Newborn Screening Quality Assurance Program

2010 ANNUAL SUMMARY REPORT

Volume 28 January 2011

INTRODUCTION

The Centers for Disease Control and Prevention's (CDC) Newborn Screening Quality Assurance Program (NSQAP) is designed to help screening laboratories achieve excellent technical proficiency and maintain confidence in their performance while processing large volumes of specimens daily. CDC continually strives to produce certified dried-blood spot (DBS) materials for reference and quality control (QC) analysis, to improve the quality and scope of services, and to provide immediate consultative assistance. By working closely with program participants, we make necessary adjustments to meet their growing and changing needs. CDC always welcomes comments and suggestions about how we may better serve the newborn screening laboratories.

A major public health responsibility, newborn screening for detection of treatable, inherited metabolic diseases is a system consisting of six parts: education, screening, follow-up, diagnosis, management, and evaluation. Effective screening of newborns by use of DBS specimens collected at birth, combined with follow-up diagnostic studies and treatment, helps prevent mental retardation and premature death. These blood specimens are collected routinely from more than 98% of all newborns in the United States. State public health laboratories or their associated laboratories routinely screen DBS specimens for inborn errors of metabolism and other disorders that require intervention. For more than 32 years, CDC, with its cosponsor the Association of Public Health Laboratories (APHL) has conducted research on materials development and assisted laboratories with quality assurance (QA) for these DBS screening tests. The QA services primarily support newborn screening tests performed by state laboratories; however, CDC also accepts other laboratories and international participants into the QA program. All laboratories in the United States that test DBS specimens participate voluntarily in NSQAP. The program provides QA services for congenital hypothyroidism (CH), phenylketonuria, galactosemia, congenital adrenal hyperplasia, maple syrup urine disease, homocystinuria, tyrosinemia, citrullinemia, argininemia, biotinidase deficiency, cystic fibrosis (CF), and hemoglobinopathies. QA services are also provided for urea cycle disorders, fatty acid oxidation disorders, and organic acid metabolic disorders.

The QA program consists of two DBS distribution components: QC materials for periodic use and quarterly proficiency testing (PT). The QC program enables laboratories to achieve high levels of technical proficiency and continuity that transcend changes in commercial assay reagents while maintaining the requisite high-volume specimen throughput. The QC materials, which supplement the participants' method- or kit-control materials, allow participants to monitor the long-term stability of their assays. The PT program provides laboratories with quarterly panels of blind-coded DBS specimens and provides an independent external assessment of each laboratory's performance. DBS materials for QC and PT are certified for homogeneity, accuracy, stability, and suitability for kits manufactured by different commercial sources.

Over the last ten years, NSQAP has grown substantially, both in the number of participants and in the scope of global participation. In 2010, 463 newborn screening laboratories in 67 countries (at least one laboratory per country) were active program participants (Figure 1); of these, 391 participated in the PT component (Figure 2) and 337 in the QC part (Figure 3). Proficiency testing data by use of tandem mass spectrometry (MS/MS)

DEPARTMENT OF HEALTH AND HUMAN SERVICES
Centers for Disease Control and Prevention (CDC)
and the
Association of Public Health Laboratories

NSQAP
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Program Information Web site:
http://www.cdc.gov/labstandards/nsqap.html

Data-reporting Web site:
https://wwwn.cdc.gov/nsqap/public/default.aspx

was reported by 222 laboratories; of these, 61 were domestic laboratories. MS/MS has made a major impact on the data reported to NSQAP. DBS materials for 38 analytes, covering primary markers for 48 disorders, were distributed to participating laboratories (Figures 2–3). This report presents an overview of all phases of the PT program and summarizes all QC data reported in 2010. For biotinidase, galactose-1-phosphate uridyltransferase (GALT) deficiency, and hemoglobins, QC materials were not distributed because of the limited availability of appropriate blood sources.

NEW ACTIVITIES

The Newborn Screening for Severe Combined Immunodeficiency (SCID): Implementation, Challenges and Updates meeting was held in Atlanta Georgia October 27–28, 2010. Following the meeting, CDC's NSQAP hosted a laboratory demonstration for the in situ method to test for T-cell Receptor Excision Circles (TREC). Attendees of the meeting represented state newborn screening laboratories, newborn screening follow-up personnel, physicians, and newborn screening stakeholders. Health and Human Services Secretary, Kathleen Sebelius, recommended in 2010 that all states screen newborns for SCID. The SCID test was the first primary molecular test to be introduced into newborn screening laboratories and will require that states gain new skills and molecular methods.

July 5–7, 2010, the Joint Advisory Committee on Agent Orange/Dioxin held a national newborn screening workshop in Hanoi, Vietnam on surveillance and prevention of birth defects. The workshop was a collaborative effort between the government of Vietnam and CDC. Dr. Joanne Mei represented NSQAP. The goal of the workshop was to review current newborn screening activities in Vietnam.

Dr. Harry Hannon was contracted to continue his work with NSMBB after his retirement as branch chief in January 2009; he completed his contractual work in August 2010.

The latest additions to the PT program in 2010 were Arginine (Arg), C4OH, C5:1 and C16OH. These analytes were also added to the UDOT program. Furthermore, NSQAP began evaluating the addition of C18:1 to its PT panels for distribution beginning January 2011. The NSQAP MS/MS panels now cover all primary biomarkers for 41 of the 42 MS/MS detectable core and secondary target disorders included in the American College of Medical Genetics (ACMG) recommended uniform panel

2010
NSQAP
BY THE NUMBERS

100 percentage of states covered

67 countries participated

717,255 DBS produced

28 employees

36 new enrollments

21 labs moved to inactive status

463 labs enrolled at year end

456 labs reported data

391 labs participated in PT

337 labs participated in QC

17 reports provided to participants

4 filter paper lots evaluated

31 US labs participated when NSQAP was established in 1978

Source: Newborn Screening Quality Assurance Program, December 2010

for newborn screening programs (hearing tests excluded) (2). The acylcarnitine C10:2 is currently being synthesized and, once received, will complete the panel of analytes required for full-coverage of the ACMG-recommended primary and secondary newborn screening disorders.

We encourage everyone to continue reporting their NSQAP QC data by the e-mail data-reporting system. Online web-based data entry is also being considered for the year 2012 to expedite data entry.

In April 2010, UDOT, a special PT panel, replaced one of the PT events within NSQAP's routine quarterly PT program. Seventy-one laboratories in the United States and Canada participated. All interactions between NSQAP and participants were handled completely by e-mail. There was a 16-day time period between shipping day and data deadline. Most participants liked UDOT because the PT simulated clinical screening practices. The report for this program can be found online at http://www.cdc.gov/labstandards/nsqap_reports.html.

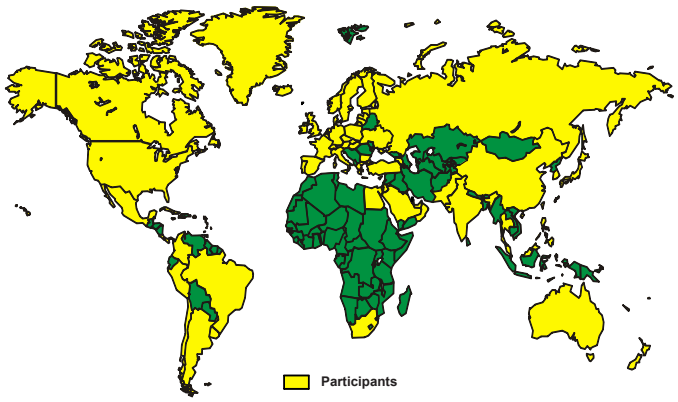
NSQAP continued a PT program for laboratories testing DBS for IgM antibodies to Toxoplasma gondii. The program had thirteen participants; most were from outside the United States. Quarterly reports for this program can be found online at http://www.cdc.gov/labstandards/nsqap_reports.html.

In 2010, the Quality Assurance/Quality Control Subcommittee of the Newborn Screening and Genetics in Public Health sponsored by APHL met twice in Atlanta. One mission component of this subcommittee is to provide guidance to the NSQAP on procedures, policies, and activities for the quality assessment of laboratory testing. We believe that input from this subcommittee will enhance our continuing efforts to better serve our participants.

NSQAP continued the pilot PT program to investigate materials and clinical interpretations, based on the ratio of 17 OHP, androstenedione, cortisol, 21-deoxycortisol, and 11-deoxycortisol for second tier Congenital Adrenal Hyperplasia (CAH) screening by use of liquid chromatography-tandem mass spectrometry. Ten laboratories participated in three quarterly surveys, and two new laboratories will be added in 2011.

In 2010, NSQAP continued the CF Mutation Detection PT program for DNA testing (CFDNA) which included 59 participants. The quarterly CFDNA data are summarized in reports posted at http://www.cdc.gov/labstandards/nsqap_reports.html. The CDC CFDNA DBS Repository now includes all 23 of the ACMG-recommended mutation

FIGURE 1. Sixty-seven Countries Participated in the Newborn Screening Quality Assurance Program in 2010



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

One or more laboratories represented for each country listed.

panel (1) for population screening and 20 other less common mutations or sequence polymorphisms.

APHL, the National Newborn Screening and Genetics Resource Center, the National Laboratory Training Network, and CDC's Newborn Screening and Molecular Biology Branch (NSMBB) co-sponsored the Newborn Screening Molecular Training Workshop: Using CF as a Model. The hands-on workshop was held in March of 2010 at the NSMBB laboratories in Atlanta, GA and covered screening and diagnostic procedures along with follow-up information for CF.

MASS SPECTROMETRY WORKGROUP

NSQAP's Mass Spectrometry Workgroup serves as a clearinghouse for MS/MS services and research for its participants. The workgroup is comprised of seven members tasked with providing NSQAP participants with QC and PT materials for amino acids, acylcarnitines, second-tier CAH and MSUD testing. In addition, workgroup members conduct research to expand NSQAP's analytical capabilities beyond the dried-blood spot.

QC and PT MS/MS panels now cover all primary biomarkers for 41 of the 42 MS/MS-detectable core and secondary target disorders listed in the ACMG-recommended uniform screening panel (2). The workgroup commissioned the synthesis of C10:2 to complete NSQAP's coverage of ACMG-recommended primary markers for all core and secondary target disorders. In addition, NSQAP will introduce C18:1 in its PT panels beginning January 2011. Furthermore, workgroup members developed blood pools that contain amino acids, acylcarnitines, and SUAC together in a single blood spot. We have a limited quantity of cards to distribute to interested NSQAP participants.

To further its mission, the workgroup has developed a pilot PT program to evaluate the use of MS/MS analyte ratios starting in January 2011. The pilot PT program will consist of ten specimens that have been prepared to simulate specific disorders which can identified through the use of concentration ratios for two or more amino acid or acylcarnitine biomarkers during routine screening. Participating laboratories in the United States and Canada that perform MS/MS analysis will be asked to identify and quantify the abnormal biomarkers present, as well as the concentration ratios used to establish a presumptive positive classification on the specimens. In addition, laboratories will be asked to comment on the specimens' presumptive disorder profiles.

Workgroup members welcome the opportunity to investigate new analytes and mass spectrometry-based methods to serve the needs of our participants. For more information about NSQAP's Mass Spectrometry Workgroup or any of its current projects, please contact Dr. Víctor R. De Jesús at vdejesus@cdc.gov.

NEWBORN SCREENING TRANSLATION RESEARCH INITIATIVE

The CDC Newborn Screening Translation Research Initiative (NSTRI) completed its fifth year of operation in 2010. NSTRI is an ongoing collaboration between the CDC Foundation and the CDC Newborn Screening and Molecular Biology Branch. The vision of NSTRI is the methodical expansion of newborn screening to detect

Figure 2. Number of Participants in Proficiency Testing Program, 2010
Total - 391

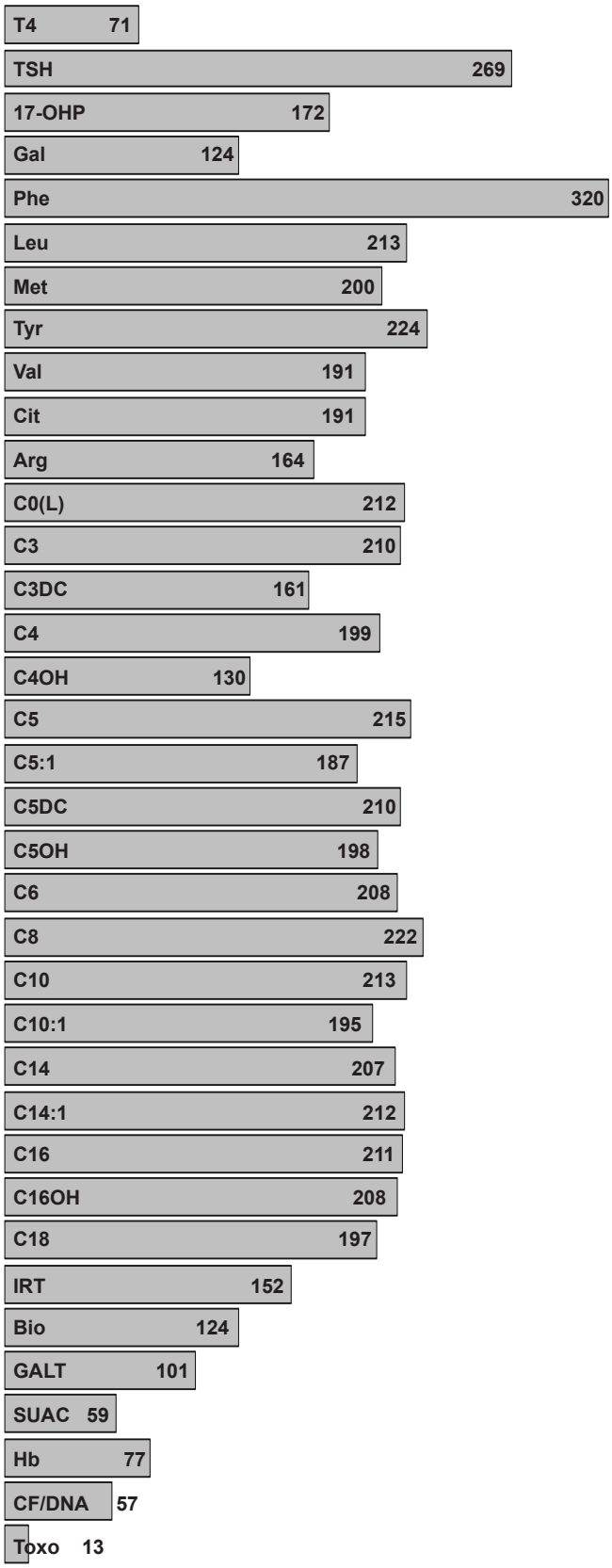
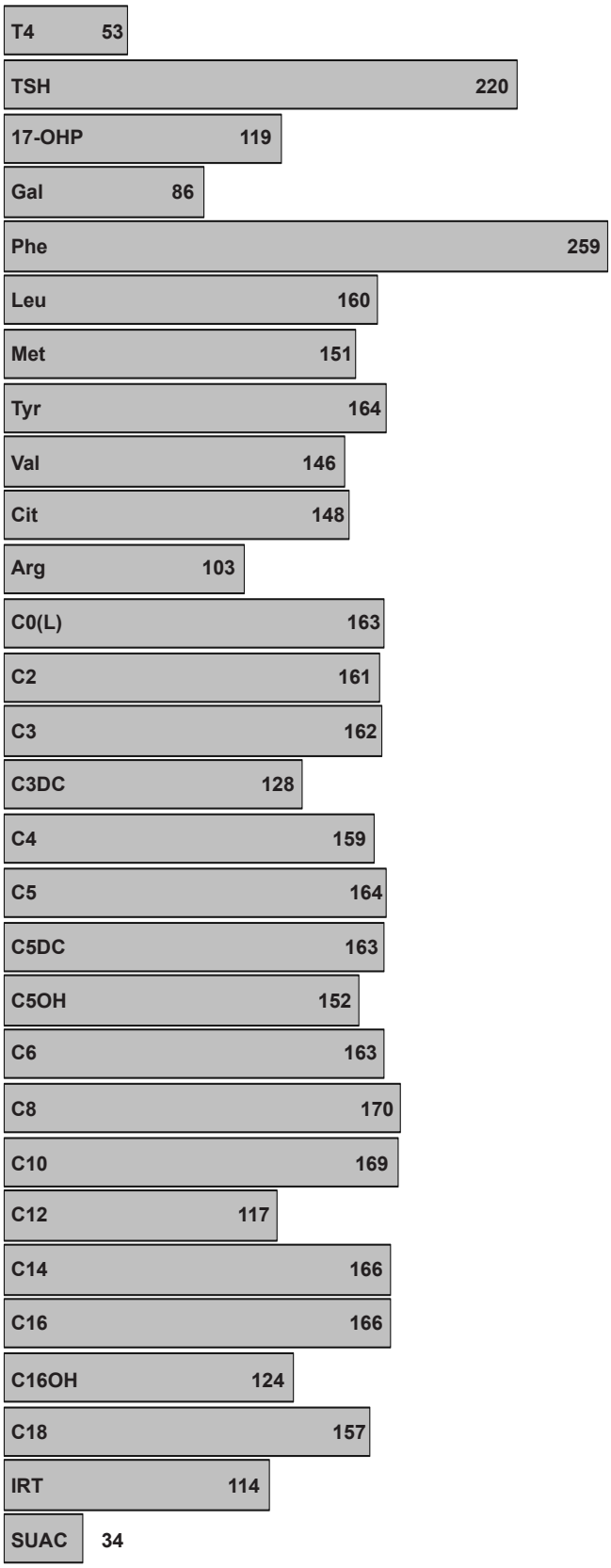


Figure 3. Number of Participants in Quality Control Program, 2010
Total - 337



more conditions in more infants around the world so that all babies with identified congenital disorders have a better chance for a healthy childhood. The mission of NSTRI is to assemble public, academic, foundation, and corporate partnerships for the scientific and financial support of translational research efforts in newborn screening.

Translation research is often described as the process of moving biomedical research findings "from bench to bedside," but a better description for NSTRI would be "from bench to bassinet." One of the most critical processes in translating laboratory research methods to practical newborn screening assays is the integration of quality assurance systems. The ultimate goal of NSTRI is to help transform research methods into routine assays that become part of NSQAP as they are adapted for routine population-based newborn screening. All NSTRI projects include collaboration with public health newborn screening programs.

During its fifth year of operation, NSTRI focused particularly on supporting the implementation of newborn screening (NBS) for SCID in public health newborn screening programs. NSTRI increased production of DBS reference materials for the TREC assay used to detect SCID and orchestrated multi-laboratory evaluations of the materials, expanding the ongoing collaboration with Wisconsin and Massachusetts to include other NBS programs. Even with the focus on SCID, work continued on developing NBS tests to detect other congenital disorders including lysosomal storage disorders, cytomegalovirus infection, and neuromental disorders such as epilepsy and autism. More than a dozen partnerships were involved in these projects, and many of the partners contributed both scientific and financial support.

For more information about NSTRI or any of its current projects, please contact Dr. Robert Vogt at rvogt@cdc.gov. Ideas for new projects and partnerships are welcomed.

NEWBORN SCREENING MOLECULAR NETWORK

The NBS Molecular Network was initiated by Drs. Suzanne Cordovado and Christopher Greene of the CDC's NSMBB in partnership with the APHL. This network was created to identify gaps and address quality assurance needs as public health NBS laboratories introduce more molecular assays into their routine testing. Molecular analysis was first introduced into NBS laboratories in 2004 as a second-tier screen for CF. In 2010, SCID was added to the recommended panel of NBS screening disorders, which hallmarks the first disorder that requires a primary molecular test. Thus, a great need now exists for molecular specific NBS laboratory support that is unique to the dried-blood spot matrix. The NBS Molecular Network was introduced to the NBS community in an evening forum at the May 2010 Newborn Screening and Genetic Testing Symposium in Orlando, FL. The intent of the NBS Molecular Network is to bring together leading public health scientists in a collaborative forum to address NBS molecular laboratory screening, quality molecular testing, and educational needs of NBS laboratories. For more information about the NBS Molecular Network, please contact Dr. Suzanne K. Cordovado at scordovado@cdc.gov.

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New countries joined NSQAP:

Bahrain, Bulgaria, El Salvador, Jordan, Kuwait, Oman, Qatar

FILTER PAPER

Each year, with the extensive cooperation of the manufacturers (Whatman Inc., Fairfield, NJ, and Ahlstrom Filtration LLC, Holly Springs, PA), we routinely evaluate new lots and compare new lots with previous lots of filter paper approved (cleared) by the Food and Drug Administration (FDA) for blood collection. The criteria for acceptable performance are the limits established in the CLSI standard (3). A manufacturer also is expected to establish its own testing program using the CLSI standard and to make available to the user its certification data for each distributed lot of paper. The independent evaluations

Filter paper lots used in the CDC production of QC and PT specimens distributed in 2010 were W051, W071, and W083 of Grade 903 and 8040201 and 0120201 of Grade 226.

Omar Retires

L. Omar Henderson, Ph.D., a research chemist working on the NSQAP team with 34 years of government service, retired January 1, 2011. Omar earned his B.S. in chemistry from Syracuse University and his M.S. and Ph.D. in Physiological Chemistry from the University of Maryland.

After working many summers with the D.C. Department of Public Health and completing his Ph.D., he accepted a job at the National Institutes of Health, NHLBI, followed by a position at Brown University Medical School as a teacher and research scientist. Omar came to CDC in 1984 hired by Dr. W. Harry Hannon. At the beginning of his time in the Division of Laboratory Sciences and NSQAP, Omar worked with Dr. Gerald Cooper continuing his research in atherosclerosis and lipoproteins in blood associated with heart disease. Since 1990, he has worked in NSQAP and with other CDC groups in the areas of immunology and immunochemistry and in developing important new quality control materials for newborn screening including QC materials for HIV screening, Type 1 diabetes, and flow cytometry . In the last several years he has been associated with the Administrative Group of NSQAP helping with administrative activities.

Omar looks forward to focusing his energy on travel with his wife Sharon and on exciting new adventures. NSQAP sends Omar "Best wishes" in his well-deserved retirement.

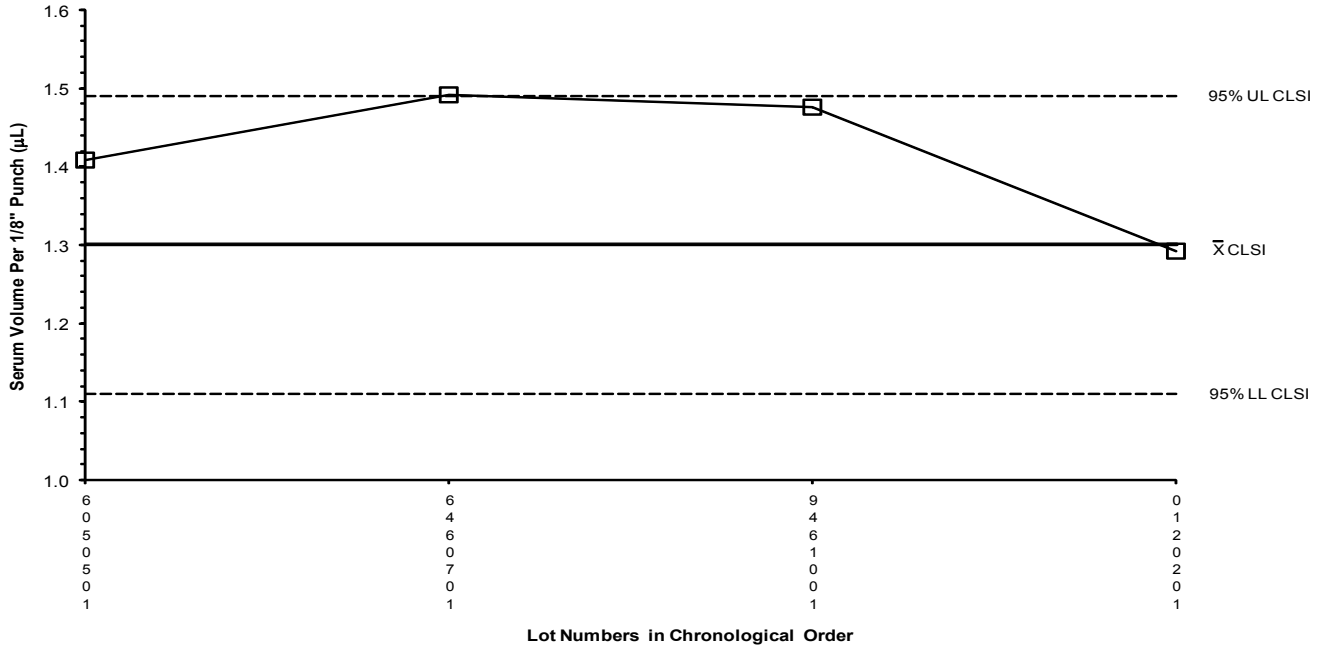
by CDC are an impartial and voluntary service offered as a function of our QA program; they do not constitute preferential endorsement of any product.

The disk that is punched from DBS specimens is a volumetric measurement that requires a degree of uniformity among and within production lots. As part of the QA program, we used an isotopic method developed at CDC to evaluate and compare different lots of filter paper (3). Mean counts per minute of added isotope-labeled thyroxine (T4) contained within a 1/8-inch disk were equated with the serum volume of the disks from the dried whole blood specimens. In comparing production lots, we used statistical analyses of the counting data to determine values for homogeneity, absorption time, and serum absorption of the disks. We also measure spot diameters to ensure that they are within acceptable Clinical and Laboratory Standards Institute (CLSI) limits (3). Lysed-cell whole blood was used initially to avoid variability contributed by uncontrolled red blood cell (RBC) lysis during the 4-day QC production span. Results of later studies concluded that RBC lysis occurring during processing of the intact-cell blood pools was not sufficient to contribute substantially to the variance. For historical reference and for maintaining uniformity of testing on all the paper production lots, we have continued using the lysed-cell procedure (Figures 4 and 6). We also measure performance with intact-cell preparations (Figures 5 and 7). Intact-cell evaluation results were confirmed by comparison to data from the lysed-cell evaluation. The published and standardized acceptable serum volumes per 1/8-inch disk are 1.30 ± 0.19 µL (mean value and 95% confidence interval [CI]) for lysed-cell blood and 1.54 ± 0.17 µL for intact-cell blood (3). The mean serum volume per 1/8-inch disk for lysed-cell blood differs from that of intact-cell blood. The mean values and CIs are the filter-paper evaluation parameters published in the CLSI (3). The CDC mean value for intact-cell evaluations for all lots is within the 95% CI defined by CLSI but below the mean value indicated by the CLSI standard (3). In 2006, the mean value and CI for the intact-cell measurements were examined and discussed during a routinely scheduled review period for revision of the LA4 standard. The CLSI committee retained the original values (not produced at CDC) for intact cells in the revised standard. The mean value and 95% CI for intact cells (Figures 5 and 7) are the values based on CDC data.

Filter paper lots used in the CDC production of QC and PT specimens distributed in 2010 were W051, W071, and W083 of Grade 903 and 8040201 of Grade 226. All filter paper lots were analyzed for agreement with the evaluation parameters according to the CLSI-approved standard (3).

The serum-absorbance volumes of 29 lots of Grade 903 filter paper (Whatman Inc.) determined from lysed RBCs (Figure 6) and for 19 lots determined from intact RBCs (Figure 7) are shown in chronological order. For W101, the most recent production lot tested of Grade 903 filter paper, we found the mean serum-absorbance volume was 1.31 µL for a 1/8-inch disk for lysed- cell blood

FIGURE 4. Ahlstrom Grade 226 Specimen Collection Paper Serum Volume by Lot Number - Lysed Red Blood Cells



Ahlstrom

FIGURE 5. Ahlstrom Grade 226 Specimen Collection Paper Serum Volume by Lot Number - Intact Red Blood Cells

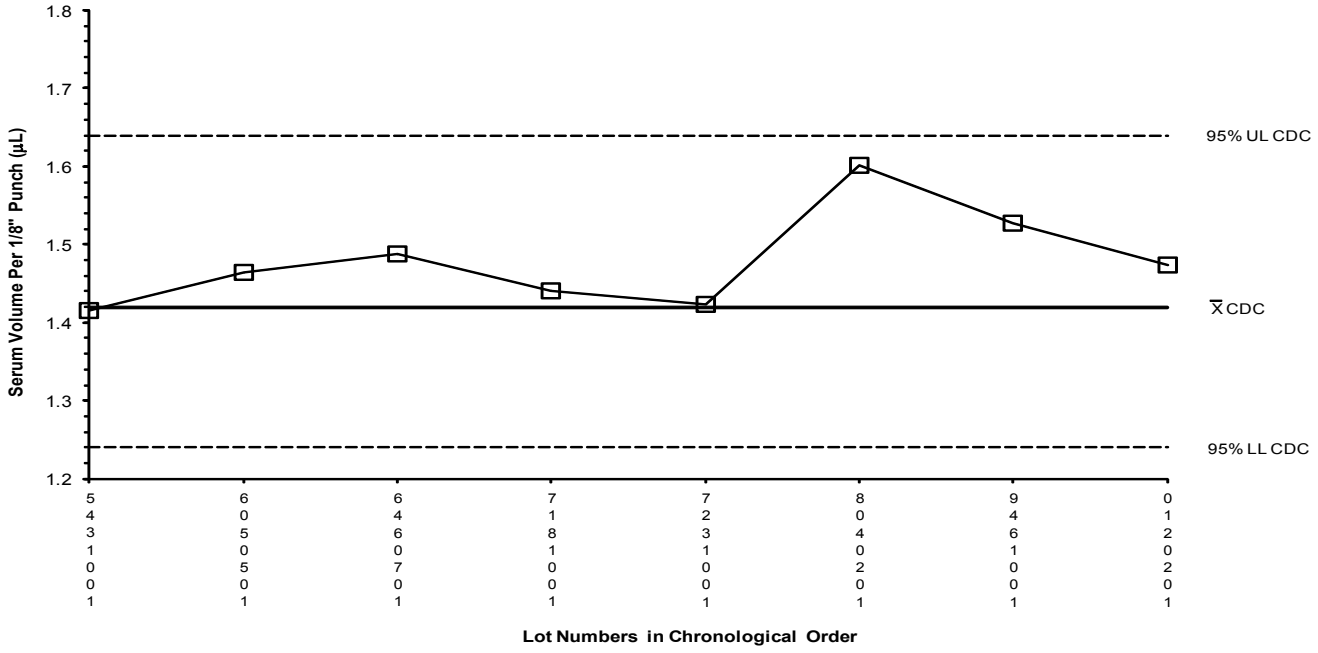
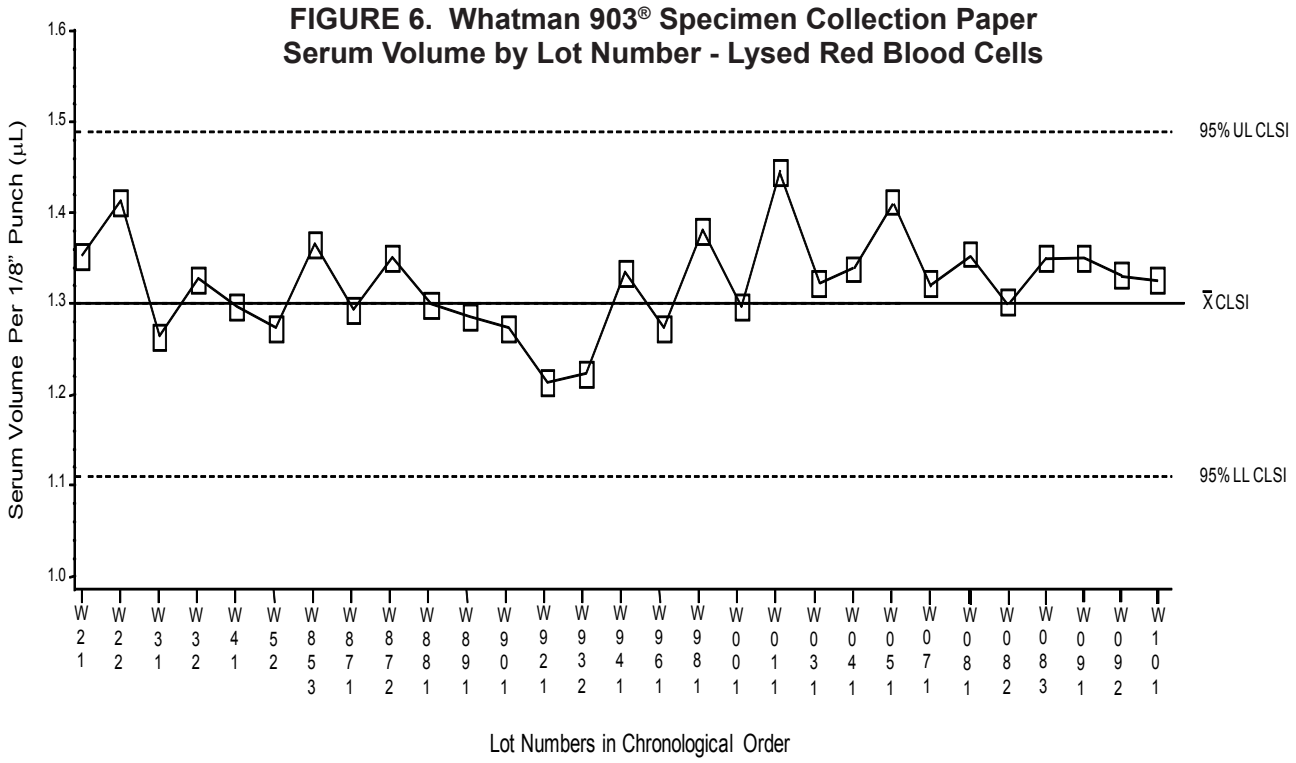


FIGURE 6. Whatman 903® Specimen Collection Paper Serum Volume by Lot Number - Lysed Red Blood Cells



Whatman Inc.

