

Newborn Screening Quality Assurance Program

2019 Quality Control Report

In co-sponsorship with Association of Public Health Laboratories (APHL)
Provided by the Newborn Screening and Molecular Biology Branch
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Introduction

AMENDED REPORT This report replaces the 2019 Quality Control Report Volume 30, No.1. It adds the method and associated statistics for Derivatized - MS/MS non-kit to C14:1 Lot A1815 on page 61. The NSQAP Quality Control (QC) dried blood spot (DBS) materials provide participants with external controls to assess method performance over time. The controls offer continuity and transcend changes in production lots of routinely used method- or kit-control materials. The external QC materials are intended to supplement the participants' method- or kit-control materials at periodic intervals to allow participants to monitor the long-term stability of their assays. NSQAP QC material is not a replacement for manufacturer kit controls or other daily QC, and should not be used for routine analysis. This report contains a summary of the 2019 Set 1 QC data submitted during the first half of the year by state, contract, and private laboratories in the United States; international participants; and manufacturers of screening test products.

QC Material Production

QC specimen lots were provided as 6-month supplies of DBS on filter paper. DBS QC lots were prepared from whole blood of 50% hematocrit. The materials were enriched with predetermined quantities of selected analytes and dispensed in 100 μ L aliquots on Grade 903 filter paper (GE Healthcare Bio-Sciences Corporation (Westborough, MA)).

NSQAP provides QC materials for analysis of thyroxine (T4), thyroid-stimulating hormone (TSH), 17 α -hydroxyprogesterone (17OHP), total galactose (TGal), galactose-1-phosphate uridylyltransferase (GALT), immunoreactive trypsinogen (IRT), phenylalanine (Phe), leucine (Leu), methionine (Met), tyrosine (Tyr), valine (Val), citrulline (Cit), alanine (Ala), arginine (Arg), ornithine (Orn), glycine (Gly), succinylacetone (SUAC). The QC pool for Tandem Mass Spectrometry (MSMS1QC) included enrichments for twenty acylcarnitines - free carnitine (C0), acetylcarnitine (C2), propionylcarnitine (C3), malonylcarnitine (C3DC), butyrylcarnitine (C4), hydroxybutyrylcarnitine (C4OH), isovalerylcarnitine (C5), tiglylcarnitine (C5:1), glutarylcarnitine (C5DC), hydroxyisovalerylcarnitine (C5OH), hexanoylcarnitine (C6), octanoylcarnitine (C8), decanoylcarnitine (C10), dodecanoylcarnitine (C12), myristoylcarnitine (C14), tetradecenoylcarnitine (C14:1), palmitoylcarnitine (C16), hydroxypalmitoylcarnitine (C16OH), stearoylcarnitine (C18), hydroxystearoylcarnitine (C18OH), 20:0-, 22:0-, 24:0- and 26:0-lysophosphatidylcholine for the detection of X-linked Adrenoleukodystrophy (XALD), creatine (CRE), guanidinoacetic acid (GUAC), creatinine (CRN). We also provide materials for galactocerebrosidase (GALC), acid α -glucosidase (GAA), α -L-iduronidase (IDUA), α -galactosidase (GLA), β -glucocerebrosidase (ABG), and acid sphingomyelinase (ASM) for the detection of Lysosomal Storage Disorder (LSD).

QC materials for T4, TSH, 17OHP and TGal, GALT consisted of DBS from three lots per analyte, with each lot containing a different concentration of analyte. QC materials for IRT, TGal, amino acids, SUAC, acylcarnitines, XALD, GAMT, and LSD consisted four lots per analyte or group of analytes. Some of the base pool analytes have been enriched to ensure concentrations at detectable levels.

NSQAP also distributed certified QC materials for newborn screening analytes and disorders designed for second-tier testing by tandem mass spectrometry (MS/MS). These programs include Second-tier Congenital Adrenal Hyperplasia (CAHQC) by LC-MS/MS for the analytes 17 α -hydroxyprogesterone (17OHP2), 4-androstenedione (4AD2), cortisol (CORT2), 11-deoxycortisol (11D2), and 21-deoxycortisol (21D2); Second-tier Maple Syrup Urine Disease and

Phenylketonuria (MSUD-PKUQC) by LC-MS/MS for the analytes alloisoleucine (ALE2), isoleucine (ILE2), leucine (LEU2), phenylalanine (PHE2), tyrosine (TYR2), and valine (VAL2); Second-tier Methylmalonic/Propionic Acidemia and Homocystinuria (MMA-tHCY) by LC-MS/MS for the analytes malonic acid (MA2), methylmalonic acid (MMA2), ethylmalonic acid (EMA2), 2-methylcitric acid (MCA2), and total homocysteine (tHCY2). QC materials for these analytes consisted of DBS from four to five lots.

QC Material Distribution

On January 15, we distributed DBS QC materials to 517 participating laboratories.

QC Data Reporting Requirements

Participants used the QC Data Report forms located at https://www.cdc.gov/labstandards/nsqap_resources.html to report results. NSQAP required the following information for each analyte; 1) laboratory information (contact name, laboratory code number, email; 2) analyte kit or method; 3) results of duplicate analysis from five independent runs with the requested analytic units and decimal places; and 4) at least nine data points for each lot of analyte. If these minimum requirements were not met, the data was not accepted unless the participant corrected their submission before the data reporting deadline.

Participant Results

For Set 1 QC materials, we compiled participant results from five runs for each QC lot, and calculated mean values and standard deviations (SD) for each analyte. Data values outside 4SD limits were reviewed, and if considered to be “blunders”, removed from the data set. For linear regression analysis, we could not include qualitative data, data submitted as inequalities or ranges, data submitted in unidentified units, or data from less than five analytic runs per specimen lot per analyte.

Several participants were required to resubmit their data because either the method was not entered from the drop-down menu as requested or data was reported in the incorrect units. To ensure that all results are entered in the CDC database, participants must convert their results to the requested units before entering them on the data report forms. For GALT analysis, where no conversion factor exists between units of U/g Hb and other reportable units, we provided a separate table with peer-group statistics. For LSDQC analysis, where mean activities differ based on method, we provided separate tables if sufficient data was submitted.

The reported QC data are summarized in tables on pages **4—101** which show the analyte by series of QC lots, the number of measurements (N), the mean values, and the 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 (aggregated) versus enriched concentrations. Methods used by less than three participants were not included in the tables.

Discussion

Summary tables show data sorted by method, method-related differences in analytic recoveries and method bias. Because we prepared each QC lot series from a single batch of hematocrit-adjusted, non-enriched blood, the endogenous concentration was the same for all specimens across the lot series and 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. A method with no analytical bias will have a slope of 1.0, with an acceptable range from 0.8 to 1.2.

Calculations of concentrations for the QC lots may vary with type of MS/MS internal standard used. Data are not sorted by internal standard type. QC materials are provided as sets of three to five analyte concentrations. A bias error in any one pool can influence the slope and intercept for a method.

Discussion (cont.)

For the purpose of our assessment, we first calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs for regression analyses. We then calculated the Y-intercept and slope listed in each table using all analyte concentrations within a lot series (**e.g., lots A1801, B1801, and C1801**). The Y-intercept is estimated by performing a weighted linear regression analysis on mean reported concentrations versus either 1) enriched concentrations; 2) assayed values (GALT, IRT; or 3) mean activity (LSD), and extrapolated the regression to the Y-axis. This parameter provides one measure of the endogenous concentration level for an analyte. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, Gly, SUAC, acylcarnitines, 20:0-, 22:0-, 24:0-, and 26:0-lysophosphatidylcholine, CRE, GALC, GALC,GAA, IDUA, GAL, ABG, ASM, and all Second-tier analytes, participants measured the endogenous concentration or activity levels by analyzing the non-enriched QC lots. For CRN and MA, no data are shown due to insufficient data reported.

We assessed the majority of analytes as demonstrating acceptable performance, with slopes falling near or within the range of acceptability (from 0.8 to 1.2). Analytes which demonstrated low slopes included **Orn, SUAC, C3DC + C4OH, C4OH, and C18OH**, but were historically consistent with previous sets. For IRT, slopes were slightly lower for all methods compared to previous lots.

Submit changes in QC enrollment using the Request for Participation Form at:

http://www.cdc.gov/labstandards/pdf/nsqap/nsqap_requestparticipation.pdf. Send forms to NSQAPDMT@cdc.gov

Domestic laboratories must submit changes no later than November 1, 2019 to receive materials in January 2020. International laboratories must submit changes no later than August 31, 2019 to receive materials in January 2020. Include your laboratory code number on the form and all correspondence with NSQAP.

2019 Quality Control Data Summaries of Statistical Analyses

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

Lot A1705 – Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	257	21.6	2.3	8.7	-2.3	0.9
AutoDelfia	277	21.6	1.8	4.0	0.9	0.8
Labsystems Diagnostics	70	29.7	1.7	9.9	6.4	0.9
Bio-Rad Quantase	30	35.0	4.3	13.0	4.6	1.3
LC-MS/MS	40	21.3	1.8	4.7	0.2	0.8
Delfia Neonatal 17-OHP (A024)	230	20.2	2.8	4.2	-3.4	0.9
AutoDelfia Neonatal 17-OHP (B024)	329	22.1	2.2	3.8	0.4	0.9
PerkinElmer GSP Neonatal	619	22.8	2.2	4.1	2.1	0.8
Zentech	50	29.8	5.6	8.8	4.2	1.0

Lot B1705 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	255	44.0	5.1	16.6	-2.3	0.9
AutoDelfia	273	42.1	3.3	8.2	0.9	0.8
Labsystems Diagnostics	70	54.1	3.4	20.1	6.4	0.9
Bio-Rad Quantase	30	70.4	8.9	25.1	4.6	1.3
LC-MS/MS	40	42.5	4.4	8.9	0.2	0.8
Delfia Neonatal 17-OHP (A024)	229	40.4	6.4	8.9	-3.4	0.9
AutoDelfia Neonatal 17-OHP (B024)	330	43.9	4.0	7.1	0.4	0.9
PerkinElmer GSP Neonatal	613	43.5	3.4	6.2	2.1	0.8
Zentech	50	54.3	8.8	11.7	4.2	1.0

Lot C1705 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	259	91.8	12.2	36.8	-2.3	0.9
AutoDelfia	274	83.5	6.5	15.6	0.9	0.8
Labsystems Diagnostics	70	100.6	13.0	31.9	6.4	0.9
Bio-Rad Quantase	30	131.3	16.2	57.2	4.6	1.3
LC-MS/MS	40	84.7	8.4	20.4	0.2	0.8
Delfia Neonatal 17-OHP (A024)	228	87.4	14.4	19.8	-3.4	0.9
AutoDelfia Neonatal 17-OHP (B024)	329	87.1	9.1	14.7	0.4	0.9
PerkinElmer GSP Neonatal	615	84.9	6.6	11.9	2.1	0.8
Zentech	50	105.3	12.6	24.6	4.2	1.0

2019 Quality Control Data Summaries of Statistical Analyses

THYROXINE (T₄ µg/dL serum)

Lot A1700 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	110	2.6	1.1	2.7	-0.5	1.0
AutoDelfia	173	1.6	0.3	0.4	-0.5	1.0
PerkinElmer GSP Neonatal	161	1.9	0.3	0.5	-0.4	1.1

Lot B1700 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	109	9.4	2.7	10.2	-0.5	1.0
AutoDelfia	179	6.3	0.7	1.0	-0.5	1.0
PerkinElmer GSP Neonatal	180	7.0	0.8	1.2	-0.4	1.1

Lot C1700 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	109	15.9	1.8	16.8	-0.5	1.0
AutoDelfia	179	10.7	1.0	1.5	-0.5	1.0
PerkinElmer GSP Neonatal	178	11.8	1.1	2.0	-0.4	1.1

2019 Quality Control Data Summaries of Statistical Analyses

THYROID-STIMULATING HORMONE (TSH μ IU/mL serum)

Lot A1801 – Enriched 25 μ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	539	25.5	3.3	7.1	-1.2	1.1
AutoDelfia	850	27.4	2.4	4.7	-1.9	1.2
Labsystems Diagnostics	160	27.5	2.9	7.8	-5.1	1.3
DiaSorin	70	25.9	3.2	4.3	-3.0	1.1
PerkinElmer GSP Neonatal	760	23.8	2.2	4.7	-6.7	1.2
Zentech	80	19.3	2.9	6.7	-5.4	1.0

Lot B1801 – Enriched 40 μ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	539	40.7	4.3	11.2	-1.2	1.1
AutoDelfia	850	43.5	3.9	7.5	-1.9	1.2
Labsystems Diagnostics	160	47.3	3.8	11.1	-5.1	1.3
DiaSorin	70	40.8	4.8	6.9	-3.0	1.1
PerkinElmer GSP Neonatal	760	39.2	3.5	7.6	-6.7	1.2
Zentech	80	33.1	4.1	10.3	-5.4	1.0

