Oracle® Healthcare Precision Medicine

User's Guide

Release 1.0

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ORACLE®

Oracle Healthcare Precision Medicine User's Guide, Release 1.0

E75998-01

Contents

Preface

This document describes how to install and setup Oracle Healthcare Precision Medicine (OHPM). The user installing Oracle Healthcare Foundation should have some knowledge of WebLogic and Linux.

Audience

This document is intended for any user working with OHPM. This includes molecular pathologists, clinical geneticists, clinicians, physicians and nurses.

Documentation Accessibility

For information about Oracle's commitment to accessibility, visit the Oracle Accessibility Program website at http://www.oracle.com/pls/topic/lookup?ctx=acc&id=docacc.

Access to Oracle Support

Oracle customers that have purchased support have access to electronic support through My Oracle Support. For information, visit http://www.oracle.com/pls/topic/lookup?ctx=acc&id=info or visit http://www.oracle.com/pls/topic/lookup?ctx=acc&id=trs if you are hearing impaired.

Finding Information and Patches on My Oracle Support

Your source for the latest information about Oracle Healthcare Analytics Data Integration is Oracle Support's self-service Web site, My Oracle Support (formerly MetaLink).

Before you install and use an Oracle software release, always visit the My Oracle Support Web site for the latest information, including alerts, release notes, documentation, and patches.

Creating a My Oracle Support Account

You must register at My Oracle Support to obtain a user name and password account before you can enter the Web site.

To register for My Oracle Support:

1. Open a Web browser to http://support.oracle.com.
2. Click the **Register here** link to create a My Oracle Support account. The registration page opens.

3. Follow the instructions on the registration page.

Signing In to My Oracle Support

To sign in to My Oracle Support:

1. Open a Web browser to http://support.oracle.com.
2. Click **Sign In**.
3. Enter your user name and password.
4. Click **Go** to open the My Oracle Support home page.

Searching for Knowledge Articles by ID Number or Text String

The fastest way to search for product documentation, release notes, and white papers is by the article ID number.

To search by the article ID number:

1. Sign in to My Oracle Support at http://support.oracle.com.
2. Locate the Search box in the upper right corner of the My Oracle Support page.
3. Click the sources icon to the left of the search box, and then select Article ID from the list.
4. Enter the article ID number in the text box.
5. Click the magnifying glass icon to the right of the search box (or press the Enter key) to execute your search.

   The Knowledge page displays the results of your search. If the article is found, click the link to view the abstract, text, attachments, and related products.

In addition to searching by article ID, you can use the following My Oracle Support tools to browse and search the knowledge base:

- Product Focus — On the Knowledge page, you can drill into a product area through the Browse Knowledge menu on the left side of the page. In the Browse any Product, By Name field, type in part of the product name, and then select the product from the list. Alternatively, you can click the arrow icon to view the complete list of Oracle products and then select your product. This option lets you focus your browsing and searching on a specific product or set of products.
- Refine Search — Once you have results from a search, use the Refine Search options on the right side of the Knowledge page to narrow your search and make the results more relevant.
- Advanced Search — You can specify one or more search criteria, such as source, exact phrase, and related product, to find knowledge articles and documentation.

Finding Patches on My Oracle Support

Be sure to check My Oracle Support for the latest patches, if any, for your product. You can search for patches by patch ID or number, or by product or family.

To locate and download a patch:

1. Sign in to My Oracle Support at http://support.oracle.com.
2. Click the **Patches & Updates** tab.

   The Patches & Updates page opens and displays the Patch Search region. You have the following options:

- In the Patch ID or Number is field, enter the primary bug number of the patch you want. This option is useful if you already know the patch number.
- To find a patch by product name, release, and platform, click the Product or Family link to enter one or more search criteria.

3. Click **Search** to execute your query. The Patch Search Results page opens.
4. Click the patch ID number. The system displays details about the patch. In addition, you can view the Read Me file before downloading the patch.
5. Click **Download**. Follow the instructions on the screen to download, save, and install the patch files.

Finding Documentation on Oracle Technology Network

The Oracle Technology Network Web site contains links to all the latest Oracle user and reference documentation. To find user documentation for Oracle products:

1. Go to the Oracle Technology Network at

   `http://www.oracle.com/technetwork/index.html` and log in.
2. Mouse over the Support tab, then click the **Documentation** hyperlink.

   Alternatively, go to Oracle Documentation page at

   `http://www.oracle.com/technology/documentation/index.html`
3. Navigate to the product you need and click the link.

   For example, scroll down to the Applications section and click Oracle Health Sciences Applications.
4. Click the link for the documentation you need.

Related Documents

For more information, see the following documents:

- *Oracle Healthcare Precision Medicine Administrator's Guide*
- *Oracle Healthcare Precision Medicine User's Guide*
- *Oracle Healthcare Precision Medicine Security Guide*
- *Oracle Healthcare Precision Medicine Release Notes*
- *Oracle Healthcare Precision Medicine Release Content Document*
- *Oracle Healthcare Precision Medicine Third Party Licenses and Notices*

Conventions

The following text conventions are used in this document:

boldface - Boldface type indicates graphical user interface elements associated with an action, or terms defined in text or the glossary.

italic - Italic type indicates book titles, emphasis, or placeholder variables for which you supply particular values.

`monospace` - Monospace type indicates commands within a paragraph, URLs, code in examples, text that appears on the screen, or text that you enter.

1 Introduction

This chapter provides an introduction to Oracle Healthcare Precision Medicine (OHPM). It contains the following topics:

1.1 Overview

Oracle Healthcare Precision Medicine is a software application designed to address the gap between treatments in the clinic and the knowledge in the research pipelines. It enables collaboration between the clinician, looking for the most appropriate treatment for his patient, and the molecular pathologist, learning patient's molecular profile and suggesting the most up-to-date treatment to follow.

The clinician orders diagnostic tests. After the specimen is collected and processed, the molecular pathologist analyzes test results and delivers treatment recommendations. OHPM helps optimize personalized patient care based on an individual's clinical and genomic profile. It also accelerates molecular laboratory testing throughput, while maintaining consistency and traceability of the generated reporting contents to fulfill compliance requirements.

1.2 Disclaimer

The Oracle Healthcare Precision Medicine software is only a search tool and is not intended to, and must not replace the clinician's judgment or experience. Furthermore, the healthcare professional using this search tool should employ their professional judgment concerning the reliability and accuracy of the information in the various knowledge databases that are employed or selected as content for reports generated using Oracle Healthcare Precision Medicine.

1.3 What Can I Do Using Oracle Healthcare Precision Medicine

The following lists the primary tasks that can be accomplished using OHPM:

- Filter through thousands of variants to identify ones which are clinically actionable or may be relevant

- Annotate variants that can be acted upon today or warrant further investigation based on sequenced data and reference information, both internal and external
- Publish a genomic report to be used in clinical practice (report can be published both to OHPM and EMR system) and therefore personalize treatment
- View the published report with full security settings, which are based on the user's access to patient records

1.4 User Roles

The following are the various user roles in OHPM:

- pm_reporter_group - for users who will be generating molecular reports and publishing them or browsing through genomic data. This includes molecular pathologists and clinical geneticists.
- pm_clinician_group - for doctors who are seeing patients and request the report to be done. This includes clinicians, physicians and nurses.
- pm_reporter_limited_group - for someone who can browse through data and do most of the reporting steps but cannot publish the report nor request report from third parties (example, Nof1). This includes molecular pathologists and clinical geneticists who may be training on the software.
- pm_admin_group - for users who can create groups of other users and manage roles of users.

Users may be given several of these roles but the roles take precedence in the order of precedence listed below:

- pm_reporter_group
- pm_reporter_limited_group
- pm_clinician_group

A user cannot have both clinician and either of the reporter roles. If this happens, the application displays an error.

The pm_admin_group role can be used in conjunction with any of the above roles.

1.5 Known Issues

Following are the known issues for this release of OHPM:

- When clicking View Patient from the Genomic Report window, the Patient Viewer does not perform. It can take several minutes to load.
- In the variant table, sorting based on chromosome position treats numbers as strings. For example, chr7 appears after chr11 when you select sorted by ascending.
- Certain variants which are present on MT or Y chromosome appear as linked to bogus 'No Gene' record.
- While filtering, certain variants are missing non-coding impact attribute when listed in the tabular view. This attribute appears correctly once the user looks at the Variant Detail screen.
- No warning or prompt is displayed before the application times out.
- Variant Effect calculations are incorrect for variants near CDS boundaries.

- There is no indication to display the default sorting and then change it.
- Mitochondrial chromosome variants are not labeled correctly when sent to Dalliance resulting in no data shown.
- The Patient Viewer tab does not load the relevant patient automatically.
- Patient Viewer only supports searching by patient ID, not patient name.
- After viewing patient details from the patient viewer, if you open another report and click Patient Viewer, you will still see the patient details from the previous report.
- Protein impact is missing from variant details in the published report and has to be added manually by the end user when publishing a report.
- Variants with chromosome position :CHRMT do not display the variant area in Dalliance.

2

Home Page

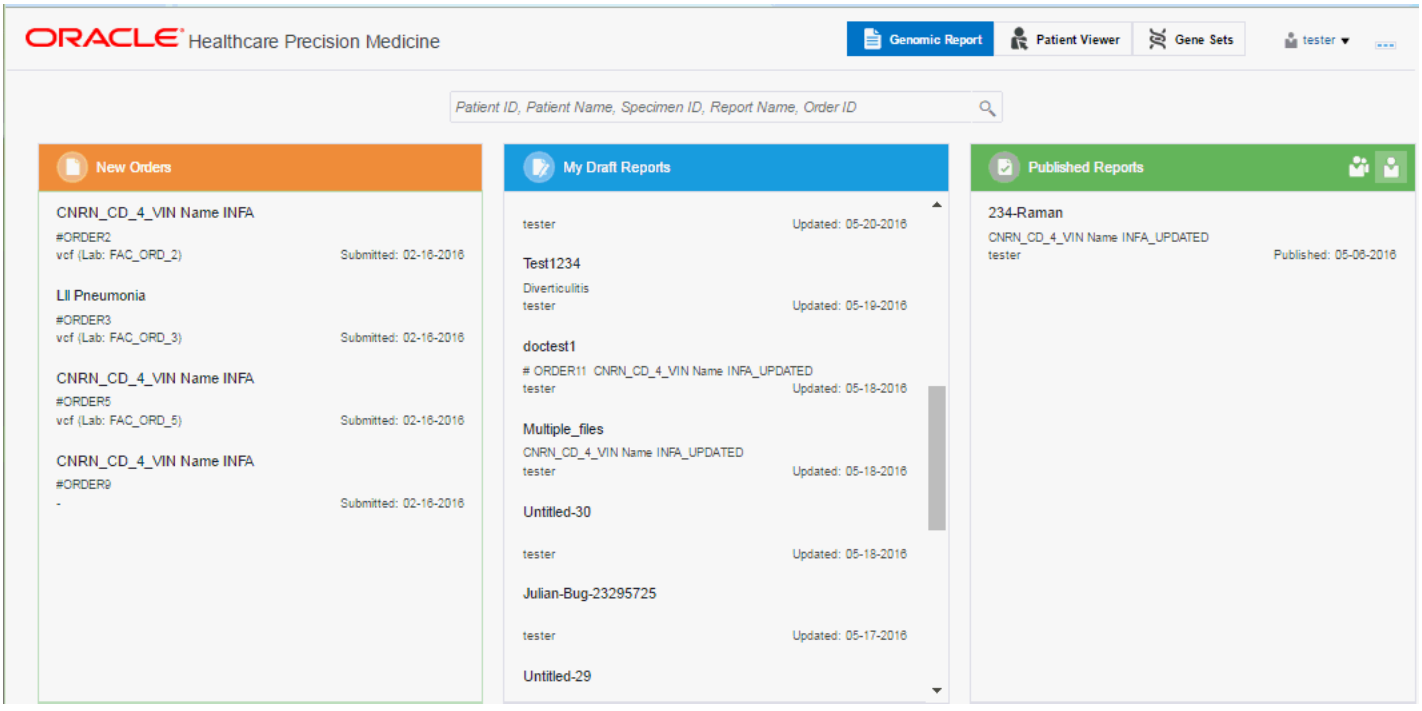
This chapter describes the features on the Home page. Depending on your role, you may have restricted access to these functions. This chapter contains the following topics:

- Section 2.1, "Molecular Pathologist Home Page"
- Section 2.2, "Clinician Home Page"

> **Note:** If you are a clinician, your page will be different from what is described here. For details, see Section 2.2, "Clinician Home Page".

2.1 Molecular Pathologist Home Page

This section describes the home page for the Molecular Pathologist.



2.1.1 Tabs

The following sections describe the home page tabs.

2.1.1.1 Genomic Report

This contains the new orders, draft reports and published reports for a user and acts as a starting point for reporting workflow.

2.1.1.2 Patient Viewer

This tab lets you view detailed patient information, including both clinical (coming from Clinical Data Model) and genomic (coming from Omics Data Bank) details. For details, see Chapter 6, "Patient Viewer".

2.1.1.3 Gene Sets

The Gene Sets tab is a way to collect genes into groupings or lists for use in filtering queries (see Section 3.4). For details on how to create and manage gene sets, see Chapter 7, "Gene Sets".

2.1.2 New Orders

This section lists out the new orders for reports with the oldest report on top. New orders have a green icon next to them. Once a draft report is created, the order is not visible in the list.

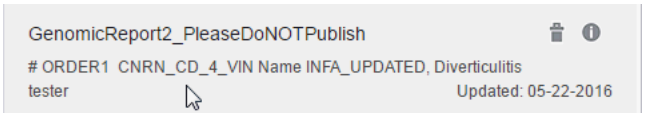
However, if you delete the draft report, the order will again appear in this list. Click an order to view the Report Review page.

The following information is displayed for each order:

- Lab from where order came
- User who submitted order
- Diagnosis that came with order
- Date when order was submitted

2.1.3 My Draft Reports

This section lists a user's draft reports with the last updated report on top. These reports are private and cannot be viewed by another user. Click a draft report to go to the Report Review page.

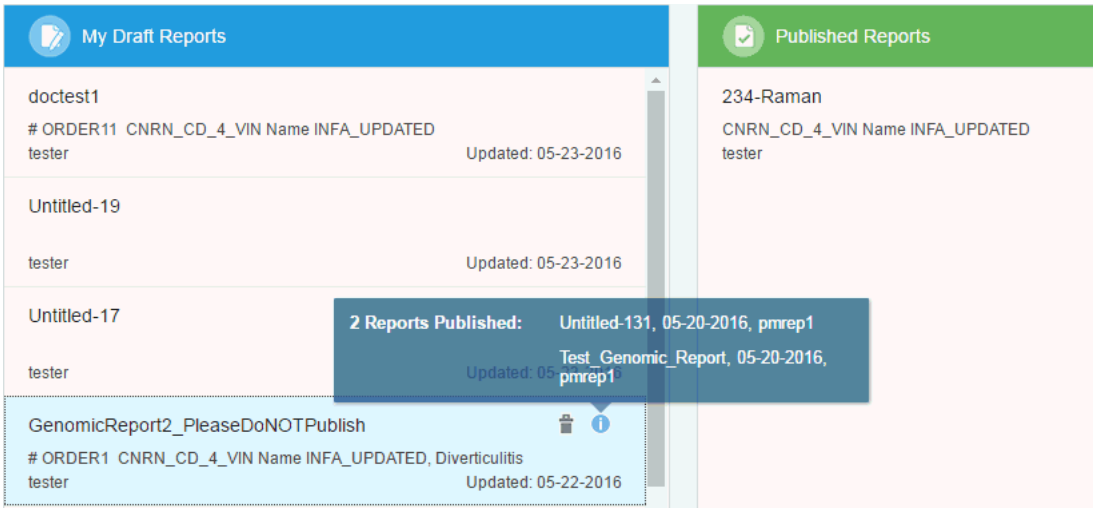


The following information is displayed for each draft report:

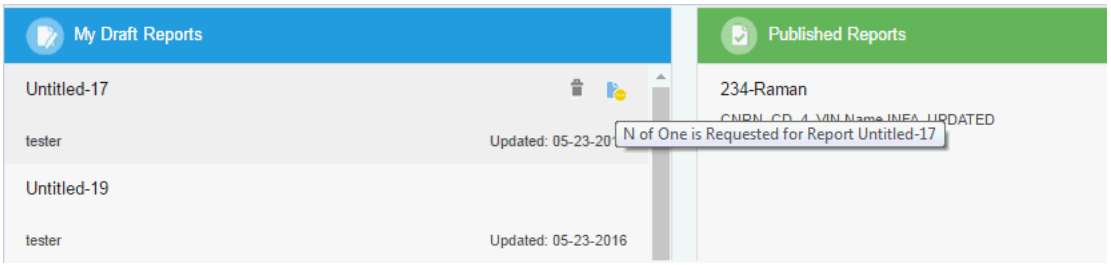
- Report name
- Date when report was last updated
- Delete icon (appears when you place the cursor over the report name)

- Indicator that other draft and published reports are available for that order ((appears when you place the cursor over the report name)

Clicking this icon results in a popup with information on the other reports for that order



- Indicator that interpretation has been requested. Place your cursor over the following icon to view a popup indicating the interpretation status.

