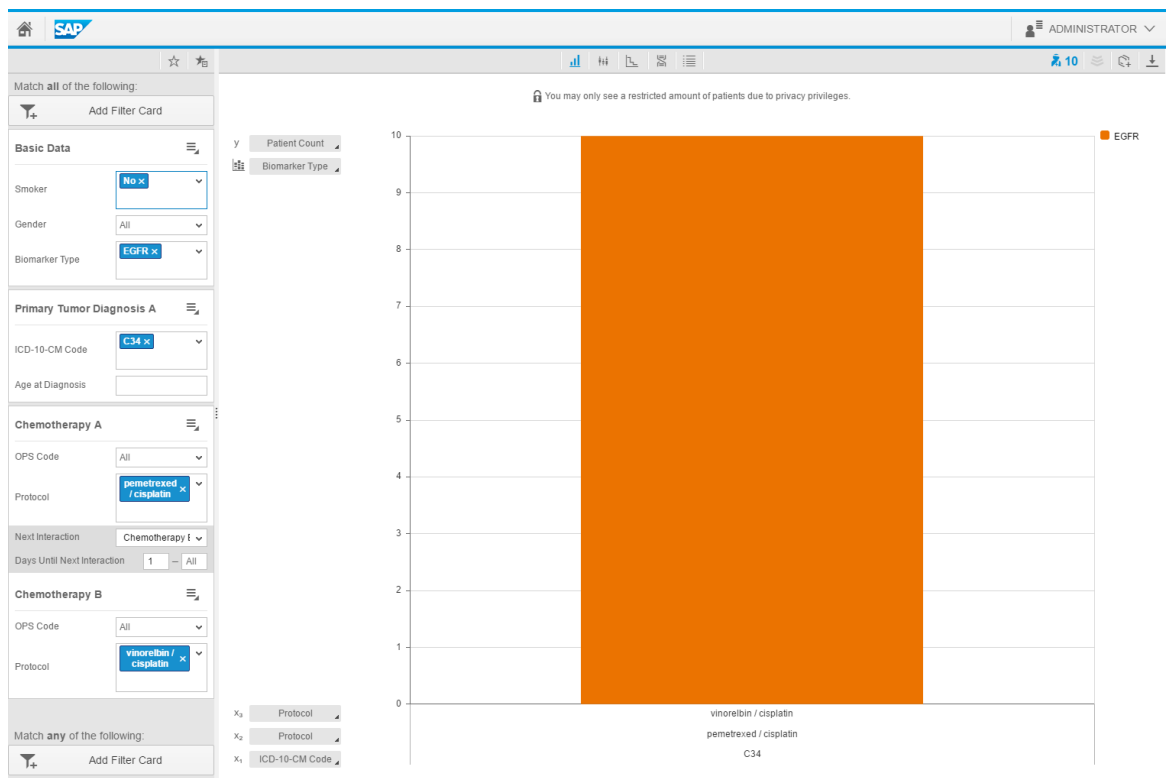
- b. Select the EGFR bar and click the  icon to drill down further.




The single bar chart shows 12 patients with the EGFR biomarker.



- c. Limit the cohort to non-smokers. To do so, in the *Basic Data* filter card, in the *Smoker* field, choose No. A total of 10 patients are non-smokers.



- d. Create a patient list by clicking the  icon. Due to privacy privileges, not all patients are visible in detail.

You may only see a restricted amount of patients due to privacy privileges.

Last Name	First Name	Date of Birth	Gender	Age at Diagnosis	ICD-10-CM Code
Burke	LORRIE	Feb 25, 1951	W	63	C34
Fields	KEVEN	Oct 20, 1952	M	61	C34
Herrera	KRYSTLE	Feb 17, 1939	W	73	C34
Holt	NESTOR	Aug 8, 1953	M	58	C34
Hopkins	JEREMIAH	Apr 20, 1963	M	51	C34
Mertens	SAMMIE	Mar 4, 1972	M	42	C34
Murphy	RICKY	Nov 6, 1939	M	75	C34
Perez	LEIGH	Aug 24, 1951	M	62	C34
Peterson	RUDOLF	May 15, 1936	M	79	C34
Ramos	BO	Oct 20, 1963	M	50	C34

Filters:

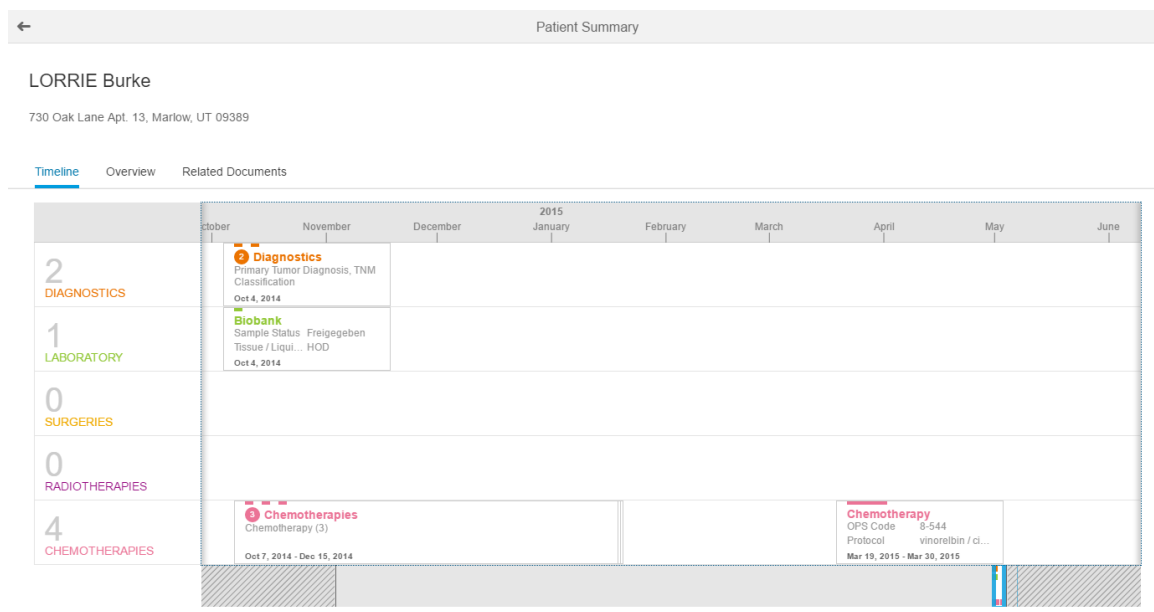
- Basic Data: Smoker (No), Gender (All), Biomarker Type (EGFR)
- Primary Tumor Diagnosis A: ICD-10-CM Code (C34)
- Chemotherapy A: OPS Code (All), Protocol (pemetrexed / cisplatin)
- Chemotherapy B: OPS Code (All), Protocol (vinorelbine / cisplatin)

13. Based on your patient analysis, create a cohort from your results and look into the details of a given patient.

- Choose [Add to Cohort](#) button and either add the patients to an existing cohort or create a new cohort. For this example, create a new cohort and give it a unique name.

You have a choice between adding just the patients you have permission to view or all the patients including those you can't see.

- From the SAP Fiori launchpad, open the [Cohorts](#) application and select your patient cohort.
- View the details for the patient Lorrie Burke by clicking her name.
- Use the navigation lane below the main timeline area to enlarge or move across the timeline and show the interactions you want to see.



3.2 Analyzing Genomic Data

Follow this step-by-step guide to get an introduction to how you can use SAP Connected Health to analyze genomic data.

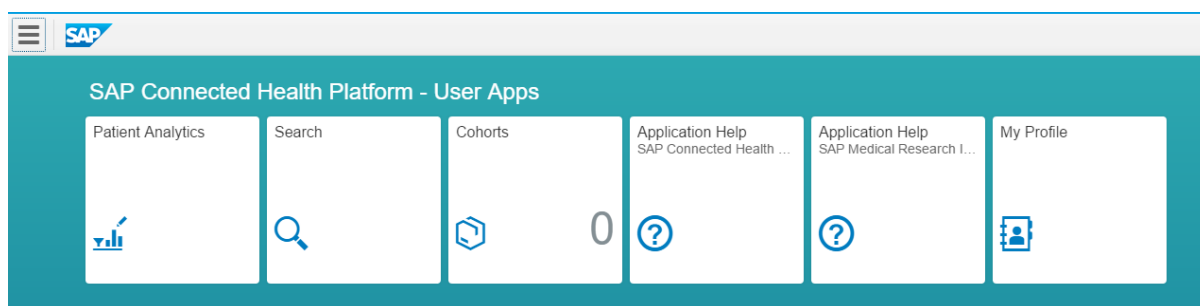
Context

Histological tumor classification does not provide exact information with respect to prognosis and recommended treatments for cancer. Understanding the molecular root cause of the disease opens ways to provide more exact treatment recommendations, build patient cohorts, and develop new drugs with higher efficacy.

