

# Oracle® Healthcare Foundation

New Features Guide

Release 7.2.1

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This guide explains the new features added to Oracle Healthcare Foundation (OHF) release 7.2.1.

- [Data Model Updates](#)
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## Data Model Updates

- [Interface Tables Added](#)
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## Interface Tables Added

The following interface tables have been added to the data model:

**Table 1** *Interface Tables Added*

Subject Area	Table Name
Accounting and Financial Reporting	HDI_BUDG_LED_GRP
Accounting and Financial Reporting	HDI_LED_GRP
Accounting and Financial Reporting	HDI_LED_GRP_LED
Patient	HDI_RELTD_PT

## Interface Tables Updated

The following interface tables have been modified:

- HDI\_ARC
- HDI\_CHRTFLD\_COMB
- HDI\_FSCL\_PD
- HDI\_JRNL

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- HDI\_JRNL\_LN
- HDI\_LED\_BAL
- HDI\_RX
- HDI\_VCHR
- HDI\_VCHR\_PAYMT

## Attributes Obsoleted

**Table 2** *Attributes Obsoleted*

Table Name	Column Name
HDI_CHRTFLD_COMB	BUDG_REF
HDI_CHRTFLD_COMB	CLAS_FLD

## Application Toolkit Updates

- [Data Lineage](#)
- [Self-Service Analytics Usage Tracking](#)

### Data Lineage

End-to-end data lineage report (from HDI to HDM to HCD to OBIEE Reports) in Self-Service Analytics to track the data transformation/data flow from Interface Tables to BI report.

### Self-Service Analytics Usage Tracking

Usage tracking for Self-Service Analytics supports tracking of who, what, when and how reports/dashboards are accessed.

## Cohort Data Mart (CDM) Updates

- [Golden Patient Record](#)
- [New Relationships for Cancer Registry Data Analysis](#)

### Golden Patient Record

Source systems may use different patient identifiers to refer to the same patient. The Golden Patient Record or Master Person Index (MPI) maps all identifiers that belong to the same patient to a common unique identifier. This Golden/MPI identifier is then used to track each patient's records across all the different source systems, enabling CDM to support a single patient record that represents the most accurate and current patient information and to view all the clinical data associated with that patient.

This section explains how to:

- [Enable or Disable the Golden Patient Record Feature](#)
- [Populate Golden Patient Mappings in HDI](#)
- [Load Golden Patient Mappings to HDM](#)

- [Load Golden Patient Mappings to CDM](#)
- [Cascading Soft Deletions and Mapping Updates](#)

For additional information, refer to the *Administrator's Guide*.

### Enable or Disable the Golden Patient Record Feature

The GOLDEN\_RECORD\_PT\_RLSHPTYP\_CODE parameter has been added to the Cohort Data Mart C\_LOAD\_PARAM table to enable or disable the extraction of Golden Patient records into the patient dimension (W\_EHA\_RESEARCH\_PATIENT\_D). By default, the feature is disabled (the parameter is set to NULL).

**Table 3 C\_LOAD\_PARAM Settings for Enabling and Disabling Golden Patient Record**

Column Name	Column Value
ENTITY_NM	W_EHA_RESEARCH_PATIENT_D
PARAM_DESC	This parameter enables or disables the Golden Patient Record functionality in the application. To enable this functionality, provide a valid code value corresponding to HDM's Related Patient.Patient Relationship Type attribute (HDM_RELTD_PT.PT_RLSHPTYP_ID). To disable this functionality keep this column Null. By default the value of this parameter is Null, indicating that the functionality is disabled.
PARAM_NM	GOLDEN_RECORD_PT_RLSHPTYP_CODE
PARAM_VAL	NULL

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**Note:** The Golden Patient Record is a one-time initial configuration and must remain consistent during incremental loads. If you decide to change the Golden Patient Record configuration between data loads, reload the CDM by truncating the entire data mart.

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### Populate Golden Patient Mappings in HDI

The HDI\_RELTD\_PT table has been added to the HDI schema to support data acquisition of non-golden (source) to golden (target) patient ID mappings.

#### Invalid mappings:

- **One-to-many mappings** - If a non-golden (source) record identifier is mapped to multiple golden (target) record identifiers, the mappings will be considered invalid and logged in the C\_ETL\_RELATED\_PT\_EXCPTN exception table during CDM load.
- **Target patient attribute contains non-golden patient identifier** - If a non-golden patient identifier is mapped to another non-golden patient identifier, the mapping is considered invalid and logged in the C\_ETL\_RELATED\_PT\_EXCPTN exception table during CDM load.
- **Golden patient identifier mapped to another golden patient identifier** - If a golden patient identifier is mapped to another golden patient identifier, the mapping is considered invalid and logged in the C\_ETL\_RELATED\_PT\_EXCPTN exception table during CDM load.
- **Switching a golden record to a non-golden record** - Switching a golden patient record to a non-golden patient record is invalid.