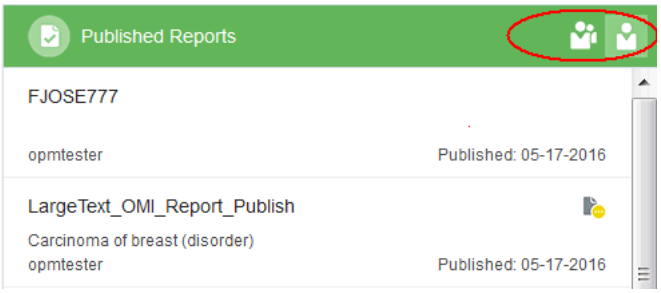


- Status of child reports

2.1.4 Published Reports

This section lists all published reports with the latest report on top. You can view all published reports or only the ones published by you using the icons on the top right.

Note: You can only view reports for patients that you have access to irrespective of whether reports have been created by you or not.



The following information is displayed for each order:

- Report name
- Report author
- Date the report was published
- Diagnosis

To view the report, click it. The PDF format of the report is displayed in a new tab.

Note: To view published reports, ensure that you have disabled the pop-up blocker in your browser.

2.1.5 Searching

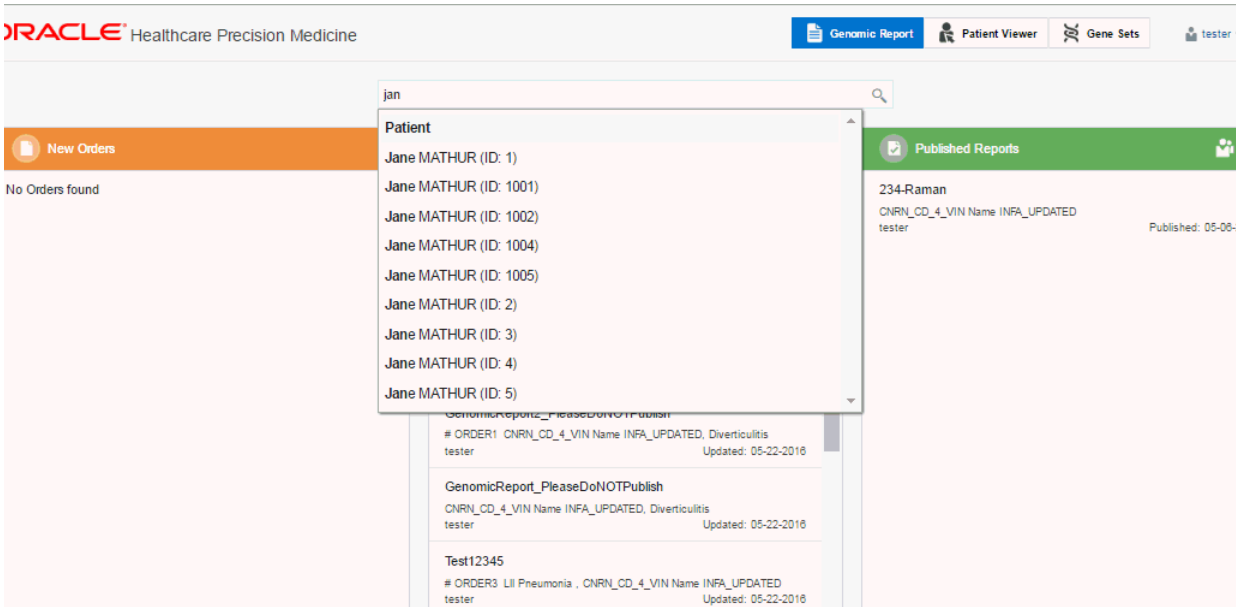
You can search for orders or reports based on any one of the following:

- Patient ID
- Patient Name
- Specimen ID
- Report Name - You can search within draft or published reports for a particular patient that you have access to.
- Order ID

Depending on the category you are using for your search, autocomplete kicks in after 1 or more characters have been entered in the search field. For example, if you are searching for a name, it is 2 characters; if it is a report, it is 1 char. Autocomplete results span all the above categories. Results are displayed with the latest report on top.

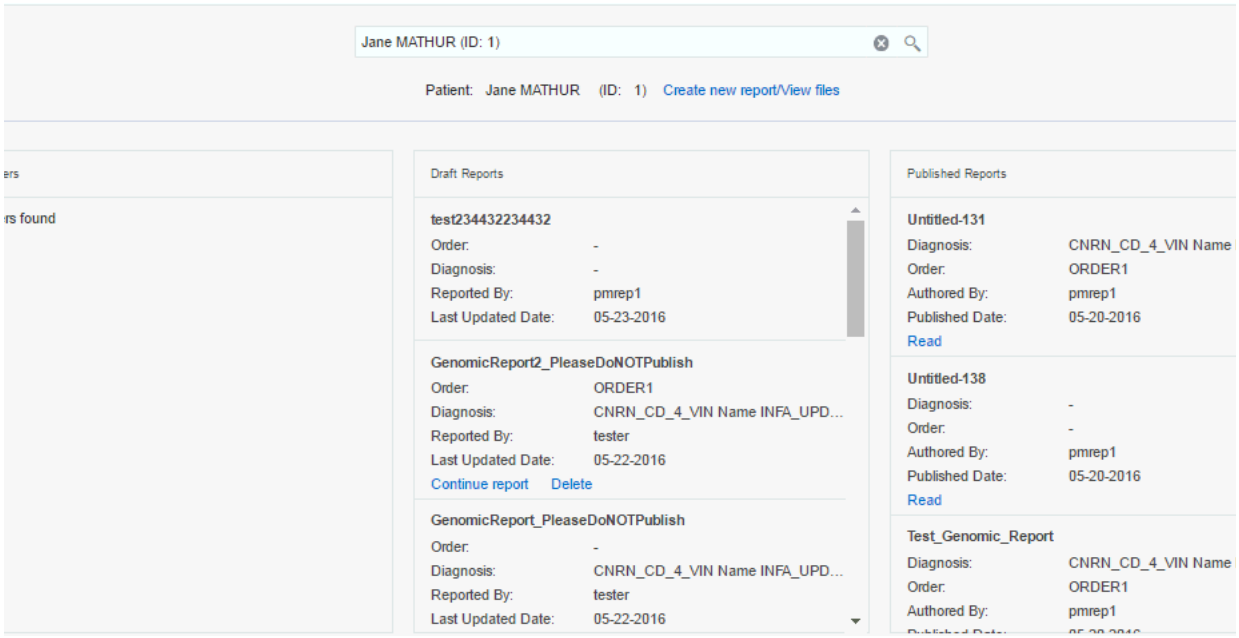
Perform the following steps to search for reports and new orders:

1. In the search bar at the top, enter the Patient ID. Matching results for the entered value are displayed in a drop-down list.



2. Select the value from the list.
3. The New Orders, Draft Reports and Published Reports for that patient are displayed.

   Click the X icon in the search bar to navigate back to the Home page.



Depending on which parameter you search for, the results will be displayed as follows:

- Selecting a Draft Report directly opens it for editing.
- Selecting an independent N-of-1 Published Report will open its PDF version in a new window.

Search All Mode

This is an alternative search mode. You can enter a search parameter and view results within all other parameters.

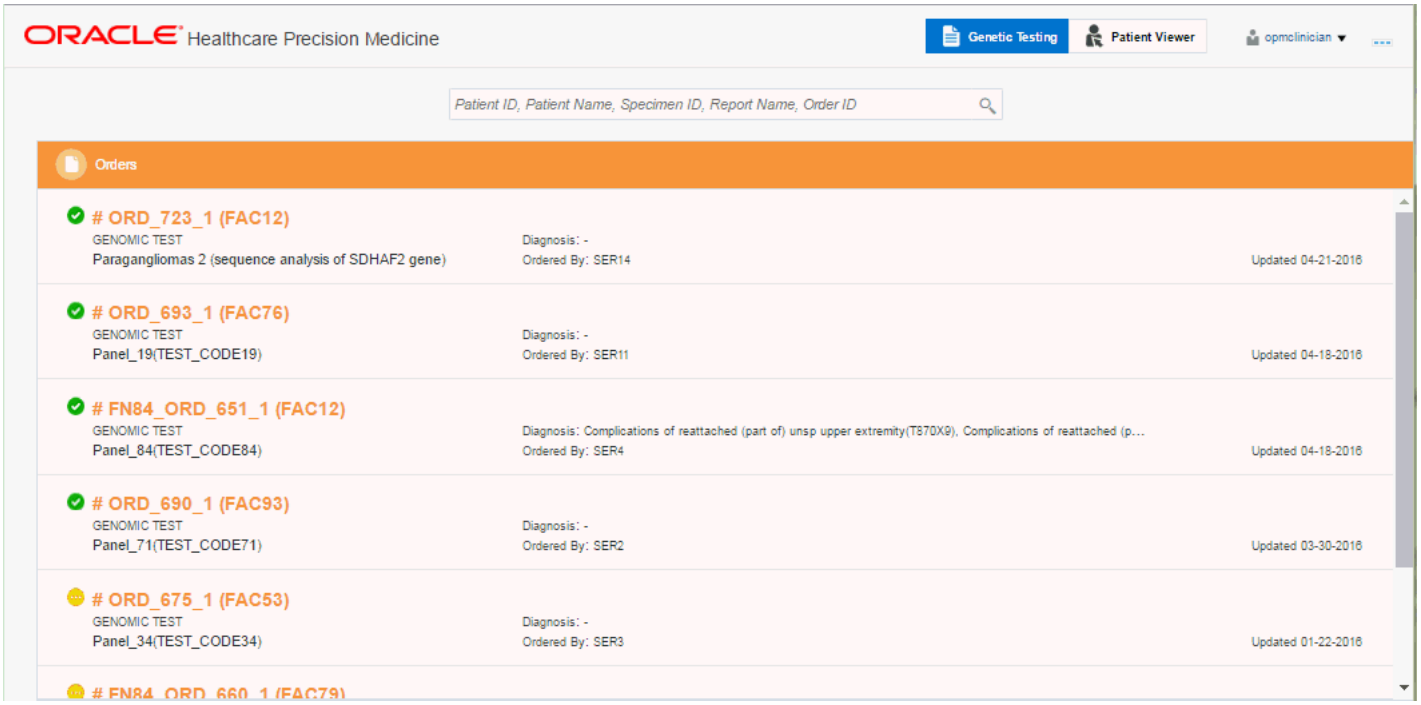
1. Enter a parameter in the search box at the top. The parameter can be the Patient ID, Patient Name, Specimen ID, Report Name or Order ID. For illustration, the patient ID has been used.
2. Click the search icon next to the search bar or press Enter.

3. The matches for different categories are displayed. Click each category to view the matches under it.

4. Select the value from the list.
5. The New Orders, Draft Reports and Published Reports for that parameter are displayed.

2.2 Clinician Home Page

If OHPM has been integrated with EMR (see the *Oracle Healthcare Precision Medicine Administrator's Guide* for information on EMR integration), clinicians can access the genomic report from EMR once it is published. However, if there is no EMR integration, you may need to access the report from OHPM. The Clinician Home Page is as follows:



2.2.1 Tabs

This section describes the tabs displayed on the Clinician home page.

2.2.1.1 Genetic Testing

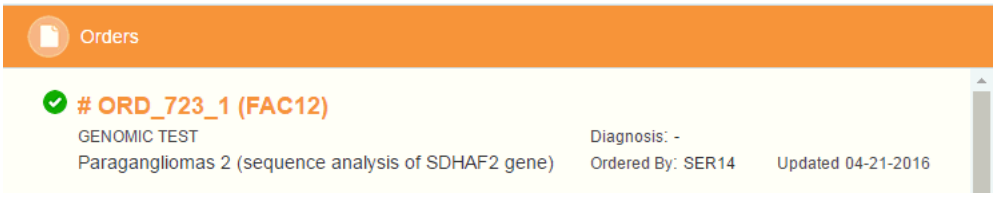
This tab displays all the Orders and can be used for searching. For details on Orders, see Section 2.2.2, "Orders".

2.2.1.2 Patient Viewer

Patient Viewer - This tab lets you view detailed patient information. For details, see Section 2.1.1.2.

2.2.2 Orders

Orders are listed with the latest order on top. The following information is displayed for each order:



- Order ID (lab)
- Ordered by - username of the user who placed the order
- Updated - When the order was last updated
- Genomic Test - Tests that have been ordered
- Diagnosis - The diagnosis that came with order

- Icons indicating whether the order has a draft report, published report or no reports
  - The green checkmark icon indicates that an order has a published report.

  - The yellow icon indicates that an order has a draft report

  - The grey icon indicates that an order has no reports.

Click an order to view its details.

2.2.3 Searching

You can search for orders or reports based on any one of the following:

- Patient ID
- Patient Name - first name or last name or both in any order
- Specimen ID
- Published Report Name - You can search only through published report names for the patients you have access to. You will not be able to view external standalone reports.
- Order ID

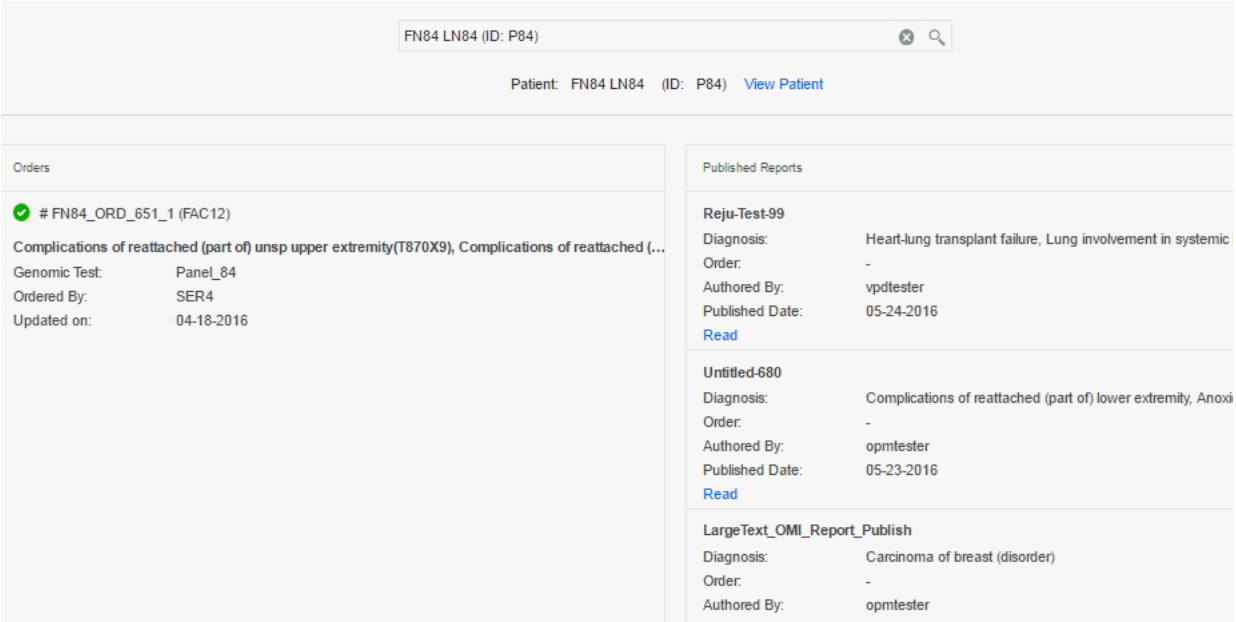
Depending on the category you are using for your search, autocomplete kicks in after 1 or more characters have been entered in the search field. For example, if you are searching for a name, it is 2 characters; if searching for a report, it is 1 char.

Autocomplete results span all the above categories. Results are displayed with the latest report on top.

Perform the following steps to search for reports and new orders:

1. In the search bar at the top, enter the Patient ID. Matching results for the entered value are displayed in a drop-down list.
2. Select the value from the list.
3. The New Orders and Published Reports for that patient are displayed.

   Click the X icon in the search bar to navigate back to the Home page.



Search All Mode

This is an alternative search mode. You can enter a search parameter and view results within all other parameters.

