March 6, 2025

MHS GENESIS Microbiology Results and Susceptibility

for the

MHS Data Repository (MDR)

(Version 1.02.07)

Future Specification

Revision History

Version	Date	Originator	Para/Tbl/Fig	Description of Change
1.00.00	4/25/2019	S. Keane	Initial Document	Baseline
1.01.00	5/30/2019	S. Keane	Whole Document	Add MHS GENESIS Microbiology Response phrases to Results file.
1.02.00	08/25/2020	S. Keane	Section VII Tables 1 & 2	Match contents with final output.
1.02.01	9/21/2020	S. Keane	Section VII Tables 1 & 2	Match contents with final output.
1.02.02	11/5/2020	S. Keane	Table 1	Update Field Lengths for: FIRST_NAME_P, LAST_NAME_P, PRSNL_COMPL_FNAME, PRSNL_COMPL_LNAME, PRSNL_ORD_FNAME, PRSNL_ORD_LNAME, PRNSL_VERIFIED_FNAME, PRSNL_VERIFIED_LNAME
1.02.03	11/20/2020	S. Keane	Table 1	Remove first/last name fields. Replace with Full Name for Patient, Personnel Verified, Personnel Completing, and Personnel Non-Physician Ordering variables.
1.02.04	02/17/2022	S. Keane	Section IV	Add Time Slicing, Frequency of processing, and Frequency of updates.
1.02.05	09/20/2023	S. Keane	Entire Document	Add Bulk Data Extract (BDE) Redshift 3.0 feed logic.
1.02.06	12/03/2024	S. Keane	Table 2.	Update business rules for BDE 3.0 MHS GENESIS Microbiology Susceptibility Results table.
1.02.07	03/06/2025	S. Keane	Table 2. and Section IX.	Hide T3 Region and add T5 Region. Add Special Outputs Section.

MHS GENESIS Microbiology Results and Susceptibility Tables

I. BACKGROUND

This specification describes the process required to create the Military Health System (MHS) Data Repository (MDR) GENESIS Microbiology Result and Susceptibility tables based on data received from Cerner PowerInsight Enterprise Data Warehouse (PI-EDW) feeds to the MDR and the MIP Redshift 3.0 feeds.

II. SOURCES

The source data files used to create the MHS GENESIS Microbiology Result and Susceptibility tables are extracted from the MHS GENESIS PI-EDW and MIP Redshift 3.0. The transfer of the raw source extracts is handled by the Solution Delivery Division (SDD) for loading into the MDR for further processing according to routine MDR operations. The format of the raw MHS GENESIS feeds to the MDR is described in the Department of Defense Healthcare Management System Modernization (DHMSM®) Program DRAFT Interface Control Document (ICD) for Bulk Data Extract (BDE).

III. TRANSMISSION (FILES AND FREQUENCY)

MHS GENESIS BDE PI-EDW feeds are provided weekly and MIP Redshift 3.0 feeds are updated daily.

IV. ORGANIZATION AND BATCHING

Source Data: The first step in MDR processing is to batch records received from MHS GENESIS. Raw data batches are stored in /mdr/raw/genesis according to routine MDR operating procedures.

Output Products: The processor outputs separate SAS data sets containing all years of data. The processor performs merges and field derivations, and must incorporate updates to records across raw data extracts. The output datasets results.sas7bdat and suscept.sas7bdat will be stored in the following directory: /mdr/pub/genesis/laboratory/results/mb/results.sas7bdat

/mdr/pub/genesis/laboratory/results/mb/suscept.sas7bdat

Time slicing: Data are organized into fiscal year files. The Fiscal Year is determined by DATE_COMPELETE.

Frequency of processing: Data are harvested weekly. Raw data batches are harvested, processed, and appended/updated to the master file. If data are received from a fiscal year not being processed that month, they will be held to batch with all other data received prior to that fiscal year's next update batch.

Frequency of updates:
Current FY: Weekly.
Prior FY: Weekly for one quarter (October, November, and December) then semiannually (April, October).

All years prior to prior FY: Annually (October) or on an as needed basis when data corrections or updates are required.

Archiving (APUB): Use routine archiving rules and procedures of the MDR.

Receiving Filters: There are no receiving filters.

