Newborn Screening Quality Assurance Program

2020 Quality Control Report

In co-sponsorship with Association of Public Health Laboratories (APHL) Volume 31, No. 1
Provided by the Newborn Screening and Molecular Biology Branch
Centers for Disease Control and Prevention
4770 Buford Highway NE, MS/F19
Atlanta, GA 30341-3724
Email: NSQAPDMT@cdc.gov

Date issued: June 1, 2020

Introduction

The NSQAP Quality Control (QC) dried blood spot (DBS) 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 materials 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 2020 Set 1 QC data submitted 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 Life Sciences Corporation (Marlborough, MA)).

NSQAP provides QC materials for analysis of thyroxine (T4), 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). The QC pool for Tandem Mass Spectrometry (MSMS1QC) included enrichments for twenty acylcarnitines - free carnitine (C0), acetylcarnitine (C2), propionylcarnitine (C3), malonylcarnitine (C3DC), butyrylcarnitine (C4), hydroxybutyrylcarnitine (C4OH), isovalerylcarnitine (C5), tiglylcarnitine (C5:1), glutarylcarnitine (C5DC), hydroxyisovalerylcarnitine (C5OH), hexanoylcarnitine (C6), octanoylcarnitine (C8), decanoylcarnitine (C10), dodecanoylcarnitine (C12), myristoylcarnitine (C14), tetradecenoylcarnitine (C14:1), palmitoylcarnitine (C16), hydroxypalmitoylcarnitine (C16OH), stearoylcarnitine (C18), hydroxystearoylcarnitine (C18OH), 20:0-, 22:0-, 24:0- and 26:0-lysophosphatidylcholine for the detection of Adrenoleukodystrophy (ALD), creatine (CRE), guanidinoacetic acid (GUAC), creatinine (CRN). We also provided materials for galactocerebrosidase (GALC), acid α-glucosidase (GAA), α-L-iduronidase (IDUA), α-galactosidase (GLA), β-glucocerebrosidase (ABG), and acid sphingomyelinase (ASM) for the detection of Lysosomal Storage Disorders (LSD).

T4, TSH, 17OHP and TGal, GALT consisted of QC materials from three lots per analyte, with each lot containing a different concentration of analyte. QC materials for IRT, TGal, amino acids, SUAC, acylcarnitines, ALD, GAMT, and LSD consisted of four lots.

NSQAP also distributed certified QC materials for newborn screening analytes and disorders tested by second-tier methods for tandem mass spectrometry (MS/MS). These programs include Second-tier Congenital Adrenal Hyperplasia (CAHQC) by LC-MS/MS for the analytes 17 α-hydroxyprogesterone (17OHP2), 4-androstenedione (4AD2), cortisol (CORT2), 11-deoxycortisol (11D2), and 21-deoxycortisol (21D2); Second-tier Maple Syrup Urine Disease and Phenylketonuria (MSUD-PKUQC) by LC-MS/MS for the analytes alloisoleucine (ALE2), isoleucine (ILE2), leucine (LEU2), phenylalanine (PHE2), tyrosine (TYR2), and valine (VAL2); Second-tier Methylmalonic/Propionic Acidemia and

QC Material Production (cont.)

Homocystinuria (MMA-tHCY) by liquid chromatography with tandem mass spectrometry (LC-MS/MS) for the analytes malonic acid (MA2), methylmalonic acid (MMA2), ethylmalonic acid (EMA2), 2-methylcitric acid (MCA2), and total homocysteine (tHCY2). QC materials for these analytes consisted of four to five lots.

QC Material Distribution

On January 14, we distributed DBS QC materials to 502 participanting laboratories worldwide.

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 and analyte. If these minimum requirements were not met, the data was not accepted unless the participant corrected their submission.

Participant Results

For Set 1 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, 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 was excluded.

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. For LSDQC analysis, where mean activities differ based on method, we provided separate tables if sufficient data was submitted.

The reported QC data are summarized in tables on pages 4—104 which show the analyte by series of QC lots, the number of measurements (N), the mean values, and the SD by kit or analytic method. In addition, we used linear regression analysis to examine the comparability by method of reported (aggregated) versus enriched concentrations. Methods where less than three participants reported data were not included in the tables.