Lot C1801 – Enriched 80 μ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	539	83.4	9.3	21.9	-1.2	1.1
AutoDelfia	850	90.5	7.0	15.1	-1.9	1.2
Labsystems Diagnostics	160	99.4	9.4	20.9	-5.1	1.3
DiaSorin	69	87.2	10.4	14.5	-3.0	1.1
PerkinElmer GSP Neonatal	760	88.0	7.5	16.8	-6.7	1.2
Zentech	80	72.6	7.4	20.2	-5.4	1.0

2019 Quality Control Data Summaries of Statistical Analyses
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT U/g Hb)

Lot F1803 – Assayed 1.4 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	293	1.2	0.3	0.5	0.0	0.8
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	50	0.9	0.1	0.2	-0.3	0.8

Lot G1803 – Assayed 3.9 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	327	3.1	0.4	0.6	0.0	0.8
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	50	2.7	0.2	0.3	-0.3	0.8

Lot H1803 – Assayed 8.6 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	326	6.9	0.8	1.2	0.0	0.8
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	50	6.3	0.5	0.7	-0.3	0.8

2019 Quality Control Data Summaries of Statistical Analyses

GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (cont.) METHODS REPORTED IN UNITS OTHER THAN U/g Hb

Lot F1803

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	4.1	1.0	4.1	0.1	14.0
Perkin Elmer GSP Neonatal (U/dL blood)	60	1.2	0.1	1.0	0.0	2.7

Lot G1803

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	32.8	5.8	31.0	1.1	83.9
Perkin Elmer GSP Neonatal (U/dL blood)	150	1.8	0.2	0.7	0.5	4.2

Lot H1803

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	92.8	19.1	88.9	3.5	229.3
Perkin Elmer GSP Neonatal (U/dL blood)	200	8.5	0.6	1.2	4.7	10.8

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

2019 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPsinOGEN (IRT ng/mL blood)

Lot A1809 – Assayed 16.6 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	188	16.5	1.9	2.1	18.3	1.0
AutoDelfia	649	17.0	1.7	1.9	21.1	1.0
MP Biomedicals ELISA Assay	40	17.6	1.9	3.1	31.4	1.8
PerkinElmer GSP Neonatal	459	16.6	1.2	1.7	19.6	1.0
Zentech	40	23.8	3.7	4.9	60.1	0.8
Labsystems - FEIA	100	24.2	3.1	6.8	26.4	1.0
Interscientific NeoMAP 4PLEX	40	20.2	3.2	8.6	18.7	0.8

Lot B1809 – Assayed 66.9 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	189	62.0	5.9	7.8	18.3	1.0
AutoDelfia	658	67.5	5.0	6.2	21.1	1.0
MP Biomedicals ELISA Assay	40	109.7	16.9	24.1	31.4	1.8
PerkinElmer GSP Neonatal	479	67.0	4.3	6.5	19.6	1.0
Zentech	40	118.2	11.1	16.4	60.1	0.8
Labsystems - FEIA	100	74.5	9.7	18.6	26.4	1.0
Interscientific NeoMAP 4PLEX	40	50.3	6.2	9.0	18.7	0.8

Lot C1809 – Assayed 122.0 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	189	122.3	13.9	15.7	18.3	1.0
AutoDelfia	659	127.7	10.2	12.7	21.1	1.0
MP Biomedicals ELISA Assay	40	247.6	39.7	93.9	31.4	1.8
PerkinElmer GSP Neonatal	476	128.5	8.4	12.0	19.6	1.0
Zentech	40	173.6	12.6	15.8	60.1	0.8
Labsystems - FEIA	98	138.1	14.2	37.6	26.4	1.0
Interscientific NeoMAP 4PLEX	40	107.4	10.7	12.1	18.7	0.8

2019 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood) cont.

Lot D1809 – Assayed 234.7 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	189	225.2	21.6	30.1	18.3	1.0
AutoDelfia	658	230.3	19.7	22.9	21.1	1.0
MP Biomedicals ELISA Assay	30	397.1	53.3	157.4	31.4	1.8
PerkinElmer GSP Neonatal	478	237.3	18.2	23.7	19.6	1.0
Zentech	40	202.3	11.5	13.3	60.1	0.8
Labsystems - FEIA	98	250.5	24.5	44.7	26.4	1.0
Interscientific NeoMAP 4PLEX	40	191.8	27.2	36.1	18.7	0.8

2019 Quality Control Data Summaries of Statistical Analyses

ALANINE (Ala $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	600	234.1	27.7	59.5	235.8	0.7
Derivatized - MS/MS PE NeoGram Kit	30	232.5	20.4	40.0	232.0	0.8
Non-derivatized - MS/MS non-kit	190	253.3	26.5	57.1	254.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	220.1	26.6	56.5	223.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	810	266.0	20.5	41.5	265.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	213.7	15.2	50.7	216.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	212.1	12.1	47.6	210.7	0.7

Lot B1815 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	600	375.9	37.1	92.9	235.8	0.7
Derivatized - MS/MS PE NeoGram Kit	30	380.8	39.9	68.5	232.0	0.8
Non-derivatized - MS/MS non-kit	190	405.2	35.7	86.0	254.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	360.9	36.5	91.3	223.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	809	423.8	31.4	66.9	265.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	343.2	22.0	87.2	216.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	343.9	28.2	69.3	210.7	0.7

Lot C1815 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	600	540.9	49.8	135.9	235.8	0.7
Derivatized - MS/MS PE NeoGram Kit	30	572.1	31.5	105.2	232.0	0.8
Non-derivatized - MS/MS non-kit	190	582.3	43.9	122.5	254.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	159	497.1	53.1	121.2	223.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	809	620.7	43.6	96.8	265.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	506.9	42.7	119.3	216.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	500.6	32.7	108.4	210.7	0.7

2019 Quality Control Data Summaries of Statistical Analyses

ALANINE (Ala $\mu\text{mol/L}$ blood) cont.

Lot D1815 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	599	663.0	65.9	166.8	235.8	0.7
Derivatized - MS/MS PE NeoGram Kit	30	701.2	50.3	148.1	232.0	0.8
Non-derivatized - MS/MS non-kit	190	715.5	48.7	157.9	254.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	623.3	51.5	150.4	223.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	810	763.6	55.4	120.8	265.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	606.5	40.6	135.0	216.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	627.0	55.3	99.5	210.7	0.7

2019 Quality Control Data Summaries of Statistical Analyses

ARGININE (Arg $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	614	7.9	1.3	4.4	6.6	0.7
Derivatized - MS/MS PE NeoGram Kit	59	6.3	1.3	1.4	4.8	0.8
Non-derivatized - MS/MS non-kit	199	8.0	1.8	5.0	6.7	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	156	8.0	1.4	2.8	9.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	861	6.0	0.7	1.3	4.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	7.5	0.9	2.1	10.9	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	5.8	1.1	2.5	5.0	0.6

Lot B1815 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	620	75.0	7.8	25.2	6.6	0.7
Derivatized - MS/MS PE NeoGram Kit	60	86.3	6.6	9.1	4.8	0.8
Non-derivatized - MS/MS non-kit	200	87.2	9.7	37.2	6.7	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	90.6	8.7	26.8	9.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	866	86.2	5.4	11.2	4.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	89.5	6.6	17.6	10.9	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	67.5	4.8	23.0	5.0	0.6

Lot C1815 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	620	147.4	13.6	49.9	6.6	0.7
Derivatized - MS/MS PE NeoGram Kit	60	171.7	10.8	19.6	4.8	0.8
Non-derivatized - MS/MS non-kit	200	172.6	19.5	75.4	6.7	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	165.8	14.5	46.2	9.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	864	167.8	10.7	21.7	4.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	160.1	12.8	30.9	10.9	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	133.2	9.7	44.6	5.0	0.6

2019 Quality Control Data Summaries of Statistical Analyses

ARGININE (Arg $\mu\text{mol/L}$ blood) cont.

Lot D1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	618	218.4	21.6	79.7	6.6	0.7
Derivatized - MS/MS PE NeoGram Kit	60	256.4	19.7	32.6	4.8	0.8
Non-derivatized - MS/MS non-kit	200	255.1	23.6	110.8	6.7	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	244.4	22.8	66.6	9.6	0.8
Non-derivatized - MS/MS PE NeoBase Kit	865	254.2	16.2	33.6	4.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	230.8	19.1	47.9	10.9	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	197.1	15.9	62.7	5.0	0.6

2019 Quality Control Data Summaries of Statistical Analyses

CITRULLINE (Cit $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	632	13.9	1.9	3.1	14.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	16.7	1.8	2.3	16.8	0.9
Non-derivatized - MS/MS non-kit	270	15.5	2.9	5.7	15.6	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	158	16.6	2.2	3.1	17.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	945	15.4	1.7	2.3	15.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	15.3	1.8	3.1	15.6	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	13.4	1.3	2.1	14.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	17.4	2.5	3.6	19.2	0.7

Lot B1815 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	638	33.8	3.9	7.2	14.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	40.3	3.6	5.3	16.8	0.9
Non-derivatized - MS/MS non-kit	268	37.7	5.1	8.3	15.6	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	160	39.8	3.9	6.0	17.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	946	38.5	3.1	4.6	15.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	37.4	2.9	6.4	15.6	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	33.0	2.0	4.6	14.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	38.3	4.8	7.4	19.2	0.7

Lot C1815 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	640	91.8	8.8	18.4	14.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	110.8	7.5	16.4	16.8	0.9
Non-derivatized - MS/MS non-kit	269	102.2	10.7	18.1	15.6	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	159	108.9	9.6	22.4	17.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	950	105.2	7.5	11.2	15.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	105.7	9.8	18.7	15.6	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	88.9	5.5	11.5	14.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	95.3	8.7	16.2	19.2	0.7

2019 Quality Control Data Summaries of Statistical Analyses

CITRULLINE (Cit $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	638	206.8	20.0	40.6	14.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	251.8	18.5	38.6	16.8	0.9
Non-derivatized - MS/MS non-kit	269	233.2	21.2	39.2	15.6	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	158	241.4	19.7	35.5	17.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	948	239.7	16.0	25.9	15.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	237.7	20.5	38.7	15.6	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	200.5	11.0	26.2	14.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	203.4	12.3	22.7	19.2	0.7

2019 Quality Control Data Summaries of Statistical Analyses

GLYCINE (Gly $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	538	310.4	23.6	77.2	308.2	0.8
Non-derivatized - MS/MS non-kit	149	271.4	40.6	97.3	272.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	309.3	27.1	60.6	303.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	658	354.4	33.8	58.4	345.6	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	234.3	19.4	39.8	231.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	49	352.4	20.5	36.7	347.3	0.9

Lot B1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	526.5	42.4	132.5	308.2	0.8
Non-derivatized - MS/MS non-kit	150	460.2	91.3	186.6	272.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	503.1	45.3	100.3	303.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	660	591.7	47.1	97.4	345.6	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	388.9	25.5	67.8	231.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	598.3	29.9	56.6	347.3	0.9

Lot C1815 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	772.1	57.9	187.3	308.2	0.8
Non-derivatized - MS/MS non-kit	149	661.6	87.7	236.2	272.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	149	718.0	55.3	147.4	303.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	660	882.2	68.9	151.6	345.6	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	593.5	52.9	107.4	231.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	871.7	55.5	76.1	347.3	0.9

2019 Quality Control Data Summaries of Statistical Analyses

GLYCINE (Gly $\mu\text{mol/L}$ blood) cont.

