

National Conversation: Tandem Mass Spectrometry in Newborn Screening

Quality Assurance & Quality Improvement

Scott M. Shone, PhD

February 6, 2015

- **Quality Assurance (QA)** – all the planned and systematic activities implemented within the quality system, and demonstrated as needed, to provide adequate confidence that an entity will fulfill requirements for quality. **NOTE:** Quality assurance may be said to comprise internal quality assurance and external quality assurance and is interrelated with quality control.
- **Quality Control (QC)** – the operational techniques and activities that are used to fulfill requirements for quality.
- **Quality Indicators (QI)** - a metric that gives an indication of process or output quality and can be used to make comparisons across different Programs

Rejecting assays is not the purpose of quality control



Materials

- Source
 - In-house
 - Commercial vendor
 - Kit
 - Non-kit
 - CDC NSQAP
- Levels
 - Decision points
 - WNL
 - Abnormal



Method

- Analyte selection
 - *m/z* range
 - Classes
 - Acquisition modes
 - Internal standards
- Establishing laboratory range
 - Replicates ≥ 20 observations
 - Instrument to Instrument
- Frequency
 - ≥ 2 per plate

Sample
C0
C2
C3
C4
C4 SRM
C5
C5 SRM
C5DC
C6
C8
C10
C12
C14
C16
C16 SRM
C18
C18 SRM
CIT
LEU
MET
PHE
TYR
ARG
C3 IS INT
C4 IS INT
C16 IS INT
CIT IS INT
LEU IS INT
PHE IS INT

Method

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PerkinElmer QUALITY CONTROL CERTIFICATE / CERTIFICAT DE CONTRÔLE DE QUALITÉ / QUALITÄTSKONTROLLZERTIFIKAT / CERTIFICADO DE CONTROL DE CALIDAD

NeoGram[®] Amino Acids and Acylcarnitines Tandem Mass Spectrometry Kit, Whatman 903

Catalog no. / Référence du catalogue / Basiskonnummer / Número de catálogo	3026-0030	Kit lot / Lot de trousse / Kit-Charge / Lote del Kit	635039	Expiry date / Date de péremption / Verfallsdatum / Fecha de caducidad	2015-09
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Component / Composant / Komponente / Componente	Lot No. / Lot n° / Ch.-Nr. / Nº de lote	Expiry date / Date de péremption / Verfallsdatum / Fecha de caducidad
Control Cards	634335	2015-09
Amino Acids Internal Standards	634893	2015-11
Acylcarnitines Internal Standards	633442	2015-09

Standard / Standard Standard / Estándar		Concentration / Concentration Konzentration / Concentración		Standard / Standard Standard / Estándar		Concentration / Concentration Konzentration / Concentración	
d ₃ -Carnitine (Free carnitine)	d ₃ -C0	0.758	µmol/L	d ₃ -Alanine	d ₃ -Ala	2.56	µmol/L
d ₃ -Acetylcarnitine	d ₃ -C2	0.094	µmol/L	d ₄ - ¹³ C-Arginine-HCl	d ₄ - ¹³ C-Arg	2.26	µmol/L
d ₃ -Propionylcarnitine	d ₃ -C3	0.049	µmol/L	d ₃ -Citrulline	d ₃ -Cit	2.12	µmol/L
d ₃ -Butyrylcarnitine	d ₃ -C4	0.038	µmol/L	¹⁵ N, ² - ¹³ C-Glycine	¹⁵ N, ² - ¹³ C-Gly	11.64	µmol/L
d ₃ -Isovalerylcarnitine	d ₃ -C5	0.036	µmol/L	d ₃ -Leucine	d ₃ -Leu	2.60	µmol/L
d ₃ -Glutaryl carnitine	d ₃ -C5DC	0.042	µmol/L	d ₃ -Methionine	d ₃ -Met	2.39	µmol/L
d ₃ -Hexanoylcarnitine	d ₃ -C6	0.040	µmol/L	d ₃ -Ornithine 2HCl	d ₃ -Orn	2.25	µmol/L
d ₃ -Octanoylcarnitine	d ₃ -C8	0.041	µmol/L	d ₃ -Phenylalanine	d ₃ -Phe	2.49	µmol/L
d ₃ -Decanoylcarnitine	d ₃ -C10	0.039	µmol/L	¹³ C ₉ -Tyrosine	¹³ C ₉ -Tyr	2.39	µmol/L
d ₃ -Lauroyl carnitine	d ₃ -C12	0.075	µmol/L	d ₃ -Valine	d ₃ -Val	2.49	µmol/L
d ₃ -Myristoylcarnitine	d ₃ -C14	0.079	µmol/L				
d ₃ -Palmitoylcarnitine	d ₃ -C16	0.071	µmol/L				
d ₃ -Octadecanoylcarnitine	d ₃ -C18	0.082	µmol/L				

