

# 2023 Call for Data



# Presenter



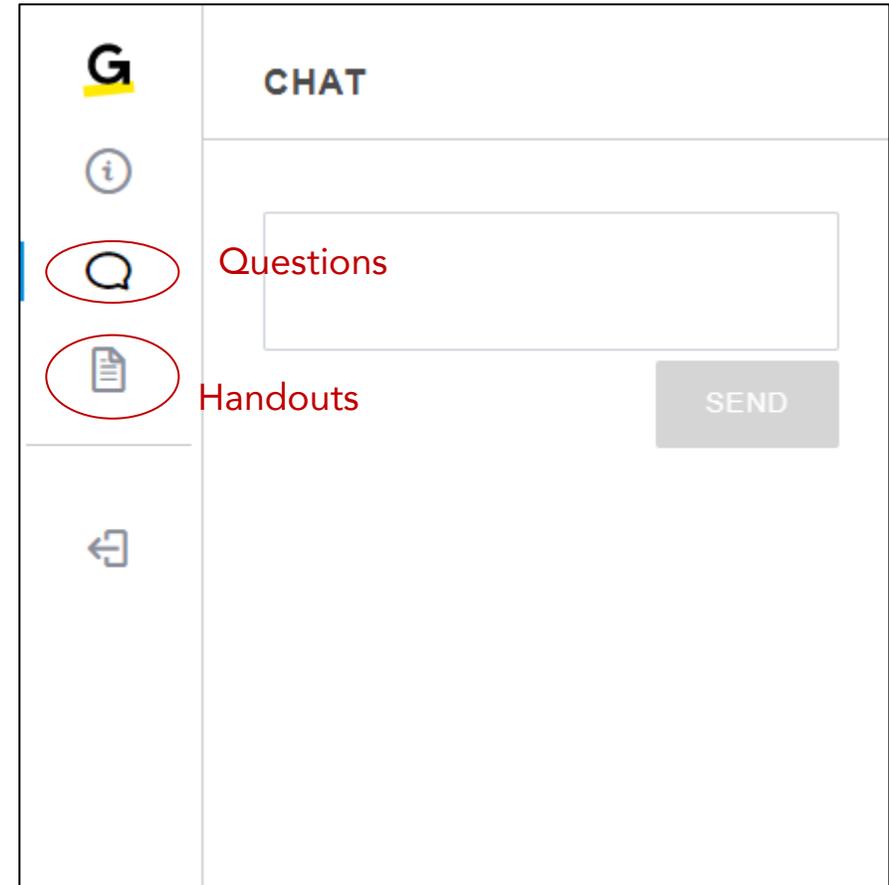
Amy Arnold, BA, CTR  
aarnold@mycrstar.com

# Housekeeping

- If you have trouble hearing the presentation and are listening through your computer, please check and adjust your volume settings. There will not be a call in feature for this webinar. If your speakers are having issues you may be able to use headphones with your computer.
- The webinar will be approximately 30 minutes in length
- CE certificates will be sent to attendees later this week to the email address you provided during registration for this webinar
- A recording of this webinar, along with handouts and the Q&A will be made available to attendees in the coming days

# Navigating GTW

- Download handouts and ask questions from the GTW control panel
- Ask questions! All questions will be answered in a follow up Q&A document



# Objectives

- To familiarize CRStar users with the processes involved in answering to the 2023 NCDB Call for Data
- To offer suggestions for Best Practices to help prepare for the Call for Data
- To demonstrate the use of the CRStar exporting application and the most up to date version of GenEDITS Plus 5.1.1.1 software

# NCDB Call for Data

- Information can be found here:  
<https://www.facs.org/quality-programs/cancer/ncdb/call-for-data>

## / Registrars

### Information for Registrars

[2023 Information for Registrars and CoC Program Standards 6.4 Documents Combined](#)

[Tool—NCDB Call for Data Submission Count Tracking by Diagnosis Year](#)

[GenEDITS Plus 5—Download and install from the CDC website](#)

## / Configuration/Setup

### Metafile and CoC User Dictionary

[NCDB and RCRS v22 Metafile](#)

[NCDB and RCRS v23 Metafile](#)

[V22 CoC User Specific Dictionary with NPI and Breast Surgical Codes](#)

[V23 CoC User Specific Dictionary](#)

# Data Submission Information

- Submission Window opens on 3/1/2023 and closes on 3/31/2023 at 11:59 CST
- Required Submission – Existing Programs
  - Analytic cases
  - All new cases diagnosed on or after 2007 through 2021
  - All updated/changed cases diagnosed on or after 2007 through 2020 (Those previously submitted in prior call for data exports)
- Required Submission – New Program
  - All analytic cases diagnosed on or after 2007 or their first accredited date (whichever is shorter) through 2021

# Prep Work

- Review instructions on NCDB website
- Review for complete staging, treatment and follow-up information
- Review FIN to verify valid number
- Carefully choose your file name so that you can easily find file for submission
- Run file through GenEDITS Plus 5.1.1.1

# Prep Work - ACoS FIN number verification

The screenshot shows the 'Hospital Lookup' page. A blue box with the number '2' and an arrow points to the 'Hospitals' tab in the top navigation bar. Another blue box with the number '1' and an arrow points to the 'Codes Maintenance' option in the left sidebar. The main content area shows search criteria for 'Hosp Nbr' and 'Hosp Name' (set to '\*Nowhere'), a 'Search' button, and a table with one record: '100048 ST NOWHERE'. A 'New Hospital' button is at the bottom right.

Hosp Nbr	Hosp Name
100048	ST NOWHERE

The screenshot shows the 'Hospital Maintenance' form. Fields include: Hospital Name (ST NOWHERE), Contact, Phone Nbr ((999) 555-1123), Rpt Hosp Id, St Name Add (123 MAIN ST), Acos Hosp Id (12345678), NPI (1699722728), and Region. A blue circle highlights the 'Acos Hosp Id' field.

