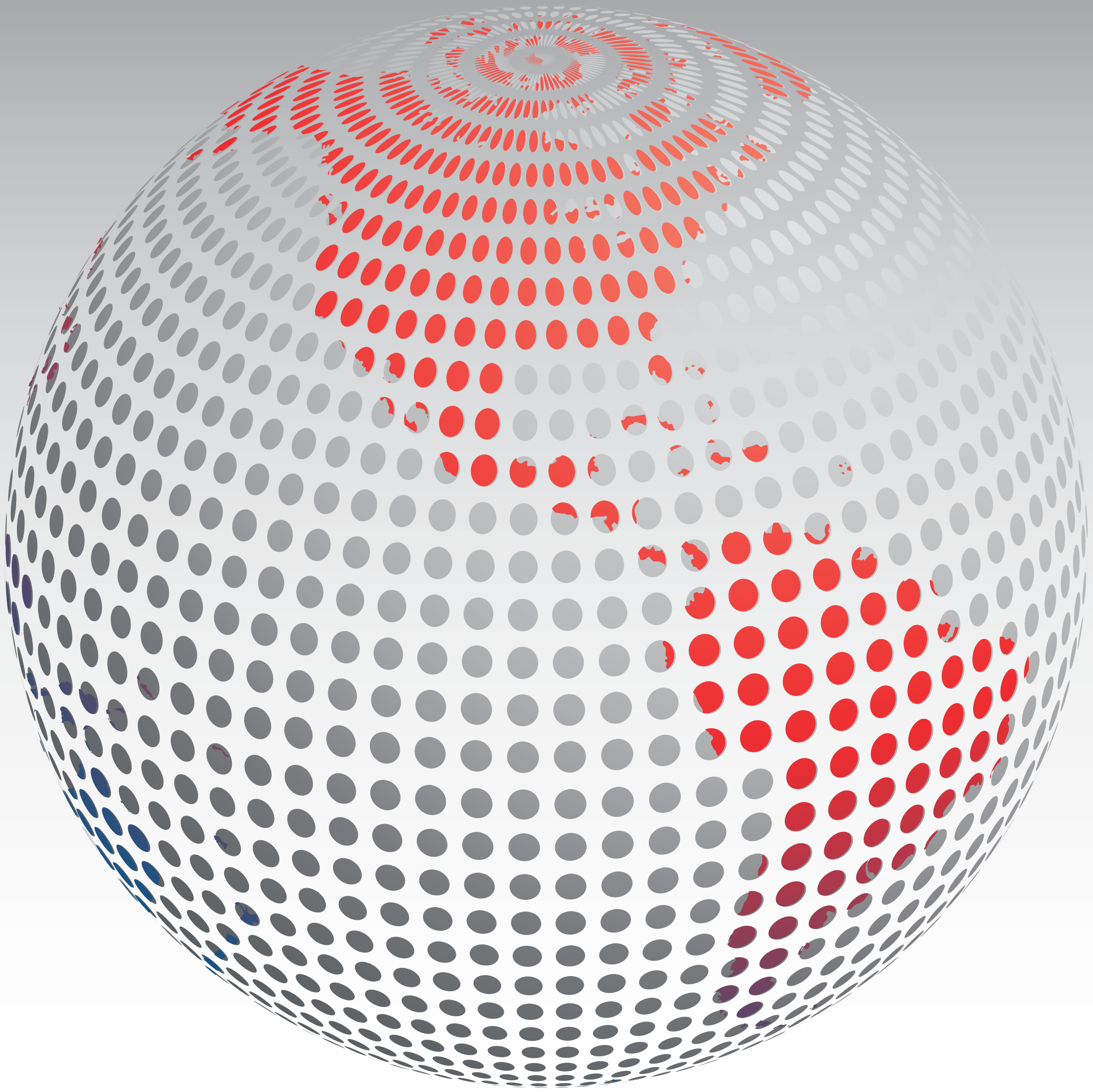
NEWBORN SCREENING

Annual Summary Report
volume 33b

2015

Quality Assurance Program



National Center for Environmental Health
Division of Laboratory Sciences

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Newborn Screening and Molecular Biology Branch
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NEWBORN SCREENING

Quality Assurance Program Annual Report 2015

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AMENDED REPORT- Version 33a of the Newborn Screening Annual Summary Report reflects a correction in domestic and foreign cutoff statistics (pages 9-14) and the sample table in Figure 4 (page21). Version 33b corrects the title of Figures 2 & 3 (page 5).

2016 Shipping Schedule for Newborn Screening Quality Assurance Program Proficiency Testing (PT) and Quality Control (QC) Materials*

*Note that shipment dates are subject to change due to unexpected temporary CDC closures

PT Panels	Enrollment Deadline	Shipping Date	Data Deadline	Report Available
Quarter 1	November 1, 2015	January 11	February 8	February 12
Quarter 2 (UDOT**)	March 1	April 4	April 25	May
Quarter 3	May 1	July 11	August 8	August 12
Quarter 4	August 1	October 3	October 31	November 4

** Domestic Laboratories only

SECOND-TIER CONGENITAL ADRENAL HYPERPLASIA, CYSTIC FIBROSIS DNA MUTATION DETECTION, LYSOSOMAL STORAGE DISORDERS, ANTI-TOXOPLASMA ANTIBODIES, T-CELL RECEPTOR EXCISION CIRCLE, AND X-LINKED ADRENOLEUKODYSTROPHY PT PANELS ONLY

CAH, CFDNA, LSD, Toxo, TREC, & XALD PT Panels	Enrollment Deadline	Shipping Date	Data Deadline	Report Available
Quarter 1	November 1, 2015	January 11	February 8	March
Quarter 2 (No CAH or XALD)	March 1	April 4	May 2	May
Quarter 3	May 1	July 11	August 8	August
Quarter 4	August 1	October 3	October 31	November

ANTI-HIV-1 ANTIBODIES PT PANELS

HIVPT & HIVQC	Enrollment Deadline	Shipping Date	Data Deadline	Report Available
Quarter 1 (HIVPT and HIVQC)	November 1, 2015	January 12	February 15	March
Quarter 2 (HIV PT only)	March 1	April 11	May 9	May
Quarter 3 (HIVPT and HIVQC)	May 1	July 12	August 8	August
Quarter 4 (HIV PT only)	August 1	*Tues:* October 11	November 7	November

SICKLE CELL AND OTHER HEMOGLOBINOPATHIES PT PANELS

Hemoglobinopathies PT Panels	Enrollment Deadline	Shipping Date	Data Deadline	Report Available
Panel 1	Waiting List	January 11	February 8	February
Panel 2	Waiting List	May 2	May 30	June
Panel 3	Waiting List	October 3	October 31	November

PRIMARY AND SECOND-TIER QUALITY CONTROL MATERIALS

All Newborn Screening QC Materials	Enrollment Deadline	Shipping Date	Data Deadline	Report Available
Set 1	November 1, 2015	January 11	April 1	July 2016
Set 2	May 1	July 12	October 1	February 2017

Introduction

Newborn screening is one of the most successful preventative public health programs in the United States. State public health laboratories or their associated laboratories routinely screen dried blood spot (DBS) specimens collected from newborns shortly after birth for certain genetic, metabolic, or endocrine disorders. Effective screening, along with follow up, diagnosis, and intervention, helps prevent mental retardation and premature death caused by these inherited diseases. Healthcare professionals collect DBS specimens from more than 98% of all newborns in the United States. The Centers for Disease Control and Prevention's (CDC) Newborn Screening Quality Assurance Program (NSQAP) assists newborn screening laboratories with these testing processes.

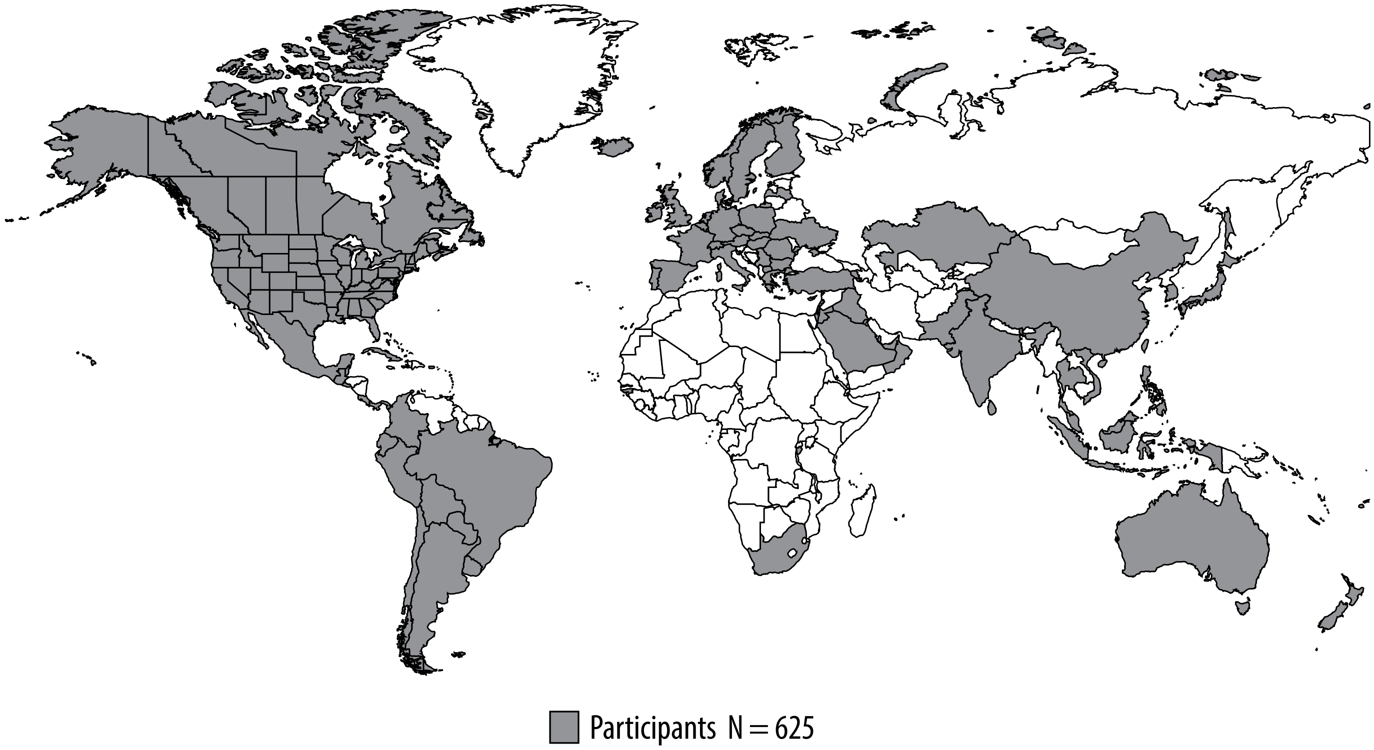
NSQAP produces certified DBS materials for proficiency testing (PT) and quality control (QC) analysis, works to improve the quality and scope of laboratory services, and provides consultative assistance to laboratories. Both state-operated and private newborn screening laboratories process large numbers of DBS specimens daily. NSQAP helps newborn screening laboratories ensure that testing accurately detects disorders, does not delay diagnosis, minimizes false positive reports, and sustains high-quality performance. Our job is to serve our participating newborn screening laboratories. We welcome comments and suggestions about how we can better serve participants' needs at NSQAPDMT@cdc.gov.

For more than 35 years, NSQAP, with its cosponsor the Association of Public Health Laboratories (APHL) has researched the development of DBS screening test materials and has assisted laboratories with DBS-related quality assurance (QA). NSQAP primarily supports U.S. newborn screening laboratories, but also allows private and international laboratories to enroll in the program. Participation is voluntary. NSQAP provides QA services for the core (primary) and secondary conditions listed in the U.S. Recommended Uniform Screening Panel (RUSP) [1]. These disorders include, but are not limited to, the following:

- congenital hypothyroidism
- congenital adrenal hyperplasia
- galactosemia
- phenylketonuria
- maple syrup urine disease
- homocystinuria
- tyrosinemia
- citrullinemia
- argininemia
- biotinidase deficiency
- cystic fibrosis
- hemoglobinopathies
- urea cycle disorders
- fatty acid oxidation disorders
- organic acid metabolic disorders
- X-linked adrenoleukodystrophy (XALD)
- severe combined immunodeficiency (SCID)

Over the years, NSQAP has grown substantially. In 2015, active program participants included 625 newborn screening laboratories in 77 countries (at least one laboratory per country) (Figure 1). Of these laboratories, 534 participated in PT (Figure 2) and 481 in QC (Figure 3). The program distributed DBS materials for 52 analytes to participating laboratories (Figures 2–3).

Figure 1. Seventy-seven Countries Participated in the Newborn Screening Quality Assurance Program in 2015



Argentina
Armenia
Australia
Austria
Bahrain
Belgium
Bolivia
Brazil
Bulgaria
Canada
Chile
China
Colombia
Costa Rica
Cuba
Czech Republic
Denmark
Ecuador
Egypt
El Salvador
Estonia
Finland
France
Germany
Greece
Guatemala
Hungary
Iceland
India
Indonesia
Iraq
Ireland
Israel
Italy
Japan
Jordan
Kazakhstan
Kuwait
Latvia
Lithuania
Luxembourg
Macedonia
Malaysia
Mexico
Morocco
Netherlands
New Zealand
Norway
Oman
Pakistan
Panama
Paraguay
Peru
Philippines
Poland
Portugal
Qatar
Romania
Saudi Arabia
Singapore
Slovak Republic
South Africa
South Korea
Spain
Sir Lanka
Sweden
Switzerland
Taiwan
Tanzania
Thailand
Turkey
Ukraine
United Arab Emirates
United Kingdom
United States
Uruguay

To offer more specialized services, NSQAP works with the Biochemical Mass Spectrometry Laboratory (BMSL), the Newborn Screening Translation Research Initiative (NSTRI), and the Molecular Quality Improvement Program (MQIP).

BMSL offers newborn screening tandem mass spectrometry (MS/MS) services, education, and research opportunities as well as overseeing amino acids, acylcarnitines, biotinidase, total galactose (TGal), galactose-1-phosphate uridyltransferase (GALT), and the filter paper evaluation program. MQIP was created to enhance molecular testing assistance provided to newborn screening laboratories. MQIP also offers the Molecular Assessment Program (MAP) which conducts onsite visits to U.S. newborn screening laboratories. These visits encompass all components of molecular testing procedures, including program-tailored guidance for laboratory-specific needs and assistance in evaluating ongoing and future molecular testing procedures. MQIP oversees the cystic fibrosis DNA mutation detection (CFDNA) PT program. NSTRI is an ongoing collaboration between the CDC Foundation and CDC's Newborn Screening Molecular Biology Branch (NSMBB) and it developed the PT program for T-cell receptor excision circle (TREC) and lysosomal storage disorders (LSD)[2].

This report summarizes all phases of NSQAP's PT activities and all QC data reported in 2015.

Figure 2. Number of Participants in Proficiency Testing Program, 2015 Total-534

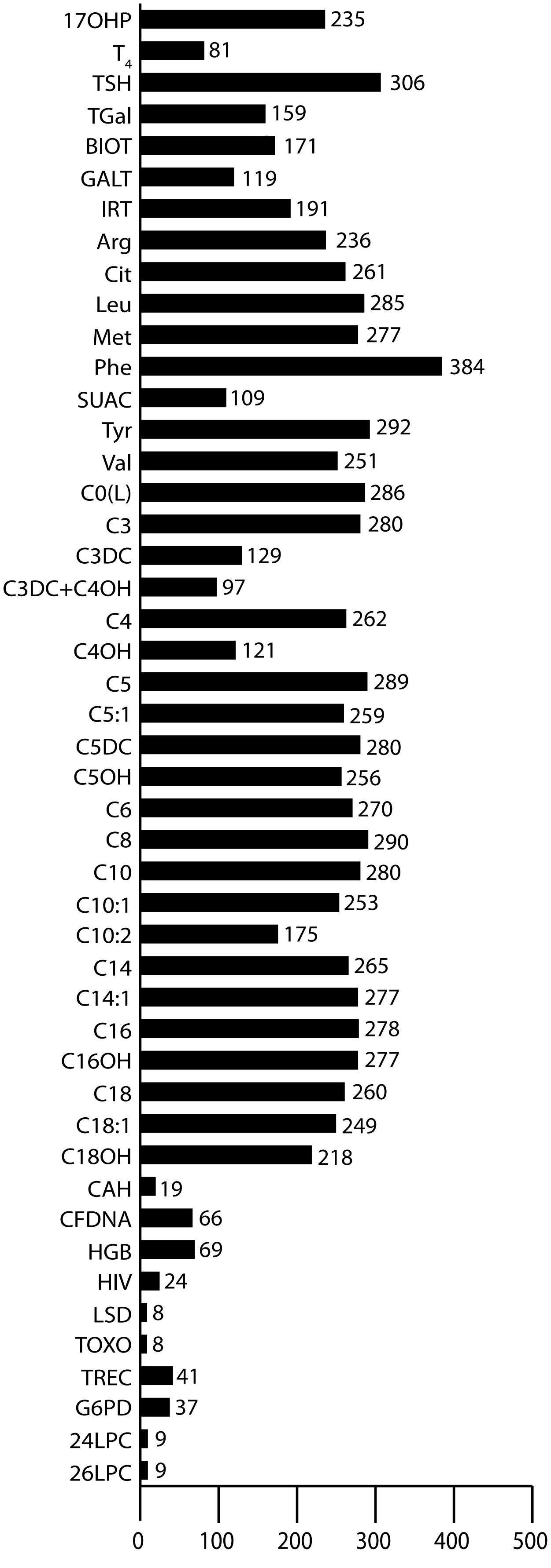
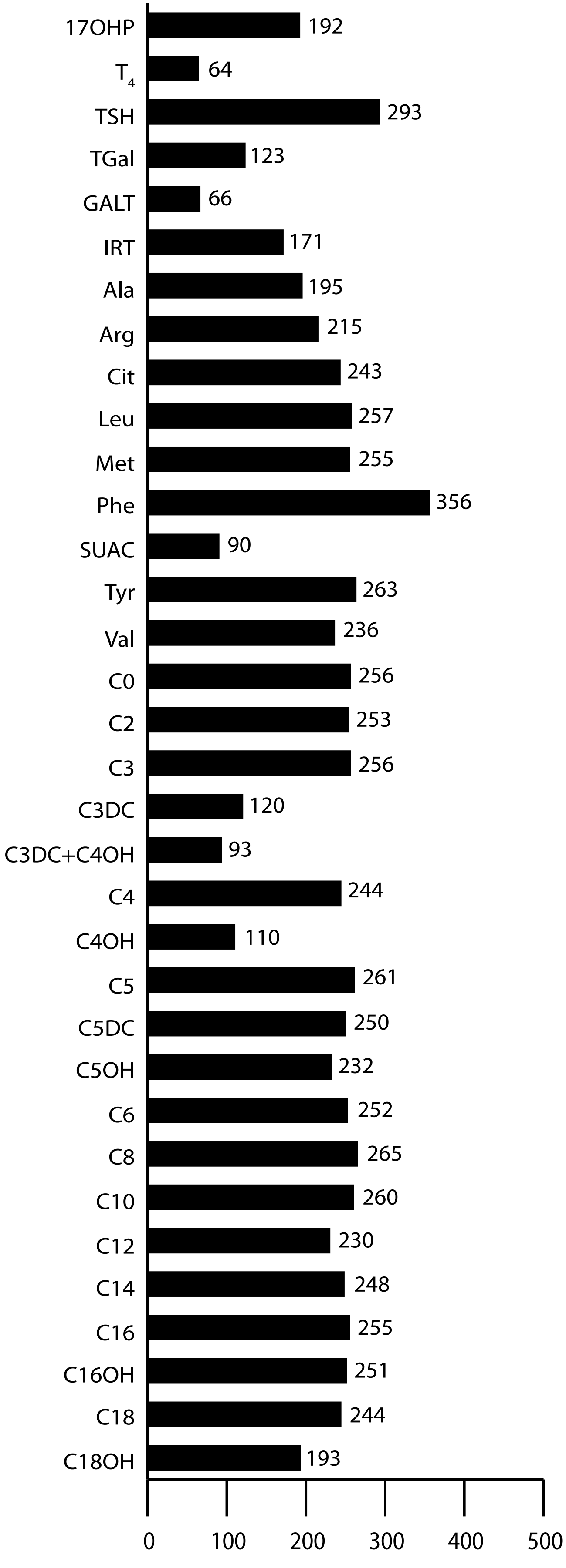


Figure 3. Number of Participants in Quality Control Program, 2015 Total- 481



2015 NEWBORN SCREENING PROGRAM HIGHLIGHTS

January
BMSL shipped the first X-linked adrenoleukodystrophy (XALD) QC materials containing 24:0- and 26:0-lysophosphatidylcholines. Summary data for these materials are included in the QC tables of this report.

February
BMSL and APHL convened a two-day workshop titled *National Conversation: Tandem Mass Spectrometry in Newborn Screening*. State newborn screening laboratorians, lab directors, and MS/MS directors attended the meeting.

March
In cooperation with APHL, MQIP hosted its annual *Newborn Screening Molecular Training Workshop*. This dynamic hands-on workshop included lectures and laboratory training activities directly related to the detection of newborn disorders using molecular methods.

April
BMSL shipped a nine-level set of QC materials to enrolled NSQAP participants. These materials are used to assess the linearity of newborn screening MS/MS assays and cover 34 amino acid and acylcarnitine analytes.

MQIP hosted the APHL Molecular Subcommittee face-to-face meeting on the CDC campus in Atlanta. Information from these meetings is used to improve molecular services to NSQAP participants.

BMSL hosted a five-day workshop: *Newborn Screening by Tandem Mass Spectrometry (MS/MS): A Hands-On Course in Understanding Laboratory Issues and Interpreting Test Results*. CDC co-sponsored the workshop at CDC's laboratories in Atlanta, GA.

NSTRI and APHL convened a two-day workshop: *Newborn Bloodspot Screening for Pompe Disease and Other Lysosomal Storage Disorders*. Attendees included physicians and scientists from newborn screening programs, medical centers, federal agencies, and APHL. You can view presentations from the workshop at **http://www.aphl.org/aphlprograms/newborn-screening-and-genetics/Pages/2015-LSDs-Workshop.aspx**

May
NSQAP and APHL hosted the QA/QC Subcommittee of the Newborn Screening and Genetics in Public Health Program in Atlanta. This subcommittee provides guidance to NSQAP on procedures, policies, and activities for quality assessment of laboratory testing. Input from this subcommittee enhances our continuing efforts to serve our participants.

June
Inter-laboratory Comparison of Assays to Measure SMN2 Copy Number in Dried Blood Spots from Patients with Spinal Muscular Atrophy, Carriers, and Controls was presented at the annual CDC Division of Laboratory Sciences Summer Symposium. The presentation focused on confirmatory testing and genetic characterization of Spinal Muscular Atrophy screen-positive results on dried blood spots.

July
NSTRI participated in the APHL NewSTEPs meeting on newborn screening for SCID. Dr. Francis Lee presented an overview of the technical and scientific support offered by the CDC including consultations, trainings, and access to reference materials. NTSRI guest researcher Dr. Lisa Kobrynski, Marcus Professor of Immunology and director of the Jeffrey Modell Foundation Center for Excellence at the Emory University School of Medicine, provided an overview of the definitions and clinical presentations associated with SCID.

September
MAP completed four site visits in 2015. These onsite visits assess a state newborn screening laboratory's molecular testing program. To request a MAP visit, go to the Newborn Screening Molecular Resources Web site at **http://www.aphl.org/aphlprograms/newborn-screening-and-genetics/Pages/Molecular-Assessment-Program.aspx**

October
PT programs for glucose-6-phosphate deficiency (G6PD) and XALD launched. Email **NSQAPDMT@cdc.gov** for more information or to register for these PT programs.

FILTER PAPER

NSQAP evaluates absorption characteristics of all filter paper lots that have Food and Drug Administration (FDA) approval as a newborn screening collection device [3]. The manufacturers must establish their own parallel evaluation. NSQAP's evaluations are an impartial and voluntary service offered as a function of our QA program; they do not constitute endorsement of any product.

The disk punched from DBS specimens is a volumetric measurement that requires a high degree of uniformity among and within production lots. NSQAP uses an isotopic method developed at CDC to evaluate and compare different lots of filter paper. Mean counts per minute of added radioisotope-labeled thyroxine (T_4) contained within a 3.2-mm disk are equated with the serum absorption volume of the disks made from washed intact red blood cells (RBCs). A description of the method is in the latest version of the Clinical and Laboratory Standards Institute (CLSI) Standard NBS01-A6, Blood Collection on Filter Paper for Newborn Screening Programs [3].

FDA-approved newborn screening filter paper manufacturers (GE Healthcare Biosciences Corporation and PerkinElmer Health Sciences) provide NSQAP with statistically valid sample sets of unprinted filter paper from each production lot. Tables 1 and 2 show serum absorption volumes from the last 10 lots of these two filter paper sources. The published and standardized acceptable serum absorption volume per 3.2-mm disk is (mean value and 95% confidence interval [CI]) 1.44 ± 0.20 µL for washed intact RBCs [3]. The testing results provided in Tables 1 and 2 are for information purposes only. Each mean value was within the acceptable range for the matrix used. All lots were homogeneous (i.e., the measured within-spot, within-sheet, and among-sheets variances were within acceptable limits).

Filter paper lots used in the CDC production of QC and PT specimens distributed in 2015 were W112, W113, and W141 of Whatman 903.

Table 1. PerkinElmer 226 Specimen Collection Paper Filter Paper Absorption Characteristics by Lot Number - Intact Red Cells

Filter Paper Lot	Date of Evaluation	Serum Absorption Volume (µL) per 3.2mm (1/8") punch		Absorption Time (sec)		Spot Diameter (mm)	
	(month/year)	Avg	StDev	Avg	StDev	Avg	StDev
105178	Aug-15	1.46	0.09	7.8	1.1	15.9	0.6
104568	Mar-15	1.56	0.10	10.1	2.1	15.9	0.7
103649	Mar-14	1.53	0.10	9.7	3.1	15.7	0.7
102928	Aug-13	1.38	0.09	8.5	0.9	16.1	0.5
102277	Dec-12	1.47	0.11	13.0	4.9	15.8	0.6
101535	Apr-12	1.49	0.08	14.7	3.1	15.7	0.5
100535	May-11	1.45	0.08	8.9	2.2	15.7	0.5
0120201	Apr-10	1.47	0.11	14.0	3.7	16.0	0.6
9461001	Feb-10	1.53	0.09	8.8	1.8	15.4	0.6
8040201	Feb-08	1.60	0.10	7.2	1.8	15.6	0.6

Table 2. Whatman 903 Specimen Collection Paper Filter Paper Absorption Characteristics by Lot Number - Intact Red Cells

Filter Paper Lot	Date of Evaluation	Serum Absorption Volume (µL) per 3.2mm (1/8”) punch		Absorption Time (sec)		Spot Diameter (mm)	
	(month/year)	Avg	StDev	Avg	StDev	Avg	StDev
W152	Aug-15	1.37	0.09	15.8	2.4	16.2	0.6
W151	Aug-15	1.39	0.08	15.2	2.6	16.2	0.8
W142	Apr-15	1.46	0.08	11.0	2.2	16.0	0.7
W141	Mar-14	1.53	0.10	13.8	3.6	15.9	0.6
W131	Aug-13	1.40	0.07	10.4	1.4	16.1	0.5
W122	May-13	1.41	0.11	14.8	2.9	16.3	0.5
W121	Jan-13	1.49	0.09	13.7	3.8	16.0	0.6
W113	Mar-12	1.44	0.08	9.9	2.0	15.8	0.6
W112	Oct-11	1.38	0.13	12.9	2.1	16.0	0.5
W111	Feb-11	1.42	0.08	10.2	1.5	16.1	0.5

PROFICIENCY TESTING

NSQAP distributes PT materials three times a year. All PT panels consist of five blind-coded, 75-µL DBS specimens. Specimen sets are packaged in a zip-closed, metalized bag with desiccant, along with instructions for analysis and reporting data. These specimens provide an independent, external assessment of each laboratory’s performance.

PT MATERIALS AND METHODS

NSQAP certifies PT specimens for homogeneity, accuracy, stability, and suitability for newborn screening assays. The PT analytes include: 17α-hydroxyprogesterone (17OHP), T_4, thyroid-stimulating hormone (TSH), biotinidase (Bio), TGal, GALT, G6PD, immunoreactive trypsinogen (IRT), arginine (Arg), citrulline (Cit), leucine (Leu), methionine (Met), phenylalanine (Phe), succinylacetone (SUAC),tyrosine (Tyr), and valine (Val), low free carnitine (C0(L)), C3, C3DC, C4, C4OH, C5, C5:1, C5OH, C5DC, C6, C8, C10, C10:1, C10:2, C14, C14:1, C16, C16OH, C18, C18:1, and C18OH, X-linked adrenoleukodystrophy (XALD).

- All PT specimens are prepared from whole blood of 50% hematocrit. PT materials are produced from single donors.
- Purified analytes or unaltered donor blood are used for PT enrichments. Enrichments made with purchased or custom-synthesized acylcarnitines are based on weighed quantities. Small variances in enrichments and recoveries might result from impurities in the purchased (synthesized) materials and endogenous analyte concentrations.
- Congenital hypothyroidism PT specimens are enriched with calculated amounts of T_4 after T_4 depletion of the base serum.
- TGal materials are enriched with galactose and galactose-1-phosphate, allowing measurement of both free galactose (galactose alone) and total galactose (free galactose plus galactose present as TGal).
- Biotinidase PT pools are made using heat-treated serum combined with compatible donor RBCs.
- Deficient GALT PT specimens are made using a 50/50 saline/serum solution combined with compatible washed RBCs and then heat-treating the pool.
- Low free carnitine (C0(L)) materials are produced by washing fresh RBCs at least six times and then combining with charcoal-stripped serum.
- CFDNA PT materials are made with blood from individual donors who express CF mutations.
- Hemoglobin specimens are made from individual umbilical cord blood units.

PT DATA HANDLING

Participants submit PT data and clinical assessments through the NSQAP data reporting website or by email. Laboratories that submit results before the data-reporting deadline will receive an individual laboratory evaluation and their data will be included in the data summary reports.

PT CUTOFFS

Participants report the decision level for sorting test results as presumptive positive (outside normal limits) from results reported as negative (within normal limits) based on their laboratory's established cutoff value. Cutoff values vary among participating laboratories because each laboratory establishes its own cutoff level. For PT evaluations, the participating laboratory's reported cutoff value is applied to our grading algorithm. If no cutoff value is reported for a particular analytical result, the grading algorithm will default to the NSQAP-assigned working cutoff values, which are based on the domestic mean cutoff value. (Figure 4)

Tables 3–5 summarize the reported cutoff values for domestic and foreign laboratories; the values for mean, median, and mode are shown for each analyte. Tables 6–9 summarize the mean, median, mode, and min/max range for reported domestic cutoffs by method.

Table 3. 2015 Summary of Non-MSMS Cutoff Values for Domestic and Foreign Laboratories

Domestic

Analyte	N	Mean	Median	Mode	Min	Max
17OHP (ng/mL serum)	43	33.7	33.0	30.0	7.0	65.0
GALT (U/g Hb)	19	3.2	3.1	3.0	2.0	5.5
IRT (ng/mL blood)	43	66.3	65.0	60.0	35.2	114.9
T_4 (µg/dL serum)	24	6.1	6.0	5.0	4.0	8.5
TGal (mg/dL blood)	24	10.7	10.0	10.0	6.0	20.0
TSH (µIU/mL serum)	43	30.8	25.0	20.0	19.0	58.0
Phe (µmol/L blood)	6	169.3	166.7	N/A*	133.0	224.2

Foreign

Analyte	N	Mean	Median	Mode	Min	Max
17OHP (ng/mL serum)	167	25.7	20.0	19.8	2.6	110.0
GALT (U/g Hb)	43	3.0	3.1	3.5	1.5	5.3
IRT (ng/mL blood)	137	65.7	65.0	60.0	40.0	99.6
T_4 (µg/dL serum)	42	6.3	6.0	6.0	1.8	22.0
TGal (mg/dL blood)	116	12.0	10.0	10.0	4.1	30.0
TSH (µIU/mL serum)	231	22.4	20.0	20.0	5.0	45.0
Phe (µmol/L blood)	65	183.4	169.9	121.2	120.0	820.8

*Not Applicable

Table 4. 2015 Summary of MS/MS Cutoff Values of Domestic Laboratories (µmol/L blood)

Analyte	N	Mean	Median	Mode	Min	Max
Arg	38	70.2	60.0	50.0	20.0	125.0
Cit	45	55.5	55.0	60.0	18.0	100.0
Leu	46	285.1	281.0	250.0	175.0	400.0
Met	46	74.5	72.5	100.0	35.0	100.0
Phe	51	141.4	140.0	130.0	75.0	182.0
SUAC	30	2.7	2.3	4.5	0.5	5.4
Tyr	52	386.7	338.0	400.0	88.0	850.0
Val	32	293.9	277.0	250.0	200.0	530.0
C0(L)	49	8.81	8.00	8.00	4.00	33.00
C3	50	5.68	6.00	6.30	2.82	8.00
C3DC	22	0.22	0.20	0.20	0.10	0.45
C3DC+C4OH	20	0.57	0.41	0.38	0.25	3.03
C4	46	1.27	1.30	1.40	0.49	1.90
C4OH	20	0.65	0.70	0.70	0.35	1.00
C5	50	0.69	0.66	1.00	0.38	1.20
C5:1	49	0.22	0.16	0.50	0.05	0.60
C5DC	49	0.35	0.32	0.50	0.05	0.80
C5OH	49	0.79	0.80	0.80	0.25	1.18
C6	47	0.39	0.29	0.24	0.16	0.95
C8	50	0.45	0.40	0.35	0.25	0.79
C10	46	0.44	0.41	0.40	0.22	0.80
C10:1	43	0.29	0.30	0.30	0.14	0.45
C10:2	30	0.16	0.12	0.10	0.06	0.50
C14	45	0.75	0.70	0.70	0.26	1.20
C14:1	50	0.61	0.65	0.60	0.17	0.80
C16	47	7.64	7.70	7.00	2.14	10.00
C16OH	50	0.13	0.12	0.10	0.07	0.25
C18	42	2.35	2.28	2.50	0.70	4.00
C18:1	44	3.48	3.00	3.00	2.00	7.00
C18OH	39	0.11	0.10	0.10	0.04	0.26

Table 5. 2015 Summary of MS/MS Cutoff Values of Foreign Laboratories (µmol/L blood)

Analyte	N	Mean	Median	Mode	Min	Max
Arg	177	56.9	51.0	70.0	10.0	150.0
Cit	194	53.6	50.0	55.0	19.5	200.0
Leu	215	308.7	300.0	300.0	147.0	600.0
Met	210	57.6	55.2	75.0	19.0	121.0
Phe	232	135.8	129.0	120.0	48.0	242.4
SUAC	69	2.4	1.6	1.5	0.1	10.0
Tyr	214	297.1	275.0	400.0	35.0	600.0
Val	199	268.2	260.0	250.0	139.3	470.0
C0(L)	221	11.71	8.80	10.00	3.50	80.00
C3	214	5.30	5.25	6.00	1.80	11.00
C3DC	101	0.31	0.28	0.30	0.04	3.70
C3DC+C4OH	66	0.58	0.50	0.50	0.19	2.20
C4	200	1.01	0.98	1.30	0.31	4.00
C4OH	91	0.60	0.61	0.65	0.05	1.40
C5	223	0.69	0.64	1.00	0.20	2.00
C5:1	192	0.17	0.15	0.25	0.01	0.50
C5DC	216	0.33	0.30	0.35	0.07	1.00
C5OH	191	0.78	0.80	1.00	0.16	2.20
C6	203	0.32	0.25	0.45	0.05	1.50
C8	228	0.36	0.32	0.30	0.07	1.42
C10	215	0.39	0.40	0.40	0.09	1.46
C10:1	188	0.30	0.28	0.30	0.06	2.03
C10:2	125	0.16	0.12	0.10	0.00	0.56
C14	200	0.63	0.60	0.80	0.14	1.50
C14:1	210	0.46	0.42	0.60	0.08	1.30
C16	213	6.62	6.90	7.50	0.51	14.00
C16OH	211	0.13	0.10	0.05	0.02	0.48
C18	199	2.18	2.03	2.50	0.71	5.00
C18:1	189	2.96	3.00	3.50	0.20	5.80
C18OH	163	0.11	0.10	0.10	0.01	2.00

Table 6. 2015 Domestic Cutoff Summary by Analyte and Method - Hormones and Galactose

