

External Quality Assessment Scheme

Semen analysis Round 1, 2023

Specimens

5 digital pictures and/or videos S001-S005 in LabScala.

Examinations

Morphology samples S001-S002

Go through the pictures and count the normal and abnormal amount of sperm (head anomaly, neck anomaly, tail anomaly) and write them down to the right slot in percentages. Please note that the sum of the results reported in the first section (normal/abnormal) must be 100%.

Two native, fresh sperm samples (S003-S004) and a native, fresh, washed sperm sample (S005)

There are three fresh semen sample videos from real native sperm in the lab. Look through the videos, count the sperm concentration and assess the motility of the sperm. In the motility calculation, progressively moving (a+b), non-progressively moving (c) and immotile (d) are evaluated.

The cell counting videos have been done using a Makler chamber, where sperms in 10 screens (squares) match the same amount in millions per mL (e.g. 200 sperms in 10 screens (squares together = 200 million sperms per mL). The videos can be watched several times. When calculating the concentration, it can be directly calculated from 10 chambers, but it is recommended to calculate e.g. 3 x 10 chambers and divide by 3.

Result reporting

Please enter the results via LabScala (www.labscala.com).

1. Give your laboratory ID (five digits) and your password.
2. Select the Semen analysis round from the front page.
3. Follow the instructions on the screen.
4. Open the videos / pictures on the sample pages and respond to the related questions.
5. Save and send the results.

If you have any questions about entering the results, please contact the EQA Coordinator. The round opens on October 24, 2023.

2023-10-24

INSTRUCTIONS

Product no. 6400
LQ700123011-015/FI

Subcontracting: Sample preparation

The results should be reported no later than
November 16, 2023.

Inquiries

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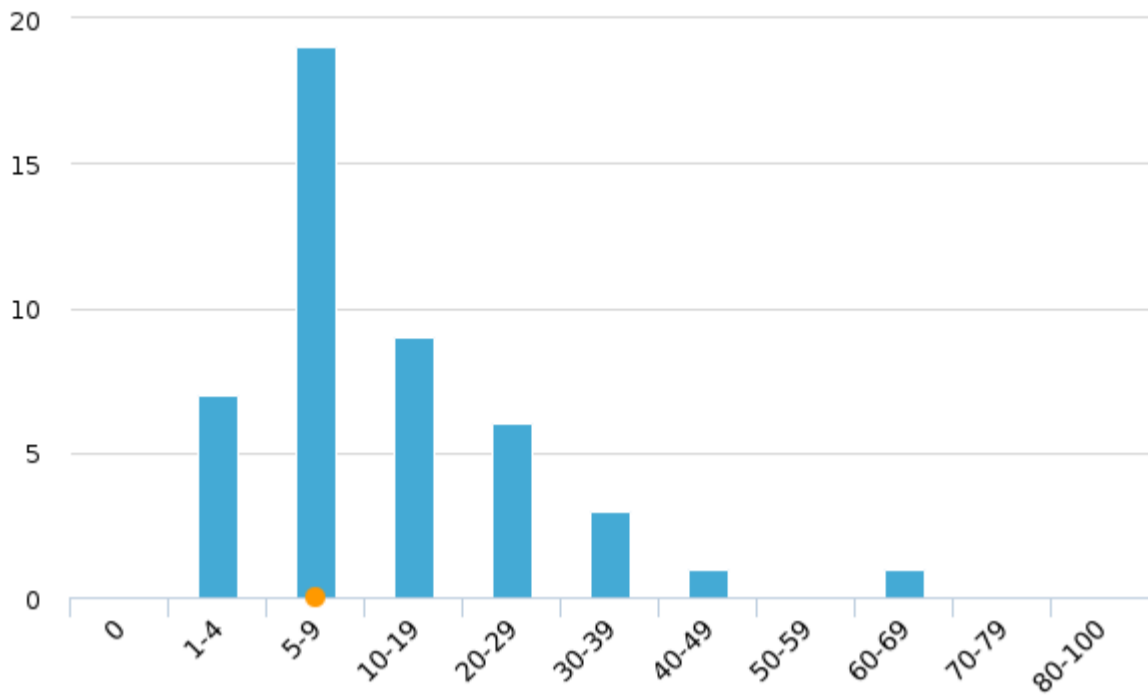
info@labquality.fi
www.labquality.com



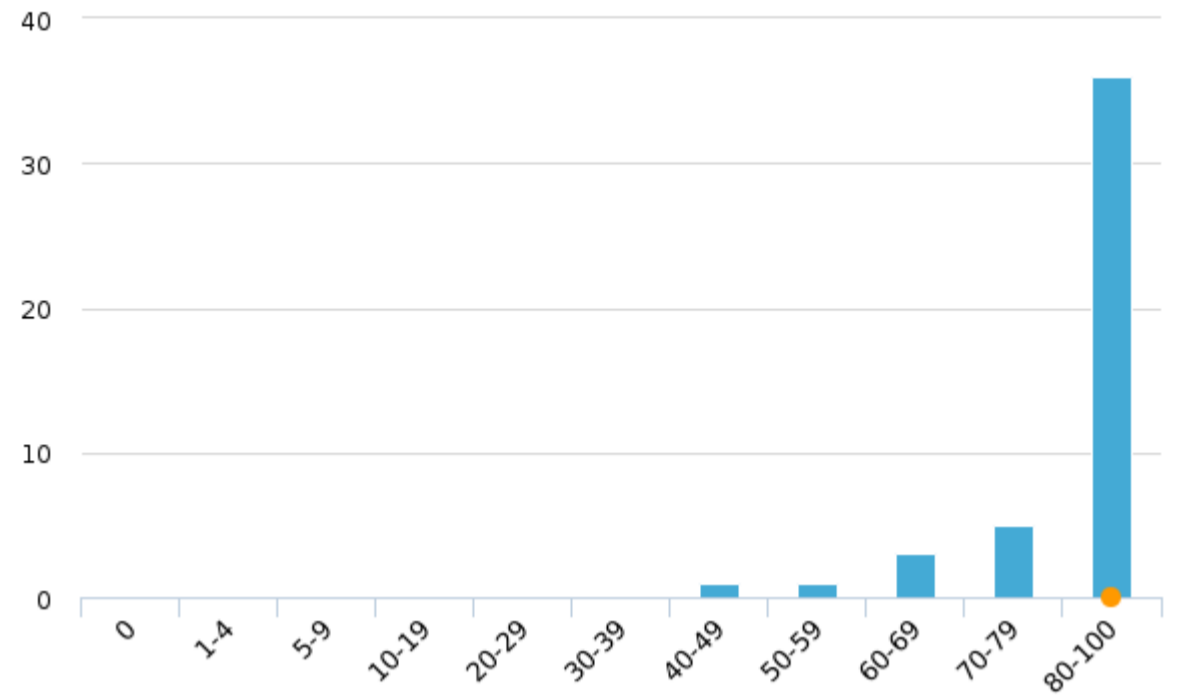
Sample S001 |

Go through the pictures and count the normal and abnormal amount of sperm (head anomaly, neck anomaly, tail anomaly) and write them down to the right slot in percentages. Please note that the sum of the results reported in the first section (normal/abnormal) must be 100%.