1. Enter a parameter in the search box at the top. The parameter can be the Patient ID, Patient Name, Specimen ID, Report Name or Order ID. For illustration, the patient ID has been used.
2. Click the search icon next to the search bar or press Enter.

3. The matches for different categories are displayed. Click each category to view the matches under it.

4. Select the value from the list.
5. The New Orders and Published Reports for that parameter are displayed.

   Click the X icon in the search bar to return to the Home page.

3

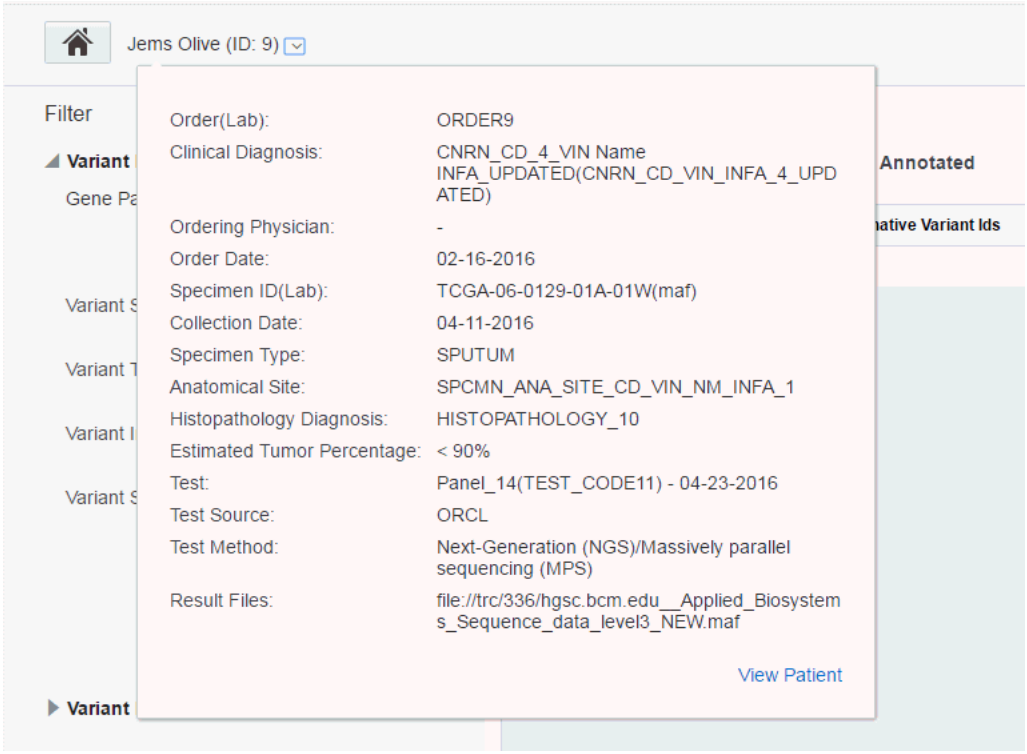
Filtering Variants and Starting Reports

This section describes the tasks you can perform with reports. It includes the following sections:

3.1 Patient Overview

You can view information about the specimen, order and data files corresponding to running genomic tests or molecular data for a given patient. Only molecular pathologists and researchers roles have access to this feature.

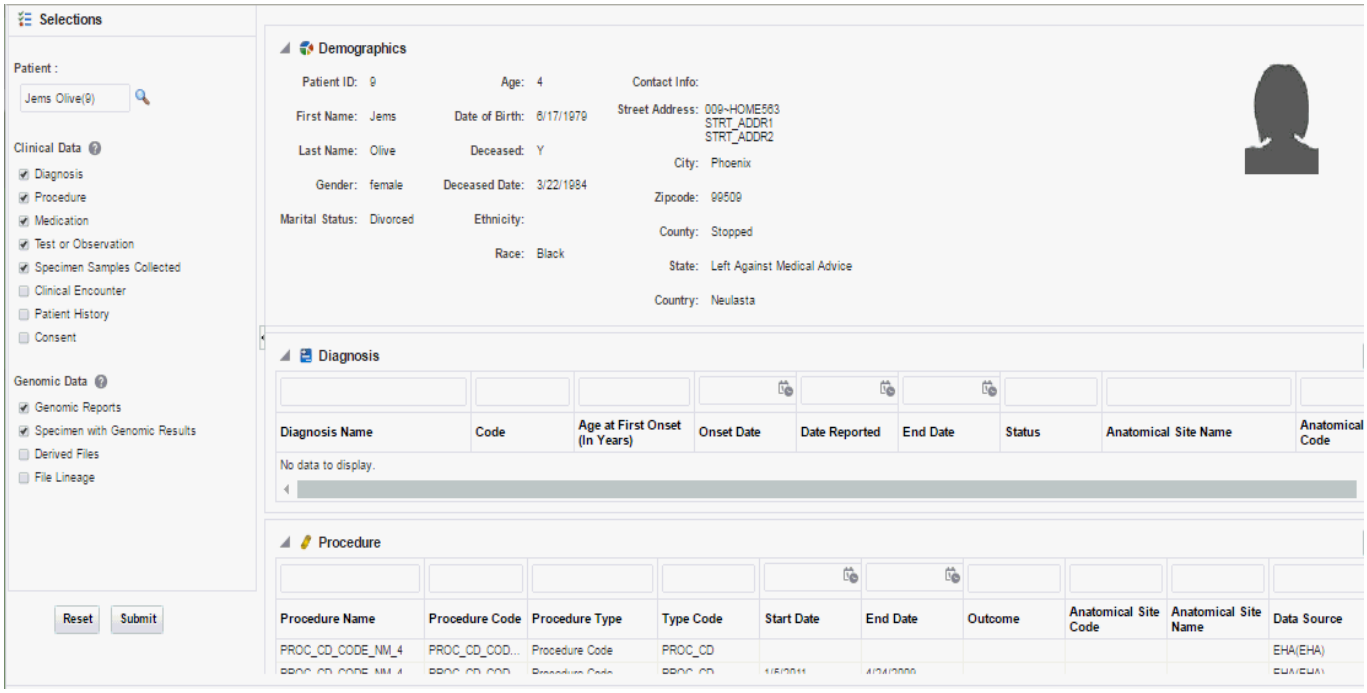
To display the overview, click the arrow next to the patient name on the top left corner.



The following information is displayed:

- Order (Lab) - Order ID and Lab that the order is coming from
- Clinical Diagnosis - The diagnosis linked to the order, can be more than one.
- Ordering Physician - The physician who placed the order
- Order Date - The date the order was placed
- Specimen ID (Lab) - Specimen number and vendor number
- Collection Date - When specimen was collected
- Specimen Type - The type of specimen, for example, blood tissue
- Anatomical Site - The site from where the specimen was taken, for example, liver.
- Histopathology Diagnosis - The diagnosis associated with specimen when returned from the pathology lab. This may or may not be same as the one associated with order, could be multiple.
- Estimated Tumor Percentage - The percentage of tumor estimated to be in tissue, for example, 10-30, >20, numeric values 0 to 100
- Test - The test(s) performed and dates each test was performed
- Test Source - Test source, from ODB reference part of the test
- Test Method - The method associated with the test in the ODB reference portion of the model
- Result Files - Sequencing files produced as a result of the test

The View Patient link on the bottom right navigates to the Patient Viewer page.



3.2 Selecting Data Files

Perform the following steps to add data files to your report:

1. Depending on which page you have navigated from, click **Create new report/View files** as shown in Figure 3–1 or **Add files** as shown in Figure 3–2.

Figure 3–1 Adding Files to a New Report

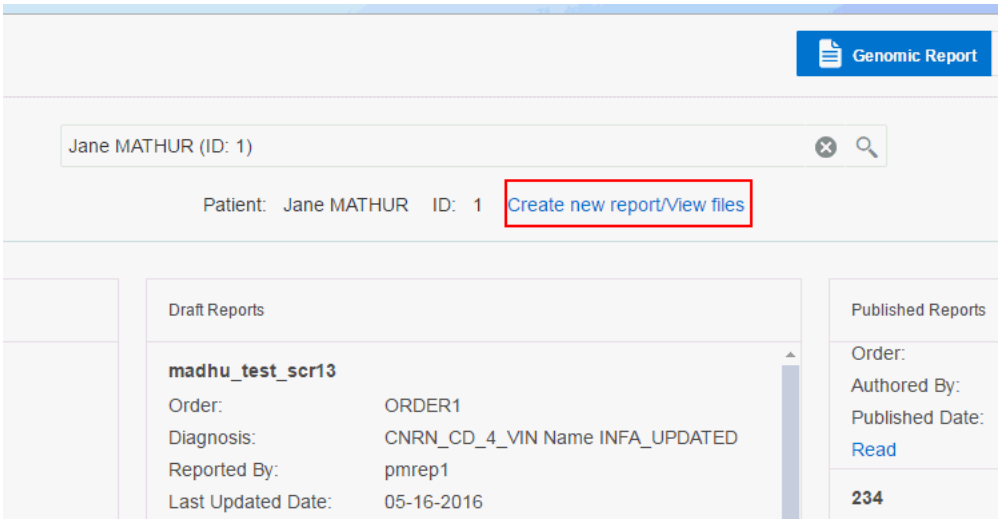
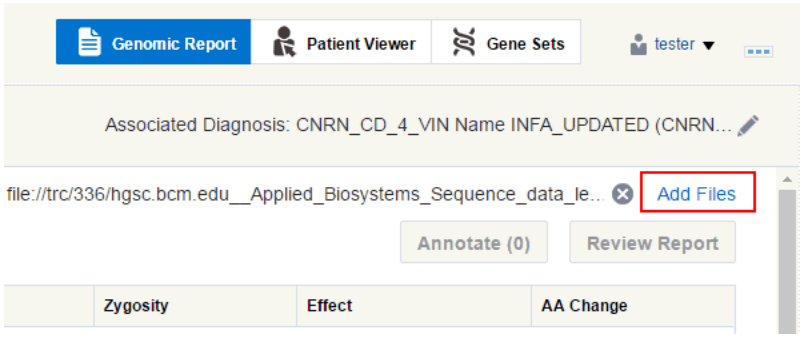


Figure 3–2 Adding Files to an Existing Order



The following details are displayed for each file:

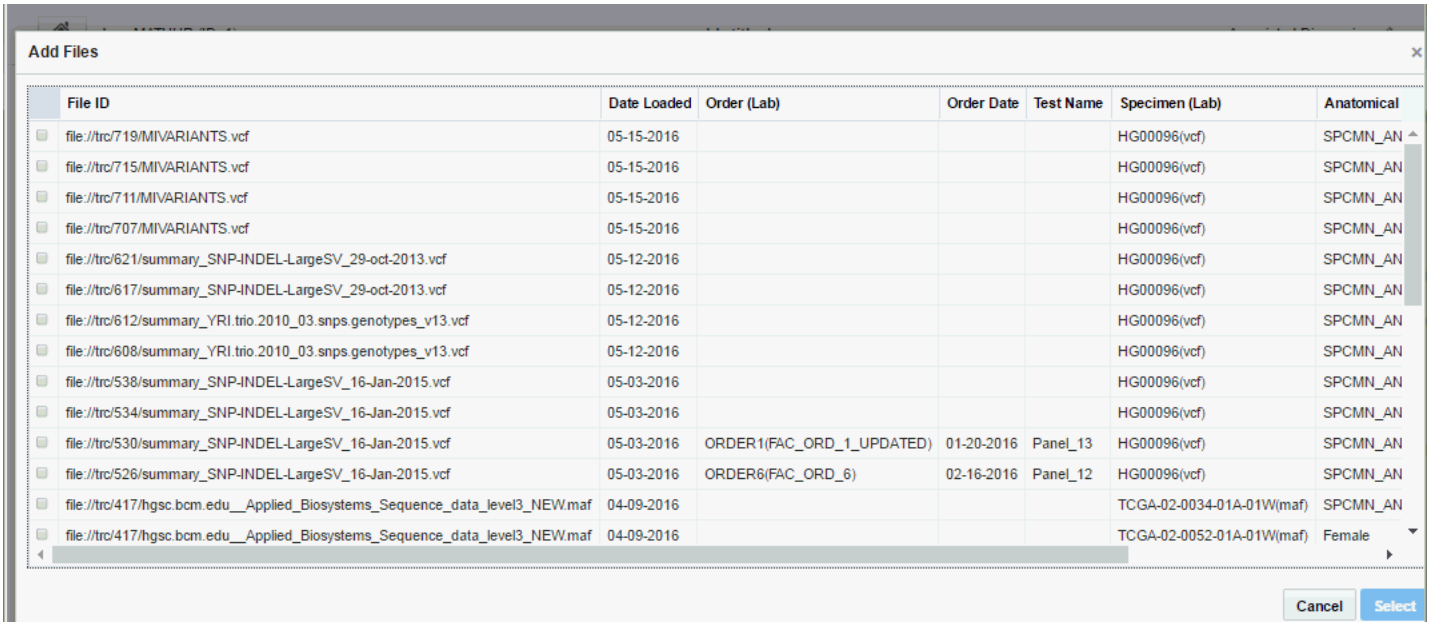
- File ID - The file ID from Omics Data Bank
- Date Loaded - Date on which the sequencing file was loaded
- Order (Lab) - The order number associated with clinician's order
- Order Date - The date when the clinician ordered the report
- Test Name - The tests that have been ordered
- Specimen (Lab) - Sample Identifier and the Lab the specimen was collected from
- Anatomical Site - Anatomical site that the specimen came from, for example, Lung or Blood
- DNA Assembly - The Assembly corresponding to results in the sequencing file

2. Select the files you want to add.

Note: All files you select must have:

- Their results aligned to the same Assembly or Alignment version. Once you select a file, all files that are not associated with the selected specimen or not aligned to same Assembly are greyed out and cannot be selected.
- Results corresponding to same (specimen, vendor) combination

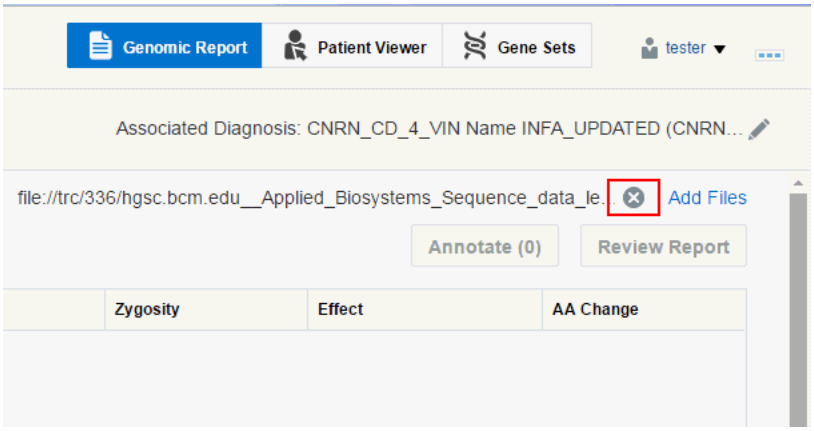
However, the associated DNA annotation version can be different.



To deselect a file, click the cross icon located next to it or you can deselect it in the previous step.

Note: If a file being deselected has Annotated variants associated with it, a warning is displayed.

If the report only has one file remaining and you try to delete it, you will be prompted to remove any annotated variant associated with the report. Only after removing the annotated variant can the file be deselected.



3. Click **Select**.

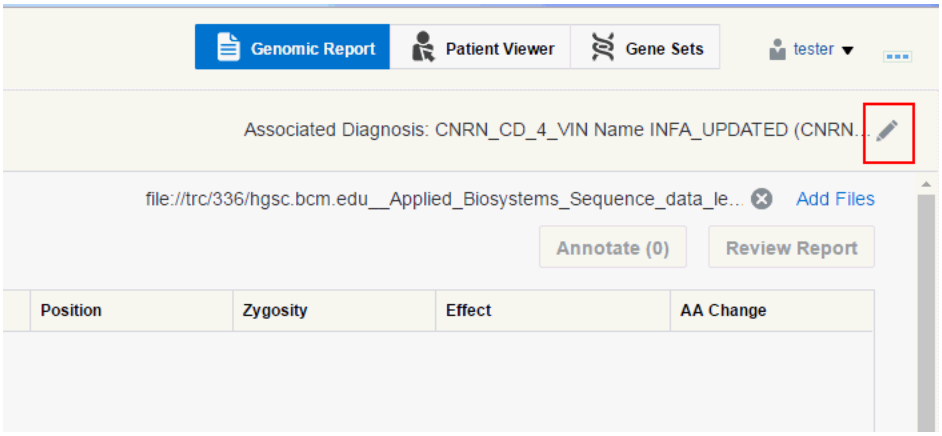
3.3 Associating Diagnoses with Reports

All the diagnoses associated with a report are visible in the top right hand corner. When a report is created, the diagnosis from the Order is automatically associated

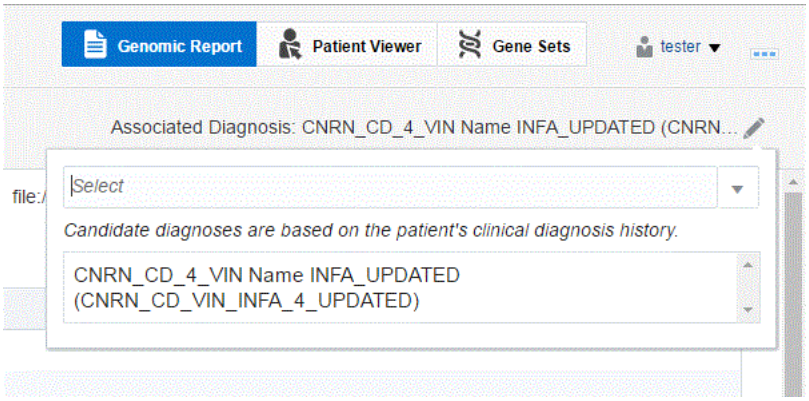
with the report. If the report is not based on an Order, you can select the diagnosis and save the report. On opening the draft report again, you can view the saved diagnosis. You can also leave the diagnosis in a report blank.