Imagine you work for the Cancer Genome Atlas Research Network, which is exploring multiple cancer types to identify molecular biomarkers. It has been shown that genetic variations correlate with treatment outcome, prognosis, or toxicity of drugs. A recent publication demonstrated that mutations, for example on the gene TP53, show strong correlation of recurrence and disease prognosis. Here we want to investigate how this finding could be potentially reproduced and used in our particular patient cohort.

Procedure

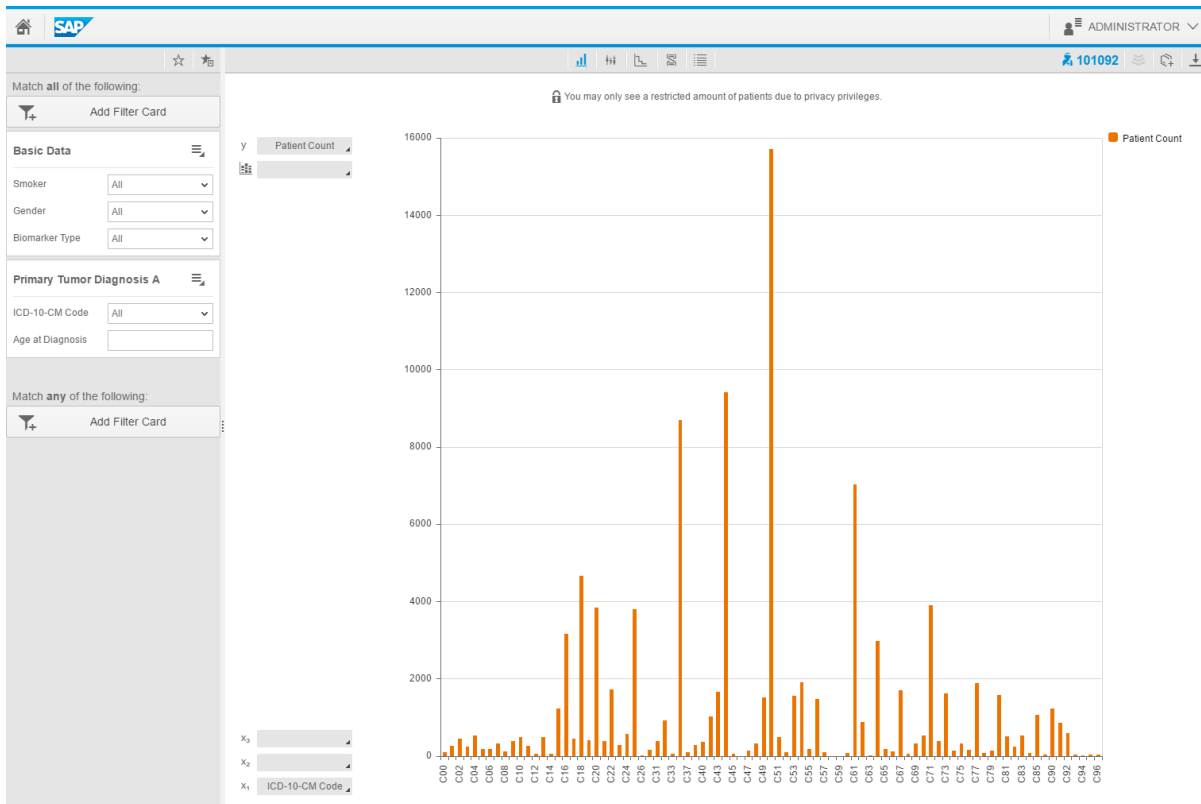
1. Open the SAP Fiori launchpad.



2. Start the analysis by clicking *Patient Analytics*.

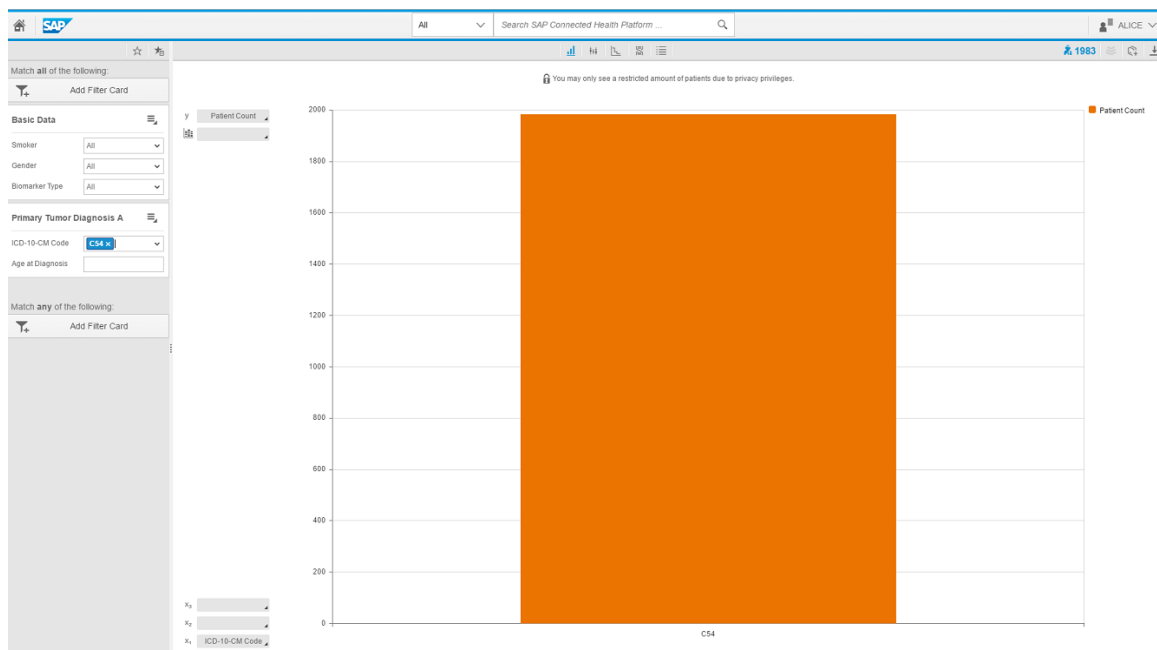
On the left hand side, filter cards for basic patient data and the primary tumor diagnosis are displayed. This is the mechanism used to build the cohort, or set of criteria to filter out unrelated patients.

When the application is loaded, a chart is displayed that shows the number of patients per diagnosis (ICD Code). The number at the top right corresponds to the amount of patients that are being aggregated for the current view.