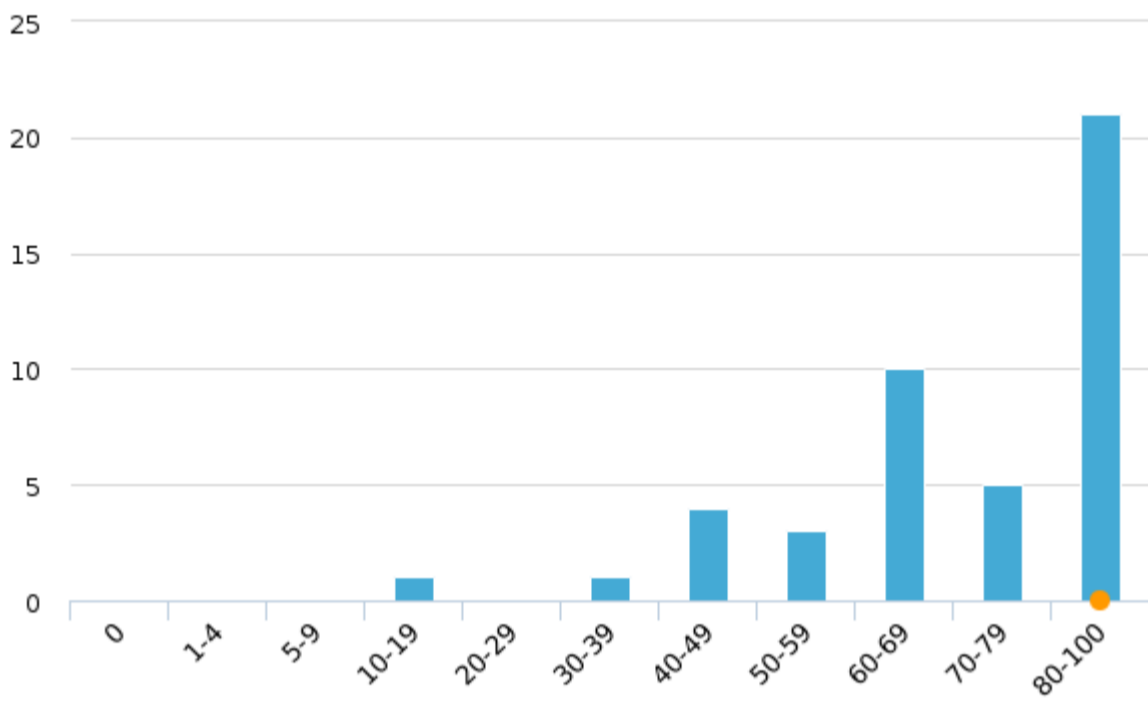
Sample S001 - Normal %



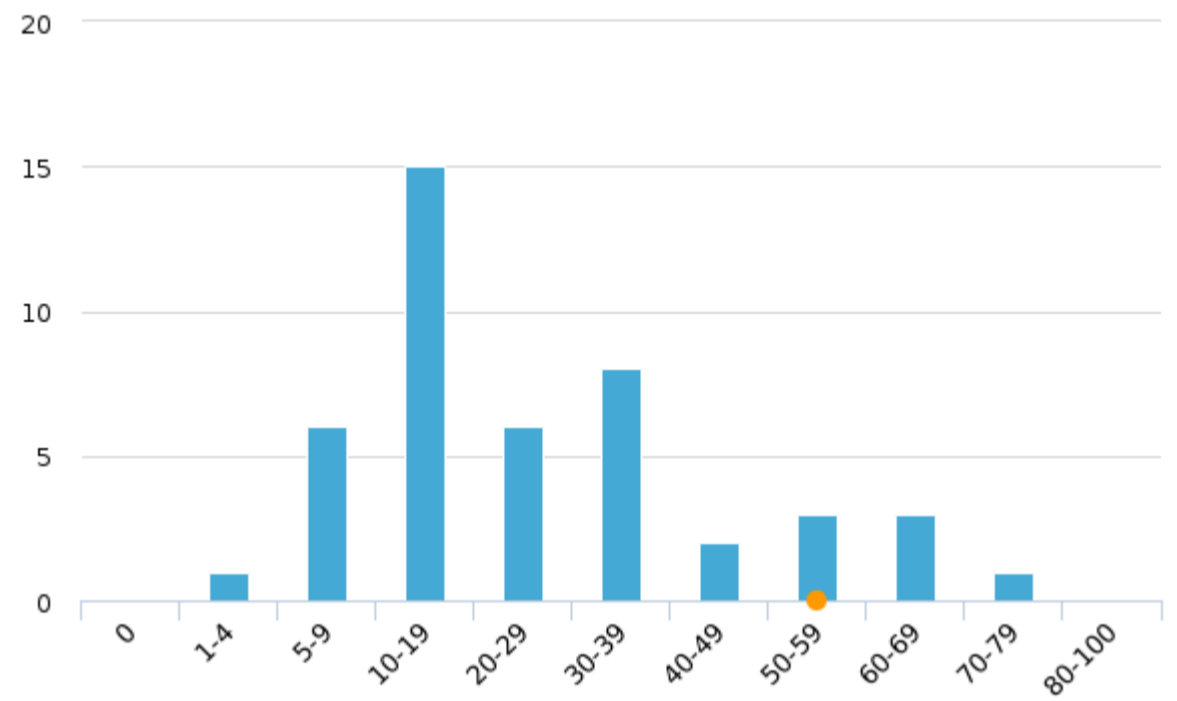
Sample S001 - Abnormal %



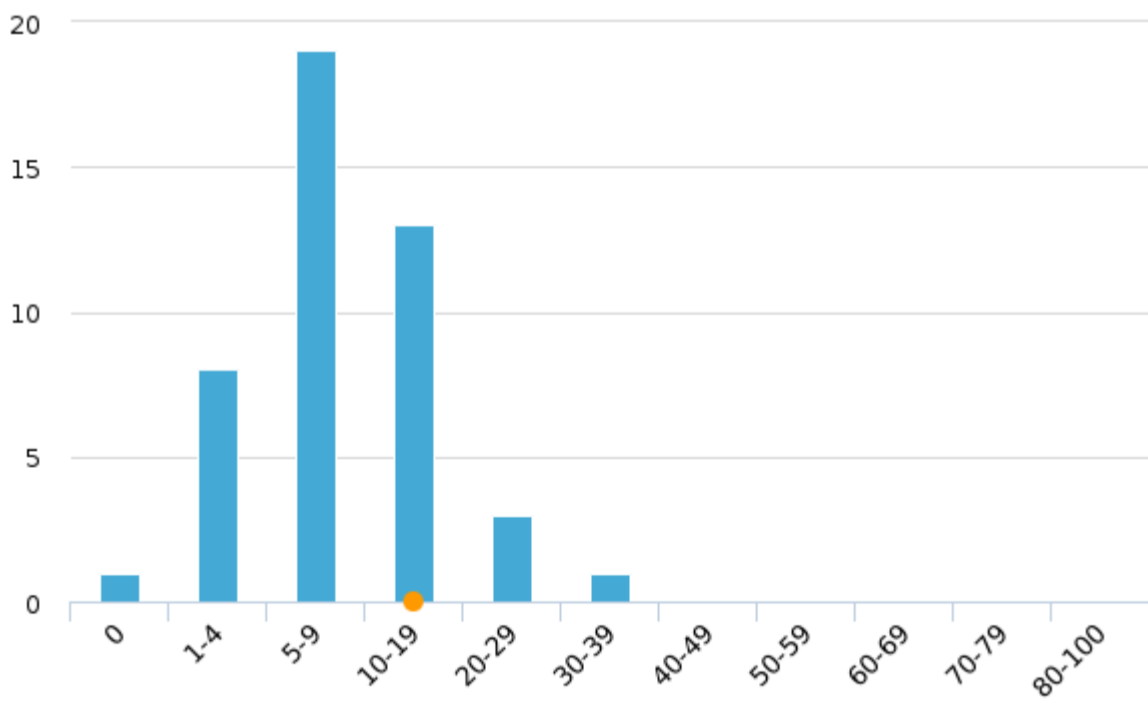
Sample S001 - Head anomaly %



Sample S001 - Neck anomaly %



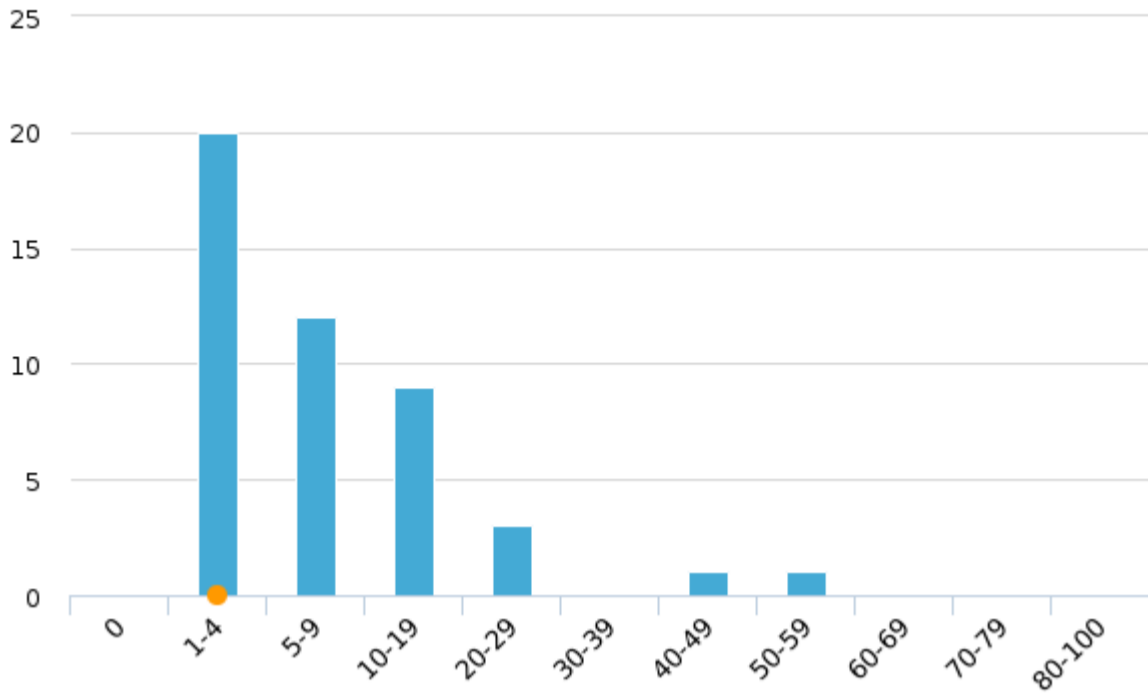
Sample S001 - Tail anomaly %