To add or edit diagnoses, perform the following steps:

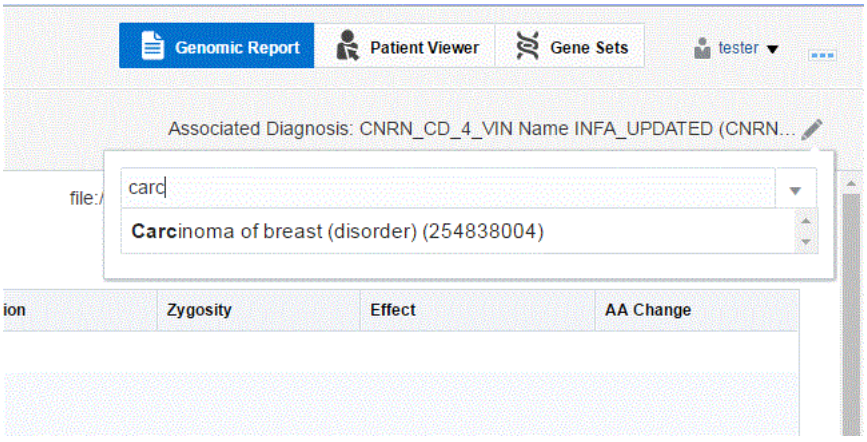
1. Click the pencil icon on the top right next to the diagnosis name.



A drop-down list of diagnoses is displayed. Diagnoses for a candidate is based on the patient's clinical diagnosis history. The candidate diagnoses, coming from patient history or order is restricted to 5 days after the Order is placed. An admin user can change this period of time to be different number.



2. You can search for a new diagnosis using the search box. Entries matching your input will be displayed.



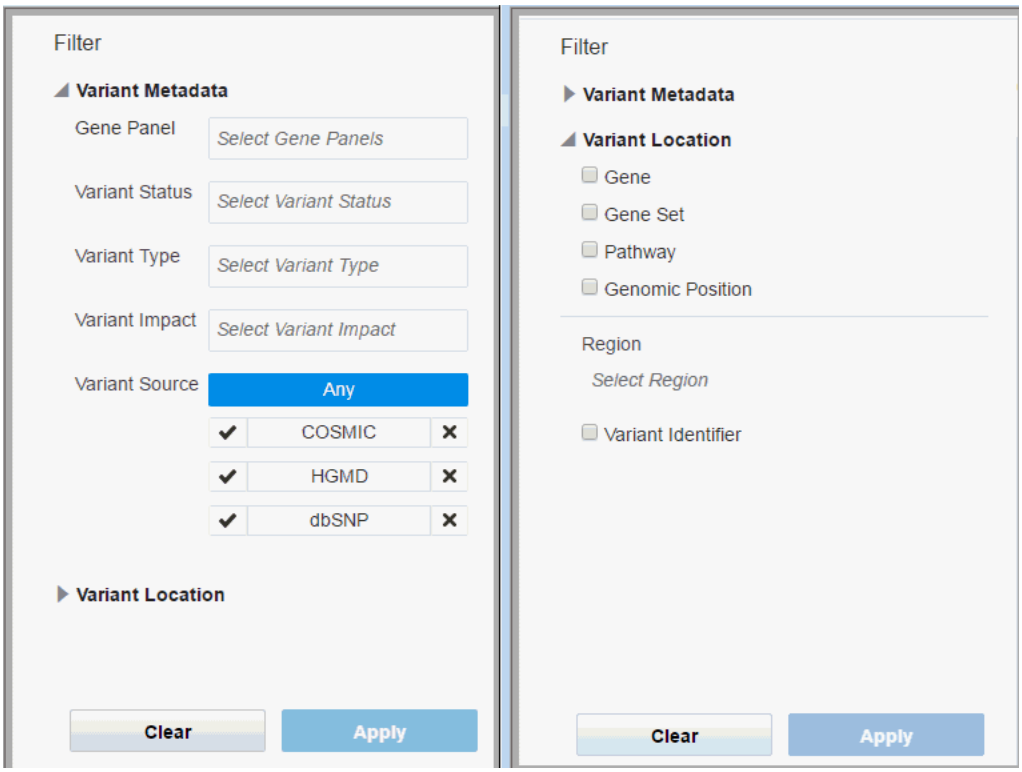
3. Select the diagnosis you want to add. You can select more than one diagnosis.
4. Click anywhere outside the panel to close it.

3.4 Filtering Variants

This section describes all the tasks associated with filtering variants. To navigate to the filter pane, perform the following steps:

1. Click a draft report to open it.
2. Click **Back to Reporting** on the bottom left. The Report View appears with the filter pane located on the left.

3.4.1 Filtering Criteria



The filter pan consists of two sections:

- Variant Metadata
  - Gene Panel - Name of the Genomic Test that was run to get the results for the patient, typically Panel Test. You can select multiple values.

    The gene panel values are preselected based on the files selected from the Add files (Section 3.2),when creating a new report.
  - Variant Status - Specifies which variant types to consider, whether the variant should be known or novel. Default considers all variants. You can select multiple values.
  - Variant Type -The type of variant. You can select multiple values.

- Variant Impact - Each variant type's impact on the resulting protein. You can select multiple values.
- Variant Source - You can filter variants based on a custom knowledge base. For details, see Section 3.4.3. To include variants from a given source, click the check mark. To exclude variants from a given source, click the x mark.

- Variant Location
  - Gene - List of one or more genes. You can select multiple values. After you enter the first three character of the gene, the autocomplete feature is enabled and displays matching values.
  - Gene Set - User-defined collection of genes that you can reference anytime instead of having to build ad-hoc lists of genes each time. You can select multiple values. After you type the first character, the autocomplete feature displays matching values.
  - Pathway - Reference to a pathway stored on the reference side of the ODB model. This in turn corresponds to a list of genes that are to be used to compare their Intensity values. You can select multiple values. After you type the first character, the autocomplete feature displays matching values.
  - Genomic Position - Specify genomic location for the variants to occur in. You can enter values in the format *chr#:from-to* or *chr#:from* where 0 < from <= to
  - Region - Types of regions supported including Exome, 3' and 5' UTR, promoter region. If you select Gene, Gene Set, Pathway, or Genomic Position, the Region filter is enabled and prepopulated with *Exome*. You can remove it before applying the filter criteria.
  - Variant Identifier - Variant identifier which is a representation of the known variant through RS ID, Cosmic ID, or coding region variants through HGVS identifier. You can search for HGVS variant identifiers by entering the gene name and the autocomplete feature displays the matching IDs. You can select multiple values.

You can use the various options to view a set of variants for a report. The Apply button is enabled only after you select at least one criteria. Click **Apply** to view the filtered variants. The **Apply** button is enabled only if the filters applied are different from the previous search. The selected criteria will be displayed the next time you open the Filter pane.

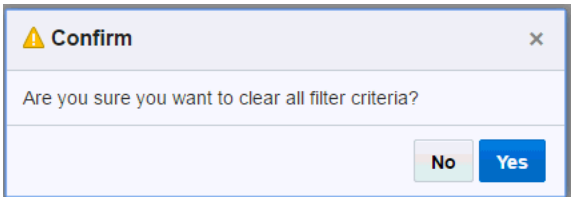
Performance will degrade if you select a large set of genes—either by selecting multiple pathways, large gene-sets or many ad-hoc gene selections. The more genes selected the more likely it is that the query performance degrades, especially with large result datasets.

Note: Filter criteria are not be saved with a Report. They will be reset when you log in again.

3.4.1.1 Clearing Filter Criteria

You can clear the filtered criteria by clicking **Clear**. You will receive a confirmation asking you if you want to clear the criteria. Click **Yes**. Click **Apply** to apply your changes.

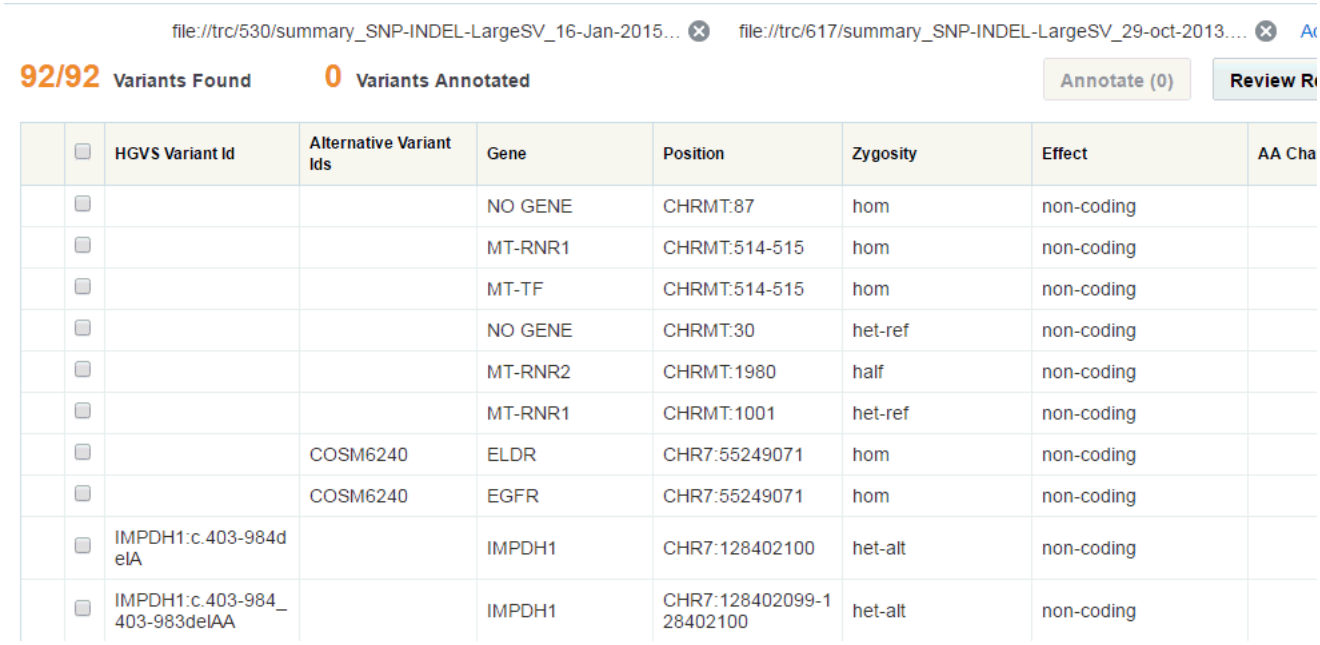
Figure 3–3 Confirmation to Clear Criteria



3.4.2 Tabular View of Variants

In the tabular view, you can select variants and then annotate them. Only 500 variants are displayed in the table. By default, filtered variants are sorted by Genomic Position. You can sort the columns either in ascending or descending order by clicking the sorting icons of the following columns:

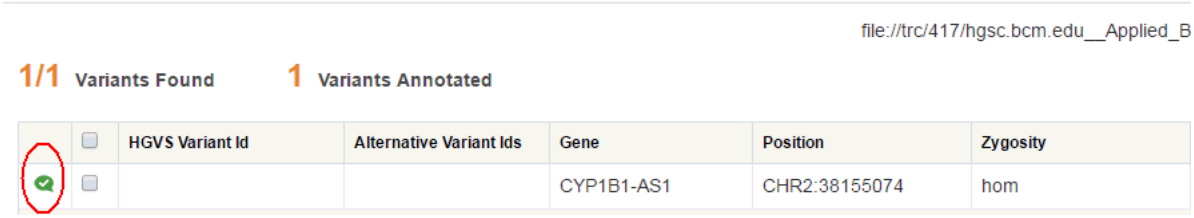
- HGVS Variant Id - Variant ID based on HGVS simple notation
- Gene - The gene name
- Position - The position on chromosome along with strand direction
- Zygosity - Variant zygosity



HGVS Variant Id	Alternative Variant Ids	Gene	Position	Zygosity	Effect	AA Cha
		NO GENE	CHRMT:87	hom	non-coding	
		MT-RNR1	CHRMT:514-515	hom	non-coding	
		MT-TF	CHRMT:514-515	hom	non-coding	
		NO GENE	CHRMT:30	het-ref	non-coding	
		MT-RNR2	CHRMT:1980	half	non-coding	
		MT-RNR1	CHRMT:1001	het-ref	non-coding	
	COSM6240	ELDR	CHR7:55249071	hom	non-coding	
	COSM6240	EGFR	CHR7:55249071	hom	non-coding	
IMPDH1:c.403-984delA		IMPDH1	CHR7:128402100	het-alt	non-coding	
IMPDH1:c.403-984_403-983delAA		IMPDH1	CHR7:128402099-128402100	het-alt	non-coding	

The **Variants Found** section denotes how many variants are displayed and how many are totally found. For example, 500/1000 Variants Found implies that 1000 variants were found but only 500 have been displayed in the table.

The Variants Annotated section denotes how many of the displayed variants have been annotated. Annotated variants have the following icon in the first column:



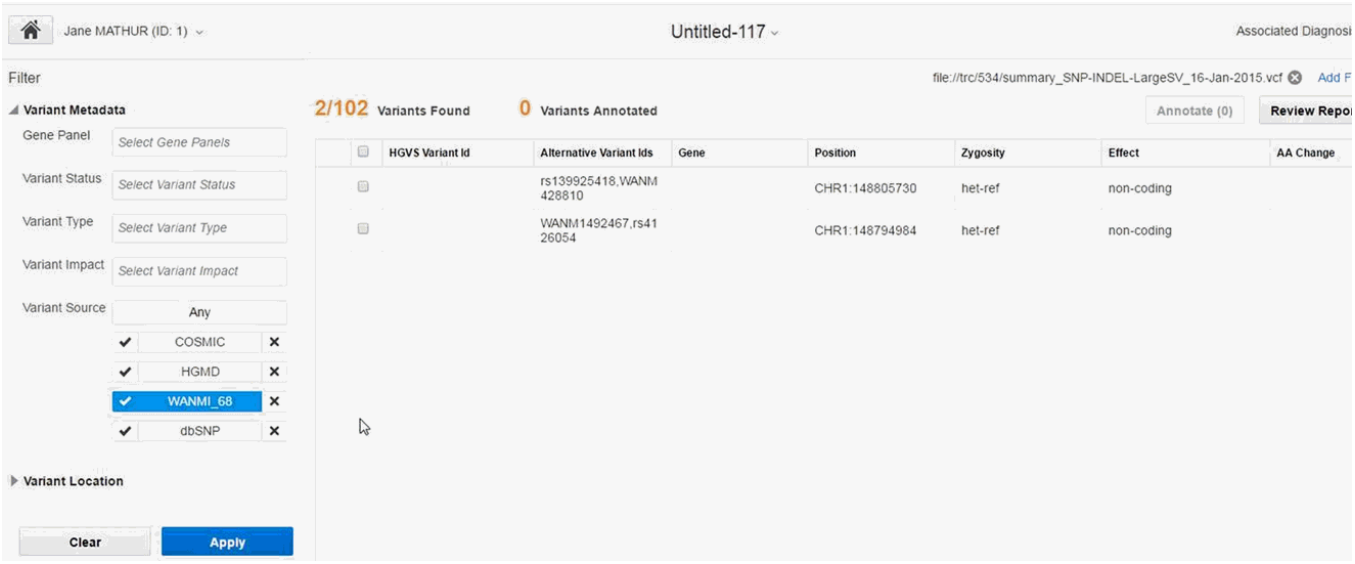
HGVS Variant Id	Alternative Variant Ids	Gene	Position	Zygosity
		CYP1B1-AS1	CHR2:38155074	hom

Note: A very small subset of variants may appear in multiple UI screens and reports to be associated with the placeholder record in the gene table with the name *NO GENE*.

