2017 Quality Control Program Report

2017 Set 2   Issued: January 31, 2018

Introduction

The NSQAP Quality Control (QC) dried blood spot materials provide participants with external controls to assess method performance over time. The controls provide 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 are 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 2017 Set 2 QC data submitted during the second 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 µL aliquots on Grade 903 filter paper (GE Healthcare Bio-Sciences Corporation (Westborough, MA)).

NSQAP provides QC materials for analysis of thyroxine (T_4), thyroid-stimulating hormone (TSH), 17 α-hydroxyprogesterone (17OHP), total galactose (TGal), galactose-1-phosphate uridyltransferase (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), eighteen acylcarnitines free carnitine (C0), acetylcarnitine (C2), propionylcarnitine (C3), malonylcarnitine (C3DC), butyrylcarnitine (C4), hydroxybutyrylcarnitine (C4OH), isovalerylcarnitine (C5), glutarylcarnitine (C5DC), hydroxyisovalerylcarnitine (C5OH), hexanoylcarnitine (C6), octanoylcarnitine (C8), decanoylcarnitine (C10), dodecanoylcarnitine (C12), myristoylcarnitine (C14), palmitoylcarnitine (C16), hydroxypalmitoylcarnitine (C16OH), stearoylcarnitine (C18), hydroxystearoylcarnitine (C18OH), 24:0- and 26:0-lysophosphatidylcholine for the detection of X-linked Adrenoleukodystrophy (XALD) and 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). T_4, TSH, 17OHP and TGal, GALT and XALD consisted of blood spot materials from three lots per analyte, with each lot containing a different concentration of analyte. The shipment for IRT, amino acids, SUAC, acylcarnitines, and LSD consisted of blood spot cards from four lots.

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- 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 methylmalonic acid (MMA2), ethylmalonic acid (EMA2), 2-methylcitric acid (MCA2), and total homocysteine (tHCY2); and guanidinoacetate methyltransferase (GAMT) by FIA-MS/MS for the analytes guanidinoacetic acid (GAA2), and creatine (CRE2).

QC Material Distribution

On July 10, 2017 we distributed dried blood spot (DBS) quality control (QC) materials to 538 participant-ing 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 QC analyte: 1) laboratory information (contact name, laboratory code number, email); 2) analyte kit or method; 3) results of duplicate sample analysis from five independent runs in the analytic units and decimal places requested, 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.

Participant Results

For Set 2 QC materials, we compiled the participant results from five analytic runs from each QC lot, and calculated mean values and standard deviations (SD). 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 appropriately 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 included a separate table to provide participants with peer-group statistics.

The reported QC data are summarized in tables on pages 4—66 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 with less than three participants reporting data were not included in the tables.

Discussion

The enriched values of the QC specimen lots do not take into account the endogenous levels of the analytes. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, Gly, SUAC, acylcarnitines, 24:0- and 26:0-lysophosphatidylcholine, G A L C , GAA, IDUA, GAL, ABG, ASM, and all Second-tier analytes, the non-enriched base pools were distributed as the first QC specimen lot in each series so that participants could measure the endogenous concentration of the series.

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.

Discussion (cont.)

Calculations of concentrations for the QC lots may vary with type of M S / M S 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.

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 A1605, B1605, and C1605). The Y-intercept provides one measure of the endogenous concentration level for an analyte. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, G l y, SUAC, acylcarnitines, 24:0- and 26:0-lysophosphatidylcholine, GALC , GAA , IDUA, GAL, ABG, ASM, and all S e c o n d - t i e r a n a l y t e s , participants measured the endogenous concentration o r a c t i v i t y levels by analyzing the non-enriched QC lots.

The majority of analytes demonstrated acceptable performance, with slopes falling near or within the range of acceptability (range from 0.8 to 1.2). Analytes which demonstrated low slopes included Arg, SUAC, C3DC + C4OH, C4OH, and C18OH, but were historically consistent with previous sets.

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 NSQAP at NSQAPDMT@cdc.gov no later than May 1, 2018 in order to receive updated materials in July 2018. Include your laboratory code number on the form and all correspondence with NSQAP.

2017 Quality Control Data Summaries of Statistical Analyses
17 α-HYDROXYPROGESTERONE (17OHP ng/mL serum)

Lot A1605 - Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	220	17.8	2.3	4.8	-1.4	0.8
Delfia Neonatal 17-OHP (A024)	240	19.3	2.3	7.4	-2.0	0.8
AutoDelfia	349	20.1	1.9	3.6	-0.3	0.8
AutoDelfia Neonatal 17-OHP (B024)	280	18.9	2.7	4.0	-0.6	0.8
Labsystems Diagnostics	50	21.9	2.8	2.9	4.7	0.7
Bio-Rad Quantase	50	19.2	3.3	9.6	0.7	0.8
TecnoSuma UMELISA	30	38.1	4.8	15.2	4.2	1.3
LC-MS/MS	30	22.0	2.5	2.7	0.5	0.9
PerkinElmer GSP Neonatal	460	19.8	1.8	2.9	1.0	0.8
Zentech	30	16.1	2.1	3.3	2.3	0.6

Lot B1605 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	218	35.8	4.8	9.0	-1.4	0.8
Delfia Neonatal 17-OHP (A024)	240	39.1	5.4	13.0	-2.0	0.8
AutoDelfia	348	41.0	3.6	7.4	-0.3	0.8
AutoDelfia Neonatal 17-OHP (B024)	279	39.1	5.2	6.4	-0.6	0.8
Labsystems Diagnostics	50	39.9	4.9	6.7	4.7	0.7
Bio-Rad Quantase	50	41.2	4.7	18.7	0.7	0.8
TecnoSuma UMELISA	30	65.7	5.9	17.3	4.2	1.3
LC-MS/MS	30	44.2	4.7	4.8	0.5	0.9
PerkinElmer GSP Neonatal	460	40.6	3.4	5.4	1.0	0.8
Zentech	30	34.3	5.1	9.7	2.3	0.6

Lot C1605 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	220	74.1	7.9	16.8	-1.4	0.8
Delfia Neonatal 17-OHP (A024)	240	81.7	11.1	26.4	-2.0	0.8
AutoDelfia	350	81.8	6.9	16.4	-0.3	0.8
AutoDelfia Neonatal 17-OHP (B024)	278	77.9	9.3	12.4	-0.6	0.8
Labsystems Diagnostics	50	74.2	10.7	13.3	4.7	0.7
Bio-Rad Quantase	50	78.3	8.8	32.0	0.7	0.8
TecnoSuma UMELISA	30	133.6	24.6	41.9	4.2	1.3
LC-MS/MS	30	87.2	11.4	11.4	0.5	0.9
PerkinElmer GSP Neonatal	467	78.2	6.1	12.2	1.0	0.8
Zentech	30	62.1	11.8	21.8	2.3	0.6

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

2017 Quality Control Data Summaries of Statistical Analyses
THYROXINE (T$_4$ µg/dL serum)

Lot A1600 - Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	70	1.8	0.5	0.7	0.0	1.0
AutoDelfia	178	1.7	0.3	0.5	-0.5	1.1
Interscientific NeoMAP Multiplex	30	1.9	0.3	0.6	-0.7	1.2
PerkinElmer GSP Neonatal	144	1.5	0.2	0.3	-0.6	1.0

Lot B1600 - Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	80	7.0	1.0	1.1	0.0	1.0
AutoDelfia	178	7.1	0.6	1.7	-0.5	1.1
Interscientific NeoMAP Multiplex	30	7.9	0.8	1.0	-0.7	1.2
PerkinElmer GSP Neonatal	200	6.6	0.6	0.7	-0.6	1.0

Lot C1600 - Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	78	10.6	1.6	1.7	0.0	1.0
AutoDelfia	179	11.5	1.0	2.9	-0.5	1.1
Interscientific NeoMAP Multiplex	30	13.1	1.0	1.0	-0.7	1.2
PerkinElmer GSP Neonatal	200	10.9	0.9	1.1	-0.6	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
THYROID-STIMULATING HORMONE (TSH μIU/mL serum)

Lot A1701 - Enriched 25 μIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	580	24.4	2.9	5.9	-0.8	1.0
AutoDelfia	898	25.6	2.5	5.5	-0.4	1.0
Labsystems Diagnostics	140	26.9	4.2	9.0	-1.9	1.1
Bio-Rad Quantase	60	21.4	1.9	7.5	-0.3	0.8
TecnoSuma UMELISA	30	24.8	1.9	1.9	-5.1	1.2
DiaSorin	70	25.9	2.9	4.9	-1.5	1.0
Interscientific NeoMAP Multiplex	30	20.6	1.3	2.0	-2.1	0.9
PerkinElmer GSP Neonatal	570	23.2	2.3	6.0	-1.0	1.0
Trimaris Neonatal	30	27.9	1.7	2.6	5.2	0.9
Zentech	39	25.0	4.6	5.9	-4.2	1.2
In House	30	29.5	3.0	4.5	7.1	0.9

Lot B1701 - Enriched 40 μIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	580	38.6	4.3	9.7	-0.8	1.0
AutoDelfia	897	40.4	3.6	8.7	-0.4	1.0
Labsystems Diagnostics	140	40.8	5.9	11.9	-1.9	1.1
Bio-Rad Quantase	60	32.4	2.3	11.5	-0.3	0.8
TecnoSuma UMELISA	30	40.6	3.6	8.0	-5.1	1.2
DiaSorin	70	35.5	4.2	7.5	-1.5	1.0
Interscientific NeoMAP Multiplex	30	32.5	2.2	5.3	-2.1	0.9
PerkinElmer GSP Neonatal	570	36.5	3.2	9.5	-1.0	1.0
Trimaris Neonatal	30	40.8	2.8	5.5	5.2	0.9
Zentech	39	42.4	8.6	9.3	-4.2	1.2
In House	30	43.2	3.9	5.4	7.1	0.9

Lot C1701 - Enriched 80 μIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Delfia	580	79.1	7.4	18.5	-0.8	1.0
AutoDelfia	900	82.1	7.1	16.4	-0.4	1.0
Labsystems Diagnostics	140	87.0	10.5	21.6	-1.9	1.1
Bio-Rad Quantase	60	67.1	4.1	20.5	-0.3	0.8
TecnoSuma UMELISA	30	88.5	8.4	22.2	-5.1	1.2
DiaSorin	70	79.7	10.0	15.4	-1.5	1.0
Interscientific NeoMAP Multiplex	30	68.8	4.8	6.7	-2.1	0.9
PerkinElmer GSP Neonatal	570	75.2	7.0	19.2	-1.0	1.0
Trimaris Neonatal	30	77.2	4.2	8.7	5.2	0.9
Zentech	39	89.2	11.3	14.8	-4.2	1.2
In House	30	79.1	8.6	14.2	7.1	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT U/g Hb)