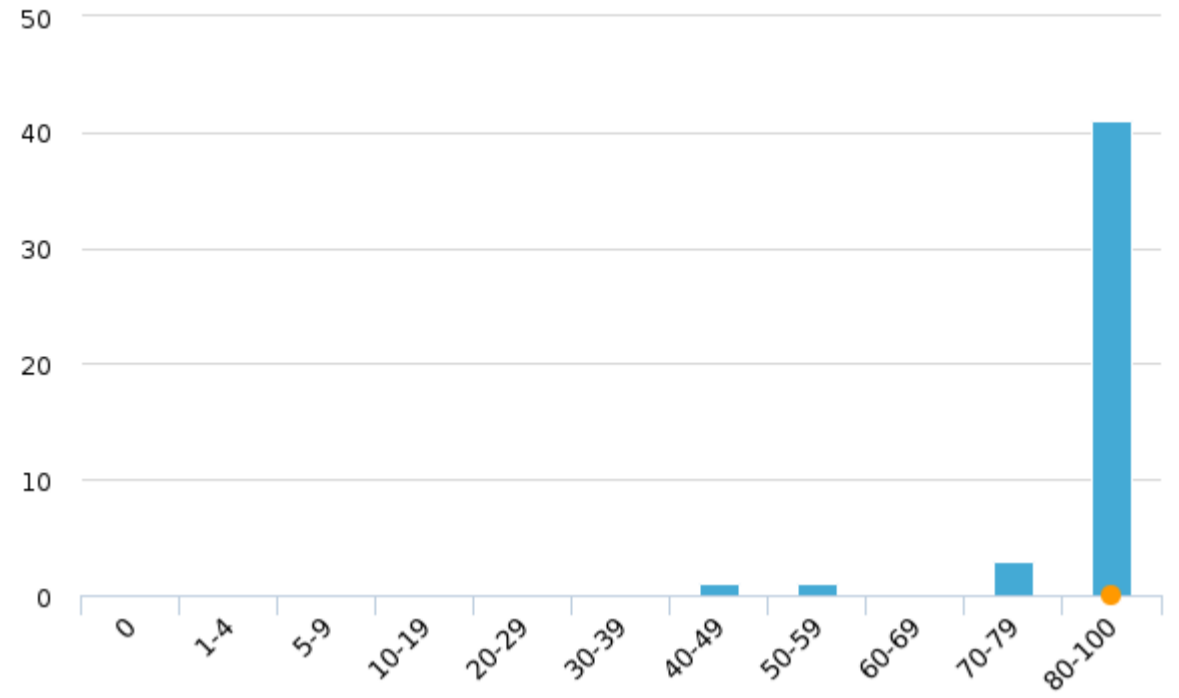
Sample S002 |

Go through the pictures and count the normal and abnormal amount of sperm (head anomaly, neck anomaly, tail anomaly) and write them down to the right slot in percentages. Please note that the sum of the results reported in the first section (normal/abnormal) must be 100%.