		CUTOFF VALUE					
Analyte	Method	N	Mean	Median	Mode	Min	Max
17OHP ng/mL serum	**ALL METHODS**	**43**	**33.7**	**33.0**	**30.0**	**7.0**	**65.0**
	AutoDelfia	7	46.6	46.2	N/A*	30.0	65.0
	AutoDelfia Neonatal 17-OHP (B024)	17	31.4	33.0	33.0	19.0	40.0
	PerkinElmer GSP Neonatal	18	32.4	30.0	25.0	25.0	60.0
TSH µIU/mL serum	**ALL METHODS**	**43**	**30.8**	**25.0**	**20.0**	**19.0**	**58.0**
	AutoDelfia	24	35.1	30.0	20.0	20.0	58.0
	PerkinElmer GSP Neonatal	18	25.7	25.0	25.0	19.0	35.0
T_4 µg/dL serum	**ALL METHODS**	**24**	**6.1**	**6.0**	**5.0**	**4.0**	**8.5**
	AutoDelfia	8	6.2	6.3	6.5	4.0	8.0
	PerkinElmer GSP Neonatal	15	6.1	5.5	5.0	4.0	8.5
TGal mg/dL blood	**ALL METHODS**	**24**	**10.7**	**10.0**	**10.0**	**6.0**	**20.0**
	Astoria-Pacific 50 Hour Reagent Kit	6	10.4	10.0	10.0	6.5	15.0
	Fluorometric manual (e.g. Hill or Misuma)	5	12.8	10.0	10.0	10.0	20.0
	PerkinElmer GSP Neonatal	3	11.4	13.0	N/A*	7.3	14.0
	PerkinElmer Neonatal Kit	5	8.0	8.0	9.5	6.0	9.5

Table 7. 2015 Domestic Cutoff Summary by Analyte and Method - GALT and IRT

		CUTOFF VALUE					
Analyte	Method	N	Mean	Median	Mode	Min	Max
GALT U/g Hb	**ALL METHODS**	**19**	**3.2**	**3.1**	**3.0**	**2.0**	**5.5**
	Astoria-Pacific Neonatal Microplate Reagent Kit	5	2.7	2.9	3.1	2.0	3.1
	PerkinElmer Neonatal Kit	13	3.2	3.2	3.0	2.4	4.0
IRT ng/mL blood	**ALL METHODS**	**43**	**66.3**	**65.0**	**60.0**	**35.2**	**114.9**
	Auto Delfia	25	69.3	66.0	67.0	37.7	114.9
	PerkinElmer GSP Neonatal	18	62.1	57.0	55.0	35.2	100.0

*N/A - Not Applicable

Table 8. 2015 Domestic Cutoff Summary by Analyte and Method - Amino Acids

Analyte µmol/ L blood	Method	CUTOFF VALUE					
		N	Mean	Median	Mode	Min	Max
Arg	**ALL MS/MS Methods**	**38**	**70.2**	**60.0**	**50.0**	**20.0**	**125.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	77.5	75.0	100.0	55.0	100.0
	Derivatized - MS/MS non-kit	13	48.3	35.0	30.0	20.0	125.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	19	83.0	100.0	50.0	50.0	125.0
Cit	**ALL MS/MS Methods**	**45**	**55.5**	**55.0**	**60.0**	**18.0**	**100.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	61.6	54.0	N/A*	40.0	100.0
	Derivatized - MS/MS non-kit	14	45.0	40.0	40.0	18.0	75.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	59.9	60.0	60.0	50.0	85.0
Leu	**ALL MS/MS Methods**	**46**	**285.1**	**281.0**	**250.0**	**175.0**	**400.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	285.0	281.0	275.0	250.0	325.0
	Derivatized - MS/MS non-kit	15	265.3	256.0	300.0	200.0	333.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	297.7	281.5	250.0	175.0	400.0
Met	**ALL MS/MS Methods**	**46**	**74.5**	**72.5**	**100.0**	**35.0**	**100.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	76.0	72.5	N/A	60.0	100.0
	Derivatized - MS/MS non-kit	15	62.5	60.0	60.0	35.0	100.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	82.2	82.5	100.0	54.5	100.0
Phe	**ALL MS/MS Methods**	**57**	**144.3**	**150.0**	**130.0**	**75.0**	**224.2**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	137.6	130.0	130.0	120.0	178.0
	Derivatized - MS/MS non-kit	18	136.5	137.0	150.0	99.0	182.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	150.2	157.5	165.0	120.0	180.0
	Non-derivatized - MS/MS non-kit	3	115.3	121.0	N/A*	75.0	150.0
SUAC	**ALL MS/MS Methods**	**30**	**2.7**	**2.3**	**4.5**	**0.5**	**5.4**
	Derivatized - MS/MS non-kit	10	2.5	2.8	3.3	0.5	5.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	19	2.6	2.0	4.5	1.0	4.5
Tyr	**ALL MS/MS Methods**	**52**	**386.7**	**358.0**	**400.0**	**88.0**	**850.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	307.3	288.0	300.0	200.0	552.0
	Derivatized - MS/MS non-kit	17	311.2	300.0	400.0	88.0	442.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	518.4	445.0	850.0	300.0	850.0
	Non-derivatized - MS/MS non-kit	3	218.3	204.0	N/A*	91.0	360.0
Val	**ALL MS/MS Methods**	**32**	**293.9**	**277.0**	**250.0**	**200.0**	**530.0**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	291.3	274.0	250.0	250.0	400.0
	Derivatized - MS/MS non-kit	11	269.7	250.0	200.0	200.0	420.0
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	14	317.2	312.5	250.0	250.0	530.0

Table 9. 2015 Domestic Cutoff Summary by Analyte and Method - Acylcarnitines

Analyte µmol/ L blood	Method	CUTOFF VALUE					
		N	Mean	Median	Mode	Min	Max
C0(L)	**ALL MS/MS Methods**	**49**	**8.81**	**8.00**	**8.00**	**4.00**	**33.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	11.12	10.00	12.00	10.00	13.00
	Derivatized - MS/MS non-kit	18	10.40	5.00	8.00	5.00	33.00
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	6.70	6.50	6.00	4.00	10.00
C3	**ALL MS/MS Methods**	**50**	**5.68**	**6.00**	**6.30**	**2.82**	**8.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	5.52	5.38	5.00	5.00	6.23
	Derivatized - MS/MS non-kit	19	5.01	5.00	5.25	2.82	7.30
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	6.26	6.30	6.30	4.00	8.00
C3DC	**ALL MS/MS Methods**	**22**	**0.22**	**0.20**	**0.20**	**0.10**	**0.45**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	0.27	0.26	0.35	0.19	0.35
	Derivatized - MS/MS non-kit	16	0.20	0.17	0.20	0.10	0.45
C3DC+C4OH	**ALL MS/MS Methods**	**20**	**0.57**	**0.41**	**0.38**	**0.25**	**3.03**
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	19	0.44	0.40	0.38	0.25	0.70
C4	**ALL MS/MS Methods**	**46**	**1.27**	**1.30**	**1.30**	**0.49**	**1.90**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	1.08	1.04	N/A*	0.81	1.40
	Derivatized - MS/MS non-kit	17	1.16	1.20	1.40	0.49	1.90
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	1.41	1.32	1.30	1.10	1.70
C4OH	**ALL MS/MS Methods**	**20**	**0.65**	**0.70**	**0.70**	**0.35**	**1.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	0.73	0.70	N/A*	0.52	1.00
	Derivatized - MS/MS non-kit	14	0.68	0.70	0.70	0.35	1.00
C5	**ALL MS/MS Methods**	**50**	**0.69**	**0.66**	**1.00**	**0.38**	**1.20**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.63	0.70	0.70	0.45	0.71
	Derivatized - MS/MS non-kit	19	0.65	0.60	0.50	0.38	1.20
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	0.76	0.70	1.00	0.50	1.00
C5:1	**ALL MS/MS Methods**	**49**	**0.22**	**0.16**	**0.50**	**0.05**	**0.60**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.20	0.18	0.25	0.15	0.25
	Derivatized - MS/MS non-kit	19	0.21	0.14	0.08	0.05	0.60
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.25	0.19	0.50	0.06	0.50
C5DC	**ALL MS/MS Methods**	**49**	**0.35**	**0.32**	**0.50**	**0.05**	**0.80**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.30	0.30	0.30	0.24	0.33
	Derivatized - MS/MS non-kit	19	0.18	0.18	0.21	0.05	0.32
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.52	0.50	0.50	0.35	0.80
C5OH	**ALL MS/MS Methods**	**49**	**0.79**	**0.80**	**0.80**	**0.25**	**1.18**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.74	0.70	0.65	0.60	1.00
	Derivatized - MS/MS non-kit	19	0.75	0.76	1.00	0.25	1.18
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.84	0.85	0.85	0.60	1.05
C6	**ALL MS/MS Methods**	**47**	**0.39**	**0.29**	**0.24**	**0.16**	**0.95**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	7	0.26	0.25	0.24	0.20	0.31
	Derivatized - MS/MS non-kit	18	0.34	0.30	0.22	0.16	0.86
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.47	0.29	0.95	0.20	0.95

Table 9. (continued)

Analyte µmol/ L blood	**Method**	**CUTOFF VALUE**					
		N	**Mean**	**Median**	**Mode**	**Min**	**Max**
C8	**ALL MS/MS Methods**	**50**	**0.45**	**0.40**	**0.35**	**0.25**	**0.79**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.39	0.38	0.38	0.32	0.55
	Derivatized - MS/MS non-kit	19	0.39	0.35	0.50	0.25	0.72
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	0.52	0.51	0.60	0.35	0.79
C10	**ALL MS/MS Methods**	**46**	**0.44**	**0.41**	**0.40**	**0.22**	**0.80**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	7	0.38	0.40	0.42	0.27	0.50
	Derivatized - MS/MS non-kit	17	0.42	0.40	0.30	0.22	0.80
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.49	0.45	0.65	0.22	0.70
C10:1	**ALL MS/MS Methods**	**43**	**0.29**	**0.30**	**0.30**	**0.14**	**0.45**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	7	0.31	0.30	0.30	0.30	0.36
	Derivatized - MS/MS non-kit	15	0.25	0.23	0.18	0.17	0.40
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	20	0.31	0.28	0.45	0.14	0.45
C10:2	**ALL MS/MS Methods**	**30**	**0.16**	**0.12**	**0.10**	**0.06**	**0.50**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	0.15	0.15	0.15	0.10	0.20
	Derivatized - MS/MS non-kit	14	0.18	0.13	0.10	0.06	0.39
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	9	0.16	0.10	0.10	0.07	0.50
C14	**ALL MS/MS Methods**	**45**	**0.75**	**0.70**	**0.70**	**0.26**	**1.20**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	7	0.69	0.70	0.70	0.52	0.78
	Derivatized - MS/MS non-kit	16	0.65	0.70	0.70	0.26	0.85
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	0.84	0.75	1.20	0.58	1.20
C14:1	**ALL MS/MS Methods**	**50**	**0.61**	**0.65**	**0.60**	**0.17**	**0.80**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.60	0.63	N/A*	0.40	0.77
	Derivatized - MS/MS non-kit	19	0.55	0.64	0.65	0.17	0.75
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	0.67	0.67	0.80	0.50	0.80
C16	**ALL MS/MS Methods**	**47**	**7.64**	**7.70**	**7.00**	**2.14**	**10.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	7.19	7.10	7.00	6.65	7.80
	Derivatized - MS/MS non-kit	18	6.67	6.88	8.00	2.14	9.00
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	8.52	8.50	10.00	7.00	10.00
C16OH	**ALL MS/MS Methods**	**50**	**0.13**	**0.12**	**0.10**	**0.07**	**0.25**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	8	0.17	0.17	0.12	0.12	0.25
	Derivatized - MS/MS non-kit	19	0.13	0.13	0.10	0.08	0.25
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	22	0.11	0.10	0.10	0.07	0.20
C18	**ALL MS/MS Methods**	**42**	**2.35**	**2.28**	**2.50**	**0.70**	**4.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	2.31	2.25	N/A*	1.89	3.00
	Derivatized - MS/MS non-kit	14	1.85	1.83	1.80	0.70	2.50
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	2.70	2.50	3.50	1.55	4.00
C18:1	**ALL MS/MS Methods**	**44**	**3.48**	**3.00**	**3.00**	**2.00**	**7.00**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	6	2.91	2.80	N/A*	2.43	3.50
	Derivatized - MS/MS non-kit	16	2.71	2.68	3.00	2.00	3.50
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	21	4.22	3.29	7.00	2.27	7.00
C18OH	**ALL MS/MS Methods**	**39**	**0.11**	**0.10**	**0.10**	**0.04**	**0.26**
	Derivatized - MS/MS PerkinElmer NeoGram Kit	7	0.14	0.14	0.10	0.10	0.20
	Derivatized - MS/MS non-kit	13	0.09	0.10	0.10	0.04	0.18
	Non-derivatized - MS/MS PerkinElmer NeoBase Kit	18	0.09	0.10	0.10	0.04	0.16

PT ERRORS

Screening programs are designed to minimize false negative reports, but this precautionary approach could result in false positive misclassifications. Laboratories should monitor false positive misclassifications to keep them as low as possible.

Tables 10 and 11 show the PT errors reported in 2015 by domestic and foreign laboratories for qualitative assessments by disorder/analyte. Because of specific clinical assessment practices, presumptive clinical classifications (qualitative assessments) of some specimens might differ by participant. As stated previously, if participants provided their cutoff values, those cutoffs were applied

Table 10. 2015 Summary of Proficiency Testing Errors by Domestic Laboratories

Disorder	Positive Specimens Assayed (N)	False Negative Errors (%)	Negative Specimens Assayed (N)	False Positive Errors (%)
Congenital Adrenal Hyperplasia	129	0.0	511	0.4
Biotinidase Deficiency	170	0.0	470	0.0
GALT Deficiency	214	0.5	426	0.0
G6PD Deficiency	2	0.0	6	0.0
Immunoreactive Trypsinogen	260	0.0	390	0.0
Congenital Hypothyroidism	264	0.0	731	0.0
Galactosemia	47	0.0	308	0.0
Arginine Screen	113	0.0	452	0.0
Citrulline Screen	138	0.0	552	0.0
Leucine Screen	140	0.0	560	0.5
Methionine Screen	138	0.0	552	0.0
Phenylalanine Screen	175	0.6	700	0.0
Succinylacetone Screen	91	0.0	364	0.0
Tyrosine Screen	162	1.2	648	0.0
Valine Screen	98	0.0	392	0.0
C0(L) Screen	146	1.4	584	0.0
C3 Screen	149	0.0	596	0.0
C3DC Screen	65	0.0	260	0.0
C3DC+C4OH Screen	120	1.7	180	0.0
C4 Screen	136	5.2	544	0.0
C4OH Screen	63	1.6	252	1.2
C5 Screen	149	0.7	596	0.2
C5:1 Screen	146	4.1	584	0.0
C5OH Screen	146	0.0	584	1.2
C6 Screen	140	3.6	560	0.0
C8 Screen	149	0.0	596	0.0
C10 Screen	137	0.0	548	0.0
C10:1 Screen	131	0.0	524	0.0
C10:2 Screen	87	1.2	348	0.0
C14 Screen	138	4.4	552	0.0
C16 Screen	140	1.4	560	0.2
C18 Screen	128	0.0	512	0.0
C5DC Screen	146	0.0	584	0.0
C14:1 Screen	149	1.3	596	0.2
C16OH Screen	198	0.0	547	0.0
C18:1 Screen	131	0.0	524	0.0
C18OH Screen	115	1.7	460	0.0
XALD screen	8	0.0	12	0.0

in the final evaluation of the error judgment. (Figure 4). The rates for false positive misclassifications are based on the number of negative specimens tested, and the rates for false negative misclassifications on the number of positive specimens tested.

A few of our PT specimens fall close to the decision level for clinical assessment, and thus, rigorously tested the ability of laboratories to make the expected cutoff decision. Most specimens near the mean cutoff value are classified as not-evaluated specimens. As such, they are not included in the error calculations.

Table 11. 2015 Summary of Proficiency Testing Errors by Foreign Laboratories

Disorder	Positive Specimens Assayed (N)	False Negative Errors (%)	Negative Specimens Assayed (N)	False Positive Errors (%)
Congenital Adrenal Hyperplasia	517	1.0	2093	1.1
Biotinidase Deficiency	453	0.9	1257	0.6
GALT Deficiency	343	0.9	682	0.2
G6PD Deficiency	30	3.3	90	1.1
Immunoreactive Trypsinogen	818	1.7	1227	0.3
Congenital Hypothyroidism	1142	0.6	3133	0.8
Galactosemia	246	0.4	1574	0.4
Arginine Screen	555	2.0	2220	0.8
Citrulline Screen	606	0.8	2424	0.6
Leucine Screen	674	0.9	2696	0.3
Methionine Screen	656	1.8	2624	0.8
Phenylalanine Screen	916	0.7	3664	1.5
Succinylacetone Screen	221	1.8	884	0.9
Tyrosine Screen	670	1.2	2680	0.4
Valine Screen	619	1.0	2476	0.5
C0(L) Screen	675	4.9	2700	1.2
C3 Screen	654	1.7	2616	0.9
C3DC Screen	308	1.3	1232	1.8
C3DC+C4OH Screen	422	5.7	633	1.3
C4 Screen	612	2.6	2448	0.9
C4OH Screen	282	3.9	1128	2.0
C5 Screen	680	1.3	2720	0.7
C5OH Screen	594	0.5	2376	3.8
C5:1 Screen	596	2.5	2384	1.0
C5DC Screen	664	1.4	2656	0.9
C6 Screen	632	1.4	2528	1.0
C8 Screen	692	1.0	2768	0.8
C10 Screen	665	1.5	2660	0.5
C10:1 Screen	594	2.7	2376	2.0
C10:2 Screen	404	2.0	1616	0.6
C14 Screen	623	2.1	2492	1.2
C14:1 Screen	652	1.7	2608	0.9
C16 Screen	657	2.0	2628	0.4
C16OH Screen	868	3.9	2387	1.1
C18 Screen	616	0.7	2464	0.7
C18:1 Screen	587	3.9	2348	0.9
C18OH Screen	504	3.0	2016	1.3
XALD Screen	4	0.0	6	0.0

SICKLE CELL DISEASE AND OTHER HEMOGLOBINOPATHIES PT PROGRAM

Table 12 show the summary of PT errors for the 2015 Sickle Cell and Hemoglobinopathy program by domestic and foreign laboratories. Table 13 shows the challenges distributed in 2015 for the sickle cell disease and other hemoglobinopathies and Table 14 shows the methods used by laboratories testing for them. Participants are evaluated on hemoglobin presumptive phenotypes and ability to provide correct presumptive clinical assessments.

Table 12: Summary of Proficiency Testing Errors for Hemoglobinopathies by Domestic and Foreign Laboratories in 2015

Testing Errors	Domestic	Foreign
Specimens assayed	725	350
Presumptive phenotype errors	2.6%	3.4%
Presumptive clinical assessment errors	0.7%	1.2%

Table 13. 2015 Hemoglobinopathies Accepted Presumptive Phenotype Distribution

Panel	Specimen 1	Specimen 2	Specimen 3	Specimen 4	Specimen 5
Panel 1	FA	FAS	FAE FAV FAC *for IEF only labs* FA + Other	FA	FA
Panel 2	FAC	FAS	FA	FA	FAS
Panel 3	FAE or FAV	FA	FAC	FA	FAS

Table 14. Frequency of Reported Hemoglobinopathy Methods

Method	Bio-Rad Screening HPLC	Isoelectric Focusing	Primus Ulta 2 HPLC	Extended Gradient HPLC	Electrophoresis – Cellulose Acetate	PCR Amplification of DNA	Electrophoresis – Citrate Agar
Primary	38	27	5	0	0	0	0
Secondary	7	23	4	3	1	1	0
Tertiary	2	1	0	0	0	0	2
Quaternary	1	0	0	0	0	0	0

CYSTIC FIBROSIS DNA MUTATION PT PROGRAM

Table 15 shows the PT errors for the CFDNA program. This program provides evaluations based on the allele identification and clinical assessment. Allele detection is dependent on the method used. Table 16 summarizes the CF mutation challenges distributed in 2015.

TABLE 15. Summary of Proficiency Testing Errors for Cystic Fibrosis DNA Mutation Detection Specimens Distributed in 2015

Quarter, Year	Specimens Assayed (N)	Number of Incorrect Genotypes	Correct Clinical Assessments	Incorrect Clinical Assessments	No Clinical Assessment Reported*	No Data Submitted
Q1, 2015	310	8	98.7%	1.3%	2.9%	3.1%
Q2, 2015	310	3	99.4%	0.6%	0.3%	4.6%
Q3, 2015	310	6	99.0%	1.0%	0.0%	7.5%
Q4, 2015	315	2	99.4%	0.6%	0.0%	6.0%
Total	1245	19	99.1%	0.9%	0.8%	5.3%

*This includes specimens where the PCR failed or participant failed to include a clinical assessment.

TABLE 16. Cystic Fibrosis DNA Mutation (CFTR gene) Challenges Distributed in 2015

Mutation (Legacy Name)	Mutation (HGVS Nomenclature)	Mutations sent
F508del	c.1521_1523delCTT	13
Wild type/no mutation	Wild type/no mutation	12
G542X	c.1624G>T	2
R1158X	c.3472C>T	1
3849+10kbC>T	c.3717+12191C>T	1
S549N	c.1646G>A	1
3272-26A>G	c.3140-26A>G	1
W1282X	c.3846G>A	2
1898+1G>A	c.1766+1G>A	1
F508C	c.1523C>G	1
3659delC	c.3528delC	1
G551D	c.1652G>A	1
R117H	c.350G>A	1
621+1G>T	c.489+1G>T	1
S492F	c. 1475C>T	1

Note: Five specimens are sent each of the four quarters and each sample has two mutations or wild type sequences.

PT BIAS PLOTS

Figures 5 – 40 are illustrated for PT analytes reported using the NSQAP data reporting website. A wide range of quantitatively measured PT challenges are selected for the bias plots. Comparisons of results by different methods are illustrated with the participants' reported PT data for one selected challenge for each analyte.

The expected value of each specimen equals the sum of the enriched value and the endogenous (non-enriched) value. GALT, G6PD, and C0(L) use CDC-assayed values due to production methods for deficient analytes. IRT standard cannot be fully recovered by any IRT analytical method; therefore, IRT PT uses CDC-assayed values.

A growing number of NSQAP participants use a non-derivatized MS/MS method for amino acids and acylcarnitine analysis. However, non-derivatized MS/MS methods cannot distinguish between analytes C3DC and C4OH (i.e., they are isobaric). Laboratories using a non-derivatized MS/MS method report C3DC+C4OH, while derivatized MS/MS method users continue to report those analytes separately.

These bias plots show the difference of the reported value (positive or negative) by laboratory and method subtracted from the expected or assayed value. To illustrate method-related differences in analyte recoveries, the PT quantitative results are grouped by kit or method.

For each plot, note the scale-changes of the Y-axis. A reported value matching the expected value falls on the plot's "0" line. For each figure, a summary of the specimen data for the selected PT challenge is tabulated in the left margin. Ideally, a reasonable bias is less than 20% of the expected value (EV).

The bias plots (Figures 5-40) illustrate the 95% CI for the participant mean. A tight scatter within this interval indicates good performance for a method or a group of methods. In general, the quantitative comparisons for PT challenges are reasonable within a method but vary among methods. Because some of the pools in a routine PT survey represent a unique donor specimen, differences in endogenous concentration levels in the donor specimens might influence differences in methods.

Figure 4. EXPLANATION OF THE NEWBORN SCREENING QUALITY ASSURANCE PROGRAM'S GRADING ALGORITHM

Part 1

The **NSQAP Expected Clinical Assessment** for PT specimens is determined by comparing the NSQAP Expected Certified Value and the NSQAP Cutoff. The **NSQAP Certified Expected Value** is the sum of the endogenous value plus the enrichment value for an individual analyte. The enrichments for each PT specimen are calculated so that the 95% confidence interval falls above or below the NSQAP cutoff value. The **NSQAP Cutoff Value** is determined annually by using the mean of all domestic laboratories' reported cutoff values as a guideline.

Part 2

The participant reports the clinical assessment as "within normal limits" or "outside normal limits." This is the **Participant *Reported* Clinical Assessment**. The **Participant *Expected* Clinical Assessment** is the assessment that is expected when the NSQAP Certified Expected Value and the participant cutoff are compared. When the Participant Reported Clinical Assessment differs from the NSQAP Expected Clinical Assessment, the grading algorithm is used to evaluate test performance. The algorithm will determine if the Participant Reported Clinical Assessment is correct, false negative, false positive or cutoff difference.

- If the NSQAP *Expected* Clinical Assessment is the same as the Participant *Expected* Clinical Assessment but the Participant *Reported* Assessment differs, the grade will be either false negative or false positive.
- If the NSQAP *Expected* Clinical Assessment and the Participant *Expected* Clinical Assessment differ, the Participant *Reported* clinical assessment will not be graded as incorrect. (If a cutoff is not provided by the participant, the evaluation will be based on the NSQAP Cutoff Value)

Part 3

Determination of a final evaluation for a specimen is based on the Clinical Laboratory Improvement Amendments (CLIA) regulations whereby the PT provider "must compare the laboratory's response for each analyte with the response that reflects agreement of either 80% of ten or more referee laboratories or 80% or more of all participating laboratories." (CLIA Regulations, 2004). An NSQAP gradable specimen must have 80% or more agreement among **domestic** laboratories. A specimen with less than 80% agreement is not-gradable/not-evaluated.

<u>Example of TSH false positive –</u>

NSQAP Certified Expected Value = 13 µIU/mL

NSQAP Cutoff = 30 µIU/mL

Participant cutoff = 35 µIU/mL

Participant's Reported Clinical Assessment =
2- Outside Normal Limits for this sample.

1. Comparison of the NSQAP Certified Expected Value and NSQAP Cutoff:

   NSQAP Certified Expected Value = 13 µIU/mL

   NSQAP Cutoff = 30 µIU/mL

   Therefore, the NSQAP Expected Clinical Assessment = *1- Within Normal Limits*

2. Comparison of the NSQAP Certified Expected Value and Participant Cutoff

   NSQAP Certified Expected Value = 13 µIU/mL

   Participant Cutoff = 35 µIU/mL

   Therefore the Participant Expected Clinical Assessment = *1- Within Normal Limits*

3. Participant Reported Clinical Assessment
   = *2-Outside Normal Limits*

   In this example, the NSQAP Expected Clinical Assessment and the Participant Expected Clinical Assessment were both "1- Within Normal Limits" but the Participant Reported Clinical Assessment is "2- Outside Normal Limits" therefore:

   Participant Evaluation Result = false positive

Sample Table: Participant Evaluation Determination

Analyte	Expected Value (EV)	NSQAP Cutoff	Participant Cutoff	Assessment: Comparison of EV and NSQAP Cutoff	Assessment: Comparison of EV and Participant Cutoff	Assessment: Participant Reported Clinical Assessment	Participant Evaluation Result
TSH	13	30	35	wnl	wnl	onl	false positive
TSH	13	30	10	wnl	onl	onl	cutoff difference
TSH	50	30	35	onl	onl	wnl	false negative
TSH	50	30	60	onl	wnl	wnl	cutoff difference

wnl- "1- Within Normal Limits"
onl -"2- Outside Normal limits"

Reference: CLIA Regulations Subpart I—Proficiency Testing Programs for Nonwaived Testing. [Updated 2004 July 7; accessed 2014 January 31]. Available from http://wwwn.cdc.gov/clia/regs/subpart_i.aspx#493.931

Grading is based on the participant reported clinical assessment, not on the reported value. Overall statistics, which are generated from all participant data, and mean reported concentrations by method are provided on the website for analytical reference only.

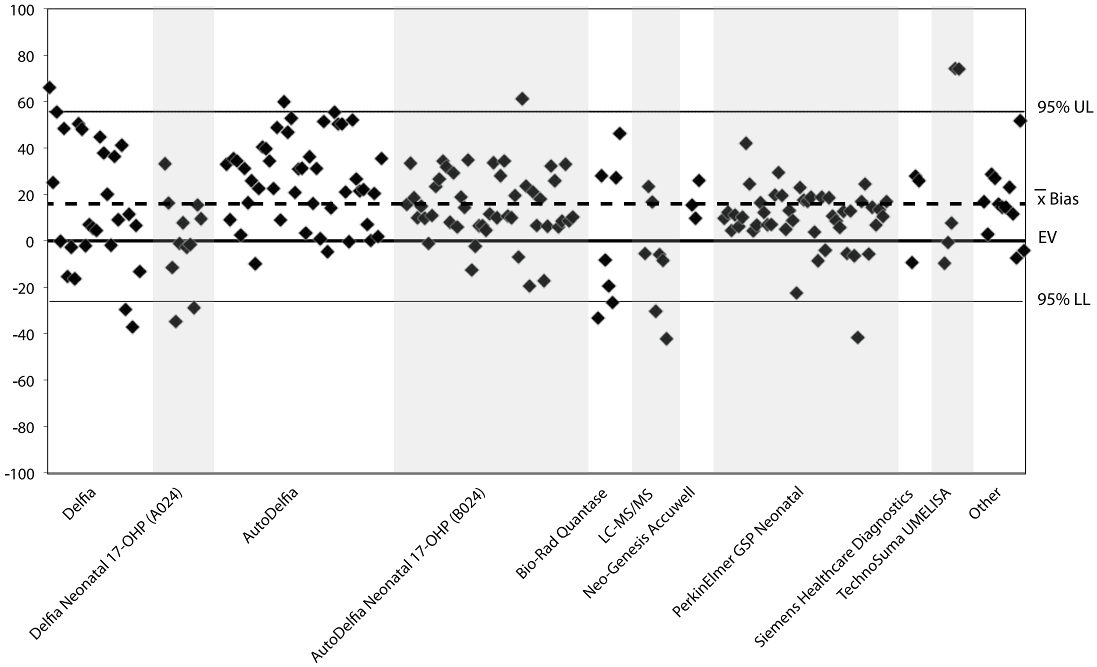
FIGURES 5-6. Reproducibility of Results by Method: 17 α-Hydroxyprogesterone (17OHP) and Thyroxine (T_4)

Bias Plot 17 of a-Hydroxyprogesterone (17OHP) Values by Method
Quarter 3, Specimen 31513
Expected Value (EV)[1] = 86.5 ng/mL serum

Quarter 3

Specimen 3

Enriched	85.0
CDC Assayed	104.2
Participant Mean	101.3
Participant Bias[2]	14.8

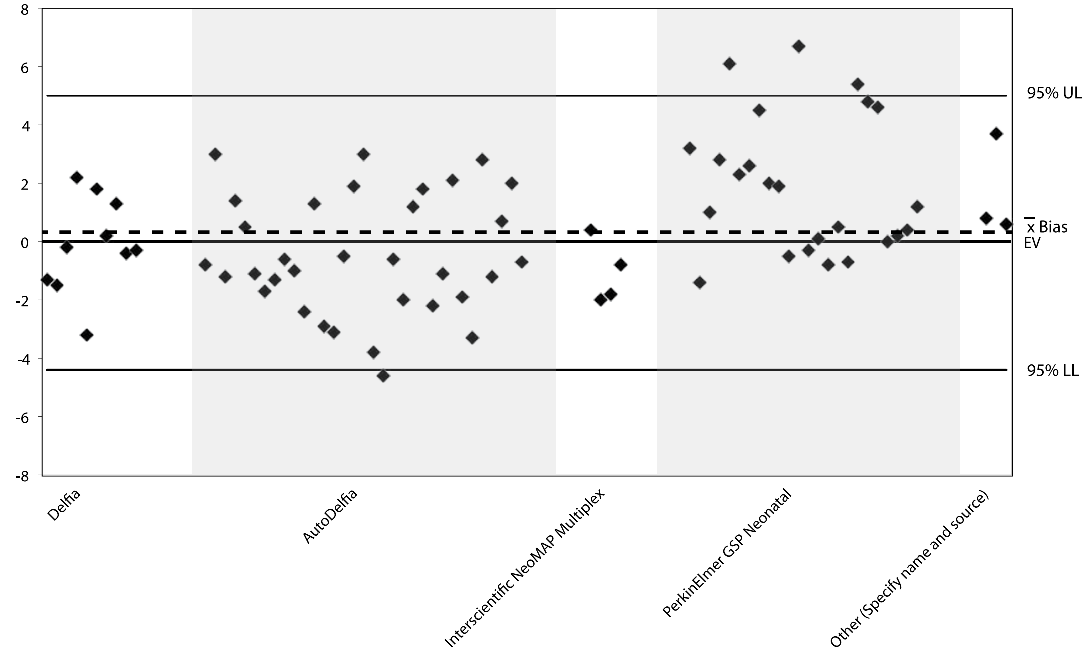


Bias Plot of Thyroxine (T_4) Values by Method
Quarter 3, Specimen 31514
Expected Value (EV)[1] = 16.4 µg/dL serum

Quarter 3

Specimen 4

Enriched	10.0
CDC Assayed	17.7
Participant Mean	16.7
Participant Bias[2]	0.3



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[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

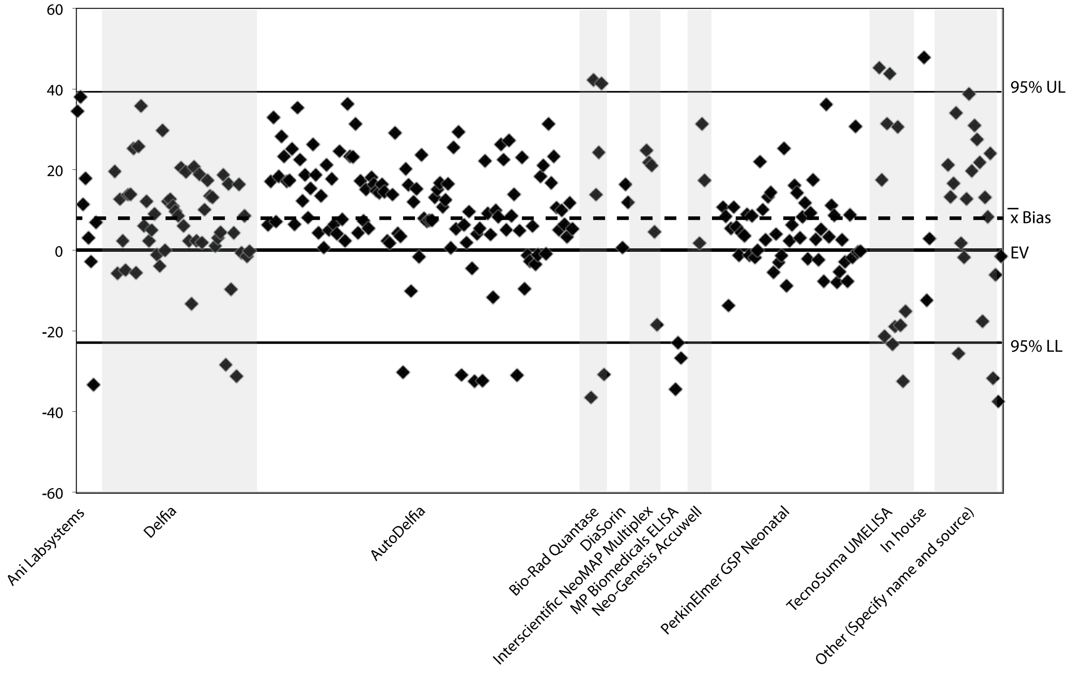
[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 7-8. Reproducibility of Results by Method: Thyroid-Stimulating Hormone (TSH) and Total Galactose (TGal)

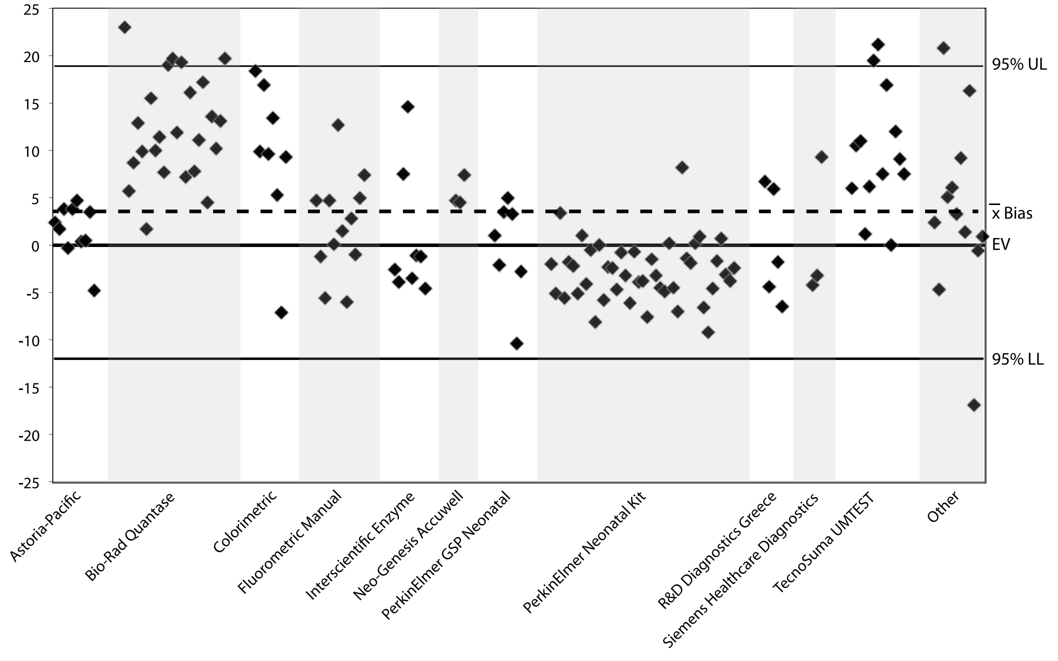
Bias Plot of Thyroid-Stimulating Hormone (TSH) Values by Method
Quarter 3, Specimen 31511
Expected Value (EV)[1] = 75.7 µIU/mL serum