Lot A1703 - Assayed 1.4 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
PerkinElmer Neonatal Kit U/g Hb	282	1.4	0.3	0.4	0.2	0.8
Astoria-Pacific Neonatal Microplate Reagent KitU/g Hb	60	0.7	0.1	0.2	-0.2	0.7

Lot B1703 - Assayed 3.8 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
PerkinElmer Neonatal Kit U/g Hb	300	3.2	0.3	0.5	0.2	0.8
Astoria-Pacific Neonatal Microplate Reagent KitU/g Hb	60	2.4	0.2	0.6	-0.2	0.7

Lot C1703 - Assayed 9.1 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
PerkinElmer Neonatal Kit U/g Hb	300	7.8	0.8	1.3	0.2	0.8
Astoria-Pacific Neonatal Microplate Reagent KitU/g Hb	60	5.9	0.5	1.2	-0.2	0.7

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

METHODS REPORTED IN UNITS OTHER THAN U/g Hb (>3 Participants)

METHOD	N	Mean	AVG WITHIN LAB SD	ALL LAB SD	MIN	MAX
Lot A1703						
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	9.1	1.9	2.9	0.3	13.8
Perkin Elmer GSP Neonatal (U/dL blood)	60	0.1	0.1	0.3	0.0	1.3
Lot B1703						
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	66.5	7.0	9.5	42.2	90.9
Perkin Elmer GSP Neonatal (U/dL blood)	131	1.8	0.2	0.4	0.8	3.3
Lot C1703						
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	40	191.7	29.0	29.6	129.9	243.0
Perkin Elmer GSP Neonatal (U/dL blood)	180	11.4	0.8	1.6	8.6	15.2

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

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

2017 Quality Control Data Summaries of Statistical Analyses
IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood)

Lot A1609 - Assayed 15.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
MP Biomedicals ELISA	39	15.5	2.6	4.0	9.8	1.2
Delfia	229	14.2	1.3	1.6	0.5	0.9
AutoDelfia	599	14.3	1.3	1.9	-1.0	1.0
PerkinElmer GSP Neonatal	360	14.4	0.9	1.2	-3.5	1.0
Zentech	40	25.8	3.3	7.1	41.2	0.8

Lot B1609 - Assayed 65.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
MP Biomedicals ELISA	40	99.2	15.5	25.7	9.8	1.2
Delfia	226	61.1	5.3	6.8	0.5	0.9
AutoDelfia	599	62.7	4.9	6.6	-1.0	1.0
PerkinElmer GSP Neonatal	379	64.7	4.1	5.9	-3.5	1.0
Zentech	40	115.0	10.6	10.8	41.2	0.8

Lot C1609 - Assayed 138.2 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
MP Biomedicals ELISA	40	195.8	23.7	56.0	9.8	1.2
Delfia	228	121.8	14.0	17.4	0.5	0.9
AutoDelfia	599	124.8	10.8	14.0	-1.0	1.0
PerkinElmer GSP Neonatal	380	128.4	8.2	11.0	-3.5	1.0
Zentech	40	174.6	17.0	20.5	41.2	0.8

Lot D1609 - Assayed 231.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
MP Biomedicals ELISA	40	286.7	38.2	70.0	9.8	1.2
Delfia	230	210.6	20.6	27.3	0.5	0.9
AutoDelfia	600	221.3	17.7	22.3	-1.0	1.0
PerkinElmer GSP Neonatal	379	236.4	17.6	23.1	-3.5	1.0
Zentech	40	205.8	19.5	30.3	41.2	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
ALANINE (Ala µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	678	202.0	23.3	50.5	207.3	0.7
Non-derivatized - MS/MS non-kit	160	200.6	19.0	48.4	214.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	200.9	21.9	52.0	206.5	0.8
Non-derivatized - MS/MS PE NeoBase Kit	679	230.7	17.6	41.5	237.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	182.7	23.2	45.1	187.4	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	193.7	12.8	54.4	196.1	0.7

Lot B1615 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	679	353.5	36.2	88.4	207.3	0.7
Non-derivatized - MS/MS non-kit	160	370.4	64.1	108.2	214.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	357.9	33.6	79.9	206.5	0.8
Non-derivatized - MS/MS PE NeoBase Kit	678	407.1	28.4	69.0	237.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	319.1	28.6	67.9	187.4	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	335.2	22.3	78.5	196.1	0.7

Lot C1615 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	680	496.4	58.8	126.2	207.3	0.7
Non-derivatized - MS/MS non-kit	160	498.6	41.5	111.9	214.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	528.8	60.0	125.5	206.5	0.8
Non-derivatized - MS/MS PE NeoBase Kit	679	576.2	38.3	84.8	237.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	444.4	35.0	92.0	187.4	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	458.5	22.2	108.9	196.1	0.7

Lot D1615 - Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	679	625.9	61.4	157.6	207.3	0.7
Non-derivatized - MS/MS non-kit	160	618.6	63.1	143.2	214.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	651.1	64.7	142.1	206.5	0.8
Non-derivatized - MS/MS PE NeoBase Kit	677	723.9	52.4	110.1	237.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	563.2	44.4	116.6	187.4	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	596.7	41.0	163.7	196.1	0.7

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

2017 Quality Control Data Summaries of Statistical Analyses
ARGININE (Arg μmol/L blood)

Lot A1615 - Non-enriched 0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	728	5.5	1.3	3.2	2.9	0.6
Non-derivatized - MS/MS non-kit	159	4.0	1.1	2.3	3.5	0.6
Derivatized - MS/MS PE NeoGram Kit	49	5.4	2.9	3.7	4.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	716	4.5	0.8	1.6	3.4	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	139	7.2	1.5	2.6	6.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	5.4	1.2	2.3	4.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	2.3	0.3	0.4	0.4	0.5

Lot B1615 - Enriched 100 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	740	60.2	7.4	20.9	2.9	0.6
Non-derivatized - MS/MS non-kit	160	59.2	8.1	21.3	3.5	0.6
Derivatized - MS/MS PE NeoGram Kit	50	72.1	4.7	13.7	4.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	717	72.3	4.4	9.1	3.4	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	139	86.6	10.9	33.9	6.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	73.7	5.0	14.2	4.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	46.7	4.1	11.6	0.4	0.5

Lot C1615 - Enriched 200 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	740	122.2	14.3	43.8	2.9	0.6
Non-derivatized - MS/MS non-kit	160	119.5	11.5	39.1	3.5	0.6
Derivatized - MS/MS PE NeoGram Kit	50	146.9	10.5	26.2	4.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	720	146.0	8.9	18.2	3.4	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	140	169.7	23.8	66.6	6.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	145.5	10.1	25.6	4.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	94.2	6.8	20.3	0.4	0.5

Lot D1615 - Enriched 300 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	737	185.9	21.1	69.6	2.9	0.6
Non-derivatized - MS/MS non-kit	160	174.7	19.1	58.8	3.5	0.6
Derivatized - MS/MS PE NeoGram Kit	50	213.9	14.3	36.8	4.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	719	216.4	14.8	30.2	3.4	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	140	251.2	35.9	94.8	6.4	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	217.1	13.7	47.2	4.4	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	146.7	12.7	36.3	0.4	0.5

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

2017 Quality Control Data Summaries of Statistical Analyses
CITRULLINE (Cit µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	789	11.8	1.6	3.0	11.4	0.7
Non-derivatized - MS/MS non-kit	199	12.7	2.0	2.9	13.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	13.8	1.2	1.7	14.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	805	12.7	1.6	2.2	13.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	138	13.9	1.8	2.1	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	13.2	1.4	2.4	12.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	12.7	1.1	1.9	12.6	0.8

Lot B1615 - Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	790	29.6	3.1	6.8	11.4	0.7
Non-derivatized - MS/MS non-kit	192	33.5	4.3	7.3	13.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	34.7	3.2	4.5	14.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	809	33.1	2.7	3.9	13.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	137	35.0	3.9	7.7	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	33.4	3.9	5.7	12.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	33.6	2.6	5.0	12.6	0.8

Lot C1615 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	790	83.7	7.9	18.6	11.4	0.7
Non-derivatized - MS/MS non-kit	200	94.9	9.6	17.1	13.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	100.8	8.0	14.9	14.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	810	95.0	6.5	9.2	13.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	98.9	9.9	20.3	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	148	93.1	6.0	11.3	12.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	91.8	5.8	11.8	12.6	0.8

Lot D1615 - Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	790	194.3	18.3	43.5	11.4	0.7
Non-derivatized - MS/MS non-kit	200	214.0	22.8	36.6	13.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	224.8	14.5	30.5	14.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	807	215.1	14.8	21.6	13.1	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	218.6	21.0	33.5	14.9	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	217.2	17.8	40.6	12.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	215.2	14.5	31.6	12.6	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
GLYCINE (Gly µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	598	248.5	26.9	66.3	249.1	0.7
Non-derivatized - MS/MS non-kit	119	190.4	42.8	86.8	190.1	0.6
Derivatized - MS/MS PE NeoGram Kit	40	286.4	21.4	61.5	287.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	500	275.9	28.4	50.4	277.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	130	254.2	23.5	39.9	257.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	181.9	23.3	52.6	178.2	0.6

Lot B1615 - Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	600	465.2	45.5	126.1	249.1	0.7
Non-derivatized - MS/MS non-kit	120	361.7	67.3	154.0	190.1	0.6
Derivatized - MS/MS PE NeoGram Kit	40	531.3	26.7	95.3	287.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	500	518.6	44.4	89.2	277.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	129	468.4	49.7	82.0	257.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	346.5	39.5	101.4	178.2	0.6

Lot C1615 - Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	600	685.8	56.3	176.1	249.1	0.7
Non-derivatized - MS/MS non-kit	120	512.4	79.3	205.3	190.1	0.6
Derivatized - MS/MS PE NeoGram Kit	40	777.9	35.3	139.5	287.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	500	753.3	61.4	115.7	277.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	130	683.4	73.0	109.6	257.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	497.5	42.8	130.0	178.2	0.6

Lot D1615 - Enriched 900 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	598	897.7	77.8	232.6	249.1	0.7
Non-derivatized - MS/MS non-kit	120	695.5	127.7	296.1	190.1	0.6
Derivatized - MS/MS PE NeoGram Kit	40	1018.6	44.8	178.7	287.1	0.8
Non-derivatized - MS/MS PE NeoBase Kit	500	992.7	89.4	161.6	277.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	130	879.3	70.6	148.6	257.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	687.6	55.9	202.0	178.2	0.6

