LABQUALITY

External Quality Assessment Scheme

Basic chemistry, POCT analyzers
Round 1, 2023

Specimens
Please find enclosed 2 human serum samples S001and S002, each 1mL.

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
Please see page 2.

Storage and use
Samples are ready for use. Please put the samples in the refrigerator immediately after arrival.

Analyse as patient samples as soon as possible, if not possible, freeze the samples.

Before analysing, let the samples warm to room temperature before use.

If the analyser is designed for whole blood samples, handle the sera as if they were whole blood.

Result reporting
Please enter the results and methods via LabScala. If you can't find your instrument or reagent from the registry, please contact the EQA Coordinator.

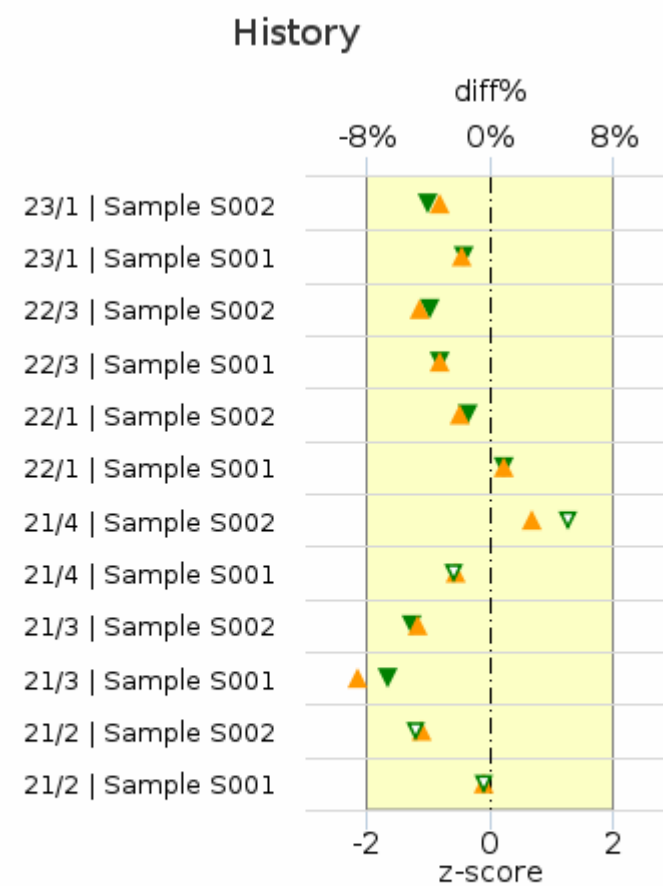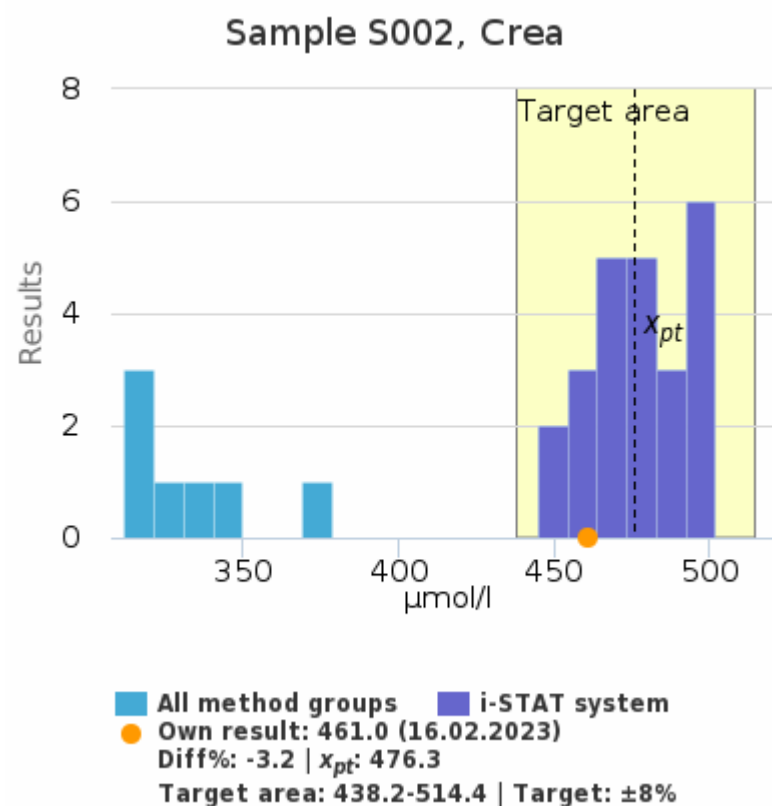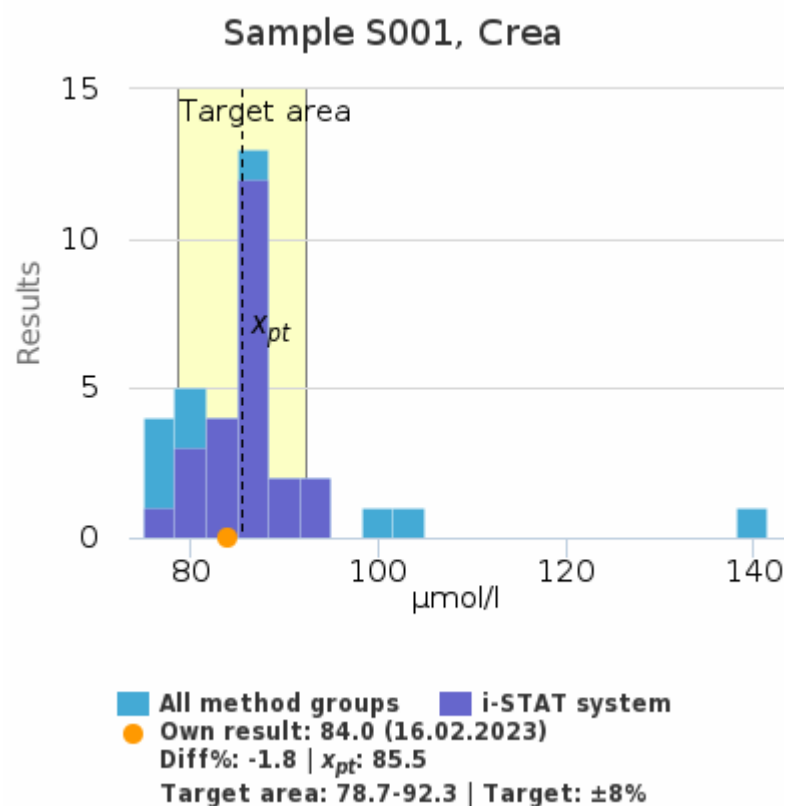S001:

LQ747423011

S002:

LQ747423012

Basic chemistry, POCT analyzers

Examinations
Alanine aminotransferase
Albumin
Alkaline phosphatase
Amylase (total and pancreatic)
Aspartate aminotransferase
Calcium
Chloride
HDL cholesterol
Cholesterol
Creatinekinase
Creatinine
Gamma glutamyltransferase
Glucose
Lactate dehydrogenase
Magnesium
Phosphorus
Potassium
Sodium
Total protein
Triglycerides
Urea
Uric acid

Crea |PNA

Sample S001, Crea

All method groups — **i-STAT system**
Own result: 84.0 (16.02.2023)
Diff%: -1.8 | x_{pt}: 85.5
Target area: 78.7-92.3 | **Target:** ±8%

	x_{pt}	sd	SEM	CV%	n
i-STAT system	85.5 µmol/l	3.6	0.7	4.2	24
All methods	85.3 µmol/l	5.8	1.0	6.8	33

Sample S002, Crea

All method groups — **i-STAT system**
Own result: 461.0 (16.02.2023)
Diff%: -3.2 | x_{pt}: 476.3
Target area: 438.2-514.4 | **Target:** ±8%

	x_{pt}	sd	SEM	CV%	n
i-STAT system	476.3 µmol/l	15.4	3.1	3.2	24
All methods	443.8 µmol/l	63.2	11.4	14.2	31

History

▲ **diff%**
▼ **z-score**
▽ **Z-score is uncertain due to the small number of observations**

Round	Sample	x_{pt}	Result	diff%	z-score
23/1	Sample S002	476.3	461.0	-3.2%	-0.99
23/1	Sample S001	85.5	84.0	-1.8%	-0.42
22/3	Sample S002	84.9	81.0	-4.6%	-0.96
22/3	Sample S001	92.0	89.0	-3.3%	-0.81
22/1	Sample S002	64.3	63.0	-2.0%	-0.36
22/1	Sample S001	85.2	86.0	0.9%	0.22
21/4	Sample S002	79.8	82.0	2.7%	1.26
21/4	Sample S001	89.0	87.0	-2.2%	-0.57
21/3	Sample S002	59.8	57.0	-4.7%	-1.28
21/3	Sample S001	90.7	83.0	-8.5%	-1.66
21/2	Sample S002	78.4	75.0	-4.4%	-1.19
21/2	Sample S001	69.3	69.0	-0.4%	-0.09

Report info

Participants

39 participants from 8 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).

Sample S001 | ALP, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	79	79	2	1.9	<1	77	80	-	3
Wet chemistry	-	-	-	-	-	76	76	-	1
All	**78**	**78**	**2**	**2.4**	**<1**	**76**	**80**	**-**	**4**

Sample S001 | ALP, U/l| histogram summaries in LabScala
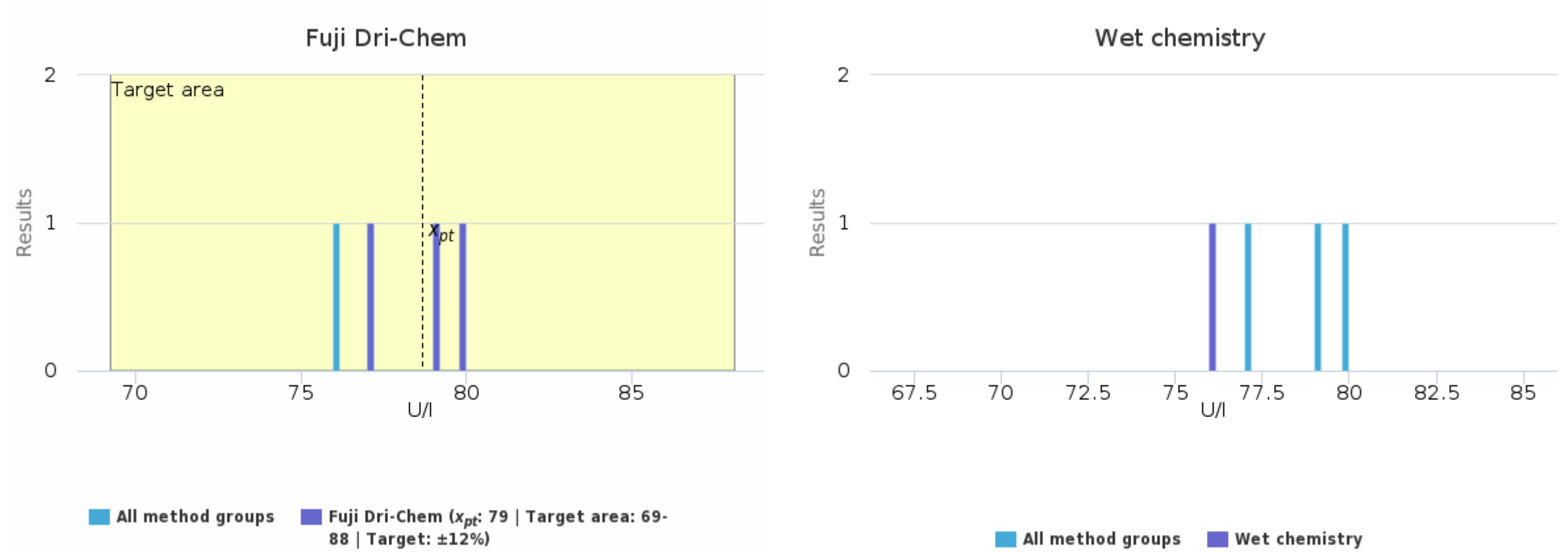
Sample S001 | ALT, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	18	18	<1	3.3	<1	17	18	-	3
Spotchem	-	-	-	-	-	20	20	-	1
Wet chemistry	-	-	-	-	-	18	18	-	1
All	**18**	**18**	**1**	**6.0**	**<1**	**17**	**20**	**-**	**5**

Sample S001 | ALT, U/l| histogram summaries in LabScala

Fuji Dri-Chem

■ All method groups ■ Fuji Dri-Chem (x_{pt}: 18 | Target area: 16-20 | Target: ±12%)


Spotchem

■ All method groups ■ Spotchem

Wet chemistry

■ All method groups ■ Wet chemistry
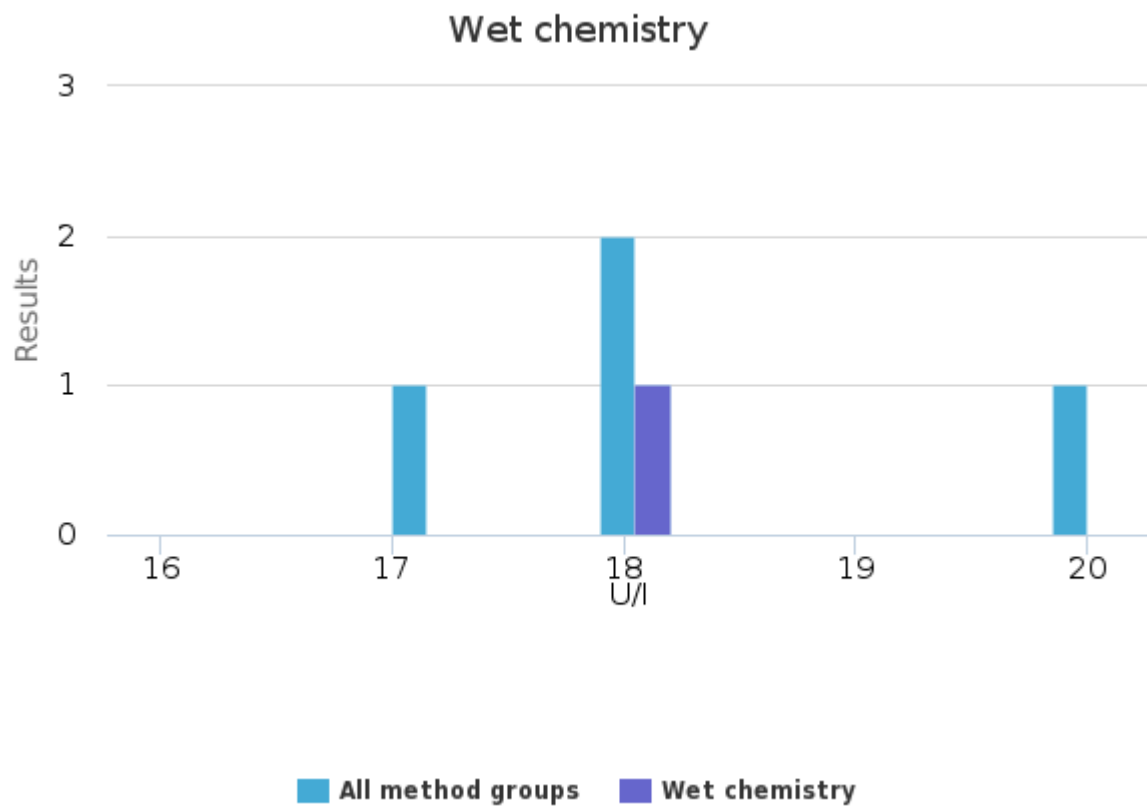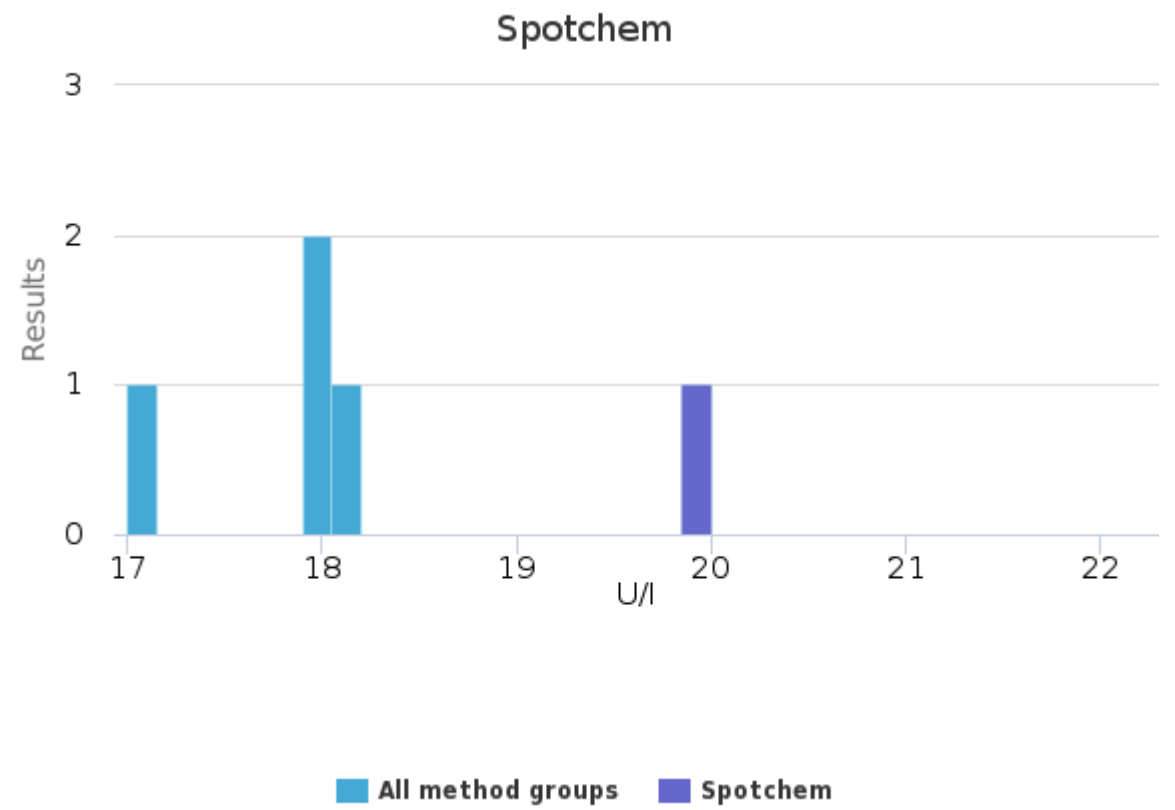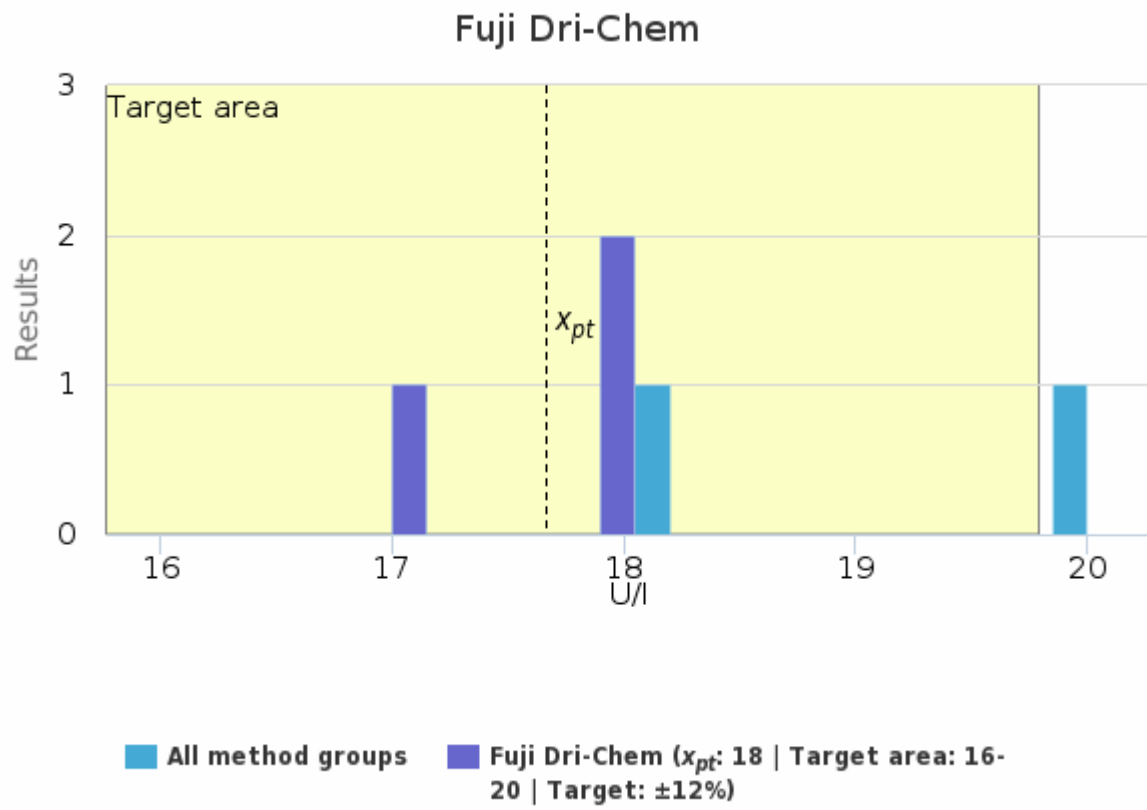
Sample S001 | Alb, g/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	41.6	41.6	-	1
All	**-**	**-**	**-**	**-**	**-**	**41.6**	**41.6**	**-**	**1**

Sample S001 | Alb, g/l| histogram summaries in LabScala

Wet chemistry

■ All method groups ■ Wet chemistry
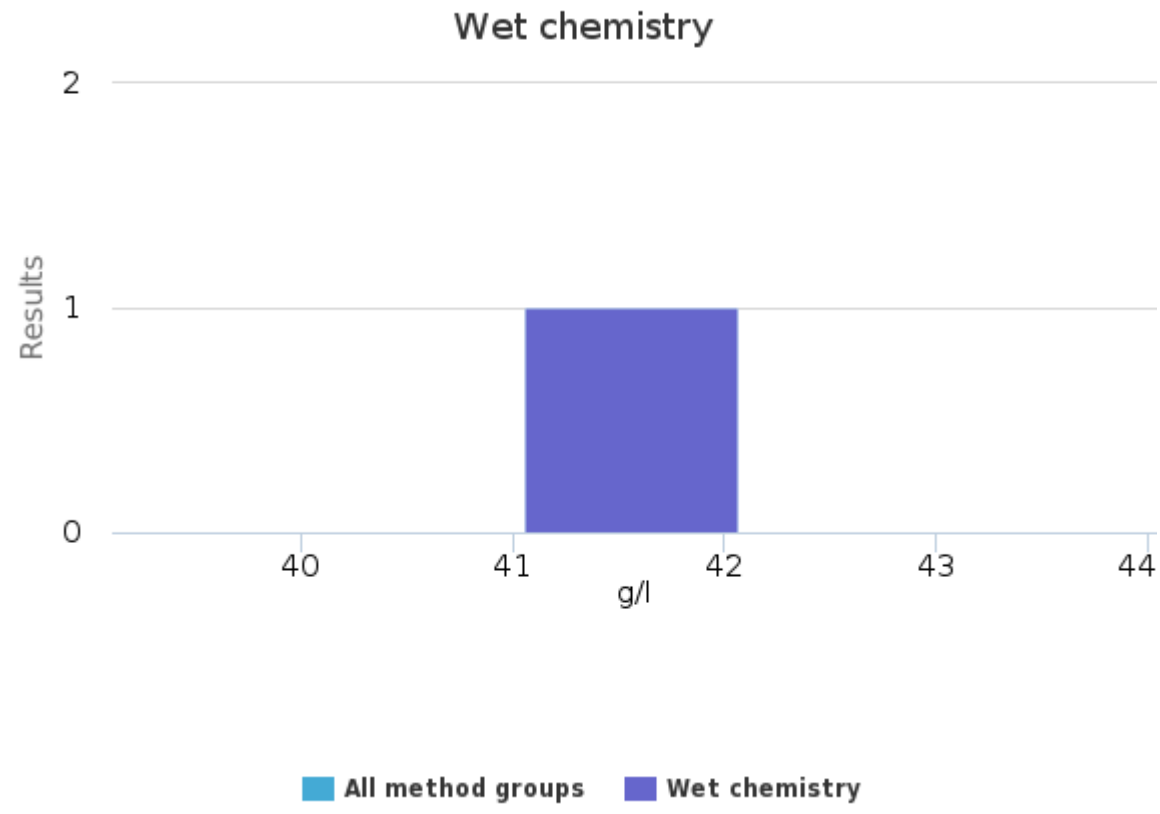
Sample S001 | Amyl, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	69	69	1	1.4	<1	68	70	-	3
Wet chemistry	-	-	-	-	-	61	61	-	1
All	**67**	**69**	**4**	**5.9**	**2**	**61**	**70**	**-**	**4**

Sample S001 | Amyl, U/l| histogram summaries in LabScala
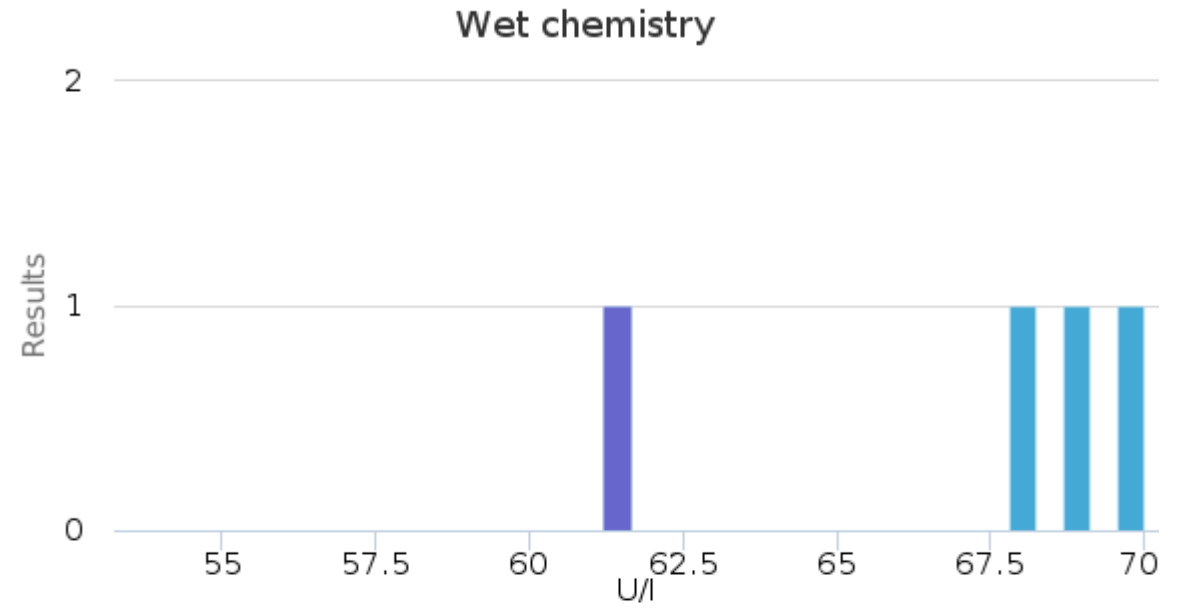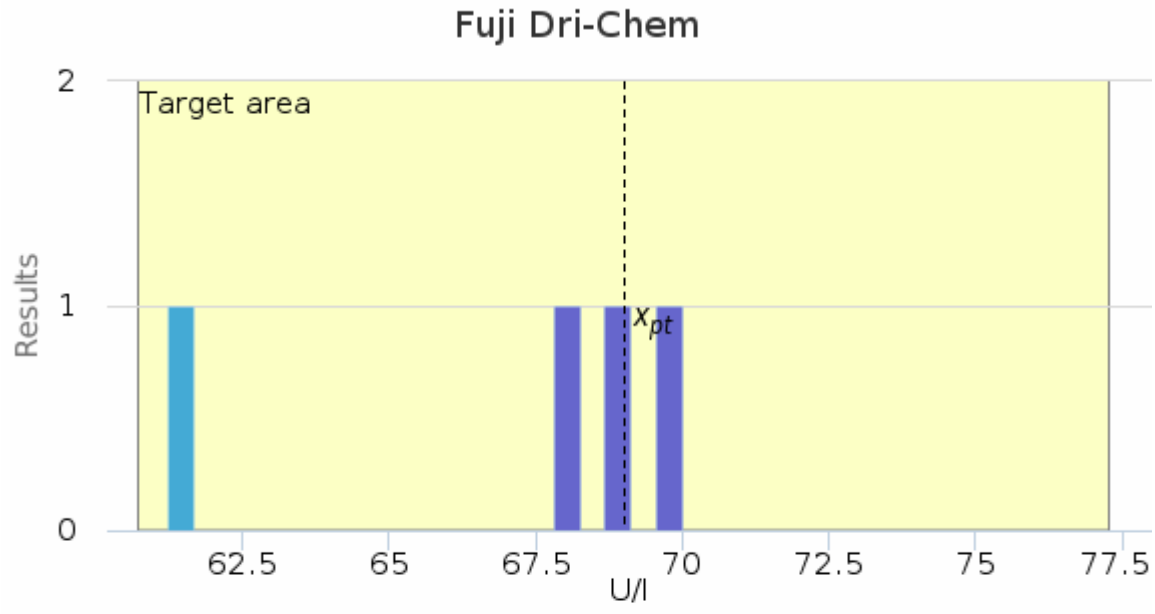
Sample S001 | AST, U/l

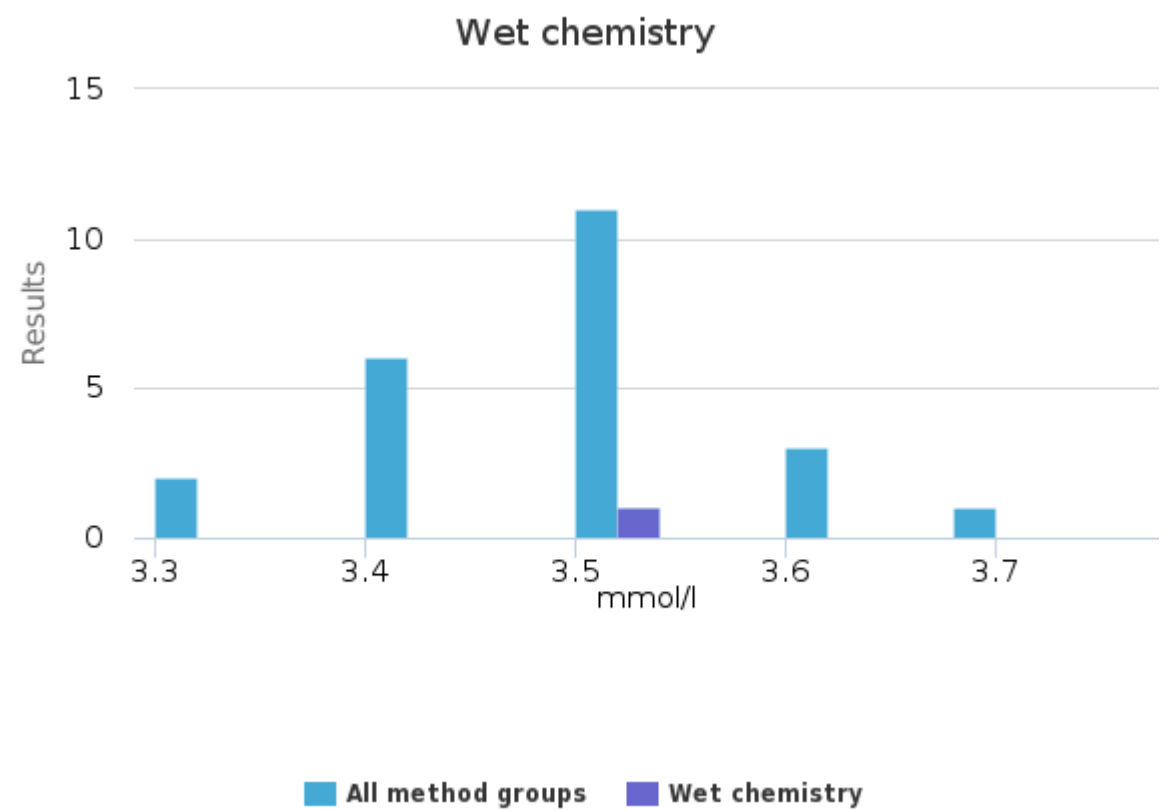| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	25	25	<1	2.3	<1	25	26	-	3
Spotchem	-	-	-	-	-	23	23	-	1
Wet chemistry	-	-	-	-	-	29	29	-	1
All	**26**	**25**	**2**	**8.2**	**<1**	**23**	**29**	**-**	**5**

Sample S001 | AST, U/l| histogram summaries in LabScala
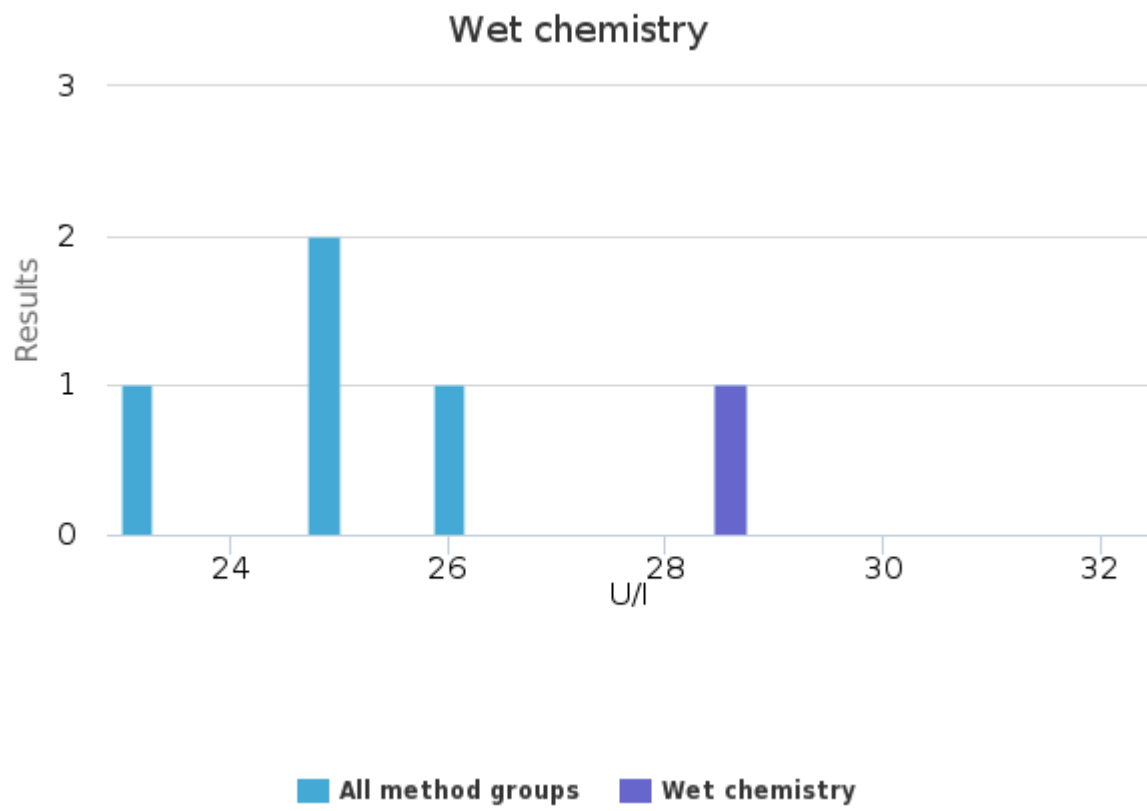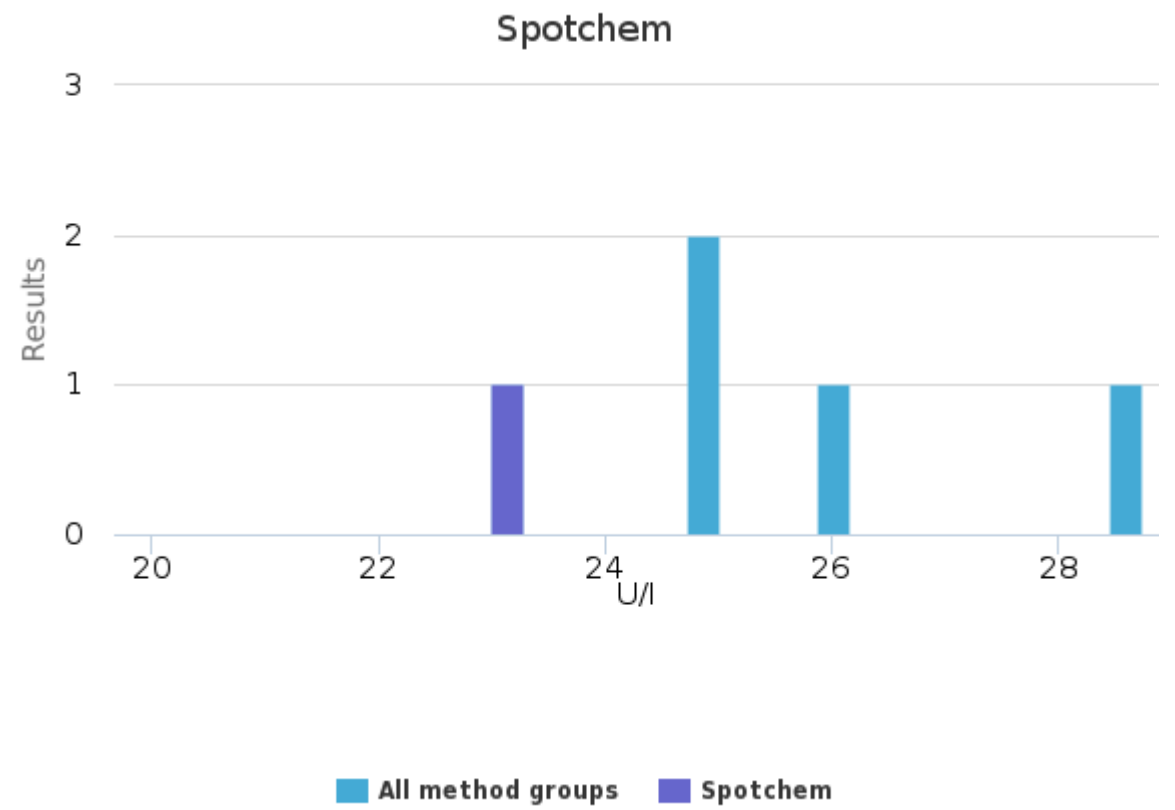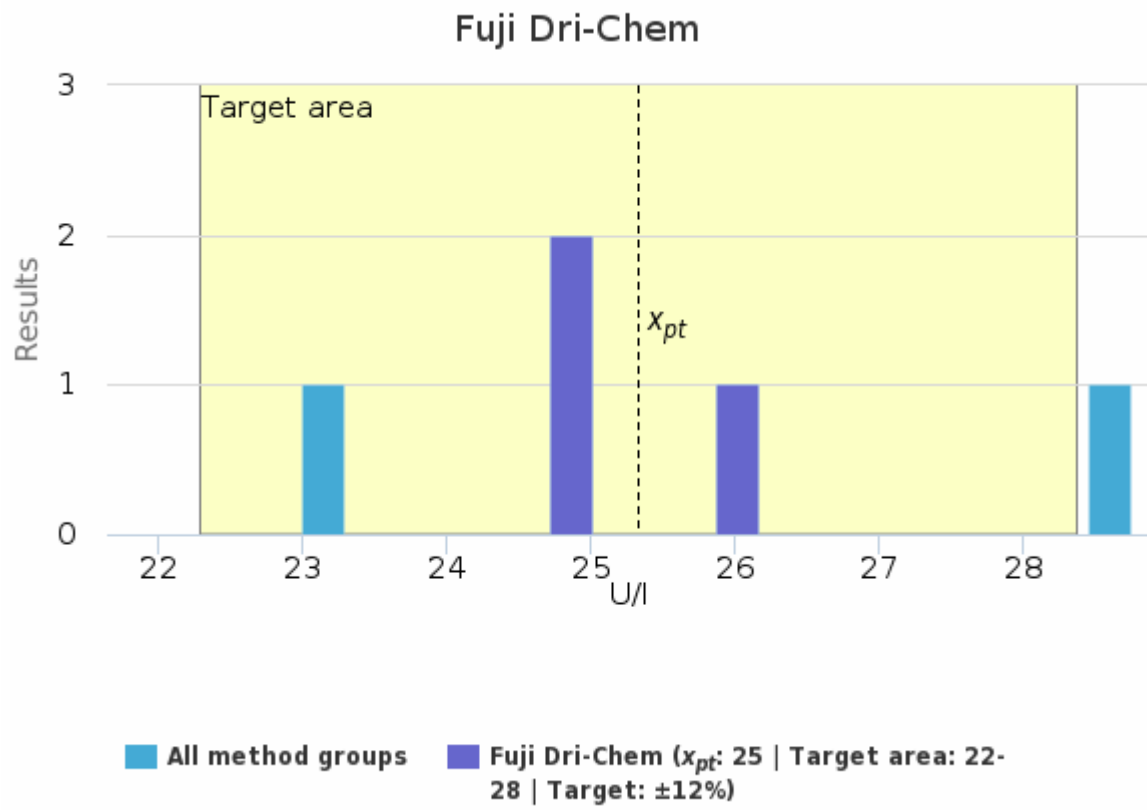
Sample S001 | Ca, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	2.39	2.39	-	1
All	**-**	**-**	**-**	**-**	**-**	**2.39**	**2.39**	**-**	**1**

