

Birmingham Quality

UK NEQAS for Holotranscobalamin

Laboratory :

Distribution : 252

Date : 19-Aug-2018

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Feedback

Quality Manager
Pathology Laboratory
Biochemistry Department
Town
County
Postcode

This Scheme is essentially web-based. We can alert you to information regarding the Scheme via email. The e-mail address (or addresses) we are currently using to contact your laboratory is shown below in red. If no e-mail address is displayed or the information shown is incorrect, please email us with an appropriate contact e-mail address as soon as possible, using the word 'feedback' in the title line.

Based on the date information you have provided, the transit time from specimen dispatch [] to receipt [] was day(s), and the subsequent time to analysis [] in your laboratory was day(s). (Missing values indicate dates not provided. "0 days" represents same day).

Any comments you made to us are shown below and have been acted upon where necessary

Any specific comments applicable only to laboratory are shown below

Any general comments applicable to all laboratories are shown below

This Distribution is part of an extensive and wide ranging study across multiple schemes and multiple UK NEQAS Chemistry Centres.

Specimens B and C have been excluded from scoring for HoloTC.

A full collated report will be available at the end of the study and we anticipate this to be end of September 2018. Thank you for your patience and for contributing to this work.

Performance Surveillance and Performance Issues

If you have a red banner for any analyte on the Performance Summary Icon (PSI) page, then you should log this in your Quality Management System.

Birmingham Quality is here to help. If you are unsure as to why you have out-of-consensus problems or if you are having difficulties with your Root Cause Analysis, then please do contact us.

It is the responsibility of the Participant to act on, investigate and hopefully resolve, all out-of-consensus performance.

It is the responsibility of the Organiser to highlight in the regular report any out-of-consensus performance by the use of scores, symbols, graphs and 'traffic lights' etc.

Likewise, for the non-numerical analytes, please check the Pie Charts and other graphical representations to see if you are out-of-consensus.

Finlay MacKenzie
Director, Birmingham Quality

Report authorised on Friday 24 August 2018 by:

Finlay MacKenzie, Director Birmingham Quality

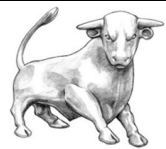


7860

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UK NEQAS
International Quality Expertise

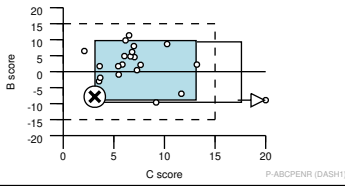
Birmingham Quality is proud to offer EQA services that adhere to the Code of Practice and have the badge of quality of UK NEQAS



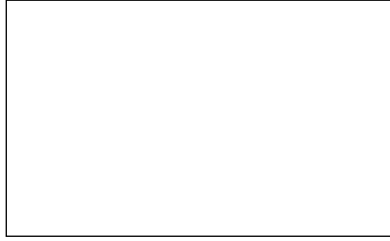
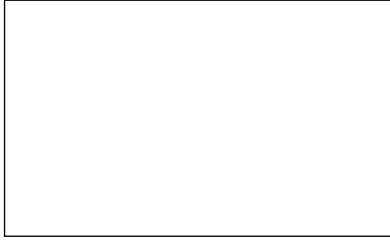
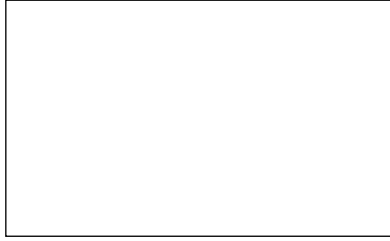
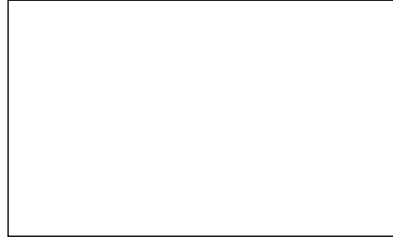
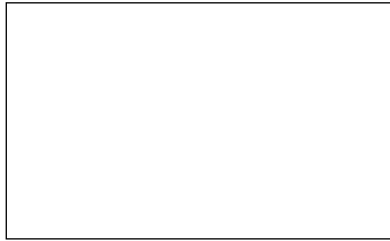
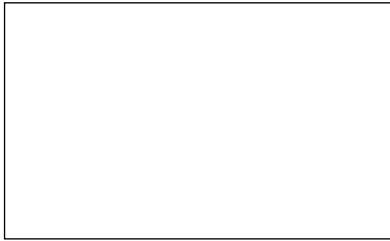
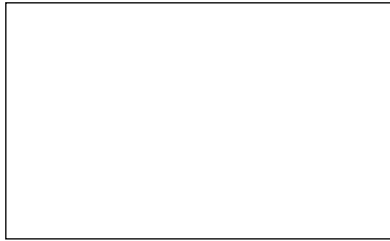
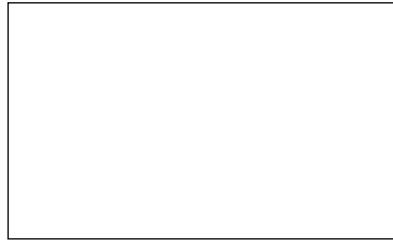
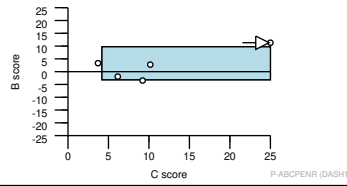
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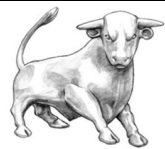
Performance Summary Icons (click graph for details)

HoloTC



Methylmalonic acid





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Participation summary

Analytical Performance over the last 6 months (rolling time window of 6 distributions)

All our time periods are 'rolling' to give you current information.

You may wish to keep you own log of Calendar Year or Financial Year time points if you require 'year-end' statements for your own internal use.

Any analytes with out of consensus performance will be highlighted in red and can be clicked for further details.

You have out of consensus performance for:	<i>None</i>
You have in consensus performance for:	HoloTC
You have no performance data for:	Methylmalonic acid

Participation and Return Rates

This scheme cycle is notionally every four weeks.

Analytically, we assess you over a six month time window (6 Distributions).

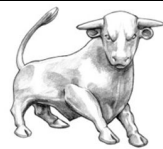
For return rates, late and amended results we assess you over a twelve month period (12 distributions).

	Distributions	Rating	Affected Distributions
Participation	8 distributions out of a possible 12	Unsatisfactory	241 242 244 245
Late Returns	0 distributions from the last 8	Satisfactory	
Amendments	0 distributions accepted from the last 8	Satisfactory	

Analytical Performance for specimens from distribution 252 only

You can judge, in association with your IQC and other QA measures, if your current performance is a blip or part of a trend.

Out of consensus for at least one specimen for:	<i>None</i>
In consensus for all specimens for:	HoloTC
You have no specimen %bias etc. for:	Methylmalonic acid
You are not registered for:	<i>None</i>



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Distribution Summary

If your laboratory is outside of the acceptable limits of performance for any its rolling time-window scores (A, B or C scores), this will be indicated by a red traffic light symbol. It is the responsibility of the laboratory to undertake an internal investigation to establish the underlying cause and put in place corrective and preventive action. Please do not wait to receive a formal notification of performance from the Scheme Organiser or the National Quality Assurance Advisory Panel (NQAAP) before logging the non-conformity and, where necessary, acting upon the data contained in your report. A green traffic light merely reflects that your laboratory is performing as well as the state-of-the-art allows; it does not necessarily mean that your assay / laboratory performance is good enough clinically.

The "A scores" for HoloTC are currently based on a 'flat 10%' degree of difficulty. Once we have accumulated more data points we will be able to calculate concentration-dependent degree of difficulty factors and put them in the same 'currency' as the A scores in other Schemes. But, for the moment, the "A scores" for HoloTC are proto A scores. Please see the online 'Explanation of the ABC of EQA' which may be found under the 'Centre' button on the UK NEQAS Results & Reports page. You will need your user-name and password to access this information. A scores, and B and C score limits are yet to be determined for MMA.

	Specimen	Pool	Result	Target	Specimen %bias	A score	B score	C score	A	B	C
HoloTC (pmol/L)	252A	277	75.2	81.8	-8.1 ◆	78	-7.8	3.1	● ↔	● ↔	● ↔
	252B	278	74.5								
	252C	279	74.5								
HoloTC Interpretation (L, I, N or H)	252A	277	N	N							
	252B	278	N	N							
	252C	279	N	N							
Methylmalonic acid (nmol/L)	252A	277	XPL	277							
	252B	278	XPL	273							
	252C	279	XPL	273							
MMA Interpretation (L, I, N or H)	252A	277		N							
	252B	278		N							
	252C	279		N							

All samples issued have been tested negative by standard methods for HIV, TPHA, Hepatitis B and C. Gentamicin, penicillin and fluconazole have been added to all specimens.

You have until the close of Distribution 253 (23/09/2018) to submit late results / request amendments to results for Distribution 252. Please enter any late results or requests to amend non-analytical errors for Distribution 252 on the web under the usual Results button ensuring the correct Distribution number has been selected. You should include your name and a valid reason.

Amending results is at the discretion of the Director and is not an automatic entitlement. We are not accepting any further requests to amend results or to change methods for Distribution 251.

Distribution 253 will be dispatched on 03/09/2018 . Results are due back in Birmingham by, notionally, 23:59 on 23/09/2018.