AC	Low control / Contrôle faible / Niedrige Kontrolle / Control bajo		High control / Contrôle élevé / Hohe Kontrolle / Control alto	
	Result / Résultat / Ergebnis / Resultado	1 SD / 1 DS / 1 SA / 1 DE	Result / Résultat / Ergebnis / Resultado	1 SD / 1 DS / 1 SA / 1 DE
C0	189.23 µmol/L	36.90	462.26 µmol/L	90.14
C2	34.12 µmol/L	6.04	73.60 µmol/L	13.03
C3	10.34 µmol/L	3.71	27.74 µmol/L	9.96
C4	3.05 µmol/L	0.74	6.13 µmol/L	1.98
C5	1.28 µmol/L	0.33	3.41 µmol/L	0.89
C5DC	0.69 µmol/L	0.16	1.80 µmol/L	0.41
C6	0.64 µmol/L	0.17	1.90 µmol/L	0.50
C8	0.69 µmol/L	0.16	2.03 µmol/L	0.53
C10	0.54 µmol/L	0.11	1.49 µmol/L	0.30
C12	1.95 µmol/L	0.43	5.45 µmol/L	1.19
C14	1.85 µmol/L	0.40	4.98 µmol/L	1.08
C16	12.74 µmol/L	2.15	32.22 µmol/L	5.45
C18	2.55 µmol/L	0.48	5.18 µmol/L	0.98

AA	Low control / Contrôle faible / Niedrige Kontrolle / Control bajo		High control / Contrôle élevé / Hohe Kontrolle / Control alto	
	Result / Résultat / Ergebnis / Resultado	1 SD / 1 DS / 1 SA / 1 DE	Result / Résultat / Ergebnis / Resultado	1 SD / 1 DS / 1 SA / 1 DE
Ala	656 µmol/L	79	1439 µmol/L	173
Cit	180 µmol/L	30	598 µmol/L	99
Gly	610 µmol/L	77	1475 µmol/L	186
Leu	467 µmol/L	66	1570 µmol/L	214
Met	88 µmol/L	17	312 µmol/L	58
Phe	226 µmol/L	28	711 µmol/L	87
Tyr	332 µmol/L	44	1150 µmol/L	152
Val	365 µmol/L	62	965 µmol/L	169

Method

- Analyte selection
 - m/z range
 - Classes
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 - ≥ 2 per plate

Trace Editor

Assay run definitions: AAAC 2/6/2014 - 2/6/2015

Activate Traces Edit Active Traces Adjust Limits Edit Trace Statuses Print

Material	Level	Test	Current Target	Target diff %	Current SD Limit	SD Limit diff %	Values from	Editable Target	Editable SD Limit	Add Limit
HC635039	HIGH	dC0	363.61	2.5	20.43	-37.0	Points (503)	354.70	32.41	<input type="checkbox"/>
		dC2	76.16	3.1	4.73	-6.6		73.89	5.06	<input type="checkbox"/>
		dC3	24.44	6.0	1.77	-10.6		23.06	1.98	<input type="checkbox"/>
		dC4	6.9	2.6	1.11	6.2		6.73	1.04	<input type="checkbox"/>
		dC4M	7.18	4.3	0.53	0.4		6.88	0.53	<input type="checkbox"/>
		dC5	2.64	4.5	0.43	7.7		2.53	0.40	<input type="checkbox"/>
		dC5M	2.75	6.1	0.23	1.1		2.59	0.23	<input type="checkbox"/>
		dC5DC	1.57	3.2	0.11	-7.8		1.52	0.12	<input type="checkbox"/>
		dC6	1.67	5.7	0.39	19.8		1.58	0.33	<input type="checkbox"/>
		dC8	1.85	8.9	0.38	14.0		1.70	0.33	<input type="checkbox"/>
		dC10	1.33	7.5	0.31	28.4		1.24	0.24	<input type="checkbox"/>
		dC12	5.2	4.2	0.74	15.4		4.99	0.64	<input type="checkbox"/>
		dC14	4.75	2.5	0.61	2.4		4.63	0.60	<input type="checkbox"/>
		dC16	30.56	1.3	3.43	2.7		30.16	3.34	<input type="checkbox"/>
		dC16M	31.48	2.7	1.98	-1.6		30.64	2.01	<input type="checkbox"/>
		dC18	5.03	3.6	0.79	21.8		4.86	0.65	<input type="checkbox"/>
		dC18M	5.02	2.6	0.32	-7.5		4.89	0.35	<input type="checkbox"/>
		dCit	522.83	4.2	35.54	-2.2		501.54	36.34	<input type="checkbox"/>
dLeu	1482.09	0.3	157.13	8.6	1477.59	144.62	<input type="checkbox"/>			
dMet	291.99	3.1	33.4	1.6	283.20	32.89	<input type="checkbox"/>			
dPhe	647.52	3.3	52.15	-3.7	626.99	54.15	<input type="checkbox"/>			
dTyr	998.39	-0.9	98.78	2.0	1007.55	96.82	<input type="checkbox"/>			
dArg	5.43	-1.4	0.76	17.9	5.51	0.64	<input type="checkbox"/>			
dC3-IS-INT	35312.62	-12.2	18339.21	-5.7	40226.34	19455.36	<input type="checkbox"/>			
dC4-IS-INT	234093.47	-15.0	150000.74	-6.0	275520.65	159502.60	<input type="checkbox"/>			
dC16-IS-INT	529902.29	-17.5	264833.73	-10.2	641977.17	294798.63	<input type="checkbox"/>			
dCit-IS-INT	116079.93	1.4	48675.31	7.9	114460.95	45100.76	<input type="checkbox"/>			

Review QC limits against running mean and SD. QC limits can also be adjusted if necessary.