Quarter 3	
Specimen 1	
Enriched	75.0
CDC Assayed	85.2
Participant Mean	83.9
Participant Bias[2]	8.2



Bias Plot of Total Galactose (TGal) Values by Method
Quarter 1, Specimen 11514
Expected Value (EV)[1] = 25.3 mg/dL whole blood

Quarter 1	
Specimen 4	
Enriched	25.0
CDC Assayed	22.3
Participant Mean	28.8
Participant Bias[2]	3.5



[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

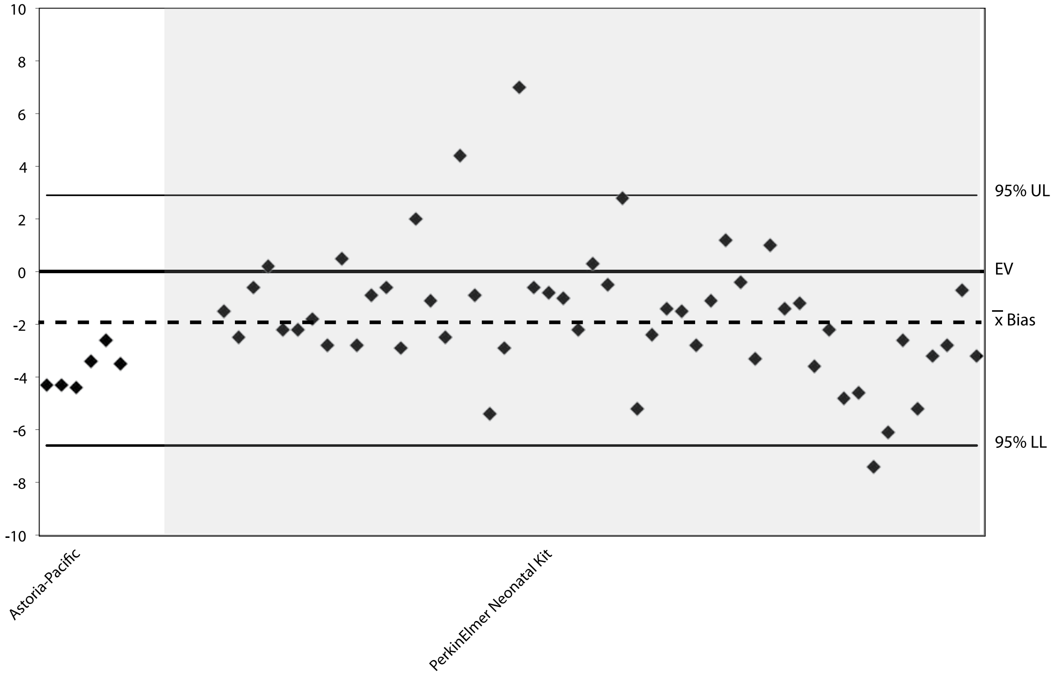
[2] Participant bias (x̄) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (x̄) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 9-10. Reproducibility of Results by Method: Galactose-1-phosphate Uridyltransferase (GALT) and Immunoreactive Trypsinogen (IRT)

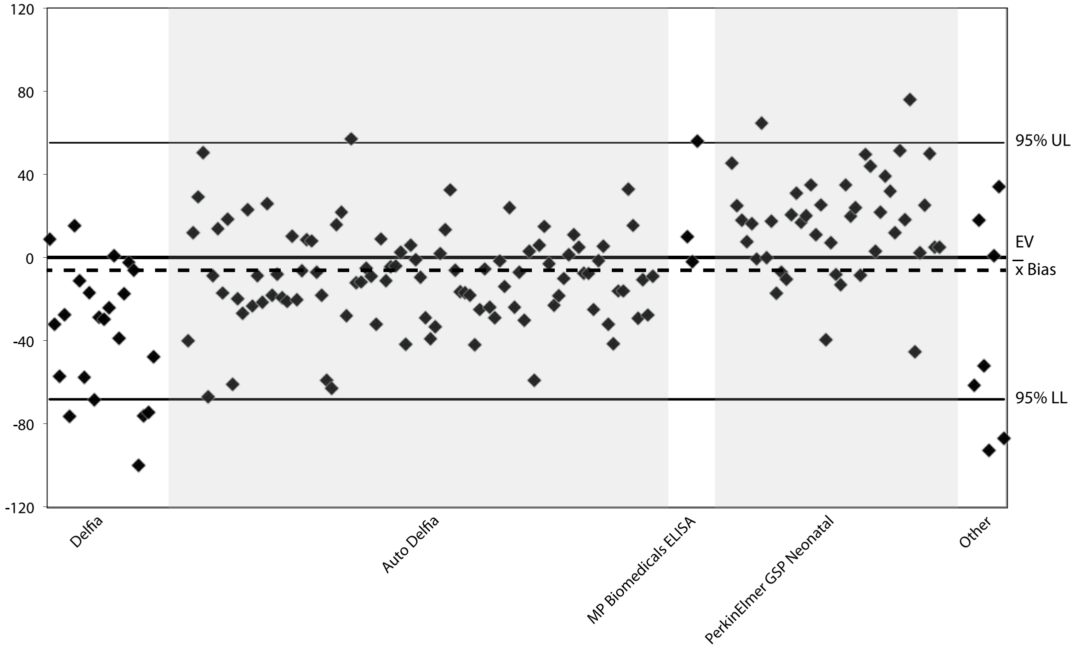
Quarter 3	
Specimen 1	
CDC Assayed	10.6
Participant Mean	8.7
Participant Bias[2]	-1.9

Bias Plot of Galactose-1-phosphate Uridyltransferase (GALT) Values by Method Quarter 3, Specimen 31591 Assayed Value (AV)[3] = 10.6 U/g Hb



Quarter 1	
Specimen 3	
CDC Assayed	239.1
Participant Mean	232.6
Participant Bias[2]	-6.5

Bias Plot of Immunoreactive Trypsinogen (IRT) Values by Method Quarter 1, Specimen 11583 Assayed Value (AV)[3] = 239.1 ng/mL blood



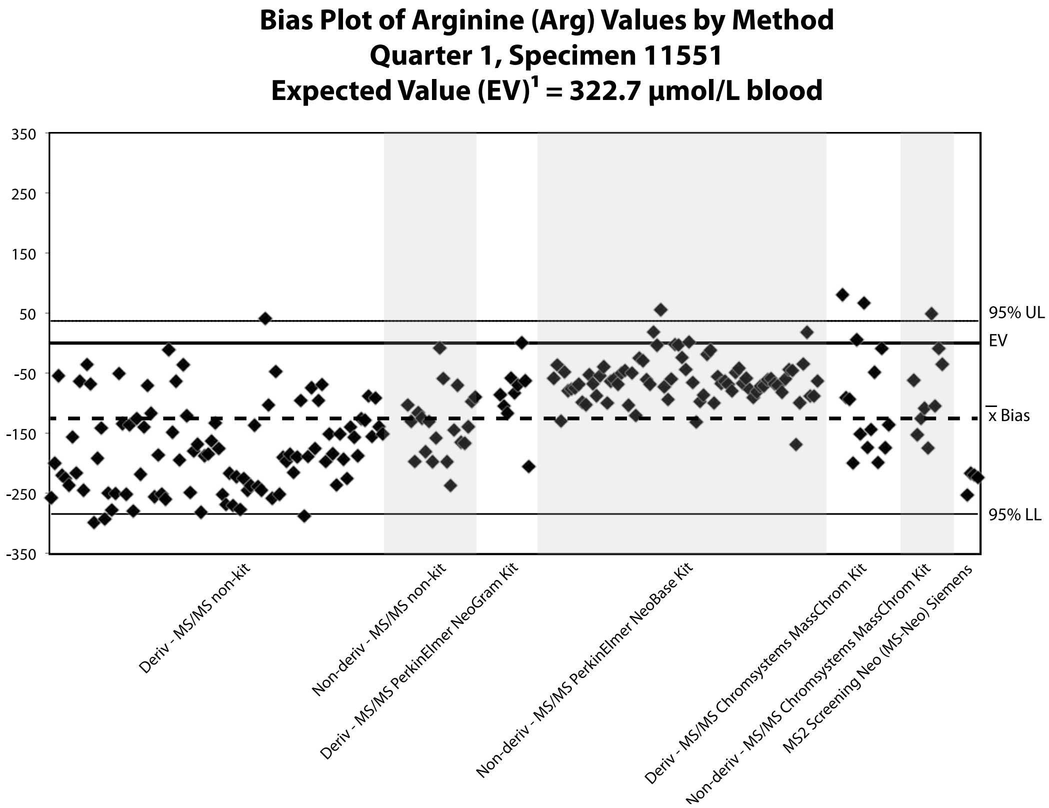
[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

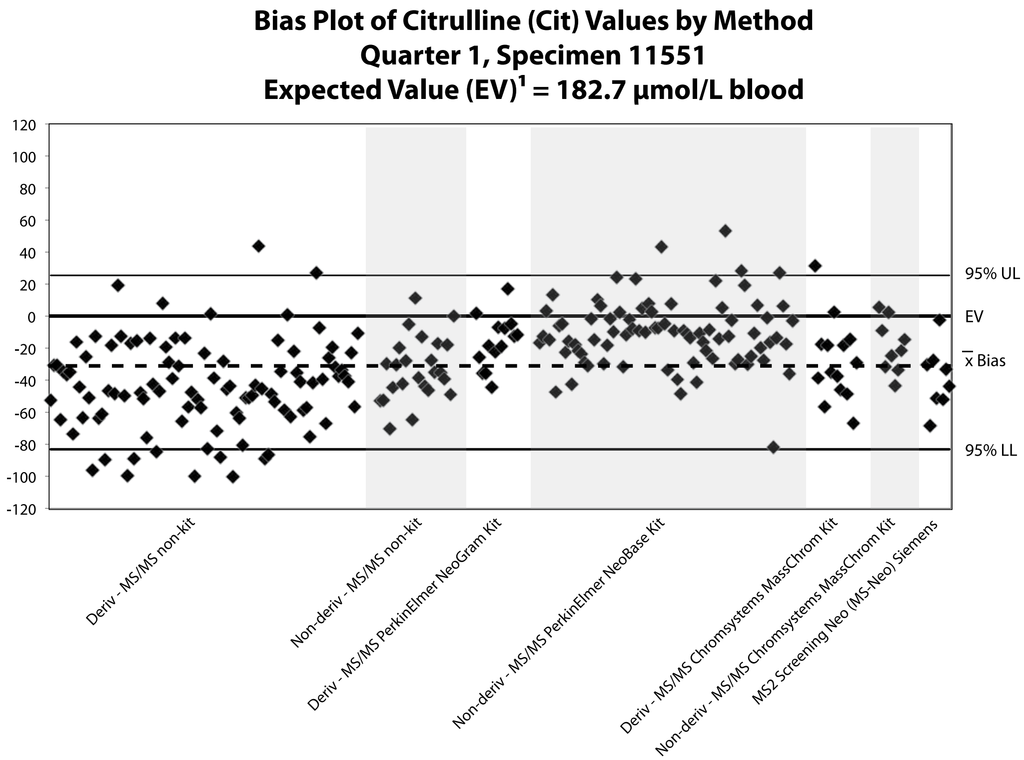
[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 11-12. Reproducibility of Results by Method: Arginine (Arg) and Citrulline (Cit)

Quarter 1	
Specimen 1	
Enriched	300.0
CDC Assayed	279.0
Participant Mean	198.7
Participant Bias[2]	-124.0


Bias Plot of Arginine (Arg) Values by Method
Quarter 1, Specimen 11551
Expected Value (EV)[1] = 322.7 µmol/L blood

Quarter 1	
Specimen 1	
Enriched	150.0
CDC Assayed	170.7
Participant Mean	153.8
Participant Bias[2]	-28.9


Bias Plot of Citrulline (Cit) Values by Method
Quarter 1, Specimen 11551
Expected Value (EV)[1] = 182.7 µmol/L blood

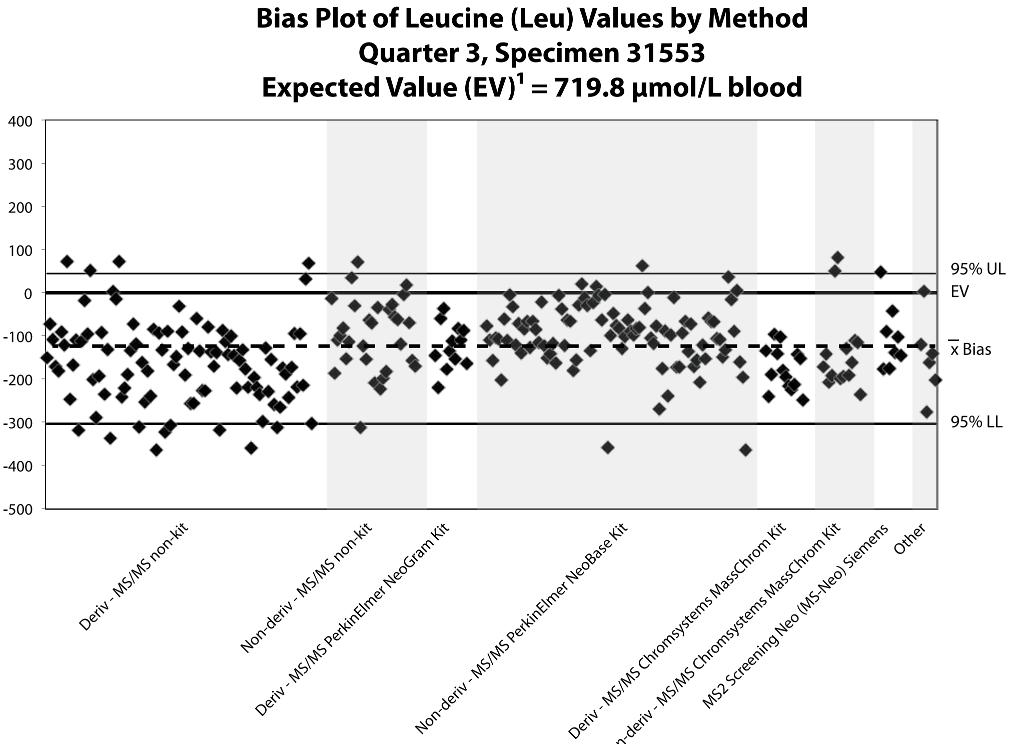
[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

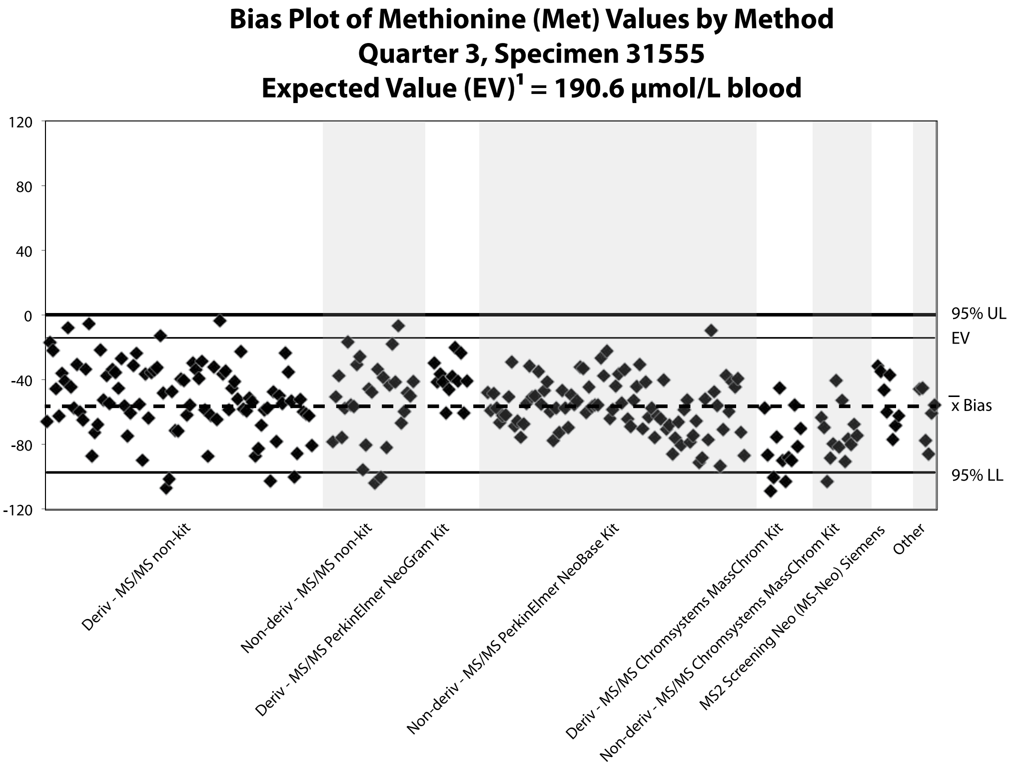
FIGURES 13-14. Reproducibility of Results by Method: Leucine (Leu) and Methionine (Met)

Quarter 3	
Specimen 3	
Enriched	600.0
CDC Assayed	608.4
Participant Mean	589.7
Participant Bias[2]	-130.1



Bias Plot of Leucine (Leu) Values by Method
Quarter 3, Specimen 31553
Expected Value (EV)[1] = 719.8 µmol/L blood

Quarter 3	
Specimen 5	
Enriched	175.0
CDC Assayed	154.2
Participant Mean	134.8
Participant Bias[2]	-55.8



Bias Plot of Methionine (Met) Values by Method
Quarter 3, Specimen 31555
Expected Value (EV)[1] = 190.6 µmol/L blood

[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

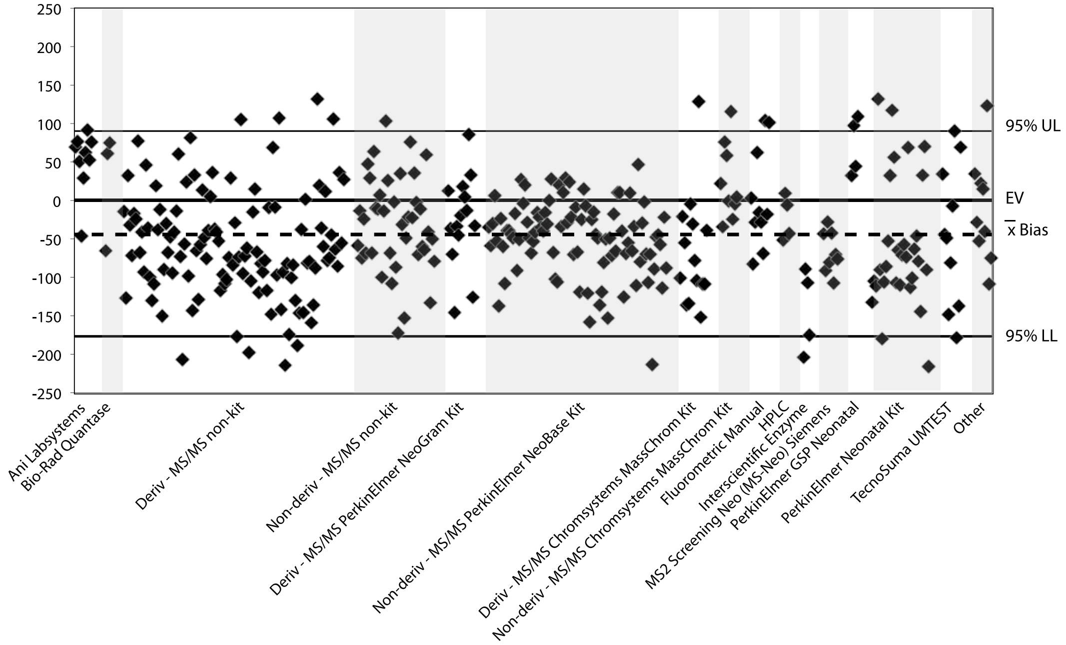
FIGURES 15-16. Reproducibility of Results by Method: Phenylalanine (Phe) and Succinylacetone (SUAC)

Quarter 1

Specimen 5

Enriched	450.0
CDC Assayed	491.5
Participant Mean	451.6
Participant Bias[2]	-43.3

Bias Plot Phenylalanine (Phe) Values by Method
Quarter 1, Specimen 11555
Expected Value (EV)[1] = 494.9 µmol/L blood

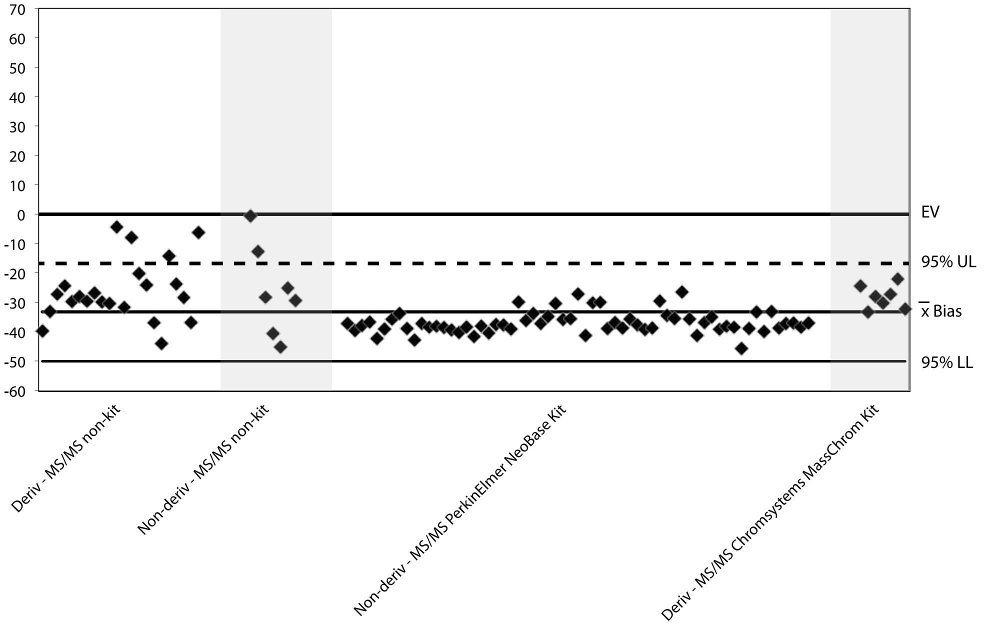


Quarter 3

Specimen 5

Enriched	50.0
CDC Assayed	22.4
Participant Mean	17.1
Participant Bias[2]	-33.3

Bias Plot of Succinylacetone (SUAC) Values by Method
Quarter 3, Specimen 31555
Expected Value (EV)[1] = 50.4 µmol/L blood



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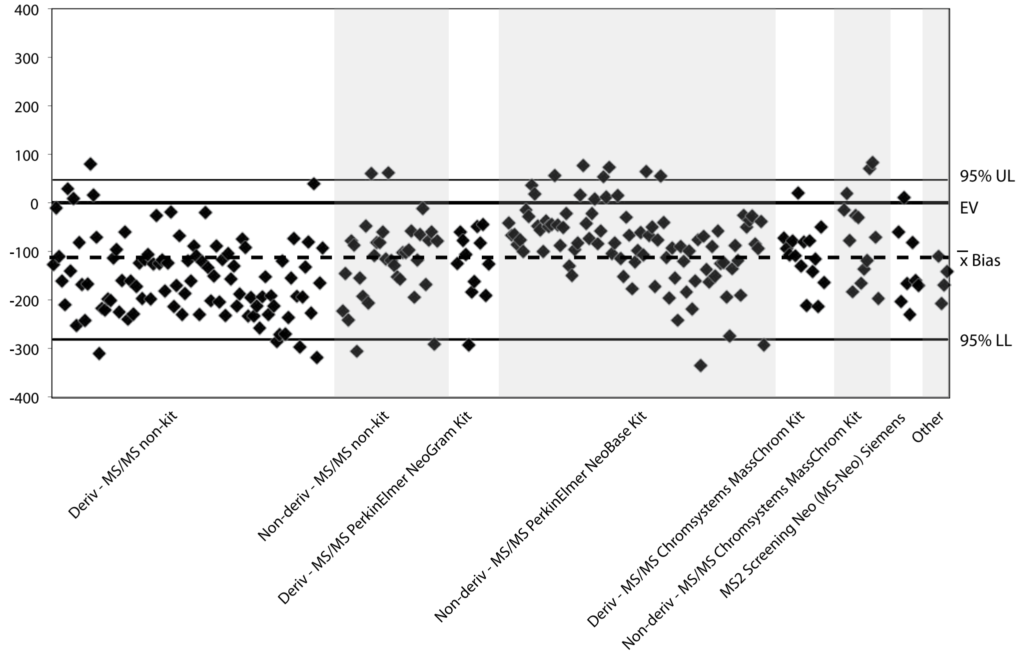
[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2]Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3]AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

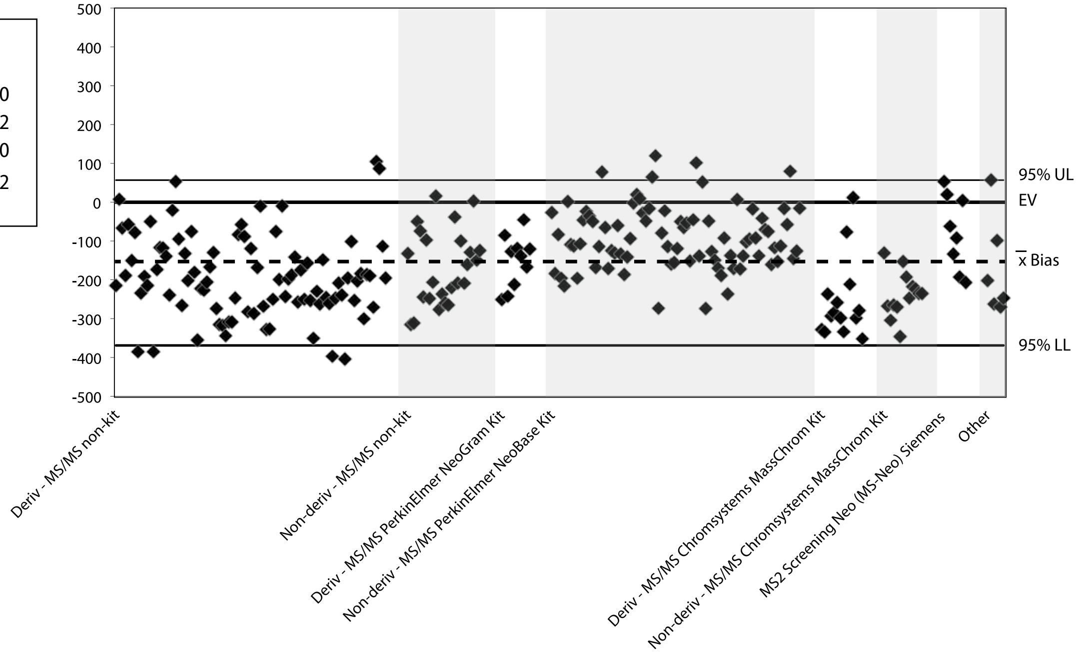
FIGURES 17-18. Reproducibility of Results by Method: Tyrosine (Tyr) and Valine (Val)

Quarter 3	
Specimen 2	
Enriched	600.0
CDC Assayed	564.9
Participant Mean	538.7
Participant Bias[2]	-117.1



Bias Plot of Tyrosine (Tyr) Values by Method
Quarter 3, Specimen 31552
Expected Value (EV)[1] = 655.8 µmol/L blood

Quarter 3	
Specimen 1	
Enriched	550.0
CDC Assayed	544.2
Participant Mean	524.0
Participant Bias[2]	-156.2



Bias Plot of Valine (Val) Values by Method
Quarter 3, Specimen 31551
Expected Value (EV)[1] = 680.2 µmol/L blood

[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

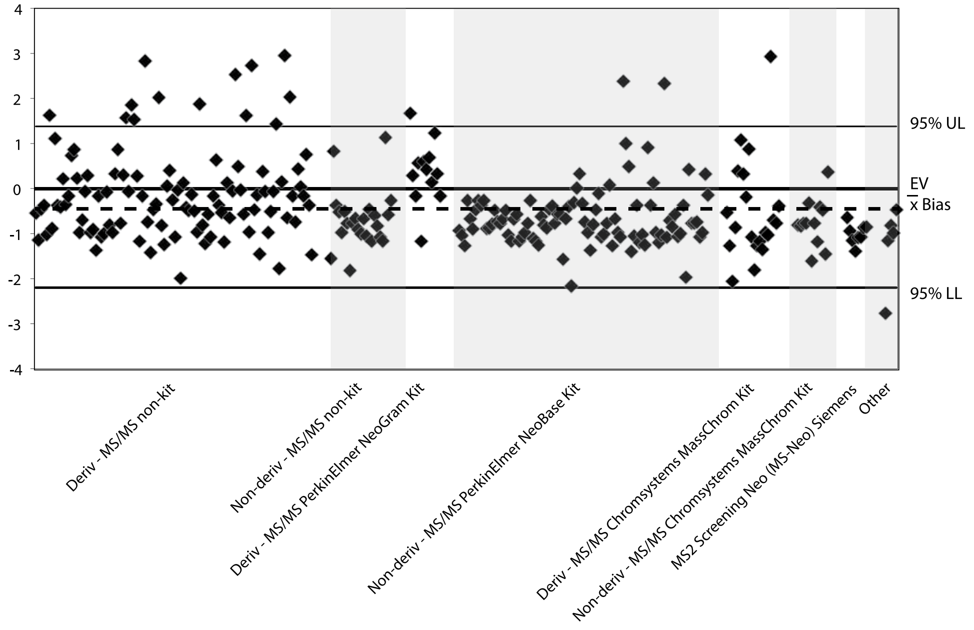
[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 19-20. Reproducibility of Results by Method: Low Free Carnitine (C0(L)) and Propionylcarnitine (C3)

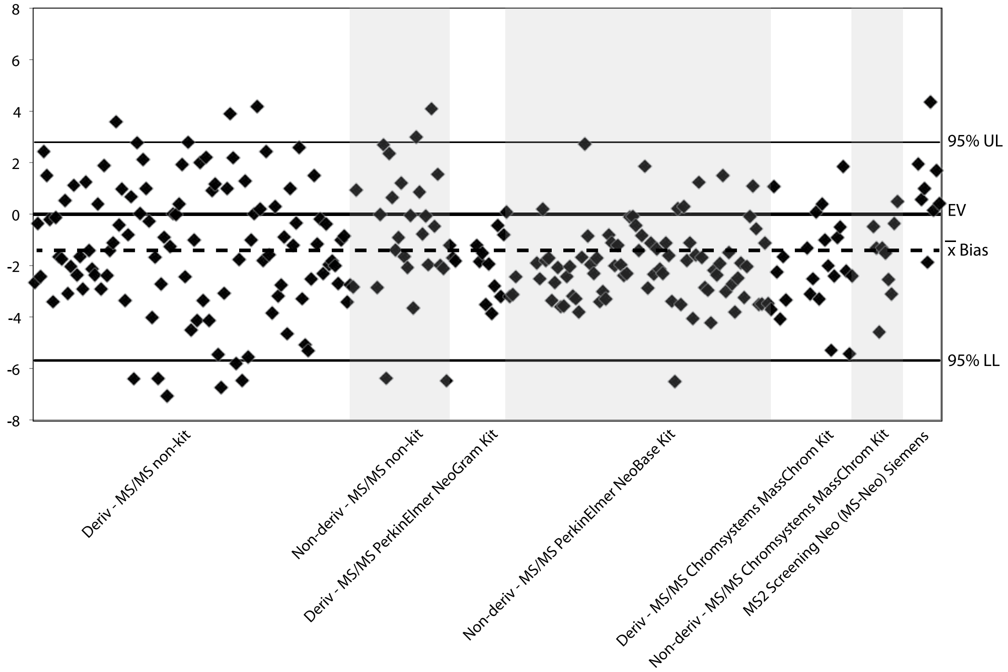
Bias Plot of Low Free Carnitine (C0(L)) Values by Method
Quarter 3, Specimen 31564
Assayed Value (AV)[3] = 3.17 μmol/L blood

Quarter 3	
Specimen 4	
Enriched	0.00
CDC Assayed	3.29
Participant Mean	2.76
Participant Bias[2]	-0.41



Bias Plot of Propionylcarnitine (C3) Values by Method
Quarter 1, Specimen 11562
Expected Value (EV)[1] = 15.01 μmol/L blood

Quarter 1	
Specimen 2	
Enriched	14.00
CDC Assayed	13.26
Participant Mean	13.56
Participant Bias[2]	-1.45



[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

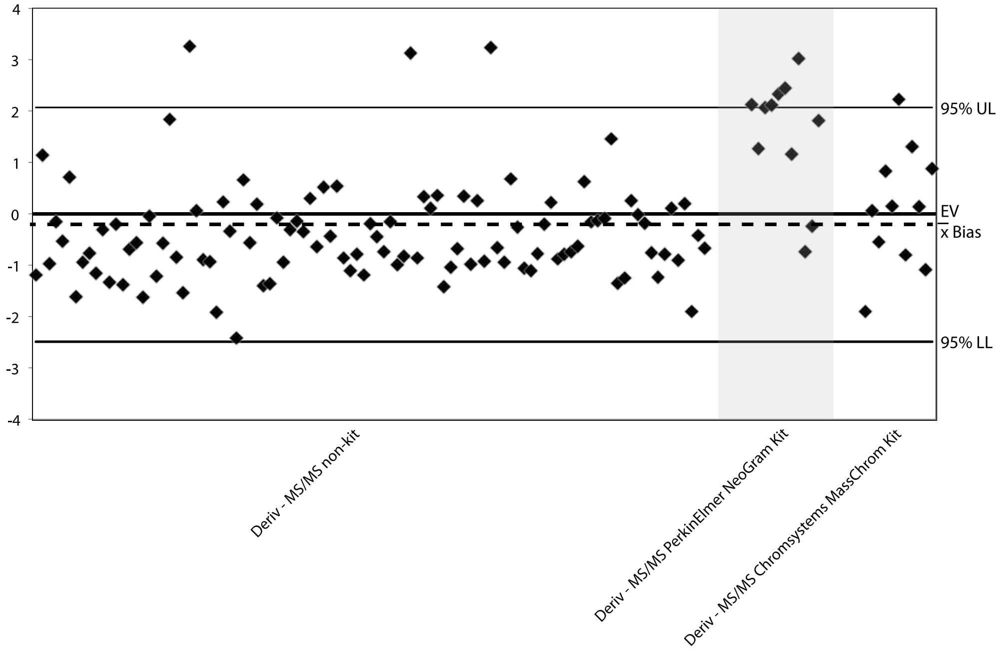
FIGURES 21-22. Reproducibility of Results by Method: Malonylcarnitine (C3DC) Derivatized and C3DC+C4OH Non-derivatized

Quarter 1

Specimen 5

Enriched	2.75
CDC Assayed	2.39
Participant Mean	2.63
Participant Bias[2]	-0.21

Bias Plot of Malonylcarnitine (C3DC) Derivatized Values by Method
Quarter 1, Specimen 11565
Expected Value (EV)[1] = 2.84 µmol/L blood

