



SQL Query Guide



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Contents

Chapter 1: Schemas and Tables	1
Data Warehouse Server	1
Schemas	1
Tables	2
Core Data Warehouse	2
Data Mart for tranSMART Search	7
Data Mart for tranSMART Dataset Explorer	8
Chapter 2: Sample SQL Queries	11
Export Microarray Data	11
Retrieve Probe Sets with Significant TEA Scores	12
Retrieve Attributes for Patients in a Study	13
Appendix A: Schema Diagrams	25
Core Data Warehouse	26
Data Mart for tranSMART Search	27
I2B2METADATA and I2B2DEMODATA	28
DEAPP	29

Chapter 1

Schemas and Tables

Data Warehouse Server

The tranSMART database warehouse server is located at the following address:

Host Name	IP
proddb.jnj.recomdata.com	174.129.240.115

Schemas

The data warehouse contains the following core schemas:

Schema	Description
BIOMART	Data accessed by tranSMART end-users. Note: You must log in as Oracle user <code>biomart_user</code> (both user ID and password) to see this database.
BIOMART_USER	tranSMART entry point into the data warehouse. Note: You must log in as Oracle user <code>biomart</code> (both user ID and password) to see this database.
DEAPP	tranSMART extension of i2b2. Includes transactional information such as biomarker data and security for clinical trials.
I2B2DEMODATA	I2B2standard database.
I2B2HIVE	I2B2standard database.
I2B2METADATA	I2B2standard database.
SEARCHAPP	Transactional information about the users who are allowed to access tranSMART, such as the queries they've run and the permissions they are granted.

The data warehouse also contains the following support schemas:

Schema	Description
CONTROL	Data integrity tests and auditing data.
REFERENCE	Reference data such as Affymetrix annotation data and MeSH disease data.

Tables

The following sections summarize the tables in the tranSMART data warehouse. The tables are grouped by core data warehouse tables, tables used by the tranSMART Search feature, and tables used by Dataset Explorer.

Core Data Warehouse

Table Name	Used For	Description
BIO_ASSAY	Assay Data and Expression Profile	Information such as ID, type, and platform about the bio assays used in a clinical trial.
BIO_ASSAY_ANALYSIS	Basic Bio Facts	Attributes of an analysis, such as analysis name, analysis description, analysis method, and assay type.
BIO_ASSAY_ANALYSIS_DATA	Basic Bio Facts	Analysis information such as results data, p-value, preferred p-value, and fold change value.
BIO_ASSAY_ANALYSIS_DATA_TEA	Basic Bio Facts	Similar to BIO_ASSAY_ANALYSIS_DATA, but includes only results ranked as statistically significant, based on the TEA algorithm.
BIO_ASSAY_DATA	Assay Data and Expression Profile	Test information such as assay ID and values. This is raw data from an experiment.
BIO_ASSAY_DATA_ANNOTATION	Assay Data and Expression Profile	Assay feature group ID and associated biomarker ID.
BIO_ASSAY_DATA_STATS	Assay Data and Expression Profile	Statistical test data such as minimum and maximum values and standard deviation.

Table Name	Used For	Description
BIO_ASSAY_DATASET	Assay Data and Expression Profile	Analysis attributes such as ID, name, description, and criteria.
BIO_ASSAY_FEATURE_GROUP	Assay Data and Expression Profile	ID, name, and type of a feature group.
BIO_ASSAY_PLATFORM	Assay Data and Expression Profile	Attributes of assay platforms (for example, Affymetrix – HG-U133-PLUS [GPL570]). Attributes include ID, name, description, organism, and vendor.
BIO_ASSAY_SAMPLE	Assay Data and Expression Profile	Assay ID, sample ID, and study timepoint ID.
BIO_ASY_ANALYSIS_DATA_ALL	Basic Bio Facts	Intermediate table that contains raw analyzed data to be processed and filtered. When these operations are complete, data is loaded into BIO_ASSAY_ANALYSIS_DATA.
BIO_ASY_ANALYSIS_DATASET	Basic Bio Facts	Link between dataset ID and analysis ID.
BIO_ASY_ANALYSIS_PLTFM	Basic Bio Facts	Analysis platform (such as Jubilant, Omicsoft, and Johnson & Johnson) and platform ID.
BIO_ASY_DATA_STATS_ALL	Assay Data and Expression Profile	Intermediate table that contains raw statistical data to be filtered. When these operations are complete, data is loaded into BIO_ASSAY_DATA_STATS.
BIO_CELL_LINE	Basic Bio Facts	Contains data related to gene signatures, such as cell line name and ID, and information about the associated disease. Data is loaded from the table CELLINESDICT in database CENTCLINRD.
BIO_CGDCP_DATA	Assay Data and Expression Profile	Cancer Gene Data Curation Project data, such as evidence code, negation indicator, and NCI disease concept code.
BIO_CLINC_TRIAL_ATTR	Experiments and Clinical Trials	Clinical trial or experiment ID, attribute code, attribute value.

Tables

Table Name	Used For	Description
BIO_CLINC_TRIAL_PT_GROUP	Experiments and Clinical Trials	Group attributes such as ID, name, description, number of patients, and type code.
BIO_CLINC_TRIAL_TIME_PT	Experiments and Clinical Trials	Time point attributes such as start and end times and dates.
BIO_CLINICAL_TRIAL	Experiments and Clinical Trials	Master metadata for clinical trials.
BIO_COMPOUND	Assay Data and Expression Profile Experiments and Clinical Trials	Master table for internal and external compounds.
BIO_CONCEPT_CODE	Assay Data and Expression Profile Biomarkers Experiments and Clinical Trials	Defines all types of concepts (for example, organism, gene, tissue type) that are used in the entire data warehouse.
BIO_CONTENT	Content and Repository	Content references for resources in files such as .pdf , .xls, and .doc.
BIO_CONTENT_REFERENCE	Content and Repository	Content references (such as bio content ID and bio data ID) that represent bio objects in the content management system.
BIO_CONTENT_REPOSITORY	Content and Repository	IDs and locations of repository resources, such as trials, internal documents, and PubMed articles.
BIO_CURATED_DATA	Basic Bio Facts	Reference IDs for curated literature resources.
BIO_CURATION_DATASET	Basic Bio Facts	Information about curated literature datasets.
BIO_DATA_ATTRIBUTE	Assay Data and Expression Profile	Bio data ID, attribute code, attribute value.
BIO_DATA_COMPOUND	Basic Bio Facts	Link between data IDs and bio compounds relating to a study or experiment.
BIO_DATA_CORREL_DESCR	Biomarkers	Correlation types (such as pathway to disease, or pathway to gene) and descriptions.

