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XN CBC Corrections

Document Type: Procedure

I. PURPOSE AND OBJECTIVE:

This procedure explains how to correct for various factors that may cause spurious values on automated Hematology cell counters.

II. PRINCIPLE:

A. A number of unusual factors present in patient samples may produce erroneous results on automated cell counters. This procedure explains how to correct for various factors that cause spurious values (e.g., high WBC counts, cold agglutinins, lipemia, icteria, cryoglobulins, nucleated RBCs, clumped platelets, platelet satellitosis, giant platelets, microcytic RBCs, RBC fragments, hemolysis, lyse resistant RBCs, and marked changes in plasma constituents).

B. Unknown interferences may also adversely affect results obtained from the instruments. It may be necessary to use a combination of correction procedures to obtain valid results.

III. ACRONYMS:

A. Laboratory Information System (LIS)

B. White Blood Cell (WBC)

C. Red Blood Cell (RBC)

D. Hemoglobin (HGB)

E. Hematocrit (HCT)

F. Mean Corpuscular Hemoglobin Concentration (MCHC)

G. Platelet (PLT)

H. Mean Cell Volume (MCV)

I. Mean Corpuscular Hemoglobin (MCH)

J. Nucleated Red blood Cell (NRBC)

IV. SPECIMEN COLLECTION AND HANDLING:

Type	Whole blood collected in a 4 mL vacutainer. This is the preferred sample. OR Capillary blood collected in a microtainer.	
Anticoagulant:	K_2EDTA	
Amount	Whole blood	Minimum sample size is 2.0 mL. Optimum sample size is 4.0 mL.
	Capillary blood	Minimum sample size is 300 mcL. Optimum sample size is 500 mcL.
Special Handling	Specimen must be well mixed for minimum of 2 minutes before being analyzed. Rim all microtainer specimens with wooden applicator sticks for clots.	
Timing	Specimen is stable for 8 hours at room temperature (72 hours at 4^{O}C).	
Criteria for Unacceptable specimens	Specimens containing clots or inappropriate volumes are unacceptable and must be redrawn.	

V. SUPPLIES:

A. Heat block: 37^{O}C.

B. XN Series Analyzers

C. HemataStat II microhematocrit centrifuge (if available).

D. **CellPack DCL:** Whole blood diluent for use in measuring the numbers and sizes of RBC and platelets for HGB concentration determination and as a Sheath fluid for FCM detector. Diluent used to make dilutions due to numerical results or interpretive messages. Run dilution in manual mode within 30 minutes. Multiply the results by the dilution factor. Verify that the RBC count matches original RBC +/- 0.20.

1. Store at 2º-35ºC, away from direct sunlight.
2. If frozen, thaw and mix thoroughly before using.
3. Cellpack DCL is clear and colorless.
    a. If it is showing signs of contamination or instability such as cloudiness or discoloration, replace.
4. Unopened, it is stable until expiration date printed on the container.
    a. Once opened, it is stable for 60 Days.

VI. CALIBRATION:

Most corrections are performed via visual, temperature, or mathematical means. See Microhematocrit procedure for respective calibration directions (site specific).

VII. QUALITY CONTROL (QC):

Since most corrections are performed via visual, temperature or mathematical means, no control materials are available. The manual microhematocrit is the only procedure where a control is run (see site specific microhematocrit procedure).

VIII. PROCEDURE:

A. **HIGH WBC COUNTS - 440.0 10*9/L or higher:**

1. High numbers of WBCs can cause a false decrease in the WBC reported.To correct a high WBC count:
    a. The middleware holds results.
    b. Perform a dilution of the specimen (1:2, 1:3, 1:5, etc.)
    c. Run in manual mode on the instrument within 30 minutes of setup. As a QC check, verify that the RBC count agrees within +/- 0.20 of undiluted sample. If not, rerun sample. If still not acceptable, remake dilution. Notify supervisor if unable to resolve.
    d. If diluted rerun was added in the middleware, the middleware will automatically calculate the results. (Refer to the Hematology Caresphere Operation procedure).
    e. Accept the WBC count if the RBC count agrees +/- 0.20 of original RBC count.
    f. In the middleware, add internal comment *"Verified by dilution"*.
        i. **NOTE:** The HGB and WBC are measured in different chambers on Sysmex analyzers, so there is no WBC interference with the HGB result.
        ii. **NOTE**: Perform manual differential.

