LABQUALITY

External Quality Assessment Scheme

# Reticulocytes, manual methods
# Round 1, 2023

### Specimens
Please find enclosed 1 human origin blood cell suspension S001, 3 mL.

### Caution
Quality control specimens derived from human blood must be handled with the same care as patient samples, i.e. as potential transmitters of serious diseases. The specimens are found to be HBsAg, HCVAb and HIVAgAb negative when tested with licensed reagents, but no known test method can offer complete assurance that the specimens will not transmit these or other infectious diseases.

### Examinations
Reticulocytes

### Storage and use
Please analyze the sample on arrival day. If this is not possible, store the sample in a refrigerator (+2…+8 °C) and analyze as soon as possible. Do not freeze. Let the vial warm up in room temperature at least 15 minutes. Gently invert the vial until the cells are completely and uniformly suspended. Do not use mechanical mixer. Prepare staining and smear.

### Result reporting
Please enter the results via LabScala (www.labscala.com). In balanced sampling method (Dacie & Lewis: Practical Haematology) at least 100 reticulocytes are counted in successive fields and the count of all red cells in every tenth field. The number of all red cells should be counted in at least ten fields. The calculation is as follows (an example): Number of the reticulocytes seen in 150 fields = 100; Number of all red cells present 15 fields = 300; the approximate number of all red cells in 150 fields = 3000; the reticulocyte percentage = 100/3000 x 100 = 3.3%.

S001

LQ711323011

**2023-04-03**

**INSTRUCTIONS**

Product no. 4140
LQ711323011/US

If the kit is incomplete or contains damaged specimens, please report immediately to info@labquality.fi

The results should be reported no later than **April 20, 2023**.

**Inquiries**
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FINAS
Finnish Accreditation Service
PT02 (EN ISO/IEC 17043)

Quality Management
DQS
ISO 9001:2015

LABQUALITY

External Quality Assessment Scheme

# Reticulocytes, automated methods
# Round 1, 2023

### Specimens

Please find enclosed 2 blood cell suspensions 3 mL each according to your order. Samples S002 and S003 are for Siemens Advia analyzers, S004 and S005 are for Sysmex analyzers, S006 and S007 are for Cell-Dyn 3200, 3500, 3700 and Ruby analyzers. Samples S008 and S009 are for Coulter GenS and Coulter LH750 analyzers. Samples S010 and S011 are for Cell-Dyn 4000, Saphire and ABX analyzers. Samples S012 and S013 are for Mindray analysers.

### Caution

Quality control specimens derived from human blood must be handled with the same care as patient samples, i.e. as potential transmitters of serious diseases. The specimens are found to be HBsAg, HCVAb and HIVAgAb negative when tested with licensed reagents, but no known test method can offer complete assurance that the specimens will not transmit these or other infectious diseases.

### Examinations

Reticulocytes

### Storage and use

Store the samples in refrigerator (+ 2…8 °C), do not freeze. Allow samples to warm up at ambient room temperature about 15 minutes. Gently invert the vials until the cells are completely suspended. Do not shake the vial or use a mechanical mixer. Analyse as patient samples.

### Result reporting

Please enter the results and methods via LabScala (www.labscala.com). If you cannot find your instrument or reagent from the registry, please contact the EQA Coordinator. Results should be given in absolute values.

**2023-04-03**

**INSTRUCTIONS**

Product no. 4150-4156
LQ711323012-113/US

If the kit is incomplete or contains damaged specimens, please report immediately to info@labquality.fi.

The results should be reported no later than **April 20, 2023**.

**Inquiries**
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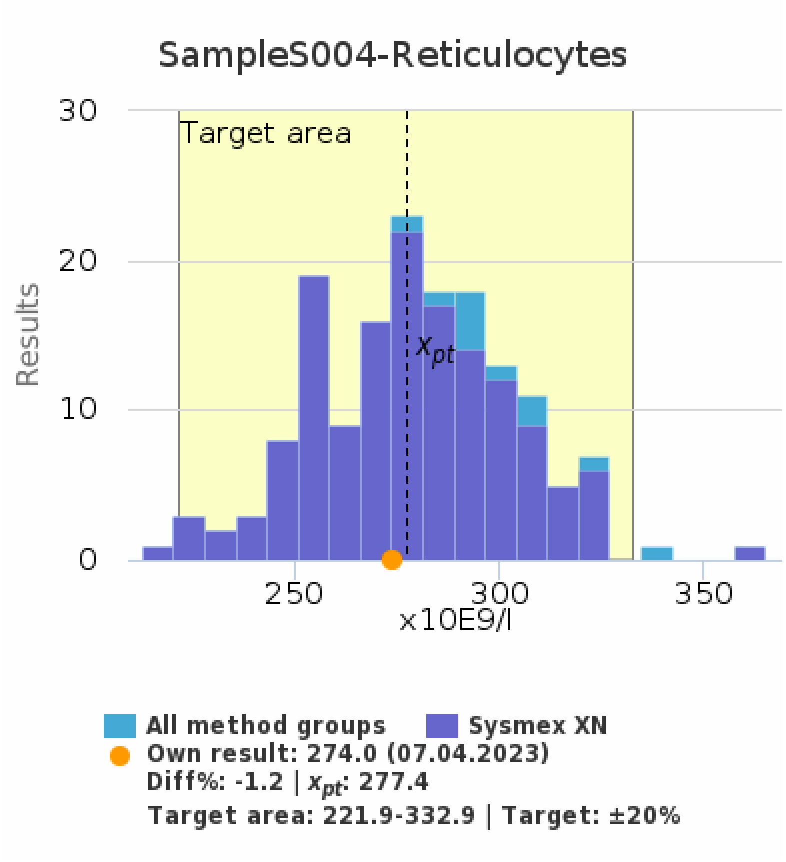
FINAS
Finnish Accreditation Service
PT02 (EN ISO/IEC 17043)

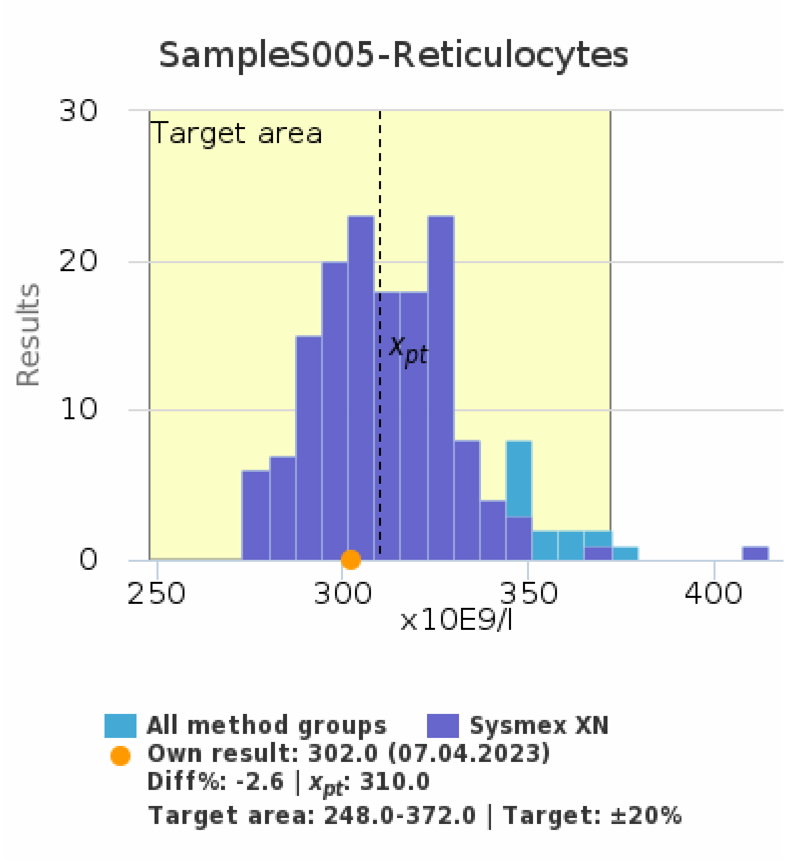
Quality Management
ISO 9001:2015

Reticulocytes, automated methods

| | |
|---|---|
| S002 | LQ711323012 |
| S003 | LQ711323013 |
| S004 | LQ711323014 |
| S005 | LQ711323015 |
| S006 | LQ711323016 |
| S007 | LQ711323017 |
| S008 | LQ711323018 |
| S009 | LQ711323019 |
| S010 | LQ7113230110 |
| S011 | LQ7113230111 |
| S012 | LQ7113230112 |
| S013 | LQ7113230113 |

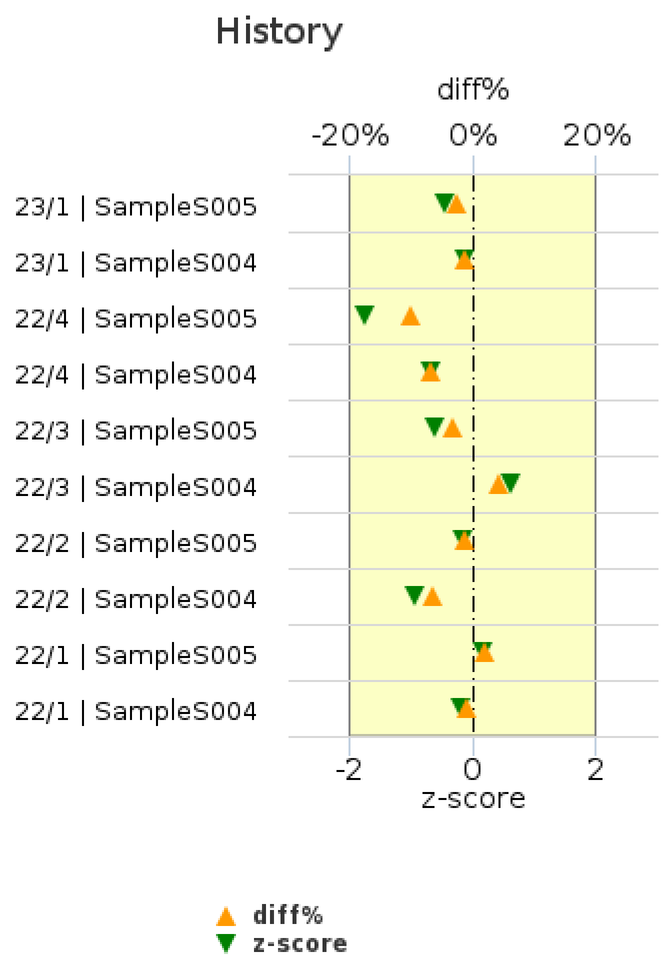
## Reticulocytes |Lionel 45156 Retic





| | $x_{pt}$ | sd | SEM | CV% | n |
|---|---|---|---|---|---|
| Sysmex XN | 277.4 x10E9/l | 23.6 | 1.9 | 8.5 | 147 |
| All methods | 279.1 x10E9/l | 23.9 | 1.9 | 8.6 | 158 |

| | $x_{pt}$ | sd | SEM | CV% | n |
|---|---|---|---|---|---|
| Sysmex XN | 310.0 x10E9/l | 17.0 | 1.4 | 5.5 | 147 |
| All methods | 313.3 x10E9/l | 20.4 | 1.6 | 6.5 | 158 |



| Round | Sample | $x_{pt}$ | Result | diff% | z-score |
|---|---|---|---|---|---|
| 23/1 | Sample S005 | 310.0 | 302.0 | -2.6% | -0.47 |
| 23/1 | Sample S004 | 277.4 | 274.0 | -1.2% | -0.14 |
| 22/4 | Sample S005 | 243.9 | 219.2 | -10.1% | -1.74 |
| 22/4 | Sample S004 | 80.8 | 75.3 | -6.8% | -0.69 |
| 22/3 | Sample S005 | 329.1 | 318.0 | -3.4% | -0.63 |
| 22/3 | Sample S004 | 284.0 | 296.0 | 4.2% | 0.60 |
| 22/2 | Sample S005 | 85.1 | 84.0 | -1.3% | -0.15 |
| 22/2 | Sample S004 | 195.8 | 183.0 | -6.5% | -0.93 |
| 22/1 | Sample S005 | 59.9 | 61.0 | 1.8% | 0.16 |
| 22/1 | Sample S004 | 243.7 | 241.0 | -1.1% | -0.18 |

## Report info

**Participants**

180 participants from 20 countries.