FIGURE 7. Whatman 903® Specimen Collection Paper Serum Volume by Lot Number - Intact Red Blood Cells

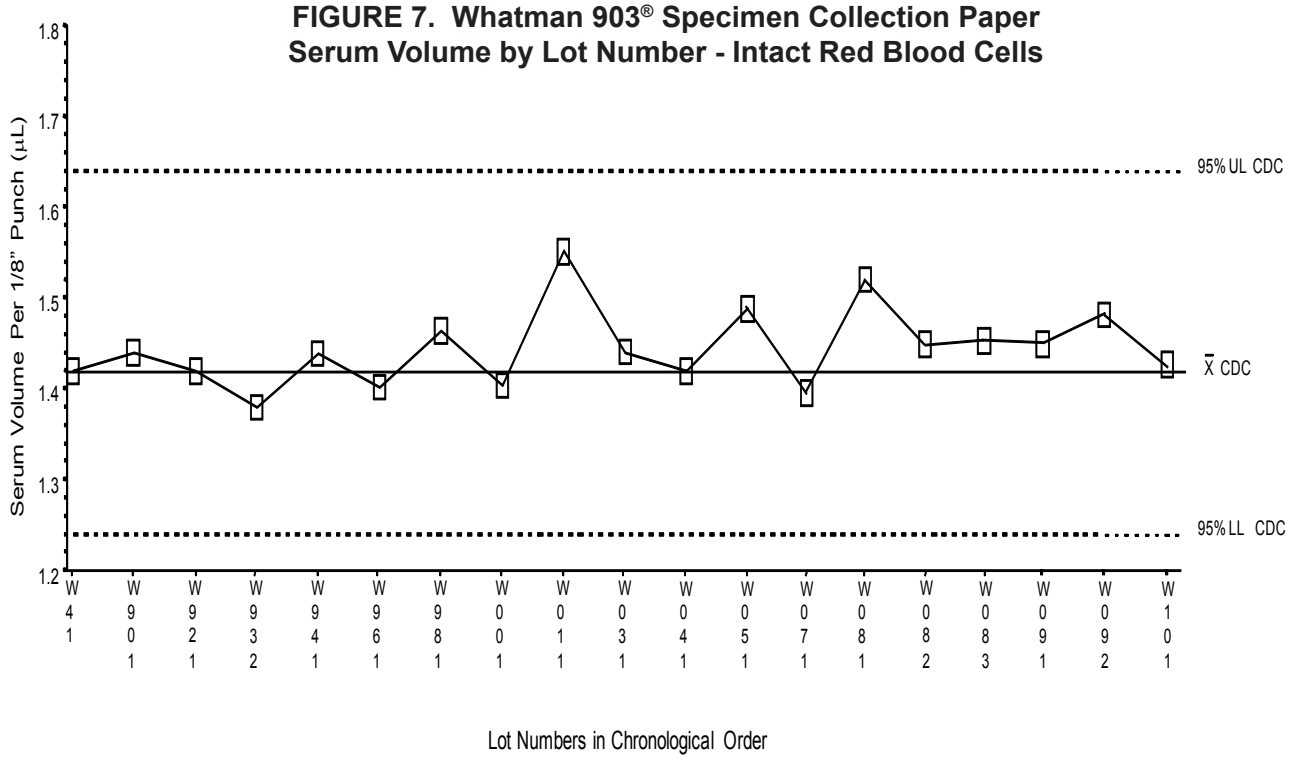


TABLE 1. 2010 Summary of Non-MS/MS Cutoff Values of Domestic and Foreign Laboratories

Domestic

Analyte	N	Mean	Median	Mode	Min/Max
T4	24	6.2	6.0	6.0	3.5-10.2
TSH	45	31.3	25.0	20.0	19.5-61
17-OHP	44	45.0	36.0	79.2	23.1-85
Galactose	20	11.5	10.5	10.0	6-20
Phenylalanine	8	158.0	151.5	181.8	121-206
IRT	48	76.6	62.0	62.0	48.8-170
GALT	22	3.0	3.1	2.3	1.1-4.1

Foreign

Analyte	N	Mean	Median	Mode	Min/Max
T4	27	6.3	6.0	6.0	4.0-20
TSH	176	24.3	21.0	20.0	7.0-50
17-OHP	101	31.6	22.0	50.0	6.6-180
Galactose	77	11.8	10.0	10.0	4.0-30
Phenylalanine	64	165.7	151.8	121.2	103-242
Leucine	8	296.0	302.5	228.9	229-382
Methionine	4	76.0	74.0	-	55-101
Tyrosine	4	326.3	348.5	-	200-408
Valine	3	288.0	282.0	-	240-342
SUAC	5	1.9	1.2	-	1.0-4
IRT	85	66.5	65.0	70.0	22-150
GALT	31	3.0	3.1	3.5	1.2-6

and 1.44 µL per 1/8-inch disk for intact-cell blood. Each mean value is within the acceptable range for the matrix used. Lot W101 was homogeneous (i.e., the measured within-spot, within-sheet, and among-sheets variances were within the acceptable limits). NSQAP's data for a production lot depend on the filter paper sample provided by the manufacturer as being representative of the entire production batch (i.e., statistically valid sampling).

In 2008, the FDA approved the filter paper, Grade 226, produced by Ahlstrom Filtration LLC (Holly Springs, PA) as a blood collection device. CDC evaluated Grade 226 according to the criteria previously described (3). The serum-absorbance volumes for eight lots of Grade 226 filter paper determined from intact RBCs (Figure 5) and four lots determined from lysed RBCs are shown in chronological order (Figure 4). For lot 0120201, the most recent production lot of Grade 226 filter paper, we found the mean serum-absorbance volume was 1.29 for lysed-cell blood and 1.47 µL for a 1/8-inch disk for intact-cell blood. Each mean value was within the acceptable range for the matrix used. Lot 0120201 was homogeneous (i.e., the measured variance was within the acceptable limits).

SPECIMEN PREPARATION AND DATA HANDLING

Tables and figures show the enriched concentrations of PT specimens and QC lots as well as the summarized quantitative data. The total concentration of each specimen or lot equaled the sum of the enriched concentration and the endogenous concentration (non-enriched). For T4 PT specimens, the CDC assayed values were reported because of differences in the blood sources used for DBS production. Some specimens were enriched above the endogenous T4 concentration, and some were enriched with T4 after T4 depletion of the base serum. All PT specimens were prepared from whole blood of 50% hematocrit. All QC lots were prepared from whole blood of 50% hematocrit. Purified analytes or unaltered donor blood were used for all enrichments with the exception of thyroid-stimulating hormone (TSH), which used the Third International Reference Preparation (81/565). For galactosemia, enrichments were made with galactose and galactose-1-phosphate so that both free galactose (galactose alone) and total galactose (free galactose plus galactose present as galactose-1-phosphate[TGal]) could be measured. For biotinidase, GALT, and CFDNA, individual donor blood from adults with these disorders was used, with the hematocrit adjusted to 50%. CDC

TABLE 2. 2010 Summary of MS/MS Cutoff Values of Domestic and Foreign Laboratories

Domestic

Analyte	N	Mean	Median	Mode	Min/Max
Phenylalanine	50	148.32	150.75	155.00	97-220
Leucine	35	296.72	300.00	300.00	222-500
Methionine	47	81.89	80.00	100.00	40-134
Tyrosine	48	414.82	359.50	850.00	88-850
Valine	40	281.00	262.00	250.00	175-445
Citrulline	35	57.79	55.00	55.00	27-100
Arginine	37	113.47	100.00	250.00	25-250
SUAC	22	2.98	3.00	3.00	0.50-5.50
C0(L)	50	8.82	8.00	7.00	3.80-15.00
C3	51	5.91	6.00	6.30	1.20-10.00
C3DC	39	0.33	0.35	0.50	0.10-0.70
C4	53	1.38	1.40	1.70	0.54-2.14
C4OH	26	0.77	0.77	1.00	0.27-1.33
C5	52	0.80	0.78	1.25	0.42-1.25
C5:1	48	0.30	0.21	0.60	0.07-1.00
C5DC	51	0.36	0.32	0.60	0.13-0.80
C5OH	51	0.85	0.86	0.90	0.19-1.70
C6	48	0.47	0.35	0.95	0.17-0.96
C8	51	0.46	0.45	0.60	0.25-0.72
C10	48	0.50	0.48	0.65	0.27-1.17
C10:1	46	0.35	0.34	0.45	0.18-0.56
C14	47	0.81	0.78	1.20	0.17-1.20
C14:1	51	0.64	0.65	0.80	0.20-0.80
C16	48	8.00	8.00	10.00	0.25-10.00
C16OH	51	0.16	0.15	0.10	0.08-0.37
C18	42	2.51	2.28	4.00	0.22-4.00

Foreign

Analyte	N	Mean	Median	Mode	Min/Max
Phenylalanine	145	150.34	145.00	120.00	49-400
Leucine	138	309.10	300.00	300.00	163-689
Methionine	124	63.16	60.00	50.00	50-103
Tyrosine	138	312.70	293.00	250.00	79.9-1000
Valine	120	285.40	287.50	250.00	147-473
Citrulline	125	56.91	50.00	40.00	19.52-200
Arginine	95	56.73	46.00	46.00	16-132
SUAC	24	3.61	2.00	1.20	0.60-10
C0(L)	106	8.78	8.00	10.00	3.05-14.00
C3	130	5.65	5.80	6.00	1.87-12.04
C3DC	93	0.37	0.30	0.30	0.08-1.40
C4	126	1.16	1.03	1.00	0.44-2.31
C4OH	78	0.64	0.60	0.66	0.23-3.03
C5	136	0.75	0.69	1.00	0.22-2.00
C5:1	110	0.23	0.24	0.25	0.02-1.50
C5DC	133	0.28	0.25	0.25	0.03-0.84
C5OH	127	0.90	0.90	1.00	0.07-4.49
C6	130	0.38	0.30	0.50	0.07-1.53
C8	143	0.42	0.40	0.50	0.11-1.00
C10	135	0.43	0.40	0.50	0.08-1.00
C10:1	119	0.34	0.30	0.30	0.08-1.00
C14	127	0.66	0.65	0.50	0.11-1.51
C14:1	130	0.53	0.50	0.40	0.02-1.50
C16	131	7.16	7.50	8.00	0.11-14.00
C16OH	126	0.21	0.16	0.20	0.03-5.59
C18	122	2.21	2.00	2.00	0.11-9.00

TABLE 3. 2010 Summary of Proficiency Testing Errors by Domestic Laboratories

	Positive Specimens Assayed (N)	False-Negative Errors (%)	Negative Specimens Assayed (N)	False-Positive Errors (%)
Hypothyroidism	234	3.8	631	0.0
Congenital Adrenal Hyperplasia	202	0.0	568	0.9
Galactosemia	113	0.0	312	0.0
Phenylketonuria	252	0.8	1008	0.1
Maple Syrup Urine Disease (Leu)	200	0.5	800	0.1
Homocystinuria (Met)	134	0.7	821	0.2
Tyrosinemia I, II, III (Tyr)	131	1.5	889	0.3
Maple Syrup Urine Disease (Val)	176	1.1	704	0.1
Citrullinemia	190	0.5	760	0.4
Argininemia	96	4.2	654	0.9
C0(L) Screen	72	11.1	876	0.1
C3 Screen	140	0.7	870	0.3
C3DC Screen	103	19.4	652	2.9
C4 Screen	120	0.0	805	0.9
C4OH Screen	68	0.0	462	0.2
C5 Screen	207	0.5	828	0.1
C5:1 Screen	124	0.0	816	0.0
C5DC Screen	205	1.0	820	0.0
C5OH Screen	126	0.0	708	2.0
C6 Screen	136	0.7	839	0.1
C8 Screen	145	0.7	905	0.1
C10 Screen	137	0.7	848	0.1
C10:1 Screen	128	0.8	797	0.1
C14 Screen	183	0.0	777	0.1
C14:1 Screen	132	0.0	883	0.1
C16 Screen	198	1.0	807	0.2
C16OH Screen	199	1.0	801	0.0
C18 Screen	128	0.8	777	0.3
Biotinidase Deficiency	191	1.6	514	1.6
GALT Deficiency	183	0.5	502	0.0
Immunoreactive Trypinogen (IRT)	367	2.5	413	0.0
Tyrosinemia I (SUAC)	14	0.0	130	0.0

assayed values were used as PT expected values for T4, immunoreactive trypsinogen (IRT), GALT, Arginine (Arg), C3DC, C4OH, C5:1, C10:1, C14:1, C16OH and C18. All reported analytic values outside the 99% CI were excluded from the summaries of quantitative results.

For obtaining data on the QC materials, we estimated the method response to endogenous materials by performing weighted linear regression analyses for mean-reported concentrations versus enriched concentrations. We then extrapolated the regression lines to the Y-axis (intercept) to obtain an estimate of the observed endogenous analyte concentration for each method category. These estimates are reliable when (2) enrichments are accurate, (3) the analytical method gives a linear response across the range of the measurements, and (3) the slopes for regression lines are approximately equal to one.

In 2010, we applied the laboratory-reported specific cutoff values, when available, to our grading algorithm for clinical assessments; if no cutoff was reported, we used the NSQAP-assigned working cutoff values based on the national mean value for this assessment.

CUTOFFS

When reporting cutoff values, we requested the decision level for sorting test results reported as presumptive positive (outside limits) from results reported as negative (within limits). The reported cutoff values are summarized in Tables 1 and 2 for domestic and foreign laboratories. The values for mean (arithmetic average), median (middle value), and mode (most frequent value) are shown for each analyte. The mean cutoff values for domestic and foreign laboratories are somewhat similar except for 17-OHP, which historically has been higher among the

TABLE 4. 2010 Summary of Proficiency Testing Errors by Foreign Laboratories

	Positive Specimens Assayed (N)	False-Negative Errors (%)	Negative Specimens Assayed (N)	False-Positive Errors (%)
Hypothyroidism	655	0.8	1805	0.9
Congenital Adrenal Hyperplasia	383	0.8	1057	1.3
Galactosemia	305	1.0	845	1.1
Phenylketonuria	563	0.5	2252	1.9
Maple Syrup Urine Disease (Leu)	354	0.3	1416	0.4
Homocystinuria (Met)	222	0.9	1438	0.5
Tyrosinemia I, II, III (Tyr)	252	0.0	1623	0.1
Maple Syrup Urine Disease (Val)	320	1.9	1280	0.5
Citrullinemia	303	1.3	1212	0.7
Argininemia	172	2.9	1088	2.5
C0(L) Screen	123	18.7	1534	3.1
C3 Screen	233	1.3	1502	1.7
C3DC Screen	167	4.2	1093	2.3
C4 Screen	224	0.9	1461	1.4
C4OH Screen	139	0.0	896	3.0
C5 Screen	363	1.4	1452	0.3
C5:1 Screen	202	0.5	1288	1.2
C5DC Screen	359	1.7	1436	1.0
C5OH Screen	218	0.5	1204	5.6
C6 Screen	234	3.4	1511	1.2
C8 Screen	252	0.4	1633	0.7
C10 Screen	241	1.7	1554	0.8
C10:1 Screen	218	1.4	1407	1.5
C14 Screen	345	0.0	1380	1.5
C14:1 Screen	234	2.1	1546	1.1
C16 Screen	349	4.3	1406	0.2
C16OH Screen	333	1.5	1357	0.8
C18 Screen	217	1.4	1368	1.0
Biotinidase Deficiency	255	0.0	690	2.9
GALT Deficiency	189	1.1	511	0.0
Immunoreactive Trypinogen (IRT)	549	2.6	626	0.3
Tyrosinemia I (SUAC)	28	0.0	192	1.6

domestic laboratories, and for Arg, which has a domestic cutoff mean more than twice the foreign cutoff mean. The range (min/max) of cutoff values was large for analytes TSH, 17-OHP, TGal, tyrosine (Tyr), valine (Val), Arg, and IRT for both domestic and foreign laboratories. The mean and median cutoff values for the MS/MS amino acids were similar for domestic and foreign laboratories; but there were two mode values, Tyr and Arg, which were very different among the domestic participants indicating a group of laboratories using a cutoff value different from the mean of the other labs.

PROFICIENCY TESTING

All PT panels contained five blind-coded 75-µL DBS specimens. Specimens in the PT panels either contained endogenous levels or were enriched with predetermined levels of T4, TSH, 17-OHP, TGal, IRT, phenylalanine (Phe), leucine (Leu), methionine (Met), Tyr, Val, citrulline (Cit), Arg, SUAC, and acylcarnitines (C0[L], C3, C3DC, C4, C4OH, C5, C5:1, C5DC, C5OH, C6, C8, C10, C10:1, C14, C14:1, C16, C16OH, and C18). CFDNA panels were made from the blood of either an adult or an adolescent CF donor. Separate panels for biotinidase deficiency and for GALT deficiency were prepared with purchased blood from donors with these enzyme deficiencies. Specimens for the hemoglobinopathies panel were prepared from umbilical cord blood.

Specimen sets were packaged in a zip-closed metalized plastic bag with desiccant, instructions for analysis, and instructions for reporting data. Ninety-nine percent of participating laboratories now report data using the Internet. We prepared and distributed quarterly reports of all results that had been received by the deadline dates. In this annual report, the comparisons of results by different methods (Figures 9–40) are illustrated with the participants' reported PT data for one selected challenge

for each analyte during the year. These are compared by using bias plots that show the difference (positive or negative) by laboratory and method of the reported value subtracted from the expected value, i.e., CDC-measured endogenous level plus enrichment; for T4, IRT, GALT, Arg, C3DC, C4OH, C5:1, C10:1, C14:1, and C16OH, the reported value has been subtracted from the CDC assayed value. Note the scale-changes of the Y-axis relative to the expected value for each plot. A reported value matching the expected value will show the illustrated value as falling on the "0" line of the plot. A reasonable bias is less than ± 20% of the expected value or within the 95% confidence interval (CI) for Figures 9–40. A summary of the specimen data for the selected quarter PT challenge in 2010 is tabulated in the left margin for each figure.

The representative PT challenge specimens selected for the bias plots (Figures 9–40) were either above or below the cutoff value for the analyte. When comparing data scatter among figures, note that the scale (Y-axis) may differ. We included the 95% CI for the mean participant bias. Good performance of a method or group of methods is indicated by a tight scatter within this interval. In general, the quantitative comparisons (Figures 9–40) for PT challenges are reasonable within a method but they vary among methods. The PT quantitative results are grouped by kit or method to illustrate any method-related differences in analyte recoveries. Because some of the pools in a routine PT survey represent a unique donor specimen, differences in endogenous materials in the donor specimens may influence method-related differences.

Representative bias plots are shown for all analytes distributed in PT challenges during 2010 that required a quantitative measurement to determine the presumptive "clinical" assessments. The bias scatter plots for T4 and TSH (Figures 9 and 10) indicate reasonable performance among all the users. Over the years, the number of T4 users has remained stable while the number of TSH users has grown. Most of the T4 and TSH methods show good agreement among users with a tight scatter of values. The recovery relative to expected value (EV) by participants is excellent with a small mean bias for all participants for T4 and TSH. In Figure 11, the bias plot for IRT shows good recovery for the participants' mean relative to the CDC assayed value. A large scatter is seen along with a method bias around the assayed values with GALT in Figure 12. For 17-OHP in Figure 13, the participant mean value is in good agreement with the EV and yields a small positive mean bias. Note, TGal in Figure 14, the scatter for one method is distinctly higher than that for all other methods and the participants' mean bias is small. The bias plot for Phe in Figure 15 shows good agreement between laboratories and among methods, but a large participant bias compared to the EV. In Figure 16, the Leu values show a tight scatter for all methods. With Met (Figure 17) most methods, except for the derivatized MS/MS kit method, show a consistently negative bias with a large participant bias difference from the EV. The scatter for the Tyr bias values (Figure 18) is small and consistent within- and among-methods. Like Phe, Val (Figure 19) illustrates a negative bias with a large participant bias. The Cit plot (Figure 20) shows some methods with a distinct difference between non-kit and kit methods, with a tight cluster of values and good agreement with the EV. Like Cit, the Arg data (Figure 21) shows the same kind of difference among the methods. The SUAC data (Figure 22) shows a highly clustered set of values with a negative bias for a non-derivatized MS/MS kit method. The bias values for SUAC have a wide scatter and a large difference among methods and users. Only a few SUAC participants show good recoveries relative to the EV. A marked difference was observed for the derivatized non-kit and kit MS/MS methods. The number of SUAC participants is still relatively small.

Bias plots for derivatized and non-dervatized MS/MS methods are shown for all acylcarnitines as selected representative PT challenges in 2010. Enrichments made with purchased or special synthesized acylcarnitines are based on weighed quantities. Slight variances in enrichments and recoveries may be attributed to impurities in the purchased (synthesized) materials and endogenous analyte concentrations. For C0 (L) (Figure 23), although the scatter of values is tight for all methods, one method is different with a clustered positive bias for all but one user. A similar observation is seen for C3DC (Figure 25) and C5DC (Figure 30). For many of the acylcarnitines, the values for the derivatized MS/MS kit method are tightly clustered and different from the other MS/MS methods. NOTE: This same type of difference is observed also with Arg (Figure 21). The users of derivatized non-kit and kit MS/MS methods show a tight scatter within a method group, but different bias values. The bias data for C3 (Figure 24) and C4 (Figure 26) show a low participant bias with consistent scatter across all methods; the mean bias for both is in excellent agreement with the EV. Figure 27 shows a small negative bias for C4OH among all methods. In Figure 28 for C5, the values are minimally scattered with good agreement with the EV. The data for C5:1 (Figure 29) show a slight negative bias for certain kit methods and the participant mean value is in good agreement with the EV. The bias plot for C5OH (Figure 31) and C6 (Figure 32) illustrate a negative cluster of values for all methods with the mean

bias in close agreement to the EV. For C8 (Figure 33), the data demonstrate a tight scatter around the expected values for all methods, and the participants' mean value is in close agreement with the EV. The MS/MS kit shows a close agreement among all users and this observation is similar for all acylcarnitines. For C10 (Figure 34) and C10:1 (Figure 35), the bias values show reasonable scatter among all laboratories and methods with good agreement for the EV; however, a negative method bias is noted between the MS/MS kit and the non-kit methods. These clustered differences are similar to the MS/MS kit method differences observed for C3DC, C5DC but in the opposite (positive) direction. For C14 (Figure 36) and C14:1 (Figure 37), all methods show reasonable scatter, but two C14 kit methods show a negatively clustered bias. The mean bias for C14 and C14:1 is in good agreement with the EV. C16 (Figure 38) data demonstrate a tight cluster of values with most laboratories showing a positive bias. For C16OH (Figure 39), the data demonstrate consistent scatter among all methods with most laboratories showing a small negative bias. Figure 40 for C18 illustrates good agreement with the EV and reasonable scatter of values within- and among-methods while showing a positive bias in all methods.

Tables 3 and 4 show the PT errors reported by domestic and foreign laboratories in 2010 for qualitative assessments reported per disorder. We applied the laboratory-reported specific cutoff values to our grading algorithm for clinical assessments (Figure 8). Presumptive clinical classifications (qualitative assessments) of some specimens may differ by participant because of specific clinical assessment practices. If participants provided us with their cutoff values, we applied these cutoffs in our final appraisal of the error judgment. We based the rates for false-positive misclassifications on the number of tested negative specimens and the rates for false-negative misclassifications on the number of positive specimens tested. False-positive misclassifications, which are a cost-benefit issue and a credibility factor for follow-up programs, should be monitored and kept as low as possible. Many of the misclassifications were in the false-positive category, with false-positive rates ranging from 0% to 5.6%. For domestic laboratories, the rate was 0.9% or lower for 29 of 32 biomarkers or disorders with C3DC having the highest rate of false-positive errors. The foreign laboratories had an error rate of 1.5% or lower for 23 of 32 biomarkers or disorders with C5OH having the highest rate of false-positive errors.

Screening programs are designed to avoid false-negative reports; however, this precautionary design contributes to false-positive reports and may cause many of the false-positive misclassifications. The false-negative rate, expected to be zero, ranged from 0% to 19.4%. For nine biomarkers or disorders, no false-negative errors were reported for the domestic laboratories. Foreign laboratories had no false-negative errors for 5 of the 32 disorders. A few of our PT specimens fell close to the decision level for classifications and thus rigorously tested the ability of laboratories to make the expected cutoff decision. Most specimens near the mean cutoff value are distributed as not-evaluated specimens, and they are not included in Tables 3 and 4. Participant data for these specimens are used to examine the relative analytical performance of the assays.

Table 5 shows the performance errors for hemoglobinopathies. The percentage of errors for qualitative assessments for sickle cell disease and other hemoglobinopathies ranged from 0.0% to 1.5% for the error categories, with 74 participants. Overall, there were 13 phenotype errors for reported data for 2010. The classification errors were essentially the same for phenotype and clinical assessments within the domestic and foreign laboratory groups. Table 6 shows the

TABLE 5. 2010 Summary of Proficiency Testing Errors for Hemoglobinopathies by Domestic and Foreign Laboratories

Hemoglobinopathies	Domestic	Foreign
Specimens assayed	740	323
Phenotype errors	1.5%	0.6%
Clinical assessment errors	1.5%	0.0%

Overall, there were 13 phenotype errors, 8 FA, 3 FAS, 2 FAC.

TABLE 6. Hemoglobin Phenotype Challenges Distributed in 2010

Phenotype	N
FA	7
FAD	1
FAC	3
FAS	4

TABLE 7. Sickle Cell and Hemoglobinopathies Methods Used in Multi-Tier Testing for Proficiency Testing in 2010

Method	Isoelectric Focusing	BioRad HPLC	Extended Gradient HPLC	Chromsystems HPLC Kit	Electrophoresis Citrate Agar	Electrophoresis Alkaline Cellulose	PCR Amplification of DNA
1st tier testing	33	35	3	1	0	0	0
2nd tier testing	17	13	6	0	1	2	2
3rd tier testing	1	0	0	0	3	0	0

phenotype challenges that were distributed in 2010 for hemoglobinopathies. In Table 7, methods that were used by participants are shown for multi-tier testing schemes to enhance the specificity of the initial screen for hemoglobinopathies. Most screening laboratories use Isoelectric Focusing and HPLC methods in only a single tier of testing. Many laboratories utilize second-tier testing with these same methods in repetitive or different combinations, and only a few used a third-tier test. Some laboratories now report the application of DNA testing for their scheme.

Table 8 shows the performance errors for CFDNA mutation detection. The percentage of errors for qualitative assessments for genotype analysis was relatively small, at 1%, for three of the PT events and 3% for one of the PT challenges. Table 9 shows the CF mutation (CFTR gene) challenges that were distributed in 2010 for CFDNA.

QUALITY CONTROL

For QC shipments of T4, TSH, 17-OHP, IRT, TGal, amino acids (Phe, Leu, Met, Tyr, Val, Cit, Arg), SUAC, and acylcarnitines (C0, C2, C3, C3DC, C4, C5, C5DC, C5OH, C6, C8, C10, C12, C14, C16, C16OH, C18), each lot within a set contained a different analyte concentration. To ensure that a laboratory received representative sheets of the production batch, we used randomizing systems to select the set of sheets from across the production batch for each laboratory. The QC materials were distributed semiannually; they included the DBS sheets, instructions for storage and analysis, and data-report forms. Data from five analytic runs of each lot and shipment were compiled in the midyear and annual summary reports distributed to each participant. Intervals between runs were not the same for all laboratories because each participant's reported data cover a different time span.

The reported QC data are summarized in Tables 10a–10cc, which show the analyte by series of QC lots, the number of measurements (N), the mean values, and the within-laboratory and total standard deviations (SD) by kit or analytic method. In addition, we used a weighted linear regression analysis to examine the comparability by method of reported versus enriched concentrations. Linear regressions (Y-intercept and slope) were calculated by method for all analytic values within an analyte QC series.

TABLE 8. Genotype Analysis of Cystic Fibrosis Mutation Detection Specimens in 2010

	Total Specimens Assayed (N)	Not Evaluated*	Sample Failure	Total Specimens Evaluated (N)	Correct Results	Incorrect Results
Q1, 2010	220	18	0	202	99%	1%
Q2, 2010	235	43	2	190	99%	1%
Q3, 2010	250	16	2	232	97%	3%
Q4, 2010	250	19	0	231	99%	1%
Total	955	96	4	855	99%	1%

*If one or both mutations are not on a laboratory's panel, the specimen is not evaluated.

Values outside the 99% CI (outliers) were excluded from the calculations.

Tables 10a–10cc provide data about method-related differences in analytic recoveries and method bias. Because we prepared each QC lot series from one batch of hematocrit-adjusted, nonenriched blood, the endogenous concentration was the same for all specimens in a lot series. We calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs for regression analyses. We calculated the Y-intercept and slope in each table, using all analyte concentrations within a lot series (e.g., lots 951, 952, and 953). Because only three or four concentrations of QC materials are available for each analyte, a bias error 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 also measured the endogenous concentrations by analyzing the nonenriched QC lots; the Y-intercepts and measured endogenous levels for these analytes were similar for most methods. Ideally, the slope should be 1.0. Most slopes were close to this value; however, the range was 0.2 to 1.8 because of a few methods and analytes.

Slope deviations may be related 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 was 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.

TABLE 9. Cystic Fibrosis Mutation (CFTR gene) Challenges Distributed in 2010

Mutation (Legacy Name)	Mutation (HGVS Nomenclature)	N
Wild type /no mutation	Wild type /no mutation	22
F508del	p.Phe508del	8
W1282X	p.Trp1282X	2
2184delA	p.Lys684AsnfsX38	1
394delTT	p.Leu88IlefsX22	1
711+1G>T	c.579+1G>T	1
CFTRdele2,3	c.54-5940_273+10250del21kb	1
G542X	p.Gly542X	1
G551D	p.Gly551Asp	1
R334W	p.Arg334Trp	1
R553X	p.Arg553X	1

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Use of trade names and commercial sources is for identification only and does not imply endorsement by the U.S. Department of Health and Human Services or the Association of Public Health Laboratories.

FIGURE 8. EXPLANATION OF NSQAP GRADING ALGORITHM

Part 1.
The expected clinical assessment (EA) for a proficiency testing (PT) specimen is determined by comparing the expected value (EV), which is the sum of endogenous and enrichment values, with the CDC cutoff. The production of a PT specimen is designed so that the 99% confidence interval (CI) for the expected value (EV) of a positive specimen falls above the CDC cutoff, and the 99% CI for the expected value (EV) of a negative specimen falls below the CDC cutoff. Specimens that do not meet this 99% CI criterion are declared not-gradable/not-evaluated (NE).

Part 2.
When your reported clinical assessment (RA) differs from the expected clinical assessment (EA), the expected value (EV) is compared with the cutoff that you provide. This determines what your laboratory expected clinical assessment (LA) should be. If the expected clinical assessment (EA) and the laboratory expected clinical assessment (LA) are the same, but different from your reported clinical assessment (RA), your grade is either false-negative or false-positive. If the expected clinical assessment (EA) and the laboratory expected clinical assessment (LA) are not the same, your reported clinical assessment (RA) will not be graded as incorrect because of a significant difference between the CDC cutoff and your cutoff (see examples below). If you do not provide a cutoff, your laboratory expected clinical assessment (LA) cannot be determined; and your grade will be based on the CDC cutoff.

Part 3.
NSQAP's determination of a final clinical assessment for a specimen is based on the Clinical Laboratory Improvement Amendments (CLIA) regulations (http://www.phppo.cdc.gov/clia/regs/subpart_i.aspx#493.929), 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." A NSQAP gradable specimen must have 80% or more agreement among domestic laboratories. A specimen with less than 80% agreement is not-gradable/not-evaluated (NE).