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

2017 Quality Control Data Summaries of Statistical Analyses
LEUCINE (Leu µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	797	64.3	6.5	13.4	67.2	0.8
Non-derivatized - MS/MS non-kit	270	70.2	5.8	11.4	73.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	65.6	5.7	7.7	68.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	75.5	5.1	9.9	77.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	138	62.9	9.5	14.9	65.5	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	73.3	4.1	11.0	75.4	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	77.2	4.5	10.0	82.0	0.8

Lot B1615 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	799	145.7	14.0	26.0	67.2	0.8
Non-derivatized - MS/MS non-kit	262	153.4	11.8	21.6	73.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	152.2	11.0	14.8	68.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	850	161.2	10.1	17.0	77.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	138	132.5	15.3	23.0	65.5	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	153.3	7.3	16.8	75.4	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	170.2	10.5	21.9	82.0	0.8

Lot C1615 - Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	799	257.0	23.1	43.9	67.2	0.8
Non-derivatized - MS/MS non-kit	270	270.2	21.9	37.6	73.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	276.1	19.0	30.1	68.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	848	279.2	16.5	31.1	77.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	233.3	20.3	35.5	65.5	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	262.7	13.8	33.1	75.4	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	285.5	17.3	31.2	82.0	0.8

Lot D1615 - Enriched 500 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	800	443.2	40.4	78.9	67.2	0.8
Non-derivatized - MS/MS non-kit	270	459.9	35.8	71.4	73.4	0.8
Derivatized - MS/MS PE NeoGram Kit	50	478.6	33.6	50.4	68.0	0.8
Non-derivatized - MS/MS PE NeoBase Kit	850	479.6	30.6	55.8	77.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	392.9	28.7	64.8	65.5	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	450.2	24.9	60.2	75.4	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	489.8	26.4	53.3	82.0	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
METHIONINE (Met µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	780	12.9	2.0	3.3	11.7	0.8
Non-derivatized - MS/MS non-kit	270	11.0	1.4	2.7	9.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	13.1	1.7	2.0	13.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	829	10.5	1.2	1.9	9.1	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	140	9.7	2.1	3.1	9.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	8.7	0.8	1.2	6.8	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	11.8	1.0	1.3	10.1	0.8

Lot B1615 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	778	49.7	5.7	10.1	11.7	0.8
Non-derivatized - MS/MS non-kit	262	44.8	4.3	8.9	9.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	53.4	5.9	6.2	13.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	823	45.3	3.2	5.5	9.1	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	139	39.9	4.4	9.1	9.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	39.3	2.7	5.9	6.8	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	47.9	3.0	4.2	10.1	0.8

Lot C1615 - Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	781	124.1	14.6	24.8	11.7	0.8
Non-derivatized - MS/MS non-kit	269	115.3	7.7	23.3	9.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	131.2	10.8	13.5	13.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	827	116.5	7.3	14.5	9.1	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	140	101.3	11.3	24.1	9.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	100.1	6.1	13.1	6.8	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	119.5	8.2	12.5	10.1	0.8

Lot D1615 - Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	779	204.5	21.8	35.4	11.7	0.8
Non-derivatized - MS/MS non-kit	270	190.7	15.4	38.3	9.6	0.7
Derivatized - MS/MS PE NeoGram Kit	50	211.2	17.1	18.8	13.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	823	194.5	12.5	23.5	9.1	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	140	162.4	18.4	41.3	9.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	172.5	10.5	26.1	6.8	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	202.0	10.9	15.7	10.1	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
ORNITHINE (Orn μmol/L blood)

Lot A1615 - Non-enriched 0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	607	70.2	10.6	37.1	68.6	0.5
Non-derivatized - MS/MS non-kit	130	85.3	12.4	19.7	86.0	0.6
Non-derivatized - MS/MS PE NeoBase Kit	476	97.2	7.2	18.5	97.8	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	130	104.1	9.8	27.9	105.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	122.1	9.7	22.4	119.6	0.8

Lot B1615 - Enriched 100 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	602	117.2	15.8	60.8	68.6	0.5
Non-derivatized - MS/MS non-kit	129	143.3	21.7	33.2	86.0	0.6
Non-derivatized - MS/MS PE NeoBase Kit	475	167.6	10.7	29.5	97.8	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	129	179.4	18.8	44.5	105.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	199.8	17.8	42.3	119.6	0.8

Lot C1615 - Enriched 200 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	605	163.5	22.4	84.1	68.6	0.5
Non-derivatized - MS/MS non-kit	130	195.4	27.0	43.4	86.0	0.6
Non-derivatized - MS/MS PE NeoBase Kit	477	229.7	14.5	41.2	97.8	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	130	250.8	25.0	66.4	105.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	267.4	18.9	53.4	119.6	0.8

Lot D1615 - Enriched 300 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	602	218.9	27.2	110.5	68.6	0.5
Non-derivatized - MS/MS non-kit	130	253.0	33.2	52.5	86.0	0.6
Non-derivatized - MS/MS PE NeoBase Kit	476	301.3	21.8	57.8	97.8	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	130	322.5	40.3	84.7	105.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	363.0	24.8	91.0	119.6	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
PHENYLALANINE (Phe µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Fluorometric Manual	79	41.3	16.2	28.3	41.0	0.8
PerkinElmer Neonatal Kit	247	23.6	6.8	18.2	23.6	0.6
Labsystems Diagnostics	101	29.3	5.3	20.4	15.0	1.0
Bio-Rad Quantase	50	48.9	19.3	35.0	14.7	1.4
PerkinElmer GSP Neonatal	30	10.2	0.1	9.2	6.3	0.6
Derivatized - MS/MS non-kit	847	24.9	2.7	5.0	24.0	0.8
Non-derivatized - MS/MS non-kit	309	24.5	2.1	3.4	24.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	26.1	2.0	3.0	25.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	829	24.7	2.1	3.3	24.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	25.4	3.5	5.2	25.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	26.6	1.7	3.9	24.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	26.4	1.6	2.7	27.1	0.9
Trimaris Neonatal	30	21.3	4.5	4.5	16.9	1.0

Lot B1615 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Fluorometric Manual	80	124.4	13.2	54.3	41.0	0.8
PerkinElmer Neonatal Kit	270	85.8	13.6	48.8	23.6	0.6
Labsystems Diagnostics	120	107.0	19.2	41.1	15.0	1.0
Bio-Rad Quantase	50	135.3	19.9	33.7	14.7	1.4
PerkinElmer GSP Neonatal	30	65.1	11.1	56.3	6.3	0.6
Derivatized - MS/MS non-kit	850	105.0	9.7	16.8	24.0	0.8
Non-derivatized - MS/MS non-kit	302	109.6	7.6	15.6	24.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	111.9	8.4	12.6	25.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	827	106.5	7.0	10.9	24.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	102.8	8.4	18.2	25.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	111.2	6.8	17.9	24.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	118.3	8.3	11.4	27.1	0.9
Trimaris Neonatal	30	118.1	12.1	13.5	16.9	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
PHENYLALANINE (Phe µmol/L blood)

Lot C1615 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Fluorometric Manual	80	207.8	20.8	88.4	41.0	0.8
PerkinElmer Neonatal Kit	270	147.9	18.7	82.2	23.6	0.6
Labsystems Diagnostics	120	210.0	15.6	73.6	15.0	1.0
Bio-Rad Quantase	50	234.3	26.7	28.8	14.7	1.4
PerkinElmer GSP Neonatal	30	119.6	19.6	103.0	6.3	0.6
Derivatized - MS/MS non-kit	850	182.4	14.5	29.2	24.0	0.8
Non-derivatized - MS/MS non-kit	310	191.6	12.0	26.0	24.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	195.9	12.4	21.5	25.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	828	184.8	11.7	19.2	24.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	179.5	15.5	31.2	25.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	189.2	10.3	25.2	24.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	200.4	13.1	18.5	27.1	0.9
Trimaris Neonatal	30	218.2	14.3	14.3	16.9	1.0

Lot D1615 - Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Fluorometric Manual	80	292.1	28.4	123.5	41.0	0.8
PerkinElmer Neonatal Kit	270	210.2	18.6	115.0	23.6	0.6
Labsystems Diagnostics	120	339.0	41.8	122.3	15.0	1.0
Bio-Rad Quantase	50	485.5	34.6	339.3	14.7	1.4
PerkinElmer GSP Neonatal	30	194.0	22.4	164.9	6.3	0.6
Derivatized - MS/MS non-kit	850	268.2	22.8	43.0	24.0	0.8
Non-derivatized - MS/MS non-kit	310	277.2	22.4	42.3	24.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	284.7	22.4	28.6	25.7	0.9
Non-derivatized - MS/MS PE NeoBase Kit	828	268.7	18.0	29.0	24.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	257.7	22.5	42.7	25.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	285.3	16.2	52.6	24.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	293.9	16.5	24.6	27.1	0.9
Trimaris Neonatal	30	335.2	28.9	30.7	16.9	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
SUCCINYLACETONE (SUAC µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	223	0.8	0.2	0.5	0.9	0.5
Non-derivatized - MS/MS non-kit	110	0.9	0.2	1.2	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	470	0.5	0.1	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	80	0.6	0.1	0.4	0.7	0.4

Lot B1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	230	2.1	0.4	1.2	0.9	0.5
Non-derivatized - MS/MS non-kit	110	2.1	0.3	1.6	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	467	1.0	0.2	0.4	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	80	1.5	0.2	0.4	0.7	0.4

Lot C1615 - Enriched 7.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	230	4.7	0.7	3.0	0.9	0.5
Non-derivatized - MS/MS non-kit	110	4.5	0.6	3.1	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	475	2.1	0.3	0.6	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	80	3.4	0.5	0.7	0.7	0.4

Lot D1615 - Enriched 15 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	230	8.3	1.5	5.5	0.9	0.5
Non-derivatized - MS/MS non-kit	110	7.6	1.0	5.3	1.0	0.4
Non-derivatized - MS/MS PE NeoBase Kit	480	3.7	0.5	1.0	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	80	6.0	0.9	1.3	0.7	0.4

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

2017 Quality Control Data Summaries of Statistical Analyses
TYROSINE (Tyr µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	824	27.3	3.1	5.1	26.3	0.8
Non-derivatized - MS/MS non-kit	289	27.9	3.9	6.9	26.5	0.8
Derivatized - MS/MS PE NeoGram Kit	50	27.9	2.8	3.4	28.4	0.8
Non-derivatized - MS/MS PE NeoBase Kit	845	30.1	2.9	4.9	29.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	31.0	6.1	7.9	31.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	31.3	2.3	5.9	27.5	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	27.1	2.4	2.5	26.7	0.8