**Report info**

Your own result should be compared to others using the same method.
Assigned values ($x_{pt}$, target values) are means of the results where results deviating more than +/- 3*standard deviation from the median are removed. The standard uncertainty (u) of the assigned value is reported as standard error of the mean (SEM). Additionally, if the measurement uncertainty of the target value is large an automatic text is printed on the report: “The uncertainty of the assigned value is not negligible, and evaluations could be affected.”
In case the client’s result is the only one in the method group, no assigned value will be calculated, no target area shown, and no statistics calculated. In case there are only a few results in the client’s own method group, the result can be compared to all method mean or to a group that is similar to the own method.
Results reported with < or > -signs cannot be included in the statistics.

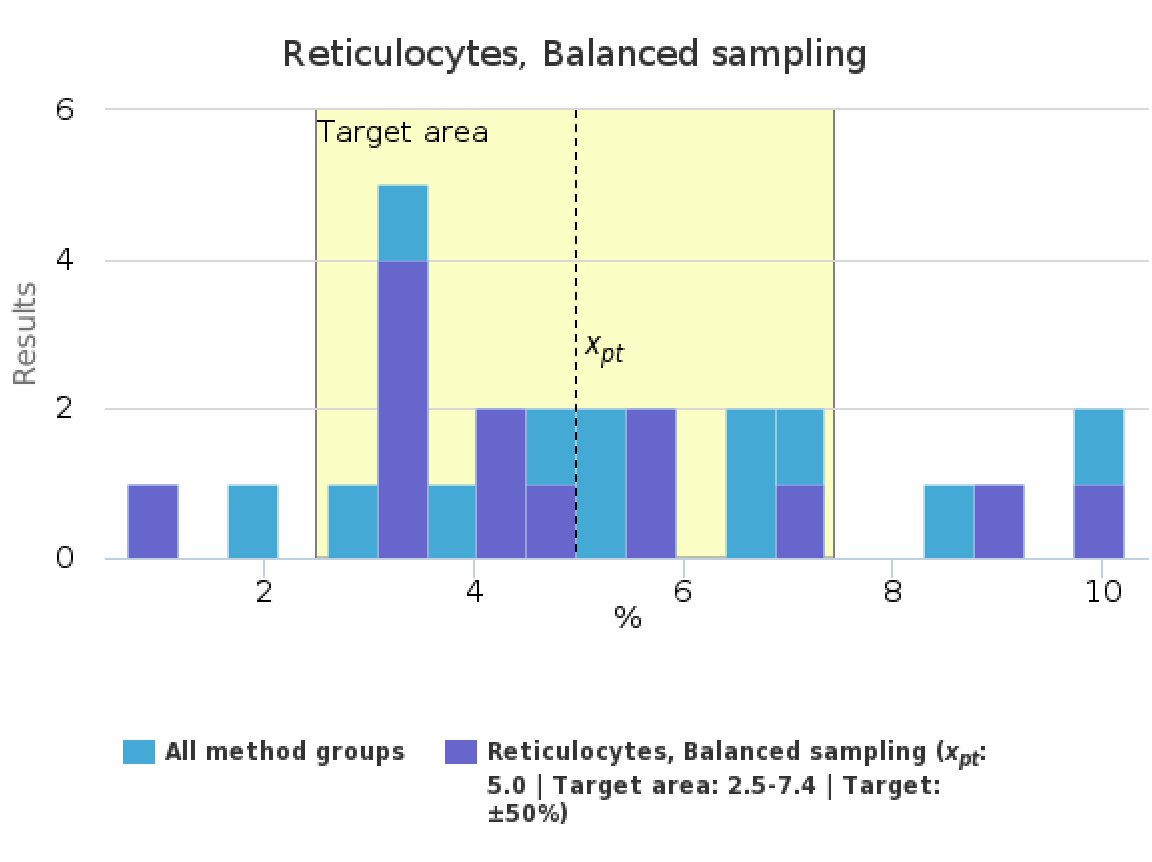
For information on report interpretation and performance evaluation, please see the " EQAS Interpretation guidelines" LabScala User instructions (top right corner ?Help link).

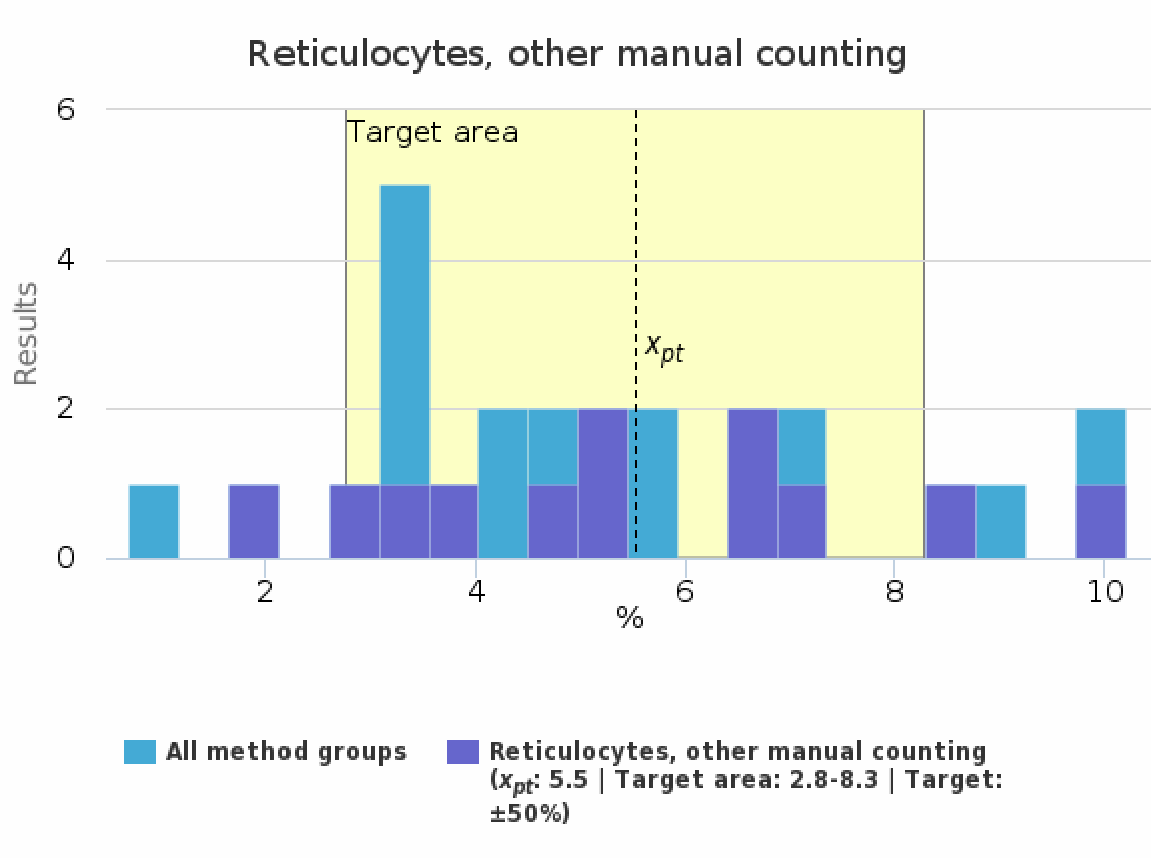
# Reticulocyte count, March, 1-2023

## Sample S001 | Reticulocytes, %

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Reticulocytes, Balanced sampling | 5.0 | 4.4 | 2.5 | 51.0 | 0.7 | 0.7 | 10.0 | - | 13 |
| Reticulocytes, other manual counting | 5.5 | 5.2 | 2.4 | 43.8 | 0.7 | 1.9 | 10.2 | - | 12 |
| **All** | **5.2** | **4.7** | **2.4** | **46.7** | **0.5** | **0.7** | **10.2** | **-** | **25** |

## Sample S001 | Reticulocytes, %| histogram summaries in LabScala

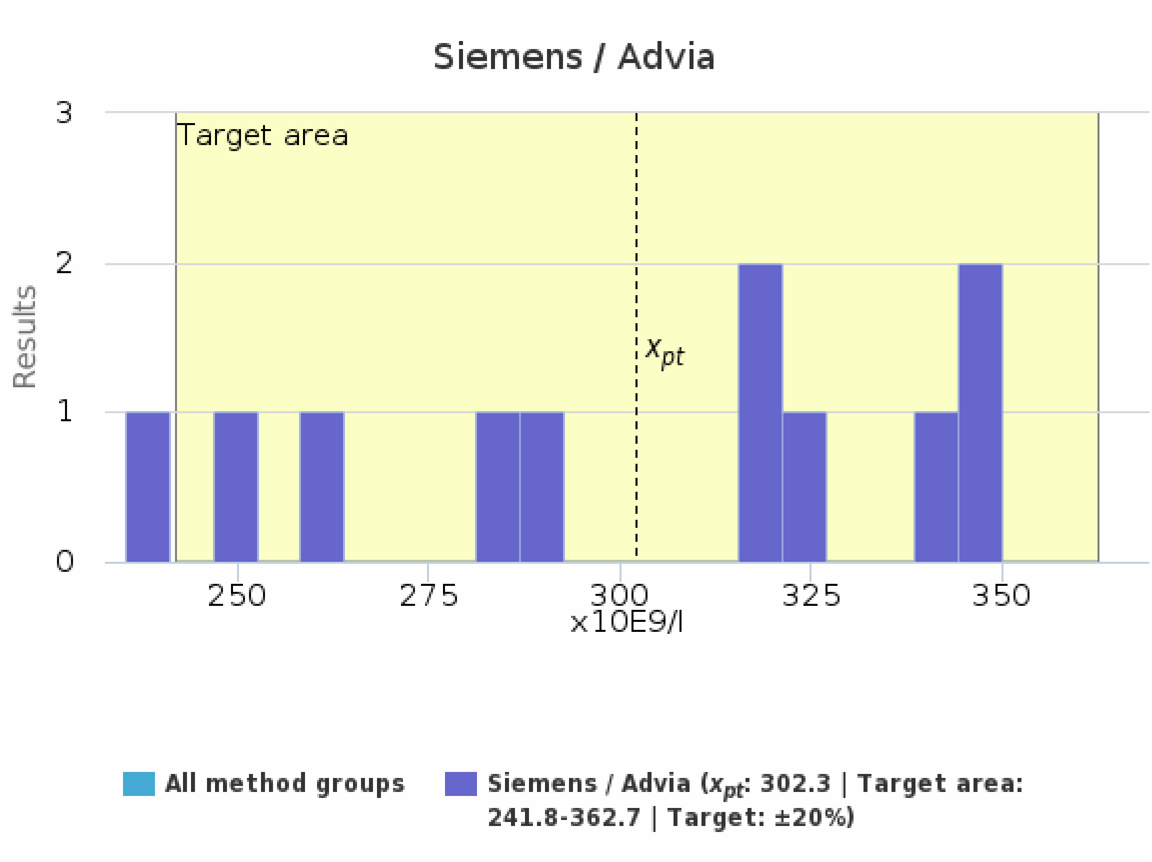




### Sample S002 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Siemens / Advia | 302.3 | 316.0 | 40.7 | 13.5 | 12.3 | 235.4 | 350.0 | - | 11 |
| **All** | **302.3** | **316.0** | **40.7** | **13.5** | **12.3** | **235.4** | **350.0** | **-** | **11** |