# Prep Work: FIN and NPI numbers

- This task can be done after selecting your export population
- Use List for a Population under Ad hoc (do not reselect the auto-selected population)
- List the fields to review including Archive FIN and NPI Archive FIN

**List for a Population**

Population Label: 01-Autoselect-NCDB-All

Report Label: FIN Number review

**Choose the Items for Your Report**

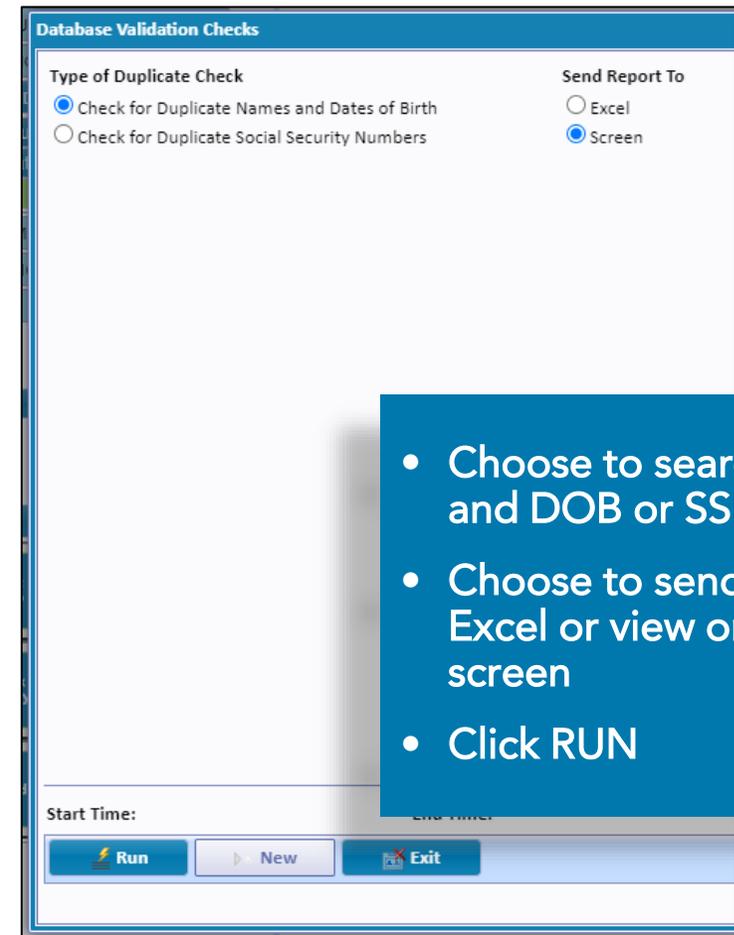
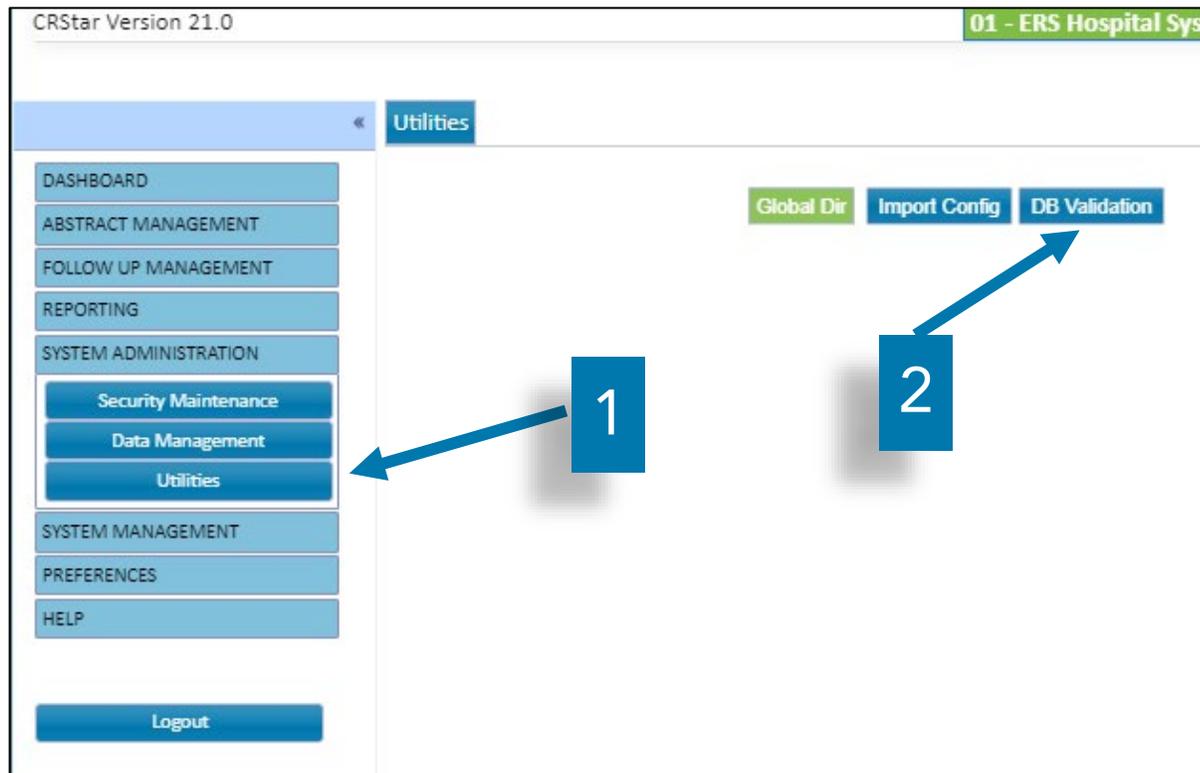
	Item Nbr	Item Description	B/S/L	C/D	Display Length
1	132	Accession Nbr	L	C	20
2	117	Site Code	L	C	20
3	118	Seq of Primary	L	C	20
4	2137	Archive Fin	L	C	20
5	3131	Npi_archive_fin	L	C	20

**Adhoc Report FIN Number review for 01-Autoselect-NCDB-All**

	Accession Nbr	Site Code	Seq of Primary	Archive Fin	Npi_archive_fin
1	01200900083	50	00	*7DS@	
2	01201300501	20	00		
3	01199600035	50	00		#12
4	01200701756	64	00		
5	03201200161	47	00	123784	1237
6	01201810027	10	12		
7	01200500694	50	00	0006530620	

# Best Practices: Database Validation

## Perform Database Validation Check/Eliminate Duplicates



- Choose to search by name and DOB or SSN
- Choose to send report to Excel or view on your screen
- Click RUN

# Best Practices: Database Validation (con't)

- Identify any duplicates. Investigate them in hospital EMR to determine which data is accurate, then combine the patients.