Discussion

Summary tables show data sorted by method, method-related differences in analytic recoveries and method bias. Because we prepared each QC lot series from a single batch of hematocrit-adjusted, non-enriched blood, the endogenous concentration was the same for all specimens across the lot series and should not affect the slope of the regression line among methods. Generally, slope values substantially different from 1.0 indicate that a method has an analytic bias. A method with no analytical bias will have a slope of 1.0, with an acceptable range from 0.8 to 1.2.

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

Discussion (cont.)

For the purpose of our assessment, we first calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs for regression analyses. We then calculated the Y-intercept and slope using all analyte concentrations within a lot series (e.g., lots A1901, B1901, and C1901)**.** The Y-intercept is estimated by performing a weighted linear regression analysis on mean reported concentrations versus either 1) enriched concentrations, 2) assayed values (GALT, IRT), or 3) mean activity (LSD), and extrapolating the regression to the Y-axis. This parameter provides one measure of the endogenous concentration level for an analyte. The endogenous concentration or activity levels of QC materials for second-tier analytes is represented by the non-enriched QC lots. For CRN and MA, no data are shown due to insufficient data.

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 Orn, SUAC, and C3DC + C4OH, but were historically consistent with previous sets. The fluorometric method reported for the LSD analytes GAA, IDUA, GLA and ABG showed high variability with markedly low slope, necessitating followup to determine if these differences are method-based, or if all results were not reported in µmol/hr/L blood.

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

https://www.cdc.gov/labstandards/nsqap_resources.html Send forms to NSQAPDMT@ cdc.gov

Domestic laboratories must submit changes no later than November 1, 2020 to receive materials in January 2021. International laboratories must submit changes no later than August 31, 2020 to receive materials in January 2021. Include your laboratory code number on the form and all correspondence with NSQAP.

2020 Quality Control Data Summaries of Statistical Analyses

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

Lot A1905 – Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	490	20.8	1.8	3.3	-1.5	0.9
Delfia	380	19.6	1.5	7.5	-5.6	1.0
Labsystems - FEIA	50	18.8	2.6	8.8	4.4	0.6
LC-MS/MS	40	20.7	1.8	2.9	-0.4	0.9
PerkinElmer GSP Neonatal	670	21.1	1.7	3.1	0.1	0.9
Zentech	40	26.0	5.1	8.5	0.4	1.1

Lot B1905 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	489	44.6	3.0	5.6	-1.5	0.9
Delfia	380	41.8	3.3	9.1	-5.6	1.0
Labsystems - FEIA	50	34.7	3.8	17.1	4.4	0.6
LC-MS/MS	40	44.5	2.9	5.6	-0.4	0.9
PerkinElmer GSP Neonatal	670	44.4	2.8	6.0	0.1	0.9
Zentech	40	55.2	9.6	18.2	0.4	1.1

Lot C1905 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	490	89.1	7.1	11.8	-1.5	0.9
Delfia	378	92.2	7.8	26.3	-5.6	1.0
Labsystems - FEIA	50	63.4	10.8	33.5	4.4	0.6
LC-MS/MS	40	86.8	5.3	12.4	-0.4	0.9
PerkinElmer GSP Neonatal	670	86.6	6.2	14.7	0.1	0.9
Zentech	40	106.4	11.1	39.9	0.4	1.1

2020 Quality Control Data Summaries of Statistical Analyses

THYROXINE (T_4 µg/dL serum)

Lot F1900 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	140	1.8	0.4	0.6	0.0	1.0
Delfia	80	1.9	0.3	0.6	0.2	1.0
PerkinElmer GSP Neonatal	152	1.9	0.2	0.5	0.1	0.9

Lot G1900 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	140	7.2	0.7	1.8	0.0	1.0
Delfia	80	7.4	0.6	0.8	0.2	1.0
PerkinElmer GSP Neonatal	170	6.8	0.6	0.8	0.1	0.9

Lot H1900 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	140	10.7	0.8	2.5	0.0	1.0
Delfia	80	10.5	1.0	1.2	0.2	1.0
PerkinElmer GSP Neonatal	170	10.3	0.9	1.2	0.1	0.9

2020 Quality Control Data Summaries of Statistical Analyses

THYROID-STIMULATING HORMONE (TSH µIU/mL serum)