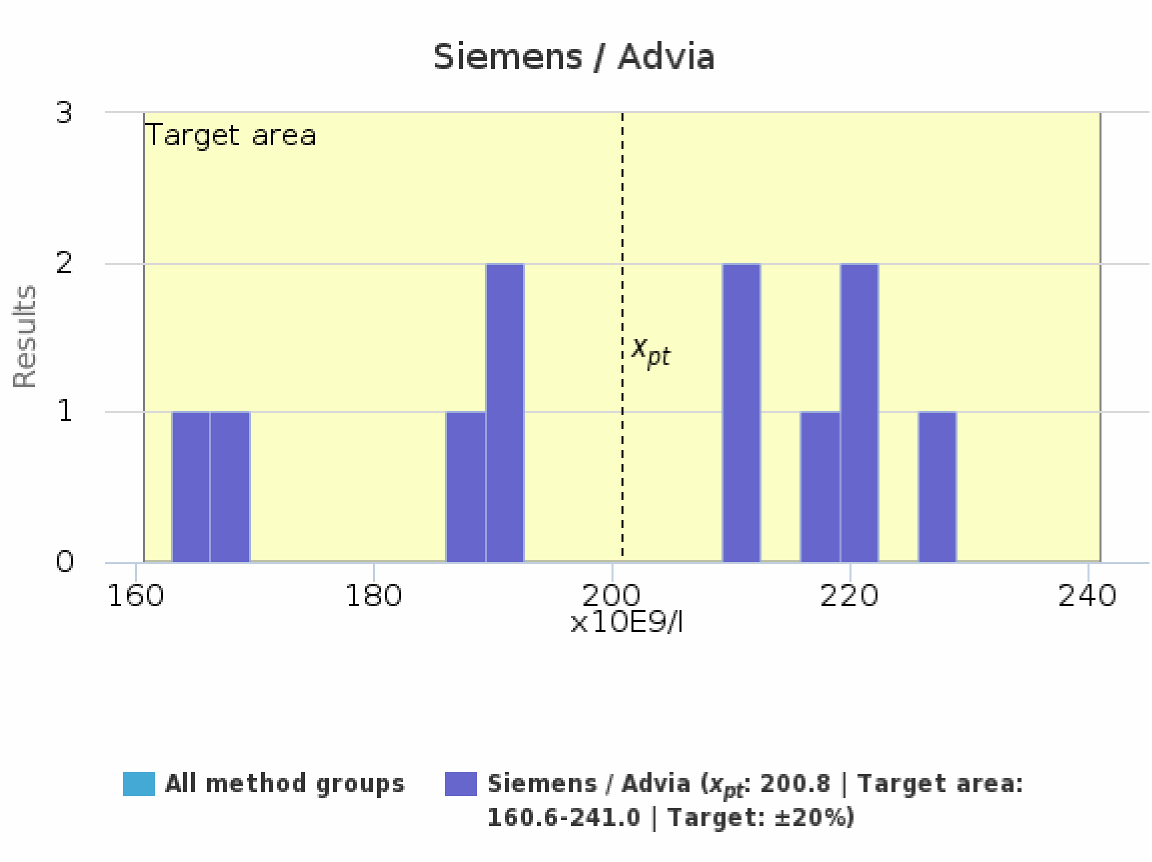
### Sample S002 | Reticulocytes, x10E9/l| histogram summaries in LabScala



### Sample S003 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Siemens / Advia | 200.8 | 209.8 | 22.1 | 11.0 | 6.7 | 163.0 | 229.0 | - | 11 |
| **All** | **200.8** | **209.8** | **22.1** | **11.0** | **6.7** | **163.0** | **229.0** | **-** | **11** |

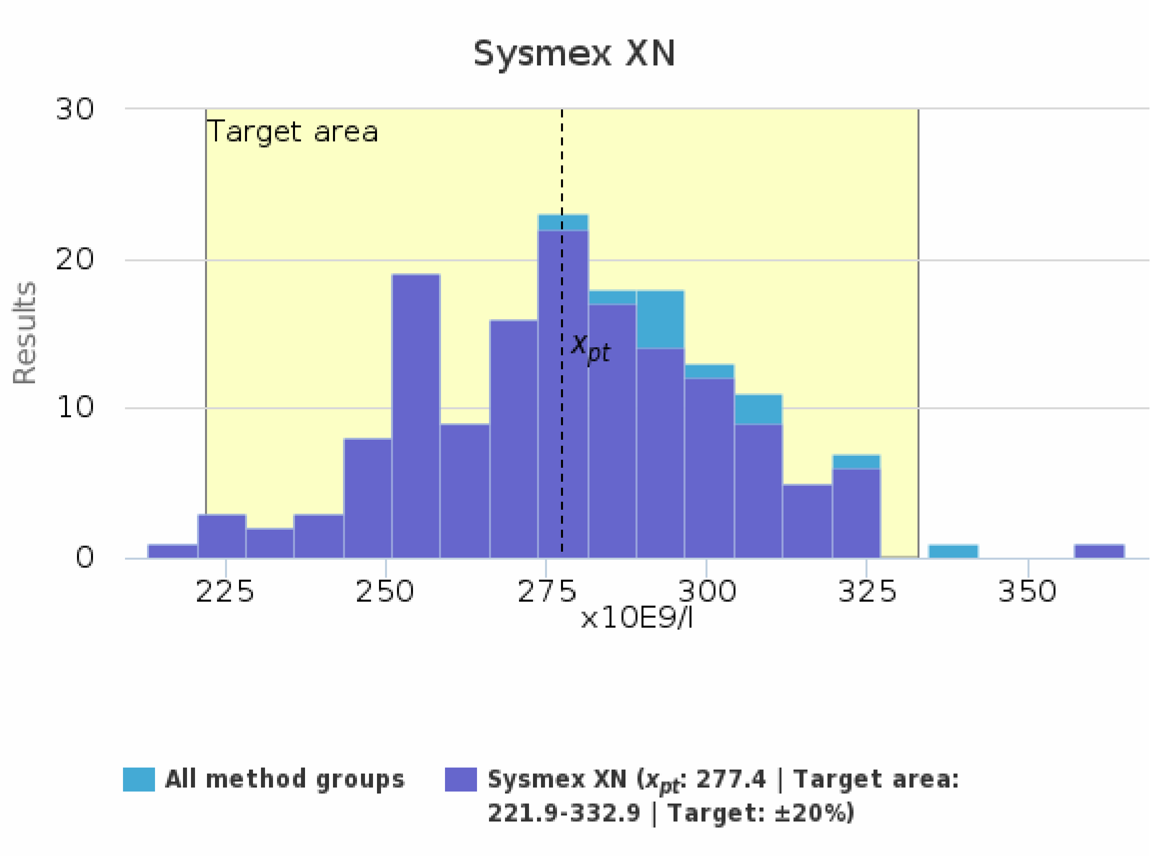
### Sample S003 | Reticulocytes, x10E9/l| histogram summaries in LabScala