Where your results appear as "XPL", it is because you did not report a numerical value for that analyte, but you did provide an explanation as to why a result was not reported.



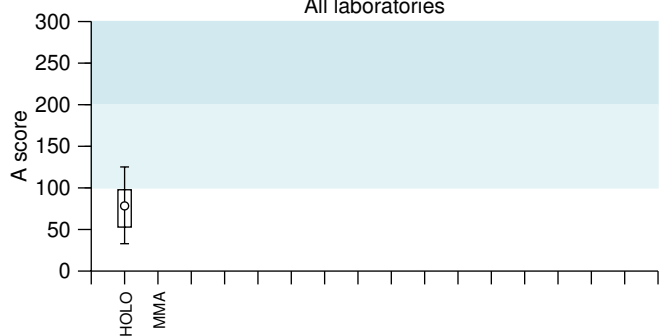
Method Summary

Our method update service is web-based and is accessed online via the 'Edit' button on the 'Results and Reports page'. You can select from a dropdown of methods or select the default option from the major manufacturer's products*.

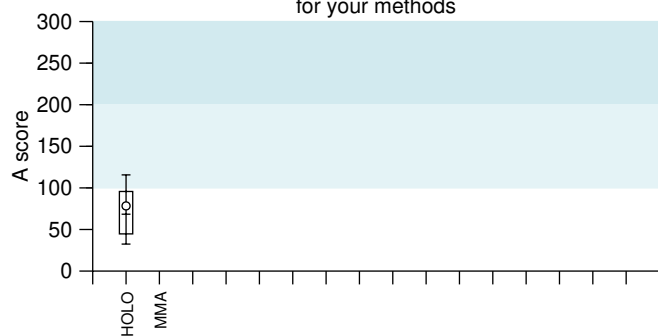
*If you are not using the system according to the manufacturer's instructions, please select the in-house category within your system's method principle.

Method Principle	Your Method	Units	A score with trend arrow	Method median A score	All lab median A score
HoloTC	Abbott Architect [AB13]	pmol/L	78 ● ↔	68	78
Methylmalonic acid	Mass spectrometry	In-house [600]			

Graphic Equalizer Plot of A scores
All laboratories



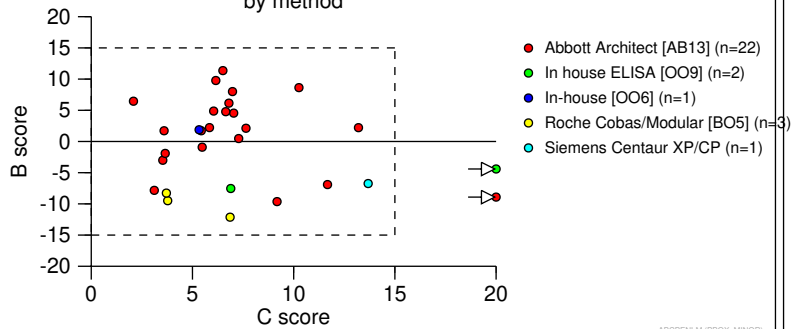
Method Graphic Equalizer Plot of A scores
for your methods



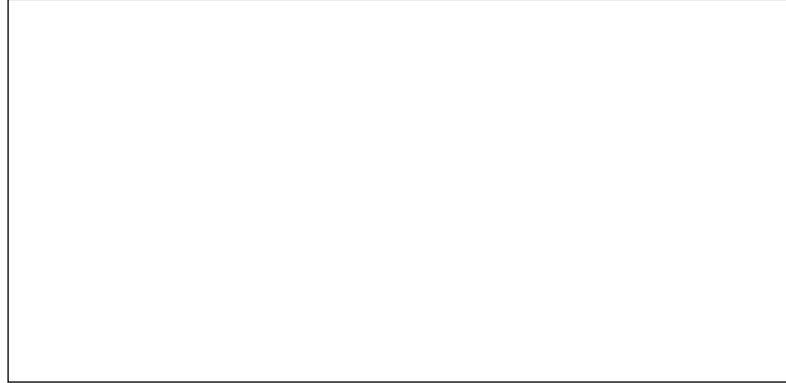
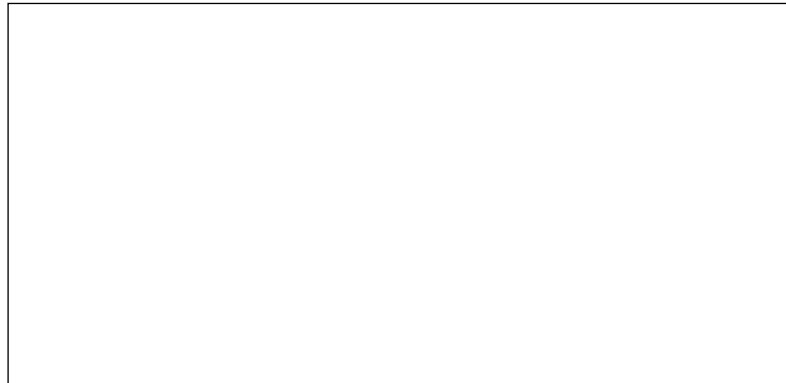
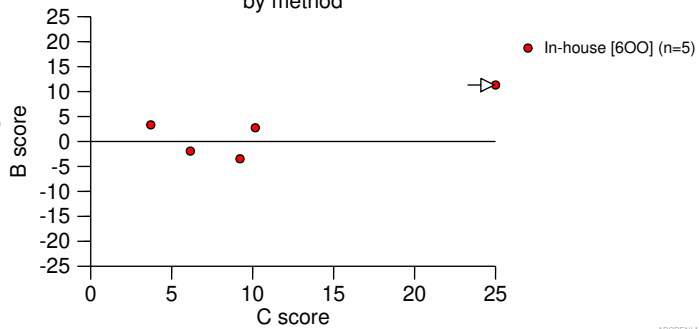


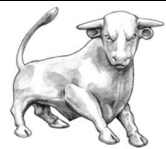
Cumulative Summary

HoloTC B and C scores by method



Methylmalonic acid B and C scores by method





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Analyte : HoloTC (pmol/L)

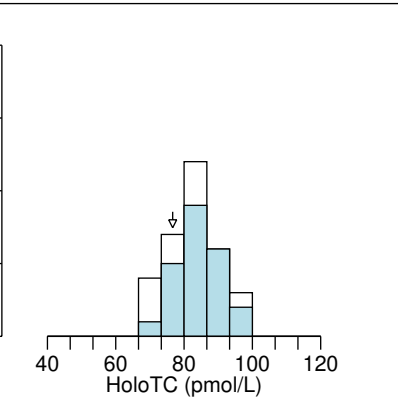
Spec.	Pool	Pool description / Treatments / Additions
252A	277	Pooled human serum
252B	278	Pooled human serum + exogenous material
252C	279	Pooled human serum + exogenous material

All methods
 Abbott Architect [AB13]

Your A score is	78	↔
Your B score is	-7.8	↔
Your C score is	3.1	↔
The A limit is	200	
The B limit is +/-	15.0	
The C limit is	15.0	

Specimen : 252A

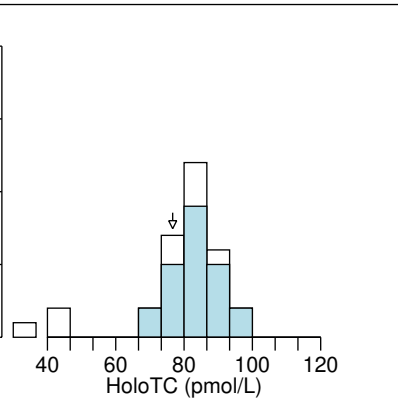
	n	Mean	SD	CV(%)
All methods [ALTM]	32	81.8	7.2	8.8
Abbott Architect [AB13]	23	83.0	6.3	7.7
In house ELISA [OO9]	3	75.5		
In-house [OO6]	1	83.6		
Roche Cobas/Modular [BO5]	4	74.7		
Siemens Centaur XP/CP	1	94.7		



Your result	75.2
Target value (ALTM)	81.8
Your Interpretation	N
Consensus	N
Standard Uncertainty	1.69
Your specimen: %bias	-8.1
Accuracy Index	81
Method mean (Abbott Architect [AB13])	83.0

Specimen : 252B

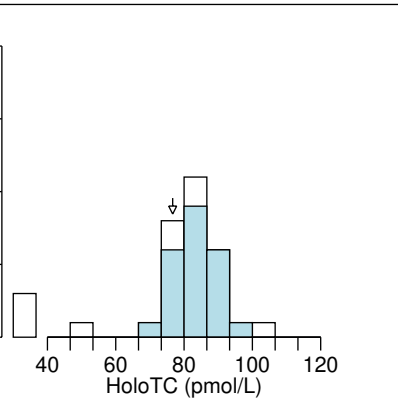
	n	Mean	SD	CV(%)
All methods [ALTM]	32	80.3	9.4	11.7
Abbott Architect [AB13]	23	82.5	6.6	8.0
In house ELISA [OO9]	3	67.7		
In-house [OO6]	1	83.1		
Roche Cobas/Modular [BO5]	4	62.3		
Siemens Centaur XP/CP	1	77.8		