Lot A1901 – Enriched 25 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	130	28.4	2.4	3.9	-2.6	1.3
AutoDelfia	700	28.2	2.1	4.7	0.3	1.1
Delfia	530	25.9	2.4	7.9	1.2	1.0
DiaSorin	70	29.6	3.9	5.0	2.1	1.2
PerkinElmer GSP Neonatal	830	26.1	2.0	5.2	-2.5	1.2
Trimaris Neonatal	30	27.6	1.1	1.6	1.7	1.1
Zentech	80	22.0	2.3	10.8	0.5	0.9

Lot B1901 – Enriched 40 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	130	53.0	4.6	8.8	-2.6	1.3
AutoDelfia	700	46.7	3.2	7.6	0.3	1.1
Delfia	529	43.1	3.5	13.1	1.2	1.0
DiaSorin	70	50.6	4.4	6.4	2.1	1.2
PerkinElmer GSP Neonatal	830	44.6	3.4	9.0	-2.5	1.2
Trimaris Neonatal	30	45.2	3.3	3.5	1.7	1.1
Zentech	80	36.7	3.5	16.9	0.5	0.9

Lot C1901 – Enriched 80 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	130	102.3	7.8	7.8	-2.6	1.3
AutoDelfia	700	91.3	6.0	15.3	0.3	1.1
Delfia	520	82.4	6.3	23.7	1.2	1.0
DiaSorin	70	94.5	8.3	11.8	2.1	1.2
PerkinElmer GSP Neonatal	830	90.3	6.6	19.3	-2.5	1.2
Trimaris Neonatal	30	86.5	4.5	8.3	1.7	1.1
Zentech	80	71.0	7.6	34.2	0.5	0.9

2020 Quality Control Data Summaries of Statistical Analyses

GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT U/g Hb)

Lot F1903 – Mean Value 1.3 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific Neonatal Microplate	60	0.6	0.1	0.2	-0.4	0.8
PerkinElmer Neonatal Kit U/g Hb	192	1.5	0.3	1.2	0.4	0.8

Lot G1903 – Mean Value 3.6 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific Neonatal Microplate	60	2.5	0.3	0.5	-0.4	0.8
PerkinElmer Neonatal Kit U/g Hb	240	3.3	0.4	0.5	0.4	0.8

Lot H1903 – Mean Value 8.9 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific Neonatal Microplate	60	6.6	0.6	1.5	-0.4	0.8
PerkinElmer Neonatal Kit U/g Hb	240	7.7	0.7	1.6	0.4	0.8

2020 Quality Control Data Summaries of Statistical Analyses

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

Lot F1903

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
In-house Quantitative Fluorometric	30	1.4	0.1	0.2	1.1	1.8
Perkin Elmer GSP Neonatal (U/dL blood)	111	0.6	0.2	0.7	0.0	2.4

Lot G1903

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
In-house Quantitative Fluorometric	30	3.2	0.3	1.1	1.9	4.9
Perkin Elmer GSP Neonatal (U/dL blood)	177	2.0	0.3	0.6	0.9	3.9

Lot H1903

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
In-house Quantitative Fluorometric	30	9.6	0.6	2.4	6.7	13.5
Perkin Elmer GSP Neonatal (U/dL blood)	230	12.1	0.8	2.3	4.5	17.0

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 curcumstances.

2020 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood)

Lot A1909 – Assayed 20.4 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	532	21.6	1.7	3.8	7.5	0.9
Delfia	160	22.6	2.3	3.2	8.7	0.9
Labsystems - FEIA	70	24.2	4.4	7.6	6.1	0.9
PerkinElmer GSP Neonatal	571	20.9	1.3	1.7	4.3	0.9
Trimaris Neonatal	30	26.8	2.2	3.7	11.9	1.0
Zentech	40	25.9	4.1	4.9	34.9	0.7

Lot B1909 – Assayed 67.0 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	550	66.7	4.6	10.8	7.5	0.9
Delfia	160	66.0	5.8	9.7	8.7	0.9
Labsystems - FEIA	70	68.8	9.2	14.5	6.1	0.9
PerkinElmer GSP Neonatal	590	66.6	3.8	5.4	4.3	0.9
Trimaris Neonatal	30	76.2	5.0	6.1	11.9	1.0
Zentech	40	96.4	15.1	17.2	34.9	0.7

Lot C1909 – Assayed 134.4 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	550	123.2	9.7	21.0	7.5	0.9
Delfia	160	133.8	12.5	38.5	8.7	0.9
Labsystems - FEIA	70	127.5	17.9	24.3	6.1	0.9
PerkinElmer GSP Neonatal	590	125.2	7.5	9.9	4.3	0.9
Trimaris Neonatal	30	146.4	15.7	22.8	11.9	1.0
Zentech	40	158.9	23.0	30.2	34.9	0.7

2020 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood) cont.