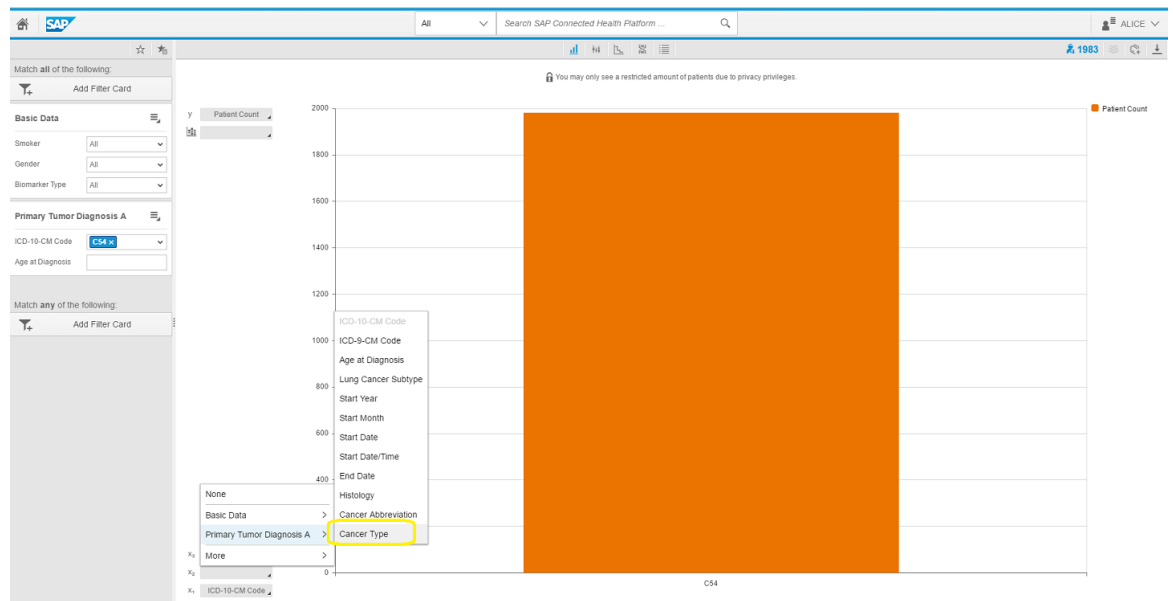



3. Search for patients diagnosed with malignant neoplasm of corpus uteri (ICD-10-CM Code: C54) and the cancer type *Uterine Corpus Endometrial Carcinoma*.
 - a. In the *Primary Tumor Diagnosis A* filter card, enter descriptive terms, such as **corpus uteri**.
 - b. Select the entry C54.

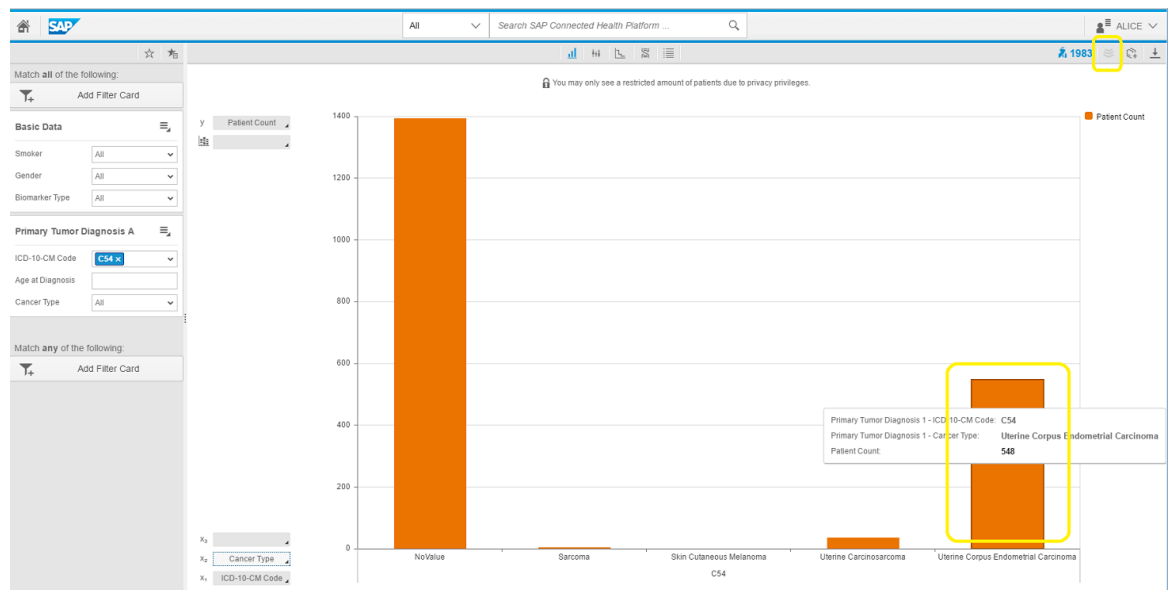
The chart now only shows a column for patients with the cancer type C54.



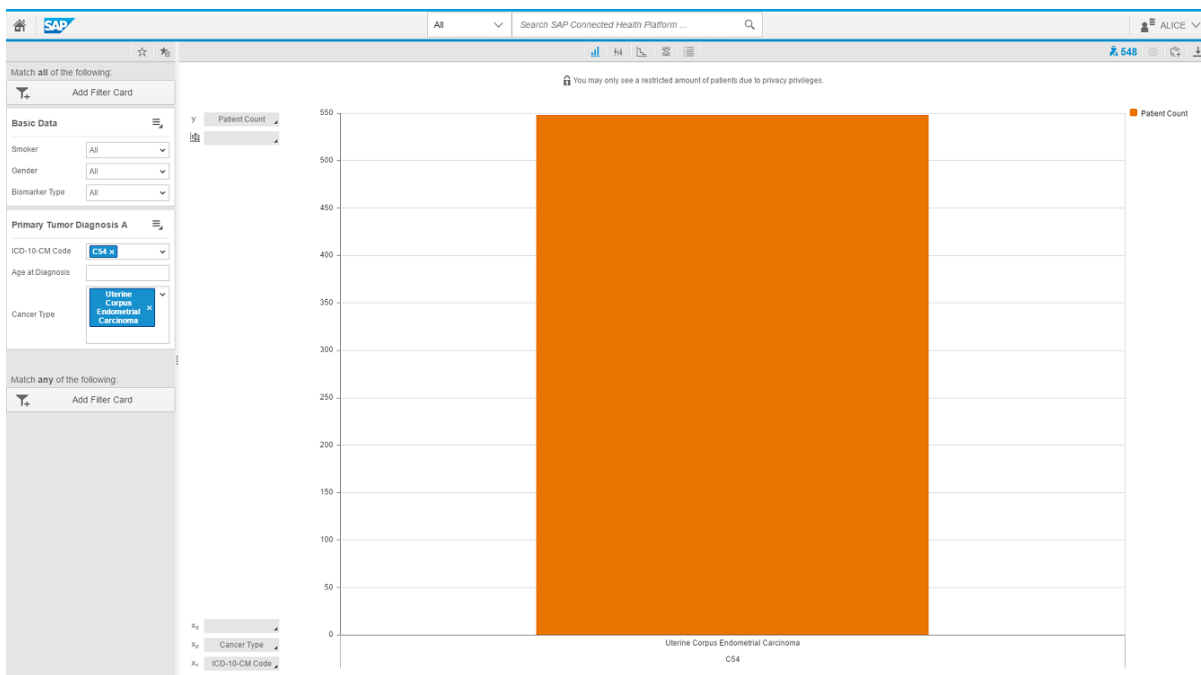
- c. On the gray button labeled X_2 in the lower left corner, choose ► *Primary Tumor Diagnosis A* ► *Cancer Type* ►.



- d. Select only patients with uterine corpus endometrial carcinoma by clicking the corresponding column and then choosing the  icon.

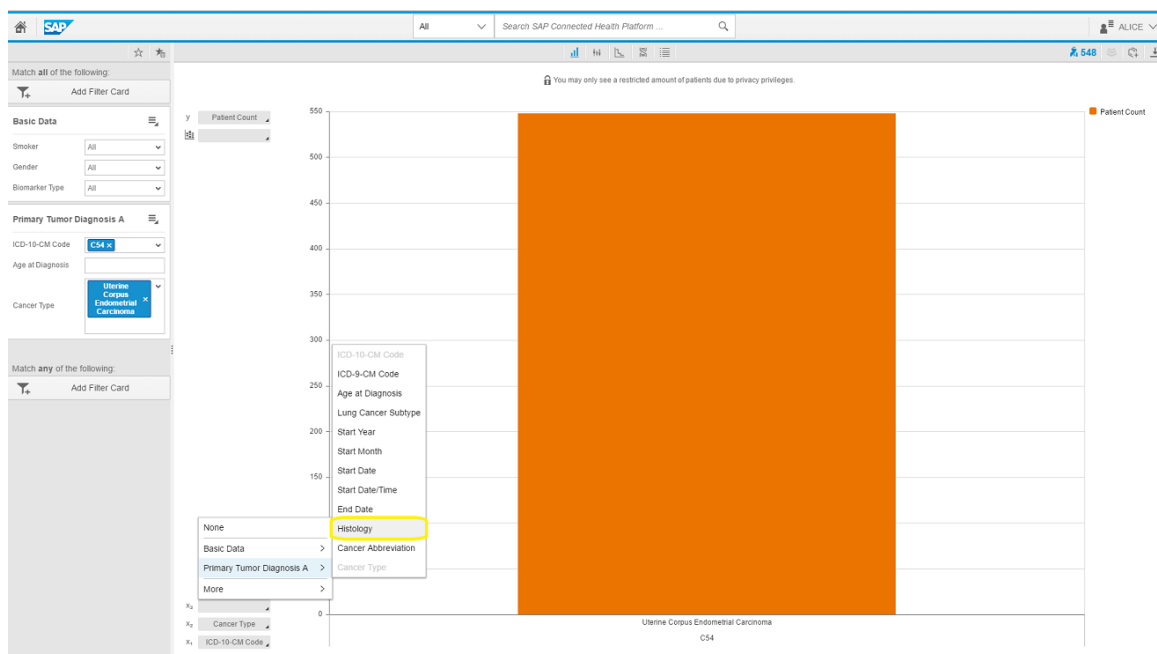


The bar chart now shows only one bar.