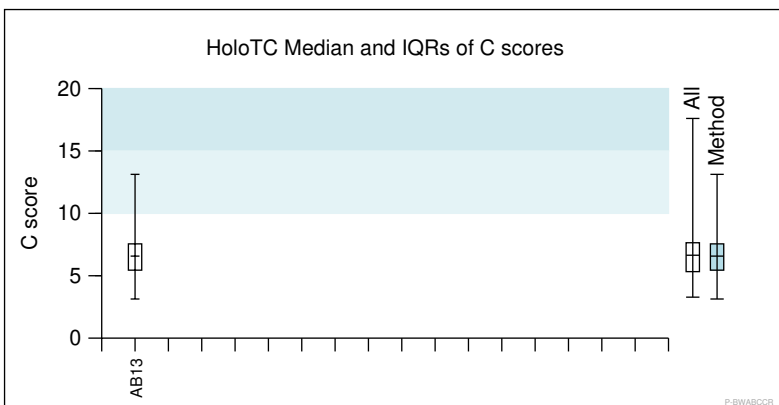
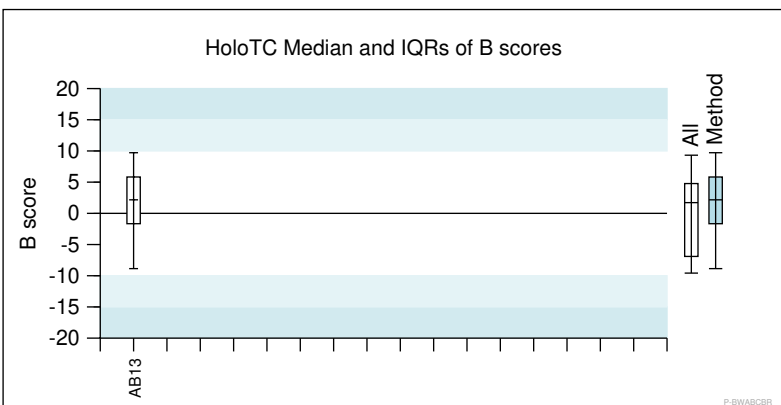
Your result	74.5
Target value ()	
Your Interpretation	N
Consensus	N
Standard Uncertainty	
Your specimen: %bias	
Accuracy Index	
Method mean (Abbott Architect [AB13])	82.5

Specimen : 252C

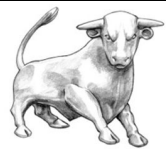
	n	Mean	SD	CV(%)
All methods [ALTM]	32	79.1	12.5	15.8
Abbott Architect [AB13]	23	83.1	6.7	8.1
In house ELISA [OO9]	3	63.4		
In-house [OO6]	1	80.9		
Roche Cobas/Modular [BO5]	4	40.9		
Siemens Centaur XP/CP	1	75.5		



Your result	74.5
Target value ()	
Your Interpretation	N
Consensus	N
Standard Uncertainty	
Your specimen: %bias	
Accuracy Index	
Method mean (Abbott Architect [AB13])	83.1



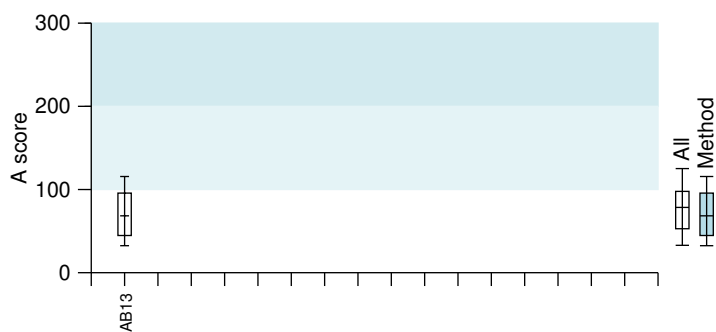
Based on the information you have provided, your reagent lot number is [10709UP00] and your calibrator lot number is [902917448].
 (Missing values indicate data not provided).
 We have excluded the HoloTC results for Specimen 252B (Pool 278) and Specimen 252C (Pool 279), please see the Feedback page for more details.



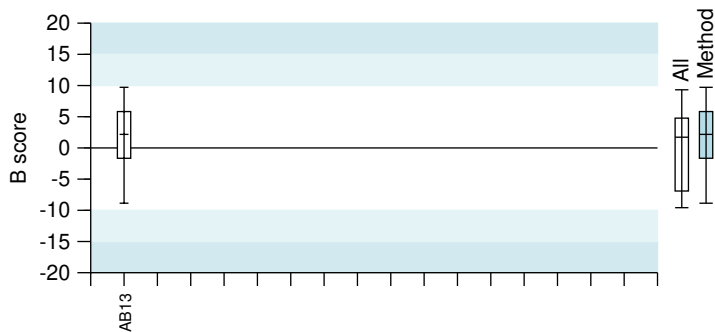
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Pool (exclusion) [Type]	Distribution 247 11-Mar-2018			Distribution 248 15-Apr-2018			Distribution 249 13-May-2018			Distribution 250 17-Jun-2018			Distribution 251 22-Jul-2018			Distribution 252 19-Aug-2018		
	result	target	%bias	result	target	%bias	result	target	%bias	result	target	%bias	result	target	%bias	result	target	%bias
(278) (266) (279) 267 246 268 269 270 271 274 272 263 261 260 277 273 276	14.2	14.76	-3.8	7.5	7.99	-6.1	15.7	17.56	-10.6	<0.5			52.3	55.4	-5.6	(74.5)	(74.5)	
				32.7	35.8	-8.7	42.3	45.3	-6.6				72.4	75.5	-4.1			
				48.8	53.3	-8.5	67.4	72.7	-7.2									
	70.7	80.6	-12.3															
	70.7	80.6	-12.3															
										82.4	90.1	-8.5	>128	125.8		75.2	81.8	-8.1
Method mean	AB13		-9.5	AB13		-7.8	AB13		-8.1	AB13		-8.5	AB13		-4.8	AB13		-8.1
A score				76			78			78			72			78		
B score				-7.6			-7.8			-7.8			-7.2			-7.8		
C score				4.0			3.4			3.1			3.1			3.1		

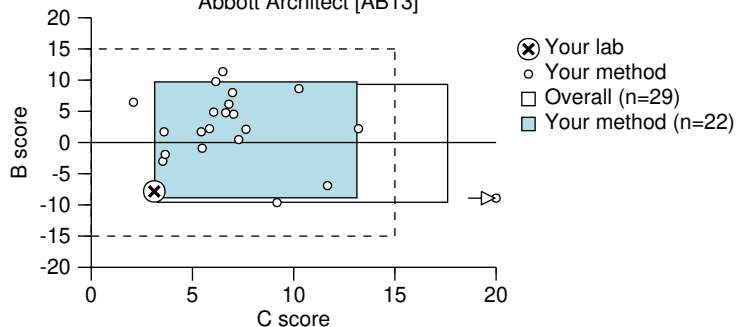
Median and IQRs of A scores



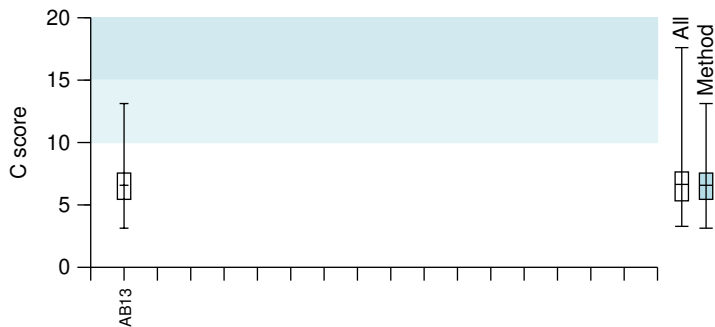
HoloTC Median and IQRs of B scores



HoloTC B score is -7.8 and C score is 3.1
Abbott Architect [AB13]



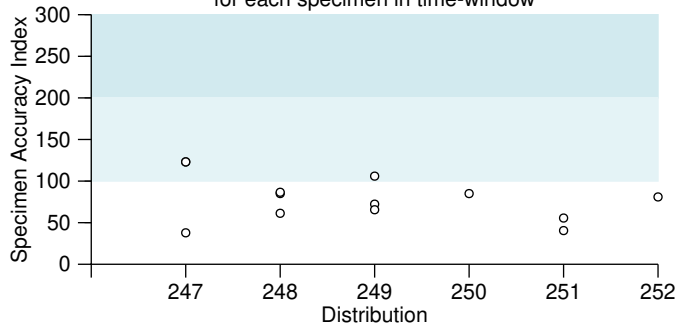
HoloTC Median and IQRs of C scores





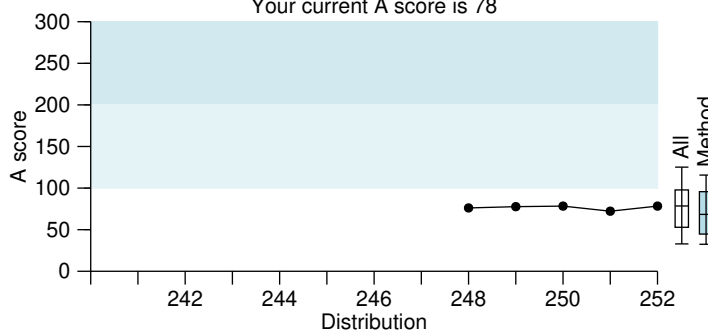
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Specimen Accuracy Index for each specimen in time-window