Lot D1909 – Assayed 250.4 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDelfia	550	217.7	16.9	38.4	7.5	0.9
Delfia	158	221.5	18.3	40.8	8.7	0.9
Labsystems - FEIA	70	235.4	43.5	54.9	6.1	0.9
PerkinElmer GSP Neonatal	590	228.7	13.0	18.1	4.3	0.9
Trimaris Neonatal	30	245.0	30.7	51.1	11.9	1.0
Zentech	40	200.5	33.3	46.0	34.9	0.7

2020 Quality Control Data Summaries of Statistical Analyses

ALANINE (Ala µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	230.5	18.2	44.6	218.6	0.7
Derivatized - MS/MS non-kit	509	254.1	25.1	59.4	241.7	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS	30	234.0	17.1	18.6	224.6	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	252.9	30.0	47.2	261.3	0.8
Non-derivatized - MS/MS Chromsystems	80	237.2	21.7	45.2	227.0	0.7
Non-derivatized - MS/MS non-kit	180	275.4	27.2	48.8	264.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	302.1	19.6	52.0	286.2	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	290.5	20.1	44.1	277.1	0.9

Lot B1915 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	330.5	34.4	75.6	218.6	0.7
Derivatized - MS/MS non-kit	509	370.7	30.6	88.9	241.7	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS	30	358.7	40.9	48.1	224.6	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	415.5	124.3	151.3	261.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom	80	343.7	21.9	54.6	227.0	0.7
Non-derivatized - MS/MS non-kit	180	417.1	35.4	72.6	264.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	439.2	24.7	68.2	286.2	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	428.6	33.2	69.3	277.1	0.9

Lot C1915 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	486.4	35.5	102.7	218.6	0.7
Derivatized - MS/MS non-kit	509	532.2	46.3	125.4	241.7	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS	30	519.3	41.4	44.0	224.6	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	577.8	79.5	137.1	261.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom	79	495.2	28.5	89.8	227.0	0.7
Non-derivatized - MS/MS non-kit	180	584.5	45.8	101.0	264.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	644.5	35.4	99.1	286.2	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	612.0	42.0	103.9	277.1	0.9

ALANINE (Ala µmol/L blood) cont.

Lot D1915 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	618.1	37.0	123.1	218.6	0.7
Derivatized - MS/MS non-kit	509	688.4	55.9	155.3	241.7	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	672.9	50.7	74.9	224.6	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	698.5	96.8	199.0	261.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	630.1	38.7	108.7	227.0	0.7
Non-derivatized - MS/MS non-kit	170	769.4	61.0	140.6	264.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	827.4	44.5	124.3	286.2	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	794.2	55.9	139.4	277.1	0.9

2020 Quality Control Data Summaries of Statistical Analyses

ARGININE (Arg µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	10.0	1.4	3.0	14.4	0.8
Derivatized - MS/MS non-kit	519	10.2	1.3	5.1	8.5	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	8.7	0.5	0.6	5.6	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS	30	6.5	0.7	0.8	4.9	0.6
Non-derivatized - Labsystems Neomass AAAC Plus	40	12.4	1.6	3.5	11.4	1.1
Non-derivatized - MS/MS Chromsystems	90	9.8	1.9	3.5	12.5	0.8
Non-derivatized - MS/MS non-kit	170	9.2	1.9	4.7	7.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	9.0	0.8	2.2	8.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	259	9.3	0.8	1.4	9.1	0.8

Lot B1915 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	94.6	6.8	24.9	14.4	0.8
Derivatized - MS/MS non-kit	519	80.0	7.0	30.4	8.5	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	85.0	4.3	6.7	5.6	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS	30	67.4	6.9	9.3	4.9	0.6
Non-derivatized - Labsystems Neomass AAAC Plus	40	117.5	21.6	35.5	11.4	1.1
Non-derivatized - MS/MS Chromsystems	90	89.5	5.3	15.5	12.5	0.8
Non-derivatized - MS/MS non-kit	170	88.1	8.7	22.7	7.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	89.8	5.1	10.6	8.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	93.0	5.8	8.9	9.1	0.8

2020 Quality Control Data Summaries of Statistical Analyses

ARGININE (Arg µmol/L blood) cont.