Lot D1815 – Enriched 900 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	540	984.1	85.2	257.9	308.2	0.8
Non-derivatized - MS/MS non-kit	149	837.6	109.7	291.6	272.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	931.6	96.5	228.6	303.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	660	1137.0	89.9	192.9	345.6	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	739.1	46.8	124.2	231.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1129.1	90.9	198.9	347.3	0.9

2019 Quality Control Data Summaries of Statistical Analyses

LEUCINE (Leu $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	643	80.0	8.5	15.8	84.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	79.7	7.3	7.6	84.4	0.9
Non-derivatized - MS/MS non-kit	338	91.0	6.1	17.8	94.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	155	84.5	14.8	33.3	88.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	958	94.8	5.8	9.9	96.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	90.6	4.7	14.6	95.2	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	96.6	4.7	8.7	102.9	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	67.3	4.8	9.2	70.3	0.8

Lot B1815 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	649	200.5	21.9	37.2	84.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	213.7	16.1	21.4	84.4	0.9
Non-derivatized - MS/MS non-kit	340	214.8	15.6	35.5	94.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	192.2	21.5	35.1	88.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	957	221.2	14.1	22.7	96.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	209.6	10.2	26.5	95.2	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	233.1	10.6	28.5	102.9	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	183.4	9.7	20.0	70.3	0.8

Lot C1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	649	332.9	28.4	59.4	84.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	363.4	25.2	40.9	84.4	0.9
Non-derivatized - MS/MS non-kit	340	353.7	23.0	56.5	94.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	314.3	30.5	53.2	88.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	958	368.9	24.3	37.2	96.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	339.3	21.8	32.5	95.2	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	377.9	19.2	38.9	102.9	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	317.8	21.4	32.3	70.3	0.8

2019 Quality Control Data Summaries of Statistical Analyses

LEUCINE (Leu $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	649	552.9	54.4	105.7	84.3	0.8
Derivatized - MS/MS PE NeoGram Kit	60	607.7	46.5	73.2	84.4	0.9
Non-derivatized - MS/MS non-kit	340	583.8	39.0	95.2	94.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	511.0	36.8	93.7	88.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	957	613.5	39.7	68.0	96.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	554.2	28.1	66.2	95.2	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	619.7	25.4	68.0	102.9	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	535.1	32.9	69.3	70.3	0.8

2019 Quality Control Data Summaries of Statistical Analyses

METHIONINE (Met $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	624	13.9	2.5	4.8	13.5	0.8
Derivatized - MS/MS PE NeoGram Kit	60	13.6	2.0	2.1	17.9	0.9
Non-derivatized - MS/MS non-kit	330	11.9	1.2	3.5	10.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	11.0	1.8	3.2	10.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	943	11.5	1.2	1.7	9.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	9.3	0.9	2.0	8.2	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	11.2	0.9	1.2	10.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	13.2	1.7	3.6	11.7	0.8

Lot B1815 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	636	53.7	5.5	8.1	13.5	0.8
Derivatized - MS/MS PE NeoGram Kit	60	63.8	20.9	29.1	17.9	0.9
Non-derivatized - MS/MS non-kit	328	49.1	4.8	8.3	10.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	160	42.9	6.5	15.1	10.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	949	48.1	3.4	5.3	9.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	43.1	2.6	8.0	8.2	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	49.3	2.4	3.1	10.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	53.2	4.5	6.1	11.7	0.8

Lot C1815 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	639	134.6	11.4	19.3	13.5	0.8
Derivatized - MS/MS PE NeoGram Kit	60	149.0	19.5	32.5	17.9	0.9
Non-derivatized - MS/MS non-kit	329	127.4	9.8	21.8	10.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	105.5	11.7	35.3	10.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	948	127.1	8.6	13.0	9.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	110.8	6.6	17.9	8.2	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	129.4	8.4	9.6	10.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	134.9	9.2	17.8	11.7	0.8

2019 Quality Control Data Summaries of Statistical Analyses

METHIONINE (Met $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	640	216.4	18.4	31.5	13.5	0.8
Derivatized - MS/MS PE NeoGram Kit	60	227.0	18.6	27.2	17.9	0.9
Non-derivatized - MS/MS non-kit	330	209.8	17.4	36.8	10.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	173.6	20.9	59.2	10.3	0.7
Non-derivatized - MS/MS PE NeoBase Kit	947	209.9	13.9	22.0	9.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	184.6	9.4	31.6	8.2	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	210.7	10.8	12.2	10.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	223.4	16.8	32.9	11.7	0.8

2019 Quality Control Data Summaries of Statistical Analyses

ORNITHINE (Orn $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	536	109.3	12.3	48.7	106.8	0.5
Non-derivatized - MS/MS non-kit	160	122.2	17.6	29.5	116.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	159.8	14.1	58.8	153.8	0.6
Non-derivatized - MS/MS PE NeoBase Kit	710	143.2	10.4	19.5	138.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	155.5	15.8	30.0	152.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	104.5	12.1	33.7	102.5	0.5

Lot B1815 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	147.1	16.8	66.8	106.8	0.5
Non-derivatized - MS/MS non-kit	160	165.3	19.7	38.7	116.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	149	209.6	20.4	75.7	153.8	0.6
Non-derivatized - MS/MS PE NeoBase Kit	710	190.8	14.0	27.8	138.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	207.2	17.9	44.8	152.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	144.1	19.8	37.5	102.5	0.5

Lot C1815 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	202.3	21.5	90.7	106.8	0.5
Non-derivatized - MS/MS non-kit	160	232.6	27.0	52.1	116.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	276.9	24.2	102.0	153.8	0.6
Non-derivatized - MS/MS PE NeoBase Kit	710	263.5	19.0	36.4	138.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	287.1	35.7	59.6	152.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	197.1	17.5	53.9	102.5	0.5

Lot D1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	244.0	27.6	109.6	106.8	0.5
Non-derivatized - MS/MS non-kit	160	291.1	33.3	75.8	116.7	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	348.3	41.2	133.2	153.8	0.6
Non-derivatized - MS/MS PE NeoBase Kit	710	321.5	22.9	45.6	138.6	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	341.8	35.0	68.1	152.1	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	240.1	20.4	54.7	102.5	0.5

2019 Quality Control Data Summaries of Statistical Analyses

PHENYLALANINE (Phe $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	130	38.5	10.7	14.7	36.4	0.8
Derivatized - MS/MS non-kit	666	33.9	3.0	5.9	34.1	0.9
Labsystems Diagnostics	128	36.8	6.3	17.3	36.0	1.1
Interscientific Enzyme	30	48.4	4.8	15.0	41.0	0.7
Derivatized - MS/MS PE NeoGram Kit	59	36.6	3.1	3.8	36.3	1.0
Non-derivatized - MS/MS non-kit	340	34.0	2.9	4.5	33.6	0.9
Fluorometric Manual	100	60.4	11.3	19.0	63.6	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	160	35.8	4.9	7.5	36.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	947	33.3	2.4	3.8	31.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	35.4	1.8	3.8	36.8	0.9
PerkinElmer GSP Neonatal	86	33.1	5.7	11.1	27.1	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	34.3	1.7	3.8	36.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	33.2	2.4	5.5	31.3	0.9

Lot B1815 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	130	158.0	16.4	22.2	36.4	0.8
Derivatized - MS/MS non-kit	666	163.1	13.2	26.4	34.1	0.9
Labsystems Diagnostics	130	197.7	15.1	24.6	36.0	1.1
Interscientific Enzyme	30	145.3	9.7	25.4	41.0	0.7
Derivatized - MS/MS PE NeoGram Kit	60	179.7	11.7	17.3	36.3	1.0
Non-derivatized - MS/MS non-kit	340	167.8	12.6	21.1	33.6	0.9
Fluorometric Manual	100	231.9	28.0	43.1	63.6	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	160	165.1	13.9	27.0	36.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	950	165.4	10.6	17.4	31.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	169.7	8.8	14.9	36.8	0.9
PerkinElmer GSP Neonatal	90	179.0	14.2	20.0	27.1	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	174.7	7.0	23.4	36.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	159.2	9.8	15.3	31.3	0.9

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PHENYLALANINE (Phe $\mu\text{mol/L}$ blood) (cont.)

Lot C1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	130	287.7	31.4	46.4	36.4	0.8
Derivatized - MS/MS non-kit	664	293.0	21.7	47.4	34.1	0.9
Labsystems Diagnostics	130	362.2	22.8	51.0	36.0	1.1
Interscientific Enzyme	30	238.0	13.6	45.4	41.0	0.7
Derivatized - MS/MS PE NeoGram Kit	60	332.4	26.6	43.5	36.3	1.0
Non-derivatized - MS/MS non-kit	340	304.6	21.3	38.4	33.6	0.9
Fluorometric Manual	100	397.9	32.3	63.3	63.6	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	159	287.8	19.4	42.4	36.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	948	301.9	20.0	31.5	31.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	305.2	17.1	26.6	36.8	0.9
PerkinElmer GSP Neonatal	90	329.8	20.0	36.4	27.1	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	309.9	16.5	35.1	36.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	287.3	17.0	29.5	31.3	0.9

Lot D1815 – Enriched 450 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit	130	412.6	40.0	70.1	36.4	0.8
Derivatized - MS/MS non-kit	670	420.6	30.9	68.6	34.1	0.9
Labsystems Diagnostics	130	525.5	36.7	78.5	36.0	1.1
Interscientific Enzyme	30	374.0	17.7	48.9	41.0	0.7
Derivatized - MS/MS PE NeoGram Kit	60	472.1	38.8	61.4	36.3	1.0
Non-derivatized - MS/MS non-kit	340	438.8	31.6	63.5	33.6	0.9
Fluorometric Manual	100	556.1	48.7	90.3	63.6	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	160	419.4	41.0	75.1	36.0	0.9
Non-derivatized - MS/MS PE NeoBase Kit	949	439.9	28.7	47.3	31.7	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	432.1	22.4	46.7	36.8	0.9
PerkinElmer GSP Neonatal	80	503.1	30.1	66.6	27.1	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	442.8	19.4	52.0	36.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	421.6	23.6	43.9	31.3	0.9

2019 Quality Control Data Summaries of Statistical Analyses

SUCCINYLACETONE (SUAC $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	230	0.8	0.2	0.5	1.1	0.5
Non-derivatized - MS/MS non-kit	119	1.0	0.3	1.4	1.2	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	127	0.3	0.1	0.2	0.6	0.3
Non-derivatized - MS/MS PE NeoBase Kit	586	0.5	0.1	0.3	0.5	0.2

Lot B1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	237	2.3	0.3	1.4	1.1	0.5
Non-derivatized - MS/MS non-kit	119	2.4	0.4	1.9	1.2	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	130	1.5	0.2	0.5	0.6	0.3
Non-derivatized - MS/MS PE NeoBase Kit	590	1.0	0.2	0.4	0.5	0.2

Lot C1815 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	235	6.2	0.7	3.9	1.1	0.5
Non-derivatized - MS/MS non-kit	119	6.2	0.9	4.7	1.2	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	129	4.2	0.6	1.1	0.6	0.3
Non-derivatized - MS/MS PE NeoBase Kit	590	2.6	0.3	0.8	0.5	0.2

Lot D1815 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	235	10.0	1.2	7.4	1.1	0.5
Non-derivatized - MS/MS non-kit	119	10.8	1.3	8.3	1.2	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	130	7.2	1.0	1.7	0.6	0.3
Non-derivatized - MS/MS PE NeoBase Kit	590	4.4	0.5	1.4	0.5	0.2

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TYROSINE (Tyr $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	639	31.3	3.2	5.9	31.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	33.5	5.0	5.6	26.8	0.9
Non-derivatized - MS/MS non-kit	310	35.5	4.2	10.6	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	160	35.9	4.9	5.7	32.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	962	34.4	3.1	4.5	30.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	33.9	2.3	4.0	32.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	30.4	2.2	2.8	31.9	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	29.3	1.8	3.5	24.8	0.8

Lot B1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	650	273.5	23.8	49.9	31.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	287.3	20.2	24.8	26.8	0.9
Non-derivatized - MS/MS non-kit	308	289.3	25.0	59.3	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	160	302.1	26.1	39.9	32.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	963	300.3	21.9	37.8	30.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	293.3	17.5	24.4	32.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	277.7	13.2	25.2	31.9	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	271.9	17.2	26.8	24.8	0.8

Lot C1815 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	656	516.3	41.9	99.5	31.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	554.5	44.5	64.6	26.8	0.9
Non-derivatized - MS/MS non-kit	310	547.4	48.9	120.5	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	160	563.8	49.2	75.6	32.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	965	576.1	39.9	70.4	30.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	555.4	32.7	53.7	32.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	522.0	26.9	36.1	31.9	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	516.6	30.2	55.7	24.8	0.8

2019 Quality Control Data Summaries of Statistical Analyses

TYROSINE (Tyr $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 900 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	656	756.0	60.9	150.2	31.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	834.9	74.3	103.0	26.8	0.9
Non-derivatized - MS/MS non-kit	308	802.1	66.9	174.0	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	160	848.1	82.0	122.3	32.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	968	858.8	61.8	109.6	30.0	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	819.5	40.7	67.9	32.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	763.4	29.4	54.0	31.9	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	780.6	55.4	69.8	24.8	0.8

2019 Quality Control Data Summaries of Statistical Analyses

VALINE (Val $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	618	80.8	10.8	20.0	85.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	78.1	7.4	8.9	82.5	0.8
Non-derivatized - MS/MS non-kit	243	67.5	5.3	20.6	68.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	79.9	11.9	25.8	85.4	0.7
Non-derivatized - MS/MS PE NeoBase Kit	945	79.9	6.4	10.4	82.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	69.7	4.9	18.5	74.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	80.0	5.1	10.1	86.7	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	60.1	4.8	14.4	59.4	0.7

Lot B1815 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	618	160.1	19.1	33.2	85.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	160.6	11.6	19.3	82.5	0.8
Non-derivatized - MS/MS non-kit	241	143.2	12.0	65.0	68.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	161.5	20.3	45.0	85.4	0.7
Non-derivatized - MS/MS PE NeoBase Kit	946	170.0	13.5	21.8	82.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	147.5	9.9	35.5	74.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	178.3	9.1	16.8	86.7	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	127.0	11.6	28.9	59.4	0.7