Table Name	Used For	Description
BIO_DATA_CORRELATION	Biomarkers	Correlation IDs.
BIO_DATA_DISEASE	Assay Data and Expression Profile Basic Bio Facts	Links between bio data IDs and bio disease IDs relating to an experiment or study. Provides a hierarchical structure of MeSH diseases.
BIO_DATA_EXT_CODE	Assay Data and Expression Profile Basic ID Facts Biomarkers	Synonyms for bio data (such as genes, pathways, and compounds), bio data sources (such as Ariadne URN), and disease terms.
BIO_DATA_LITERATURE	Basic Bio Facts	Link between BIO_DATA_ID and the IDs BIO_LIT_REF_DATA_ID (table BIO_LIT_REF_DATA) and BIO_CURATION_DATASET_ID (tables BIO_CURATED_DATA and BIO_CURATION_DATASET).
BIO_DATA_OMIC_MARKER	Basic Bio Facts	Link between bio data IDs and biomarker ID. This is the tranSMART annotation table.
BIO_DATA_UID	Assay Data and Expression Profile Biomarkers Experiments and Clinical Trials	Link between bio data IDs and unique IDs (such as EXP:Omicsoft: GSE2123).
BIO_DISEASE	Assay Data and Expression Profile Basic Bio Facts Experiments and Clinical Trials	A disease master table with cross reference to ICD 9/10 and MeSH coding systems.
BIO_EXPERIMENT	Experiments and Clinical Trials	Metadata about a particular experiment with attributes such as investigator, experiment type, and completion date.
BIO_LIT_ALT_DATA	Basic Bio Facts	Alterations data from curated asthma and oncology literature.
BIO_LIT_AMD_DATA	Basic Bio Facts	Molecule alterations data from curated oncology literature.
BIO_LIT_INH_DATA	Basic Bio Facts	Inhibitors data from curated oncology literature.

Tables

Table Name	Used For	Description
BIO_LIT_INT_DATA	Basic Bio Facts	Interactions data from curated asthma and oncology literature.
BIO_LIT_INT_MODEL_MV	Basic Bio Facts	Materialized view that associates IDs for Jubilant interactions data and experimental model types (such as homo sapiens or cavia porcellus).
BIO_LIT_MODEL_DATA	Basic Bio Facts	Information about the experiment that generated the asthma or oncology data described in the curated literature.
BIO_LIT_PE_DATA	Basic Bio Facts	Protein effects data from curated asthma literature.
BIO_LIT_REF_DATA	Basic Bio Facts	Information about the referenced literature, such as title, description, and disease type.
BIO_LIT_SUM_DATA	Basic Bio Facts	Summary of alterations data from curated oncology literature.
BIO_MARKER	Basic Bio Facts Biomarkers	Master table for biomarkers, with attributes such as ID, type, organism, and description.
BIO_MARKER_CORREL_MV	Basic Bio Facts Biomarkers	Materialized view that associates biomarker IDs by correlation type, such as gene and homologue.
BIO_PATIENT	Experiments and Clinical Trials	Master table for patient data with attributes such as subject ID, experiment ID, gender, and race.
BIO_PATIENT_EVENT	Experiments and Clinical Trials	Information about a patient event, including event code, type, date, timepoint ID, and site.
BIO_PATIENT_EVENT_ATTR	Experiments and Clinical Trials	Link between patient attribute ID, patient event ID, clinical trial ID, and the patient event attributes.
BIO_SAMPLE	Experiments and Clinical Trials	Sample name, type, and ID, and associated experiment ID, subject ID, and patient event ID.
BIO_SUBJECT	Experiments and Clinical Trials	Subject ID and type, and site subject ID.

To view a schema diagram of the core data warehouse, see [Core Data Warehouse](#) on page 26.

Data Mart for tranSMART Search

Table Name	Description
SEARCH_APP_ACCESS_LOG	Information about tranSMART search events, including type of search and the user running the search.
SEARCH_AUTH_USER	Administrative data about the user running a search, including user email and tranSMART user type (such as Administrator, Study Owner, Study Spectator). Used for authentication.
SEARCH_AUTH_USER_SEC_ACCESS	User access ID and object ID.
SEARCH_BIO_MKR_CORREL_FAST_MV	Materialized view that associates a domain object ID with the associated biomarker ID and the correlation type.
SEARCH_CUSTOM_FILTER	Saved search filter ID, name, and description, and ID of user who created the filter.
SEARCH_CUSTOM_FILTER_ITEM	Saved search filter ID and the IDs of one or more components of the search filter.
SEARCH_GENE_SIG_FILE_SCHEMA	Description of the format of a gene signature file – for example, <i>Gene Symbol</i> <tab> <i>Metric Indicator</i> .
SEARCH_GENE_SIGNATURE	Complete definition of a gene signature, as defined on the pages of the gene signature wizard.
SEARCH_GENE_SIGNATURE_ITEM	Link between gene signature search IDs and biomarker IDs, bio data IDs, and fold change metrics.
SEARCH_KEYWORD	Name, ID, bio data ID, category, and other information about the keywords displayed in the autocomplete dropdown.
SEARCH_KEYWORD_TERM	Name, ID, rank, length, and other information about the keyword displayed in the autocomplete dropdown.
SEARCH_REQUEST_MAP	Link between request map ID, configuration attribute (such as role administrator or anonymous authentication), and target URL. Used for authentication.
SEARCH_ROLE	ID and authority description of the tranSMART search roles (administrator, study owner, spectator). Used for authentication.
SEARCH_ROLE_AUTH_USER	Link between role IDs and authorities IDs. Used for authentication.

Table Name	Description
SEARCH_SEC_ACCESS_LEVEL	Access level name, value, and ID.
SEARCH_SECURE_OBJECT	Object ID and associated biodata ID and display name (such as a particular clinical trial).
SEARCH_SECURE_OBJECT_PATH	Secure object ID and the object's path in the navigation tree.
SEARCH_USER_FEEDBACK	Log of user feedback about tranSMART, including user ID, date issued, and feedback text.

To view a schema diagram of the tables in the tranSMART Search Data Mart, see [Data Mart for tranSMART Search](#) on page 27.

Data Mart for tranSMART Dataset Explorer

The Dataset Explorer data mart is a subset of data from the core data warehouse that is converted into an i2b2 schema for data exploration.

The following tables describe the i2b2-based schemas you need to be aware of.

I2B2METADATA and I2B2DEMODATA Schemas

The i2b2metadata schema contains ontology data. The i2b2demodata schema contains ontology and fact data. The tables and their relationships with i2b2 fields are listed below:

Schema.Table	Description	Relationships
I2B2DEMODATA. CONCEPT_COUNTS	Stores the counts that are displayed at all branch-level nodes in the navigation tree.	CONCEPT_PATH to: I2B2.C_FULLNAME CONCEPT_DIMENSION.CONCEPT_PATH
I2B2DEMODATA. CONCEPT_DIMENSION	Stores all paths. (Similar to i2b2 with small differences.)	CONCEPT_PATH to: CONCEPT_COUNTS.CONCEPT_PATH I2B2.C_FULLNAME CONCEPT_CD to: OBSERVATION_FACT.CONCEPT_CD
I2B2DEMODATA. OBSERVATION_FACT	Stores all measurements recorded for patients during the trial.	CONCEPT_CD to: CONCEPT_DIMENSION.CONCEPT_CD I2B2.C_BASECODE PATIENT_NUM to: PATIENT_DIMENSION.PATIENT_NUM

Schema.Table	Description	Relationships
I2B2DEMOTDATA. PATIENT_DIMENSION	Stores patient demographic data.	PATIENT_NUM to: OBSERVATION_FACT.PATIENT_NUM
I2B2DEMOTDATA. PATIENT_TRIAL	Maps a patient to a trial (contains one record for each trial/patient association).	PATIENT_NUM to: PATIENT_DIMENSION.PATIENT_NUM TRIAL to: wildcard match with CONCEPT_PATH or C_FULLNAME.
I2B2METADATA. I2B2	Stores detailed information about the i2b2 navigation tree.	C_BASECODE to: OBSERVATION_FACT.CONCEPT_CD I2B2.CONCEPT_CD C_FULLNAME to: CONCEPT_DIMNENSION.CONCEPT_PATH I2B2.C_FULLNAME
I2B2METADATA. I2B2_SECURE	Allows security access to be set at the node level of the navigation tree. This is a copy of the i2b2 table with the additional security field SECURE_OBJ_TOKEN.	See relationships for table i2b2.
I2B2METADATA. I2B2_TAGS	Used to map a search Type (Area, Compound, or Disease) to a trial in the Search by Subject tab.	PATH to: I2B2.C_FULLNAME

To view a diagram of the tables in the i2b2metadata and i2b2demodata schemas, see [I2B2METADATA and I2B2DEMOTDATA](#) on page 28.