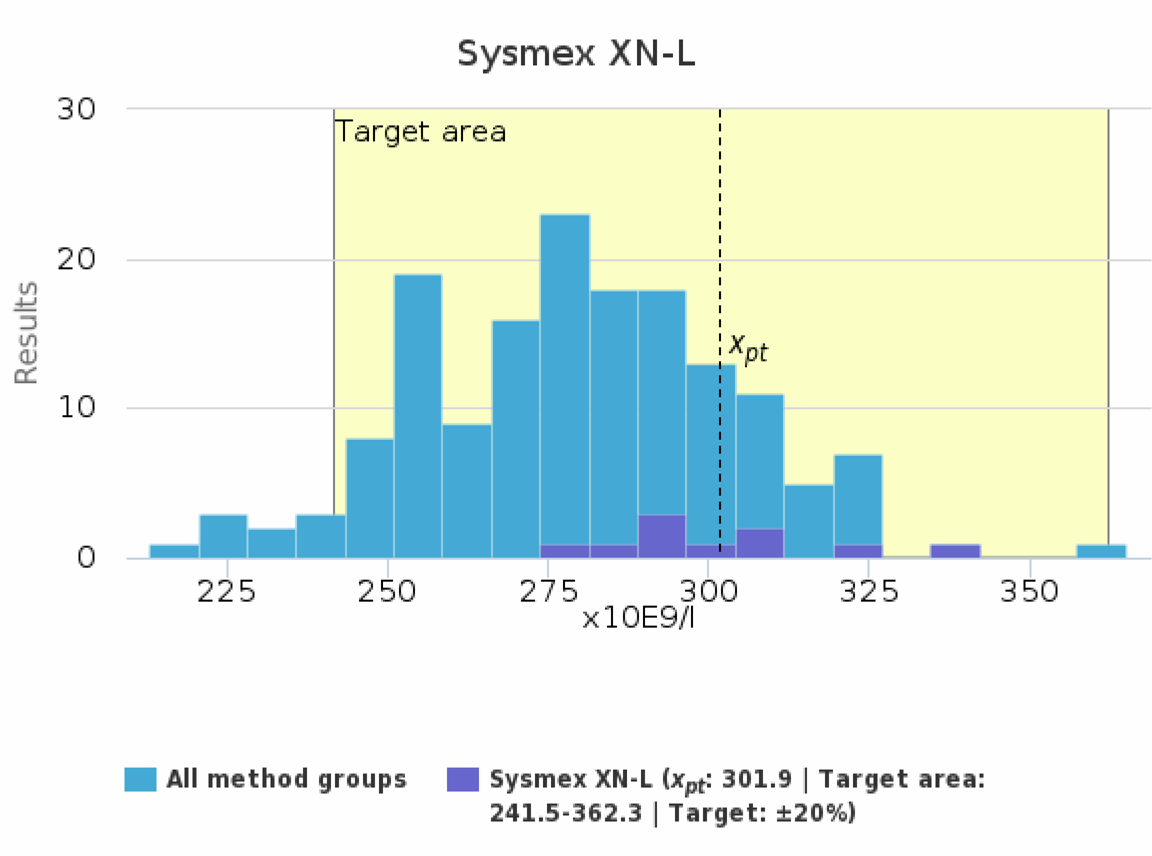


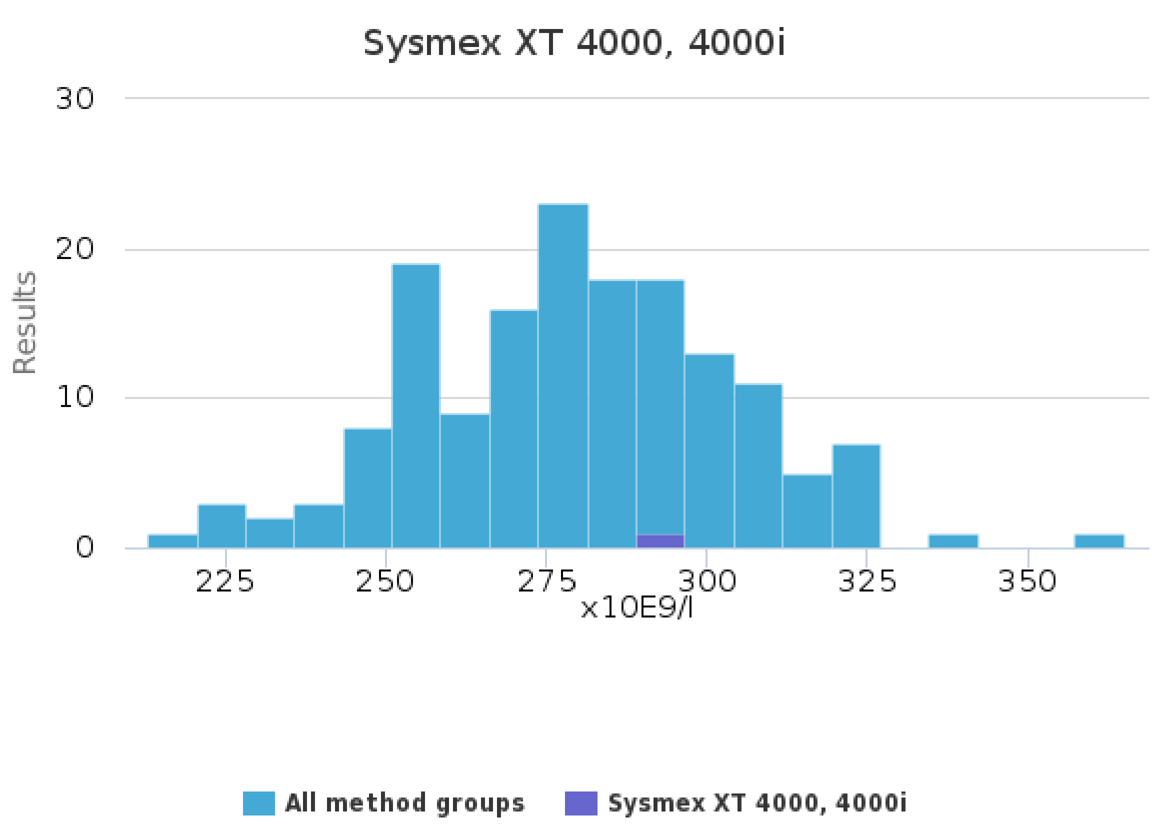
### Sample S004 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Sysmex XN | 277.4 | 278.4 | 23.6 | 8.5 | 1.9 | 213.0 | 325.4 | 1 | 147 |
| Sysmex XN-L | 301.9 | 298.0 | 18.0 | 6.0 | 5.7 | 277.0 | 338.1 | - | 10 |
| Sysmex XT 4000, 4000i | - | - | - | - | - | 295.1 | 295.1 | - | 1 |
| **All** | **279.1** | **279.3** | **23.9** | **8.6** | **1.9** | **213.0** | **338.1** | **1** | **158** |

### Sample S004 | Reticulocytes, x10E9/l| histogram summaries in LabScala



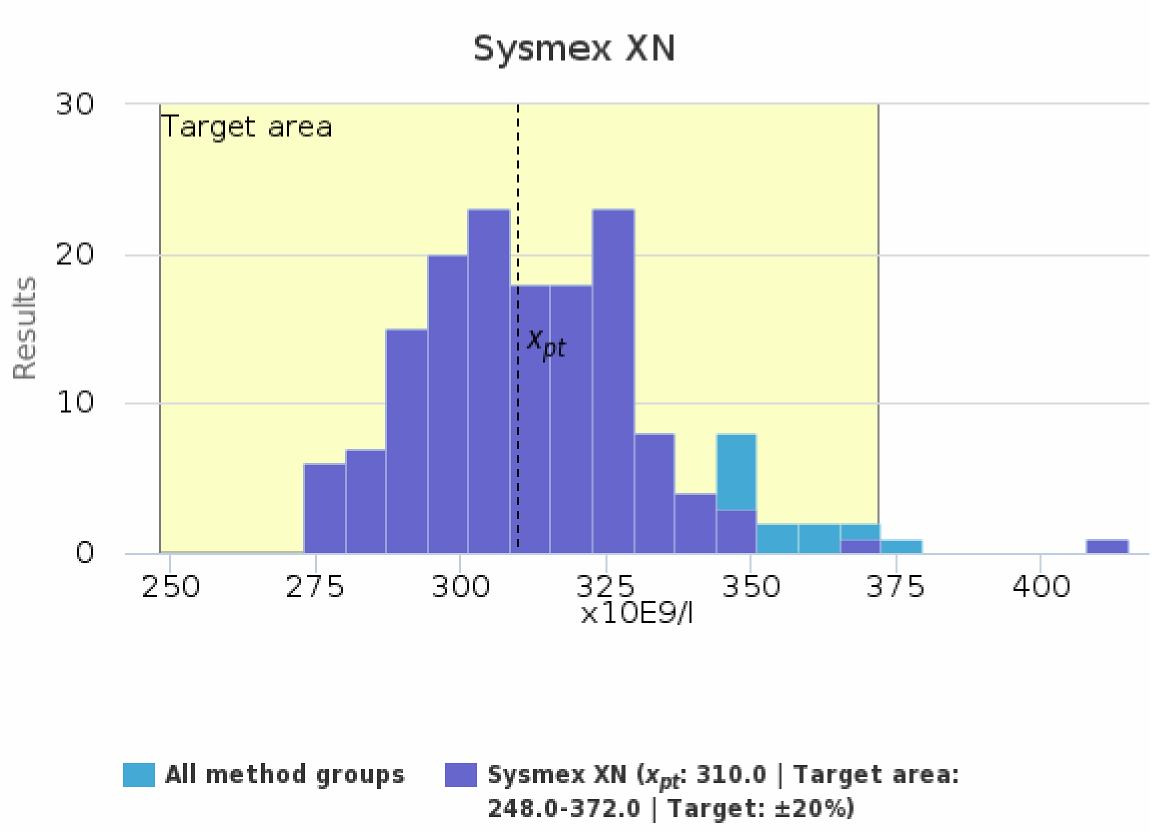




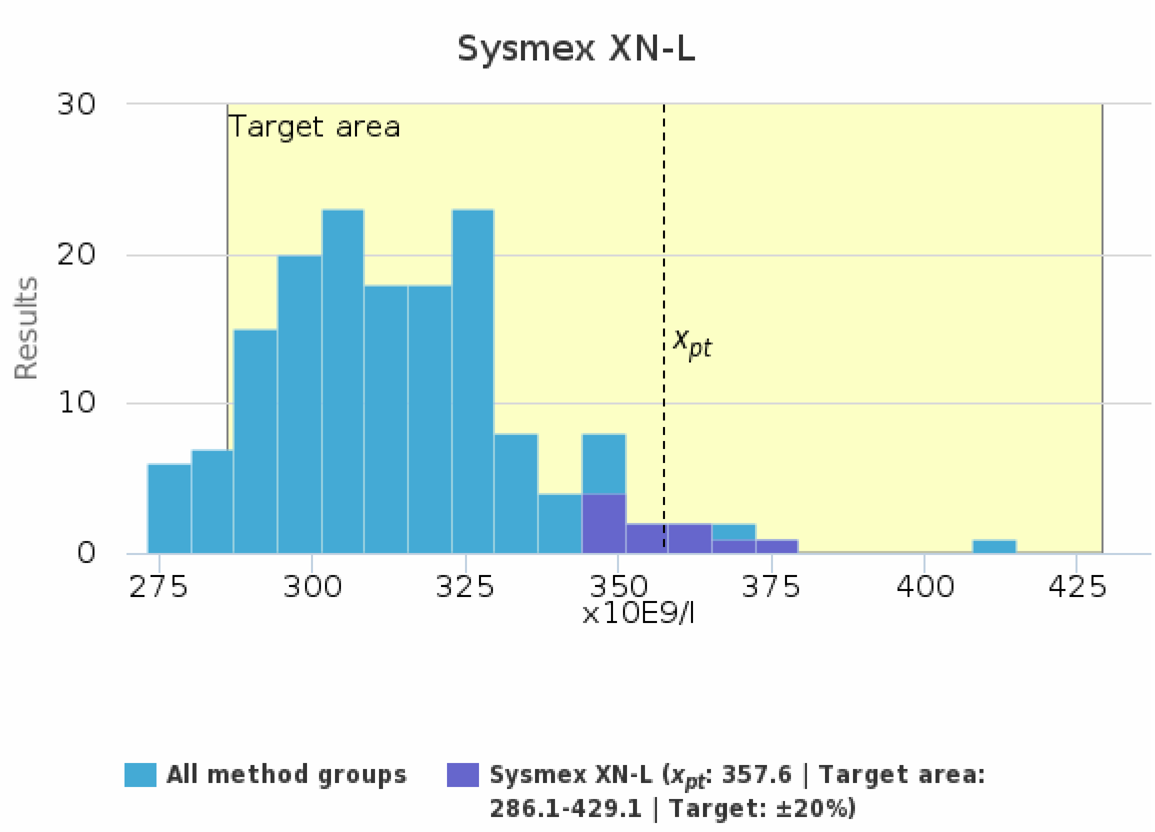
## Sample S005 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Sysmex XN | 310.0 | 309.2 | 17.0 | 5.5 | 1.4 | 273.0 | 365.4 | 1 | 147 |
| Sysmex XN-L | 357.6 | 353.8 | 9.7 | 2.7 | 3.1 | 347.6 | 374.8 | - | 10 |
| Sysmex XT 4000, 4000i | - | - | - | - | - | 345.1 | 345.1 | - | 1 |
| **All** | **313.3** | **310.6** | **20.4** | **6.5** | **1.6** | **273.0** | **374.8** | **1** | **158** |

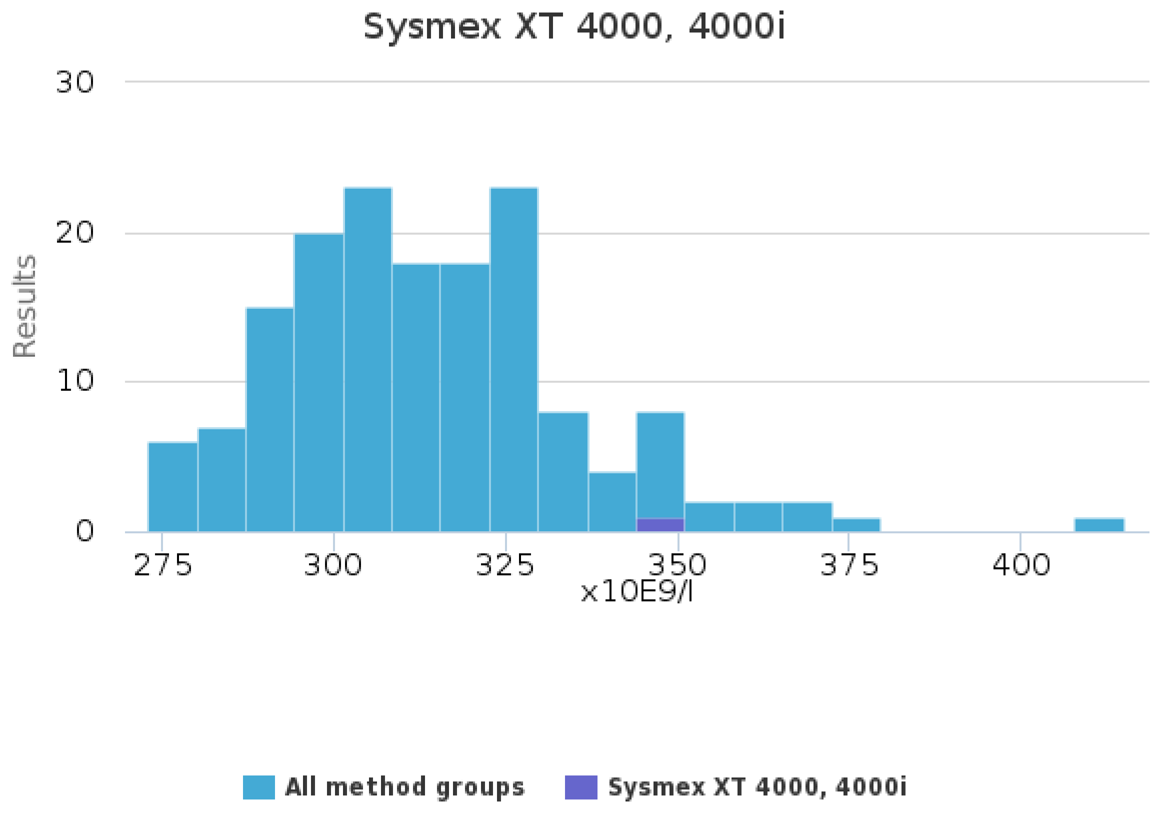
## Sample S005 | Reticulocytes, x10E9/l| histogram summaries in LabScala