WESLEY	LYMPH NODES	03/03/1963	827653495
WILLANETTE	BREAST	12/16/1936	834366172
WILLANETTE	BREAST	12/16/1936	834366172
WILLIAM	PROSTATE	08/17/1946	834466676
WILLIAM	PROSTATE	08/17/1946	834466676
WILLIAM	SKIN	07/04/1953	834538743
WILLIAM	SKIN	07/04/1953	834539743
WILLIE	PROSTATE	10/19/1923	834236676
WILLIE	PROSTATE	10/19/1923	834238676

Print Exit

# Best Practices: Database Validation (con't)

## Combine patients

The screenshot displays the 'Abstract Utilities' menu on the left, with 'Abstract Utilities' selected. The main area shows 'Delete Abstract', 'Copy Abstract', and 'Combine Patients' buttons. A 'Merge Patients' dialog box is open, showing two patient selection lists. The left list is titled 'Select Patient 1' and the right 'Select Patient 2'. A 'Merge Primaries into Patient 1 and Delete Patient 2' button is between them. A 'New' button and 'Exit' button are at the bottom.

Numbered callouts and text boxes:

- 1**: Points to the 'Abstract Utilities' menu item.
- 2**: Points to the 'Combine Patients' button.
- 3**: Points to the 'Name' field in the 'Select Patient 1' list, with a text box: **Correct pt info verified in EMR**.
- 4**: Points to the 'Name' field in the 'Select Patient 2' list, with a text box: **Incorrect pt info verified in EMR**.
- 5**: Points to the 'Merge Primaries into Patient 1 and Delete Patient 2' button.

# Best Practices: Follow Up

- Before starting the Call for Data process, get ahead by doing a thorough job of Follow-Up
  - Include applicable follow-up, recurrence, death and updated treatment data
  - Accurately input
  - Edits run
- Serves three purposes:
  - Ensures the most updated cases are submitted
  - Less errors in Follow-Up data
- No harm in pausing FU activities when it's time to submit

# Best Practices: GenEdits Plus 5 & Metafile

- The metafile for the 2023 Call for Data is: NCDB v22b
- It is important that everyone on your team has the correct metafile before trying to reconcile any errors identified by the GenEDITS Plus 5.1.1.1 software *(Note: this is a new version)*
- Utilize one person to run the GenEDITS
  - More than one person can process the edits
- Assign one person to run final GenEDITS and submit data

# Best Practices: General

- File storage
- Pause all Follow-up and Import activities while completing the final run of edits and submission
- RCRS Platform
  - Make sure the appropriate people have access
  - Check your facility profile for accurate information

# Common Errors

- **Conflicts in Follow-Up info**
  - Recurrence type 70 and Cancer status 1
  - Recurrence type blank and Cancer status 2
  - Recurrence date entered with no Recurrence type
- **Conflicts in Class of Case info**
  - Class 00 without Referred to facility
  - Class 20-22 without Referred from facility
- **Conflicts in Staging data**
  - Having both (p) values and (yp) values on same case

# What could cause my file to be rejected?

- Your FIN is incorrect in the transmission file or more than one FIN in the file
- File is not formatted for v22 or v23
- Submitted incorrect state export file instead of NCDB export
- More than one period in the file before extension (.xml)
- Special characters in file name. Only hyphen (-) and underscore (\_) are accepted
- Zip Files - These are not accepted

# GenEDITS Plus 5.1.1.1

- **Instructions**

<https://www.facs.org/media/udac4mdm/2022-genedits-plus-5.pdf>

- **Download**

<https://www.cdc.gov/cancer/npcr/tools/edits/edits50.htm>

- **Metafile Installation -**

<https://www.facs.org/quality-programs/cancer-programs/national-cancer-database/ncdb-call-for-data/>

**Hint: Hospital Firewalls can interfere with download**

# Creating Your Data File

The screenshot shows the ERS Data Exports interface. On the left is a navigation menu with categories: DASHBOARD, ABSTRACT MANAGEMENT, FOLLOW UP MANAGEMENT, REPORTING, SYSTEM ADMINISTRATION, SYSTEM MANAGEMENT, PREFERENCES, HELP, and CRStar REPORTING. A 'Logout' button is at the bottom. The 'Data Exports' section is active, showing 'State Export', 'NCDB Export', and 'Export V...'. Callout 1 points to 'Data Exports' in the menu. Callout 2 points to 'NCDB Export'. Callout 3 points to the 'Export NCDB Data' modal window. Callout 4 points to the 'Run' button in the modal.

**Export NCDB Data**

Auto Select  Use Existing Population

**Auto Selection Criteria**

Hospital:

Cases Diagnosed in 2021  
 Cases Diagnosed in

Exclude Cases Prior to Reference Year  
Year:

Filename:

Export Data For:  
 NCDB  
 RCRS

Start Time:  End Time:

# Creating Your Data File

- The 2023 Export file is created and a list of cases is displayed
- At the bottom of the list, a summary of the contents is displayed
- The export list can be printed or saved (printed) as a PDF for reference
- Click on the download indicator at the bottom left of your screen to go to the file

**Export NCDB Data**

Auto Select  Use Existing

Auto Selection Criteria

Hospital: 01 ERS H

Cases Diagnosed in 2023  
 Cases Diagnosed in

Exclude Cases Prior to  
Year: 2008

Filename: NCDB Export

Export Data For:  
 NCDB  
 RCRS

Start Time: 9:09:41 AM

Run New

**Data Exported**

Cases Exported for the NCDB Total Number of Cases: 306 January 25, 2023

Acc Nbr	Med Rec Nbr	Last Name	First Name	Site	Seq	Dx Date
200900083	418563001	LARYNX	BETTY	50	00	01/14/2019
201300501	426314811	RECTUM	INGEBORG	20	00	03/29/2018
199600035	419186790	PANCREAS	LYDA	50	00	01/13/2018
201300196	417549355	STOMACH	JE			
201200161	422561588	Check	Te			
201810027	263332489	CHECK	B'			
201100178	363600777	CERVIX	SH			
200500694	419963222	BREAST	De			
201510000	434747222	BREAST	LA			
200100771	418521575	PROSTATE	JO			
201100424	419211750	BREAST	PA			
200500091	428663431	PROSTATE	KE			
201300232	420642490	THYROID	PH			
200900007	230218790	BREAST	KA			
200000148	422174939	RECTUM	RA			
200801779	420069017	PROSTATE	JA			
201201270	526349134	VULVA	CA			
201600983	425155656	CERVIX	CH			
201000018	422565214	BONE MARROW	CA			
200701330	225307169	PROSTATE	HA			
201200241	419027473	BREAST	M			
199000815	424380390	BREAST	M			
201795874	087467524	smith	jo			
201200028	418562586	PROSTATE	DO			
200600347	423620755	BREAST	PA			