Examples of Grading Scenarios

Analyte	CDC Cutoff	Expected Value (EV)	Lab Cutoff	Assessment: (EA) EV/CDC cutoff	Assessment: (LA) EV/Lab cutoff	Assessment: (RA) Lab reported	Lab Grade
TSH	25	13	30	Neg	Neg	Pos	FP
TSH	25	13	10	Neg	Pos	Pos	CD
Leu	4.1	6.7	4.5	Pos	Pos	Neg	FN
Leu	4.1	6.7	8.0	Pos	Neg	Neg	CD

FN = False negative
FP = False positive
CD = Cutoff Difference - clinical assessment is not judged as incorrect

TSH = Thyroid-stimulating Hormone
Leu = Leucine

Note that the grade is based on the reported clinical assessment, not on the reported value. Overall Statistics, which are generated from all participants' data, and Mean Reported Concentrations by method are provided on the Web site for analytical reference only.

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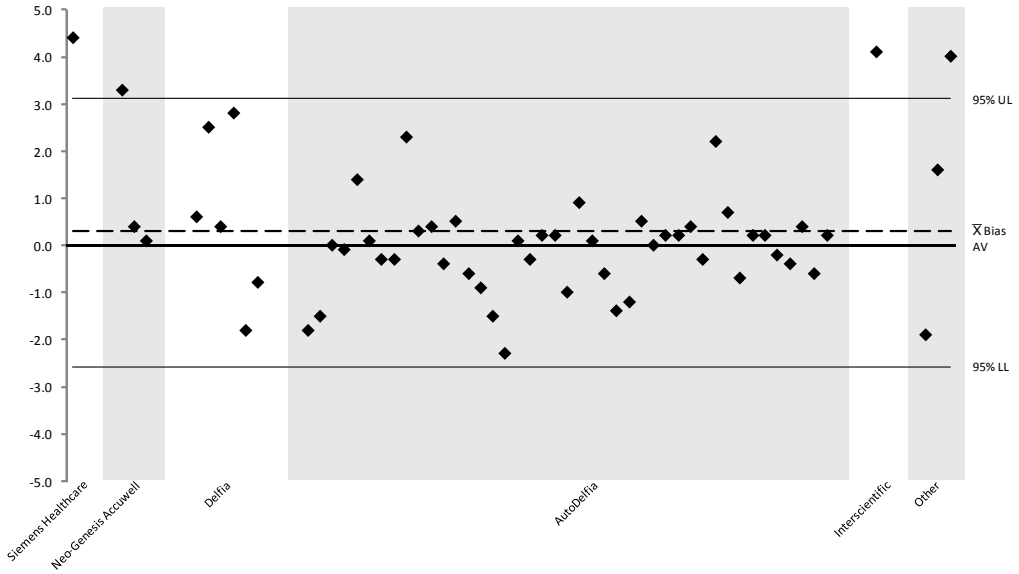
FIGURES 9-10. Reproducibility of Results by Different Methods – Thyroxine and Thyroid-Stimulating Hormone

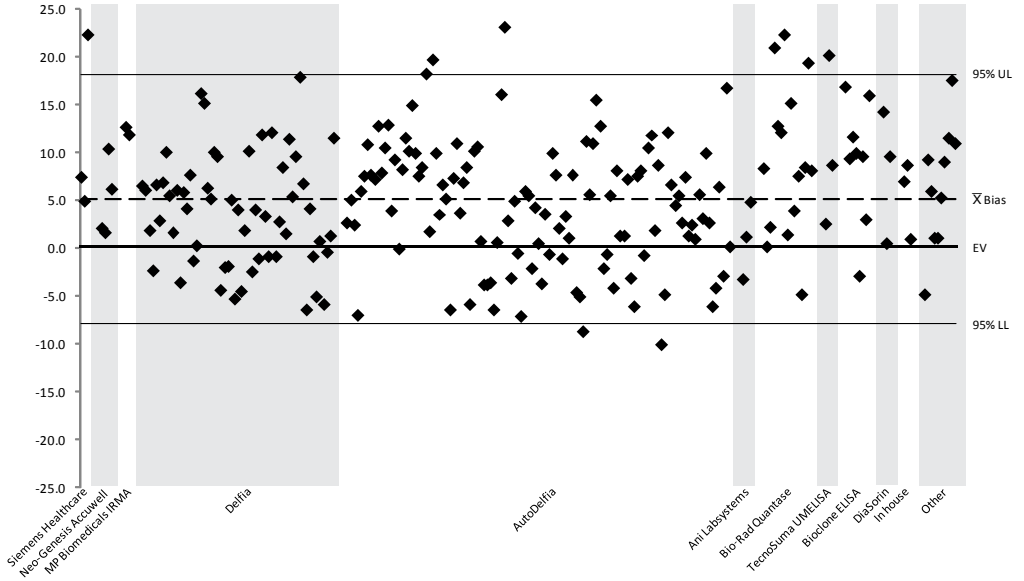
Quarter 3	
Specimen 2	
CDC Assayed	7.0
Participant Mean	7.3
Participant Bias[2]	0.3

Figure 9. Bias Plot of Thyroxine Values by Method
Quarter 3, Specimen 2
Assayed Value (AV)[3] 7.0 µg/dL serum



Quarter 1	
Specimen 1	
Enriched	45.0
CDC Assayed	47.5
Participant Mean	50.2
Participant Bias[2]	5.0

Figure 10. Bias Plot of Thyroid-Stimulating Hormone Values by Method
Quarter 1, Specimen 1
Expected Value (EV)[1] 45.2 µIU/mL serum



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Immunoreactive Trypsinogen (IRT) and Galactose-1-Phosphate Uridyltransferase (GALT)

Figure 11. Bias Plot of Immunoreactive Trypsinogen (IRT) Values by Method
Quarter 3, Specimen 3
Assayed Value (AV)[3] 164.8 ng/mL whole blood

Quarter 3	
Specimen 3	
CDC Assayed	164.8
Participant Mean	155.3
Participant Bias[2]	-9.5

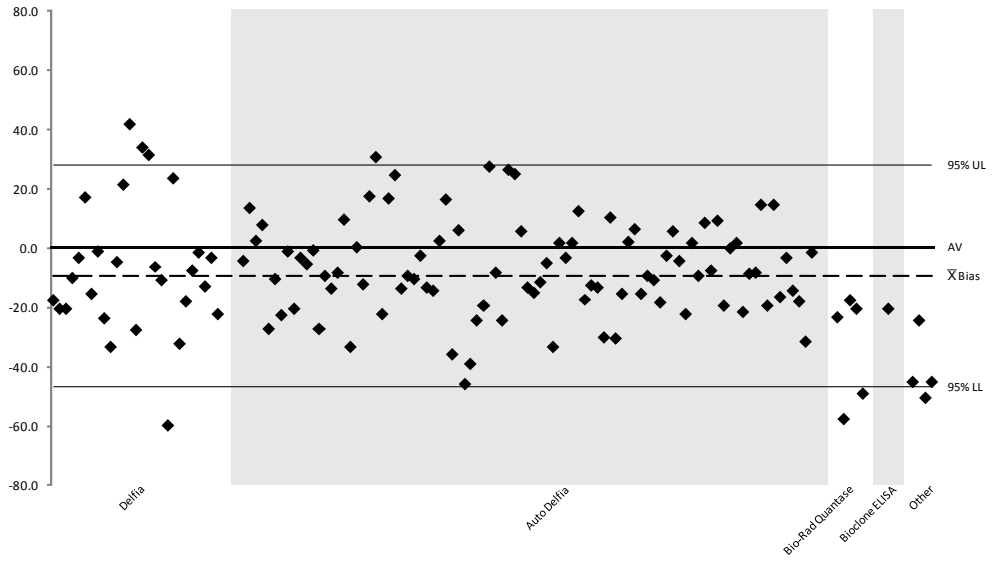
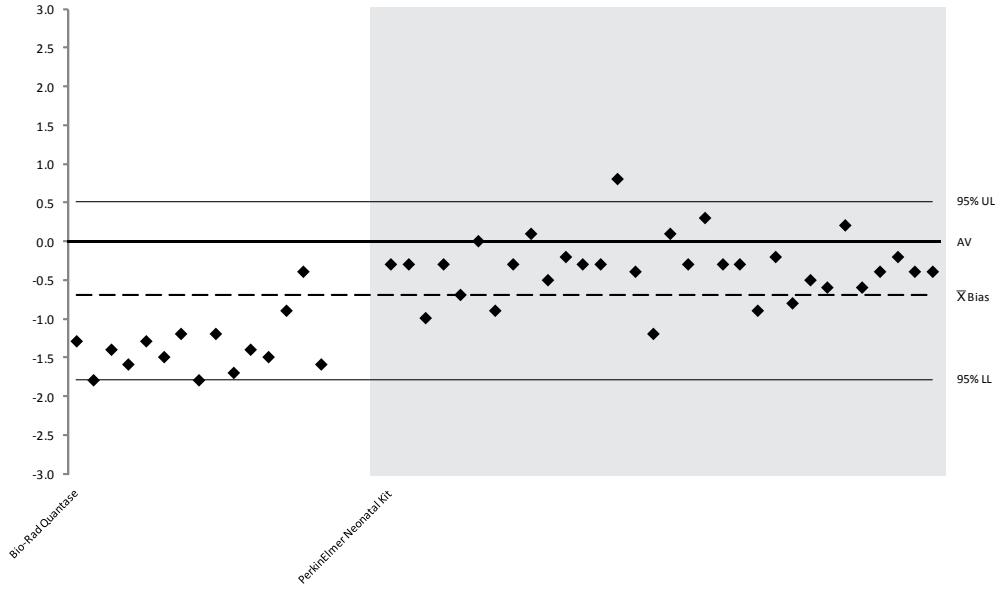


Figure 12. Bias Plot of Galactose-1-Phosphate Uridyltransferase (GALT) Values by Method
Quarter 1, Specimen 4
Assayed Value (AV)[3] 1.8 U/g Hb

Quarter 1	
Specimen 4	
CDC Assayed	1.8
Participant Mean	1.1
Participant Bias[2]	-0.7

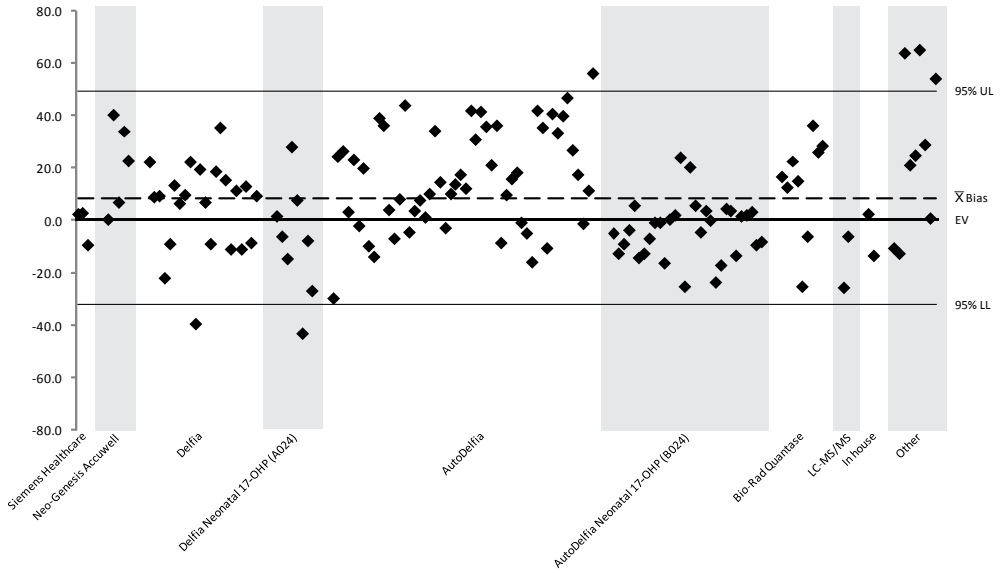


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – 17 α-Hydroxyprogesterone and Total Galactose

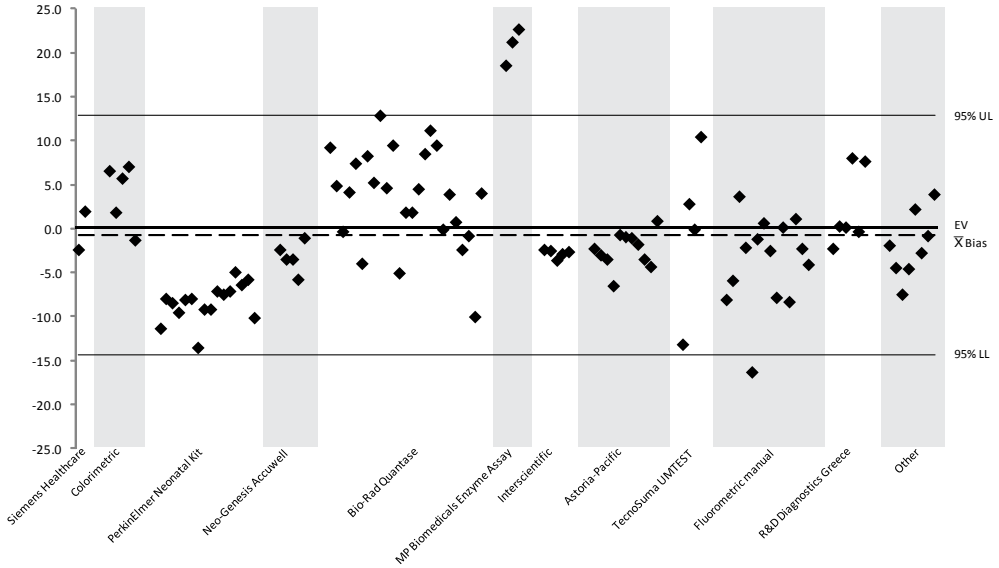
Quarter 1	
Specimen 3	
Enriched	106.0
CDC Assayed	103.4
Participant Mean	114.6
Participant Bias[2]	8.2

Figure 13. Bias Plot of 17 α-Hydroxyprogesterone Values by Method
Quarter 1, Specimen 3
Expected Value (EV)[1] 106.4 ng/mL serum



Quarter 3	
Specimen 3	
Enriched	25.0
CDC Assayed	25.7
Participant Mean	25.6
Participant Bias[2]	-0.8

Figure 14. Bias Plot of Total Galactose Values by Method
Quarter 3, Specimen 3
Expected Value (EV)[1] 26.4 mg/dL whole blood

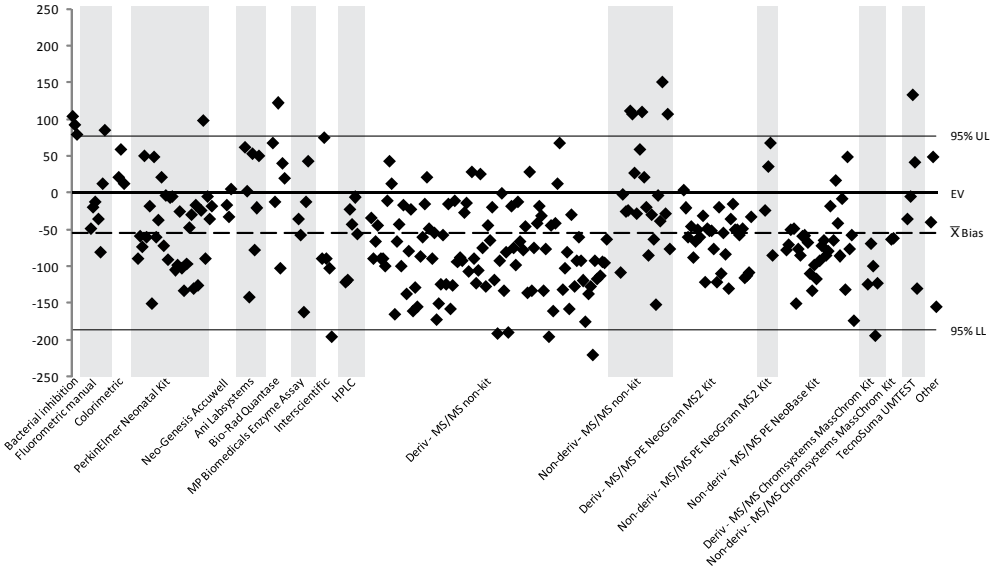


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – Phenylalanine and Leucine

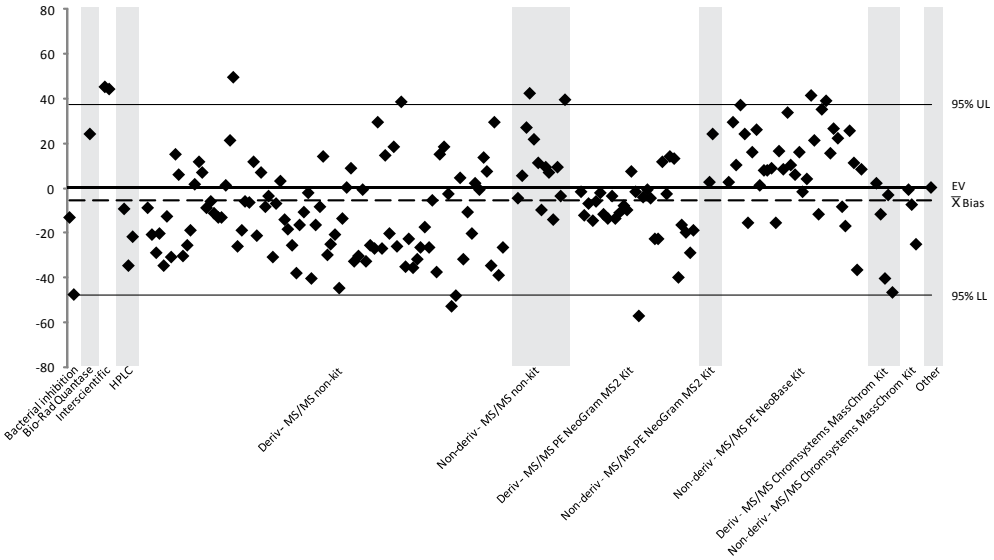
Quarter 1	
Specimen 4	
Enriched	424.20
CDC Assayed	406.02
Participant Mean	416.65
Participant Bias[2]	-56.03

Figure 15. Bias Plot of Phenylalanine Values by Method
Quarter 1, Specimen 4
Expected Value (EV)[1] 472.68 µmol/L whole blood



Quarter 3	
Specimen 5	
Enriched	0.00
CDC Assayed	114.03
Participant Mean	118.48
Participant Bias[2]	-5.49

Figure 16. Bias Plot of Leucine Values by Method
Quarter 3, Specimen 5
Expected Value (EV)[1] 123.97 µmol/L whole blood

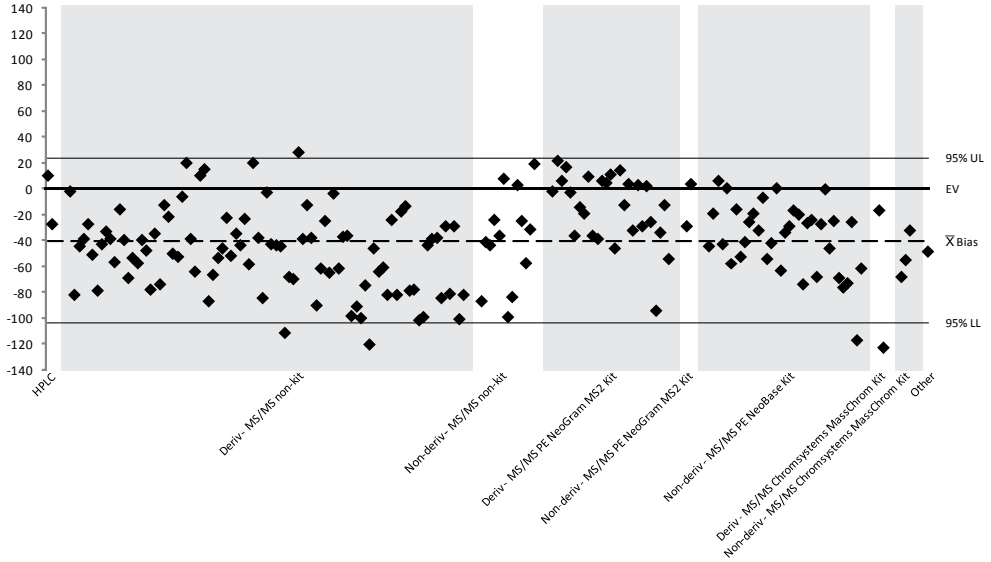


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – Methionine and Tyrosine

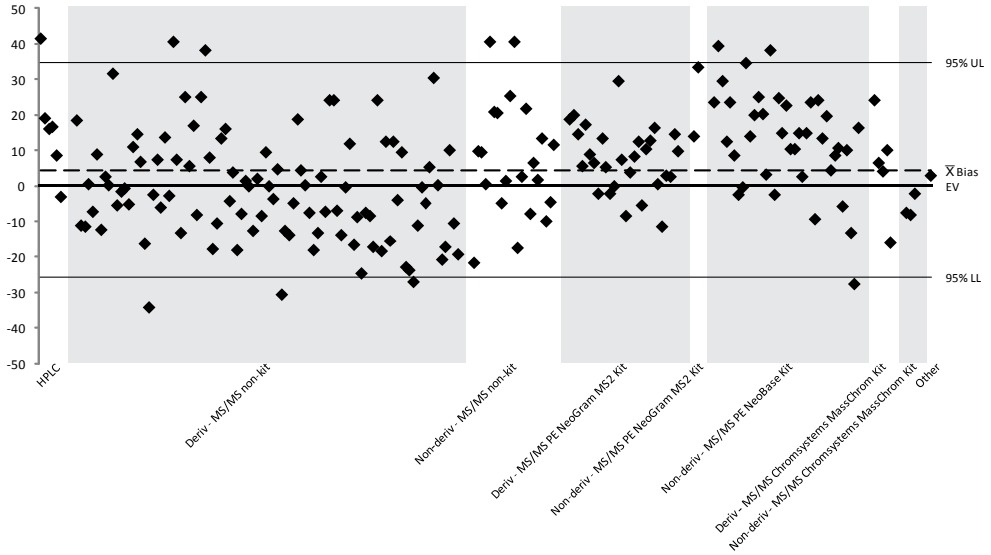
Quarter 3	
Specimen 4	
Enriched	225.00
CDC Assayed	193.49
Participant Mean	200.84
Participant Bias[2]	-40.56

Figure 17. Bias Plot of Methionine Values by Method
Quarter 3, Specimen 4
Expected Value (EV)[1] 241.40 µmol/L whole blood



Quarter 3	
Specimen 3	
Enriched	0.00
CDC Assayed	72.16
Participant Mean	81.05
Participant Bias[2]	4.35

Figure 18. Bias Plot of Tyrosine Values by Method
Quarter 3, Specimen 3
Expected Value (EV)[1] 76.70 µmol/L whole blood

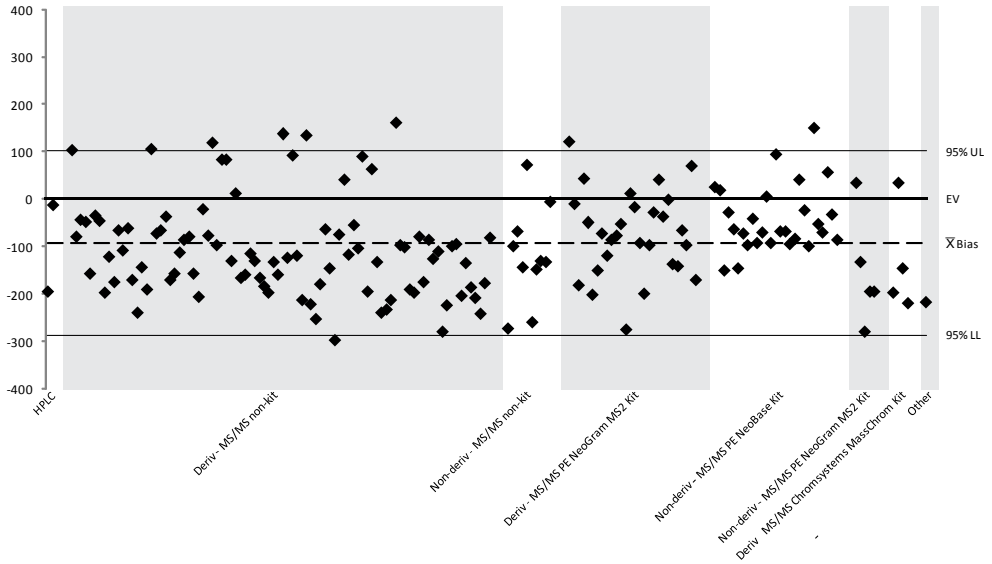


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – Valine and Citrulline

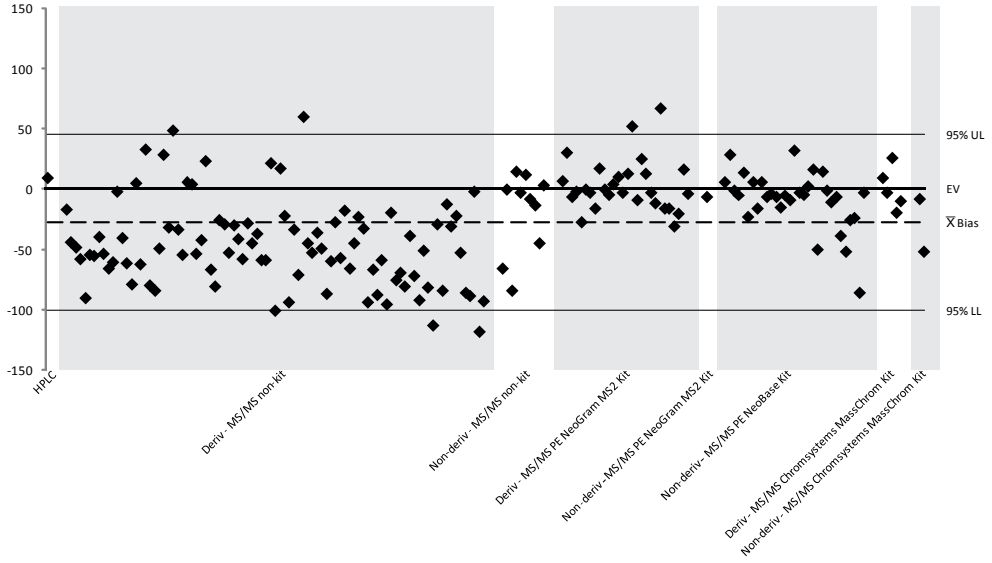
Quarter 1	
Specimen 3	
Enriched	513.00
CDC Assayed	521.55
Participant Mean	572.32
Participant Bias[2]	-94.58

Figure 19. Bias Plot of Valine Values by Method
Quarter 1, Specimen 3
Expected Value (EV)[1] 666.90 µmol/L whole blood



Quarter 3	
Specimen 2	
Enriched	160.00
CDC Assayed	154.91
Participant Mean	152.28
Participant Bias[2]	-28.19

Figure 20. Bias Plot of Citrulline Values by Method
Quarter 3, Specimen 2
Expected Value (EV)[1] 180.47 µmol/L whole 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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Arginine and Succinylacetone (SUAC)

Figure 21. Bias Plot of Arginine Values by Method
Quarter 1, Specimen 1
Assayed Value (AV)[3] 94.73 µmol/L whole blood

Quarter 1	
Specimen 1	
CDC Assayed	94.73
Participant Mean	129.06
Participant Bias[2]	34.33

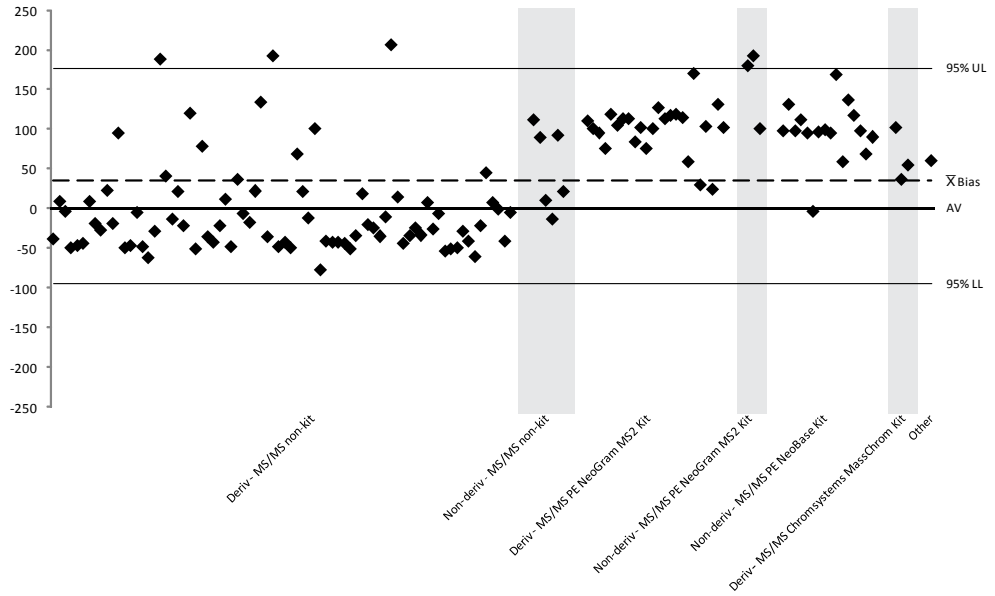
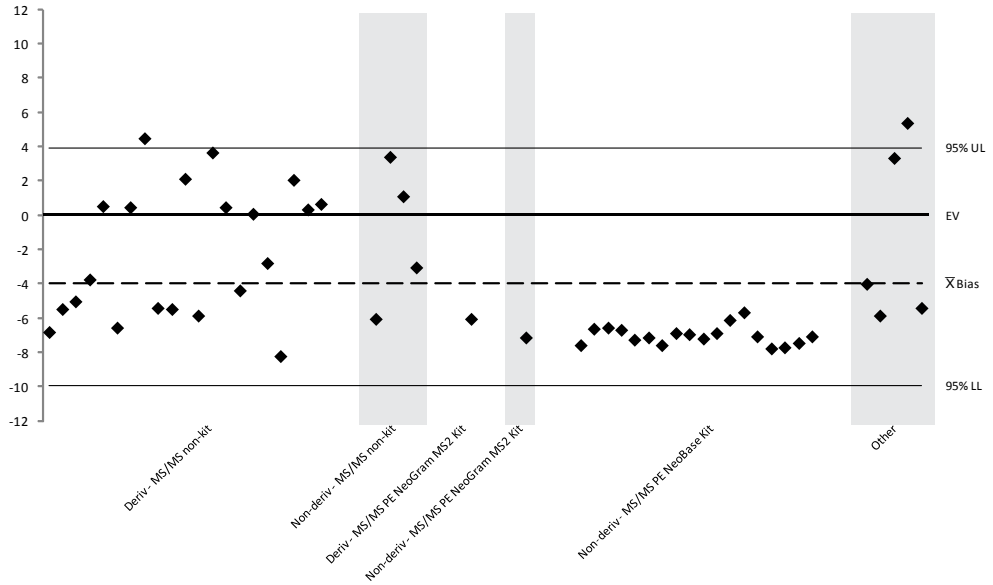


Figure 22. Bias Plot of Succinylacetone (SUAC) Values by Method
Quarter 3, Specimen 5
Expected Value (EV)[1] 10.00 µmol/L whole blood

Quarter 3	
Specimen 5	
Enriched	10.00
CDC Assayed	11.07
Participant Mean	6.02
Participant Bias[2]	-3.98



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Free Carnitine (C0(L)) and Propionylcarnitine (C3)

Figure 23. Bias Plot of Free Carnitine (C0(L)) Values by Method
Quarter 1, Specimen 3
Expected Value (EV)[1] 7.69 µmol/L whole blood

Quarter 1	
Specimen 3	
Enriched	0.00
CDC Assayed	7.18
Participant Mean	8.04
Participant Bias[2]	0.35