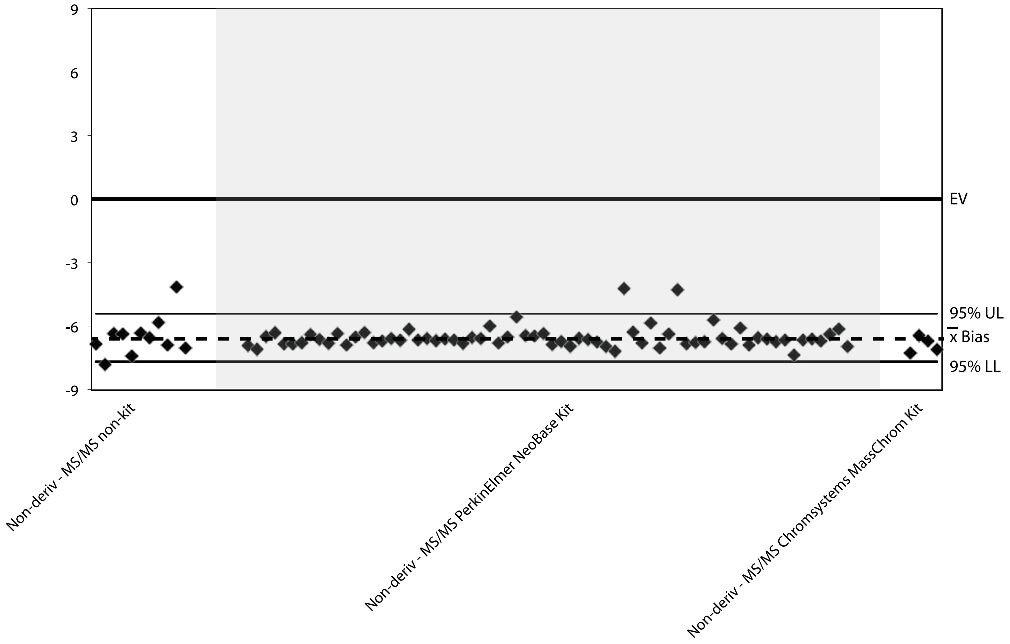


Quarter 3

Specimen 3

Enriched	8.00
CDC Assayed	0.64
Participant Mean	1.50
Participant Bias[2]	-6.55

Bias Plot of C3DC+C4OH Non-derivatized Values by Method
Quarter 3, Specimen 31563
Expected Value (EV)[1] = 8.05 µmol/L blood



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[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

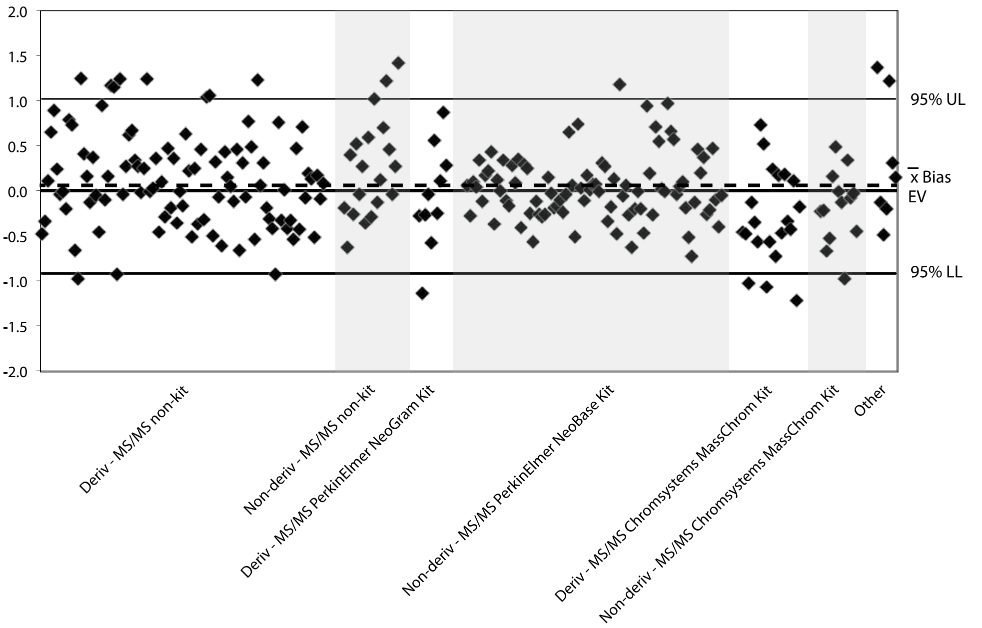
[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 23-24. Reproducibility of Results by Method: Butyrylcarnitine (C4) and Hydroxybutyrylcarnitine (C4OH) Derivatized

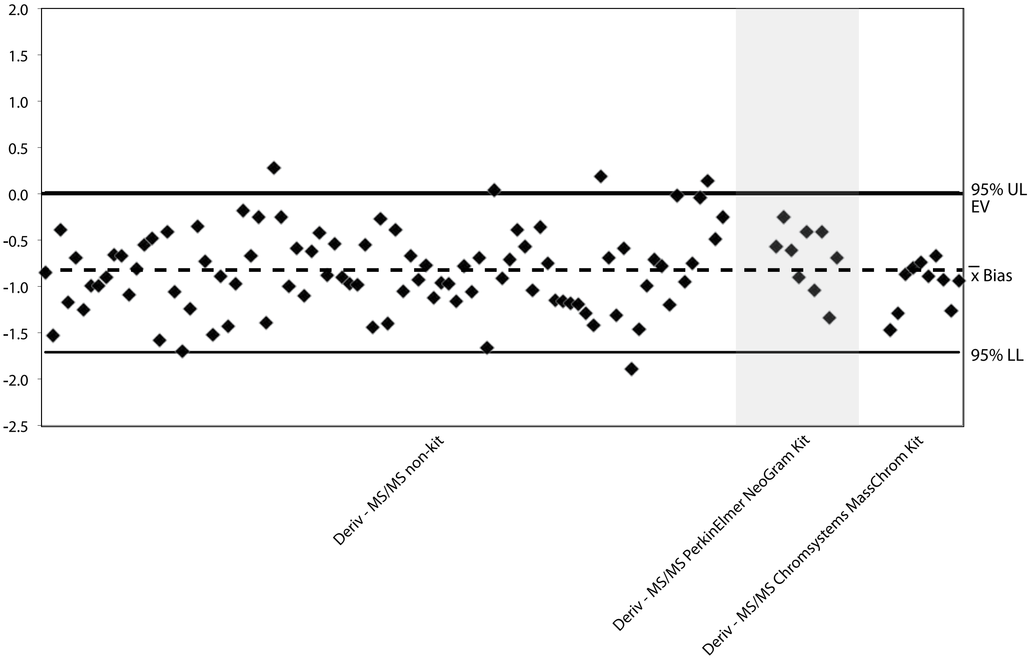
Quarter 3	
Specimen 2	
Enriched	3.00
CDC Assayed	3.92
Participant Mean	3.48
Participant Bias[2]	0.05

Bias Plot of Butyrylcarnitine (C4) Values by Method
Quarter 3, Specimen 31562
Expected Value (EV)[1] = 3.43 µmol/L blood



Quarter 1	
Specimen 2	
Enriched	2.30
CDC Assayed	1.56
Participant Mean	1.64
Participant Bias[2]	-0.85

Bias Plot of Hydroxybutyrylcarnitine (C4OH) Derivatized Values by Method
Quarter 1, Specimen 11562
Expected Value (EV)[1] = 2.49 µmol/L blood



[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

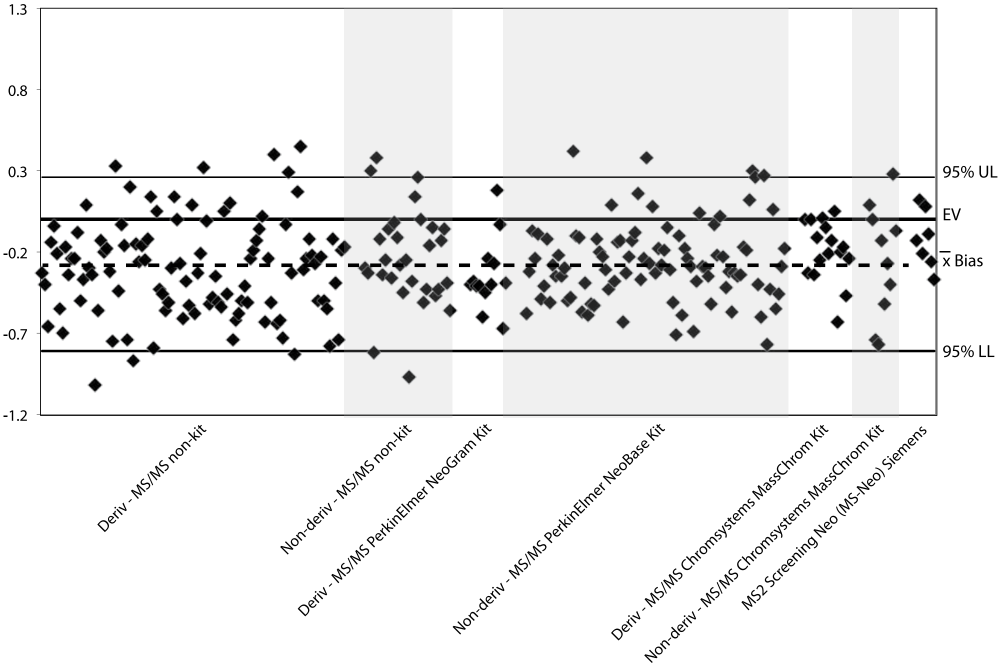
FIGURES 25-26. Reproducibility of Results by Method: Isovalerylcarnitine (C5) and Tiglylcarnitine (C5:1)

Quarter 1

Specimen 2

Enriched	2.00
CDC Assayed	1.84
Participant Mean	1.86
Participant Bias[2]	-0.27

Bias Plot of Isovalerylcarnitine (C5) Values by Method
Quarter 1, Specimen 11562
Expected Value (EV)[1] = 2.13 µmol/L blood

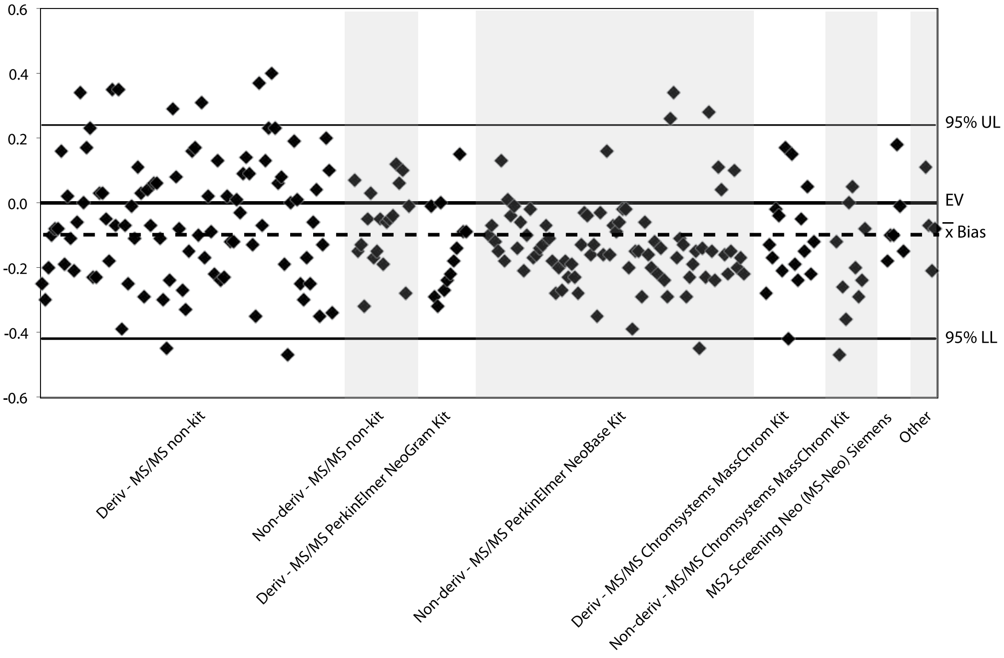


Quarter 3

Specimen 5

Enriched	0.75
CDC Assayed	0.97
Participant Mean	0.70
Participant Bias[2]	-0.09

Bias Plot of Tiglylcarnitine (C5:1) Values by Method
Quarter 3, Specimen 31565
Expected Value (EV)[1] = 0.79 µmol/L blood



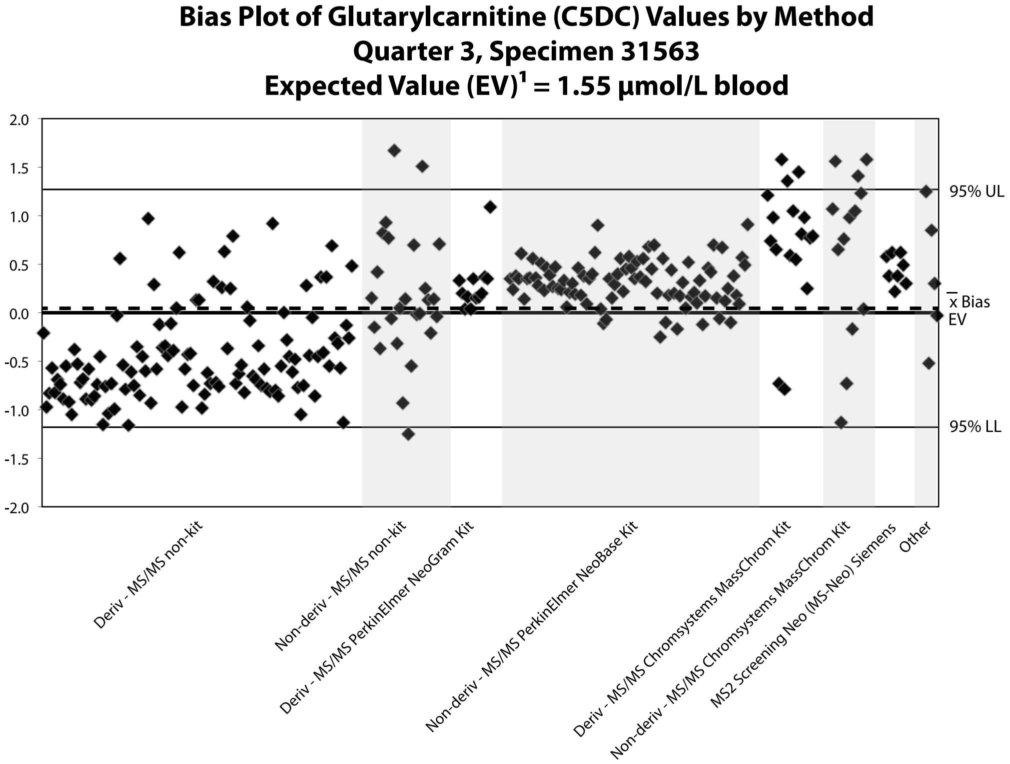
[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

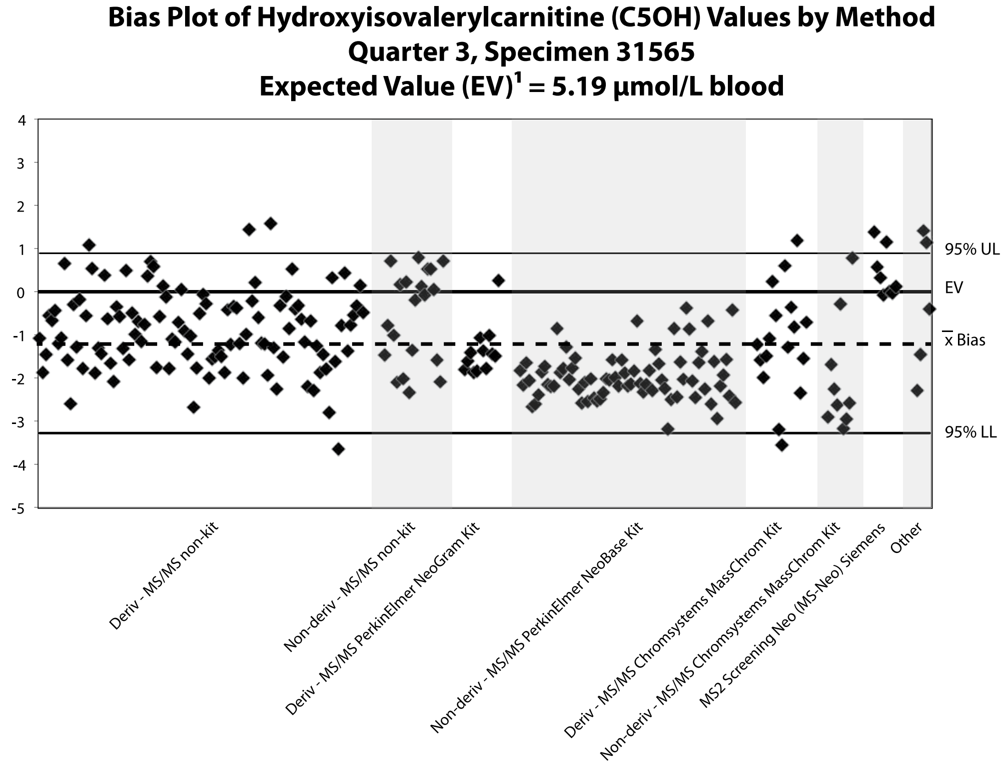
FIGURES 27-28. Reproducibility of Results by Method: Glutarylcarnitine (C5DC) and Hydroxyisovalerylcarnitine (C5OH)

Quarter 3	
Specimen 3	
Enriched	1.50
CDC Assayed	1.38
Participant Mean	1.59
Participant Bias[2]	0.04



Bias Plot of Glutarylcarnitine (C5DC) Values by Method
Quarter 3, Specimen 31563
Expected Value (EV)[1] = 1.55 µmol/L blood

Quarter 3	
Specimen 5	
Enriched	4.00
CDC Assayed	5.50
Participant Mean	3.99
Participant Bias[2]	-1.20



Bias Plot of Hydroxyisovalerylcarnitine (C5OH) Values by Method
Quarter 3, Specimen 31565
Expected Value (EV)[1] = 5.19 µmol/L blood

[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

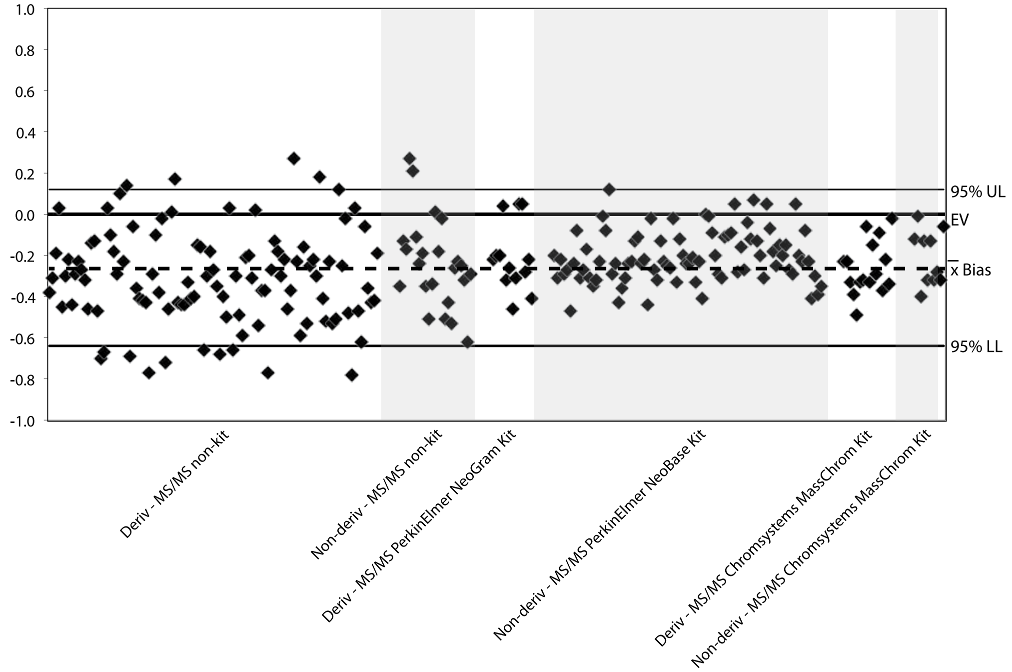
FIGURES 29-30. Reproducibility of Results by Method: Hexanoylcarnitine (C6) and Octanoylcarnitine (C8)

Quarter 1

Specimen 3

Enriched	1.50
CDC Assayed	1.36
Participant Mean	1.27
Participant Bias[2]	-0.26

Bias Plot of Hexanoylcarnitine (C6) Values by Method
Quarter 1, Specimen 11563
Expected Value (EV)[1] = 1.53 µmol/L blood

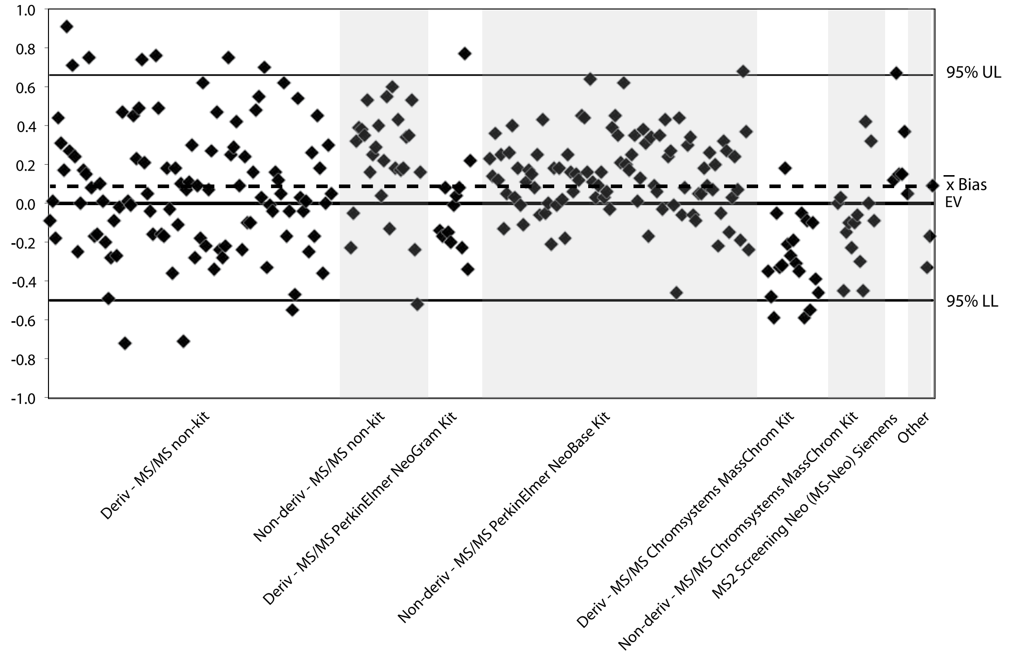


Quarter 3

Specimen 1

Enriched	2.00
CDC Assayed	2.44
Participant Mean	2.13
Participant Bias[2]	0.08

Bias Plot of Octanoylcarnitine (C8) Values by Method
Quarter 3, Specimen 31561
Expected Value (EV)[1] = 2.05 µmol/L blood



[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

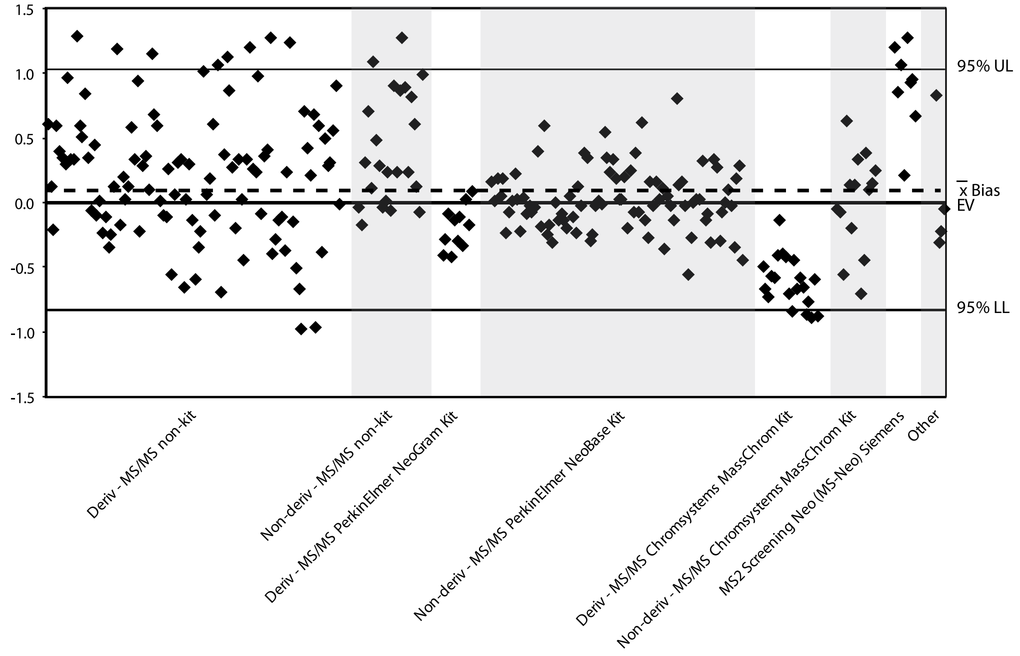
[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 31-32. Reproducibility of Results by Method: Decanoylcarnitine (C10) and Decenoylcarnitine (C10:1)

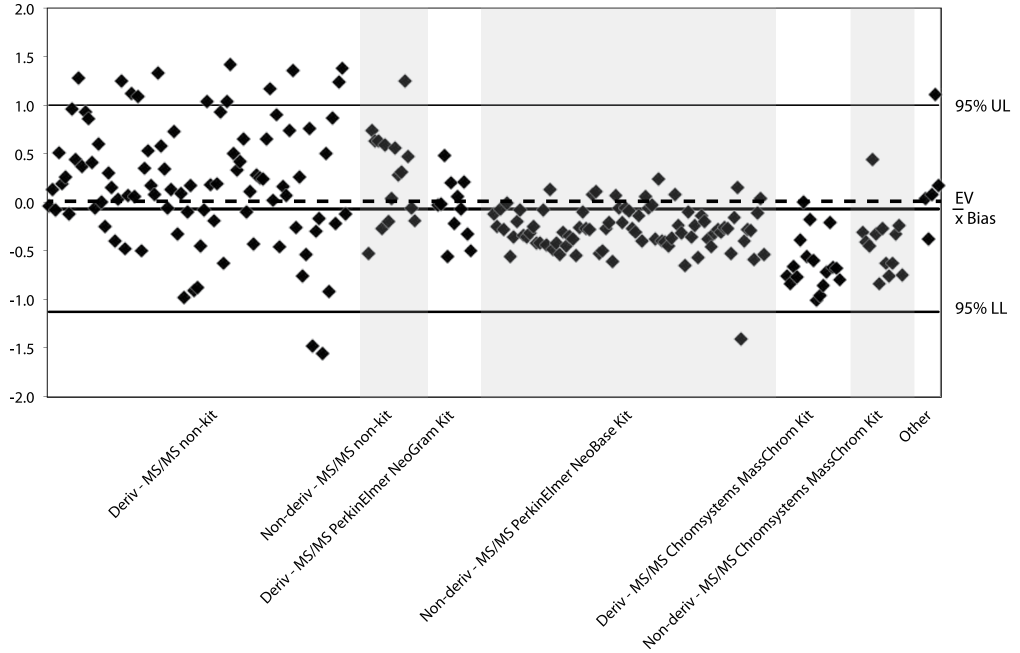
Quarter 3	
Specimen 1	
Enriched	2.00
CDC Assayed	2.54
Participant Mean	2.17
Participant Bias[2]	0.10

Bias Plot of Decanoylcarnitine (C10) Values by Method
Quarter 3, Specimen 31561
Expected Value (EV)[1] = 2.07 µmol/L blood



Quarter 3	
Specimen 1	
Enriched	2.00
CDC Assayed	2.65
Participant Mean	1.99
Participant Bias[2]	-0.07

Bias Plot of Decenoylcarnitine (C10:1) Values by Method
Quarter 3, Specimen 31561
Expected Value (EV)[1] = 2.06 µmol/L blood



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[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

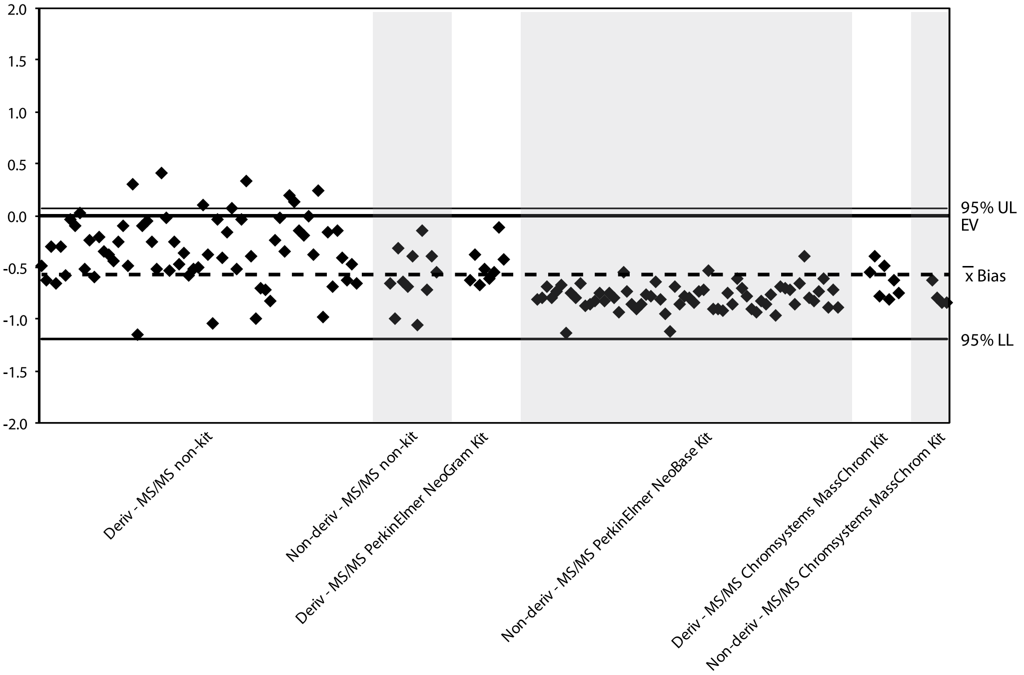
FIGURES 33-34. Reproducibility of Results by Method: Decadienoylcarnitine (C10:2) and Myristoylcarnitine (C14)

Quarter 1

Specimen 5

Enriched	1.50
CDC Assayed	1.20
Participant Mean	0.96
Participant Bias[2]	-0.56

Bias Plot of Decadienoylcarnitine (C10:2) Values by Method
Quarter 1, Specimen 11565
Expected Value (EV)[1] = 1.52 µmol/L blood

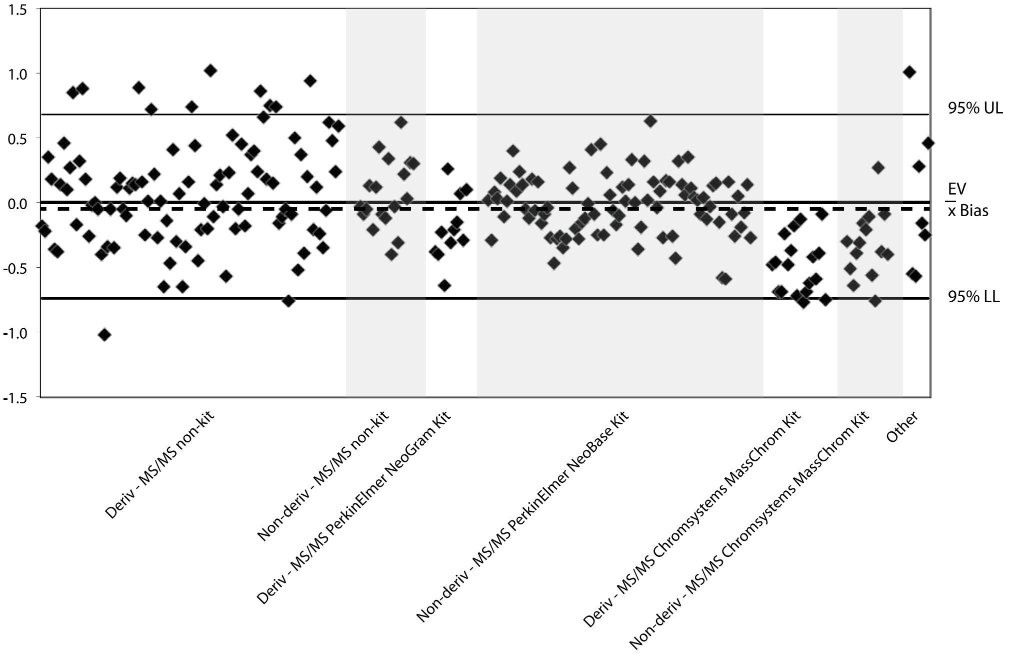


Quarter 3

Specimen 2

Enriched	2.25
CDC Assayed	2.75
Participant Mean	2.36
Participant Bias[2]	-0.03

Bias Plot of Myristoylcarnitine (C14) Values by Method
Quarter 3, Specimen 31562
Expected Value (EV)[1] = 2.39 µmol/L blood



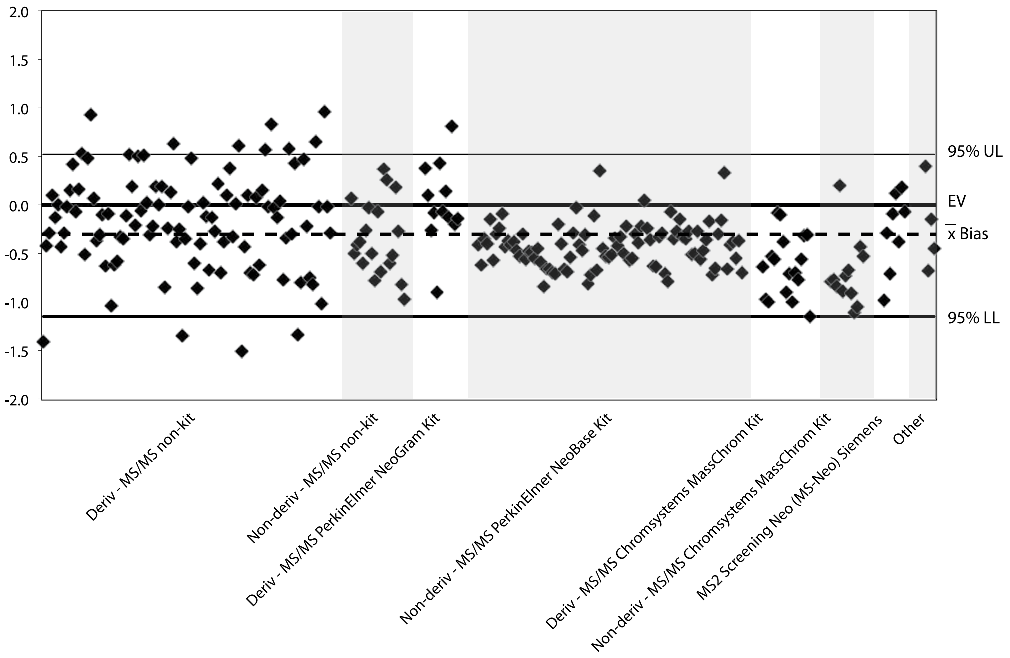
[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

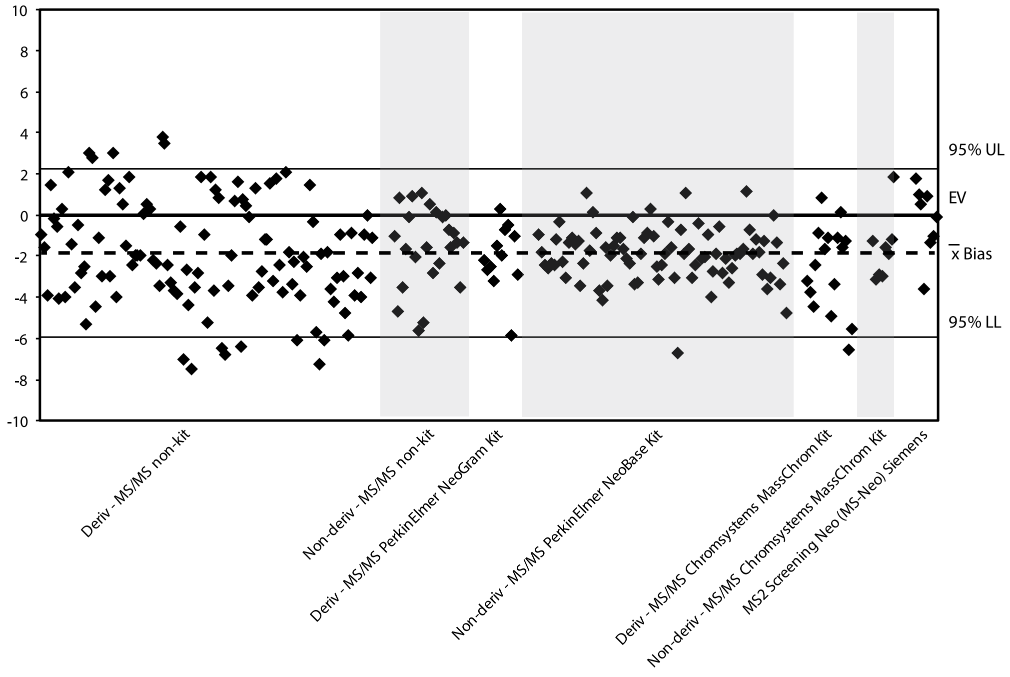
FIGURES 35-36. Reproducibility of Results by Method: Tetradecenoylcarnitine (C14:1) and Palmitoylcarnitine (C16)