Lot B1615 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	828	175.7	15.4	28.9	26.3	0.8
Non-derivatized - MS/MS non-kit	282	180.4	13.0	30.9	26.5	0.8
Derivatized - MS/MS PE NeoGram Kit	50	186.6	16.0	17.7	28.4	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	195.1	13.1	21.4	29.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	187.9	18.5	26.5	31.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	190.4	13.0	28.0	27.5	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	182.5	13.8	15.9	26.7	0.8

Lot C1615 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	824	323.1	29.5	53.7	26.3	0.8
Non-derivatized - MS/MS non-kit	287	334.7	23.5	51.8	26.5	0.8
Derivatized - MS/MS PE NeoGram Kit	50	342.3	27.9	28.1	28.4	0.8
Non-derivatized - MS/MS PE NeoBase Kit	848	358.3	22.0	40.0	29.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	352.2	28.3	51.5	31.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	347.8	18.9	54.1	27.5	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	331.2	25.0	30.6	26.7	0.8

Lot D1615 - Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	825	476.9	40.6	77.3	26.3	0.8
Non-derivatized - MS/MS non-kit	289	493.6	38.6	83.2	26.5	0.8
Derivatized - MS/MS PE NeoGram Kit	50	499.8	31.5	38.9	28.4	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	527.0	35.5	58.6	29.5	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	139	505.2	49.5	76.8	31.0	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	527.1	30.0	78.0	27.5	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	492.0	35.8	40.4	26.7	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
VALINE (Val µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	736	76.0	11.0	21.3	76.5	0.7
Non-derivatized - MS/MS non-kit	218	59.8	6.6	13.8	60.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	72.6	8.1	13.2	71.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	819	69.1	5.9	10.2	68.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	140	70.2	11.6	18.3	68.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	158	53.2	3.4	12.2	52.7	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	71.3	5.7	10.7	73.8	0.8

Lot B1615 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	748	213.8	23.8	41.0	76.5	0.7
Non-derivatized - MS/MS non-kit	214	199.6	21.7	43.0	60.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	213.3	19.0	39.3	71.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	819	233.3	17.9	31.8	68.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	137	200.6	24.8	48.0	68.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	160	179.5	11.5	35.9	52.7	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	240.5	20.8	31.9	73.8	0.8

Lot C1615 - Enriched 350 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	750	314.8	35.4	57.3	76.5	0.7
Non-derivatized - MS/MS non-kit	220	304.3	23.7	61.7	60.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	314.3	27.7	61.7	71.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	819	353.4	26.1	48.2	68.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	138	299.3	30.6	65.4	68.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	160	275.5	18.4	63.4	52.7	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	350.5	29.0	42.0	73.8	0.8

Lot D1615 - Enriched 500 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	748	417.0	44.4	78.6	76.5	0.7
Non-derivatized - MS/MS non-kit	220	404.6	33.0	85.7	60.7	0.7
Derivatized - MS/MS PE NeoGram Kit	40	425.8	39.6	75.5	71.9	0.7
Non-derivatized - MS/MS PE NeoBase Kit	819	479.6	36.2	68.3	68.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	138	406.2	44.8	89.2	68.2	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	372.2	28.8	72.7	52.7	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	475.2	33.3	44.1	73.8	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
TOTAL GALACTOSE (TGal mg/dL blood)

Lot A1605 - Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Siemens Healthcare Diagnostics	40	5.1	0.3	0.5	1.8	0.8
Fluorometric Manual	90	5.1	0.8	1.0	0.2	1.0
Colorimetric	40	5.9	1.1	1.2	-0.1	1.1
PerkinElmer Neonatal Kit	323	5.0	0.8	2.6	1.1	0.8
Labsystems Diagnostics	49	6.1	1.1	1.5	0.0	1.2
Bio-Rad Quantase	140	6.7	1.0	3.5	0.1	1.2
PerkinElmer GSP Neonatal	190	5.9	0.5	0.9	2.0	0.8
Astoria-Pacific 50 Hour Reagent Kit	40	6.5	0.5	0.9	1.7	0.9
TecnoSuma UMTEST	50	5.6	1.2	1.5	-1.8	1.4
Zentech	30	5.1	1.3	3.2	1.2	0.7

Lot B1605 - Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Siemens Healthcare Diagnostics	40	10.0	0.6	0.8	1.8	0.8
Fluorometric Manual	90	9.9	1.1	1.6	0.2	1.0
Colorimetric	40	10.6	1.3	1.9	-0.1	1.1
PerkinElmer Neonatal Kit	323	9.3	1.2	3.9	1.1	0.8
Labsystems Diagnostics	50	11.2	1.7	2.6	0.0	1.2
Bio-Rad Quantase	140	12.0	1.6	5.3	0.1	1.2
PerkinElmer GSP Neonatal	190	10.3	0.9	1.2	2.0	0.8
Astoria-Pacific 50 Hour Reagent Kit	40	10.8	0.8	1.2	1.7	0.9
TecnoSuma UMTEST	50	11.4	1.8	2.1	-1.8	1.4
Zentech	30	7.9	1.1	3.3	1.2	0.7

Lot C1605 - Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Siemens Healthcare Diagnostics	40	24.3	1.2	4.1	1.8	0.8
Fluorometric Manual	90	29.5	2.3	3.6	0.2	1.0
Colorimetric	40	33.8	7.4	10.1	-0.1	1.1
PerkinElmer Neonatal Kit	323	25.4	2.7	8.7	1.1	0.8
Labsystems Diagnostics	50	34.8	4.0	8.3	0.0	1.2
Bio-Rad Quantase	140	37.4	4.4	7.9	0.1	1.2
PerkinElmer GSP Neonatal	190	26.1	2.8	3.8	2.0	0.8
Astoria-Pacific 50 Hour Reagent Kit	40	29.5	2.0	3.9	1.7	0.9
TecnoSuma UMTEST	50	39.6	5.7	7.5	-1.8	1.4
Zentech	30	22.6	3.0	5.1	1.2	0.7

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

2017 Quality Control Data Summaries of Statistical Analyses
FREE CARNITINE (C0 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	849	18.66	1.87	4.00	18.18	1.3
Non-derivatized - MS/MS non-kit	190	15.69	1.32	3.14	15.58	1.0
Derivatized - MS/MS PE NeoGram Kit	50	22.18	1.63	2.59	22.06	1.7
Non-derivatized - MS/MS PE NeoBase Kit	827	15.64	1.29	2.26	15.44	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	148	15.78	2.15	3.96	15.69	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	13.92	1.16	2.21	13.65	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	16.22	1.06	2.15	16.13	1.0

Lot B1615 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	848	31.14	3.02	6.53	18.18	1.3
Non-derivatized - MS/MS non-kit	188	25.64	3.05	5.95	15.58	1.0
Derivatized - MS/MS PE NeoGram Kit	50	39.18	2.89	4.64	22.06	1.7
Non-derivatized - MS/MS PE NeoBase Kit	830	25.13	2.02	3.68	15.44	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	148	27.02	3.60	6.94	15.69	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	22.00	1.43	3.12	13.65	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	26.51	1.84	3.19	16.13	1.0

Lot C1615 - Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	849	44.26	4.55	9.42	18.18	1.3
Non-derivatized - MS/MS non-kit	190	35.82	2.74	7.27	15.58	1.0
Derivatized - MS/MS PE NeoGram Kit	50	56.37	4.83	7.70	22.06	1.7
Non-derivatized - MS/MS PE NeoBase Kit	830	34.77	2.44	4.94	15.44	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	149	37.24	3.50	8.11	15.69	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	29.32	2.19	4.45	13.65	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	36.11	2.81	3.99	16.13	1.0

Lot D1615 - Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	849	58.81	5.88	12.34	18.18	1.3
Non-derivatized - MS/MS non-kit	188	46.20	4.12	9.95	15.58	1.0
Derivatized - MS/MS PE NeoGram Kit	50	73.84	5.96	10.06	22.06	1.7
Non-derivatized - MS/MS PE NeoBase Kit	820	45.18	3.47	6.43	15.44	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	150	49.46	5.57	10.96	15.69	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	39.11	2.55	6.50	13.65	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	47.17	3.48	4.96	16.13	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
ACETYLCARNITINE (C2 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	803	12.63	1.43	3.48	12.56	0.8
Non-derivatized - MS/MS non-kit	190	10.92	0.81	2.02	11.08	0.9
Derivatized - MS/MS PE NeoGram Kit	40	12.35	0.76	1.54	12.73	0.6
Non-derivatized - MS/MS PE NeoBase Kit	809	9.77	0.71	1.07	9.65	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	148	11.11	1.74	2.61	10.95	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	9.95	0.87	3.62	9.78	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	12.12	0.65	0.99	11.98	1.0

Lot B1615 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	804	20.78	2.30	4.70	12.56	0.8
Non-derivatized - MS/MS non-kit	187	20.20	2.33	4.59	11.08	0.9
Derivatized - MS/MS PE NeoGram Kit	40	19.18	0.93	2.50	12.73	0.6
Non-derivatized - MS/MS PE NeoBase Kit	804	17.50	1.12	1.87	9.65	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	148	18.60	1.90	2.66	10.95	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	17.85	1.11	6.19	9.78	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	22.13	1.30	1.71	11.98	1.0

Lot C1615 - Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	808	28.25	2.92	6.34	12.56	0.8
Non-derivatized - MS/MS non-kit	190	28.56	1.79	4.93	11.08	0.9
Derivatized - MS/MS PE NeoGram Kit	40	24.96	1.55	3.19	12.73	0.6
Non-derivatized - MS/MS PE NeoBase Kit	810	24.89	1.62	2.57	9.65	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	150	25.89	2.34	3.32	10.95	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	25.18	1.34	9.77	9.78	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	30.58	1.81	2.86	11.98	1.0

Lot D1615 - Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	806	37.07	3.52	7.90	12.56	0.8
Non-derivatized - MS/MS non-kit	190	37.49	2.55	6.08	11.08	0.9
Derivatized - MS/MS PE NeoGram Kit	40	30.42	2.14	4.33	12.73	0.6
Non-derivatized - MS/MS PE NeoBase Kit	807	33.40	2.39	3.87	9.65	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	150	34.26	2.88	3.91	10.95	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	34.26	2.09	12.55	9.78	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	42.04	2.32	4.03	11.98	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
PROPIONYLCARNITINE (C3 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	834	1.17	0.17	0.28	1.14	0.8
Non-derivatized - MS/MS non-kit	189	1.11	0.10	0.25	1.14	0.8
Derivatized - MS/MS PE NeoGram Kit	49	0.97	0.09	0.11	1.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	828	0.98	0.08	0.10	0.95	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.99	0.14	0.20	0.98	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.01	0.09	0.21	0.95	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.15	0.07	0.11	1.11	0.9