Apply Close

Method

- Analyte selection
 - m/z range
 - Classes
 - Acquisition modes
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MS	Year	[D]ay	(P)late# 1	Processed Date								
	1	2	3	4	5	6	7	8	9	10	11	12
A	ac&aa_b 1	ac&aa_b 2	ac&aa_b 3	ac&aa_b 4	ac&aa_b 5	ac&aa_b 6			ACodc_1466 8	ACodc_1467 9	AAodc_1426 10	AAodc_1427 11
B	ac&aa_b 13	ac&aa_h 14	0001 15	0002 16	0003 17	0004 18	0005 19	0006 20	0007 21	0008 22	0009 23	0010 24
C	0011 25	0012 26	0013 27	0014 28	0015 29	0016 30	0017 31	0018 32	0019 33	0020 34	0021 35	0022 36
D	0023 37	0024 38	0025 39	0026 40	0027 41	0028 42	0029 43	0030 44	0031 45	0032 46	0033 47	0034 48
E	0035 49	0036 50	0037 51	0038 52	0039 53	0040 54	0041 55	0042 56	0043 57	0044 58	0045 59	0046 60
F	0047 61	0048 62	0049 63	0050 64	0051 65	0052 66	0053 67	0054 68	0055 69	0056 70	0057 71	0058 72
G	0059 73	0060 74	0061 75	0062 76	0063 77	0064 78	0065 79	0066 80	0067 81	0068 82	0069 83	0070 84
H	0071 85	0072 86	0073 87	0074 88	0075 89	0076 90	0077 91	0078 92	0079 93	0080 94	ac&aa_h 95	ac&aa_b 96

AA&AC IS#			Retest Spec punched by:
Control sheet#	Punched by:		
Extraction	Tech Initials		Retest Spec # verified by:
1st Drying Time	Added Butanol Tech Initials		Dryer #
Incubation Time			
2nd Drying Time	Added Recon sol'n Tech Initials		Dryer #
Comments			Comments

Monitor & Corrective Action

- Acceptance Criteria
 - Modified Westgard
 - Controls
 - Individual vs. Multiple analytes
 - Individual vs. Multiple Controls
 - Patients
 - Mean
 - Median
- Frequency
- Trends
- Shifts

Sample	2015035P1-LOW1	2015035P1-LOW2	Range	2015035P1-HIGH1	2015035P1-HIGH2	Range
C0	139.46	157.12	(123.52 - 181.60)	358.85	342.54	(302.32 - 424.90)
C2	32.49	35.83	(29.79 - 42.99)	73.68	73.62	(61.97 - 90.35)
C3	8.33	9.44	(7.46 - 11.60)	23.56	22.56	(19.13 - 29.75)
C4	1.68	2.65	(1.39 - 4.09)	7.73	5.95	(3.57 - 10.23)
C4 MRM	2.31	2.63	(2.21 - 3.35)	6.68	6.27	(5.59 - 8.77)
C5	1.23	1.06	(0.50 - 1.58)	2.29	2.26	(1.35 - 3.93)
C5 MRM	0.94	1.05	(0.87 - 1.23)	2.49	2.55	(2.06 - 3.44)
C5DC	0.63	0.67	(0.48 - 0.72)	1.53	1.48	(1.24 - 1.90)
C6	0.42	0.63	(0.17 - 1.07)	2.19	1.46	(0.50 - 2.84)
C8	0.8	0.62	(0.24 - 1.08)	1.79	1.4	(0.71 - 2.99)
C10	0.55	0.49	(0.14 - 0.86)	1.28	0.61	(0.40 - 2.26)
C12	2.11	1.9	(1.08 - 2.82)	4.1	5.22	(2.98 - 7.42)
C14	1.99	2.19	(1.06 - 2.62)	3.65	5.43	(2.92 - 6.58)
C16	10.86	10.86	(8.09 - 17.09)	24.34	27.81	(20.27 - 40.85)
C16 MRM	11.7	13.62	(10.62 - 14.70)	31.59	29.63	(25.54 - 37.42)
C18	2.26	2.35	(1.59 - 3.33)	5.2	5.98	(2.66 - 7.40)
C18 MRM	2.36	2.56	(2.02 - 2.98)	4.87	4.67	(4.06 - 5.98)
CIT	161.82	174.12	(128.98 - 191.02)	526.25	509.94	(416.21 - 629.45)
LEU	379.78	575.87	(363.63 - 613.17)	1614.49	1485.48	(1010.70 - 1953.48)
MET	94.2	109.52	(54.32 - 112.76)	321.77	253.68	(191.79 - 392.19)
PHE	192.89	227.81	(167.78 - 254.48)	539.97	656.16	(491.07 - 803.97)
TYR	281.85	391.81	(215.61 - 389.97)	1107.64	999.54	(702.05 - 1294.73)
ARG	6.88	6.33	(3.36 - 7.08)	5.61	5.1	(3.15 - 7.71)