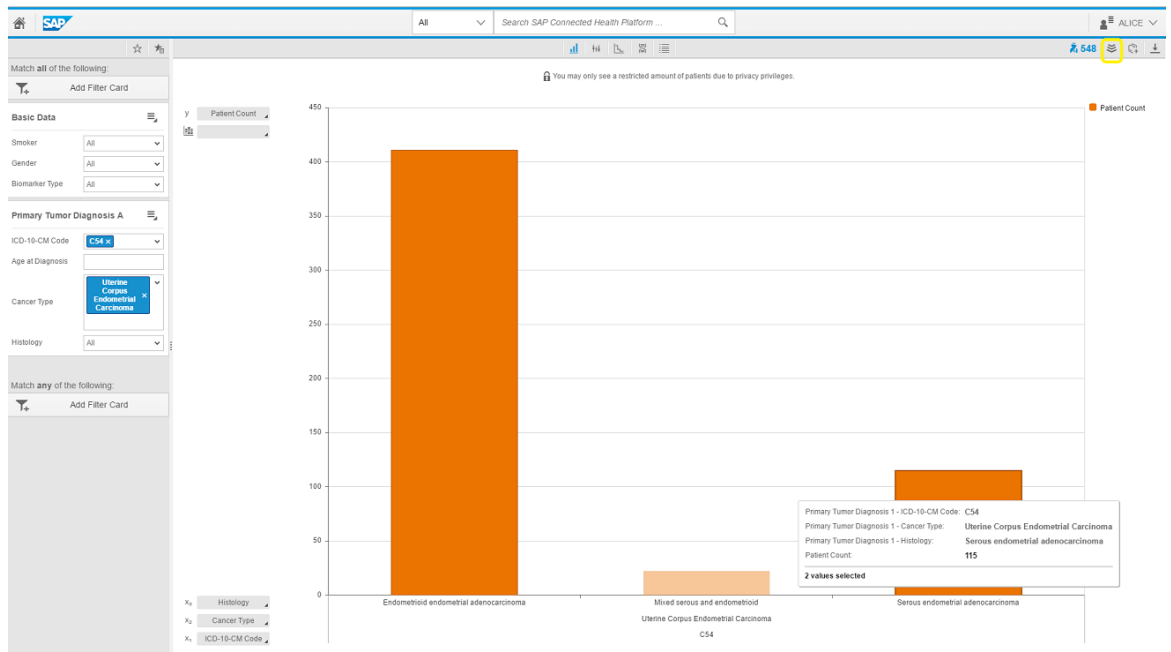


4. Break down the cohort by histology.

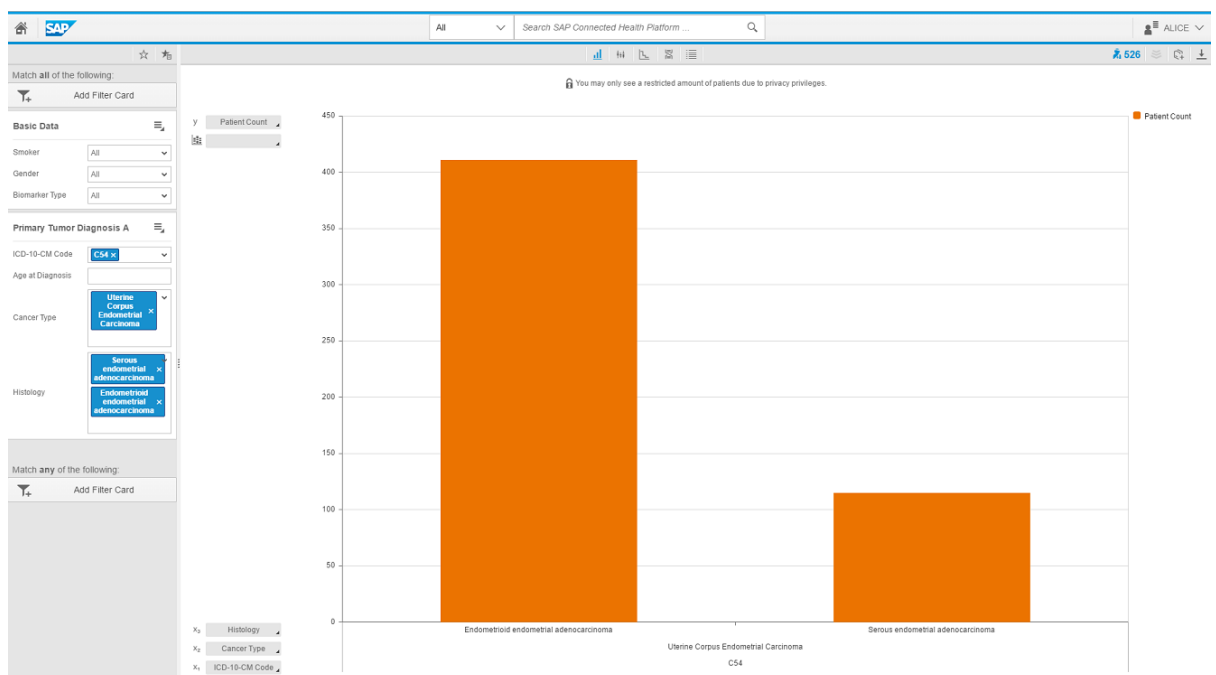
- On the gray button labeled X_3 in the lower left corner of the graphic, choose **Primary Tumor Diagnosis A** **Histology**.




- Remove any irrelevant data or border-line cases and filter according to endometrioid and serous histological findings. To do so, select **Endometrioid endometrial adenocarcinoma** and **Serous endometrial adenocarcinoma** and click the **≡** icon.

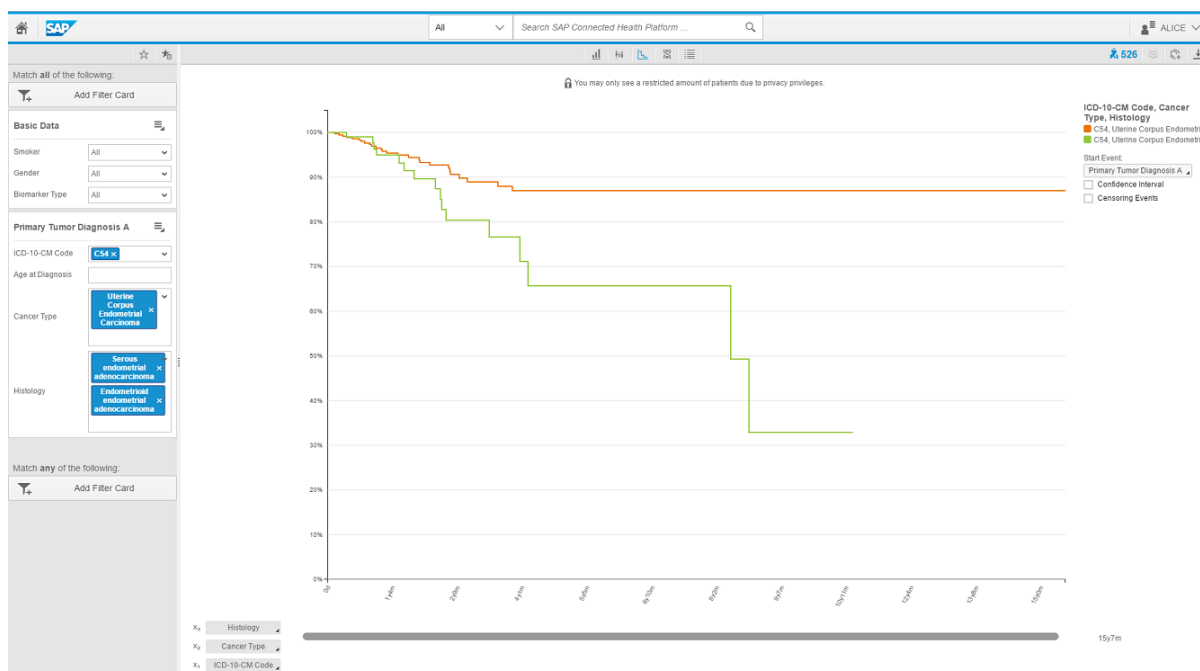


The result is shown in a graph with 2 bars.




