INSTRUCTIONS for using the NC reporting template (TemplateA.xlsx).

1. Open the template and save the file with a *new name* – or copy the file and *give the copy a new name*.

    Important: Each file must have a *different*, *unique* name or it will be **overwritten** with a previously submitted file with the same name.

    a. The file name should be *unique* to your facility as there are 200+ facilities uploading one or more files per week.
    b. Please do **not** put commas (,) number symbols (#) slashes (/) or apostrophes (') in the file name.

Suggestion: start the filename with your CLIA number or abbreviated facility name and include a date reference (e.g., **CPB-2023-05-05.xlsx**)

2. Fields marked with an asterisk* are required
    a. The Medicaid ID is *required,* if applicable. If child is NOT enrolled in Medicaid, leave the Medicaid ID field blank.

3. Some of the fields have a drop-down pick list with choices to select
    a. If none of the choices are applicable, please leave blank

4. **Sample number** (a.k.a. laboratory sample number, Specimen ID, Accession number)
    a. This should be a *unique* identifier for the blood lead specimen. A sample ID should never be used again

Suggestion: Use the patient number combined with the sample date as yymmdd.
Example: If the patient id is **126995** and the date of the test is **07/16/2023** the sample number would be **126995-230716**

5. **Blood lead test result**: The reportable range of the LeadCare II test is 3.3 to 65 µg/dL.
    a. **"Low"** means the result is less than 3.3 - enter **< 3.3** in the result field
    b. If the result is between 3.3 and 65 - enter the number (e.g., **3.6, 4.7, 11.2**) in the result field
    c. **"High"** means the result is greater than 65, enter **> 65** in the result field

(**Please note**: Result values other than these will be rejected.)

    d. **DO NOT** enter test results *analyzed by another laboratory* (e.g., NC State Laboratory of Public Health, LabCorp, Mayo, Quest Diagnostics, etc.)
    e. **DO NOT** enter a result as "normal". "Normal" is an *interpretation.* "Normal" is not the test result.
    f. **DO NOT** put units of measurement in the result field (e.g. µg/dL, mcg)

Please see examples below:

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Sample number* (unique - never use same number again)	Specimen date* (mm/dd/yyyy)	Result*	Specimen type C* (DO NOT analyze venous specimens)
256498-230103	01/03/2023	<3.3	C
364589-230103	01/03/2023	<3.3	C
678154-230104	01/04/2023	<3.3	C
957128-230104	01/04/2023	<3.3	C
951623-230104	01/04/2023	3.6	C
845796-230105	01/05/2023	<3.3	C

Correct

Sample number* (unique - never use same number again)	Specimen date* (mm/dd/yyyy)	Result*	Specimen type C* (DO NOT analyze venous specimens)
256498-230103	01/03/2023	NORMAL	C
364589-230103	01/03/2023	<1	C
678154-230104	01/04/2023	3.6 µg/dL	C
957128-230104	01/04/2023	Negative	C
951623-230104	01/04/2023	<2	C
845796-230105	01/05/2023	3.2	C

Incorrect