Diagnosis Year Nbr of Cases

2021	76
2020	34
2019	15
2018	53
2017	16
2016	16
2015	15
2014	2
2013	4
2012	12
2011	12
2010	7
2009	21
2008	23

Print Download Exit

NCDB\_Data (2).zip

# Your Auto-Selected Population

- If you need to run other reports on the auto-selected population, it is available in your Population Label drop-down menu, BUT, if you open it, there will be no selection criteria listed
- Do NOT reselect the population here, it will come up with zero cases
- You can, however, create a new label and run a subpopulation as shown in this example:

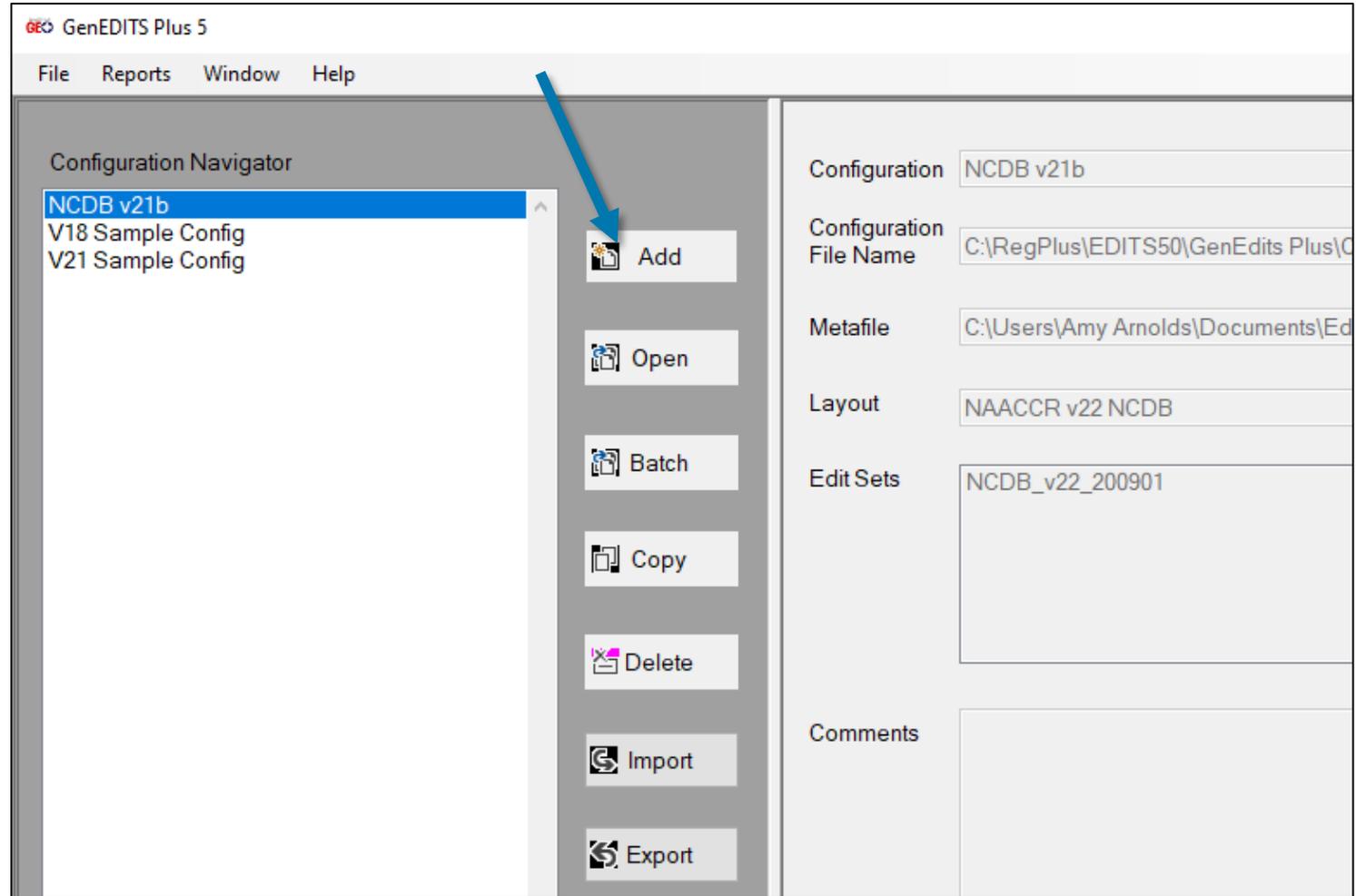
The screenshot shows a software interface for population selection. At the top, there's a 'Population' header. Below it, a 'Population Label' dropdown menu is set to '01-Autoselect-NCDB-All'. A 'New Label' input field contains 'Sample Sub Population' and is circled in red. Below this is a 'Site Codes' section with a table:

	Site	Site Description
▶ 1	50	BREAST
2		
3		

At the bottom, there's a toolbar with buttons: 'Select' (with a red 'X' over it), 'Delete Label', 'Edit Selection', 'New', and 'Exit'. 'Start Time:' and 'End Time:' labels are also present above the toolbar.

# Create v22b Configuration

- Open GenEdits 5.1.1.1
- Click Add
- Choose "Browse" by Metafile Name



# Create v22b Configuration (Con't)

- Select NCDBv22b Metafile

The screenshot shows the 'New configuration' dialog box with the following fields:

- Metafile Name: C:\RegPlus\EDITS50\GenEdits Plus\MetaFiles\NCDB\_v22b\_230120.smf
- Record Layout: NAACCR v22 NCDB (RL00005) (COC)
- Edit Sets: NCDB\_v22\_200901
- Datafile Name: (empty)

The file explorer window shows the following table of files:

Name	Date modified	Type	Size
NAACCR_v22B_20220404.smf	1/25/2023 9:51 AM	SMF File	84,514 KB
NAACCR_v23testing_20220809_nolayout....	1/5/2023 7:48 AM	SMF File	85,591 KB
NCDB_v21b_211011.smf	2/25/2022 10:57 AM	SMF File	84,514 KB
NCDB_v22b_230120.smf	1/25/2023 9:50 AM	SMF File	84,514 KB

The 'Run Edits' button is highlighted in the bottom right corner of the dialog box.