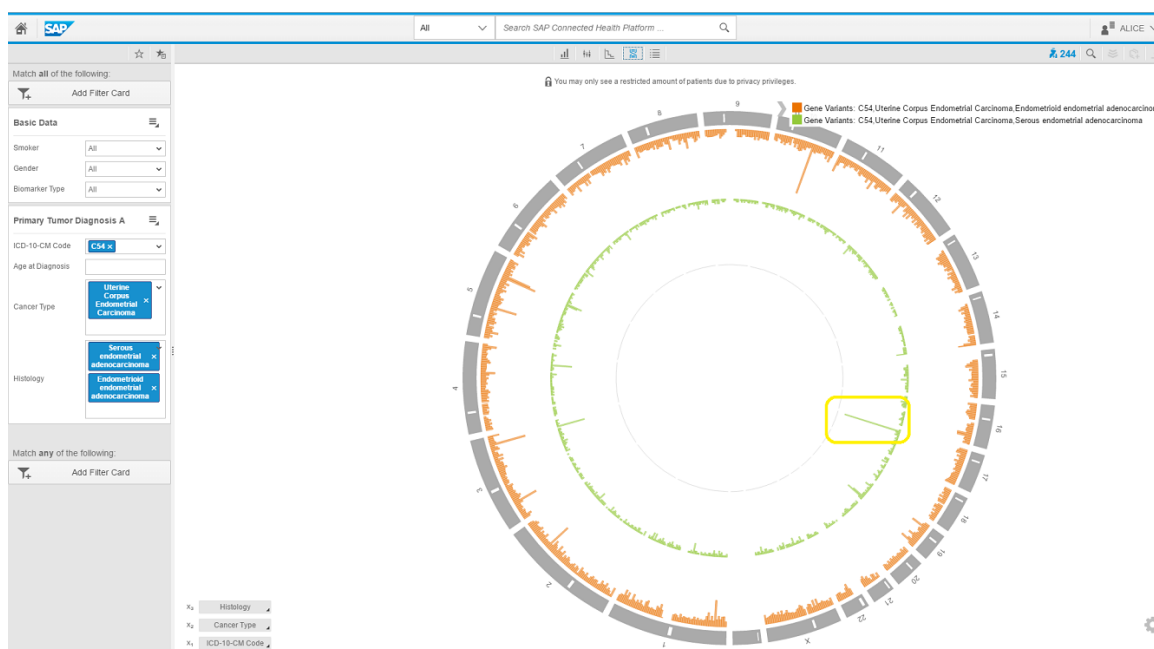
5. Check the survival rates to see if there is any correlation. To do so, switch to the Kaplan-Meier chart by clicking the  icon.

The Kaplan-Meier chart gives us an overview of how long the patients with the filtered histological findings lived after the primary tumor diagnosis was made. As we can see, there is a strong correlation of survival rate and histological classes. Patients with the endometrioid carcinoma have a noticeable higher life expectancy.



6. Check how the genetic variations (mutations) in the tissue biopsy correlate with the histological classes.

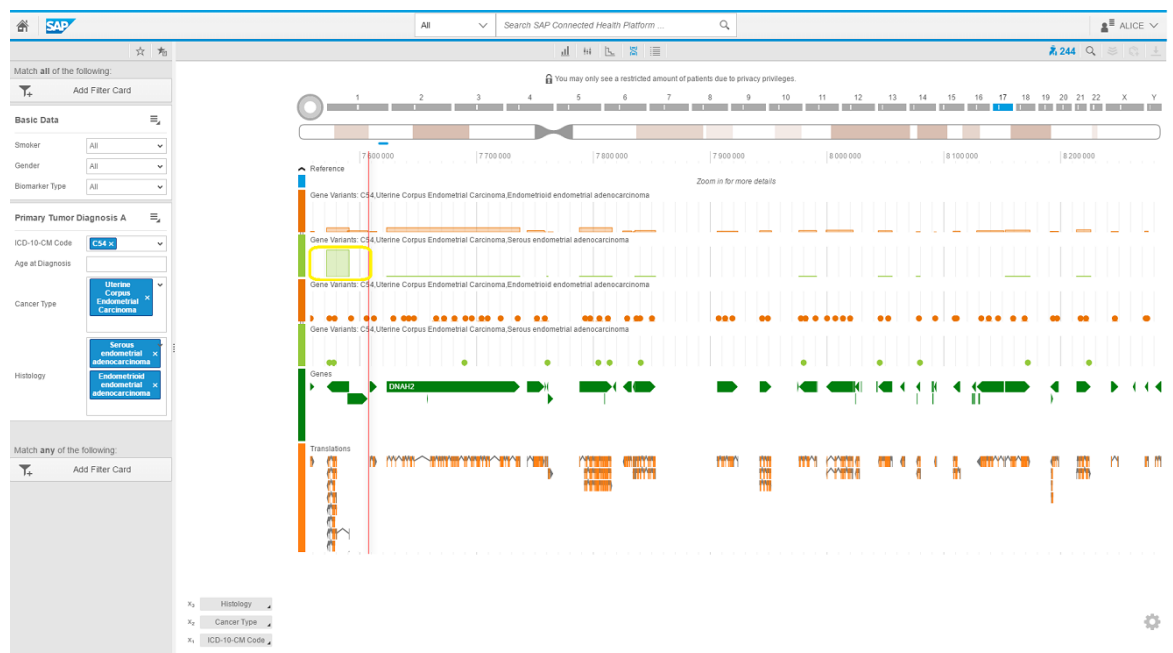
- Start the Variant Browser by clicking the  icon.
- Investigate the peak in chromosome 17 by clicking the peak to open the chromosome view.



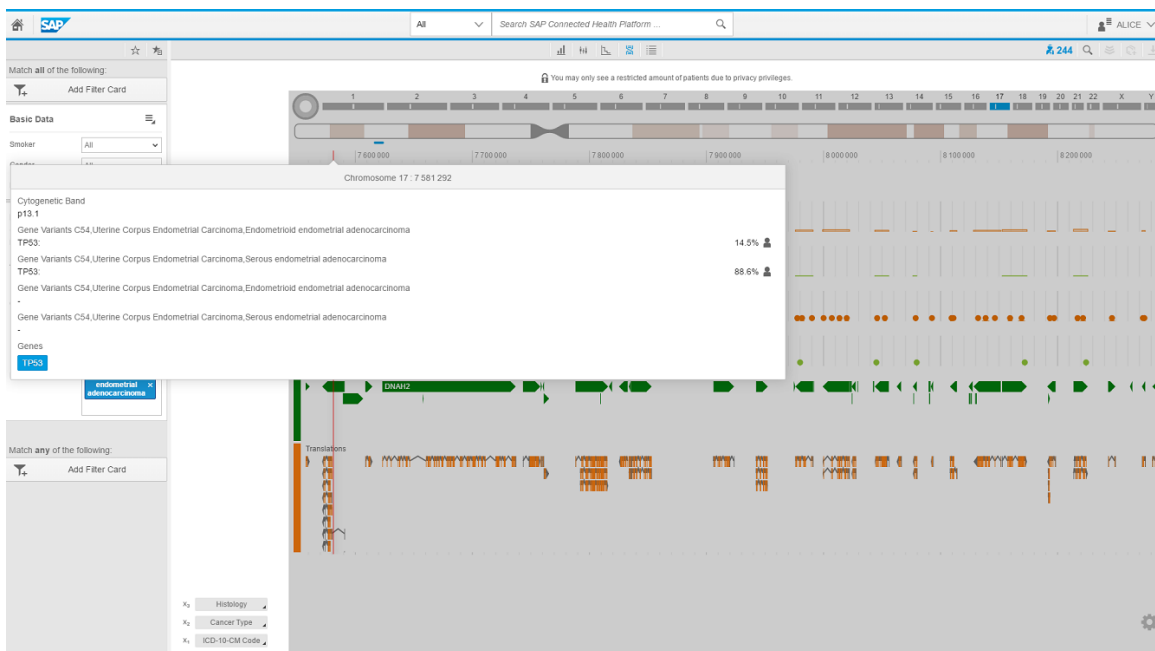
The detailed view of the genetic variations in chromosome 17 is now shown for both histological classes. You can zoom in and out by using the mouse wheel.