A NO GENE gene is not a regular coding gene and can be safely ignored when displayed, with any mapped variant assumed to be *intergenic* unless mapped to another valid gene region.

3.4.3 Filtering Variants Based on Custom Knowledge Bases

You can filter variants based on custom knowledge bases in OHPM. You can include criteria from custom variant sources while filtering variants.


Jane MATHUR (ID: 1)
Untitled-117
Associated Diagnosi
Filter
file://trc/534/summary_SNP-INDEL-LargeSV_16-Jan-2015.vcf
Add F
Variant Metadata
2/102 Variants Found
0 Variants Annotated
Annotate (0)
Review Repo
Gene Panel
Select Gene Panels
Variant Status
Select Variant Status
Variant Type
Select Variant Type
Variant Impact
Select Variant Impact
Variant Source
Any
COSMIC
HGMD
WANMI_68
dbSNP
Variant Location
Clear
Apply
HGVS Variant Id
Alternative Variant Ids
Gene
Position
Zygosity
Effect
AA Change
rs139925418,WANM 428810
CHR1:148805730
het-ref
non-coding
WANM1492467,rs41 26054
CHR1:148794984
het-ref
non-coding

4

Reporting Workflow

This chapter describes how to perform various tasks to create reports. It includes the following topics:

4.1 Naming a Report

This task can be performed only by molecular pathologists.

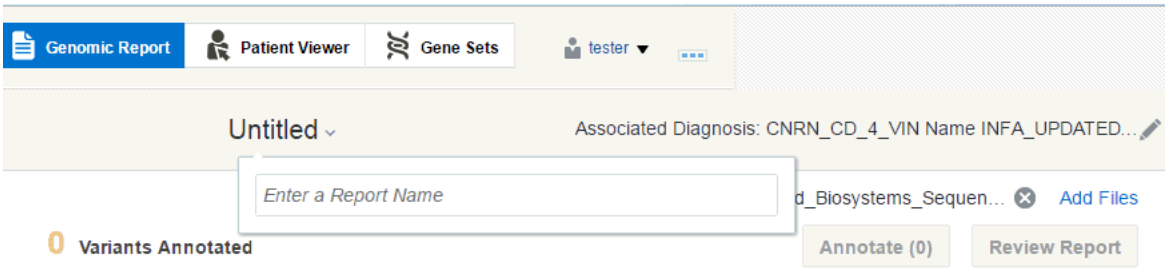
Before saving your report, it appears with the default name *Untitled*. It is auto-saved with an auto-generated name. Your report is a draft and is private to you until it is published.

The report name should be unique. It should not consist of alphanumeric characters and . - _ + : $ symbols.

Perform the following steps to name a draft genomic report:

1. When you first open a draft report, the name appears as shown:

2. Click the downward arrow next to the default user name.



3. Enter the report name. Click anywhere outside the box or presenter key to save the report.
4. The system validates the report name and saves it. It appears in the draft report section on the Home page.

4.1.1 Overwriting a Draft Report

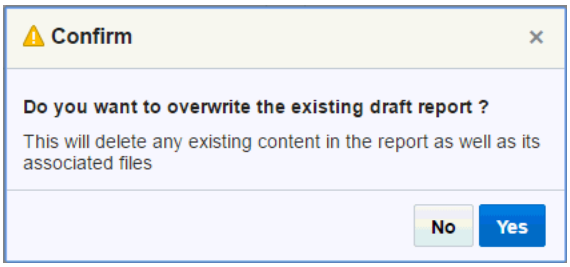
You can overwrite a draft report by:

Note:

- A draft report cannot be overwritten if the Target Report has an external N-of-1 report associated with it.
- Published reports cannot be renamed.

---

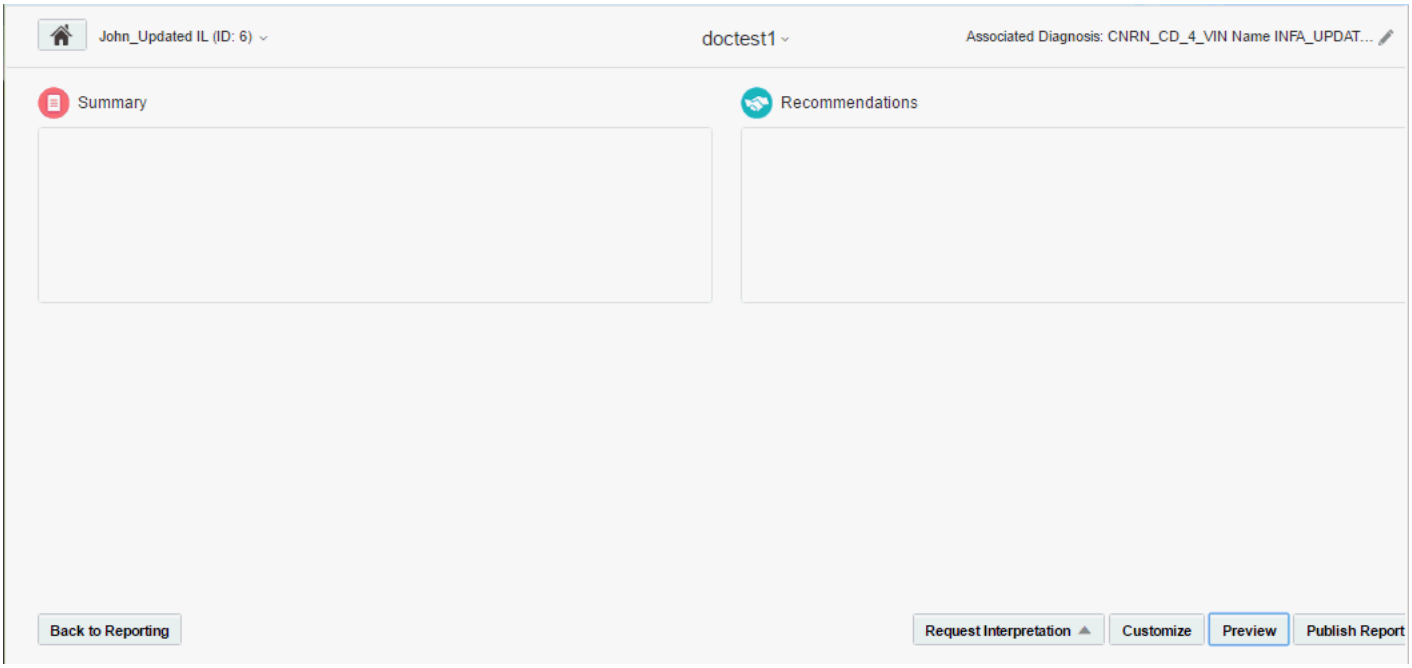
1. Create a new report for an order.
2. Enter a name of an existing report that you have created. Click anywhere outside the box or presenter key.
3. The following confirmation box appears:



4. Click **Yes** to overwrite the existing report. This will delete all content from the existing report and its associated files.

4.2 Viewing a Report

To view a report, click it in the Draft report section on the home page. On opening a draft report, the gene panels are not preselected.



The following options are available:

- **Summary** - Lets you enter a report summary.
- **Recommendations** - Lets you enter recommendations, if any.
- **Back to Reporting** - This option navigates to the Reporting pane where you can work with the report.
- **Request Interpretation** - This option lets you request external interpretation for selected variants in the report. Currently, the only external interpretation integrated in OHPM is N-of-One.
- **Customize** - This option lets you select the information that will appear when you publish the report.
- **Preview** - This option lets you preview the report before publishing it.
- **Publish** - This option publishes the report. Depending on whether you have set up the EHR integration, the report may also be sent to EMR and published there. While you will not see any difference, the actual report is sent to EMR and the physician can log in there to view the report.

4.3 Editing a Report

To edit a report, perform the following steps:

1. Click a draft report to open it in the Report Review pane.

   If you are in the Variant Filtering pane, click **Review Report** on the top right corner of the Variants list, to navigate the Report Review pane.

2. Click the pencil icon shown below to edit each section for a variant.

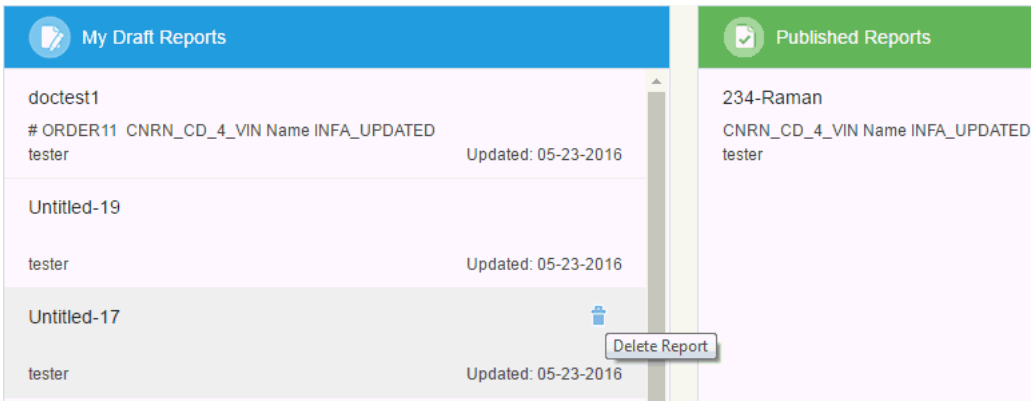
4.4 Customizing a Report

You can use this option to customize the published report and the Nof1 report when published standalone by clicking **Customize** on the bottom right of the draft report. The Customize Report screen appears.

Select the information that you want to add into the report and click **Apply**.

4.5 Deleting a Report

To delete a report, click the trashcan icon in the draft reports section.

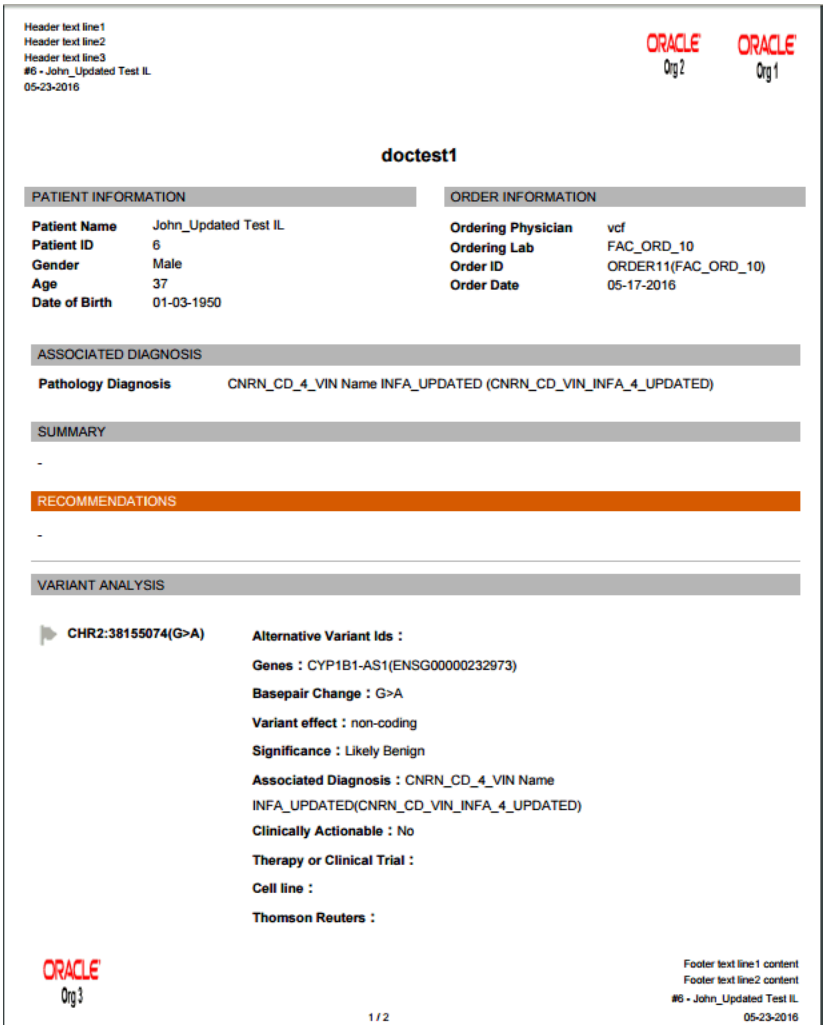


Note: You cannot delete a draft report that has an N-of-One report associated with it.

4.6 Previewing a Report

You can preview a report before publishing it by clicking **Preview** on the bottom right of a draft report. A PDF version of the report opens in a new window.

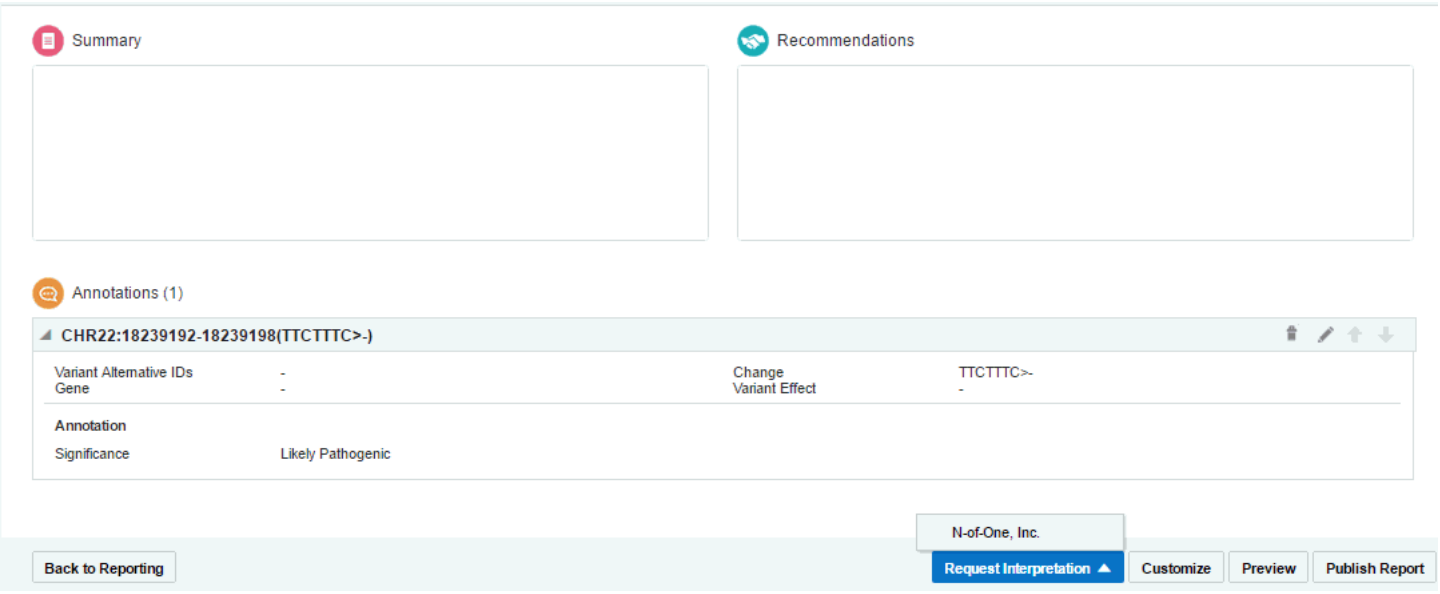
You can customize the report header and footer logo and text. For details, see the *Oracle® Healthcare Precision Medicine Administrator's Guide*.