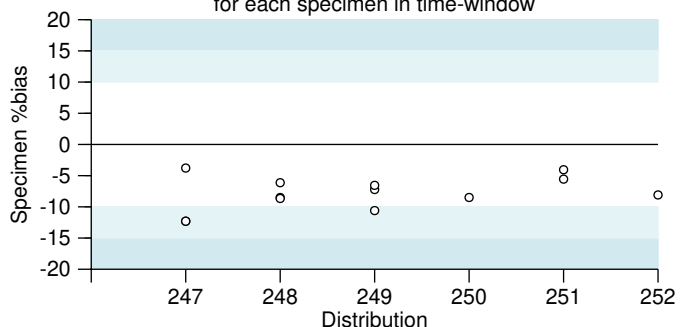
P-ABCAT5 (ABC1)

A score by distribution Your current A score is 78



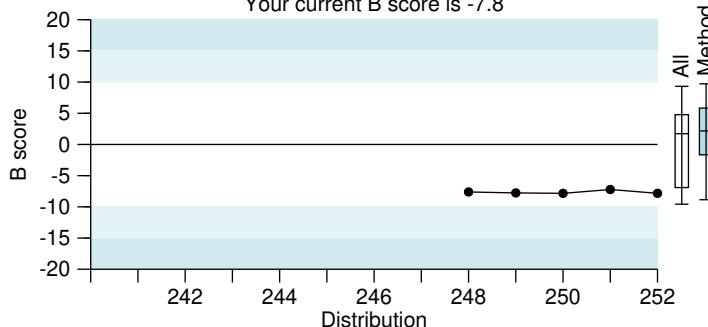
P-ABCAT (ABC1)

Specimen %bias for each specimen in time-window



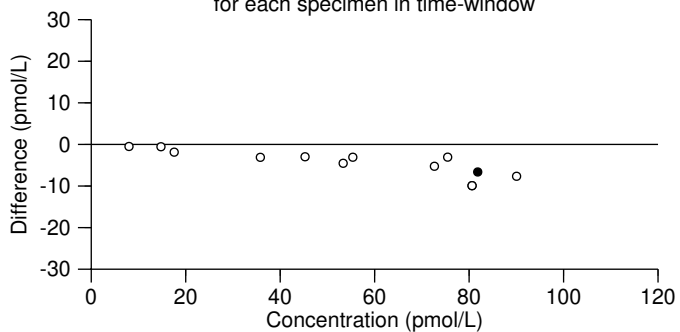
P-ABCBRS (ABC1)

B score by distribution Your current B score is -7.8



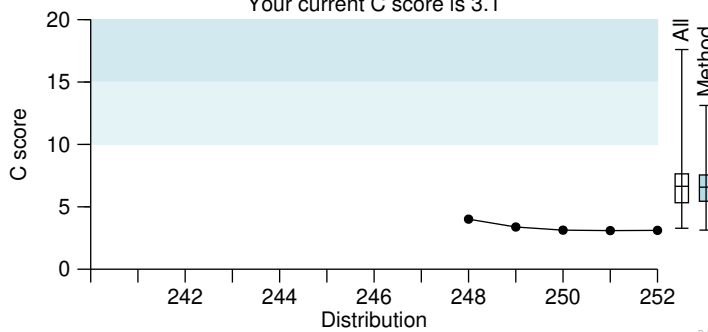
P-ABCBR (ABC1)

Difference (result - target) for each specimen in time-window



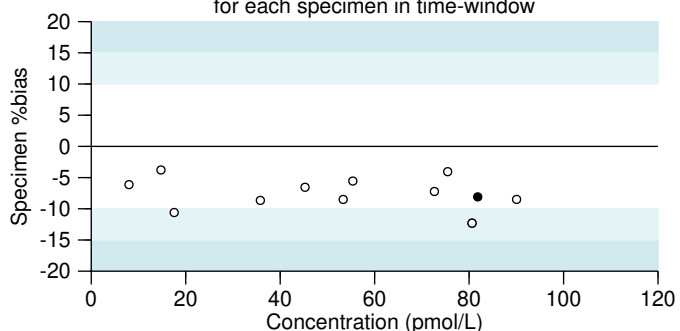
P-BA1F5IA (ABC1)

C score by distribution Your current C score is 3.1



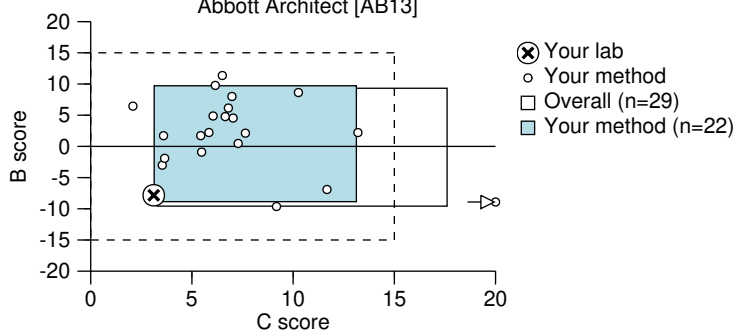
P-ABCCR (ABC1)

Specimen %bias for each specimen in time-window



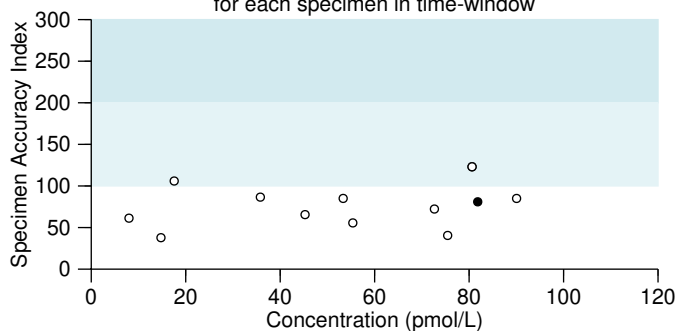
P-BA1F5IP (ABC1)

HoloTC B score is -7.8 and C score is 3.1 Abbott Architect [AB13]



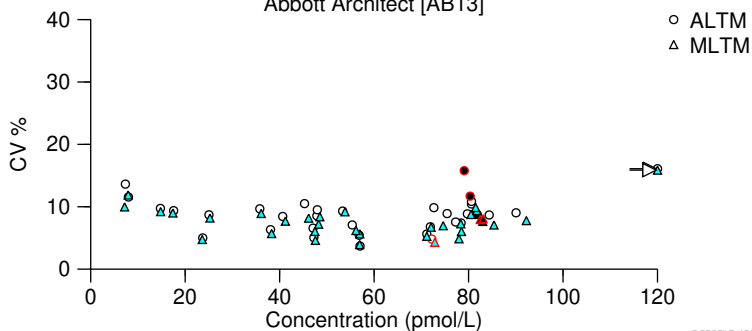
P-ABCPENR (ABC1)

Specimen Accuracy Index for each specimen in time-window



P-YSTMDD (ABC1)

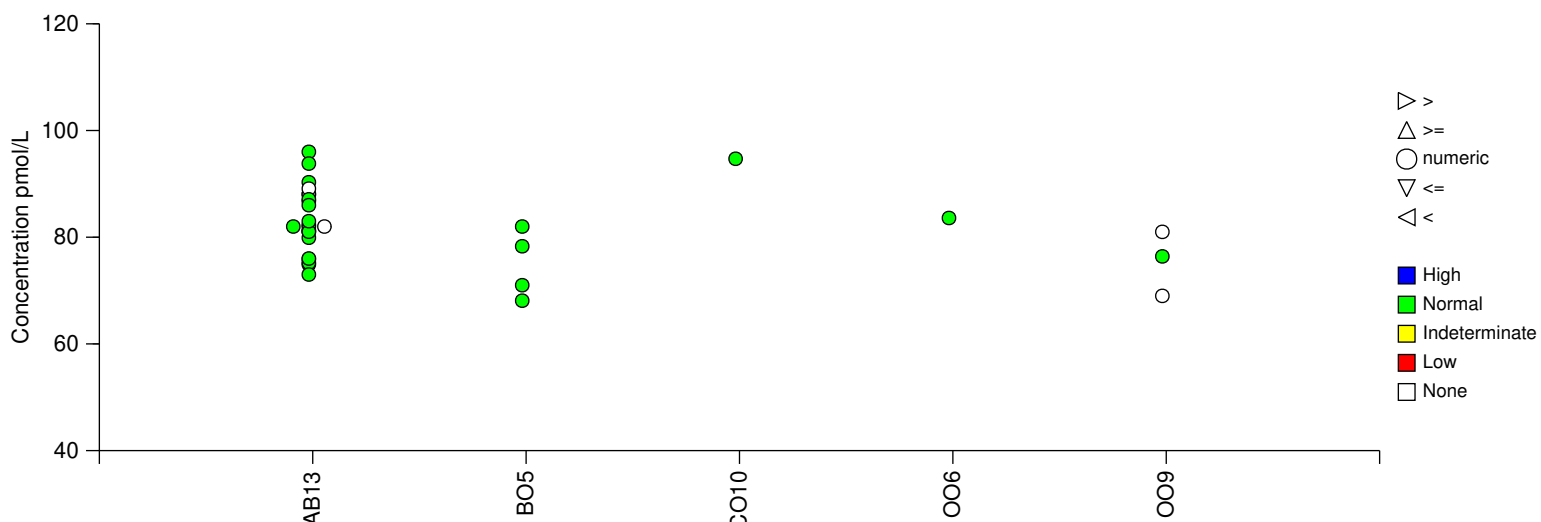
HoloTC Between-laboratory agreement Abbott Architect [AB13]