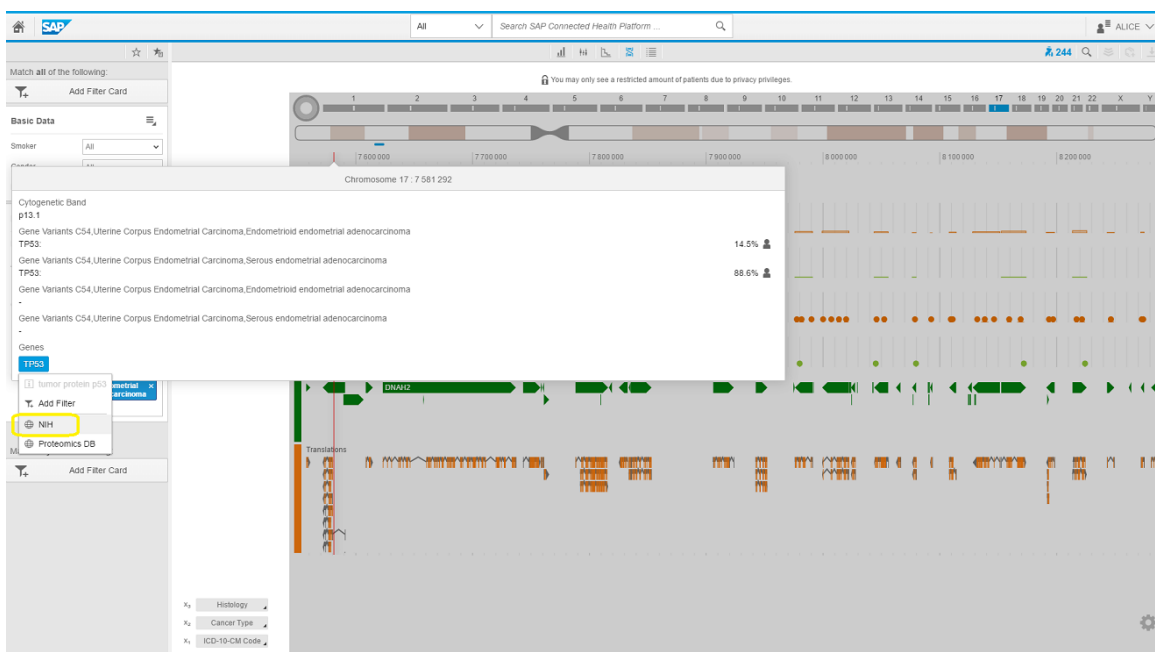
c. Find out which gene the mutation is located in. To do so, click the peak.



The gene is displayed, as well as the percentage share of mutations in the two histological classes.



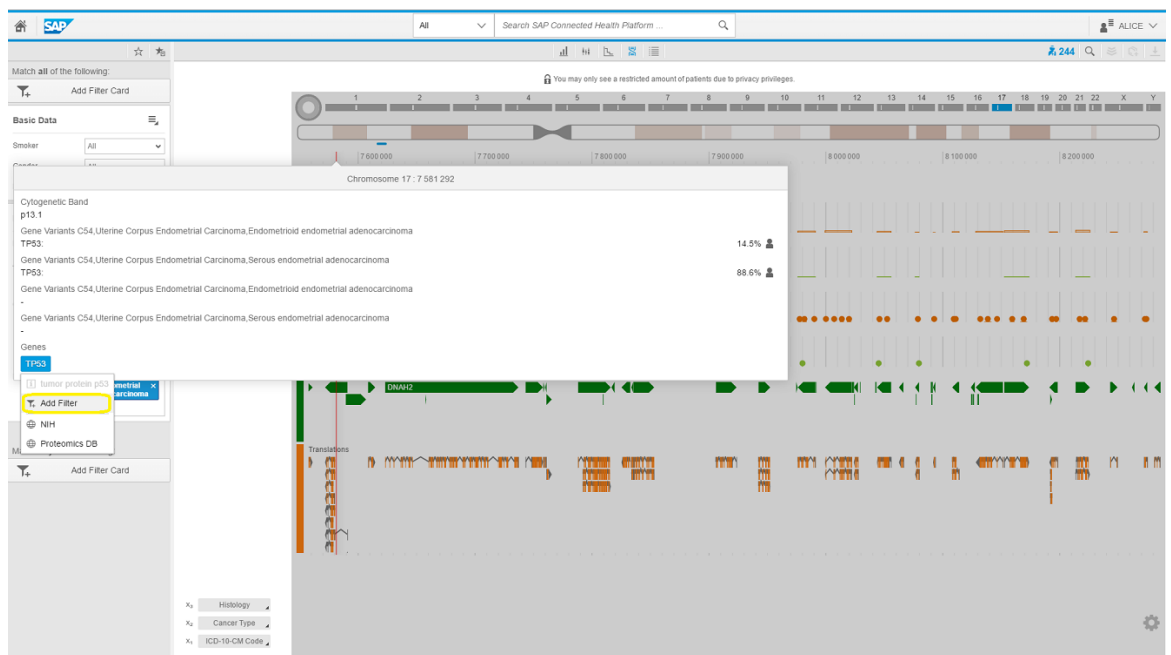
- d. From the gene, you can go directly to external sources, such as the National Center for Biotechnology Information (NCBI), for more general information.



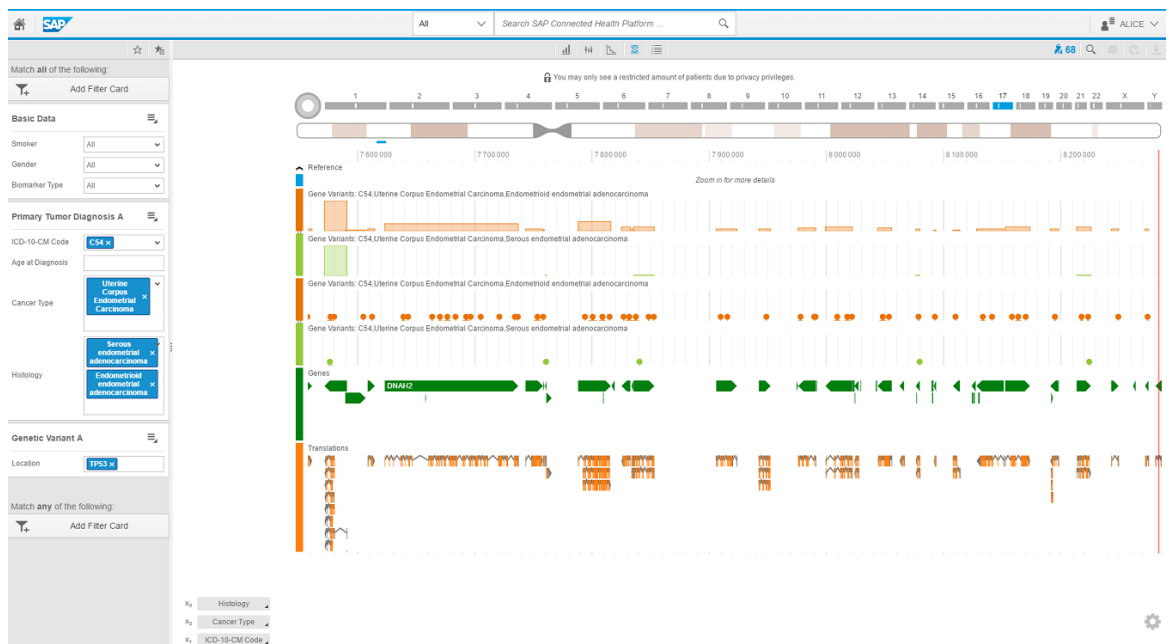
7. Check whether our patient cohort reflects the Cancer Genome Atlas Research Network publication results.