Monitor & Corrective Action

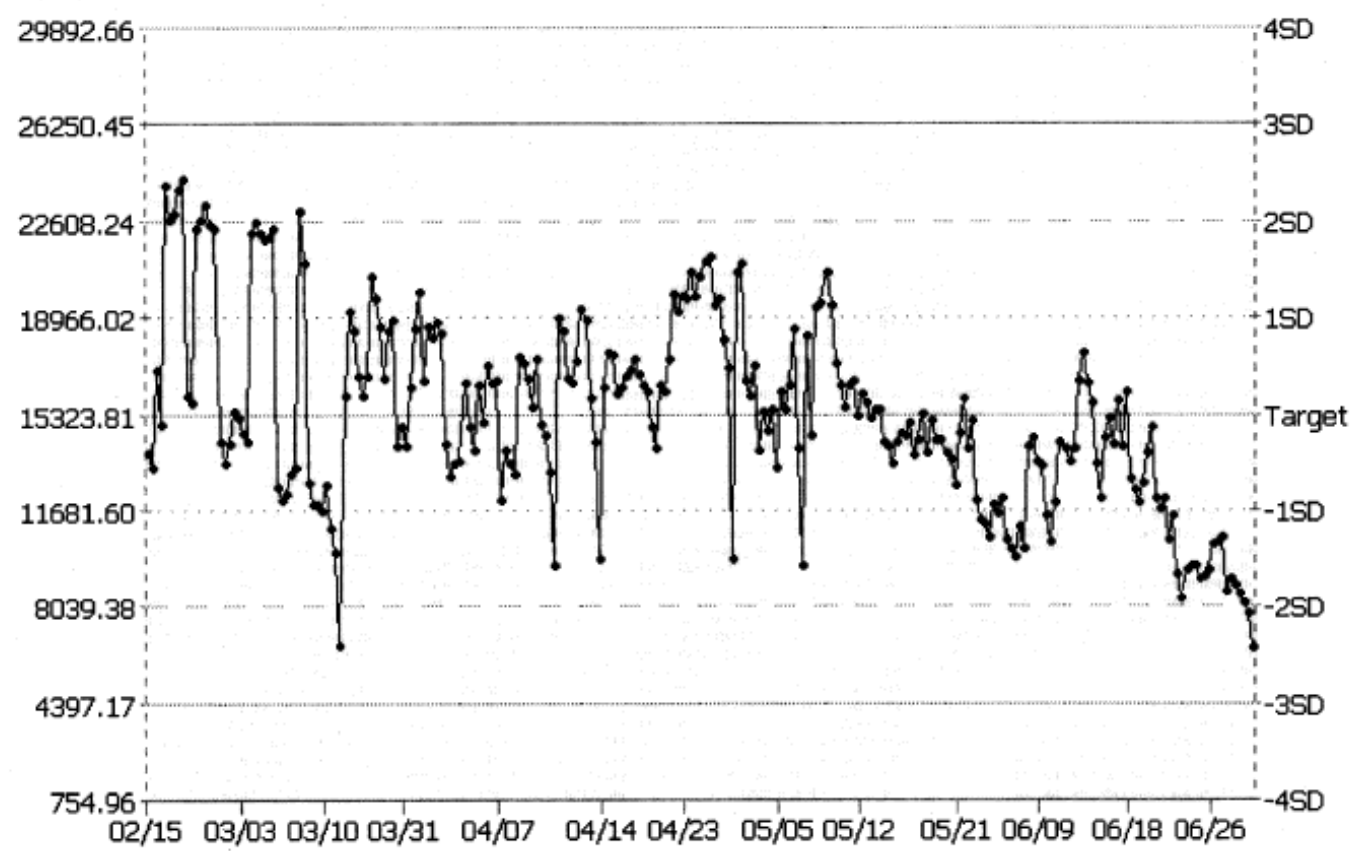
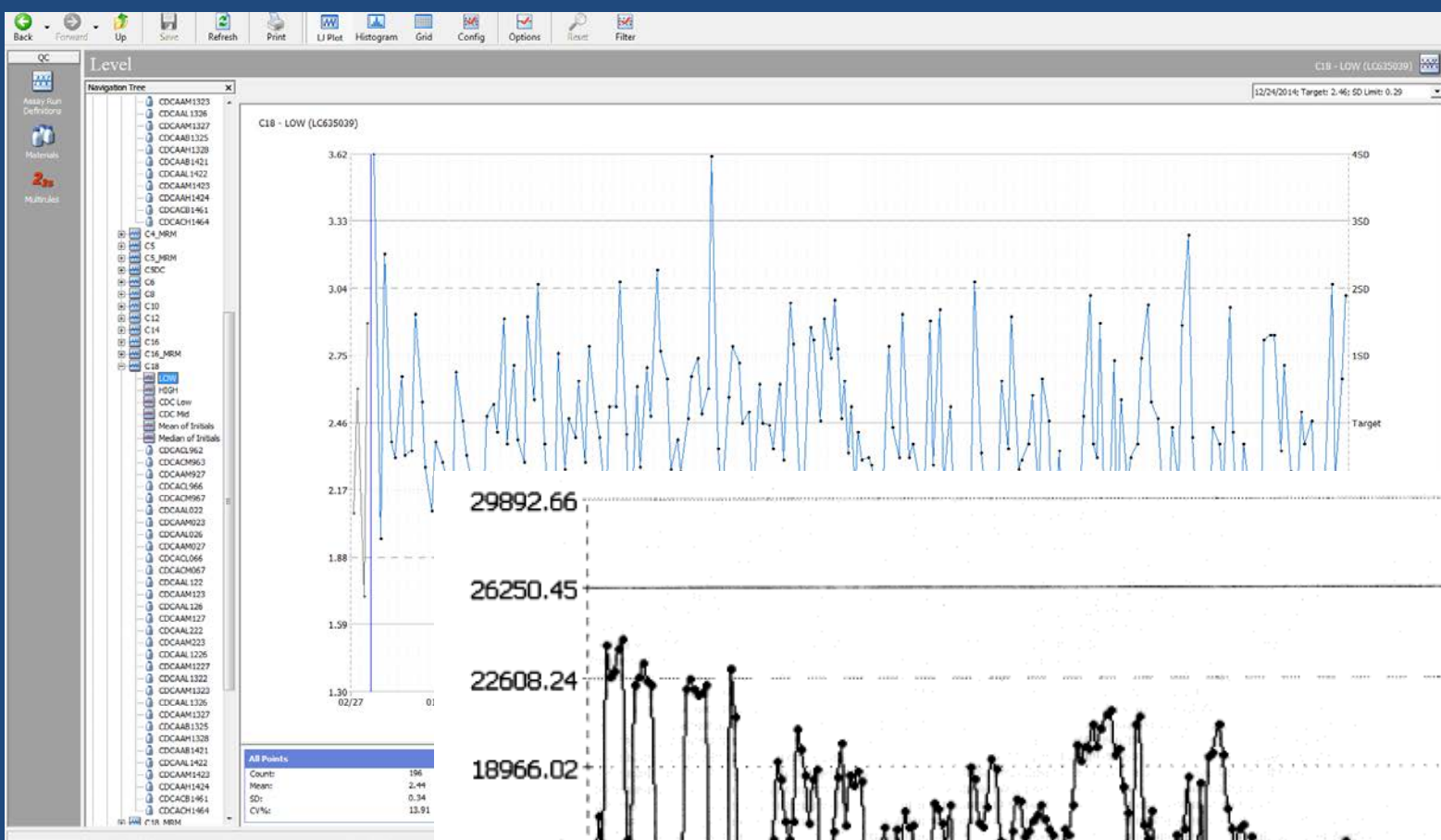
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Sample	2015035P1-LOW1	2015035P1-LOW2	Range	2015035P1-HIGH1	2015035P1-HIGH2	Range
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C4	1.68	2.65	(1.39 - 4.09)	7.73	5.95	(3.57 - 10.23)
C4 MRM	2.31	2.63	(2.21 - 3.35)	6.68	6.27	(5.59 - 8.77)
C5	1.23	1.06	(0.50 - 1.58)	2.29	2.26	(1.35 - 3.93)
C5 MRM	0.94	1.05	(0.87 - 1.23)	2.49	2.55	(2.06 - 3.44)
C5DC	0.63	0.67	(0.48 - 0.72)	1.53	1.48	(1.24 - 1.90)
C6	0.42	0.63	(0.17 - 1.07)	2.19	1.46	(0.50 - 2.84)
C8	0.8	0.62	(0.24 - 1.08)	1.79	1.4	(0.71 - 2.99)