Lot B1615 - Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	835	4.54	0.49	0.90	1.14	0.8
Non-derivatized - MS/MS non-kit	182	4.52	0.38	0.94	1.14	0.8
Derivatized - MS/MS PE NeoGram Kit	50	4.01	0.41	0.47	1.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	827	3.97	0.27	0.40	0.95	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	147	3.92	0.46	0.64	0.98	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	3.93	0.26	0.71	0.95	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	4.77	0.31	0.46	1.11	0.9

Lot C1615 - Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	837	7.77	0.85	1.63	1.14	0.8
Non-derivatized - MS/MS non-kit	189	7.98	0.61	1.60	1.14	0.8
Derivatized - MS/MS PE NeoGram Kit	50	6.87	0.61	0.70	1.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	830	6.80	0.42	0.70	0.95	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	149	6.71	0.63	1.06	0.98	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	6.72	0.43	1.40	0.95	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	7.94	0.47	0.69	1.11	0.9

Lot D1615 - Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	825	11.36	1.19	2.27	1.14	0.8
Non-derivatized - MS/MS non-kit	187	11.20	0.84	2.09	1.14	0.8
Derivatized - MS/MS PE NeoGram Kit	50	9.76	0.87	0.98	1.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	830	10.03	0.64	1.04	0.95	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	148	9.73	1.06	1.50	0.98	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	10.00	0.59	2.16	0.95	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	11.98	0.72	1.25	1.11	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE (C3DC µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	708	0.04	0.03	0.05	0.04	0.5
Derivatized - MS/MS PE NeoGram Kit	48	0.04	0.02	0.03	0.06	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	120	0.04	0.02	0.03	0.06	0.7

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	732	0.31	0.06	0.14	0.04	0.5
Derivatized - MS/MS PE NeoGram Kit	50	0.70	0.10	0.11	0.06	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	119	0.42	0.06	0.17	0.06	0.7

Lot C1615 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	732	0.83	0.15	0.38	0.04	0.5
Derivatized - MS/MS PE NeoGram Kit	50	1.90	0.18	0.30	0.06	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	120	1.19	0.15	0.44	0.06	0.7

Lot D1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	732	1.64	0.25	0.70	0.04	0.5
Derivatized - MS/MS PE NeoGram Kit	50	3.75	0.39	0.49	0.06	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	120	2.23	0.24	0.92	0.06	0.7

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

2017 Quality Control Data Summaries of Statistical Analyses
MALONYLCARNITINE + HYDROXYBUTYRYLCARNITINE (C3DC+C4OH µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Non-derivatized - MS/MS non-kit	119	0.09	0.03	0.08	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	597	0.07	0.01	0.04	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	0.10	0.01	0.11	0.08	0.4

Lot B1615 - Enriched 1.0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Non-derivatized - MS/MS non-kit	130	0.54	0.17	0.44	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	600	0.41	0.06	0.25	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.50	0.04	0.63	0.08	0.4

Lot C1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Non-derivatized - MS/MS non-kit	130	1.09	0.20	0.79	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	601	0.82	0.10	0.50	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.01	0.14	1.28	0.08	0.4

Lot D1615 - Enriched 5.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Non-derivatized - MS/MS non-kit	130	2.40	0.37	1.75	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	602	1.84	0.18	1.08	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	2.28	0.38	2.93	0.08	0.4

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

2017 Quality Control Data Summaries of Statistical Analyses
BUTYRYLCARNITINE (C4 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	811	0.13	0.05	0.08	0.13	0.7
Non-derivatized - MS/MS non-kit	178	0.11	0.02	0.03	0.11	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.12	0.03	0.03	0.15	0.7
Non-derivatized - MS/MS PE NeoBase Kit	815	0.12	0.02	0.03	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.10	0.03	0.03	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.10	0.02	0.03	0.08	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.10	0.01	0.01	0.05	0.8

Lot B1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	825	0.86	0.12	0.18	0.13	0.7
Non-derivatized - MS/MS non-kit	172	0.82	0.08	0.11	0.11	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.79	0.12	0.14	0.15	0.7
Non-derivatized - MS/MS PE NeoBase Kit	817	0.79	0.06	0.08	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.73	0.08	0.13	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.75	0.05	0.09	0.08	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.88	0.06	0.07	0.05	0.8

Lot C1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	829	2.27	0.27	0.44	0.13	0.7
Non-derivatized - MS/MS non-kit	180	2.26	0.19	0.26	0.11	0.7
Derivatized - MS/MS PE NeoGram Kit	50	2.17	0.30	0.36	0.15	0.7
Non-derivatized - MS/MS PE NeoBase Kit	819	2.11	0.13	0.24	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	149	2.01	0.28	0.45	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.03	0.12	0.26	0.08	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.33	0.13	0.18	0.05	0.8

Lot D1615 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	827	3.76	0.41	0.68	0.13	0.7
Non-derivatized - MS/MS non-kit	180	3.68	0.29	0.45	0.11	0.7
Derivatized - MS/MS PE NeoGram Kit	50	3.33	0.39	0.43	0.15	0.7
Non-derivatized - MS/MS PE NeoBase Kit	820	3.52	0.24	0.39	0.11	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	149	3.28	0.41	0.63	0.09	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	3.43	0.22	0.49	0.08	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.24	0.25	0.34	0.05	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
HYDROXYBUTYRYLCARNITINE (C4OH µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	682	0.09	0.03	0.05	0.09	0.6
Derivatized - MS/MS PE NeoGram Kit	50	0.09	0.02	0.03	0.11	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	109	0.08	0.02	0.03	0.09	0.6

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	697	0.39	0.07	0.13	0.09	0.6
Derivatized - MS/MS PE NeoGram Kit	50	0.43	0.07	0.09	0.11	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.37	0.06	0.08	0.09	0.6

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	697	0.71	0.11	0.24	0.09	0.6
Derivatized - MS/MS PE NeoGram Kit	50	0.77	0.10	0.15	0.11	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	109	0.69	0.14	0.17	0.09	0.6

Lot D1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	699	1.60	0.21	0.50	0.09	0.6
Derivatized - MS/MS PE NeoGram Kit	50	1.66	0.18	0.25	0.11	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	109	1.54	0.25	0.37	0.09	0.6

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

2017 Quality Control Data Summaries of Statistical Analyses
ISOVALERYLCARNITINE (C5 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	825	0.09	0.03	0.05	0.09	0.8
Non-derivatized - MS/MS non-kit	218	0.06	0.01	0.01	0.07	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.07	0.02	0.02	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	843	0.06	0.01	0.01	0.06	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.10	0.04	0.07	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	148	0.07	0.01	0.02	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.07	0.01	0.02	0.07	0.9

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	847	0.47	0.06	0.10	0.09	0.8
Non-derivatized - MS/MS non-kit	212	0.45	0.04	0.07	0.07	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.44	0.07	0.08	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	849	0.43	0.03	0.05	0.06	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	147	0.44	0.10	0.12	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.43	0.03	0.07	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.50	0.03	0.05	0.07	0.9

Lot C1615 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	845	1.22	0.14	0.23	0.09	0.8
Non-derivatized - MS/MS non-kit	220	1.23	0.09	0.18	0.07	0.8
Derivatized - MS/MS PE NeoGram Kit	50	1.18	0.20	0.20	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	849	1.14	0.08	0.14	0.06	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	149	1.17	0.16	0.21	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	1.14	0.07	0.14	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.33	0.10	0.12	0.07	0.9

Lot D1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	845	2.37	0.24	0.44	0.09	0.8
Non-derivatized - MS/MS non-kit	218	2.37	0.17	0.29	0.07	0.8
Derivatized - MS/MS PE NeoGram Kit	50	2.29	0.32	0.32	0.07	0.7
Non-derivatized - MS/MS PE NeoBase Kit	847	2.24	0.16	0.26	0.06	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	149	2.26	0.23	0.34	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.30	0.15	0.34	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	2.64	0.14	0.18	0.07	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
GLUTARYLCARNITINE (C5DC µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	786	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS non-kit	209	0.04	0.01	0.03	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	49	0.04	0.02	0.03	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	719	0.05	0.01	0.02	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	138	0.05	0.02	0.04	0.05	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.08	0.02	0.06	0.06	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.05	0.01	0.01	0.05	0.9

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	839	0.32	0.06	0.14	0.02	0.6
Non-derivatized - MS/MS non-kit	212	0.43	0.06	0.19	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.55	0.08	0.11	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	726	0.52	0.05	0.08	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	139	0.63	0.12	0.19	0.05	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.72	0.08	0.24	0.06	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.49	0.03	0.05	0.05	0.9

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	838	0.61	0.10	0.27	0.02	0.6
Non-derivatized - MS/MS non-kit	220	0.85	0.10	0.35	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	1.03	0.16	0.18	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	727	1.00	0.09	0.15	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	139	1.25	0.22	0.40	0.05	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.32	0.15	0.46	0.06	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.89	0.07	0.09	0.05	0.9

Lot D1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	838	1.52	0.20	0.66	0.02	0.6
Non-derivatized - MS/MS non-kit	220	2.03	0.24	0.81	0.04	0.8
Derivatized - MS/MS PE NeoGram Kit	50	2.56	0.26	0.44	0.04	1.0
Non-derivatized - MS/MS PE NeoBase Kit	729	2.44	0.20	0.38	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	140	2.97	0.33	0.82	0.05	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	3.35	0.28	1.04	0.06	1.3
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	2.21	0.14	0.22	0.05	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
HYDROXYISOVALERYLCARNITINE (C5OH µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	826	0.37	0.06	0.11	0.36	0.7
Non-derivatized - MS/MS non-kit	180	0.53	0.05	0.15	0.53	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.36	0.05	0.06	0.37	0.8
Non-derivatized - MS/MS PE NeoBase Kit	597	0.43	0.06	0.14	0.44	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	137	0.36	0.08	0.11	0.37	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.38	0.03	0.14	0.37	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.60	0.04	0.06	0.59	0.9

Lot B1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	826	1.09	0.14	0.25	0.36	0.7
Non-derivatized - MS/MS non-kit	174	1.23	0.15	0.38	0.53	0.7
Derivatized - MS/MS PE NeoGram Kit	50	1.16	0.15	0.26	0.37	0.8
Non-derivatized - MS/MS PE NeoBase Kit	592	0.97	0.10	0.39	0.44	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	137	0.99	0.12	0.26	0.37	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.88	0.08	0.37	0.37	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.50	0.09	0.15	0.59	0.9

Lot C1615 - Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	829	1.81	0.23	0.43	0.36	0.7
Non-derivatized - MS/MS non-kit	180	1.96	0.16	0.56	0.53	0.7
Derivatized - MS/MS PE NeoGram Kit	50	1.85	0.24	0.37	0.37	0.8
Non-derivatized - MS/MS PE NeoBase Kit	592	1.46	0.10	0.60	0.44	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	140	1.61	0.25	0.43	0.37	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	1.34	0.09	0.57	0.37	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	2.32	0.14	0.21	0.59	0.9