Quarter 3	
Specimen 2	
Enriched	2.25
CDC Assayed	2.54
Participant Mean	1.99
Participant Bias[2]	-0.31



Bias Plot of Tetradecenoylcarnitine (C14:1) Values by Method
Quarter 3, Specimen 31562
Expected Value (EV)[1] = 2.30 µmol/L blood

Quarter 1	
Specimen 4	
Enriched	16.00
CDC Assayed	15.07
Participant Mean	14.84
Participant Bias[2]	-1.85



Bias Plot of Palmitoylcarnitine (C16) Values by Method
Quarter 1, Specimen 11564
Expected Value (EV)[1] = 16.69 µmol/L blood

[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

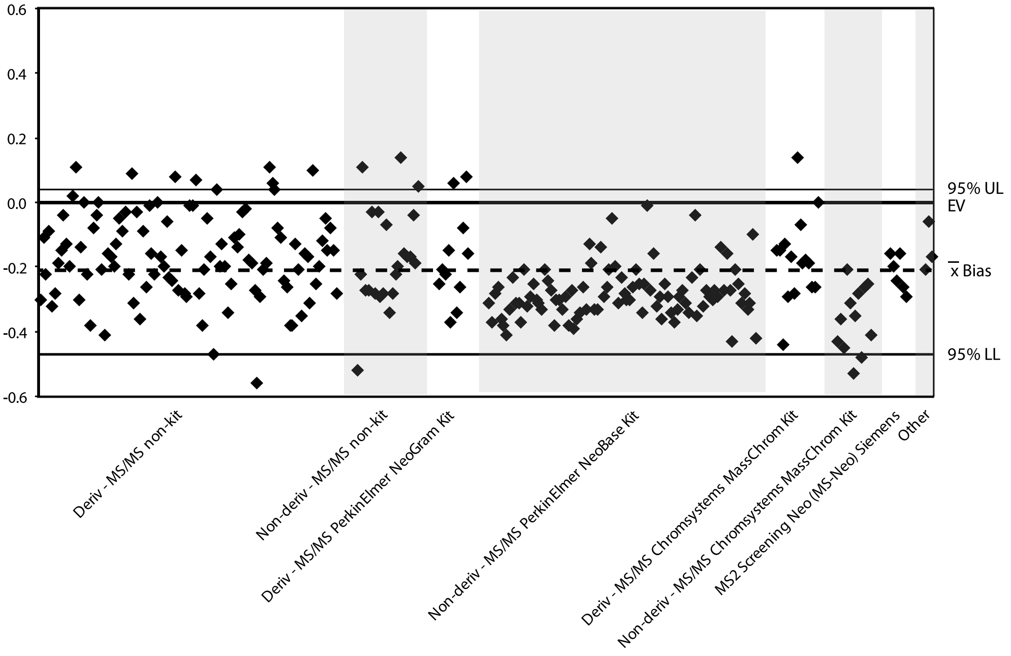
FIGURES 37-38. Reproducibility of Results by Method: Hydroxypalmitoylcarnitine (C16OH) and Stearoylcarnitine (C18)

Quarter 3

Specimen 3

Enriched	0.80
CDC Assayed	0.63
Participant Mean	0.60
Participant Bias[2]	-0.21

Bias Plot of Hydroxypalmitoylcarnitine (C16OH) Values by Method
Quarter 3, Specimen 31563
Expected Value (EV)[1] = 0.81 µmol/L blood

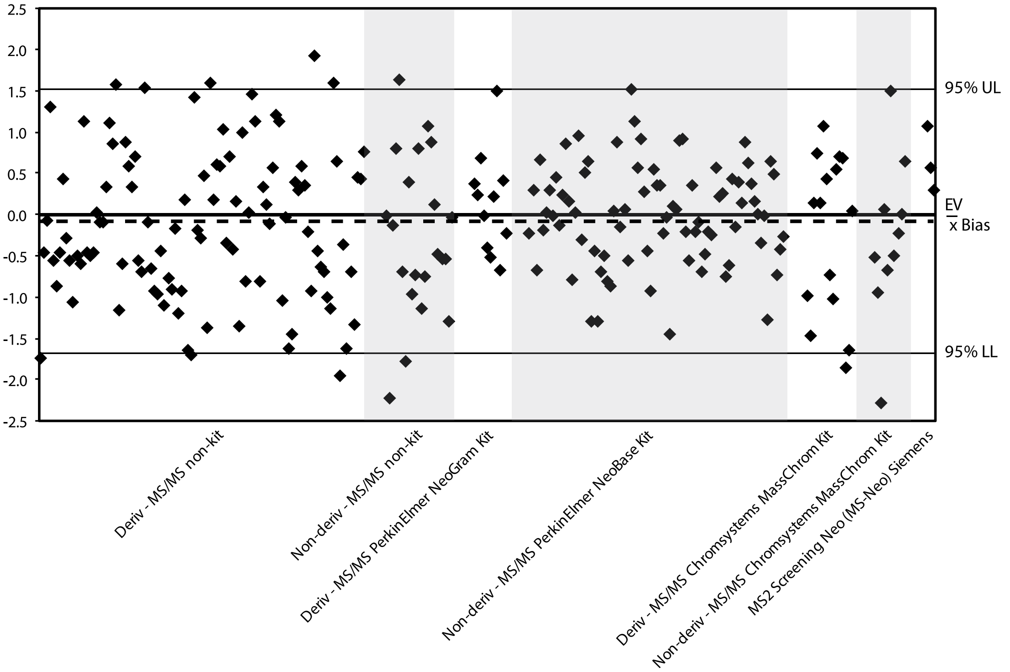


Quarter 1

Specimen 5

Enriched	6.00
CDC Assayed	6.21
Participant Mean	6.29
Participant Bias[2]	-0.08

Bias Plot of Stearoylcarnitine (C18) Values by Method
Quarter 1, Specimen 11565
Expected Value (EV)[1] = 6.37 µmol/L blood



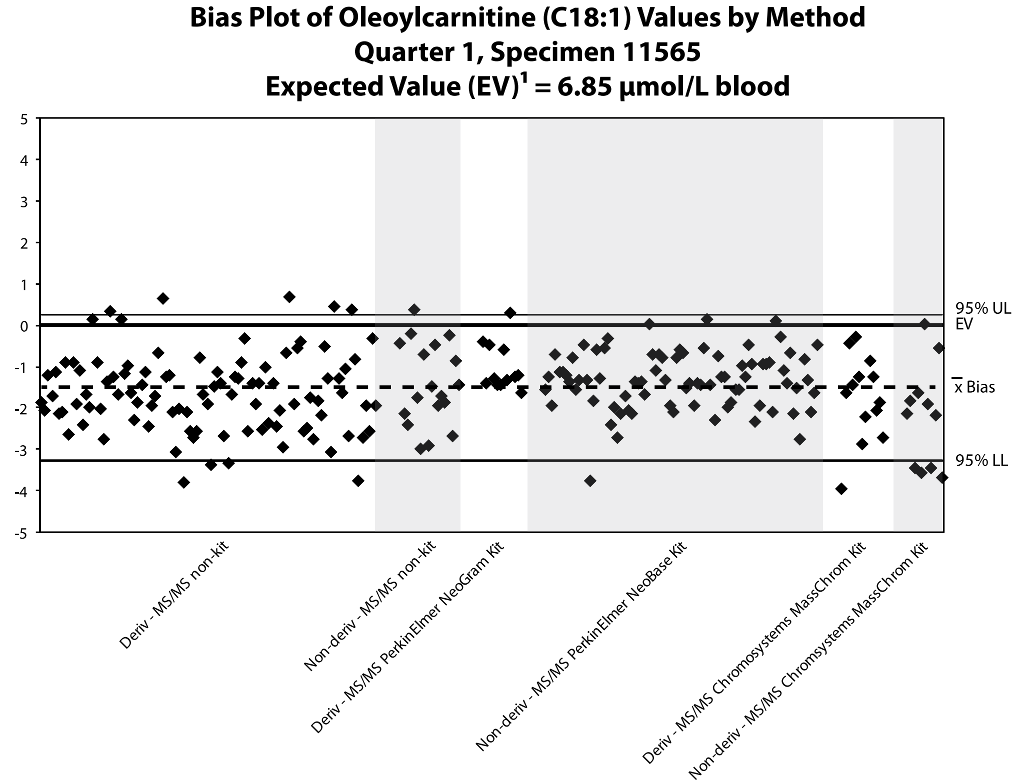
[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

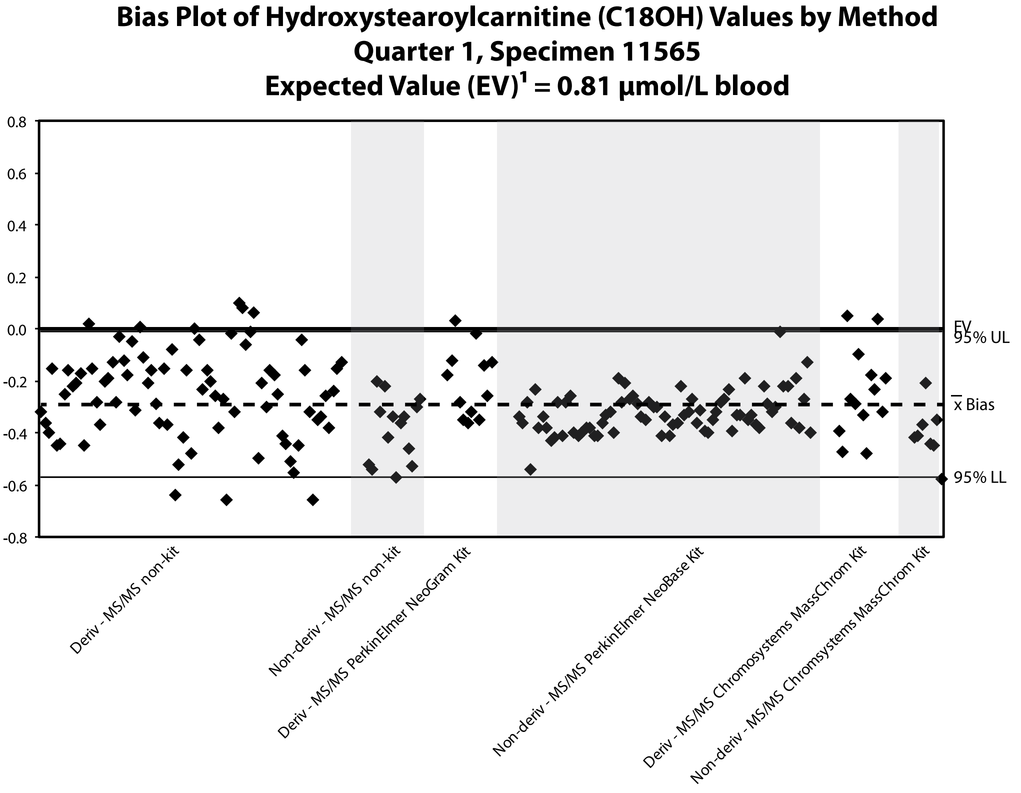
[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

FIGURES 39-40. Reproducibility of Results by Method: Oleoylcarnitine (C18:1) and Hydroxystearoylcarnitine (C18OH)

Quarter 1	
Specimen 5	
Enriched	6.00
CDC Assayed	5.32
Participant Mean	5.34
Participant Bias[2]	-1.51


Bias Plot of Oleoylcarnitine (C18:1) Values by Method
Quarter 1, Specimen 11565
Expected Value (EV)[1] = 6.85 µmol/L blood

Quarter 1	
Specimen 5	
Enriched	0.80
CDC Assayed	0.59
Participant Mean	0.52
Participant Bias[2]	-0.29


Bias Plot of Hydroxystearoylcarnitine (C18OH) Values by Method
Quarter 1, Specimen 11565
Expected Value (EV)[1] = 0.81 µmol/L blood

[1] EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.

[2] Participant bias (X) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias (X) excludes outlier values. The 95% confidence interval is shown.

[3] AV is the CDC assayed value. The solid line represents perfect agreement with the AV or zero bias.

QUALITY CONTROL

The QC program helps laboratories maintain high levels of technical proficiency and continuity, particularly during lot-to-lot changes in commercial assay systems or reagents. The QC materials, which supplement the participants' method- or kit-control materials, allow participants to monitor long-term assay stability. QC materials are distributed semiannually.

QC MATERIALS AND METHODS

NSQAP certifies QC analysis materials for homogeneity, accuracy, stability, and suitability for newborn screening assays. We distribute QC analysis materials (DBS cards), instructions for storage, analysis, and certification sheets in each shipment. Download QC certification sheets and data report forms from our website at: **http://www.cdc.gov/labstandards/nsqap_resources.html**

QC materials are produced by combining blood from multiple donors. The RBCs are washed several times, combined with purified serum to achieve a 50% hematocrit, and then lysed. Each lot within a set of QC shipments contains a different analyte concentration of the following: T_4, TSH, 17OHP, IRT, TGal, GALT, amino acids (alanine, Arg, Cit, Leu, Met, Phe, SUAC, Tyr, Val), and acylcarnitines (C0, C2, C3, C3DC, C4, C4OH, C5, C5DC, C5OH, C6, C8, C10, C12, C14, C16, C16OH, C18, C18OH), and XALD.

- Purified analyte standards are used for most QC material enrichments, with the exception of TSH, for which the Third International Reference Preparation (81/565) is used.
- T_4 QC materials are enriched with calculated amounts of T_4 after T_4 depletion of the base serum.
- TGal materials are enriched with galactose and galactose-1-phosphate, allowing measurement of both free galactose (galactose alone) and total galactose (free galactose plus galactose present as TGal).
- GALT QC materials are made using a 50/50 saline/serum solution combined with compatible washed RBCs and then heat-treating the pool.

To ensure laboratories receive representative sheets of QC materials from each lot, we use a system to randomize blood spot cards from across the production batch.

QC DATA HANDLING

For each semiannual QC event, data points from five independent runs of each QC analyte lot level are compiled and tabulated.

Tables 17a–17jj show the reported QC data. The tables show the analyte by series of QC lots, number of measurements (N), mean values, within-laboratory standard deviations (SD), and total SDs by kit or analytic method. In addition, we use a weighted linear-regression analysis to examine the comparability by method of reported versus enriched concentrations. We calculate linear regressions (Y-intercept and slope) by method for all analytic values within an analyte QC series. Values outside the 99% CI (outliers) are excluded from the calculations.

Tables 17a–17jj show data for method-related differences in analytic recoveries and method biases. For regression analyses, we calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs. We calculated the Y-intercept and slope in each table, using all analyte concentrations within a lot series (e.g., lots 1425, 1426, 1427, 1428). Because only three or four concentrations of QC materials are available for each analyte, a bias in any one pool can markedly influence the slope and intercept. The Y-intercept provides one measure of the endogenous concentration level for an analyte. For amino acids and acylcarnitines, participants measure the endogenous concentrations by analyzing the non-enriched QC lots; for most methods, the Y-intercepts and measured endogenous levels were similar. Ideally, the slope should be 1.0. Slope deviations might relate to analytic (dose-response) ranges for calibration curves or to poor recoveries for one or more specimens in a three- or four-specimen QC set. Because the endogenous concentration is the same for all QC lots within a series, it should not affect the slope of the regression line among methods. Generally, slope values substantially different from 1.0 indicate that a method has an analytic bias.

In certain circumstances, where no unit conversion factor exists to allow for direct comparison of enrichment values to observed concentrations, we provide basic peer group statistics to assist in laboratory self assessment.

REFERENCES

1. "Newborn Screening: Towards a Uniform Screening Panel and System." Genetic Medicine 2006;8(5) Suppl: S12–S252, as authored by the American College of Medical Genetics and commissioned by the Health Resources and Services Administration.

2. De Jesús VR, Mei JV, Cordovado SK, Cuthbert CD. The Newborn Screening Quality Assurance Program at the Centers for Disease Control and Prevention: Thirty-Five Year Experience Assuring Newborn Screening Laboratory Quality. International Journal of Newborn Screening 2015, 1; 13-26.

3. Clinical and Laboratory Standards Institute. Blood collection on filter paper for newborn screening programs: Approved Standard—Sixth Edition. CLSI Document NBS01-A6. Wayne, PA: Clinical and Laboratory Standards Institute; 2014.

Table 17a. 2015 Quality Control Data Summaries of Statistical Analyses
17 α-HYDROXYPROGESTERONE (ng 17OHP/mL serum)

Lot 1351 - Enriched 25.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	21.9	1.7	3.5	5.9	0.7
Neo-Genesis Accuwell	30	23.5	3.0	5.7	-2.0	1.0
Delfia	140	19.0	2.4	5.1	-2.2	0.9
Delfia Neonatal 17-OHP (A024)	89	17.9	2.3	3.3	-2.4	0.8
AutoDelfia	262	20.4	2.4	3.8	-0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	345	20.5	2.1	3.0	0.5	0.8
Bio-Rad Quantase	90	21.4	2.9	5.3	3.0	0.8
TecnoSuma UMELISA	20	23.8	2.6	2.7	-5.6	1.2
LC-MS/MS	39	21.8	1.9	3.5	1.0	0.8
PerkinElmer GSP Neonatal	320	21.4	1.9	2.3	1.6	0.8
In House	20	24.1	6.3	6.3	2.8	0.8

Lot 1352 - Enriched 50.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	43.0	3.0	7.0	5.9	0.7
Neo-Genesis Accuwell	29	47.0	6.1	6.4	-2.0	1.0
Delfia	140	40.6	3.7	8.7	-2.2	0.9
Delfia Neonatal 17-OHP (A024)	89	38.8	4.8	7.2	-2.4	0.8
AutoDelfia	263	44.7	3.9	8.4	-0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	345	43.0	3.8	6.1	0.5	0.8
Bio-Rad Quantase	90	47.7	4.9	15.6	3.0	0.8
TecnoSuma UMELISA	20	57.0	6.6	12.0	-5.6	1.2
LC-MS/MS	40	43.2	3.8	5.9	1.0	0.8
PerkinElmer GSP Neonatal	324	44.1	3.3	4.5	1.6	0.8
In House	20	42.1	4.9	9.3	2.8	0.8

Lot 1353 - Enriched 100.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	75.0	4.9	13.7	5.9	0.7
Neo-Genesis Accuwell	30	97.9	16.2	19.8	-2.0	1.0
Delfia	144	83.0	9.3	23.9	-2.2	0.9
Delfia Neonatal 17-OHP (A024)	90	79.3	11.3	18.1	-2.4	0.8
AutoDelfia	252	85.9	8.9	15.1	-0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	341	83.0	8.6	12.5	0.5	0.8
Bio-Rad Quantase	78	84.5	8.9	18.9	3.0	0.8
TecnoSuma UMELISA	20	115.6	7.7	18.3	-5.6	1.2
LC-MS/MS	40	84.7	4.8	9.9	1.0	0.8
PerkinElmer GSP Neonatal	319	83.8	7.2	8.9	1.6	0.8
In House	20	84.6	6.2	23.3	2.8	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
17 α-HYDROXYPROGESTERONE (ng 17OHP/mL serum)

Lot 1551 - Enriched 25.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	29.6	2.4	3.6	5.8	1.0
Neo-Genesis Accuwell	30	26.6	2.8	3.1	-2.6	1.1
Delfia	217	22.8	2.4	4.4	-0.6	0.9
Delfia Neonatal 17-OHP (A024)	80	22.7	2.9	5.0	-0.4	0.9
AutoDelfia	217	23.8	2.0	2.7	-0.7	1.0
AutoDelfia Neonatal 17-OHP (B024)	368	23.8	2.4	4.3	-1.3	1.0
Bio-Rad Quantase	77	22.5	3.2	7.7	1.5	0.9
TecnoSuma UMELISA	10	26.5	1.3	1.3	1.7	1.0
LC-MS/MS	60	24.8	2.8	6.5	2.9	0.9
PerkinElmer GSP Neonatal	351	25.0	2.0	2.8	0.4	1.0
In House	19	28.6	3.6	3.6	7.4	0.9

Lot 1552 - Enriched 50.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	54.4	4.0	8.7	5.8	1.0
Neo-Genesis Accuwell	30	48.4	4.7	6.5	-2.6	1.1
Delfia	214	44.4	4.6	7.3	-0.6	0.9
Delfia Neonatal 17-OHP (A024)	76	44.1	4.6	10.0	-0.4	0.9
AutoDelfia	213	46.6	4.1	4.8	-0.7	1.0
AutoDelfia Neonatal 17-OHP (B024)	361	46.8	4.0	7.9	-1.3	1.0
Bio-Rad Quantase	78	45.7	6.2	17.3	1.5	0.9
TecnoSuma UMELISA	10	49.7	3.7	3.7	1.7	1.0
LC-MS/MS	60	47.4	4.0	11.5	2.9	0.9
PerkinElmer GSP Neonatal	347	47.9	3.5	4.2	0.4	1.0
In House	18	54.5	3.8	4.9	7.4	0.9

Lot 1553 - Enriched 100.0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	30	102.0	8.4	16.6	5.8	1.0
Neo-Genesis Accuwell	30	106.9	11.1	13.6	-2.6	1.1
Delfia	217	91.2	10.0	15.9	-0.6	0.9
Delfia Neonatal 17-OHP (A024)	75	90.4	9.9	19.6	-0.4	0.9
AutoDelfia	222	95.5	9.2	12.9	-0.7	1.0
AutoDelfia Neonatal 17-OHP (B024)	367	97.0	9.7	18.2	-1.3	1.0
Bio-Rad Quantase	77	87.7	15.7	35.0	1.5	0.9
TecnoSuma UMELISA	10	99.3	9.3	9.3	1.7	1.0
LC-MS/MS	60	91.3	5.6	23.8	2.9	0.9
PerkinElmer GSP Neonatal	349	96.9	7.9	11.6	0.4	1.0
In House	20	96.8	7.2	28.9	7.4	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17b. 2015 Quality Control Data Summaries of Statistical Analyses
THYROID-STIMULATING HORMONE (µIU TSH/mL serum)

Lot 1411 - Enriched 25.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	35.4	4.2	5.1	-1.0	1.4
Neo-Genesis Accuwell	40	25.2	4.3	4.9	-0.4	1.1
MP Biomedicals ELISA	20	15.9	2.2	4.1	-6.6	0.9
Delfia	427	26.3	2.8	5.3	-0.7	1.1
AutoDelfia	862	28.0	2.5	4.5	-0.2	1.1
Ani Labsystems	89	25.6	2.2	3.7	-5.1	1.2
Bio-Rad Quantase	70	32.8	4.0	11.8	1.3	1.3
TecnoSuma UMELISA	29	32.9	4.0	4.5	-2.5	1.4
Bioclone ELISA	10	25.7	0.9	0.9	-0.3	1.1
DiaSorin	88	25.0	2.1	3.0	1.5	1.0
Interscientific NeoMAP Multiplex	50	24.6	1.7	2.3	-3.0	1.1
PerkinElmer GSP Neonatal	431	26.7	2.2	2.9	0.0	1.1
In House	40	25.7	1.8	2.7	1.1	1.0

Lot 1412 - Enriched 40.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	55.7	5.0	7.0	-1.0	1.4
Neo-Genesis Accuwell	40	42.7	4.8	7.3	-0.4	1.1
MP Biomedicals ELISA	20	26.6	3.2	7.6	-6.6	0.9
Delfia	427	44.0	4.8	8.1	-0.7	1.1
AutoDelfia	841	45.9	3.5	5.0	-0.2	1.1
Ani Labsystems	88	43.4	4.1	6.2	-5.1	1.2
Bio-Rad Quantase	70	54.2	5.5	21.8	1.3	1.3
TecnoSuma UMELISA	28	53.4	4.4	5.1	-2.5	1.4
Bioclone ELISA	10	43.6	2.2	2.2	-0.3	1.1
DiaSorin	90	40.0	3.6	6.6	1.5	1.0
Interscientific NeoMAP Multiplex	50	41.7	2.5	3.2	-3.0	1.1
PerkinElmer GSP Neonatal	433	42.7	3.2	4.5	0.0	1.1
In House	40	41.3	3.1	5.2	1.1	1.0

Lot 1413 - Enriched 80.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	114.0	11.5	11.9	-1.0	1.4
Neo-Genesis Accuwell	39	83.5	9.7	10.9	-0.4	1.1
MP Biomedicals ELISA	20	62.7	8.0	19.2	-6.6	0.9
Delfia	412	87.1	7.8	15.4	-0.7	1.1
AutoDelfia	838	91.0	7.1	10.0	-0.2	1.1
Ani Labsystems	88	92.6	6.3	12.6	-5.1	1.2
Bio-Rad Quantase	70	104.5	11.5	47.6	1.3	1.3
TecnoSuma UMELISA	29	110.0	7.0	7.0	-2.5	1.4
Bioclone ELISA	10	85.0	2.9	2.9	-0.3	1.1
DiaSorin	89	77.6	5.3	11.2	1.5	1.0
Interscientific NeoMAP Multiplex	48	85.9	5.1	6.4	-3.0	1.1
PerkinElmer GSP Neonatal	435	85.5	6.6	9.2	0.0	1.1
In House	40	80.7	5.2	15.4	1.1	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
THYROID-STIMULATING HORMONE (µIU TSH/mL serum)

Lot 1511 - Enriched 25.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	33.4	3.1	4.5	-0.5	1.4
Neo-Genesis Accuwell	39	26.9	2.8	4.1	-1.8	1.2
MP Biomedicals ELISA	20	20.5	1.8	4.0	-2.9	1.0
Delfia	415	27.8	2.5	3.6	-0.5	1.2
AutoDelfia	880	27.8	2.2	5.8	-1.2	1.2
Ani Labsystems	80	26.9	2.1	2.7	-1.9	1.2
Bio-Rad Quantase	70	23.7	2.1	9.0	0.8	0.9
TecnoSuma UMELISA	20	36.9	5.3	14.2	-6.0	1.8
Bioclone ELISA	20	17.9	1.4	11.2	1.2	0.7
DiaSorin	79	29.5	3.0	3.9	-1.8	1.3
Interscientific NeoMAP Multiplex	49	27.0	1.8	1.9	1.4	1.1
PerkinElmer GSP Neonatal	462	26.7	1.9	2.4	-2.7	1.2
In House	49	29.0	2.4	4.1	0.0	1.2

Lot 1512 - Enriched 40.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	59.3	4.5	6.6	-0.5	1.4
Neo-Genesis Accuwell	40	46.2	5.0	5.0	-1.8	1.2
MP Biomedicals ELISA	20	38.2	3.8	3.8	-2.9	1.0
Delfia	420	48.0	4.3	5.8	-0.5	1.2
AutoDelfia	865	48.1	3.5	9.8	-1.2	1.2
Ani Labsystems	76	48.7	3.5	3.6	-1.9	1.2
Bio-Rad Quantase	70	38.0	3.6	15.1	0.8	0.9
TecnoSuma UMELISA	20	67.3	10.1	23.5	-6.0	1.8
Bioclone ELISA	20	29.8	2.9	19.1	1.2	0.7
DiaSorin	76	54.0	5.4	6.6	-1.8	1.3
Interscientific NeoMAP Multiplex	49	48.9	3.3	3.6	1.4	1.1
PerkinElmer GSP Neonatal	464	47.2	3.1	4.9	-2.7	1.2
In House	49	46.5	3.0	4.3	0.0	1.2

Lot 1513 - Enriched 80.0 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	20	113.2	8.5	10.5	-0.5	1.4
Neo-Genesis Accuwell	40	92.0	7.3	7.4	-1.8	1.2
MP Biomedicals ELISA	20	75.5	13.2	15.7	-2.9	1.0
Delfia	418	93.2	8.9	11.9	-0.5	1.2
AutoDelfia	877	94.3	6.9	19.9	-1.2	1.2
Ani Labsystems	78	94.4	5.9	9.2	-1.9	1.2
Bio-Rad Quantase	70	74.7	9.3	32.9	0.8	0.9
TecnoSuma UMELISA	20	135.8	23.2	64.7	-6.0	1.8
Bioclone ELISA	20	56.5	5.3	37.7	1.2	0.7
DiaSorin	74	103.5	9.1	10.1	-1.8	1.3
Interscientific NeoMAP Multiplex	49	89.5	7.2	8.0	1.4	1.1
PerkinElmer GSP Neonatal	465	94.1	6.5	8.7	-2.7	1.2
In House	50	92.7	7.1	13.5	0.0	1.2

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis

Table 17c. 2015 Quality Control Data Summaries of Statistical Analyses
THYROXINE (µg T_4/dL serum)

Lot 1401 - Enriched 2.0 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Neo-Genesis Accuwell	37	1.3	0.2	0.2	-0.3	0.9
Delfia	175	1.8	0.3	0.4	-0.2	1.0
AutoDelfia	411	1.9	0.3	0.3	-0.1	1.0
Interscientific NeoMAP Multiplex	99	1.8	0.3	0.3	-0.2	1.0
PerkinElmer GSP Neonatal	374	1.8	0.2	0.2	-0.3	1.0

Lot 1402 - Enriched 7.0 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Neo-Genesis Accuwell	40	6.4	1.0	2.1	-0.3	0.9
Delfia	176	6.5	0.7	0.9	-0.2	1.0
AutoDelfia	420	6.6	0.6	0.7	-0.1	1.0
Interscientific NeoMAP Multiplex	99	6.3	0.5	0.5	-0.2	1.0
PerkinElmer GSP Neonatal	380	6.8	0.7	0.7	-0.3	1.0

Lot 1403 - Enriched 11.0 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Neo-Genesis Accuwell	40	9.2	0.9	1.8	-0.3	0.9
Delfia	174	10.6	0.9	1.5	-0.2	1.0
AutoDelfia	420	10.6	1.0	1.1	-0.1	1.0
Interscientific NeoMAP Multiplex	100	10.5	0.9	0.9	-0.2	1.0
PerkinElmer GSP Neonatal	368	11.2	1.2	1.3	-0.3	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

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Table 17d. 2015 Quality Control Data Summaries of Statistical Analyses
TOTAL GALACTOSE (mg TGal/dL blood)

Lot 1425 - Enriched 5.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	5.6	0.5	0.6	1.4	0.9
Fluorometric Manual	99	4.6	0.5	1.3	0.8	0.9
Colorimetric	64	6.3	0.9	1.5	1.3	1.1
PerkinElmer Neonatal Kit	255	5.2	0.6	1.0	1.4	0.8
Neo-Genesis Accuwell	29	6.6	0.5	1.4	0.6	1.2
Bio-Rad Quantase	129	6.8	1.2	1.7	-0.9	1.4
Interscientific Enzyme	30	5.3	0.4	0.5	1.2	0.8
Astoria-Pacific 50 Hour Reagent Kit	97	6.7	0.5	0.7	1.6	1.0
TecnoSuma UMTEST	30	8.2	1.7	2.1	2.5	1.1

Lot 1426 - Enriched 10.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	11.0	0.6	0.6	1.4	0.9
Fluorometric Manual	96	9.4	0.7	2.0	0.8	0.9
Colorimetric	68	12.7	1.3	2.4	1.3	1.1
PerkinElmer Neonatal Kit	257	9.5	0.9	1.4	1.4	0.8
Neo-Genesis Accuwell	29	13.1	1.0	2.1	0.6	1.2
Bio-Rad Quantase	128	12.7	2.0	2.8	-0.9	1.4
Interscientific Enzyme	30	9.1	1.0	1.0	1.2	0.8
Astoria-Pacific 50 Hour Reagent Kit	100	11.9	0.8	1.2	1.6	1.0
TecnoSuma UMTEST	30	12.6	1.4	3.0	2.5	1.1

Lot 1427 - Enriched 15.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	15.5	1.0	1.2	1.4	0.9
Fluorometric Manual	90	15.4	1.2	1.2	0.8	0.9
Colorimetric	70	18.2	2.0	3.6	1.3	1.1
PerkinElmer Neonatal Kit	257	13.6	1.3	2.1	1.4	0.8
Neo-Genesis Accuwell	30	18.3	1.3	2.4	0.6	1.2
Bio-Rad Quantase	130	19.3	2.3	4.4	-0.9	1.4
Interscientific Enzyme	30	13.8	1.1	1.3	1.2	0.8
Astoria-Pacific 50 Hour Reagent Kit	99	16.9	1.1	2.1	1.6	1.0
TecnoSuma UMTEST	30	20.2	1.9	3.1	2.5	1.1

Lot 1428 - Enriched 30.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	29.0	2.1	10.1	1.4	0.9
Fluorometric Manual	100	26.9	1.8	6.4	0.8	0.9
Colorimetric	70	34.2	3.6	8.6	1.3	1.1
PerkinElmer Neonatal Kit	266	25.2	2.3	3.6	1.4	0.8
Neo-Genesis Accuwell	28	37.1	2.3	2.9	0.6	1.2
Bio-Rad Quantase	140	41.2	5.3	10.2	-0.9	1.4
Interscientific Enzyme	30	25.5	2.2	2.5	1.2	0.8
Astoria-Pacific 50 Hour Reagent Kit	100	32.2	1.9	3.6	1.6	1.0
TecnoSuma UMTEST	30	35.5	2.8	6.1	2.5	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
TOTAL GALACTOSE (mg TGal/dL blood)

Lot 1521 - Enriched 5.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	5.4	0.4	0.5	1.6	0.8
Fluorometric Manual	99	5.1	0.7	1.2	0.4	1.0
Colorimetric	57	5.9	0.8	1.2	0.2	1.1
PerkinElmer Neonatal Kit	259	5.3	0.7	1.1	1.2	0.8
Neo-Genesis Accuwell	28	6.4	0.6	1.1	0.7	1.2
Bio-Rad Quantase	153	6.5	0.7	1.4	0.5	1.1
Interscientific Enzyme	39	6.1	0.6	0.7	1.7	0.8
PerkinElmer GSP Neonatal	105	5.5	0.4	0.7	1.0	0.9
Astoria-Pacific 50 Hour Reagent Kit	87	6.6	0.5	0.9	1.7	0.9
TecnoSuma UMTEST	18	7.7	0.4	0.4	1.7	1.1

Lot 1522 - Enriched 10.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	9.7	0.6	0.8	1.6	0.8
Fluorometric Manual	90	10.0	0.7	1.5	0.4	1.0
Colorimetric	60	11.3	1.4	2.9	0.2	1.1
PerkinElmer Neonatal Kit	263	8.9	1.0	1.6	1.2	0.8
Neo-Genesis Accuwell	30	12.9	1.1	3.2	0.7	1.2
Bio-Rad Quantase	149	11.0	1.3	2.2	0.5	1.1
Interscientific Enzyme	39	9.6	0.8	1.3	1.7	0.8
PerkinElmer GSP Neonatal	110	9.9	1.0	1.3	1.0	0.9
Astoria-Pacific 50 Hour Reagent Kit	90	10.9	0.8	1.3	1.7	0.9
TecnoSuma UMTEST	20	12.5	1.3	1.7	1.7	1.1

Lot 1523 - Enriched 15.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	13.9	0.9	1.2	1.6	0.8
Fluorometric Manual	90	15.0	1.2	1.8	0.4	1.0
Colorimetric	60	16.7	2.0	4.4	0.2	1.1
PerkinElmer Neonatal Kit	264	12.9	1.1	2.1	1.2	0.8
Neo-Genesis Accuwell	28	18.0	1.1	2.7	0.7	1.2
Bio-Rad Quantase	147	15.9	1.6	3.0	0.5	1.1
Interscientific Enzyme	40	13.8	0.8	2.4	1.7	0.8
PerkinElmer GSP Neonatal	108	13.7	1.2	1.5	1.0	0.9
Astoria-Pacific 50 Hour Reagent Kit	89	15.1	0.9	1.3	1.7	0.9
TecnoSuma UMTEST	20	18.8	1.9	4.1	1.7	1.1

Lot 1524 - Enriched 30.0 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Siemens Healthcare Diagnostics	40	25.5	1.3	5.9	1.6	0.8
Fluorometric Manual	94	29.0	2.5	3.6	0.4	1.0
Colorimetric	60	33.5	3.3	10.0	0.2	1.1
PerkinElmer Neonatal Kit	261	24.7	2.0	3.5	1.2	0.8
Neo-Genesis Accuwell	30	35.9	2.9	6.2	0.7	1.2
Bio-Rad Quantase	151	33.0	3.1	7.2	0.5	1.1
Interscientific Enzyme	39	26.4	2.3	4.4	1.7	0.8
PerkinElmer GSP Neonatal	107	27.5	2.7	3.2	1.0	0.9
Astoria-Pacific 50 Hour Reagent Kit	88	29.5	1.5	3.1	1.7	0.9
TecnoSuma UMTEST	20	35.6	3.6	7.9	1.7	1.1

Table 17e. 2015 Quality Control Data Summaries of Statistical Analyses
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (U GALT/g Hb)

Lot 1431 - Assayed 1.3 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	295	1.3	0.3	0.5	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	40	0.6	0.1	0.2	-0.6	0.7

Lot 1432 - Assayed 4.1 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	293	3.0	0.4	0.5	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	39	2.1	0.2	0.3	-0.6	0.7

Lot 1433 - Assayed 9.5 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	295	7.2	0.9	1.2	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	40	6.6	0.7	1.0	-0.6	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Methods Reported in Units Other Than U/g Hb (>3 Participants)*

Lot Number	Method	N	Mean	Avg Within Lab SD	All Lab SD	Min Concentration	Max Concentration
1431	Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	70	14.7	1.9	3.9	8.1	23.2
	Perkin Elmer GSP Neonatal (U/dL blood)	70	0.5	0.2	1.0	0.0	2.5
1432	Astoria-Pacific 50 Hour Reage nt Kit (µmol/L blood)	70	66.3	6.5	10.0	45.0	94.6
	Perkin Elmer GSP Neonatal (U/dL blood)	70	1.5	0.3	0.6	0.5	2.5
1433	Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	70	193.0	28.9	44.4	90.0	303.4
	Perkin Elmer GSP Neonatal (U/dL blood)	70	8.2	0.7	1.3	5.3	10.2

*Outlier data was removed based on the 99% confidence interval

Table 17e. 2015 Quality Control Data Summaries of Statistical Analyses
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (U GALT/g Hb)

Lot 1531 - Assayed 1.4 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	261	1.3	0.3	0.4	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	70	0.7	0.1	0.2	-0.4	0.7

Lot 1532 - Assayed 3.4 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	267	2.6	0.3	0.5	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	70	2.1	0.2	0.5	-0.4	0.7

Lot 1533 - Assayed 7.7 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
PerkinElmer Neonatal Kit	277	5.9	0.6	0.9	0.2	0.7
Astoria-Pacific Neonatal Microplate Reagent Kit	70	5.3	0.6	1.0	-0.4	0.7

Methods Reported in Units Other Than U/g Hb (>3 Participants)*

Lot Number	Method	N	Mean	Avg Within Lab SD	All Lab SD	Min Concentration	Max Concentration
1531	Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	60	16.9	2.6	3.1	10.0	24.7
	Perkin Elmer GSP Neonatal (U/dL blood)	91	0.7	0.1	1.0	0.0	2.5
1532	Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	60	63.8	8.5	13.4	36.0	87.3
	Perkin Elmer GSP Neonatal (U/dL blood)	100	1.7	0.3	0.6	0.2	2.8
1533	Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	60	171.3	25.2	53.6	52.0	266.9
	Perkin Elmer GSP Neonatal (U/dL blood)	100	7.5	0.6	1.1	5.2	4.7

*Outlier data was removed based on the 99% confidence interval

Several laboratories reported their GALT results in either µmol/L blood or U/dL blood according to their analytic method.NSQAP's certified units for GALT are U/g hemoglobin. Due to the lack of a conversion factor between U/g hemoglobin and µmol/L blood or U/dL blood, the linear regression parameters cannot be calculated for these units of measure. Basic peer-group statistics are provided to assist in self-assessment under those circumstances.