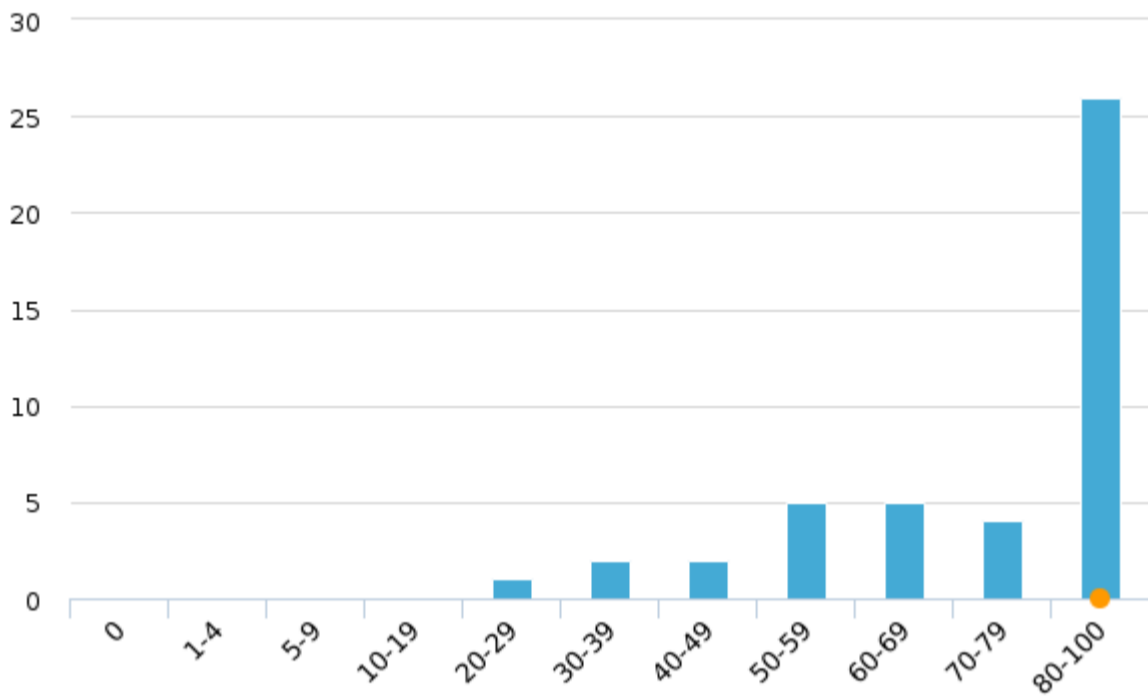
Sample S002 - Normal %



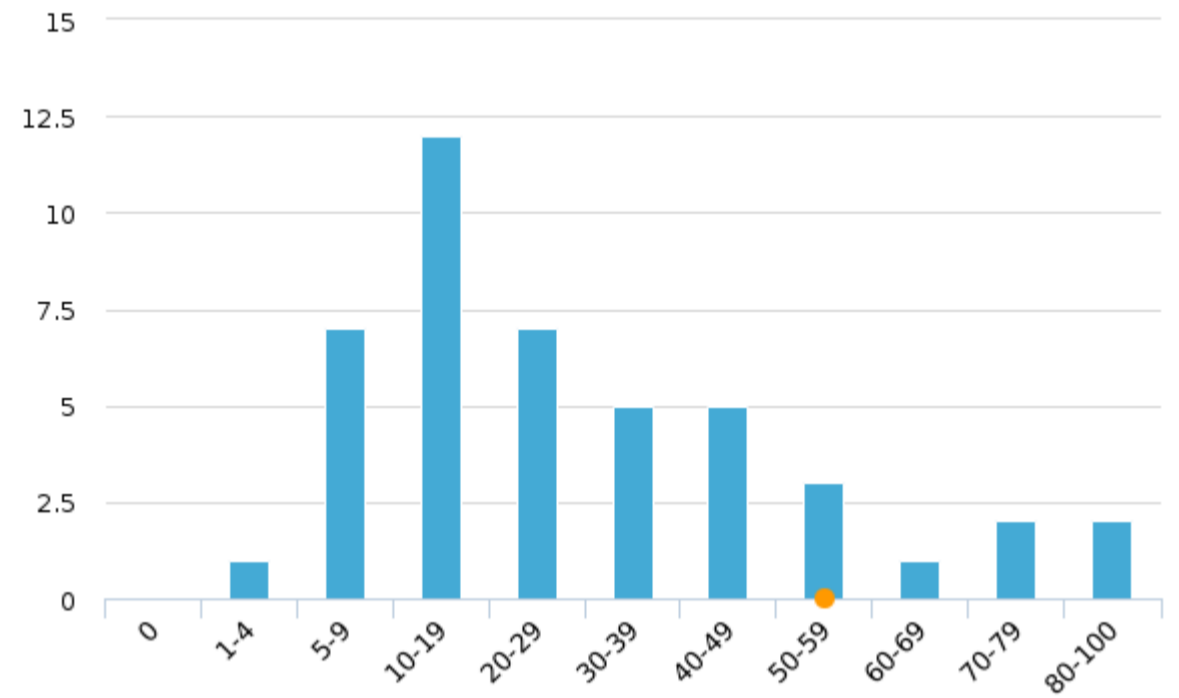
Sample S002 - Abnormal %



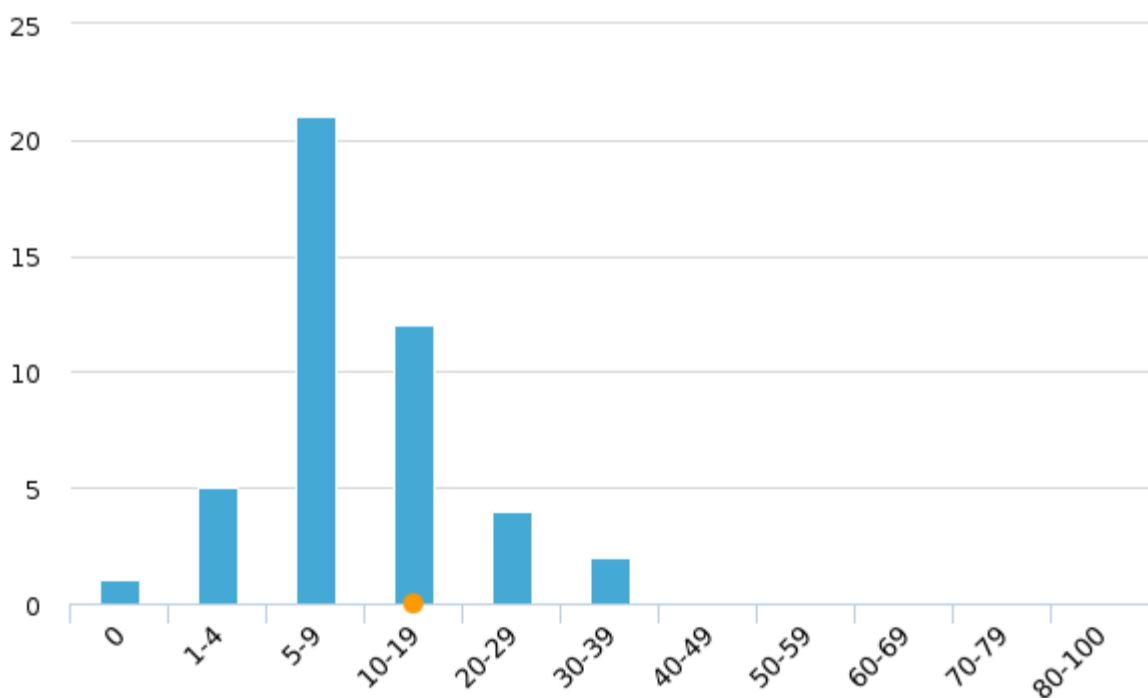
Sample S002 - Head anomaly %



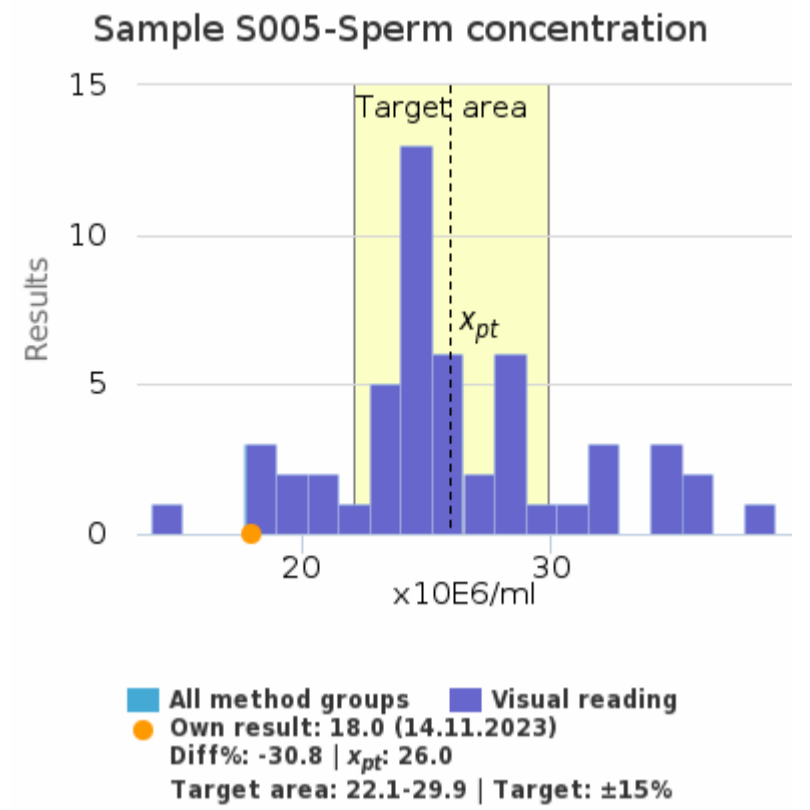
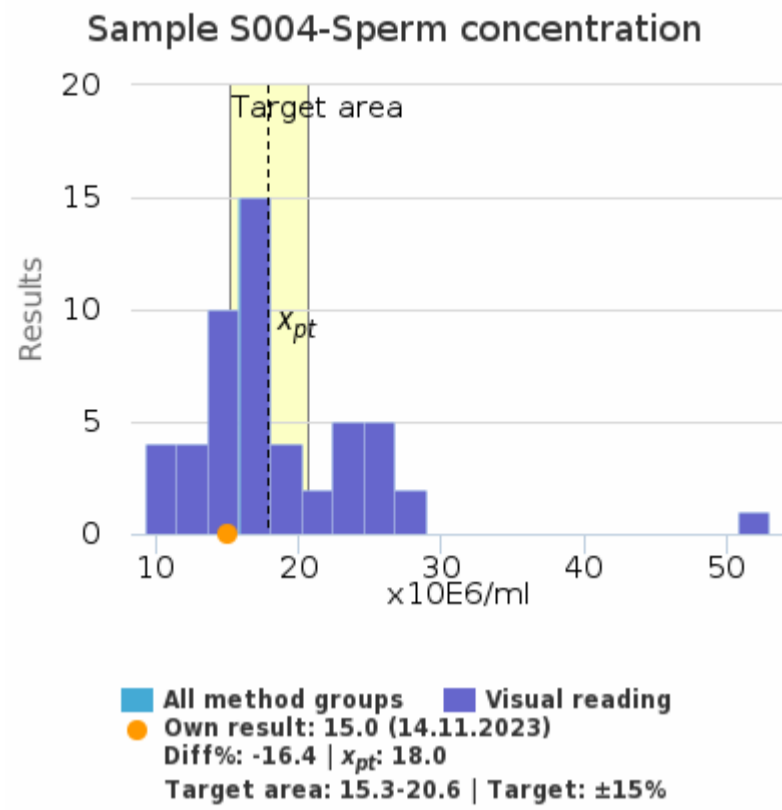