Lot C1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	627	310.0	32.5	56.8	85.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	321.3	28.9	52.7	82.5	0.8
Non-derivatized - MS/MS non-kit	244	298.3	23.8	98.0	68.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	158	319.4	44.0	88.4	85.4	0.7
Non-derivatized - MS/MS PE NeoBase Kit	949	351.6	27.5	44.1	82.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	299.7	22.7	54.6	74.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	358.5	22.4	27.9	86.7	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	268.1	28.5	66.2	59.4	0.7

2019 Quality Control Data Summaries of Statistical Analyses

VALINE (Val $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 500 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	625	442.0	38.4	76.7	85.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	461.2	39.6	86.9	82.5	0.8
Non-derivatized - MS/MS non-kit	248	441.4	28.9	127.5	68.8	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	156	451.0	53.6	113.1	85.4	0.7
Non-derivatized - MS/MS PE NeoBase Kit	937	517.6	41.8	67.0	82.3	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	426.5	31.1	63.5	74.7	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	518.6	28.7	32.3	86.7	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	404.6	42.5	85.6	59.4	0.7

2019 Quality Control Data Summaries of Statistical Analyses

TOTAL GALACTOSE (TGal mg/dL blood)

Lot A1705 – Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Siemens Healthcare Diagnostics	40	6.0	0.3	0.4	2.4	0.8
Colorimetric	40	7.3	1.3	2.0	0.5	1.3
PerkinElmer Neonatal Kit	349	5.2	0.6	0.9	1.1	0.9
Bio-Rad Quantase	120	6.7	1.0	1.6	-0.1	1.4
Interscientific Enzyme	40	4.7	0.6	0.7	2.2	0.6
Astoria-Pacific 50 Hour Reagent Kit	40	6.2	0.4	0.8	1.7	0.9
TecnoSuma UMTEST	30	6.3	1.3	1.3	-0.1	1.3
Fluorometric Manual	160	7.5	0.6	8.0	2.4	0.8
PerkinElmer GSP Neonatal	240	6.3	0.6	1.0	1.4	1.0
Zentech	50	6.4	0.7	1.3	2.9	0.9

Lot B1705 – Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Siemens Healthcare Diagnostics	40	11.1	0.7	0.8	2.4	0.8
Colorimetric	40	13.4	1.7	3.9	0.5	1.3
PerkinElmer Neonatal Kit	350	9.8	0.9	1.3	1.1	0.9
Bio-Rad Quantase	119	13.8	1.9	2.3	-0.1	1.4
Interscientific Enzyme	40	8.0	0.7	0.8	2.2	0.6
Astoria-Pacific 50 Hour Reagent Kit	40	10.6	0.7	1.2	1.7	0.9
TecnoSuma UMTEST	30	13.2	2.1	2.5	-0.1	1.3
Fluorometric Manual	160	9.7	1.0	1.4	2.4	0.8
PerkinElmer GSP Neonatal	240	11.4	0.9	1.3	1.4	1.0
Zentech	50	12.4	1.1	1.7	2.9	0.9

Lot C1705 – Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Siemens Healthcare Diagnostics	40	26.9	1.9	5.3	2.4	0.8
Colorimetric	40	40.2	4.0	14.9	0.5	1.3
PerkinElmer Neonatal Kit	349	26.5	2.6	3.5	1.1	0.9
Bio-Rad Quantase	120	41.2	5.0	9.2	-0.1	1.4
Interscientific Enzyme	40	18.5	1.7	2.1	2.2	0.6
Astoria-Pacific 50 Hour Reagent Kit	40	28.4	4.2	4.8	1.7	0.9
TecnoSuma UMTEST	30	39.4	6.0	7.3	-0.1	1.3
Fluorometric Manual	160	27.7	2.3	5.4	2.4	0.8
PerkinElmer GSP Neonatal	240	31.3	3.8	4.8	1.4	1.0
Zentech	50	28.4	2.0	3.0	2.9	0.9

2019 Quality Control Data Summaries of Statistical Analyses

FREE CARNITINE (C0 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	668	17.50	1.62	3.31	17.38	1.4
Derivatized - MS/MS PE NeoGram Kit	60	18.99	1.21	3.66	18.46	1.9
Non-derivatized - MS/MS non-kit	268	15.88	1.46	3.33	15.73	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	169	15.70	1.85	4.28	15.36	1.3
Non-derivatized - MS/MS PE NeoBase Kit	948	15.11	1.07	1.90	14.91	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	14.05	0.85	2.20	14.07	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	16.61	1.09	1.58	16.83	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	17.08	1.84	3.23	16.62	1.5

Lot B1815 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	662	31.87	2.64	7.17	17.38	1.4
Derivatized - MS/MS PE NeoGram Kit	60	36.53	2.35	8.04	18.46	1.9
Non-derivatized - MS/MS non-kit	268	27.51	3.43	6.51	15.73	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	170	27.96	3.75	7.62	15.36	1.3
Non-derivatized - MS/MS PE NeoBase Kit	949	25.89	1.89	3.18	14.91	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	23.96	1.33	3.78	14.07	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	29.56	1.83	3.82	16.83	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	31.29	3.48	5.72	16.62	1.5

Lot C1815 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	670	45.54	4.10	10.43	17.38	1.4
Derivatized - MS/MS PE NeoGram Kit	60	54.63	2.76	12.17	18.46	1.9
Non-derivatized - MS/MS non-kit	268	39.01	4.01	8.38	15.73	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	170	39.57	4.23	10.14	15.36	1.3
Non-derivatized - MS/MS PE NeoBase Kit	949	36.46	2.65	4.40	14.91	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	34.26	2.82	5.52	14.07	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	40.66	2.10	4.33	16.83	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	44.92	4.56	7.92	16.62	1.5

2019 Quality Control Data Summaries of Statistical Analyses

FREE CARNITINE (C0 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	669	60.86	5.61	14.27	17.38	1.4
Derivatized - MS/MS PE NeoGram Kit	60	74.53	4.75	16.68	18.46	1.9
Non-derivatized - MS/MS non-kit	268	51.45	4.78	11.14	15.73	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	170	53.86	6.74	15.07	15.36	1.3
Non-derivatized - MS/MS PE NeoBase Kit	948	48.32	3.38	5.83	14.91	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	43.89	2.64	7.16	14.07	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	53.44	2.19	5.67	16.83	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	61.71	5.59	7.89	16.62	1.0

2019 Quality Control Data Summaries of Statistical Analyses

ACETYLCARNITINE (C2 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	634	12.42	1.33	3.70	12.40	1.0
Derivatized - MS/MS PE NeoGram Kit	60	12.19	0.85	1.68	12.18	0.7
Non-derivatized - MS/MS non-kit	256	9.46	0.97	2.31	8.87	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	169	9.95	1.25	2.40	9.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	921	8.36	0.60	1.20	8.32	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	8.29	0.47	1.23	8.33	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	9.29	0.45	0.73	9.49	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	9.69	0.85	2.26	9.46	0.9

Lot B1815 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	634	22.45	2.18	5.38	12.40	1.0
Derivatized - MS/MS PE NeoGram Kit	60	18.66	1.44	2.59	12.18	0.7
Non-derivatized - MS/MS non-kit	256	20.48	2.43	5.40	8.87	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	170	18.94	1.87	3.11	9.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	921	17.88	1.22	2.81	8.32	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	17.40	0.94	2.60	8.33	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	20.30	0.90	2.28	9.49	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	18.24	1.34	2.65	9.46	0.9

Lot C1815 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	634	31.96	2.93	7.01	12.40	1.0
Derivatized - MS/MS PE NeoGram Kit	60	25.42	1.45	2.91	12.18	0.7
Non-derivatized - MS/MS non-kit	256	30.83	3.49	7.50	8.87	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	170	27.64	2.19	4.07	9.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	923	27.18	1.82	3.87	8.32	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	26.94	1.62	4.78	8.33	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	30.31	1.37	2.36	9.49	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	26.61	1.83	4.04	9.46	0.9

2019 Quality Control Data Summaries of Statistical Analyses

ACETYLCARNITINE (C2 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	633	42.37	4.11	9.87	12.40	1.0
Derivatized - MS/MS PE NeoGram Kit	60	31.80	2.71	3.90	12.18	0.7
Non-derivatized - MS/MS non-kit	259	45.10	4.64	14.82	8.87	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	168	37.08	3.64	6.14	9.89	0.9
Non-derivatized - MS/MS PE NeoBase Kit	916	37.01	2.34	5.61	8.32	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	35.65	1.97	5.82	8.33	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	40.82	1.57	3.60	9.49	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	36.39	2.77	5.91	9.46	0.9

2019 Quality Control Data Summaries of Statistical Analyses

PROPIONYLCARNITINE (C3 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	646	1.18	0.18	0.33	1.16	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.86	0.09	0.09	0.80	0.8
Non-derivatized - MS/MS non-kit	270	1.09	0.11	0.22	1.03	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.98	0.14	0.26	0.86	0.9
Non-derivatized - MS/MS PE NeoBase Kit	948	0.98	0.08	0.15	0.92	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.93	0.07	0.15	0.95	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.00	0.06	0.07	1.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.93	0.09	0.17	0.81	0.9

Lot B1815 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	658	5.06	0.59	1.15	1.16	1.0
Derivatized - MS/MS PE NeoGram Kit	60	3.79	0.29	0.50	0.80	0.8
Non-derivatized - MS/MS non-kit	270	4.93	0.47	0.97	1.03	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	4.20	0.43	0.86	0.86	0.9
Non-derivatized - MS/MS PE NeoBase Kit	949	4.41	0.32	0.69	0.92	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	4.17	0.24	0.63	0.95	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.68	0.25	0.43	1.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	4.28	0.35	0.78	0.81	0.9

Lot C1815 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	659	8.93	0.89	2.09	1.16	1.0
Derivatized - MS/MS PE NeoGram Kit	60	6.82	0.47	0.84	0.80	0.8
Non-derivatized - MS/MS non-kit	270	8.76	0.78	1.86	1.03	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	7.45	0.60	1.73	0.86	0.9
Non-derivatized - MS/MS PE NeoBase Kit	947	7.79	0.49	1.12	0.92	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	7.47	0.50	1.18	0.95	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	8.17	0.39	0.47	1.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	7.69	0.65	1.50	0.81	0.9

2019 Quality Control Data Summaries of Statistical Analyses

PROPIONYLCARNITINE (C3 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	659	12.95	1.38	2.95	1.16	1.0
Derivatized - MS/MS PE NeoGram Kit	60	10.01	0.69	1.43	0.80	0.8
Non-derivatized - MS/MS non-kit	269	12.89	1.15	2.73	1.03	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	11.22	1.15	2.43	0.86	0.9
Non-derivatized - MS/MS PE NeoBase Kit	942	11.52	0.78	1.68	0.92	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	10.61	0.64	1.53	0.95	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	11.93	0.54	0.78	1.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	11.60	1.23	1.77	0.81	0.9

2019 Quality Control Data Summaries of Statistical Analyses

MALONYLCARNITINE (C3DC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	584	0.10	0.03	0.05	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.17	0.03	0.03	0.03	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.12	0.03	0.05	0.03	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	49	0.05	0.01	0.02	-0.01	0.5

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	596	0.35	0.06	0.16	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.68	0.06	0.10	0.03	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	150	0.44	0.08	0.18	0.03	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.22	0.03	0.06	-0.01	0.5

Lot C1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	596	0.99	0.16	0.41	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	60	1.96	0.19	0.30	0.03	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	150	1.24	0.16	0.47	0.03	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.65	0.08	0.23	-0.01	0.5

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	595	1.96	0.28	0.78	0.03	0.6
Derivatized - MS/MS PE NeoGram Kit	60	3.98	0.35	0.60	0.03	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	150	2.49	0.33	0.98	0.03	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.40	0.22	0.60	-0.01	0.5

2019 Quality Control Data Summaries of Statistical Analyses

MALONYLCARNITINE + HYDROXYBUTYRYLCARNITINE (C3DC+C4OH $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	160	0.18	0.05	0.13	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	791	0.13	0.02	0.04	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.23	0.13	0.28	0.10	0.6

Lot B1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	160	0.57	0.11	0.42	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	795	0.42	0.04	0.09	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.68	0.08	0.81	0.10	0.6

Lot C1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	160	1.13	0.16	0.83	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	798	0.86	0.07	0.2	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	1.40	0.15	1.69	0.10	0.6

Lot D1815 – Enriched 5.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	160	2.64	0.4	1.97	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	796	1.96	0.16	0.45	0.05	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	3.17	0.3	3.67	0.10	0.6

2019 Quality Control Data Summaries of Statistical Analyses

BUTYRYLCARNITINE (C4 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	643	0.13	0.04	0.07	0.11	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.12	0.04	0.05	0.07	0.7
Non-derivatized - MS/MS non-kit	246	0.11	0.03	0.05	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	156	0.10	0.05	0.06	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	936	0.10	0.02	0.03	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.08	0.01	0.02	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.09	0.01	0.02	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.09	0.02	0.03	0.05	0.8