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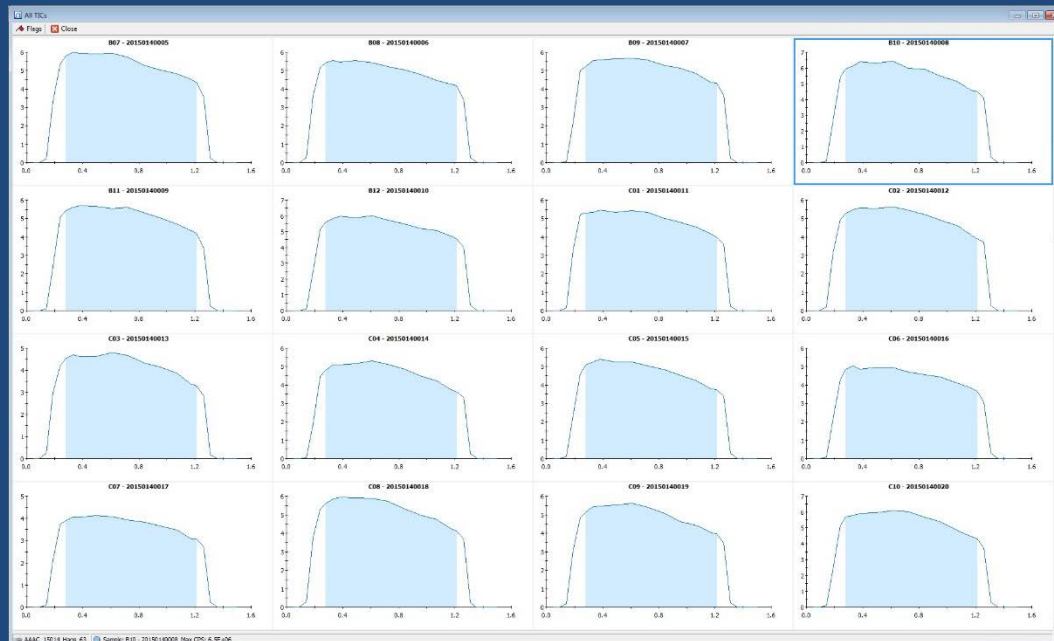
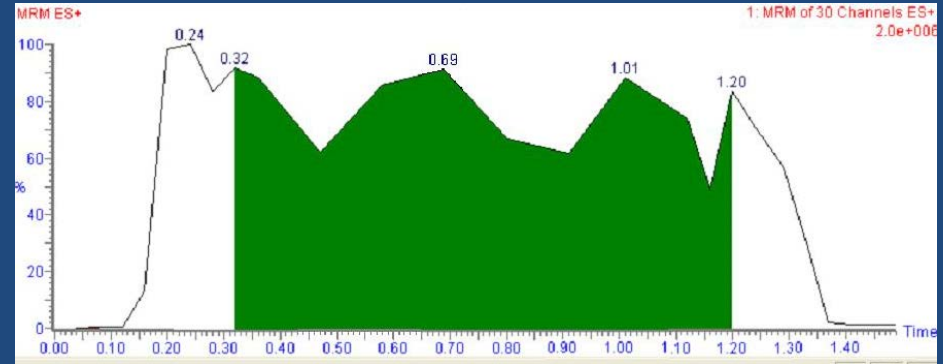
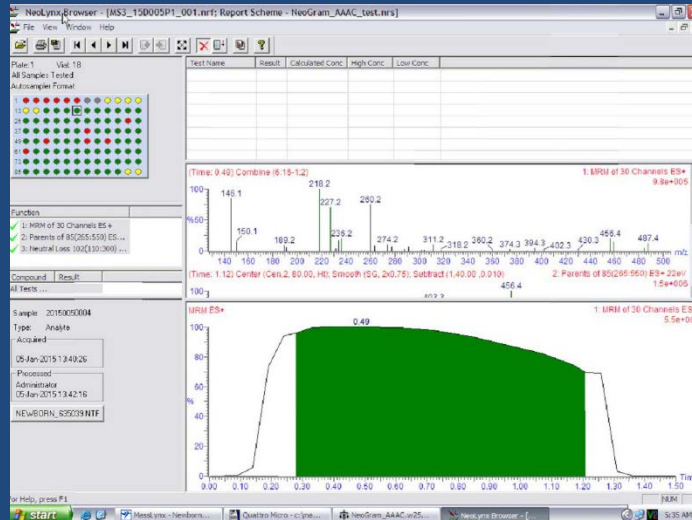
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C3	8.33	9.44	(7.46 - 11.60)	23.56	22.56	(19.13 - 29.75)
C4	1.68	2.65	(1.39 - 4.09)	7.73	5.95	(3.57 - 10.23)
C4 MRM	2.31	2.63	(2.21 - 3.35)	6.68	6.27	(5.59 - 8.77)
C5	1.23	1.06	(0.50 - 1.58)	2.29	2.26	(1.35 - 3.93)
C5 MRM	0.94	1.05	(0.87 - 1.23)	2.49	2.55	(2.06 - 3.44)
C5DC	0.63	0.67	(0.48 - 0.72)	1.53	1.48	(1.24 - 1.90)
C6	0.42	0.63	(0.17 - 1.07)	2.19	1.46	(0.50 - 2.84)
C8	0.8	0.62	(0.24 - 1.08)	1.79	1.4	(0.71 - 2.99)
C10	0.55	0.49	(0.14 - 0.86)	1.28	0.61	(0.40 - 2.26)
C12	2.11	1.9	(1.08 - 2.82)	4.1	5.22	(2.98 - 7.42)
C14	1.99	2.19	(1.06 - 2.62)	3.65	5.43	(2.92 - 6.58)
C16	10.86	10.86	(8.09 - 17.09)	24.34	27.81	(20.27 - 40.85)
C16 MRM	11.7	13.62	(10.62 - 14.70)	31.59	29.63	(25.54 - 37.42)
C18	2.26	2.35	(1.59 - 3.33)	5.2	5.98	(2.66 - 7.40)
C18 MRM	2.36	2.56	(2.02 - 2.98)	4.87	4.67	(4.06 - 5.98)
CIT	161.82	174.12	(128.98 - 191.02)	526.25	509.94	(416.21 - 629.45)
LEU	379.78	575.87	(363.63 - 613.17)	1614.49	1485.48	(1010.70 - 1953.48)
MET	94.2	109.52	(54.32 - 112.76)	321.77	253.68	(191.79 - 392.19)
PHE	192.89	227.81	(167.78 - 254.48)	539.97	656.16	(491.07 - 803.97)
TYR	281.85	389.96	(215.61 - 389.97)	1107.64	999.54	(702.05 - 1294.73)
ARG	6.88	6.33	(3.36 - 7.08)	5.61	5.1	(3.15 - 7.71)