### Load Golden Patient Mappings to HDM

The new HDM\_RELTD\_PT table has been added to the HDM schema to support non-golden to golden patient ID mappings.

Use the new wf\_SIL\_DI\_HDI\_RELTD\_PT ETL to load data from HDI\_RELTD\_PT to HDM\_RELTD\_PT.

### Load Golden Patient Mappings to CDM

The C\_ETL\_RELATED\_PT intermediate table has been added to the HDM schema to support processing of the mapping records in HDM\_RELTD\_PT, before loading the CDM dimension and bridge tables.

The C\_ETL\_RELATED\_PT\_EXCPTN exception table has been added to the HDM schema to log invalid mapping records.

Use the new wf\_SIL\_CDM\_C\_ETL\_RELATED\_PT ETL to load the data from HDM\_RELTD\_PT to C\_ETL\_RELATED\_PT, which will then be referred in CDM datamart ETLs to resolve the non-golden to golden patient records. The C\_ETL\_RELATED\_PT table must be loaded before the W\_EHA\_RESEARCH\_PATIENT\_D dimension, as it is a driving entity.

The following CDM ETLs have been updated:

**Table 4 Updated CDM ETLs**

Table Name	ETLs
W_EHA_RESEARCH_PATIENT_D	wf_SIL_CDM_W_EHA_RESEARCH_PATIENT_D_FULL wf_SIL_CDM_W_EHA_RESEARCH_PATIENT_D
W_EHA_SUBADMN_PATIENT_H	wf_SIL_CDM_W_EHA_SUBADMN_PATIENT_H_FULL wf_SIL_CDM_W_EHA_SUBADMN_PATIENT_H
W_EHA_PT_GRP_PATIENT_H	wf_SIL_CDM_W_EHA_PT_GRP_PATIENT_H_FULL wf_SIL_CDM_W_EHA_PT_GRP_PATIENT_H
W_EHA_OBSV_PATIENT_H	wf_SIL_CDM_W_EHA_ORDER_PATIENT_H_FULL wf_SIL_CDM_W_EHA_ORDER_PATIENT_H
W_EHA_PT_FAM_RLSHP_DHL	wf_SIL_CDM_W_EHA_FAMBR_RLSHP_TYPE_D_FULL wf_SIL_CDM_W_EHA_FAMBR_RLSHP_TYPE_D
W_EHA_SPECIMEN_PATIENT_H	wf_SIL_CDM_W_EHA_SPECIMEN_PATIENT_H_FULL wf_SIL_CDM_W_EHA_SPECIMEN_PATIENT_H
W_EHA_PT_HISTORY_PT_H	wf_SIL_CDM_W_EHA_PT_HISTORY_PT_H_FULL wf_SIL_CDM_W_EHA_PT_HISTORY_PT_H
W_EHA_SUBJECT_D	wf_SIL_CDM_W_EHA_SUBJECT_D_FULL wf_SIL_CDM_W_EHA_SUBJECT_D
W_EHA_ORDER_PATIENT_H	wf_SIL_CDM_W_EHA_ORDER_PATIENT_H_FULL wf_SIL_CDM_W_EHA_ORDER_PATIENT_H
W_EHA_APPT_PATIENT_H	wf_SIL_CDM_W_EHA_APPT_PATIENT_H_FULL wf_SIL_CDM_W_EHA_APPT_PATIENT_H

**Table 4 (Cont.) Updated CDM ETLs**

<b>Table Name</b>	<b>ETLs</b>
W_EHA_CONSENT_PATIENT_H	wf_SIL_CDM_W_EHA_CONSENT_PATIENT_H_FULL wf_SIL_CDM_W_EHA_CONSENT_PATIENT_H
W_EHA_ENC_PATIENT_H	wf_SIL_CDM_W_EHA_ENC_PATIENT_H_FULL wf_SIL_CDM_W_EHA_ENC_PATIENT_H
W_EHA_DX_PATIENT_H	wf_SIL_CDM_W_EHA_DX_PATIENT_H_FULL wf_SIL_CDM_W_EHA_DX_PATIENT_H

**Note:** Demographic attributes and entities are populated based on the values associated in HDM with the golden patient record for the following CDM entities:

- W\_EHA\_RESEARCH\_PATIENT\_D
- W\_EHA\_ETHN\_PATIENT\_H
- W\_EHA\_RACE\_PATIENT\_H

## **Cascading Soft Deletions and Mapping Updates**

### **Soft Deletion of Golden Patient Record**

If a golden patient record in HDM\_RELTD\_PT is soft deleted, then the corresponding patient record in W\_EHA\_RESEARCH\_PATIENT\_D is soft deleted and all clinical records associated with the corresponding patient will be soft deleted in CDM.