Sample S001 | Ca, mmol/l| histogram summaries in LabScala

Wet chemistry

■ All method groups ■ Wet chemistry

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
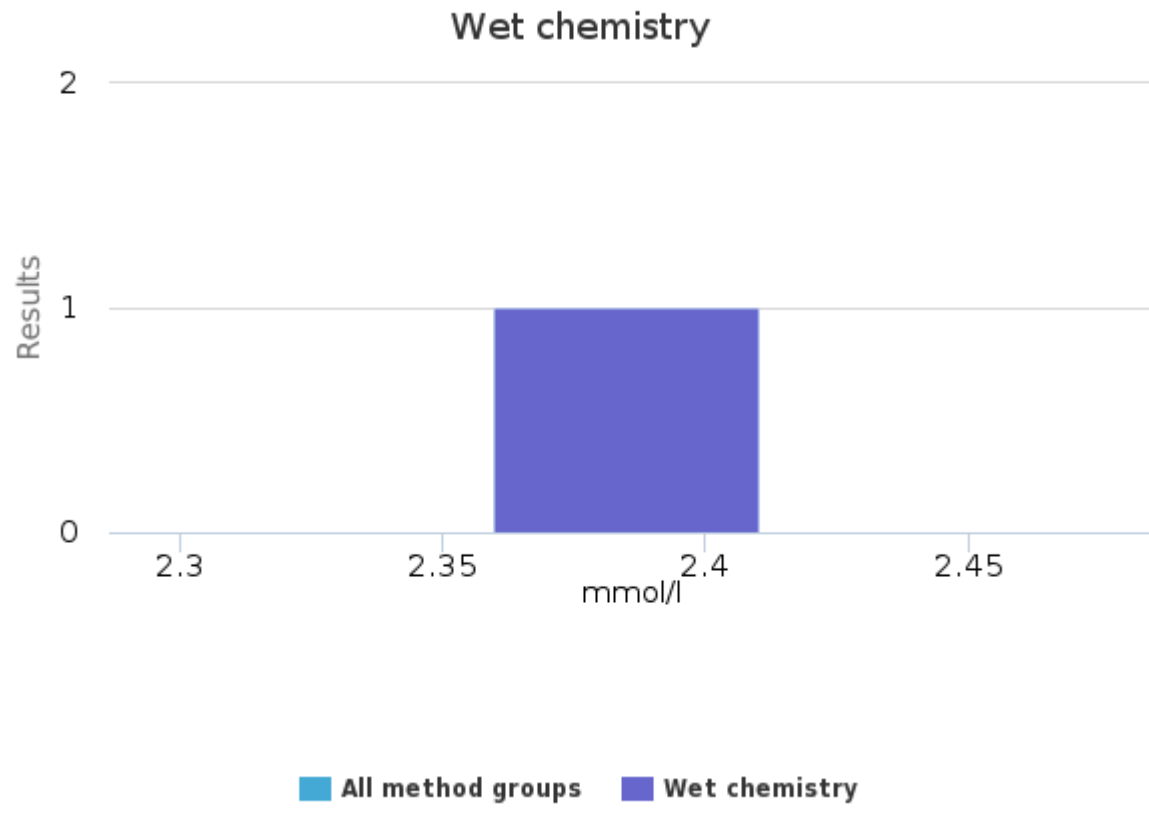
Sample S001 | CK, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	-	-	-	-	-	159.00	159.00	-	1
Wet chemistry	-	-	-	-	-	151.00	151.00	-	1
All	**155.00**	**155.00**	**5.66**	**3.6**	**4.00**	**151.00**	**159.00**	**-**	**2**

Sample S001 | CK, U/l| histogram summaries in LabScala
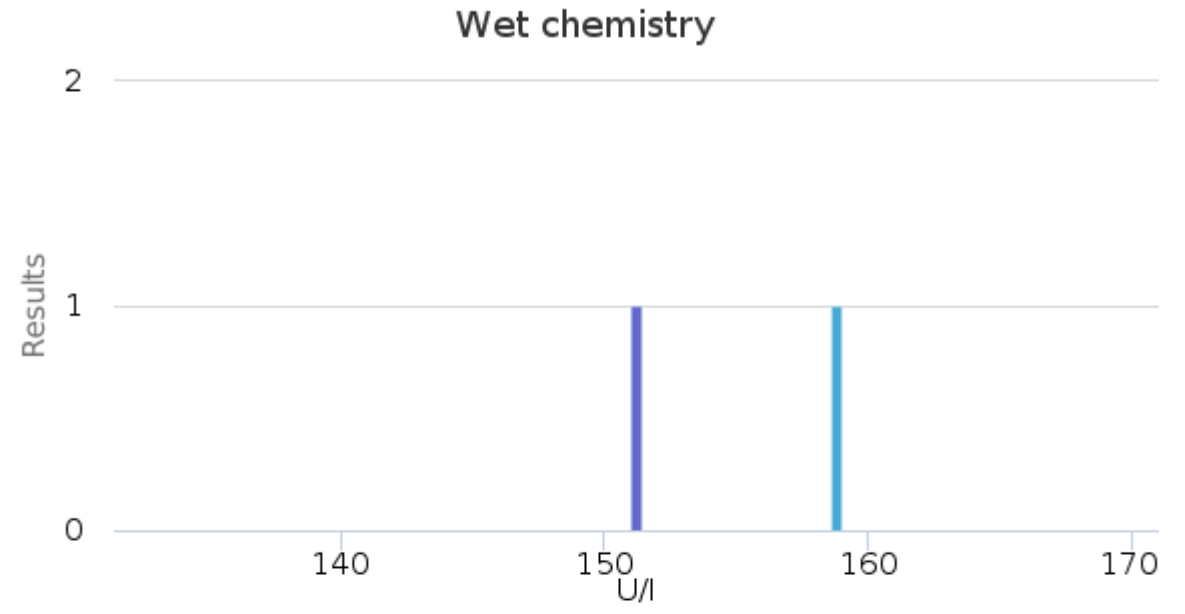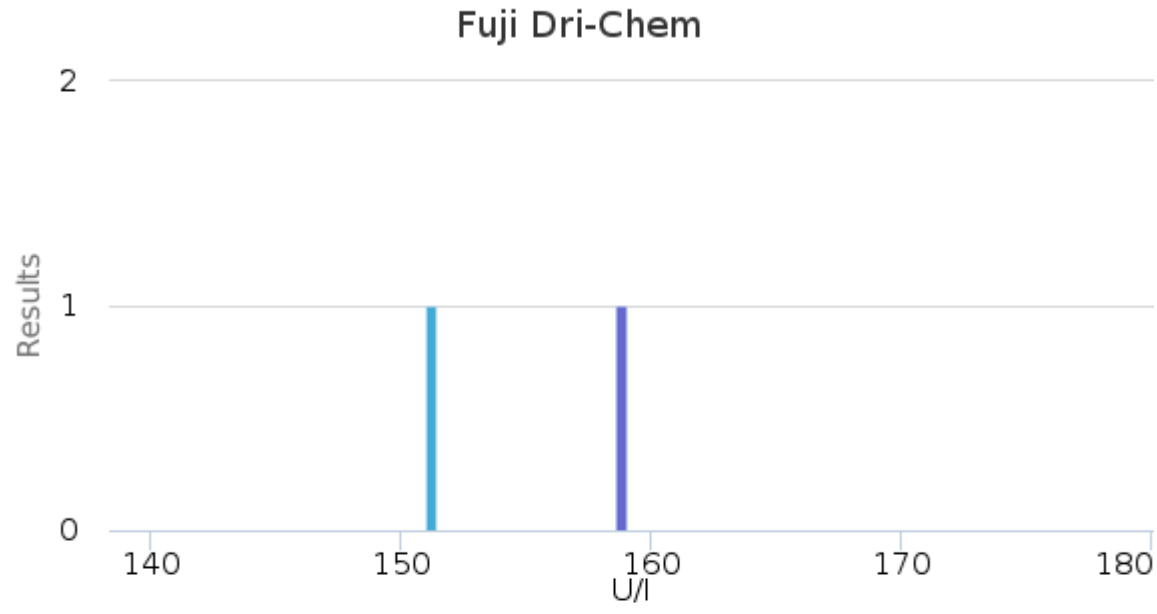
Sample S001 | Cl, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	-	-	-	-	-	98.0	98.0	-	1
i-STAT system	100.6	100.0	0.9	0.9	0.2	99.0	102.0	-	16
Spotchem	-	-	-	-	-	106.0	106.0	-	1
All	**100.4**	**100.0**	**1.1**	**1.1**	**0.3**	**98.0**	**102.0**	**1**	**18**

Sample S001 | Cl, mmol/l| histogram summaries in LabScala
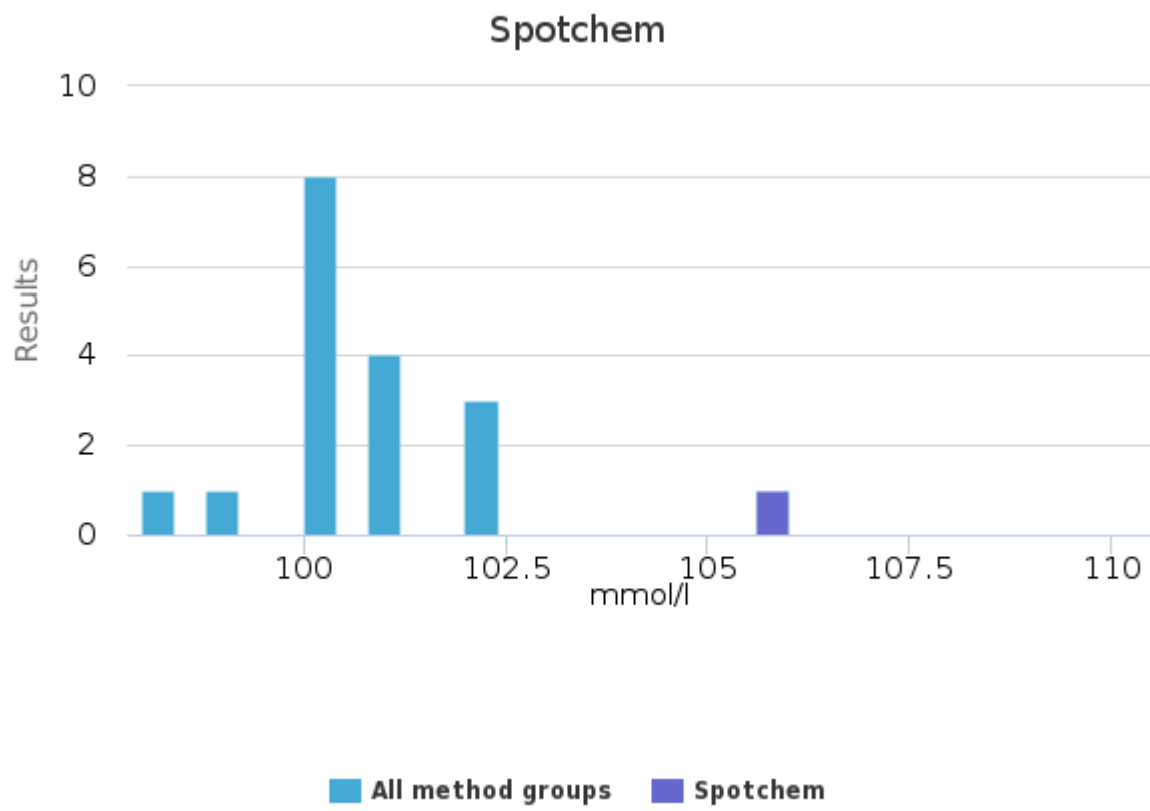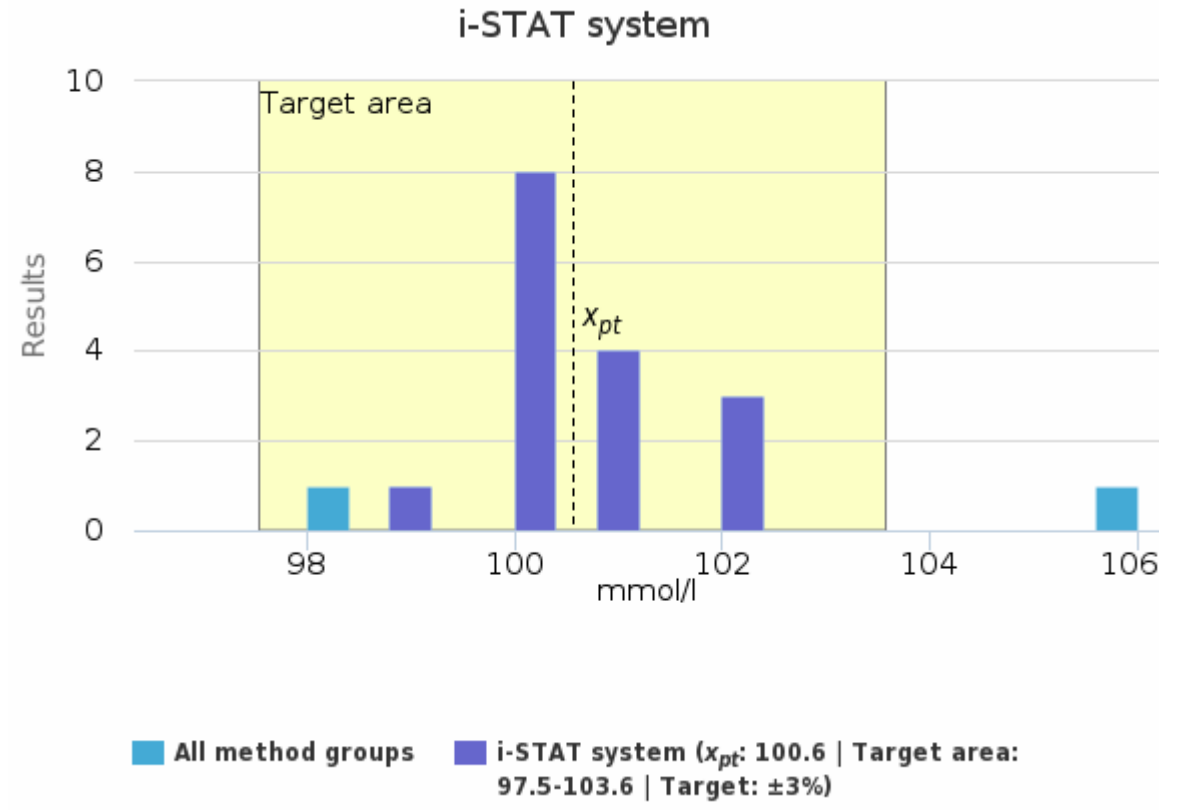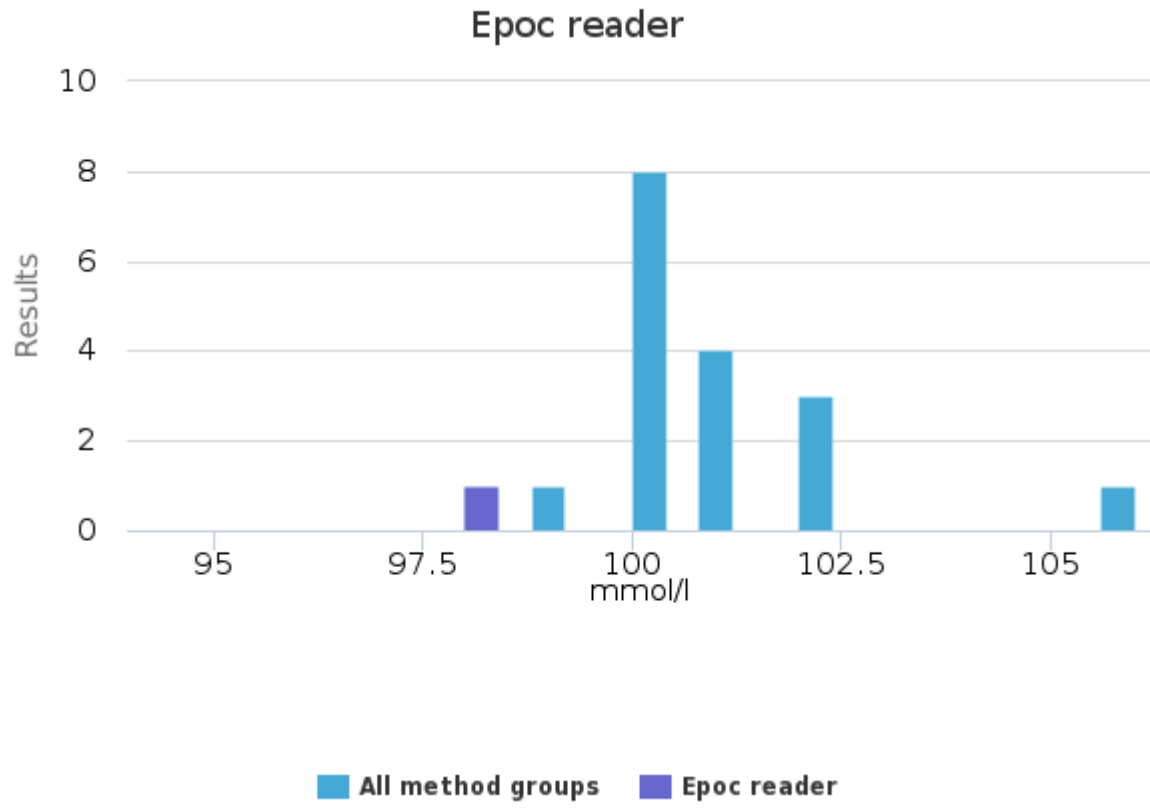
Sample S001 | Glucose, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	-	-	-	-	-	3.30	3.30	-	1
Fuji Dri-Chem	-	-	-	-	-	3.70	3.70	-	1
i-STAT system	3.48	3.50	0.08	2.2	0.02	3.30	3.60	-	21
Wet chemistry	-	-	-	-	-	3.52	3.52	-	1
All	**3.48**	**3.50**	**0.09**	**2.7**	**0.02**	**3.30**	**3.70**	**-**	**24**

Sample S001 | Glucose, mmol/l| histogram summaries in LabScala
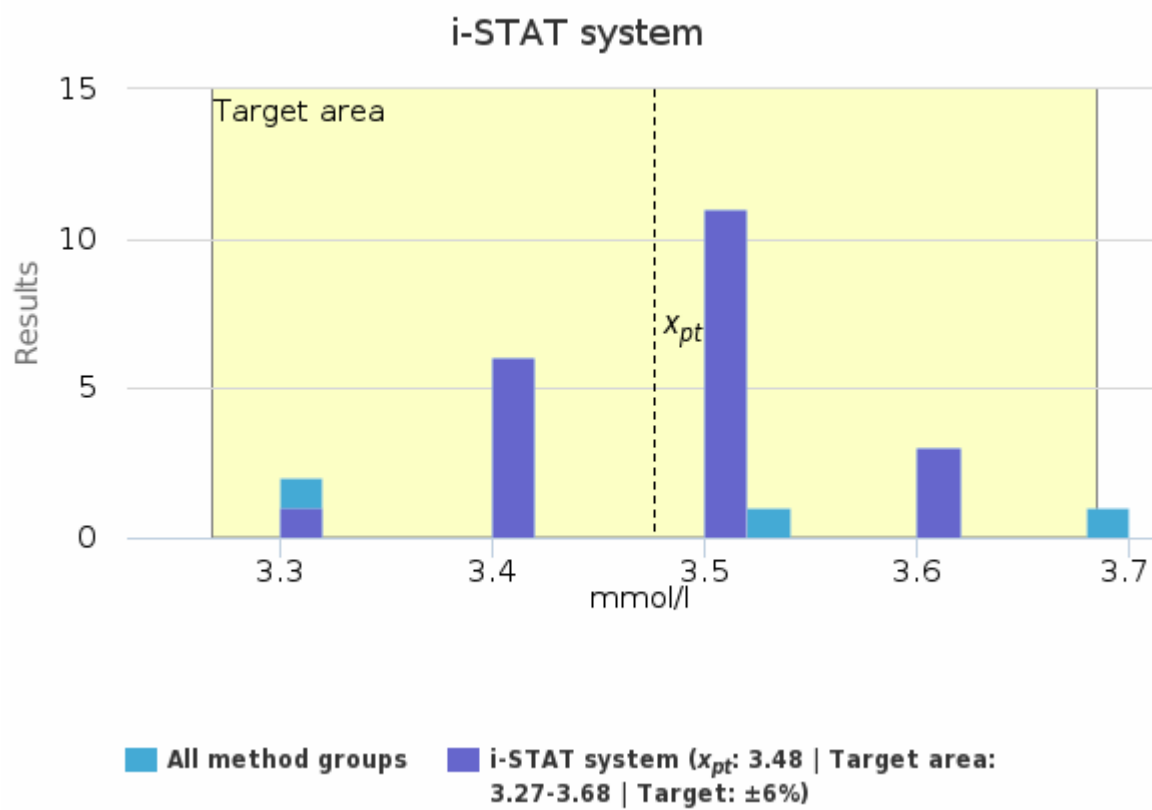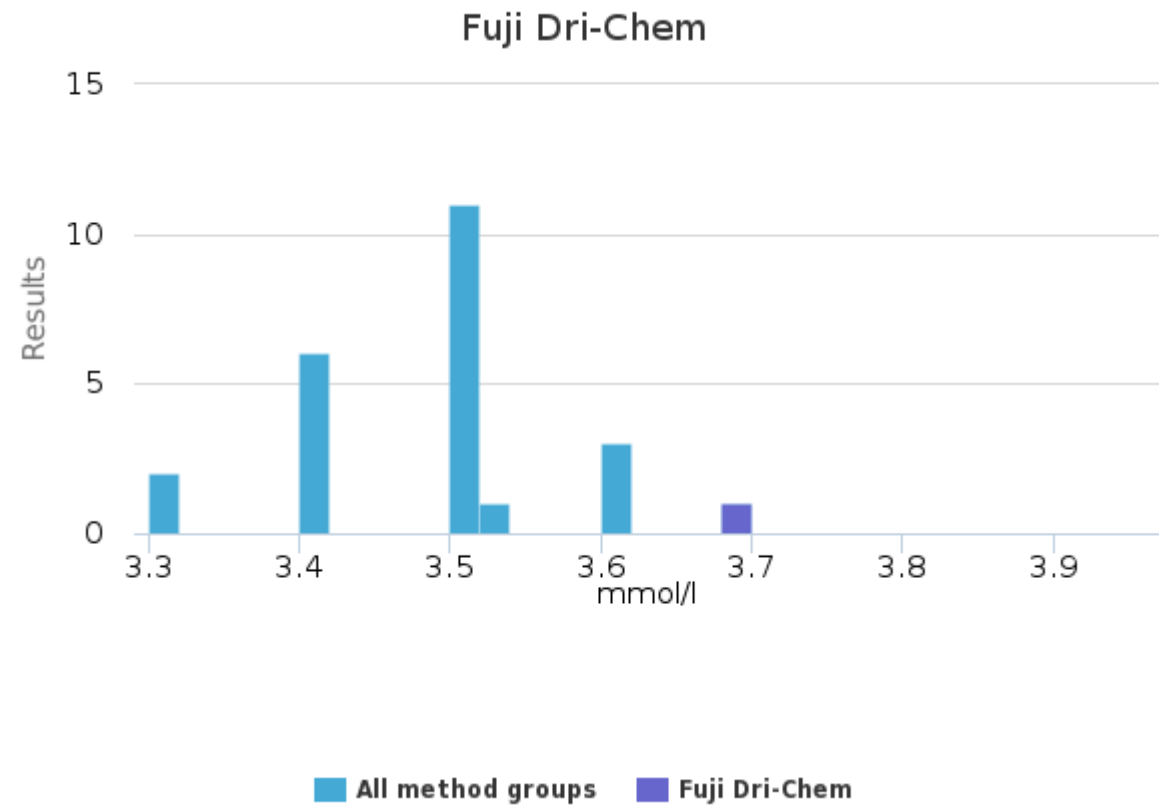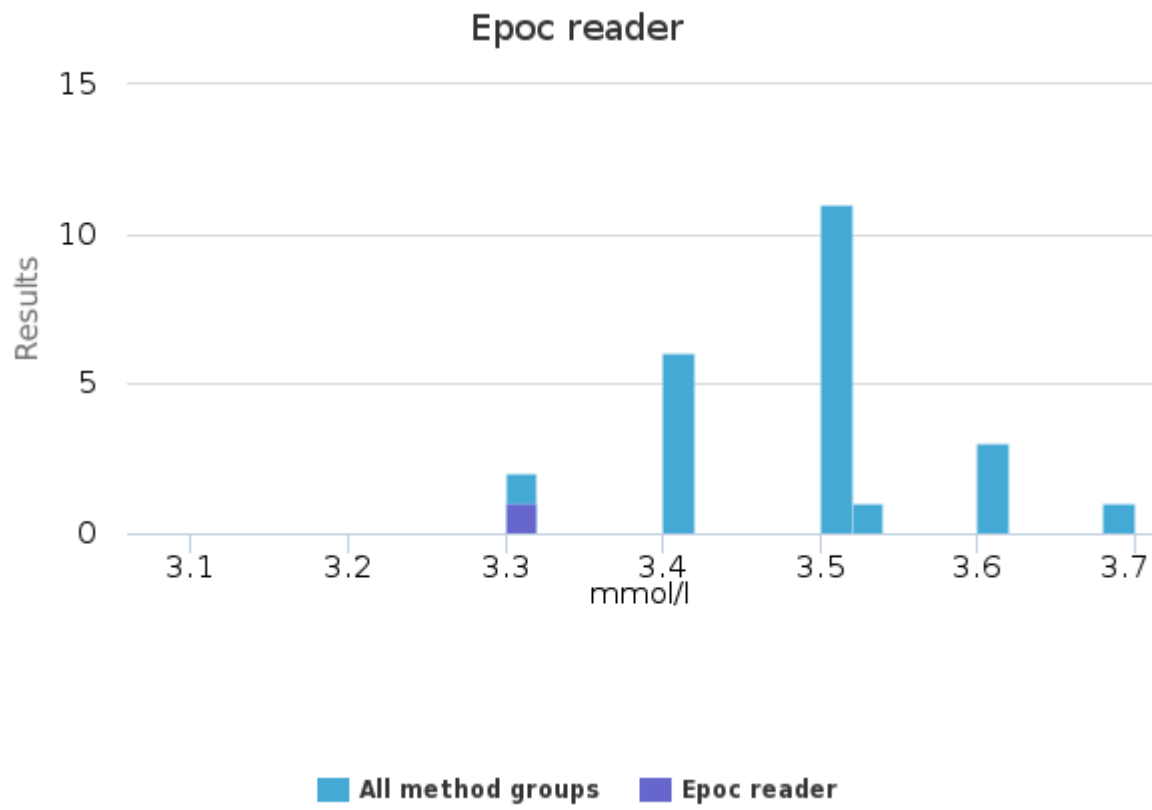
Sample S001 | GT, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	48	48	<1	1.2	<1	48	49	-	3
Wet chemistry	-	-	-	-	-	45	45	-	1
All	**48**	**48**	**2**	**3.4**	**<1**	**45**	**49**	**-**	**4**

Sample S001 | GT, U/l| histogram summaries in LabScala
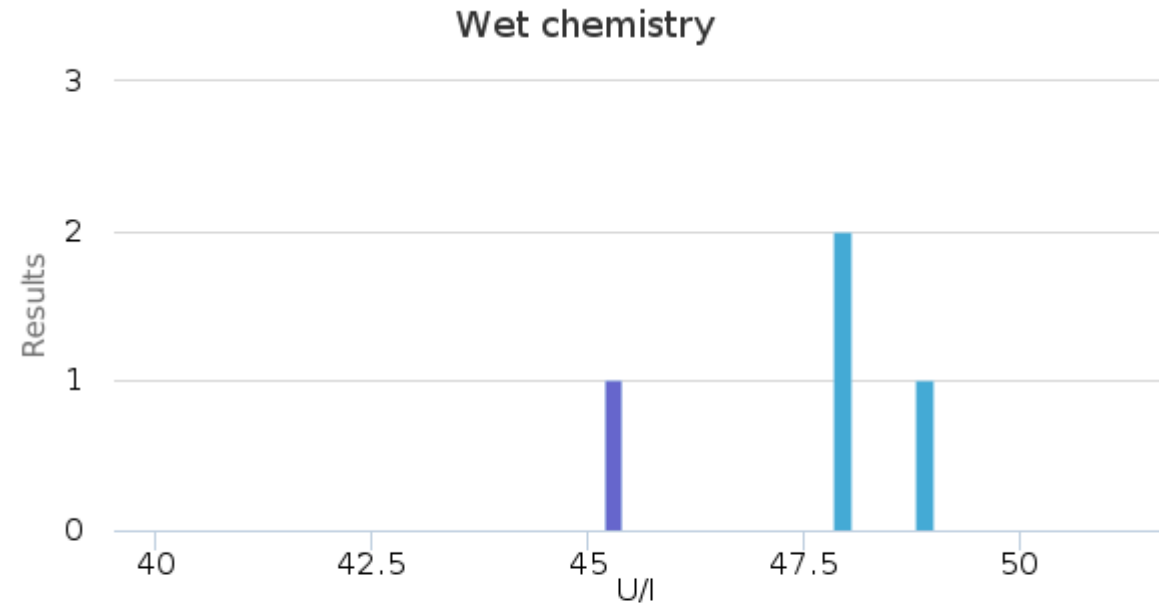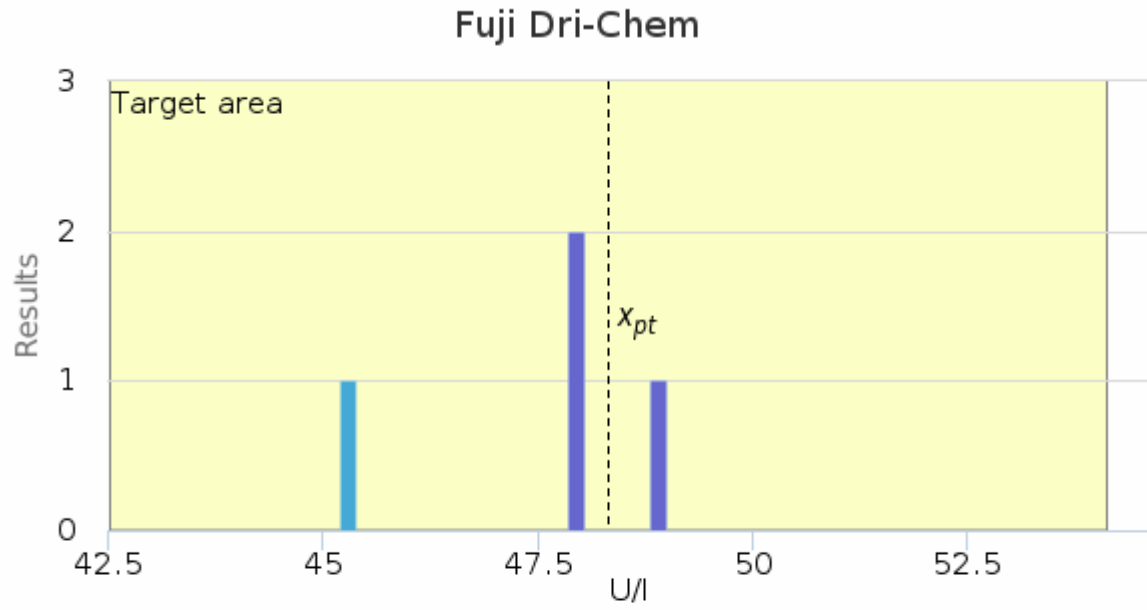
Sample S001 | K, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	7.70	7.70	0.14	1.8	0.10	7.60	7.80	-	2
Fuji Dri-Chem	7.07	7.10	0.06	0.8	0.03	7.00	7.10	-	3
i-STAT system	6.93	6.90	0.05	0.7	0.01	6.90	7.00	1	22
Spotchem	-	-	-	-	-	6.70	6.70	-	1
Wet chemistry	-	-	-	-	-	7.17	7.17	-	1
All	**6.95**	**6.90**	**0.09**	**1.4**	**0.02**	**6.70**	**7.17**	**2**	**29**

Sample S001 | K, mmol/l| histogram summaries in LabScala

Wet chemistry

Legend: ■ All method groups   ■ Wet chemistry

Sample S001 | Chol, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Accutrend	4.77	4.77	0.16	3.4	0.12	4.65	4.88	-	2
Afinion	4.69	4.65	0.13	2.9	0.05	4.56	4.94	-	7
cobas b101	-	-	-	-	-	4.52	4.52	-	1
Spotchem	-	-	-	-	-	4.20	4.20	-	1
Wet chemistry	-	-	-	-	-	4.47	4.47	-	1
All	**4.63**	**4.64**	**0.19**	**4.2**	**0.06**	**4.20**	**4.94**	**-**	**12**

Sample S001 | Chol, mmol/l | histogram summaries in LabScala

Wet chemistry
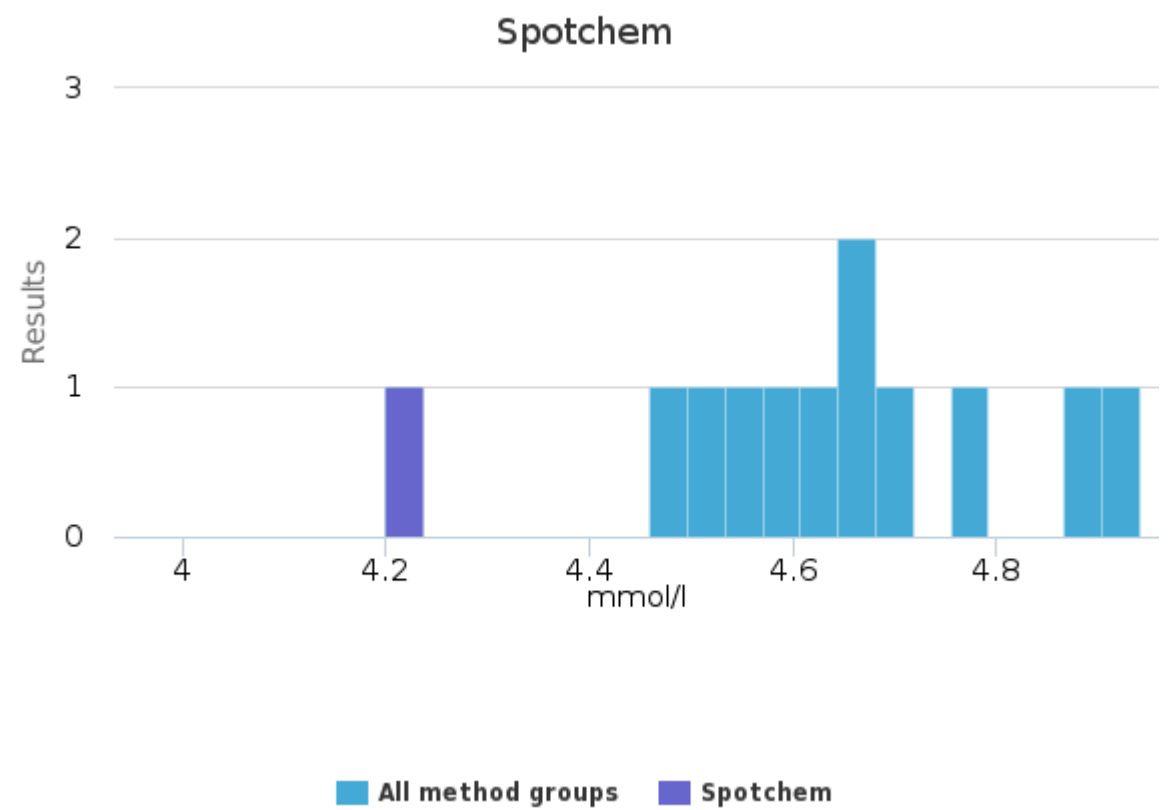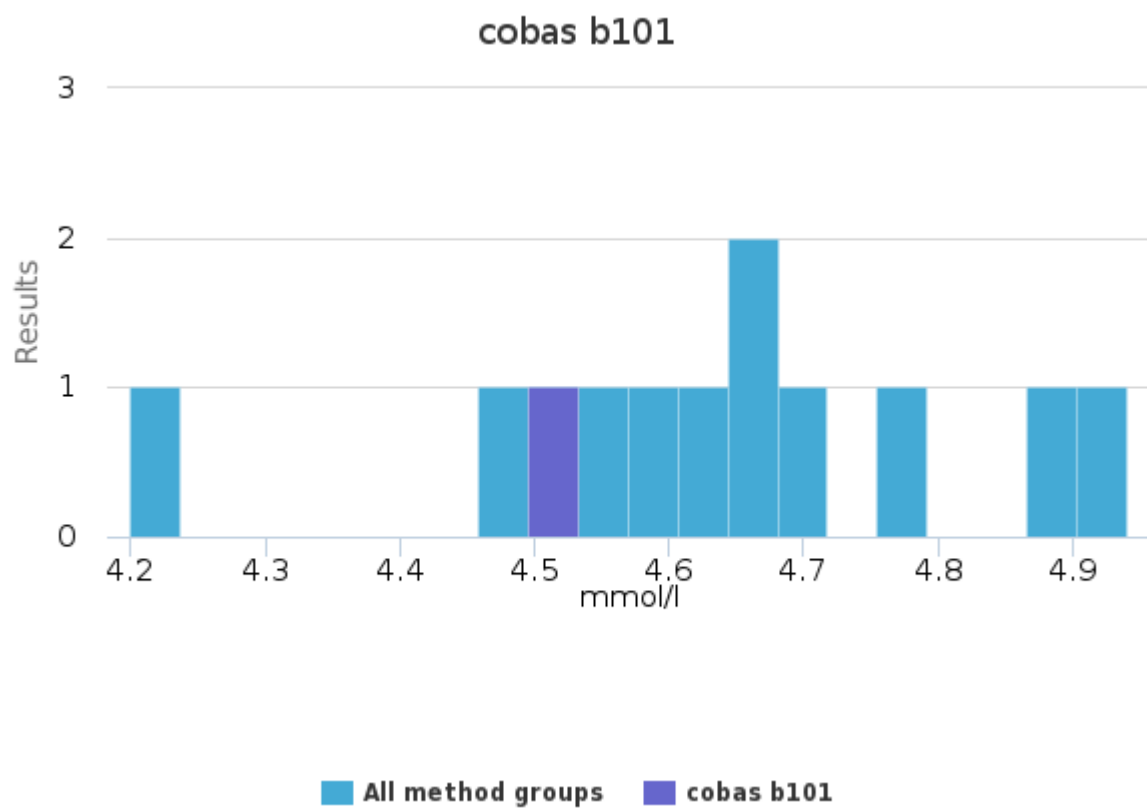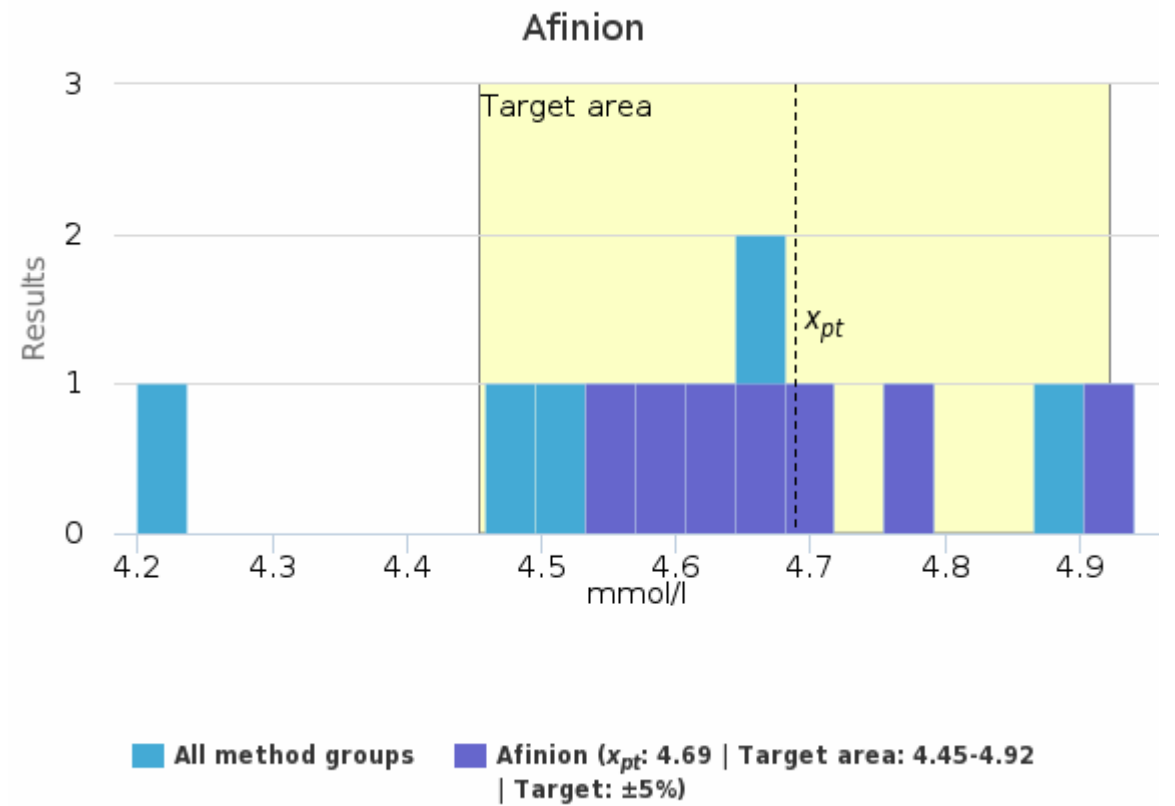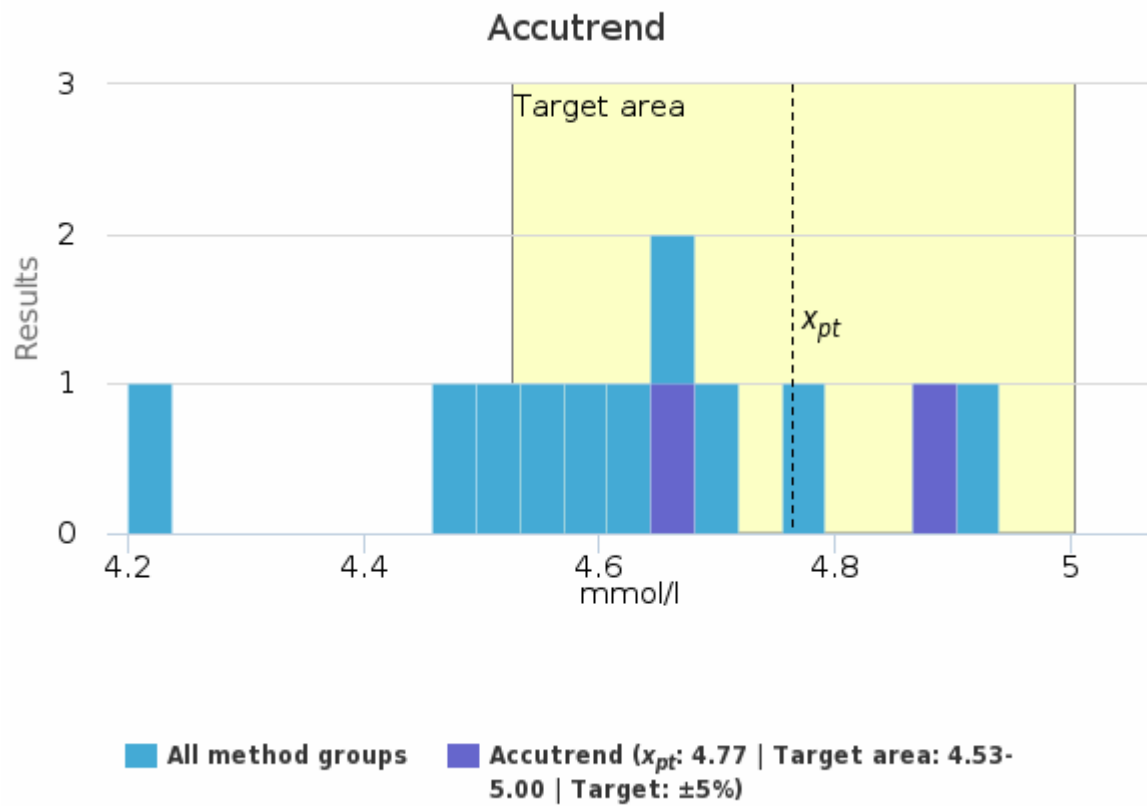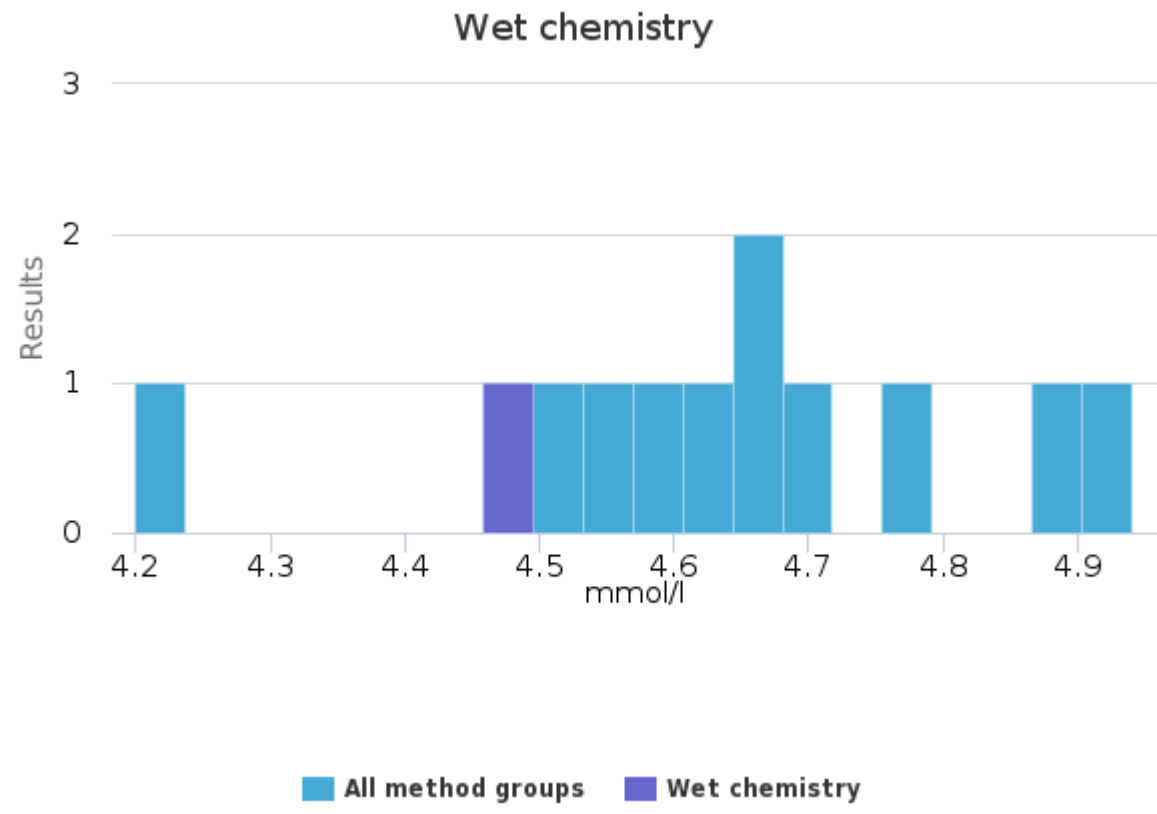
Sample S001 | Chol-HDL, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Afinion	1.20	1.20	0.04	3.5	0.03	1.17	1.23	-	2
cobas b101	-	-	-	-	-	1.33	1.33	-	1
Spotchem	-	-	-	-	-	1.23	1.23	-	1
Wet chemistry	-	-	-	-	-	1.22	1.22	-	1
All	**1.24**	**1.23**	**0.06**	**4.6**	**0.03**	**1.17**	**1.33**	**-**	**5**