MHS GENESIS Microbiology Result and Susceptibility tables will contain result-records for orders in the MHS GENESIS Laboratory table where Activity Type = "Microbiology". Select result records that match order records on primary key. All records were provided with the initial batch of data. Thereafter, new and changed records are sent each week.

V. UPDATE PROCESSES

New raw feeds contain either insert or update records. These records shall be used to update the master The processor shall delete duplicates before updating the table. Duplicate records, defined as those with the same primary key. When choosing among duplicate records, the processor shall select the record with the most recent value for the variable: UPDT_DT_TM (update date/time (UPDT_DT_TM) for multiple of records with the same primary key. Table A lists the final two (2) datasets and each table's primary key. ORDER_SK is used to link the tables.

Table A: Final Datasets

Microbiology Results Final Datasets	Primary Key
MHS GENESIS Microbiology Results	ORDER_SK
MHS GENESIS Microbiology Susceptibility Results	SUSCEPT_RESULTS_SK

VI. FILE MERGES

Tables B and C describe the data merges that are necessary to append many of the fields in the MHS GENESIS Microbiology Result and Susceptibility files.

Table B: File Merges from PI-EDW Source Tables

Merge	Key Matching
MHS GENESIS Laboratory Orders	Select records where ACTIVITY_TYPE = 'Microbiology'. Match on ORDER_SK.
MHS GENESIS Microbiology Order	Match on ORDER_SK. Use MICRO_ORDER_SK for additional matching.
MHS GENESIS Microbiology Task	Match on MICRO_ORDER_SK. Use MICRO_TASK_SK for additional matching.
MHS GENESIS Microbiology Susceptibility Results	Match on MICRO_TASK_SK.
MHS GENESIS Microbiology Report Response	Match on MICRO_TASK_SK.
MHS GENESIS Clinical Event	Match on ORDER_SK. Select records where EVENT_CLASS_REF in ('230'). Use EVENT_SK for additional matching.
MHS GENESIS Clinical Event Result Associations	Match on EVENT_SK.
MHS GENESIS Personnel	Match on VERIFIED_PRSNL.

Table C: File Merges from MIP Redshift 3.0 Source Views

Source Table Name	View Name	Date Matching	Key Matching
MHS GENESIS Microbiology Order	genesis_vw.mic_order_lab		encntr_id, order_id
	genesis_vw.ce_microbiology		event_id
MHS GENESIS Microbiology Task	genesis_vw.mic_task_log		order_id, task_log_id
MHS GENESIS Microbiology Susceptibility Results	genesis_vw.ce_susceptibility		event_id
MHS GENESIS Microbiology Report Response	genesis_vw.mic_report_response		task_log_id
MHS GENESIS Clinical Event	genesis_vw.clinical_event	valid_until_dt_tm > sysdate	encntr_id, order_id, event_id
MHS GENESIS Clinical Event Specimen	genesis_vw.ce_specimen_coll		event_id
MHS GENESIS Container	genesis_vw.container		container_id

VII. FILE LAYOUT

Table 1 describes the file layout and derivation rules for the MHS GENESIS Microbiology Results file. Unless specified, business rules apply to both source tables. Listed by Source table then by Variable Name.

Table 1 MHS GENESIS Microbiology Results

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
MHS GENESIS Microbiology Order					
Date Time Culture Start	CULTURE_START_DT_TM	E8601DT	culture_start_dt_tm	culture_start_dt_tm	Format e8601dt.
Date Time Culture Start Local	CULTURE_START_DT_TM_local	E8601DT	culture_start_dt_tm	culture_start_dt_tm	Format e8601dt. Convert to local Time.
Date Time Specimen Collected	FIRST_CTNR_DRAWN_DT_TM	E8601DT	first_ctnr_drawn_dt_tm	collect_dt_tm	Format e8601dt.
Date Time Specimen Collected Local	FIRST_CTNR_DRAWN_DT_TM_local	E8601DT	first_ctnr_drawn_dt_tm	collect_dt_tm	Format e8601dt. Convert to local Time.
Nosocomial Infection Indicator	NOSOCOIMAL_IND	N(8)		non_socomial_ind	2.4 No Transformation. 3.0 Rename NON_SOCOMIAL_IND = NOSOCOMIAL_IND.
Number of Containers	NBR_OF_CONTAINERS	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Number of Specimens	NBR_OF_SPECIMENS	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Order Comment	ORDER_COMMENT	$255.00	source_site_freetext	source_text	2.4 rename SOURCE_SITE_FREETEXT = ORDER_COMMENT. 3.0 rename SOURCE_TEXT = ORDER_COMMENT.
Order Status	ORDER_STATUS	$20.00	status_ref	status_cd	put(STATUS_REF, $MICSI.) as ORDER_STATUS (code set 1031).