Lot B1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	649	0.95	0.13	0.22	0.11	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.78	0.10	0.11	0.07	0.7
Non-derivatized - MS/MS non-kit	248	0.92	0.12	0.22	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.77	0.11	0.14	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	938	0.84	0.06	0.11	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.77	0.04	0.09	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.93	0.06	0.16	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.85	0.10	0.16	0.05	0.8

Lot C1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	650	2.57	0.30	0.50	0.11	0.8
Derivatized - MS/MS PE NeoGram Kit	60	2.15	0.31	0.34	0.07	0.7
Non-derivatized - MS/MS non-kit	245	2.52	0.33	0.59	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	169	2.15	0.26	0.40	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	940	2.37	0.16	0.28	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.18	0.15	0.27	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.63	0.16	0.42	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	2.38	0.24	0.42	0.05	0.8

2019 Quality Control Data Summaries of Statistical Analyses

BUTYRYLCARNITINE (C4 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	645	4.31	0.47	0.77	0.11	0.8
Derivatized - MS/MS PE NeoGram Kit	60	3.74	0.39	0.55	0.07	0.7
Non-derivatized - MS/MS non-kit	250	4.33	0.39	0.89	0.08	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	168	3.66	0.32	0.65	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	938	4.06	0.28	0.48	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	3.65	0.23	0.41	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.46	0.21	0.66	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	4.17	0.44	0.79	0.05	0.8

2019 Quality Control Data Summaries of Statistical Analyses

HYDROXYBUTYRYLCARNITINE (C4OH $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	565	0.16	0.04	0.06	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.14	0.02	0.02	0.07	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	120	0.14	0.03	0.04	0.07	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.11	0.02	0.03	0.04	0.6

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	569	0.45	0.08	0.15	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.42	0.05	0.07	0.07	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	120	0.39	0.06	0.09	0.07	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.34	0.05	0.09	0.04	0.6

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	566	0.82	0.11	0.27	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.79	0.10	0.17	0.07	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	120	0.72	0.09	0.17	0.07	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.62	0.09	0.14	0.04	0.6

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	568	1.89	0.24	0.62	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	1.86	0.19	0.33	0.07	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	120	1.69	0.19	0.42	0.07	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.53	0.19	0.40	0.04	0.6

2019 Quality Control Data Summaries of Statistical Analyses

ISOVALERYLCARNITINE (C5 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	644	0.19	0.04	0.06	0.09	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.15	0.03	0.03	0.05	0.8
Non-derivatized - MS/MS non-kit	293	0.16	0.02	0.07	0.06	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	157	0.18	0.03	0.06	0.07	1.0
Non-derivatized - MS/MS PE NeoBase Kit	957	0.15	0.02	0.02	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	0.16	0.02	0.04	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.16	0.01	0.02	0.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	49	0.15	0.03	0.04	0.03	1.0

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	655	0.56	0.08	0.14	0.09	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.47	0.07	0.07	0.05	0.8
Non-derivatized - MS/MS non-kit	298	0.58	0.07	0.11	0.06	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.55	0.08	0.09	0.07	1.0
Non-derivatized - MS/MS PE NeoBase Kit	949	0.50	0.04	0.06	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.53	0.04	0.10	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.54	0.03	0.06	0.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.52	0.07	0.11	0.03	1.0

Lot C1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	656	1.50	0.18	0.34	0.09	1.0
Derivatized - MS/MS PE NeoGram Kit	60	1.27	0.13	0.19	0.05	0.8
Non-derivatized - MS/MS non-kit	298	1.56	0.16	0.26	0.06	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.45	0.16	0.22	0.07	1.0
Non-derivatized - MS/MS PE NeoBase Kit	959	1.39	0.10	0.16	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	1.44	0.11	0.22	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.47	0.09	0.13	0.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.45	0.13	0.22	0.03	1.0

2019 Quality Control Data Summaries of Statistical Analyses

ISOVALERYLCARNITINE (C5 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	655	2.93	0.30	0.65	0.09	1.0
Derivatized - MS/MS PE NeoGram Kit	60	2.59	0.27	0.39	0.05	0.8
Non-derivatized - MS/MS non-kit	298	3.11	0.31	0.48	0.06	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	2.93	0.28	0.45	0.07	1.0
Non-derivatized - MS/MS PE NeoBase Kit	959	2.81	0.19	0.34	0.04	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	2.85	0.16	0.45	0.06	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.94	0.13	0.27	0.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	2.98	0.26	0.32	0.03	1.0

2019 Quality Control Data Summaries of Statistical Analyses

TIGLYLCARNITINE (C5:1 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	557	0.12	0.03	0.05	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.09	0.02	0.03	0.03	0.6
Non-derivatized - MS/MS non-kit	200	0.20	0.11	0.27	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	158	0.12	0.04	0.06	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	765	0.08	0.01	0.02	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.08	0.01	0.07	-0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.09	0.01	0.02	0.02	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	0.10	0.02	0.04	0.00	0.7

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	558	0.45	0.07	0.14	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.32	0.04	0.07	0.03	0.6
Non-derivatized - MS/MS non-kit	198	0.68	0.07	0.85	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	160	0.44	0.07	0.13	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	769	0.33	0.03	0.06	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.36	0.03	0.22	-0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.38	0.02	0.06	0.02	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	0.37	0.06	0.09	0.00	0.7

Lot C1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	558	1.25	0.18	0.36	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.95	0.13	0.23	0.03	0.6
Non-derivatized - MS/MS non-kit	197	1.95	0.18	2.51	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	159	1.22	0.14	0.38	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	770	0.98	0.09	0.16	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.99	0.10	0.36	-0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.08	0.09	0.14	0.02	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	1.07	0.12	0.20	0.00	0.7

2019 Quality Control Data Summaries of Statistical Analyses

TIGLYLCARNITINE (C5:1 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	546	2.48	0.28	0.70	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	1.86	0.18	0.42	0.03	0.6
Non-derivatized - MS/MS non-kit	197	3.80	0.47	4.92	0.07	1.3
Derivatized - MS/MS Chromsystems MassChrom Kit	160	2.48	0.28	0.64	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	770	1.97	0.17	0.32	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	2.13	0.17	0.91	-0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	2.18	0.11	0.25	0.02	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	2.24	0.25	0.31	0.00	0.7

2019 Quality Control Data Summaries of Statistical Analyses

GLUTARYLCARNITINE (C5DC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	658	0.10	0.03	0.05	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	59	0.14	0.02	0.04	0.01	1.1
Non-derivatized - MS/MS non-kit	256	0.15	0.03	0.06	0.04	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.17	0.05	0.07	0.04	1.3
Non-derivatized - MS/MS PE NeoBase Kit	836	0.15	0.02	0.04	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.19	0.03	0.06	0.03	1.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.14	0.01	0.02	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.17	0.02	0.08	0.04	1.4

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	668	0.39	0.08	0.17	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	59	0.57	0.06	0.10	0.01	1.1
Non-derivatized - MS/MS non-kit	260	0.58	0.08	0.16	0.04	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	166	0.71	0.12	0.20	0.04	1.3
Non-derivatized - MS/MS PE NeoBase Kit	839	0.56	0.05	0.08	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.72	0.08	0.16	0.03	1.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.51	0.03	0.07	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.75	0.09	0.41	0.04	1.4

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	668	0.73	0.12	0.33	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.11	0.09	0.18	0.01	1.1
Non-derivatized - MS/MS non-kit	260	1.11	0.13	0.31	0.04	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.32	0.20	0.37	0.04	1.3
Non-derivatized - MS/MS PE NeoBase Kit	839	1.08	0.08	0.15	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	1.43	0.13	0.35	0.03	1.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.94	0.06	0.14	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.46	0.22	0.77	0.04	1.4

2019 Quality Control Data Summaries of Statistical Analyses

GLUTARYLCARNITINE (C5DC $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	668	1.83	0.27	0.84	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	60	2.82	0.25	0.51	0.01	1.1
Non-derivatized - MS/MS non-kit	260	2.73	0.35	0.75	0.04	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	170	3.32	0.42	0.95	0.04	1.3
Non-derivatized - MS/MS PE NeoBase Kit	839	2.70	0.20	0.39	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	3.53	0.39	0.72	0.03	1.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.27	0.12	0.35	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	3.56	0.59	1.92	0.04	1.4

2019 Quality Control Data Summaries of Statistical Analyses

HYDROXYISOVALERYLCARNITINE (C5OH $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	663	0.40	0.07	0.11	0.49	0.7
Derivatized - MS/MS PE NeoGram Kit	59	0.33	0.04	0.05	0.40	0.6
Non-derivatized - MS/MS non-kit	216	0.61	0.06	0.25	0.70	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	160	0.38	0.05	0.09	0.46	0.6
Non-derivatized - MS/MS PE NeoBase Kit	756	0.45	0.04	0.09	0.51	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.36	0.03	0.14	0.43	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.61	0.04	0.04	0.74	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.28	0.03	0.07	0.34	0.5

Lot B1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	670	1.31	0.19	0.33	0.49	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.10	0.13	0.20	0.40	0.6
Non-derivatized - MS/MS non-kit	219	1.61	0.23	0.44	0.70	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	160	1.22	0.18	0.32	0.46	0.6
Non-derivatized - MS/MS PE NeoBase Kit	760	1.12	0.09	0.21	0.51	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.97	0.06	0.38	0.43	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.72	0.09	0.18	0.74	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.98	0.11	0.23	0.34	0.5

Lot C1815 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	669	1.71	0.20	0.42	0.49	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.47	0.23	0.31	0.40	0.6
Non-derivatized - MS/MS non-kit	218	2.05	0.28	0.58	0.70	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	160	1.59	0.17	0.37	0.46	0.6
Non-derivatized - MS/MS PE NeoBase Kit	758	1.42	0.10	0.26	0.51	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.23	0.07	0.48	0.43	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.15	0.12	0.15	0.74	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.26	0.13	0.30	0.34	0.5

2019 Quality Control Data Summaries of Statistical Analyses
HYDROXYISOVALERYLCARNITINE (C5OH $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	669	2.43	0.26	0.56	0.49	0.7
Derivatized - MS/MS PE NeoGram Kit	60	2.09	0.27	0.42	0.40	0.6
Non-derivatized - MS/MS non-kit	220	2.85	0.34	0.77	0.70	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	160	2.24	0.22	0.51	0.46	0.6
Non-derivatized - MS/MS PE NeoBase Kit	759	1.95	0.14	0.33	0.51	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.67	0.12	0.60	0.43	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.95	0.13	0.23	0.74	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.83	0.23	0.49	0.34	0.5

2019 Quality Control Data Summaries of Statistical Analyses

HEXANOYL CARNITINE (C6 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	643	0.12	0.03	0.05	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.12	0.03	0.03	0.05	0.6
Non-derivatized - MS/MS non-kit	259	0.11	0.02	0.04	0.02	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	159	0.11	0.03	0.03	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	944	0.10	0.01	0.02	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	0.10	0.01	0.02	0.03	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.11	0.01	0.01	0.02	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.10	0.02	0.03	0.04	0.6

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	656	0.41	0.06	0.11	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.37	0.05	0.05	0.05	0.6
Non-derivatized - MS/MS non-kit	260	0.43	0.05	0.09	0.02	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.36	0.04	0.06	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	948	0.40	0.03	0.05	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.39	0.02	0.04	0.03	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.43	0.02	0.04	0.02	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.36	0.07	0.08	0.04	0.6

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	660	0.80	0.09	0.20	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.68	0.08	0.09	0.05	0.6
Non-derivatized - MS/MS non-kit	260	0.85	0.08	0.16	0.02	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.67	0.08	0.13	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	947	0.79	0.05	0.08	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.79	0.05	0.10	0.03	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	0.85	0.05	0.05	0.02	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.67	0.11	0.12	0.04	0.6

2019 Quality Control Data Summaries of Statistical Analyses

HEXANOYLCARNITINE (C6 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	657	1.94	0.22	0.45	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	60	1.63	0.18	0.21	0.05	0.6
Non-derivatized - MS/MS non-kit	259	2.11	0.20	0.39	0.02	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.55	0.12	0.29	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	950	1.97	0.13	0.21	0.02	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.88	0.10	0.20	0.03	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	40	2.09	0.09	0.13	0.02	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.62	0.14	0.19	0.04	0.6

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OCTANOYLCARNITINE (C8 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	643	0.14	0.04	0.06	0.05	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.12	0.03	0.03	0.03	0.9
Non-derivatized - MS/MS non-kit	300	0.16	0.02	0.05	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	158	0.12	0.05	0.08	0.03	0.8
Non-derivatized - MS/MS PE NeoBase Kit	956	0.14	0.01	0.02	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.12	0.01	0.03	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.13	0.01	0.01	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.10	0.02	0.02	0.00	0.8