Sample S001 | Chol-HDL, mmol/l| histogram summaries in LabScala
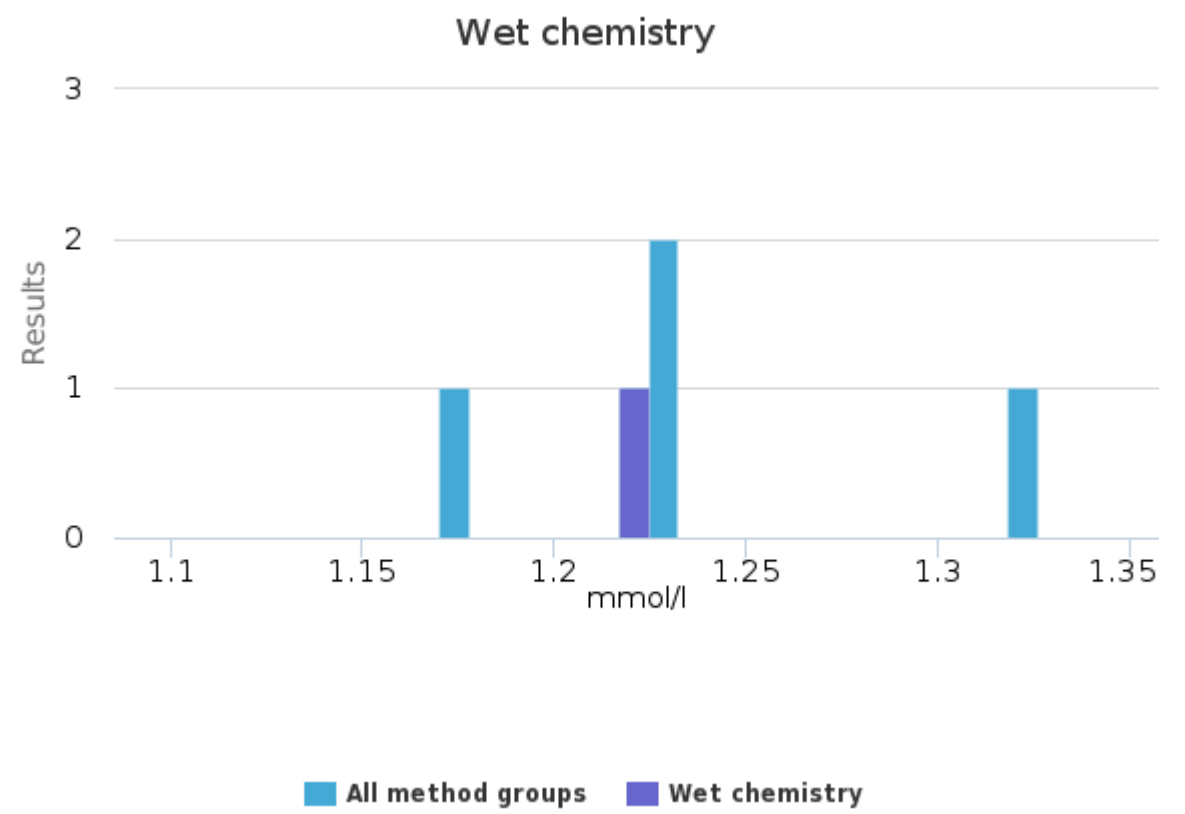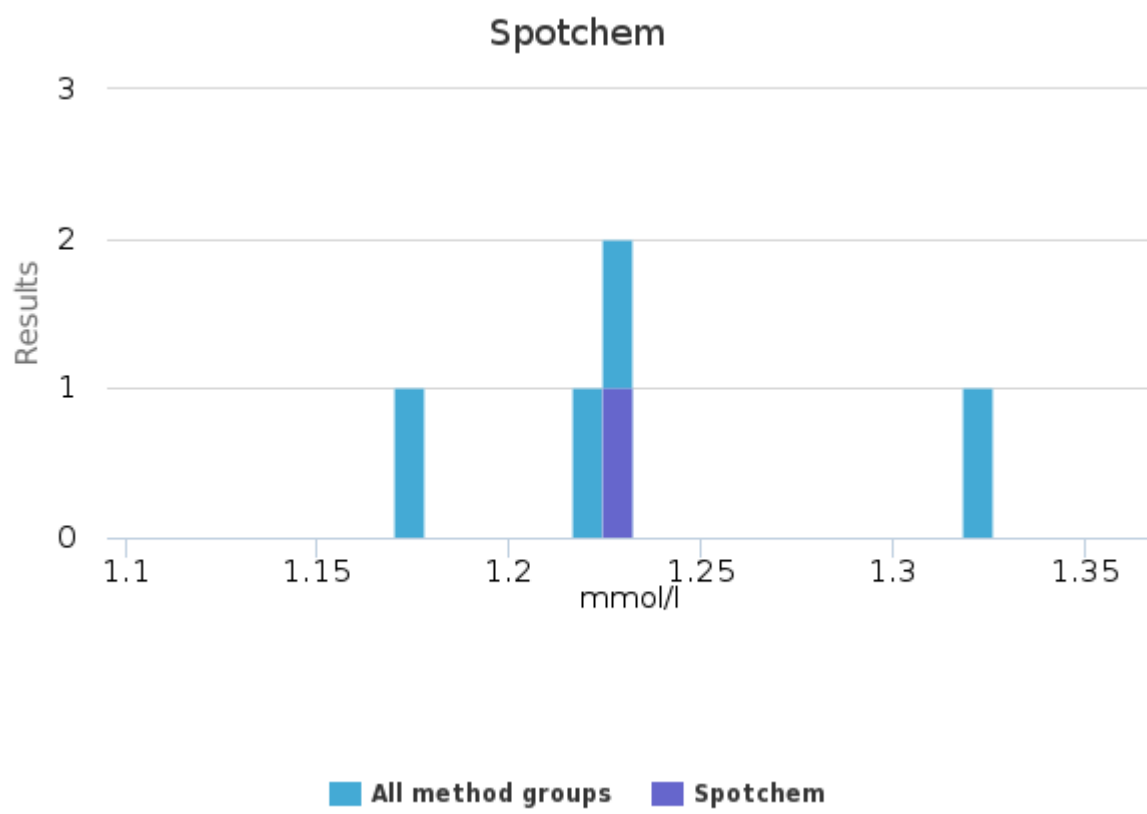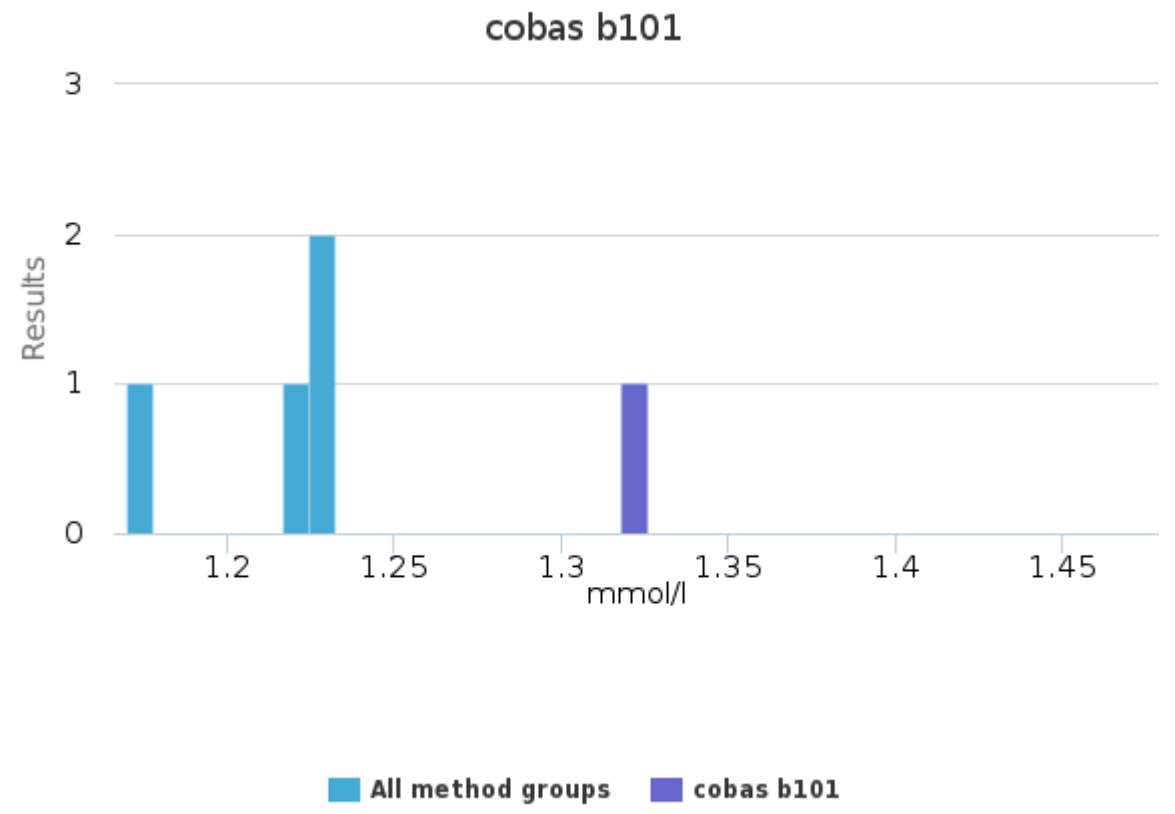
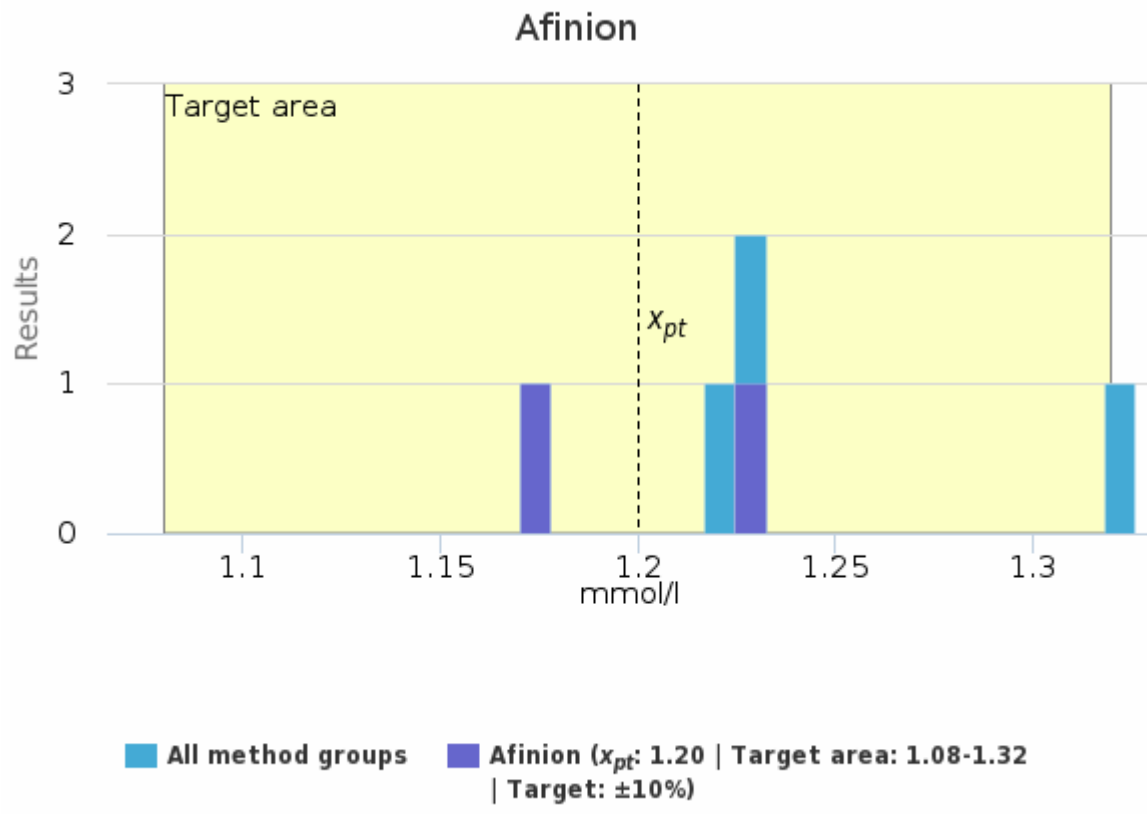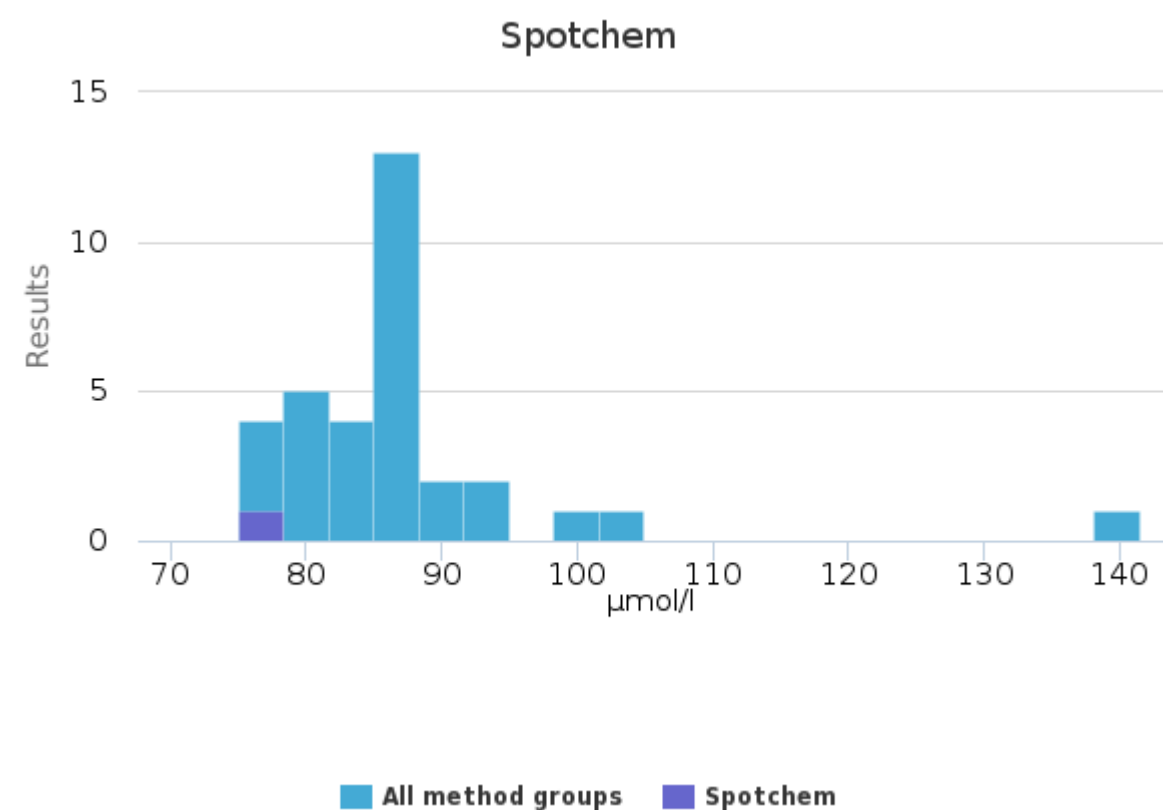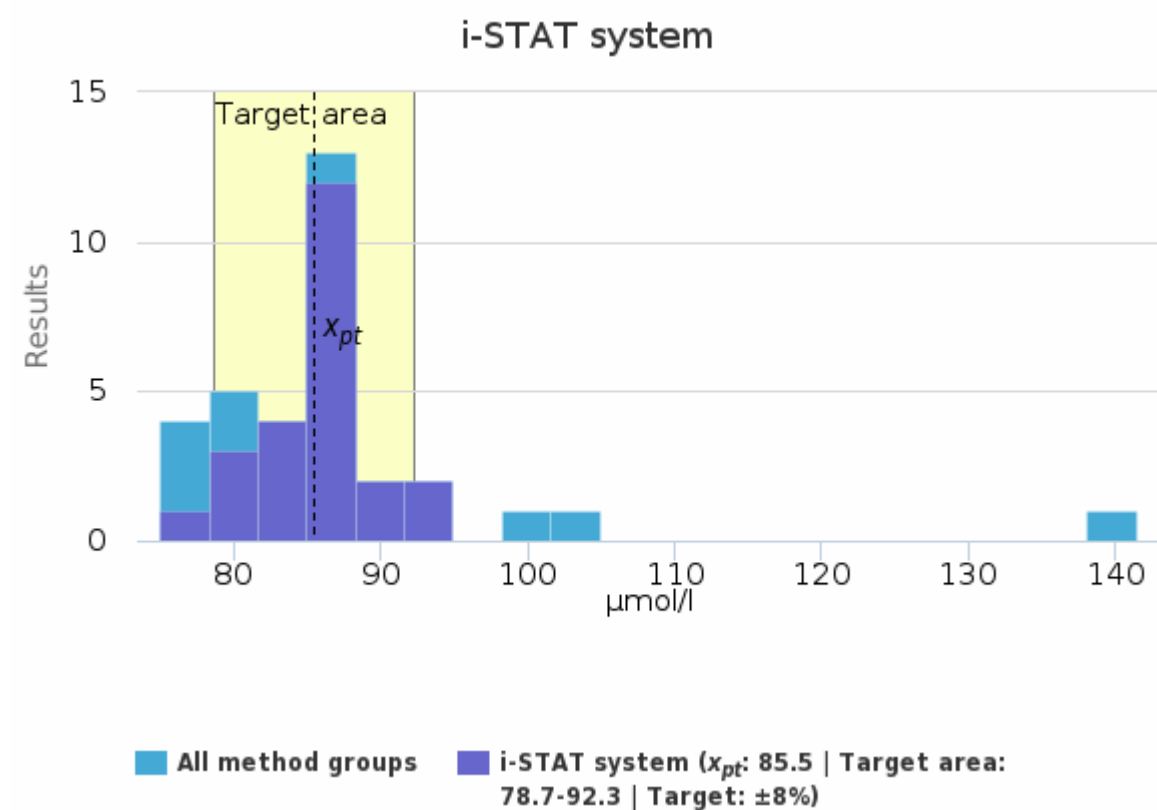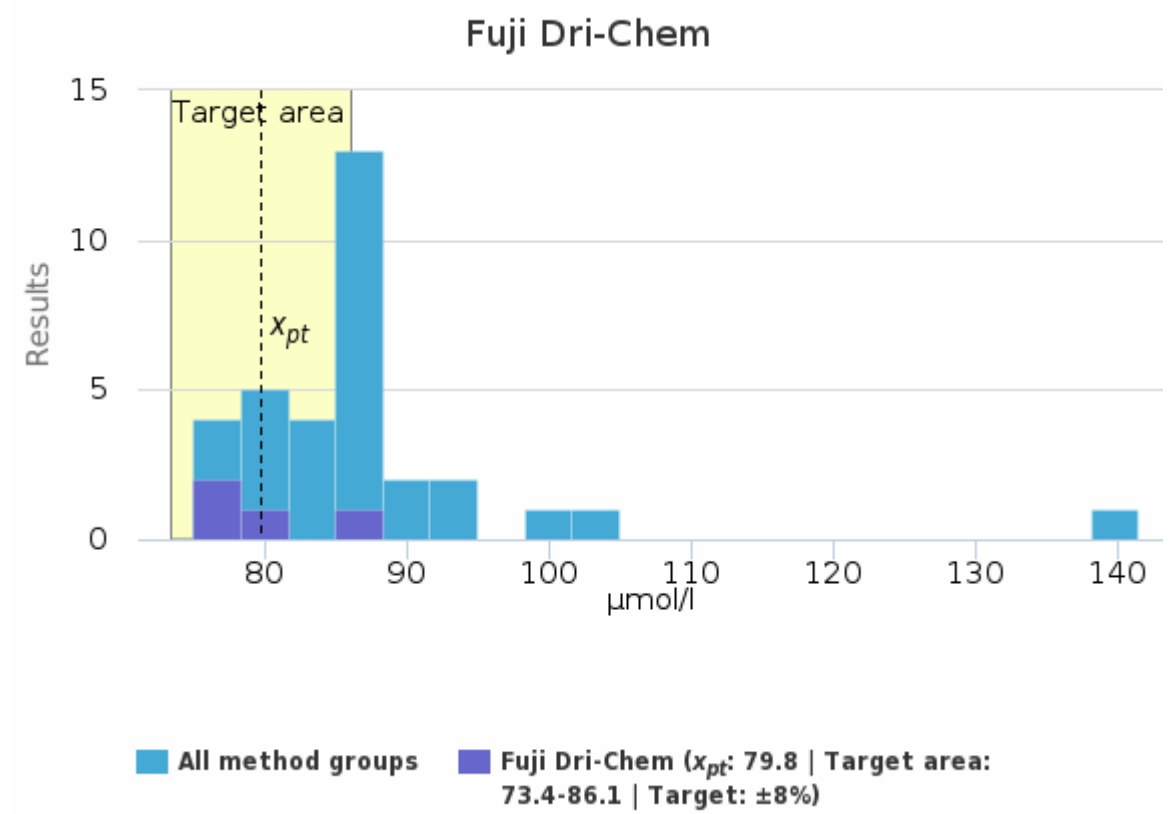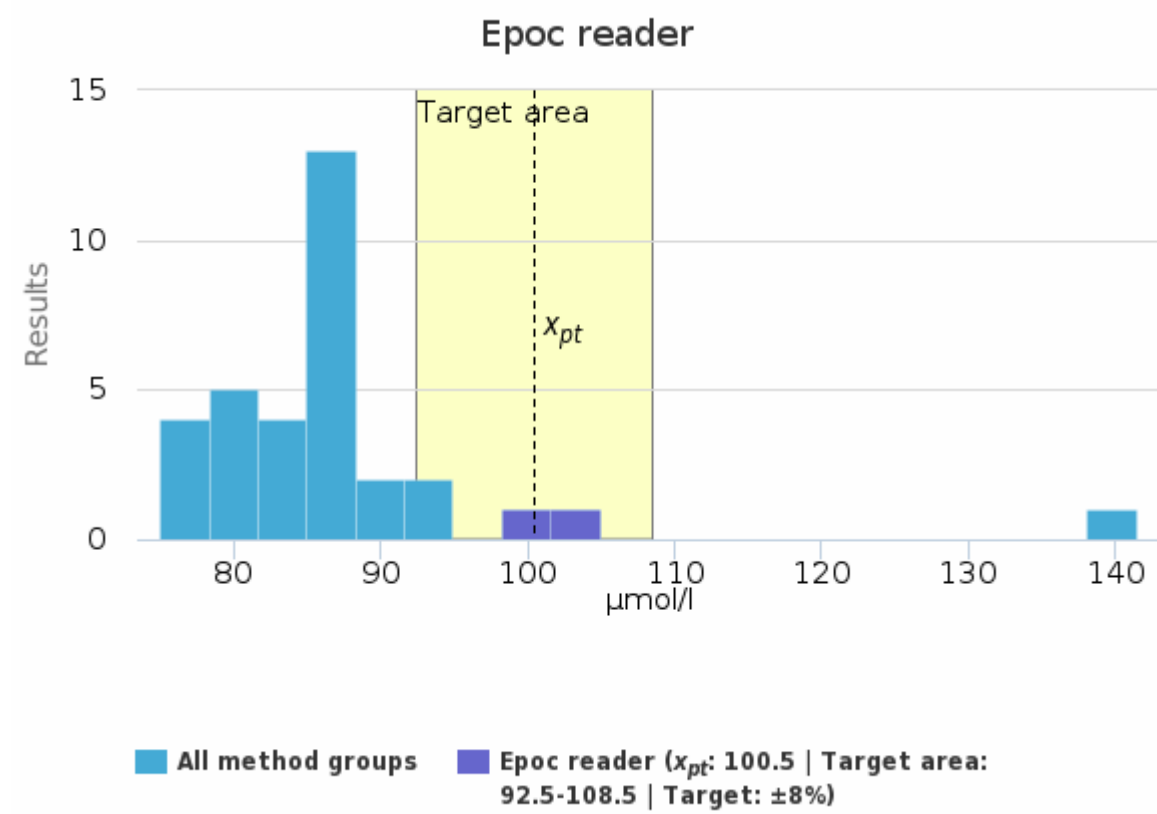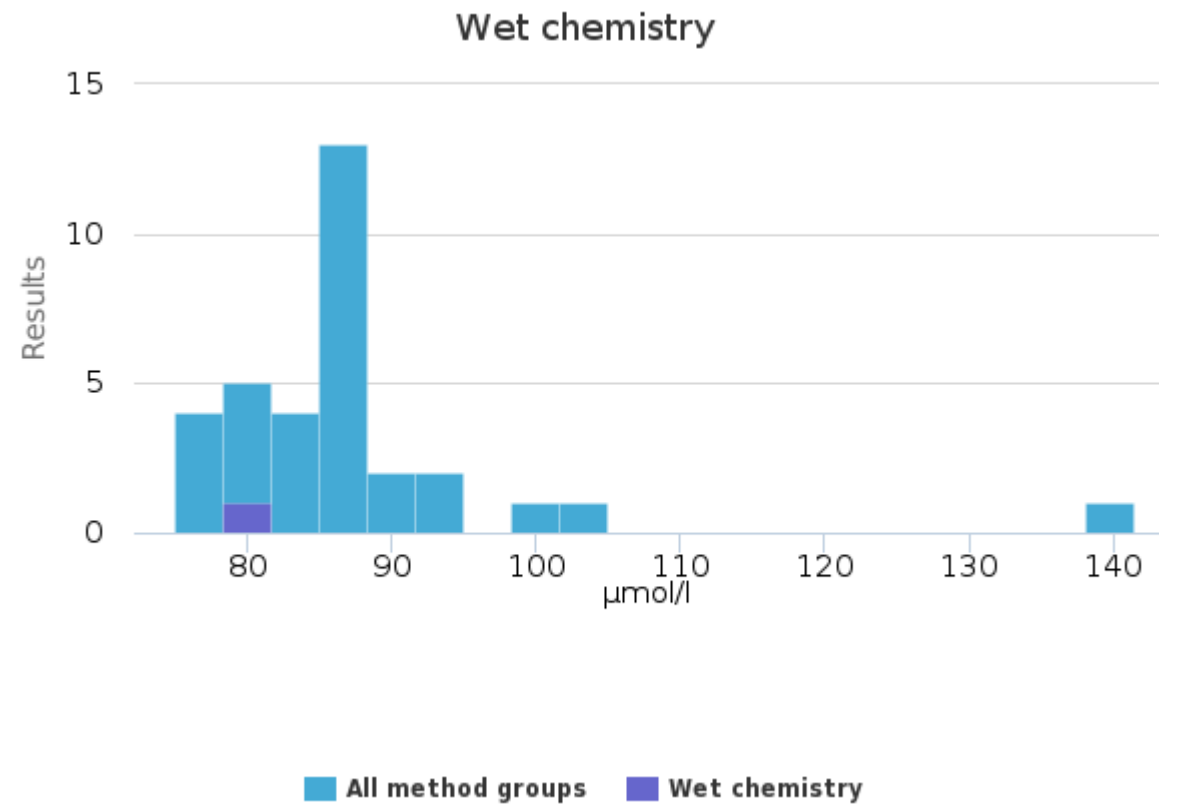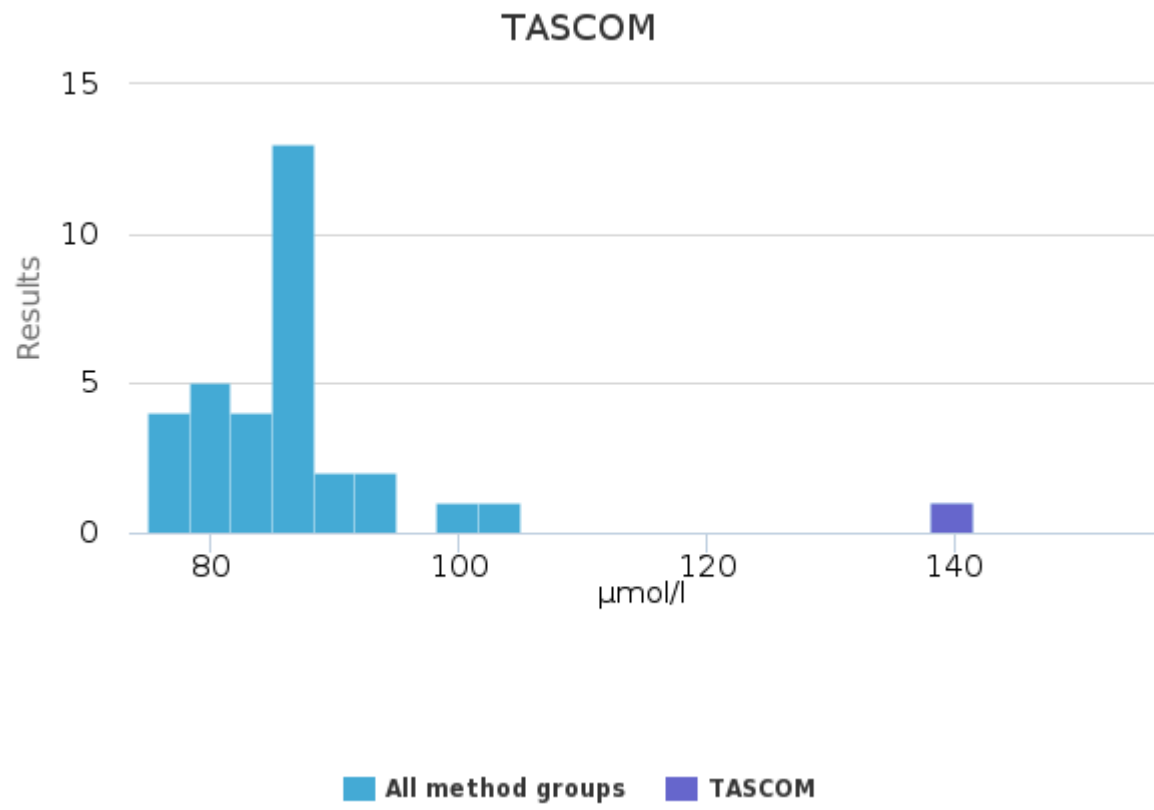**Sample S001 | Crea, µmol/l**

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	100.5	100.5	2.1	2.1	1.5	99.0	102.0	-	2
Fuji Dri-Chem	79.8	79.0	4.6	5.8	2.3	75.0	86.0	-	4
i-STAT system	85.5	85.5	3.6	4.2	0.7	78.0	92.0	-	24
Spotchem	-	-	-	-	-	76.0	76.0	-	1
TASCOM	-	-	-	-	-	141.4	141.4	-	1
Wet chemistry	-	-	-	-	-	81.0	81.0	-	1
All	**85.3**	**85.0**	**5.8**	**6.8**	**1.0**	**75.0**	**102.0**	**1**	**33**

Sample S001 | Crea, µmol/l| histogram summaries in LabScala

TASCOM

Wet chemistry

Sample S001 | LD, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	166.83	166.83	-	1
All	**-**	**-**	**-**	**-**	**-**	**166.83**	**166.83**	**-**	**1**

Sample S001 | LD, U/l| histogram summaries in LabScala
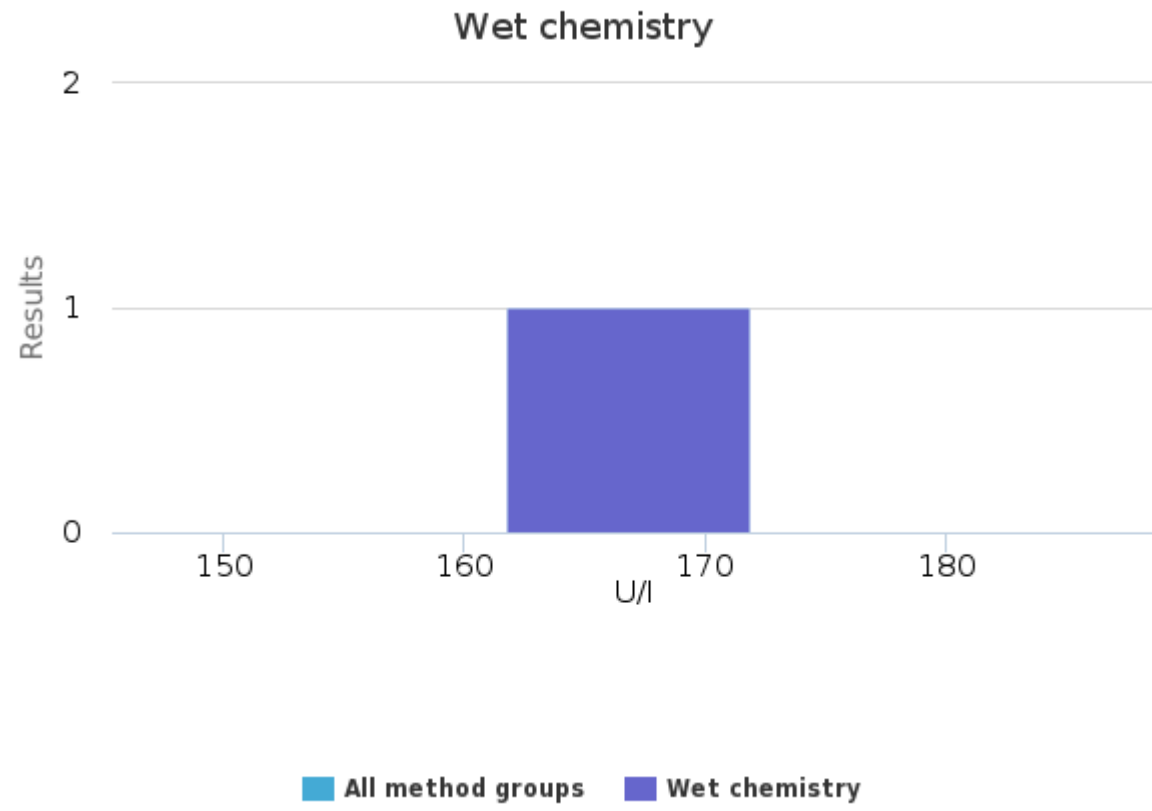
Sample S001 | Mg, mmol/l

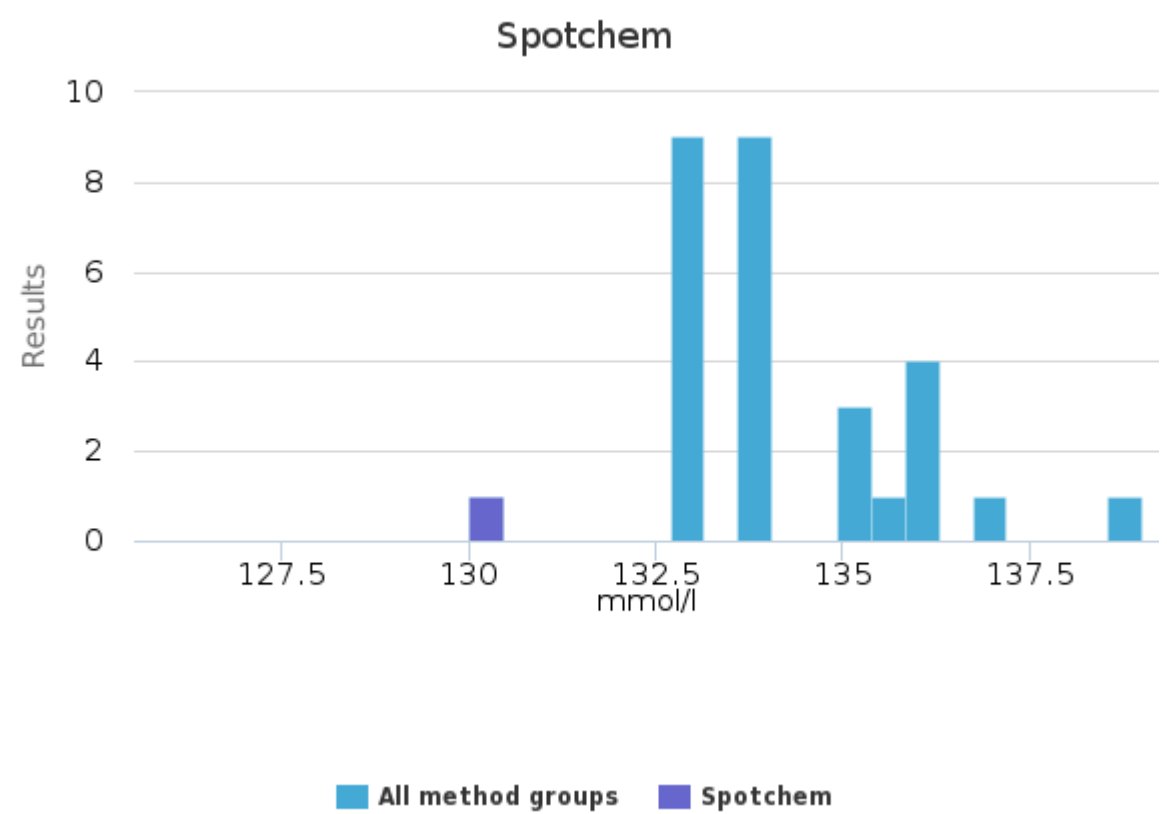| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	0.86	0.86	-	1
All	**-**	**-**	**-**	**-**	**-**	**0.86**	**0.86**	**-**	**1**