Lot C1915 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	169.3	13.1	42.7	14.4	0.8
Derivatized - MS/MS non-kit	519	152.1	13.5	58.0	8.5	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	161.1	7.8	12.4	5.6	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	129.0	13.0	17.7	4.9	0.6
Non-derivatized - Labsystems Neomass AAAC Plus	40	225.0	22.3	67.7	11.4	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	164.8	9.3	31.6	12.5	0.8
Non-derivatized - MS/MS non-kit	170	167.7	13.3	42.9	7.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	171.2	8.7	19.9	8.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	174.1	9.6	17.3	9.1	0.8

Lot D1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	237.0	16.3	63.0	14.4	0.8
Derivatized - MS/MS non-kit	509	229.3	19.9	92.9	8.5	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	252.8	10.7	21.3	5.6	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	197.8	14.8	39.9	4.9	0.6
Non-derivatized - Labsystems Neomass AAAC Plus	40	333.9	33.2	99.1	11.4	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	233.0	11.5	49.1	12.5	0.8
Non-derivatized - MS/MS non-kit	160	256.6	21.3	68.4	7.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	255.5	12.9	29.3	8.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	258	260.0	12.8	25.8	9.1	0.8

2020 Quality Control Data Summaries of Statistical Analyses

CITRULLINE (Cit µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	13.2	2.0	2.8	13.0	0.8
Derivatized - MS/MS non-kit	549	14.2	1.5	3.5	13.8	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	14.8	0.8	0.9	13.5	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	14.9	1.5	2.0	16.7	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	15.5	2.4	3.0	21.4	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	13.4	1.8	2.5	14.2	0.8
Non-derivatized - MS/MS non-kit	260	15.3	3.2	5.6	15.4	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	14.2	1.4	2.2	14.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	13.5	1.5	1.8	12.7	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	269	13.8	1.6	2.3	13.8	0.8

Lot B1915 – Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	33.2	4.5	6.5	13.0	0.8
Derivatized - MS/MS non-kit	549	34.4	3.0	7.1	13.8	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	36.5	1.7	2.2	13.5	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	33.0	3.5	4.3	16.7	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	51.5	6.1	12.3	21.4	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	34.7	2.7	5.5	14.2	0.8
Non-derivatized - MS/MS non-kit	260	39.0	4.4	7.9	15.4	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	36.5	2.6	4.1	14.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	32.8	2.2	2.6	12.7	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	35.7	2.9	4.2	13.8	0.8

CITRULLINE (Cit µmol/L blood) (cont.)

Lot C1915 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	92.3	9.4	15.3	13.0	0.8
Derivatized - MS/MS non-kit	549	93.1	7.8	19.6	13.8	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	100.5	4.1	6.5	13.5	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	86.3	6.9	15.1	16.7	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	126.2	16.1	20.3	21.4	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	95.8	7.6	15.3	14.2	0.8
Non-derivatized - MS/MS non-kit	260	106.5	10.7	22.1	15.4	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	101.2	6.2	10.7	14.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	90.5	4.9	6.0	12.7	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	96.7	6.7	10.4	13.8	0.8

Lot D1915 – Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	213.2	20.7	35.7	13.0	0.8
Derivatized - MS/MS non-kit	549	215.4	19.1	49.1	13.8	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	239.6	12.3	19.4	13.5	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	180.6	12.3	28.8	16.7	0.7
Non-derivatized - Labsystems Neomass AAAC Plus	40	274.5	30.6	34.5	21.4	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	215.8	14.6	31.2	14.2	0.8
Non-derivatized - MS/MS non-kit	250	245.5	22.9	51.0	15.4	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	233.5	13.2	21.5	14.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	212.2	9.4	14.6	12.7	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	224.7	13.3	21.3	13.8	0.8