Table 17f. 2015 Quality Control Data Summaries of Statistical Analyses
IMMUNOREACTIVE TRYPSINOGEN (ng IRT/mL blood)

Lot 1491 - Assayed 19.7 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
MP Biomedicals ELISA	89	24.3	3.0	8.1	29.7	1.1
Delfia	400	19.3	2.4	2.7	2.1	0.9
AutoDelfia	1410	19.5	1.7	2.0	2.0	1.0
Bio-Rad Quantase	40	50.4	5.0	21.7	58.2	0.9
PerkinElmer GSP Neonatal	647	19.6	1.4	1.5	0.4	1.0

Lot 1492 - Assayed 70.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
MP Biomedicals ELISA	83	114.7	14.3	32.7	29.7	1.1
Delfia	412	67.8	6.5	7.8	2.1	0.9
AutoDelfia	1399	70.2	5.6	6.7	2.0	1.0
Bio-Rad Quantase	40	138.0	5.2	49.2	58.2	0.9
PerkinElmer GSP Neonatal	664	71.6	4.3	4.5	0.4	1.0

Lot 1493 - Assayed 145.6 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
MP Biomedicals ELISA	88	237.9	41.2	83.3	29.7	1.1
Delfia	406	140.2	13.9	15.8	2.1	0.9
AutoDelfia	1367	143.5	9.5	10.6	2.0	1.0
Bio-Rad Quantase	40	217.7	7.9	66.7	58.2	0.9
PerkinElmer GSP Neonatal	663	148.8	8.8	9.8	0.4	1.0

Lot 1494 - Assayed 259.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
MP Biomedicals ELISA	65	281.5	40.7	98.1	29.7	1.1
Delfia	408	242.8	22.0	27.1	2.1	0.9
AutoDelfia	1390	249.7	18.1	20.4	2.0	1.0
Bio-Rad Quantase	40	275.3	27.9	85.6	58.2	0.9
PerkinElmer GSP Neonatal	651	261.8	16.9	17.5	0.4	1.0

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Table 17g. 2015 Quality Control Data Summaries of Statistical Analyses
ALANINE (µmol Ala/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	663	360.6	36.2	78.6	359.1	0.7
Non-derivatized - MS/MS non-kit	94	352.5	27.0	82.9	350.9	0.7
Derivatized - MS/MS PE NeoGram Kit	88	354.9	35.7	78.1	354.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	458	424.9	32.0	66.3	426.0	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	95	345.7	24.9	34.4	346.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	313.0	26.0	52.0	313.8	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	392.7	14.2	14.2	387.3	0.9

Lot 1426 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	658	497.6	45.7	95.5	359.1	0.7
Non-derivatized - MS/MS non-kit	94	483.8	43.1	113.9	350.9	0.7
Derivatized - MS/MS PE NeoGram Kit	90	507.3	56.3	117.7	354.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	461	605.8	46.2	94.8	426.0	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	97	487.5	37.5	56.5	346.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	440.0	42.1	80.3	313.8	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	542.0	19.4	19.4	387.3	0.9

Lot 1427 - Enriched 400.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	654	626.4	57.2	123.7	359.1	0.7
Non-derivatized - MS/MS non-kit	94	615.0	39.3	134.2	350.9	0.7
Derivatized - MS/MS PE NeoGram Kit	90	641.3	59.5	152.4	354.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	466	766.1	58.3	120.4	426.0	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	95	615.6	41.7	65.3	346.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	561.4	36.0	105.1	313.8	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	753.6	25.1	25.1	387.3	0.9

Lot 1428 - Enriched 600.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	651	774.9	64.7	149.3	359.1	0.7
Non-derivatized - MS/MS non-kit	95	754.5	68.2	200.2	350.9	0.7
Derivatized - MS/MS PE NeoGram Kit	90	806.0	75.3	183.0	354.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	465	951.8	67.9	146.8	426.0	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	96	759.1	50.9	96.9	346.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	687.2	39.0	117.8	313.8	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	899.0	37.2	37.2	387.3	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
ALANINE (µmol Ala/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	690	349.9	32.1	88.7	349.9	0.7
Non-derivatized - MS/MS non-kit	148	348.9	36.4	77.0	353.1	0.7
Derivatized - MS/MS PE NeoGram Kit	78	386.2	44.9	63.7	389.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	538	421.8	31.4	66.1	422.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	120	341.5	27.2	92.5	342.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	324.9	22.1	89.7	326.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	383.7	16.4	16.4	363.0	0.8

Lot 1522 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	679	492.7	43.5	112.4	349.9	0.7
Non-derivatized - MS/MS non-kit	149	499.6	57.0	124.8	353.1	0.7
Derivatized - MS/MS PE NeoGram Kit	78	542.4	56.3	94.8	389.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	539	602.8	42.6	91.9	422.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	477.3	34.2	124.7	342.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	470.1	32.1	132.3	326.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	500.0	24.1	24.1	363.0	0.8

Lot 1523 - Enriched 400.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	677	639.8	55.4	140.8	349.9	0.7
Non-derivatized - MS/MS non-kit	147	652.4	65.9	145.3	353.1	0.7
Derivatized - MS/MS PE NeoGram Kit	79	692.8	73.3	106.1	389.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	547	786.2	59.8	120.6	422.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	601.4	52.8	154.1	342.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	599.9	37.5	166.7	326.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	659.9	37.2	37.2	363.0	0.8

Lot 1428 - Enriched 600.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	685	780.2	74.9	178.2	349.9	0.7
Non-derivatized - MS/MS non-kit	150	781.2	72.4	192.8	353.1	0.7
Derivatized - MS/MS PE NeoGram Kit	80	837.4	93.1	166.2	389.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	548	960.3	68.9	136.8	422.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	740.5	52.5	176.0	342.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	744.0	44.3	199.7	326.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	10	858.1	46.5	46.5	363.0	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17h. 2015 Quality Control Data Summaries of Statistical Analyses
ARGININE (µmol Arg/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	687	8.8	1.4	3.8	10.1	0.6
Non-derivatized - MS/MS non-kit	108	7.7	1.9	3.9	8.0	0.7
Derivatized - MS/MS PE NeoGram Kit	116	9.9	1.0	2.1	9.2	0.8
Non-derivatized - MS/MS PE NeoBase Kit	550	8.9	0.9	1.7	10.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	10.8	1.4	2.8	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	10.0	1.2	2.6	16.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	29	5.5	0.9	1.8	4.6	0.5

Lot 1426 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	711	74.1	8.2	28.2	10.1	0.6
Non-derivatized - MS/MS non-kit	119	77.1	6.9	18.7	8.0	0.7
Derivatized - MS/MS PE NeoGram Kit	116	90.9	6.7	16.8	9.2	0.8
Non-derivatized - MS/MS PE NeoBase Kit	560	96.2	6.2	10.6	10.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	100.0	13.2	23.1	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	90.5	7.7	18.0	16.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	48.7	3.0	3.7	4.6	0.5

Lot 1427 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	701	135.5	14.2	50.7	10.1	0.6
Non-derivatized - MS/MS non-kit	118	145.6	15.8	33.7	8.0	0.7
Derivatized - MS/MS PE NeoGram Kit	116	171.5	11.8	31.8	9.2	0.8
Non-derivatized - MS/MS PE NeoBase Kit	547	175.2	10.1	18.2	10.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	96	182.2	12.6	34.9	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	163.3	12.9	32.2	16.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	97.8	5.3	14.8	4.6	0.5

Lot 1428 - Enriched 600.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	690	196.1	18.5	74.3	10.1	0.6
Non-derivatized - MS/MS non-kit	119	214.3	21.7	48.5	8.0	0.7
Derivatized - MS/MS PE NeoGram Kit	119	256.2	18.3	47.5	9.2	0.8
Non-derivatized - MS/MS PE NeoBase Kit	553	257.3	15.2	28.6	10.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	96	254.2	17.0	56.0	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	91	215.0	14.1	39.8	16.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	142.5	11.1	24.2	4.6	0.5

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
ARGININE (µmol Arg/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	734	7.3	1.5	3.5	7.1	0.7
Non-derivatized - MS/MS non-kit	150	5.4	1.2	3.0	5.1	0.7
Derivatized - MS/MS PE NeoGram Kit	107	6.5	1.1	1.4	5.1	0.7
Non-derivatized - MS/MS PE NeoBase Kit	629	6.5	1.2	2.2	5.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	119	8.6	1.3	2.3	10.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	101	5.2	1.1	1.6	7.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	38	4.8	1.3	3.7	3.2	0.5

Lot 1522 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	777	71.3	9.4	27.1	7.1	0.7
Non-derivatized - MS/MS non-kit	158	77.1	8.4	18.7	5.1	0.7
Derivatized - MS/MS PE NeoGram Kit	109	77.2	8.2	14.9	5.1	0.7
Non-derivatized - MS/MS PE NeoBase Kit	628	86.9	5.9	12.9	5.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	120	97.9	8.2	18.9	10.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	104	82.8	7.3	12.1	7.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	47.2	4.7	6.4	3.2	0.5

Lot 1523 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	780	139.2	17.6	54.2	7.1	0.7
Non-derivatized - MS/MS non-kit	157	152.9	16.2	39.0	5.1	0.7
Derivatized - MS/MS PE NeoGram Kit	110	154.3	17.4	33.2	5.1	0.7
Non-derivatized - MS/MS PE NeoBase Kit	632	168.6	11.6	25.8	5.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	117	180.5	15.0	29.3	10.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	154.0	11.3	25.8	7.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	92.8	7.3	9.6	3.2	0.5

Lot 1524 - Enriched 300.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	773	202.2	25.8	80.1	7.1	0.7
Non-derivatized - MS/MS non-kit	156	223.7	24.3	56.7	5.1	0.7
Derivatized - MS/MS PE NeoGram Kit	107	228.7	24.4	42.3	5.1	0.7
Non-derivatized - MS/MS PE NeoBase Kit	626	251.6	17.9	36.4	5.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	120	263.8	24.2	48.6	10.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	222.7	15.7	40.5	7.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	141.5	11.2	19.4	3.2	0.5

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17i. 2015 Quality Control Data Summaries of Statistical Analyses
CITRULLINE (µmol Cit/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	738	26.1	2.6	4.5	27.0	0.8
Non-derivatized - MS/MS non-kit	196	27.7	3.1	6.4	29.1	0.8
Derivatized - MS/MS PE NeoGram Kit	126	29.3	2.0	3.6	29.4	0.9
Non-derivatized - MS/MS PE NeoBase Kit	635	29.1	2.6	3.5	30.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	99	28.7	2.7	4.5	29.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	96	28.7	4.4	4.9	29.4	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	27.1	2.2	2.3	27.5	0.9

Lot 1426 - Enriched 25.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	737	46.9	4.5	8.2	27.0	0.8
Non-derivatized - MS/MS non-kit	198	50.6	4.4	9.0	29.1	0.8
Derivatized - MS/MS PE NeoGram Kit	129	53.4	3.8	6.8	29.4	0.9
Non-derivatized - MS/MS PE NeoBase Kit	630	54.3	4.0	5.8	30.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	97	51.9	4.1	6.5	29.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	96	52.4	8.4	9.1	29.4	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	47.7	4.5	4.9	27.5	0.9

Lot 1427 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	746	106.4	9.4	18.6	27.0	0.8
Non-derivatized - MS/MS non-kit	197	114.6	10.0	18.0	29.1	0.8
Derivatized - MS/MS PE NeoGram Kit	128	118.4	6.4	14.6	29.4	0.9
Non-derivatized - MS/MS PE NeoBase Kit	635	122.3	8.1	12.9	30.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	95	115.6	7.7	11.6	29.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	118.1	11.8	17.7	29.4	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	115.1	8.6	12.3	27.5	0.9

Lot 1428 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	745	222.4	17.2	36.6	27.0	0.8
Non-derivatized - MS/MS non-kit	198	238.2	18.6	33.8	29.1	0.8
Derivatized - MS/MS PE NeoGram Kit	128	257.1	16.4	32.8	29.4	0.9
Non-derivatized - MS/MS PE NeoBase Kit	631	258.7	16.7	25.8	30.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	97	243.7	14.1	27.2	29.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	251.2	27.7	35.4	29.4	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	239.8	15.9	22.7	27.5	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
CITRULLINE (µmol Cit/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	799	26.3	2.7	5.7	27.2	0.8
Non-derivatized - MS/MS non-kit	240	29.1	3.6	5.1	30.8	0.9
Derivatized - MS/MS PE NeoGram Kit	109	30.1	2.8	3.9	30.2	0.9
Non-derivatized - MS/MS PE NeoBase Kit	685	30.1	2.9	4.2	31.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	30.8	2.8	3.8	32.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	116	30.9	3.1	4.4	32.0	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	27.4	2.8	3.2	28.0	0.8

Lot 1522 - Enriched 25.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	799	46.6	4.4	9.8	27.2	0.8
Non-derivatized - MS/MS non-kit	245	52.4	5.0	8.3	30.8	0.9
Derivatized - MS/MS PE NeoGram Kit	107	51.0	4.4	6.6	30.2	0.9
Non-derivatized - MS/MS PE NeoBase Kit	689	54.7	4.5	6.7	31.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	54.5	4.2	7.5	32.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	53.9	4.3	7.3	32.0	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	47.8	3.1	4.1	28.0	0.8

Lot 1523 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	797	108.0	10.2	23.6	27.2	0.8
Non-derivatized - MS/MS non-kit	244	123.8	11.2	19.2	30.8	0.9
Derivatized - MS/MS PE NeoGram Kit	108	117.2	11.4	15.9	30.2	0.9
Non-derivatized - MS/MS PE NeoBase Kit	688	124.4	9.6	14.5	31.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	116	119.7	7.6	14.4	32.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	129	120.7	9.1	16.8	32.0	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	112.2	7.6	8.2	28.0	0.8

Lot 1524 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	790	223.3	21.4	46.3	27.2	0.8
Non-derivatized - MS/MS non-kit	250	251.9	22.9	40.2	30.8	0.9
Derivatized - MS/MS PE NeoGram Kit	108	244.2	23.9	37.9	30.2	0.9
Non-derivatized - MS/MS PE NeoBase Kit	684	259.5	18.0	28.5	31.4	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	249.0	17.2	26.1	32.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	127	249.2	17.6	35.0	32.0	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	232.7	15.5	25.6	28.0	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17j. 2015 Quality Control Data Summaries of Statistical Analyses
LEUCINE (µmol Leu/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	767	146.3	11.7	23.6	147.7	0.8
Non-derivatized - MS/MS non-kit	275	178.8	11.5	25.7	180.8	0.9
Derivatized - MS/MS PE NeoGram Kit	125	143.5	13.0	15.9	142.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	626	177.3	10.6	17.1	179.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	93	140.5	13.0	22.2	140.1	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	168.3	12.7	23.2	170.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	170.8	14.8	22.8	170.4	0.9

Lot 1426 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	765	232.3	18.8	31.8	147.7	0.8
Non-derivatized - MS/MS non-kit	261	274.3	19.6	42.2	180.8	0.9
Derivatized - MS/MS PE NeoGram Kit	127	235.6	19.7	26.8	142.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	628	273.0	16.8	28.1	179.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	95	222.3	18.7	27.9	140.1	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	95	258.7	14.9	29.3	170.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	56	264.9	17.2	26.8	170.4	0.9

Lot 1427 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	755	350.0	27.7	46.8	147.7	0.8
Non-derivatized - MS/MS non-kit	272	398.5	27.1	58.4	180.8	0.9
Derivatized - MS/MS PE NeoGram Kit	127	359.9	24.5	39.5	142.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	623	400.6	24.3	38.7	179.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	94	327.7	26.3	33.1	140.1	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	384.1	25.1	51.5	170.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	402.6	41.2	62.8	170.4	0.9

Lot 1428 - Enriched 500.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	772	556.8	43.7	83.1	147.7	0.8
Non-derivatized - MS/MS non-kit	277	624.1	46.8	98.3	180.8	0.9
Derivatized - MS/MS PE NeoGram Kit	129	597.3	43.8	69.9	142.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	630	628.6	38.4	66.4	179.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	98	532.8	36.0	54.1	140.1	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	599.0	45.6	89.1	170.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	57	639.7	41.5	70.5	170.4	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
LEUCINE (µmol Leu/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	808	142.7	12.3	26.7	143.0	0.9
Non-derivatized - MS/MS non-kit	326	169.8	11.9	20.1	170.4	0.9
Derivatized - MS/MS PE NeoGram Kit	107	139.3	11.6	14.3	139.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	681	169.2	9.6	16.5	168.5	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	112	139.4	9.1	16.5	140.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	168.0	9.2	25.9	169.9	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	169.4	10.6	25.7	167.8	0.9

Lot 1522 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	811	230.4	18.1	35.6	143.0	0.9
Non-derivatized - MS/MS non-kit	324	260.9	18.2	29.5	170.4	0.9
Derivatized - MS/MS PE NeoGram Kit	110	227.1	18.4	26.1	139.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	675	259.8	15.8	25.7	168.5	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	115	219.0	17.2	25.4	140.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	126	258.6	13.0	33.8	169.9	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	261.2	12.7	31.9	167.8	0.9

Lot 1523 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	827	360.3	31.4	53.7	143.0	0.9
Non-derivatized - MS/MS non-kit	321	390.1	26.7	45.0	170.4	0.9
Derivatized - MS/MS PE NeoGram Kit	109	359.0	35.9	38.5	139.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	674	389.0	25.4	39.2	168.5	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	116	328.0	21.6	28.9	140.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	134	372.4	20.4	44.9	169.9	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	392.8	22.6	51.7	167.8	0.9

Lot 1524 - Enriched 500.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	819	577.8	46.1	92.6	143.0	0.9
Non-derivatized - MS/MS non-kit	325	613.9	41.2	82.2	170.4	0.9
Derivatized - MS/MS PE NeoGram Kit	109	580.3	56.5	67.7	139.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	670	619.0	41.2	58.5	168.5	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	115	520.9	34.7	45.9	140.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	129	586.3	31.0	49.2	169.9	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	630.4	38.5	84.6	167.8	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17k. 2015 Quality Control Data Summaries of Statistical Analyses
METHIONINE (µmol Met/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	779	23.6	3.1	4.9	23.6	0.8
Non-derivatized - MS/MS non-kit	281	22.0	1.8	3.6	21.5	0.8
Derivatized - MS/MS PE NeoGram Kit	116	24.5	2.9	3.5	24.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	623	22.1	1.6	2.9	21.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	18.4	2.9	5.0	16.8	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	96	18.6	2.2	3.4	18.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	22.5	1.6	1.9	20.5	0.9

Lot 1426 - Enriched 50.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	764	64.1	5.7	9.4	23.6	0.8
Non-derivatized - MS/MS non-kit	272	62.9	4.6	12.1	21.5	0.8
Derivatized - MS/MS PE NeoGram Kit	116	67.4	6.8	8.7	24.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	625	63.2	4.2	8.0	21.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	97	48.5	7.8	14.5	16.8	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	54.7	4.4	9.6	18.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	61.9	4.3	5.2	20.5	0.9

Lot 1427 - Enriched 150.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	769	143.6	12.4	22.1	23.6	0.8
Non-derivatized - MS/MS non-kit	280	142.2	9.1	24.8	21.5	0.8
Derivatized - MS/MS PE NeoGram Kit	119	149.4	12.3	17.6	24.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	626	141.1	9.4	17.6	21.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	97	107.2	14.3	32.4	16.8	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	126.1	16.5	25.6	18.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	146.5	10.4	13.3	20.5	0.9

Lot 1428 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	769	224.7	17.6	33.5	23.6	0.8
Non-derivatized - MS/MS non-kit	279	227.9	15.0	41.8	21.5	0.8
Derivatized - MS/MS PE NeoGram Kit	119	233.7	19.4	28.8	24.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	631	229.8	14.6	29.2	21.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	177.0	23.5	47.9	16.8	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	198.2	18.8	32.5	18.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	235.8	11.6	17.6	20.5	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
METHIONINE (µmol Met/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	810	22.0	2.5	4.1	21.5	0.8
Non-derivatized - MS/MS non-kit	316	18.5	2.0	3.4	17.7	0.8
Derivatized - MS/MS PE NeoGram Kit	107	21.9	3.1	3.4	22.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	689	16.8	1.5	2.5	15.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	119	16.3	2.7	5.5	15.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	14.8	1.4	2.7	13.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	20.5	1.5	2.1	19.1	0.8

Lot 1522 - Enriched 50.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	805	62.2	5.7	9.9	21.5	0.8
Non-derivatized - MS/MS non-kit	307	58.5	5.0	9.8	17.7	0.8
Derivatized - MS/MS PE NeoGram Kit	110	63.6	7.3	9.1	22.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	672	55.0	3.7	7.3	15.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	120	44.1	6.2	16.1	15.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	48.7	3.3	8.3	13.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	59.8	3.4	5.7	19.1	0.8

Lot 1523 - Enriched 150.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	807	146.4	12.5	22.5	21.5	0.8
Non-derivatized - MS/MS non-kit	315	142.6	12.1	25.6	17.7	0.8
Derivatized - MS/MS PE NeoGram Kit	108	151.9	17.1	18.5	22.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	692	136.7	9.6	19.8	15.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	119	101.8	13.8	37.5	15.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	127	116.7	8.4	16.8	13.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	145.4	11.4	15.6	19.1	0.8

Lot 1524 - Enriched 250.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	808	229.1	19.7	36.9	21.5	0.8
Non-derivatized - MS/MS non-kit	318	226.1	18.2	39.9	17.7	0.8
Derivatized - MS/MS PE NeoGram Kit	109	230.0	24.9	31.5	22.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	684	217.9	15.6	30.2	15.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	120	161.3	21.0	58.5	15.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	192.0	14.0	32.3	13.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	230.7	12.5	23.6	19.1	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17l. 2015 Quality Control Data Summaries of Statistical Analyses PHENYLALANINE (µmol Phe/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	108	106.7	11.6	27.1	105.3	1.1
PerkinElmer Neonatal Kit	222	83.3	10.6	13.4	82.9	0.9
Ani Labsystems	117	92.2	11.9	22.2	91.6	1.3
Bio-Rad Quantase	30	98.8	14.6	17.9	99.4	1.1
Interscientific Enzyme	40	75.7	4.1	7.0	67.4	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	112.7	10.1	10.1	122.3	1.1
HPLC	10	79.7	4.2	4.2	76.5	1.0
Derivatized - MS/MS non-kit	844	74.1	5.8	10.2	74.0	0.9
Non-derivatized - MS/MS non-kit	345	77.8	5.5	11.6	78.3	1.0
Derivatized - MS/MS PE NeoGram Kit	156	78.3	6.3	9.8	76.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	640	75.6	4.9	7.5	76.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	81	77.6	6.2	13.5	80.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	84.7	6.3	10.2	84.6	1.0
TecnoSuma UMTEST	20	120.5	9.7	52.0	114.2	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	75.6	4.4	7.6	74.5	1.0

Lot 1426 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	108	213.0	19.5	32.6	105.3	1.1
PerkinElmer Neonatal Kit	221	170.8	14.8	21.9	82.9	0.9
Ani Labsystems	119	226.8	21.1	36.4	91.6	1.3
Bio-Rad Quantase	28	210.9	17.0	20.8	99.4	1.1
Interscientific Enzyme	39	151.9	8.1	50.0	67.4	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	234.0	12.0	12.0	122.3	1.1
HPLC	10	172.2	9.4	9.4	76.5	1.0
Derivatized - MS/MS non-kit	836	164.4	12.4	21.9	74.0	0.9
Non-derivatized - MS/MS non-kit	338	177.2	10.1	24.2	78.3	1.0
Derivatized - MS/MS PE NeoGram Kit	157	174.0	11.4	20.2	76.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	640	170.9	11.3	17.2	76.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	87	171.6	16.0	31.9	80.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	188.2	15.4	24.5	84.6	1.0
TecnoSuma UMTEST	20	235.7	15.0	97.0	114.2	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	167.5	10.8	15.8	74.5	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
PHENYLALANINE (µmol Phe/L blood)

Lot 1427 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	97	320.1	29.4	45.2	105.3	1.1
PerkinElmer Neonatal Kit	221	261.2	20.2	31.3	82.9	0.9
Ani Labsystems	120	352.5	25.6	58.9	91.6	1.3
Bio-Rad Quantase	30	317.9	15.8	26.3	99.4	1.1
Interscientific Enzyme	40	261.9	10.2	18.8	67.4	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	350.6	21.5	21.5	122.3	1.1
HPLC	10	272.9	9.8	9.8	76.5	1.0
Derivatized - MS/MS non-kit	845	253.2	20.3	35.3	74.0	0.9
Non-derivatized - MS/MS non-kit	342	269.4	16.4	39.0	78.3	1.0
Derivatized - MS/MS PE NeoGram Kit	155	268.4	16.7	30.8	76.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	638	262.4	16.4	27.3	76.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	82	251.7	17.0	35.8	80.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	288.7	14.9	26.9	84.6	1.0
TecnoSuma UMTEST	20	375.6	16.9	91.0	114.2	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	267.4	18.4	22.4	74.5	1.0

Lot 1428 - Enriched 300.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	108	433.2	43.4	53.3	105.3	1.1
PerkinElmer Neonatal Kit	219	349.2	28.8	46.0	82.9	0.9
Ani Labsystems	120	494.6	28.7	79.5	91.6	1.3
Bio-Rad Quantase	27	429.3	18.3	33.8	99.4	1.1
Interscientific Enzyme	30	364.7	10.5	20.8	67.4	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	426.2	20.9	20.9	122.3	1.1
HPLC	10	377.1	15.3	15.3	76.5	1.0
Derivatized - MS/MS non-kit	853	344.5	25.2	52.5	74.0	0.9
Non-derivatized - MS/MS non-kit	346	370.0	24.0	56.0	78.3	1.0
Derivatized - MS/MS PE NeoGram Kit	155	372.9	27.9	44.6	76.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	636	357.1	21.4	35.0	76.1	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	83	339.7	24.0	62.5	80.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	394.0	23.8	32.2	84.6	1.0
TecnoSuma UMTEST	20	509.6	42.8	121.1	114.2	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	360.7	17.6	26.9	74.5	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
PHENYLALANINE (µmol Phe/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	79	93.9	8.9	18.3	90.7	1.1
PerkinElmer Neonatal Kit	155	75.1	9.4	11.3	74.9	0.9
Ani Labsystems	79	82.3	9.2	12.8	81.0	1.3
Bio-Rad Quantase	29	84.2	10.9	10.9	82.7	1.1
Interscientific Enzyme	30	78.1	3.8	3.8	70.9	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	100.9	3.5	3.5	97.7	1.1
HPLC	10	81.8	4.0	4.0	84.2	0.9
Derivatized - MS/MS non-kit	888	71.4	5.8	11.0	70.8	0.9
Non-derivatized - MS/MS non-kit	384	74.5	5.1	9.8	74.8	1.0
Derivatized - MS/MS PE NeoGram Kit	119	73.8	7.5	11.0	73.2	1.0
Non-derivatized - MS/MS PE NeoBase Kit	708	71.1	4.4	7.7	69.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	68.7	5.8	8.0	68.8	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	79.9	4.7	8.5	80.3	1.0
TecnoSuma UMTEST	10	74.6	9.9	9.9	69.8	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	74.3	5.1	7.1	73.0	1.0

Lot 1522 - Enriched 100.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	77	197.6	17.4	19.4	90.7	1.1
PerkinElmer Neonatal Kit	159	165.4	20.1	25.9	74.9	0.9
Ani Labsystems	79	212.0	16.2	30.8	81.0	1.3
Bio-Rad Quantase	30	191.2	26.0	38.1	82.7	1.1
Interscientific Enzyme	30	166.8	5.6	13.0	70.9	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	196.2	6.1	6.1	97.7	1.1
HPLC	10	175.4	8.1	8.1	84.2	0.9
Derivatized - MS/MS non-kit	888	162.9	12.0	24.2	70.8	0.9
Non-derivatized - MS/MS non-kit	388	173.6	11.0	21.5	74.8	1.0
Derivatized - MS/MS PE NeoGram Kit	120	167.3	15.6	25.9	73.2	1.0
Non-derivatized - MS/MS PE NeoBase Kit	707	163.5	10.0	18.3	69.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	111	155.5	12.8	26.1	68.8	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	183.6	9.8	18.5	80.3	1.0
TecnoSuma UMTEST	10	173.4	20.0	20.0	69.8	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	168.8	8.7	17.6	73.0	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
PHENYLALANINE (µmol Phe/L blood)

Lot 1523 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	68	318.0	28.3	32.1	90.7	1.1
PerkinElmer Neonatal Kit	150	244.7	21.1	33.3	74.9	0.9
Ani Labsystems	80	337.4	27.3	53.0	81.0	1.3
Bio-Rad Quantase	29	286.0	21.8	25.7	82.7	1.1
Interscientific Enzyme	30	264.4	6.2	27.8	70.9	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	320.0	8.8	8.8	97.7	1.1
HPLC	10	274.4	15.7	15.7	84.2	0.9
Derivatized - MS/MS non-kit	889	254.3	19.5	39.8	70.8	0.9
Non-derivatized - MS/MS non-kit	384	271.2	17.7	31.4	74.8	1.0
Derivatized - MS/MS PE NeoGram Kit	119	263.5	27.9	39.3	73.2	1.0
Non-derivatized - MS/MS PE NeoBase Kit	709	254.1	16.5	27.2	69.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	237.0	16.8	37.7	68.8	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	278.6	17.5	29.4	80.3	1.0
TecnoSuma UMTEST	10	291.3	48.0	48.0	69.8	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	263.2	15.0	26.5	73.0	1.0

Lot 1524 - Enriched 300.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Fluorometric Manual	80	429.5	31.3	62.1	90.7	1.1
PerkinElmer Neonatal Kit	155	342.0	33.5	47.8	74.9	0.9
Ani Labsystems	80	475.9	38.3	74.2	81.0	1.3
Bio-Rad Quantase	29	406.7	20.9	25.9	82.7	1.1
Interscientific Enzyme	28	385.2	7.8	11.8	70.9	1.0
Astoria-Pacific 50 Hour Reagent Kit	10	417.3	15.3	15.3	97.7	1.1
HPLC	10	353.5	18.5	18.5	84.2	0.9
Derivatized - MS/MS non-kit	893	348.9	27.8	56.6	70.8	0.9
Non-derivatized - MS/MS non-kit	388	369.6	24.8	47.6	74.8	1.0
Derivatized - MS/MS PE NeoGram Kit	120	358.8	39.1	55.8	73.2	1.0
Non-derivatized - MS/MS PE NeoBase Kit	708	353.1	23.3	37.5	69.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	111	325.9	25.2	58.2	68.8	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	384.6	22.8	47.6	80.3	1.0
TecnoSuma UMTEST	10	404.5	36.1	36.1	69.8	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	363.9	23.1	37.8	73.0	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17m. 2015 Quality Control Data Summaries of Statistical Analyses
SUCCINYLACETONE (µmol SUAC/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	237	0.7	0.2	0.5	0.8	0.5
Non-derivatized - MS/MS non-kit	68	1.0	0.3	0.9	1.1	0.5
Non-derivatized - MS/MS PE NeoBase Kit	395	0.5	0.1	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.5	0.2	0.4	0.6	0.4

Lot 1426 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	233	2.1	0.3	1.2	0.8	0.5
Non-derivatized - MS/MS non-kit	70	2.4	0.4	0.9	1.1	0.5
Non-derivatized - MS/MS PE NeoBase Kit	395	1.0	0.2	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	38	1.6	0.2	0.2	0.6	0.4

Lot 1427 - Enriched 7.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	238	5.0	0.6	2.8	0.8	0.5
Non-derivatized - MS/MS non-kit	70	4.9	0.7	1.8	1.1	0.5
Non-derivatized - MS/MS PE NeoBase Kit	393	2.0	0.3	0.7	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	38	3.6	0.4	0.5	0.6	0.4

Lot 1428 - Enriched 15.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	237	8.8	1.0	4.9	0.8	0.5
Non-derivatized - MS/MS non-kit	70	8.8	1.2	3.7	1.1	0.5
Non-derivatized - MS/MS PE NeoBase Kit	389	3.5	0.4	1.1	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	39	6.2	0.5	1.3	0.6	0.4

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
SUCCINYLACETONE (µmol SUAC/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	241	0.7	0.2	0.5	0.9	0.5
Non-derivatized - MS/MS non-kit	76	0.9	0.3	0.8	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	390	0.5	0.1	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	70	0.5	0.1	0.3	0.6	0.4

Lot 1522 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	235	2.3	0.3	1.2	0.9	0.5
Non-derivatized - MS/MS non-kit	80	2.2	0.4	1.1	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	396	1.0	0.2	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	70	1.7	0.2	0.5	0.6	0.4

Lot 1523 - Enriched 7.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	240	5.0	0.7	2.8	0.9	0.5
Non-derivatized - MS/MS non-kit	80	4.3	0.7	2.4	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	404	2.0	0.3	0.7	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	70	3.5	0.4	0.8	0.6	0.4

Lot 1524 - Enriched 15.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	236	8.7	1.2	4.8	0.9	0.5
Non-derivatized - MS/MS non-kit	79	7.4	1.2	4.8	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	390	3.6	0.4	1.1	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	70	6.4	0.4	1.7	0.6	0.4

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17n. 2015 Quality Control Data Summaries of Statistical Analyses
TYROSINE (µmol Tyr/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	83.1	3.7	3.7	82.1	0.9
Derivatized - MS/MS non-kit	809	55.1	4.7	7.7	57.4	0.8
Non-derivatized - MS/MS non-kit	301	56.8	4.5	7.8	59.4	0.8
Derivatized - MS/MS PE NeoGram Kit	128	56.2	5.5	8.0	56.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	631	61.7	4.3	7.1	63.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	95	61.2	6.6	9.0	64.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	62.8	7.1	10.6	61.9	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	68	55.3	3.7	5.2	56.6	0.8