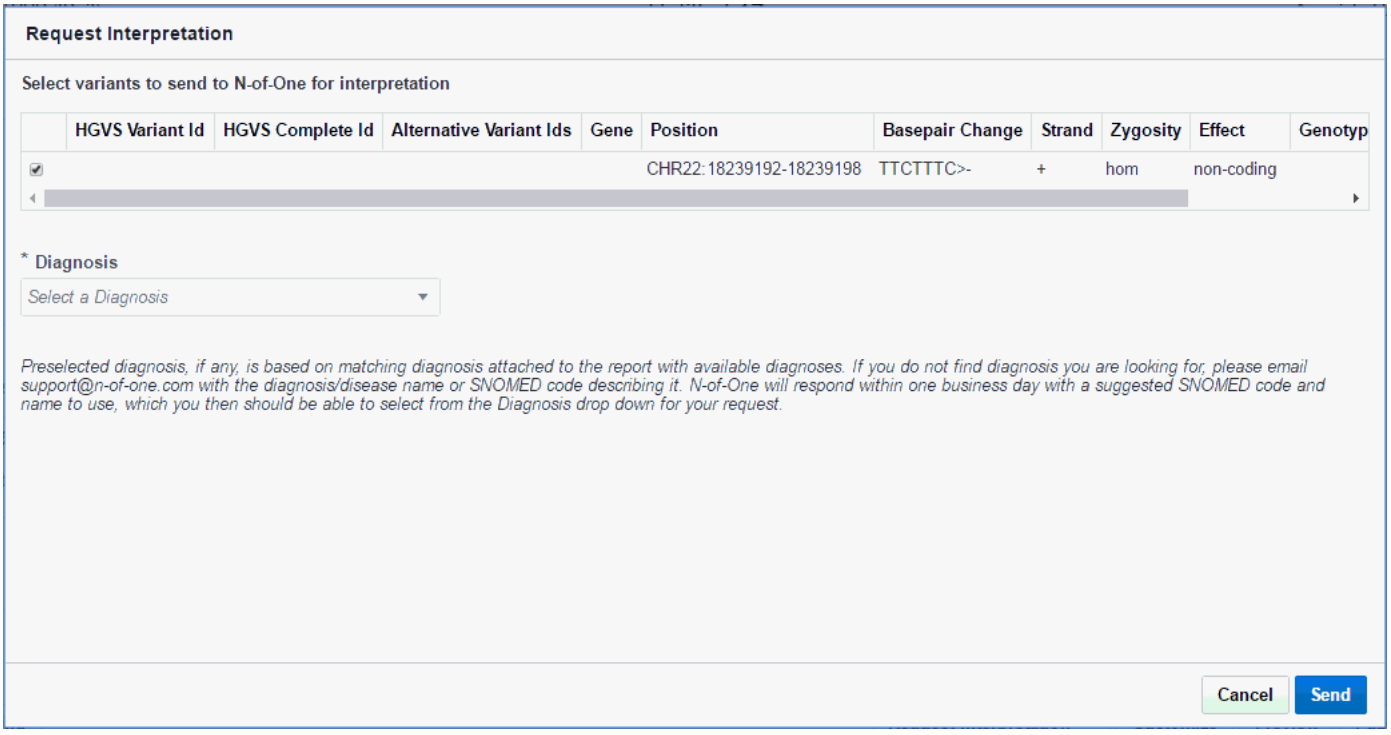
4.7 Requesting Interpretation

You can request third party interpretation (for example, Nof1) for your report. Perform the following steps to request interpretation.

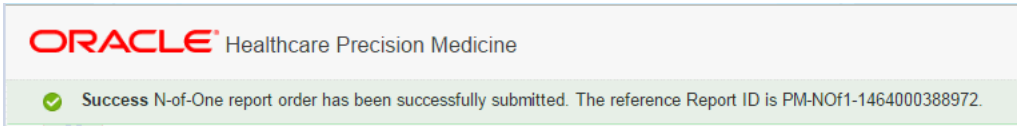
1. Open a draft report.
2. Click **Request Interpretation**.



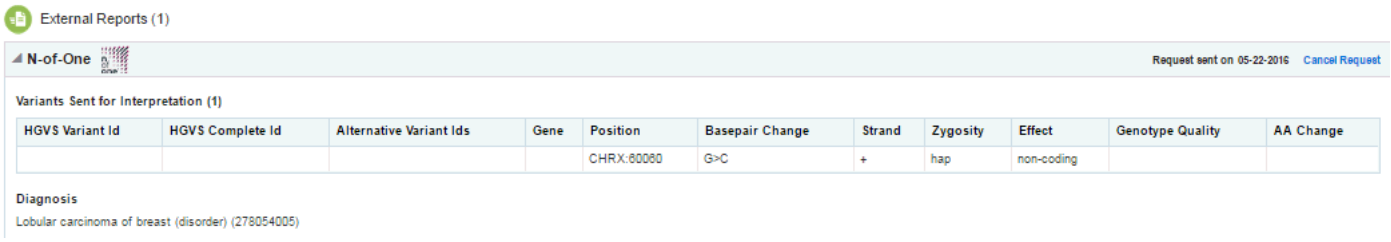
3. Select **N-of-1**. The Request Interpretation screen appears.



4. Select variants to send to N-of-1 interpretation.
5. Select a **Diagnosis**. If the diagnosis in the parent report matches ones from N-of-One, it gets automatically selected.
6. Click **Send**. You will receive a confirmation that your report has been submitted along with a reference number.

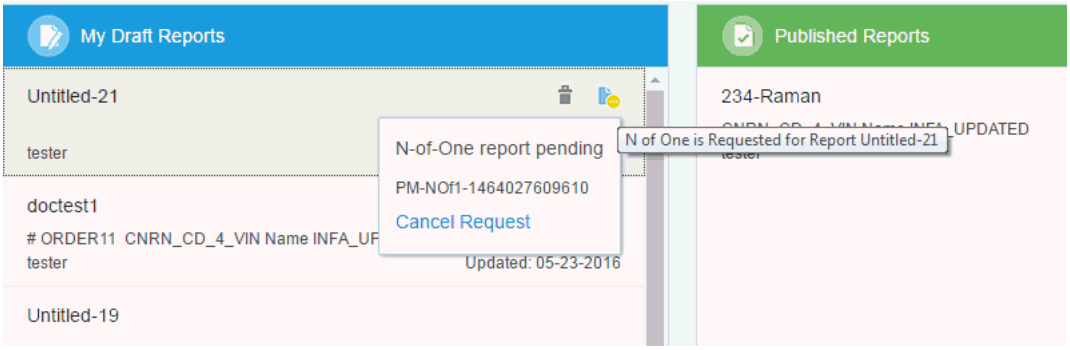


Also an entry is made in the Review Report view as follows:



You can cancel this interpretation request by clicking **Cancel Request** on the top right of the above entry. You will receive a confirmation message. Click **Yes**.

Also, the following icon appears in the draft reports section after requesting an external report. Clicking it displays the external report details.



4.8 Publishing a Report

You can publish your report by clicking **Publish** on the bottom right of the report. The published report then appears in the Published Reports section of the Home page. The report moves out of the Draft Report section once it is published.

Once published, your report will be visible to everyone with full access to the corresponding patient.

4.9 Summary and Recommendations

You can include your summary and recommendations for the clinician in the report. To edit these fields, open the report in the Report Review view. Click the field and enter your input.

5 Annotation

This section describes all the tasks related to annotating variants. It includes the following sections:

- Section 5.1, "Annotating Variants"
- Section 5.3, "Annotation Pane"
- Section 5.2, "Detailed Variant View"

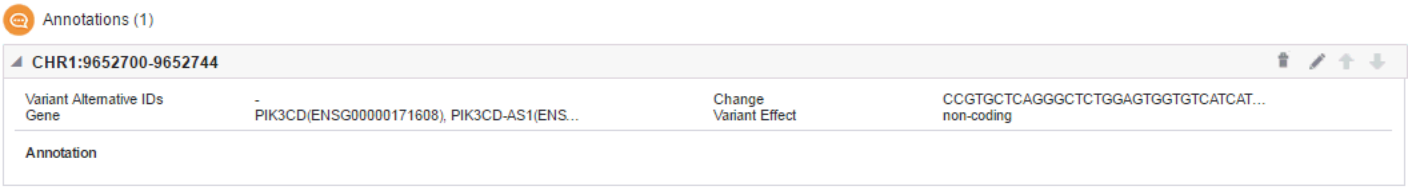
5.1 Annotating Variants

To annotate variants, perform the following steps:

1. Open the report in the reporting view.
2. Select the variants you want to annotate.
3. Click **Annotate** on the top right. The Annotation Pane appears.

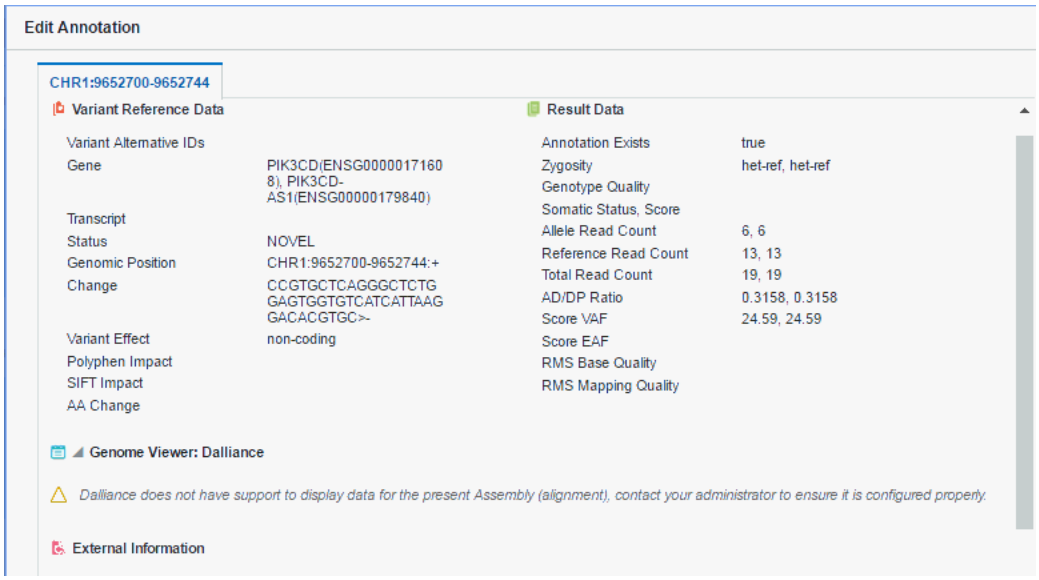
4. Enter details in the annotation pane.
5. Click **Save Annotation**. You will receive a confirmation.
6. Click **Yes**. The variant is annotated and the following icon appears next to it in the Reporting View.

The following entry appears in the Report Review pane.



You can delete or edit this information using the icons on the top right of this section.

5.2 Detailed Variant View



This view displays:

- important reference details and metadata about each variant
- details about the given variant based on the result file it appeared in

Only molecular pathologists and researchers have access to this feature.

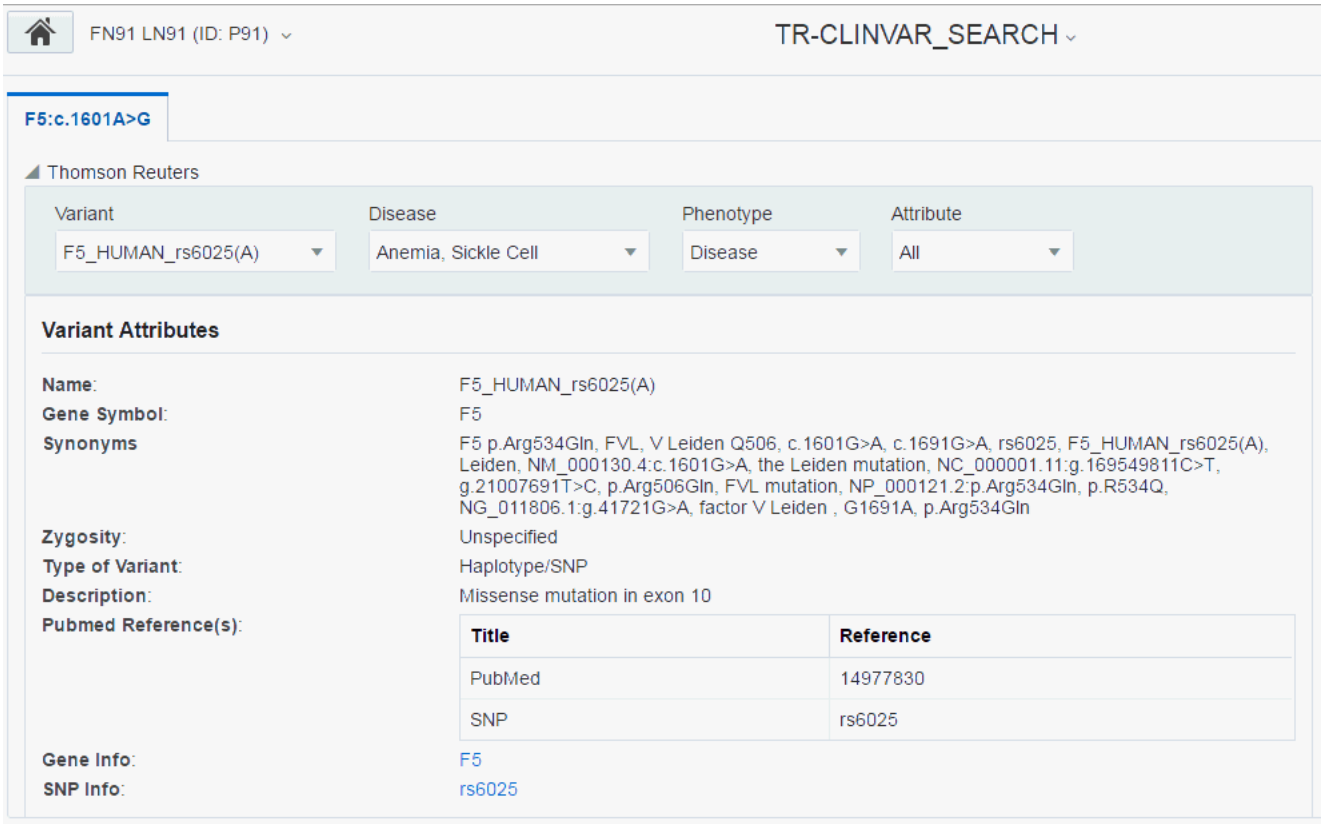
> **Note:** A very small subset of variants may appear in multiple UI screens and reports to be associated with the placeholder record in the gene table with the name *NO GENE*.
>
> A NO GENE gene is not a regular coding gene and can be safely ignored when displayed, with any mapped variant assumed to be *intergenic* unless mapped to another valid gene region.

It lists the following information:

- Variant Reference Data

  - Variant Alternative IDs - Displays any other names that the variant may have
  - Gene - The gene containing the variant
  - Transcript - The transcript being used to determine the impact
  - Status - Can be either known or novel
  - Position - The position of the variant within the chromosome
  - Change - Basepair change
  - Effect - Based on the preferred transcript, it is the effect the variant has on resulting protein. Among the effects are missense, nonsense, noncoding, frameshit and so on.
  - Polyphen Impact - The PolyPhen Impact of the variant
  - SIFT Impact - The SIFT impact of the variant
  - AA Change - Amino acid change
- Result Data
  - Annotation exists - Indicates whether variant is already annotated in the report
  - Zygosity - Variant zygosity. Similarity of alleles in an organism to reference.
  - Genotype Quality - Genotype Quality
  - Somatic Status, Score - Calculated ration of somatic likelihood
  - Allele Read Count - Number of reads that support the given allele
  - Reference Read Count - Number of reads that support the reference sequence
  - Total Read Count - Total number of reads
  - AD/DP Ratio
  - Score VAF - Positive or negative integer representing confidence in the call from CGI masterVar file
  - Score EAF - Positive integer representing confidence in the call from CGI masterVar file
  - RMS Base Quality - RMS base quality at this position
  - RMS Mapping Quality - RMS mapping quality at this position
- Genome Viewer: Dalliance - view variant and gene in embedded genomic browser screen against the annotation and reference or assembly information. The system checks if the Dalliance version of DNA display matches what is actively used for the given report, that is, the Preferred Version of DNA used for a given Assembly set.

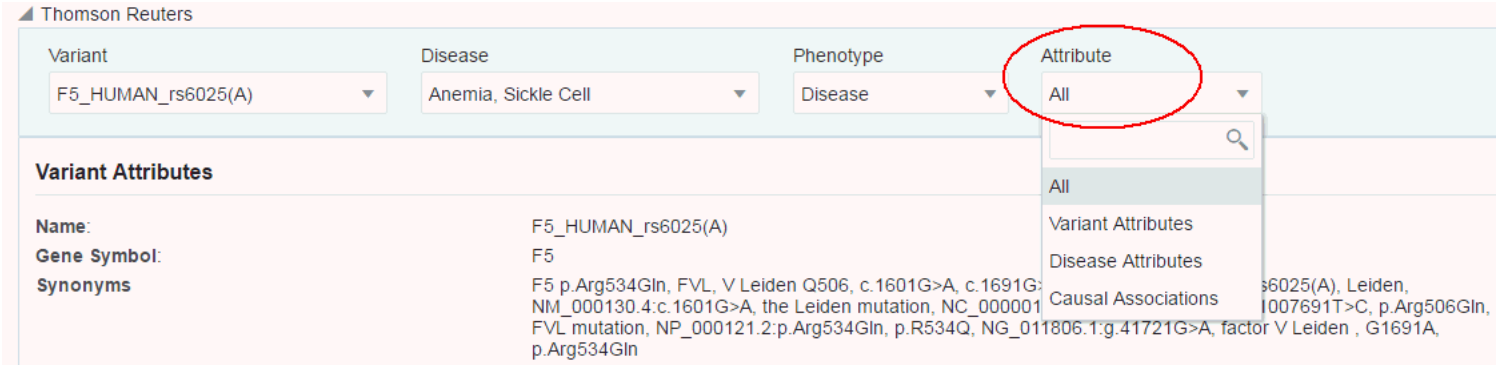
- External Information:
  - Thomson Reuters - If subscribed, displays the reference information for a selected variant. To view the view Thomson Reuters reference information, select the Variant and Disease from the respective drop-down lists.