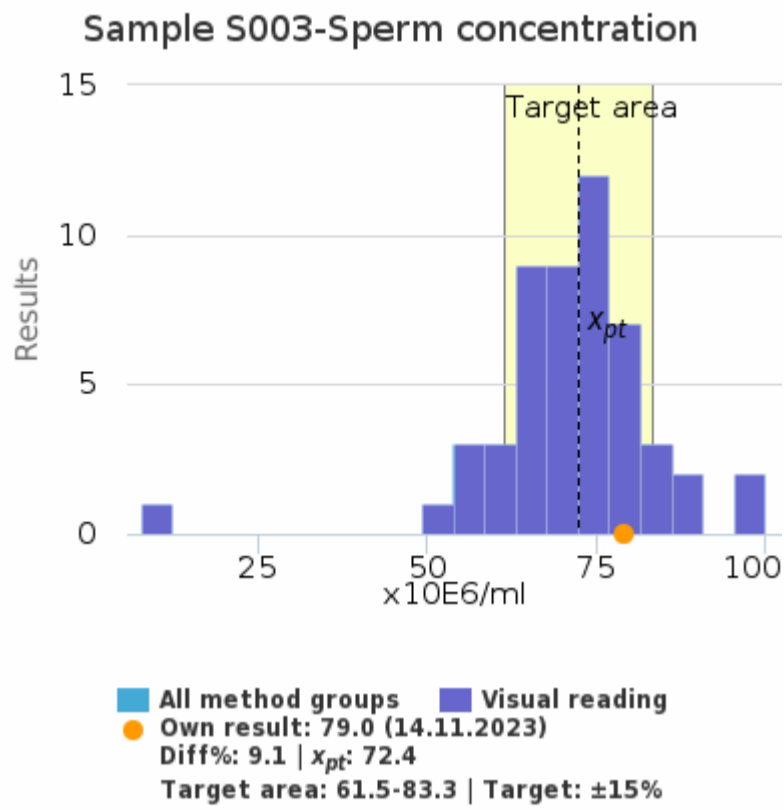
Sample S002 - Neck anomaly %



Sample S002 - Tail anomaly %



Sperm concentration |001

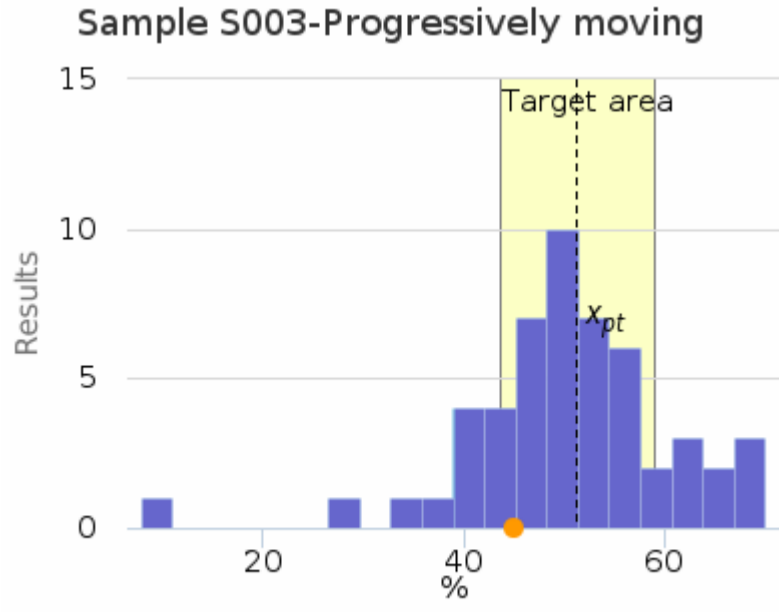


	x_{pt}	sd	SEM	CV%	n
Visual reading	72.4 x10E6/ml	9.9	1.4	13.6	52
All methods	72.4 x10E6/ml	9.9	1.4	13.6	52