Sample S001 | Mg, mmol/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
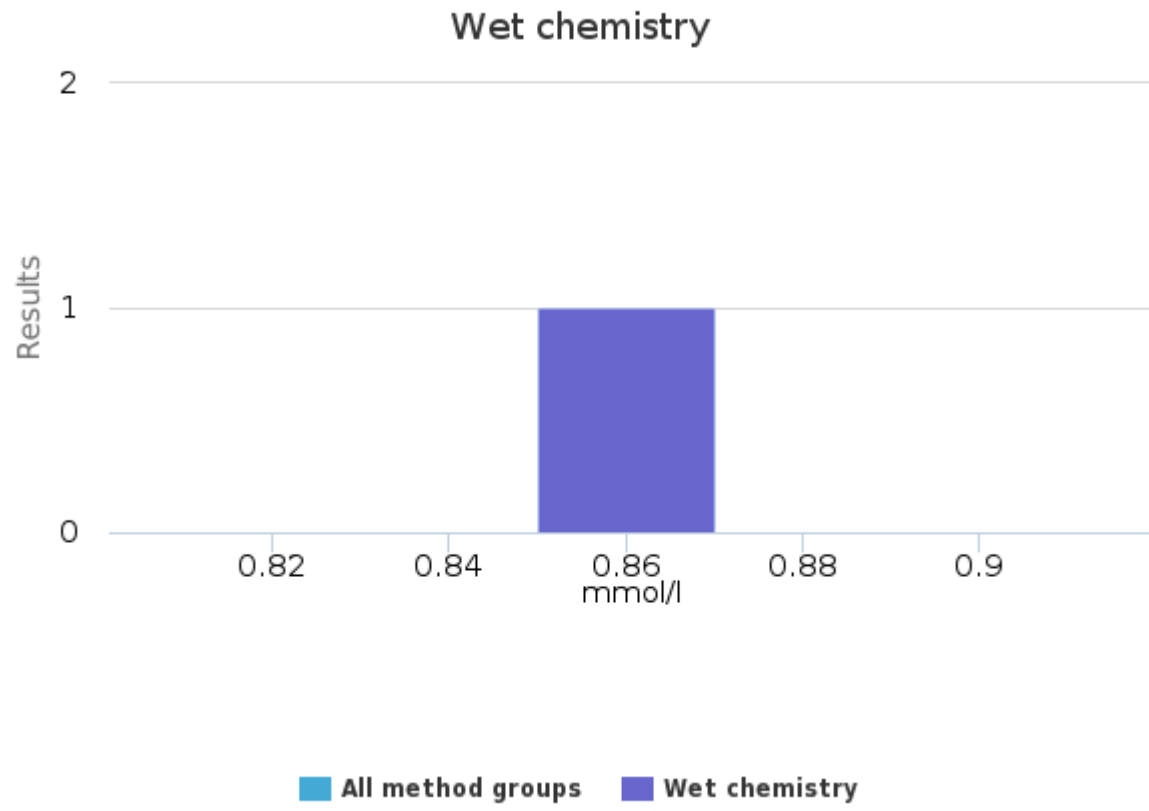
Sample S001 | Na, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	138	138	1	1.0	1	137	139	-	2
Fuji Dri-Chem	136	136	<1	<0.1	<1	136	136	-	3
i-STAT system	134	134	<1	0.6	<1	133	136	-	22
Spotchem	-	-	-	-	-	130	130	-	1
Wet chemistry	-	-	-	-	-	136	136	-	1
All	**134**	**134**	**2**	**1.2**	**<1**	**130**	**139**	**-**	**29**

Sample S001 | Na, mmol/l| histogram summaries in LabScala

Epoc reader

■ All method groups ■ Epoc reader (x_{pt}: 138 | Target area: 135-141 | Target: ±2%)

Fuji Dri-Chem

■ All method groups ■ Fuji Dri-Chem (x_{pt}: 136 | Target area: 133-139 | Target: ±2%)

i-STAT system

■ All method groups ■ i-STAT system (x_{pt}: 134 | Target area: 131-136 | Target: ±2%)

Spotchem

■ All method groups ■ Spotchem

Wet chemistry

Legend: ■ All method groups ■ Wet chemistry
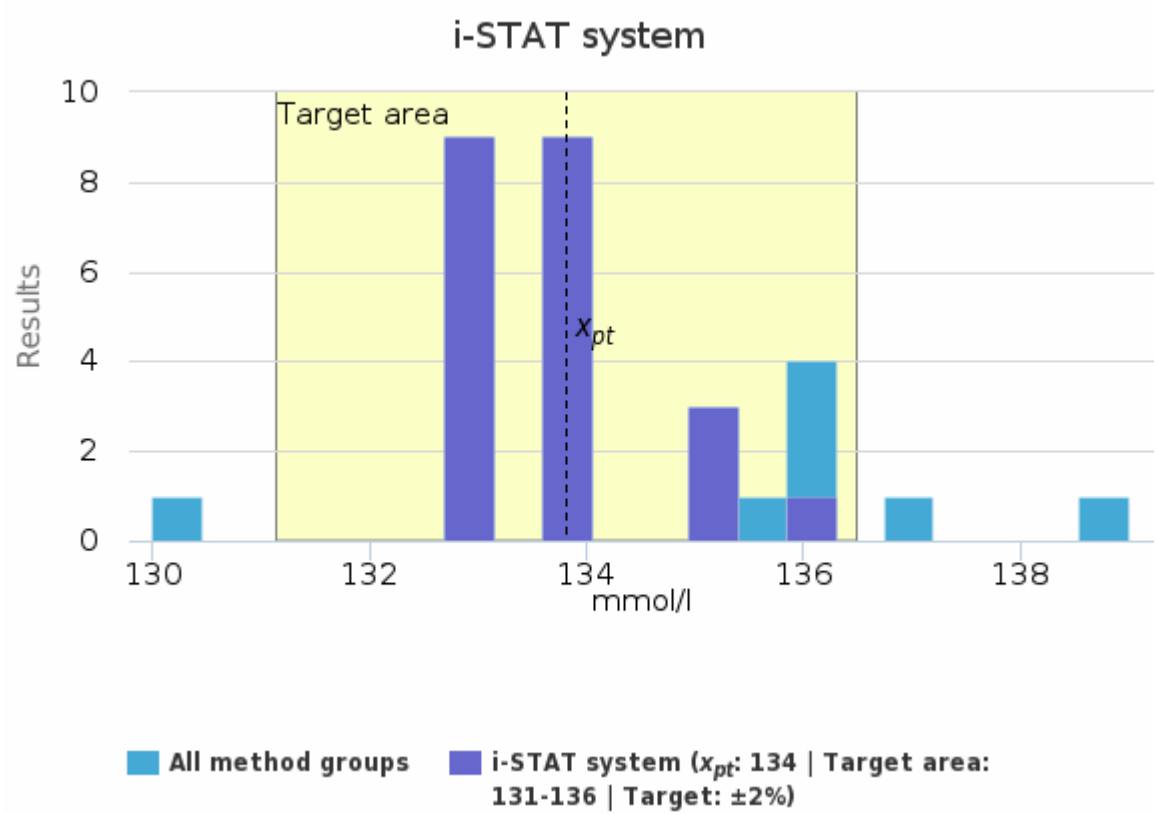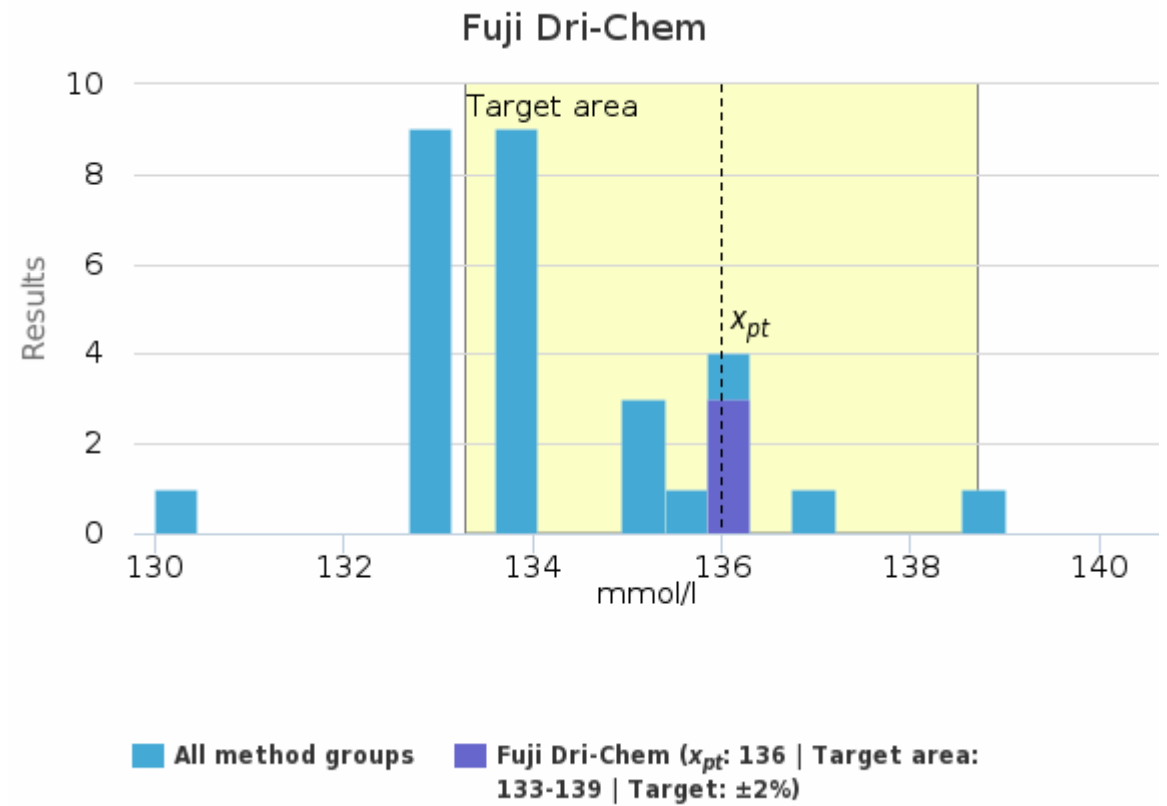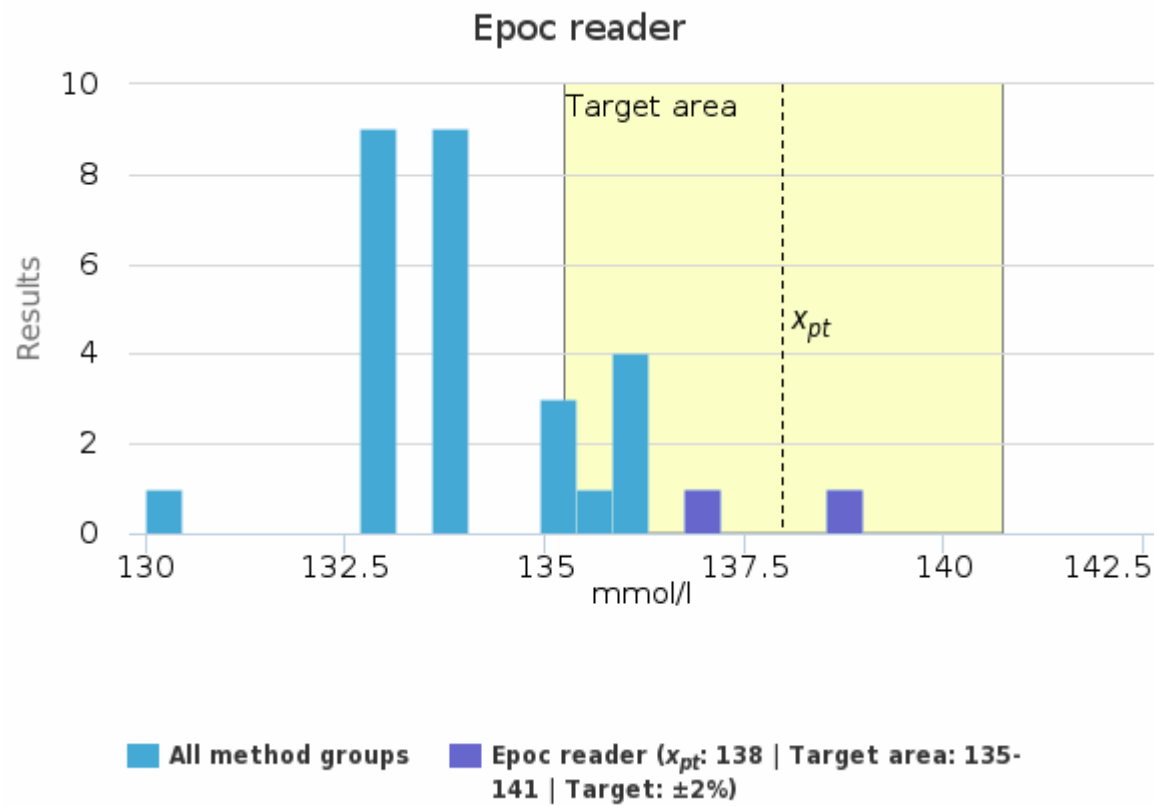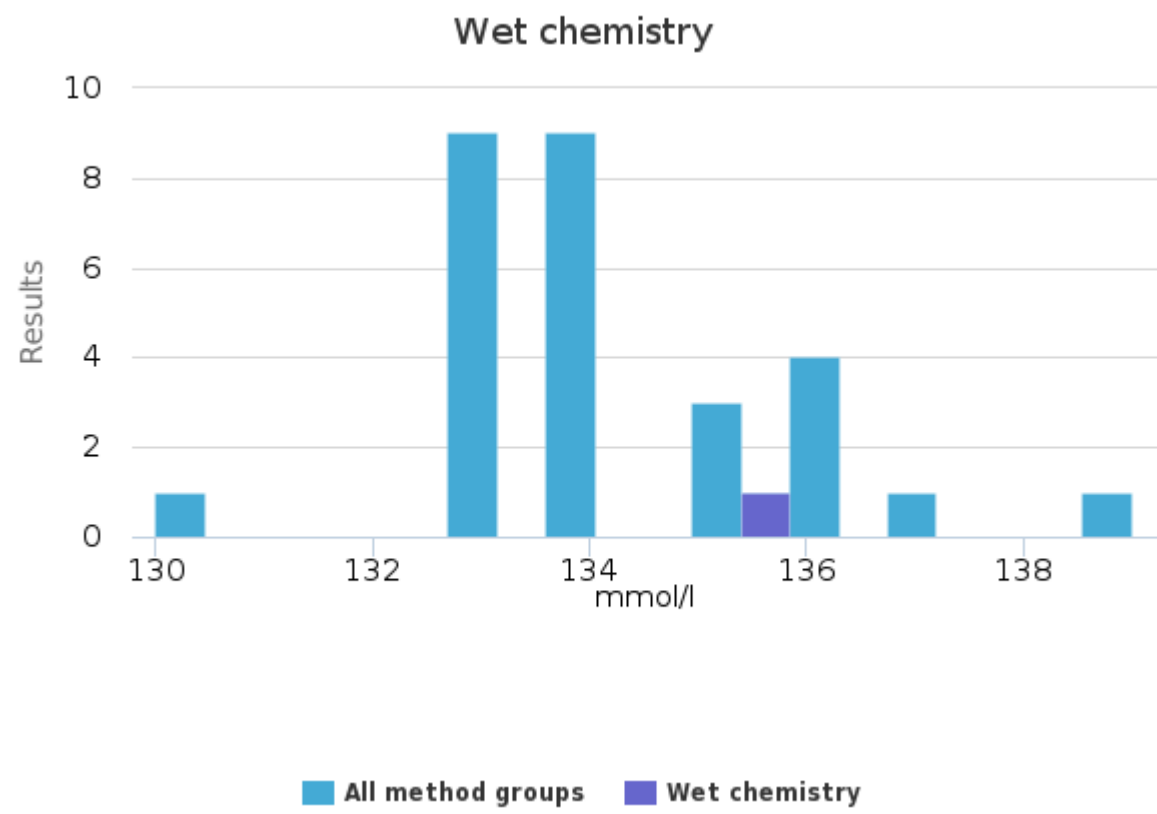
Sample S001 | Pi, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	1.11	1.11	-	1
All	**-**	**-**	**-**	**-**	**-**	**1.11**	**1.11**	**-**	**1**

Sample S001 | Pi, mmol/l| histogram summaries in LabScala

■ All method groups ■ Wet chemistry

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
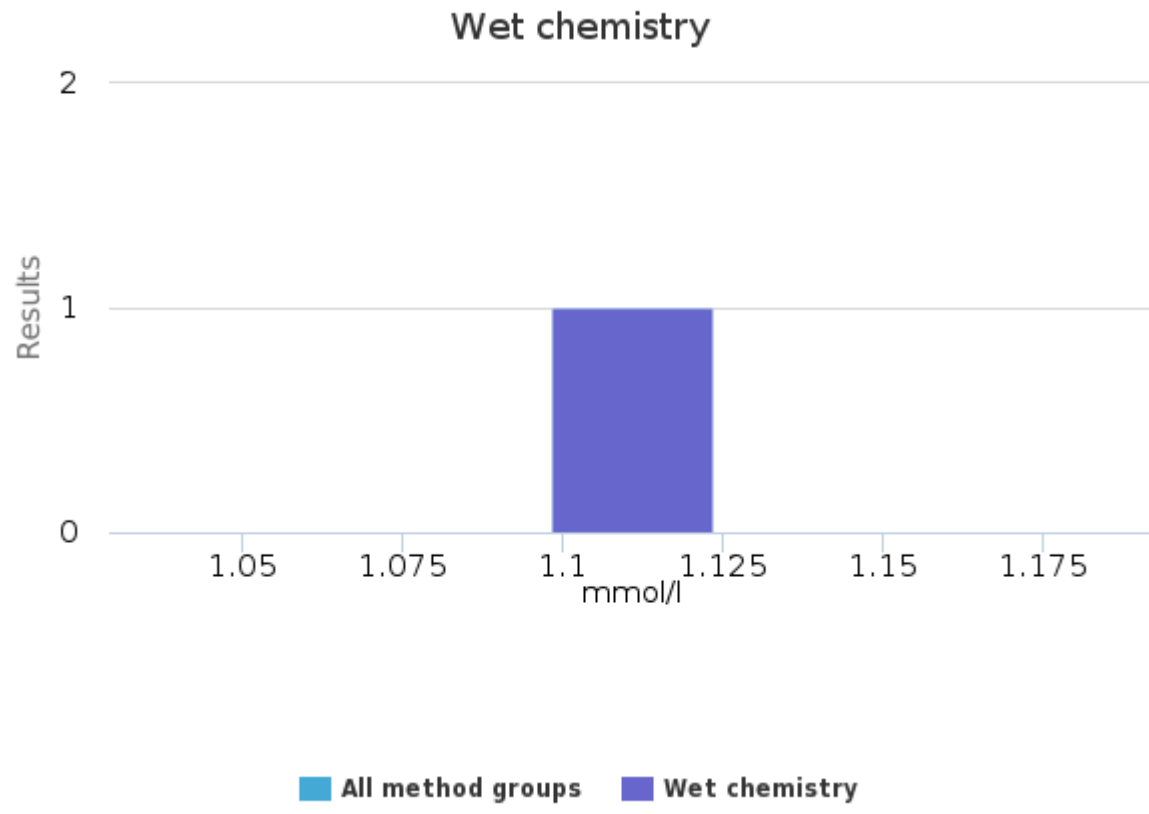
Sample S001 | Prot, g/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	70.9	70.9	-	1
All	**-**	**-**	**-**	**-**	**-**	**70.9**	**70.9**	**-**	**1**

Sample S001 | Prot, g/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
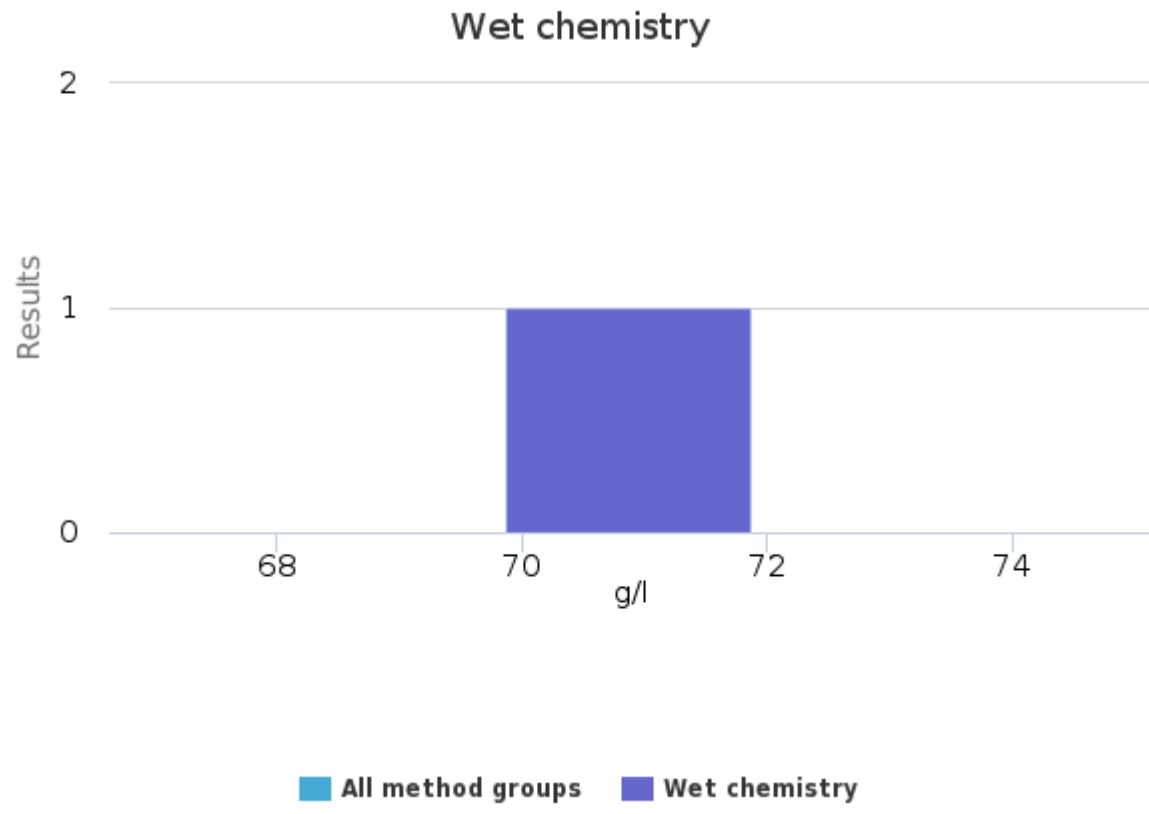
Sample S001 | Trigly, mmol/l

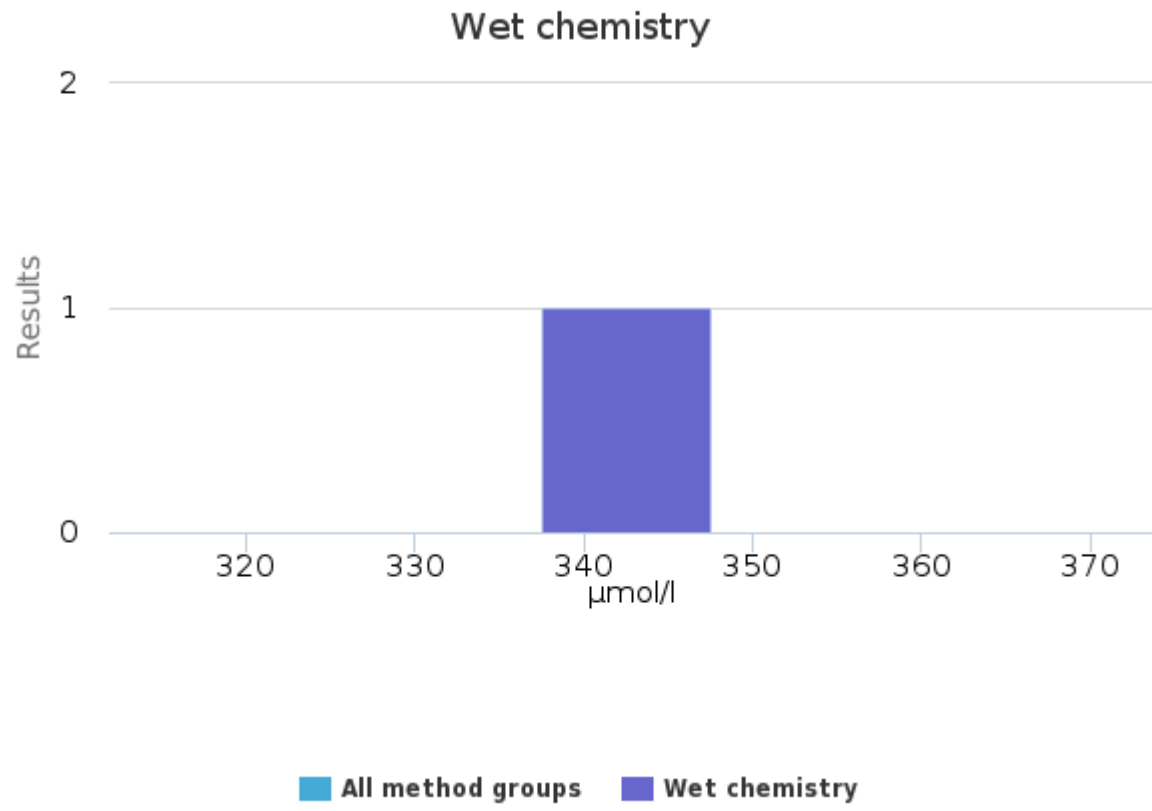| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Afinion	1.62	1.62	0.06	3.8	0.02	1.54	1.74	-	7
cobas b101	-	-	-	-	-	1.55	1.55	-	1
Spotchem	-	-	-	-	-	1.56	1.56	-	1
Wet chemistry	-	-	-	-	-	1.57	1.57	-	1
All	**1.60**	**1.59**	**0.06**	**3.6**	**0.02**	**1.54**	**1.74**	**-**	**10**

Sample S001 | Trigly, mmol/l| histogram summaries in LabScala
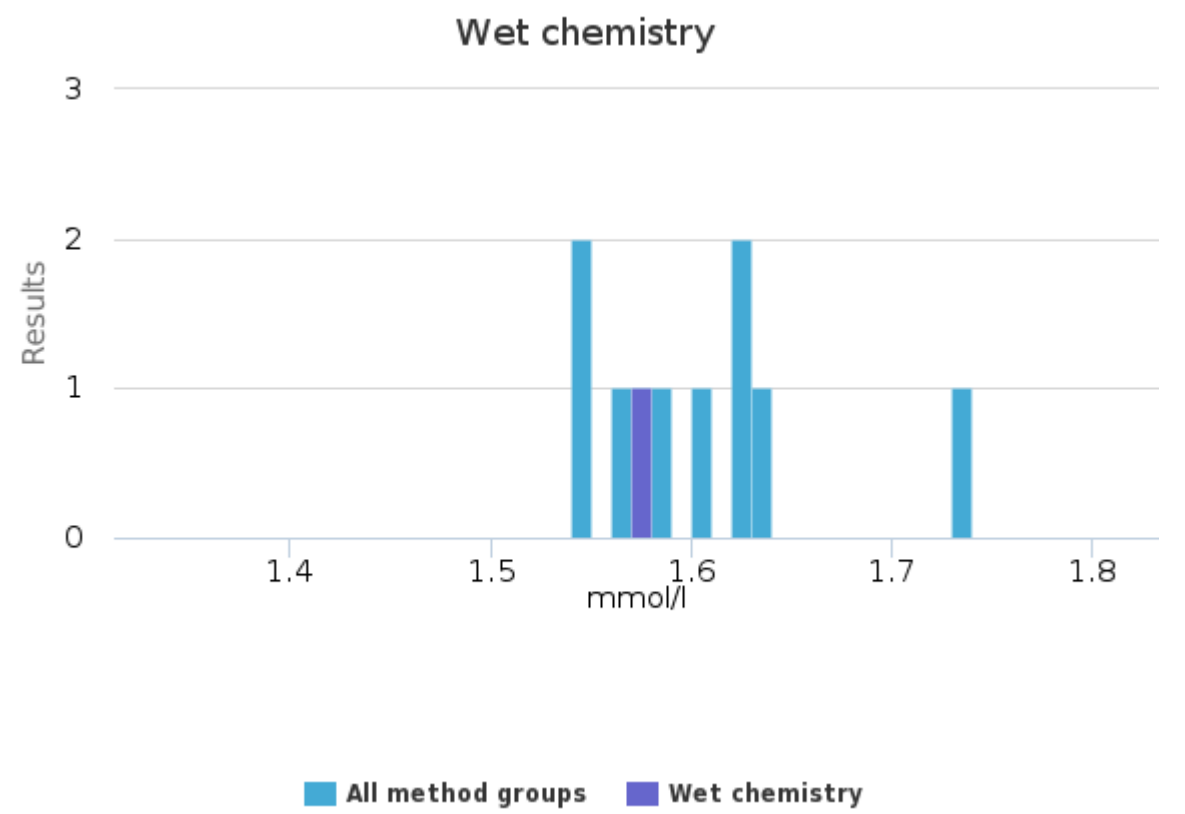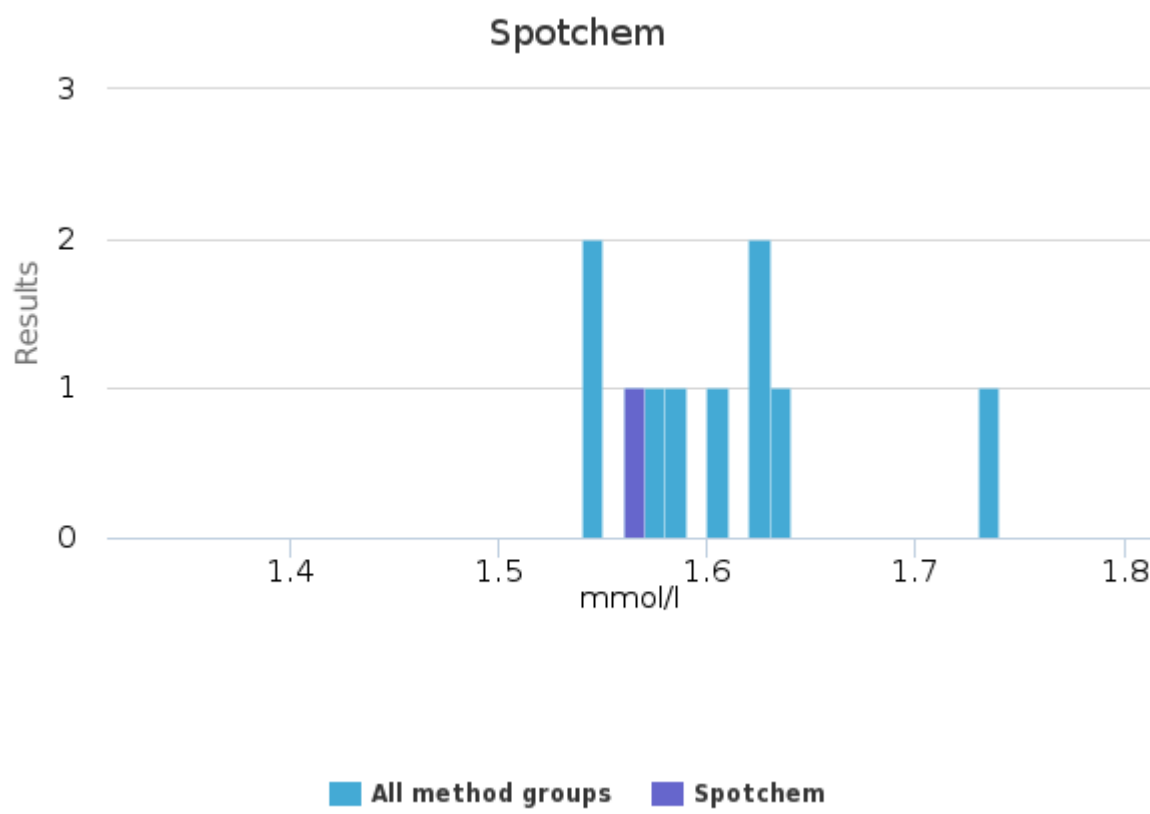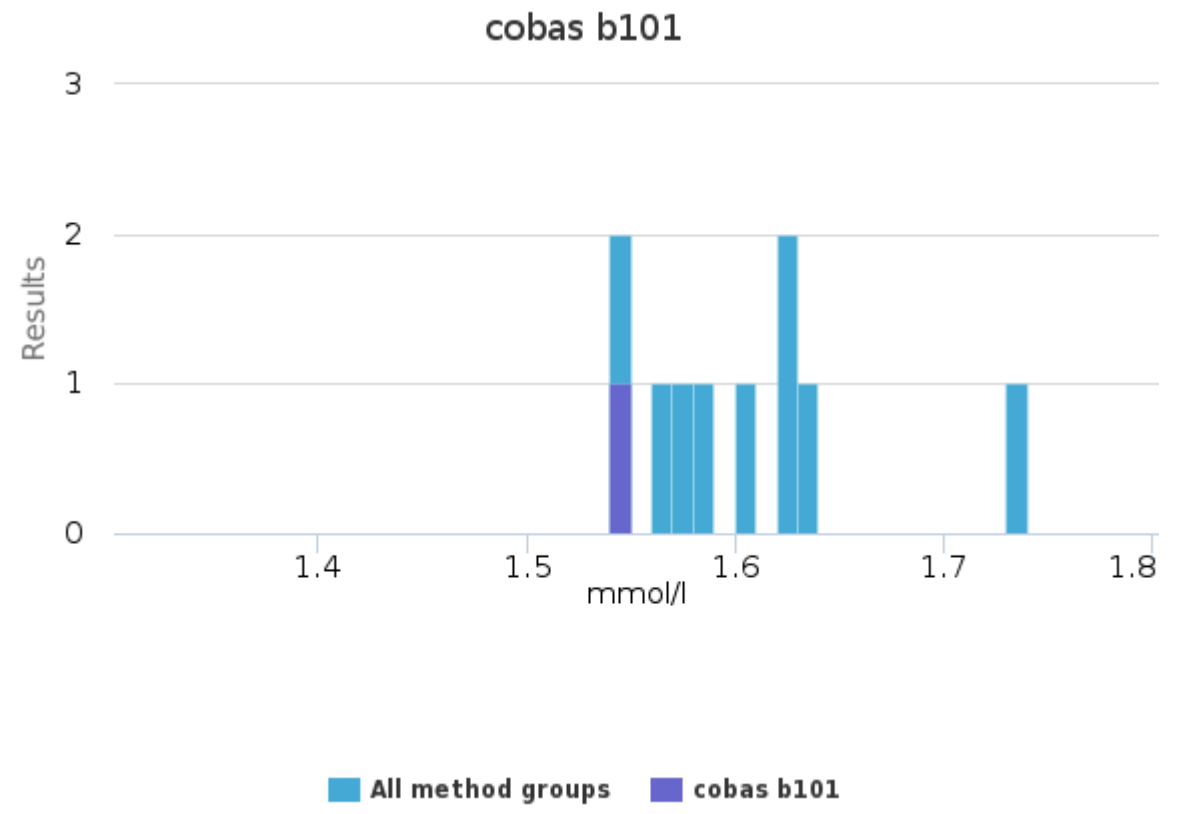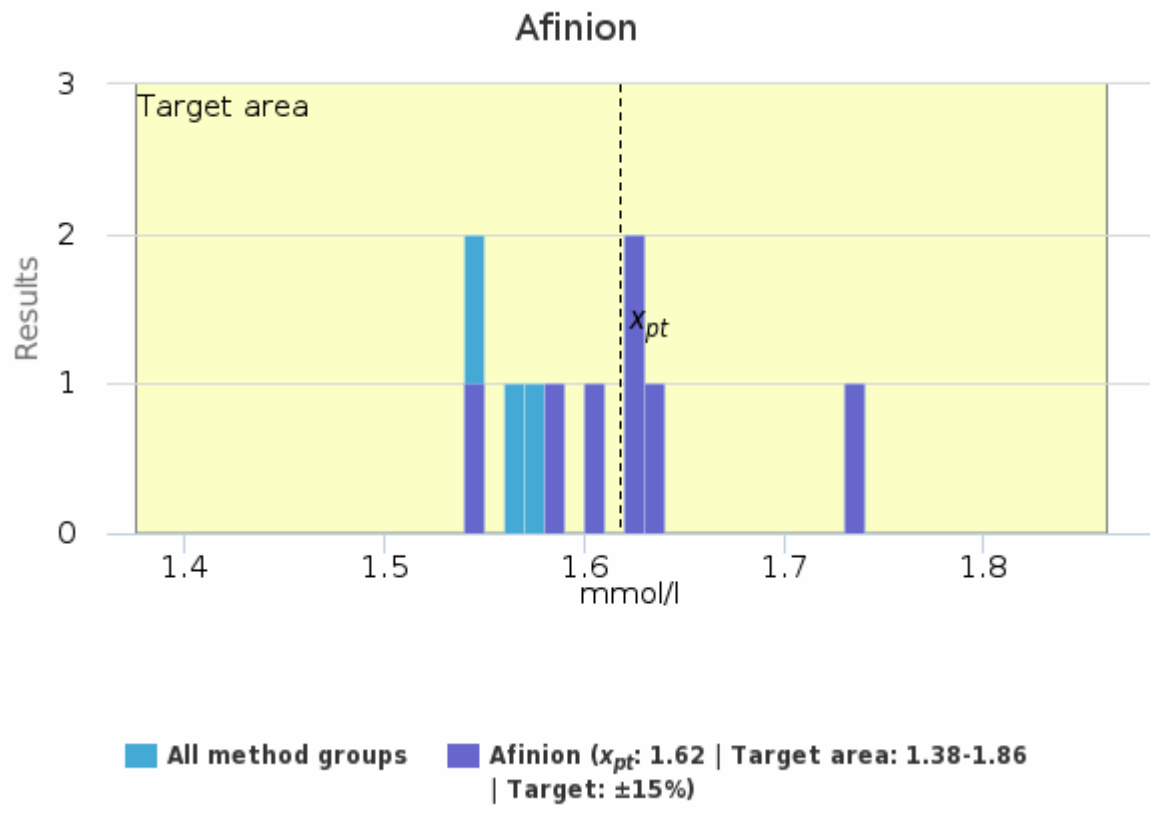
Sample S001 | Uric acid, µmol/l