DEAPP Schema

The DEAPP schema contains biomarker data such as RBM, Affymetrix expressions, ELISA, and SNP. The tables in the schema are listed below:

Table Name	Description
DE_PATHWAY	Provides autosearch data to the Select a Gene/Pathway field of the Compare subsets-Pathway Selection dialog. Includes pathway name, description, ID, and source.
DE_PATHWAY_GENE	Provides autosearch data to the Select a Gene/Pathway field of the Compare subsets-Pathway Selection dialog. Includes gene symbol and ID, and pathway ID,
DE_SAVED_COMPARISON	Contains the IDs of the subset definitions saved with the Dataset Explorer Save button.

Tables

Table Name	Description
DE_SUBJECT_MICROARRAY_DATA	Gene expression data used in heat maps. Includes patient, subject, and assay IDs, and gene symbol, probe set, timepoint, and intensity values.
DE_SUBJECT_PROTEIN_DATA	Protein data, including patient, subject, assay, and gene IDs, and gene symbol, timepoint, and intensity values.
DE_SUBJECT_RBM_DATA	RBM data used in heat maps. Includes patient, assay, and gene IDs, gene symbol and antigen names, and intensity values.
DE_SUBJECT_SAMPLE_MAPPING	Mapping table for RBM and microarray data. Each RBM dataset has an observed score and a z-score. Generally, DE_SUBJECT_SAMPLE_MAPPING will have two records for every record in DE_SUBJECT_RBM_DATA – one for the observed score and one for the z-score.
DE_XTRIAL_CHILD_MAP	Information for mapping a concept from a specific trial to a “parent concept” that exists across trials.
DE_XTRIAL_PARENT_NAMES	Information about concepts that are mapped across trials.
HAPLOVIEW_DATA	SNP data for haploviews. Includes i2b2 and JnJ IDs, and trial, gene, and chromosome names.
SNP_INFO	SNP data, including SNP ID, gene symbol, chromosome, and SNP reference.
STG_RBM_ANTIGEN_GENE	RBM antigen name, gene ID, and gene symbol.

To view a diagram of the tables in the DEAPP schema, see [DEAPP](#) on page 29.

Chapter 2

Sample SQL Queries

This chapter has the following sample queries:

- [Export Microarray Data](#) (page 11)
- [Retrieve Probe Sets with Significant TEA Score](#) (page 12)
- [Retrieve Attributes for Patients in a Study](#) (page 13)

Export Microarray Data

This query exports all microarray data for the BRC Depression Study. A temporary table is used for export due to the amount of data retrieved.

```
create table exp_brc_ds_mRNA
as
select
distinct
dssm.patient_id,
dssm.subject_id,
dssm.sample_type,
dssm.timepoint,
dsma.probeset,
dsma.gene_symbol,
dsma.raw_intensity,
dsma.pvalue,
dsma.zscore
from deapp.de_subject_sample_mapping dssm,
deapp.de_subject_microarray_data dsma
where
dsma.trial_name = 'BRC:mRNA:DS'
and
dsma.assay_id = dssm.assay_id
and dssm.platform_cd = 'IT62514';
/
```

Retrieve Probe Sets with Significant TEA Scores

This query retrieves all probe sets with a significant TEA score for a given GEO dataset:

```
--
-- For a given GEO dataset (GSE2113), find all probesets (and gene
-- annotations) with significant TEA scores
--
select
distinct
baadt.feature_group_name as probeset_name,
bm.bio_marker_name as gene_symbol,
bm.primary_external_id as gene_id,
baadt.fold_change_ratio as fold_change,
baadt.tea_normalized_pvalue,
baadt.adjusted_pvalue,
baadt.raw_pvalue,
baa.analysis_name,
be.title as experiment,
be.accession as experiment_accession,
bap.platform_name,
bap.platform_organism
from
biomart.bio_assay_analysis_data_tea baadt
join
biomart.bio_assay_analysis baa
on baadt.bio_assay_analysis_id = baa.bio_assay_analysis_id
join
biomart.bio_experiment be
on baadt.bio_experiment_id = be.bio_experiment_id
join
biomart.bio_assay_platform bap
on baadt.bio_assay_platform_id = bap.bio_assay_platform_id
join
bio_assay_data_annotation bada
on bada.bio_assay_feature_group_id = baadt.bio_assay_feature_group_id
join
bio_marker bm
on bada.bio_marker_id = bm.bio_marker_id
where be.accession = 'GSE2113'
```


Retrieve Attributes for Patients in a Study

This query retrieves all clinical attributes for each patient in the BRC Depression Study. Note that a query is used to generate the `max(decode)` selection clause.

```
select c_name ,
       c_fullname ,
       max(decode(patient_num,48097,tval_char,null)) "48097",
       max(decode(patient_num,48098,tval_char,null)) "48098",
       max(decode(patient_num,48099,tval_char,null)) "48099",
       max(decode(patient_num,48100,tval_char,null)) "48100",
       max(decode(patient_num,48101,tval_char,null)) "48101",
       max(decode(patient_num,48102,tval_char,null)) "48102",
       max(decode(patient_num,48103,tval_char,null)) "48103",
       max(decode(patient_num,48104,tval_char,null)) "48104",
       max(decode(patient_num,48105,tval_char,null)) "48105",
       max(decode(patient_num,48106,tval_char,null)) "48106",
       max(decode(patient_num,48107,tval_char,null)) "48107",
       max(decode(patient_num,48108,tval_char,null)) "48108",
       max(decode(patient_num,48109,tval_char,null)) "48109",
       max(decode(patient_num,48110,tval_char,null)) "48110",
       max(decode(patient_num,48111,tval_char,null)) "48111",
       max(decode(patient_num,48112,tval_char,null)) "48112",
       max(decode(patient_num,48113,tval_char,null)) "48113",
       max(decode(patient_num,48114,tval_char,null)) "48114",
       max(decode(patient_num,48115,tval_char,null)) "48115",
       max(decode(patient_num,48116,tval_char,null)) "48116",
       max(decode(patient_num,48117,tval_char,null)) "48117",
       max(decode(patient_num,48118,tval_char,null)) "48118",
       max(decode(patient_num,48119,tval_char,null)) "48119",
       max(decode(patient_num,48120,tval_char,null)) "48120",
       max(decode(patient_num,48121,tval_char,null)) "48121",
       max(decode(patient_num,48122,tval_char,null)) "48122",
       max(decode(patient_num,48123,tval_char,null)) "48123",
       max(decode(patient_num,48124,tval_char,null)) "48124",
       max(decode(patient_num,48125,tval_char,null)) "48125",
       max(decode(patient_num,48126,tval_char,null)) "48126",
       max(decode(patient_num,48127,tval_char,null)) "48127",
       max(decode(patient_num,48128,tval_char,null)) "48128",
       max(decode(patient_num,48129,tval_char,null)) "48129",
       max(decode(patient_num,48130,tval_char,null)) "48130",
       max(decode(patient_num,48131,tval_char,null)) "48131",
       max(decode(patient_num,48132,tval_char,null)) "48132",
       max(decode(patient_num,48133,tval_char,null)) "48133",
       max(decode(patient_num,48134,tval_char,null)) "48134",
       max(decode(patient_num,48135,tval_char,null)) "48135",
       max(decode(patient_num,48136,tval_char,null)) "48136",
       max(decode(patient_num,48137,tval_char,null)) "48137",
       max(decode(patient_num,48138,tval_char,null)) "48138",
       max(decode(patient_num,48139,tval_char,null)) "48139",
       max(decode(patient_num,48140,tval_char,null)) "48140",
       max(decode(patient_num,48141,tval_char,null)) "48141",
```