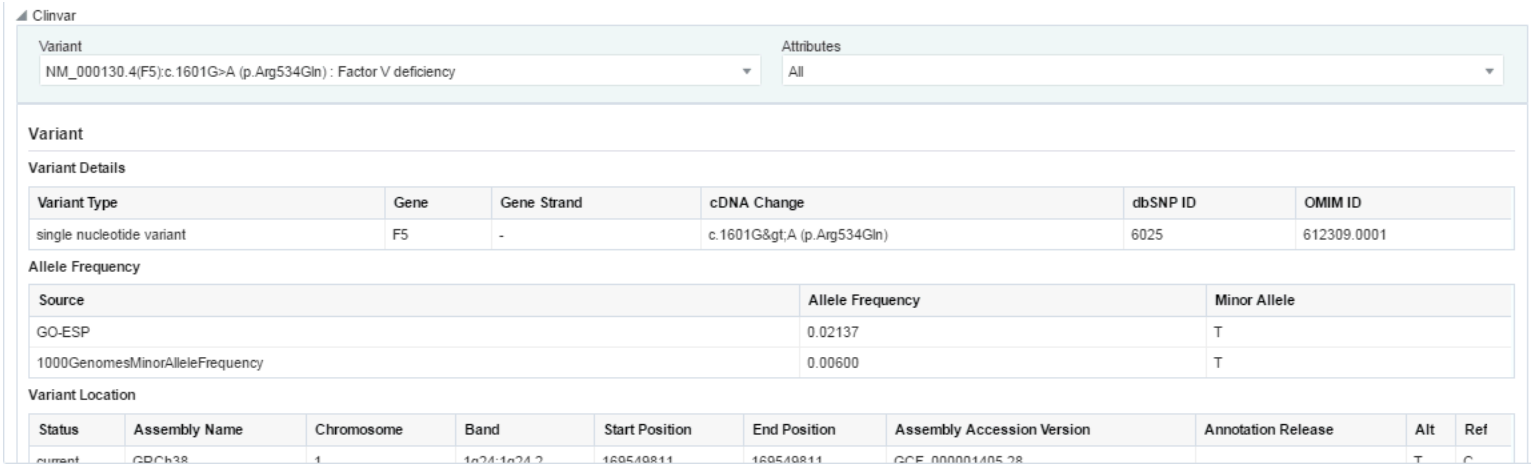
The following sections are displayed:

* Variant Attributes
* Disease Attributes
* Casual Associations

You can select which sections you want to view using the **Attributes** drop-down list. By default, all sections are displayed.



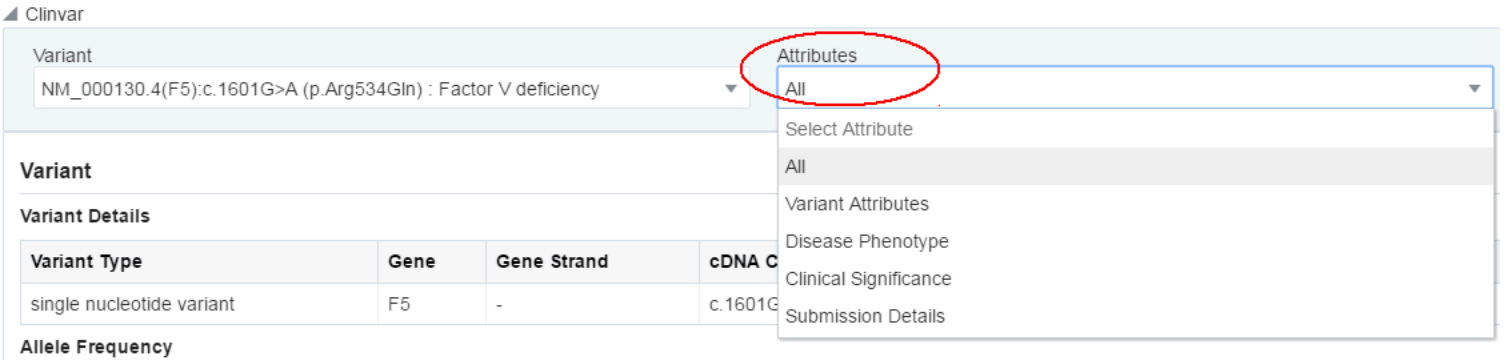
– ClinVar - If subscribed, displays the reference information for a selected variant. Select a variant from the Variant drop-down list to view ClinVar reference information.



The following sections are displayed:

* Variant - displays Variant Attributes including Variant Details, Allele Frequency, Variant Location
* Disease Phenotype
* Clinical Significance
* ClinVar Submission Details

You can select which sections you want to view using the **Attributes** drop-down list. By default, all sections are displayed.



5.3 Annotation Pane

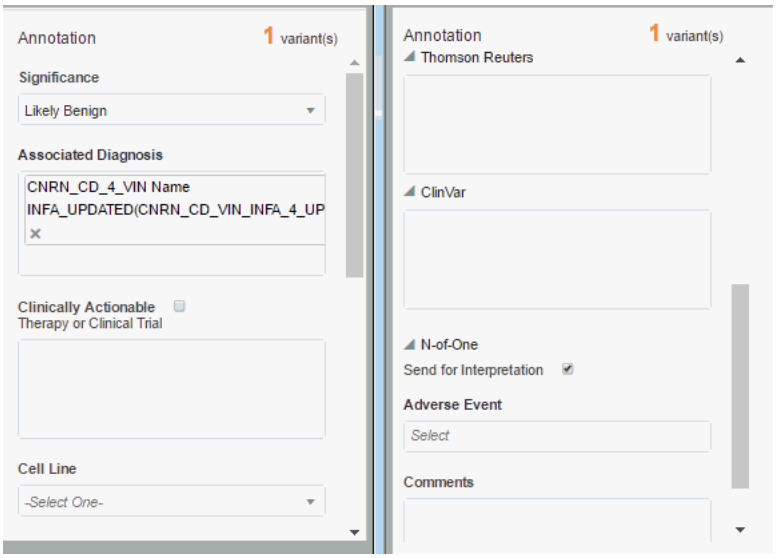
The Annotation Pane lets you annotate variants with your comments, functional labels and so on. This pane contains the following default fields and can be fully customized by the administrator:

- Significance - has the values Pathogenic, Likely Pathogenic, Benign, Likely Benign, Unknown Significance. You can select any one or leave this blank.
- Associated Diagnosis - diagnosis that is associated with the variant.
- Clinically Actionable - this marks a variant as clinically important and highlights at the top of the report

- Therapy or Clinical Trial - Enter any clinical trials or therapies that are currently available
- Cell Line - has the values Somatic, Germline, Unknown. You can select one of them.
- Annotation for Thomson Reuters, ClinVar - you can select relevant information from Thomson Reuters and ClinVar in the Tabular View and add this information to the annotations.

> **Note:** You must subscribe to Thomson Reuters and ClinVar to access their reference information.

- N-of-One - Selecting the check box **Send for Interpretation** will mark this variant as a candidate to send for N-of-One interpretation.
- Adverse Events - select adverse events, if any, for example, Severe Allergic Reaction.
- Comments - enter your comments on the report



6

Patient Viewer

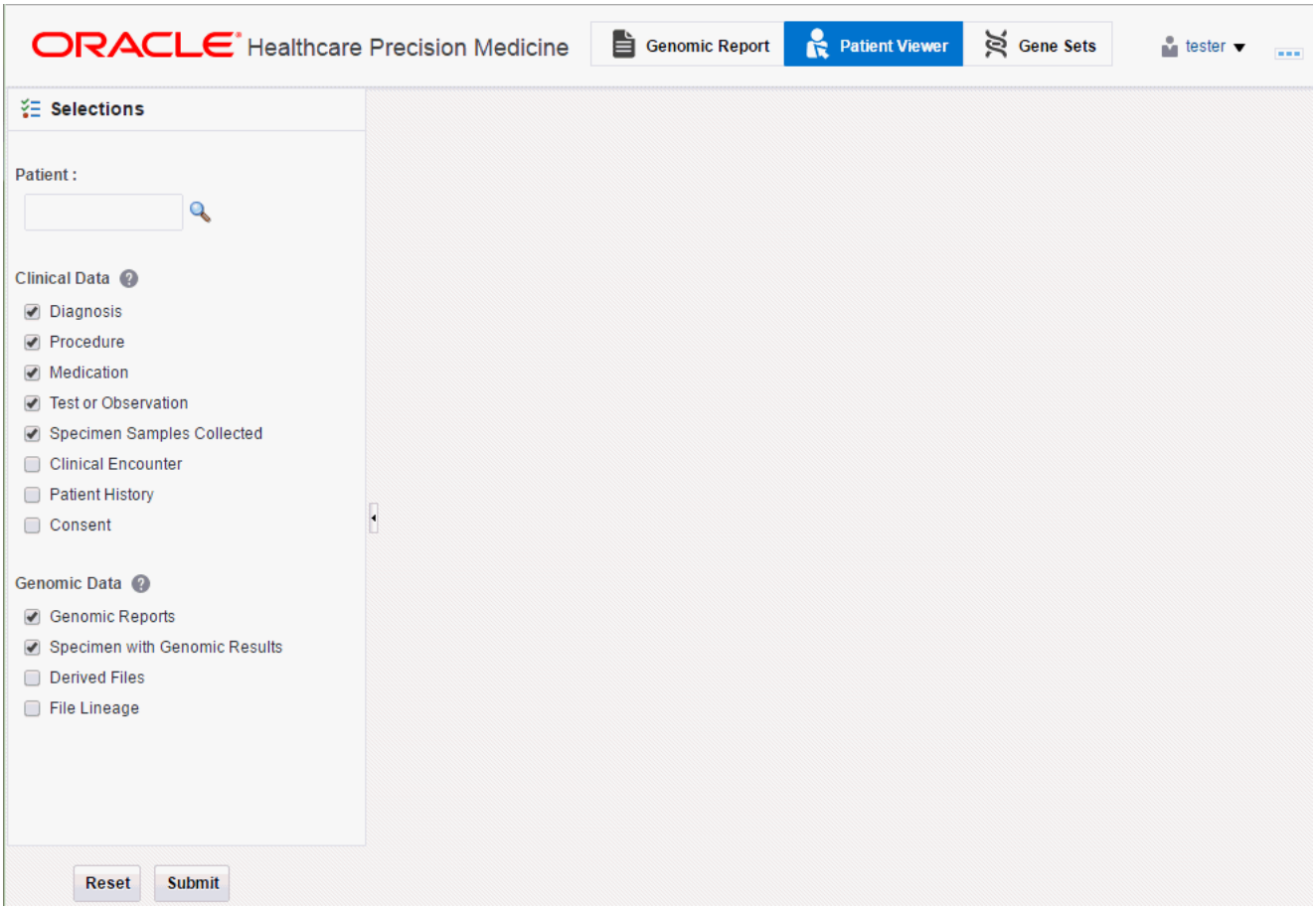
This chapter describes the patient viewer tab in OHPM. It contains the following sections:

6.1 Introduction

This tab lets you view detailed patient information.

When you click the Patient Viewer tab from the reporting view, you will not see patient details. You must search for the patient to see their details.

6.2 Viewing Patient Details



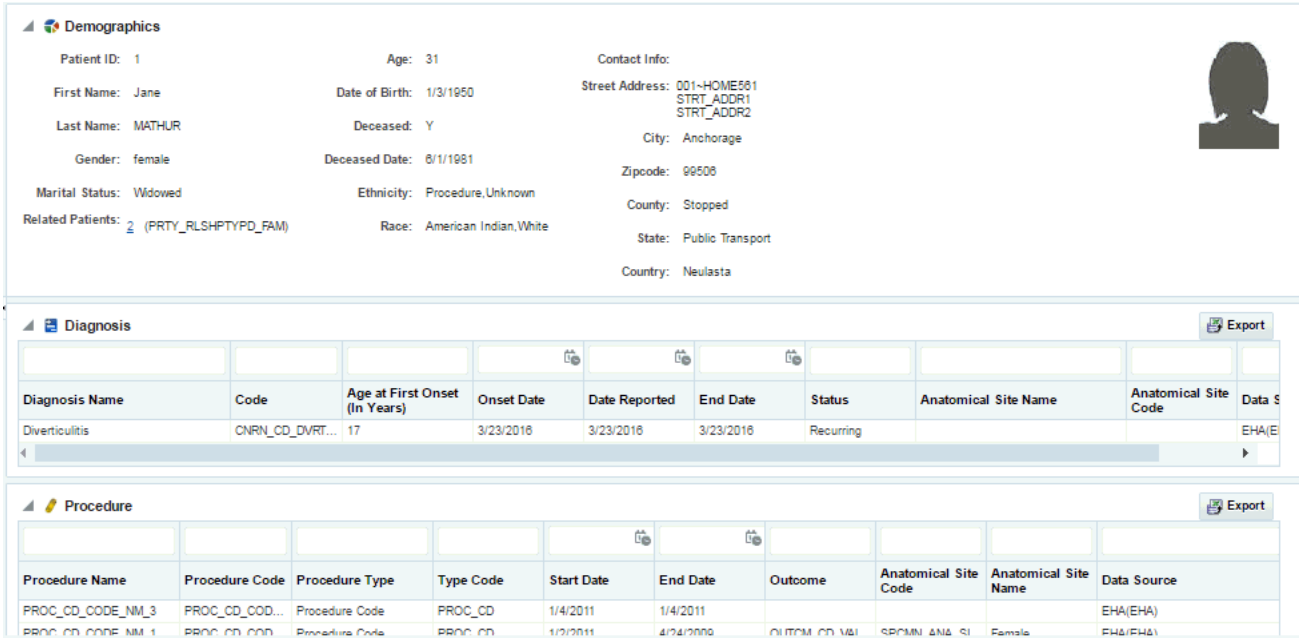
1. Enter a patient ID in the **Patient** field. A drop-down list displays matching results.

   You can search for a patient by clicking the Search icon.

2. Select the **Clinical Data** and **Genomic Data** categories you want to view for the patient.

3. Click **Submit**. The patient data is displayed.

   You can export information from each of these reports to a Microsoft Excel format by clicking **Export**.



6.3 Reports Available in the Patient Viewer

The following reports can be viewed for a patient in the patient viewer.