# Create v22b Configuration (Con't)

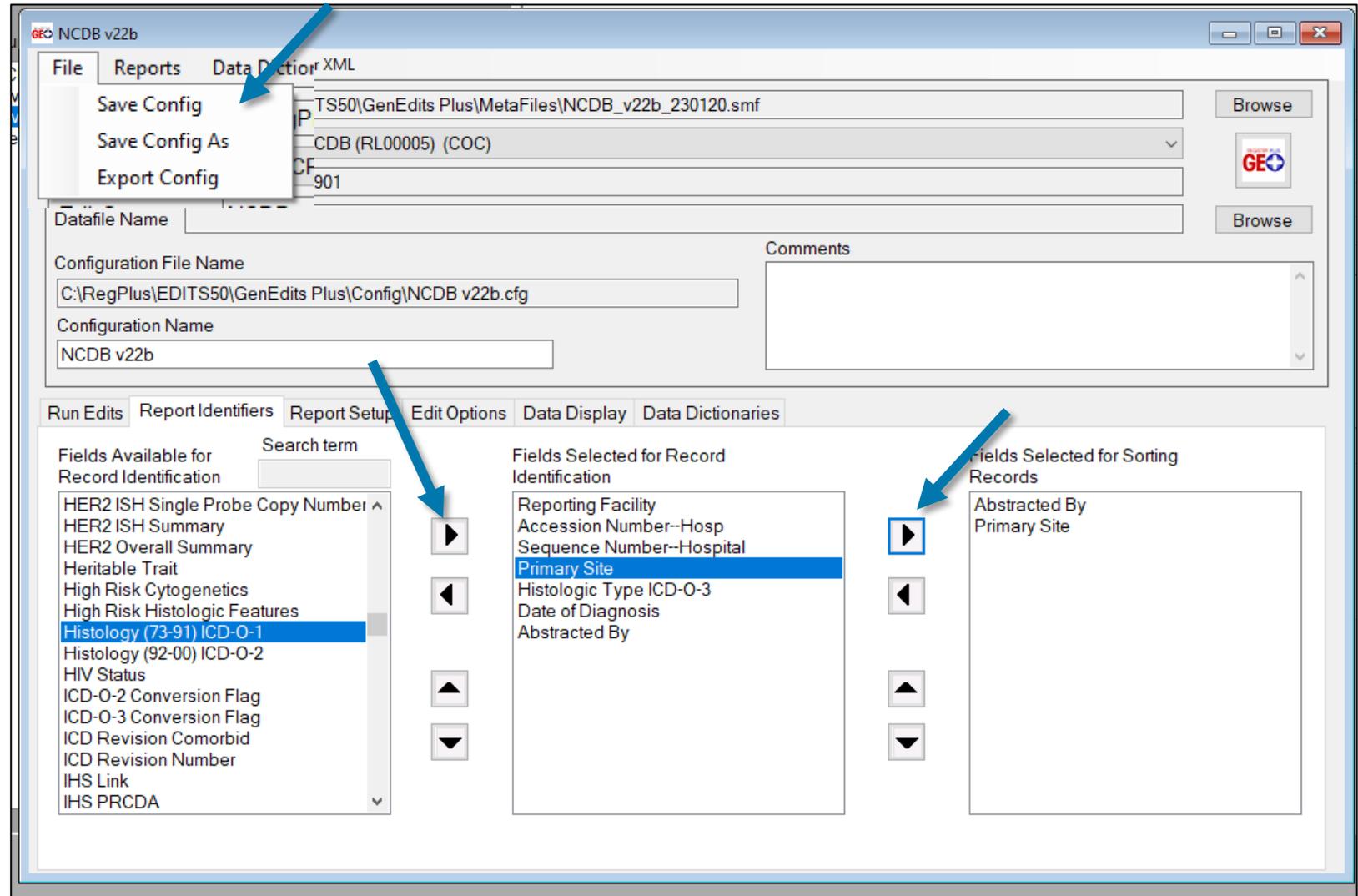
- Enter your configuration name
- Choose Edit Sets
- Data Dictionaries for XML
  - Base Data Dictionary - NAACCR
  - User Data Dictionary

The screenshot shows the 'New configuration' dialog box with the following details:

- Metafile Name:** naaccr-dictionary-220.mf
- Record Layout:** NAACCR V22 NCDB (RL00005) (COC)
- Edit Sets:** NAACCR V22 NCDB (RL00005) (COC)
- Configuration Name:** NCDB v22b
- Active Tab:** Data Dictionaries for XML
- Edit Sets List:**
  - NCDB\_v22\_200901 (2108231) (COC)
  - RCRS\_v22\_200901 (2008232) (COC)
- Run Edits Button:** A button labeled 'Run Edits' is highlighted with a black border.