Retrieve Attributes for Patients in a Study

```
max(decode(patient_num,48142,tval_char,null)) "48142",
max(decode(patient_num,48143,tval_char,null)) "48143",
max(decode(patient_num,48144,tval_char,null)) "48144",
max(decode(patient_num,48145,tval_char,null)) "48145",
max(decode(patient_num,48146,tval_char,null)) "48146",
max(decode(patient_num,48147,tval_char,null)) "48147",
max(decode(patient_num,48148,tval_char,null)) "48148",
max(decode(patient_num,48149,tval_char,null)) "48149",
max(decode(patient_num,48150,tval_char,null)) "48150",
max(decode(patient_num,48151,tval_char,null)) "48151",
max(decode(patient_num,48152,tval_char,null)) "48152",
max(decode(patient_num,48153,tval_char,null)) "48153",
max(decode(patient_num,48154,tval_char,null)) "48154",
max(decode(patient_num,48155,tval_char,null)) "48155",
max(decode(patient_num,48156,tval_char,null)) "48156",
max(decode(patient_num,48157,tval_char,null)) "48157",
max(decode(patient_num,48158,tval_char,null)) "48158",
max(decode(patient_num,48159,tval_char,null)) "48159",
max(decode(patient_num,48160,tval_char,null)) "48160",
max(decode(patient_num,48161,tval_char,null)) "48161",
max(decode(patient_num,48162,tval_char,null)) "48162",
max(decode(patient_num,48163,tval_char,null)) "48163",
max(decode(patient_num,48164,tval_char,null)) "48164",
max(decode(patient_num,48165,tval_char,null)) "48165",
max(decode(patient_num,48166,tval_char,null)) "48166",
max(decode(patient_num,48167,tval_char,null)) "48167",
max(decode(patient_num,48168,tval_char,null)) "48168",
max(decode(patient_num,48169,tval_char,null)) "48169",
max(decode(patient_num,48170,tval_char,null)) "48170",
max(decode(patient_num,48171,tval_char,null)) "48171",
max(decode(patient_num,48172,tval_char,null)) "48172",
max(decode(patient_num,48173,tval_char,null)) "48173",
max(decode(patient_num,48174,tval_char,null)) "48174",
max(decode(patient_num,48175,tval_char,null)) "48175",
max(decode(patient_num,48176,tval_char,null)) "48176",
max(decode(patient_num,48177,tval_char,null)) "48177",
max(decode(patient_num,48178,tval_char,null)) "48178",
max(decode(patient_num,48179,tval_char,null)) "48179",
max(decode(patient_num,48180,tval_char,null)) "48180",
max(decode(patient_num,48181,tval_char,null))
"48181",max(decode(patient_num,48182,tval_char,null)) "48182",
max(decode(patient_num,48183,tval_char,null))
"48183",max(decode(patient_num,48184,tval_char,null)) "48184",
max(decode(patient_num,48185,tval_char,null))
"48185",max(decode(patient_num,48186,tval_char,null)) "48186",
max(decode(patient_num,48187,tval_char,null))
"48187",max(decode(patient_num,48188,tval_char,null)) "48188",
max(decode(patient_num,48189,tval_char,null))
"48189",max(decode(patient_num,48190,tval_char,null)) "48190",
max(decode(patient_num,48191,tval_char,null))
"48191",max(decode(patient_num,48192,tval_char,null)) "48192",
max(decode(patient_num,48193,tval_char,null))
"48193",max(decode(patient_num,48194,tval_char,null)) "48194",
max(decode(patient_num,48195,tval_char,null))
"48195",max(decode(patient_num,48196,tval_char,null)) "48196",
max(decode(patient_num,48197,tval_char,null))
"48197",max(decode(patient_num,48198,tval_char,null)) "48198",
```

```

max(decode(patient_num,48199,tval_char,null))
"48199",max(decode(patient_num,48200,tval_char,null)) "48200",
max(decode(patient_num,48201,tval_char,null))
"48201",max(decode(patient_num,48202,tval_char,null)) "48202",
max(decode(patient_num,48203,tval_char,null))
"48203",max(decode(patient_num,48204,tval_char,null)) "48204",
max(decode(patient_num,48205,tval_char,null))
"48205",max(decode(patient_num,48206,tval_char,null)) "48206",
max(decode(patient_num,48207,tval_char,null))
"48207",max(decode(patient_num,48208,tval_char,null)) "48208",
max(decode(patient_num,48209,tval_char,null))
"48209",max(decode(patient_num,48210,tval_char,null)) "48210",
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max(decode(patient_num,48350,tval_char,null))
"48350",max(decode(patient_num,48351,tval_char,null)) "48351",
max(decode(patient_num,48352,tval_char,null)) "48352"
from
i2b2demodata.observation_fact a
join i2b2metadata.i2b2 b
on a.concept_cd = b.c_basecode
where
c_fullname like '%BRC Depression Study%'
and c_columndatatype = 'T'
and c_visualattributes not like '%H%'
group by c_name, c_fullname
UNION ALL
select c_name,
c_fullname ,
max(decode(patient_num,48097,cast(nval_num as varchar2(20)),null))
"48097",max(decode(patient_num,48098,cast(nval_num as
varchar2(20)),null)) "48098",max(decode(patient_num,48099,cast(nval_num

```

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as varchar2(20)),null))
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as varchar2(20)),null))
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as varchar2(20)),null))
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as varchar2(20)),null))
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```

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"48174",max(decode(patient_num,48175,cast(nval_num as

```

```

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as varchar2(20)),null))