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Positive Response Indicator	ORDER_POSITIVE_IND	N(8)		positive_ind	None.
Specimen	SPECIMEN	$38.00	first_specimen_type_ref	specimen_type_cd	put(FIRST_SPECIMEN_TYPE_REF, $SPECT.) as SPECIMEN (code set 2052).
Specimen Collected Indicator	COLLECTED_IND	N(8)		specimen_id	2.4 No Transformation. 3.0 If specimen_id is null then 0; else 1.
Specimen Collection Method	COLLECTION_METHOD	$13.00	first_ctnr_coll_method_ref	collection_method_cd	put(FIRST_CTNR_COLL_METHOD_REF, $COLLM.) as COLLECTION_METHOD (code set 2058).
Specimen Collection Priority	PRIORITY	$11.00	collection_priority_ref	collect_priority_cd	put(COLLECTION_PRIORITY_REF, $collection_priority.) as PRIORITY, (code set 2054).
Specimen Container	CONTAINER_TYPE	$59.00	first_ctnr_type_ref	spec_cntnr_cd	put(FIRST_CTNR_TYPE_REF, $SPECC.) as CONTAINER_TYPE (code set 2051).
Specimen Container Units	CONTAINER_UNITS	$60.00	first_cntr_units_ref	units_cd	2.4 put(FIRST_CNTR_UNITS_REF, $UNITII.) as CONTAINER_UNITS (code set 240). 3.0 Apply code set 54.
Specimen Site	SPECIMEN_SITE	$38.00	first_specimen_site_ref	body_site_cd	put(FIRST_SPECIMEN_SITE_REF, $BODYS.) as SPECIMEN_SITE (code set 1028).
Volume	VOLUME	N(8)	first_cntr_volume	collect_volume	2.4 rename FIRST_CNTR_VOLUME = VOLUME. 3.0 rename COLLECT_VOLUME = VOLUME.
MHS GENESIS Clinical Event					
Accession Number Clinical Events	ACCESSION_NBR	$100.00		accession_nbr	None.
Date Time Verified	VERIFIED_DT_TM	E8601DT		verified_dt_tm	None.
Date Time Verified Local	VERIFIED_DT_TM_local	E8601DT	verified_dt_tm	verified_dt_tm	Format e8601dt. Convert to local Time.
Event SK	EVENT_SK	$100.00		event_id	None.
MHS Genesis Test Ordered Desc Clinical Events	EVENT_CODE	$60.00	event_code_ref	event_cd	put(event_code_ref,$ev_code.) as EVENT_CODE(code set 72).
Normalcy Indicator	EVENT_NORMACY	$14.00	event_normacy_ref	normalcy_cd	put(EVENT_NORMACY_REF, $ev_norm.) as EVENT_NORMACY (code set 52).
Order SK	ORDER_SK	$100.00		order_id	None.
MHS GENESIS Microbiology Task					
Organism n (where n = 1-8)	ORGANISM	$60.00	organism_ref	organism_cd	put(ORGANISM_REF, $ORGAO.) as ORGANISMn (code set 1021). Transpose Organism.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
MHS GENESIS Clinical Even Result Asssociations					
LOINC Code	LOINC_CODE	$60.00	value	source_identifier	2.4 Obtain value AS LOINC_CODE match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain source_identifier as LOINC_CODE match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.
LOINC Description	LOINC_DESCRIPTION	$255.00	description	source_string	2.4 Obtain description as LOINC_DESCRIPTION match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain source_string as LOINC_DESCRIPTION match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.
LOINC Lab Test Name	LAB_OBSERVATION_NAME	$60.00	display	short_string	2.4 Obtain display AS LAB_OBSERVATION_NAME match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain short_string as LAB_OBSERVATION_NAME match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.
MHS GENESIS Personnel					
Personnel Verified EDIPN	PRSNL_VERIFIED_EDIPN	$10.00	prsnl_verified_edipn	prsnl_verified_edipn	2.4 Obtain PRSNL_EDIPN from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Personnel Verified HIPAA	PRSNL_VERIFIED_HIPAA	$10.00	prsnl_verified_hipaa	prsnl_verified_hipaa	2.4 Obtain HIPAA1 from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.