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	659	0.53	0.08	0.13	0.05	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.46	0.07	0.07	0.03	0.9
Non-derivatized - MS/MS non-kit	300	0.56	0.06	0.15	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.40	0.05	0.07	0.03	0.8
Non-derivatized - MS/MS PE NeoBase Kit	959	0.48	0.04	0.06	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.44	0.03	0.09	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.50	0.03	0.05	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.40	0.07	0.08	0.00	0.8

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	652	1.00	0.11	0.21	0.05	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.88	0.10	0.13	0.03	0.9
Non-derivatized - MS/MS non-kit	300	1.05	0.10	0.30	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.80	0.10	0.15	0.03	0.8
Non-derivatized - MS/MS PE NeoBase Kit	960	0.94	0.07	0.10	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.83	0.06	0.16	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.95	0.05	0.08	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.78	0.09	0.14	0.00	0.8

2019 Quality Control Data Summaries of Statistical Analyses

OCTANOYLCARNITINE (C8 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	658	2.44	0.30	0.53	0.05	1.0
Derivatized - MS/MS PE NeoGram Kit	60	2.17	0.19	0.33	0.03	0.9
Non-derivatized - MS/MS non-kit	300	2.60	0.21	0.74	0.04	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.98	0.24	0.38	0.03	0.8
Non-derivatized - MS/MS PE NeoBase Kit	959	2.35	0.16	0.27	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	2.06	0.12	0.42	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.34	0.10	0.21	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	2.02	0.21	0.36	0.00	0.8

2019 Quality Control Data Summaries of Statistical Analyses

DECANOYLCARNITINE (C10 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	641	0.12	0.03	0.05	-0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.10	0.02	0.02	-0.02	0.9
Non-derivatized - MS/MS non-kit	278	0.15	0.02	0.07	0.01	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	160	0.07	0.01	0.03	-0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	937	0.11	0.01	0.02	-0.02	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.12	0.02	0.06	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.11	0.01	0.01	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.08	0.02	0.02	-0.02	0.8

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	657	0.47	0.08	0.13	-0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.36	0.05	0.05	-0.02	0.9
Non-derivatized - MS/MS non-kit	276	0.51	0.06	0.15	0.01	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	161	0.27	0.05	0.13	-0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	950	0.42	0.04	0.06	-0.02	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.40	0.02	0.12	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.44	0.03	0.04	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.34	0.04	0.05	-0.02	0.8

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	654	1.02	0.13	0.24	-0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.81	0.11	0.14	-0.02	0.9
Non-derivatized - MS/MS non-kit	275	1.06	0.10	0.29	0.01	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.55	0.06	0.20	-0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	955	0.92	0.07	0.11	-0.02	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.83	0.06	0.21	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.94	0.06	0.09	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.76	0.09	0.12	-0.02	0.8

2019 Quality Control Data Summaries of Statistical Analyses

DECANOYLCARNITINE (C10 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	657	2.58	0.32	0.56	-0.01	1.0
Derivatized - MS/MS PE NeoGram Kit	60	2.10	0.20	0.34	-0.02	0.9
Non-derivatized - MS/MS non-kit	275	2.69	0.24	0.71	0.01	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.45	0.19	0.55	-0.01	0.6
Non-derivatized - MS/MS PE NeoBase Kit	958	2.36	0.16	0.29	-0.02	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	2.08	0.14	0.52	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.41	0.13	0.20	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.95	0.20	0.30	-0.02	0.8

2019 Quality Control Data Summaries of Statistical Analyses

DODECANOYLCARNITINE (C12 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	610	0.12	0.03	0.05	0.00	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.12	0.03	0.03	-0.01	0.9
Non-derivatized - MS/MS non-kit	239	0.12	0.02	0.05	0.00	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	158	0.12	0.04	0.06	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	909	0.10	0.01	0.02	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.09	0.01	0.02	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.10	0.01	0.01	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.10	0.02	0.03	-0.01	0.8

Lot B1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	628	0.89	0.13	0.21	0.00	0.9
Derivatized - MS/MS PE NeoGram Kit	59	0.88	0.12	0.12	-0.01	0.9
Non-derivatized - MS/MS non-kit	239	1.00	0.11	0.41	0.00	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.78	0.10	0.16	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	904	0.83	0.06	0.09	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.77	0.05	0.13	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.93	0.06	0.10	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.77	0.07	0.10	-0.01	0.8

Lot C1815 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	629	1.86	0.23	0.41	0.00	0.9
Derivatized - MS/MS PE NeoGram Kit	59	1.81	0.22	0.28	-0.01	0.9
Non-derivatized - MS/MS non-kit	237	2.07	0.19	0.84	0.00	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.62	0.20	0.31	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	907	1.77	0.13	0.18	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.66	0.12	0.25	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.93	0.13	0.18	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.60	0.21	0.30	-0.01	0.8

2019 Quality Control Data Summaries of Statistical Analyses

DODECANOYLCARNITINE (C12 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	628	2.79	0.33	0.60	0.00	0.9
Derivatized - MS/MS PE NeoGram Kit	60	2.82	0.26	0.41	-0.01	0.9
Non-derivatized - MS/MS non-kit	235	3.06	0.30	1.19	0.00	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	168	2.45	0.23	0.48	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	910	2.70	0.19	0.27	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.45	0.15	0.33	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.95	0.16	0.29	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	2.46	0.22	0.31	-0.01	0.8

2019 Quality Control Data Summaries of Statistical Analyses

MYRISTOYL CARNITINE (C14 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	625	0.09	0.03	0.04	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.08	0.02	0.02	0.01	0.9
Non-derivatized - MS/MS non-kit	256	0.08	0.01	0.05	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	156	0.08	0.02	0.04	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	927	0.06	0.01	0.01	-0.01	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.05	0.01	0.01	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.06	0.00	0.01	0.00	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.05	0.01	0.01	-0.01	0.7

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	634	0.52	0.07	0.12	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.48	0.06	0.07	0.01	0.9
Non-derivatized - MS/MS non-kit	257	0.52	0.06	0.14	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.42	0.05	0.08	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	936	0.46	0.04	0.05	-0.01	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	0.42	0.03	0.07	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.49	0.03	0.05	0.00	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.35	0.04	0.07	-0.01	0.7

Lot C1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	638	1.53	0.20	0.35	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	60	1.45	0.12	0.21	0.01	0.9
Non-derivatized - MS/MS non-kit	254	1.58	0.19	0.71	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	169	1.19	0.14	0.19	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	938	1.40	0.10	0.14	-0.01	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.26	0.08	0.18	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.40	0.09	0.10	0.00	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.04	0.12	0.22	-0.01	0.7

2019 Quality Control Data Summaries of Statistical Analyses

MYRISTOYL CARNITINE (C14 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	636	2.91	0.30	0.57	0.03	1.0
Derivatized - MS/MS PE NeoGram Kit	60	2.78	0.21	0.37	0.01	0.9
Non-derivatized - MS/MS non-kit	254	3.02	0.33	1.16	0.01	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	170	2.33	0.24	0.35	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	939	2.75	0.20	0.28	-0.01	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.46	0.17	0.37	-0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.74	0.15	0.19	0.00	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	2.10	0.19	0.40	-0.01	0.7

2019 Quality Control Data Summaries of Statistical Analyses

TETRADECENOYLCARNITINE (C14:1 $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	529	0.09	0.02	0.04	-0.01	1.1
Derivatized - MS/MS PE NeoGram Kit	49	0.08	0.03	0.03	-0.06	1.1
Non-derivatized - MS/MS non-kit	220	0.08	0.01	0.03	-0.02	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	159	0.08	0.02	0.04	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	777	0.07	0.01	0.02	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	88	0.06	0.01	0.02	-0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.08	0.01	0.01	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	0.06	0.02	0.04	-0.03	0.8

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	528	0.53	0.08	0.13	-0.01	1.1
Derivatized - MS/MS PE NeoGram Kit	50	0.52	0.07	0.08	-0.06	1.1
Non-derivatized - MS/MS non-kit	220	0.49	0.07	0.14	-0.02	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	160	0.45	0.08	0.12	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	777	0.43	0.03	0.06	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.40	0.04	0.12	-0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.52	0.03	0.05	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	0.37	0.04	0.09	-0.03	0.8

Lot C1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	521	1.55	0.19	0.28	-0.01	1.1
Derivatized - MS/MS PE NeoGram Kit	50	1.58	0.16	0.27	-0.06	1.1
Non-derivatized - MS/MS non-kit	220	1.53	0.18	0.40	-0.02	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	160	1.18	0.14	0.23	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	774	1.30	0.10	0.17	-0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	1.21	0.17	0.42	-0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.43	0.09	0.12	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	1.08	0.13	0.31	-0.03	0.8

2019 Quality Control Data Summaries of Statistical Analyses

TETRADECENOYL CARNITINE (C14:1 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	521	3.15	0.34	0.50	-0.01	1.1
Derivatized - MS/MS PE NeoGram Kit	49	3.37	0.29	0.48	-0.06	1.1
Non-derivatized - MS/MS non-kit	220	3.02	0.36	0.78	-0.02	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	160	2.48	0.32	0.48	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	775	2.71	0.21	0.37	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	2.46	0.28	0.80	-0.02	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	2.61	0.11	0.20	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	2.31	0.25	0.44	-0.03	0.8

2019 Quality Control Data Summaries of Statistical Analyses

PALMITOYL CARNITINE (C16 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	652	0.84	0.14	0.19	0.85	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.76	0.10	0.11	0.72	0.8
Non-derivatized - MS/MS non-kit	260	0.80	0.08	0.13	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.70	0.10	0.20	0.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	919	0.80	0.08	0.11	0.73	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.72	0.06	0.10	0.69	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.76	0.05	0.10	0.75	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.92	0.18	0.29	0.84	0.9

Lot B1815 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	652	3.98	0.43	0.67	0.85	0.8
Derivatized - MS/MS PE NeoGram Kit	60	3.63	0.30	0.32	0.72	0.8
Non-derivatized - MS/MS non-kit	260	4.01	0.36	0.63	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	3.58	0.41	1.03	0.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	927	3.95	0.30	0.50	0.73	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	3.57	0.22	0.46	0.69	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.04	0.23	0.54	0.75	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	4.06	0.36	0.85	0.84	0.9

Lot C1815 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	654	7.24	0.66	1.22	0.85	0.8
Derivatized - MS/MS PE NeoGram Kit	60	6.74	0.51	0.81	0.72	0.8
Non-derivatized - MS/MS non-kit	260	7.42	0.64	1.07	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	6.46	0.62	1.65	0.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	930	7.41	0.51	0.83	0.73	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	6.84	0.48	0.88	0.69	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	7.32	0.46	0.81	0.75	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	7.68	0.76	1.69	0.84	0.9

2019 Quality Control Data Summaries of Statistical Analyses

PALMITOYL CARNITINE (C16 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	649	10.24	0.90	1.67	0.85	0.8
Derivatized - MS/MS PE NeoGram Kit	60	9.66	0.67	1.26	0.72	0.8
Non-derivatized - MS/MS non-kit	260	10.62	0.82	1.49	0.78	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	9.48	0.86	2.24	0.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	927	10.72	0.78	1.31	0.73	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	9.60	0.71	1.16	0.69	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	58	10.66	0.51	1.07	0.75	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	11.00	1.00	2.29	0.84	0.9

2019 Quality Control Data Summaries of Statistical Analyses

HYDROXPALMITOYL CARNITINE (C16OH $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	625	0.09	0.03	0.04	0.01	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.07	0.02	0.02	0.00	0.7
Non-derivatized - MS/MS non-kit	250	0.08	0.01	0.03	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.08	0.02	0.03	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	929	0.07	0.01	0.02	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.06	0.01	0.02	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.07	0.01	0.01	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.06	0.01	0.03	-0.02	0.7

Lot B1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	635	0.21	0.04	0.06	0.01	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.17	0.03	0.04	0.00	0.7
Non-derivatized - MS/MS non-kit	250	0.20	0.03	0.07	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.19	0.04	0.06	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	939	0.16	0.02	0.04	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.15	0.02	0.06	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.18	0.01	0.02	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	48	0.14	0.02	0.07	-0.02	0.7

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	628	0.80	0.11	0.23	0.01	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.67	0.08	0.15	0.00	0.7
Non-derivatized - MS/MS non-kit	250	0.81	0.08	0.26	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	0.72	0.10	0.20	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	931	0.67	0.06	0.14	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.62	0.06	0.20	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.72	0.05	0.10	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.67	0.15	0.31	-0.02	0.7