Sysmex XN



Sysmex XN-L

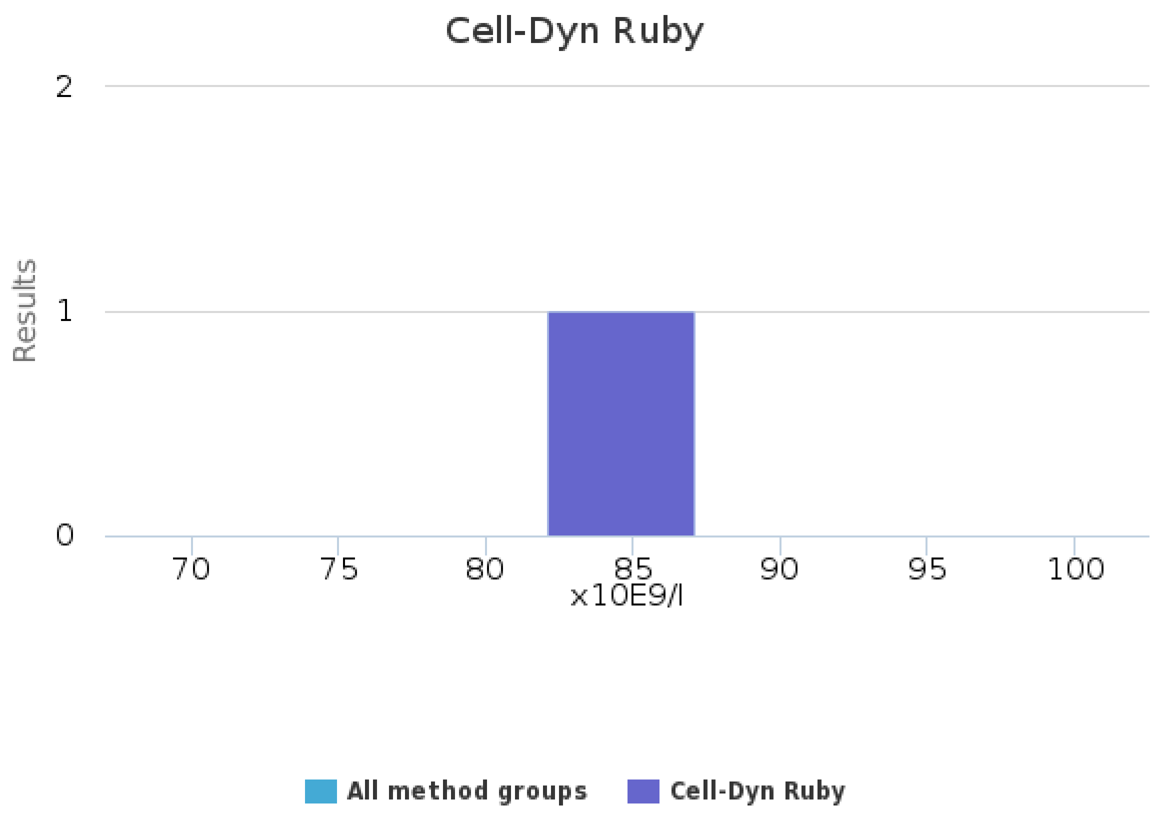


Sysmex XT 4000, 4000i

### Sample S006 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Cell-Dyn Ruby | - | - | - | - | - | 84.6 | 84.6 | - | 1 |
| **All** | **-** | **-** | **-** | **-** | **-** | **84.6** | **84.6** | **-** | **1** |

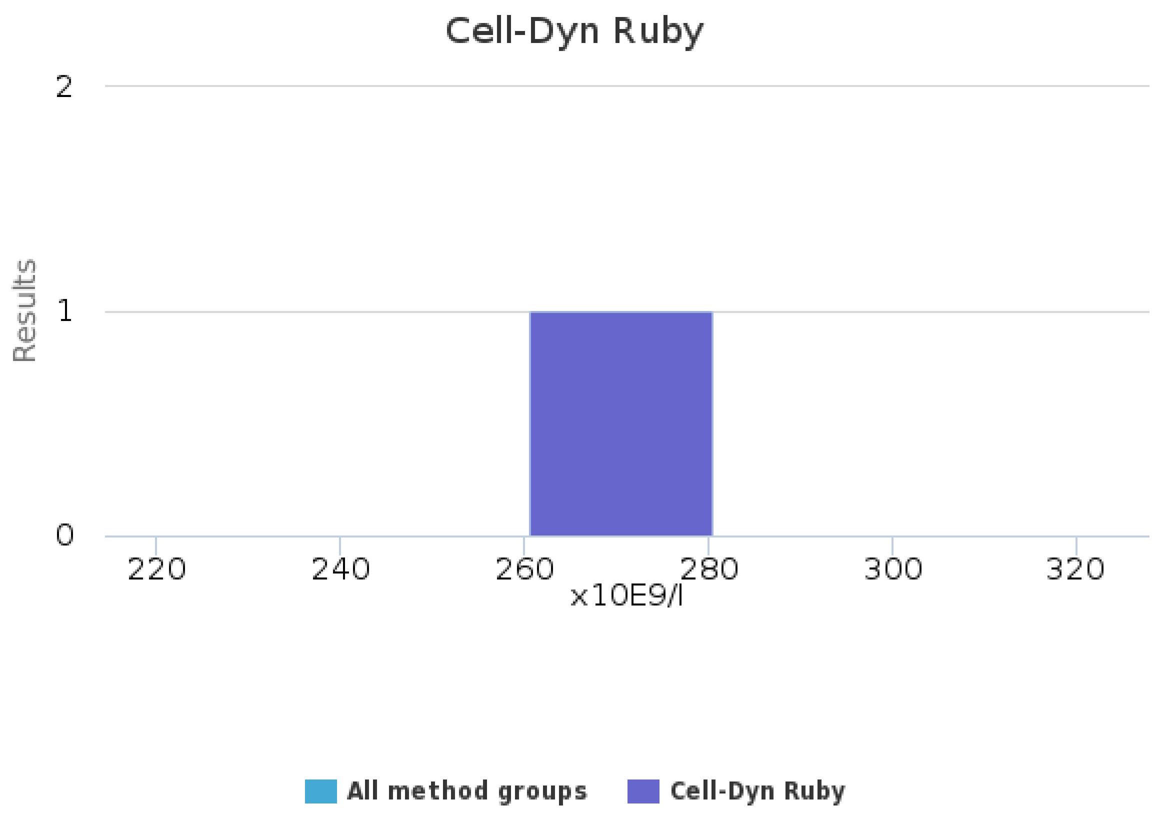
### Sample S006 | Reticulocytes, x10E9/l| histogram summaries in LabScala



### Sample S007 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Cell-Dyn Ruby | - | - | - | - | - | 270.5 | 270.5 | - | 1 |
| **All** | **-** | **-** | **-** | **-** | **-** | **270.5** | **270.5** | **-** | **1** |

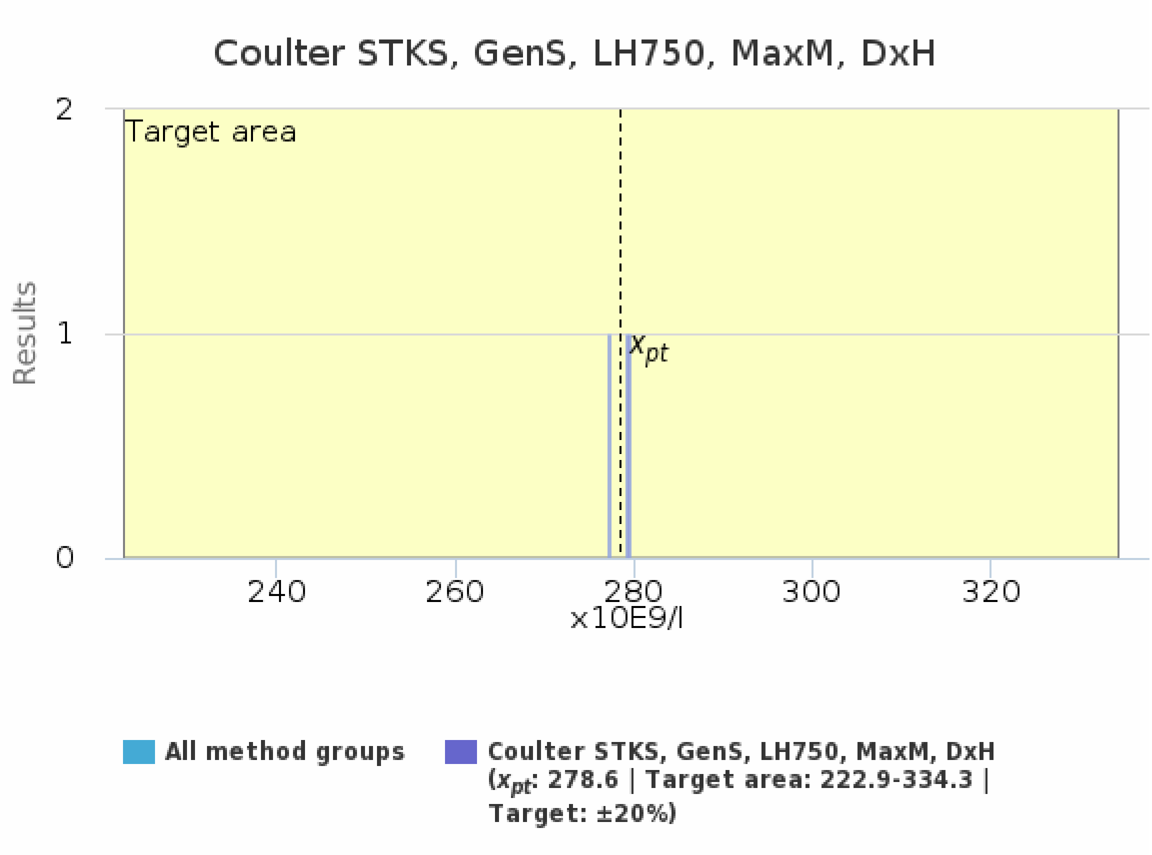
### Sample S007 | Reticulocytes, x10E9/l| histogram summaries in LabScala