Personnel Verified Name	PRNSL_VERIFIED_NAME	$61.00	prsnl_verified_name	prsnl_verified_name	2.4 Obtain FULL_NAME from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.
Personnel Verified MD Flag	PRSNL_VERIFIED_MD_FLAG	N(8)	prsnl_verified_md_flag	prsnl_verified_md_flag	2.4 Obtain PHYSICIAN_IND from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.
Personnel Verified NPI	PRSNL_VERIFIED_NPI	$10.00	prsnl_verified_npi	prsnl_verified_npi	2.4 Obtain NPI from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.
Personnel Verified Test Indicator	PRSNL_VERIFIED_FLAG	$1.00	prsnl_verified_flag	prsnl_verified_flag	2.4 Obtain TEST_RECORD_IND from Personnel; Match on VERIFIED_PRSNL from clev_ccevent = PRSNL_SK from personnel. 3.0 Use verified_prsnl_id as verified_prsnl.
MHS GENESIS Laboratory Orders					
Accession Number	ACCESSION	$100.00			None.
Ben Cat Common	COMBEN_D	$1.00			None.
Beneficiary Category	BENCAT_D	$3.00			None.
Beneficiary Zip Code	ZIP_D	$5.00			None.
Date Complete	DATE_COMPLETE	$8.00			None.
Date Time Order Local	ORDER_DT_TM_LOCAL	DATETIME			None.
Eligibility Group	ELG_GRP	$1.00			None.
Encounter PI-EDW Key	ENCOUNTER_KEY	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Encounter SK	ENCOUNTER_SK	$100.00		n/a	2.4 No Transformation. 3.0 NULL.
Encounter Type	ENCOUNTER_TYPE	$22.00			None.
Enrollment Group	ENR_GRP	$1.00			None.
Financial Information Number (FIN)	FIN_E	$40.00			None.
Fiscal Month	FM	$2.00			None.
Fiscal Year	FY	$4.00			None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Genesis Go Live Date	gen_begin_dt	MMDDYY			None.
Inpatient Indicator	INPT	$1.00			None.
Medical Record Number	MRN	$40.00			None.
MEPRS4 Code, Ordering	MEPRS_CD	$4.00			None.
MHS Genesis Flag	MHS_GENESIS_FLAG	$1.00			None.
MHS Genesis Test Ordered Description	ORDERABLE_DISP	$100.00			None.
MTF	MTF	$4.00			None.
MTF Display Name	UNIT_DISPLAY	$45.00			None.
MTF Name	UNIT_NAME	$100.00			None.
Parent MTF Name	ORGANIZATION_NAME	$40.00			None.
Patient Age	PATAGE	N(8)			None.
Patient Date of Birth	PATDOB	YYMMDDN			None.
Patient EDIPN	EDIPN	$10.00			None.
Patient Name	NAME	$61.00			None.
Patient Gender	GENDER_D	$1.00			None.
Patient Race	RACE	$1.00			None.
Patient SSN	SSN	$9.00			None.
Person SK	PERSON_SK	$100.00			None.
Personnel Completing EDIPN	PRSNL_COMPL_EDIPN	$10.00			None.
Personnel Completing HIPAA Taxonomy	PRSNL_COMPL_HIPAA	$10.00			None.
Personnel Completing Name	PRSNL_COMPL_NAME	$61.00			None.
Personnel Completing MD Flag	PRSNL_COMPL_MD_FLAG	N(8)			None.
Personnel Completing NPI	PRSNL_COMPL_NPI	$100.00			None.
Personnel Non-Physician Ordering EDIPN	PRSNL_ORD_EDIPN	$10.00			None.
Personnel Non-Physician Ordering HIPAA	PRSNL_ORD_HIPAA	$10.00			None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Personnel Non-Physician Ordering Name	PRSNL_ORD_NAME	$61.00			None.
Personnel Non-Physician Ordering MD Flag	PRSNL_ORD_MD_FLAG	N(8)			None.
Personnel Non-Physician Ordering NPI	PRSNL_ORD_NPI	$100.00			None.
Sponsor ID	SPONSSN	$9.00			None.
Sponsor Service	SPONSVC	$1.00			None.
Sponsor Service, Aggregate	SVCAGG	$1.00			None.
Tmt MTF Military Service	MTF_SVC	$1.00			None.
Tmt MTF Parent of Record	MTF_PARENT_REC	$4.00			None.
Tmt MTF T17 Region	MTF_T17_REG	$2.00			None.
Tmt MTF T3 Region	MTF_T3_REG	$2.00			Hide. Not populated as of Jan 2025.
Tmt MTF T3 Region	MTF_T5_REG	$2.00			Populated FY23+.
Internally Derived					
Related Suscept-Result Flag	RESULT_FLAG_SUSCEPT	N(8)			2.4 If micro_order_sk in (Results, Suscept) then 1; else 0. 3.0 If order_id in (Results, Suscept) then 1; else 0.