2019 Quality Control Data Summaries of Statistical Analyses
HYDROXPALMITOYLCARNITINE (C16OH $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	631	1.19	0.17	0.36	0.01	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.99	0.09	0.24	0.00	0.7
Non-derivatized - MS/MS non-kit	250	1.20	0.11	0.36	0.00	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.08	0.13	0.27	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	927	1.00	0.09	0.22	0.00	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.94	0.10	0.33	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.08	0.07	0.15	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.03	0.18	0.44	-0.02	0.7

2019 Quality Control Data Summaries of Statistical Analyses

STEAROYLCARNITINE (C18 $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	603	0.59	0.09	0.15	0.64	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.59	0.07	0.07	0.62	0.8
Non-derivatized - MS/MS non-kit	260	0.57	0.06	0.12	0.60	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	169	0.54	0.08	0.12	0.57	0.7
Non-derivatized - MS/MS PE NeoBase Kit	905	0.56	0.05	0.06	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.51	0.04	0.07	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.54	0.03	0.05	0.60	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.56	0.08	0.14	0.59	0.8

Lot B1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	608	1.42	0.20	0.32	0.64	0.8
Derivatized - MS/MS PE NeoGram Kit	60	1.46	0.15	0.16	0.62	0.8
Non-derivatized - MS/MS non-kit	254	1.48	0.15	0.32	0.60	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	170	1.32	0.15	0.26	0.57	0.7
Non-derivatized - MS/MS PE NeoBase Kit	908	1.44	0.11	0.15	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.34	0.07	0.21	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.43	0.09	0.14	0.60	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.39	0.19	0.36	0.59	0.8

Lot C1815 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	606	3.04	0.31	0.61	0.64	0.8
Derivatized - MS/MS PE NeoGram Kit	60	3.24	0.27	0.35	0.62	0.8
Non-derivatized - MS/MS non-kit	254	3.22	0.31	0.66	0.60	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	170	2.83	0.31	0.57	0.57	0.7
Non-derivatized - MS/MS PE NeoBase Kit	907	3.16	0.22	0.32	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	3.00	0.23	0.43	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	3.06	0.18	0.25	0.60	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	3.12	0.36	0.84	0.59	0.8

2019 Quality Control Data Summaries of Statistical Analyses

STEAROYL Carnitine (C18 $\mu\text{mol/L}$ blood) (cont.)

Lot D1815 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	610	4.42	0.48	0.88	0.64	0.8
Derivatized - MS/MS PE NeoGram Kit	60	4.77	0.39	0.54	0.62	0.8
Non-derivatized - MS/MS non-kit	250	4.86	0.41	0.58	0.60	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	170	4.23	0.61	0.83	0.57	0.7
Non-derivatized - MS/MS PE NeoBase Kit	908	4.71	0.35	0.47	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	4.36	0.30	0.58	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.52	0.24	0.38	0.60	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	4.59	0.50	1.08	0.59	0.8

2019 Quality Control Data Summaries of Statistical Analyses

HYDROXYSTEAROYL CARNITINE (C18OH $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	499	0.08	0.03	0.04	0.02	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.07	0.02	0.02	0.00	0.6
Non-derivatized - MS/MS non-kit	180	0.05	0.02	0.03	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.06	0.02	0.04	0.00	0.6
Non-derivatized - MS/MS PE NeoBase Kit	866	0.06	0.01	0.01	0.00	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.05	0.01	0.01	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.07	0.02	0.03	0.01	0.6

Lot B1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	503	0.18	0.05	0.10	0.02	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.16	0.02	0.03	0.00	0.6
Non-derivatized - MS/MS non-kit	177	0.15	0.05	0.10	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	0.16	0.04	0.08	0.00	0.6
Non-derivatized - MS/MS PE NeoBase Kit	868	0.15	0.02	0.02	0.00	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.14	0.01	0.04	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.15	0.03	0.07	0.01	0.6

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	502	0.64	0.09	0.30	0.02	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.63	0.08	0.15	0.00	0.6
Non-derivatized - MS/MS non-kit	178	0.62	0.08	0.44	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	0.59	0.08	0.25	0.00	0.6
Non-derivatized - MS/MS PE NeoBase Kit	870	0.57	0.05	0.07	0.00	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.53	0.05	0.12	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.55	0.08	0.31	0.01	0.6

2019 Quality Control Data Summaries of Statistical Analyses

HYDROXYSTEAROYL CARNITINE (C18OH $\mu\text{mol/L}$ blood) cont.

Lot D1815 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	501	0.94	0.15	0.48	0.02	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.97	0.10	0.23	0.00	0.6
Non-derivatized - MS/MS non-kit	176	0.85	0.29	0.55	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	0.92	0.15	0.41	0.00	0.6
Non-derivatized - MS/MS PE NeoBase Kit	870	0.87	0.07	0.11	0.00	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.80	0.05	0.17	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.86	0.25	0.53	0.01	0.6

2019 Quality Control Data Summaries of Statistical Analyses

20:0-LYSOPHOSPHATIDYLCHOLINE (20LPC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	49	0.25	0.04	0.08	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	68	0.40	0.10	0.21	0.17	0.9

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	0.42	0.08	0.13	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	68	0.61	0.14	0.31	0.17	0.9

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	0.77	0.14	0.25	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	70	1.14	0.30	0.66	0.17	0.9

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	1.80	0.40	0.57	0.08	0.7
Non-derivatized - MS/MS PE NeoBase Kit	69	2.51	0.45	1.20	0.17	0.9

2019 Quality Control Data Summaries of Statistical Analyses

22:0-LYSOPHOSPHATIDYLCHOLINE (22LPC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	0.30	0.07	0.11	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	68	0.34	0.09	0.17	0.08	1.0

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	0.52	0.13	0.20	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	68	0.56	0.08	0.23	0.08	1.0

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	0.99	0.14	0.30	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	70	1.10	0.30	0.61	0.08	1.0

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	50	2.45	0.39	0.74	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	69	2.57	0.50	1.11	0.08	1.0

2019 Quality Control Data Summaries of Statistical Analyses

24:0-LYSOPHOSPHATIDYLCHOLINE (24LPC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	68	0.36	0.05	0.06	0.12	1.1
Non-derivatized - MS/MS PE NeoBase Kit	68	0.47	0.09	0.20	0.17	1.1

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	70	0.59	0.09	0.11	0.12	1.1
Non-derivatized - MS/MS PE NeoBase Kit	68	0.68	0.10	0.27	0.17	1.1

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	70	1.30	0.34	0.45	0.12	1.1
Non-derivatized - MS/MS PE NeoBase Kit	69	1.38	0.39	0.72	0.17	1.1

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	69	2.74	0.43	0.64	0.12	1.1
Non-derivatized - MS/MS PE NeoBase Kit	69	3.01	0.59	1.11	0.17	1.1

2019 Quality Control Data Summaries of Statistical Analyses

26:0-LYSOPHOSPHATIDYLCHOLINE (26LPC $\mu\text{mol/L}$ blood)

Lot A1815 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	88	0.36	0.06	0.11	0.07	1.1
Non-derivatized - MS/MS PE NeoBase Kit	77	0.41	0.06	0.17	0.12	1.2

Lot B1815 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	90	0.58	0.08	0.15	0.07	1.1
Non-derivatized - MS/MS PE NeoBase Kit	78	0.63	0.09	0.23	0.12	1.2

Lot C1815 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	89	1.25	0.27	0.42	0.07	1.1
Non-derivatized - MS/MS PE NeoBase Kit	78	1.39	0.47	0.61	0.12	1.2

Lot D1815 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	89	2.89	0.44	0.83	0.07	1.1
Non-derivatized - MS/MS PE NeoBase Kit	78	3.01	0.74	1.08	0.12	1.2

2019 Quality Control Data Summaries of Statistical Analyses

CREATINE (CRE $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	60	205.35	12.01	79.53	205.08	0.9

Lot B1815 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	60	292.57	25.90	109.8	205.08	0.9

Lot C1815 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	60	477.24	38.51	169.1	205.08	0.9

Lot D1815 – Enriched 500 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	60	651.24	47.60	246.34	205.08	0.9

2019 Quality Control Data Summaries of Statistical Analyses

GUANIDINOACETIC ACID (GUAC $\mu\text{mol/L}$ blood)

Lot A1815 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	90	1.48	0.15	0.68	1.35	0.9

Lot B1815 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	90	5.46	0.54	1.87	1.35	0.9

Lot C1815 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	90	10.02	1.05	3.26	1.35	0.9

Lot D1815 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	90	18.64	1.72	6.40	1.35	0.9

2019 Quality Control Data Summaries of Statistical Analyses

CREATININE (CRN $\mu\text{mol/L}$ blood)

Creatinine is not shown due to insufficient data reported.

2019 Quality Control Data Summaries of Statistical Analyses
GALACTOCEREBROSIDASE (GALC $\mu\text{mol/hr/L}$ blood)

Lot A1808 – Mean Activity 0.16 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	89	0.15	0.10	0.12	0.02	0.9
FIA-MS/MS multiplexed enzyme reaction	89	0.28	0.19	0.25	0.16	1.0

Lot B1808 – Mean Activity 0.39 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	88	0.36	0.12	0.12	0.02	0.9
FIA-MS/MS multiplexed enzyme reaction	99	0.57	0.26	0.32	0.16	1.0

Lot C1808 – Mean Activity 2.89 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	89	2.50	0.34	0.62	0.02	0.9
FIA-MS/MS multiplexed enzyme reaction	100	3.13	0.47	0.61	0.16	1.0

Lot D1808 – Mean Activity 5.58 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	90	4.83	0.56	1.01	0.02	0.9
FIA-MS/MS multiplexed enzyme reaction	99	5.79	0.45	0.73	0.16	1.0

2019 Quality Control Data Summaries of Statistical Analyses

ACID α -GLUCOSIDASE (GAA $\mu\text{mol/hr/L}$ blood)

Lot A1808 – Mean Activity 0.16 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	118	0.21	0.09	0.14	-0.08	1.4
FIA-MS/MS multiplexed enzyme reaction	100	0.20	0.09	0.13	0.07	1.0
Fluorometric	30	0.36	0.12	0.41	0.12	0.7

Lot B1808 – Mean Activity 0.58 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	0.82	0.26	0.33	-0.08	1.4
FIA-MS/MS non-kit multiplexed enzyme reaction	119	0.73	0.22	0.32	0.07	1.0
Fluorometric	30	0.79	0.20	0.78	0.12	0.7

Lot C1808 – Mean Activity 4.98 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	6.49	0.93	1.87	-0.08	1.4
FIA-MS/MS non-kit multiplexed enzyme reaction	120	5.00	0.65	1.23	0.07	1.0
Fluorometric	50	2.73	0.64	2.63	0.12	0.7

Lot D1808 – Mean Activity 7.87 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	11.21	1.10	3.29	-0.08	1.4
FIA-MS/MS non-kit multiplexed enzyme reaction	120	8.07	0.66	1.93	0.07	1.0
Fluorometric	50	5.65	0.78	4.23	0.12	0.7

2019 Quality Control Data Summaries of Statistical Analyses

ACID α -GLUCOSIDASE (GAA $\mu\text{mol/hr/L}$ blood) (cont.) METHOD REPORT FOR DIGITAL MICROFLUIDICS

Lot A1808 – Mean Activity 1.44 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	40	1.62	0.35	0.42	0.81	1.0

Lot B1808 – Mean Activity 2.43 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	67	3.13	0.72	0.84	0.81	1.0

Lot C1808 – Mean Activity 15.42 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	70	16.46	2.07	2.28	0.81	1.0

Lot D1808 – Mean Activity 28.23 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	70	27.71	2.90	3.56	0.81	1.0

2019 Quality Control Data Summaries of Statistical Analyses

α-L-IDURONIDASE (IDUA μmol/hr/L blood)

Lot A1808 – Mean Activity 0.12 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	0.15	0.08	0.10	-0.08	1.3
FIA-MS/MS multiplexed enzyme reaction	108	0.14	0.04	0.07	0.07	0.9

Lot B1808 – Mean Activity 0.45 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	0.60	0.15	0.24	-0.08	1.3
FIA-MS/MS multiplexed enzyme reaction	117	0.56	0.15	0.21	0.07	0.9

Lot C1808 – Mean Activity 4.36 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	4.98	0.69	1.62	-0.08	1.3
FIA-MS/MS multiplexed enzyme reaction	120	4.12	0.41	0.61	0.07	0.9
Fluorometric	30	2.90	0.61	1.29	-3.10	1.4

Lot D1808 – Mean Activity 8.03 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	10.20	1.17	3.79	-0.08	1.3
FIA-MS/MS multiplexed enzyme reaction	120	7.65	0.61	1.05	0.07	0.9
Fluorometric	30	7.96	1.38	6.82	-3.10	1.4

2019 Quality Control Data Summaries of Statistical Analyses

α -L-IDURONIDASE (IDUA $\mu\text{mol/hr/L}$ blood)

Lot A1808 – Mean Activity 2.44 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	55	2.69	0.38	0.93	0.38	0.9

Lot B1808 – Mean Activity 4.23 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	69	4.02	0.66	1.09	0.38	0.9