Since the original paper predicted that TP53 is one strong predictive marker (in combination of other markers such as copy number variations, methylation), we want to explore whether our patients with the TP53 variant would have a bad prognosis irrespective of the histology. We filter all patients in our patient cohort according to gene TP53 and analyze whether the mutations in the TP53 gene correlate to disease prognosis and life expectation.

- a. Filter the genetic variant location TP53 by clicking [Add Filter](#).



Now in both cohorts only patients with variations in gene TP53 are shown. The number of patients reduces significantly.



b. Switch to the Kaplan-Meier chart.

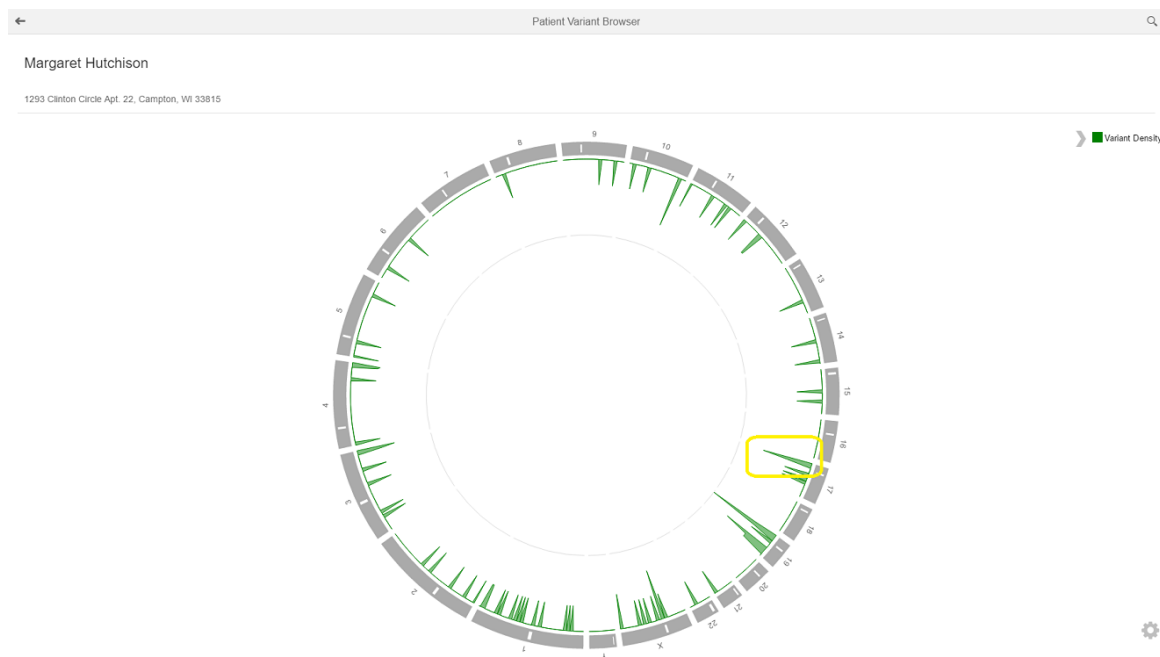
If TP53 alone were a sufficient marker, we would expect both histology groups to have a low survival rate in the Kaplan-Meier analysis. In our cohort, this is not the case. We conclude that for building cohorts, TP53 alone is not a sufficient biomarker.



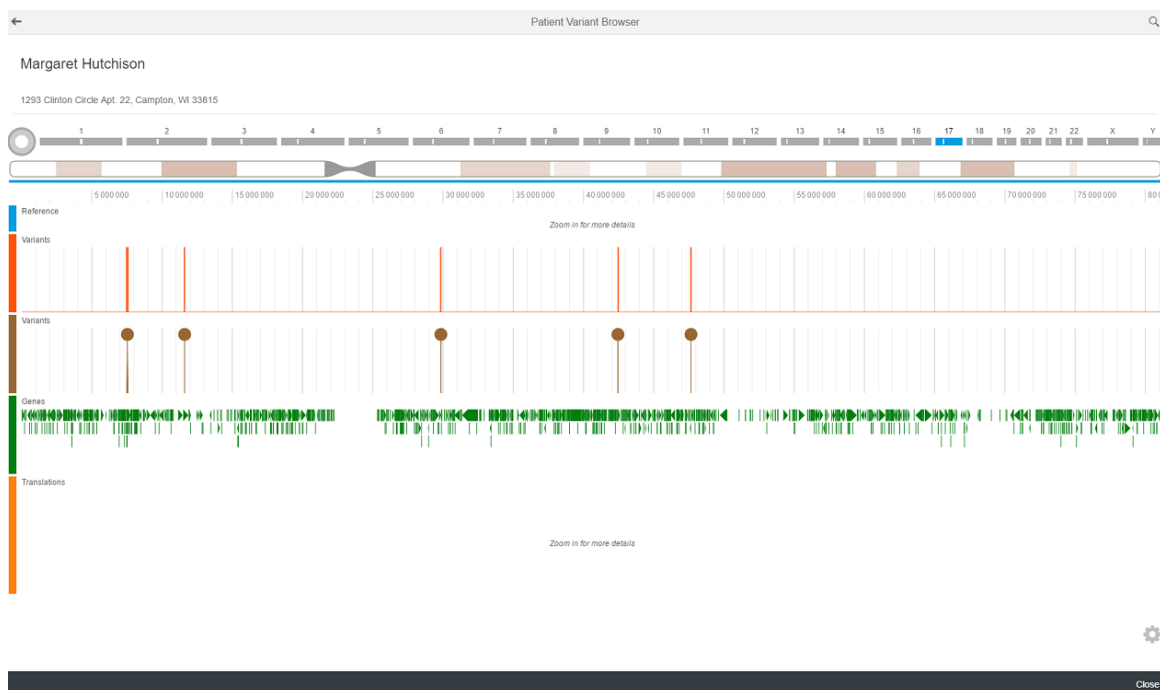
8. Look into the details of a specific patient in the cohort.
 - a. Open the patient list view by clicking the icon.
 - b. Select the patient Margaret Hutchinson.
 - c. Choose [Overview](#).
 - d. One of Margaret's interactions has a genomic sample associated with it. View this genomic information in the Variant Browser.

Patient Summary			
Margaret Hutchison			
1293 Clinton Circle Apt. 22, Campion, WI 53815			
Timeline Overview Related Documents			
<div> <div>✓ 1 Diagnostics</div> <div>✓ 1 Laboratory</div> <div>0 Surgeries</div> <div>✓ 1 Radiotherapies</div> <div>✓ 1 Chemotherapies</div> </div>			
Jun 29, 2010	Vital Status Diagnostics	Age at Last Contact: 78	
Feb 24, 2010 - Feb 25, 2010	Genome Sequencing Laboratory	Genome Reference: GRCh37 Sample Class: Primary Tumor Sample Id: 9000654	View in Variant Browser
Oct 26, 2008 - Feb 13, 2009	Chemotherapy Chemotherapies	OPS Code: 8-543 Protocol: paclitaxel / carboplatin Start Date/Time: Oct 26, 2008, 12:00:00 AM	
May 30, 2008 - Jun 27, 2008	Radiotherapy Radiotherapies	Radio Dosage (Gy): 18 Start Date/Time: May 30, 2008, 12:00:00 AM	
Mar 20, 2008	Primary Tumor Diagnosis Diagnostics	ICD-10-CM Code: C54 Age at Diagnosis: 76 Histology: Serous endometrial adenocarcinoma Diagnosis Free Text: Uterine Corpus Endometrial Carcinoma Start Date/Time: Mar 20, 2008, 12:00:00 AM	
Mar 20, 2008	TNM Classification Diagnostics	M-Component: No Value N-Component: No Value T-Component: No Value	

- e. Open the detailed view of genetic variations (mutations) for this patient by clicking the peak in the overview.