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```

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"48233",max(decode(patient_num,48234,cast(nval_num as
varchar2(20)),null)) "48234",max(decode(patient_num,48235,cast(nval_num
as varchar2(20)),null))
"48235",max(decode(patient_num,48236,cast(nval_num as
varchar2(20)),null)) "48236",max(decode(patient_num,48237,cast(nval_num
as varchar2(20)),null))
"48237",max(decode(patient_num,48238,cast(nval_num as
varchar2(20)),null)) "48238",max(decode(patient_num,48239,cast(nval_num
as varchar2(20)),null))
"48239",max(decode(patient_num,48240,cast(nval_num as
varchar2(20)),null)) "48240",max(decode(patient_num,48241,cast(nval_num
as varchar2(20)),null))
"48241",max(decode(patient_num,48242,cast(nval_num as
varchar2(20)),null)) "48242",max(decode(patient_num,48243,cast(nval_num
as varchar2(20)),null))
"48243",max(decode(patient_num,48244,cast(nval_num as
varchar2(20)),null)) "48244",max(decode(patient_num,48245,cast(nval_num
as varchar2(20)),null))
"48245",max(decode(patient_num,48246,cast(nval_num as
varchar2(20)),null)) "48246",max(decode(patient_num,48247,cast(nval_num
as varchar2(20)),null))
"48247",max(decode(patient_num,48248,cast(nval_num as
varchar2(20)),null)) "48248",max(decode(patient_num,48249,cast(nval_num
as varchar2(20)),null))
"48249",max(decode(patient_num,48250,cast(nval_num as
varchar2(20)),null)) "48250",max(decode(patient_num,48251,cast(nval_num
as varchar2(20)),null))

```

Retrieve Attributes for Patients in a Study

```
"48251",max(decode(patient_num,48252,cast(nval_num as
varchar2(20)),null)) "48252",max(decode(patient_num,48253,cast(nval_num
as varchar2(20)),null))
"48253",max(decode(patient_num,48254,cast(nval_num as
varchar2(20)),null)) "48254",max(decode(patient_num,48255,cast(nval_num
as varchar2(20)),null)) "48255",
max(decode(patient_num,48256,cast(nval_num as varchar2(20)),null))
"48256",max(decode(patient_num,48257,cast(nval_num as
varchar2(20)),null)) "48257",max(decode(patient_num,48258,cast(nval_num
as varchar2(20)),null))
"48258",max(decode(patient_num,48259,cast(nval_num as
varchar2(20)),null)) "48259",max(decode(patient_num,48260,cast(nval_num
as varchar2(20)),null))
"48260",max(decode(patient_num,48261,cast(nval_num as
varchar2(20)),null)) "48261",max(decode(patient_num,48262,cast(nval_num
as varchar2(20)),null))
"48262",max(decode(patient_num,48263,cast(nval_num as
varchar2(20)),null)) "48263",max(decode(patient_num,48264,cast(nval_num
as varchar2(20)),null))
"48264",max(decode(patient_num,48265,cast(nval_num as
varchar2(20)),null)) "48265",max(decode(patient_num,48266,cast(nval_num
as varchar2(20)),null))
"48266",max(decode(patient_num,48267,cast(nval_num as
varchar2(20)),null)) "48267",max(decode(patient_num,48268,cast(nval_num
as varchar2(20)),null))
"48268",max(decode(patient_num,48269,cast(nval_num as
varchar2(20)),null)) "48269",max(decode(patient_num,48270,cast(nval_num
as varchar2(20)),null))
"48270",max(decode(patient_num,48271,cast(nval_num as
varchar2(20)),null)) "48271",max(decode(patient_num,48272,cast(nval_num
as varchar2(20)),null))
"48272",max(decode(patient_num,48273,cast(nval_num as
varchar2(20)),null)) "48273",max(decode(patient_num,48274,cast(nval_num
as varchar2(20)),null))
"48274",max(decode(patient_num,48275,cast(nval_num as
varchar2(20)),null)) "48275",max(decode(patient_num,48276,cast(nval_num
as varchar2(20)),null))
"48276",max(decode(patient_num,48277,cast(nval_num as
varchar2(20)),null)) "48277",max(decode(patient_num,48278,cast(nval_num
as varchar2(20)),null))
"48278",max(decode(patient_num,48279,cast(nval_num as
varchar2(20)),null)) "48279",max(decode(patient_num,48280,cast(nval_num
as varchar2(20)),null))
"48280",max(decode(patient_num,48281,cast(nval_num as
varchar2(20)),null)) "48281",max(decode(patient_num,48282,cast(nval_num
as varchar2(20)),null))
"48282",max(decode(patient_num,48283,cast(nval_num as
varchar2(20)),null)) "48283",max(decode(patient_num,48284,cast(nval_num
as varchar2(20)),null))
"48284",max(decode(patient_num,48285,cast(nval_num as
varchar2(20)),null)) "48285",max(decode(patient_num,48286,cast(nval_num
as varchar2(20)),null))
"48286",max(decode(patient_num,48287,cast(nval_num as
varchar2(20)),null)) "48287",max(decode(patient_num,48288,cast(nval_num
as varchar2(20)),null))
"48288",max(decode(patient_num,48289,cast(nval_num as
varchar2(20)),null)) "48289",max(decode(patient_num,48290,cast(nval_num
```

```

as varchar2(20)),null))
"48290",max(decode(patient_num,48291,cast(nval_num as
varchar2(20)),null)) "48291",max(decode(patient_num,48292,cast(nval_num
as varchar2(20)),null))
"48292",max(decode(patient_num,48293,cast(nval_num as
varchar2(20)),null)) "48293",max(decode(patient_num,48294,cast(nval_num
as varchar2(20)),null))
"48294",max(decode(patient_num,48295,cast(nval_num as
varchar2(20)),null)) "48295",max(decode(patient_num,48296,cast(nval_num
as varchar2(20)),null))
"48296",max(decode(patient_num,48297,cast(nval_num as
varchar2(20)),null)) "48297",max(decode(patient_num,48298,cast(nval_num
as varchar2(20)),null))
"48298",max(decode(patient_num,48299,cast(nval_num as
varchar2(20)),null)) "48299",max(decode(patient_num,48300,cast(nval_num
as varchar2(20)),null))
"48300",max(decode(patient_num,48301,cast(nval_num as
varchar2(20)),null)) "48301",max(decode(patient_num,48302,cast(nval_num
as varchar2(20)),null))
"48302",max(decode(patient_num,48303,cast(nval_num as
varchar2(20)),null)) "48303",max(decode(patient_num,48304,cast(nval_num
as varchar2(20)),null))
"48304",max(decode(patient_num,48305,cast(nval_num as
varchar2(20)),null)) "48305",max(decode(patient_num,48306,cast(nval_num
as varchar2(20)),null))
"48306",max(decode(patient_num,48307,cast(nval_num as
varchar2(20)),null)) "48307",max(decode(patient_num,48308,cast(nval_num
as varchar2(20)),null)) "48308",
max(decode(patient_num,48309,cast(nval_num as varchar2(20)),null))
"48309",max(decode(patient_num,48310,cast(nval_num as
varchar2(20)),null)) "48310",max(decode(patient_num,48311,cast(nval_num
as varchar2(20)),null))
"48311",max(decode(patient_num,48312,cast(nval_num as
varchar2(20)),null)) "48312",max(decode(patient_num,48313,cast(nval_num
as varchar2(20)),null))
"48313",max(decode(patient_num,48314,cast(nval_num as
varchar2(20)),null)) "48314",max(decode(patient_num,48315,cast(nval_num
as varchar2(20)),null))
"48315",max(decode(patient_num,48316,cast(nval_num as
varchar2(20)),null)) "48316",max(decode(patient_num,48317,cast(nval_num
as varchar2(20)),null))
"48317",max(decode(patient_num,48318,cast(nval_num as
varchar2(20)),null)) "48318",max(decode(patient_num,48319,cast(nval_num
as varchar2(20)),null))
"48319",max(decode(patient_num,48320,cast(nval_num as
varchar2(20)),null)) "48320",max(decode(patient_num,48321,cast(nval_num
as varchar2(20)),null))
"48321",max(decode(patient_num,48322,cast(nval_num as
varchar2(20)),null)) "48322",max(decode(patient_num,48323,cast(nval_num
as varchar2(20)),null))
"48323",max(decode(patient_num,48324,cast(nval_num as
varchar2(20)),null)) "48324",max(decode(patient_num,48325,cast(nval_num
as varchar2(20)),null))
"48325",max(decode(patient_num,48326,cast(nval_num as
varchar2(20)),null)) "48326",max(decode(patient_num,48327,cast(nval_num
as varchar2(20)),null))
"48327",max(decode(patient_num,48328,cast(nval_num as

```

Retrieve Attributes for Patients in a Study