B. **HIGH RBC, HGB, PLT/PLT-F, or hematocrit**

1. Linearity Values
    a. RBC: 8.60 10*12/L or higher
    b. HGB: 26.0g/dL or higher
    c. HCT: 75.0% or higher
    d. PLT/PLT-F: 5000 10*9/L or higher
2. Parameters that exceed the manufacturer's limits are flagged with @ beside the result. The sample must be diluted and rerun in manual mode. Do NOT use the Pre-dilute mode on the XN.
3. These values should be diluted as per the WBC procedure and compared to the original value.

4. In the middleware, add internal comment "*Verified by dilution*."
    a. **NOTE**: Do not use differential results from run on diluted specimen.

C. **COLD AGGLUTININS:**

1. Cold agglutinins cause the spontaneous agglutination of RBCs at temperatures lower than 37^{O}C. The degree of agglutination is dependent on the cold agglutinin titer.
2. Due to the fact that the Heat Reaction Chamber on the Sysmex XN analyzers is warmed to 37^{O}C, only strong cold agglutinins will be apparent. The strong cold agglutinins will cause spurious low RBC counts due to counting micro-agglutinates as single cells. Also, the MCV will be falsely elevated due to micro-agglutinates being sized as a single large cell. The hemoglobin reading is usually correct. Also, with a correct hemoglobin value and low hematocrit, the MCHC and the MCH will be spuriously elevated.
3. Check for cold agglutination on all bloods with:
    a. "MCHC" greater than 38.0 g/dL;
    b. Smear and hematology analyzer MCV do not agree (**NOTE:** MCV does not necessarily have to be macrocytic to be suspicious of a cold agglutinin);
    c. Smears with RBC agglutinates; or
    d. Any blood you are suspicious of because of a "lacy" appearance in the tube or on the slide. If b, c, or d is present, follow cold agglutinin procedure, regardless of MCHC value.
4. To correct for the effect of a cold agglutinin:
    a. Place the blood in a 37^{O}C incubator (e.g., heating block or water bath) for **at least 15 minutes.**
    b. Mix specimen thoroughly and rerun the blood through the manual mode of the hematology analyzer. (So specimen doesn't cool down).
    c. Report the 37^{O}C results (for all parameters) if the MCHC is feasible.
    d. In the middleware, add *"Possible Cold Agglutinin"* comment next to MCHC result, then SAVE.
    e. For a cold agglutinin specimen that has instrument flags/lab values requiring microscopic review: If RBC agglutinates are present, make warmed smears to see if the agglutinates go away upon warming. Regardless of which smears (room temp or warmed) exhibit agglutinates, report *"RBC agglutinates present"*. If case needs further review by a pathologist, submit both sets of clearly marked slides to the pathologist.
        i. **NOTE:** Cold agglutinins must **always** be incubated at 37^{O}C before being reported as such.
5. If a cold agglutinin does not resolve using these measures, some parameters may be reported:
    a. Determine if there is **no optical interference with the HGB** by spinning an aliquot of the sample (no interference due to lipemia, icteria, or hemolysis).
        i. Sites able to perform a spun HCT: the HGB may be reported out from

the **warmed** sample. A **spun HCT** will be performed, and the **recalculated MCHC must be less than or equal to 38** to check the reliability of these parameters. Ensure that the HGB and HCT values are consistent with each other and review for consistency with patient history. The warmed HGB, spun HCT, and recalculated MCHC may then be reported. WBC, PLT, and differential may be reported. **Verify the WBC, PLT, and differential on smear for the first occurrence** and on future occurrences if any delta checks or flags pertaining to these parameters are present. Refer to the calculations and interpretations section for the calculation formulas. The MCV and MCH cannot be reported, as these calculations require the RBC, which cannot be obtained if the effect from the cold agglutinin has not been resolved.