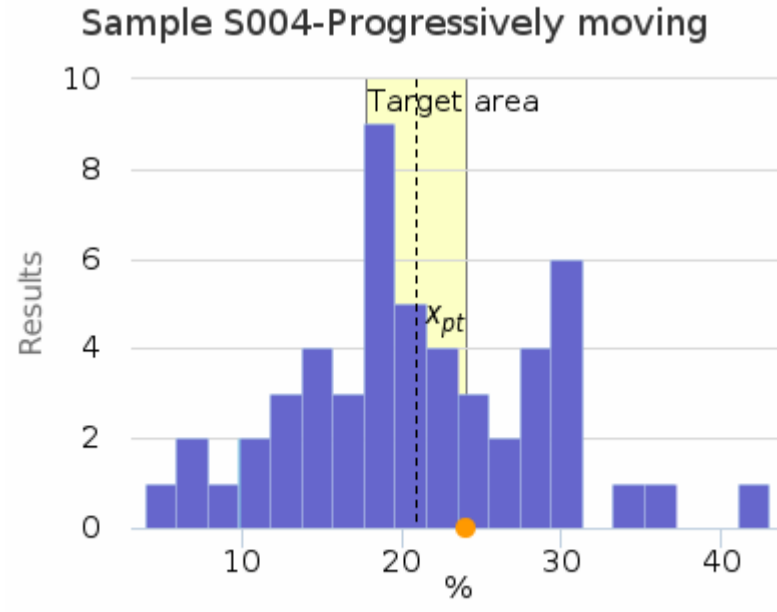
	x_{pt}	sd	SEM	CV%	n
Visual reading	18.0 x10E6/ml	4.7	0.7	26.4	52
All methods	18.0 x10E6/ml	4.7	0.7	26.4	52

	x_{pt}	sd	SEM	CV%	n
Visual reading	26.0 x10E6/ml	5.0	0.7	19.4	52
All methods	26.0 x10E6/ml	5.0	0.7	19.4	52

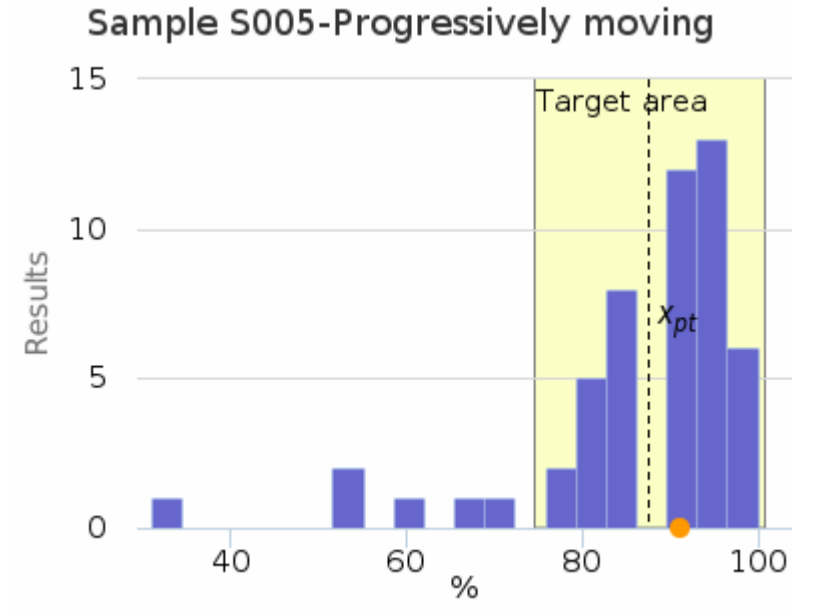
Progressively moving |001



■ All method groups ■ Visual reading
● Own result: 45 (14.11.2023)
 Diff%: -12 | x_{pt} : 51
 Target area: 44-59 | Target: $\pm 15\%$



■ All method groups ■ Visual reading
● Own result: 24 (14.11.2023)
 Diff%: 15 | x_{pt} : 21
 Target area: 18-24 | Target: $\pm 15\%$



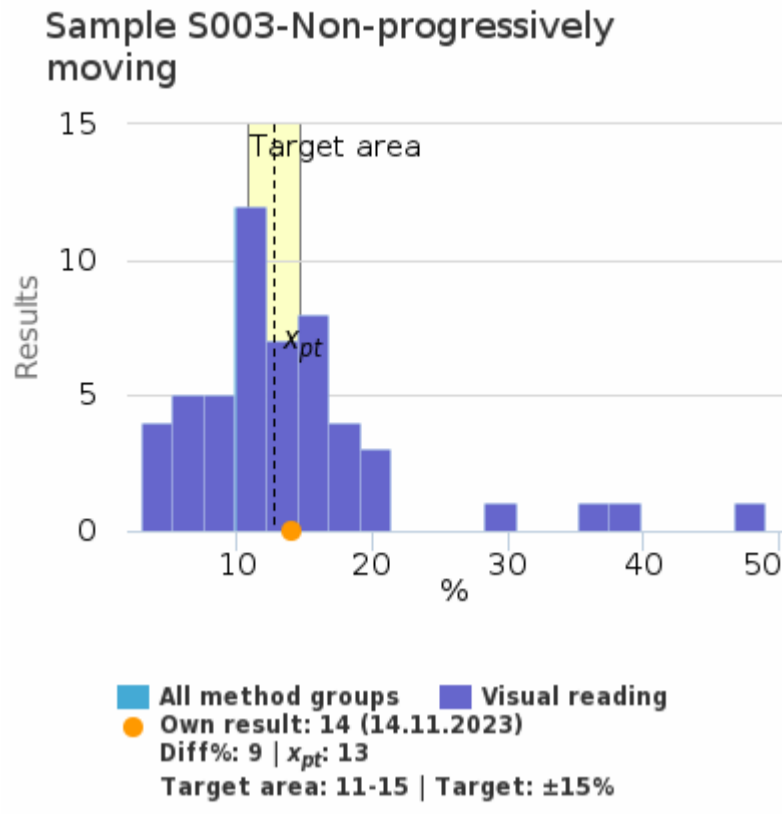
■ All method groups ■ Visual reading
● Own result: 91 (14.11.2023)
 Diff%: 4 | x_{pt} : 88
 Target area: 75-101 | Target: $\pm 15\%$

	x_{pt}	sd	SEM	CV%	n
Visual reading	51 %	9	1	16.8	52
All methods	51 %	9	1	16.8	52

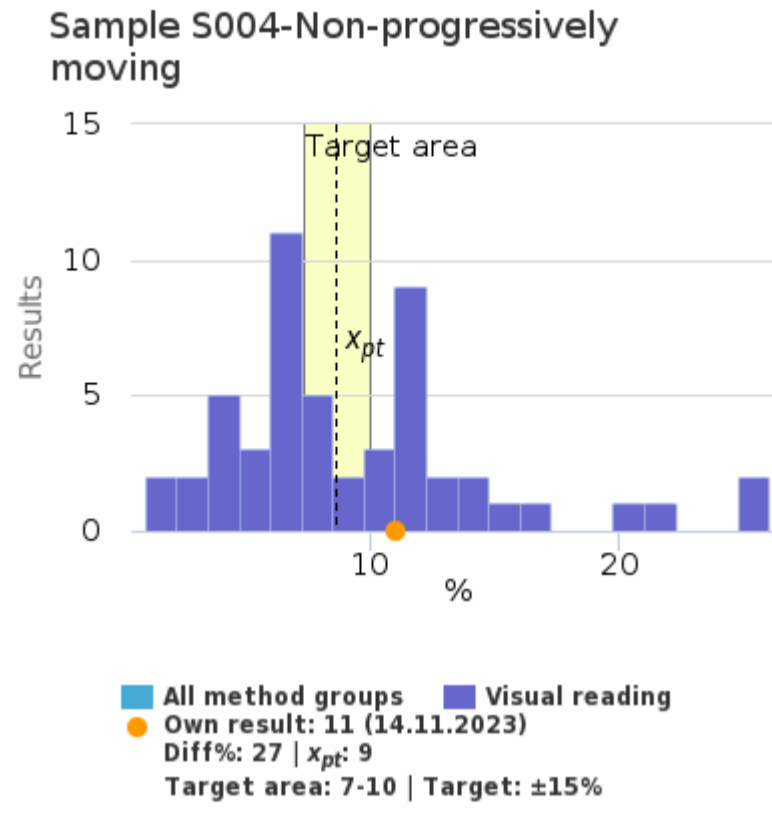
	x_{pt}	sd	SEM	CV%	n
Visual reading	21 %	8	1	38.3	52
All methods	21 %	8	1	38.3	52

	x_{pt}	sd	SEM	CV%	n
Visual reading	88 %	11	1	12.1	52
All methods	88 %	11	1	12.1	52