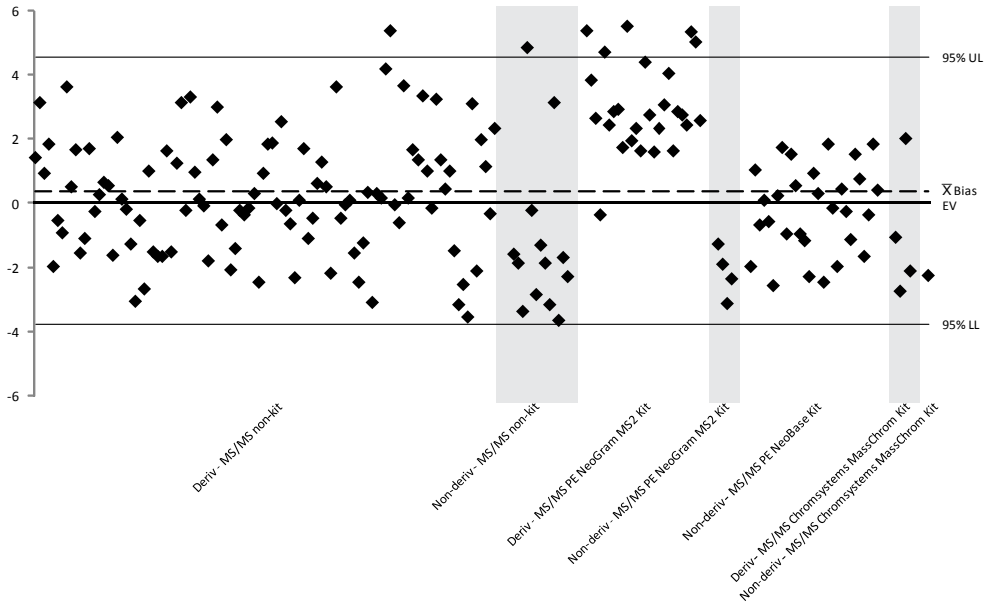
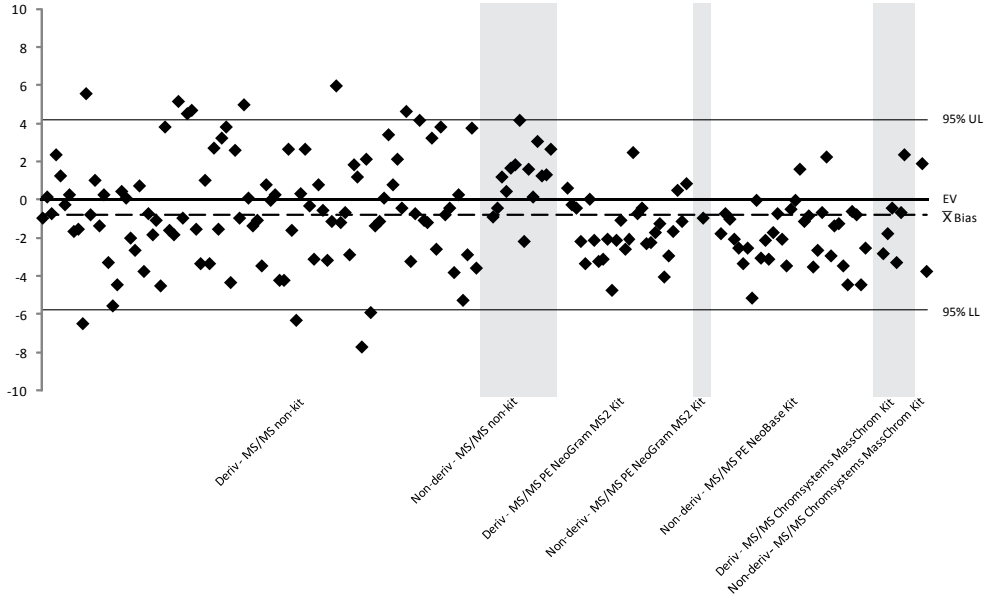


Figure 24. Bias Plot of Propionylcarnitine (C3) Values by Method
Quarter 3, Specimen 5
Expected Value (EV)[1] 15.66 µmol/L whole blood

Quarter 3	
Specimen 5	
Enriched	10.00
CDC Assayed	16.38
Participant Mean	14.84
Participant Bias[2]	-0.82

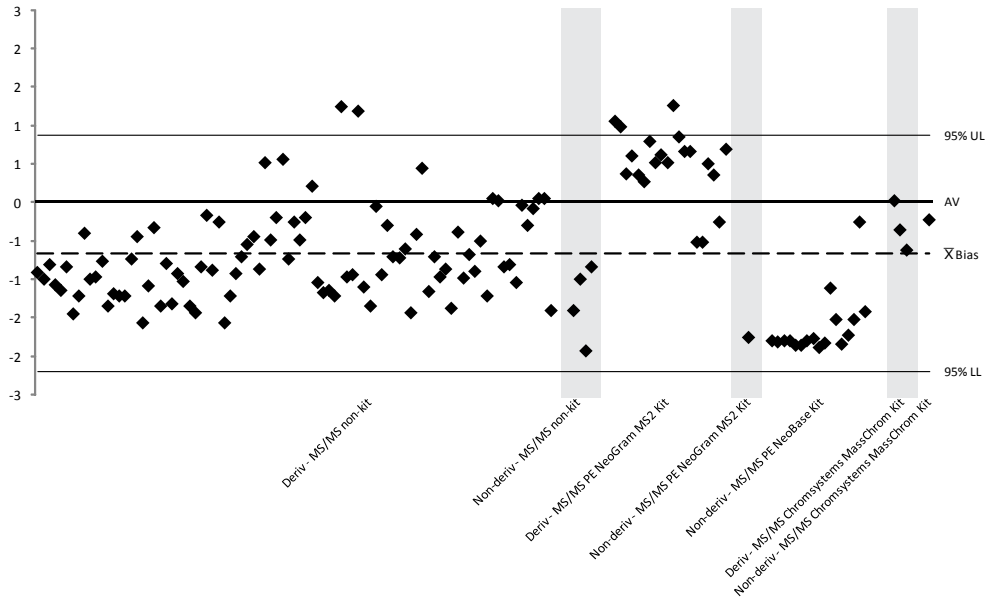


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – Malonylcarnitine (C3DC) and Butyrylcarnitine (C4)

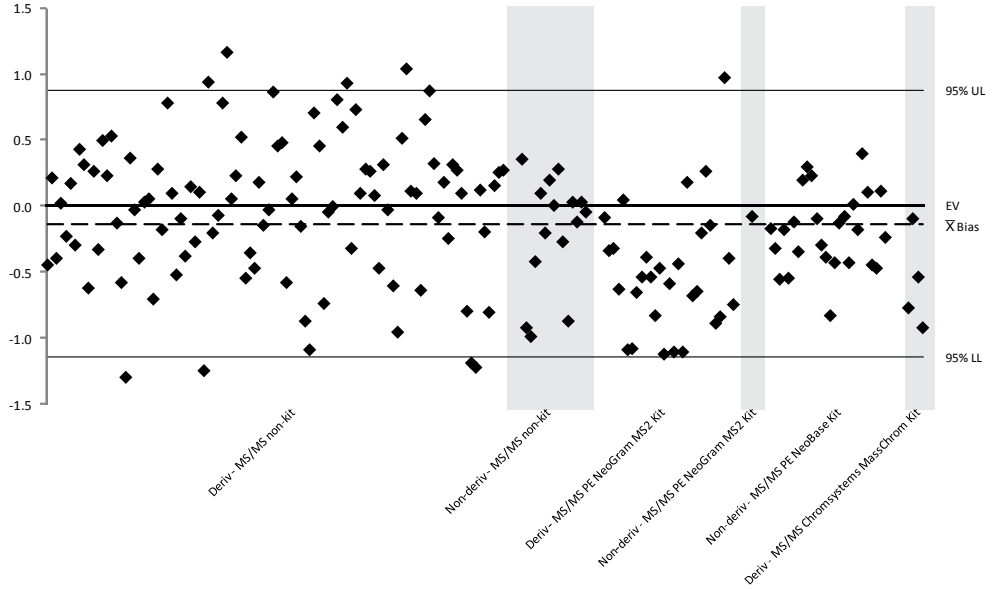
Quarter 3	
Specimen 5	
CDC Assayed	2.21
Participant Mean	1.54
Participant Bias[2]	-0.67

Figure 25. Bias Plot of Malonylcarnitine (C3DC) Values by Method
Quarter 3, Specimen 5
Assayed Value (AV)[3] 2.21 µmol/L whole blood



Quarter 1	
Specimen 5	
Enriched	3.00
CDC Assayed	1.97
Participant Mean	3.08
Participant Bias[2]	-0.14

Figure 26. Bias Plot of Butyrylcarnitine (C4) Values by Method
Quarter 1, Specimen 5
Expected Value (EV)[1] 3.22 µmol/L whole blood

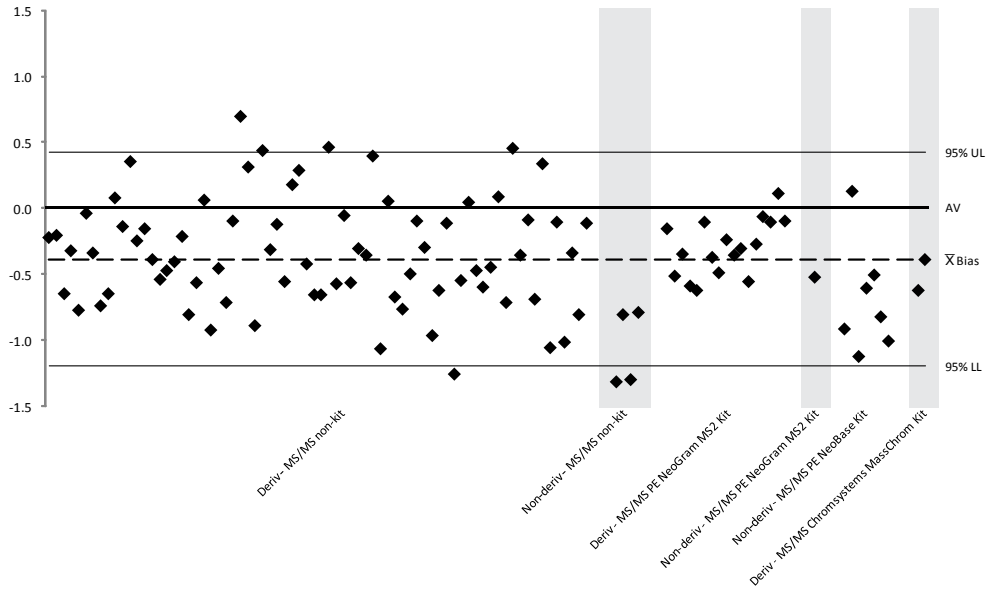


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\overline{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\overline{X}$) excludes 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 Different Methods – Hydroxybutyrylcarnitine (C4OH) and Isovalerylcarnitine (C5)

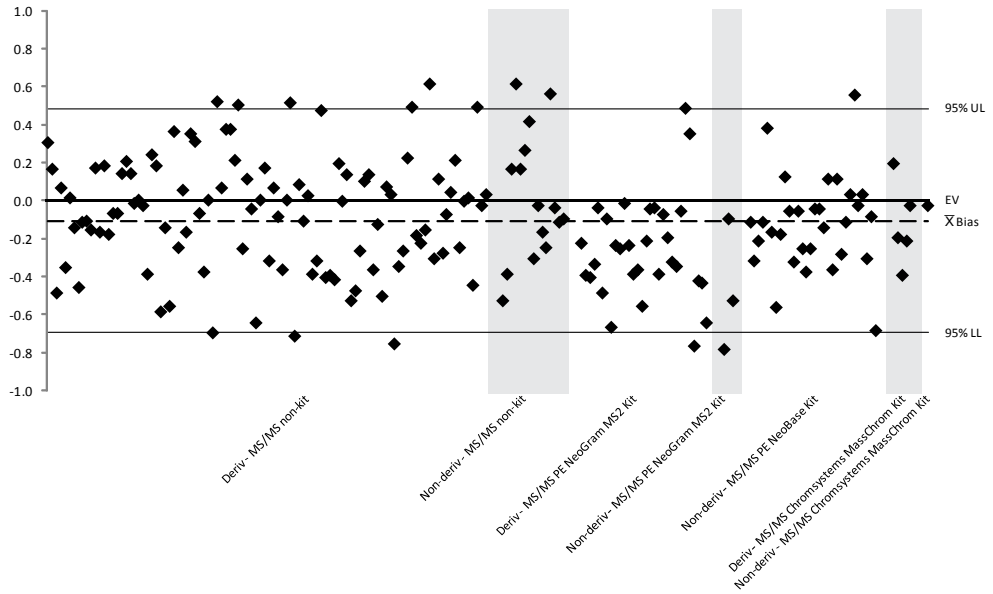
Quarter 1	
Specimen 2	
CDC Assayed	1.87
Participant Mean	1.48
Participant Bias[2]	-0.39

Figure 27. Bias Plot of Hydroxybutyrylcarnitine (C4OH) Values by Method
Quarter 1, Specimen 2
Assayed Value (AV)[3] 1.87 µmol/L whole blood



Quarter 1	
Specimen 5	
Enriched	2.00
CDC Assayed	1.44
Participant Mean	2.08
Participant Bias[2]	-0.11

Figure 28. Bias Plot of Isovalerylcarnitine (C5) Values by Method
Quarter 1, Specimen 5
Expected Value (EV)[1] 2.19 µmol/L whole blood

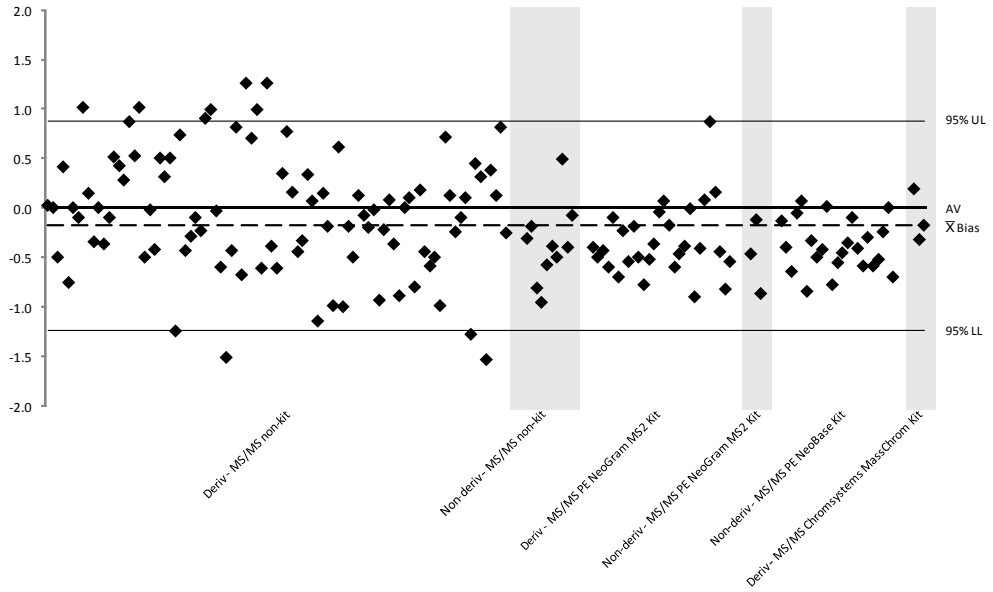


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – Tiglylcarnitine (C5:1) and Glutarylcarnitine (C5DC)

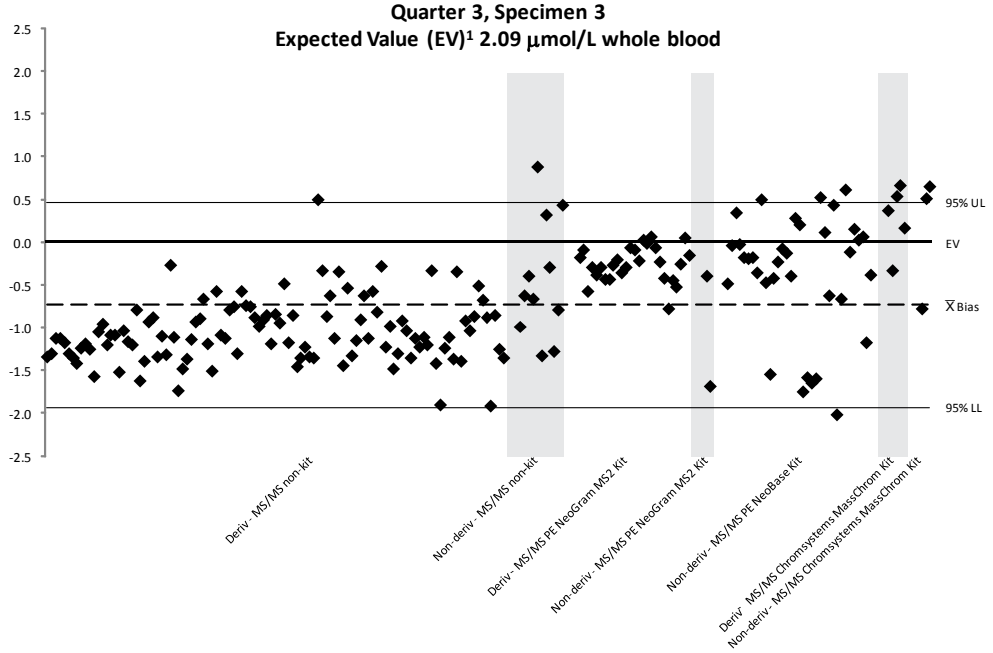
Quarter 1	
Specimen 1	
CDC Assayed	2.19
Participant Mean	2.01
Participant Bias[2]	-0.18

Figure 29. Bias Plot of Tiglylcarnitine (C5:1) Values by Method
Quarter 1, Specimen 1
Assayed Value (AV)[3] 2.19 µmol/L whole blood



Quarter 3	
Specimen 3	
Enriched	2.00
CDC Assayed	1.47
Participant Mean	1.35
Participant Bias[2]	-0.74

Figure 30. Bias Plot of Glutarylcarnitine (C5DC) Values by Method
Quarter 3, Specimen 3
Expected Value (EV)[1] 2.09 µmol/L whole blood

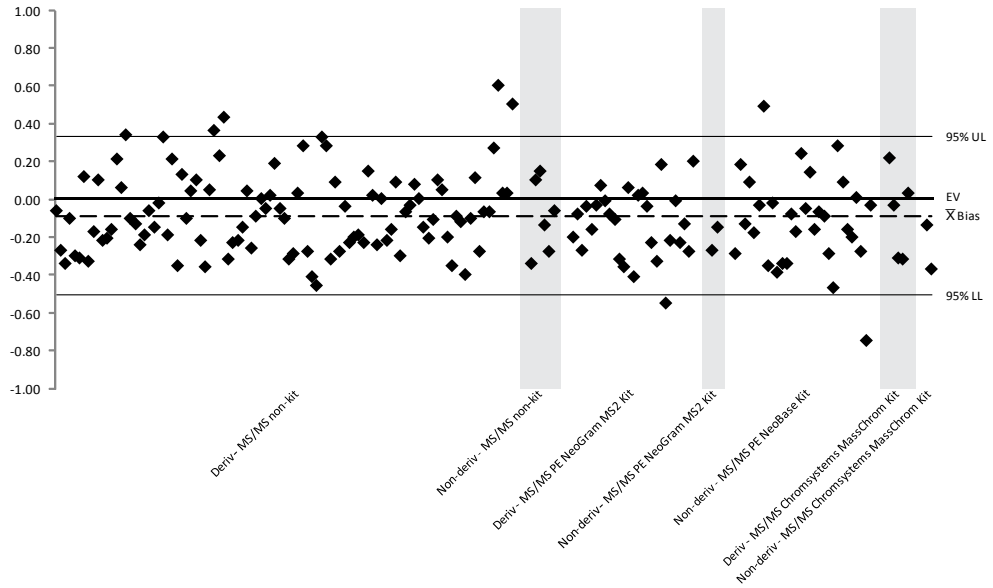


[1]EV is the sum of the endogenous and enrichment values. The solid line represents perfect agreement with the EV or zero bias.
[2]Participant bias ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) excludes outlier 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 Different Methods – 3-Hydroxyisovalerylcarnitine (C5OH) and Hexanoylcarnitine (C6)

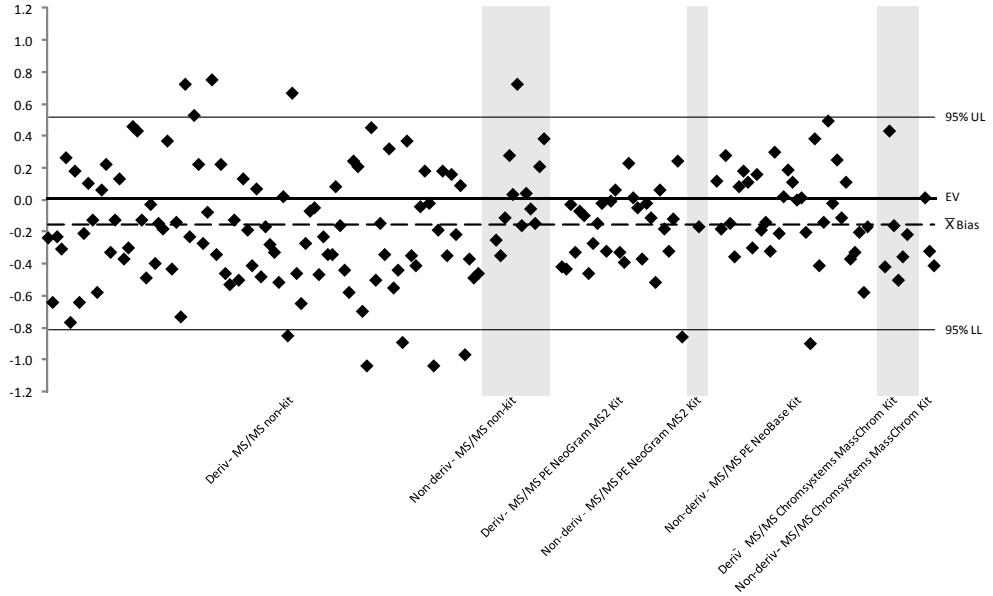
Quarter 3	
Specimen 4	
Enriched	0.00
CDC Assayed	1.05
Participant Mean	0.96
Participant Bias[2]	-0.09

Figure 31. Bias Plot of 3-Hydroxyisovalerylcarnitine (C5OH) Values by Method
Quarter 3, Specimen 4
Expected Value (EV)[1] 1.05 µmol/L whole blood



Quarter 3	
Specimen 1	
Enriched	2.00
CDC Assayed	1.89
Participant Mean	1.86
Participant Bias[2]	-0.16

Figure 32. Bias Plot of Hexanoylcarnitine (C6) Values by Method
Quarter 3, Specimen 1
Expected Value (EV)[1] 2.02 µmol/L whole 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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Octanoylcarnitine (C8) and Decanoylcarnitine (C10)

Figure 33. Bias Plot of Octanoylcarnitine (C8) Values by Method
Quarter 3, Specimen 1
Expected Value (EV)[1] 4.04 µmol/L whole blood

Quarter 3	
Specimen 1	
Enriched	4.00
CDC Assayed	4.06
Participant Mean	3.83
Participant Bias[2]	-0.21

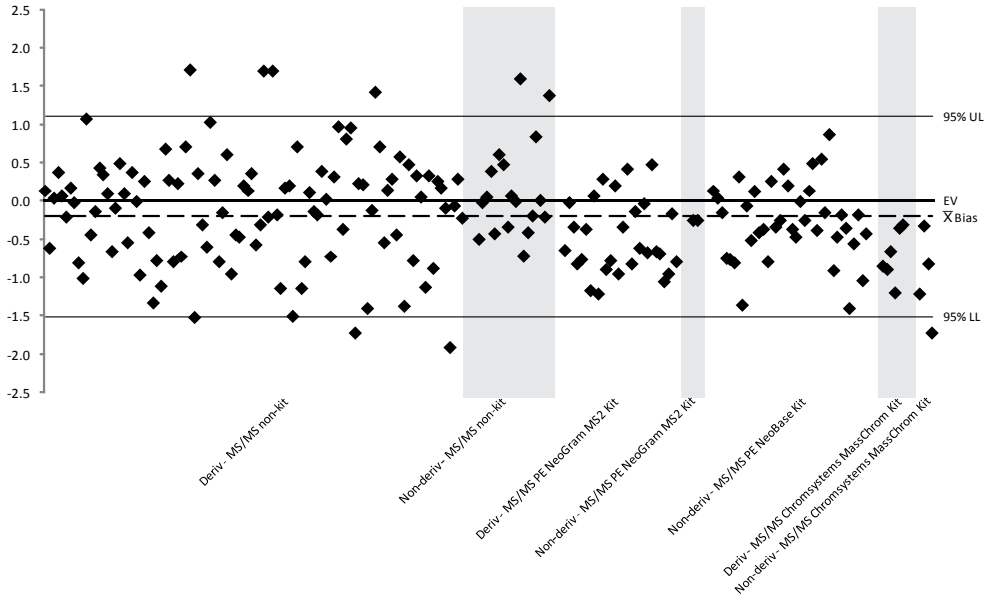
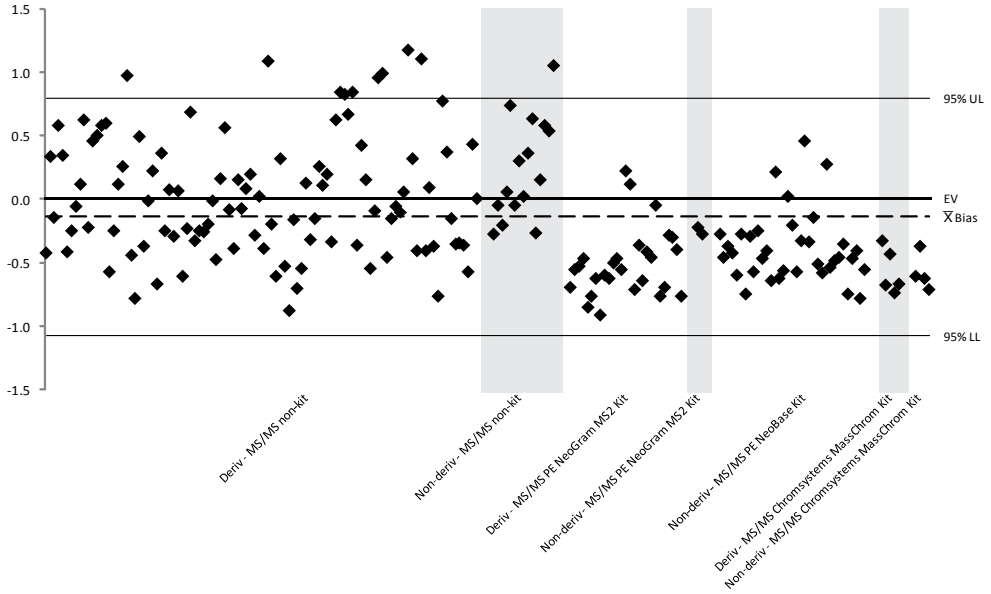


Figure 34. Bias Plot of Decanoylcarnitine (C10) Values by Method
Quarter 3, Specimen 1
Expected Value (EV)[1] 2.05 µmol/L whole blood

Quarter 3	
Specimen 1	
Enriched	2.00
CDC Assayed	1.96
Participant Mean	1.91
Participant Bias[2]	-0.14



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Decenoylcarnitine (C10:1) and Myristoylcarnitine (C14)

Figure 35. Bias Plot of Decenoylcarnitine (C10:1) Values by Method
Quarter 3, Specimen 1
Assayed Value (AV)[3] 3.66 µmol/L whole blood

Quarter 3	
Specimen 1	
CDC Assayed	3.66
Participant Mean	3.27
Participant Bias[2]	-0.39

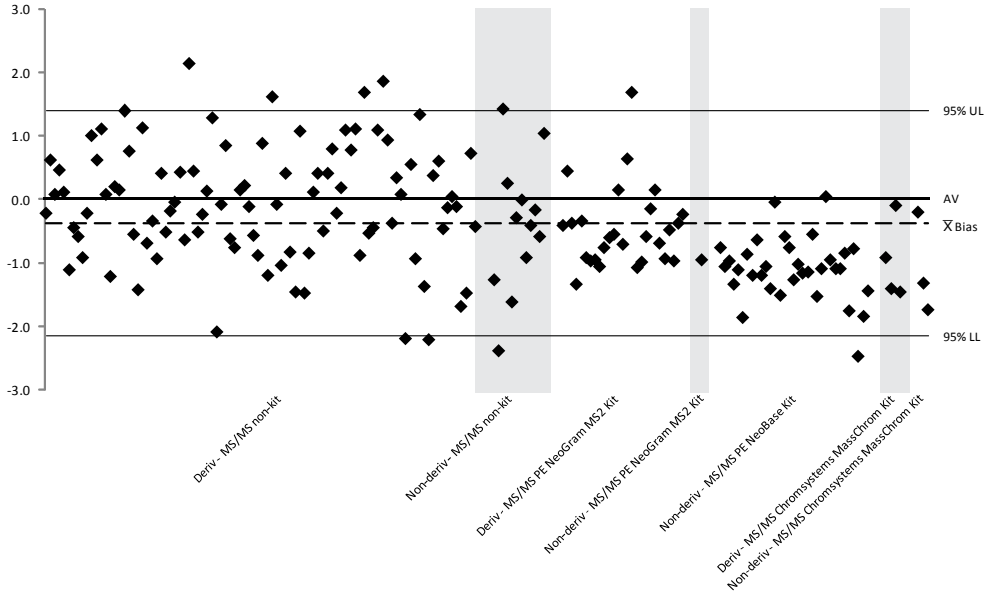
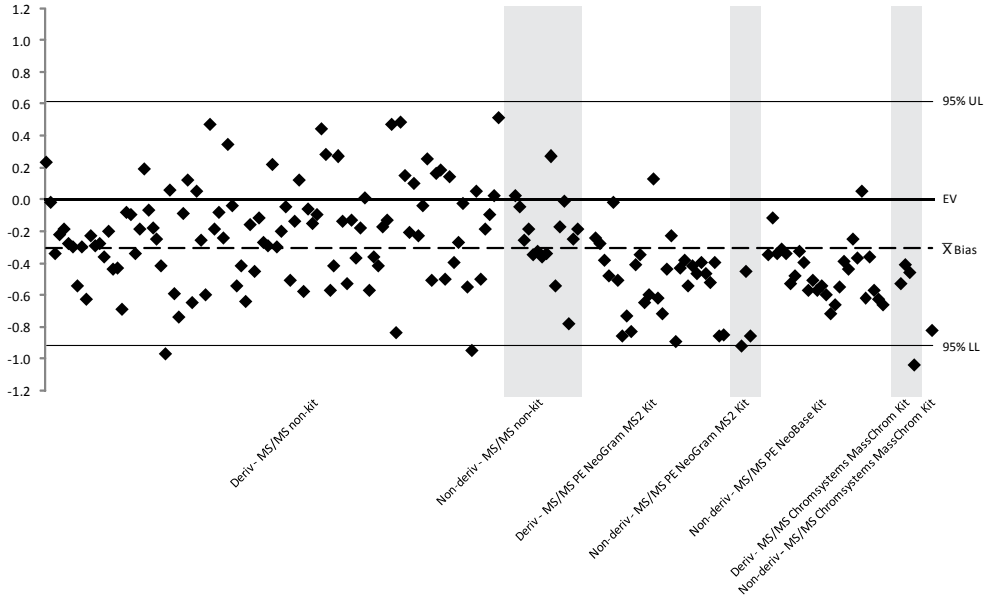


Figure 36. Bias Plot of Myristoylcarnitine (C14) Values by Method
Quarter 1, Specimen 4
Expected Value (EV)[1] 1.85 µmol/L whole blood

Quarter 1	
Specimen 4	
Enriched	1.50
CDC Assayed	1.53
Participant Mean	1.54
Participant Bias[2]	-0.31



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – Tetradecenoylcarnitine (C14:1) and Palmitoylcarnitine (C16)

Figure 37. Bias Plot of Tetradecenoylcarnitine (C14:1) Values by Method
Quarter 1, Specimen 4
Assayed Value (AV)[3] 1.44 µmol/L whole blood

Quarter 1	
Specimen 4	
CDC Assayed	1.44
Participant Mean	1.31
Participant Bias[2]	-0.13

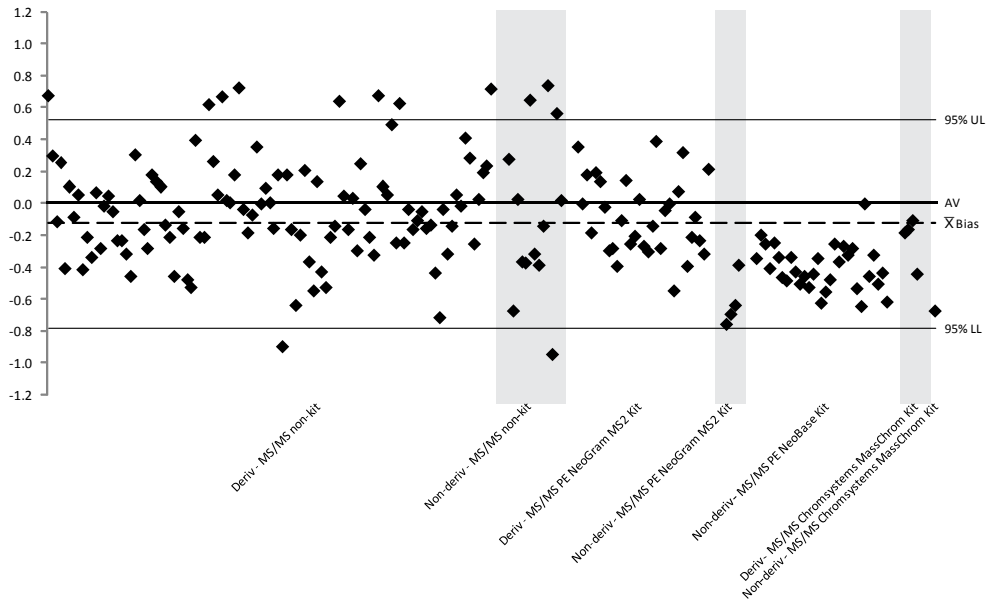
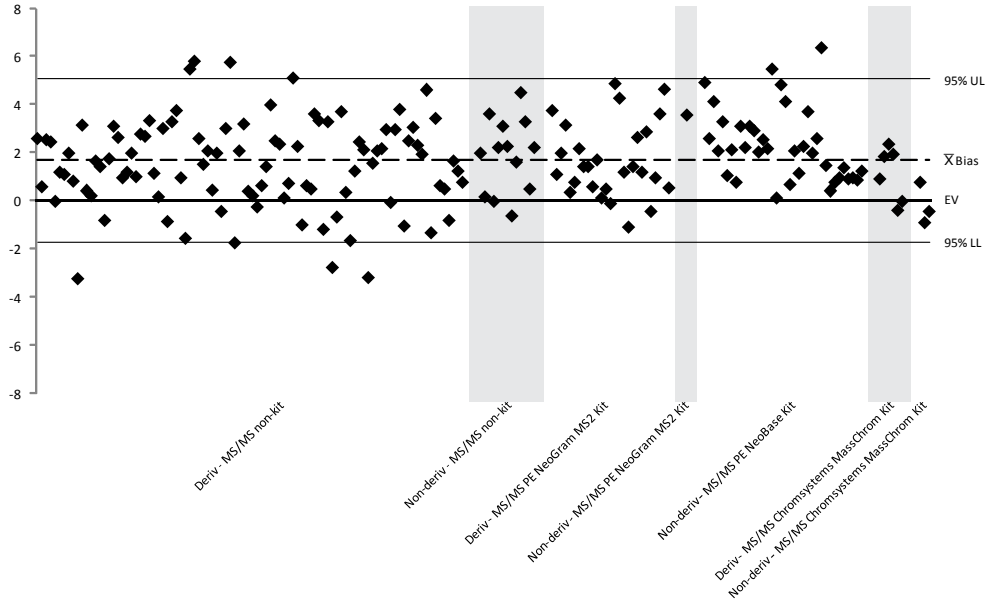