```
varchar2(20)),null)) "48328",max(decode(patient_num,48329,cast(nval_num
as varchar2(20)),null))
"48329",max(decode(patient_num,48330,cast(nval_num as
varchar2(20)),null)) "48330",max(decode(patient_num,48331,cast(nval_num
as varchar2(20)),null))
"48331",max(decode(patient_num,48332,cast(nval_num as
varchar2(20)),null)) "48332",max(decode(patient_num,48333,cast(nval_num
as varchar2(20)),null))
"48333",max(decode(patient_num,48334,cast(nval_num as
varchar2(20)),null)) "48334",max(decode(patient_num,48335,cast(nval_num
as varchar2(20)),null))
"48335",max(decode(patient_num,48336,cast(nval_num as
varchar2(20)),null)) "48336",max(decode(patient_num,48337,cast(nval_num
as varchar2(20)),null))
"48337",max(decode(patient_num,48338,cast(nval_num as
varchar2(20)),null)) "48338",max(decode(patient_num,48339,cast(nval_num
as varchar2(20)),null))
"48339",max(decode(patient_num,48340,cast(nval_num as
varchar2(20)),null)) "48340",max(decode(patient_num,48341,cast(nval_num
as varchar2(20)),null))
"48341",max(decode(patient_num,48342,cast(nval_num as
varchar2(20)),null)) "48342",max(decode(patient_num,48343,cast(nval_num
as varchar2(20)),null))
"48343",max(decode(patient_num,48344,cast(nval_num as
varchar2(20)),null)) "48344",max(decode(patient_num,48345,cast(nval_num
as varchar2(20)),null))
"48345",max(decode(patient_num,48346,cast(nval_num as
varchar2(20)),null)) "48346",max(decode(patient_num,48347,cast(nval_num
as varchar2(20)),null))
"48347",max(decode(patient_num,48348,cast(nval_num as
varchar2(20)),null)) "48348",max(decode(patient_num,48349,cast(nval_num
as varchar2(20)),null))
"48349",max(decode(patient_num,48350,cast(nval_num as
varchar2(20)),null)) "48350",max(decode(patient_num,48351,cast(nval_num
as varchar2(20)),null))
"48351",max(decode(patient_num,48352,cast(nval_num as
varchar2(20)),null)) "48352"
from
i2b2demodata.observation_fact a
join i2b2metadata.i2b2 b
on a.concept_cd = b.c_basecode
where
c_fullname like '%BRC Depression Study%'
and c_columndatatype = 'N'
and c_visualattributes not like '%H%'
group by c_name, c_fullname order by c_fullname;
```

Appendix A

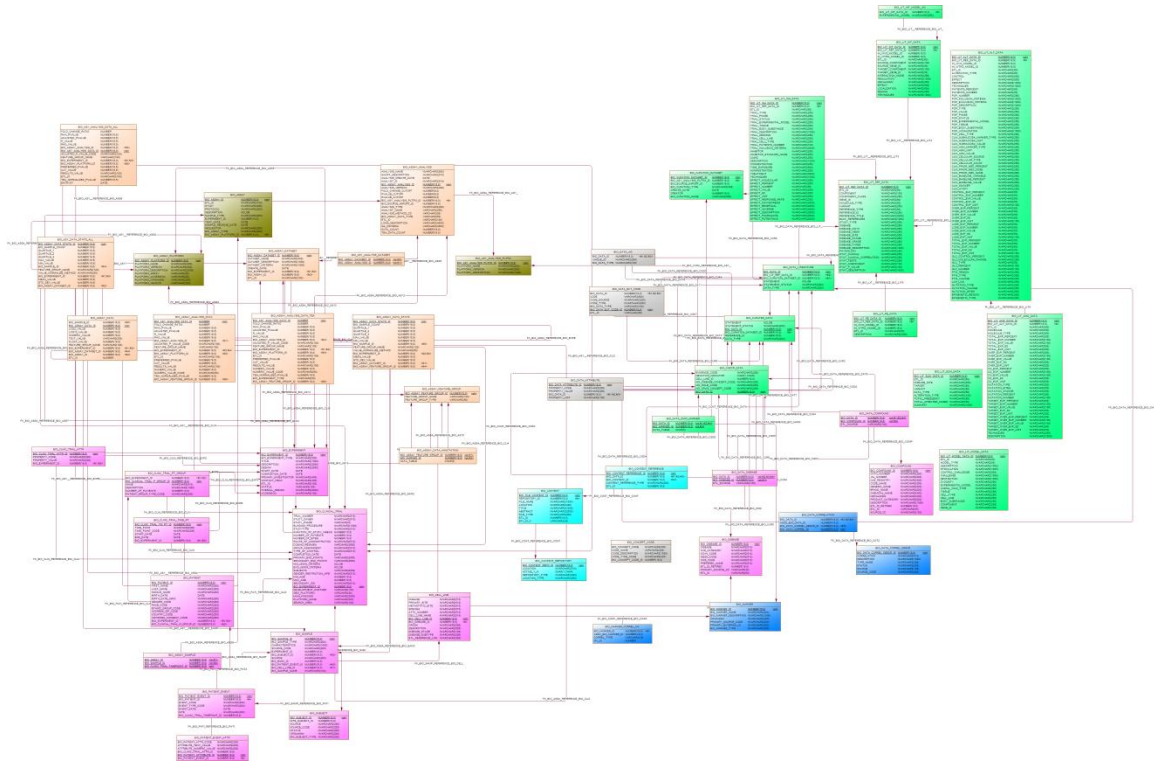
Schema Diagrams

This appendix contains illustrations of the following categories of tables in the tranSMART data warehouse:

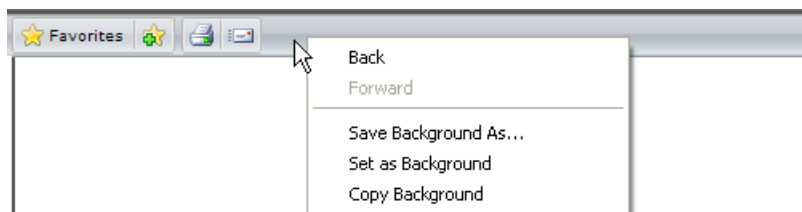
- [Core Data Warehouse](#) (page 26)
- [Data Mart for tranSMART Search](#) (page 27)
- Dataset Explorer:
 - [I2B2METADATA and I2B2DEMODATA](#) (page 28)
 - [DEAPP](#) (page 29)

Core Data Warehouse

Click the image to display a larger version of the diagram.

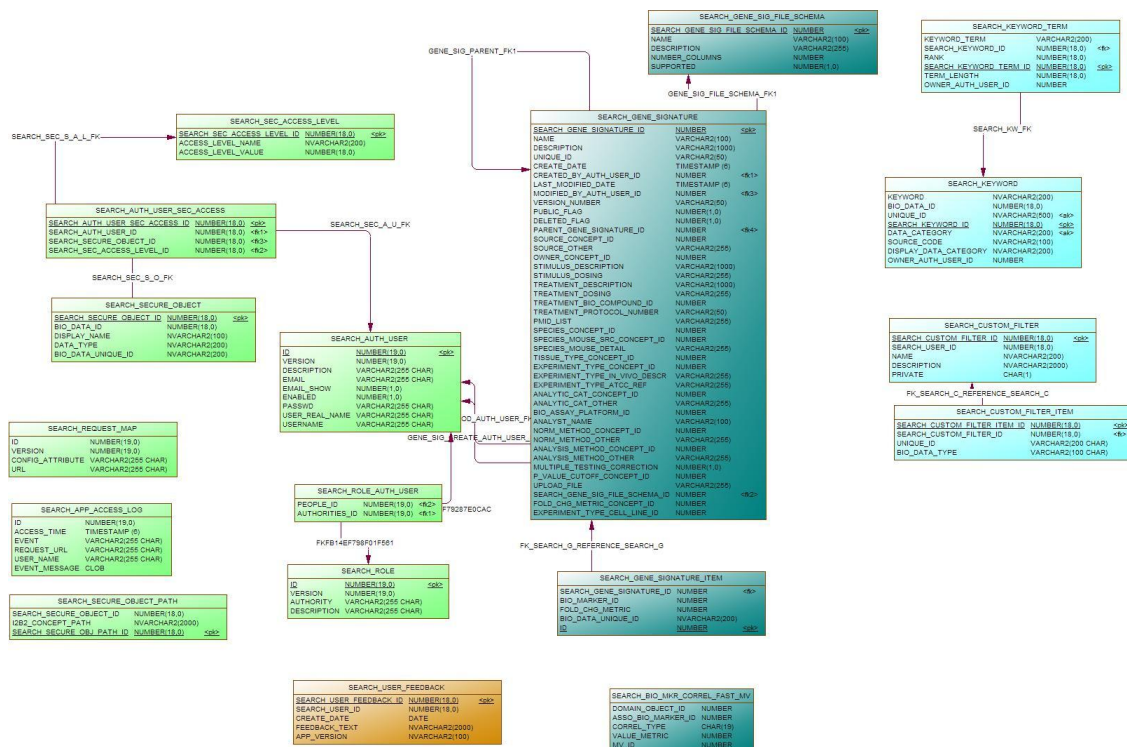