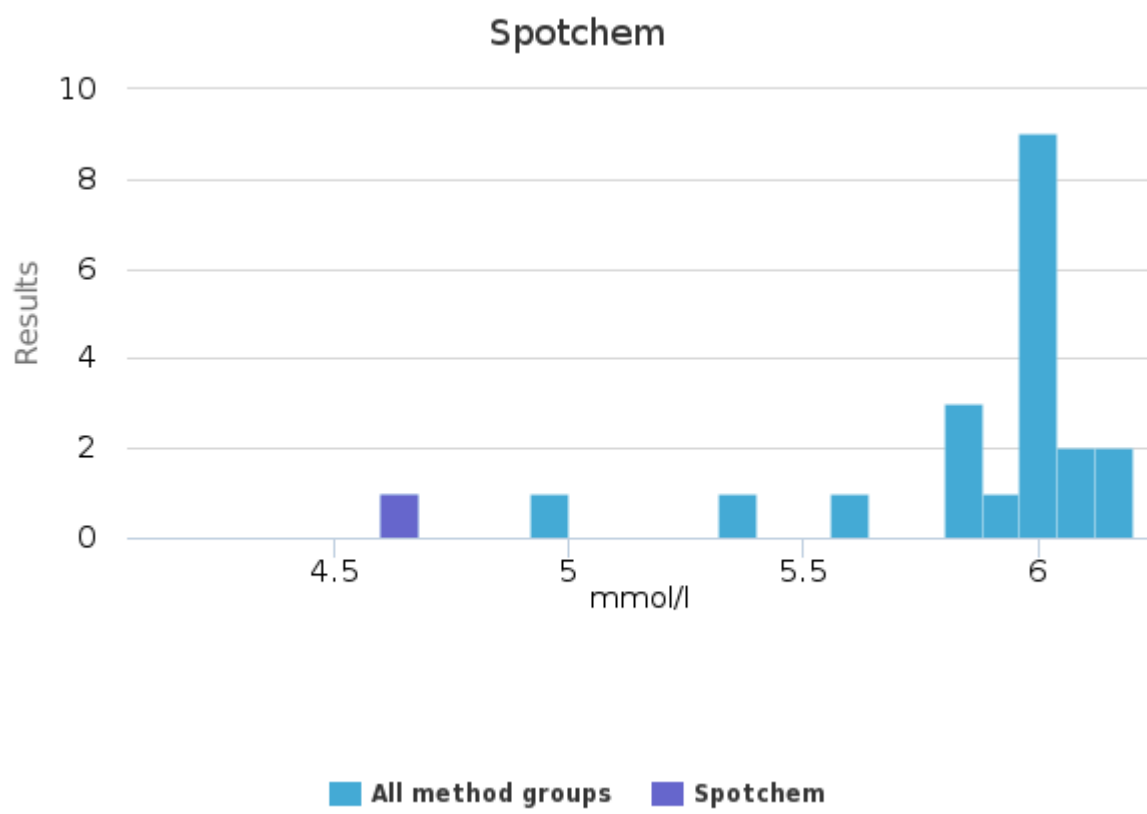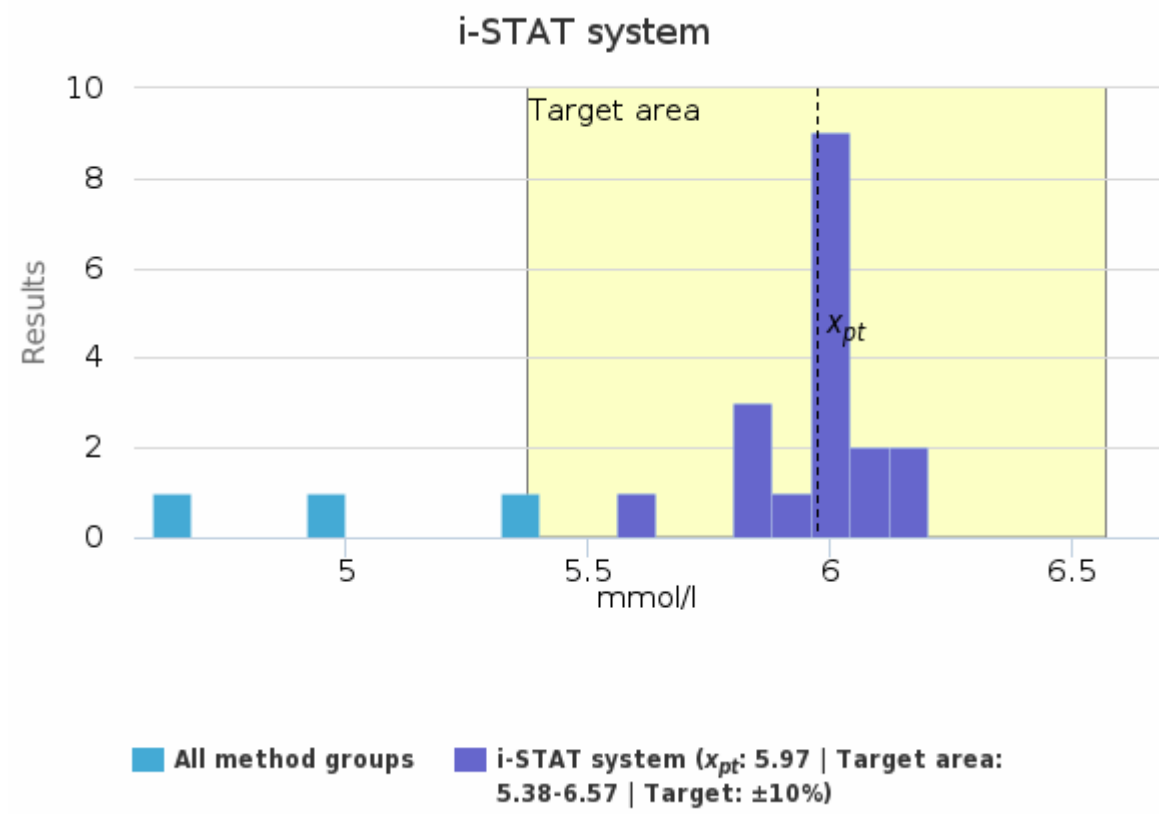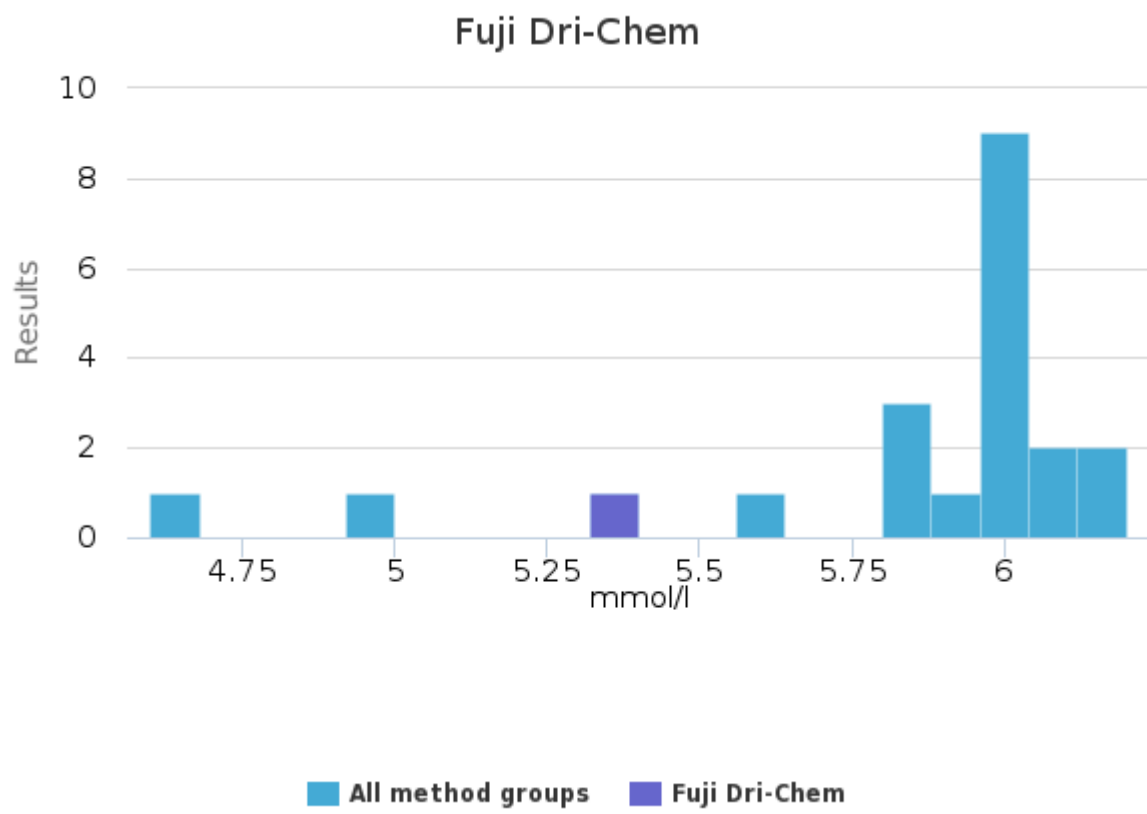| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	343	343	-	1
All	**-**	**-**	**-**	**-**	**-**	**343**	**343**	**-**	**1**

Sample S001 | Uric acid, µmol/l| histogram summaries in LabScala

Sample S001 | Urea, mmol/l

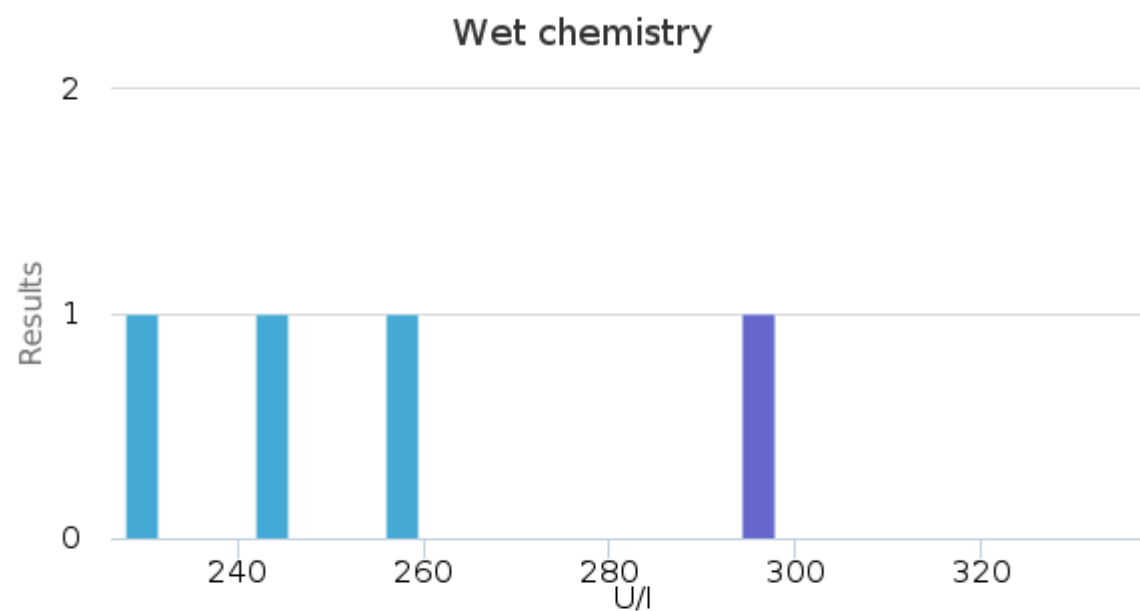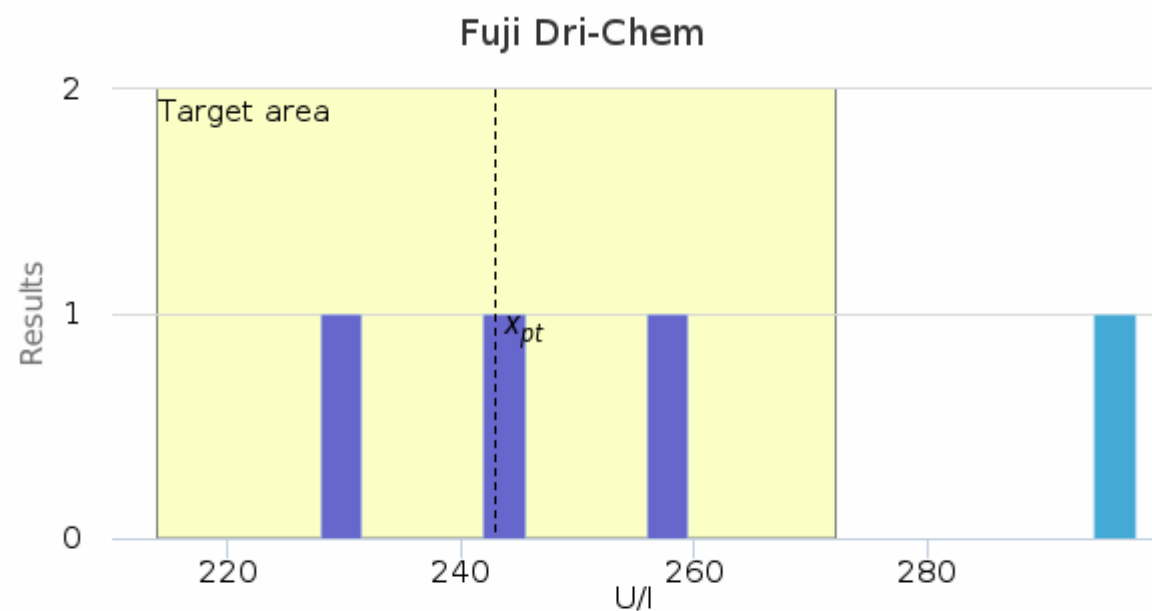| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	-	-	-	-	-	5.35	5.35	-	1
i-STAT system	5.97	6.00	0.15	2.5	0.04	5.60	6.20	-	18
Spotchem	-	-	-	-	-	4.60	4.60	-	1
Wet chemistry	-	-	-	-	-	4.97	4.97	-	1
All	**5.89**	**6.00**	**0.29**	**5.0**	**0.07**	**4.97**	**6.20**	**1**	**21**

Sample S001 | Urea, mmol/l| histogram summaries in LabScala
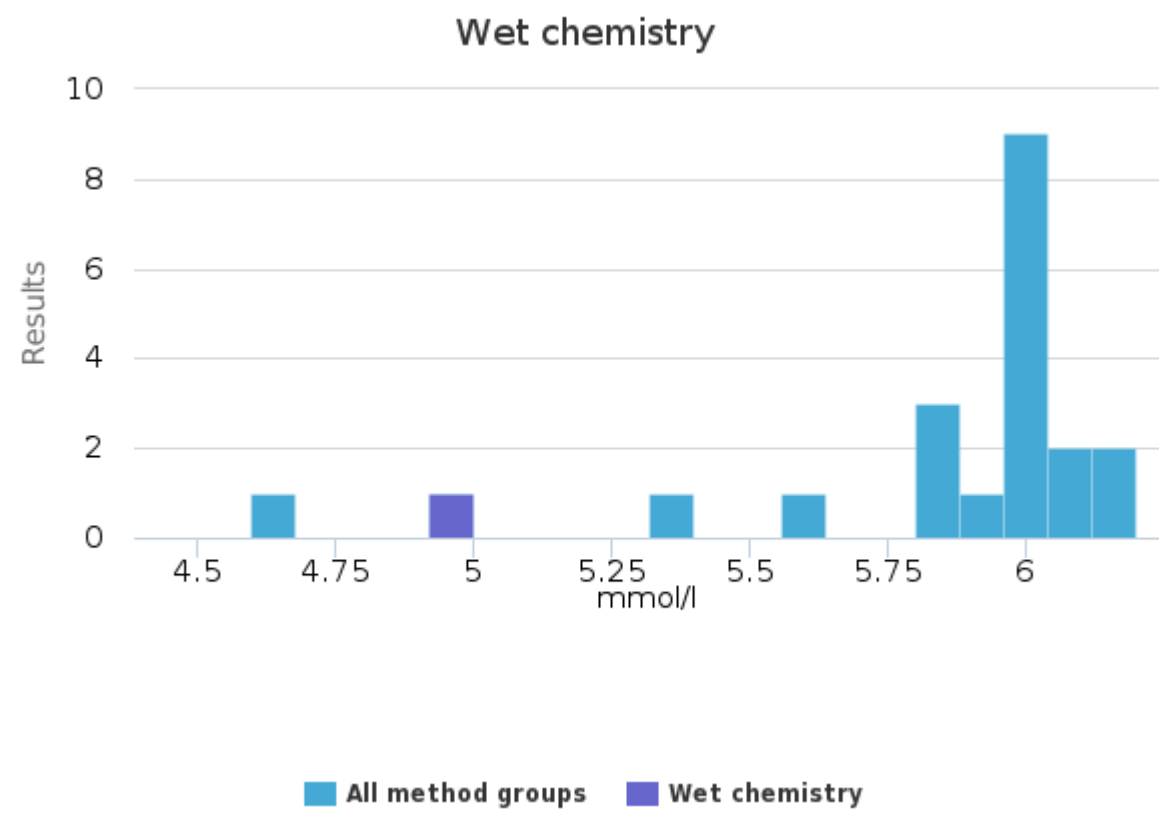
Sample S002 | ALP, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	243.00	244.00	14.53	6.0	8.39	228.00	257.00	-	3
Wet chemistry	-	-	-	-	-	297.89	297.89	-	1
All	**256.72**	**250.50**	**29.90**	**11.6**	**14.95**	**228.00**	**297.89**	**-**	**4**

Sample S002 | ALP, U/l| histogram summaries in LabScala

Sample S002 | ALT, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	124.67	125.00	2.52	2.0	1.45	122.00	127.00	-	3
Spotchem	-	-	-	-	-	114.00	114.00	-	1
Wet chemistry	-	-	-	-	-	113.73	113.73	-	1
All	**120.35**	**122.00**	**6.18**	**5.1**	**2.76**	**113.73**	**127.00**	**-**	**5**

Sample S002 | ALT, U/l| histogram summaries in LabScala
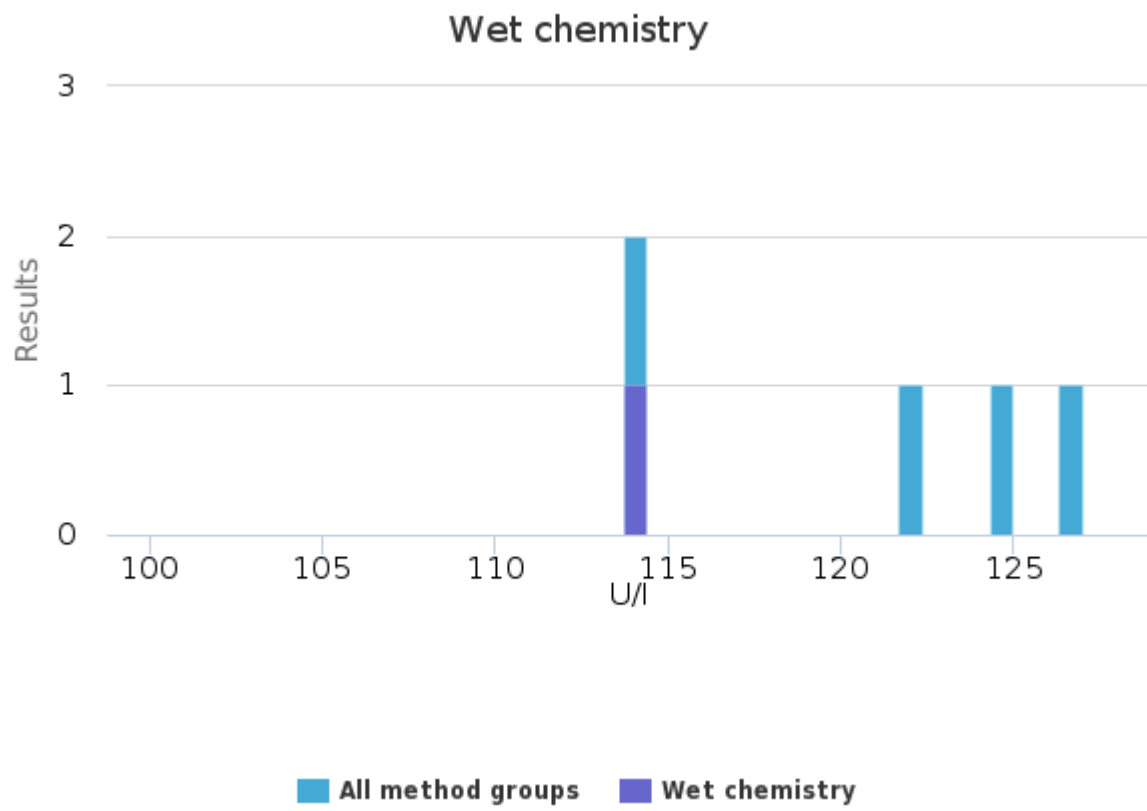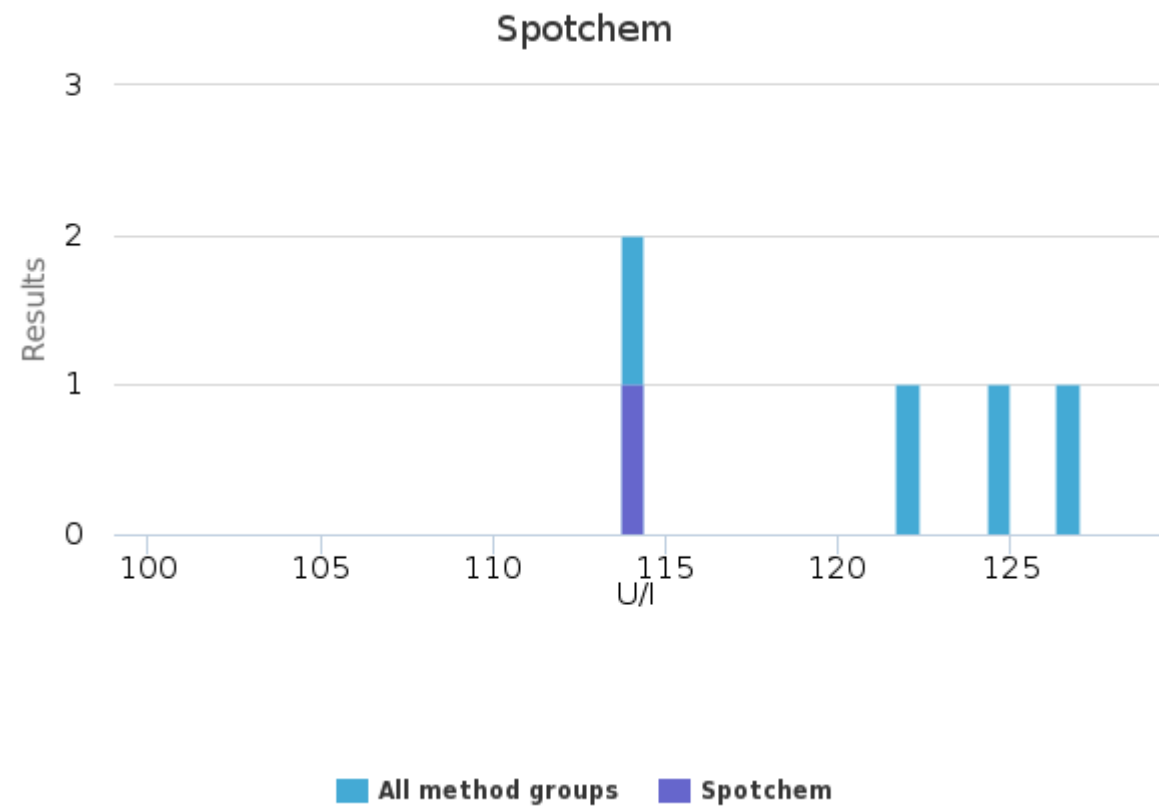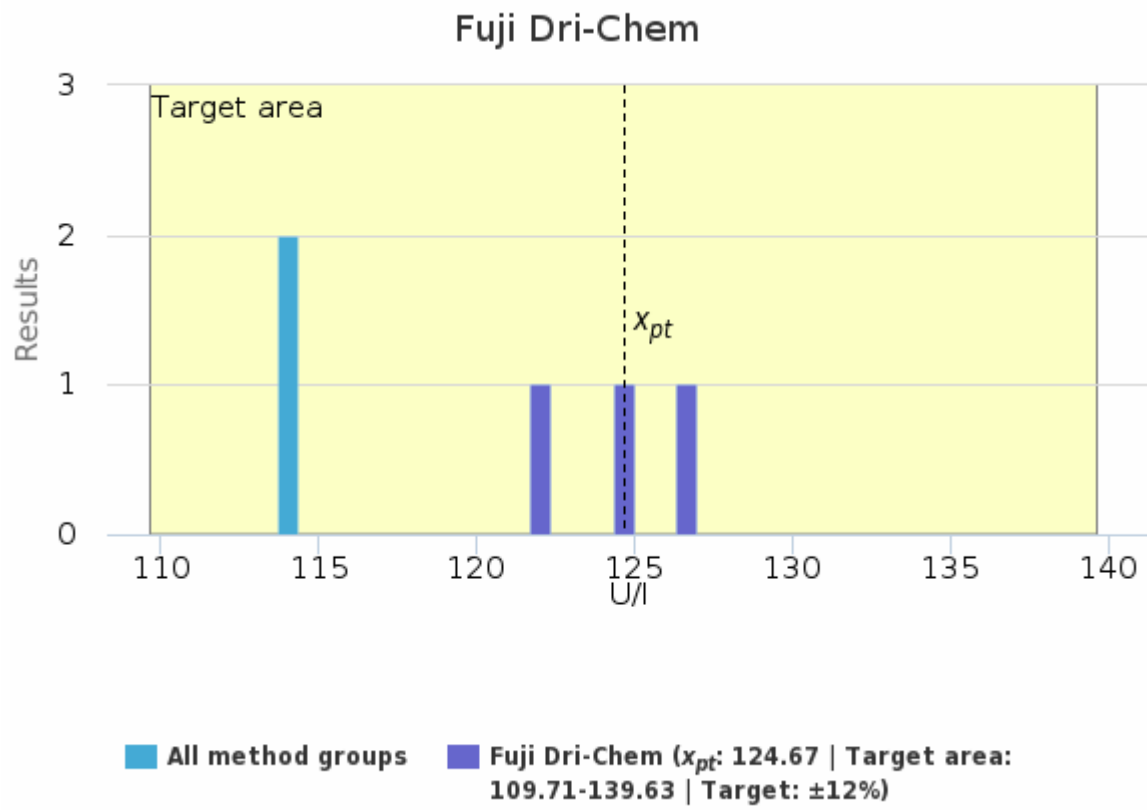
Sample S002 | Alb, g/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	51.61	51.61	-	1
All	**-**	**-**	**-**	**-**	**-**	**51.61**	**51.61**	**-**	**1**

Sample S002 | Alb, g/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	51.61	51.61	-	1
All	**-**	**-**	**-**	**-**	**-**	**51.61**	**51.61**	**-**	**1**
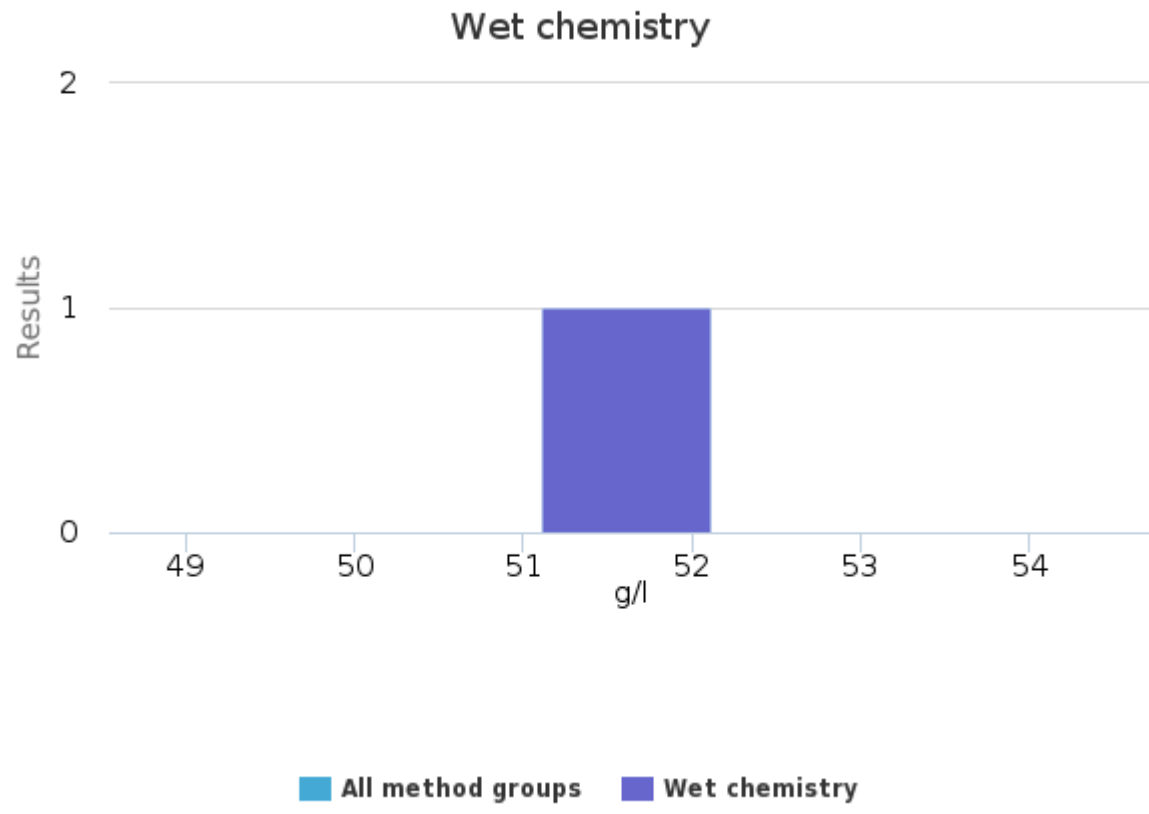
Sample S002 | Amyl, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	282.00	281.00	4.58	1.6	2.65	278.00	287.00	-	3
Wet chemistry	-	-	-	-	-	389.13	389.13	-	1
All	**308.78**	**284.00**	**53.70**	**17.4**	**26.85**	**278.00**	**389.13**	**-**	**4**

Sample S002 | Amyl, U/l| histogram summaries in LabScala
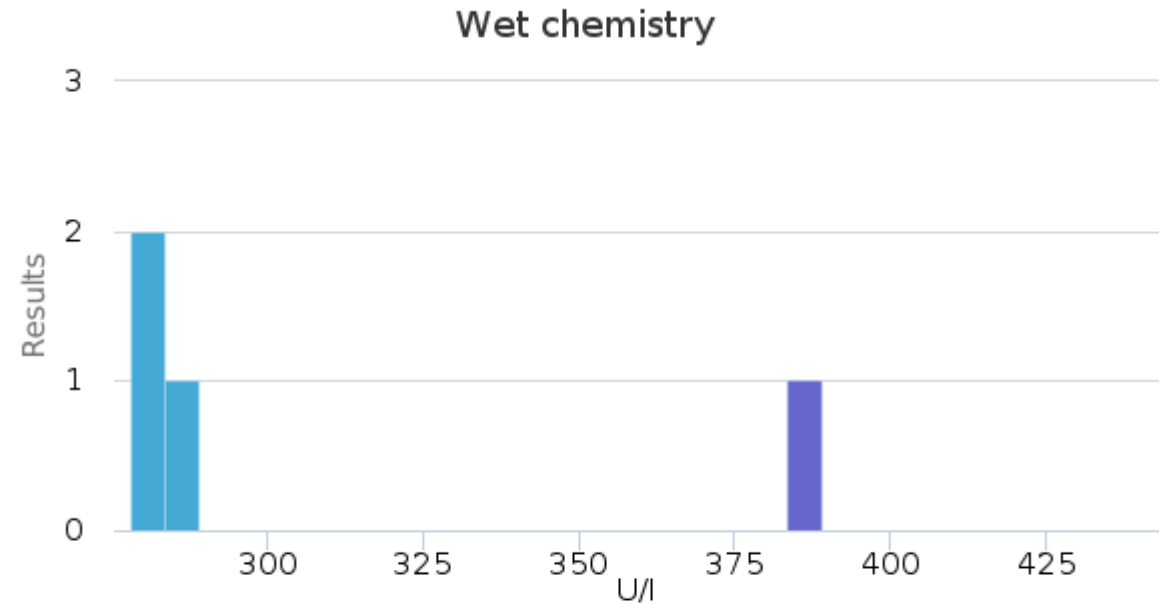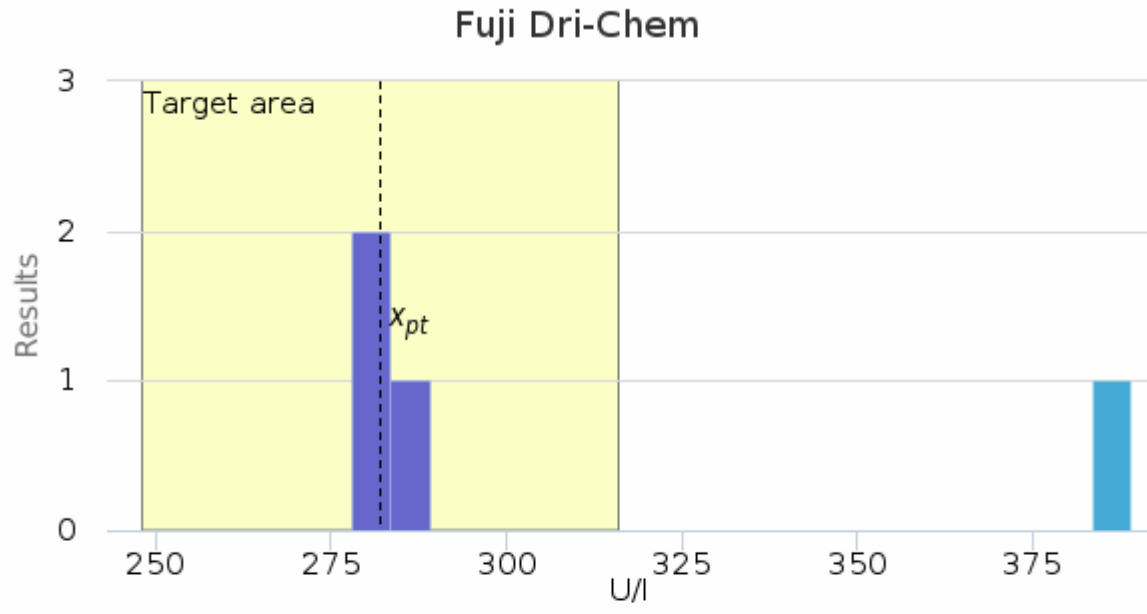
Sample S002 | AST, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	197.00	196.00	4.58	2.3	2.65	193.00	202.00	-	3
Spotchem	-	-	-	-	-	188.00	188.00	-	1
Wet chemistry	-	-	-	-	-	209.84	209.84	-	1
All	**197.77**	**196.00**	**8.44**	**4.3**	**3.77**	**188.00**	**209.84**	**-**	**5**

Sample S002 | AST, U/l| histogram summaries in LabScala

Fuji Dri-Chem

- All method groups
- Fuji Dri-Chem (x_{pt}: 197.00 | Target area: 173.36-220.64 | Target: ±12%)

Spotchem

- All method groups
- Spotchem

Wet chemistry

- All method groups
- Wet chemistry
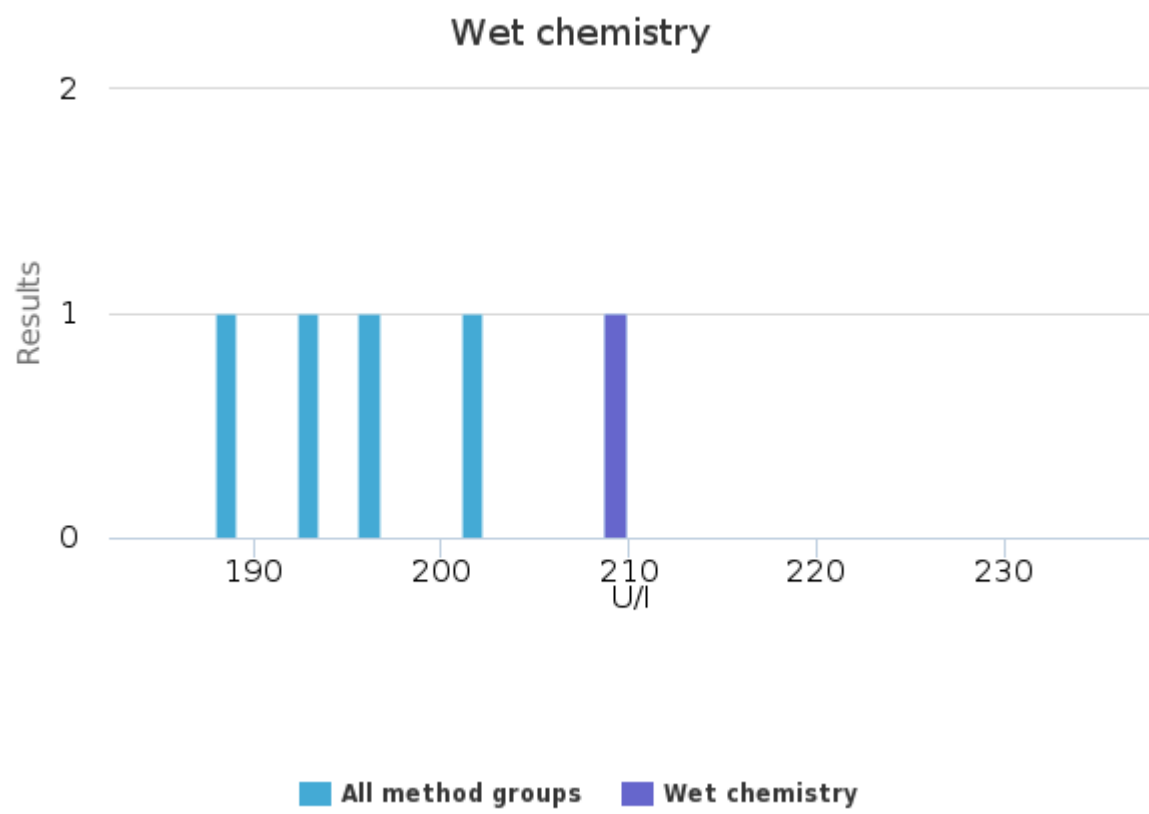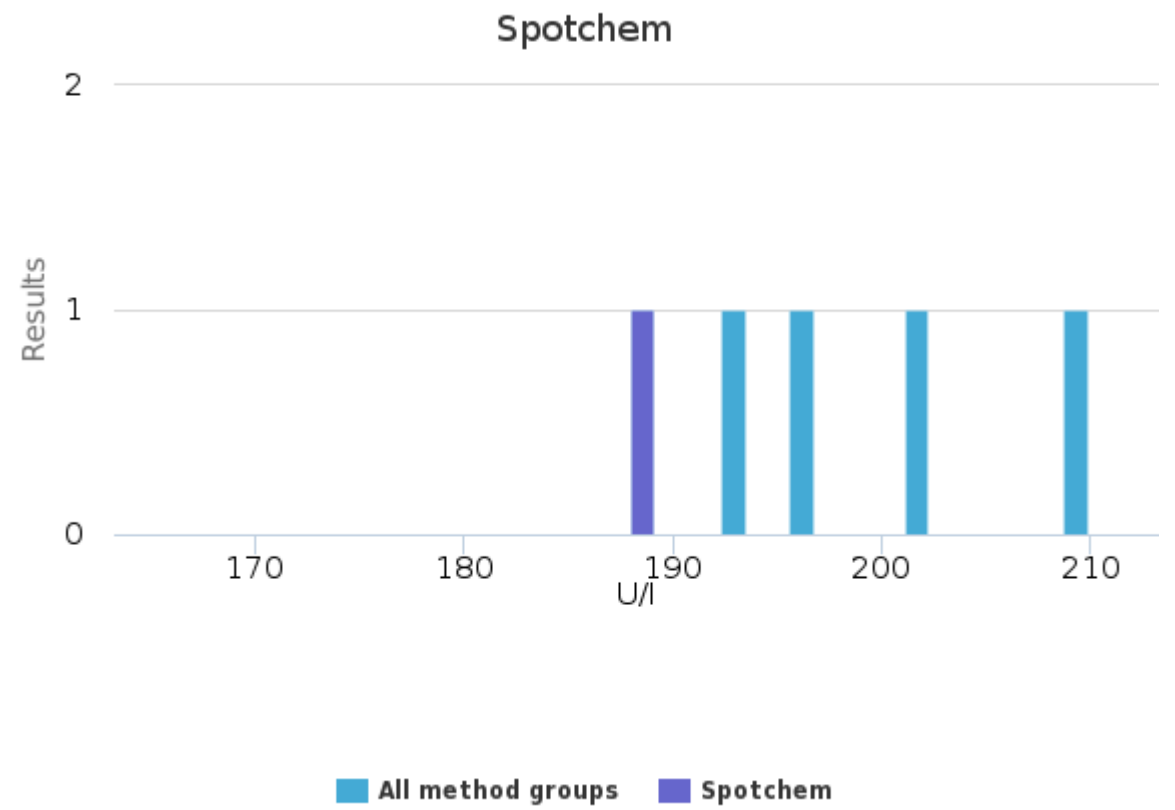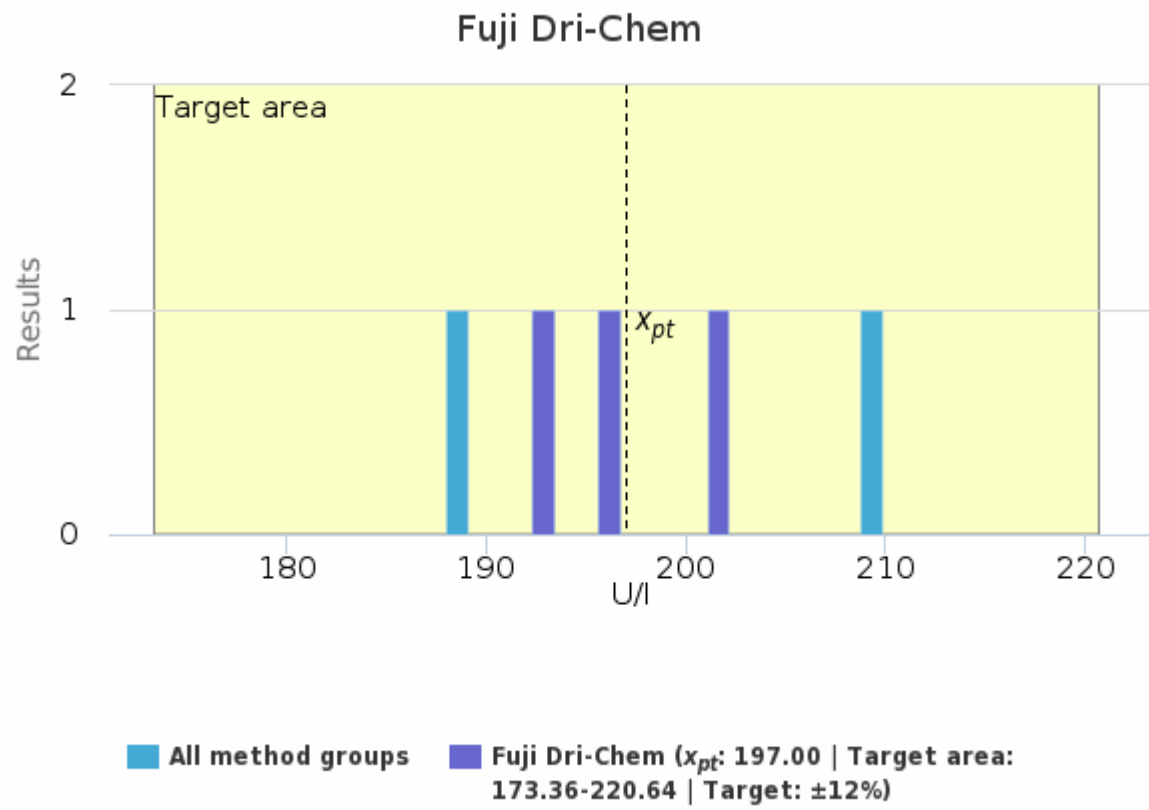
Sample S002 | Ca, mmol/l