Total Ion Chromatograms



Cutoffs

- Frequency
- Percentiles
- Individual vs. Pattern

Analyte					
	Mean	SD	Median	UWL	UCL
C0 (low)	30.83	10.90	28.83		
C0 (high)				107.00	137.00
C0/(C16+C18)high	9.28	3.91	8.59	37.97	53.42
C0/(C16+C18)low					
C3	1.65	0.72	1.51	6.86	9.00
C3/C16 (R)	0.65	0.34	0.57	2.43	2.73
C3/C2 (R)	0.06	0.07	0.06	0.20	0.26
C3DC	0.08	0.03	0.08	0.22	0.30
C4	0.45	0.30	0.38	1.10	1.30
C4/C2 (R)	0.0110	0.0040	0.0100	0.04	0.07
C4/C3 (R)	0.16	0.08	0.14	0.76	0.94
C4OH	0.20	0.09	0.02	0.65	0.75
C4OH/C16	0.076	0.070	0.072	0.200	0.298
C5	0.14	0.08	0.12	0.70	0.90

Analyte	Previous Median	7/09 to 12/09 Median	Current Bord Value	Calculate Bord Value	Current Bord %ile	Calculate Bord %ile	Current Pre Value	Calculate Pre Value	Current Pre %ile	Calculate Pre %ile
Arg		9.87	100.00			0.9991	200.00			0.9998
C0 (low)		34.40	10.46		0.0007	0.0010	5.23		0.0005	0.0008
C0 (high)	35.30		107.00	103.09	0.9986	0.9989	137.00	128.02	0.9997	0.9998
C0/C16	12.59	12.12	32.87	38.02	0.9884	0.9838	66.84	76.99	0.9986	0.9975
C0/C18	43.97	43.99	100.00	106.45	0.9909	0.9878	170.00	182.18	0.9990	0.9987
C10:1	0.07	0.06	0.30	0.24	0.9988	0.9990	0.62	0.75	0.9995	0.9994

Views

- Filter
- Histogram
- Scatter Chart
- 3D Chart
- Data Sheet

Filter

Filter by any or all of the criteria below.

Test: C5-OH

Filter profile: (New)

Site: (all) Instrument: (all)

Measured: 12/29/2009 - 3/16/2012

Concentration: 0.00 - 13.96 Barcode like: 2011%

Age at collection: 0 - 144 h

Weight: - 9250 g

Test phase: Initial

KitLot:

Results of other tests:

Test	Concentration

Filter

Data Set

Statistics	
N:	101628
Mean:	0.17
Median:	0.16
Std Dev:	0.09
Min:	0.00
Max:	9.93

Std Dev:	
2SD:	0.35
3SD:	0.44
4SD:	0.53
5SD:	0.61


Percentiles	
1.0%	0.05
1.0%	0.05
10.0%	0.09
50.0%	0.16
90.0%	0.27
99.0%	0.44
99.5%	0.50
99.9%	0.70

Cut-Off	
Absolute:	0.67
Percentage:	99.88%
n SD:	5.56

Detection Rates	
Within limits:	101508
Outside limits:	120
False positives:	116
False negatives:	0

Proficiency Testing

- External
- Internal
- Specimen exchange



Department of Health and Human Services
Centers for Disease Control and Prevention

CDC en Español

Newborn Screening Quality Assurance Program

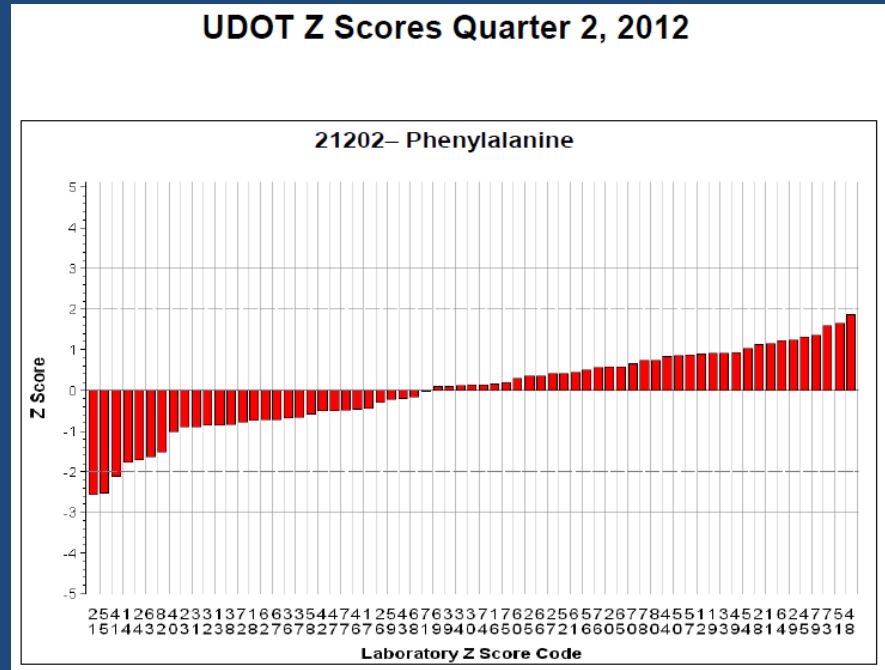
PROFICIENCY TESTING
Quarterly Report

This program is cosponsored by the Centers for Disease Control and Prevention and the Association of Public Health Laboratories.
Volume 27, No. 4 November 2014

Newborn Screening Quality Assurance Program
UDOT Statistics - Mean Concentration by Method
Year: 2012 Quarter: 2

Specimen No. 21206		C16OH		
		Expected Value 0.80 μmol/L blood		
		N	Mean	SD
Method Code	Method Name			
22	Deriv-MS/MS non-kit	23	0.55	0.12
35	Deriv-MS/MS PE NeoGram MS2 Kit	12	0.50	0.05
60	Non-deriv MS/MS PE NeoBase Kit	19	0.41	0.04