Lot D1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	828	2.59	0.32	0.61	0.36	0.7
Non-derivatized - MS/MS non-kit	180	2.64	0.21	0.75	0.53	0.7
Derivatized - MS/MS PE NeoGram Kit	50	2.67	0.40	0.57	0.37	0.8
Non-derivatized - MS/MS PE NeoBase Kit	593	2.02	0.15	0.62	0.44	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	140	2.18	0.25	0.61	0.37	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	1.90	0.11	0.79	0.37	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	3.33	0.19	0.28	0.59	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
HEXANOYLCARNITINE (C6 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	787	0.04	0.02	0.04	0.04	0.7
Non-derivatized - MS/MS non-kit	178	0.02	0.01	0.01	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.03	0.02	0.02	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	810	0.02	0.01	0.02	0.02	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	146	0.08	0.05	0.12	0.10	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.03	0.01	0.03	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.01	0.00	0.00	-0.01	0.7

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	836	0.37	0.07	0.11	0.04	0.7
Non-derivatized - MS/MS non-kit	182	0.34	0.03	0.06	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.33	0.07	0.07	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	820	0.34	0.03	0.04	0.02	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.33	0.06	0.13	0.10	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	0.38	0.03	0.13	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.32	0.03	0.06	-0.01	0.7

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	836	0.68	0.09	0.18	0.04	0.7
Non-derivatized - MS/MS non-kit	190	0.67	0.05	0.10	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.58	0.10	0.11	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	820	0.66	0.04	0.07	0.02	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.59	0.09	0.14	0.10	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.72	0.04	0.20	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.61	0.06	0.13	-0.01	0.7

Lot D1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	835	1.67	0.21	0.44	0.04	0.7
Non-derivatized - MS/MS non-kit	190	1.65	0.14	0.27	0.01	0.7
Derivatized - MS/MS PE NeoGram Kit	50	1.25	0.17	0.20	0.07	0.5
Non-derivatized - MS/MS PE NeoBase Kit	828	1.63	0.10	0.17	0.02	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	150	1.25	0.14	0.21	0.10	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.79	0.10	0.62	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.65	0.13	0.32	-0.01	0.7

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

2017 Quality Control Data Summaries of Statistical Analyses
OCTANOYLCARNITINE (C8 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	807	0.04	0.02	0.03	0.04	0.9
Non-derivatized - MS/MS non-kit	218	0.03	0.01	0.02	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.03	0.01	0.02	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	841	0.02	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.03	0.01	0.02	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.02	0.00	0.02	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.02	0.00	0.00	0.01	1.0

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	854	0.49	0.07	0.11	0.04	0.9
Non-derivatized - MS/MS non-kit	221	0.47	0.05	0.13	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.47	0.06	0.08	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	848	0.44	0.03	0.05	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.40	0.07	0.09	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	158	0.42	0.03	0.06	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.53	0.04	0.06	0.01	1.0

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	855	0.94	0.13	0.21	0.04	0.9
Non-derivatized - MS/MS non-kit	227	0.93	0.09	0.24	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.91	0.13	0.15	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	848	0.87	0.06	0.08	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.79	0.13	0.16	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	160	0.78	0.05	0.11	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.00	0.07	0.11	0.01	1.0

Lot D1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	854	2.30	0.28	0.46	0.04	0.9
Non-derivatized - MS/MS non-kit	226	2.27	0.18	0.53	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	50	2.14	0.42	0.44	0.04	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	2.18	0.15	0.23	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	1.86	0.24	0.33	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	160	2.01	0.14	0.28	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	2.56	0.14	0.27	0.01	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
DECANOYLCARNITINE (C10 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	777	0.03	0.02	0.03	0.02	1.0
Non-derivatized - MS/MS non-kit	217	0.05	0.02	0.04	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	50	0.03	0.02	0.02	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	844	0.03	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.03	0.01	0.02	0.01	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	138	0.04	0.01	0.02	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.03	0.01	0.01	0.00	1.3

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	826	0.52	0.08	0.15	0.02	1.0
Non-derivatized - MS/MS non-kit	212	0.55	0.07	0.14	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	50	0.43	0.07	0.08	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	845	0.44	0.04	0.05	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.31	0.05	0.09	0.01	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.43	0.03	0.08	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.67	0.07	0.11	0.00	1.3

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	827	1.01	0.14	0.28	0.02	1.0
Non-derivatized - MS/MS non-kit	219	1.05	0.12	0.23	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	50	0.86	0.13	0.15	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	844	0.84	0.06	0.10	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	150	0.61	0.08	0.18	0.01	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.81	0.06	0.17	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.26	0.11	0.21	0.00	1.3

Lot D1615 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	825	2.53	0.32	0.66	0.02	1.0
Non-derivatized - MS/MS non-kit	219	2.61	0.26	0.48	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	50	2.10	0.26	0.35	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	2.19	0.17	0.26	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	1.57	0.24	0.47	0.01	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.13	0.13	0.44	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	3.30	0.20	0.51	0.00	1.3

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

2017 Quality Control Data Summaries of Statistical Analyses
DODECANOYLCARNITINE (C12 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	753	0.05	0.02	0.04	0.04	0.9
Non-derivatized - MS/MS non-kit	168	0.02	0.01	0.01	0.06	1.0
Derivatized - MS/MS PE NeoGram Kit	50	0.04	0.02	0.02	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	743	0.02	0.01	0.01	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	147	0.06	0.03	0.05	0.05	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	139	0.01	0.00	0.01	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.01	0.00	0.00	0.02	1.0

Lot B1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	770	0.97	0.16	0.25	0.04	0.9
Non-derivatized - MS/MS non-kit	178	1.09	0.21	0.54	0.06	1.0
Derivatized - MS/MS PE NeoGram Kit	50	0.99	0.11	0.18	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	758	0.86	0.06	0.09	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.81	0.11	0.23	0.05	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.82	0.07	0.12	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.03	0.09	0.12	0.02	1.0

Lot C1615 - Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	769	1.83	0.26	0.45	0.04	0.9
Non-derivatized - MS/MS non-kit	178	1.99	0.21	0.94	0.06	1.0
Derivatized - MS/MS PE NeoGram Kit	50	1.89	0.29	0.33	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	753	1.67	0.11	0.18	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	150	1.57	0.17	0.41	0.05	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.48	0.12	0.30	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.91	0.15	0.20	0.02	1.0

Lot D1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	769	2.78	0.38	0.68	0.04	0.9
Non-derivatized - MS/MS non-kit	178	2.96	0.29	1.32	0.06	1.0
Derivatized - MS/MS PE NeoGram Kit	50	2.73	0.33	0.40	0.06	0.9
Non-derivatized - MS/MS PE NeoBase Kit	747	2.56	0.18	0.28	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	150	2.36	0.24	0.58	0.05	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.38	0.19	0.34	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.94	0.18	0.20	0.02	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
MYRISTOYLCARNITINE (C14 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	812	0.08	0.02	0.04	0.08	0.9
Non-derivatized - MS/MS non-kit	169	0.06	0.01	0.03	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.08	0.02	0.02	0.09	0.9
Non-derivatized - MS/MS PE NeoBase Kit	815	0.06	0.03	0.03	0.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.08	0.02	0.04	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	137	0.04	0.01	0.01	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.06	0.01	0.01	0.06	1.0

Lot B1615 - Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	830	0.54	0.09	0.14	0.08	0.9
Non-derivatized - MS/MS non-kit	173	0.53	0.07	0.13	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.54	0.09	0.12	0.09	0.9
Non-derivatized - MS/MS PE NeoBase Kit	809	0.48	0.04	0.05	0.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.43	0.05	0.09	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.44	0.04	0.06	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.59	0.05	0.06	0.06	1.0

Lot C1615 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	830	1.39	0.19	0.31	0.08	0.9
Non-derivatized - MS/MS non-kit	179	1.40	0.16	0.30	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	50	1.44	0.18	0.24	0.09	0.9
Non-derivatized - MS/MS PE NeoBase Kit	814	1.30	0.09	0.14	0.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	1.14	0.14	0.21	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.14	0.08	0.13	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.52	0.12	0.15	0.06	1.0

Lot D1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	829	2.76	0.33	0.61	0.08	0.9
Non-derivatized - MS/MS non-kit	180	2.73	0.25	0.49	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	50	2.77	0.36	0.48	0.09	0.9
Non-derivatized - MS/MS PE NeoBase Kit	820	2.60	0.19	0.26	0.05	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	150	2.17	0.28	0.40	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.35	0.17	0.30	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	3.05	0.18	0.19	0.06	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
PALMITOYLCARNITINE (C16 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	854	0.88	0.12	0.18	0.93	0.8
Non-derivatized - MS/MS non-kit	200	0.83	0.10	0.16	0.90	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.82	0.09	0.12	0.87	0.8
Non-derivatized - MS/MS PE NeoBase Kit	816	0.82	0.08	0.12	0.85	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	148	0.80	0.14	0.21	0.86	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	0.77	0.06	0.10	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.91	0.06	0.08	1.01	0.9

Lot B1615 - Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	859	4.13	0.45	0.69	0.93	0.8
Non-derivatized - MS/MS non-kit	192	4.11	0.42	0.66	0.90	0.8
Derivatized - MS/MS PE NeoGram Kit	50	3.92	0.34	0.51	0.87	0.8
Non-derivatized - MS/MS PE NeoBase Kit	808	4.04	0.30	0.47	0.85	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	147	3.84	0.45	0.57	0.86	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	3.78	0.29	0.41	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	4.62	0.34	0.44	1.01	0.9

Lot C1615 - Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	858	7.10	0.66	1.14	0.93	0.8
Non-derivatized - MS/MS non-kit	199	7.28	0.64	1.08	0.90	0.8
Derivatized - MS/MS PE NeoGram Kit	50	6.82	0.72	1.05	0.87	0.8
Non-derivatized - MS/MS PE NeoBase Kit	820	7.03	0.49	0.86	0.85	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	150	6.64	0.69	1.00	0.86	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	6.53	0.41	0.70	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	7.82	0.53	0.62	1.01	0.9