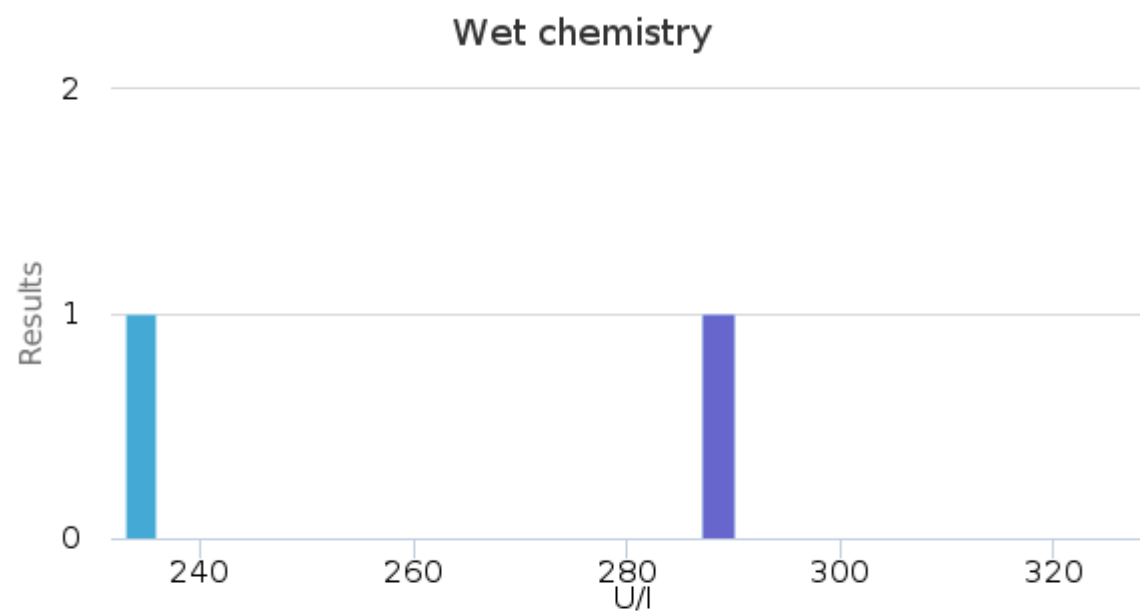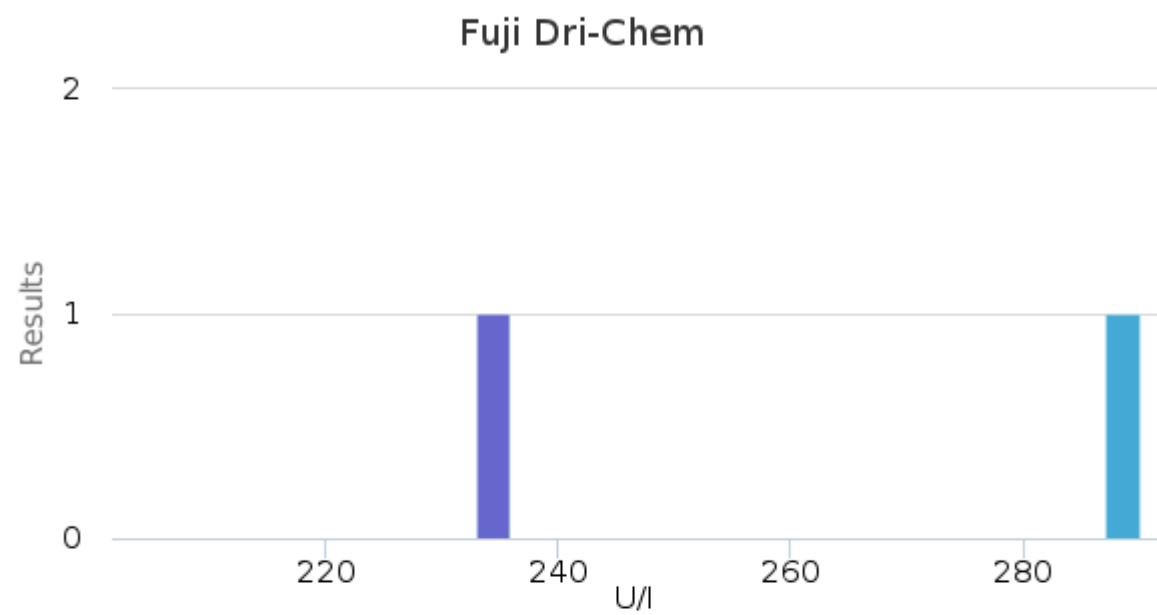| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	3.09	3.09	-	1
All	**-**	**-**	**-**	**-**	**-**	**3.09**	**3.09**	**-**	**1**

Sample S002 | Ca, mmol/l| histogram summaries in LabScala
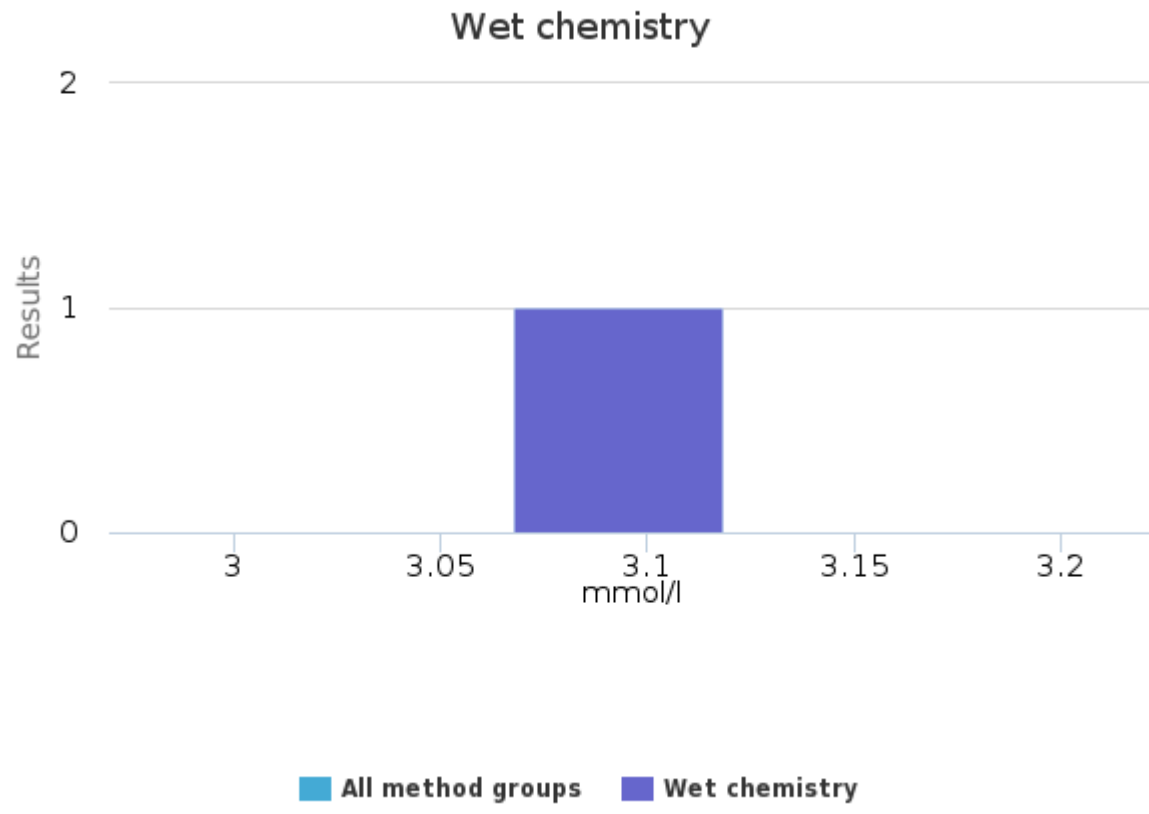
Sample S002 | CK, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	-	-	-	-	-	233.00	233.00	-	1
Wet chemistry	-	-	-	-	-	290.00	290.00	-	1
All	**261.50**	**261.50**	**40.31**	**15.4**	**28.50**	**233.00**	**290.00**	**-**	**2**

Sample S002 | CK, U/l| histogram summaries in LabScala

Sample S002 | Cl, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	-	-	-	-	-	140.0	140.0	-	1
Spotchem	-	-	-	-	-	171.0	171.0	-	1
All	**155.5**	**155.5**	**21.9**	**14.1**	**15.5**	**140.0**	**171.0**	**-**	**2**

Sample S002 | Cl, mmol/l| histogram summaries in LabScala
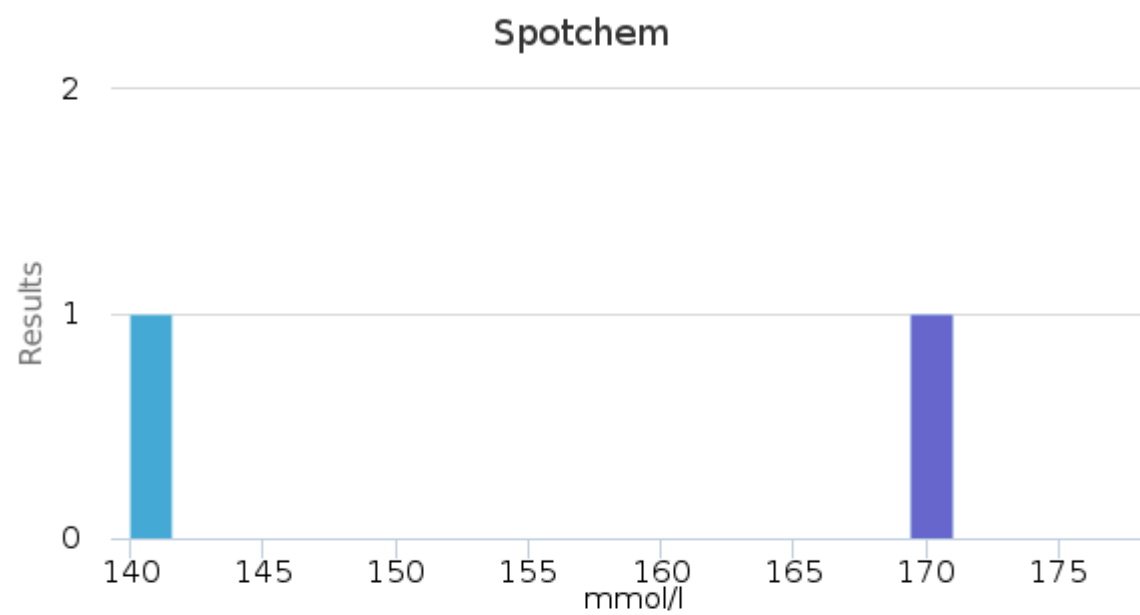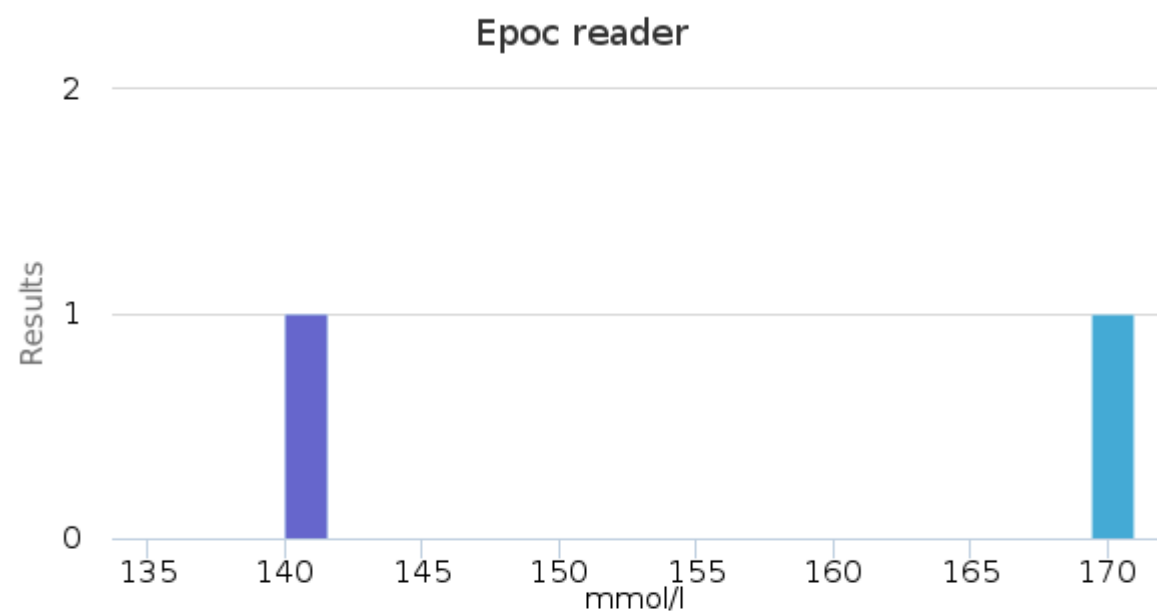
Sample S002 | Glucose, mmol/l
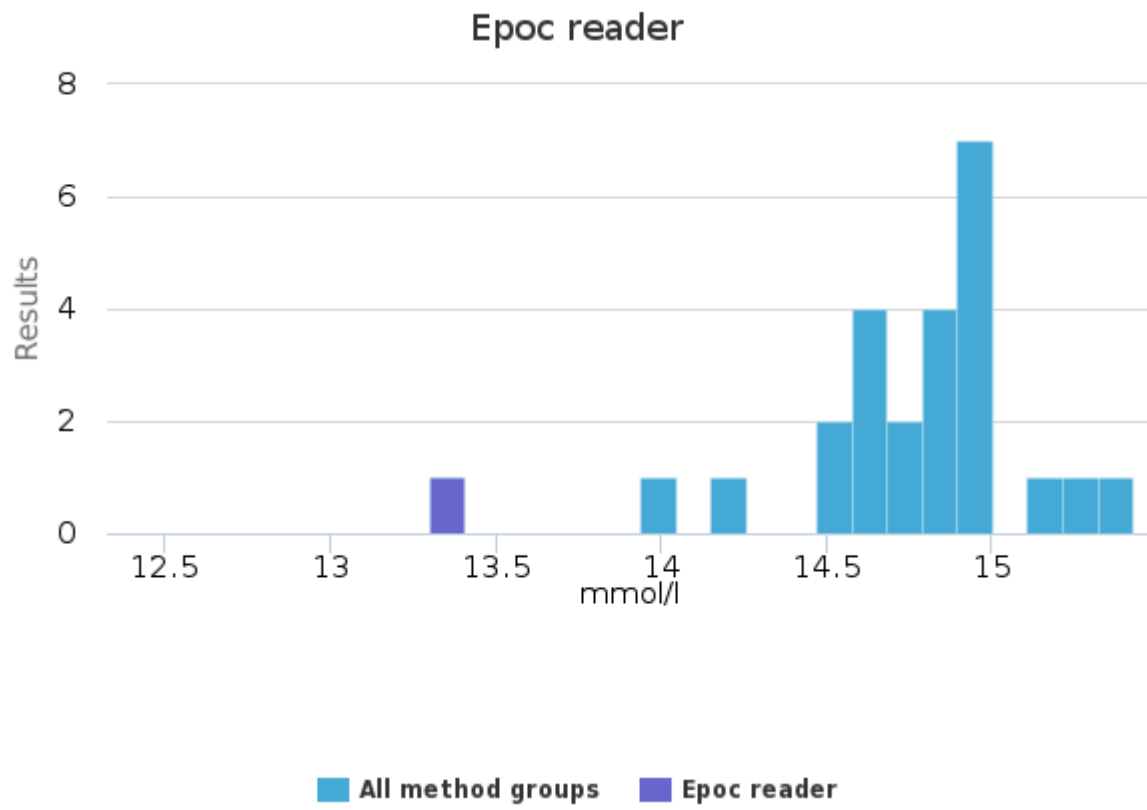
Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	-	-	-	-	-	13.30	13.30	-	1
Fuji Dri-Chem	-	-	-	-	-	15.30	15.30	-	1
i-STAT system	14.73	14.80	0.28	1.9	0.06	14.00	15.20	-	22
Wet chemistry	-	-	-	-	-	15.43	15.43	-	1
All	**14.78**	**14.80**	**0.32**	**2.2**	**0.07**	**14.00**	**15.43**	**1**	**25**

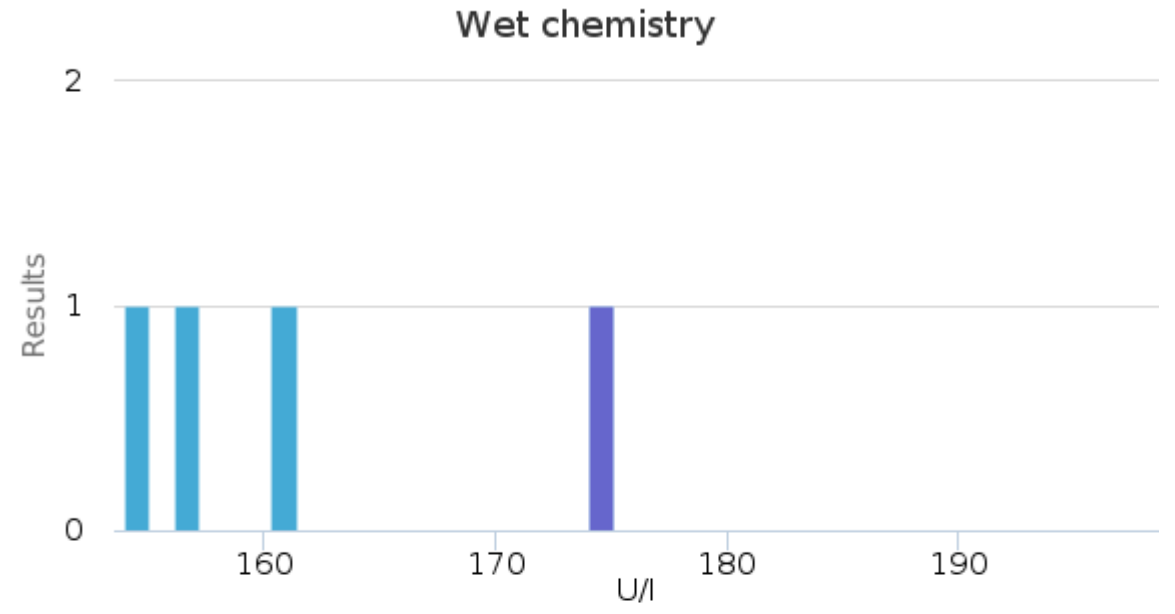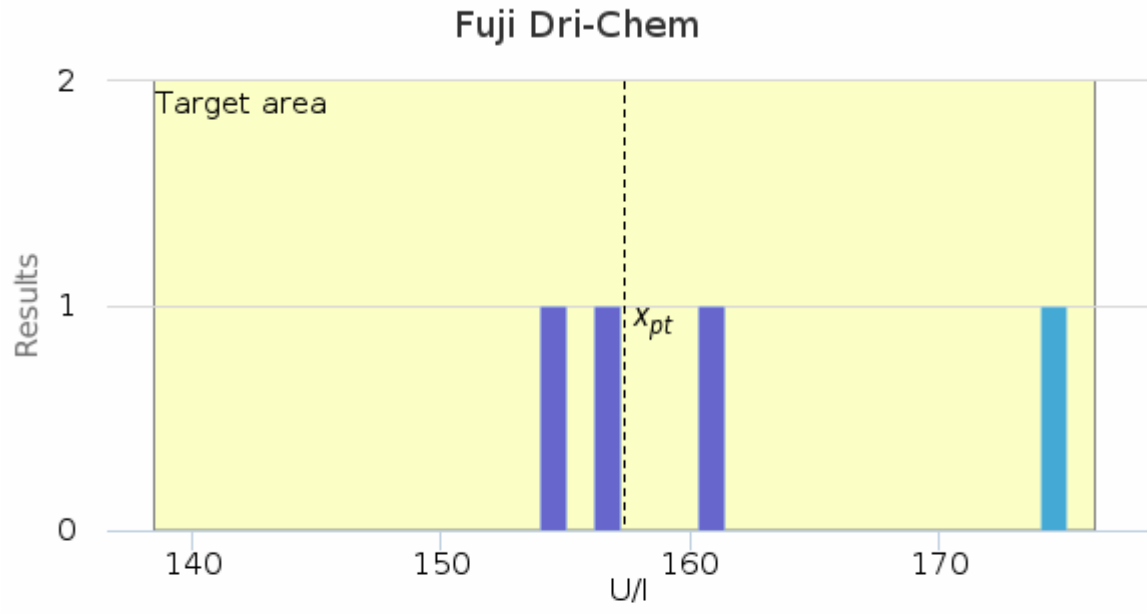**Sample S002 | Glucose, mmol/l| histogram summaries in LabScala**
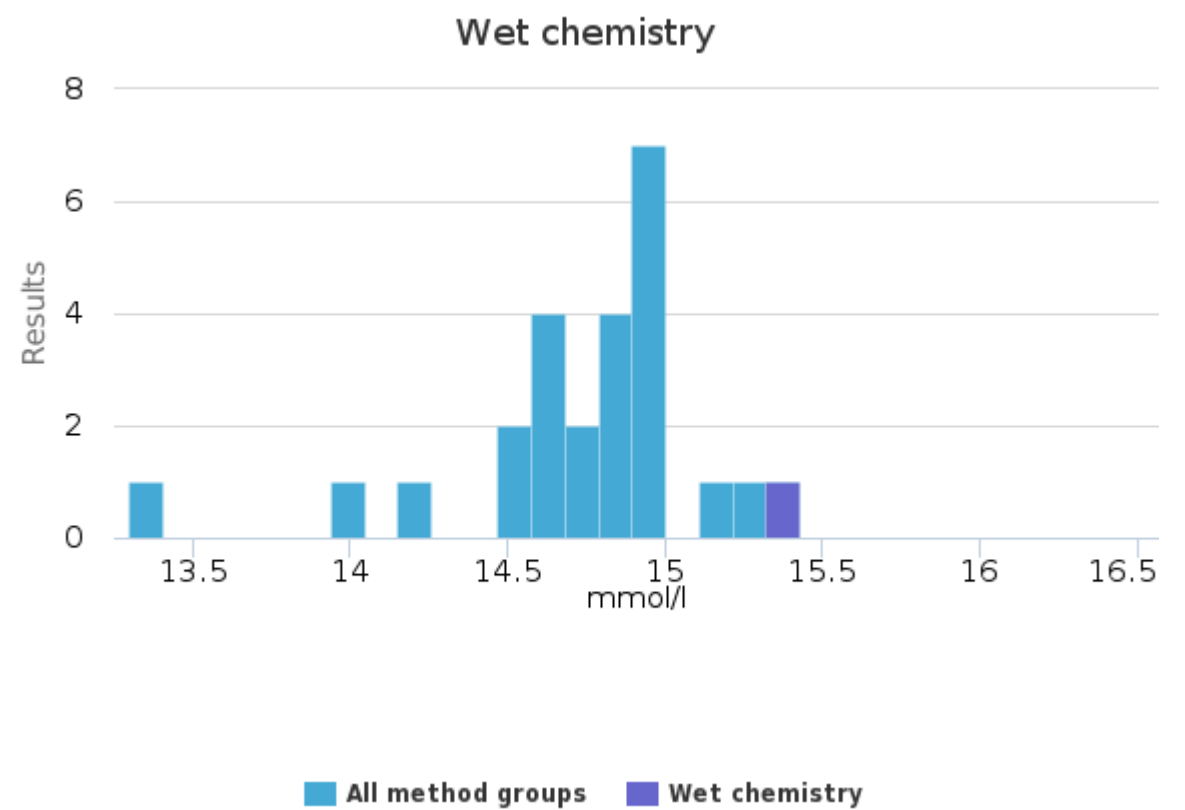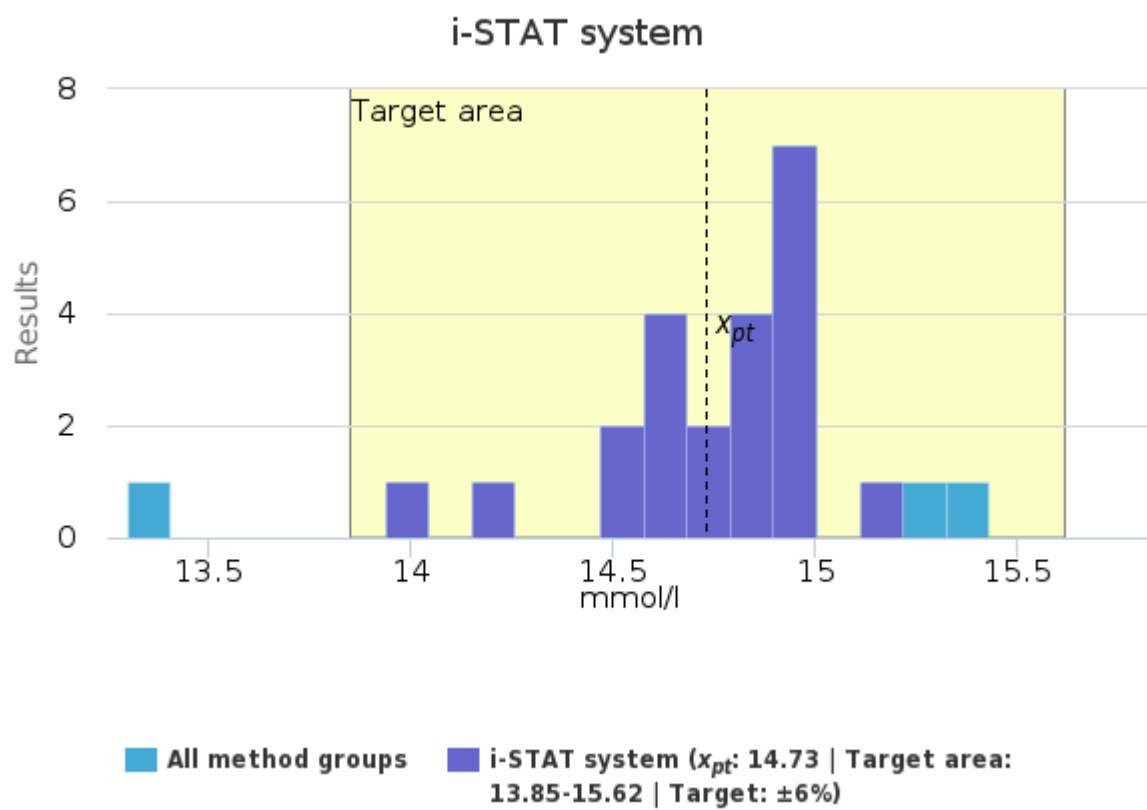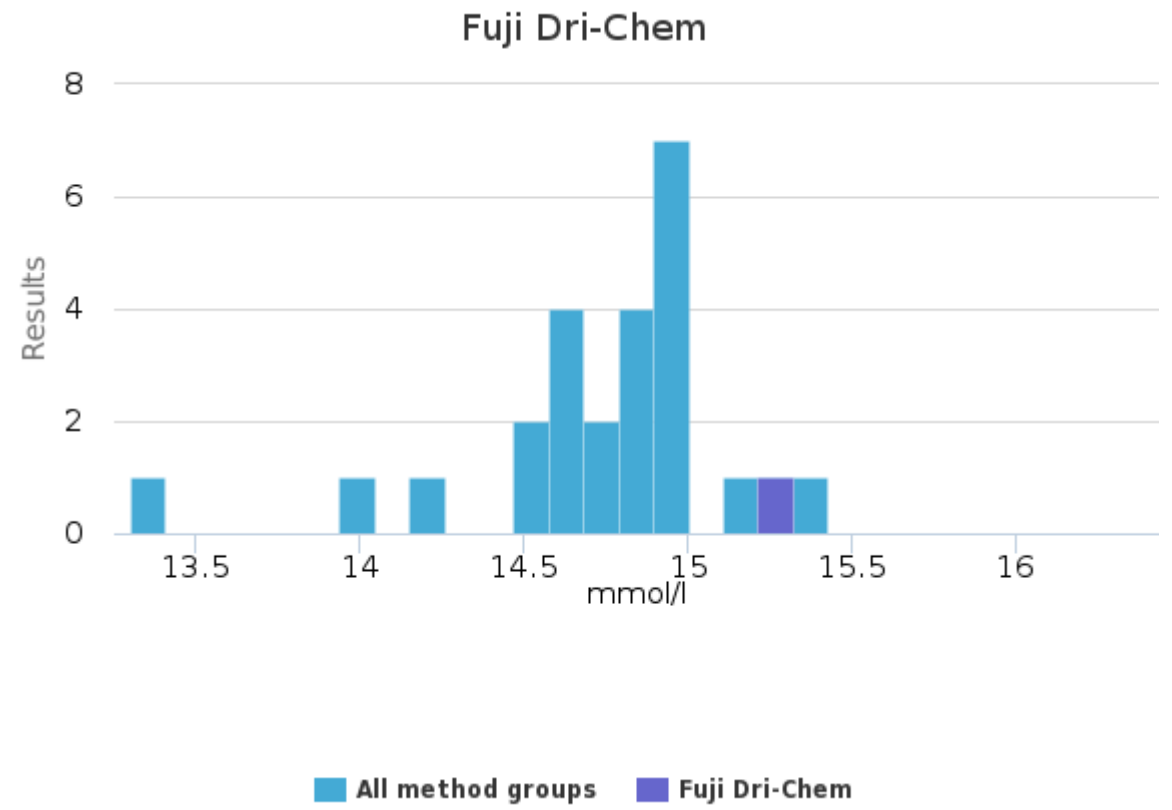
Sample S002 | GT, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	157.33	157.00	3.51	2.2	2.03	154.00	161.00	-	3
Wet chemistry	-	-	-	-	-	175.13	175.13	-	1
All	**161.78**	**159.00**	**9.35**	**5.8**	**4.67**	**154.00**	**175.13**	**-**	**4**

Sample S002 | GT, U/l| histogram summaries in LabScala

Sample S002 | K, mmol/l

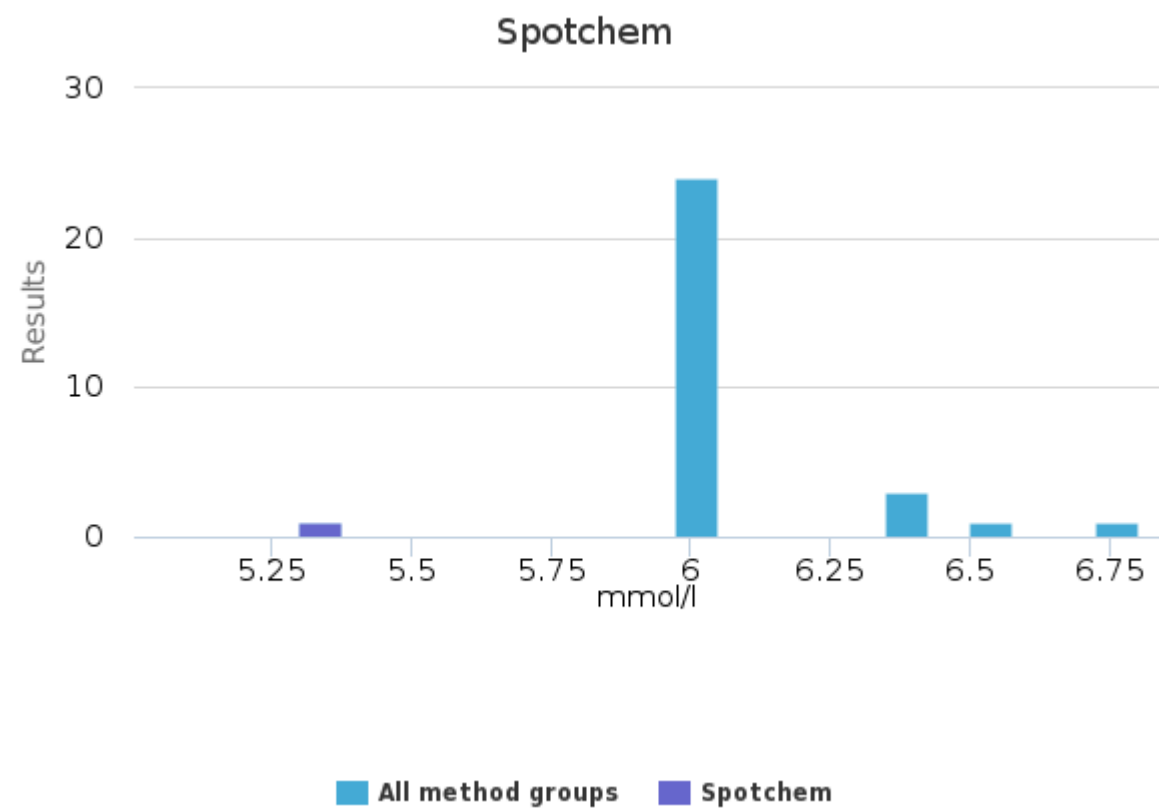| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	6.65	6.65	0.21	3.2	0.15	6.50	6.80	-	2
Fuji Dri-Chem	6.40	6.40	<0.01	<0.1	<0.01	6.40	6.40	-	3
i-STAT system	6.00	6.00	<0.01	<0.1	<0.01	6.00	6.00	-	23
Spotchem	-	-	-	-	-	5.30	5.30	-	1
Wet chemistry	-	-	-	-	-	5.98	5.98	-	1
All	**6.03**	**6.00**	**0.21**	**3.4**	**0.04**	**5.30**	**6.50**	**1**	**30**

Sample S002 | K, mmol/l| histogram summaries in LabScala
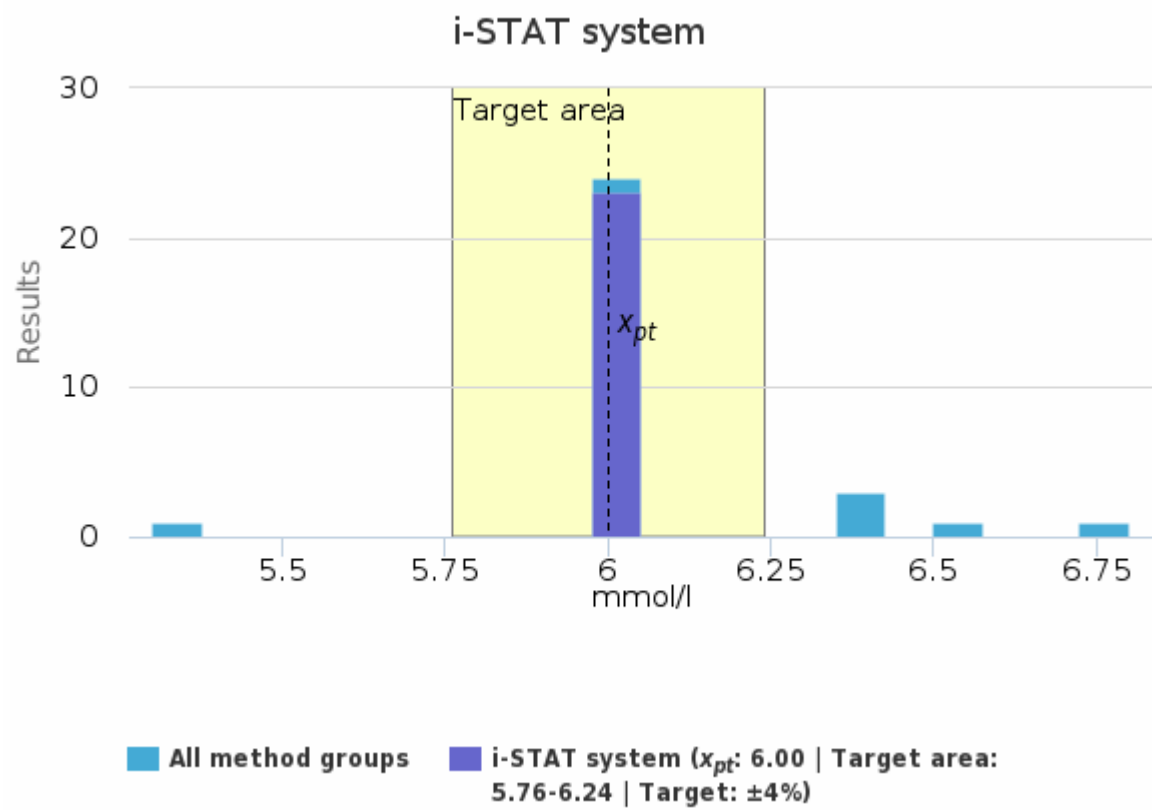
Wet chemistry

Legend: All method groups ■ Wet chemistry ■
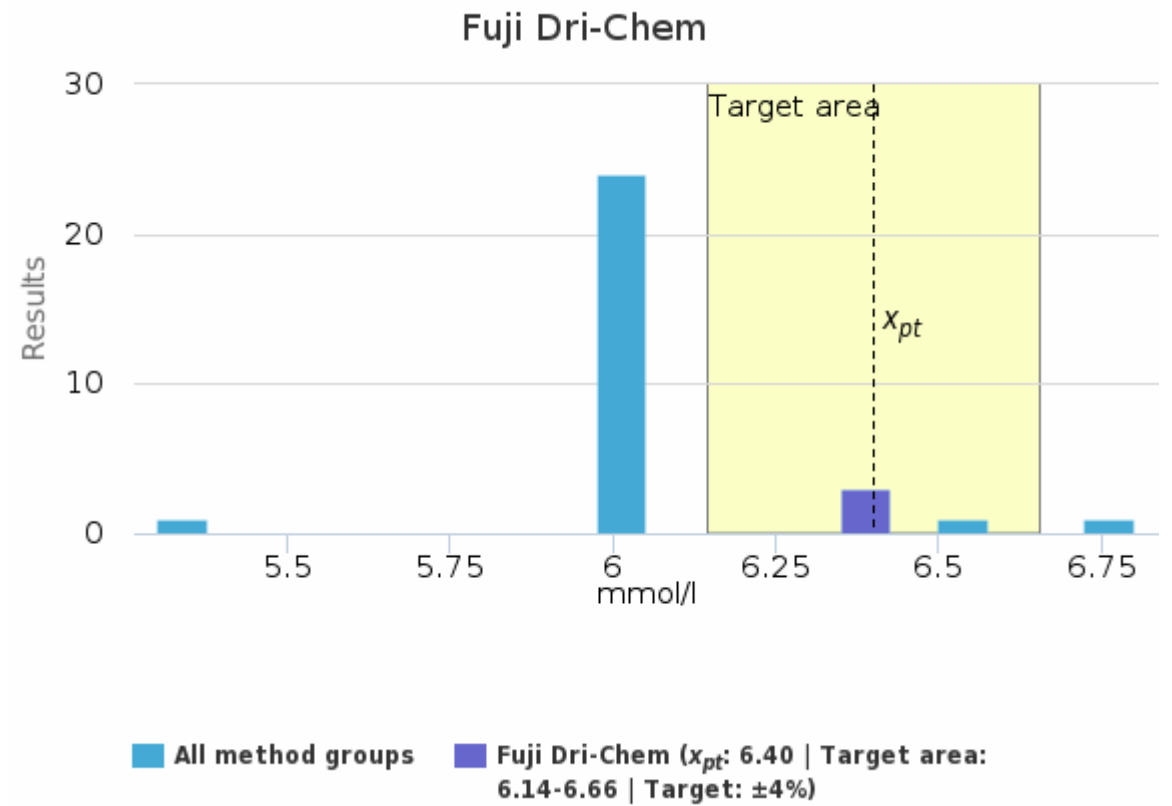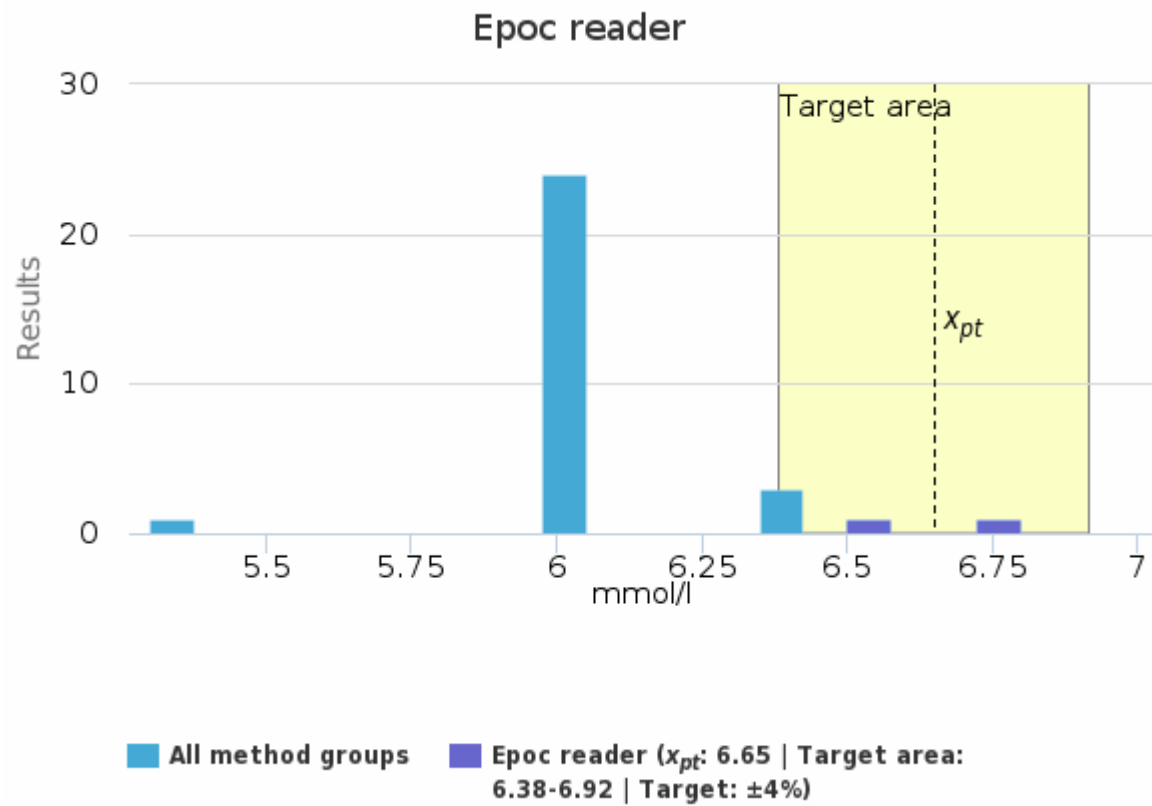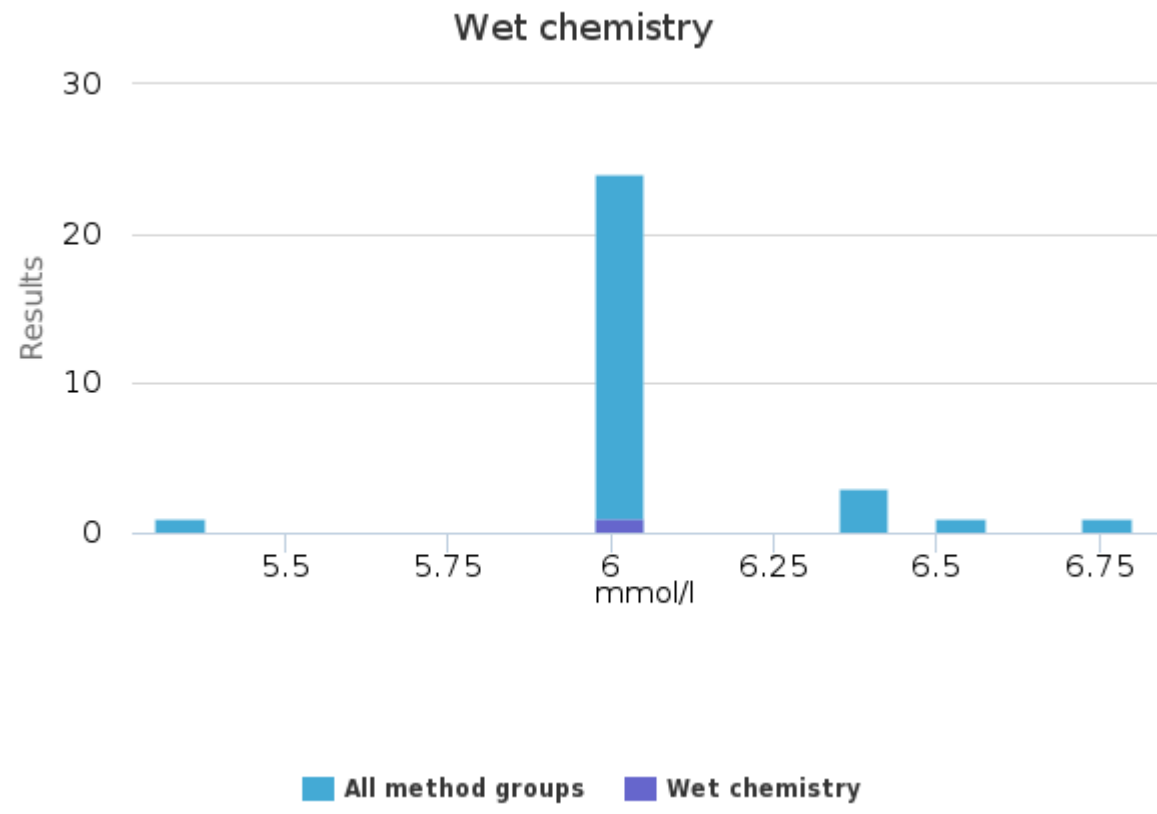
Sample S002 | Chol, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Accutrend	5.65	5.65	0.39	6.9	0.28	5.37	5.92	-	2
Afinion	5.69	5.70	0.17	3.1	0.07	5.41	5.93	-	7
cobas b101	-	-	-	-	-	5.12	5.12	-	1
Spotchem	-	-	-	-	-	5.00	5.00	-	1
Wet chemistry	-	-	-	-	-	5.13	5.13	-	1
All	**5.53**	**5.62**	**0.32**	**5.8**	**0.09**	**5.00**	**5.93**	**-**	**12**