### **Soft Deletion of Mapping Record**

If a non-golden patient record mapping in HDM\_RELTD\_PT is soft deleted and not linked to any other golden record, then CDM clinical records which were earlier linked to the golden patient record will be soft deleted.

### **Mapping Update**

If a non-golden patient record mapping is updated to a different golden patient record in HDM\_RELTD\_PT, the mapping update is cascaded to all CDM clinical records to associate clinical records to the new golden patient.

### **Non-Golden Patient Identifier not Mapped to Golden Patient Identifier**

If a non-golden patient identifier is not mapped to any golden patient identifier, then clinical records associated with the non-golden patient identifier in HDM will not be loaded to CDM.

### **ODB Linkage of Soft-Deleted and Re-Mapped Records**

When a patient specimen record is soft-deleted in the <CDM\_schema>.W\_EHA\_SPECIMEN\_PATIENT\_H table, all linked ODB specimens are also soft-deleted in the <ODB\_schema>.W\_EHA\_SPEC\_PATIENT table. When a new specimen is created in CDM by the ETL process, the system attempts to find a corresponding ODB specimen and re-map it using the specimen number and vendor number values. The patient aggregates are updated automatically to reflect new and removed specimen data in ODB.

## Permanently Remove Soft-Deleted Records from CDM

If golden record re-mappings occur often and the number of soft-deleted records starts to impact performance or storage capacity, you may choose to enable a purge job as follows:

1. Configure the `cdm_keep_deleted_prct` parameter in the `<Enterprise_schema>.W_EHA_CONFIG_PARAMETER` table. This parameter determines the percentage of soft-deleted rows in a bridge table that will trigger the purge job to clean up the table. For example, a value of 5 means that when more than 5 percent of the rows have `delete_flg = 'Y'` in any given bridge table, all those records will be permanently deleted by the purge job.
2. Configure the `cdm_cleanup_DOP` parameter in the `<Enterprise_schema>.W_EHA_CONFIG_PARAMETER` table. This parameter determines the degree of parallelism used by the purge job. You may choose a value that is lower or equal to the `max_parallel_degree` parameter.
3. Schedule or run the job on-demand as follows:

```
BEGIN
  CLEANUP_UTIL.cleanup_job;
END;
```

## New Relationships for Cancer Registry Data Analysis

The following relationships have been added to the CDM data model to support cancer registry data analysis:

- [Patient Diagnosis to Patient Observation Relationship](#)
- [Patient Diagnosis to Patient Procedure Relationship](#)
- [Patient Diagnosis to Patient Substance Administration Relationship](#)
- [Patient Diagnosis to Patient Specimen Relationship](#)
- [Patient Specimen to Patient Observation Relationship](#)

### Patient Diagnosis to Patient Observation Relationship

A patient diagnosis record (`W_EHA_DX_PATIENT_H`) can be associated with multiple patient observation records (`W_EHA_OBSV_PATIENT_H`) via the new `W_EHA_OBSV_PATIENT_H.DX_PATIENT_WID` column.

To select the patient diagnosis record linked to a patient observation in HDM, the CDM ETL for `W_EHA_OBSV_PATIENT_H` uses a parameterized filter on the Observation Concern Relationship Type attribute in the HDM Observation Concern intersection table (`HDM_OBSV_CNRN.OBSV_CNRN_RLSHPTYP_ID`). If this parameter is set to null (default), the ETL selects all the associations between the patient diagnosis and the patient observation in HDM.

After applying the above filter, if the CDM ETL finds a patient observation that is linked to multiple patient diagnoses in HDM, it replicates the corresponding number of records in `W_EHA_OBSV_PATIENT_H` with different `DX_PATIENT_WID` values.

### Patient Diagnosis to Patient Procedure Relationship

A patient diagnosis record (`W_EHA_DX_PATIENT_H`) can be associated with multiple patient procedure records (`W_EHA_PROC_PATIENT_H`) via the new `W_EHA_PROC_PATIENT_H.DX_PATIENT_WID` column.