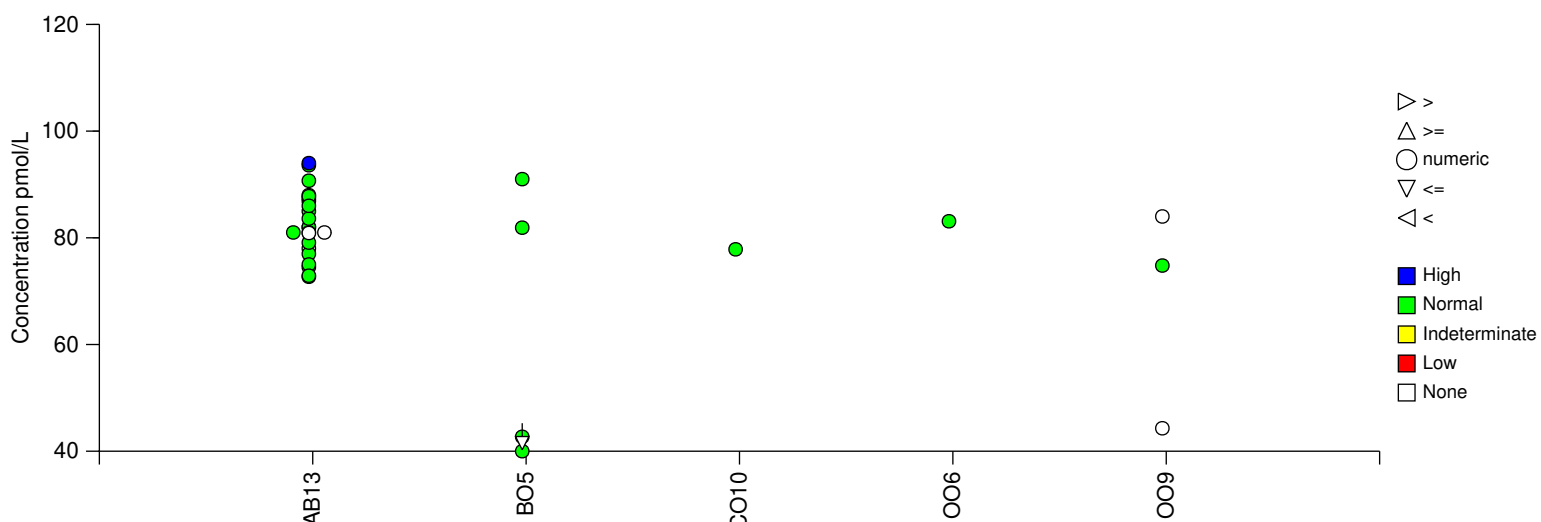
P-PROFILE (ABC1)



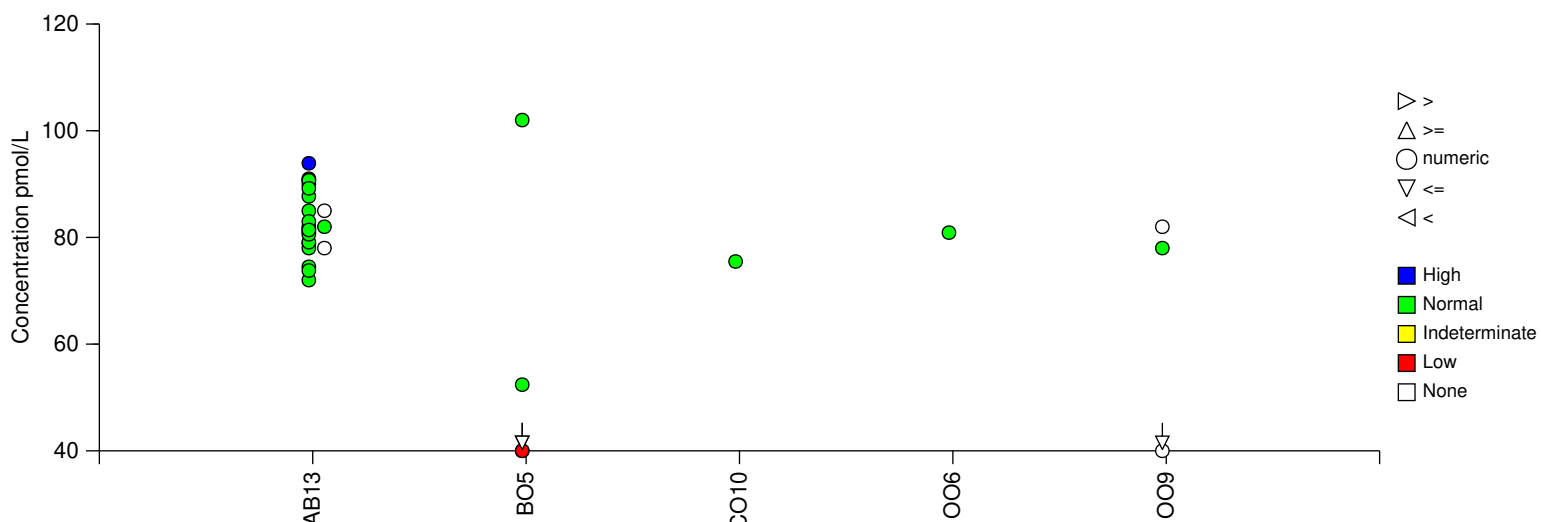
HoloTC - Specimen 252A



HoloTC - Specimen 252B

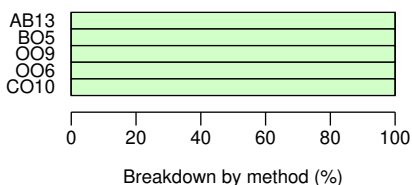
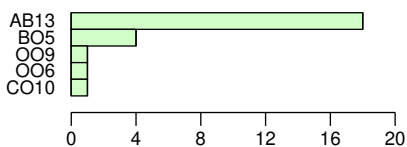
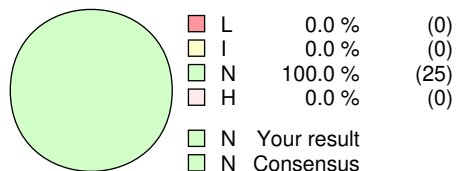


HoloTC - Specimen 252C

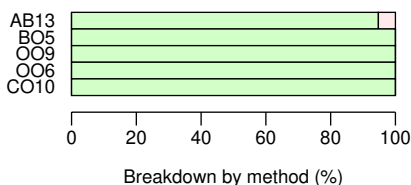
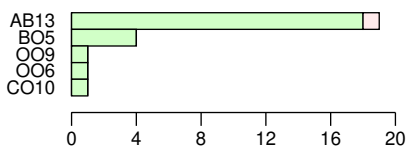
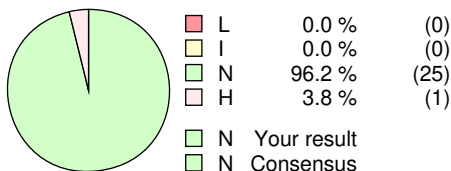




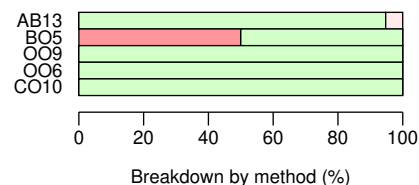
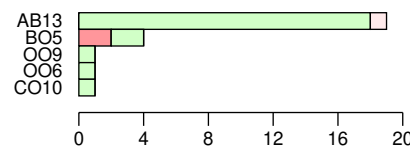
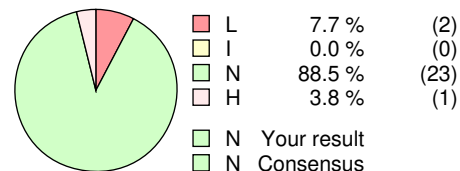
Specimen : 252A



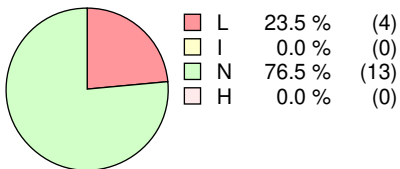
Specimen : 252B



Specimen : 252C

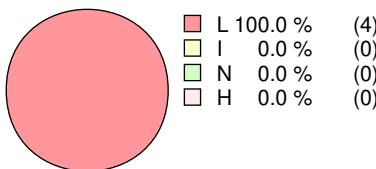


Specimens distributed in each category

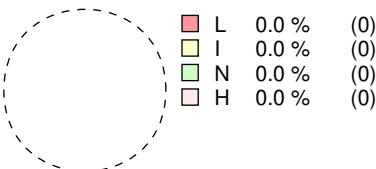


Your interpretation for each category

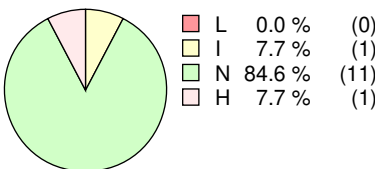
Low



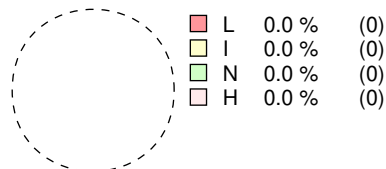
Indeterminate

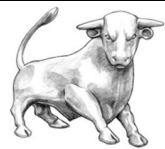


Normal



High





Birmingham Quality

UK NEQAS for Holotranscobalamin

Laboratory :