Sample S002 | Chol, mmol/l| histogram summaries in LabScala
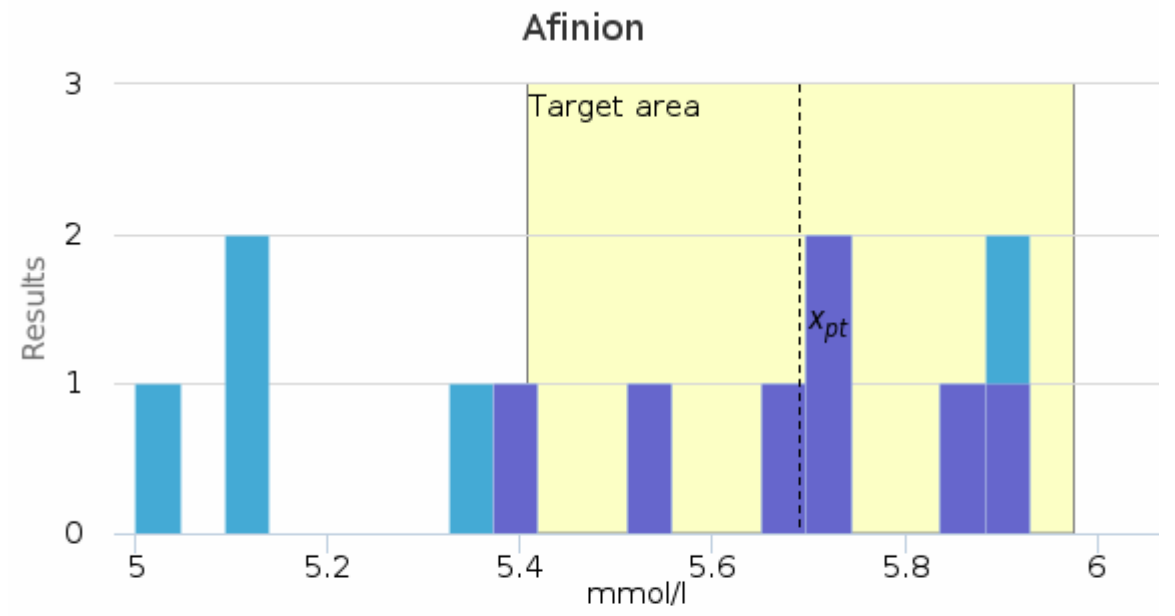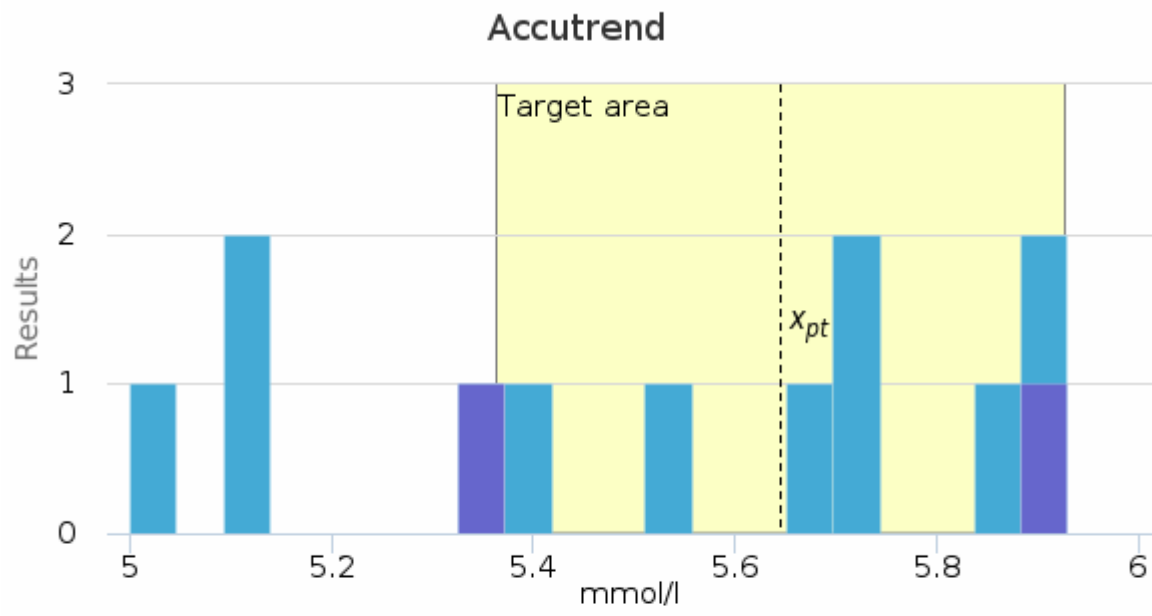
Wet chemistry

Results

mmol/l

■ All method groups ■ Wet chemistry
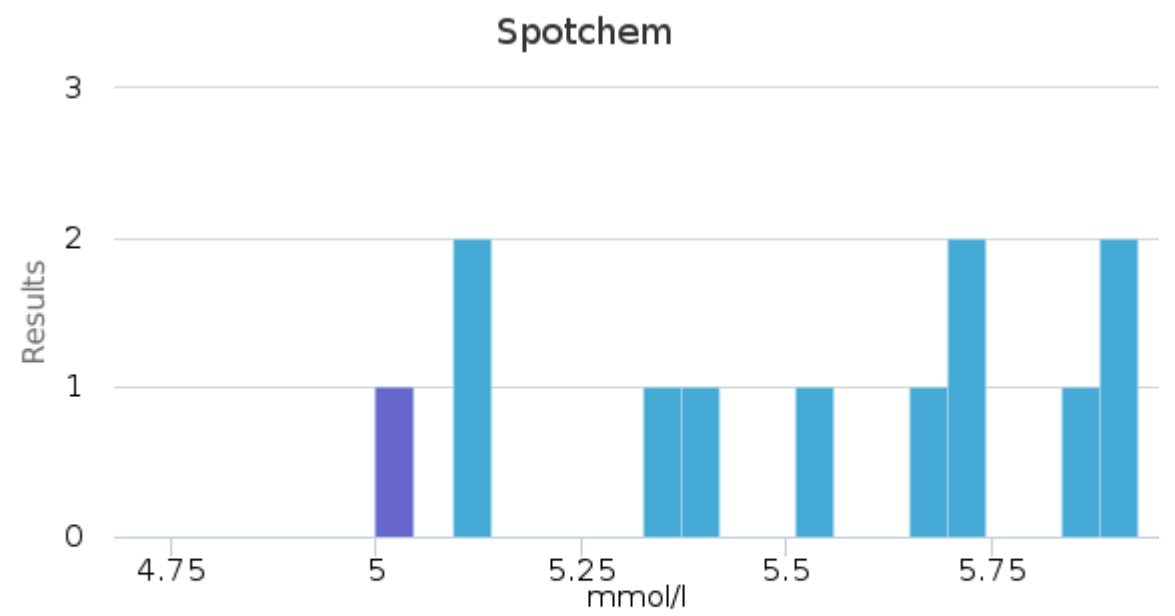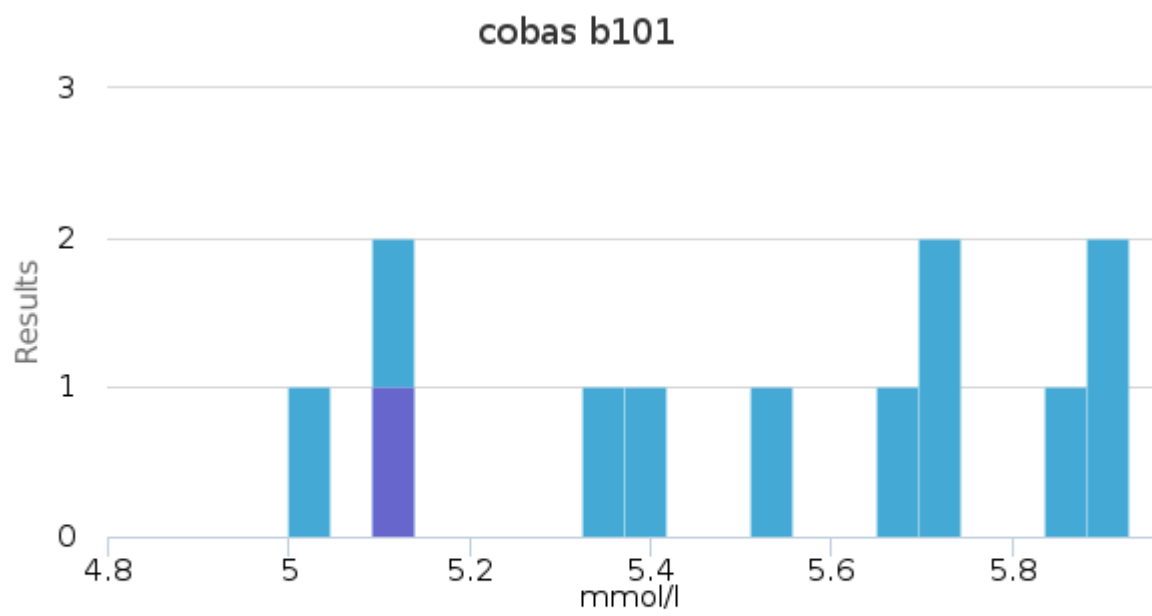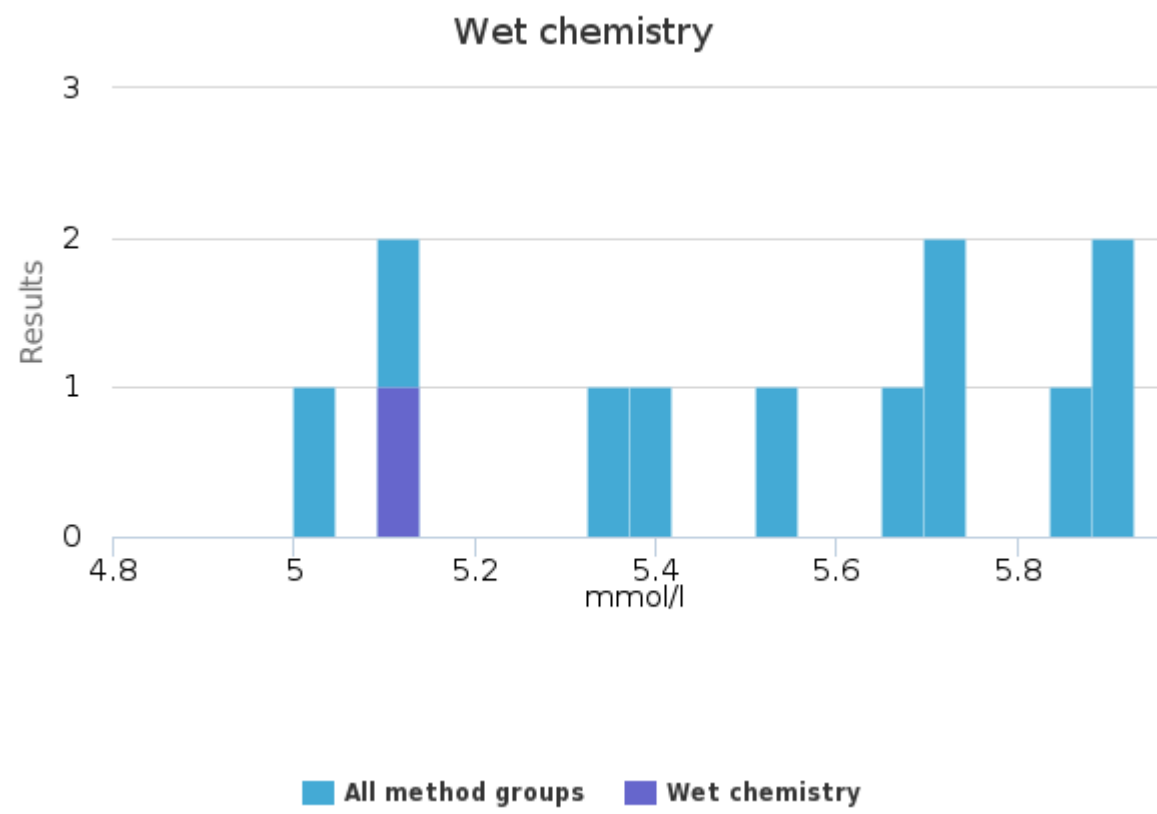
Sample S002 | Chol-HDL, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Afinion	1.08	1.08	0.03	2.6	0.02	1.06	1.10	-	2
cobas b101	-	-	-	-	-	0.83	0.83	-	1
Spotchem	-	-	-	-	-	0.85	0.85	-	1
Wet chemistry	-	-	-	-	-	0.97	0.97	-	1
All	**0.96**	**0.97**	**0.12**	**12.5**	**0.05**	**0.83**	**1.10**	**-**	**5**

Sample S002 | Chol-HDL, mmol/l| histogram summaries in LabScala
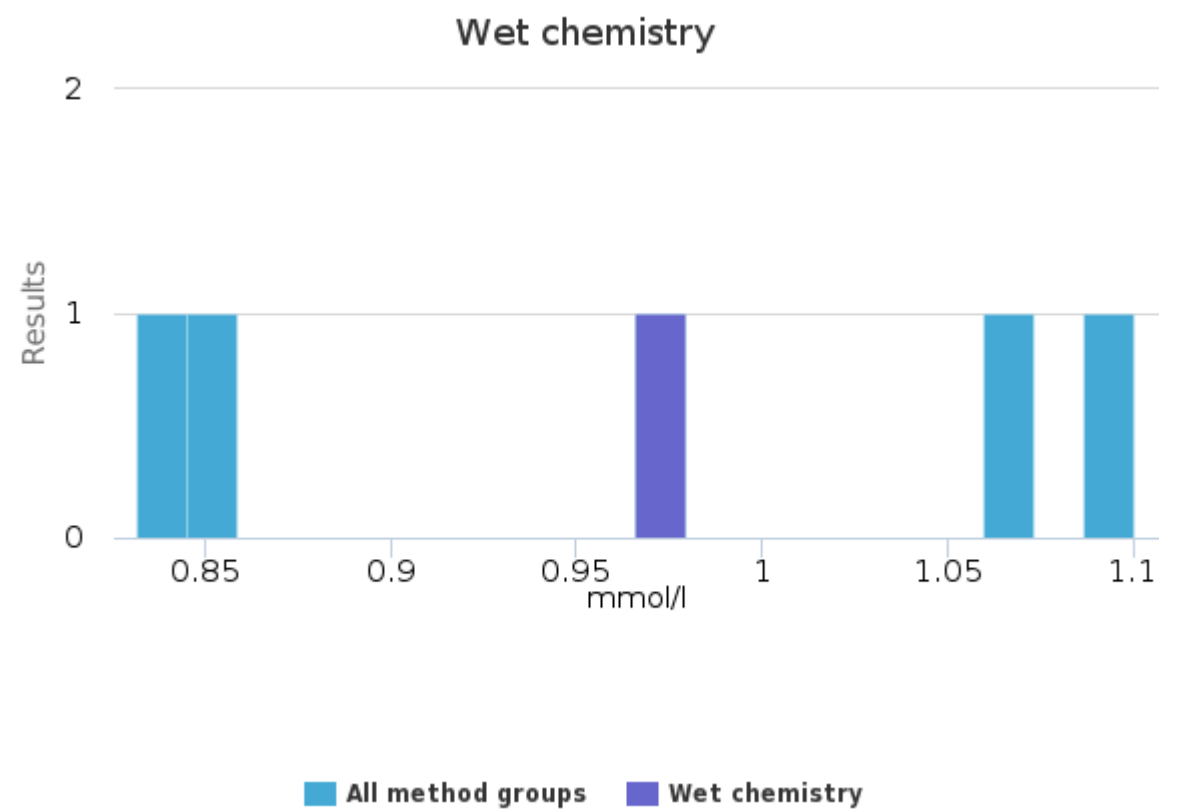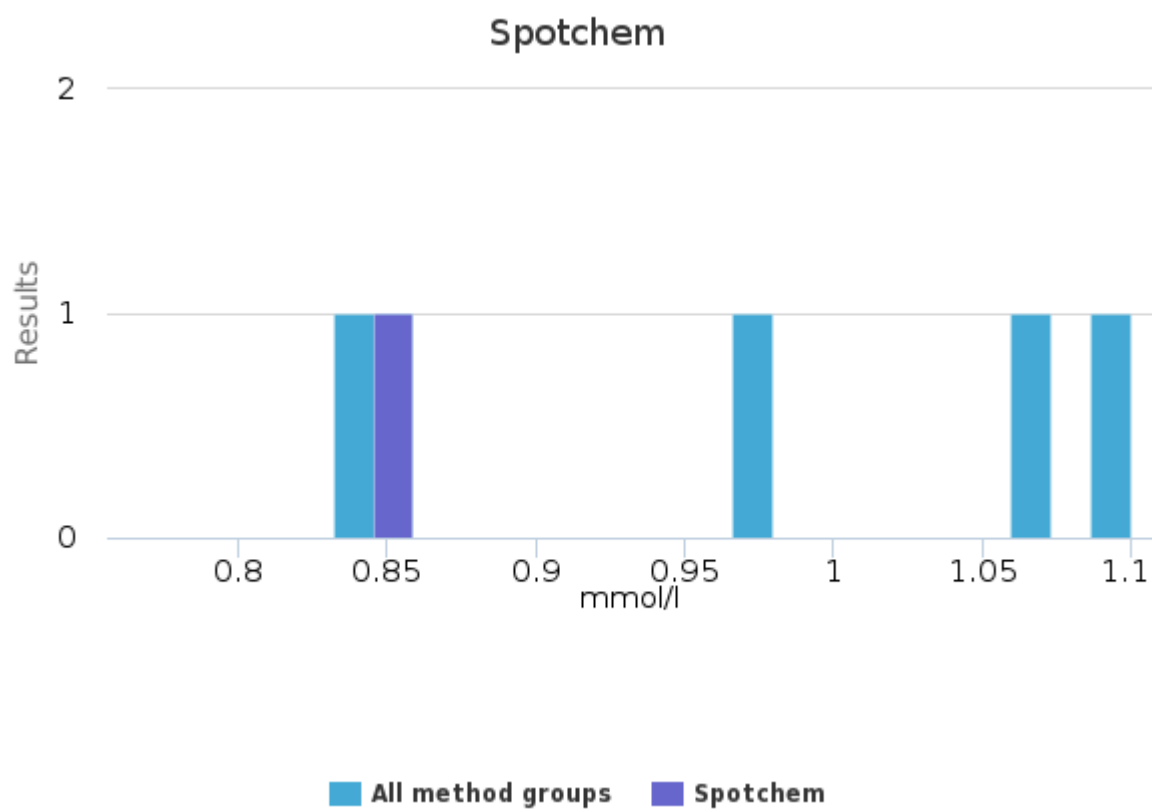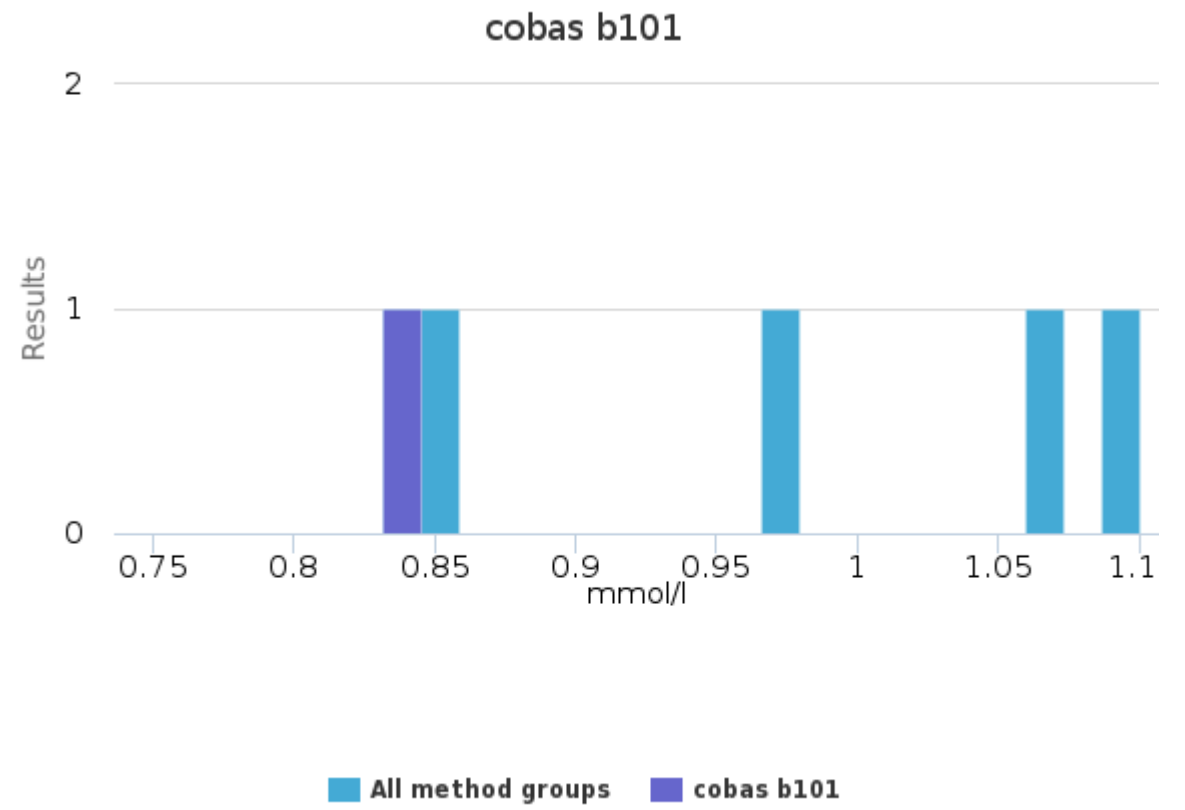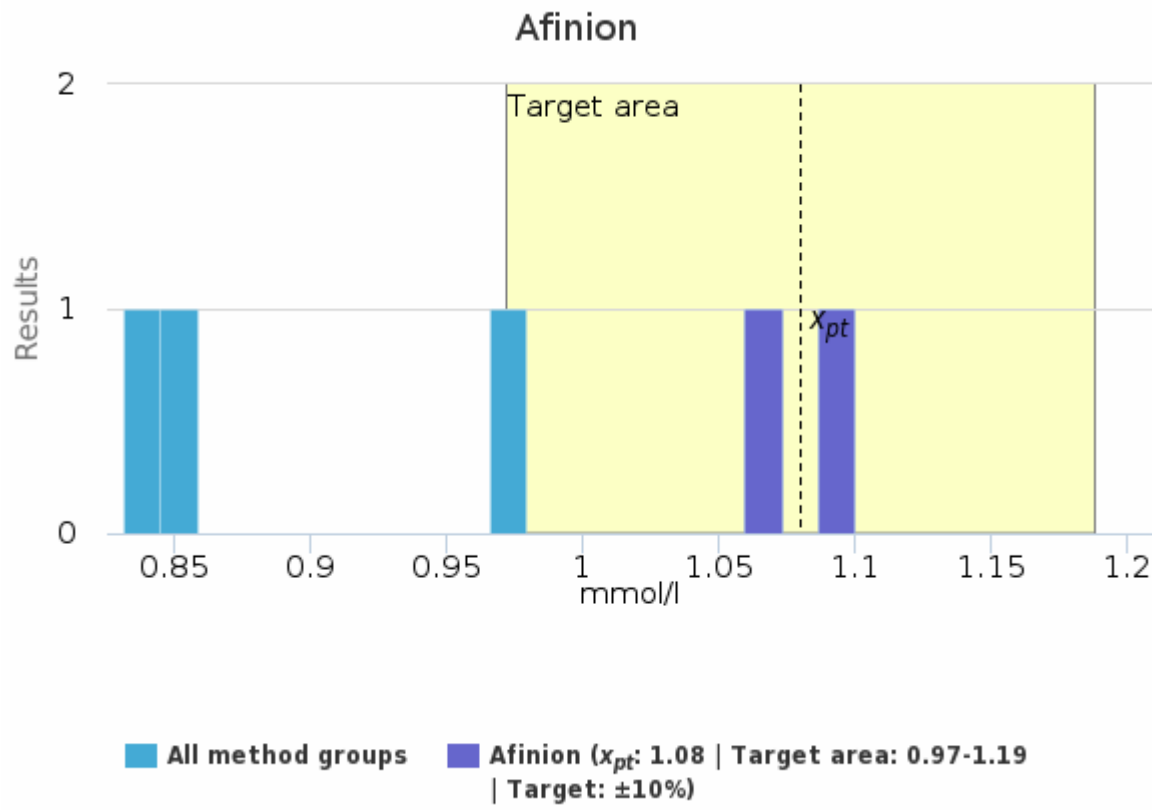
Sample S002 | Crea, µmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	325.3	323.5	13.2	4.1	6.6	312.0	342.0	-	4
i-STAT system	476.3	476.5	15.4	3.2	3.1	448.0	502.0	-	24
Spotchem	-	-	-	-	-	337.0	337.0	-	1
TASCOM	-	-	-	-	-	318.2	318.2	-	1
Wet chemistry	-	-	-	-	-	372.0	372.0	-	1
All	**443.8**	**469.0**	**63.2**	**14.2**	**11.4**	**312.0**	**502.0**	**-**	**31**

Sample S002 | Crea, µmol/l| histogram summaries in LabScala
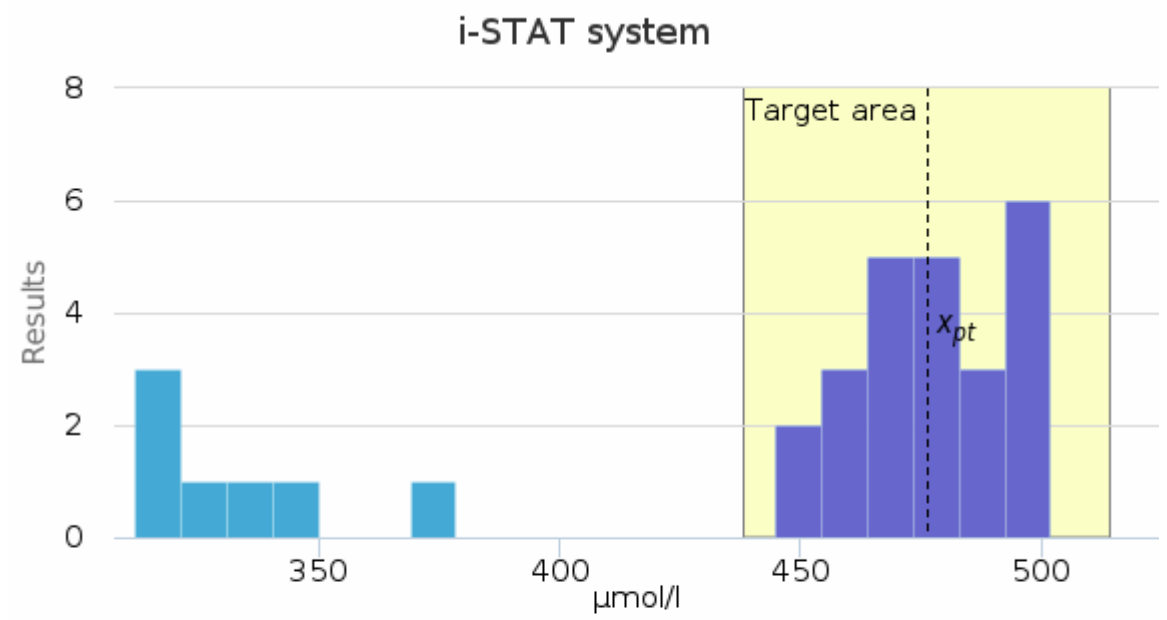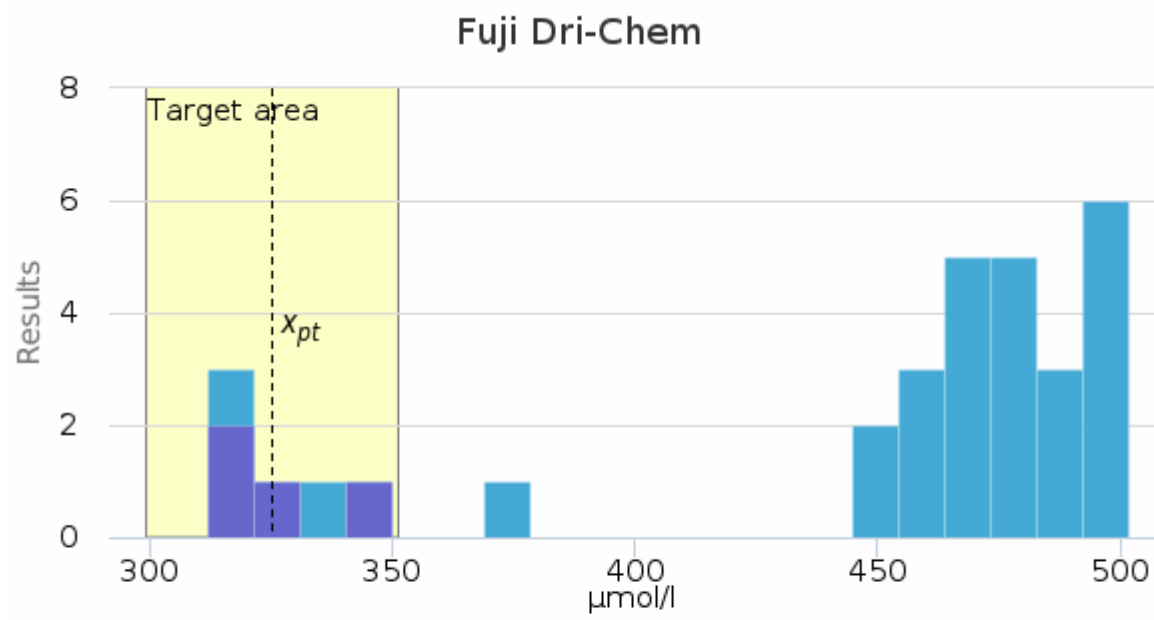
Copyright © Labquality Oy
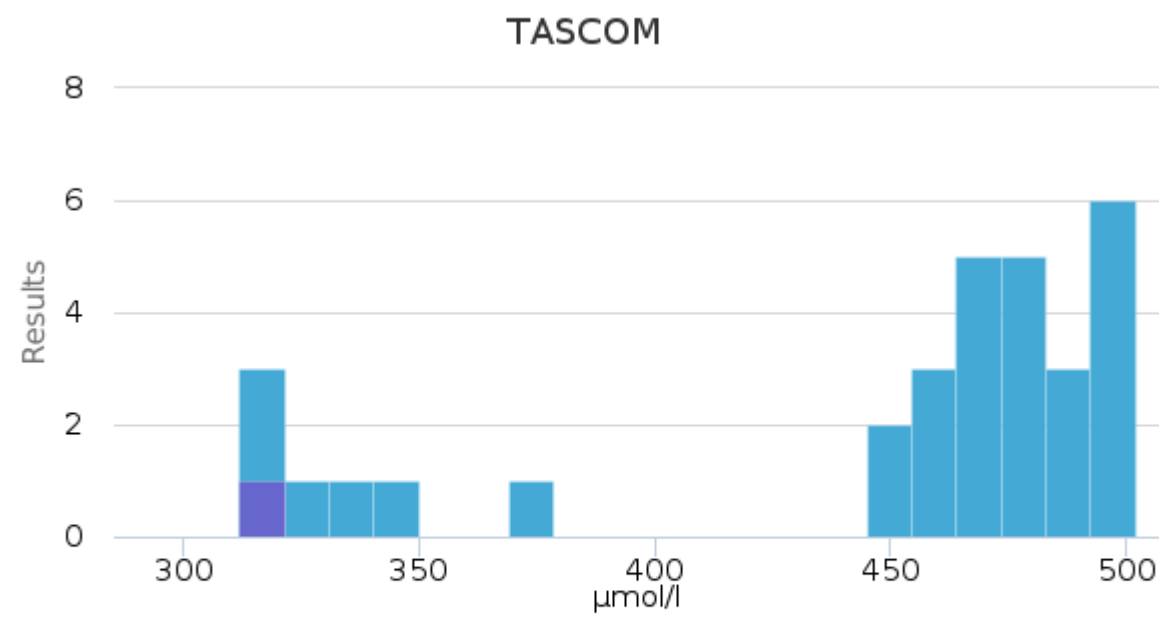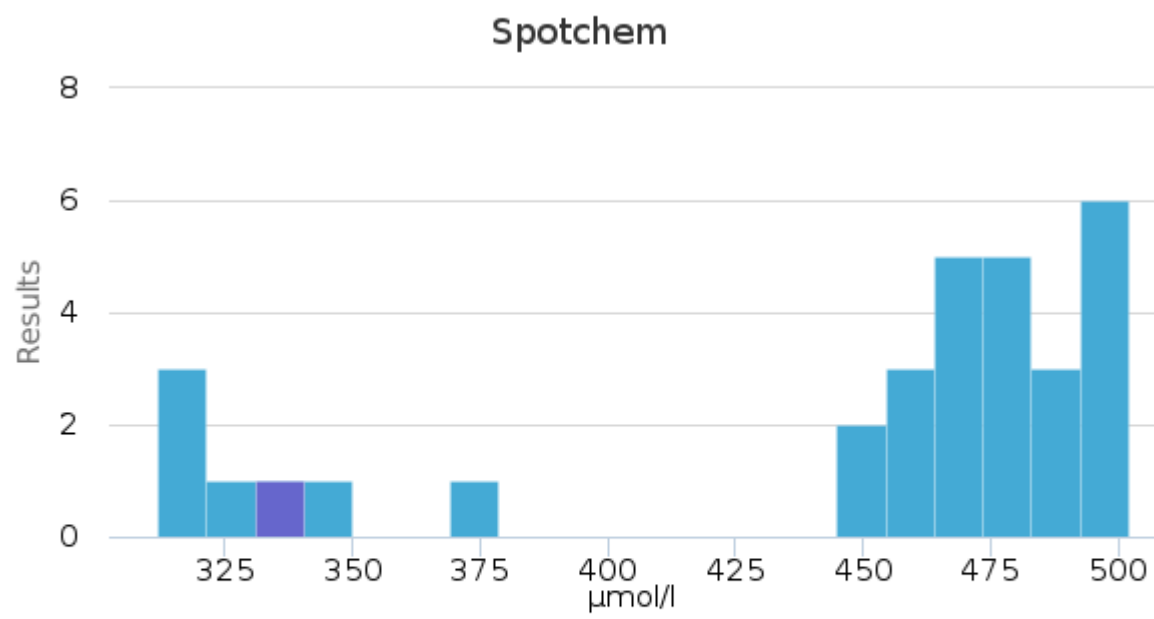
Wet chemistry

Legend: All method groups | Wet chemistry
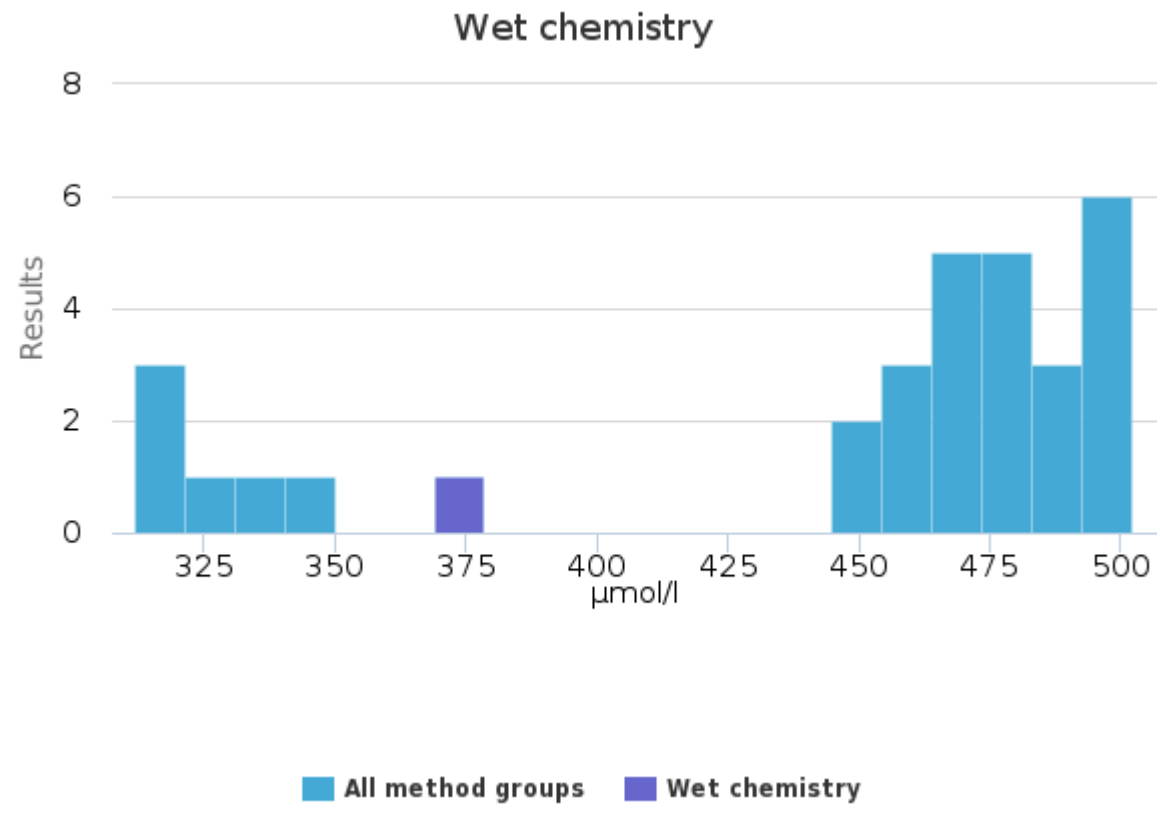
Sample S002 | LD, U/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	233.27	233.27	-	1
All	**-**	**-**	**-**	**-**	**-**	**233.27**	**233.27**	**-**	**1**