a. NOTE: For all parameters that can not be reported, remove the result from the middleware and enter NM in the result field.

ii. Sites unable to perform a spun HCT: Report the warmed HGB. WBC, PLT, and differential may be reported. **Verify the WBC, PLT, and differential on smear for the first occurrence** and on future occurrences if any delta checks or flags pertaining to these parameters are present.

a. NOTE: For all parameters that can not be reported, remove the result from the middleware and enter NM in the result field.

6. NOTE: When RBC result is unable to be obtained on a strong cold agglutinin sample, #NM the retic parameters if a reticulocyte is ordered.

D. **LIPEMIA**

1. Lipemic plasma can cause a falsely elevated hemoglobin due to a cloudy SLS-hemoglobin solution which decreases the amount of transmitted light through the solution to the photocell. (Lipemia usually occurs in patients with hyperchylomicronemia whose triglycerides are greater than 1,000 mg/dL.)
2. Lipemia should be suspected on all bloods with: (a) a lacy appearance of blood smear or (b) an MCHC over 38.0 g/dL. Action must be taken on MCHCs greater than 38.0 g/dL.
3. To check for lipemia, spin down a portion of the blood for approximately 5 minutes (or let settle for approximately 10-15 minutes) and visually check plasma layer for characteristic milky appearance.
4. To correct for lipemia perform either of the following procedures:
    a. **Plasma Replacement:**
        i. Spin down a **PORTION** of a well mixed blood specimen at **2000** rpm for 5 minutes.
        ii. Mark the top (meniscus) of the plasma level.
        iii. Carefully remove **most, but not all,** of the plasma.
        iv. Replace the plasma with the same amount of Cell Pack DCL diluent

(add diluent up to the mark) and mix.

v. If the aliquot still appears lipemic after plasma replacement, repeat the plasma replacement steps on the aliquot until it no longer appears lipemic. This may need to be performed multiple times to correct for interference.

vi. Place XN in manual mode.

vii. Barcode sample into XN or manually enter order ID.

viii. Check "Cap Open."

ix. Mix sample then REMOVE cap and place in proper manual mode holder.

x. Cycle the sample through the instrument.

xi. Use the RBC result as a guide to verify proper re-dilution of the specimen.

xii. If the RBC result is within +/- 0.20 of the original RBC, report the HGB from the re-diluted sample.

xiii. Recalculate the MCH and MCHC using the **new** HGB and **original** RBC and HCT.

xiv. In the middleware, add *"Corrected for Lipemia"* comment next to the MCHC result field, then SAVE.

a. **NOTE:** To avoid any math errors, have second technologist verify calculations.

b. **Plasma Blank:**

i. Spin down a **PORTION** of a well mixed blood specimen at **2000** rpm for 5 minutes.

ii. Perform a hemoglobin on the **PLASMA** using the hematology analyzer manual mode.

iii. Place XN in manual mode.

iv. Barcode sample into XN or manually enter order ID.

v. Check "Cap Open."

vi. REMOVE cap and place in proper manual mode holder.

vii. Cycle the sample through the instrument.

viii. Use the following formula to calculate the correct hemoglobin:

a. **Corrected HGB = Original HGB - [(1-{Original HCT/100}) x Plasma HGB]**

b. **Example:**

Results on Original Run

WBC	5.1
RBC	4.03

HGB	16.1
HCT	39.3
MCV	97.5
MCH	40.0
MCHC	41.3
PLT	250

Calculation for Corrected Hemoglobin (HGB)