### Sample S008 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Coulter STKS, GenS, LH750, MaxM, DxH | 278.6 | 279.2 | 1.3 | 0.5 | 0.7 | 277.1 | 279.4 | - | 3 |
| **All** | **278.6** | **279.2** | **1.3** | **0.5** | **0.7** | **277.1** | **279.4** | **-** | **3** |

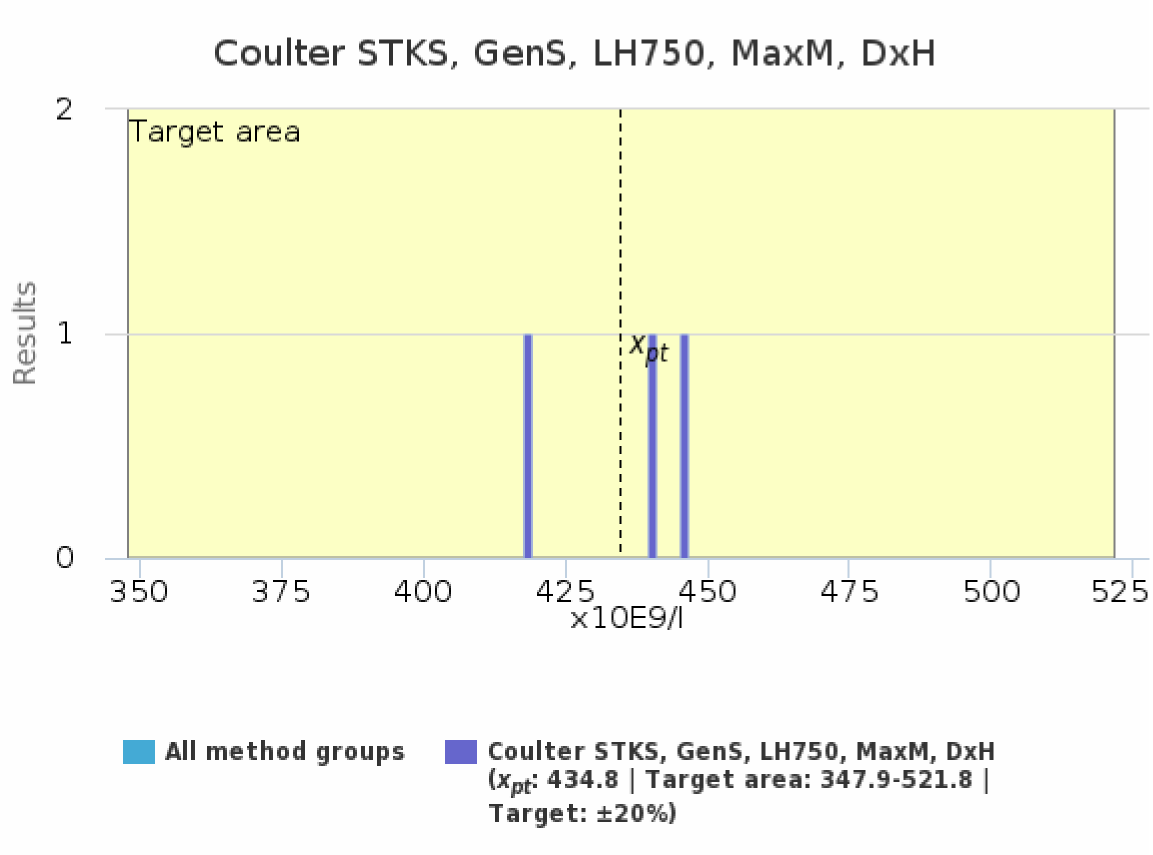
### Sample S008 | Reticulocytes, x10E9/l| histogram summaries in LabScala



## Sample S009 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Coulter STKS, GenS, LH750, MaxM, DxH | 434.8 | 440.1 | 15.3 | 3.5 | 8.8 | 417.6 | 446.8 | - | 3 |
| **All** | **434.8** | **440.1** | **15.3** | **3.5** | **8.8** | **417.6** | **446.8** | **-** | **3** |

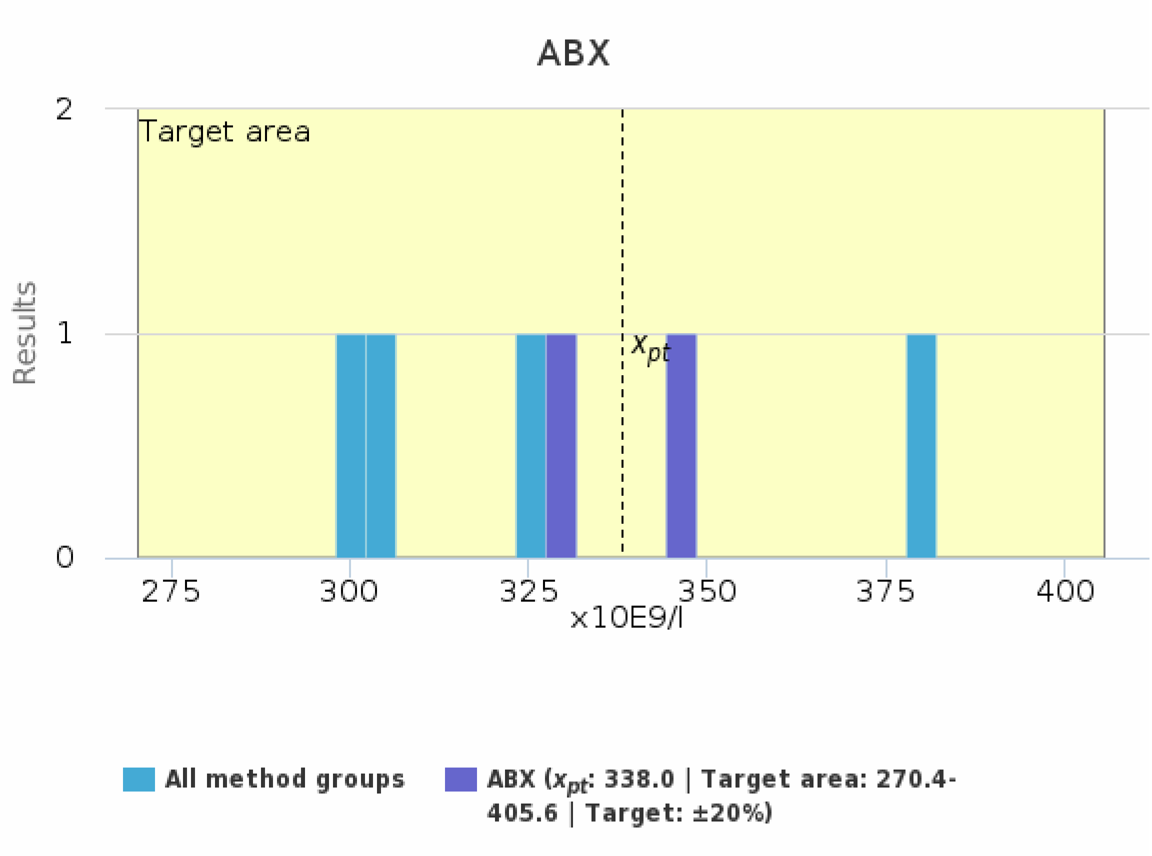
## Sample S009 | Reticulocytes, x10E9/l| histogram summaries in LabScala