To select the patient diagnosis record linked to a patient procedure in HDM, the CDM ETL for W\_EHA\_PROC\_PATIENT\_H uses a parameterized filter on the Intervention Concern Relationship Type attribute in the HDM Intervention Concern intersection table (HDM\_INTVN\_CNRRN.INTVN\_CNRRN\_RLSHPTYP\_ID). If this parameter is set to null (default), the ETL selects all the associations between the patient diagnosis and the patient procedure in HDM.

After applying the above filter, if the CDM ETL finds a patient procedure that is linked to multiple patient diagnoses in HDM, it replicates the corresponding number of records in W\_EHA\_PROC\_PATIENT\_H with different DX\_PATIENT\_WID values.

### **Patient Diagnosis to Patient Substance Administration Relationship**

A patient diagnosis record (W\_EHA\_DX\_PATIENT\_H) can be associated with multiple patient substance administration records (W\_EHA\_SUBADMN\_PATIENT\_H) via the new **W\_EHA\_SUBADMN\_PATIENT\_H.DX\_PATIENT\_WID** column.

To select the patient diagnosis record linked to a patient substance administration in HDM, the CDM ETL for W\_EHA\_SUBADMN\_PATIENT\_H uses a parameterized filter on the Intervention Concern Relationship Type attribute in the HDM Intervention Concern intersection table (HDM\_INTVN\_CNRRN.INTVN\_CNRRN\_RLSHPTYP\_ID). If this parameter is set to null (default), the ETL selects all the associations between the patient diagnosis and the patient substance administration in HDM.

After applying the above filter, if the CDM ETL finds a patient substance administration that is linked to multiple patient diagnoses in HDM, it replicates the corresponding number of records in W\_EHA\_SUBADMN\_PATIENT\_H with different DX\_PATIENT\_WID values.

### **Patient Diagnosis to Patient Specimen Relationship**

A patient diagnosis record (W\_EHA\_DX\_PATIENT\_H) can be associated with multiple patient specimen records (W\_EHA\_SPECIMEN\_PATIENT\_H) via the new Patient Specimen Diagnosis association **W\_EHA\_SPECIMEN\_DX\_PATIENT\_H**. This table supports associations between one patient specimen record and multiple patient diagnosis records, and vice versa.

To populate W\_EHA\_SPECIMEN\_DX\_PATIENT\_H, its CDM ETL sources records from the HDM Specimen Concern intersection table (HDM\_SPCMN\_CNRRN). The ETL provides an optional parameterized filter on the HDM attribute Specimen Concern Relationship Type (HDM\_SPCMN\_CNRRN.SPCMN\_CNRRN\_RLSHPTYP\_ID). If the parameter for this filter is set to Null (default), the ETL selects all the associations between the patient specimen and the patient diagnosis in HDM.

### **Patient Specimen to Patient Observation Relationship**

A patient specimen record (W\_EHA\_SPECIMEN\_PATIENT\_H) can be associated with multiple patient observation records (W\_EHA\_OBSV\_PATIENT\_H) via the new **W\_EHA\_OBSV\_PATIENT\_H.SPECIMEN\_PATIENT\_WID** column.

To select the patient specimen record linked to a patient observation in HDM, the CDM ETL for W\_EHA\_OBSV\_PATIENT\_H uses a parameterized filter on the Observation Specimen Relationship Type attribute in the HDM Observation Specimen intersection table (HDM\_OBSV\_SPCMN.OBSV\_SPCMN\_RLSHPTYP\_ID). If this parameter is set to null (default), the ETL selects all the associations between the patient specimen and the patient observation in HDM.

After applying the above filter, if the CDM ETL finds a patient observation that is linked to multiple patient specimens in HDM, it replicates the corresponding number of records in W\_EHA\_OBSV\_PATIENT\_H with different SPECIMEN\_PATIENT\_WID values.

## Omics Data Bank (ODB) Updates

- [VCF Loader Enhancements](#)
- [Omics Data Access Control](#)
- [RNA-seq Data Model and Loader Updates](#)
- [Alias Based Linking of Omics and Clinical Specimens](#)
- [Automated ODB - CDM Specimen Linkage Refresh after a Full CDM Refresh](#)
- [Protein Effect for Frameshift Mutations Calculation](#)
- [Splicing Mutations Identification](#)

### VCF Loader Enhancements

The VCF loader has been enhanced to load the sequence variant data in VCF 4.2 format. The loader is backward compatible and still works with the VCF 4.1 format.

### Omics Data Access Control

The omics data access can now be controlled through applications like OHTR as the data access control policies have been upgraded to restrict or provide access to genomics data residing in the ODB schema. You can create policies where you can define if you grant access or restrict access to genomic data at patient or subject level. You can also define the access control expiration date for this genomic data.