Plasma HGB	4.5
Corrected HGB	= 16.1 - [(1-[39.3/100]) x 4.5] = 16.1 - [(1-0.393) x 4.5] = 16.1 - [0.607 x 4.5] = 16.1 - 2.7315 = 13.4

ix. Recalculate the MCH and MCHC using **new** HGB, **original** RBC, and **original** HCT.

a. **Example**:

Corrected Report

WBC	5.1
RBC	4.03
HGB	13.4
HCT	39.3
MCV	97.5
MCH	33.3
MCHC	34.1
PLT	250

x. In the middleware, add *"Corrected for Lipemia"* comment next to the MCHC result field, then SAVE.

a. **NOTE:** To avoid any math errors, have second technologist verify calculations.

E. **ICTERIA (HYPERBILIRUBINEMIA):**

1. If interference from bilirubin is suspected, a correct hemoglobin value may be obtained by performing one of the correction procedures described above for LIPEMIA and free-texting *"Corrected for ICTERIA"* as an internal comment.

F. **CRYOGLOBULINS:**

1. Cold-precipitated plasma immunoglobulins (cryoglobulin) or fibrinogen (cryofibrinogen) in a blood sample can cause a falsely increased WBC count with excessively high takeoff at 35 fL resulting in a voteout (-----) and/or * code for the WBC parameter. Also, the RBC count, hemoglobin, hematocrit and platelet count may be slightly increased along with a slightly decreased MCV.
2. Aggregates of blue staining amorphous material may be seen on Wright stained smears. Increased levels of cryoglobulin may be associated with myeloma, macroglobulinemia, lymphoproliferative disorders (e.g. CLL), metastastic tumors, autoimmune disorders, infection, and as an idiopathic disease. Cryofibrinogen has been observed in association with many disorders including myeloma, carcinoma, leukemia, aneurysm, pregnancy, the use of oral contraceptives, thromboembolic phenomena, diabetes, and as an essential disease.
3. To correct for the effects of a cryoglobulin:
    a. Warm specimen to 37^{O}C for a **minimum** of 15 minutes.
    b. Rerun through the hematology analyzer manual mode.
    c. Report the 37^{O}C results (for all parameters) if the results are feasible **and** no parameter flags are present.
    d. In the middleware, free-text internal comment *"Possible cryoglobulin"*.

G. **NUCLEATED RBCS:**

1. NRBCs are a reportable parameter from the Sysmex XN-Series analyzers. The XN analyzer provides a "corrected WBC" taking into account the NRBCs counted. The comment *"WBC corrected for NRBCs"* will automatically be added to the WBC field by the middleware. XN-Series NRBC counts are linear to 600 per 100 WBC.
    a. **NOTE:** To report NRBCs from the Sysmex XN-450 analyzers, refer to the attachment.
2. If performing a scan and there is a significant discrepancy of NRBCs on the slide versus the analyzer count (+/- 10), report corrected WBC as follows:
    a. Perform a manual differential in the middleware. The corrected WBC will need to be manually resulted in the middleware using the equations below. Add comment *"WBC corrected or adjusted for the presence of nRBCs"* to the WBC field. Call corrected WBC to physician or nursing unit as applicable.
    b. Calculations:

Calculations

Original absolute # x $\frac{\text{Corrected WBC}}{\text{Original WBC}}$ = New absolute #
$\frac{\text{Original absolute \#}}{100 + \text{NRBC}}$ x 100 = New absolute #

3. NOTE: Refer to the Caresphere Workflow attachment to the Hematology Caresphere Operation procedure for more detailed information.