Table 2 describes the file layout and derivation rules for the MHS GENESIS Microbiology Susceptibility file.

Table 2 MHS GENESIS Microbiology Susceptibility Results

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
MHS GENESIS Microbiology Order					
Order SK	ORDER_SK	$100.00	order_sk	order_id	None.
Body Site	SPECIMEN_SITE	$38.00	first_specimen_site_ref	body_site_cd	put(FIRST_SPECIMEN_SITE_REF, $BODYS.) as SPECIMEN_SITE (code set 1028).
Number of Containers	NBR_OF_CONTAINERS	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Order Positive Indicator	ORDER_POSITIVE_IND	N(8)		positive_ind	None.
Specimen	SPECIMEN	$38.00	first_specimen_type_ref	specimen_type_cd	put(FIRST_SPECIMEN_TYPE_REF, $SPECT.) as SPECIMEN (code set 2052).

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Specimen Container	CONTAINER_TYPE	$59.00	first_ctnr_type_ref	spec_cntnr_cd	put(FIRST_CTNR_TYPE_REF, $SPECC.) as CONTAINER_TYPE (code set 2051).
Specimen Container Units	CONTAINER_UNITS	$60.00	first_cntr_units_ref	units_cd	2.4 put(FIRST_CNTR_UNITS_REF, $UNITII.) as CONTAINER_UNITS (code set 240). 3.0 Apply code set 54.
Volume	VOLUME	N(8)	first_cntr_volume	collect_volume	2.4 rename FIRST_CNTR_VOLUME = VOLUME. 3.0 rename COLLECT_VOLUME = VOLUME.
MHS GENESIS Microbiology Task					
Organism	ORGANISM	$60.00	organism_ref	organism_cd	put(ORGANISM_REF, $ORGAO.) as ORGANISM (code set 1021).
MHS GENESIS Microbiology Susceptibility Results					
Abnormal Response Indicator	ABNORMAL_RESPONSE_IND	N(8)		abnormal_flag	None.
Alpha Numeric Result	ALPHA_NUMERIC_RESULT	$20.00	alpha_numeric_result_ref	result_cd	2.4 put(ALPHA_NUMERIC_RESULT_REF, $ALPSR.) as ALPHA_NUMERIC_RESULT (code set 1025). 3.0 apply code sets 64, 1025 where suscept_seq_nbr = 1.
Antibiotic Medication	ANTIBIOTIC_MEDICATION	$32.00	antibiotic_medication_ref	antibiotic_cd	put(ANTIBIOTIC_MEDICATION_REF, $ANTIA.) as ANTIBIOTIC_MEDICATION 3.0 apply code sets (code sets 39, 1011).
Chartable Indicator	CHARTABLE_IND	N(8)		chartable_flag	None.
Detail Test Type	DETAIL_TEST_TYPE	$30.00	detail_test_type_ref	detail_susceptibility_cd	put(DETAIL_TEST_TYPE_REF, $SUSCD.) as DETAIL_TEST_TYPE (code set 1004). 3.0 Apply code set 1004 where suscept_seq_nbr =2.
Interpretation Result	INTERPRETATION_RESULT	$28.00	interpretation_result_ref	result_cd	2.4 put(INTERPRETATION_RESULT_REF, $SUSIR.) as INTERPRETATION_RESULT (code set 64). 3.0 Apply code sets (64, 1025) where suscept_seq_nbr = 2.
MIC Dilution	MIC_DILUT	$100.00	result_txt	result_cd	2.4 If RESULT_TYPE_FLAG = 7 then RESULT_TXT = MIC_INTERP; else RESULT_TXT = MIC_DILUT. 3.0 Apply code sets (64, 1025) where suscept_seq_nbr = 1.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
MIC Interpretation	MIC_INTERP	$100.00	result_txt	result CD	2.4 If RESULT_TYPE_FLAG = 7 then RESULT_TXT = MIC_INTERP; else RESULT_TXT = MIC_DILUT. 3.0 Apply code sets (6,1025) where suscept_seq_nbr = 2.