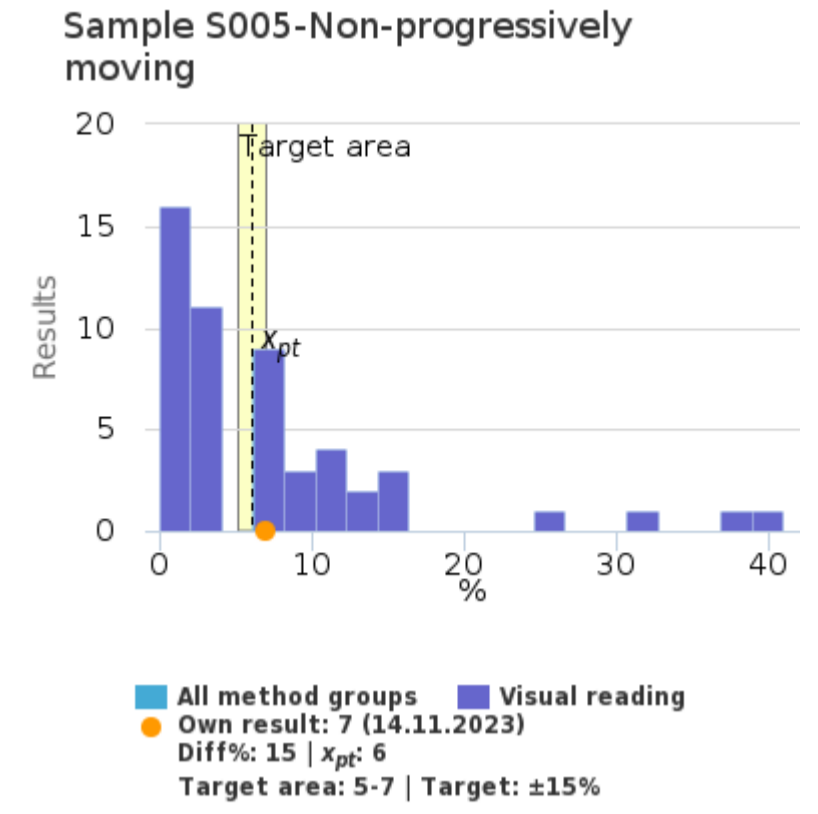
Non-progressively moving |001



	x_{pt}	sd	SEM	CV%	n
Visual reading	13 %	6	<1	49.3	52
All methods	13 %	6	<1	49.3	52

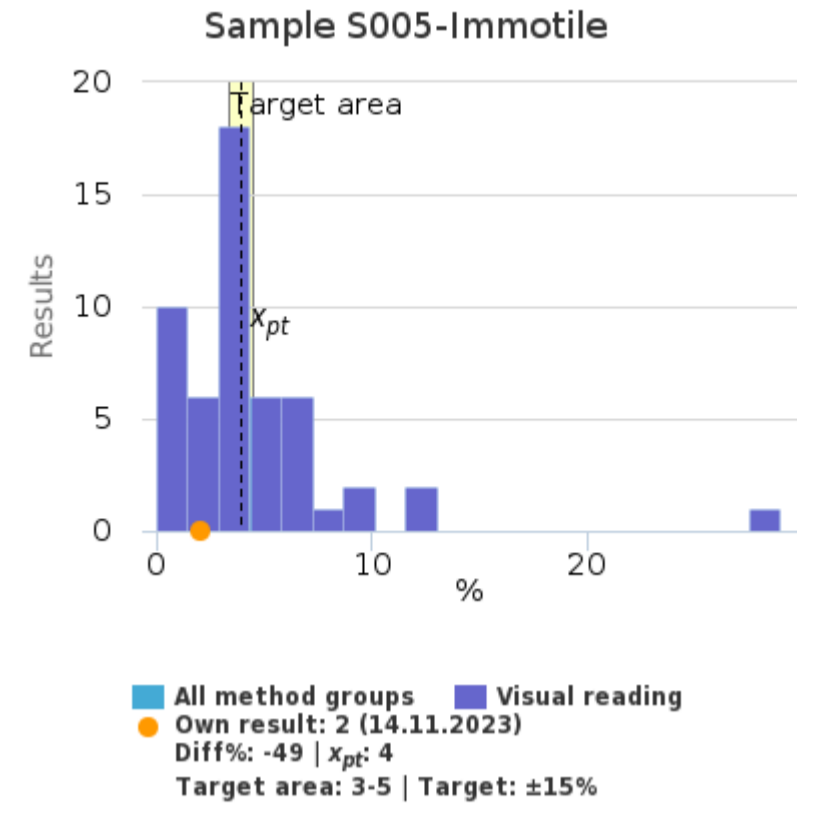
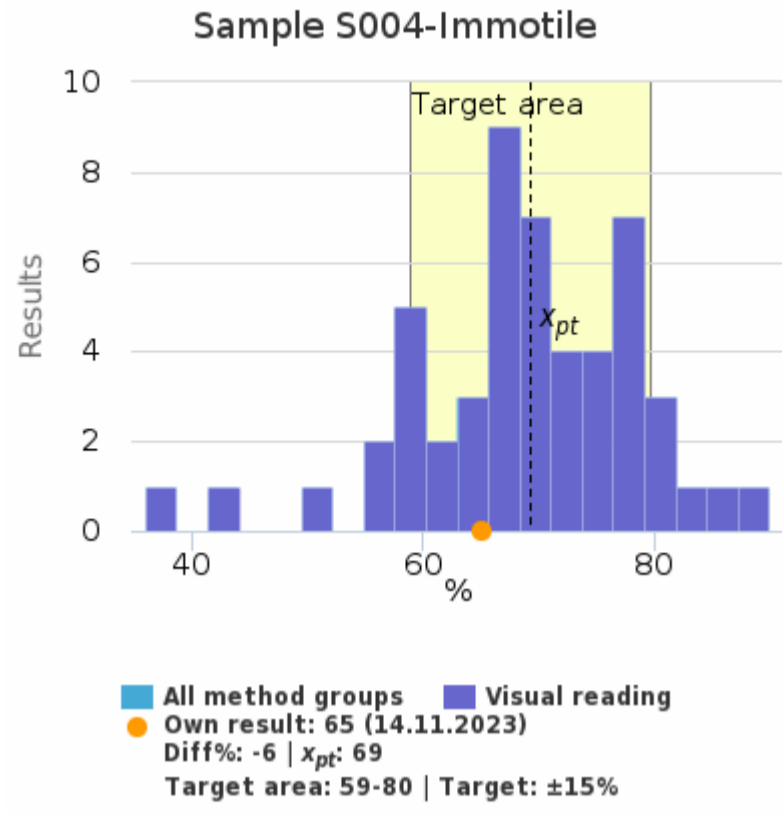
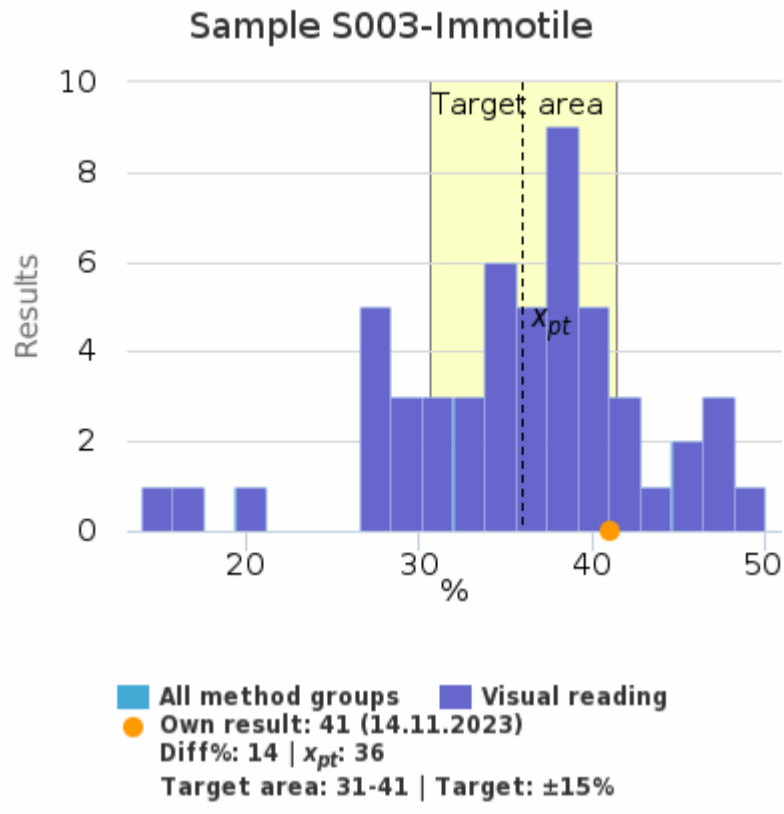