H. **PLATELET CLUMPING:**

1. Platelet clumping can result in **spurious low** and **widely fluctuating platelet counts** on hematology instruments.
2. Platelet clumping may occur because of poor collection technique resulting in the presence of micro clots, delays in mixing the blood and anticoagulant, the presence of platelet agglutinins, or EDTA-induced clumping.
3. Check for platelet clumping by first checking for a clot. Document as internal comment in the middleware. Then examine a peripheral smear on all bloods with the following instrument flags or results:
    a. platelet count less than 75 10*9/L
    b. The PLT-F rerun retains the platelet clump(s) flag (Not applicable to the XN-L sites)
    c. platelet delta check (decrease only)
4. The middleware holds results.
5. To correct for platelet clumping:
    a. Examine Wright stained smear for clumping - particularly at the **feathered** and **side (lateral) edges**.
    b. If platelet clumps are seen:
        i. Scan peripheral smear to determine if WBC estimate matches instrument count.
        ii. If estimate does not match instrument count, add comment *"WBC may be inaccurate due to WBC/PLT interference"* to **WBC comment field.**
        iii. Note approximate platelet estimate from stained smear (ADQ , INC, DEC).
        iv. In the middleware, remove the platelet result and select the appropriate clumped platelet comment that correlates with the platelet estimate (will need to enter comment twice in the middleware):
            a. *"Platelets clumped in EDTA, appear adequate on smear."*
            b. *"Platelets clumped in EDTA, appear decreased on smear."*
            c. *"Platelets clumped in EDTA, appear increased on smear."*
        v. Click Validate All.
        vi. See example below (Figure 1).
        vii. **Note:** If platelet clumps are present but are insignificant, report instrument count and add internal middleware comment: *"Insignificant platelet clumps present."*
        viii. **Note:** If platelet clumping was discovered after results have been validated in the middleware, a corrected report will need to be made in the LIS.

c. **See Section X, Note C for another technique for handling platelet clumping.**

Complete Blood Count (CBC) W Diff

Complete Blood Count w/ Diff (Final result)

Test Name	Result		Ref. Range	Units	Resulting Lab:
WBC	**12.1**	**(H)**	3.5-10.1	bil/L	BLRYO
RBC	**4.17**	**(L)**	4.31-5.48	tril/L	BLRYO
Hemoglobin	**10.6**	**(L)**	13.5-17.0	g/dL	BLRYO
Hematocrit	**31.7**	**(L)**	40.1-50.1	%	BLRYO
MCV	**76**	**(L)**	80-100	fL	BLRYO
MCH	**25**	**(L)**	28-33	pg	BLRYO
MCHC	33		32-36	g/dL	BLRYO
RDW-CV	**18**	**(H)**	12-15	%	BLRYO
Platelets					BLRYO
Platelets Clumped in EDTA, appear adequate on smear					
Neutrophils	**8.8**	**(H)**	1.6-7.2	bil/L	BLRYO
Lymphocytes	2.1		1.1-4.0	bil/L	BLRYO
Monocytes	**1.0**	**(H)**	0.0-0.9	bil/L	BLRYO
Eosinophils	0.1		0.0-0.4	bil/L	BLRYO
Basophils	0.0		0.0-0.1	bil/L	BLRYO
Immature Granulocytes	**0.09**	**(H)**	0.00-0.04	bil/L	BLRYO
Immature Granulocyte %	0.7			%	BLRYO

Results verified at 7/13/2021 1014.

Non-Automated Differential/Morphology (Final result)

Test Name	Result	Ref. Range	Units	Resulting Lab:
RBC Morphology	Unremarkable			BLRYO
Platelet Estimate	Adequate	Adequate		BLRYO

Figure 1 - LIS Final Report with PLT Clumping Comment

I. **PLATELET SATELLITOSIS:**

1. Platelet satellitosis is the adherence of platelets to neutrophils and is seen only in EDTA-anticoagulated blood. Platelet satellitosis can cause spurious low or fluctuating platelet counts on hematology instruments. In addition, spurious neutropenia can occur in white cell differentials performed on wedge blood smears.
2. Check for platelet satellitosis by examining **feathered edges** and **side (lateral) edges** of a blood smear on all bloods with:
    a. Platelet counts less than 75 10*9/L or
    b. Widely different platelet results from previously reported values.
3. To correct for platelet satellitosis:
    a. Note approximate platelet estimate (ADQ, INC, DEC) from stained smear.
    b. Delete PLT result from middleware and replace with the statement (will need to enter the comment twice in the middleware): ***"Platelet satellitosis in EDTA - Appear (platelet estimate)".***
    c. Report hematology analyzer differential if scan agrees; otherwise perform manual differential.