Numeric Result	NUMERIC_RESULT	N(8)		result_numeric_value	None.
Panel	PANEL	$27.00	panel_ref	panel_antibiotic_cd	2.4 put(PANEL_REF, $MICRT.) as PANEL (code set 1010). 3.0 apply code sets 1010, 132038.
Panel Complete Required Indicator	PANEL_COMPLETE_REQUIRED_IND	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Result Status	RESULT_STATUS	$45.00	result_status_ref	susceptibility_status_cd	put(RESULT_STATUS_REF, $MICSII.) as RESULT_STATUS (code set 1901).
Result Unit	RESULT_UNIT	$60.00	result_unit_ref	result_unit_cd	put(RESULT_UNIT_REF, $unit_ref.) as RESULT_UNIT (code set 54).
Susceptibility Results SK	SUSCEPT_RESULTS_SK	$100.00		event_id, micro_seq_nbr,suscept_seq_nbr	2.4 No Transformation. 3.0 Order by event_id,micro_seq_nbr, suscept_seq_nbr then concatenate(event_id,~, micro_seq_nbr, ~, row_num (1-n) for every unique suscept_seq_nbr) .
MHS GENESIS Clinical Event					
Date Time Verified Local	VERIFIED_DT_TM_local	E8601DT	verified_dt_tm	verfied_dt_tm, verified_tz	Format e8601dt. Convert to local Time.
Encounter SK	ENCOUNTER_SK	$100.00		n/a	2.4 No Transformation. 3.0 NULL.
MHS Genesis Test Ordered Desc Clinical Events	EVENT_CODE	$60.00	event_code_ref	event_cd	put(event_code_ref,$ev_code.) as EVENT_CODE (code set 72).
MHS GENESIS Laboratory Orders					
Accession Number	ACCESSION	$100.00			None.
Ben Cat Common	COMBEN_D	$1.00			None.
Beneficiary Category	BENCAT_D	$3.00			None.
Date Complete	DATE_COMPLETE	$8.00			None.
Date Time Order Local	ORDER_DT_TM_LOCAL	DATETIME			None.
Encounter Type	ENCOUNTER_TYPE	$22.00			None.
Financial Information Number (FIN)	FIN_E	$40.00			None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Fiscal Month	FM	$2.00			None.
Fiscal Year	FY	$4.00			None.
Inpatient Indicator	INPT	$1.00			None.
Medical Record Number	MRN	$40.00			None.
MEPRS4 Code, Ordering	MEPRS_CD	$4.00			None.
MHS Genesis Test Ordered Desc	ORDERABLE_DISP	$100.00			None.
MTF	MTF	$4.00			None.
MTF Display Name	UNIT_DISPLAY	$45.00			None.
MTF Name	UNIT_NAME	$100.00			None.
Parent MTF Name	ORGANIZATION_NAME	$40.00			None.
Patient EDIPN	EDIPN	$10.00			None.

VIII. EXCLUSIONS

Here are the conditions required to exclude and/or remove records from the MHS GENESIS Microbiology Results and Susceptibility files. If any of the following conditions are met, either delete the record or output to an error file.

If primary key is missing or zero.

IX. SPECIAL OUTPUTS

This file serves as the input to the MIP Core MHS GENESIS Microbiology Results table. In accordance with Technical Data Standards, the data should be made available to users with the same file names, field names and formats as the source data, with underscores replacing spaces in the names, if desired. The MIP core MHS GENESIS Microbiology Results table should be updated at the same cadency of the M2 file and row counts should be validated against the MDR Export transmittals.