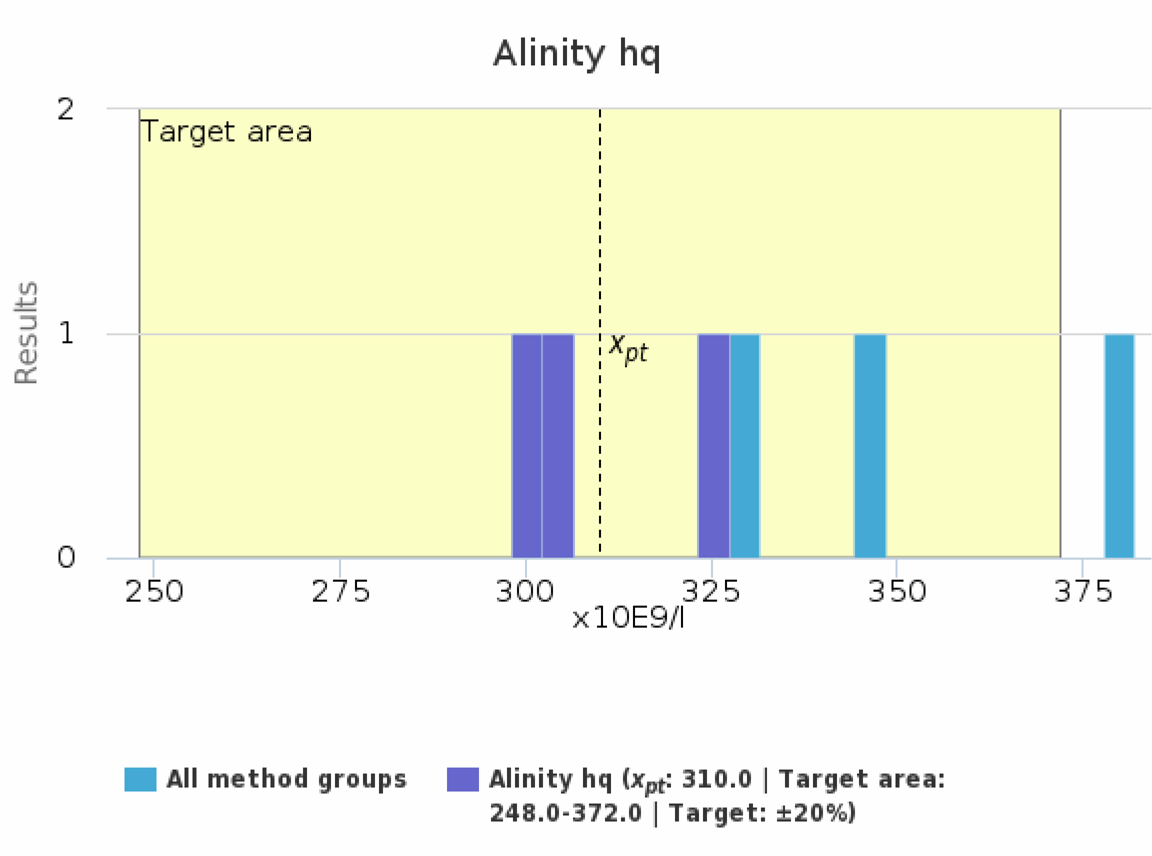


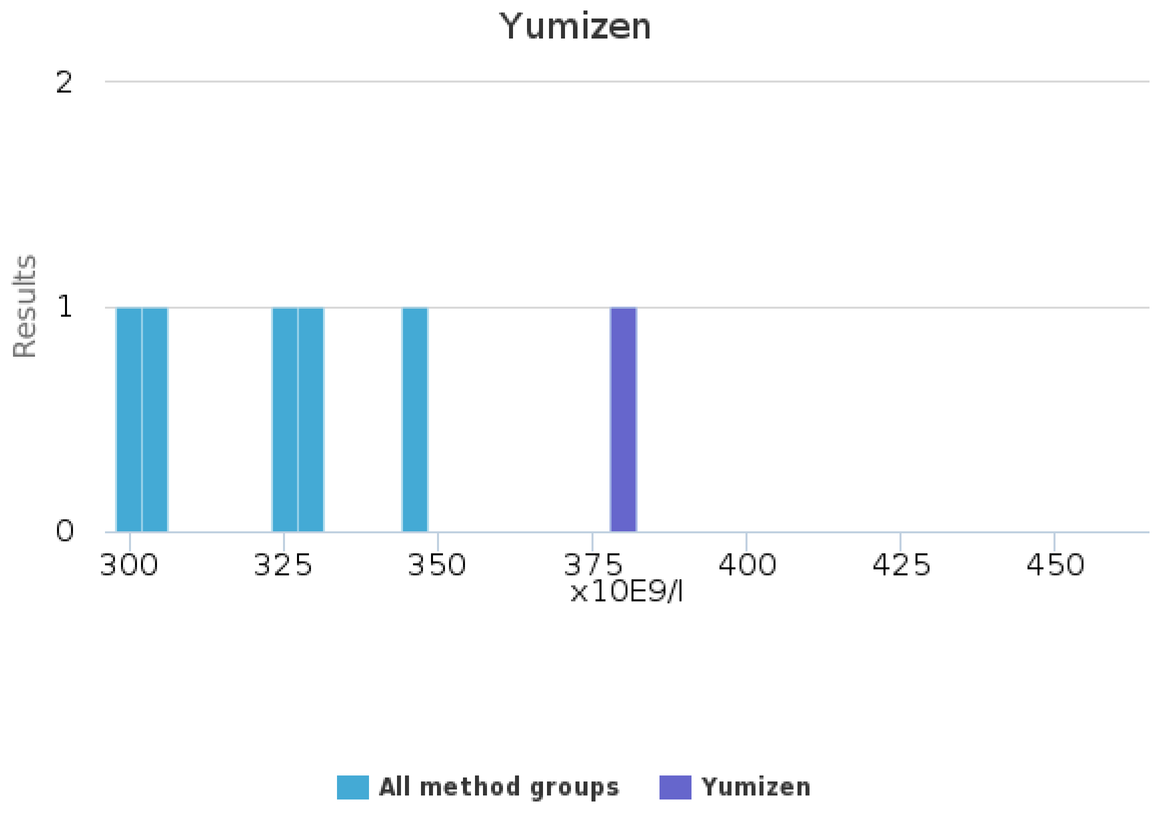
### Sample S010 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| ABX | 338.0 | 338.0 | 9.9 | 2.9 | 7.0 | 331.0 | 345.0 | - | 2 |
| Alinity hq | 310.0 | 306.0 | 14.4 | 4.7 | 8.3 | 298.0 | 326.0 | - | 3 |
| Yumizen | - | - | - | - | - | 382.0 | 382.0 | - | 1 |
| **All** | **331.3** | **328.5** | **30.1** | **9.1** | **12.3** | **298.0** | **382.0** | **-** | **6** |

### Sample S010 | Reticulocytes, x10E9/l| histogram summaries in LabScala



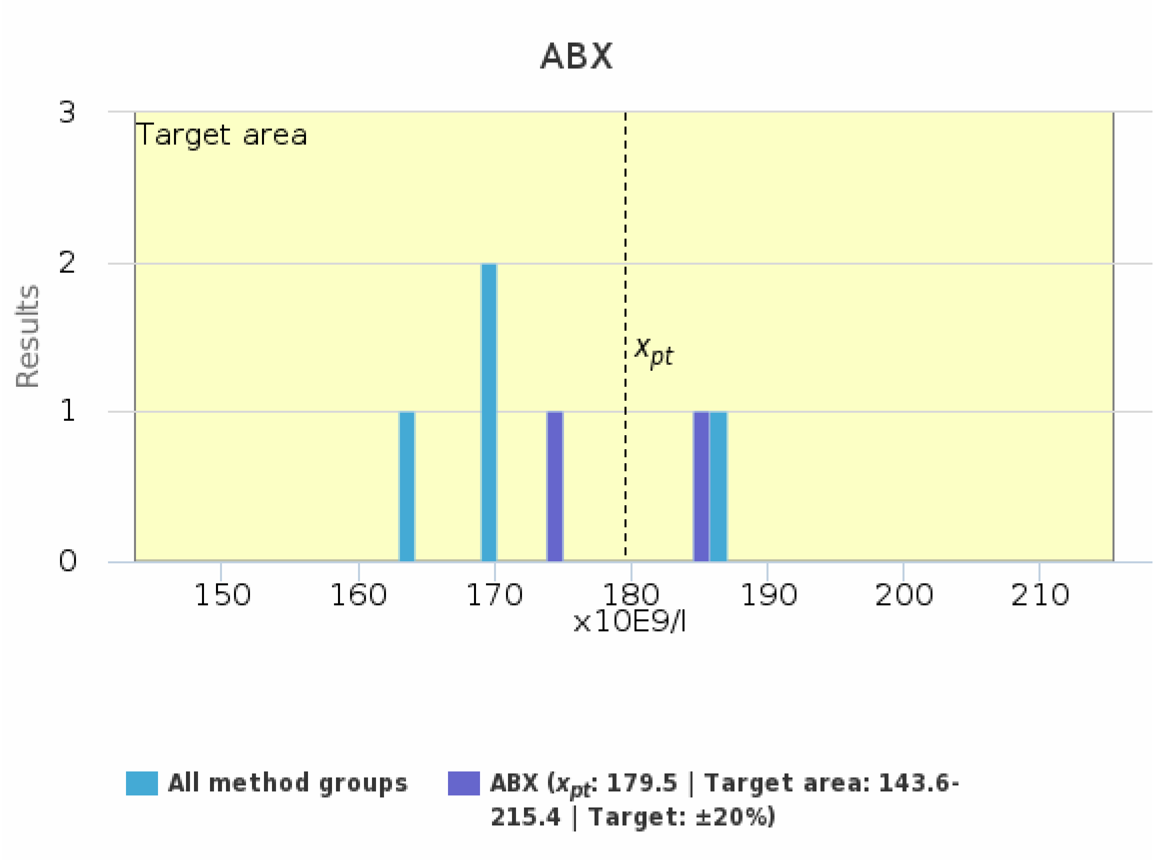


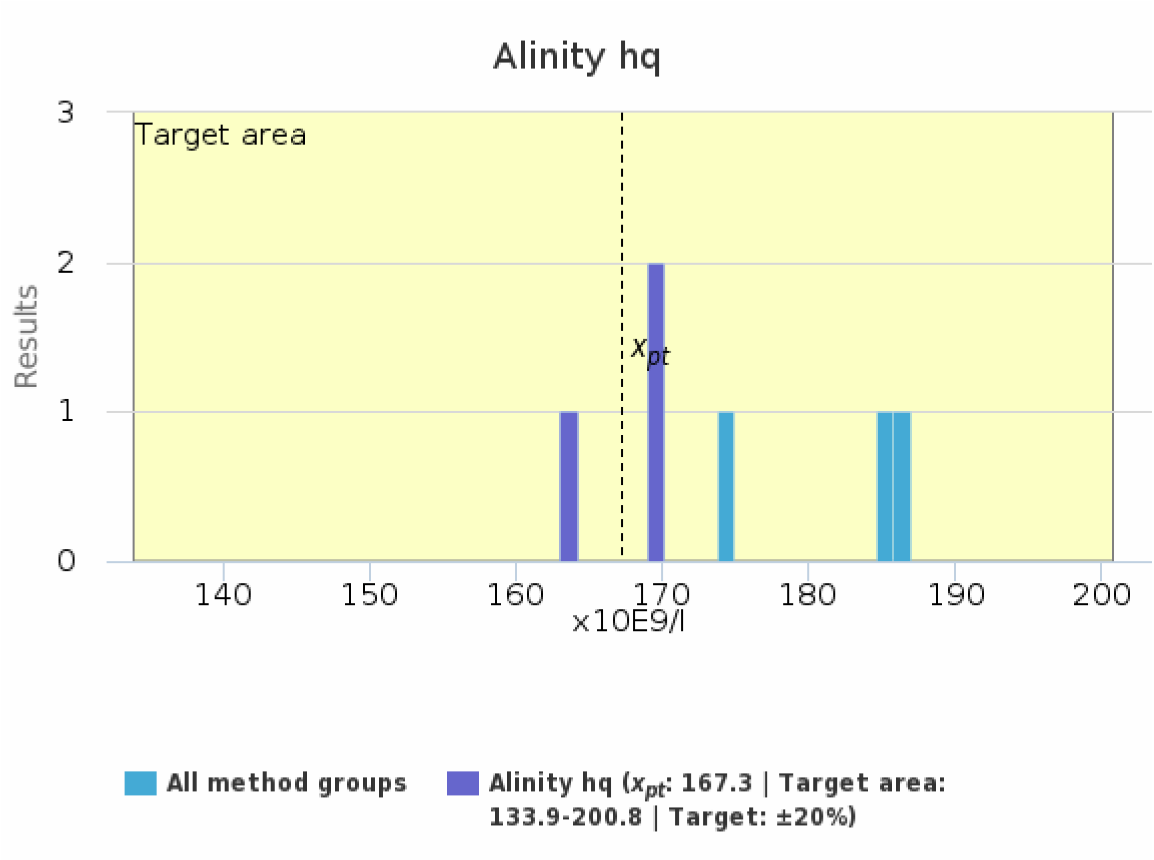


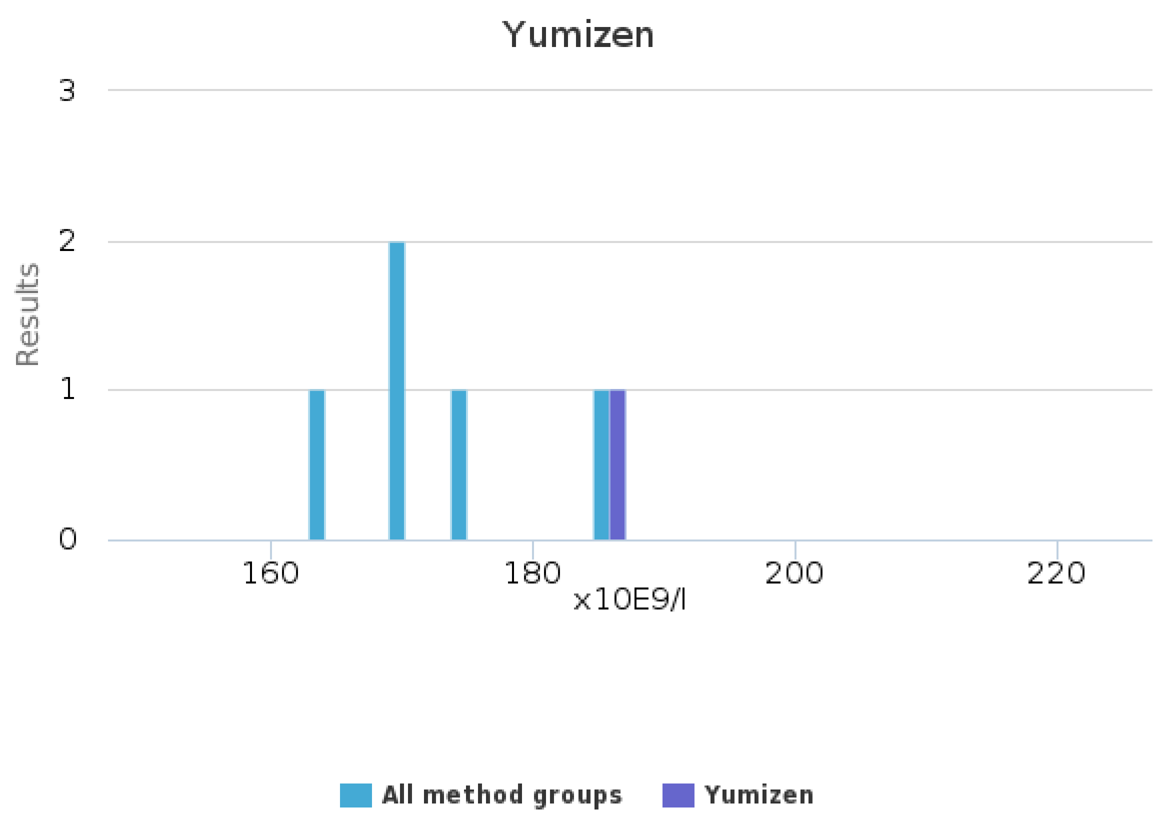
### Sample S011 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| ABX | 179.5 | 179.5 | 7.8 | 4.3 | 5.5 | 174.0 | 185.0 | - | 2 |
| Alinity hq | 167.3 | 169.0 | 3.8 | 2.3 | 2.2 | 163.0 | 170.0 | - | 3 |
| Yumizen | - | - | - | - | - | 187.0 | 187.0 | - | 1 |
| **All** | **174.7** | **172.0** | **9.5** | **5.4** | **3.9** | **163.0** | **187.0** | **-** | **6** |