J. **MICROCYTIC RBC OR RBC FRAGMENTS:**

1. Scan the peripheral smear for the presence of fragmented RBCs and other RBC abnormalities.
2. If extremely microcytic RBC are present:
    a. Estimate the PLT count.

b. Utilize the fluorescent platelet (PLT-F) if needed. (Not applicable to the XN-L sites)

K. **MCHC >38.0**: Refer to the cold agglutinin section above.

L. **GIANT PLATELETS SEEN (With PLT Abnormal Distribution Flag or with PLT clumps):**

1. Giant Platelets and clumped platelets may falsely elevate the WBC and falsely decrease the platelet count. The PLT will be asterisked.
    a. Perform PLT-F.
        i. For the XN-L sites, perform a rerun on the second analyzer.
    b. A visual estimate of the WBC count must be performed. If there is a discrepancy between the analyzer and WBC estimate, add the comment, "*WBC may be inaccurate due to WBC/PLT interference*".

M. **HEMOLYSIS:**

1. In vitro hemolysis of red cells after sample collection may lead to a spuriously low RBC count and hematocrit. If possible recollect sample.
2. Extensive **in vivo** hemolysis may lead to a falsely elevated hemoglobin value that represents both plasma and red cell hemoglobin. Thus the MCH and MCHC may be spuriously elevated. (Measured values for red cell count and hematocrit are still correct.) If in **vivo** hemolysis is suspected:
    a. Perform the plasma replacement procedure described under "LIPEMIA" above and recalculate the MCH and MCHC with the **new** corrected hemoglobin.
    b. Verify platelet count on blood smear.
    c. Free-text the internal comment: *"Corrected for hemolysis"*.
    d. Add sample comment *"Sample is markedly hemolyzed. Suggest clinical correlation to assess whether due to in-vitro or in-vivo hemolysis."*

N. **RBC LYSE RESISTANCE:**

1. Red blood cells containing large amounts of abnormal hemoglobin S or C may be more resistant to lysis. Due to RBC lyse resistance, the WBC count from the DIFF scattergram may be suspect. However, a correct count is derived from the WBC channel, which has a stronger lysing reagent.
2. To correct for the presence of RBC lyse resistance, verify the hematology analyzer WBC against a WBC estimate from the peripheral smear.

O. **MARKED CHANGES IN PLASMA CONSTITUENTS**: Marked changes in plasma constituents (i.e. very low sodium or very high glucose) may cause cells to swell or shrink. When it is determined the interference is not due to cold agglutinin, lipemia, icteria, hemolysis, or RBC lyse resistance, review the sodium and glucose results if testing is ordered for patient.

1. The middleware holds results for MCHC >38.0.
    a. If applicable, perform a spun hematocrit. If the spun hematocrit is greater than the value obtained from the analyzer, report the spun hematocrit if the recalculated MCHC is less than or equal to 38. Recalculate the MCV and MCHC. Refer to the calculations and interpretations section for the calculation formulas. See site specific microhematocrit procedure.

b. Alternatively, a dilution may be performed.
    i. Perform a dilution of the specimen (1:2, 1:3, 1:5, etc.) Allow to equilibrate for 5 minutes before analysis.
    ii. Run in manual mode on the instrument within 20 minutes of setup.
    iii. As a QC check, verify that the RBC count agrees within +/- 0.20 of undiluted sample.
    iv. If diluted rerun was added in the middleware, the middleware will automatically calculate the results. (Refer to the *Hematology Caresphere Operation* procedure).
    v. Document the steps taken in the middleware as an internal comment, ie., *"Run 2 performed by dilution."*
    vi. **NOTE: Do not use differential results from run on diluted specimen.**

IX. CALCULATIONS AND INTERPRETATIONS:

A. **Mean corpuscular volume (MCV)** is the volume of the average RBC of a given sample of blood. Results are expressed in femtoliters (fL), formerly known as cubic microns or μ^3.