Figure 38. Bias Plot of Palmitoylcarnitine (C16) Values by Method
Quarter 3, Specimen 2
Expected Value (EV)[1] 10.86 µmol/L whole blood

Quarter 3	
Specimen 2	
Enriched	10.00
CDC Assayed	12.71
Participant Mean	12.51
Participant Bias[2]	1.65



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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 Different Methods – 3-Hydroxypalmitoylcarnitine (C16OH) and Stearoylcarnitine (C18)

Figure 39. Bias Plot of 3-Hydroxypalmitoylcarnitine (C16OH) Values by Method
Quarter 3, Specimen 3
Assayed Value (AV)[3] 1.80 µmol/L whole blood

Quarter 3	
Specimen 3	
CDC Assayed	1.80
Participant Mean	1.38
Participant Bias[2]	-0.42

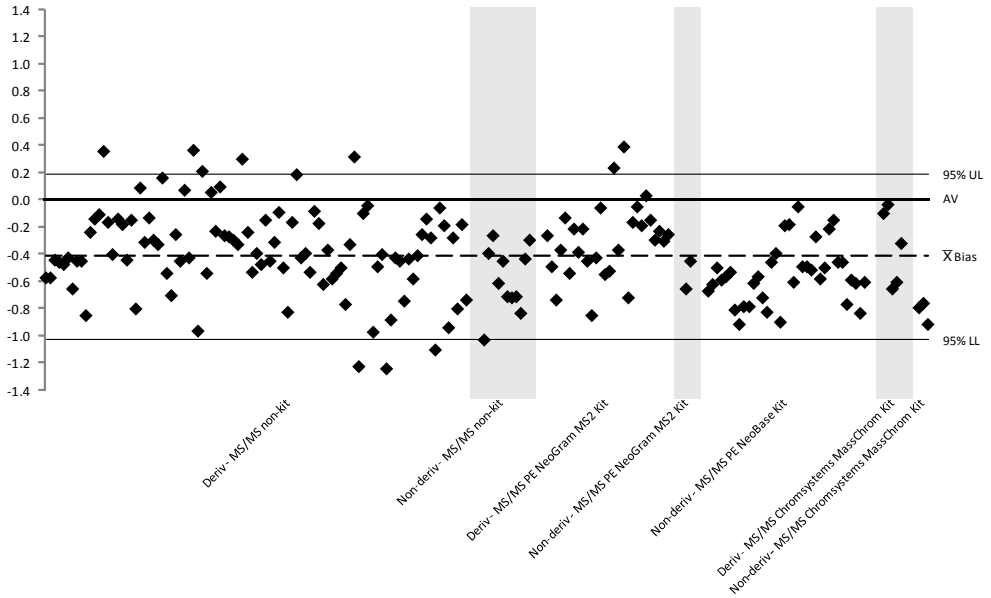
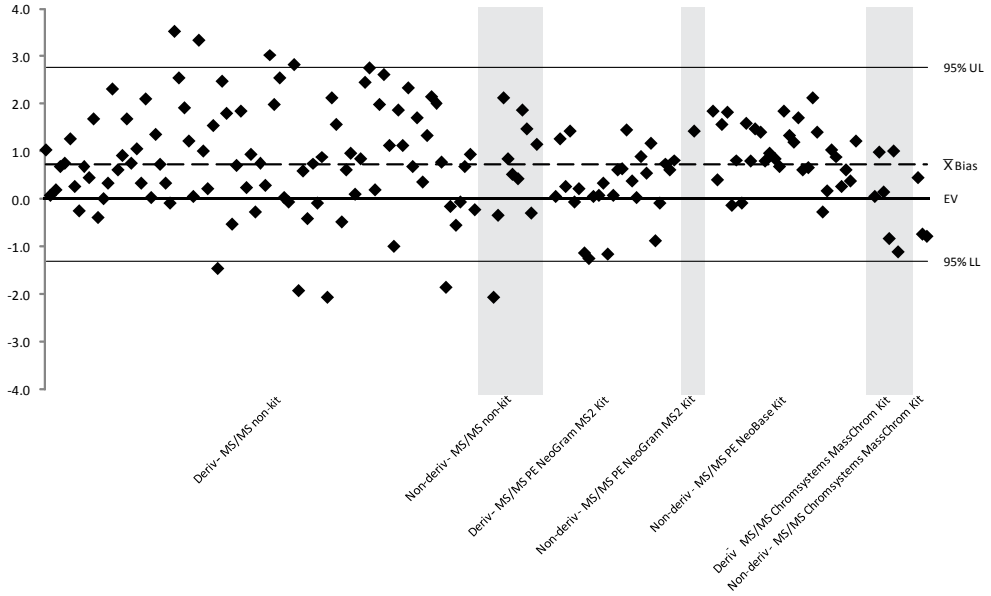


Figure 40. Bias Plot of Stearoylcarnitine (C18) Values by Method
Quarter 3, Specimen 2
Expected Value (EV)[1] 5.46 µmol/L whole blood

Quarter 3	
Specimen 2	
Enriched	5.00
CDC Assayed	6.04
Participant Mean	6.17
Participant Bias[2]	0.71



[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 ($\bar{X}$) is the mean value of all participants' assayed values minus EV; represented by the broken line. Participant bias ($\bar{X}$) 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.

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Table 10a. 2010 Quality Control Data
Summaries of Statistical Analyses

17 α-HYDROXYPROGESTERONE (ng 17-OHP/mL serum)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 951 - Enriched 25 ng/mL serum						
Siemens Healthcare Diagnostics	30	24.2	1.9	2.2	2.2	0.9
Neo-Genesis Accuwell	67	33.3	4.6	4.8	5.7	1.2
Delfia	250	22.3	4.0	6.4	-3.7	1.0
Delfia Neonatal 17-OHP (A024)	99	22.3	3.3	4.7	-2.1	1.0
AutoDelfia	650	23.9	2.4	3.7	-2.3	1.0
AutoDelfia Neonatal 17-OHP (B024)	536	22.1	1.9	2.6	-1.8	1.0
Bio-Rad Quantase	119	29.3	5.6	8.7	2.4	1.1
LC-MS/MS	60	30.3	5.2	7.2	3.5	1.1
In House	58	28.8	2.6	7.9	0.9	1.1
Other	180	25.4	3.9	6.4	1.5	1.0
Lot 952 - Enriched 50 ng/mL serum						
Siemens Healthcare Diagnostics	30	48.1	4.0	5.9	2.2	0.9
Neo-Genesis Accuwell	70	71.5	7.8	11.5	5.7	1.2
Delfia	258	48.3	8.3	14.2	-3.7	1.0
Delfia Neonatal 17-OHP (A024)	97	47.9	5.8	8.7	-2.1	1.0
AutoDelfia	653	50.2	4.8	7.9	-2.3	1.0
AutoDelfia Neonatal 17-OHP (B024)	542	45.8	3.9	5.0	-1.8	1.0
Bio-Rad Quantase	117	55.4	10.4	14.5	2.4	1.1
LC-MS/MS	60	59.0	8.4	14.8	3.5	1.1
In House	58	55.8	5.3	17.0	0.9	1.1
Other	174	52.0	7.3	11.7	1.5	1.0
Lot 953 - Enriched 100 ng/mL serum						
Siemens Healthcare Diagnostics	30	92.1	9.6	12.0	2.2	0.9
Neo-Genesis Accuwell	66	126.9	13.8	13.8	5.7	1.2
Delfia	260	100.3	16.0	33.1	-3.7	1.0
Delfia Neonatal 17-OHP (A024)	100	96.8	14.1	22.1	-2.1	1.0
AutoDelfia	650	102.6	9.7	16.6	-2.3	1.0
AutoDelfia Neonatal 17-OHP (B024)	538	93.6	8.2	10.0	-1.8	1.0
Bio-Rad Quantase	116	109.2	19.2	28.4	2.4	1.1
LC-MS/MS	60	112.7	12.9	22.3	3.5	1.1
In House	58	111.6	10.3	34.5	0.9	1.1
Other	173	99.7	11.8	23.1	1.5	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.

Table 10b. 2010 Quality Control Data
Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPSINOGEN (ng IRT/mL whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 991 - Assayed 26.2 ng/mL whole blood						
MP Biomedicals (ICN) ELISA	20	32.7	2.9	3.8	25.7	0.3
Delfia	293	24.4	3.0	3.7	1.1	0.9
AutoDelfia	1264	22.8	2.0	2.6	-2.4	1.0
Bio-Rad Quantase	108	24.3	3.5	5.6	3.4	0.8
Bioclone ELISA	50	19.2	3.1	5.5	3.2	0.6
Other	103	25.4	2.9	6.1	5.8	0.8
Lot 992 - Assayed 64.3 ng/mL whole blood						
MP Biomedicals (ICN) ELISA	20	47.7	6.0	7.5	25.7	0.3
Delfia	286	62.8	5.3	6.1	1.1	0.9
AutoDelfia	1258	61.9	4.7	5.8	-2.4	1.0
Bio-Rad Quantase	106	53.5	9.1	16.1	3.4	0.8
Bioclone ELISA	50	45.0	6.0	15.1	3.2	0.6
Other	107	59.9	5.8	13.9	5.8	0.8
Lot 993 - Assayed 113.7 ng/mL whole blood						
MP Biomedicals (ICN) ELISA	20	58.0	9.8	9.8	25.7	0.3
Delfia	281	108.1	9.6	11.9	1.1	0.9
AutoDelfia	1259	108.1	7.8	9.9	-2.4	1.0
Bio-Rad Quantase	107	85.6	14.8	27.2	3.4	0.8
Bioclone ELISA	50	76.2	8.6	31.0	3.2	0.6
Other	108	93.6	8.8	26.2	5.8	0.8
Lot 994 - Assayed 177.0 ng/mL whole blood						
MP Biomedicals (ICN) ELISA	20	79.8	9.2	10.8	25.7	0.3
Delfia	284	166.4	15.8	17.9	1.1	0.9
AutoDelfia	1272	171.6	12.6	16.1	-2.4	1.0
Bio-Rad Quantase	100	140.5	25.2	38.5	3.4	0.8
Bioclone ELISA	48	115.7	18.9	66.2	3.2	0.6
Other	110	147.0	18.5	44.7	5.8	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.

Table 10c. 2010 Quality Control Data
Summaries of Statistical Analyses

THYROXINE (μg T4/dL serum)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 801 - Enriched 2 μg/dL serum						
Siemens Healthcare Diagnostics	20	2.6	0.5	0.6	0.4	1.1
Neo-Genesis Accuwell	29	1.9	0.6	0.8	-0.3	1.1
Delfia	58	2.0	0.5	0.9	-0.6	1.1
AutoDelfia	323	1.9	0.3	0.3	-0.1	0.9
Interscientific NeoMAP Multiplex	30	1.5	0.4	0.4	-0.6	1.0
Other	38	2.3	0.3	0.8	-0.3	1.2
Lot 802 - Enriched 7 μg/dL serum						
Siemens Healthcare Diagnostics	20	8.4	0.7	0.8	0.4	1.1
Neo-Genesis Accuwell	30	6.9	1.0	1.6	-0.3	1.1
Delfia	57	6.6	0.9	1.4	-0.6	1.1
AutoDelfia	322	6.5	0.6	0.7	-0.1	0.9
Interscientific NeoMAP Multiplex	30	6.1	0.6	0.6	-0.6	1.0
Other	37	7.5	1.1	1.8	-0.3	1.2
Lot 803 - Enriched 11 μg/dL serum						
Siemens Healthcare Diagnostics	20	12.6	1.4	1.4	0.4	1.1
Neo-Genesis Accuwell	30	11.4	1.4	2.7	-0.3	1.1
Delfia	56	12.3	1.6	3.4	-0.6	1.1
AutoDelfia	323	10.3	0.9	1.0	-0.1	0.9
Interscientific NeoMAP Multiplex	30	10.5	1.2	1.2	-0.6	1.0
Other	39	13.1	1.9	4.7	-0.3	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.

THYROXINE (μg T4/dL serum)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 901 - Enriched 2 μg/dL serum						
Siemens Healthcare Diagnostics	10	2.0	0.5	0.5	-0.2	1.0
Neo-Genesis Accuwell	30	1.9	0.5	0.6	-0.6	1.0
Delfia	77	1.4	0.4	0.4	-0.3	0.8
AutoDelfia	283	1.4	0.3	0.4	-0.3	0.8
Interscientific NeoMAP Multiplex	10	2.1	0.2	0.2	0.9	0.6
Other	47	1.7	0.3	0.4	-0.4	0.9
Lot 902 - Enriched 7 μg/dL serum						
Siemens Healthcare Diagnostics	10	6.4	1.1	1.1	-0.2	1.0
Neo-Genesis Accuwell	28	5.6	0.9	0.9	-0.6	1.0
Delfia	78	4.7	0.7	0.7	-0.3	0.8
AutoDelfia	273	4.8	0.5	0.6	-0.3	0.8
Interscientific NeoMAP Multiplex	10	5.3	0.2	0.2	0.9	0.6
Other	58	5.4	1.0	1.6	-0.4	0.9
Lot 903 - Enriched 11 μg/dL serum						
Siemens Healthcare Diagnostics	10	11.0	1.0	1.0	-0.2	1.0
Neo-Genesis Accuwell	30	11.3	2.6	3.3	-0.6	1.0
Delfia	77	8.2	1.1	1.3	-0.3	0.8
AutoDelfia	281	8.4	0.9	1.0	-0.3	0.8
Interscientific NeoMAP Multiplex	10	7.6	0.3	0.3	0.9	0.6
Other	59	9.9	1.6	3.2	-0.4	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 10d. 2010 Quality Control Data
Summaries of Statistical Analyses

THYROID-STIMULATING HORMONE (μIU TSH/mL serum)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 911 - Enriched 25 μIU/mL serum						
Siemens Healthcare Diagnostics	20	32.9	3.2	5.0	2.5	1.2
Neo-Genesis Accuwell	30	28.2	3.5	5.7	-2.7	1.2
MP Biomedicals IRMA	20	34.2	2.4	2.4	3.1	1.3
Delfia	467	27.1	2.4	3.7	-1.6	1.2
AutoDelfia	853	28.1	2.1	3.0	-1.4	1.2
Ani Labsystems	49	27.4	2.3	2.9	-3.0	1.3
Bio-Rad Quantase	96	25.9	3.5	5.4	-2.6	1.2
TecnoSuma UMELISA	30	26.3	3.7	3.7	-8.2	1.3
Bioclone ELISA	39	31.4	5.4	8.4	-1.2	1.3
DiaSorin	107	29.2	4.0	5.0	-2.5	1.3
In House	30	27.9	3.7	5.9	-3.7	1.3
Other	138	26.5	2.5	5.1	-2.6	1.2
Lot 912 - Enriched 40 μIU/mL serum						
Siemens Healthcare Diagnostics	20	51.8	4.7	4.7	2.5	1.2
Neo-Genesis Accuwell	29	45.3	4.1	7.5	-2.7	1.2
MP Biomedicals IRMA	20	54.2	4.9	5.2	3.1	1.3
Delfia	460	44.7	3.8	5.2	-1.6	1.2
AutoDelfia	852	46.1	3.5	4.7	-1.4	1.2
Ani Labsystems	49	48.0	3.6	3.9	-3.0	1.3
Bio-Rad Quantase	99	43.4	7.5	8.9	-2.6	1.2
TecnoSuma UMELISA	29	43.0	5.2	5.2	-8.2	1.3
Bioclone ELISA	39	50.2	5.6	11.0	-1.2	1.3
DiaSorin	107	47.6	5.5	6.5	-2.5	1.3
In House	30	47.2	6.3	7.0	-3.7	1.3
Other	139	44.5	4.1	8.4	-2.6	1.2
Lot 913 - Enriched 80 μIU/mL serum						
Siemens Healthcare Diagnostics	20	100.3	4.6	11.6	2.5	1.2
Neo-Genesis Accuwell	29	94.8	8.3	11.2	-2.7	1.2
MP Biomedicals IRMA	20	103.7	6.7	9.1	3.1	1.3
Delfia	460	90.6	7.5	11.9	-1.6	1.2
AutoDelfia	861	93.3	6.6	9.8	-1.4	1.2
Ani Labsystems	46	96.5	5.4	7.6	-3.0	1.3
Bio-Rad Quantase	94	89.0	10.9	16.1	-2.6	1.2
TecnoSuma UMELISA	29	98.4	8.6	16.9	-8.2	1.3
Bioclone ELISA	40	102.4	9.9	26.6	-1.2	1.3
DiaSorin	109	98.3	11.5	17.3	-2.5	1.3
In House	30	97.8	11.3	11.9	-3.7	1.3
Other	130	90.9	6.4	10.3	-2.6	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.

THYROID-STIMULATING HORMONE (μIU TSH/mL serum)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 011 - Enriched 25 μIU/mL serum						
Siemens Healthcare Diagnostics	10	28.1	3.0	3.0	-4.2	1.3
Neo-Genesis Accuwell	50	24.3	3.4	6.5	-5.2	1.2
MP Biomedicals IRMA	20	33.0	2.7	3.9	4.2	1.1
Delfia	391	27.2	2.2	2.5	0.2	1.1
AutoDelfia	855	27.3	1.9	2.7	-1.1	1.1
Ani Labsystems	60	26.8	3.2	4.1	-1.5	1.1
Bio-Rad Quantase	78	30.9	2.5	6.2	-0.3	1.2
TecnoSuma UMELISA	30	26.0	2.3	3.3	-6.6	1.3
Bioclone ELISA	70	37.8	4.9	13.2	1.6	1.4
DiaSorin	93	26.6	2.9	5.9	2.8	1.0
In House	30	27.2	3.0	3.6	1.4	1.1
Other	158	25.9	2.5	4.6	-2.8	1.1
Lot 012 - Enriched 40 μIU/mL serum						
Siemens Healthcare Diagnostics	10	46.0	4.4	4.4	-4.2	1.3
Neo-Genesis Accuwell	50	42.8	5.0	7.3	-5.2	1.2
MP Biomedicals IRMA	20	48.7	5.2	7.4	4.2	1.1
Delfia	395	43.3	3.7	4.2	0.2	1.1
AutoDelfia	855	43.7	3.2	4.2	-1.1	1.1
Ani Labsystems	59	44.9	3.5	3.9	-1.5	1.1
Bio-Rad Quantase	78	46.0	3.9	10.3	-0.3	1.2
TecnoSuma UMELISA	30	43.0	4.6	6.0	-6.6	1.3
Bioclone ELISA	69	58.6	8.8	22.9	1.6	1.4
DiaSorin	99	42.8	4.4	8.9	2.8	1.0
In House	30	44.6	3.3	4.1	1.4	1.1
Other	159	43.1	4.6	8.5	-2.8	1.1
Lot 013 - Enriched 80 μIU/mL serum						
Siemens Healthcare Diagnostics	10	97.7	13.0	13.0	-4.2	1.3
Neo-Genesis Accuwell	50	89.9	7.5	9.9	-5.2	1.2
MP Biomedicals IRMA	20	95.0	6.5	8.6	4.2	1.1
Delfia	404	86.5	6.5	11.1	0.2	1.1
AutoDelfia	854	89.2	6.2	8.0	-1.1	1.1
Ani Labsystems	60	90.2	4.9	10.4	-1.5	1.1
Bio-Rad Quantase	79	96.0	9.3	31.2	-0.3	1.2
TecnoSuma UMELISA	29	95.5	9.3	9.9	-6.6	1.3
Bioclone ELISA	69	116.5	15.6	39.9	1.6	1.4
DiaSorin	95	80.9	8.2	17.6	2.8	1.0
In House	29	85.7	5.1	8.8	1.4	1.1
Other	158	89.0	8.6	16.4	-2.8	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 10e. 2010 Quality Control Data
Summaries of Statistical Analyses

TOTAL GALACTOSE (mg Gal/dL whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Enriched 5 mg/dL whole blood						
Fluorometric Manual	120	4.7	0.7	2.0	0.0	1.0
Colorimetric	38	6.0	0.8	0.8	-0.3	1.2
PerkinElmer Neonatal Kit	110	4.7	0.4	0.5	0.8	0.8
Neo-Genesis Accuwell	39	5.5	0.3	0.4	0.8	1.0
Bio-Rad Quantase	132	6.3	1.3	1.7	0.7	1.2
MP Biomedicals Enzyme Assay	30	10.1	0.8	1.8	3.1	1.6
Interscientific Enzyme	39	5.6	0.6	1.1	1.2	0.9
Astoria-Pacific	110	7.0	0.6	1.1	1.6	1.0
TecnoSuma UMTEST	10	6.7	0.7	0.7	1.6	1.0
R&D Diagnostics Greece	36	5.1	0.5	1.6	0.2	1.0
Other	65	4.9	0.8	1.2	0.2	1.0
Lot 926 - Enriched 10 mg/dL whole blood						
Fluorometric Manual	109	9.8	0.8	2.0	0.0	1.0
Colorimetric	40	12.4	1.5	2.4	-0.3	1.2
PerkinElmer Neonatal Kit	119	9.1	0.9	1.0	0.8	0.8
Neo-Genesis Accuwell	40	10.3	0.5	0.5	0.8	1.0
Bio-Rad Quantase	134	12.2	1.4	2.2	0.7	1.2
MP Biomedicals Enzyme Assay	30	19.7	1.3	4.2	3.1	1.6
Interscientific Enzyme	39	10.4	0.7	3.1	1.2	0.9
Astoria-Pacific	109	11.6	0.9	1.4	1.6	1.0
TecnoSuma UMTEST	10	10.9	0.8	0.8	1.6	1.0
R&D Diagnostics Greece	40	10.8	1.0	2.0	0.2	1.0
Other	68	10.1	1.5	2.2	0.2	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.

TOTAL GALACTOSE (mg Gal/dL whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 927 - Enriched 15 mg/dL whole blood						
Fluorometric Manual	102	14.7	1.0	2.4	0.0	1.0
Colorimetric	40	17.8	1.8	4.1	-0.3	1.2
PerkinElmer Neonatal Kit	115	12.9	1.1	1.3	0.8	0.8
Neo-Genesis Accuwell	39	15.0	1.0	1.2	0.8	1.0
Bio-Rad Quantase	135	18.9	2.6	3.2	0.7	1.2
MP Biomedicals Enzyme Assay	29	29.5	1.6	5.7	3.1	1.6
Interscientific Enzyme	40	15.1	1.7	5.0	1.2	0.9
Astoria-Pacific	110	16.8	1.4	2.4	1.6	1.0
TecnoSuma UMTEST	10	17.0	1.9	1.9	1.6	1.0
R&D Diagnostics Greece	38	15.8	1.9	2.5	0.2	1.0
Other	65	14.0	1.4	2.0	0.2	1.0
Lot 928 - Enriched 30 mg/dL whole blood						
Fluorometric Manual	108	29.0	2.0	4.4	0.0	1.0
Colorimetric	40	37.1	3.0	8.7	-0.3	1.2
PerkinElmer Neonatal Kit	119	25.1	2.1	2.8	0.8	0.8
Neo-Genesis Accuwell	39	29.4	1.8	2.3	0.8	1.0
Bio-Rad Quantase	135	35.7	5.0	7.7	0.7	1.2
MP Biomedicals Enzyme Assay	29	51.4	2.6	4.0	3.1	1.6
Interscientific Enzyme	38	28.4	1.7	7.8	1.2	0.9
Astoria-Pacific	105	32.6	2.2	3.1	1.6	1.0
TecnoSuma UMTEST	10	31.2	3.4	3.4	1.6	1.0
R&D Diagnostics Greece	39	31.2	4.0	4.0	0.2	1.0
Other	66	28.8	2.5	4.4	0.2	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.

TOTAL GALACTOSE (mg Gal/dL whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Enriched 5 mg/dL whole blood						
Siemens Healthcare Diagnostics	10	5.6	0.2	0.2	-1.6	1.3
Fluorometric Manual	110	5.6	0.5	0.7	1.2	0.9
Colorimetric	28	5.9	1.0	1.0	-0.3	1.2
PerkinElmer Neonatal Kit	123	4.6	0.6	0.7	1.1	0.8
Neo-Genesis Accuwell	56	6.1	0.4	1.2	0.8	1.0
Bio-Rad Quantase	86	5.4	1.1	1.2	-1.1	1.3
MP Biomedicals Enzyme Assay	28	10.0	0.7	0.9	1.4	1.8
Interscientific Enzyme	10	6.1	0.7	0.7	1.1	0.8
Astoria-Pacific	88	7.5	0.6	1.2	3.0	0.9
TecnoSuma UMTEST	20	6.7	1.0	2.2	0.3	1.2
R&D Diagnostics Greece	60	6.1	0.8	1.2	0.6	1.1
Other	87	5.9	0.7	1.1	1.3	1.0
Lot 022 - Enriched 10 mg/dL whole blood						
Siemens Healthcare Diagnostics	10	11.3	0.8	0.8	-1.6	1.3
Fluorometric Manual	117	10.2	0.8	1.3	1.2	0.9
Colorimetric	30	11.9	2.1	2.2	-0.3	1.2
PerkinElmer Neonatal Kit	127	8.7	0.7	1.1	1.1	0.8
Neo-Genesis Accuwell	55	10.8	0.7	1.1	0.8	1.0
Bio-Rad Quantase	84	12.0	2.0	2.3	-1.1	1.3
MP Biomedicals Enzyme Assay	30	19.9	2.0	3.2	1.4	1.8
Interscientific Enzyme	10	8.7	0.7	0.7	1.1	0.8
Astoria-Pacific	89	12.5	1.0	1.6	3.0	0.9
TecnoSuma UMTEST	20	12.3	1.4	3.8	0.3	1.2
R&D Diagnostics Greece	58	11.2	1.1	1.3	0.6	1.1
Other	90	11.4	1.1	2.1	1.3	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.

TOTAL GALACTOSE (mg Gal/dL whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 023 - Enriched 15 mg/dL whole blood						
Siemens Healthcare Diagnostics	10	15.8	1.5	1.5	-1.6	1.3
Fluorometric Manual	114	14.4	1.0	1.8	1.2	0.9
Colorimetric	30	18.4	2.8	3.4	-0.3	1.2
PerkinElmer Neonatal Kit	126	12.7	0.9	1.3	1.1	0.8
Neo-Genesis Accuwell	57	15.6	0.9	2.3	0.8	1.0
Bio-Rad Quantase	85	17.7	3.0	3.6	-1.1	1.3
MP Biomedicals Enzyme Assay	30	27.4	2.1	4.9	1.4	1.8
Interscientific Enzyme	10	13.4	1.8	1.8	1.1	0.8
Astoria-Pacific	84	16.3	1.0	1.4	3.0	0.9
TecnoSuma UMTEST	20	19.1	2.1	3.6	0.3	1.2
R&D Diagnostics Greece	59	16.5	1.7	2.4	0.6	1.1
Other	88	15.9	1.2	2.4	1.3	1.0
Lot 024 - Enriched 30 mg/dL whole blood						
Siemens Healthcare Diagnostics	10	37.3	2.6	2.6	-1.6	1.3
Fluorometric Manual	110	27.7	1.7	4.2	1.2	0.9
Colorimetric	30	36.8	5.9	9.6	-0.3	1.2
PerkinElmer Neonatal Kit	130	23.6	1.8	3.2	1.1	0.8
Neo-Genesis Accuwell	58	31.2	1.5	5.1	0.8	1.0
Bio-Rad Quantase	89	37.7	5.4	6.7	-1.1	1.3
MP Biomedicals Enzyme Assay	30	54.7	4.4	7.0	1.4	1.8
Interscientific Enzyme	10	26.7	3.8	3.8	1.1	0.8
Astoria-Pacific	87	30.5	1.8	2.9	3.0	0.9
TecnoSuma UMTEST	20	37.5	3.6	9.8	0.3	1.2
R&D Diagnostics Greece	57	32.9	2.3	2.8	0.6	1.1
Other	89	30.4	2.2	4.9	1.3	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.