Lot D1615 - Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	851	10.25	0.94	1.70	0.93	0.8
Non-derivatized - MS/MS non-kit	200	10.29	0.89	1.44	0.90	0.8
Derivatized - MS/MS PE NeoGram Kit	50	9.80	0.99	1.42	0.87	0.8
Non-derivatized - MS/MS PE NeoBase Kit	818	10.24	0.75	1.20	0.85	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	149	9.46	0.92	1.49	0.86	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	149	9.80	0.62	1.27	0.74	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	11.28	0.70	0.87	1.01	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
HYDROXYPALMITOYLCARNITINE (C16OH µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	762	0.02	0.01	0.02	0.02	0.7
Non-derivatized - MS/MS non-kit	166	0.03	0.01	0.12	0.05	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.02	0.01	0.01	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	801	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	139	0.02	0.01	0.01	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	129	0.01	0.00	0.01	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.01	0.00	0.00	0.01	0.7

Lot B1615 - Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	826	0.20	0.04	0.06	0.02	0.7
Non-derivatized - MS/MS non-kit	187	0.28	0.13	0.34	0.05	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.19	0.03	0.03	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	798	0.16	0.02	0.04	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	139	0.18	0.03	0.07	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.16	0.03	0.09	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.17	0.02	0.03	0.01	0.7

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	828	0.75	0.10	0.21	0.02	0.7
Non-derivatized - MS/MS non-kit	186	0.84	0.10	0.49	0.05	0.8
Derivatized - MS/MS PE NeoGram Kit	50	0.69	0.10	0.13	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	798	0.63	0.06	0.15	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	140	0.67	0.09	0.22	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.61	0.08	0.31	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.66	0.05	0.11	0.01	0.7

Lot D1615 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	826	1.13	0.14	0.32	0.02	0.7
Non-derivatized - MS/MS non-kit	186	1.24	0.18	0.89	0.05	0.8
Derivatized - MS/MS PE NeoGram Kit	50	1.02	0.18	0.23	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	805	0.95	0.10	0.24	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	140	0.99	0.19	0.35	0.02	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.96	0.10	0.54	0.00	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.99	0.09	0.16	0.01	0.7

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

2017 Quality Control Data Summaries of Statistical Analyses
STEAROYLCARNITINE (C18 µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	800	0.69	0.09	0.16	0.70	0.8
Non-derivatized - MS/MS non-kit	169	0.70	0.08	0.11	0.71	0.9
Derivatized - MS/MS PE NeoGram Kit	50	0.72	0.10	0.11	0.74	0.9
Non-derivatized - MS/MS PE NeoBase Kit	806	0.66	0.06	0.08	0.66	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	149	0.60	0.12	0.16	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.59	0.05	0.09	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	0.68	0.04	0.08	0.70	0.9

Lot B1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	806	1.56	0.19	0.32	0.70	0.8
Non-derivatized - MS/MS non-kit	162	1.60	0.15	0.23	0.71	0.9
Derivatized - MS/MS PE NeoGram Kit	50	1.63	0.20	0.25	0.74	0.9
Non-derivatized - MS/MS PE NeoBase Kit	808	1.56	0.11	0.16	0.66	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	145	1.40	0.18	0.25	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	1.38	0.11	0.22	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	1.65	0.12	0.16	0.70	0.9

Lot C1615 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	809	3.17	0.35	0.65	0.70	0.8
Non-derivatized - MS/MS non-kit	169	3.38	0.27	0.43	0.71	0.9
Derivatized - MS/MS PE NeoGram Kit	50	3.49	0.43	0.47	0.74	0.9
Non-derivatized - MS/MS PE NeoBase Kit	809	3.25	0.23	0.32	0.66	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	2.97	0.38	0.55	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	2.88	0.22	0.48	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	3.36	0.25	0.33	0.70	0.9

Lot D1615 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	807	4.88	0.52	1.04	0.70	0.8
Non-derivatized - MS/MS non-kit	169	5.10	0.42	0.70	0.71	0.9
Derivatized - MS/MS PE NeoGram Kit	50	5.18	0.47	0.58	0.74	0.9
Non-derivatized - MS/MS PE NeoBase Kit	806	5.07	0.36	0.53	0.66	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	148	4.59	0.54	0.88	0.60	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	150	4.64	0.38	0.77	0.56	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	70	5.24	0.34	0.42	0.70	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
HYDROXYSTEAROYLCARNITINE (C18OH µmol/L blood)

Lot A1615 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	585	0.02	0.01	0.02	0.01	0.6
Non-derivatized - MS/MS non-kit	99	0.01	0.00	0.01	0.02	0.5
Derivatized - MS/MS PE NeoGram Kit	50	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	692	0.00	0.00	0.01	0.00	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	117	0.01	0.01	0.01	0.01	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.00	0.00	0.01	-0.01	0.5

Lot B1615 - Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	637	0.16	0.03	0.06	0.01	0.6
Non-derivatized - MS/MS non-kit	120	0.18	0.09	0.16	0.02	0.5
Derivatized - MS/MS PE NeoGram Kit	50	0.17	0.04	0.04	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	709	0.13	0.02	0.03	0.00	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	119	0.13	0.04	0.06	0.01	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.11	0.02	0.04	-0.01	0.5

Lot C1615 - Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	633	0.57	0.08	0.19	0.01	0.6
Non-derivatized - MS/MS non-kit	119	0.55	0.06	0.30	0.02	0.5
Derivatized - MS/MS PE NeoGram Kit	50	0.63	0.09	0.11	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	708	0.53	0.04	0.08	0.00	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	120	0.52	0.10	0.23	0.01	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.45	0.07	0.17	-0.01	0.5

Lot D1615 - Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
Derivatized - MS/MS non-kit	634	0.88	0.12	0.33	0.01	0.6
Non-derivatized - MS/MS non-kit	118	0.81	0.10	0.45	0.02	0.5
Derivatized - MS/MS PE NeoGram Kit	50	0.94	0.13	0.18	0.02	0.6
Non-derivatized - MS/MS PE NeoBase Kit	710	0.82	0.07	0.12	0.00	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	119	0.81	0.14	0.33	0.01	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	140	0.72	0.13	0.28	-0.01	0.5

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

2017 Quality Control Data Summaries of Statistical Analyses
GALACTOCEREBROSIDASE (GALC µmol/hr/L blood)

Lot A1508 - Mean Activity 0.05 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	49	0.08	0.07	0.09	0.06	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	30	0.09	0.03	0.03	0.08	1.4

Lot B1508 - Mean Activity 0.30 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	49	0.26	0.09	0.13	0.06	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	40	0.43	0.07	0.13	0.08	1.4

Lot C1508 - Mean Activity 2.31 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	50	1.64	0.18	0.76	0.06	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	40	3.42	0.42	1.01	0.08	1.4

Lot D1508 - Mean Activity 4.81 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	50	3.31	0.35	1.65	0.06	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	40	6.57	0.63	1.10	0.08	1.4

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

2017 Quality Control Data Summaries of Statistical Analyses
ACID α-GLUCOSIDASE (GAAµmol/hr/L blood)

Lot A1508 - Mean Activity 0.05 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.07	0.06	0.12	0.20	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	40	0.07	0.02	0.04	0.21	0.5

Lot B1508 - Mean Activity 0.84 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.74	0.16	0.36	0.20	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	0.56	0.09	0.17	0.21	0.5

Lot C1508 - Mean Activity 8.21 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	6.38	0.58	2.93	0.20	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	4.75	0.43	1.86	0.21	0.5

Lot D1508 - Mean Activity 16.54 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	11.63	0.90	5.27	0.20	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	8.47	0.69	3.51	0.21	0.5

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

2017 Quality Control Data Summaries of Statistical Analyses
α-L-IDURONIDASE (IDUA µmol/hr/L blood)

Lot A1508 - Mean Activity 0.28 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.15	0.07	0.13	0.07	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	45	0.09	0.02	0.03	0.07	0.6

Lot B1508 - Mean Activity 0.86 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.64	0.11	0.29	0.07	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	0.53	0.10	0.16	0.07	0.6

Lot C1508 - Mean Activity 7.28 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	5.57	1.14	2.88	0.07	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	4.64	0.56	1.40	0.07	0.6

Lot D1508 - Mean Activity 16.06 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	11.38	1.98	5.68	0.07	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	60	9.46	0.98	3.07	0.07	0.6

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

2017 Quality Control Data Summaries of Statistical Analyses
α-GALACTOSIDASE (GLA µmol/hr/L blood)

Lot A1508 - Mean Activity 0.17 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.22	0.11	0.18	0.32	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	46	0.31	0.10	0.29	0.20	1.1

Lot B1508 - Mean Activity 0.52 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	0.75	0.20	0.62	0.32	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	50	0.82	0.13	0.35	0.20	1.1

Lot C1508 - Mean Activity 4.13 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	4.91	0.41	3.38	0.32	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	50	4.74	0.42	1.33	0.20	1.1

Lot D1508 - Mean Activity 9.41 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	9.16	0.93	6.12	0.32	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	50	10.47	0.51	2.70	0.20	1.1

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

2017 Quality Control Data Summaries of Statistical Analyses
ß-GLUCOCEREBROSIDASE (ABG µmol/hr/L blood)

Lot A1508 - Mean Activity 0.18 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	53	0.30	0.16	0.20	0.30	0.5
FIA-MS/MS non-kit multiplexed enzyme reaction	58	0.16	0.06	0.07	0.10	0.8

Lot B1508 - Mean Activity 0.63 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	59	0.56	0.17	0.26	0.30	0.5
FIA-MS/MS non-kit multiplexed enzyme reaction	60	0.66	0.16	0.35	0.10	0.8

Lot C1508 - Mean Activity 6.05 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	3.71	0.46	2.09	0.30	0.5
FIA-MS/MS non-kit multiplexed enzyme reaction	60	4.63	0.64	1.88	0.10	0.8

Lot D1508 - Mean Activity 12.56 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	60	6.70	0.56	3.87	0.30	0.5
FIA-MS/MS non-kit multiplexed enzyme reaction	60	9.60	0.87	3.61	0.10	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
ACID SPHINGOMYELINASE (ASM µmol/hr/L blood)

Lot A1508 - Mean Activity 0.08 µmol/hr/L blood

METHOD[ɪ]	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope**
LC-MS/MS	50	0.03	0.05	0.07	0.02	0.7

Lot B1508 - Mean Activity 0.19 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	50	0.18	0.09	0.11	0.02	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	30	0.21	0.04	0.14	-0.03	1.0

Lot C1508 - Mean Activity 1.50 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	50	1.14	0.14	0.61	0.02	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	30	1.31	0.27	0.76	-0.03	1.0

Lot D1508 - Mean Activity 3.06 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	50	2.20	0.28	1.24	0.02	0.7
FIA-MS/MS non-kit multiplexed enzyme reaction	30	2.95	0.56	2.29	-0.03	1.0

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

[ɪ]Data for methods with less than 3 participants have been removed from the data set