Lot 1426 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	262.3	12.2	12.2	82.1	0.9
Derivatized - MS/MS non-kit	831	220.0	17.6	30.1	57.4	0.8
Non-derivatized - MS/MS non-kit	292	229.6	14.9	37.8	59.4	0.8
Derivatized - MS/MS PE NeoGram Kit	127	225.8	19.9	28.5	56.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	638	252.1	16.7	29.3	63.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	98	242.5	17.6	27.7	64.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	251.3	28.3	42.0	61.9	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	223.8	15.2	21.8	56.6	0.8

Lot 1427 - Enriched 400.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	9	444.1	14.7	14.7	82.1	0.9
Derivatized - MS/MS non-kit	816	379.3	28.3	49.5	57.4	0.8
Non-derivatized - MS/MS non-kit	302	392.6	26.9	68.6	59.4	0.8
Derivatized - MS/MS PE NeoGram Kit	130	389.2	26.4	45.5	56.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	638	432.3	27.8	51.2	63.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	98	412.6	32.1	43.5	64.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	94	439.5	40.9	79.3	61.9	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	396.5	21.9	30.3	56.6	0.8

Lot 1428 - Enriched 600.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	627.0	26.2	26.2	82.1	0.9
Derivatized - MS/MS non-kit	821	535.6	37.4	76.0	57.4	0.8
Non-derivatized - MS/MS non-kit	307	557.1	44.8	95.8	59.4	0.8
Derivatized - MS/MS PE NeoGram Kit	129	562.9	42.0	69.0	56.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	637	617.0	37.6	69.1	63.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	97	581.4	47.4	83.3	64.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	98	632.7	46.0	98.0	61.9	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	69	556.5	25.1	40.2	56.6	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
TYROSINE (µmol Tyr/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	91.4	5.5	5.5	95.4	0.8
Derivatized - MS/MS non-kit	824	53.3	4.9	7.9	52.3	0.8
Non-derivatized - MS/MS non-kit	346	56.7	4.7	8.3	55.3	0.9
Derivatized - MS/MS PE NeoGram Kit	107	54.5	6.0	7.2	54.8	0.8
Non-derivatized - MS/MS PE NeoBase Kit	712	58.9	4.6	8.6	56.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	59.9	4.9	9.1	59.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	61.2	4.0	6.7	59.4	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	52.7	2.5	5.5	48.9	0.8

Lot 1522 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	262.5	10.9	10.9	95.4	0.8
Derivatized - MS/MS non-kit	828	216.9	16.7	32.2	52.3	0.8
Non-derivatized - MS/MS non-kit	346	232.9	17.1	32.9	55.3	0.9
Derivatized - MS/MS PE NeoGram Kit	108	218.9	20.9	25.8	54.8	0.8
Non-derivatized - MS/MS PE NeoBase Kit	704	240.0	15.7	30.8	56.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	120	242.7	20.3	41.4	59.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	251.3	17.6	32.1	59.4	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	209.1	9.4	18.9	48.9	0.8

Lot 1523 - Enriched 400.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	441.7	27.7	27.7	95.4	0.8
Derivatized - MS/MS non-kit	837	386.8	30.8	57.9	52.3	0.8
Non-derivatized - MS/MS non-kit	338	407.5	28.5	52.4	55.3	0.9
Derivatized - MS/MS PE NeoGram Kit	108	390.0	40.8	51.8	54.8	0.8
Non-derivatized - MS/MS PE NeoBase Kit	710	423.7	27.5	52.9	56.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	413.4	33.5	56.6	59.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	127	429.2	33.5	55.8	59.4	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	370.6	18.3	36.4	48.9	0.8

Lot 1524 - Enriched 600.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
HPLC	10	588.6	29.0	29.0	95.4	0.8
Derivatized - MS/MS non-kit	839	552.3	43.9	87.5	52.3	0.8
Non-derivatized - MS/MS non-kit	342	591.5	42.1	80.3	55.3	0.9
Derivatized - MS/MS PE NeoGram Kit	107	549.4	50.5	71.7	54.8	0.8
Non-derivatized - MS/MS PE NeoBase Kit	712	613.7	41.5	81.8	56.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	602.2	40.1	87.2	59.9	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	633.4	44.5	78.6	59.4	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	543.6	26.3	62.3	48.9	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17o. 2015 Quality Control Data Summaries of Statistical Analyses
VALINE (µmol Val/L blood)

Lot 1425 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	711	158.6	15.7	28.0	160.9	0.7
Non-derivatized - MS/MS non-kit	188	144.3	8.4	25.4	146.6	0.7
Derivatized - MS/MS PE NeoGram Kit	115	165.2	19.1	22.9	168.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	627	175.6	13.4	23.2	179.8	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	93	135.9	12.5	22.3	138.9	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	131.2	10.9	19.6	136.0	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	176.4	11.3	21.2	175.7	0.9

Lot 1426 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	717	305.8	28.6	52.7	160.9	0.7
Non-derivatized - MS/MS non-kit	186	294.8	19.2	50.0	146.6	0.7
Derivatized - MS/MS PE NeoGram Kit	118	323.1	38.8	48.2	168.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	630	365.9	29.1	51.9	179.8	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	99	281.2	33.4	57.0	138.9	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	272.0	19.8	46.9	136.0	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	354.5	23.9	45.4	175.7	0.9

Lot 1427 - Enriched 350.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	715	402.1	40.5	68.6	160.9	0.7
Non-derivatized - MS/MS non-kit	188	392.9	22.2	65.4	146.6	0.7
Derivatized - MS/MS PE NeoGram Kit	118	425.0	39.0	61.1	168.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	632	484.1	40.2	70.5	179.8	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	96	357.9	38.8	72.3	138.9	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	364.3	22.1	57.6	136.0	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	498.7	27.9	60.2	175.7	0.9

Lot 1428 - Enriched 500.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	716	509.8	45.1	83.2	160.9	0.7
Non-derivatized - MS/MS non-kit	189	503.0	33.6	89.8	146.6	0.7
Derivatized - MS/MS PE NeoGram Kit	117	538.5	55.8	80.9	168.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	627	621.1	46.9	84.4	179.8	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	96	472.5	42.8	91.3	138.9	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	454.6	24.6	73.0	136.0	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	629.7	34.2	66.2	175.7	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
VALINE (µmol Val/L blood)

Lot 1521 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	771	164.1	15.8	30.2	160.2	0.7
Non-derivatized - MS/MS non-kit	238	147.1	11.4	29.6	145.5	0.7
Derivatized - MS/MS PE NeoGram Kit	97	173.7	21.1	26.6	169.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	686	172.8	13.5	23.8	166.7	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	143.4	18.4	35.7	140.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	124.8	8.2	13.8	121.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	186.0	10.3	20.3	180.3	0.9

Lot 1522 - Enriched 200.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	775	302.1	30.1	55.2	160.2	0.7
Non-derivatized - MS/MS non-kit	239	289.1	22.4	58.8	145.5	0.7
Derivatized - MS/MS PE NeoGram Kit	97	307.5	36.7	50.8	169.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	709	334.0	29.4	56.5	166.7	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	265.4	26.4	65.8	140.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	251.9	15.3	34.6	121.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	355.2	17.5	35.6	180.3	0.9

Lot 1523 - Enriched 350.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	790	418.1	42.4	84.2	160.2	0.7
Non-derivatized - MS/MS non-kit	237	405.7	32.6	84.4	145.5	0.7
Derivatized - MS/MS PE NeoGram Kit	100	427.6	50.5	69.7	169.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	684	471.8	37.1	67.2	166.7	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	109	359.2	42.6	88.7	140.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	354.2	25.0	50.5	121.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	491.5	30.0	50.0	180.3	0.9

Lot 1524 - Enriched 500.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	790	533.2	57.7	108.9	160.2	0.7
Non-derivatized - MS/MS non-kit	240	513.9	37.6	106.8	145.5	0.7
Derivatized - MS/MS PE NeoGram Kit	100	534.5	69.4	95.7	169.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	679	611.7	49.8	86.9	166.7	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	463.1	43.9	116.3	140.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	459.5	29.0	58.2	121.6	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	640.4	44.0	68.7	180.3	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17p. 2015 Quality Control Data Summaries of Statistical Analyses
FREE CARNITINE (µmol C0/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	846	16.46	1.67	2.87	16.17	1.3
Non-derivatized - MS/MS non-kit	209	15.73	1.23	2.91	15.47	1.1
Derivatized - MS/MS PE NeoGram Kit	130	21.19	1.82	3.29	20.18	1.8
Non-derivatized - MS/MS PE NeoBase Kit	633	15.29	1.29	1.94	15.09	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	106	14.84	1.76	3.05	14.80	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	13.43	1.01	1.71	13.71	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	16.13	0.79	1.66	15.97	1.1

Lot 1466 - Enriched 10.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	847	28.71	2.71	4.67	16.17	1.3
Non-derivatized - MS/MS non-kit	206	25.92	1.84	4.12	15.47	1.1
Derivatized - MS/MS PE NeoGram Kit	128	37.58	2.79	5.94	20.18	1.8
Non-derivatized - MS/MS PE NeoBase Kit	633	25.29	2.02	3.08	15.09	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	26.00	2.86	5.54	14.80	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	23.52	1.49	3.14	13.71	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	26.83	2.13	3.26	15.97	1.1

Lot 1467 - Enriched 20.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	833	41.50	3.90	6.83	16.17	1.3
Non-derivatized - MS/MS non-kit	203	36.24	2.51	5.70	15.47	1.1
Derivatized - MS/MS PE NeoGram Kit	129	56.03	4.46	9.98	20.18	1.8
Non-derivatized - MS/MS PE NeoBase Kit	630	35.50	2.70	4.04	15.09	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	108	37.49	3.48	8.47	14.80	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	31.40	2.43	4.88	13.71	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	37.28	2.04	3.70	15.97	1.1

Lot 1468 - Enriched 30.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	850	54.96	4.76	9.71	16.17	1.3
Non-derivatized - MS/MS non-kit	207	47.68	3.38	8.54	15.47	1.1
Derivatized - MS/MS PE NeoGram Kit	130	76.46	5.95	12.97	20.18	1.8
Non-derivatized - MS/MS PE NeoBase Kit	644	46.38	3.98	6.16	15.09	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	108	48.68	4.70	10.45	14.80	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	41.22	2.87	6.61	13.71	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	48.91	3.11	6.59	15.97	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
FREE CARNITINE (µmol C0/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	913	16.87	1.80	3.47	16.74	1.4
Non-derivatized - MS/MS non-kit	256	15.27	1.41	3.04	15.40	1.1
Derivatized - MS/MS PE NeoGram Kit	109	19.67	1.75	3.02	19.23	1.9
Non-derivatized - MS/MS PE NeoBase Kit	700	13.96	1.11	2.00	14.15	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	128	14.23	1.34	3.31	14.01	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	13.29	0.87	1.56	13.41	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	14.77	1.19	2.09	14.88	1.1

Lot 1562 - Enriched 10.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	914	31.10	3.02	5.88	16.74	1.4
Non-derivatized - MS/MS non-kit	259	26.67	2.49	5.85	15.40	1.1
Derivatized - MS/MS PE NeoGram Kit	110	37.93	3.72	6.72	19.23	1.9
Non-derivatized - MS/MS PE NeoBase Kit	698	24.64	1.90	3.36	14.15	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	129	25.55	2.51	6.10	14.01	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	23.32	1.21	2.40	13.41	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	25.90	1.44	3.44	14.88	1.1

Lot 1563 - Enriched 20.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	913	44.86	3.99	8.03	16.74	1.4
Non-derivatized - MS/MS non-kit	260	37.64	2.75	7.67	15.40	1.1
Derivatized - MS/MS PE NeoGram Kit	110	55.59	4.72	10.52	19.23	1.9
Non-derivatized - MS/MS PE NeoBase Kit	704	35.00	2.41	4.76	14.15	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	130	37.66	3.70	9.22	14.01	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	32.52	2.21	3.86	13.41	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	37.07	2.26	4.32	14.88	1.1

Lot 1564 - Enriched 30.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	911	59.98	5.70	11.54	16.74	1.4
Non-derivatized - MS/MS non-kit	260	48.62	3.77	9.71	15.40	1.1
Derivatized - MS/MS PE NeoGram Kit	107	76.34	6.58	12.83	19.23	1.9
Non-derivatized - MS/MS PE NeoBase Kit	696	44.89	3.29	5.95	14.15	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	129	49.66	4.24	12.30	14.01	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	42.37	2.49	4.14	13.41	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	47.64	3.06	5.56	14.88	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17q. 2015 Quality Control Data Summaries of Statistical Analyses
ACETYLCARNITINE (µmol C2/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	813	11.52	1.34	2.99	11.76	0.9
Non-derivatized - MS/MS non-kit	200	9.05	0.71	1.75	9.17	1.0
Derivatized - MS/MS PE NeoGram Kit	130	14.44	1.05	2.86	14.40	0.6
Non-derivatized - MS/MS PE NeoBase Kit	640	8.38	0.56	0.94	8.49	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	105	11.18	1.32	2.40	11.39	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	7.50	0.58	1.06	7.68	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	11.06	0.62	1.83	11.08	1.1

Lot 1466 - Enriched 10.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	817	20.89	2.19	4.75	11.76	0.9
Non-derivatized - MS/MS non-kit	198	19.02	1.36	3.29	9.17	1.0
Derivatized - MS/MS PE NeoGram Kit	128	20.99	1.27	2.84	14.40	0.6
Non-derivatized - MS/MS PE NeoBase Kit	652	17.58	1.10	2.06	8.49	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	108	20.32	1.99	2.94	11.39	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	16.56	1.03	1.92	7.68	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	22.09	1.45	3.00	11.08	1.1

Lot 1467 - Enriched 20.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	814	29.33	2.91	5.72	11.76	0.9
Non-derivatized - MS/MS non-kit	196	27.90	1.89	4.85	9.17	1.0
Derivatized - MS/MS PE NeoGram Kit	127	26.74	1.62	3.36	14.40	0.6
Non-derivatized - MS/MS PE NeoBase Kit	646	26.44	1.67	2.95	8.49	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	28.28	2.51	4.05	11.39	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	23.74	1.61	2.98	7.68	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	32.91	2.11	3.65	11.08	1.1

Lot 1468 - Enriched 30.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	816	37.99	3.50	7.30	11.76	0.9
Non-derivatized - MS/MS non-kit	198	37.81	2.63	7.15	9.17	1.0
Derivatized - MS/MS PE NeoGram Kit	130	33.88	2.03	4.03	14.40	0.6
Non-derivatized - MS/MS PE NeoBase Kit	642	35.24	2.31	4.02	8.49	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	36.97	3.16	4.13	11.39	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	32.89	2.10	3.57	7.68	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	43.95	2.63	4.14	11.08	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
ACETYLCARNITINE (µmol C2/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	890	12.98	1.63	3.48	12.73	1.0
Non-derivatized - MS/MS non-kit	250	11.24	0.97	1.96	10.88	1.1
Derivatized - MS/MS PE NeoGram Kit	106	14.44	1.47	2.18	14.52	0.7
Non-derivatized - MS/MS PE NeoBase Kit	674	9.07	0.54	1.00	8.74	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	121	10.74	0.75	1.73	10.28	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	8.69	0.65	1.22	8.51	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	11.05	0.58	0.76	10.68	1.1

Lot 1562 - Enriched 10.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	868	22.24	2.10	4.09	12.73	1.0
Non-derivatized - MS/MS non-kit	245	21.41	1.47	3.17	10.88	1.1
Derivatized - MS/MS PE NeoGram Kit	105	21.76	2.29	3.00	14.52	0.7
Non-derivatized - MS/MS PE NeoBase Kit	680	17.92	1.09	1.90	8.74	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	122	19.35	1.41	2.99	10.28	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	16.95	1.07	1.89	8.51	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	21.60	1.02	1.65	10.68	1.1

Lot 1563 - Enriched 20.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	880	31.48	2.98	6.24	12.73	1.0
Non-derivatized - MS/MS non-kit	246	32.31	2.50	5.00	10.88	1.1
Derivatized - MS/MS PE NeoGram Kit	105	27.72	2.10	3.57	14.52	0.7
Non-derivatized - MS/MS PE NeoBase Kit	685	26.99	1.58	2.82	8.74	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	121	27.93	1.99	3.51	10.28	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	106	25.21	1.49	2.92	8.51	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	33.24	1.98	2.39	10.68	1.1

Lot 1564 - Enriched 30.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	875	42.01	3.52	7.50	12.73	1.0
Non-derivatized - MS/MS non-kit	248	43.92	3.07	6.29	10.88	1.1
Derivatized - MS/MS PE NeoGram Kit	107	35.32	3.36	4.14	14.52	0.7
Non-derivatized - MS/MS PE NeoBase Kit	676	37.39	2.17	3.95	8.74	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	128	38.84	2.53	5.65	10.28	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	95	34.40	2.24	3.59	8.51	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	45.10	2.32	3.06	10.68	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17r. 2015 Quality Control Data Summaries of Statistical Analyses
PROPIONYLCARNITINE (µmol C3/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	819	0.95	0.12	0.18	1.02	0.9
Non-derivatized - MS/MS non-kit	205	0.92	0.09	0.17	0.94	1.0
Derivatized - MS/MS PE NeoGram Kit	125	0.78	0.08	0.11	0.77	0.8
Non-derivatized - MS/MS PE NeoBase Kit	636	0.78	0.06	0.09	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	105	0.90	0.16	0.20	0.86	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.80	0.08	0.14	0.80	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	1.01	0.07	0.10	1.02	1.0

Lot 1466 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	819	3.88	0.42	0.64	1.02	0.9
Non-derivatized - MS/MS non-kit	206	3.90	0.27	0.63	0.94	1.0
Derivatized - MS/MS PE NeoGram Kit	127	3.25	0.24	0.37	0.77	0.8
Non-derivatized - MS/MS PE NeoBase Kit	650	3.30	0.22	0.36	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	106	3.39	0.32	0.42	0.86	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	3.36	0.34	0.53	0.80	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	4.12	0.29	0.36	1.02	1.0

Lot 1467 - Enriched 7.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	822	8.14	0.89	1.41	1.02	0.9
Non-derivatized - MS/MS non-kit	201	8.16	0.66	1.29	0.94	1.0
Derivatized - MS/MS PE NeoGram Kit	126	6.76	0.47	0.83	0.77	0.8
Non-derivatized - MS/MS PE NeoBase Kit	647	7.00	0.47	0.74	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	7.00	0.70	0.78	0.86	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	7.01	0.56	1.22	0.80	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	8.66	0.54	0.58	1.02	1.0

Lot 1468 - Enriched 12.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	829	12.20	1.26	2.14	1.02	0.9
Non-derivatized - MS/MS non-kit	202	12.57	1.01	2.25	0.94	1.0
Derivatized - MS/MS PE NeoGram Kit	129	10.61	0.85	1.21	0.77	0.8
Non-derivatized - MS/MS PE NeoBase Kit	645	10.82	0.68	1.15	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	10.97	1.07	1.37	0.86	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	10.94	0.78	1.59	0.80	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	13.32	0.76	0.85	1.02	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
PROPIONYLCARNITINE (µmol C3/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	894	1.02	0.12	0.19	0.90	1.0
Non-derivatized - MS/MS non-kit	251	1.01	0.10	0.17	0.91	1.1
Derivatized - MS/MS PE NeoGram Kit	103	0.78	0.08	0.11	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	704	0.82	0.06	0.10	0.71	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	117	0.92	0.11	0.12	0.77	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.86	0.08	0.15	0.70	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	47	1.03	0.04	0.08	0.89	1.1

Lot 1562 - Enriched 4.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	893	5.04	0.51	0.85	0.90	1.0
Non-derivatized - MS/MS non-kit	244	5.11	0.40	0.82	0.91	1.1
Derivatized - MS/MS PE NeoGram Kit	103	4.08	0.42	0.57	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	709	4.24	0.28	0.49	0.71	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	117	4.49	0.38	0.50	0.77	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	4.32	0.27	0.57	0.70	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	5.37	0.26	0.53	0.89	1.1

Lot 1563 - Enriched 8.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	901	8.91	0.89	1.45	0.90	1.0
Non-derivatized - MS/MS non-kit	251	9.39	0.78	1.66	0.91	1.1
Derivatized - MS/MS PE NeoGram Kit	103	7.04	0.56	1.28	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	704	7.59	0.45	0.83	0.71	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	116	8.06	0.62	0.83	0.77	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	106	7.77	0.48	1.17	0.70	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	9.64	0.48	0.87	0.89	1.1

Lot 1564 - Enriched 12.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	902	13.61	1.36	2.18	0.90	1.0
Non-derivatized - MS/MS non-kit	248	13.95	1.01	2.18	0.91	1.1
Derivatized - MS/MS PE NeoGram Kit	107	11.01	1.04	1.96	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	702	11.61	0.70	1.29	0.71	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	117	12.39	0.91	1.44	0.77	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	12.08	0.79	1.67	0.70	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	14.68	0.79	1.32	0.89	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17s. 2015 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE (µmol C3DC/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	750	0.03	0.01	0.02	0.05	0.5
Derivatized - MS/MS PE NeoGram Kit	112	0.04	0.01	0.01	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	96	0.04	0.02	0.03	0.06	0.6

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	746	0.31	0.06	0.10	0.05	0.5
Derivatized - MS/MS PE NeoGram Kit	120	0.68	0.07	0.19	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	97	0.36	0.08	0.14	0.06	0.6

Lot 1467 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	744	0.91	0.15	0.28	0.05	0.5
Derivatized - MS/MS PE NeoGram Kit	120	2.16	0.19	0.59	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	96	1.06	0.20	0.35	0.06	0.6

Lot 1468 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	737	1.62	0.22	0.50	0.05	0.5
Derivatized - MS/MS PE NeoGram Kit	120	3.91	0.33	1.05	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	93	1.89	0.43	0.65	0.06	0.6

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE (µmol C3DC/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	803	0.03	0.02	0.03	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	82	0.03	0.01	0.02	0.01	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	123	0.03	0.02	0.03	0.02	0.7

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	808	0.33	0.06	0.12	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	86	0.70	0.08	0.15	0.01	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	123	0.35	0.07	0.12	0.02	0.7

Lot 1563 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	815	0.92	0.13	0.32	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	88	1.93	0.20	0.47	0.01	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	124	1.00	0.17	0.35	0.02	0.7

Lot 1564 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	811	1.83	0.25	0.59	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	86	4.03	0.43	0.88	0.01	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	124	2.01	0.35	0.67	0.02	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17t. 2015 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE + HYDROXYBUTYRYLCARNITINE
(µmol C3DC+C4OH/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	119	0.09	0.02	0.05	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	493	0.06	0.01	0.03	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	48	0.12	0.04	0.15	0.08	0.6

Lot 1466 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	118	0.55	0.08	0.26	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	479	0.39	0.04	0.11	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.78	0.14	0.88	0.08	0.6

Lot 1467 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	120	1.17	0.17	0.63	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	473	0.79	0.07	0.20	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	1.51	0.19	1.81	0.08	0.6

Lot 1468 - Enriched 5.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	120	2.50	0.31	1.35	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	479	1.78	0.14	0.41	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	3.65	0.70	4.33	0.08	0.6

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE + HYDROXYBUTYRYLCARNITINE
(µmol C3DC+C4OH/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	139	0.08	0.02	0.05	0.08	0.5
Non-derivatized - MS/MS PE NeoBase Kit	521	0.05	0.01	0.02	0.04	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.09	0.04	0.12	0.16	0.3

Lot 1562 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	136	0.60	0.09	0.34	0.08	0.5
Non-derivatized - MS/MS PE NeoBase Kit	531	0.39	0.03	0.14	0.04	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	65	0.49	0.04	0.76	0.16	0.3

Lot 1563 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	137	1.21	0.19	0.69	0.08	0.5
Non-derivatized - MS/MS PE NeoBase Kit	510	0.79	0.06	0.14	0.04	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	63	0.86	0.12	1.54	0.16	0.3

Lot 1564 - Enriched 5.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Non-derivatized - MS/MS non-kit	134	2.73	0.32	1.52	0.08	0.5
Non-derivatized - MS/MS PE NeoBase Kit	509	1.83	0.12	0.30	0.04	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	1.60	0.25	0.43	0.16	0.3

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17u. 2015 Quality Control Data Summaries of Statistical Analyses
BUTYRYLCARNITINE (µmol C4/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	803	0.14	0.03	0.05	0.14	0.8
Non-derivatized - MS/MS non-kit	173	0.13	0.02	0.02	0.14	0.8
Derivatized - MS/MS PE NeoGram Kit	122	0.15	0.04	0.04	0.13	0.7
Non-derivatized - MS/MS PE NeoBase Kit	621	0.13	0.02	0.04	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	101	0.14	0.05	0.09	0.11	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	0.12	0.02	0.04	0.11	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.13	0.01	0.01	0.14	0.9

Lot 1466 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	814	0.97	0.12	0.18	0.14	0.8
Non-derivatized - MS/MS non-kit	168	1.00	0.10	0.12	0.14	0.8
Derivatized - MS/MS PE NeoGram Kit	129	0.85	0.13	0.15	0.13	0.7
Non-derivatized - MS/MS PE NeoBase Kit	621	0.90	0.06	0.11	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.88	0.13	0.18	0.11	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.89	0.09	0.14	0.11	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.01	0.06	0.06	0.14	0.9

Lot 1467 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	812	2.16	0.22	0.35	0.14	0.8
Non-derivatized - MS/MS non-kit	168	2.24	0.22	0.27	0.14	0.8
Derivatized - MS/MS PE NeoGram Kit	127	1.94	0.23	0.29	0.13	0.7
Non-derivatized - MS/MS PE NeoBase Kit	627	2.05	0.14	0.24	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	1.84	0.24	0.34	0.11	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	1.92	0.18	0.30	0.11	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	2.31	0.14	0.15	0.14	0.9

Lot 1468 - Enriched 5.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	833	4.23	0.43	0.68	0.14	0.8
Non-derivatized - MS/MS non-kit	178	4.32	0.40	0.71	0.14	0.8
Derivatized - MS/MS PE NeoGram Kit	127	3.78	0.45	0.52	0.13	0.7
Non-derivatized - MS/MS PE NeoBase Kit	629	4.05	0.30	0.48	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	3.84	0.40	0.69	0.11	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	3.90	0.35	0.45	0.11	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	28	4.43	0.20	0.22	0.14	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
BUTYRYLCARNITINE (μmol C4/L blood)

Lot 1561 - Nonenriched 0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	885	0.11	0.03	0.05	0.03	1.0
Non-derivatized - MS/MS non-kit	214	0.10	0.02	0.02	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	90	0.12	0.04	0.05	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	670	0.10	0.02	0.03	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	122	0.10	0.03	0.03	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	101	0.08	0.01	0.01	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.09	0.01	0.02	0.03	1.0

Lot 1562 - Enriched 1.0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	884	1.00	0.12	0.18	0.03	1.0
Non-derivatized - MS/MS non-kit	227	1.00	0.10	0.16	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	99	0.87	0.16	0.17	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	674	0.92	0.07	0.11	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	128	0.85	0.11	0.15	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	104	0.87	0.06	0.08	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	1.00	0.05	0.13	0.03	1.0

Lot 1563 - Enriched 3.0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	882	2.73	0.28	0.44	0.03	1.0
Non-derivatized - MS/MS non-kit	230	2.87	0.22	0.43	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	97	2.31	0.36	0.42	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	658	2.57	0.18	0.26	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	130	2.41	0.25	0.41	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	105	2.44	0.17	0.23	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	2.81	0.16	0.31	0.03	1.0

Lot 1564 - Enriched 5.0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	906	4.98	0.48	0.83	0.03	1.0
Non-derivatized - MS/MS non-kit	230	5.10	0.42	0.73	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	100	4.25	0.67	0.83	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	670	4.62	0.30	0.50	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	129	4.33	0.42	0.71	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	4.40	0.32	0.40	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	5.00	0.27	0.58	0.03	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17v. 2015 Quality Control Data Summaries of Statistical Analyses HYDROXYBUTYRYLCARNITINE (µmol C4OH/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	691	0.08	0.02	0.03	0.08	0.7
Derivatized - MS/MS PE NeoGram Kit	106	0.10	0.03	0.05	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	67	0.06	0.02	0.03	0.06	0.7

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	703	0.41	0.06	0.11	0.08	0.7
Derivatized - MS/MS PE NeoGram Kit	109	0.47	0.08	0.19	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	70	0.40	0.05	0.08	0.06	0.7

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	703	0.74	0.10	0.19	0.08	0.7
Derivatized - MS/MS PE NeoGram Kit	106	0.85	0.14	0.38	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	70	0.70	0.09	0.14	0.06	0.7

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	714	1.75	0.21	0.42	0.08	0.7
Derivatized - MS/MS PE NeoGram Kit	107	1.93	0.25	0.77	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	68	1.69	0.19	0.36	0.06	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYBUTYRYLCARNITINE (µmol C4OH/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	757	0.08	0.02	0.03	0.07	0.7
Derivatized - MS/MS PE NeoGram Kit	94	0.08	0.03	0.05	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	96	0.06	0.02	0.02	0.05	0.7

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	758	0.44	0.07	0.12	0.07	0.7
Derivatized - MS/MS PE NeoGram Kit	99	0.45	0.09	0.14	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	96	0.36	0.05	0.08	0.05	0.7

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	756	0.81	0.11	0.21	0.07	0.7
Derivatized - MS/MS PE NeoGram Kit	100	0.83	0.14	0.27	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	98	0.72	0.10	0.15	0.05	0.7

Lot 1564 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	754	1.92	0.23	0.48	0.07	0.7
Derivatized - MS/MS PE NeoGram Kit	99	2.02	0.35	0.67	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	95	1.70	0.17	0.31	0.05	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17w. 2015 Quality Control Data Summaries of Statistical Analyses
ISOVALERYLCARNITINE (µmol C5/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	846	0.09	0.02	0.03	0.10	0.8
Non-derivatized - MS/MS non-kit	232	0.08	0.01	0.02	0.09	0.9
Derivatized - MS/MS PE NeoGram Kit	127	0.08	0.02	0.03	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	638	0.07	0.01	0.01	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	113	0.10	0.03	0.05	0.10	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	0.07	0.01	0.03	0.07	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	0.08	0.01	0.02	0.09	0.9

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	848	0.53	0.06	0.10	0.10	0.8
Non-derivatized - MS/MS non-kit	246	0.56	0.05	0.07	0.09	0.9
Derivatized - MS/MS PE NeoGram Kit	126	0.49	0.07	0.08	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	635	0.52	0.04	0.07	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	118	0.56	0.07	0.12	0.10	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.50	0.05	0.10	0.07	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.58	0.04	0.05	0.09	0.9

Lot 1467 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	846	1.32	0.14	0.23	0.10	0.8
Non-derivatized - MS/MS non-kit	243	1.40	0.11	0.17	0.09	0.9
Derivatized - MS/MS PE NeoGram Kit	127	1.23	0.15	0.19	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	638	1.31	0.09	0.16	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	115	1.35	0.18	0.24	0.10	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	1.19	0.11	0.22	0.07	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.46	0.07	0.10	0.09	0.9

Lot 1466 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	851	2.59	0.25	0.42	0.10	0.8
Non-derivatized - MS/MS non-kit	245	2.77	0.20	0.31	0.09	0.9
Derivatized - MS/MS PE NeoGram Kit	128	2.47	0.25	0.36	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	638	2.59	0.18	0.31	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	119	2.71	0.31	0.44	0.10	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	2.44	0.19	0.44	0.07	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	2.88	0.15	0.22	0.09	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
ISOVALERYLCARNITINE (µmol C5/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	913	0.07	0.02	0.03	0.07	0.9
Non-derivatized - MS/MS non-kit	289	0.06	0.01	0.02	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	107	0.07	0.02	0.02	0.07	0.8
Non-derivatized - MS/MS PE NeoBase Kit	685	0.06	0.01	0.02	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	126	0.07	0.02	0.03	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	113	0.06	0.01	0.01	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	0.06	0.01	0.01	0.06	1.0

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	906	0.52	0.07	0.10	0.07	0.9
Non-derivatized - MS/MS non-kit	297	0.52	0.05	0.09	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	105	0.45	0.07	0.08	0.07	0.8
Non-derivatized - MS/MS PE NeoBase Kit	687	0.48	0.04	0.06	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	123	0.51	0.08	0.10	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	0.49	0.05	0.07	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	0.54	0.02	0.04	0.06	1.0

Lot 1563 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	904	1.36	0.15	0.24	0.07	0.9
Non-derivatized - MS/MS non-kit	288	1.47	0.12	0.23	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	110	1.23	0.17	0.23	0.07	0.8
Non-derivatized - MS/MS PE NeoBase Kit	686	1.31	0.10	0.17	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	127	1.35	0.14	0.19	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	1.34	0.09	0.23	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	1.47	0.06	0.10	0.06	1.0

Lot 1564 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	911	2.67	0.27	0.46	0.07	0.9
Non-derivatized - MS/MS non-kit	285	2.84	0.20	0.42	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	107	2.38	0.37	0.42	0.07	0.8
Non-derivatized - MS/MS PE NeoBase Kit	689	2.57	0.17	0.28	0.06	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	128	2.72	0.31	0.49	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	2.64	0.17	0.40	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.91	0.18	0.28	0.06	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17x. 2015 Quality Control Data Summaries of Statistical Analyses
GLUTARYLCARNITINE (µmol C5DC/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	843	0.02	0.01	0.02	0.03	0.7
Non-derivatized - MS/MS non-kit	229	0.04	0.01	0.02	0.07	1.0
Derivatized - MS/MS PE NeoGram Kit	117	0.03	0.01	0.01	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	562	0.05	0.01	0.02	0.07	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	101	0.04	0.02	0.05	0.02	1.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	83	0.06	0.03	0.04	0.08	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	56	0.07	0.01	0.01	0.08	1.1

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	840	0.36	0.07	0.15	0.03	0.7
Non-derivatized - MS/MS non-kit	240	0.55	0.06	0.16	0.07	1.0
Derivatized - MS/MS PE NeoGram Kit	120	0.52	0.05	0.06	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	569	0.57	0.05	0.07	0.07	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.65	0.13	0.27	0.02	1.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.71	0.09	0.21	0.08	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	0.62	0.05	0.05	0.08	1.1

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	840	0.70	0.12	0.31	0.03	0.7
Non-derivatized - MS/MS non-kit	236	1.05	0.11	0.31	0.07	1.0
Derivatized - MS/MS PE NeoGram Kit	123	1.04	0.09	0.14	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	585	1.10	0.09	0.15	0.07	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	109	1.25	0.28	0.53	0.02	1.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	1.36	0.25	0.46	0.08	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.16	0.07	0.08	0.08	1.1

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	840	1.65	0.25	0.72	0.03	0.7
Non-derivatized - MS/MS non-kit	236	2.45	0.23	0.72	0.07	1.0
Derivatized - MS/MS PE NeoGram Kit	124	2.48	0.20	0.26	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	590	2.58	0.21	0.34	0.07	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	109	3.16	0.44	1.34	0.02	1.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	3.21	0.44	1.06	0.08	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.74	0.19	0.20	0.08	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
GLUTARYLCARNITINE (µmol C5DC/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	881	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS non-kit	286	0.04	0.01	0.03	0.05	0.9
Derivatized - MS/MS PE NeoGram Kit	102	0.03	0.01	0.02	0.02	1.1
Non-derivatized - MS/MS PE NeoBase Kit	632	0.05	0.01	0.02	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.04	0.02	0.03	0.06	1.4
Non-derivatized - MS/MS Chromsystems MassChrom Kit	112	0.07	0.03	0.05	0.07	1.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	0.06	0.01	0.01	0.06	1.2

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	883	0.34	0.06	0.14	0.02	0.6
Non-derivatized - MS/MS non-kit	281	0.54	0.07	0.18	0.05	0.9
Derivatized - MS/MS PE NeoGram Kit	105	0.56	0.07	0.09	0.02	1.1
Non-derivatized - MS/MS PE NeoBase Kit	628	0.56	0.05	0.09	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	128	0.75	0.18	0.28	0.06	1.4
Non-derivatized - MS/MS Chromsystems MassChrom Kit	116	0.91	0.15	0.30	0.07	1.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	0.64	0.04	0.05	0.06	1.2

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	882	0.63	0.09	0.26	0.02	0.6
Non-derivatized - MS/MS non-kit	278	0.97	0.11	0.35	0.05	0.9
Derivatized - MS/MS PE NeoGram Kit	107	1.05	0.11	0.14	0.02	1.1
Non-derivatized - MS/MS PE NeoBase Kit	645	1.05	0.09	0.18	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	129	1.41	0.22	0.47	0.06	1.4
Non-derivatized - MS/MS Chromsystems MassChrom Kit	113	1.63	0.21	0.47	0.07	1.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	47	1.20	0.07	0.09	0.06	1.2