Distribution : **252**

Date : 19-Aug-2018

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Analyte : Methylmalonic acid (nmol/L)

Spec.	Pool	Pool description / Treatments / Additions
252A	277	Pooled human serum
252B	278	Pooled human serum + exogenous material
252C	279	Pooled human serum + exogenous material

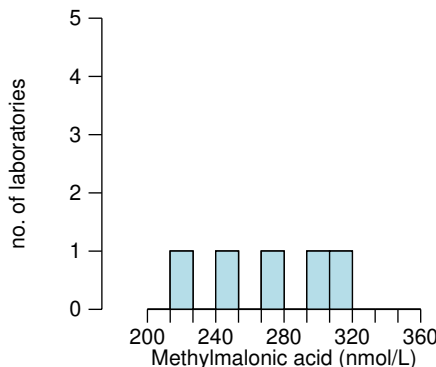
- All methods
- Mass spectrometry
- In-house [600]

Your A score is
Your B score is
Your C score is

The A limit is
The B limit is +/-
The C limit is

Specimen : 252A

	n	Mean	SD	CV(%)
All methods [ALTM]	5	277	50	18.0
Mass spectrometry	5	277	50	18.0
In-house [600]	5	277	50	18.0



Your result XPL
Target value 277
(ALTM)

Your Interpretation Consensus N

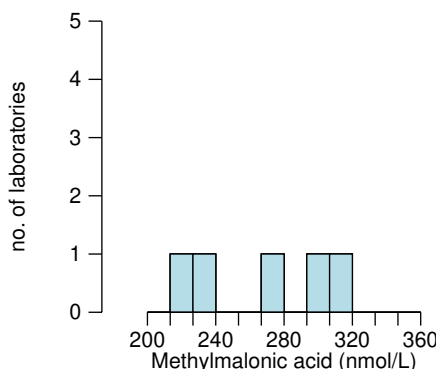
Standard Uncertainty 36

Your specimen:
%bias
Accuracy Index

Method mean (In-house [600]) 277

Specimen : 252B

	n	Mean	SD	CV(%)
All methods [ALTM]	5	273	60	21.9
Mass spectrometry	5	273	60	21.9
In-house [600]	5	273	60	21.9



Your result XPL
Target value 273
(ALTM)

Your Interpretation Consensus N

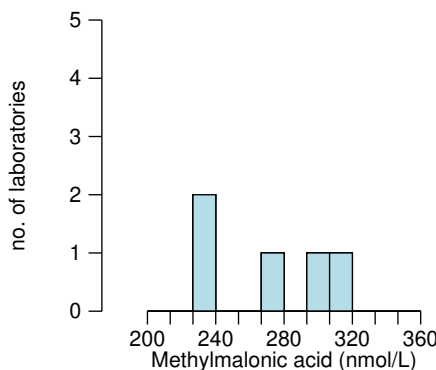
Standard Uncertainty 43

Your specimen:
%bias
Accuracy Index

Method mean (In-house [600]) 273

Specimen : 252C

	n	Mean	SD	CV(%)
All methods [ALTM]	5	273	60	21.9
Mass spectrometry	5	273	60	21.9
In-house [600]	5	273	60	21.9



Your result XPL
Target value 273
(ALTM)

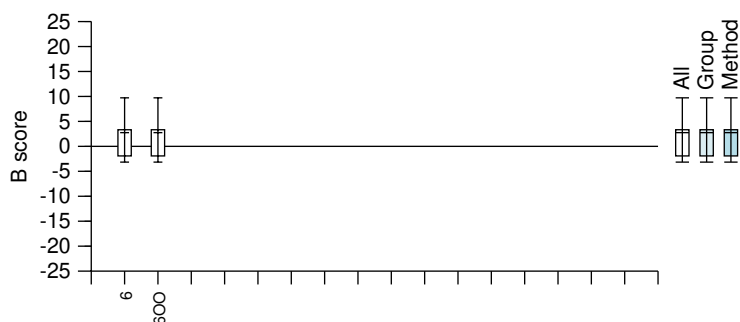
Your Interpretation Consensus N

Standard Uncertainty 43

Your specimen:
%bias
Accuracy Index

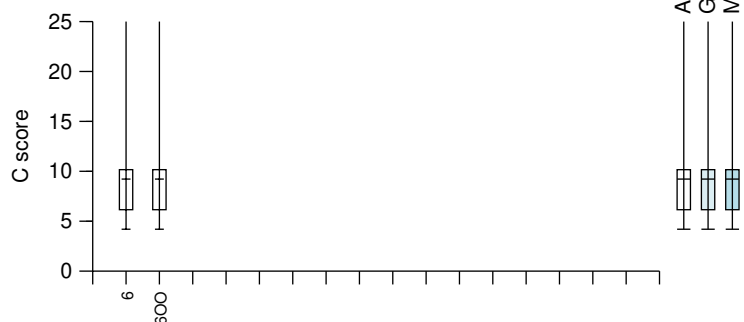
Method mean (In-house [600]) 273

Methylmalonic acid Median and IQRs of B scores



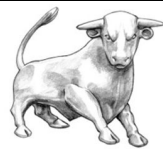
P:BWABCBP

Methylmalonic acid Median and IQRs of C scores



P:BWABCBP

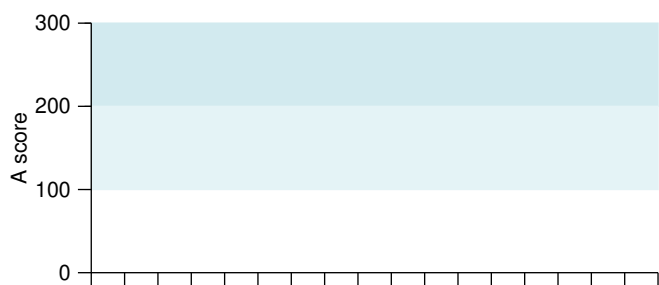
A scores, and B and C score limits are not yet available for this analyte.



Birmingham Quality

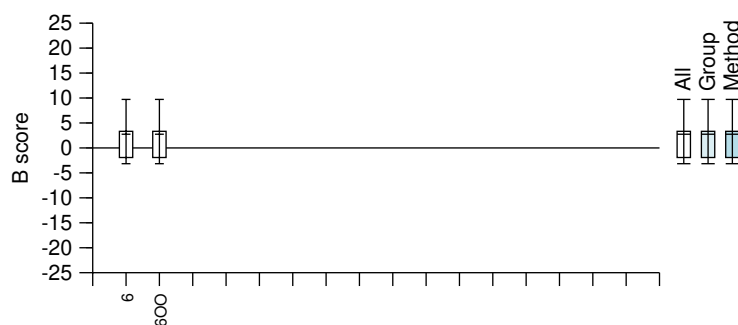
Pool (exclusion) [Type]	Distribution 247 11-Mar-2018 result target %bias	Distribution 248 15-Apr-2018 result target %bias	Distribution 249 13-May-2018 result target %bias	Distribution 250 17-Jun-2018 result target %bias	Distribution 251 22-Jul-2018 result target %bias	Distribution 252 19-Aug-2018 result target %bias
246 276 274 260 278 279 263 277 273 271 272 270 261 268 269 267 266	XPL 25 XPL 234 XPL 646	 XPL 480 XPL 708 XPL 834	 XPL 499 XPL 557 XPL 673	 XPL 347 XPL 943	 XPL 198 XPL 221 XPL 275	 XPL 273 XPL 273 XPL 277
Method	600	600	600	600	600	600
A score B score C score						

Median and IQRs of A scores



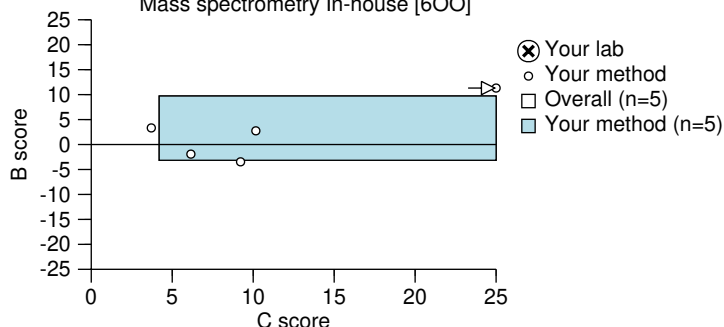
P-BWABCAT

Methylmalonic acid Median and IQRs of B scores



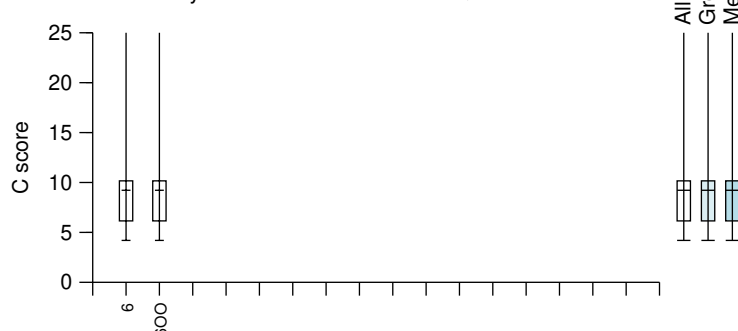
P-BWABCGR

Methylmalonic acid B score is and C score is
Mass spectrometry In-house [600]