### RNA-seq Data Model and Loader Updates

The RNA-seq data model and loader have been upgraded to support exon, gene and transcript based normalization. Both the model and loader also support loading RPKM/FPKM/FPKM\_UQ/TPM quantification types.

### Alias Based Linking of Omics and Clinical Specimens

Omics specimens loaded in OHF are linked by default to the clinical specimens in CDM based on their Specimen Number (loaded in Omics data files) and Specimen Vendor Number (provided as a loader input parameter).

The linking process has been enhanced to also support specimen identification based on the combination between the Specimen Alias and Issuing Service Provided, both of which are loaded into the HDM interface tables:

1. The loader first attempts to use Specimen Number/Specimen Vendor Number to link Omics specimens to CDM specimens. If successful, the process stops here.
2. If a matching Specimen Number/Specimen Vendor number combination is not found in CDM, the loader switches to a lookup by Specimen Alias. In this second pass, the loader tries to match the Specimen Identifier from a result file with the Specimen Alias and the input value of the Specimen Vendor Number with the Issuing Service Provider name.



3. If a matching record is found in the CDM alias tables, the loader verifies if the corresponding CDM specimen has been previously linked with an Omics specimen.
  - If an Omics specimen has been linked previously, the loader reuses its record.
  - If an Omics specimen hasn't been linked previously, the loader creates a new Omics specimen record.

The association of specimen aliases to the loaded genomic files is tracked in the Omics database.

### Automated ODB - CDM Specimen Linkage Refresh after a Full CDM Refresh

You no longer have to manually update CDM references for OMICS specimens when the CDM schema is reloaded with a full refresh ETL. The CDM references are updated automatically after each ETL to ensure the consistency of ODB - CDM specimen links.

You must still update OMICS study references if the CDM is reloaded with a full load ETL. To do this, in the ODB schema, execute the following SQL statement:

```
update w_aha_rslt_study rs set external_study_wid = (
select row_wid from cdm.w_aha_study_d sd
where rs.result_study_name = sd. study_name
);
```

### Protein Effect for Frameshift Mutations Calculation

The protein effect for frameshift mutations is now calculated using the short format HGVS recommendations. For example, p.N123fs indicates: the prefix reference sequence (protein), the first amino acid changed (nitrogen), its position (123), and the type of mutation (frameshift).

### Splicing Mutations Identification

You can now query mutations based on their proximity to the intron/exon boundary.

The IS\_SPLICING attribute has been added to the W\_EHA\_VARIANT\_EFFECT table. The value of this attribute is set to "Y" for variants in close proximity to intron/exon border.

Two system parameters define the length of the splice regions on the intron and exon sides of the border:

- splice\_region\_length\_intron - length of the intronic portion of the splice region (default 2).
- splice\_region\_length\_exon - length of the exonic portion of the splice region (default 2).

You can control the initialization parameters using the PL/SQL API:

#### Verify Current Settings

```
SQL> select config_util.get_config_parameter (i_name=>'splice_region_
length_exon') as splice_region_length_exon from dual;
```

```
SPLICE_REGION_LENGTH_EXON
-----
-----
```

2

```
SQL> select config_util.get_config_parameter (i_name=>'splice_region_
length_intron') as splice_region_length_intron from dual;
```

```
SPLICE_REGION_LENGTH_INTRON
```

```
-----
-----
```

```
2
```

### Set New Parameter Values

```
SQL> exec config_util.set_config_parameter (i_name=>'splice_region_length_
exon',i_value=>3);
```

PL/SQL procedure successfully completed.

```
SQL> exec config_util.set_config_parameter (i_name=>'splice_region_length_
intron',i_value=>8);
```

PL/SQL procedure successfully completed.

```
SQL> commit;
```

Commit complete.

### Reload the Contents of the W\_EHA\_VARIANT\_EFFECT Table

```
BEGIN
```

```
  DBMS_SCHEDULER.create_job (
    job_name          => 'VARIANT_EFFECT_FULL_REFRESH',
    job_type          => 'PLSQL_BLOCK',
    job_action        => q'[BEGIN odb_var_effect_util.process_var_effect(i_
full_refresh=>'Y'); END;]',
    enabled           => true,
    comments          => 'Fully refresh variant_effect table contents');
```

```
END;
```

```
/
```

## Where to Find the Product Documentation

The product documentation is available at the following locations:

- My Oracle Support: <https://support.oracle.com> — What's New, What's Fixed, and Known Issues.
- Oracle Help Center: <https://docs.oracle.com/en/industries/health-sciences/oracle-healthcare-foundation/index.html> — The most current documentation set.

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