Sample S002 | LD, U/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n

LABQUALITY
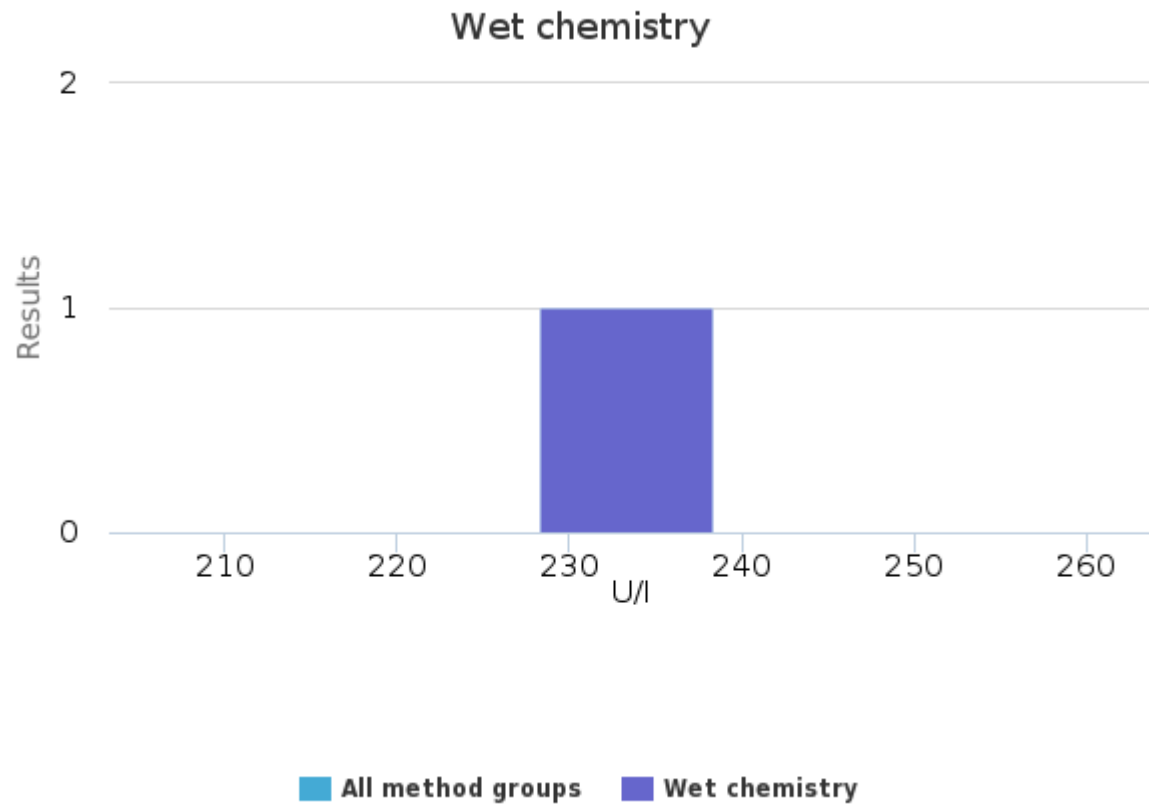
Sample S002 | Mg, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	1.53	1.53	-	1
All	**-**	**-**	**-**	**-**	**-**	**1.53**	**1.53**	**-**	**1**

Sample S002 | Mg, mmol/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	1.53	1.53	-	1
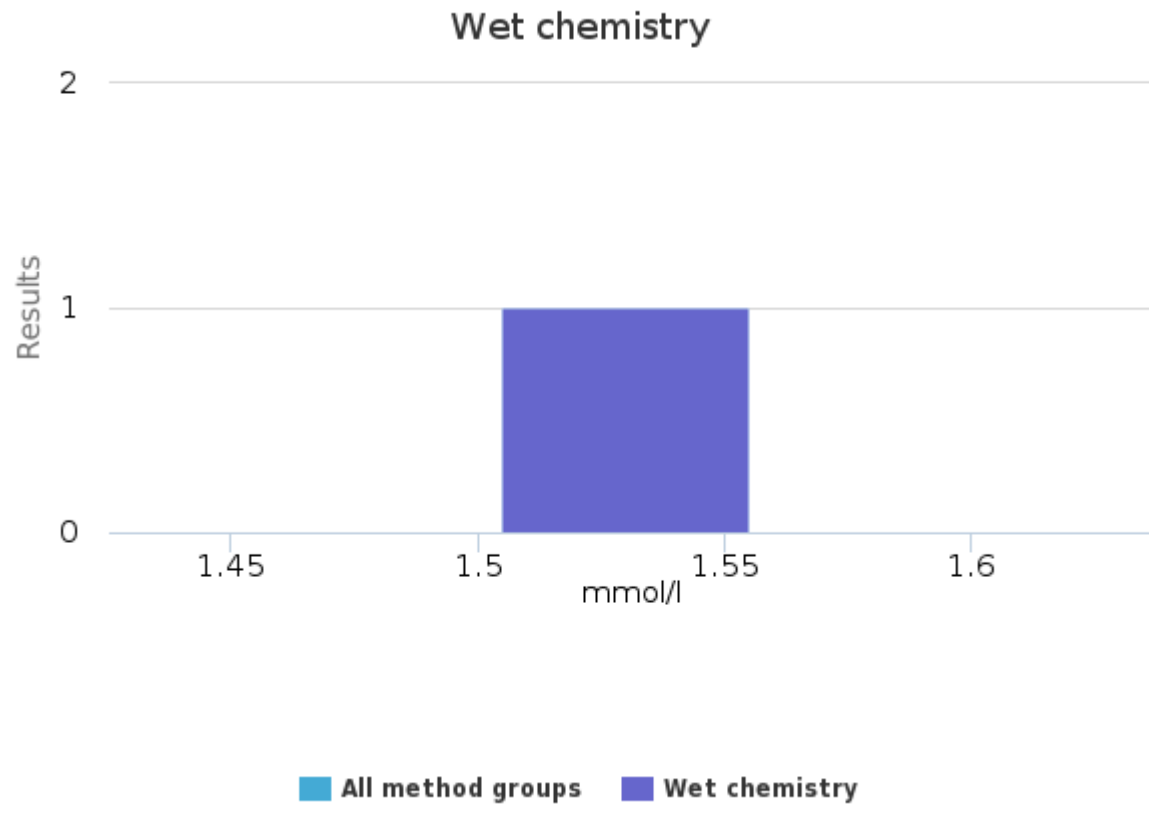
Sample S002 | Na, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Epoc reader	165.0	165.0	2.8	1.7	2.0	163.0	167.0	-	2
Fuji Dri-Chem	161.7	162.0	0.6	0.4	0.3	161.0	162.0	-	3
i-STAT system	153.7	154.0	0.6	0.4	0.1	153.0	155.0	-	23
Spotchem	-	-	-	-	-	150.0	150.0	-	1
Wet chemistry	-	-	-	-	-	149.6	149.6	-	1
All	**154.6**	**154.0**	**3.2**	**2.1**	**0.6**	**149.6**	**163.0**	**1**	**30**

Sample S002 | Na, mmol/l| histogram summaries in LabScala
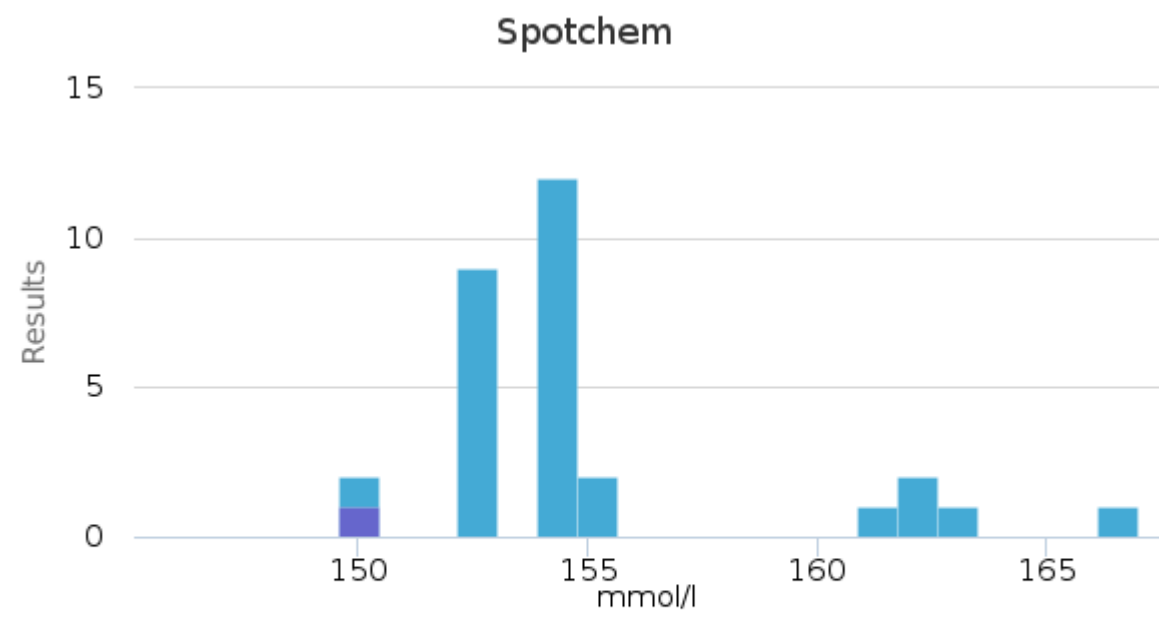
Wet chemistry

Legend: All method groups, Wet chemistry
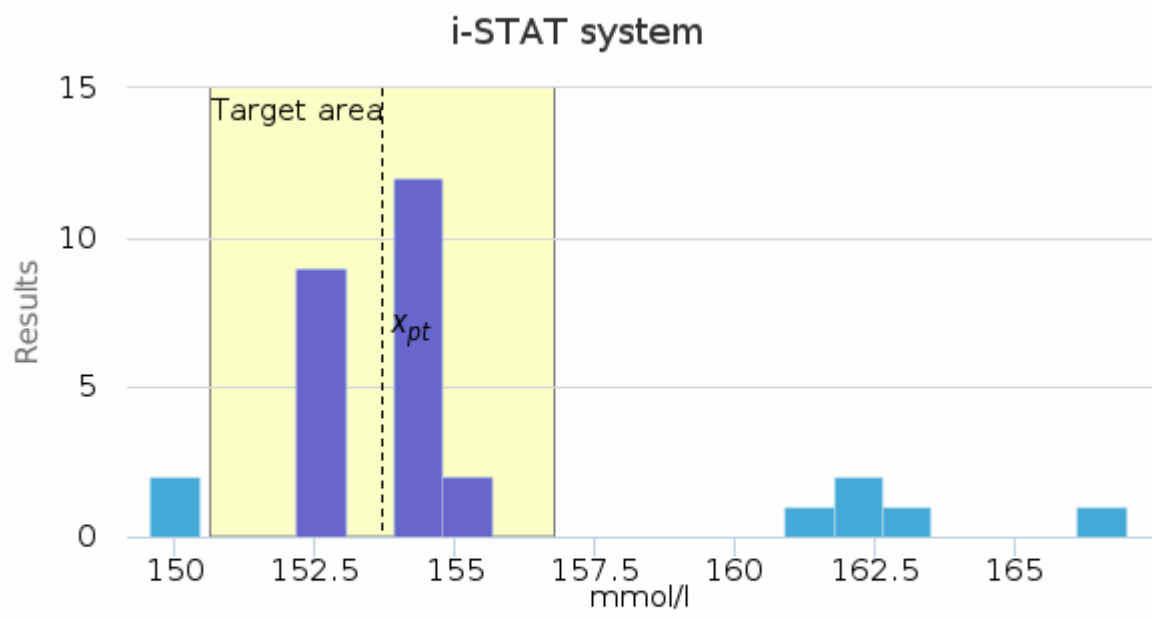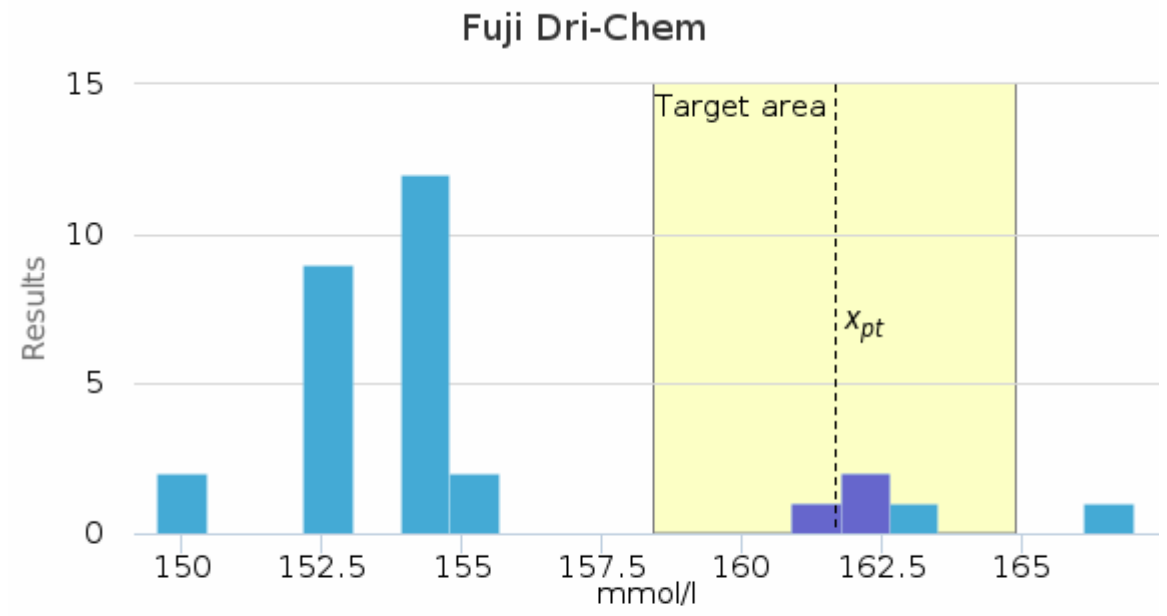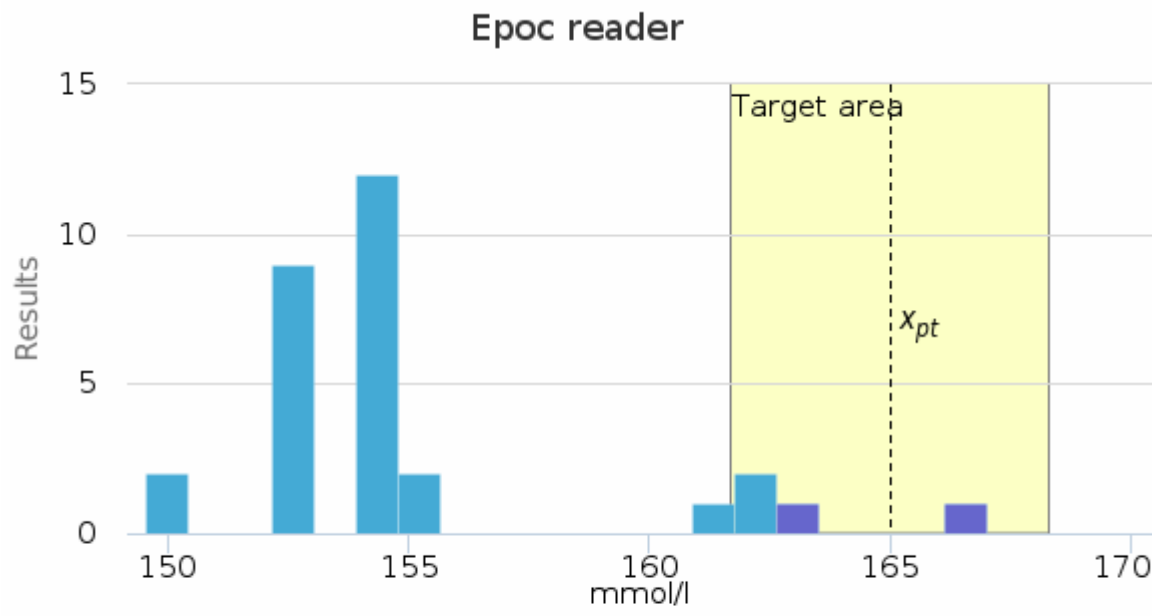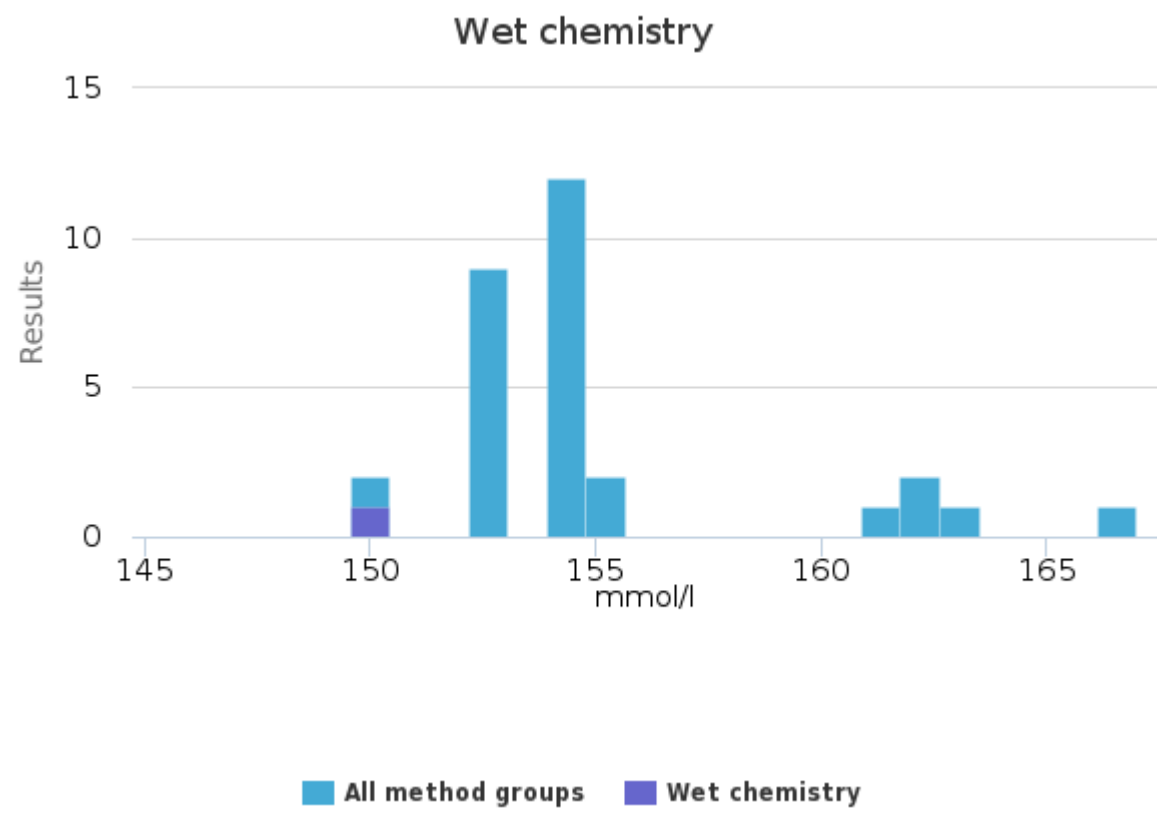
Sample S002 | Pi, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	2.74	2.74	-	1
All	**-**	**-**	**-**	**-**	**-**	**2.74**	**2.74**	**-**	**1**

Sample S002 | Pi, mmol/l| histogram summaries in LabScala

Wet chemistry

All method groups   Wet chemistry

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	2.74	2.74	-	1
All	-	-	-	-	-	2.74	2.74	-	1
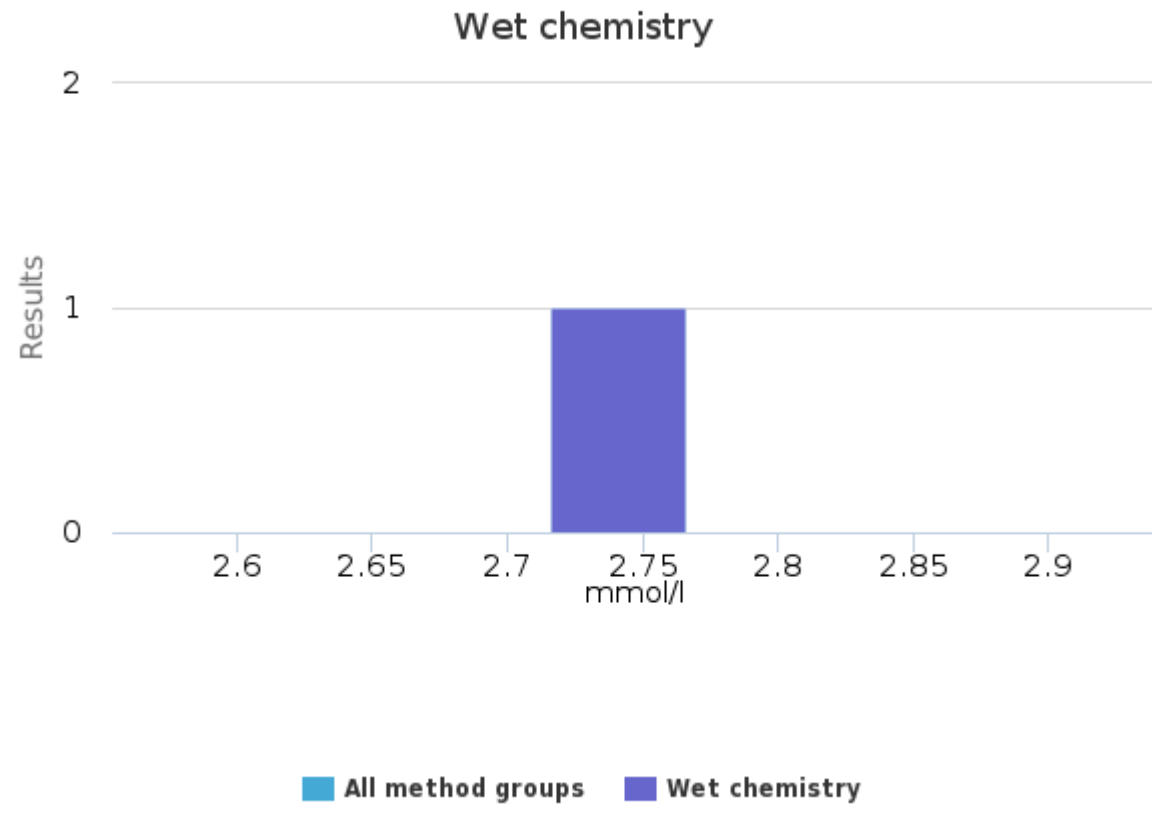
Sample S002 | Prot, g/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	87.50	87.50	-	1
All	**-**	**-**	**-**	**-**	**-**	**87.50**	**87.50**	**-**	**1**

Sample S002 | Prot, g/l| histogram summaries in LabScala

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	87.50	87.50	-	1
All	**-**	**-**	**-**	**-**	**-**	**87.50**	**87.50**	**-**	**1**
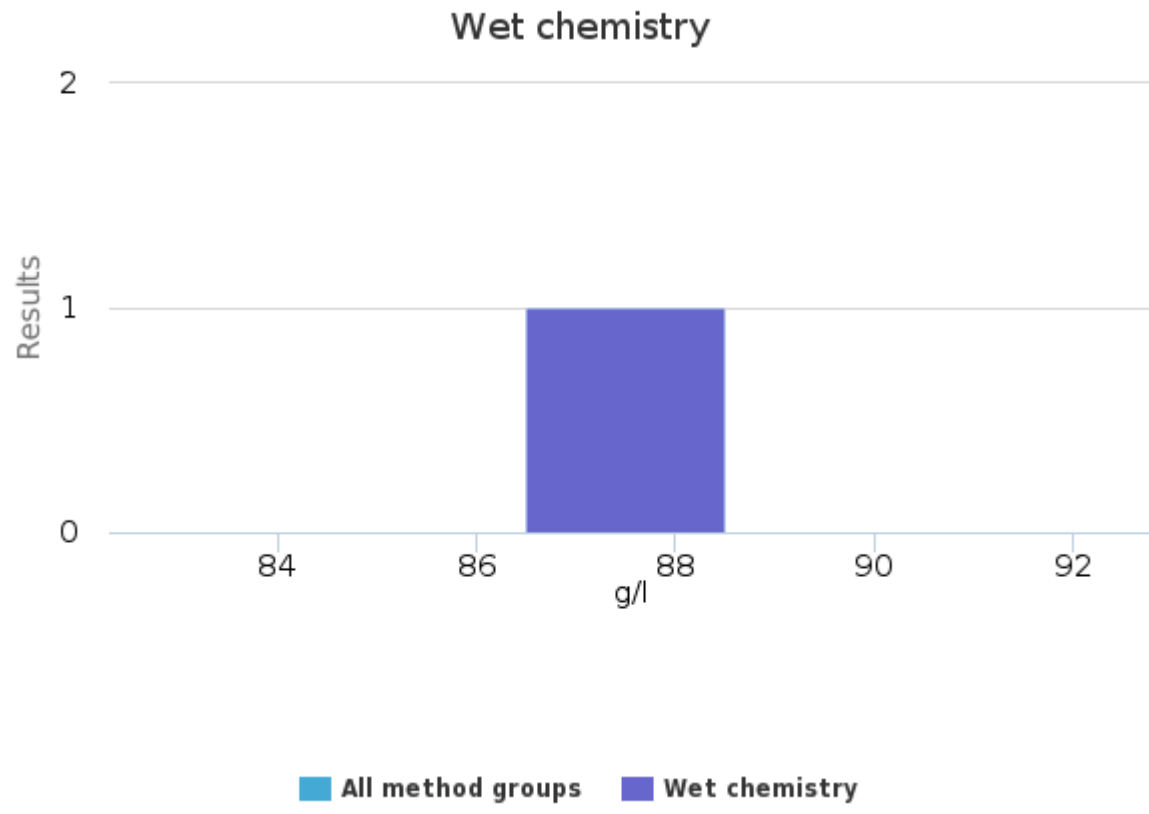
Sample S002 | Trigly, mmol/l

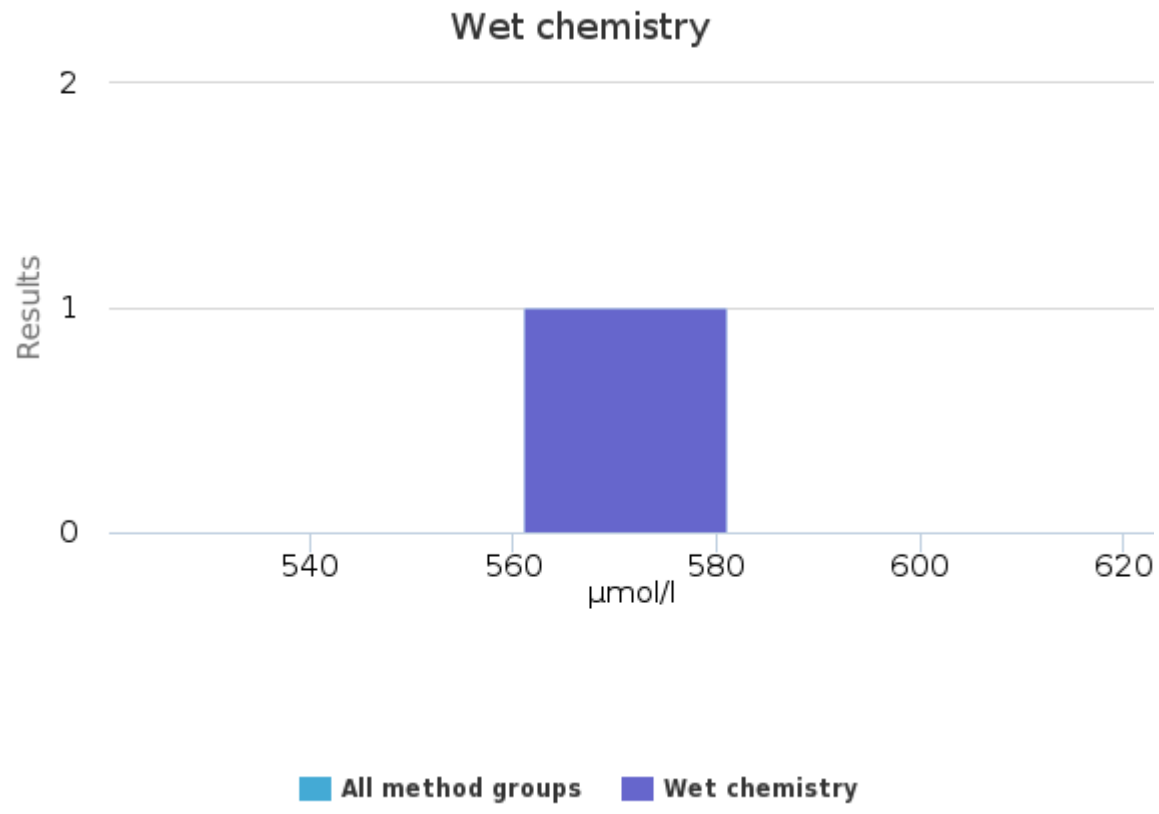| Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Afinion	3.50	3.55	0.09	2.7	0.04	3.34	3.59	-	7
cobas b101	-	-	-	-	-	3.13	3.13	-	1
Wet chemistry	-	-	-	-	-	3.04	3.04	-	1
All	**3.41**	**3.48**	**0.20**	**5.9**	**0.07**	**3.04**	**3.59**	**-**	**9**

Sample S002 | Trigly, mmol/l| histogram summaries in LabScala
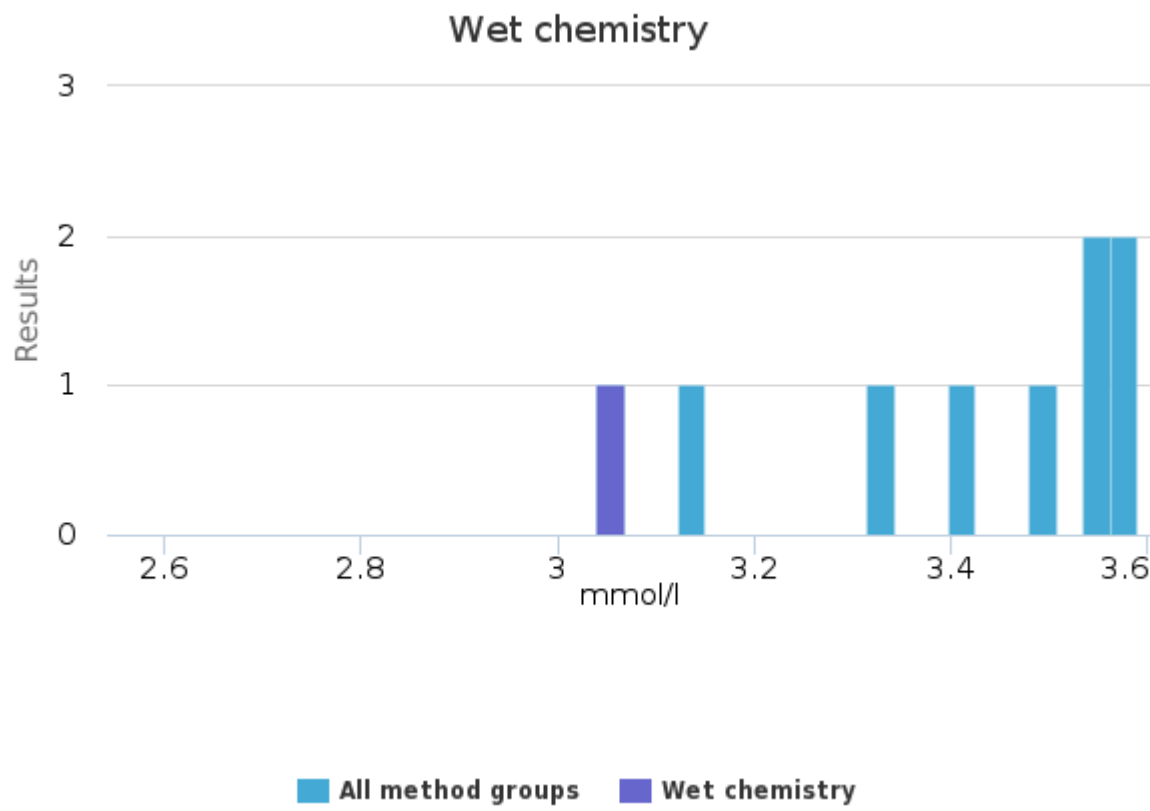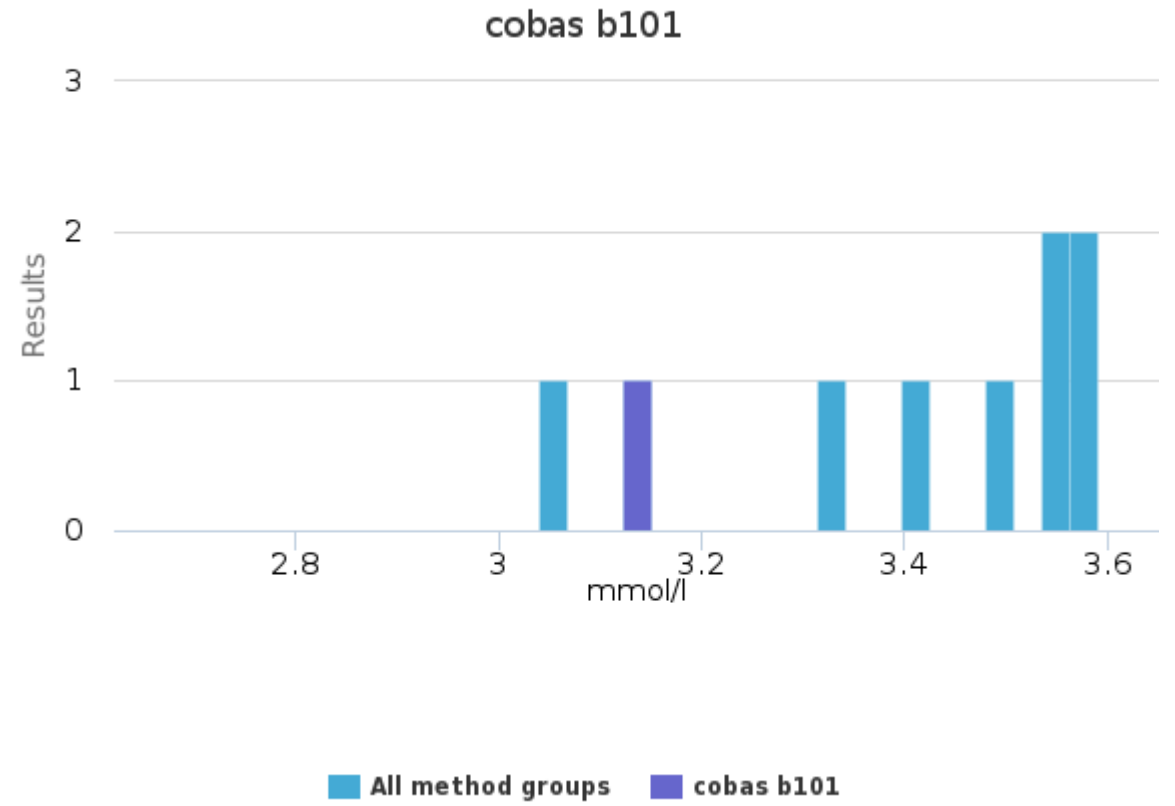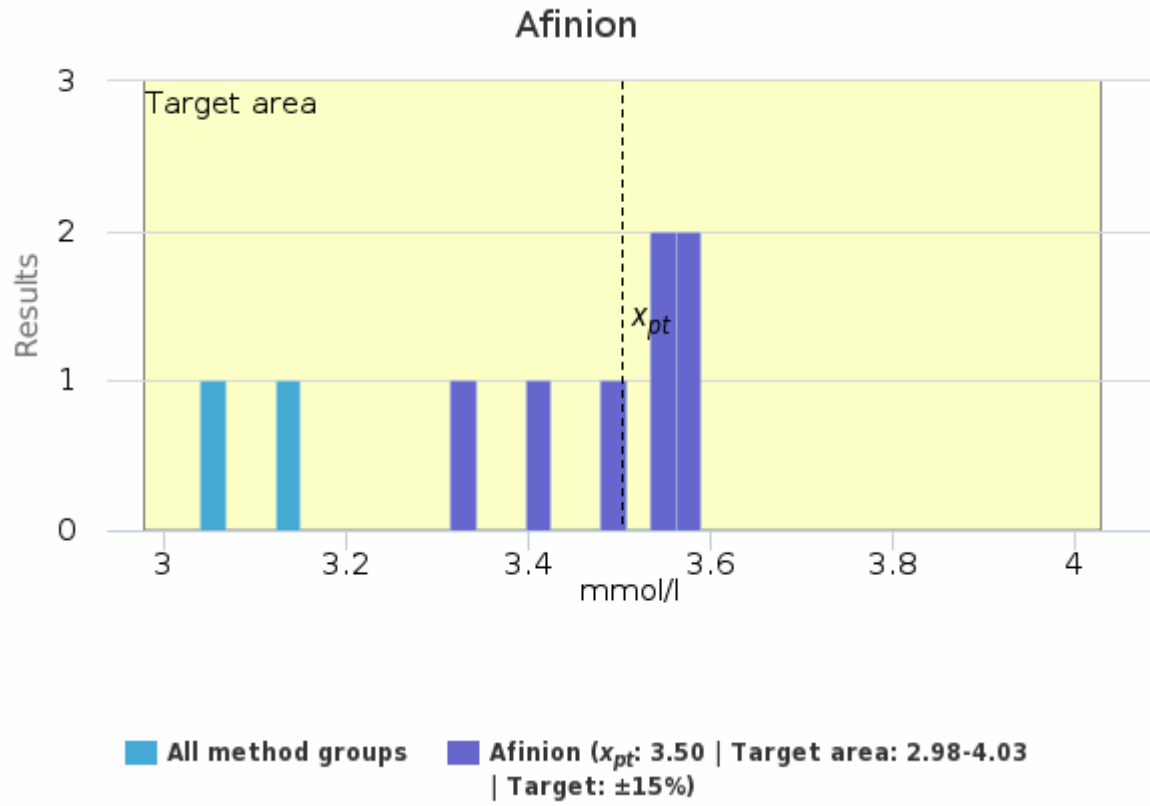
Sample S002 | Uric acid, µmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Wet chemistry	-	-	-	-	-	571.08	571.08	-	1
All	**-**	**-**	**-**	**-**	**-**	**571.08**	**571.08**	**-**	**1**

Sample S002 | Uric acid, µmol/l| histogram summaries in LabScala

Basic chemistry, POCT analyzers, February, 1-2023
Quantitative report

Sample S002 | Urea, mmol/l

Methodics	x_{pt}	Median	sd	CV%	SEM	min	max	Outliers	n
Fuji Dri-Chem	-	-	-	-	-	21.15	21.15	-	1
i-STAT system	25.27	25.40	0.50	2.0	0.12	24.00	26.10	-	18
Spotchem	-	-	-	-	-	18.30	18.30	-	1
Wet chemistry	-	-	-	-	-	20.49	20.49	-	1
All	**24.82**	**25.35**	**1.45**	**5.8**	**0.32**	**20.49**	**26.10**	**1**	**21**

Sample S002 | Urea, mmol/l| histogram summaries in LabScala

Fuji Dri-Chem

■ All method groups ■ Fuji Dri-Chem

i-STAT system

Target area

x_{pt}

■ All method groups ■ i-STAT system (x_{pt}: 25.27 | Target area: 22.74-27.79 | Target: ±10%)

Spotchem

■ All method groups ■ Spotchem

Wet chemistry

■ All method groups ■ Wet chemistry

Report info

Participants

39 participants from 8 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).

LABQUALITY

External Quality Assessment Scheme

Basic chemistry, POCT analyzers
Round 1, 2023

Specimens

Sample S001 (LQ747423011) and Sample S002 (LQ747423012) were human liquid sera.

Based on the previous tests and the results of this round, the samples are 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 – Expert

Wet chemistry values were obtained by Roche methods.

Sample S001 represented a normal level except for very high potassium and low glucose. Sample S002 represented a high level sample.

The overall result of the round was very good.

More detailed information about the results

A target area will only be given if there are two or more results in each method group. All results are mainly within the target range, except for a few slightly different results. Only one result has been reported for several device types and thus target area cannot be given. These results also largely correspond to the level of results reported with other devices, except for the high glucose in both Reflotron samples.

Glucose
The level of sample 001 was low. Client results varied from 3.3 – 3.7 mmol/L. The level of sample S002, on the other hand, was very high and the results varied between 13.3–15.4 mmol/L. All customers reported consistent results, i.e. hypo/hyperglycemia would have been detected.

Potassium
Potassium levels in sample S001 and S002 002 were pathologically high being higher than 6 mmol/L. The results of all participants agree well with each other.

Calcium
This round again included iSTAT devices that incorrectly reported ionized calcium results for the total calcium of the round. These results were excluded from the result processing. Device users should pay attention what they report on the round and what is requested on Labscala result sheet. Reporting a result to wrong analyte for a patient could cause a serious treatment error. However, all these reported results were consistent with each other.

Chloride
Sample S002 represented a high-level sample. A total of 17 results had been reported for chloride, of which only two gave a numerical result. The other 15 participants reported results above the measurement range (>140 mmol/L),

which correspond well to the two numerical results obtained, with an average of 155.5 mmol/L. The results obtained with the different methods of other analytes were also very similar.

<u>HDL cholesterol</u>
Very high results had been reported for HDL cholesterol, which might be total cholesterol results. We ask customers to check the original result on the device if the % difference between the result and the target value is very large.

End of report