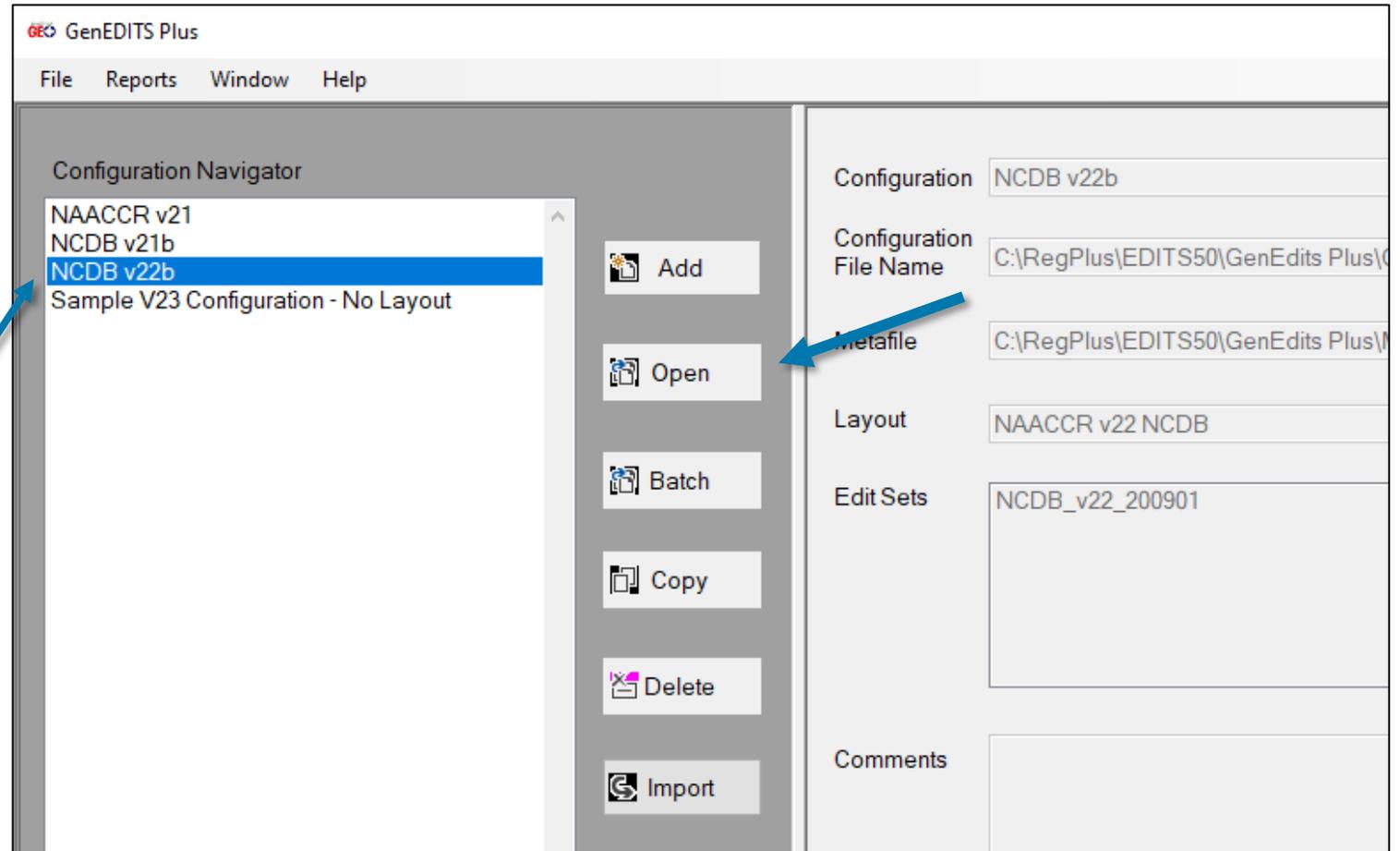
# Create v22b Configuration (Con't)

- Choose Field and click arrow to add to the Report
- Choose Field and add to the sorting section as desired



# Cleaning Up Your Data

- Choose v22b Configuration
- Click open



# Cleaning Up your Data (Con't)

- Click Browse and choose your data file ensuring it populates in the Datafile Name box
- Confirm your NAACCR Version and Record Count
- Click Run Edits

File Reports Data Dictionaries for XML

Metafile Name C:\RegPlus\EDITS50\GenEdits Plus\MetaFiles\NCDB\_v22b\_230120.smf Browse

Record Layout NAACCR v22 NCDB (RL00005) (COC)

Edit Sets NCDB\_v22\_200901

Datafile Name C:\RegPlus\EDITS50\GenEdits Plus\Data\NCDB Export90943AM.xml Browse

Configuration File Name C:\RegPlus\EDITS50\GenEdits Plus\Config\NCDB v22b.cfg

Configuration Name NCDB v22b

Comments

Run Edits Report Identifiers Report Setup Edit Options Data Display Data Dictionaries

Record Type I NAACCR Version 220 Record Count 306

Edit Set Options

Skip Empty  Skip Failed  Suppress Warnings

Start editing at record 1 Stop editing after record 306

Report Counts Only Detailed Error Limit

Progress

Run Edits

Records Processed Errors Reported

Records With Errors Time Remaining

# Cleaning Up Your Data (con't)

- GenEDITS Plus 5.1.1.1 generates your edit reports as you specified
- The summary report shows you how many of each edit type you have
- The detail report shows you each case that has edits with identifying information so you can clean those edits up in CRStar

# Cleaning Up Your Data

- Edit numbers can be looked up in GenEDITS Plus 5.1.1.1 to help clarify what all of this means

RX Summ--Treatment Stat, Treatment (CC) [N1601]		
<b>E: Conflict between RX Summ--Treatment Status and treatment codes</b>		
RX Summ--Treatment Status #1285	(Start Pos: 2224)	Value: [0]
RX Summ--Surg Prim Site #1290	(Start Pos: 2225)	Value: [50]
RX Summ--Surg Oth Reg/Dis #1294	(Start Pos: 2228)	Value: [0]
RX Summ--BRM #1410	(Start Pos: 2247)	Value: [00]
RX Summ--Chemo #1390	(Start Pos: 2243)	Value: [03]
RX Summ--Hormone #1400	(Start Pos: 2245)	Value: [01]
RX Summ--Transplnt/Endocr #3250	(Start Pos: 2241)	Value: [00]
RX Summ--Other #1420	(Start Pos: 2249)	Value: [0]
Reason for No Radiation #1430	(Start Pos: 2250)	Value: [0]
Phase I Radiation Primary Treatment Volume #1504	(Start Pos: 2281)	Value: [40]
Rad--Regional RX Modality #1570	(Start Pos: 2264)	Value: --blank--
Date of Diagnosis #390	(Start Pos: 544)	Value: [20180219]
RX Summ--Scope Reg LN Sur #1292	(Start Pos: 2227)	Value: [5]

# Cleaning Up Your Data - Finding 4 digit Edit

1. Go to Edit Options tab
2. Double-click on Edit tag to sort the edit tag numbers numerically
3. Find the edit in the list and highlight it
4. Click Edit Details

The screenshot shows the GEC NCDB v21b application window. The 'Edit Options' tab is selected. The configuration panel at the top shows the Metafile Name as 'C:\RegPlus\EDITS50\GenEdits Plus\MetaFiles\NCDB\_v21b\_210505.smf', Record Layout as 'NAACCR v21 NCDB (RL00005) (COC)', and Edit Sets as 'NCDB\_v21\_200901'. The 'Edit Options' table below has columns for Edit Name, Edit Tag, Agency, Use Edit Set Options (1482), Suppress Edit, Skip Empty, Skip Failed, and No Skips. The 'Edit Tag' column is sorted numerically. The row 'RX Summ-- Treatm Stat, Treatment (COC)' with Edit Tag 'N1601' is highlighted. The 'Edit Details' button is also highlighted.