Clinical Data

- Demographics
- Diagnosis
- Procedure
- Medications Taken
- Test or Observation
- Specimen Samples Collected
- Clinical Encounter
- Patient History
- Consent

Genomic Data

- Genomic Reports
- Specimen with Genomic Results
- Derived Files
- File Lineage

6.3.1 Clinical Data

The attributes displayed for each section are listed below:

- **Demographics**

Patient ID, First Name, Last Name, Gender, Marital Status, Related Patients, Age, Date of Birth, Deceased, Deceased Date, Ethnicity, Race, Street Address, City, Zip code, County, State, Country

- **Diagnosis**

  Diagnosis Name, Code, Age at First Onset (in Years), Onset Date, Date Reported, End Date, Status, Anatomical Site Name, Anatomical Site Code, Data Source

- **Procedure**

  Procedure Name, Procedure Code, Procedure Type, Type Code, Start Date, End Date, Outcome, Anatomical Site Name, Anatomical Site Code, Data Source

- **Medications Taken**

  Medication Name, Medication Code, Description, Start Date, End Date, Dosage, Dosage Units, Outcome, Data Source

- **Test or Observation**

  Test or Observation Name, Test or Observation Code, Type, Date, Numeric Result (Units) [Reference Range], Result (text), Data Source

- **Specimen Samples Collected**

  Specimen Type Name, Specimen Type Code, Date Collected, Anatomical Site Name, Anatomical Site Code, Amount, Units, Data Source

- **Clinical Encounter**

  Encounter Id, Encounter Type, Start Data, End Date, Additional Details (clicking this provides more details about the encounter like Event Name, Event Type, Start Date, End Date, Location Name (Location Type)), Data Source

- **Patient History**

  History or Risk Name, History or Risk Code, Type, Start Date, End Date, Frequency (Units), Amount (Units), Text Value of Code, Applicable To, Data Source

- **Consent Forms Signed**

  Consent Type Name, Consent Type Code, Description, Consent Status Name, Status Code, Start Date, End Date, Data Source

6.3.2 Genomic Data

Genomic data is displayed in four sections as follows:

Table 6–1 Genomic Report

Column Heading	Definition	Sample Value or Values
Report Id	Report Name	Titled Report
Diagnosis	Diagnosis in the order	Diverticulitis
Genetic Test	Genomic tests performed	Panel_13
Report Author	User that created the report	user1
Publish Date	Date the report was published	6/20/2016
Order ID (Lab)	Order ID from the lab	Order1

Table 6–2 Specimens with Genomic Results

Column Heading	Definition	Sample Value or Values
Specimen Id	Specimen belonging to the selected patient or subject	HG00096
Specimen Vendor Id	Specimen Vendor for that specimen	Vcf
Version Label	Represents Assembly Version (DNA reference version against which this data was loaded)	GRCh37(V68)
Sequence Variants Results	Whether the sample has sequence variants results	Yes / No
Copy Number Variation Results	Whether the sample has copy number variants results	Yes / No
Single Channel Microarray Results	Whether the sample has single channel results	Yes / No
Dual Channel Microarray Results	Whether the sample has dual channel results	Yes / No
Rna-Seq Expression Results	Whether the sample has rna sequencing results	Yes / No

Table 6–3 Derived Files

Column Heading	Definition	Sample Value or Values
Filename	Filename including path of the genomic file stored including path	C:/John_specimen01.vcf
File Size in MB	Size of the File in MB	Numeric, positive integer
File URI	URI of the file	File://trc/abc.maf
Alternate Filepath	The FTP path of the file	
File Type, Version	Type of file and Version	Variant Call Format, 4.1
Result Type	Type of result data in the file	Sequencing, Copy Number Variation, Gene Expression (2-channel or single channel)
Alignment Version (DNA Reference Version)	Represents Assembly Version (DNA reference version against which this data was loaded)	GRCh37(v68)
Total Number of Specimen in File	Total number of specimen that the file contains where not all specimen belong to the selected patient	Numeric, positive integer
Last Updated	When record was last updated	19-Mar-2012

Table 6–4 File Lineage

Column Heading	Definition	Sample Value or Values
Parent Filename	Parent Filename including path of the genomic file stored including path	C:/John_specimen01.BAM
File Size in MB	Size of the File in MB	Numeric
File URI	URI of the file	File://trc/abc.maf
Alternate Filepath	The FTP path of the file	

Table 6–4 (Cont.) File Lineage

Column Heading	Definition	Sample Value or Values
File Type, Version	Type of file and Version	Binary Alignment Map, 1.0
Alignment Version (DNA Reference Version)	Represents Assembly Version (DNA reference version against which this data was loaded)	GrCH37
Last Updated	When record was last updated	19-Mar-2012
Derived Child Files: File - Specimen Id, Vendor Id	Information about Derived Results files that have their lineage based on the particular Low Level file.	C:/John_specimen01.vcf - HG00096_1,HarvardLab1

7

Gene Sets

This section describes the gene set tab in OHPM. It contains the following sections:

7.1 Introduction

The Gene Sets tab is a way to collect genes into groupings or lists. There will be a list of genes you work with regularly, which may be as small as a couple of genes or large, consisting of hundreds of genes.

Often you may keep several such sets, each characterizing a group of genes with particular attributes; for example, transcription factors, genes involved in some regulation mechanism, genes that have been implicated to contribute to a particular characteristic and so on. The concept of Gene Set lets you group genes into convenient *collections* for reuse.

7.2 Gene Sets List

My Gene Sets section lists the recently updated gene sets. Clicking the selected gene sets loads it in the Manage Gene Sets/Manage window.

7.3 Adding or Editing Gene Sets

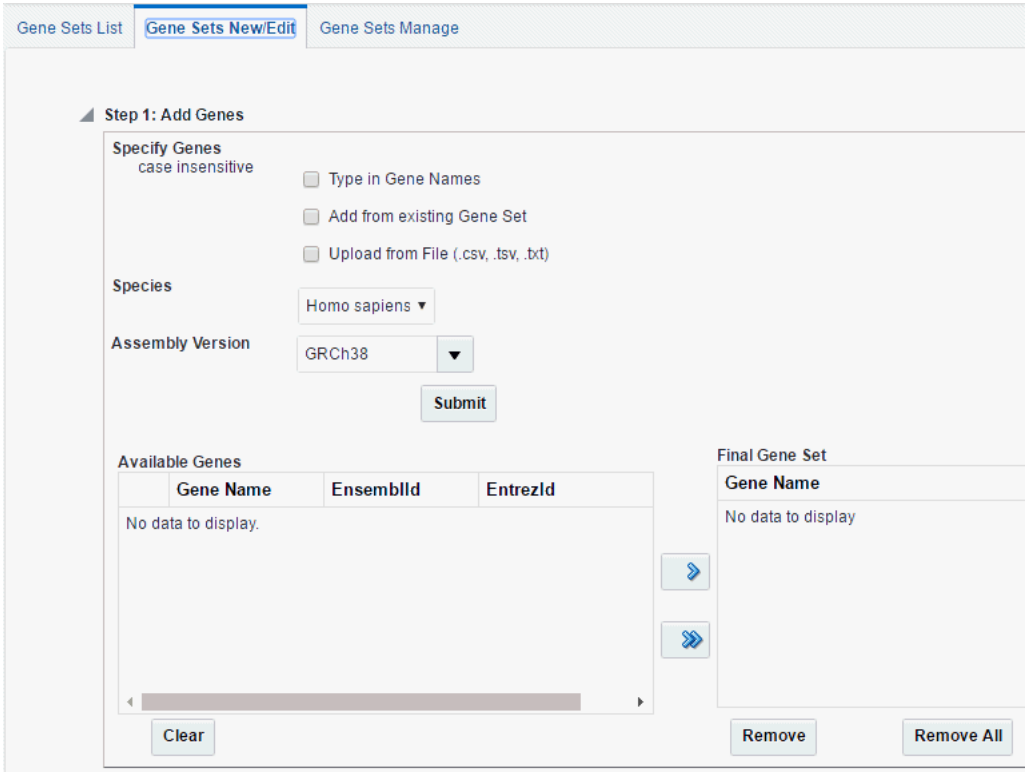
The Gene Sets New/Edit section helps you group genes as a set. You can group a few genes for quick search retrieval or for use in a cohort query. For example, if you have a set of 10 genes that you plan to work with or always search for results based on genes from within this particular array of 10, you can create a new Gene Set to collect these 10 genes into one group.

A gene can be part of many different Gene Sets. Also, you can create many different gene sets, each gene set with a different combinations of genes.

Note:

1. There are no restrictions regarding genes that can be included in any particular Gene Set. You can mix genes from multiple species, or assembly versions.
2. Gene Sets are Private only and cannot be shared among users.
3. Gene Set names are not case- sensitive.
4. The file size limit for the **Upload from File** option is less than 5MB when genes are matched using Equals. When using Contains or Starts With option, the list of genes cannot be longer than 512 characters.

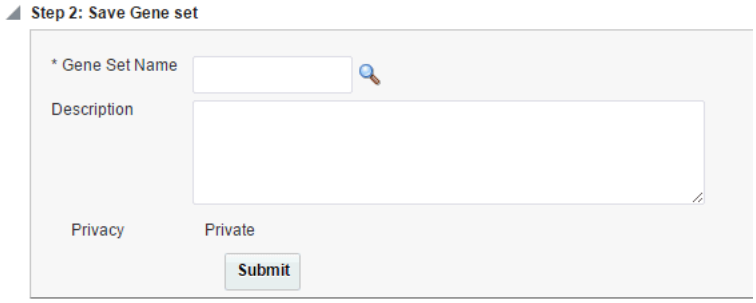
Perform the following steps to create a new gene set:



1. Specify genes either by:
   - selecting **Type in Gene Set**. You can search for genes using their Ensembl or HUGO names. You can enter multiple gene names separated by space, comma or semicolon.
   - selecting **Add from Existing Gene Set**.
   - selecting **Upload from File**. Select a file from your desktop where the genes are delimited by comma, space or tab.
2. Select the **Species**.
3. Select the **Assembly Version**.
4. Click **Submit**.
5. A list of genes appears in the **Available Genes** section. Using the arrow buttons, move the required genes to the **Final Gene Set** section. These are the genes that will comprise a gene set.

You can select to move all genes from the left hand side panel to the right hand side panel using the following icon:

6. After you have selected all required genes, enter a **Gene Set Name**. You can either preserve the selection as a new Genet Set or save over an existing one.

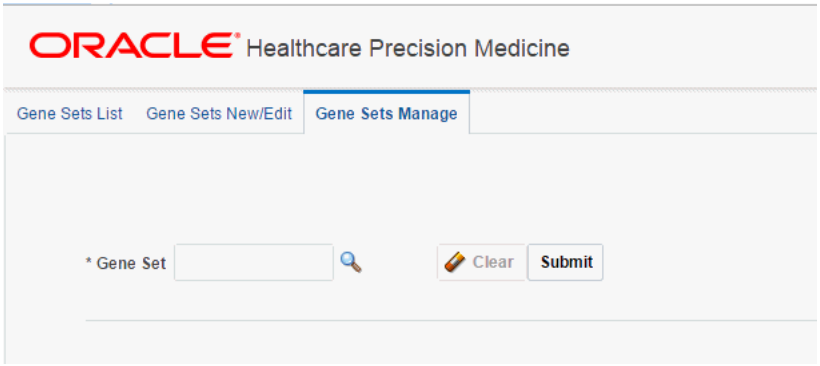


7. Enter a description for the gene set.
8. Click **Submit**. Your gene set is created.

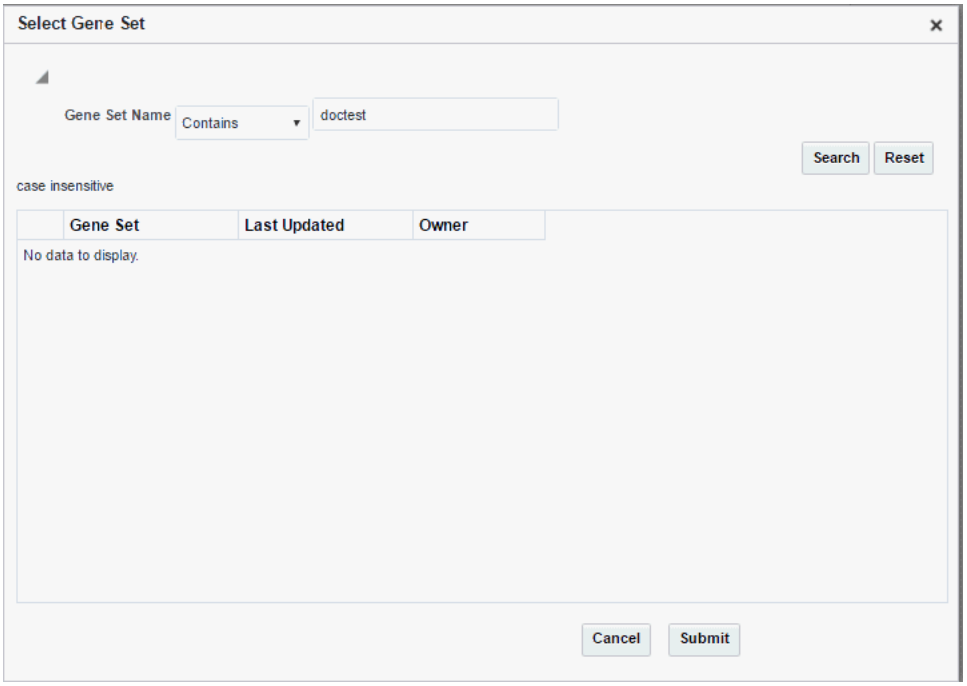
7.4 Managing Gene Sets

The Gene Sets Manage screen lets you view the individual genes (members) included in a given Gene Set and its metadata. You can select a specific Gene Set to view by using its name and click **Submit** to view the Gene Set's detailed information.

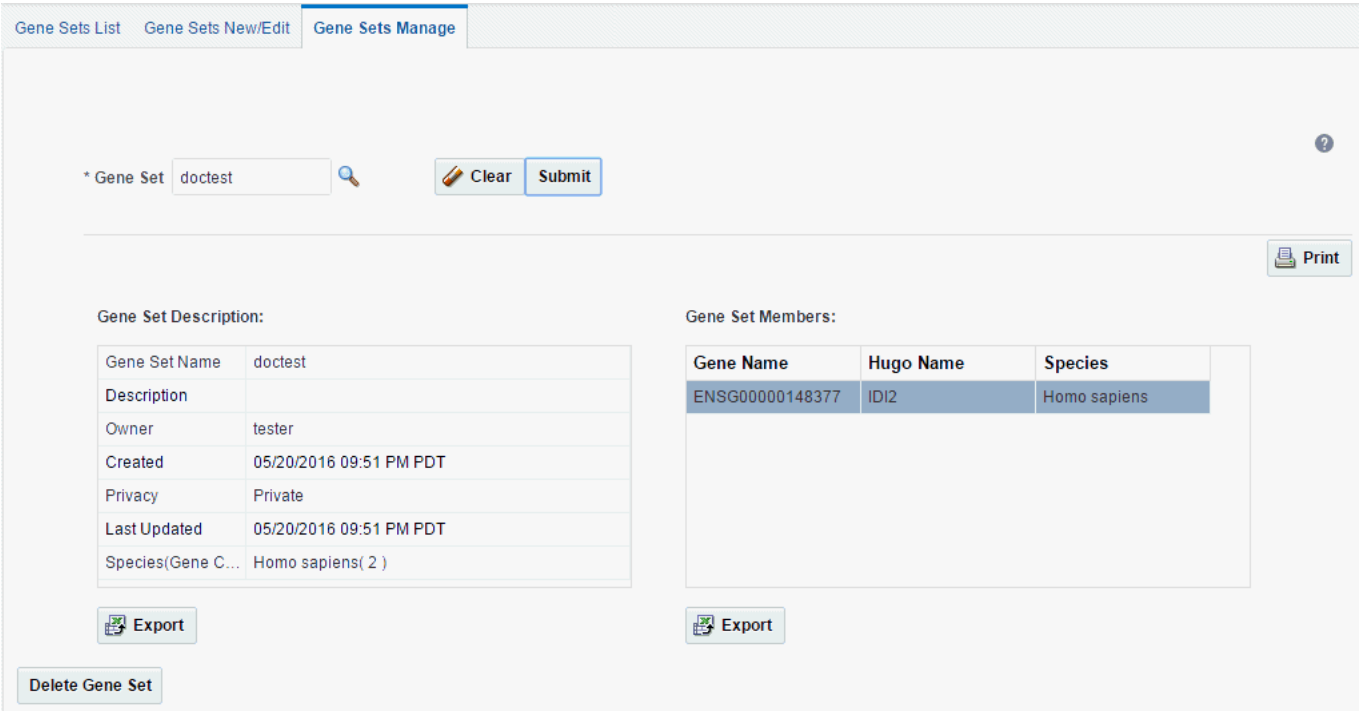
1. Enter a **Gene Set**.



You can search for a gene set by clicking the magnifying glass icon.



2. After selecting the gene set, click **Submit**. Detailed information for the gene set is displayed.



Each Gene Set's metadata includes the name, description given by the user, owner of the gene set, privacy setting, the creation and update dates and summary of how many genes are in a gene set.

7.4.1 Exporting a Gene Set

You can export the gene set data to a Microsoft Excel worksheet (.xls) file. Perform the following steps to export a gene set:

1. In the Gene Set Manage tab, search for the gene set you want to export.
2. Click **Export** to export the Gene Set Description or Gene Set Data.
3. You will receive a warning that the export process will take a while. Click **OK** to proceed or **Cancel** to stop the export.

Finally, you can delete a Gene Set using the **Delete** button. A confirmation box appears to ensure you are performing the proper action.

7.4.2 Printing Gene Set Data

Perform the following steps to print gene set data:

1. In the Gene Set Manage tab, search for the gene set you want to print.
2. Click **Print** on the right. Your printer settings appear.
3. Select the printer and click **OK**.

7.4.3 Deleting a Gene Set

Perform the following steps to delete a gene set:

1. In the Gene Set Manage tab, search for the gene set you want to delete.
2. Click **Delete Gene Set**.
3. A confirmation box appears. Click **Yes** to delete the gene set.

> **Note:** This deletion will only soft-delete a Gene Set. This implies that the actual Gene Set record is still in the database, but it can only be restored with the help of a System Administrator.