Lot 1564 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	875	1.59	0.21	0.63	0.02	0.6
Non-derivatized - MS/MS non-kit	277	2.40	0.24	0.86	0.05	0.9
Derivatized - MS/MS PE NeoGram Kit	105	2.64	0.30	0.39	0.02	1.1
Non-derivatized - MS/MS PE NeoBase Kit	649	2.65	0.21	0.43	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	128	3.43	0.47	1.10	0.06	1.4
Non-derivatized - MS/MS Chromsystems MassChrom Kit	114	4.10	0.37	1.22	0.07	1.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.94	0.19	0.32	0.06	1.2

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17y. 2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYISOVALERYLCARNITINE (µmol C5OH/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	833	0.39	0.06	0.10	0.39	0.8
Non-derivatized - MS/MS non-kit	199	0.55	0.05	0.10	0.56	0.8
Derivatized - MS/MS PE NeoGram Kit	125	0.36	0.07	0.08	0.36	0.7
Non-derivatized - MS/MS PE NeoBase Kit	522	0.43	0.04	0.08	0.43	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	98	0.42	0.08	0.12	0.42	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	57	0.31	0.05	0.07	0.33	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	0.66	0.05	0.09	0.63	1.0

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	819	0.77	0.09	0.16	0.39	0.8
Non-derivatized - MS/MS non-kit	199	0.97	0.08	0.19	0.56	0.8
Derivatized - MS/MS PE NeoGram Kit	129	0.70	0.10	0.14	0.36	0.7
Non-derivatized - MS/MS PE NeoBase Kit	524	0.70	0.05	0.13	0.43	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	96	0.77	0.12	0.16	0.42	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	0.56	0.07	0.13	0.33	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	55	1.11	0.06	0.12	0.63	1.0

Lot 1467 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	822	1.53	0.18	0.33	0.39	0.8
Non-derivatized - MS/MS non-kit	198	1.74	0.15	0.34	0.56	0.8
Derivatized - MS/MS PE NeoGram Kit	125	1.35	0.18	0.25	0.36	0.7
Non-derivatized - MS/MS PE NeoBase Kit	522	1.21	0.09	0.22	0.43	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	99	1.49	0.21	0.31	0.42	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	58	0.98	0.09	0.26	0.33	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	57	2.08	0.12	0.27	0.63	1.0

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	816	2.28	0.23	0.47	0.39	0.8
Non-derivatized - MS/MS non-kit	198	2.54	0.20	0.51	0.56	0.8
Derivatized - MS/MS PE NeoGram Kit	128	2.07	0.25	0.36	0.36	0.7
Non-derivatized - MS/MS PE NeoBase Kit	526	1.75	0.13	0.32	0.43	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	99	2.17	0.26	0.48	0.42	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	56	1.36	0.16	0.26	0.33	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	3.11	0.14	0.37	0.63	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYISOVALERYLCARNITINE (µmol C5OH/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	909	0.48	0.07	0.12	0.45	0.9
Non-derivatized - MS/MS non-kit	239	0.66	0.08	0.16	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	109	0.44	0.07	0.09	0.42	0.8
Non-derivatized - MS/MS PE NeoBase Kit	525	0.50	0.05	0.10	0.49	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	138	0.44	0.06	0.12	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.44	0.10	0.18	0.40	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.73	0.04	0.06	0.70	1.1

Lot 1562 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	890	1.30	0.16	0.26	0.45	0.9
Non-derivatized - MS/MS non-kit	240	1.51	0.13	0.36	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	108	1.20	0.14	0.21	0.42	0.8
Non-derivatized - MS/MS PE NeoBase Kit	522	1.08	0.08	0.22	0.49	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	139	1.18	0.14	0.32	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.04	0.18	0.40	0.40	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.75	0.10	0.15	0.70	1.1

Lot 1563 - Enriched 2.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	893	2.12	0.23	0.41	0.45	0.9
Non-derivatized - MS/MS non-kit	236	2.44	0.23	0.56	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	108	1.92	0.24	0.34	0.42	0.8
Non-derivatized - MS/MS PE NeoBase Kit	523	1.67	0.12	0.35	0.49	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	139	1.90	0.23	0.49	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.67	0.10	0.52	0.40	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.80	0.14	0.23	0.70	1.1

Lot 1564 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	900	3.09	0.34	0.66	0.45	0.9
Non-derivatized - MS/MS non-kit	240	3.36	0.28	0.81	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	109	2.80	0.39	0.48	0.42	0.8
Non-derivatized - MS/MS PE NeoBase Kit	519	2.30	0.14	0.45	0.49	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	137	2.66	0.32	0.77	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	79	2.42	0.21	0.79	0.40	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	3.95	0.23	0.35	0.70	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17z. 2015 Quality Control Data Summaries of Statistical Analyses
HEXANOYLCARNITINE (µmol C6/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	846	0.03	0.01	0.03	0.04	0.8
Non-derivatized - MS/MS non-kit	198	0.02	0.01	0.01	0.02	0.8
Derivatized - MS/MS PE NeoGram Kit	120	0.03	0.02	0.02	0.07	0.6
Non-derivatized - MS/MS PE NeoBase Kit	631	0.02	0.01	0.01	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	103	0.06	0.03	0.05	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	84	0.02	0.01	0.01	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.01	0.00	0.00	0.01	0.7

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	837	0.43	0.06	0.09	0.04	0.8
Non-derivatized - MS/MS non-kit	196	0.44	0.05	0.09	0.02	0.8
Derivatized - MS/MS PE NeoGram Kit	128	0.42	0.06	0.08	0.07	0.6
Non-derivatized - MS/MS PE NeoBase Kit	659	0.42	0.03	0.05	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.46	0.07	0.08	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.46	0.05	0.07	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.36	0.02	0.04	0.01	0.7

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	837	0.79	0.10	0.17	0.04	0.8
Non-derivatized - MS/MS non-kit	196	0.84	0.09	0.18	0.02	0.8
Derivatized - MS/MS PE NeoGram Kit	129	0.68	0.09	0.10	0.07	0.6
Non-derivatized - MS/MS PE NeoBase Kit	649	0.80	0.06	0.09	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.77	0.11	0.12	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.82	0.07	0.13	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.69	0.04	0.10	0.01	0.7

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	839	1.93	0.19	0.36	0.04	0.8
Non-derivatized - MS/MS non-kit	189	2.05	0.23	0.43	0.02	0.8
Derivatized - MS/MS PE NeoGram Kit	129	1.56	0.16	0.21	0.07	0.6
Non-derivatized - MS/MS PE NeoBase Kit	652	1.96	0.15	0.23	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	1.75	0.20	0.23	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	2.01	0.14	0.22	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.73	0.12	0.23	0.01	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
HEXANOYLCARNITINE (µmol C6/L blood)

Lot 1561 - Nonenriched 0 µmol/L whole blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	881	0.03	0.01	0.02	0.04	0.8
Non-derivatized - MS/MS non-kit	228	0.01	0.00	0.01	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	101	0.03	0.02	0.02	0.08	0.6
Non-derivatized - MS/MS PE NeoBase Kit	692	0.01	0.01	0.01	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	128	0.04	0.01	0.02	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	102	0.01	0.01	0.01	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	37	0.01	0.00	0.00	0.03	0.8

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	901	0.48	0.06	0.11	0.04	0.8
Non-derivatized - MS/MS non-kit	236	0.47	0.05	0.09	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	106	0.41	0.07	0.08	0.08	0.6
Non-derivatized - MS/MS PE NeoBase Kit	716	0.46	0.04	0.05	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	129	0.45	0.07	0.07	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.48	0.03	0.05	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.45	0.03	0.05	0.03	0.8

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	894	0.86	0.10	0.18	0.04	0.8
Non-derivatized - MS/MS non-kit	239	0.87	0.09	0.16	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	107	0.66	0.09	0.14	0.08	0.6
Non-derivatized - MS/MS PE NeoBase Kit	703	0.83	0.05	0.09	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.72	0.08	0.10	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	0.86	0.06	0.09	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.82	0.06	0.12	0.03	0.8

Lot 1562 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	896	2.14	0.23	0.45	0.04	0.8
Non-derivatized - MS/MS non-kit	239	2.18	0.19	0.40	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	107	1.46	0.17	0.28	0.08	0.6
Non-derivatized - MS/MS PE NeoBase Kit	706	2.04	0.12	0.20	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	126	1.61	0.21	0.35	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	2.18	0.15	0.32	0.02	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	2.02	0.14	0.30	0.03	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17aa. 2015 Quality Control Data Summaries of Statistical Analyses
OCTANOYLCARNITINE (µmol C8/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	865	0.03	0.01	0.02	0.03	0.9
Non-derivatized - MS/MS non-kit	260	0.02	0.01	0.01	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	119	0.02	0.02	0.02	0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	643	0.02	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	101	0.03	0.02	0.04	0.03	0.8
Non-derivatized - MS/MSChromsystems MassChrom Kit	88	0.02	0.01	0.01	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	56	0.03	0.01	0.01	0.02	1.0

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	856	0.50	0.06	0.11	0.03	0.9
Non-derivatized - MS/MS non-kit	262	0.50	0.04	0.07	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	125	0.45	0.08	0.09	0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	640	0.47	0.04	0.06	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	105	0.45	0.07	0.08	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	0.42	0.04	0.06	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.51	0.04	0.05	0.02	1.0

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	857	0.95	0.12	0.19	0.03	0.9
Non-derivatized - MS/MS non-kit	266	0.98	0.09	0.15	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	126	0.86	0.12	0.14	0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	644	0.92	0.07	0.10	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.86	0.11	0.13	0.03	0.8
Non-derivatized - MS/MSChromsystems MassChrom Kit	90	0.78	0.06	0.10	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	0.99	0.06	0.09	0.02	1.0

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	858	2.35	0.25	0.41	0.03	0.9
Non-derivatized - MS/MS non-kit	267	2.45	0.20	0.33	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	129	2.21	0.25	0.33	0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	642	2.35	0.17	0.26	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	2.12	0.23	0.30	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	2.04	0.16	0.24	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	59	2.51	0.15	0.17	0.02	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
OCTANOYLCARNITINE (µmol C8/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	909	0.03	0.01	0.02	0.03	1.0
Non-derivatized - MS/MS non-kit	305	0.02	0.01	0.01	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	104	0.02	0.01	0.02	0.03	0.9
Non-derivatized - MS/MS PE NeoBase Kit	711	0.01	0.01	0.01	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	128	0.02	0.01	0.01	0.03	0.9
Non-derivatized - MS/MSChromsystems MassChrom Kit	115	0.02	0.01	0.01	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.02	0.01	0.01	0.02	1.1

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	898	0.57	0.07	0.11	0.03	1.0
Non-derivatized - MS/MS non-kit	315	0.54	0.05	0.07	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	105	0.51	0.08	0.09	0.03	0.9
Non-derivatized - MS/MS PE NeoBase Kit	700	0.52	0.04	0.05	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	124	0.48	0.06	0.07	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	0.47	0.03	0.05	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.61	0.03	0.09	0.02	1.1

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	889	1.05	0.12	0.18	0.03	1.0
Non-derivatized - MS/MS non-kit	304	1.04	0.09	0.13	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	110	0.94	0.14	0.17	0.03	0.9
Non-derivatized - MS/MS PE NeoBase Kit	701	0.98	0.07	0.10	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	123	0.89	0.10	0.12	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	0.89	0.06	0.10	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	1.14	0.07	0.18	0.02	1.1

Lot 1564 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	889	2.61	0.25	0.41	0.03	1.0
Non-derivatized - MS/MS non-kit	307	2.61	0.19	0.28	0.02	1.0
Derivatized - MS/MS PE NeoGram Kit	110	2.34	0.35	0.39	0.03	0.9
Non-derivatized - MS/MS PE NeoBase Kit	712	2.48	0.14	0.24	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	125	2.17	0.21	0.29	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.27	0.15	0.26	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.87	0.19	0.45	0.02	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17bb. 2015 Quality Control Data Summaries of Statistical Analyses
DECANOYLCARNITINE (µmol C10/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	813	0.02	0.01	0.02	0.00	1.0
Non-derivatized - MS/MS non-kit	245	0.02	0.01	0.01	0.00	1.0
Derivatized - MS/MS PE NeoGram Kit	124	0.02	0.01	0.02	0.00	0.7
Non-derivatized - MS/MS PE NeoBase Kit	649	0.02	0.01	0.01	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	97	0.02	0.01	0.02	0.00	0.7
Non-derivatized - MS/MSChromsystems MassChrom Kit	85	0.02	0.01	0.01	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	57	0.02	0.01	0.01	-0.01	1.1

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	833	0.48	0.07	0.12	0.00	1.0
Non-derivatized - MS/MS non-kit	246	0.52	0.04	0.09	0.00	1.0
Derivatized - MS/MS PE NeoGram Kit	127	0.37	0.06	0.07	0.00	0.7
Non-derivatized - MS/MS PE NeoBase Kit	644	0.42	0.04	0.06	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	105	0.38	0.06	0.08	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	0.38	0.04	0.05	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.55	0.04	0.12	-0.01	1.1

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	829	0.93	0.13	0.22	0.00	1.0
Non-derivatized - MS/MS non-kit	244	0.98	0.10	0.19	0.00	1.0
Derivatized - MS/MS PE NeoGram Kit	128	0.72	0.11	0.13	0.00	0.7
Non-derivatized - MS/MS PE NeoBase Kit	650	0.81	0.07	0.10	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.70	0.10	0.14	0.00	0.7
Non-derivatized - MS/MSChromsystems MassChrom Kit	86	0.71	0.06	0.11	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.06	0.08	0.18	-0.01	1.1

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	836	2.40	0.29	0.53	0.00	1.0
Non-derivatized - MS/MS non-kit	248	2.58	0.23	0.48	0.00	1.0
Derivatized - MS/MS PE NeoGram Kit	126	1.86	0.20	0.28	0.00	0.7
Non-derivatized - MS/MS PE NeoBase Kit	638	2.15	0.15	0.26	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	1.86	0.23	0.33	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	1.94	0.14	0.23	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.78	0.21	0.39	-0.01	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
DECANOYLCARNITINE (µmol C10/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	872	0.02	0.01	0.02	0.02	1.0
Non-derivatized - MS/MS non-kit	284	0.02	0.01	0.02	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	108	0.03	0.02	0.03	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	715	0.02	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	127	0.03	0.01	0.02	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	116	0.02	0.01	0.01	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	0.02	0.00	0.01	0.01	1.3

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	876	0.55	0.07	0.12	0.02	1.0
Non-derivatized - MS/MS non-kit	294	0.59	0.06	0.09	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	106	0.42	0.07	0.08	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	700	0.47	0.04	0.06	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.37	0.05	0.08	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	115	0.45	0.05	0.09	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.63	0.06	0.11	0.01	1.3

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	881	1.07	0.14	0.22	0.02	1.0
Non-derivatized - MS/MS non-kit	283	1.16	0.11	0.17	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	106	0.79	0.11	0.15	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	716	0.92	0.06	0.11	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.75	0.09	0.16	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	0.92	0.08	0.20	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.27	0.11	0.21	0.01	1.3

Lot 1564 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	884	2.63	0.28	0.52	0.02	1.0
Non-derivatized - MS/MS non-kit	280	2.87	0.22	0.38	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	107	2.04	0.28	0.34	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	718	2.34	0.15	0.26	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	124	1.76	0.17	0.34	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	117	2.25	0.16	0.44	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	3.14	0.28	0.54	0.01	1.3

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17cc. 2015 Quality Control Data Summaries of Statistical Analyses
DODECANOYLCARNITINE (µmol C12/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	745	0.03	0.02	0.03	0.05	0.9
Non-derivatized - MS/MS non-kit	162	0.01	0.00	0.01	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	128	0.03	0.02	0.02	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	595	0.01	0.00	0.00	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	105	0.07	0.03	0.06	0.11	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	85	0.01	0.01	0.01	0.00	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.01	0.00	0.00	0.02	0.9

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	761	0.48	0.09	0.14	0.05	0.9
Non-derivatized - MS/MS non-kit	161	0.45	0.04	0.09	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	125	0.45	0.07	0.09	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	604	0.41	0.04	0.05	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	104	0.51	0.09	0.14	0.11	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	0.38	0.04	0.05	0.00	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.48	0.04	0.07	0.02	0.9

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	756	0.94	0.15	0.26	0.05	0.9
Non-derivatized - MS/MS non-kit	158	0.87	0.09	0.17	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	127	0.89	0.11	0.17	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	616	0.80	0.07	0.09	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	105	1.05	0.19	0.33	0.11	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	0.71	0.06	0.13	0.00	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.96	0.09	0.11	0.02	0.9

Lot 1468 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	773	2.22	0.29	0.53	0.05	0.9
Non-derivatized - MS/MS non-kit	160	2.14	0.23	0.43	0.02	0.9
Derivatized - MS/MS PE NeoGram Kit	125	2.09	0.24	0.30	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	609	2.04	0.15	0.22	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	102	2.20	0.25	0.41	0.11	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	1.84	0.12	0.18	0.00	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	2.31	0.21	0.21	0.02	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
DODECANOYLCARNITINE (µmol C12/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	780	0.03	0.01	0.03	0.02	1.0
Non-derivatized - MS/MS non-kit	202	0.01	0.00	0.01	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	100	0.04	0.02	0.03	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	650	0.01	0.00	0.01	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	124	0.05	0.02	0.03	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	106	0.01	0.00	0.01	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	36	0.01	0.00	0.00	0.00	1.1

Lot 1562 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	791	0.98	0.14	0.25	0.02	1.0
Non-derivatized - MS/MS non-kit	190	1.01	0.12	0.22	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	99	0.94	0.14	0.15	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	669	0.92	0.06	0.09	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.95	0.11	0.22	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	104	0.85	0.06	0.09	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	39	1.06	0.06	0.13	0.00	1.1

Lot 1563 - Enriched 2.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	793	1.89	0.23	0.46	0.02	1.0
Non-derivatized - MS/MS non-kit	190	2.02	0.22	0.49	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	100	1.83	0.25	0.30	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	659	1.82	0.11	0.16	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	124	1.82	0.16	0.32	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	106	1.68	0.13	0.21	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	2.13	0.15	0.29	0.00	1.1

Lot 1564 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	792	2.94	0.35	0.68	0.02	1.0
Non-derivatized - MS/MS non-kit	190	3.01	0.29	0.62	0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	98	2.81	0.39	0.43	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	667	2.83	0.18	0.26	-0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	122	2.78	0.29	0.48	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	105	2.62	0.18	0.27	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	3.24	0.19	0.46	0.00	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17dd. 2015 Quality Control Data Summaries of Statistical Analyses MYRISTOYLCARNITINE (µmol C14/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	819	0.06	0.02	0.03	0.05	1.0
Non-derivatized - MS/MS non-kit	175	0.04	0.01	0.01	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	126	0.06	0.02	0.02	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	622	0.04	0.01	0.01	0.02	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	113	0.08	0.03	0.05	0.08	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	0.03	0.01	0.01	0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	28	0.04	0.00	0.00	0.01	1.1

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	820	0.53	0.07	0.10	0.05	1.0
Non-derivatized - MS/MS non-kit	179	0.53	0.05	0.07	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	125	0.50	0.07	0.08	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	628	0.48	0.04	0.05	0.02	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	0.49	0.08	0.08	0.08	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.43	0.04	0.08	0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.54	0.03	0.04	0.01	1.1

Lot 1467 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	826	1.47	0.17	0.27	0.05	1.0
Non-derivatized - MS/MS non-kit	180	1.49	0.14	0.23	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	128	1.36	0.15	0.20	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	635	1.40	0.10	0.15	0.02	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	1.30	0.17	0.19	0.08	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	1.22	0.09	0.20	0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.62	0.12	0.13	0.01	1.1

Lot 1468 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	824	2.94	0.34	0.51	0.05	1.0
Non-derivatized - MS/MS non-kit	179	3.02	0.26	0.44	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	127	2.73	0.28	0.41	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	626	2.81	0.20	0.30	0.02	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	114	2.54	0.25	0.34	0.08	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	2.51	0.14	0.34	0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	3.30	0.29	0.30	0.01	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
MYRISTOYLCARNITINE (µmol C14/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	870	0.06	0.02	0.03	0.06	1.0
Non-derivatized - MS/MS non-kit	226	0.05	0.01	0.01	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	108	0.07	0.02	0.02	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	684	0.04	0.01	0.01	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	0.07	0.02	0.03	0.07	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	0.03	0.01	0.01	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.04	0.01	0.01	0.04	1.0

Lot 1562 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	872	0.56	0.07	0.11	0.06	1.0
Non-derivatized - MS/MS non-kit	235	0.55	0.05	0.10	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	109	0.50	0.09	0.10	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	688	0.48	0.04	0.06	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	125	0.47	0.05	0.08	0.07	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	0.44	0.03	0.04	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	39	0.54	0.03	0.04	0.04	1.0

Lot 1563 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	868	1.52	0.18	0.26	0.06	1.0
Non-derivatized - MS/MS non-kit	230	1.57	0.14	0.30	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	108	1.33	0.16	0.21	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	674	1.38	0.09	0.13	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	129	1.18	0.12	0.24	0.07	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	1.27	0.08	0.12	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	1.56	0.11	0.15	0.04	1.0

Lot 1564 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	866	3.00	0.31	0.50	0.06	1.0
Non-derivatized - MS/MS non-kit	233	3.10	0.26	0.51	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	107	2.76	0.27	0.37	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	685	2.76	0.17	0.25	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	118	2.34	0.21	0.31	0.07	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	106	2.52	0.17	0.25	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	3.06	0.19	0.32	0.04	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17ee. 2015 Quality Control Data Summaries of Statistical Analyses PALMITOYLCARNITINE (µmol C16/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	845	0.79	0.10	0.15	0.86	0.9
Non-derivatized - MS/MS non-kit	196	0.81	0.07	0.13	0.87	0.9
Derivatized - MS/MS PE NeoGram Kit	130	0.74	0.10	0.13	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	654	0.72	0.06	0.08	0.76	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	106	0.81	0.11	0.15	0.87	0.8
Non-derivatized - MS/MSChromsystems MassChrom Kit	89	0.70	0.06	0.09	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.86	0.06	0.11	0.92	0.9

Lot 1466 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	858	3.44	0.33	0.45	0.86	0.9
Non-derivatized - MS/MS non-kit	199	3.64	0.30	0.56	0.87	0.9
Derivatized - MS/MS PE NeoGram Kit	124	3.07	0.29	0.41	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	656	3.27	0.23	0.34	0.76	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	106	3.44	0.33	0.42	0.87	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	3.28	0.26	0.40	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	3.66	0.25	0.35	0.92	0.9

Lot 1467 - Enriched 8.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	864	7.81	0.77	1.13	0.86	0.9
Non-derivatized - MS/MS non-kit	197	8.25	0.76	1.19	0.87	0.9
Derivatized - MS/MS PE NeoGram Kit	126	7.27	0.69	0.96	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	650	7.55	0.55	0.77	0.76	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	109	7.68	0.74	1.04	0.87	0.8
Non-derivatized - MS/MSChromsystems MassChrom Kit	85	7.41	0.53	0.62	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	8.34	0.55	0.70	0.92	0.9

Lot 1468 - Enriched 12.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	860	11.00	0.99	1.51	0.86	0.9
Non-derivatized - MS/MS non-kit	200	11.70	0.87	1.69	0.87	0.9
Derivatized - MS/MS PE NeoGram Kit	129	10.27	0.97	1.42	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	653	10.68	0.75	1.10	0.76	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	107	10.93	0.99	1.23	0.87	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	10.72	0.73	1.01	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	11.75	0.84	1.21	0.92	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
PALMITOYLCARNITINE (µmol C16/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	921	0.74	0.09	0.13	0.72	0.9
Non-derivatized - MS/MS non-kit	244	0.75	0.07	0.11	0.73	0.9
Derivatized - MS/MS PE NeoGram Kit	108	0.63	0.10	0.11	0.60	0.8
Non-derivatized - MS/MS PE NeoBase Kit	702	0.65	0.05	0.07	0.57	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	126	0.69	0.08	0.11	0.62	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.64	0.05	0.07	0.63	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	0.75	0.04	0.05	0.71	1.0

Lot 1562 - Enriched 4.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	925	4.28	0.41	0.61	0.72	0.9
Non-derivatized - MS/MS non-kit	249	4.45	0.37	0.70	0.73	0.9
Derivatized - MS/MS PE NeoGram Kit	109	3.76	0.45	0.58	0.60	0.8
Non-derivatized - MS/MS PE NeoBase Kit	709	3.91	0.25	0.36	0.57	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	128	3.96	0.35	0.46	0.62	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	3.93	0.22	0.33	0.63	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	49	4.60	0.25	0.36	0.71	1.0

Lot 1563 - Enriched 8.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	912	7.47	0.68	1.03	0.72	0.9
Non-derivatized - MS/MS non-kit	243	8.01	0.73	1.22	0.73	0.9
Derivatized - MS/MS PE NeoGram Kit	109	6.54	0.69	1.10	0.60	0.8
Non-derivatized - MS/MS PE NeoBase Kit	710	7.03	0.42	0.63	0.57	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	127	7.06	0.50	0.79	0.62	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	7.09	0.49	0.68	0.63	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	8.33	0.50	0.76	0.71	1.0

Lot 1564 - Enriched 12.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	925	11.30	1.01	1.57	0.72	0.9
Non-derivatized - MS/MS non-kit	249	11.89	0.89	1.72	0.73	0.9
Derivatized - MS/MS PE NeoGram Kit	107	10.00	1.06	1.65	0.60	0.8
Non-derivatized - MS/MS PE NeoBase Kit	705	10.78	0.64	0.96	0.57	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	127	10.77	0.78	1.21	0.62	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	10.49	0.64	0.87	0.63	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	12.44	0.74	1.14	0.71	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17ff. 2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYPALMITOYLCARNITINE (µmol C16OH/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	830	0.02	0.01	0.02	0.01	0.7
Non-derivatized - MS/MS non-kit	179	0.01	0.00	0.01	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	126	0.02	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	642	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	96	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	84	0.01	0.00	0.01	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.01	0.00	0.00	0.00	0.7

Lot 1466 - Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	823	0.19	0.03	0.05	0.01	0.7
Non-derivatized - MS/MS non-kit	178	0.18	0.02	0.03	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	124	0.17	0.03	0.03	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	627	0.15	0.01	0.02	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	98	0.19	0.04	0.07	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	86	0.17	0.04	0.07	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.16	0.01	0.05	0.00	0.7

Lot 1467 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	823	0.35	0.06	0.10	0.01	0.7
Non-derivatized - MS/MS non-kit	178	0.34	0.04	0.06	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	128	0.33	0.05	0.07	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	626	0.29	0.03	0.04	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	99	0.37	0.06	0.09	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	85	0.30	0.06	0.13	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	69	0.34	0.02	0.07	0.00	0.7

Lot 1468 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	828	0.70	0.09	0.18	0.01	0.7
Non-derivatized - MS/MS non-kit	183	0.70	0.09	0.14	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	130	0.67	0.09	0.14	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	626	0.60	0.05	0.08	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	91	0.72	0.09	0.13	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.65	0.09	0.25	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.69	0.05	0.14	0.00	0.7

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYPALMITOYLCARNITINE (µmol C16OH/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	879	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS non-kit	233	0.01	0.00	0.01	0.00	0.8
Derivatized - MS/MS PE NeoGram Kit	94	0.01	0.01	0.01	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	718	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	123	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	93	0.00	0.00	0.00	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.00	0.00	0.00	0.00	0.8

Lot 1562 - Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	878	0.20	0.03	0.05	0.01	0.7
Non-derivatized - MS/MS non-kit	242	0.20	0.03	0.06	0.00	0.8
Derivatized - MS/MS PE NeoGram Kit	99	0.19	0.04	0.04	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	696	0.16	0.02	0.03	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	121	0.19	0.03	0.05	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	0.15	0.01	0.05	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.21	0.02	0.06	0.00	0.8

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	876	0.74	0.08	0.15	0.01	0.7
Non-derivatized - MS/MS non-kit	239	0.78	0.09	0.23	0.00	0.8
Derivatized - MS/MS PE NeoGram Kit	100	0.68	0.09	0.12	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	710	0.62	0.04	0.08	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	118	0.71	0.07	0.12	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	93	0.56	0.04	0.14	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.80	0.05	0.26	0.00	0.8

Lot 1564 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	884	1.13	0.12	0.24	0.01	0.7
Non-derivatized - MS/MS non-kit	237	1.18	0.13	0.33	0.00	0.8
Derivatized - MS/MS PE NeoGram Kit	98	1.04	0.16	0.23	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	704	0.94	0.07	0.12	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	116	1.06	0.13	0.20	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	94	0.88	0.07	0.25	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.21	0.08	0.39	0.00	0.8

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17gg. 2015 Quality Control Data Summaries of Statistical Analyses
STEAROYLCARNITINE (µmol C18/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	796	0.64	0.08	0.13	0.67	0.9
Non-derivatized - MS/MS non-kit	157	0.64	0.06	0.08	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	119	0.63	0.08	0.11	0.63	0.9
Non-derivatized - MS/MS PE NeoBase Kit	646	0.63	0.05	0.06	0.64	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	104	0.65	0.09	0.11	0.65	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.59	0.06	0.13	0.60	0.9

Lot 1466 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	810	1.54	0.18	0.29	0.67	0.9
Non-derivatized - MS/MS non-kit	158	1.56	0.14	0.21	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	117	1.49	0.15	0.19	0.63	0.9
Non-derivatized - MS/MS PE NeoBase Kit	646	1.57	0.11	0.14	0.64	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	108	1.52	0.22	0.29	0.65	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	1.44	0.14	0.31	0.60	0.9

Lot 1467 - Enriched 2.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	811	2.42	0.26	0.44	0.67	0.9
Non-derivatized - MS/MS non-kit	154	2.46	0.22	0.32	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	118	2.44	0.24	0.34	0.63	0.9
Non-derivatized - MS/MS PE NeoBase Kit	656	2.52	0.18	0.25	0.64	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	2.42	0.29	0.39	0.65	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	2.32	0.21	0.47	0.60	0.9

Lot 1468 - Enriched 5.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	804	4.97	0.50	0.88	0.67	0.9
Non-derivatized - MS/MS non-kit	154	5.17	0.37	0.75	0.64	0.9
Derivatized - MS/MS PE NeoGram Kit	118	5.01	0.49	0.64	0.63	0.9
Non-derivatized - MS/MS PE NeoBase Kit	654	5.30	0.38	0.54	0.64	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	104	5.02	0.50	0.68	0.65	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	4.84	0.40	0.82	0.60	0.9

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
STEAROYLCARNITINE (µmol C18/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	862	0.64	0.09	0.14	0.63	0.9
Non-derivatized - MS/MS non-kit	203	0.64	0.06	0.10	0.63	0.9
Derivatized - MS/MS PE NeoGram Kit	105	0.63	0.10	0.12	0.61	0.9
Non-derivatized - MS/MS PE NeoBase Kit	685	0.60	0.04	0.06	0.58	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	119	0.58	0.09	0.19	0.55	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	0.55	0.05	0.07	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	0.62	0.04	0.04	0.60	1.0

Lot 1562 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	856	1.55	0.17	0.31	0.63	0.9
Non-derivatized - MS/MS non-kit	205	1.58	0.13	0.23	0.63	0.9
Derivatized - MS/MS PE NeoGram Kit	109	1.52	0.20	0.23	0.61	0.9
Non-derivatized - MS/MS PE NeoBase Kit	704	1.55	0.11	0.16	0.58	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	116	1.44	0.16	0.33	0.55	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	1.42	0.09	0.12	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	47	1.59	0.08	0.09	0.60	1.0

Lot 1563 - Enriched 3.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	844	3.19	0.33	0.59	0.63	0.9
Non-derivatized - MS/MS non-kit	205	3.40	0.25	0.44	0.63	0.9
Derivatized - MS/MS PE NeoGram Kit	110	3.12	0.31	0.41	0.61	0.9
Non-derivatized - MS/MS PE NeoBase Kit	690	3.30	0.22	0.31	0.58	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	116	3.04	0.28	0.68	0.55	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	3.11	0.21	0.29	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	3.49	0.23	0.24	0.60	1.0

Lot 1564 - Enriched 5.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	851	5.09	0.53	0.93	0.63	0.9
Non-derivatized - MS/MS non-kit	210	5.35	0.37	0.73	0.63	0.9
Derivatized - MS/MS PE NeoGram Kit	109	5.06	0.60	0.72	0.61	0.9
Non-derivatized - MS/MS PE NeoBase Kit	695	5.33	0.32	0.47	0.58	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	117	4.97	0.52	1.00	0.55	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	107	4.82	0.33	0.44	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	48	5.55	0.32	0.34	0.60	1.0

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17hh. 2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYSTEAROYLCARNITINE (µmol C18OH/L blood)

Lot 1465 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	609	0.01	0.01	0.02	0.01	0.6
Non-derivatized - MS/MS non-kit	95	0.01	0.00	0.01	0.01	0.5
Derivatized - MS/MS PE NeoGram Kit	121	0.01	0.01	0.01	0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	542	0.00	0.00	0.00	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	84	0.01	0.01	0.01	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	85	0.01	0.00	0.01	0.01	0.5

Lot 1466 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	614	0.31	0.06	0.11	0.01	0.6
Non-derivatized - MS/MS non-kit	98	0.27	0.03	0.11	0.01	0.5
Derivatized - MS/MS PE NeoGram Kit	128	0.31	0.05	0.07	0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	535	0.28	0.02	0.04	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.35	0.10	0.15	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.26	0.04	0.12	0.01	0.5

Lot 1467 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	615	0.61	0.09	0.22	0.01	0.6
Non-derivatized - MS/MS non-kit	96	0.52	0.07	0.23	0.01	0.5
Derivatized - MS/MS PE NeoGram Kit	127	0.60	0.08	0.12	0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	537	0.55	0.05	0.08	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	87	0.67	0.11	0.20	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	0.48	0.08	0.23	0.01	0.5

Lot 1468 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	594	0.94	0.13	0.27	0.01	0.6
Non-derivatized - MS/MS non-kit	98	0.80	0.08	0.40	0.01	0.5
Derivatized - MS/MS PE NeoGram Kit	130	0.91	0.11	0.18	0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	540	0.85	0.07	0.13	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	86	0.99	0.11	0.30	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	87	0.73	0.10	0.37	0.01	0.5

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

2015 Quality Control Data Summaries of Statistical Analyses
HYDROXYSTEAROYLCARNITINE (µmol C18OH/L blood)

Lot 1561 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	627	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS non-kit	136	0.01	0.00	0.01	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	96	0.01	0.01	0.01	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	586	0.00	0.00	0.01	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	99	0.01	0.00	0.01	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	93	0.00	0.00	0.00	0.00	0.5

Lot 1562 - Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	631	0.18	0.03	0.06	0.01	0.7
Non-derivatized - MS/MS non-kit	135	0.17	0.03	0.12	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	99	0.18	0.04	0.04	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	566	0.15	0.02	0.02	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.19	0.03	0.07	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	96	0.12	0.02	0.04	0.00	0.5

Lot 1563 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	648	0.68	0.09	0.20	0.01	0.7
Non-derivatized - MS/MS non-kit	135	0.70	0.11	0.45	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	98	0.66	0.09	0.12	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	568	0.60	0.04	0.07	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.69	0.10	0.19	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	0.52	0.05	0.15	0.00	0.5

Lot 1564 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
Derivatized - MS/MS non-kit	628	1.00	0.12	0.26	0.01	0.7
Non-derivatized - MS/MS non-kit	135	1.02	0.10	0.70	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	99	0.97	0.14	0.20	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	592	0.89	0.06	0.12	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.96	0.12	0.29	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	97	0.76	0.09	0.19	0.00	0.5

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17ii. 2015 Quality Control Data Summaries of Statistical Analyses
24:0-LYSOPHOSPHATIDYLCHOLINE (µmol 24LPC/L blood)

Lot 14101 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	50	0.09	0.02	0.08	0.12	1.0
FIA-MS/MS	30	0.30	0.09	0.12	0.28	1.4

Lot 14102 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	49	1.10	0.20	0.46	0.12	1.0
FIA-MS/MS	30	1.65	0.29	0.29	0.28	1.4

Lot 14103 - Enriched 5.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	50	4.87	1.05	2.00	0.12	1.0
FIA-MS/MS	30	7.25	1.23	1.23	0.28	1.4

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

Table 17jj. 2015 Quality Control Data Summaries of Statistical Analyses
26:0 LYSOPHOSPHATIDYLCHOLINE (µmol 26LPC/L blood)

Lot 14101 - Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	50	0.06	0.01	0.08	0.08	0.9
FIA-MS/MS	40	0.26	0.11	0.12	0.27	1.1

Lot 14102 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	50	1.00	0.14	0.24	0.08	0.9
FIA-MS/MS	40	1.34	0.32	0.40	0.27	1.1

Lot 14103 - Enriched 5.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept*	Slope
LC-MS/MS	50	4.51	0.46	0.84	0.08	0.9
FIA-MS/MS	39	5.61	0.99	1.55	0.27	1.1

*Estimated by performing a weighted linear regression analysis of mean reported concentrations versus enriched concentrations and extrapolating the regression to the Y-axis.

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