Note: To return to this PDF page after viewing the full-size diagram, click your browser's Back button, if it is displayed, or right-click the solid bar above the diagram, then click Back.

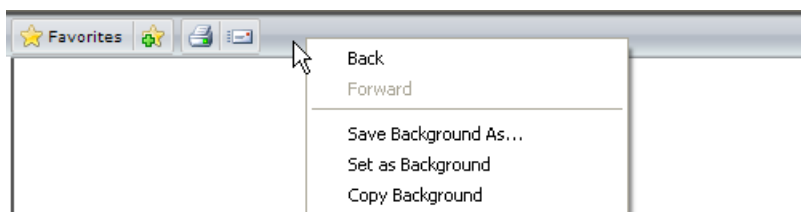


Data Mart for tranSMART Search

Click the image to display a larger version of the diagram.



Note: To return to this PDF page after viewing the full-size diagram, click your browser's Back button, if it is displayed, or right-click the solid bar above the diagram, then click Back.



I2B2METADATA and I2B2DEMODATA

I2B2METADATA

I2B2	
C_HLEVEL	NUMBER(22,0)
C_FULLNAME	VARCHAR2(900)
C_NAME	VARCHAR2(2000)
C_SYNONYM_CD	CHAR(1)
C_VISUALATTRIBUTES	CHAR(3)
C_TOTALNUM	NUMBER(22,0)
C_BASECODE	VARCHAR2(450)
C_METADATAXML	CLOB
C_FACTTABLECOLUMN	VARCHAR2(50)
C_TABLENAME	VARCHAR2(50)
C_COLUMNNAME	VARCHAR2(50)
C_COLUMNDATATYPE	VARCHAR2(50)
C_OPERATOR	VARCHAR2(10)
C_DIMCODE	VARCHAR2(900)
C_COMMENT	CLOB
C_TOOLTIP	VARCHAR2(900)
UPDATE_DATE	DATE
DOWNLOAD_DATE	DATE
IMPORT_DATE	DATE
SOURCESYSTEM_CD	VARCHAR2(50)
VALUETYPE_CD	VARCHAR2(50)

I2B2_TAGS	
TAG_ID	NUMBER(18,0) <small><pk></small>
PATH	NVARCHAR2(200)
TAG	NVARCHAR2(200)
TAG_TYPE	NVARCHAR2(200)

I2B2_SECURE	
C_HLEVEL	NUMBER(22,0)
C_FULLNAME	VARCHAR2(900)
C_NAME	VARCHAR2(2000)
C_SYNONYM_CD	CHAR(1)
C_VISUALATTRIBUTES	CHAR(3)
C_TOTALNUM	NUMBER(22,0)
C_BASECODE	VARCHAR2(450)
C_METADATAXML	CLOB
C_FACTTABLECOLUMN	VARCHAR2(50)
C_TABLENAME	VARCHAR2(50)
C_COLUMNNAME	VARCHAR2(50)
C_COLUMNDATATYPE	VARCHAR2(50)
C_OPERATOR	VARCHAR2(10)
C_DIMCODE	VARCHAR2(900)
C_COMMENT	CLOB
C_TOOLTIP	VARCHAR2(900)
UPDATE_DATE	DATE
DOWNLOAD_DATE	DATE
IMPORT_DATE	DATE
SOURCESYSTEM_CD	VARCHAR2(50)
VALUETYPE_CD	VARCHAR2(50)
SECURE_OBJ_TOKEN	VARCHAR2(50)

I2B2DEMODATA

OBSERVATION_FACT	
ENCOUNTER_NUM	
PATIENT_NUM	
CONCEPT_CD	
PROVIDER_ID	
START_DATE	
MODIFIER_CD	
VALTYPE_CD	
TVAL_CHAR	
NVAL_NUM	
VALUEFLAG_CD	
QUANTITY_NUM	
UNITS_CD	
END_DATE	
LOCATION_CD	
CONFIDENCE_NUM	
UPDATE_DATE	
DOWNLOAD_DATE	
IMPORT_DATE	
SOURCESYSTEM_CD	
UPLOAD_ID	
OBSERVATION_BLOB	

PATIENT_DIMENSION	
PK	PATIENT_NUM
VITAL_STATUS_CD	
BIRTH_DATE	
DEATH_DATE	
SEX_CD	
AGE_IN_YEARS_NUM	
LANGUAGE_CD	
RACE_CD	
MARITAL_STATUS_CD	
RELIGION_CD	
ZIP_CD	
STATECITYZIP_PATH	
UPDATE_DATE	
DOWNLOAD_DATE	
IMPORT_DATE	
SOURCESYSTEM_CD	
UPLOAD_ID	
PATIENT_BLOB	

CONCEPT_COUNTS	
CONCEPT_PATH	
PARENT_CONCEPT_PATH	
PATIENT_COUNT	

CONCEPT_DIMENSION	
PK	CONCEPT_PATH
CONCEPT_CD	
NAME_CHAR	
CONCEPT_BLOB	
UPDATE_DATE	
DOWNLOAD_DATE	
IMPORT_DATE	
SOURCESYSTEM_CD	
UPLOAD_ID	
TABLE_NAME	

PROVIDER_DIMENSION	
PK	PROVIDER_ID
PK	PROVIDER_PATH
NAME_CHAR	
PROVIDER_BLOB	
UPDATE_DATE	
DOWNLOAD_DATE	
IMPORT_DATE	
SOURCESYSTEM_CD	