P-ABCPEUR

Methylmalonic acid Median and IQRs of C scores



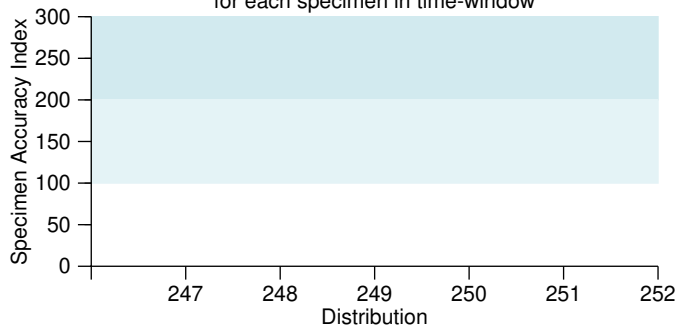
P-BWABCCR



Birmingham Quality

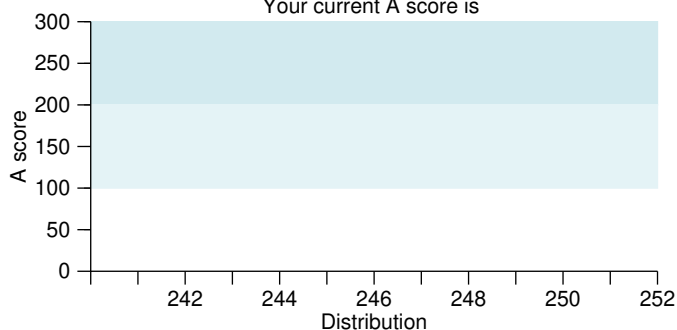
Methylmalonic acid nmol/L

Specimen Accuracy Index for each specimen in time-window



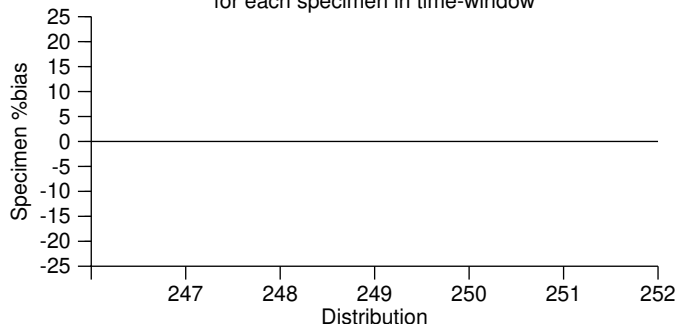
P-ABCATS (ABC1)

A score by distribution Your current A score is



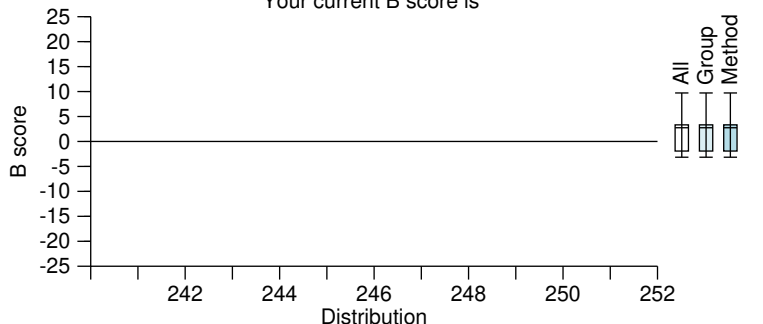
P-ABCAT (ABC1)

Specimen %bias for each specimen in time-window



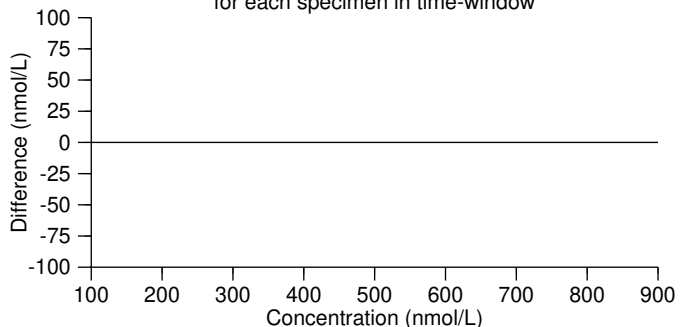
P-ABCBS (ABC1)

B score by distribution Your current B score is



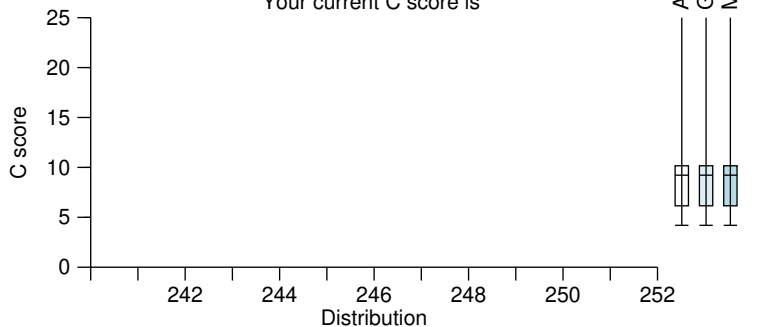
P-ABCB (ABC1)

Difference (result - target) for each specimen in time-window



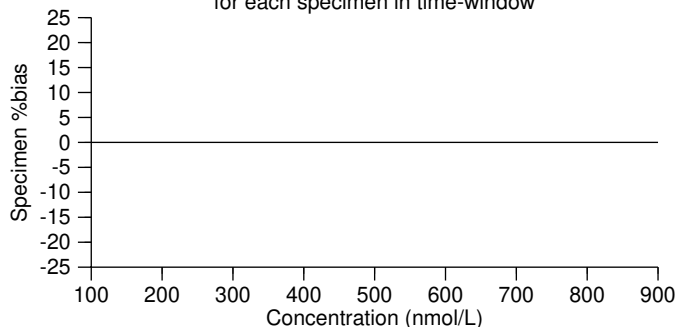
P-BA1FSA (ABC1)

C score by distribution Your current C score is



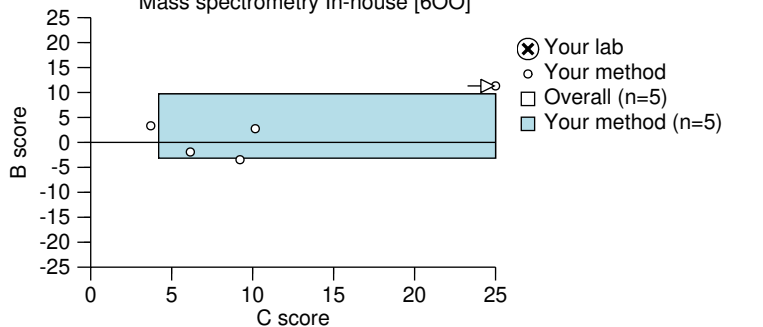
P-ABCC (ABC1)

Specimen %bias for each specimen in time-window



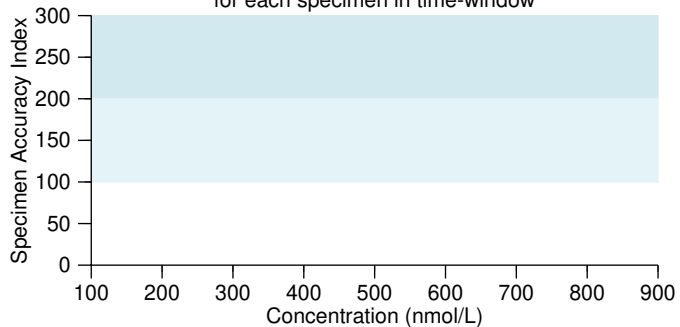
P-BA1FSP (ABC1)

Methylmalonic acid B score is and C score is Mass spectrometry In-house [600]



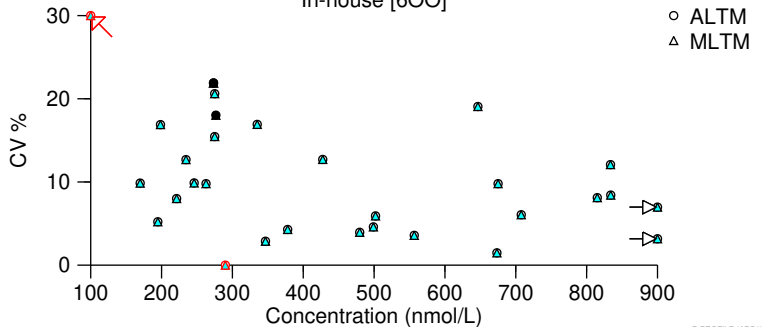
P-ABCPENR (ABC1)

Specimen Accuracy Index for each specimen in time-window



P-YSTMOD (ABC1)