Table 10f. 2010 Quality Control Data
Summaries of Statistical Analyses

PHENYLALANINE (μmol Phe/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
Bacterial Inhibition Assays	20	75.74	10.01	15.29	82.84	0.8
Fluorometric Manual	69	121.46	11.98	30.99	125.97	1.1
Colorimetric	79	90.04	13.02	16.04	95.64	1.4
PerkinElmer Neonatal Kit	269	79.41	11.74	14.52	75.99	0.9
Neo-Genesis Accuwell	10	75.75	14.07	14.07	74.97	1.0
Ani Labsystems	110	90.54	10.07	18.90	99.27	1.1
Bio-Rad Quantase	60	79.75	24.17	45.78	71.99	1.0
MP Biomedicals Enzyme Assay	20	45.68	20.73	32.11	56.08	1.2
Interscientific Enzyme	20	78.82	7.01	7.01	83.19	0.8
Astoria-Pacific	30	61.29	2.95	51.66	60.01	0.6
HPLC	30	88.75	11.20	16.04	87.72	0.9
Derivatized - MS/MS Non-kit	790	76.52	6.48	10.15	75.01	0.9
Non-derivatized - MS/MS Non-kit	209	88.89	6.58	15.90	86.92	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	236	80.85	6.80	8.98	80.28	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	109.78	7.96	7.96	92.26	1.3
Non-derivatized - MS/MS PE NeoBase Kit	174	80.86	5.55	8.67	75.46	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	75.17	9.72	12.86	74.91	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	82.92	5.19	6.97	86.25	0.9
TecnoSuma UMTEST	20	119.69	29.58	35.62	115.06	1.1
Other	19	79.26	3.19	3.29	71.80	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 926 - Enriched 121 μmol/L whole blood						
Bacterial Inhibition Assays	20	187.46	18.67	21.08	82.84	0.8
Fluorometric Manual	70	252.46	18.57	46.34	125.97	1.1
Colorimetric	80	265.41	19.00	45.21	95.64	1.4
PerkinElmer Neonatal Kit	274	186.41	19.54	25.53	75.99	0.9
Neo-Genesis Accuwell	10	180.59	20.76	20.76	74.97	1.0
Ani Labsystems	110	234.56	23.03	38.64	99.27	1.1
Bio-Rad Quantase	60	189.05	31.87	101.43	71.99	1.0
MP Biomedicals Enzyme Assay	30	174.35	37.42	48.67	56.08	1.2
Interscientific Enzyme	20	183.60	13.40	13.40	83.19	0.8
Astoria-Pacific	30	136.20	5.36	113.39	60.01	0.6
HPLC	30	199.19	10.57	17.82	87.72	0.9
Derivatized - MS/MS Non-kit	799	177.95	14.76	24.21	75.01	0.9
Non-derivatized - MS/MS Non-kit	210	207.34	13.64	36.63	86.92	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	239	190.46	14.79	20.83	80.28	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	233.16	18.04	18.04	92.26	1.3
Non-derivatized - MS/MS PE NeoBase Kit	172	184.32	13.77	23.28	75.46	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	174.55	19.61	28.55	74.91	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	201.55	13.11	19.41	86.25	0.9
TecnoSuma UMTEST	19	221.11	44.96	44.96	115.06	1.1
Other	20	183.17	13.51	19.70	71.80	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 927 - Enriched 303 μmol/L whole blood						
Bacterial Inhibition Assays	20	333.25	15.60	37.27	82.84	0.8
Fluorometric Manual	58	454.15	30.41	86.18	125.97	1.1
Colorimetric	80	540.98	30.33	81.74	95.64	1.4
PerkinElmer Neonatal Kit	271	355.11	29.09	41.72	75.99	0.9
Neo-Genesis Accuwell	10	398.14	21.77	21.77	74.97	1.0
Ani Labsystems	110	432.03	37.38	68.55	99.27	1.1
Bio-Rad Quantase	60	366.79	37.91	185.97	71.99	1.0
MP Biomedicals Enzyme Assay	30	446.35	51.41	59.03	56.08	1.2
Interscientific Enzyme	20	335.72	19.83	19.83	83.19	0.8
Astoria-Pacific	30	251.18	12.84	209.83	60.01	0.6
HPLC	30	371.66	22.92	27.07	87.72	0.9
Derivatized - MS/MS Non-kit	786	338.30	24.89	43.60	75.01	0.9
Non-derivatized - MS/MS Non-kit	210	392.04	26.21	69.93	86.92	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	237	361.36	28.82	38.19	80.28	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	471.22	40.93	40.93	92.26	1.3
Non-derivatized - MS/MS PE NeoBase Kit	174	352.73	24.06	37.77	75.46	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	320.42	30.72	55.61	74.91	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	367.63	30.07	37.97	86.25	0.9
TecnoSuma UMTEST	18	495.45	59.21	59.21	115.06	1.1
Other	20	323.36	27.14	27.28	71.80	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 928 - Enriched 666 μmol/L whole blood						
Bacterial Inhibition Assays	20	622.05	75.04	83.78	82.84	0.8
Fluorometric Manual	69	820.29	43.23	132.05	125.97	1.1
Colorimetric	72	1037.42	45.78	110.65	95.64	1.4
PerkinElmer Neonatal Kit	274	697.57	56.15	79.37	75.99	0.9
Neo-Genesis Accuwell	10	732.05	60.32	60.32	74.97	1.0
Ani Labsystems	110	809.13	68.01	109.69	99.27	1.1
Bio-Rad Quantase	60	742.62	72.37	403.69	71.99	1.0
MP Biomedicals Enzyme Assay	29	802.35	63.92	72.32	56.08	1.2
Interscientific Enzyme	20	623.56	57.03	57.03	83.19	0.8
Astoria-Pacific	30	483.83	20.97	404.77	60.01	0.6
HPLC	30	710.52	47.70	63.66	87.72	0.9
Derivatized - MS/MS Non-kit	788	653.18	49.32	96.80	75.01	0.9
Non-derivatized - MS/MS Non-kit	206	760.33	62.65	125.69	86.92	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	240	694.96	56.99	79.35	80.28	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	955.20	45.11	45.11	92.26	1.3
Non-derivatized - MS/MS PE NeoBase Kit	177	697.42	39.51	73.33	75.46	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	619.12	92.57	127.61	74.91	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	39	701.29	50.99	61.75	86.25	0.9
TecnoSuma UMTEST	19	854.92	141.90	150.12	115.06	1.1
Other	20	672.84	39.15	105.80	71.80	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
Bacterial Inhibition Assays	20	82.15	14.48	16.09	94.80	0.8
Fluorometric Manual	70	119.07	11.19	41.74	125.13	0.9
Colorimetric	80	116.26	16.64	23.00	111.30	1.4
PerkinElmer Neonatal Kit	272	94.72	11.55	18.00	96.96	0.9
Neo-Genesis Accuwell	20	97.63	11.43	30.36	101.37	1.0
Ani Labsystems	79	93.77	9.04	16.47	99.88	1.1
Bio-Rad Quantase	30	111.16	16.33	16.33	109.30	1.1
MP Biomedicals Enzyme Assay	20	45.18	14.29	15.65	48.36	1.1
Interscientific Enzyme	40	55.53	9.57	63.23	55.59	0.4
Astoria-Pacific	20	105.30	3.28	28.59	112.52	0.9
HPLC	40	94.42	6.31	12.02	99.86	0.9
Derivatized - MS/MS Non-kit	740	82.49	6.85	11.46	85.48	0.8
Non-derivatized - MS/MS Non-kit	159	95.68	6.84	14.98	99.18	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	205	89.43	7.27	10.54	91.61	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	95.58	2.85	2.85	97.31	1.0
Non-derivatized - MS/MS PE NeoBase Kit	186	87.34	6.19	9.26	90.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	84.94	8.60	10.32	87.99	0.8
TecnoSuma UMTEST	30	96.00	21.84	84.46	104.41	0.7
Other	70	84.55	10.96	55.84	83.66	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 022 - Enriched 182 μmol/L whole blood						
Bacterial Inhibition Assays	18	257.73	16.72	19.20	94.80	0.8
Fluorometric Manual	70	302.29	25.15	56.53	125.13	0.9
Colorimetric	80	374.37	34.04	56.64	111.30	1.4
PerkinElmer Neonatal Kit	274	266.95	24.78	38.80	96.96	0.9
Neo-Genesis Accuwell	20	290.18	18.48	25.66	101.37	1.0
Ani Labsystems	80	302.56	25.58	39.07	99.88	1.1
Bio-Rad Quantase	30	316.50	19.72	31.58	109.30	1.1
MP Biomedicals Enzyme Assay	20	257.48	41.62	41.62	48.36	1.1
Interscientific Enzyme	40	126.10	12.46	141.31	55.59	0.4
Astoria-Pacific	20	288.84	8.95	50.19	112.52	0.9
HPLC	40	269.67	15.49	23.41	99.86	0.9
Derivatized - MS/MS Non-kit	723	242.28	17.62	30.65	85.48	0.8
Non-derivatized - MS/MS Non-kit	159	286.60	20.83	44.21	99.18	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	263.63	20.73	30.99	91.61	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	291.54	16.47	16.47	97.31	1.0
Non-derivatized - MS/MS PE NeoBase Kit	186	256.99	18.17	29.34	90.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	49	241.37	24.69	27.86	87.99	0.8
TecnoSuma UMTEST	30	248.08	47.28	214.57	104.41	0.7
Other	70	238.39	28.41	159.22	83.66	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 023 - Enriched 424 μmol/L whole blood						
Bacterial Inhibition Assays	20	453.33	38.70	54.12	94.80	0.8
Fluorometric Manual	67	518.76	32.65	70.21	125.13	0.9
Colorimetric	79	669.24	49.64	106.66	111.30	1.4
PerkinElmer Neonatal Kit	272	479.32	36.74	61.48	96.96	0.9
Neo-Genesis Accuwell	20	550.47	29.81	42.84	101.37	1.0
Ani Labsystems	80	574.43	54.52	81.39	99.88	1.1
Bio-Rad Quantase	30	533.22	50.98	97.03	109.30	1.1
MP Biomedicals Enzyme Assay	20	468.90	41.80	41.80	48.36	1.1
Interscientific Enzyme	40	220.20	15.88	246.67	55.59	0.4
Astoria-Pacific	20	522.99	25.23	91.63	112.52	0.9
HPLC	40	491.06	25.74	44.78	99.86	0.9
Derivatized - MS/MS Non-kit	720	437.14	34.00	59.69	85.48	0.8
Non-derivatized - MS/MS Non-kit	159	530.15	39.24	88.33	99.18	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	481.32	33.34	54.39	91.61	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	515.62	33.49	33.49	97.31	1.0
Non-derivatized - MS/MS PE NeoBase Kit	186	466.93	33.52	52.97	90.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	436.53	33.75	48.33	87.99	0.8
TecnoSuma UMTEST	30	397.44	56.64	344.14	104.41	0.7
Other	70	443.36	63.60	305.39	83.66	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.

PHENYLALANINE (μmol Phe/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 024 - Enriched 666 μmol/L whole blood						
Bacterial Inhibition Assays	19	630.99	41.10	73.87	94.80	0.8
Fluorometric Manual	66	740.66	49.89	79.20	125.13	0.9
Colorimetric	74	1059.03	53.10	151.97	111.30	1.4
PerkinElmer Neonatal Kit	266	702.99	53.94	87.16	96.96	0.9
Neo-Genesis Accuwell	20	785.07	57.58	82.74	101.37	1.0
Ani Labsystems	80	822.24	67.31	90.88	99.88	1.1
Bio-Rad Quantase	30	837.79	119.18	131.23	109.30	1.1
MP Biomedicals Enzyme Assay	19	762.38	46.64	66.53	48.36	1.1
Interscientific Enzyme	40	313.61	16.11	351.29	55.59	0.4
Astoria-Pacific	20	732.71	15.33	102.09	112.52	0.9
HPLC	38	699.56	35.32	39.35	99.86	0.9
Derivatized - MS/MS Non-kit	724	640.37	45.80	95.04	85.48	0.8
Non-derivatized - MS/MS Non-kit	159	769.49	53.20	126.16	99.18	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	706.92	55.00	86.11	91.61	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	781.10	46.41	46.41	97.31	1.0
Non-derivatized - MS/MS PE NeoBase Kit	188	684.44	52.66	81.59	90.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	633.07	53.71	66.98	87.99	0.8
TecnoSuma UMTEST	30	575.61	78.43	491.84	104.41	0.7
Other	70	652.49	86.68	447.36	83.66	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 10g. 2010 Quality Control Data
Summaries of Statistical Analyses

LEUCINE (μmol Leu/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
Bacterial Inhibition Assays	20	132.76	15.00	31.46	70.81	1.4
Bio-Rad Quantase	10	232.49	15.30	15.30	200.08	1.1
Interscientific Enzyme	20	188.45	16.08	16.08	183.80	0.8
HPLC	10	137.80	10.24	10.24	130.60	1.0
Derivatized - MS/MS Non-kit	783	163.87	14.82	27.79	156.39	0.9
Non-derivatized - MS/MS Non-kit	100	193.56	15.57	22.78	183.10	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	246	159.22	12.73	17.38	150.90	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	202.58	11.57	11.57	191.33	0.9
Non-derivatized - MS/MS PE NeoBase Kit	156	204.12	14.86	21.33	193.17	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	153.01	15.31	19.09	150.80	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	171.25	10.93	31.02	172.78	0.7
Other	20	146.12	8.18	37.20	147.11	0.7
Lot 926 - Enriched 229 μmol/L whole blood						
Bacterial Inhibition Assays	20	341.06	25.71	62.17	70.81	1.4
Bio-Rad Quantase	10	389.13	55.50	55.50	200.08	1.1
Interscientific Enzyme	20	360.12	19.97	19.97	183.80	0.8
HPLC	10	350.98	20.06	20.06	130.60	1.0
Derivatized - MS/MS Non-kit	789	344.79	28.97	52.20	156.39	0.9
Non-derivatized - MS/MS Non-kit	100	369.48	31.63	47.79	183.10	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	248	347.60	26.90	34.22	150.90	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	396.73	21.90	21.90	191.33	0.9
Non-derivatized - MS/MS PE NeoBase Kit	155	395.89	28.81	47.24	193.17	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	321.84	33.16	47.57	150.80	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	349.21	18.12	41.57	172.78	0.7
Other	18	319.47	12.58	15.87	147.11	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.

LEUCINE (μmol Leu/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 927 - Enriched 534 μmol/L whole blood						
Bacterial Inhibition Assays	20	645.50	60.12	135.59	70.81	1.4
Bio-Rad Quantase	10	763.92	29.42	29.42	200.08	1.1
Interscientific Enzyme	20	567.67	38.10	38.10	183.80	0.8
HPLC	10	637.03	45.35	45.35	130.60	1.0
Derivatized - MS/MS Non-kit	797	600.81	46.69	95.59	156.39	0.9
Non-derivatized - MS/MS Non-kit	99	619.46	43.98	82.95	183.10	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	245	610.00	48.60	54.46	150.90	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	669.32	40.04	40.04	191.33	0.9
Non-derivatized - MS/MS PE NeoBase Kit	156	673.19	47.16	76.88	193.17	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	524.38	55.46	79.66	150.80	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	557.37	32.68	68.92	172.78	0.7
Other	19	516.47	27.38	27.65	147.11	0.7
Lot 928 - Enriched 686 μmol/L whole blood						
Bacterial Inhibition Assays	20	1139.54	86.36	361.71	70.81	1.4
Bio-Rad Quantase	10	930.13	59.55	59.55	200.08	1.1
Interscientific Enzyme	20	727.14	50.11	50.11	183.80	0.8
HPLC	10	820.68	66.31	66.31	130.60	1.0
Derivatized - MS/MS Non-kit	788	754.02	59.07	114.77	156.39	0.9
Non-derivatized - MS/MS Non-kit	99	787.47	53.34	89.88	183.10	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	246	776.28	61.20	77.59	150.90	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	855.42	58.15	58.15	191.33	0.9
Non-derivatized - MS/MS PE NeoBase Kit	159	849.28	56.37	90.29	193.17	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	667.85	59.40	97.69	150.80	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	689.66	33.52	53.23	172.78	0.7
Other	20	651.42	47.76	47.76	147.11	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.

LEUCINE (μmol Leu/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
Bacterial Inhibition Assays	20	128.80	13.57	32.63	93.63	1.2
Bio-Rad Quantase	10	246.83	11.83	11.83	264.27	1.0
Interscientific Enzyme	20	186.20	10.11	11.57	201.22	0.7
HPLC	10	150.82	14.65	14.65	157.18	0.9
Derivatized - MS/MS Non-kit	711	175.18	16.47	32.24	179.13	0.8
Non-derivatized - MS/MS Non-kit	79	203.33	14.52	26.47	211.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	215	174.01	13.91	18.74	180.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	197.36	13.65	13.65	202.51	0.8
Non-derivatized - MS/MS PE NeoBase Kit	177	214.44	14.38	23.10	220.53	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	180.55	13.27	16.08	190.92	0.8
Other	50	163.47	9.83	25.73	168.29	0.7
Lot 022 - Enriched 229 μmol/L whole blood						
Bacterial Inhibition Assays	20	351.16	21.04	39.18	93.63	1.2
Bio-Rad Quantase	10	512.13	22.35	22.35	264.27	1.0
Interscientific Enzyme	20	376.93	32.29	32.29	201.22	0.7
HPLC	10	378.27	24.68	24.68	157.18	0.9
Derivatized - MS/MS Non-kit	696	366.64	33.00	59.46	179.13	0.8
Non-derivatized - MS/MS Non-kit	79	405.09	28.44	59.37	211.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	213	384.91	27.57	37.75	180.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	392.94	12.26	12.26	202.51	0.8
Non-derivatized - MS/MS PE NeoBase Kit	176	423.12	27.46	45.62	220.53	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	371.48	33.16	40.79	190.92	0.8
Other	50	330.61	24.51	44.53	168.29	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.

LEUCINE (μmol Leu/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 023 - Enriched 534 μmol/L whole blood						
Bacterial Inhibition Assays	20	682.36	63.02	131.28	93.63	1.2
Bio-Rad Quantase	10	755.98	27.19	27.19	264.27	1.0
Interscientific Enzyme	20	597.10	25.84	26.57	201.22	0.7
HPLC	10	628.44	27.09	27.09	157.18	0.9
Derivatized - MS/MS Non-kit	707	605.39	50.00	109.13	179.13	0.8
Non-derivatized - MS/MS Non-kit	79	659.30	58.37	123.32	211.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	216	642.23	42.70	70.32	180.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	650.55	8.88	8.88	202.51	0.8
Non-derivatized - MS/MS PE NeoBase Kit	177	681.91	46.94	79.62	220.53	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	596.81	41.33	72.87	190.92	0.8
Other	50	529.33	26.38	73.70	168.29	0.7
Lot 024 - Enriched 686 μmol/L whole blood						
Bacterial Inhibition Assays	20	1150.98	63.26	308.56	93.63	1.2
Bio-Rad Quantase	10	1059.27	92.30	92.30	264.27	1.0
Interscientific Enzyme	20	784.75	37.65	37.65	201.22	0.7
HPLC	10	918.04	48.60	48.60	157.18	0.9
Derivatized - MS/MS Non-kit	699	845.54	68.01	158.67	179.13	0.8
Non-derivatized - MS/MS Non-kit	79	889.18	70.72	149.00	211.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	214	900.08	70.67	98.01	180.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	884.91	45.87	45.87	202.51	0.8
Non-derivatized - MS/MS PE NeoBase Kit	175	934.89	60.43	101.39	220.53	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	808.82	67.33	91.80	190.92	0.8
Other	50	735.69	56.66	94.25	168.29	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 10h. 2010 Quality Control Data
Summaries of Statistical Analyses

METHIONINE (μmol Met/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
HPLC	10	17.78	1.74	1.74	12.30	0.9
Derivatized - MS/MS Non-kit	774	23.38	2.93	4.42	18.60	0.8
Non-derivatized - MS/MS Non-kit	104	21.48	3.02	4.05	17.76	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	226	27.09	3.23	4.05	22.90	1.0
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	27.69	6.35	6.35	15.35	0.9
Non-derivatized - MS/MS PE NeoBase Kit	151	20.85	2.10	2.72	14.91	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	29	16.46	2.37	4.15	10.67	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	10	13.53	1.11	1.11	9.86	0.7
Other	20	22.14	5.22	18.14	20.44	0.7
Lot 926 - Enriched 67 μmol/L whole blood						
HPLC	10	70.92	4.55	4.55	12.30	0.9
Derivatized - MS/MS Non-kit	786	71.82	7.20	11.11	18.60	0.8
Non-derivatized - MS/MS Non-kit	106	69.12	5.99	11.36	17.76	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	237	85.84	7.91	11.54	22.90	1.0
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	67.45	15.53	15.53	15.35	0.9
Non-derivatized - MS/MS PE NeoBase Kit	152	71.96	6.21	8.87	14.91	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	29	52.92	6.00	11.81	10.67	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	10	56.09	3.51	3.51	9.86	0.7
Other	20	65.98	4.13	9.83	20.44	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.

METHIONINE (μmol Met/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 927 - Enriched 201 μmol/L whole blood						
HPLC	10	183.05	15.50	15.50	12.30	0.9
Derivatized - MS/MS Non-kit	778	177.30	14.61	24.70	18.60	0.8
Non-derivatized - MS/MS Non-kit	106	173.70	11.67	27.68	17.76	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	237	208.79	18.75	25.43	22.90	1.0
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	175.68	24.54	24.54	15.35	0.9
Non-derivatized - MS/MS PE NeoBase Kit	151	182.79	14.18	19.06	14.91	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	120.65	27.52	30.13	10.67	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	10	127.69	14.76	14.76	9.86	0.7
Other	20	153.20	12.18	17.40	20.44	0.7
Lot 928 - Enriched 335 μmol/L whole blood						
HPLC	10	320.54	29.82	29.82	12.30	0.9
Derivatized - MS/MS Non-kit	770	300.56	25.45	43.92	18.60	0.8
Non-derivatized - MS/MS Non-kit	105	288.86	24.65	50.68	17.76	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	232	349.34	28.52	38.73	22.90	1.0
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	322.31	26.53	26.53	15.35	0.9
Non-derivatized - MS/MS PE NeoBase Kit	152	318.23	20.59	31.53	14.91	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	228.07	40.82	44.58	10.67	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	10	237.17	24.45	24.45	9.86	0.7
Other	20	251.00	26.09	34.50	20.44	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.

METHIONINE (μmol Met/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
Neo-Genesis Accuwell	10	21.99	2.43	2.43	28.90	0.8
Bio-Rad Quantase	10	37.16	13.16	13.16	27.45	0.5
HPLC	10	19.28	3.37	3.37	19.49	0.8
Derivatized - MS/MS Non-kit	692	24.21	2.97	4.30	25.58	0.8
Non-derivatized - MS/MS Non-kit	87	23.66	2.28	3.49	25.62	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	195	27.36	3.33	4.03	28.60	0.9
Non-derivatized - MS/MS PE NeoBase Kit	178	23.88	2.49	3.01	24.73	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	50	19.59	4.02	8.45	20.43	0.7
Other	40	34.23	9.35	14.06	27.05	0.6
Lot 022 - Enriched 67 μmol/L whole blood						
Neo-Genesis Accuwell	10	81.93	3.75	3.75	28.90	0.8
Bio-Rad Quantase	10	52.48	9.53	9.53	27.45	0.5
HPLC	10	77.52	8.93	8.93	19.49	0.8
Derivatized - MS/MS Non-kit	685	78.67	7.71	12.48	25.58	0.8
Non-derivatized - MS/MS Non-kit	89	82.77	6.75	13.05	25.62	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	200	90.12	8.92	11.89	28.60	0.9
Non-derivatized - MS/MS PE NeoBase Kit	178	82.38	6.55	8.52	24.73	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	50	65.03	12.69	24.00	20.43	0.7
Other	40	63.93	6.14	6.64	27.05	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.

METHIONINE (μmol Met/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 023 - Enriched 201 μmol/L whole blood						
Neo-Genesis Accuwell	10	187.49	10.57	10.57	28.90	0.8
Bio-Rad Quantase	10	136.15	32.59	32.59	27.45	0.5
HPLC	10	173.51	10.12	10.12	19.49	0.8
Derivatized - MS/MS Non-kit	683	183.05	15.02	28.37	25.58	0.8
Non-derivatized - MS/MS Non-kit	88	191.85	15.86	28.93	25.62	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	196	206.94	16.36	23.79	28.60	0.9
Non-derivatized - MS/MS PE NeoBase Kit	175	184.90	12.42	16.21	24.73	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	50	154.14	25.51	51.52	20.43	0.7
Other	40	147.12	7.31	7.37	27.05	0.6
Lot 024 - Enriched 403 μmol/L whole blood						
Neo-Genesis Accuwell	10	324.64	20.63	20.63	28.90	0.8
Bio-Rad Quantase	10	248.47	49.36	49.36	27.45	0.5
HPLC	10	344.81	26.39	26.39	19.49	0.8
Derivatized - MS/MS Non-kit	676	338.31	27.54	54.53	25.58	0.8
Non-derivatized - MS/MS Non-kit	89	357.07	27.66	53.12	25.62	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	196	387.57	30.50	40.17	28.60	0.9
Non-derivatized - MS/MS PE NeoBase Kit	176	354.13	23.65	29.18	24.73	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	50	285.82	44.73	81.46	20.43	0.7
Other	40	283.28	20.41	23.47	27.05	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.

Table 10i. 2010 Quality Control Data
Summaries of Statistical Analyses

TYROSINE (μmol Tyr/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
Fluorometric Manual	10	130.20	6.78	6.78	119.00	1.0
HPLC	19	67.61	4.87	4.87	67.44	1.0
Derivatized - MS/MS Non-kit	774	56.89	5.23	9.08	52.97	0.8
Non-derivatized - MS/MS Non-kit	182	64.16	5.01	12.09	58.82	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	232	62.46	6.16	7.99	59.33	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	77.99	16.90	16.90	65.02	1.0
Non-derivatized - MS/MS PE NeoBase Kit	175	67.29	5.46	9.00	62.15	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	28	60.59	7.29	8.38	58.66	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	54.46	3.58	7.36	53.06	0.8
Other	20	52.69	3.58	11.40	56.05	0.7
Lot 926 - Enriched 276 μmol/L whole blood						
Fluorometric Manual	10	359.90	36.69	36.69	119.00	1.0
HPLC	20	331.47	16.48	22.27	67.44	1.0
Derivatized - MS/MS Non-kit	778	272.12	22.27	38.06	52.97	0.8
Non-derivatized - MS/MS Non-kit	184	310.26	22.95	63.89	58.82	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	234	298.11	23.05	28.17	59.33	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	331.87	35.83	35.83	65.02	1.0
Non-derivatized - MS/MS PE NeoBase Kit	176	312.60	25.73	46.95	62.15	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	29	298.09	24.63	33.86	58.66	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	39	277.03	14.02	28.05	53.06	0.8
Other	20	253.71	23.20	25.94	56.05	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.

TYROSINE (μmol Tyr/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 927 - Enriched 497 μmol/L whole blood						
Fluorometric Manual	10	595.90	59.37	59.37	119.00	1.0
HPLC	20	539.74	35.95	35.95	67.44	1.0
Derivatized - MS/MS Non-kit	776	451.25	35.04	61.30	52.97	0.8
Non-derivatized - MS/MS Non-kit	183	504.21	34.08	102.26	58.82	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	233	489.83	43.56	49.06	59.33	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	543.50	46.00	46.00	65.02	1.0
Non-derivatized - MS/MS PE NeoBase Kit	176	512.31	37.02	66.87	62.15	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	470.86	62.21	68.16	58.66	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	438.93	25.80	55.11	53.06	0.8
Other	20	421.50	33.33	35.56	56.05	0.7
Lot 928 - Enriched 773 μmol/L whole blood						
Fluorometric Manual	10	855.20	103.87	103.87	119.00	1.0
HPLC	20	805.71	59.51	70.08	67.44	1.0
Derivatized - MS/MS Non-kit	776	681.87	51.44	97.05	52.97	0.8
Non-derivatized - MS/MS Non-kit	184	776.71	75.08	156.67	58.82	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	233	738.79	57.00	68.94	59.33	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	854.80	92.27	92.27	65.02	1.0
Non-derivatized - MS/MS PE NeoBase Kit	177	780.28	54.91	99.85	62.15	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	724.55	77.95	84.33	58.66	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	39	675.32	28.16	62.95	53.06	0.8
Other	20	603.66	53.89	80.16	56.05	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.

TYROSINE (μmol Tyr/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
Fluorometric Manual	10	142.70	6.53	6.53	130.13	1.0
Bio-Rad Quantase	10	30.30	5.93	5.93	22.29	0.4
HPLC	30	68.31	5.32	7.51	72.19	0.9
Derivatized - MS/MS Non-kit	710	58.13	5.57	10.40	61.49	0.8
Non-derivatized - MS/MS Non-kit	139	69.74	6.32	13.71	73.73	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	204	64.29	6.51	9.17	64.51	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	75.43	3.62	3.62	79.85	1.1
Non-derivatized - MS/MS PE NeoBase Kit	194	71.10	5.83	8.97	75.42	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	61.42	6.27	8.12	65.50	0.8
Other	40	48.58	2.70	2.81	53.40	0.7
Lot 022 - Enriched 276 μmol/L whole blood						
Fluorometric Manual	10	404.60	40.70	40.70	130.13	1.0
Bio-Rad Quantase	10	135.69	16.53	16.53	22.29	0.4
HPLC	30	332.12	23.97	39.38	72.19	0.9
Derivatized - MS/MS Non-kit	702	282.54	23.63	42.64	61.49	0.8
Non-derivatized - MS/MS Non-kit	148	334.74	24.10	70.01	73.73	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	197	308.12	26.05	38.22	64.51	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	390.65	28.87	28.87	79.85	1.1
Non-derivatized - MS/MS PE NeoBase Kit	193	343.56	24.22	47.40	75.42	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	296.04	30.81	48.67	65.50	0.8
Other	37	242.79	12.07	12.90	53.40	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.

TYROSINE (μmol Tyr/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 023 - Enriched 497 μmol/L whole blood						
Fluorometric Manual	10	626.30	50.43	50.43	130.13	1.0
Bio-Rad Quantase	10	222.10	22.26	22.26	22.29	0.4
HPLC	29	521.45	19.54	46.19	72.19	0.9
Derivatized - MS/MS Non-kit	695	441.15	34.53	65.20	61.49	0.8
Non-derivatized - MS/MS Non-kit	148	540.74	43.23	115.47	73.73	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	203	500.49	37.02	60.49	64.51	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	591.90	47.25	47.25	79.85	1.1
Non-derivatized - MS/MS PE NeoBase Kit	196	537.55	42.65	75.77	75.42	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	459.70	38.71	76.73	65.50	0.8
Other	40	370.49	20.32	29.97	53.40	0.7
Lot 024 - Enriched 773 μmol/L whole blood						
Fluorometric Manual	10	942.10	80.39	80.39	130.13	1.0
Bio-Rad Quantase	10	364.37	39.26	39.26	22.29	0.4
HPLC	30	776.80	35.17	55.66	72.19	0.9
Derivatized - MS/MS Non-kit	690	659.00	51.76	98.10	61.49	0.8
Non-derivatized - MS/MS Non-kit	149	790.57	58.18	157.90	73.73	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	204	744.50	58.51	89.79	64.51	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	909.03	65.66	65.66	79.85	1.1
Non-derivatized - MS/MS PE NeoBase Kit	198	800.30	64.53	112.05	75.42	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	685.84	54.59	77.37	65.50	0.8
Other	40	552.91	60.84	68.84	53.40	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 10j. 2010 Quality Control Data
Summaries of Statistical Analyses

VALINE (μmol Val/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
HPLC	10	202.47	14.72	14.72	193.57	1.0
Derivatized - MS/MS Non-kit	722	186.99	20.53	31.17	179.52	0.8
Non-derivatized - MS/MS Non-kit	90	179.47	13.23	22.52	167.70	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	225	182.21	19.85	28.69	172.33	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	171.91	14.35	14.35	150.88	0.8
Non-derivatized - MS/MS PE NeoBase Kit	163	202.56	17.07	30.68	192.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	156.20	15.74	40.20	147.92	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	133.19	6.62	17.42	135.58	0.6
Lot 926 - Enriched 256 μmol/L whole blood						
HPLC	10	431.01	24.61	24.61	193.57	1.0
Derivatized - MS/MS Non-kit	727	364.51	40.34	59.03	179.52	0.8
Non-derivatized - MS/MS Non-kit	90	367.88	26.42	51.70	167.70	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	223	361.47	38.82	58.16	172.33	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	329.82	25.97	25.97	150.88	0.8
Non-derivatized - MS/MS PE NeoBase Kit	165	419.85	40.15	80.74	192.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	300.21	24.09	56.24	147.92	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	288.58	15.85	26.95	135.58	0.6
Lot 927 - Enriched 598 μmol/L whole blood						
HPLC	10	754.97	52.77	52.77	193.57	1.0
Derivatized - MS/MS Non-kit	726	630.28	59.89	101.34	179.52	0.8
Non-derivatized - MS/MS Non-kit	90	647.31	52.58	96.23	167.70	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	222	627.15	65.83	105.03	172.33	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	608.00	43.41	43.41	150.88	0.8
Non-derivatized - MS/MS PE NeoBase Kit	166	732.71	70.02	130.28	192.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	507.61	47.23	105.38	147.92	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	482.36	31.74	58.07	135.58	0.6
Lot 928 - Enriched 939 μmol/L whole blood						
HPLC	10	1099.28	87.87	87.87	193.57	1.0
Derivatized - MS/MS Non-kit	726	895.11	85.05	144.08	179.52	0.8
Non-derivatized - MS/MS Non-kit	90	949.89	80.14	121.24	167.70	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	225	908.37	98.85	149.15	172.33	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	903.70	75.63	75.63	150.88	0.8
Non-derivatized - MS/MS PE NeoBase Kit	169	1068.35	102.96	201.49	192.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	737.47	65.91	133.85	147.92	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	682.00	42.47	63.09	135.58	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.