UPLOAD_ID	

DEAPP

DE_SUBJECT_MICROARRAY_DATA	
TRIAL_NAME	VARCHAR2(50)
PROBESET_ID	NUMBER(22,0)
ASSAY_ID	NUMBER(18,0)
PATIENT_ID	NUMBER(18,0)
TIMEPOINT	VARCHAR2(100)
PVALUE	FLOAT(128)
REFSEQ	VARCHAR2(50)
SUBJECT_ID	VARCHAR2(50)
RAW_INTENSITY	NUMBER
LOG_INTENSITY	NUMBER
MEAN_INTENSITY	NUMBER
STDDEV_INTENSITY	NUMBER
MEDIAN_INTENSITY	NUMBER
ZSCORE	NUMBER

DE_SUBJECT_RBM_DATA	
TRIAL_NAME	VARCHAR2(15)
ANTIGEN_NAME	VARCHAR2(100)
N_VALUE	NUMBER
PATIENT_ID	NUMBER(38,0)
GENE_SYMBOL	VARCHAR2(100)
GENE_ID	NUMBER(10,0)
ASSAY_ID	NUMBER
NORMALIZED_VALUE	NUMBER(18,5)
CONCEPT_CD	NVARCHAR2(100)
TIMEPOINT	VARCHAR2(100)
DATA_UID	VARCHAR2(100)
VALUE	NUMBER
LOG_INTENSITY	NUMBER
MEAN_INTENSITY	NUMBER
STDDEV_INTENSITY	NUMBER
MEDIAN_INTENSITY	NUMBER
ZSCORE	NUMBER

DE_SUBJECT_PROTEIN_DATA	
TRIAL_NAME	VARCHAR2(15)
COMPONENT	VARCHAR2(15)
INTENSITY	NUMBER
PATIENT_ID	NUMBER(38,0)
SUBJECT_ID	VARCHAR2(10)
GENE_SYMBOL	VARCHAR2(100)
GENE_ID	NUMBER(10,0)
ASSAY_ID	NUMBER
TIMEPOINT	VARCHAR2(20)
N_VALUE	NUMBER
MEAN_INTENSITY	NUMBER
STDDEV_INTENSITY	NUMBER
MEDIAN_INTENSITY	NUMBER
ZSCORE	NUMBER

HAPLOVIEW_DATA	
I2B2_ID	NUMBER(20,0)
JNJ_ID	VARCHAR2(20)
FATHER_ID	NUMBER(5,0)
MOTHER_ID	NUMBER(5,0)
SEX	NUMBER(1,0)
AFFECTION_STATUS	NUMBER(1,0)
CHROMOSOME	VARCHAR2(10)
GENE	VARCHAR2(50)
RELEASE	NUMBER(4,0)
RELEASE_DATE	DATE
TRIAL_NAME	VARCHAR2(50)
SNP_DATA	CLOB

SNP_INFO	
SNP	VARCHAR2(50)
GENE	VARCHAR2(50)
POSITION	NUMBER(20,0)
CHROMOSOME	VARCHAR2(8)
REFSNP	VARCHAR2(20)
STRAND	VARCHAR2(10)
SNP_IDX	NUMBER(4,0)

DE_SUBJECT_SAMPLE_MAPPING	
PATIENT_ID	NUMBER(18,0)
SITE_ID	NVARCHAR2(100)
SUBJECT_ID	NVARCHAR2(100)
SUBJECT_TYPE	NVARCHAR2(100)
CONCEPT_CODE	VARCHAR2(1000 CHAR)
ASSAY_ID	NUMBER(18,0)
PATIENT_UID	VARCHAR2(50)
SAMPLE_TYPE	VARCHAR2(100)
ASSAY_UID	NVARCHAR2(100)
TRIAL_NAME	VARCHAR2(30)
TIMEPOINT	VARCHAR2(100)
TIMEPOINT_CD	VARCHAR2(50)
SAMPLE_TYPE_CD	VARCHAR2(50)
TISSUE_TYPE_CD	VARCHAR2(50)
PLATFORM	VARCHAR2(50)
PLATFORM_CD	VARCHAR2(50)
TISSUE_TYPE	VARCHAR2(20)
DATA_UID	VARCHAR2(100)
GPL_ID	VARCHAR2(20)

DE_MRNA_ANNOTATION	
GPL_ID	VARCHAR2(100)
PROBE_ID	VARCHAR2(100)
GENE_SYMBOL	VARCHAR2(100)
GENE_ID	VARCHAR2(100)
PROBESET_ID	NUMBER(38,0)

DEAPP_ANNOTATION	
ANNOTATION_TYPE	VARCHAR2(50)
ANNOTATION_VALUE	VARCHAR2(100)
GENE_ID	NUMBER
GENE_SYMBOL	VARCHAR2(200)

DEAPP_PROBESET	
PROBESET_ID	NUMBER(38,0)
PROBESET	VARCHAR2(100)
PLATFORM	VARCHAR2(100)

DE_XTRIAL_CHILD_MAP	
CONCEPT_CD	VARCHAR2(50) <pk>
PARENT_CD	NUMBER <fk>
MANUALLY_MAPPED	NUMBER
STUDY_ID	VARCHAR2(50)

DE_XTRIAL_PARENT_NAMES	
PARENT_CD	NUMBER <pk>
ACROSS_PATH	VARCHAR2(500) <pk>
MANUALLY_CREATED	NUMBER

DE_SAVED_COMPARISON	
COMPARISON_ID	NUMBER
QUERY_ID1	NUMBER
QUERY_ID2	NUMBER