Lot C1808 – Mean Activity 15.79 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	60	14.15	1.59	2.23	0.38	0.9

Lot D1808 – Mean Activity 30.52 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	60	27.30	2.29	3.92	0.38	0.9

2019 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA μmol/hr/L blood)

Lot A1808 – Mean Activity 0.72 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	117	0.62	0.21	0.26	-0.17	1.1
FIA-MS/MS multiplexed enzyme reaction	79	0.69	0.13	0.18	0.06	0.9
Fluorometric	30	0.73	0.22	0.61	-0.05	1.0

Lot B1808 – Mean Activity 1.31 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	118	1.29	0.29	0.42	-0.17	1.1
FIA-MS/MS multiplexed enzyme reaction	90	1.30	0.18	0.25	0.06	0.9
Fluorometric	30	1.36	0.23	0.95	-0.05	1.0

Lot C1808 – Mean Activity 7.88 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	8.12	0.64	1.87	-0.17	1.1
FIA-MS/MS multiplexed enzyme reaction	90	7.50	0.54	0.92	0.06	0.9
Fluorometric	40	7.73	0.83	4.71	-0.05	1.0

Lot D1808 – Mean Activity 14.98 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	15.92	1.23	3.21	-0.17	1.1
FIA-MS/MS multiplexed enzyme reaction	90	14.10	0.73	1.54	0.06	0.9
Fluorometric	40	15.21	1.18	7.29	-0.05	1.0

2019 Quality Control Data Summaries of Statistical Analyses

α -GALACTOSIDASE (GLA $\mu\text{mol/hr/L}$ blood)

Lot A1808 – Mean Activity 3.66 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	42	4.31	0.68	0.93	2.10	0.9

Lot B1808 – Mean Activity 5.59 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	7.31	1.50	1.98	2.10	0.9

Lot C1808 – Mean Activity 32.42 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	32.73	2.96	3.83	2.10	0.9

Lot D1808 – Mean Activity 64.28 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	59.31	3.54	4.95	2.10	0.9

2019 Quality Control Data Summaries of Statistical Analyses

β-GLUCOCEREBROSIDASE (ABG μmol/hr/L blood)

Lot A1808 – Mean Activity 0.60 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	115	0.54	0.22	0.36	0.00	0.9
FIA-MS/MS multiplexed enzyme reaction	73	0.70	0.32	0.46	0.22	0.8

Lot B1808 – Mean Activity 1.06 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	1.12	0.61	0.87	0.00	0.9
FIA-MS/MS multiplexed enzyme reaction	89	1.03	0.30	0.43	0.22	0.8

Lot C1808 – Mean Activity 5.74 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	5.21	0.96	2.70	0.00	0.9
FIA-MS/MS multiplexed enzyme reaction	90	4.60	0.71	1.16	0.22	0.8
Fluorometric	30	2.52	0.29	1.99	-0.33	0.5

Lot D1808 – Mean Activity 11.29 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	10.69	1.15	6.98	0.00	0.9
FIA-MS/MS multiplexed enzyme reaction	90	8.88	0.77	1.93	0.22	0.8
Fluorometric	30	5.28	0.51	3.62	-0.33	0.5

2019 Quality Control Data Summaries of Statistical Analyses

β-GLUCOCEREBROSIDASE (ABG μmol/hr/L blood)

Lot A1808 – Mean Activity 2.17 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	47	2.45	0.43	0.52	0.64	0.9

Lot B1808 – Mean Activity 2.36 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	2.85	0.47	0.60	0.64	0.9

Lot C1808 – Mean Activity 6.61 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	7.06	0.85	1.01	0.64	0.9

Lot D1808 – Mean Activity 11.66 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Digital Microfluidics	50	11.30	0.80	1.42	0.64	0.9

2019 Quality Control Data Summaries of Statistical Analyses

ACID SPHINGOMYELINASE (ASM $\mu\text{mol/hr/L}$ blood)

Lot A1808 – Mean Activity 0.16 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	69	0.14	0.05	0.07	-0.02	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	73	0.15	0.04	0.06	-0.02	1.0

Lot B1808 – Mean Activity 0.30 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	68	0.26	0.07	0.09	-0.02	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	90	0.28	0.06	0.06	-0.02	1.0

Lot C1808 – Mean Activity 1.45 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	69	1.44	0.27	0.43	-0.02	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	89	1.4	0.18	0.22	-0.02	1.0

Lot D1808 – Mean Activity 2.67 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	69	2.63	0.44	0.86	-0.02	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	90	2.65	0.22	0.31	-0.02	1.0

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER 17 α -HYDROXYPROGESTERONE (17OHP2 ng/mL serum)

Lot A1811 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	151	1.01	0.78	0.92	1.79	1.0

Lot B1811 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	219	10.95	1.43	2.97	1.79	1.0

Lot C1811 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	50.73	5.41	12.68	1.79	1.0

Lot D1811 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	103.68	9.81	25.78	1.79	1.0

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	498.46	42.81	116.39	1.79	1.0

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER 4-ANDROSTENEDIONE (4AD2 ng/mL serum)

Lot A1811 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	144	0.6	0.44	0.67	0.66	1.0

Lot B1811 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	10.44	1.15	2.31	0.66	1.0

Lot C1811 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	51.73	4.42	11.5	0.66	1.0

Lot D1811 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	104.65	9.13	23.16	0.66	1.0

Lot E1811 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	514.93	42.8	112.63	0.66	1.0

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER CORTISOL (CORT2 ng/mL serum)

Lot A1811 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	145	2.23	1.31	2.87	-1.64	1.0

Lot B1811 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	180	3.14	1.32	3.4	-1.64	1.0

Lot C1811 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	51.96	4.77	10.87	-1.64	1.0

Lot D1811 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	98.2	8.75	20.93	-1.64	1.0

Lot E1811 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	220	503.99	38.46	98.74	-1.64	1.0

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER 11-DEOXYCORTISOL (11D2 ng/mL serum)

Lot A1811 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	112	0.56	0.44	0.63	3.71	1.0

Lot B1811 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	11.07	1.33	3.58	3.71	1.0

Lot C1811 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	55.46	5.73	14.67	3.71	1.0

Lot D1811 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	110.22	13.27	29.7	3.71	1.0

Lot E1811 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	510.07	66.51	150.89	3.71	1.0

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER 21-DEOXYCORTISOL (21D2 ng/mL serum)

Lot A1811 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	102	0.33	0.32	0.49	0.69	0.9

Lot B1811 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	8.94	1.31	2.71	0.69	0.9

Lot C1811 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	46.36	4.84	11.91	0.69	0.9

Lot D1811 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	98.4	10.97	25.27	0.69	0.9

Lot E1811 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	471.63	53.31	119.72	0.69	0.9

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER ALLO-ISOLEUCINE (ALE2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	142	1.27	1.14	2.58	3.15	0.9
UPLC	30	0.67	0.29	0.29	-2.92	1.1

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	93.15	10.26	16.60	3.15	0.9
UPLC	60	109.22	6.74	26.39	-2.92	1.1

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	184.93	24.65	35.17	3.15	0.9
UPLC	60	219.21	14.72	66.42	-2.92	1.1

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	357.17	32.00	67.12	3.15	0.9
UPLC	60	447.81	38.65	120.2	-2.92	1.1

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	160	717.62	62.46	139.8	3.15	0.9
UPLC	60	896.72	106.67	282.0	-2.92	1.1

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER ISOLEUCINE (ILE2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	148	11.42	3.31	6.32	12.69	0.9
UPLC	50	13.71	2.28	4.58	17.19	1.2

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	101.48	11.98	23.95	12.69	0.9
UPLC	60	130.19	7.38	59.9	17.19	1.2

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	185.66	26.93	41.7	12.69	0.9
UPLC	60	245.09	21.16	108.5 3	17.19	1.2

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	358.24	35.03	74.19	12.69	0.9
UPLC	60	490.98	31.24	210.0	17.19	1.2

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	705.80	70.12	153.5	12.69	0.9
UPLC	60	932.68	86.58	359.9	17.19	1.2

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER LEUCINE (LEU2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	29.01	5.61	12.1	33.27	0.9
UPLC	60	36.57	5.69	14.82	39.08	1.1

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	125.77	12.94	26.14	33.27	0.9
UPLC	60	151.69	8.48	51.86	39.08	1.1

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	222.86	28.98	46.94	33.27	0.9
UPLC	60	269.09	13.58	87.98	39.08	1.1

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	395.14	42.65	79.66	33.27	0.9
UPLC	60	497.51	35.47	174.1	39.08	1.1

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	764.31	51.66	149.4	33.27	0.9
UPLC	60	947.07	67.09	299.8	39.08	1.1

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER PHENYLALANINE (PHE2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	127	18.24	3.89	10.28	22.29	0.9
UPLC	30	13.85	2.82	3.06	11.62	1.1

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	128	113.89	12.57	18.35	22.29	0.9
UPLC	30	115.86	9.22	22.93	11.62	1.1

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	127	207.63	32.75	37.75	22.29	0.9
UPLC	30	222.48	13.55	32.35	11.62	1.1

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	129	385.84	34.9	56.96	22.29	0.9
UPLC	30	435.26	26.73	65.34	11.62	1.1

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	129	746.59	54.23	97.17	22.29	0.9
UPLC	30	859.46	50.23	140.2	11.62	1.1

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER TYROSINE (TYR2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	118	23.80	5.22	9.77	25.90	0.9
UPLC	30	21.46	3.37	3.48	15.14	1.0

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	118	114.15	10.18	17.88	25.90	0.9
UPLC	30	116.44	7.74	18.49	15.14	1.0

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	118	205.96	26.85	39.71	25.90	0.9
UPLC	30	217.26	14.26	28.59	15.14	1.0

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	374.59	44.43	66.42	25.90	0.9
UPLC	30	421.18	28.11	63.26	15.14	1.0

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	119	729.34	62.56	111.9	25.90	0.9
UPLC	30	840.71	52.91	141.6	15.14	1.0

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER VALINE (VAL2 $\mu\text{mol/L}$ blood)

Lot A1813 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	169	42.19	6.95	16.02	42.07	0.9
UPLC	40	48.59	3.98	8.53	47.61	1.0

Lot B1813 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	169	130.50	14.84	31.38	42.07	0.9
UPLC	40	151.05	7.51	23.57	47.61	1.0

Lot C1813 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	169	224.03	32.24	54.70	42.07	0.9
UPLC	40	255.56	12.70	33.42	47.61	1.0

Lot D1813 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	169	394.92	43.00	80.47	42.07	0.9
UPLC	40	456.52	27.31	65.98	47.61	1.0

Lot E1813 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	170	757.18	71.99	147.8	42.07	0.9
UPLC	40	875.70	35.83	133.6	47.61	1.0

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER MALONIC ACID (MA2 $\mu\text{mol/L}$ blood)

MA2 is not shown due to insufficient data reported.

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER METHYLMALONIC ACID (MMA2 $\mu\text{mol/L}$ blood)

Lot A1814 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	207	2.23	0.44	0.74	0.45	0.9

Lot B1814 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	220	4.62	0.58	1.13	0.45	0.9

Lot C1814 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	220	18.09	1.72	4.52	0.45	0.9

Lot D1814 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	220	43.97	5.19	10.91	0.45	0.9

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER ETHYLMALONIC ACID (EMA2 $\mu\text{mol/L}$ blood)

Lot A1814 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	108	2.07	0.31	0.63	0.29	1.0

Lot B1814 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	110	5.1	0.63	0.89	0.29	1.0

Lot C1814 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	110	20.04	1.75	4.3	0.29	1.0

Lot D1814 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	110	48.74	4.7	11.3	0.29	1.0

2019 Quality Control Data Summaries of Statistical Analyses

2ND TIER 2-METHYLCITRIC ACID (MCA2 $\mu\text{mol/L}$ blood)

Lot A1814 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	160	1.00	0.21	0.55	0.13	0.8

Lot B1814 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	170	2.02	0.30	0.67	0.13	0.8

Lot C1814 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	170	7.73	0.85	2.24	0.13	0.8

Lot D1814 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	170	19.38	1.95	5.69	0.13	0.8

2019 Quality Control Data Summaries of Statistical Analyses
2ND TIER TOTAL HOMOCYSTEINE (tHcy2 $\mu\text{mol/L}$ blood)

Lot A1814 – Enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	190	13.37	1.41	7.06	13.41	1.2

Lot B1814 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	190	25.44	2.97	13.41	13.41	1.2

Lot C1814 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	190	71.00	7.64	38.43	13.41	1.2

Lot D1814 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	130.11	14.84	66.71	13.41	1.2

This *NEWBORN SCREENING QUALITY ASSURANCE PROGRAM* report is an internal publication distributed to program participants and selected program colleagues. The laboratory quality assurance program is a project cosponsored by the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laboratories.

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