Specimen No. 21207		Cit		
		Expected Value 165.16 μmol/L blood		
		N	Mean	SD
Method Code	Method Name			
22	Deriv-MS/MS non-kit	22	108.49	29.40
35	Deriv-MS/MS PE NeoGram MS2 Kit	13	156.36	15.43
60	Non-deriv MS/MS PE NeoBase Kit	21	143.20	14.22



Overall Statistics

(Calculations based on All Labs, All Methods)

Year: 2014 Quarter: 4

Acylcarnitines

Specimen 41461	C0(L)	C3	C3DC	C3DC+ C4OH	C4	C4OH	C5	C5:1	C5DC	C5OH	C8
N*	272	255	131	85	243	115	287	231	273	246	243
Outliers	7	18	2	7	12	4	15	17	4	8	18
Mean	45.36	2.35	2.64	0.75	0.39	0.21	0.18	0.03	1.47	0.49	0.05
UL (95%)	62.18	3.03	5.16	1.62	0.55	0.42	0.26	0.07	2.65	0.75	0.09
LL (95%)	28.54	1.66	0.12	0.00	0.23	0.00	0.11	0.00	0.29	0.22	0.00

Specimen 41462	C0(L)	C3	C3DC	C3DC+ C4OH	C4	C4OH	C5	C5:1	C5DC	C5OH	C8
N*	267	255	125	85	240	112	266	235	264	249	245
Outliers	12	18	8	7	15	7	16	13	13	5	16
Mean	45.57	2.34	0.07	0.13	0.38	0.14	0.18	0.03	0.11	0.50	0.05
UL (95%)	60.87	3.00	0.15	0.28	0.51	0.26	0.24	0.07	0.22	0.75	0.10
LL (95%)	30.27	1.68	0.00	0.00	0.25	0.03	0.12	0.00	0.00	0.25	0.00

	31351							31352						
	Mean	LL	UL	SD	Rep Value	SDI		Mean	LL	UL	SD	Rep Value	SDI	
PHE	43.90	24.81	62.98	9.54	38.34	-1		71.19	38.06	104.32	16.57	63.37	0	
LEU	115.99	73.68	158.31	21.16	84.73	-1		167.53	103.85	231.22	31.85	130.22	-1	
MET	20.53	13.37	27.69	3.58	20.80	0		247.10	166.82	327.38	40.14	238.32	0	
TYR	49.52	34.55	64.49	7.49	53.35	1		720.81	533.62	908.00	93.60	671.14	-1	
CIT	153.75	102.46	205.05	25.65	164.09	0		20.31	12.53	28.09	3.89	21.30	0	
ARG	199.57	38.35	360.79	80.61	295.07	1		9.08	0.39	17.77	4.35	9.19	0	

	31361							31362						
	Mean	LL	UL	SD	Rep Value	SDI		Mean	LL	UL	SD	Rep Value	SDI	
C0	22.35	13.94	30.76	4.21	31.93	2		36.92	10.79	23.79	-6.57	46.61	-1	
C3	1.79	1.20	2.37	0.29	1.48	-1		1.64	0.93	1.86	0.11	1.26	-3	
C3DC	0.07	0.00	0.15	0.04	0.06	0		0.08	0.00	0.09	0.01	0.07	-2	
C4	0.14	0.02	0.26	0.06	0.00	-2		0.15	0.02	0.37	0.11	0.07	-1	
C4OH	0.08	0.01	0.15	0.04	0.07	0		0.09	0.04	0.18	0.05	0.08	0	
C5	0.08	0.03	0.13	0.03	0.03	-2		0.11	0.03	0.14	0.02	0.11	0	
C5:1	0.02	0.00	0.07	0.03	0.02	0		0.03	0.00	0.06	0.02	0.10	5	
C5DC	0.09	0.00	0.19	0.05	0.06	-1		0.09	0.00	0.10	0.01	0.07	-4	
C5OH	0.38	0.18	0.58	0.10	0.32	-1		0.72	0.23	0.74	0.01	0.63	-9	

MS/MS COLLABORATIVE PROJECT

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Calculate a condition-specific score for a case based on all clinically significant analytes and ratios

CURRENT DATA POSTED BY YOUR LABORATORY

[Cutoff Values](#)

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[Last Update](#)

COMPARE YOUR LABORATORY DATA WITH OTHER PARTICIPANTS

[Cutoff Values Comparison](#)

[Percentiles Comparison](#)

[Performance Metrics Comparison](#)

[Disease Range](#)

[Disease Range \(MoM\)](#)

[Analyte Comparison](#)

[Profile Comparison](#)

CUMULATIVE PROJECT DATA

[Participant Profile](#)

Participant profile summary of all responses

[Score Cards](#)

Tabular summary of all data (sorted by analyte type)

[Plots by Target Range](#)

Display of evidence-based and actual cutoff distribution for one analyte



QUALITY INDICATORS

The eight newborn screening Quality Indicators have been developed by representatives from state newborn screening programs and have undergone careful evaluation by stakeholders to assure agreement on definitions. These will be used to provide longitudinal comparisons within a program as well as comparisons to aggregate data across programs.

Quality Indicator 6 Percent of out of range results.

Quality Indicator 7 Frequency of condition detected by newborn screening for each disorder.

Quality Indicator 8 Percent of missed cases (false negatives), reported by disorder.