Edit Name	Edit Tag	Agency	Use Edit Set Options (1482)	Suppress Edit	Skip Empty	Skip Failed	No Skips
CS SSF 8, SSF 9, Testis (CS)	N1590	CS	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
CS SSF 9, SSF 15, Testis (CS)	N1591	CS	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<b>RX Summ-- Treatm Stat, Treatment (COC)</b>	<b>N1601</b>	<b>COC</b>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Surgery, RX Date Surgery, ICDO3 (COC)	N1606	COC	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Multiplicity Ctr, Lymphoma/Leukem/Unk Site (NAACCR)	N1615	NAACCR	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Summ Stg 2000, Site, Hist ICDO3, Class (NAACCR)	N1617	NAACCR	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Mult Tum Rpt, Lymphoma/Leukemia/Unk Site (NAAC...	N1619	NAACCR	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Date of Mult Tum, Lymphoma/Leukem/Unk Site (NAA...	N1620	NAACCR	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
CS SSF 16, MerkelCell Schemas (CS)	N1632	CS	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
CS SSF 17, MerkelCell Schemas (CS)	N1633	CS	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

# Cleaning Up Your Data

Look for keywords like “must equal”, “cannot be”, etc

**Edit Name:** RX Summ--Treatment Stat, Treatment (COC) (N1601)

**Agency:** COC

Description Admin Notes Edit Logic

The purpose of this edit is to verify that RX Summ--Treatment Status and treatment fields are coded consistently.

This edit is skipped under the following conditions:

- a. RX Summ--Treatment Status is blank
- b. Date of Diagnosis is blank (unknown) or invalid

1. If any of the treatment fields indicate treatment given, then RX Summ--Treatment Status must equal 1 (treatment given). Treatment is considered "given" if any of the following is true:

RX Summ--Surg Prim Site = 10-90  
RX Summ--Surg Oth Reg/Dis = 1-5  
RX Summ--BRM = 01  
RX Summ--Chemo = 01-03  
RX Summ--Hormone = 01  
RX Summ--Transplnt/Endocr = 10-40  
RX Summ--Other = 1, 2, 3, 6  
Reason for No Radiation = 0

2. If Treatment Status = 1 (treatment given), at least one of the following fields must equal treatment given. Treatment is considered "given" if any of the following is true:

RX Summ--Surg Prim Site = 10-90  
RX Summ--Scope Reg LN Sur = 1-7  
RX Summ--Surg Oth Reg/Dis = 1-5  
RX Summ--BRM = 01  
RX Summ--Chemo = 01-03  
RX Summ--Hormone = 01  
RX Summ--Transplnt/Endocr = 10-40  
RX Summ--Other = 1, 2, 3, 6  
Reason for No Radiation = 0

# Cleaning Up Your Data

- Run edits on every case you touch during the cleanup process
- Review and clear all edits
- Run export again and pass through GenEDITS
- If edits are clear, data can be submitted
- If edits aren't clear they will need to be worked on then re-exported until clear

# Submitting the Call for Data

- Instructions to Submit Data: <https://www.facs.org/-/media/files/quality-programs/cancer/ncdb/how-to-submit-data.ashx>
- Questions or Issues? [ACSTechsupport@iqvia.com](mailto:ACSTechsupport@iqvia.com)

# Determining Submission Completeness

- Keep track of how many cases were in each Export batch you created
- Errors & Rejected Cases - Any rejected cases are considered not submitted. Correct them and re-submit prior to the deadline 3/31/2023
- Compare to the number of cases received by the NCDB after submitting
- View and screenshot the Upload History Report from the RCRS Dashboard
  - Instructions can be found in the on the CoC's Call for Data Website

2023 Information for Registrars and CoC Program Standards 6.4 Documents Combined

# Determining Submission Completeness

The NCDB uses this formula and these percentages to determine if a facility's data submission meets the expectations for submission based on year.

Percent of Case Submission Expectations for Standard 6.4 Compliance:

**Diagnosis Years 2021, 2022**

**To Calculate Actual % for the first row (For CFD 2023)**

**Formula is:** 
$$\frac{\text{Total submitted cases in CFD2023 for dx 2021}}{\text{Total submitted cases in CFD2022 for dx 2020}} \times 100 = \text{Actual\%}$$

**To Calculate Actual % for the other rows (For CFD 2023)**

Compare Total number of cases submitted for each diagnosis year in current CFD vs. prior (last year) CFD for the same diagnosis year

**Formula is:** 
$$\frac{\text{(# Cases submitted in current year for the diagnosis year xxxx)}}{\text{(# Cases submitted in prior year for the diagnosis year xxxx)}} \times 100 = \text{Actual\%}$$

Year	Percentage
2021	100
2020	85
2019	50
2018	30
2017	25
2016	20
2015	15
2014	10
2007-2013	5

# Determining Submission Completeness

## Call for Data Submission Count Tracking by Diagnosis Year

*NOTE: Document updated by ERS to assist clients due to no updated template provided by CoC - this is not an official CoC document*

Call for Data 2023			
Dx year	CFD 2023 # Cases	CFD 2022 # Cases	% Annual Caseload
First dx year	Enter # of cases submitted for dx 2021	Enter # of cases submitted for dx 2020	#VALUE!

Enter the number of cases submitted for each diagnosis year for 2022 CFD and 2021 CFD in corresponding # Cases columns. The estimated percentage of your program's annual caseload will be automatically calculated.