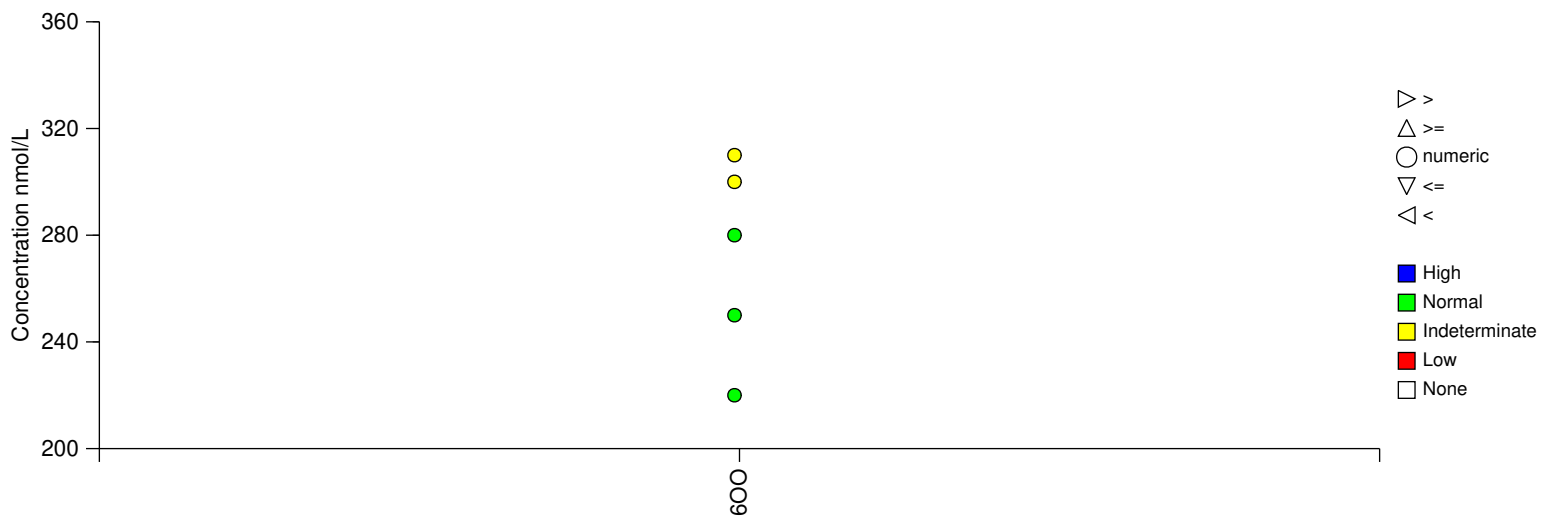
Methylmalonic acid Between-laboratory agreement In-house [600]



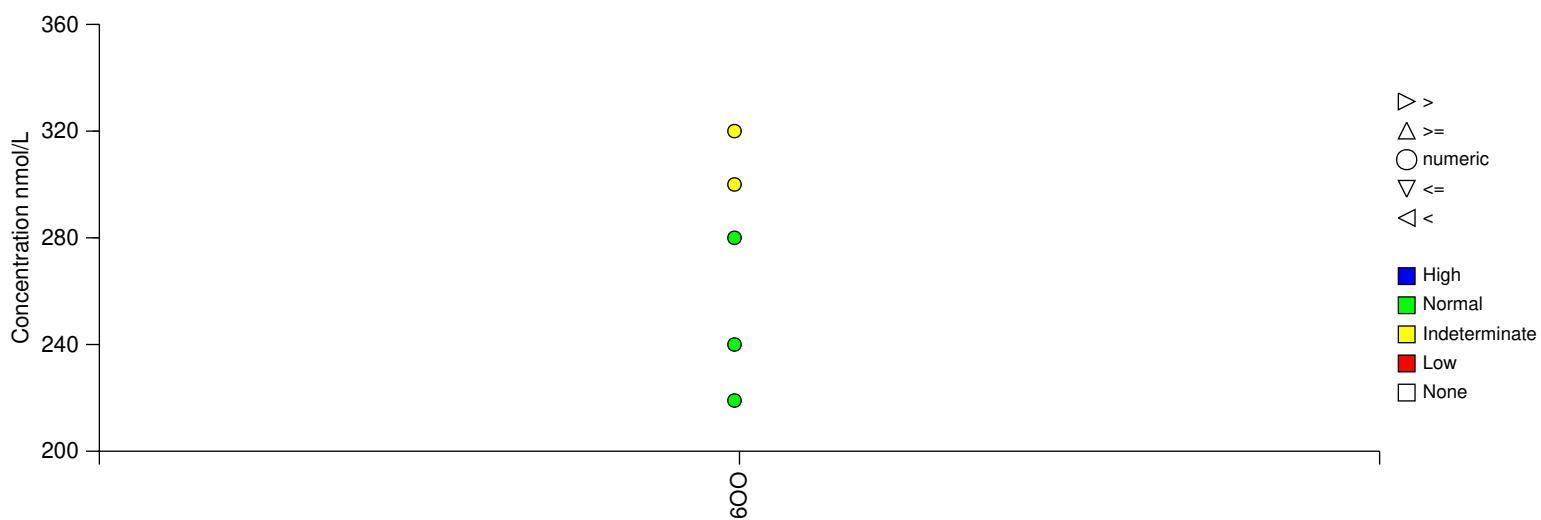
P-PROFILE (ABC1)



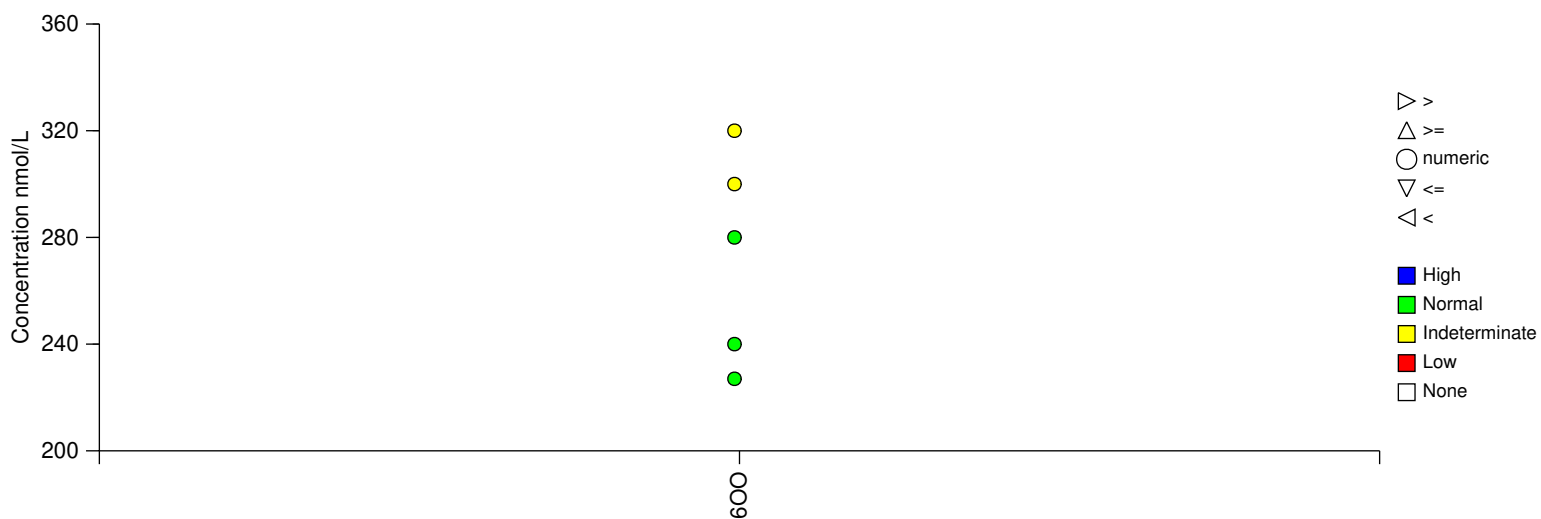
Methylmalonic acid - Specimen 252A



Methylmalonic acid - Specimen 252B

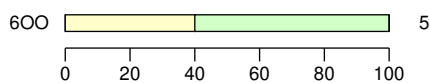
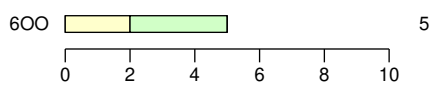
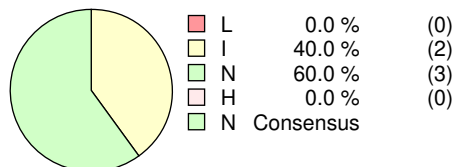


Methylmalonic acid - Specimen 252C

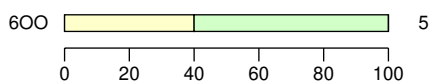
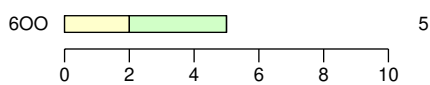
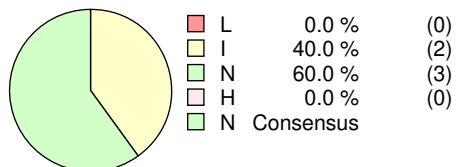




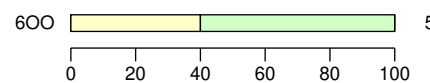
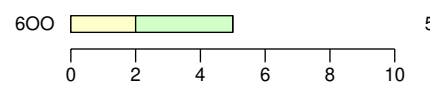
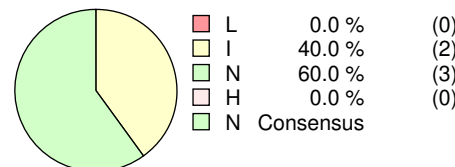
Specimen : 252A



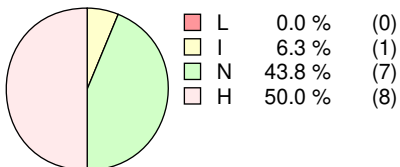
Specimen : 252B



Specimen : 252C



Specimens distributed in each category



Your interpretation for each category

Low

Indeterminate

Normal

High