	x_{pt}	sd	SEM	CV%	n
Visual reading	9 %	4	<1	51.1	52
All methods	9 %	4	<1	51.1	52



	x_{pt}	sd	SEM	CV%	n
Visual reading	6 %	6	<1	91.1	52
All methods	6 %	6	<1	91.1	52

Immotile |001



	x_{pt}	sd	SEM	CV%	n
Visual reading	36 %	7	<1	18.8	52
All methods	36 %	7	<1	18.8	52

	x_{pt}	sd	SEM	CV%	n
Visual reading	69 %	9	1	13.1	52
All methods	69 %	9	1	13.1	52

	x_{pt}	sd	SEM	CV%	n
Visual reading	4 %	3	<1	73.9	52
All methods	4 %	3	<1	73.9	52

External Quality Assessment Scheme

Semen analysis Round 1, 2023

Specimens

The survey material consisted of sample pictures and videos (S001-S005). Three parameters were included in the survey:

Morphological classification: from the pictures S001-S002 participants evaluated the normal and abnormal sperm (abnormal head, midpiece, tail). The samples were stained using Papanicolaou technique.

Sperm concentration: video specimens (S003-S005) for the concentrations to be estimated. The concentration was assessed by counting the sperm in 10 screens which matches the same amount in millions per mL.

Motility assessment: The same video samples as in the sperm concentration evaluation were used (samples S003-S005). The motility of the sperm was evaluated (progressive motility (a+b), non-progressive motility (c), immotile (d)) according to the WHO manual.

Report info

Please see the description of the data analysis on the last page of this letter as an annex (Annex 1). It is important to read the Final report first, because it contains important information of the samples and results in each round.

Comments – Expert

For the results obtained to be comparable against each other it is important for all participating laboratories to use the same criteria in measuring sperm concentration, assessment of motility and morphology. This survey is based on the evaluation criteria written in the WHO standard.

Morphology

Morphology was assessed by 46 laboratories. The participants were asked to evaluate especially the head anomalies as well as the midpiece and tail.

Sample S001 was normal (8%). In four laboratories too strict criteria were used and the sample was evaluated as abnormal. In other laboratories the sample was assessed as normal, variation being huge. 24% of the results were within the acceptable range.

Sample S002 was normal (5%). One third of the participants evaluated the sample as abnormal. In total, 26% of the assessments were within the acceptable range. Again, the assessments showed a notable variation.

In general, head and tail anomalies were better recognized than midpiece anomalies.

Expected results:

Sample S001: normal 8% (7-10% acceptable range)

Sample S002: normal 5% (4-6% acceptable range)

Sperm concentration

Sperm concentration was assessed by 52 laboratories.

The thickest sample S003 was assessed moderately well by all participants and more than 70% of the results were as expected. Clearly too low concentration was assessed by one laboratory.

2023-12-12

FINAL REPORT

Product no. 6400

Subcontracting: Sample preparation

Samples sent	2023-10-24
Round closed	2023-11-16
Final report	2023-12-12

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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With the sample S004 more than one third of the results were in the acceptable range. One of the assessments was clearly out of the range (too high).

Almost two thirds of the reported results for the sample S005 were as expected. Minimum (14 million/mL) and maximum (39 million/mL) values were quite far apart from each other, though.

Expected results:

Sample S003: results are according to the criteria of the clinic if they are 62-83 million/mL

Sample S004: results are according to the criteria of the clinic if they are 15-21 million/mL

Sample S005: results are according to the criteria of the clinic if they are 22-30 million/mL

Sperm motility

Sperm motility was assessed by 52 laboratories.

The assessment of the progressive motility (a+b) is the most important criteria. If the percentage of non-progressively motile (c) and immotile (d) spermatozoa is high, it may have an effect on fertilization.

For the native sample S003 and washed sample S005 one laboratory assessed the progressive motility to be very low. With the sample S003 ca 60% of the assessments were as expected. Sample S004 was the most challenging one to evaluate and only one third of the assessments were in acceptable range. Reported results for the washed sample S005 were uniform 88% of the assessments being in acceptable range. This was expected as assessing washed samples should be easiest and most obvious.

Expected results:

Sample S003: results are according to the criteria of the clinic if percentage of a+b is ca 51% (44-59%)

Sample S004: results are according to the criteria of the clinic if percentage of a+b is ca 21% (18-24%)

Sample S005: results are according to the criteria of the clinic if percentage of a+b is ca 88% (75-99%)

End of report

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Annex 1.

Results for morphology were processed using the results of the normal and abnormal (head anomaly, neck anomaly, tail anomaly) forms. Each laboratory's own results are marked in the table with the name entered on the result form. The participants should be precise when assessing the normal sperm and extra attention should be given when assessing the head anomalies. The results of the morphology assessment are shown in histograms, where laboratory's own result is marked with an orange dot.

Results for concentration and motility are presented in histograms. The result of your laboratory is illustrated by an orange dot. The target for sperm concentrations is the mean +15%. The corrected mean is calculated with results that fall within the median + 3 x uncorrected standard deviation. The enclosed table gives the corrected mean, the number of results reported, the standard deviation between laboratories and the coefficient of variation.

For information on report interpretation and performance evaluation, please see the "EQAS Interpretation guidelines" in LabScala User instructions. In case you have any questions regarding the reports, please contact the EQA Coordinator.