Call for Data 2023			
Dx year	CFD 2023 # Cases	CFD 2022 # Cases	% Annual Caseload
2021			
2020			#DIV/0!
2019			#DIV/0!
2018			#DIV/0!
2017			#DIV/0!
2016			#DIV/0!
2015			#DIV/0!
2014			#DIV/0!
2013			#DIV/0!
2012			#DIV/0!
2011			#DIV/0!
2010			#DIV/0!
2009			#DIV/0!
2008			#DIV/0!
2007			#DIV/0!

# Responsibilities During the Call For Data (Vendor Responsibilities)

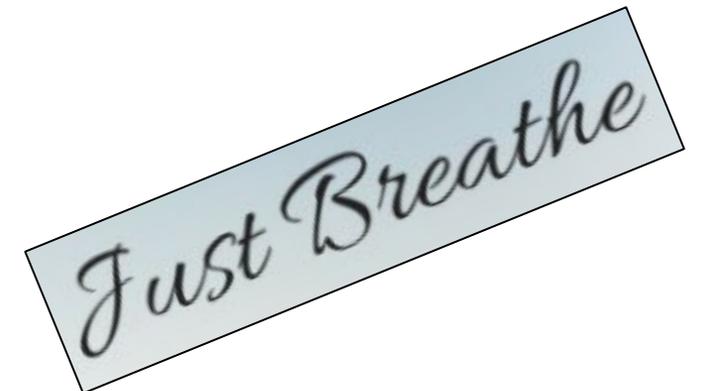
- Support tickets will be answered in the order received. We may need to limit the amount of time spent on each call
- ERS will not provide support for GenEDITS Plus 5.1.1.1 software
- ERS will gladly assist with any *software related edits*. However, we are unable to provide clean-up services for data entry errors
- ERS will assist with global data changes if applicable and the amount of any one edit is over 75 errors.
  - The edits below require manual review and globals are not indicated:
    - Recurrence Type – 1st, Cancer Status (COC)
    - Date Case Completed - CoC, Date of Diagnosis (NCDB)
    - Rx Summ - Treat Stat, Date 1<sup>st</sup> Crs RX COC (COC)

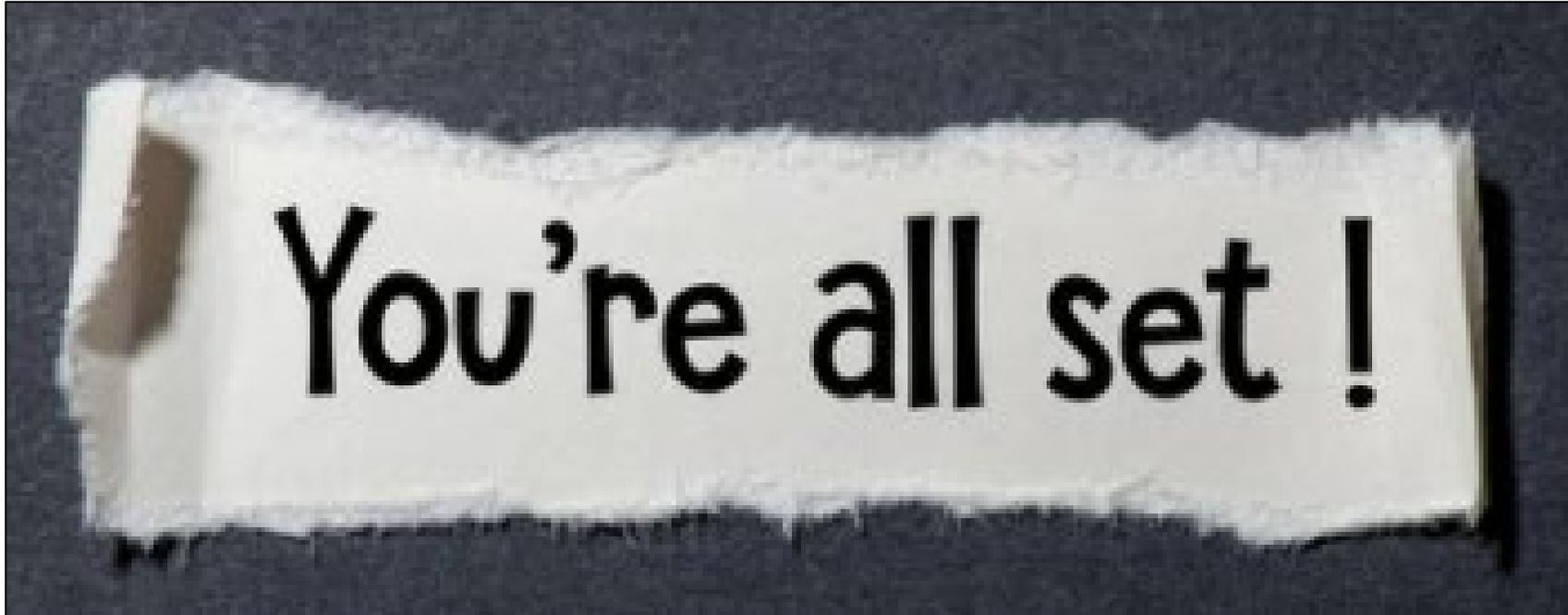
# Responsibilities During the Call for Data (Client Responsibilities)

- Please submit a support ticket if assistance is needed with an ERS issue. Please do not email or call the support staff directly
- For assistance with GenEDITS Plus 5.1.1.1 software, contact the CDC as this software is developed and supported by the CDC. For assistance with the NCDB submission portal, contact the NCDB
- During this time, it is imperative for Registrars and Follow-Up clerks to run NCDB edits after entering Follow-Up and subsequent treatment information. If new FU is entered, the case becomes eligible for this Call for Data. Make sure it passes edits
- A backup of the database must be done prior to any global changes

# Quick Review

- Get organized. Review the 2022 Call for Data Requirements
- Do some preliminary data reviews
- Check for incorrect FIN and NPI numbers
- Install GenEDITS Plus 5.1.1.1
- Download the NCDB v22b metafiles and import them into GenEDITS
- Create the NCDB 2023 CFD Configuration
- Create the 2021 and earlier Data Export files in CRStar
- Run edits on the Export files in GenEDITS Plus 5.1.1.1 (repeat until clean) and save a copy of the final clean report
- Submit data through NCDB Datalinks portal
- Determine Submission Completeness







**THANK YOU**

Amy Arnold, BA, CTR  
Manager, Strategic Services  
aarnold@mycrstar.com