**Level A slope data not available for method results <LOD

2017 Quality Control Data Summaries of Statistical Analyses
24:0-LYSOPHOSPHATIDYLCHOLINE (24LPC μmol/L blood)

Lot A1610 - Non-enriched 0 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	70	0.12	0.02	0.08	0.09	1.0
FIA-MS/MS	30	0.28	0.06	0.11	0.25	1.0

Lot B1610 - Enriched 1.00 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	70	1.07	0.13	0.29	0.09	1.0
FIA-MS/MS	30	1.22	0.18	0.24	0.25	1.0

Lot C1610 - Enriched 5.00 μmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	70	5.19	0.47	1.28	0.09	1.0
FIA-MS/MS	29	5.38	0.50	0.58	0.25	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
26:0 LYSOPHOSPHATIDYLCHOLINE (26LPC µmol/L blood)

Lot A1610 - Non-enriched 0 µmol/L blood

METHOD[i]	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope**
LC-MS/MS	80	0.06	0.02	0.09	0.06	1.0

Lot B1610 - Enriched 1.00 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	1.04	0.14	0.19	0.06	1.0
FIA-MS/MS	30	1.19	0.10	0.34	0.08	1.1

Lot C1610 - Enriched 5.00 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	4.96	0.45	0.69	0.06	1.0
FIA-MS/MS	30	5.67	0.73	1.43	0.08	1.1

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

[i]Data for methods with less than 3 participants have been removed from the data set

**Level A slope data not available for method results <LOD

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER 17 α-HYDROXYPROGESTERONE (17OHP2 ng/mL serum)

Lot A1711 - Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	1.3	0.7	2.1	-0.6	0.9

Lot B1711 - Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	179	9.5	1.2	2.8	-0.6	0.9

Lot C1711 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	180	44.1	4.4	9.4	-0.6	0.9

Lot D1711 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	179	90.8	9.0	20.3	-0.6	0.9

Lot E1711 - Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	180	461.6	53.9	109.8	-0.6	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER 4-ANDROSTENEDIONE (4AD2 ng/mL serum)

Lot A1711 - Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	112	0.5	0.4	0.5	-2.1	1.0

Lot B1711 - Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	169	10.4	1.4	3.0	-2.1	1.0

Lot C1711 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	169	44.5	4.7	10.4	-2.1	1.0

Lot D1711 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	169	93.2	9.9	21.9	-2.1	1.0

Lot E1711 - Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	170	488.8	60.6	115.4	-2.1	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER CORTISOL (CORT2 ng/mL serum)

Lot A1711 - Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	1.2	0.8	2.3	-4.1	1.0

Lot B1711 - Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	170	8.8	1.4	2.9	-4.1	1.0

Lot C1711 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	170	41.5	4.5	8.3	-4.1	1.0

Lot D1711 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	169	85.6	7.2	15.1	-4.1	1.0

Lot E1711 - Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	170	476.1	38.6	77.7	-4.1	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER 11-DEOXYCORTISOL (11D2 ng/mL serum)

Lot A1711 - Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	94	2.2	0.3	2.9	0.8	0.9

Lot B1711 - Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	9.7	1.0	3.4	0.8	0.9

Lot C1711 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	45.8	4.0	8.5	0.8	0.9

Lot D1711 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	129	88.6	6.6	17.8	0.8	0.9

Lot E1711 - Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	448.2	37.4	123.0	0.8	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER 21-DEOXYCORTISOL (21D2 ng/mL serum)

Lot A1711 - Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	90	1.0	0.7	1.4	-4.4	1.0

Lot B1711 - Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	9.1	1.7	3.5	-4.4	1.0

Lot C1711 - Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	46.4	6.3	10.5	-4.4	1.0

Lot D1711 - Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	129	88.7	12.0	20.1	-4.4	1.0

Lot E1711 - Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	506.7	61.3	99.6	-4.4	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER ALLOISOLEUCINE (ALE2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	114	1.7	0.4	2.7	6.1	0.8
UPLC	30	0.3	0.1	0.5	5.1	0.9

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	149	91.5	7.9	17.4	6.1	0.8
UPLC	50	97.4	6.5	13.5	5.1	0.9

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	150	176.9	18.1	34.1	6.1	0.8
UPLC	50	189.8	12.6	22.5	5.1	0.9

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	150	343.6	37.1	70.7	6.1	0.8
UPLC	50	373.2	25.9	43.9	5.1	0.9

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	149	678.5	69.8	125.2	6.1	0.8
UPLC	50	736.0	67.6	106.8	5.1	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER ISOLEUCINE (ILE2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	38.0	3.9	7.7	39.3	0.9
UPLC	49	35.9	3.7	4.9	39.7	0.9

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	128.1	8.9	24.5	39.3	0.9
UPLC	50	129.3	7.8	13.5	39.7	0.9

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	209.5	20.2	44.9	39.3	0.9
UPLC	50	216.6	14.4	19.9	39.7	0.9

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	374.9	33.6	77	39.3	0.9
UPLC	50	386.6	27.5	38.3	39.7	0.9

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	721.1	73.6	133.8	39.3	0.9
UPLC	50	735.9	65.6	87.4	39.7	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER LEUCINE (LEU2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	139	186.4	12.6	45.5	191.8	0.9
UPLC	50	183.9	15.4	22.7	187.3	0.9

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	138	283.1	16.6	66.2	191.8	0.9
UPLC	50	276.4	18.6	31.9	187.3	0.9

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	139	368.4	31.8	90.9	191.8	0.9
UPLC	50	357.3	27.4	40.5	187.3	0.9

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	553.3	53.8	138.3	191.8	0.9
UPLC	50	526.7	38.6	64.5	187.3	0.9

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	139	897.0	81	212.4	191.8	0.9
UPLC	50	866.8	84.1	126.4	187.3	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER PHENYLALANINE (PHE2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	84.2	5.9	13.1	88.9	0.8

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	172.1	11.3	24	88.9	0.8

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	248.2	18	38.2	88.9	0.8

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	412.2	34	64.6	88.9	0.8

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	130	725.1	45.4	93.8	88.9	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER TYROSINE (TYR2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	63.7	6.1	12.8	67.3	0.8

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	146.4	10.3	24.8	67.3	0.8

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	222.1	14.5	40.7	67.3	0.8

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	379.6	25.3	68.7	67.3	0.8

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	120	683.2	44.7	99.7	67.3	0.8

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER VALINE (VAL2 µmol/L blood)

Lot A1713 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	180.4	14.5	33.6	180.4	0.8
UPLC	40	209.9	14.7	24.7	213.2	0.9

Lot B1713 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	261.3	18.4	55	180.4	0.8
UPLC	40	301.0	15.5	34.4	213.2	0.9

Lot C1713 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	337.7	30.8	80.9	180.4	0.8
UPLC	40	383.7	23	32.7	213.2	0.9

Lot D1713 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	496.6	57.4	114.7	180.4	0.8
UPLC	40	560.6	37.7	54	213.2	0.9

Lot E1713 - Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	815.1	76.5	167.1	180.4	0.8
UPLC	40	896.7	65.3	106.6	213.2	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER METHYLMALONIC ACID (MMA2 µmol/L blood)

Lot F1614 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	141	0.48	0.35	0.59	0.07	0.9

Lot G1614 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	4.41	0.88	1.51	0.07	0.9

Lot H1614 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	190	8.77	1.34	2.14	0.07	0.9

Lot I1614 - Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	20.88	2.96	5.49	0.07	0.9

Lot J1614 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	188	43.55	5.62	9.15	0.07	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER ETHYLMALONIC ACID (EMA2 µmol/L blood)

Lot F1614 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	52	0.18	0.19	0.26	-0.04	1.0

Lot G1614 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	4.77	0.65	0.87	-0.04	1.0

Lot H1614 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	9.36	0.72	1.36	-0.04	1.0

Lot I1614 - Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	23.78	1.92	3.80	-0.04	1.0

Lot J1614 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	80	47.84	3.32	7.70	-0.04	1.0

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER 2-METHYLCITRIC ACID (MCA2 µmol/L blood)

Lot F1614 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	94	0.45	0.71	0.94	0.12	0.9

Lot G1614 - Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	138	2.21	0.57	0.90	0.12	0.9

Lot H1614 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	138	4.27	0.74	1.29	0.12	0.9

Lot I1614 - Enriched 12.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	10.56	1.29	2.68	0.12	0.9

Lot J1614 - Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	140	21.52	2.51	5.12	0.12	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
2ND TIER TOTAL HOMOCYSTEINE (tHCY2 µmol/L blood)

Lot F1614 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	6.18	1.28	3.40	5.61	0.9

Lot G1614 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	15.27	3.20	6.21	5.61	0.9

Lot H1614 - Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	21.14	3.08	8.18	5.61	0.9

Lot I1614 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	189	48.26	7.16	18.23	5.61	0.9

Lot J1614 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	188	92.05	13.70	35.01	5.61	0.9

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

2017 Quality Control Data Summaries of Statistical Analyses
GUANIDINOACETIC ACID (GAA2 µmol/L blood)

Lot A1612 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	40	1.33	0.25	0.87	1.22	0.80
Derivatized MS/MS non-kit	20	1.09	0.06	0.10	0.96	0.70

Lot B1612 - Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	40	3.37	0.49	1.31	1.22	0.80
Derivatized MS/MS non-kit	20	3.00	0.28	0.29	0.96	0.70

Lot C1612 - Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	40	5.06	0.39	1.80	1.22	0.80
Derivatized MS/MS non-kit	20	4.45	0.21	0.47	0.96	0.70

Lot D1612 - Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	40	6.83	0.86	2.48	1.22	0.80
Derivatized MS/MS non-kit	20	6.25	0.35	0.35	0.96	0.70

Lot E1612 - Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	40	9.02	0.76	2.81	1.22	0.80
Derivatized MS/MS non-kit	20	8.29	0.42	0.62	0.96	0.70

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

2017 Quality Control Data Summaries of Statistical Analyses
CREATINE (CRE2 µmol/L blood)

Lot A1612 - Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	30	243.09	28.52	82.24	246.12	0.80
Derivatized MS/MS non-kit	20	195.66	7.53	8.67	195.89	0.70

Lot B1612 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	30	297.74	31.18	86.85	246.12	0.80
Derivatized MS/MS non-kit	20	242.14	14.07	16.13	195.89	0.70

Lot C1612 - Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	30	357.33	25.35	121.79	246.12	0.80
Derivatized MS/MS non-kit	20	296.79	12.05	39.10	195.89	0.70

Lot D1612 - Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	30	470.85	34.22	165.72	246.12	0.80
Derivatized MS/MS non-kit	20	412.40	23.28	27.89	195.89	0.70

Lot E1612 - Enriched 450 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept*	Slope
LC-MS/MS	30	607.40	48.60	170.51	246.12	0.80
Derivatized MS/MS non-kit	20	533.22	18.77	57.31	195.89	0.70

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