### Sample S011 | Reticulocytes, x10E9/l| histogram summaries in LabScala



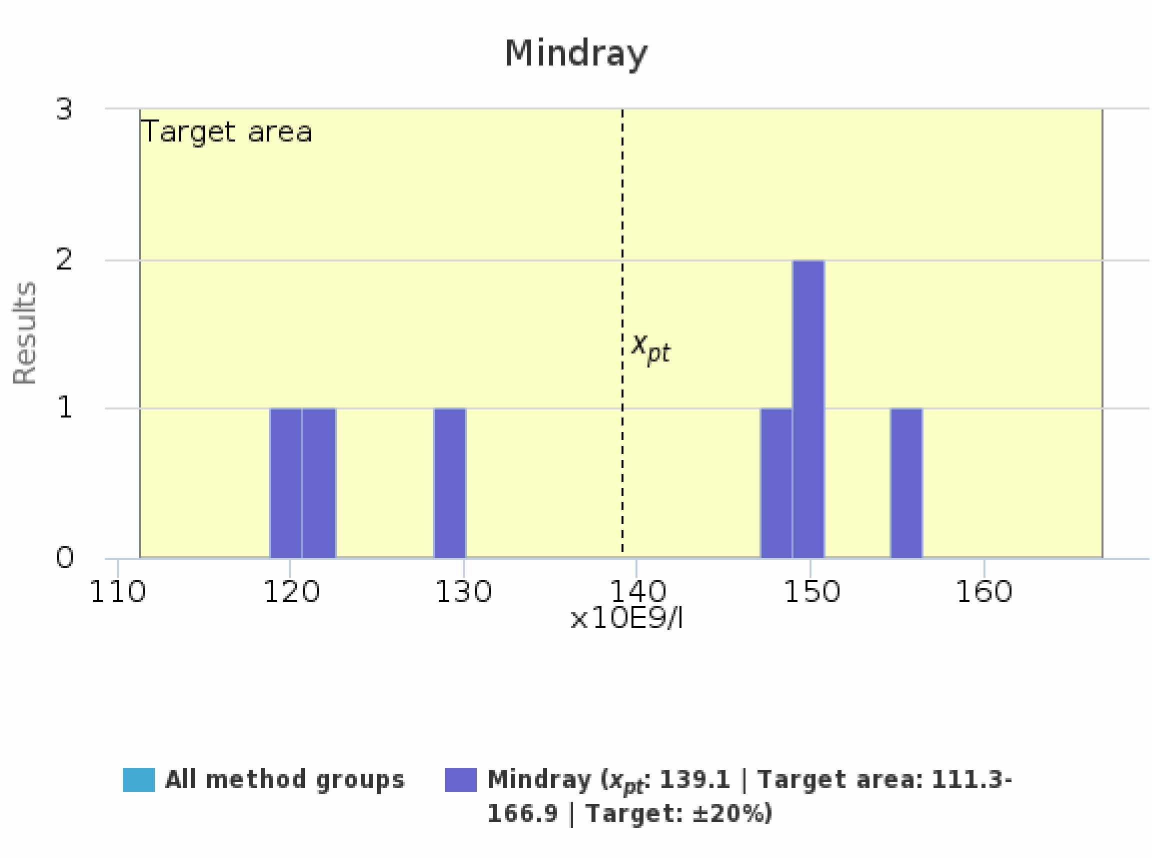




### Sample S012 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Mindray | 139.1 | 147.7 | 15.3 | 11.0 | 5.8 | 118.9 | 156.5 | - | 7 |
| **All** | **139.1** | **147.7** | **15.3** | **11.0** | **5.8** | **118.9** | **156.5** | **-** | **7** |

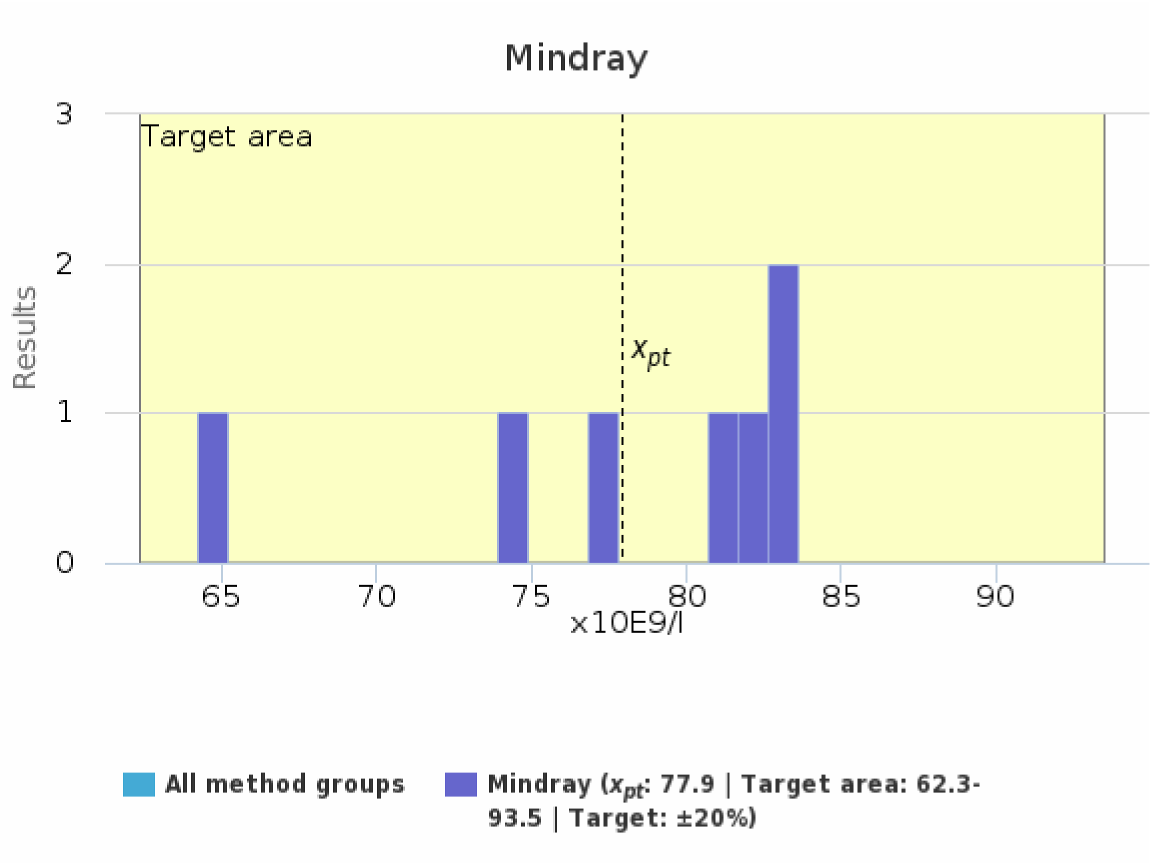
### Sample S012 | Reticulocytes, x10E9/l| histogram summaries in LabScala



### Sample S013 | Reticulocytes, x10E9/l

| Methodics | $x_{pt}$ | Median | sd | CV% | SEM | min | max | Outliers | n |
|---|---|---|---|---|---|---|---|---|---|
| Mindray | 77.9 | 81.1 | 6.9 | 8.9 | 2.6 | 64.2 | 83.6 | - | 7 |
| **All** | **77.9** | **81.1** | **6.9** | **8.9** | **2.6** | **64.2** | **83.6** | **-** | **7** |

### Sample S013 | Reticulocytes, x10E9/l| histogram summaries in LabScala



## Report info

**Participants**

180 participants from 20 countries.

**Report info**

Your own result should be compared to others using the same method.
Assigned values ($x_{pt}$, target values) are means of the results where results deviating more than +/- 3*standard deviation from the median are removed. The standard uncertainty (u) of the assigned value is reported as standard error of the mean (SEM). Additionally, if the measurement uncertainty of the target value is large an automatic text is printed on the report: “The uncertainty of the assigned value is not negligible, and evaluations could be affected.”
In case the client’s result is the only one in the method group, no assigned value will be calculated, no target area shown, and no statistics calculated. In case there are only a few results in the client’s own method group, the result can be compared to all method mean or to a group that is similar to the own method.
Results reported with < or > -signs cannot be included in the statistics.

For information on report interpretation and performance evaluation, please see the " EQAS Interpretation guidelines" LabScala User instructions (top right corner ?Help link).

External Quality Assessment Scheme

# Reticulocytes
# Round 1, 2023

## Specimens

All samples were blood cell suspensions. Sample S001 (LQ711323011) was for manual methods. Laboratories were asked to stain the sample themselves. Samples S002 (LQ711323012) and S003 (LQ711323013) were for Siemens Advia analysers. Samples S004 (LQ711323014) and S005 (LQ711323015) were for Sysmex analysers. Samples S006 (LQ711323016) and S007 (LQ711323017) were for Cell-Dyn 3200, 3500, 3700 and Ruby analysers. Samples S008 (LQ711323018) and S009 (LQ711323019) were for Coulter analysers. Sample S010 (LQ7113230110) and S011 (LQ7113230111) were for ABX, Cell-Dyn 4000 and Saphire analysers. Sample S012 (LQ7113230112) and S013 (LQ7113230113) were for Mindray analysers. Note! You can only compare your own results with the results of samples intended for your own analyzer.

Based on the previous tests and the results of this round, the samples were homogeneous, stable and suitable for the external quality assessment scheme.

The materials were sent without temperature control packaging.

## Report info

Please see the description of the data analysis on the last page of the laboratory-specific histograms and Numerical Summary reports. It is important to read the Final report first, because it contains important information of the samples and results in each round.

## Comments – EQA Coordinator

The results from automated analysers were asked in absolute values. The results have been reported in unit x 10E9/L. Different analysers can give results in different units. There were results given in wrong units. These results have been discarded from target value calculation. Please pay attention to choosing the correct unit, so that the results do not have to be unnecessarily removed from result processing. One customer had also clearly mixed the samples with each other, these results have been removed from the results processing. Apart from this and the results given in clearly wrong units, the round went well.

## End of Report

**2023-04-24**

**FINAL REPORT**

Product no. 4140, 4150-4156

| | |
|---|---|
| Samples sent | 2023-04-03 |
| Round closed | 2023-04-20 |
| Final report | 2023-04-24 |

**Request for correction**

Typing errors in laboratory’s result forms are on laboratory’s responsibility. Labquality accepts responsibility only for result processing. Requests must be notified by writing within three weeks from the date of this letter.

**Authorized by**

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