The genetic variants of the single patient are shown.



3.3 Analyzing Content Extracted from Documents

Follow this step-by-step guide to get an introduction to how you can use SAP Connected Health to analyze content extracted from documents.

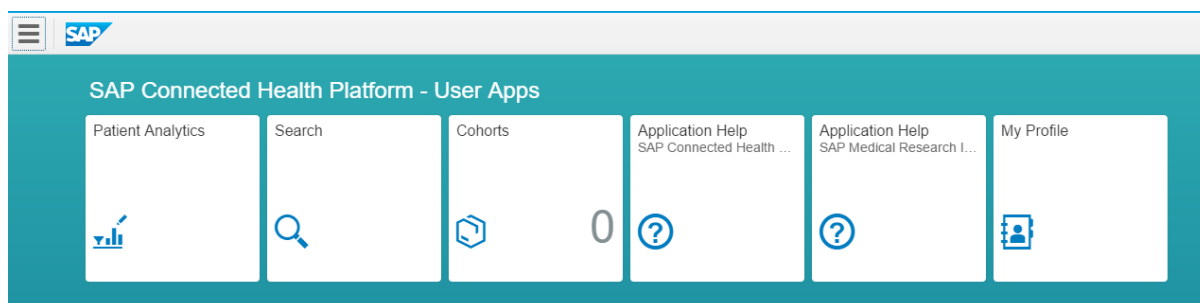
Context

Unstructured documents that are often stored externally as Microsoft Word or PDF files are integrated into SAP Connected Health as binary content. This content is stored in the clinical data warehouse and can be consumed directly by analytic applications such as *Patient Search* and *Patient Analytics*.

Your system is pre-configured with the interaction information extracted from the unstructured document. In this scenario, your system is configured with patients who received medication with the medicinal ingredient Pantoprazol. The following procedure guides you to use filter cards feature in the *Patient Analytics* application to analyze the unstructured data:

Procedure

1. Open the SAP Fiori launchpad.



2. Click *Patient Analytics*.

When the application is loaded, a chart is displayed that shows the number of patients based on the pre-configured filter card interaction named *Medication*.

To filter for patients who received medication with the specific medicinal ingredient, you proceed as follows:

3. In the *Match All* section, for *Medication* filter card, open the *Select Filter Attributes* menu.
4. Choose the medicinal ingredient *Pantoprazol*.

Choose  (Patient List) to display a list of patients who match your current filter criteria.

Note

Depending on your authorizations, you might not be able to see all patients who match your filter criteria in the patient list. You can only see the patients that you are authorized to access.

Choose an entry from the list to view more details about the patient, such as the patient's interactions or documents related to the patient in the [Patient Summary](#) application.

4 Additional Demo Using MIMIC

If you have the necessary licenses, you can enhance the provided example patient data with the openly-available MIMIC-III patient data set.

MIMIC-III (Medical Information Mart for Intensive Care III) is a large, openly-available database comprising de-identified health-related data associated with over forty thousand patients who stayed in critical care units of the Beth Israel Deaconess Medical Center between 2001 and 2012. The database includes information such as demographics, vital sign measurements made at the bedside (~1 data point per hour), laboratory test results, procedures, medications, caregiver notes, imaging reports, and mortality (both in and out of hospital).

i Note

Not all data available in the MIMIC data set is supported by the trial version of this product.

To integrate and use the MIMIC data set, you must log on as the user **MIMIC** with the password **Tour1234**. All necessary data integration profiles and configurations are provided for you.

When you integrate the MIMIC data set, the following data types are loaded and available for use in the various applications:

Table 8:

MIMIC Data Type	Mapped Clinical Data Model Entity	Number of Entries
PATIENTS	Entity Patient	46,520
		i Note Patients are assigned fictitious names and addresses.
ADMISSIONS	Entity Interaction Attributes - EAV Interaction Details	58,976
DIAGNOSES_ICD	Entity Interaction Attributes - EAV Interaction Details	651,047
PROCEDURES_ICD	Entity Interaction Attributes - EAV Interaction Details	240,095
ICUSTAYS	Entity Interaction <ul style="list-style-type: none">String Attributes - EAV Interaction-DetailsNumeric Attributes - EAV InteractionMeasures	61,532

MIMIC Data Type	Mapped Clinical Data Model Entity	Number of Entries
MICROBIOLOGYEVENTS	Entity Interaction Attributes - EAV Interaction Details	328,446
D_ICD_DIAGNOSES	Lookup Table (Ref.Codes)	14,567
D_ICD_PROCEDURES	Lookup Table (Ref.Codes)	14,567
PRESCRIPTIONS	Entity Interaction Attributes - EAV Interaction Details	4,156,848
LABEVENTS	Entity Interaction <ul style="list-style-type: none"> String Attributes - EAV Interaction-Details Numeric Attributes - EAV InteractionMeasures 	27,872,575
CHARTEVENTS	Entity Interaction <ul style="list-style-type: none"> String Attributes - EAV Interaction-Details Numeric Attributes - EAV InteractionMeasures 	263,201,375

Related Information

[Integrating MIMIC Data \[page 45\]](#)

4.1 Integrating MIMIC Data

Context

Before you can view the MIMIC data in any of the applications, you must download the data from Physionet and integrate it into the system using the [Data Integration Cockpit](#).

Procedure

1. Obtain a license for the MIMIC-III data set.

This process involves passing an exam and sending the certificate to Physionet.

For more information, go to <https://mimic.physionet.org/https://mimic.physionet.org/gettingstarted/access//> and <https://mimic.physionet.org/https://mimic.physionet.org/gettingshttps://physionet.org/works/MIMICIIIClinicalDatabase/access.html//>.

2. Download the MIMIC-III data set and unzip the CSV files.
3. Copy the CSV files to the folder `/hana/shared/ffh-data/mimic/`.

To do so, use an FTP client, such as WinSCP.

4. Launch the trial version of SAP Connected Health platform and SAP Medical Research Insights.
5. Log on to the system as the **ADMINISTRATOR** with the password **Tour1234**.
6. Open the *Data Integration Cockpit* application.
7. Select the data import extension for MIMIC data and run the pre-configured profile.

➔ Tip

We recommend that you don't change any of the profile parameters of the pre-configured profile. After the profile run you can examine the number of records imported for each table.

8. Select the transform extension for MIMIC data and run the pre-configured profile.

➔ Recommendation

We recommend you don't change any of the parameters of the pre-configured profile. These are set to ensure you can use the data set in the applications. For example, the data must have the OrgID 102 for the MIMIC user to see it and not all tables in the MIMIC data set are supported by this trial version.

9. Select the basic extension for clinical data and run the pre-configured profiles for patients and interactions.

i Note

The pre-configured profile for interactions only loads one entity at a time. Therefore, you must run the profile repeatedly until no new data is integrated.

➔ Tip

If you make an error, you can rollback a data integration run by selecting the profile and choosing *Clean Up*.

10. Log on to the system as the user **MIMIC** with the password **Tour1234**

Results

After the data is integrated, you can view the data in the applications, such as *Patient Analytics* or *Search*.

5 Additional Guides

For additional information on any of the applications and their associated features within this product, please see the following guides:

Table 9:

Feature/App	Guide	Link
Patient Analytics	SAP Medical Research Insights Application Help	http://help.sap.com/med_res-insights201
Patient Search	SAP Foundation for Health Application Help	http://help.sap.com/platform_health101
Cohorts	SAP Foundation for Health Application Help	http://help.sap.com/platform_health101
Clinical Data Model Configuration	SAP Foundation for Health Implementation Guide	http://help.sap.com/platform_health101
Data Integration Cockpit	SAP Foundation for Health Implementation Guide	http://help.sap.com/platform_health101
Clinical Data Warehouse Cockpit	SAP Foundation for Health Administration Guide	http://help.sap.com/platform_health101
Ontology Services	SAP Foundation for Health Implementation Guide	http://help.sap.com/platform_health101
Document Processing	SAP Foundation for Health Implementation Guide	http://help.sap.com/platform_health101
User Management	SAP Foundation for Health Implementation Guide	http://help.sap.com/platform_health101
Patient Analytics Configuration	SAP Medical Research Insights Administration Guide	http://help.sap.com/med_res-insights201

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