VALINE (μmol Val/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
HPLC	10	194.48	19.86	19.86	195.99	0.9
Derivatized - MS/MS Non-kit	674	192.89	22.82	37.66	194.50	0.8
Non-derivatized - MS/MS Non-kit	69	174.18	15.02	29.95	180.04	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	192	187.38	20.50	29.05	187.90	0.8
Non-derivatized - MS/MS PE NeoBase Kit	179	204.80	19.21	27.89	207.67	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	158.31	16.89	43.58	164.29	0.7
Other	40	174.71	8.65	20.76	173.11	0.7
Lot 022 - Enriched 256 μmol/L whole blood						
HPLC	10	447.98	27.16	27.16	195.99	0.9
Derivatized - MS/MS Non-kit	661	391.13	39.90	69.65	194.50	0.8
Non-derivatized - MS/MS Non-kit	69	393.48	36.00	77.86	180.04	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	197	399.40	42.47	60.65	187.90	0.8
Non-derivatized - MS/MS PE NeoBase Kit	173	449.64	35.83	53.13	207.67	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	342.50	38.02	92.26	164.29	0.7
Other	40	355.81	16.77	16.77	173.11	0.7
Lot 023 - Enriched 598 μmol/L whole blood						
HPLC	10	722.88	35.89	35.89	195.99	0.9
Derivatized - MS/MS Non-kit	676	644.33	62.47	117.13	194.50	0.8
Non-derivatized - MS/MS Non-kit	68	670.74	65.22	156.38	180.04	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	195	655.93	61.96	110.66	187.90	0.8
Non-derivatized - MS/MS PE NeoBase Kit	178	770.88	68.49	103.28	207.67	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	558.94	58.16	167.35	164.29	0.7
Other	40	577.58	32.78	35.94	173.11	0.7
Lot 024 - Enriched 940 μmol/L whole blood						
HPLC	10	1078.00	81.83	81.83	195.99	0.9
Derivatized - MS/MS Non-kit	662	904.99	83.03	164.27	194.50	0.8
Non-derivatized - MS/MS Non-kit	69	938.73	95.66	202.00	180.04	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	197	946.81	104.79	159.32	187.90	0.8
Non-derivatized - MS/MS PE NeoBase Kit	179	1084.83	99.74	147.34	207.67	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	784.72	83.28	213.96	164.29	0.7
Other	40	835.72	82.54	84.01	173.11	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 10k. 2010 Quality Control Data
Summaries of Statistical Analyses

CITRULLINE (μmol Cit/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 925 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	761	23.96	2.99	5.09	22.54	0.7
Non-derivatized - MS/MS Non-kit	105	28.47	3.84	7.31	26.02	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	230	28.59	1.96	3.15	28.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	34.08	6.38	6.38	29.05	1.2
Non-derivatized - MS/MS PE NeoBase Kit	157	30.57	3.25	4.77	28.76	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	29	28.43	3.72	6.01	29.38	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	23.88	1.59	4.01	23.26	0.7
Other	20	17.18	1.26	10.22	9.92	0.9
Lot 926 - Enriched 57 μmol/L whole blood						
Derivatized - MS/MS Non-kit	759	63.05	6.47	12.33	22.54	0.7
Non-derivatized - MS/MS Non-kit	106	74.14	8.14	16.71	26.02	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	237	78.11	4.74	7.90	28.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	93.83	7.56	7.56	29.05	1.2
Non-derivatized - MS/MS PE NeoBase Kit	155	77.99	6.55	10.03	28.76	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	80.79	7.56	9.33	29.38	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	67.68	4.51	11.96	23.26	0.7
Other	20	50.72	3.72	15.56	9.92	0.9
Lot 927 - Enriched 171 μmol/L whole blood						
Derivatized - MS/MS Non-kit	754	144.80	13.85	26.90	22.54	0.7
Non-derivatized - MS/MS Non-kit	108	170.47	20.09	43.61	26.02	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	239	178.18	11.34	16.33	28.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	220.01	15.46	15.46	29.05	1.2
Non-derivatized - MS/MS PE NeoBase Kit	157	175.34	13.79	21.92	28.76	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	172.61	25.57	25.57	29.38	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	143.74	9.67	34.94	23.26	0.7
Other	18	151.53	8.95	9.31	9.92	0.9
Lot 928 - Enriched 285 μmol/L whole blood						
Derivatized - MS/MS Non-kit	757	230.65	22.44	44.45	22.54	0.7
Non-derivatized - MS/MS Non-kit	108	275.08	35.10	70.59	26.02	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	234	280.10	15.87	24.67	28.06	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	367.83	24.31	24.31	29.05	1.2
Non-derivatized - MS/MS PE NeoBase Kit	158	280.38	19.84	33.12	28.76	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	274.43	38.07	41.30	29.38	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	237.31	17.01	30.09	23.26	0.7
Other	20	254.98	21.72	40.94	9.92	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.

CITRULLINE (μmol Cit/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	702	22.78	2.76	5.80	16.49	0.8
Non-derivatized - MS/MS Non-kit	68	27.35	4.44	6.34	19.34	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	205	28.73	1.88	3.11	20.27	1.1
Non-derivatized - MS/MS PE NeoBase Kit	185	28.76	2.93	3.52	21.33	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	28.33	3.30	4.04	22.15	1.0
Other	50	18.38	0.92	5.67	10.31	0.7
Lot 022 - Enriched 57 μmol/L whole blood						
Derivatized - MS/MS Non-kit	684	64.83	6.75	14.22	16.49	0.8
Non-derivatized - MS/MS Non-kit	69	79.29	12.13	19.43	19.34	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	206	82.51	5.08	8.91	20.27	1.1
Non-derivatized - MS/MS PE NeoBase Kit	188	79.97	7.24	9.48	21.33	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	81.31	7.71	11.11	22.15	1.0
Other	50	52.64	3.90	17.62	10.31	0.7
Lot 023 - Enriched 171 μmol/L whole blood						
Derivatized - MS/MS Non-kit	692	143.49	14.00	33.36	16.49	0.8
Non-derivatized - MS/MS Non-kit	69	179.13	21.36	46.00	19.34	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	209	184.78	10.54	21.65	20.27	1.1
Non-derivatized - MS/MS PE NeoBase Kit	184	176.81	12.15	19.76	21.33	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	174.51	13.15	23.87	22.15	1.0
Other	50	116.23	5.99	45.42	10.31	0.7
Lot 024 - Enriched 343 μmol/L whole blood						
Derivatized - MS/MS Non-kit	675	266.31	25.91	54.73	16.49	0.8
Non-derivatized - MS/MS Non-kit	69	330.66	33.61	73.97	19.34	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	205	342.98	21.57	38.33	20.27	1.1
Non-derivatized - MS/MS PE NeoBase Kit	185	324.25	24.52	36.75	21.33	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	319.47	36.96	47.60	22.15	1.0
Other	50	233.35	18.98	74.11	10.31	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 10l. 2010 Quality Control Data
Summaries of Statistical Analyses

ARGININE (μmol Arg/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Assayed 7.93 μmol/L whole blood						
Derivatized - MS/MS Non-kit	585	10.70	1.73	5.24	1.85	1.1
Non-derivatized - MS/MS Non-kit	40	14.95	1.98	6.36	4.19	1.8
Derivatized - MS/MS PE NeoGram MS2 Kit	139	13.78	1.37	2.40	-2.29	1.8
Non-derivatized - MS/MS PE NeoBase Kit	157	13.34	1.10	1.55	-0.55	1.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	13.47	1.25	4.22	3.10	1.5
Other	30	5.45	0.26	0.26	5.06	0.5
Lot 022 - Assayed 28.12 μmol/L whole blood						
Derivatized - MS/MS Non-kit	573	29.11	4.17	12.38	1.85	1.1
Non-derivatized - MS/MS Non-kit	40	45.69	4.05	19.74	4.19	1.8
Derivatized - MS/MS PE NeoGram MS2 Kit	139	39.93	3.22	7.35	-2.29	1.8
Non-derivatized - MS/MS PE NeoBase Kit	158	43.02	3.47	5.77	-0.55	1.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	40.86	5.20	10.13	3.10	1.5
Other	30	17.23	1.57	1.57	5.06	0.5
Lot 023 - Assayed 34.69 μmol/L whole blood						
Derivatized - MS/MS Non-kit	563	43.12	5.60	20.71	1.85	1.1
Non-derivatized - MS/MS Non-kit	40	87.28	14.99	51.29	4.19	1.8
Derivatized - MS/MS PE NeoGram MS2 Kit	140	67.82	4.30	15.45	-2.29	1.8
Non-derivatized - MS/MS PE NeoBase Kit	156	63.89	6.32	9.44	-0.55	1.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	63.92	5.49	14.53	3.10	1.5
Other	30	27.27	2.27	2.27	5.06	0.5
Lot 024 - Assayed 65.90 μmol/L whole blood						
Derivatized - MS/MS Non-kit	557	72.92	8.67	30.53	1.85	1.1
Non-derivatized - MS/MS Non-kit	40	119.86	10.16	49.68	4.19	1.8
Derivatized - MS/MS PE NeoGram MS2 Kit	139	116.68	9.12	24.66	-2.29	1.8
Non-derivatized - MS/MS PE NeoBase Kit	159	111.60	8.66	12.64	-0.55	1.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	100.10	9.60	22.86	3.10	1.5
Other	30	31.97	4.64	4.64	5.06	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 10m. 2010 Quality Control Data
Summaries of Statistical Analyses

SUCCINYLACETONE (μmol SUAC/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 021 - Assayed 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	198	0.84	0.31	0.97	0.96	0.6
Non-derivatized - MS/MS Non-kit	30	3.19	0.53	2.80	3.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	90	0.74	0.19	0.44	0.75	0.2
Lot 022 - Assayed 2.61 μmol/L whole blood						
Derivatized - MS/MS Non-kit	197	2.72	0.46	1.69	0.96	0.6
Non-derivatized - MS/MS Non-kit	29	5.20	0.40	1.24	3.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	90	1.19	0.25	0.48	0.75	0.2
Lot 023 - Assayed 6.08 μmol/L whole blood						
Derivatized - MS/MS Non-kit	200	4.75	0.63	2.61	0.96	0.6
Non-derivatized - MS/MS Non-kit	30	8.37	0.80	1.55	3.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	90	1.70	0.28	0.57	0.75	0.2
Lot 024 - Assayed 11.88 μmol/L whole blood						
Derivatized - MS/MS Non-kit	201	8.30	1.15	4.83	0.96	0.6
Non-derivatized - MS/MS Non-kit	30	12.47	0.76	1.02	3.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	90	2.63	0.42	0.67	0.75	0.2

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

Table 10n. 2010 Quality Control Data
Summaries of Statistical Analyses

FREE CARNITINE (μmol C0/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	848	15.64	1.59	2.67	15.25	1.3
Non-derivatized - MS/MS Non-kit	118	14.08	2.24	3.50	13.95	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	232	20.71	1.70	3.36	20.39	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	12.26	1.25	1.25	11.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	163	15.51	1.37	2.09	15.51	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	39	13.72	1.26	2.99	13.50	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	29	12.92	0.99	1.68	12.99	1.0
Lot 966 - Enriched 10 μmol/L whole blood						
Derivatized - MS/MS Non-kit	854	27.57	2.72	5.03	15.25	1.3
Non-derivatized - MS/MS Non-kit	118	23.97	3.14	5.19	13.95	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	233	38.40	3.14	5.89	20.39	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	20.97	1.73	1.73	11.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	162	25.80	2.05	3.20	15.51	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	23.92	2.15	4.84	13.50	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	22.74	1.64	2.48	12.99	1.0
Lot 967 - Enriched 20 μmol/L whole blood						
Derivatized - MS/MS Non-kit	859	40.22	3.72	6.89	15.25	1.3
Non-derivatized - MS/MS Non-kit	118	35.39	4.23	8.37	13.95	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	237	56.44	5.08	8.89	20.39	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	30.34	2.56	2.56	11.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	161	36.56	3.12	4.67	15.51	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	36.48	4.30	9.37	13.50	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	31.97	1.82	3.05	12.99	1.0
Lot 968 - Enriched 30 μmol/L whole blood						
Derivatized - MS/MS Non-kit	859	53.71	5.25	9.64	15.25	1.3
Non-derivatized - MS/MS Non-kit	116	45.16	5.29	10.03	13.95	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	236	75.55	6.24	12.34	20.39	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	40.59	2.56	2.56	11.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	160	46.64	4.47	6.74	15.51	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	40	46.59	4.93	11.54	13.50	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	41.76	2.30	5.58	12.99	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.

FREE CARNITINE (μmol C0/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	783	19.48	1.89	2.99	18.98	1.3
Non-derivatized - MS/MS Non-kit	87	19.71	1.91	4.02	19.10	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	199	26.33	2.42	4.14	25.82	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	20.05	2.01	2.01	19.55	1.1
Non-derivatized - MS/MS PE NeoBase Kit	197	20.30	1.87	3.12	19.99	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	40	18.94	2.14	4.57	18.48	1.0
Lot 062 - Enriched 10 μmol/L whole blood						
Derivatized - MS/MS Non-kit	812	31.23	2.97	5.46	18.98	1.3
Non-derivatized - MS/MS Non-kit	88	28.93	3.03	5.37	19.10	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	199	43.75	3.89	7.24	25.82	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	29.96	2.34	2.34	19.55	1.1
Non-derivatized - MS/MS PE NeoBase Kit	190	30.38	2.95	4.97	19.99	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	38	28.01	2.95	5.05	18.48	1.0
Lot 063 - Enriched 20 μmol/L whole blood						
Derivatized - MS/MS Non-kit	798	43.29	4.07	6.79	18.98	1.3
Non-derivatized - MS/MS Non-kit	88	39.76	3.66	6.87	19.10	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	195	61.49	5.43	9.56	25.82	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	39.03	3.34	3.34	19.55	1.1
Non-derivatized - MS/MS PE NeoBase Kit	191	40.79	3.18	6.17	19.99	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	38	37.72	2.92	7.09	18.48	1.0
Lot 064 - Enriched 30 μmol/L whole blood						
Derivatized - MS/MS Non-kit	811	57.32	5.27	9.48	18.98	1.3
Non-derivatized - MS/MS Non-kit	89	51.23	4.40	9.07	19.10	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	197	81.29	5.84	12.24	25.82	1.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	51.86	3.01	3.01	19.55	1.1
Non-derivatized - MS/MS PE NeoBase Kit	190	52.30	5.32	9.35	19.99	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	38	48.85	5.57	8.08	18.48	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 10o. 2010 Quality Control Data
Summaries of Statistical Analyses

ACETYLCARNITINE (μmol C2/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	835	12.11	1.33	2.79	12.17	0.9
Non-derivatized - MS/MS Non-kit	117	9.55	0.99	1.81	9.76	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	226	12.93	1.22	2.49	13.09	0.5
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	10.53	0.84	0.84	11.26	1.2
Non-derivatized - MS/MS PE NeoBase Kit	151	7.33	0.56	0.89	7.47	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	29	10.94	1.46	1.46	10.38	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	9.60	1.07	1.29	10.04	1.0
Lot 966 - Enriched 10 μmol/L whole blood						
Derivatized - MS/MS Non-kit	837	21.55	2.17	4.23	12.17	0.9
Non-derivatized - MS/MS Non-kit	120	19.89	2.28	3.54	9.76	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	224	18.71	1.22	2.46	13.09	0.5
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	23.99	2.09	2.09	11.26	1.2
Non-derivatized - MS/MS PE NeoBase Kit	151	15.37	1.04	1.80	7.47	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	28	19.40	1.58	2.30	10.38	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	21.20	2.33	3.91	10.04	1.0
Lot 967 - Enriched 20 μmol/L whole blood						
Derivatized - MS/MS Non-kit	837	30.39	2.85	5.77	12.17	0.9
Non-derivatized - MS/MS Non-kit	119	29.59	2.98	5.41	9.76	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	223	23.91	1.61	2.79	13.09	0.5
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	35.35	2.86	2.86	11.26	1.2
Non-derivatized - MS/MS PE NeoBase Kit	152	23.55	1.78	3.13	7.47	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	28	30.01	1.80	3.36	10.38	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	30.65	2.27	4.64	10.04	1.0
Lot 968 - Enriched 30 μmol/L whole blood						
Derivatized - MS/MS Non-kit	844	39.85	3.97	7.96	12.17	0.9
Non-derivatized - MS/MS Non-kit	120	39.18	3.90	6.81	9.76	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	219	29.16	1.88	3.92	13.09	0.5
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	46.20	4.04	4.04	11.26	1.2
Non-derivatized - MS/MS PE NeoBase Kit	149	30.79	2.37	3.79	7.47	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	30	40.25	3.57	9.76	10.38	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	41.12	3.94	6.28	10.04	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.

ACETYLCARNITINE (μmol C2/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	771	15.64	1.62	3.57	15.81	0.9
Non-derivatized - MS/MS Non-kit	85	13.63	1.04	2.38	14.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	203	16.58	1.45	2.69	17.00	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	9	11.38	0.30	0.30	11.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	177	10.77	0.75	1.79	10.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	14.99	1.64	4.20	15.22	0.9
Lot 062 - Enriched 10 μmol/L whole blood						
Derivatized - MS/MS Non-kit	770	25.24	2.43	5.24	15.81	0.9
Non-derivatized - MS/MS Non-kit	86	24.41	2.18	4.05	14.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	202	23.17	1.44	2.74	17.00	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	19.49	1.20	1.20	11.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	176	19.29	1.30	3.17	10.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	24.33	2.21	4.07	15.22	0.9
Lot 063 - Enriched 21 μmol/L whole blood						
Derivatized - MS/MS Non-kit	766	34.30	3.31	6.52	15.81	0.9
Non-derivatized - MS/MS Non-kit	89	36.42	2.81	6.52	14.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	199	28.55	1.72	3.37	17.00	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	27.45	2.38	2.38	11.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	179	27.77	1.98	4.28	10.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	33.01	3.38	4.50	15.22	0.9
Lot 064 - Enriched 31 μmol/L whole blood						
Derivatized - MS/MS Non-kit	773	43.40	4.01	8.50	15.81	0.9
Non-derivatized - MS/MS Non-kit	83	44.73	3.55	7.90	14.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	198	33.71	1.65	3.29	17.00	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	36.25	1.88	1.88	11.26	0.8
Non-derivatized - MS/MS PE NeoBase Kit	176	36.33	2.10	5.54	10.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	41.64	4.19	5.45	15.22	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 10p. 2010 Quality Control Data
Summaries of Statistical Analyses

PROPIONYLCARNITINE (μmol C3/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	878	1.30	0.20	0.35	1.29	1.0
Non-derivatized - MS/MS Non-kit	126	1.13	0.13	0.19	1.16	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	227	0.96	0.06	0.09	1.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.00	0.12	0.12	1.13	1.0
Non-derivatized - MS/MS PE NeoBase Kit	167	1.02	0.08	0.14	1.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	1.06	0.12	0.13	0.93	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	1.21	0.13	0.13	1.19	1.0
Lot 966 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	858	4.30	0.53	0.87	1.29	1.0
Non-derivatized - MS/MS Non-kit	130	4.20	0.47	0.72	1.16	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	224	3.54	0.25	0.36	1.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	4.07	0.32	0.32	1.13	1.0
Non-derivatized - MS/MS PE NeoBase Kit	163	3.64	0.25	0.48	1.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	3.76	0.32	0.53	0.93	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	4.33	0.41	0.62	1.19	1.0
Lot 967 - Enriched 7.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	854	8.73	0.97	1.68	1.29	1.0
Non-derivatized - MS/MS Non-kit	129	8.70	0.92	1.41	1.16	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	230	7.19	0.48	0.69	1.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	8.41	0.35	0.35	1.13	1.0
Non-derivatized - MS/MS PE NeoBase Kit	163	7.60	0.49	0.97	1.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	8.27	1.00	1.67	0.93	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	8.97	0.82	0.91	1.19	1.0
Lot 968 - Enriched 12.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	877	13.31	1.62	3.24	1.29	1.0
Non-derivatized - MS/MS Non-kit	129	13.16	1.42	2.26	1.16	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	229	10.72	0.64	1.12	1.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	12.39	0.99	0.99	1.13	1.0
Non-derivatized - MS/MS PE NeoBase Kit	167	11.28	0.81	1.61	1.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	30	12.88	1.32	3.38	0.93	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	13.75	1.23	1.23	1.19	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.

PROPIONYLCARNITINE (μmol C3/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	812	1.84	0.26	0.43	1.80	1.0
Non-derivatized - MS/MS Non-kit	99	1.81	0.21	0.34	1.86	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	1.50	0.11	0.16	1.54	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.63	0.17	0.17	1.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	187	1.53	0.11	0.22	1.55	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.63	0.21	0.33	1.58	0.9
Lot 062 - Enriched 3.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	803	5.26	0.61	1.04	1.80	1.0
Non-derivatized - MS/MS Non-kit	99	5.47	0.51	0.98	1.86	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	4.54	0.32	0.47	1.54	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	4.80	0.32	0.32	1.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	188	4.60	0.34	0.69	1.55	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	4.73	0.54	0.58	1.58	0.9
Lot 063 - Enriched 8.7 μmol/L whole blood						
Derivatized - MS/MS Non-kit	796	10.25	1.14	2.06	1.80	1.0
Non-derivatized - MS/MS Non-kit	99	10.79	0.91	2.00	1.86	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	209	8.96	0.55	0.88	1.54	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	9.29	0.82	0.82	1.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	187	9.02	0.62	1.19	1.55	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	9.48	0.75	0.89	1.58	0.9
Lot 064 - Enriched 13.9 μmol/L whole blood						
Derivatized - MS/MS Non-kit	788	15.58	1.73	2.84	1.80	1.0
Non-derivatized - MS/MS Non-kit	98	16.03	1.45	3.04	1.86	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	13.30	0.76	1.15	1.54	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	14.41	0.96	0.96	1.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	184	13.55	0.86	1.69	1.55	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	14.29	1.08	1.53	1.58	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 10q. 2010 Quality Control Data
Summaries of Statistical Analyses

MALONYLCARNITINE (μmol C3DC/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	694	0.04	0.02	0.04	0.08	0.6
Non-derivatized - MS/MS Non-kit	58	0.07	0.04	0.05	0.09	0.2
Derivatized - MS/MS PE NeoGram MS2 Kit	200	0.03	0.01	0.01	0.12	1.1
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.09	0.12	0.12	0.22	1.3
Non-derivatized - MS/MS PE NeoBase Kit	100	0.12	0.02	0.07	0.15	0.3
Derivatized - MS/MS Chromsystems MassChrom Kit	20	0.03	0.01	0.01	0.09	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	19	0.05	0.01	0.01	0.05	0.1
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	697	0.40	0.09	0.18	0.08	0.6
Non-derivatized - MS/MS Non-kit	57	0.21	0.07	0.11	0.09	0.2
Derivatized - MS/MS PE NeoGram MS2 Kit	209	0.72	0.08	0.16	0.12	1.1
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.97	0.16	0.16	0.22	1.3
Non-derivatized - MS/MS PE NeoBase Kit	100	0.34	0.04	0.19	0.15	0.3
Derivatized - MS/MS Chromsystems MassChrom Kit	20	0.60	0.10	0.27	0.09	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.13	0.02	0.02	0.05	0.1
Lot 967 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	693	0.91	0.16	0.38	0.08	0.6
Non-derivatized - MS/MS Non-kit	58	0.42	0.10	0.20	0.09	0.2
Derivatized - MS/MS PE NeoGram MS2 Kit	210	1.74	0.19	0.37	0.12	1.1
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.19	0.17	0.17	0.22	1.3
Non-derivatized - MS/MS PE NeoBase Kit	98	0.62	0.09	0.36	0.15	0.3
Derivatized - MS/MS Chromsystems MassChrom Kit	20	1.52	0.20	0.64	0.09	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.25	0.03	0.03	0.05	0.1
Lot 968 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	695	1.72	0.27	0.71	0.08	0.6
Non-derivatized - MS/MS Non-kit	58	0.72	0.14	0.35	0.09	0.2
Derivatized - MS/MS PE NeoGram MS2 Kit	209	3.23	0.33	0.69	0.12	1.1
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	3.95	0.45	0.45	0.22	1.3
Non-derivatized - MS/MS PE NeoBase Kit	98	1.08	0.13	0.67	0.15	0.3
Derivatized - MS/MS Chromsystems MassChrom Kit	20	2.79	0.29	1.31	0.09	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.45	0.05	0.05	0.05	0.1

Note that for both kit and non-kit users, the calculation of concentrations for the quality control lots varied with type of internal standard. Data are not sorted by internal standard type. In a survey, participants reported using d6-C5DC, d3-C5DC, d3-C8, d3-C3, or d3-C16.

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

MALONYLCARNITINE (μmol C3DC/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	653	0.04	0.02	0.03	0.08	0.5
Non-derivatized - MS/MS Non-kit	20	0.13	0.03	0.03	0.14	0.3
Derivatized - MS/MS PE NeoGram MS2 Kit	171	0.04	0.01	0.01	0.12	1.2
Non-derivatized - MS/MS PE NeoBase Kit	131	0.10	0.02	0.06	0.12	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.04	0.02	0.03	0.08	0.9
Lot 062 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	660	0.37	0.07	0.14	0.08	0.5
Non-derivatized - MS/MS Non-kit	20	0.29	0.07	0.09	0.14	0.3
Derivatized - MS/MS PE NeoGram MS2 Kit	177	0.76	0.07	0.12	0.12	1.2
Non-derivatized - MS/MS PE NeoBase Kit	131	0.24	0.05	0.14	0.12	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.56	0.08	0.22	0.08	0.9
Lot 063 - Enriched 1.6 μmol/L whole blood						
Derivatized - MS/MS Non-kit	663	0.98	0.16	0.35	0.08	0.5
Non-derivatized - MS/MS Non-kit	20	0.66	0.09	0.19	0.14	0.3
Derivatized - MS/MS PE NeoGram MS2 Kit	173	2.15	0.16	0.40	0.12	1.2
Non-derivatized - MS/MS PE NeoBase Kit	134	0.52	0.06	0.34	0.12	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.61	0.20	0.60	0.08	0.9
Lot 064 - Enriched 3.3 μmol/L whole blood						
Derivatized - MS/MS Non-kit	666	1.81	0.28	0.67	0.08	0.5
Non-derivatized - MS/MS Non-kit	20	1.11	0.14	0.37	0.14	0.3
Derivatized - MS/MS PE NeoGram MS2 Kit	177	4.06	0.33	0.78	0.12	1.2
Non-derivatized - MS/MS PE NeoBase Kit	131	0.88	0.11	0.57	0.12	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	40	3.12	0.41	1.37	0.08	0.9

Note that for both kit and non-kit users, the calculation of concentrations for the quality control lots varied with type of internal standard. Data are not sorted by internal standard type. In a survey, participants reported using d6-C5DC, d3-C5DC, d3-C8, d3-C3, or d3-C16.

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

Table 10r. 2010 Quality Control Data
Summaries of Statistical Analyses

BUTYRYLCARNITINE (μmol C4/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	843	0.15	0.05	0.07	0.15	0.8
Non-derivatized - MS/MS Non-kit	119	0.12	0.04	0.06	0.13	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	220	0.13	0.04	0.04	0.16	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.24	0.11	0.11	0.28	0.8
Non-derivatized - MS/MS PE NeoBase Kit	148	0.11	0.02	0.03	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	30	0.09	0.02	0.03	0.27	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.10	0.01	0.01	0.14	0.8
Lot 966 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	833	0.98	0.13	0.19	0.15	0.8
Non-derivatized - MS/MS Non-kit	127	0.91	0.12	0.17	0.13	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	228	0.86	0.15	0.17	0.16	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.04	0.19	0.19	0.28	0.8
Non-derivatized - MS/MS PE NeoBase Kit	160	0.84	0.07	0.14	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	30	1.15	0.15	0.73	0.27	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.98	0.08	0.10	0.14	0.8
Lot 967 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	835	2.30	0.27	0.43	0.15	0.8
Non-derivatized - MS/MS Non-kit	130	2.21	0.26	0.42	0.13	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	229	1.98	0.30	0.34	0.16	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.28	0.27	0.27	0.28	0.8
Non-derivatized - MS/MS PE NeoBase Kit	159	2.10	0.16	0.31	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	30	1.52	0.14	0.76	0.27	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	19	2.25	0.14	0.14	0.14	0.8
Lot 968 - Enriched 5.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	835	4.36	0.48	0.83	0.15	0.8
Non-derivatized - MS/MS Non-kit	130	4.13	0.51	0.90	0.13	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	225	3.65	0.45	0.63	0.16	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	4.06	1.04	1.04	0.28	0.8
Non-derivatized - MS/MS PE NeoBase Kit	157	3.87	0.28	0.48	0.12	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	30	3.08	0.29	0.98	0.27	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	4.20	0.36	0.36	0.14	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.

BUTYRYLCARNITINE (μmol C4/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	760	0.18	0.04	0.06	0.18	0.8
Non-derivatized - MS/MS Non-kit	94	0.14	0.03	0.03	0.15	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	193	0.17	0.04	0.05	0.18	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.14	0.03	0.03	0.12	0.8
Non-derivatized - MS/MS PE NeoBase Kit	175	0.15	0.02	0.03	0.14	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.15	0.04	0.05	0.12	0.7
Lot 062 - Enriched 0.9 μmol/L whole blood						
Derivatized - MS/MS Non-kit	776	0.92	0.14	0.18	0.18	0.8
Non-derivatized - MS/MS Non-kit	99	0.90	0.10	0.13	0.15	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	195	0.84	0.16	0.16	0.18	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.83	0.06	0.06	0.12	0.8
Non-derivatized - MS/MS PE NeoBase Kit	177	0.85	0.07	0.12	0.14	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.78	0.08	0.10	0.12	0.7
Lot 063 - Enriched 2.3 μmol/L whole blood						
Derivatized - MS/MS Non-kit	780	1.99	0.25	0.34	0.18	0.8
Non-derivatized - MS/MS Non-kit	100	2.11	0.21	0.34	0.15	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	196	1.74	0.26	0.28	0.18	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.79	0.17	0.17	0.12	0.8
Non-derivatized - MS/MS PE NeoBase Kit	179	1.85	0.14	0.23	0.14	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.71	0.23	0.28	0.12	0.7
Lot 064 - Enriched 4.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	783	3.79	0.43	0.64	0.18	0.8
Non-derivatized - MS/MS Non-kit	97	3.91	0.36	0.56	0.15	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	195	3.32	0.43	0.47	0.18	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	3.57	0.24	0.24	0.12	0.8
Non-derivatized - MS/MS PE NeoBase Kit	175	3.60	0.26	0.42	0.14	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	38	3.38	0.30	0.37	0.12	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 10s. 2010 Quality Control Data
Summaries of Statistical Analyses

ISOVALERYLCARNITINE (μmol C5/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	840	0.08	0.02	0.04	0.09	0.9
Non-derivatized - MS/MS Non-kit	124	0.06	0.02	0.02	0.06	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	232	0.07	0.02	0.03	0.08	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.12	0.04	0.04	0.20	0.7
Non-derivatized - MS/MS PE NeoBase Kit	168	0.07	0.01	0.02	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.06	0.03	0.03	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.07	0.01	0.01	0.07	0.9
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	864	0.54	0.08	0.11	0.09	0.9
Non-derivatized - MS/MS Non-kit	125	0.52	0.07	0.08	0.06	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	235	0.50	0.08	0.10	0.08	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.61	0.17	0.17	0.20	0.7
Non-derivatized - MS/MS PE NeoBase Kit	161	0.48	0.04	0.06	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.47	0.06	0.06	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.54	0.05	0.12	0.07	0.9
Lot 967 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	847	1.39	0.15	0.23	0.09	0.9
Non-derivatized - MS/MS Non-kit	125	1.46	0.15	0.19	0.06	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	234	1.31	0.16	0.18	0.08	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.38	0.26	0.26	0.20	0.7
Non-derivatized - MS/MS PE NeoBase Kit	167	1.37	0.10	0.15	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.38	0.21	0.22	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	1.45	0.08	0.30	0.07	0.9
Lot 968 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	857	2.72	0.28	0.42	0.09	0.9
Non-derivatized - MS/MS Non-kit	127	2.84	0.28	0.34	0.06	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	235	2.53	0.28	0.33	0.08	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.32	0.49	0.49	0.20	0.7
Non-derivatized - MS/MS PE NeoBase Kit	166	2.60	0.21	0.30	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	2.62	0.35	0.58	0.06	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	2.84	0.17	0.57	0.07	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.

ISOVALERYLCARNITINE (μmol C5/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	813	0.11	0.03	0.04	0.12	0.9
Non-derivatized - MS/MS Non-kit	92	0.09	0.03	0.03	0.09	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	187	0.10	0.03	0.03	0.10	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.09	0.02	0.02	0.08	0.9
Non-derivatized - MS/MS PE NeoBase Kit	187	0.09	0.02	0.02	0.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	47	0.10	0.02	0.03	0.10	0.9
Lot 062 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	808	0.57	0.07	0.11	0.12	0.9
Non-derivatized - MS/MS Non-kit	99	0.57	0.05	0.06	0.09	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	194	0.52	0.08	0.09	0.10	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.52	0.05	0.05	0.08	0.9
Non-derivatized - MS/MS PE NeoBase Kit	188	0.53	0.05	0.08	0.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	49	0.55	0.08	0.09	0.10	0.9
Lot 063 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	814	1.45	0.18	0.26	0.12	0.9
Non-derivatized - MS/MS Non-kit	97	1.54	0.14	0.19	0.09	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	197	1.32	0.16	0.20	0.10	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.32	0.13	0.13	0.08	0.9
Non-derivatized - MS/MS PE NeoBase Kit	188	1.39	0.11	0.20	0.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	1.43	0.17	0.20	0.10	0.9
Lot 064 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	809	2.78	0.31	0.49	0.12	0.9
Non-derivatized - MS/MS Non-kit	96	2.96	0.23	0.39	0.09	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	195	2.57	0.32	0.38	0.10	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.68	0.18	0.18	0.08	0.9
Non-derivatized - MS/MS PE NeoBase Kit	190	2.69	0.22	0.39	0.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	47	2.80	0.30	0.34	0.10	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 10t. 2010 Quality Control Data
Summaries of Statistical Analyses

GLUTARYLCARNITINE (μmol C5DC/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	835	0.02	0.01	0.02	0.03	0.4
Non-derivatized - MS/MS Non-kit	128	0.03	0.02	0.02	0.01	0.5
Derivatized - MS/MS PE NeoGram MS2 Kit	226	0.02	0.01	0.01	0.03	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.04	0.04	0.04	0.04	1.5
Non-derivatized - MS/MS PE NeoBase Kit	139	0.06	0.02	0.03	0.05	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.02	0.02	0.02	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.06	0.02	0.04	0.07	0.8
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	856	0.21	0.05	0.08	0.03	0.4
Non-derivatized - MS/MS Non-kit	130	0.28	0.06	0.11	0.01	0.5
Derivatized - MS/MS PE NeoGram MS2 Kit	236	0.38	0.03	0.05	0.03	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.79	0.08	0.08	0.04	1.5
Non-derivatized - MS/MS PE NeoBase Kit	138	0.39	0.05	0.07	0.05	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.47	0.13	0.14	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.50	0.06	0.19	0.07	0.8
Lot 967 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	857	0.40	0.07	0.15	0.03	0.4
Non-derivatized - MS/MS Non-kit	128	0.52	0.09	0.20	0.01	0.5
Derivatized - MS/MS PE NeoGram MS2 Kit	225	0.72	0.05	0.07	0.03	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.49	0.13	0.13	0.04	1.5
Non-derivatized - MS/MS PE NeoBase Kit	143	0.75	0.08	0.15	0.05	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.94	0.15	0.23	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.89	0.11	0.31	0.07	0.8
Lot 968 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	852	0.94	0.14	0.32	0.03	0.4
Non-derivatized - MS/MS Non-kit	130	1.35	0.22	0.55	0.01	0.5
Derivatized - MS/MS PE NeoGram MS2 Kit	227	1.75	0.11	0.15	0.03	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	3.75	0.44	0.44	0.04	1.5
Non-derivatized - MS/MS PE NeoBase Kit	146	1.80	0.17	0.33	0.05	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	2.40	0.34	0.44	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	2.12	0.33	0.78	0.07	0.8

Note that for both kit and non-kit users, the calculation of concentrations for the quality control lots varied with type of internal standard. Data are not sorted by internal standard type. In a survey, participants reported using d3-C5, d9-C5, d3-C8, or d6-C5DC, d3-C5DC as an internal standard for C5DC.