1. $$MCV = \frac{Hct\ \% \times 10}{RBC\ (trill/L)}$$

B. **Mean corpuscular hemoglobin (MCH)** is the average weight of hemoglobin contained in an average erythrocyte. Results are expressed as picograms (pg) which is the same as micromicrograms (µµg).

1. $$MCH = \frac{Hgb\ (gm/dL) \times 10}{RBC\ (trill/L)}$$

C. **Mean corpuscular hemoglobin concentration (MCHC)** is the average concentration of hemoglobin in a given volume of packed red cells. Results expressed as % or gm/dL.

1. $$MCHC = \frac{Hgb\ (gm/dL) \times 100}{Hct\ \%}$$

X. EXPECTED VALUES:

The presence of elevated WBC counts, lipemia, icteria, cold agglutinins, cryoglobulins, nucleated RBCs, or platelet clumping/satellitosis, giant platelets, microcytic / fragmented / RBC lyse resistance, hemolysis, and

marked changes in plasma constituents is not found in normal blood.

XI. NOTES:

A. In some situations a corrected value may be unable to be obtained. If a corrected value cannot be obtained by manual methods, add the comment *"Unable to perform due to unknown interference"* to the affected parameter in the middleware or LIS. Consult supervisor if further direction is needed.

B. Instrument voteouts will come across into the middleware as "#nm". This translates to *"Unable to perform"* in the LIS.

C. Abnormal paraproteins found in Multiple Myeloma patients can falsely increase the HGB. To correct HGB, perform plasma replacement or plasma blank procedure.

D. MCHCs over 37.0 gm/dL may be a result of **falsely high** HGBs or **falsely low** HCTs.

1. Falsely high HGB possible causes:
    a. Lipemia
    b. Increased bilirubin
    c. Abnormal proteins
2. Falsely low HCT possible causes:
    a. Cold agglutinin
    b. Gross hemolysis
    c. Instrument failure
    d. Incorrect RBC count

XII. REFERENCES:

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D. Koepke JA. Tips on Technology. MLO, July 1995.

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G. XN Flagging Guide, Sysmex, January 2015, Document -1166-LSS

Attachments

Attachment-MCHC GREATER THAN 38 WORKFLOW.pdf

Attachment-Nucleated Red Blood Cells Correction On The XN-L Analyzers.pdf

Approval Signatures

Step Description	Approver	Date
	Hassan Kanaan: OUWB Clinical Faculty	10/29/2024
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	Ann Marie Blenc: System Med Dir, Hematopath	10/26/2024
	Jeremy Powers: Chief, Pathology	10/23/2024
	John Pui: Chief, Pathology	10/23/2024
	Ryan Johnson: OUWB Clinical Faculty	10/22/2024
	Masood Siddiqui: Staff Pathologist	10/22/2024
Policy and Forms Steering Committee Approval (if needed)	Megan Masakowski: Mgr, Division Laboratory	10/22/2024
	Udayasree Bartley: Medical Technologist Lead	10/22/2024
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	Ashley Beesley: Mgr, Laboratory	10/14/2024
	Katherine Persinger: Mgr, Laboratory	10/11/2024
	Megan Masakowski: Mgr, Division Laboratory	10/10/2024

Applicability

Dearborn, Farmington Hills, Grosse Pointe, Royal Oak, Taylor, Trenton, Troy, Wayne