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

GLUTARYLCARNITINE (µmol C5DC/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 µmol/L whole blood						
Derivatized - MS/MS Non-kit	798	0.02	0.01	0.02	0.04	0.5
Non-derivatized - MS/MS Non-kit	89	0.05	0.02	0.03	0.06	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	201	0.03	0.01	0.01	0.05	1.0
Non-derivatized - MS/MS PE NeoBase Kit	168	0.07	0.02	0.03	0.10	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	47	0.04	0.03	0.04	0.05	1.2
Lot 062 - Enriched 0.5 µmol/L whole blood						
Derivatized - MS/MS Non-kit	822	0.30	0.06	0.10	0.04	0.5
Non-derivatized - MS/MS Non-kit	90	0.60	0.10	0.24	0.06	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	203	0.60	0.04	0.08	0.05	1.0
Non-derivatized - MS/MS PE NeoBase Kit	174	0.64	0.07	0.16	0.10	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.72	0.20	0.24	0.05	1.2
Lot 063 - Enriched 1.1 µmol/L whole blood						
Derivatized - MS/MS Non-kit	828	0.57	0.10	0.21	0.04	0.5
Non-derivatized - MS/MS Non-kit	90	1.14	0.17	0.48	0.06	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	197	1.15	0.07	0.12	0.05	1.0
Non-derivatized - MS/MS PE NeoBase Kit	179	1.19	0.11	0.27	0.10	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	50	1.36	0.28	0.34	0.05	1.2
Lot 064 - Enriched 2.7 µmol/L whole blood						
Derivatized - MS/MS Non-kit	825	1.36	0.20	0.46	0.04	0.5
Non-derivatized - MS/MS Non-kit	90	2.79	0.27	1.21	0.06	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	200	2.79	0.17	0.28	0.05	1.0
Non-derivatized - MS/MS PE NeoBase Kit	176	2.79	0.24	0.55	0.10	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	49	3.38	0.75	0.92	0.05	1.2

Note that for both kit and non-kit users, the calculation of concentrations for the quality control lots varied with type of internal standard. Data are not sorted by internal standard type. In a survey, participants reported using d3-C5, d9-C5, d3-C8, or d6-C5DC, d3-C5DC as an internal standard for C5DC.

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

Table10u. 2010 Quality Control Data
Summaries of Statistical Analyses

3-HYDROXYISOVALERYLCARNITINE (μmol C5OH/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	834	0.49	0.07	0.11	0.49	0.8
Non-derivatized - MS/MS Non-kit	77	0.57	0.08	0.23	0.58	0.7
Derivatized - MS/MS PE NeoGram MS2 Kit	227	0.42	0.07	0.09	0.44	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.57	0.17	0.17	0.60	0.5
Non-derivatized - MS/MS PE NeoBase Kit	117	0.60	0.06	0.31	0.59	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	20	0.37	0.05	0.06	0.38	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.44	0.05	0.14	0.44	0.5
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	841	0.87	0.12	0.19	0.49	0.8
Non-derivatized - MS/MS Non-kit	79	0.97	0.11	0.39	0.58	0.7
Derivatized - MS/MS PE NeoGram MS2 Kit	229	0.78	0.12	0.16	0.44	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.85	0.13	0.13	0.60	0.5
Non-derivatized - MS/MS PE NeoBase Kit	113	0.83	0.08	0.37	0.59	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	20	0.68	0.08	0.14	0.38	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.70	0.09	0.20	0.44	0.5
Lot 967 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	840	1.61	0.20	0.35	0.49	0.8
Non-derivatized - MS/MS Non-kit	78	1.65	0.19	0.65	0.58	0.7
Derivatized - MS/MS PE NeoGram MS2 Kit	225	1.41	0.18	0.20	0.44	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.32	0.22	0.22	0.60	0.5
Non-derivatized - MS/MS PE NeoBase Kit	120	1.42	0.12	0.41	0.59	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	20	1.38	0.13	0.30	0.38	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	1.14	0.12	0.34	0.44	0.5
Lot 968 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	847	2.37	0.29	0.51	0.49	0.8
Non-derivatized - MS/MS Non-kit	80	2.45	0.26	0.96	0.58	0.7
Derivatized - MS/MS PE NeoGram MS2 Kit	226	2.03	0.26	0.34	0.44	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.75	0.28	0.28	0.60	0.5
Non-derivatized - MS/MS PE NeoBase Kit	120	1.90	0.19	0.46	0.59	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	20	1.94	0.17	0.49	0.38	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	1.63	0.19	0.54	0.44	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.

3-HYDROXYISOVALERYLCARNITINE (µmol C5OH/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 µmol/L whole blood						
Derivatized - MS/MS Non-kit	766	0.54	0.08	0.13	0.53	0.8
Non-derivatized - MS/MS Non-kit	70	0.74	0.11	0.24	0.75	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	206	0.52	0.10	0.11	0.51	0.7
Non-derivatized - MS/MS PE NeoBase Kit	148	0.62	0.05	0.13	0.62	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.59	0.09	0.21	0.58	0.8
Lot 062 - Enriched 0.3 µmol/L whole blood						
Derivatized - MS/MS Non-kit	768	0.74	0.11	0.17	0.53	0.8
Non-derivatized - MS/MS Non-kit	70	0.97	0.14	0.27	0.75	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	205	0.69	0.10	0.11	0.51	0.7
Non-derivatized - MS/MS PE NeoBase Kit	150	0.77	0.06	0.12	0.62	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	49	0.80	0.11	0.31	0.58	0.8
Lot 063 - Enriched 0.8 µmol/L whole blood						
Derivatized - MS/MS Non-kit	772	1.16	0.15	0.26	0.53	0.8
Non-derivatized - MS/MS Non-kit	70	1.42	0.18	0.41	0.75	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	203	1.06	0.15	0.19	0.51	0.7
Non-derivatized - MS/MS PE NeoBase Kit	149	1.06	0.09	0.16	0.62	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	50	1.27	0.15	0.43	0.58	0.8
Lot 064 - Enriched 1.4 µmol/L whole blood						
Derivatized - MS/MS Non-kit	787	1.61	0.23	0.39	0.53	0.8
Non-derivatized - MS/MS Non-kit	70	1.84	0.21	0.57	0.75	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	209	1.45	0.21	0.25	0.51	0.7
Non-derivatized - MS/MS PE NeoBase Kit	148	1.36	0.11	0.18	0.62	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	50	1.76	0.21	0.59	0.58	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 10v. 2010 Quality Control Data
Summaries of Statistical Analyses

HEXANOYLCARNITINE (μmol C6/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	839	0.04	0.02	0.03	0.04	0.8
Non-derivatized - MS/MS Non-kit	119	0.02	0.02	0.03	0.03	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	231	0.03	0.02	0.02	0.08	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.01	0.01	0.01	0.04	0.7
Non-derivatized - MS/MS PE NeoBase Kit	158	0.02	0.01	0.01	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.02	0.01	0.01	0.05	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	29	0.01	0.00	0.00	0.04	0.8
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	856	0.43	0.06	0.10	0.04	0.8
Non-derivatized - MS/MS Non-kit	119	0.43	0.07	0.08	0.03	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	236	0.38	0.07	0.08	0.08	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.39	0.04	0.04	0.04	0.7
Non-derivatized - MS/MS PE NeoBase Kit	158	0.40	0.03	0.06	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.35	0.05	0.05	0.05	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.44	0.03	0.05	0.04	0.8
Lot 967 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	848	0.85	0.11	0.18	0.04	0.8
Non-derivatized - MS/MS Non-kit	125	0.89	0.09	0.15	0.03	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	233	0.70	0.10	0.11	0.08	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.80	0.03	0.03	0.04	0.7
Non-derivatized - MS/MS PE NeoBase Kit	159	0.81	0.07	0.10	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.70	0.08	0.10	0.05	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.84	0.05	0.07	0.04	0.8
Lot 968 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	860	2.03	0.23	0.46	0.04	0.8
Non-derivatized - MS/MS Non-kit	128	2.11	0.21	0.33	0.03	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	227	1.47	0.18	0.22	0.08	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.80	0.21	0.21	0.04	0.7
Non-derivatized - MS/MS PE NeoBase Kit	156	1.89	0.12	0.19	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.53	0.13	0.23	0.05	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	1.95	0.12	0.19	0.04	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.

HEXANOYLCARNITINE (μmol C6/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	767	0.04	0.02	0.03	0.06	0.8
Non-derivatized - MS/MS Non-kit	94	0.01	0.01	0.01	0.04	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	204	0.03	0.02	0.02	0.07	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.01	0.00	0.00	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	170	0.02	0.01	0.01	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.04	0.02	0.02	0.07	0.8
Lot 062 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	812	0.48	0.07	0.12	0.06	0.8
Non-derivatized - MS/MS Non-kit	96	0.50	0.06	0.07	0.04	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	206	0.46	0.09	0.10	0.07	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.46	0.04	0.04	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	183	0.45	0.04	0.05	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.48	0.08	0.12	0.07	0.8
Lot 063 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	817	0.91	0.12	0.21	0.06	0.8
Non-derivatized - MS/MS Non-kit	97	0.99	0.08	0.12	0.04	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	202	0.79	0.11	0.13	0.07	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.88	0.08	0.08	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	187	0.86	0.06	0.11	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.85	0.08	0.20	0.07	0.8
Lot 064 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	808	2.15	0.26	0.44	0.06	0.8
Non-derivatized - MS/MS Non-kit	98	2.32	0.22	0.37	0.04	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	206	1.82	0.24	0.26	0.07	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.19	0.17	0.17	0.02	0.9
Non-derivatized - MS/MS PE NeoBase Kit	186	2.09	0.16	0.24	0.03	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.99	0.24	0.43	0.07	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 10w. 2010 Quality Control Data
Summaries of Statistical Analyses

OCTANOYLCARNITINE (μmol C8/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	862	0.04	0.02	0.03	0.04	1.0
Non-derivatized - MS/MS Non-kit	175	0.03	0.02	0.03	0.05	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	225	0.02	0.01	0.02	0.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	9	0.04	0.02	0.02	0.13	0.8
Non-derivatized - MS/MS PE NeoBase Kit	161	0.02	0.01	0.01	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	37	0.01	0.01	0.01	0.01	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	38	0.02	0.00	0.01	0.02	0.8
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	868	0.52	0.07	0.11	0.04	1.0
Non-derivatized - MS/MS Non-kit	183	0.51	0.07	0.10	0.05	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	235	0.43	0.08	0.09	0.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.63	0.18	0.18	0.13	0.8
Non-derivatized - MS/MS PE NeoBase Kit	167	0.45	0.04	0.07	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.37	0.05	0.05	0.01	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	0.43	0.03	0.05	0.02	0.8
Lot 967 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	877	1.02	0.13	0.21	0.04	1.0
Non-derivatized - MS/MS Non-kit	185	0.99	0.10	0.16	0.05	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	236	0.83	0.12	0.13	0.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.94	0.16	0.16	0.13	0.8
Non-derivatized - MS/MS PE NeoBase Kit	166	0.90	0.08	0.13	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.78	0.12	0.13	0.01	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	0.84	0.05	0.09	0.02	0.8
Lot 968 - Enriched 2.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	874	2.45	0.29	0.48	0.04	1.0
Non-derivatized - MS/MS Non-kit	184	2.34	0.22	0.38	0.05	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	233	1.98	0.28	0.37	0.04	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.11	0.29	0.29	0.13	0.8
Non-derivatized - MS/MS PE NeoBase Kit	165	2.15	0.20	0.33	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	1.91	0.27	0.30	0.01	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	2.07	0.13	0.22	0.02	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.

OCTANOYLCARNITINE (μmol C8/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	809	0.05	0.02	0.03	0.04	1.0
Non-derivatized - MS/MS Non-kit	127	0.03	0.01	0.02	0.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	199	0.03	0.02	0.02	0.04	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	9	0.01	0.00	0.00	-0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	172	0.02	0.01	0.02	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	47	0.02	0.01	0.02	0.03	0.8
Lot 062 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	821	0.57	0.08	0.11	0.04	1.0
Non-derivatized - MS/MS Non-kit	126	0.58	0.06	0.08	0.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	209	0.51	0.08	0.09	0.04	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.48	0.04	0.04	-0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	187	0.52	0.05	0.07	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.48	0.07	0.08	0.03	0.8
Lot 063 - Enriched 1.1 μmol/L whole blood						
Derivatized - MS/MS Non-kit	824	1.09	0.14	0.22	0.04	1.0
Non-derivatized - MS/MS Non-kit	127	1.14	0.10	0.15	0.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	206	0.95	0.14	0.17	0.04	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.97	0.10	0.10	-0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	185	1.01	0.09	0.12	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	0.92	0.14	0.16	0.03	0.8
Lot 064 - Enriched 2.6 μmol/L whole blood						
Derivatized - MS/MS Non-kit	827	2.63	0.31	0.52	0.04	1.0
Non-derivatized - MS/MS Non-kit	126	2.74	0.24	0.37	0.03	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	205	2.28	0.32	0.34	0.04	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.48	0.15	0.15	-0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	187	2.45	0.19	0.27	0.03	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	2.19	0.21	0.23	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 10x. 2010 Quality Control Data
Summaries of Statistical Analyses

DECANOYLCARNITINE (μmol C10/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	845	0.02	0.01	0.02	0.03	0.9
Non-derivatized - MS/MS Non-kit	140	0.02	0.01	0.03	0.03	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	241	0.01	0.01	0.01	0.02	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.04	0.01	0.01	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	160	0.01	0.01	0.01	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	36	0.02	0.01	0.01	0.02	0.8
Lot 966 - Enriched 0.3 μmol/L whole blood						
Derivatized - MS/MS Non-kit	854	0.27	0.05	0.08	0.03	0.9
Non-derivatized - MS/MS Non-kit	144	0.26	0.04	0.05	0.03	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	243	0.19	0.03	0.04	0.02	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.29	0.08	0.08	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	155	0.19	0.03	0.04	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.18	0.03	0.03	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	38	0.22	0.02	0.04	0.02	0.8
Lot 967 - Enriched 0.8 μmol/L whole blood						
Derivatized - MS/MS Non-kit	858	0.72	0.11	0.17	0.03	0.9
Non-derivatized - MS/MS Non-kit	145	0.71	0.09	0.13	0.03	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	239	0.47	0.07	0.09	0.02	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.58	0.12	0.12	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	153	0.53	0.05	0.09	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.54	0.09	0.09	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	0.59	0.04	0.06	0.02	0.8
Lot 968 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	856	1.42	0.20	0.35	0.03	0.9
Non-derivatized - MS/MS Non-kit	148	1.37	0.17	0.29	0.03	0.9
Derivatized - MS/MS PE NeoGram MS2 Kit	241	0.94	0.13	0.18	0.02	0.6
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.07	0.20	0.20	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	156	1.04	0.12	0.20	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.02	0.12	0.16	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	39	1.20	0.07	0.15	0.02	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.

DECANOYLCARNITINE (μmol C10/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	808	0.03	0.02	0.03	0.03	1.1
Non-derivatized - MS/MS Non-kit	124	0.03	0.01	0.03	0.02	1.2
Derivatized - MS/MS PE NeoGram MS2 Kit	203	0.03	0.02	0.02	0.02	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.02	0.01	0.01	-0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	178	0.02	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	37	0.03	0.02	0.04	0.01	0.8
Lot 062 - Enriched 0.3 μmol/L whole blood						
Derivatized - MS/MS Non-kit	817	0.37	0.06	0.09	0.03	1.1
Non-derivatized - MS/MS Non-kit	129	0.37	0.04	0.08	0.02	1.2
Derivatized - MS/MS PE NeoGram MS2 Kit	204	0.25	0.05	0.05	0.02	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.26	0.02	0.02	-0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	182	0.28	0.02	0.04	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.26	0.03	0.05	0.01	0.8
Lot 063 - Enriched 0.9 μmol/L whole blood						
Derivatized - MS/MS Non-kit	821	1.00	0.14	0.24	0.03	1.1
Non-derivatized - MS/MS Non-kit	128	1.03	0.11	0.22	0.02	1.2
Derivatized - MS/MS PE NeoGram MS2 Kit	202	0.70	0.12	0.13	0.02	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.73	0.06	0.06	-0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	187	0.79	0.07	0.10	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.72	0.10	0.11	0.01	0.8
Lot 064 - Enriched 1.7 μmol/L whole blood						
Derivatized - MS/MS Non-kit	816	1.93	0.25	0.45	0.03	1.1
Non-derivatized - MS/MS Non-kit	128	2.03	0.23	0.48	0.02	1.2
Derivatized - MS/MS PE NeoGram MS2 Kit	203	1.36	0.17	0.20	0.02	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.52	0.10	0.10	-0.01	0.9
Non-derivatized - MS/MS PE NeoBase Kit	184	1.57	0.10	0.16	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.43	0.17	0.22	0.01	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 10y. 2010 Quality Control Data
Summaries of Statistical Analyses

MYRISTOYLCARNITINE (μmol C14/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	825	0.04	0.02	0.03	0.03	0.8
Non-derivatized - MS/MS Non-kit	125	0.04	0.02	0.04	0.02	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	234	0.03	0.01	0.02	0.02	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.04	0.02	0.02	0.06	0.5
Non-derivatized - MS/MS PE NeoBase Kit	166	0.02	0.00	0.01	0.00	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.02	0.02	0.02	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	28	0.01	0.00	0.00	0.00	0.7
Lot 966 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	855	0.46	0.07	0.12	0.03	0.8
Non-derivatized - MS/MS Non-kit	119	0.43	0.06	0.09	0.02	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	233	0.40	0.06	0.07	0.02	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.32	0.06	0.06	0.06	0.5
Non-derivatized - MS/MS PE NeoBase Kit	164	0.37	0.04	0.07	0.00	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.33	0.05	0.07	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	28	0.34	0.03	0.03	0.00	0.7
Lot 967 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	841	1.25	0.17	0.24	0.03	0.8
Non-derivatized - MS/MS Non-kit	120	1.22	0.12	0.21	0.02	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	232	1.04	0.14	0.15	0.02	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.79	0.17	0.17	0.06	0.5
Non-derivatized - MS/MS PE NeoBase Kit	166	1.10	0.09	0.18	0.00	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.01	0.11	0.18	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	28	0.96	0.06	0.06	0.00	0.7
Lot 968 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	846	2.55	0.31	0.47	0.03	0.8
Non-derivatized - MS/MS Non-kit	121	2.50	0.28	0.65	0.02	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	234	2.18	0.24	0.30	0.02	0.7
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.51	0.18	0.18	0.06	0.5
Non-derivatized - MS/MS PE NeoBase Kit	164	2.23	0.21	0.34	0.00	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	39	1.97	0.14	0.30	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	2.01	0.14	0.29	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.

MYRISTOYLCARNITINE (μmol C14/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	789	0.09	0.03	0.03	0.10	1.0
Non-derivatized - MS/MS Non-kit	98	0.07	0.02	0.02	0.08	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	201	0.10	0.03	0.03	0.10	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.06	0.01	0.01	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	188	0.07	0.01	0.01	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	38	0.09	0.04	0.04	0.11	0.8
Lot 062 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	793	0.61	0.08	0.13	0.10	1.0
Non-derivatized - MS/MS Non-kit	98	0.58	0.06	0.10	0.08	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	210	0.56	0.09	0.10	0.10	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.54	0.03	0.03	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	184	0.54	0.04	0.06	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	0.51	0.07	0.09	0.11	0.8
Lot 063 - Enriched 1.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	794	1.60	0.20	0.30	0.10	1.0
Non-derivatized - MS/MS Non-kit	96	1.60	0.17	0.26	0.08	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	206	1.48	0.17	0.19	0.10	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.45	0.12	0.12	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	185	1.49	0.11	0.17	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.27	0.14	0.23	0.11	0.8
Lot 064 - Enriched 3.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	813	3.09	0.39	0.65	0.10	1.0
Non-derivatized - MS/MS Non-kit	98	3.06	0.28	0.42	0.08	1.0
Derivatized - MS/MS PE NeoGram MS2 Kit	208	2.84	0.31	0.36	0.10	0.9
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.87	0.18	0.18	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	188	2.89	0.20	0.30	0.07	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	2.45	0.33	0.41	0.11	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 10z. 2010 Quality Control Data
Summaries of Statistical Analyses

PALMITOYLCARNITINE (μmol C16/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	863	0.56	0.08	0.12	0.58	0.8
Non-derivatized - MS/MS Non-kit	123	0.53	0.07	0.10	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	232	0.51	0.08	0.09	0.54	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.57	0.09	0.09	0.56	0.8
Non-derivatized - MS/MS PE NeoBase Kit	159	0.51	0.04	0.04	0.52	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.49	0.10	0.15	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	0.51	0.05	0.08	0.48	0.8
Lot 966 - Enriched 4.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	881	3.79	0.39	0.61	0.58	0.8
Non-derivatized - MS/MS Non-kit	126	3.81	0.39	0.63	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	233	3.59	0.36	0.41	0.54	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	3.80	0.46	0.46	0.56	0.8
Non-derivatized - MS/MS PE NeoBase Kit	162	3.65	0.25	0.37	0.52	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	3.29	0.28	0.40	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	3.89	0.22	0.91	0.48	0.8
Lot 967 - Enriched 8.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	858	7.06	0.66	1.05	0.58	0.8
Non-derivatized - MS/MS Non-kit	123	6.95	0.66	1.13	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	232	6.54	0.70	0.77	0.54	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	6.76	0.76	0.76	0.56	0.8
Non-derivatized - MS/MS PE NeoBase Kit	166	7.02	0.48	0.79	0.52	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	39	6.35	0.93	1.26	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	20	7.11	0.30	1.61	0.48	0.8
Lot 968 - Enriched 12.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	866	10.15	0.97	1.55	0.58	0.8
Non-derivatized - MS/MS Non-kit	127	10.24	0.90	1.48	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	238	9.54	0.94	1.23	0.54	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	10.17	1.12	1.12	0.56	0.8
Non-derivatized - MS/MS PE NeoBase Kit	163	9.98	0.76	1.07	0.52	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	40	9.24	0.85	1.18	0.44	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	19	10.70	0.53	2.23	0.48	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.

PALMITOYLCARNITINE (µmol C16/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 µmol/L whole blood						
Derivatized - MS/MS Non-kit	817	1.03	0.15	0.23	1.13	0.8
Non-derivatized - MS/MS Non-kit	97	1.04	0.08	0.11	1.18	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	206	1.02	0.13	0.15	1.12	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.01	0.09	0.09	1.10	0.9
Non-derivatized - MS/MS PE NeoBase Kit	184	1.03	0.09	0.13	1.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.94	0.16	0.25	1.04	0.7
Lot 062 - Enriched 4.2 µmol/L whole blood						
Derivatized - MS/MS Non-kit	818	4.66	0.46	0.75	1.13	0.8
Non-derivatized - MS/MS Non-kit	97	4.88	0.29	0.40	1.18	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	203	4.65	0.49	0.55	1.12	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	9	4.93	0.35	0.35	1.10	0.9
Non-derivatized - MS/MS PE NeoBase Kit	181	4.72	0.36	0.56	1.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	4.23	0.46	0.59	1.04	0.7
Lot 063 - Enriched 8.4 µmol/L whole blood						
Derivatized - MS/MS Non-kit	817	7.91	0.75	1.26	1.13	0.8
Non-derivatized - MS/MS Non-kit	98	8.35	0.70	0.94	1.18	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	205	8.03	0.72	0.92	1.12	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	8.37	0.60	0.60	1.10	0.9
Non-derivatized - MS/MS PE NeoBase Kit	182	8.26	0.65	0.95	1.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	50	7.42	0.72	1.20	1.04	0.7
Lot 064 - Enriched 12.7 µmol/L whole blood						
Derivatized - MS/MS Non-kit	817	11.32	1.05	1.75	1.13	0.8
Non-derivatized - MS/MS Non-kit	98	11.76	0.94	1.55	1.18	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	206	11.36	0.97	1.20	1.12	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	12.14	0.73	0.73	1.10	0.9
Non-derivatized - MS/MS PE NeoBase Kit	186	11.80	0.84	1.32	1.09	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	49	10.33	1.25	1.54	1.04	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 10aa. 2010 Quality Control Data
Summaries of Statistical Analyses

STEAROYLCARNITINE (μmol C18/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 965 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	806	0.66	0.09	0.15	0.65	0.9
Non-derivatized - MS/MS Non-kit	94	0.51	0.08	0.13	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	232	0.58	0.08	0.09	0.58	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	0.73	0.19	0.19	0.79	0.8
Non-derivatized - MS/MS PE NeoBase Kit	167	0.56	0.04	0.05	0.57	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.51	0.08	0.09	0.47	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	0.50	0.05	0.06	0.48	0.8
Lot 966 - Enriched 1.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	796	1.55	0.17	0.27	0.65	0.9
Non-derivatized - MS/MS Non-kit	98	1.32	0.17	0.27	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	235	1.41	0.17	0.19	0.58	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	1.62	0.18	0.18	0.79	0.8
Non-derivatized - MS/MS PE NeoBase Kit	162	1.40	0.09	0.13	0.57	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	1.20	0.11	0.14	0.47	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	1.28	0.07	0.14	0.48	0.8
Lot 967 - Enriched 2.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	789	2.43	0.26	0.42	0.65	0.9
Non-derivatized - MS/MS Non-kit	100	2.12	0.28	0.44	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	236	2.24	0.25	0.28	0.58	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	2.27	0.35	0.35	0.79	0.8
Non-derivatized - MS/MS PE NeoBase Kit	169	2.29	0.16	0.23	0.57	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	39	2.01	0.29	0.33	0.47	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	2.04	0.12	0.27	0.48	0.8
Lot 968 - Enriched 5.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	788	5.16	0.55	0.88	0.65	0.9
Non-derivatized - MS/MS Non-kit	98	4.39	0.52	0.83	0.54	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	236	4.73	0.49	0.61	0.58	0.8
Non-derivatized - MS/MS PE NeoGram MS2 Kit	10	4.52	0.38	0.38	0.79	0.8
Non-derivatized - MS/MS PE NeoBase Kit	168	4.80	0.34	0.46	0.57	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	40	4.32	0.52	0.55	0.47	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	30	4.48	0.20	0.37	0.48	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.

STEAROYLCARNITINE (μmol C18/L whole blood)
- continued -

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	761	0.83	0.11	0.19	0.81	0.8
Non-derivatized - MS/MS Non-kit	83	0.76	0.10	0.12	0.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	195	0.73	0.10	0.11	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	196	0.74	0.06	0.08	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	49	0.67	0.10	0.17	0.69	0.7
Lot 062 - Enriched 1.2 μmol/L whole blood						
Derivatized - MS/MS Non-kit	754	1.80	0.21	0.34	0.81	0.8
Non-derivatized - MS/MS Non-kit	84	1.69	0.15	0.23	0.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	194	1.65	0.20	0.23	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	192	1.67	0.11	0.16	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	49	1.49	0.19	0.27	0.69	0.7
Lot 063 - Enriched 2.3 μmol/L whole blood						
Derivatized - MS/MS Non-kit	742	2.70	0.30	0.49	0.81	0.8
Non-derivatized - MS/MS Non-kit	86	2.62	0.29	0.42	0.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	197	2.58	0.25	0.31	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	192	2.57	0.18	0.27	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	50	2.38	0.33	0.49	0.69	0.7
Lot 064 - Enriched 5.8 μmol/L whole blood						
Derivatized - MS/MS Non-kit	752	5.62	0.60	1.07	0.81	0.8
Non-derivatized - MS/MS Non-kit	89	5.49	0.57	0.80	0.74	0.8
Derivatized - MS/MS PE NeoGram MS2 Kit	193	5.31	0.47	0.53	0.73	0.8
Non-derivatized - MS/MS PE NeoBase Kit	194	5.50	0.39	0.55	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	48	4.72	0.58	0.89	0.69	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 10bb. 2010 Quality Control Data
Summaries of Statistical Analyses

DODECANOYLCARNITINE (μmol C12/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	634	0.04	0.02	0.03	0.06	1.3
Non-derivatized - MS/MS Non-kit	72	0.01	0.00	0.00	0.02	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	173	0.04	0.02	0.02	0.07	1.2
Non-derivatized - MS/MS PE NeoBase Kit	149	0.01	0.00	0.01	0.02	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	37	0.06	0.04	0.04	0.10	1.1
Lot 062 - Enriched 0.2 μmol/L whole blood						
Derivatized - MS/MS Non-kit	635	0.37	0.07	0.12	0.06	1.3
Non-derivatized - MS/MS Non-kit	80	0.26	0.03	0.07	0.02	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	175	0.34	0.07	0.07	0.07	1.2
Non-derivatized - MS/MS PE NeoBase Kit	156	0.27	0.02	0.03	0.02	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.36	0.07	0.07	0.10	1.1
Lot 063 - Enriched 0.5 μmol/L whole blood						
Derivatized - MS/MS Non-kit	639	0.69	0.13	0.21	0.06	1.3
Non-derivatized - MS/MS Non-kit	80	0.54	0.06	0.15	0.02	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	174	0.65	0.10	0.12	0.07	1.2
Non-derivatized - MS/MS PE NeoBase Kit	156	0.53	0.05	0.06	0.02	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	40	0.67	0.14	0.14	0.10	1.1
Lot 064 - Enriched 1.1 μmol/L whole blood						
Derivatized - MS/MS Non-kit	644	1.50	0.23	0.41	0.06	1.3
Non-derivatized - MS/MS Non-kit	80	1.24	0.12	0.34	0.02	1.1
Derivatized - MS/MS PE NeoGram MS2 Kit	177	1.37	0.15	0.19	0.07	1.2
Non-derivatized - MS/MS PE NeoBase Kit	157	1.26	0.09	0.11	0.02	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	39	1.31	0.17	0.19	0.10	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 10cc. 2010 Quality Control Data
Summaries of Statistical Analyses

3-HYDROXYPALMITOYLCARNITINE (μmol C16OH/L whole blood)

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Lot 061 - Nonenriched 0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	685	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS Non-kit	79	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS PE NeoGram MS2 Kit	188	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	168	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.01	0.01	0.01	0.02	0.6
Lot 062 - Enriched 0.4 μmol/L whole blood						
Derivatized - MS/MS Non-kit	698	0.27	0.04	0.07	0.02	0.6
Non-derivatized - MS/MS Non-kit	77	0.24	0.04	0.07	0.01	0.6
Derivatized - MS/MS PE NeoGram MS2 Kit	191	0.27	0.05	0.06	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	166	0.24	0.02	0.04	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	48	0.24	0.05	0.07	0.02	0.6
Lot 063 - Enriched 0.8 μmol/L whole blood						
Derivatized - MS/MS Non-kit	708	0.51	0.07	0.12	0.02	0.6
Non-derivatized - MS/MS Non-kit	79	0.49	0.09	0.16	0.01	0.6
Derivatized - MS/MS PE NeoGram MS2 Kit	195	0.53	0.08	0.11	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	167	0.47	0.05	0.08	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	50	0.47	0.07	0.13	0.02	0.6
Lot 064 - Enriched 2.0 μmol/L whole blood						
Derivatized - MS/MS Non-kit	704	1.22	0.13	0.28	0.02	0.6
Non-derivatized - MS/MS Non-kit	79	1.18	0.16	0.40	0.01	0.6
Derivatized - MS/MS PE NeoGram MS2 Kit	197	1.29	0.16	0.25	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	167	1.16	0.09	0.16	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	50	1.11	0.16	0.32	0.02	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.

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