2020 Quality Control Data Summaries of Statistical Analyses

GLYCINE (Gly µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	362.9	26.2	62.3	348.0	0.8
Derivatized - MS/MS non-kit	449	375.4	25.1	115.0	355.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	349.1	25.1	26.0	344.6	0.8
Non-derivatized - Labsystems Neomass AAAC Plus	40	393.6	106.3	136.7	352.7	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	254.0	21.7	39.1	246.1	0.5
Non-derivatized - MS/MS non-kit	130	319.5	40.3	102.1	303.7	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	520	399.1	27.5	78.2	382.8	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	199	383.7	32.1	56.8	367.4	0.8

Lot B1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	548.1	67.2	110.8	348.0	0.8
Derivatized - MS/MS non-kit	449	571.7	37.0	174.1	355.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	560.6	52.1	54.9	344.6	0.8
Non-derivatized - Labsystems Neomass AAAC Plus	39	655.8	200.4	281.7	352.7	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	381.5	28.7	50.2	246.1	0.5
Non-derivatized - MS/MS non-kit	130	494.5	48.0	150.9	303.7	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	520	609.2	37.6	113.8	382.8	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	582.2	45.7	76.7	367.4	0.8

Lot C1915 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	812.9	65.2	134.7	348.0	0.8
Derivatized - MS/MS non-kit	449	824.1	60.9	251.9	355.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	809.1	59.9	63.8	344.6	0.8
Non-derivatized - Labsystems Neomass AAAC Plus	38	960.3	216.6	311.6	352.7	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	547.9	33.5	69.1	246.1	0.5
Non-derivatized - MS/MS non-kit	130	710.5	67.4	228.4	303.7	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	520	888.1	55.3	152.6	382.8	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	199	833.6	61.9	109.4	367.4	0.8

GLYCINE (Gly µmol/L blood) cont.

Lot D1915 – Enriched 900 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	1032.9	71.9	166.4	348.0	0.8
Derivatized - MS/MS non-kit	449	1094.3	71.1	368.7	355.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1024.9	63.8	103.4	344.6	0.8
Non-derivatized - Labsystems Neomass AAAC Plus	40	1406.0	322.4	637.5	352.7	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	695.3	42.0	86.7	246.1	0.5
Non-derivatized - MS/MS non-kit	120	943.6	85.7	293.8	303.7	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	520	1145.5	73.9	200.0	382.8	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	1087.2	72.0	121.6	367.4	0.8

2020 Quality Control Data Summaries of Statistical Analyses

LEUCINE (Leu µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	97.7	14.8	29.6	94.1	0.7
Derivatized - MS/MS non-kit	569	98.9	7.5	17.9	91.7	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	97.6	4.6	5.7	85.1	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	84.8	5.2	8.7	80.9	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	108.2	7.2	7.1	108.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	114.1	12.1	30.0	112.5	0.7
Non-derivatized - MS/MS non-kit	290	112.0	8.9	20.2	103.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	117.4	6.5	13.5	108.8	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	123.6	7.2	17.1	112.9	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	107.7	6.6	11.0	101.5	0.8

Lot B1915 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	200.8	18.5	27.6	94.1	0.7
Derivatized - MS/MS non-kit	569	214.1	16.5	34.5	91.7	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	214.9	8.4	15.1	85.1	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	202.1	13.9	22.0	80.9	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	228.2	41.1	51.7	108.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	221.8	12.0	35.5	112.5	0.7
Non-derivatized - MS/MS non-kit	290	234.3	16.9	33.7	103.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	240.4	13.1	26.7	108.8	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	238.7	13.6	30.6	112.9	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	220.0	14.2	23.5	101.5	0.8

LEUCINE (Leu µmol/L blood) (cont.)

Lot C1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	314.7	31.3	45.7	94.1	0.7
Derivatized - MS/MS non-kit	569	346.1	23.8	55.9	91.7	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	350.9	15.5	26.1	85.1	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	340.9	24.5	27.8	80.9	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	364.9	63.0	103.3	108.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	333.1	13.5	36.8	112.5	0.7
Non-derivatized - MS/MS non-kit	290	372.4	27.3	57.1	103.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	380.0	19.8	39.6	108.8	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	374.4	19.0	49.7	112.9	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	339.5	18.3	38.3	101.5	0.8

Lot D1915 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	538.8	36.0	64.0	94.1	0.7
Derivatized - MS/MS non-kit	569	612.4	39.8	104.9	91.7	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	647.9	37.0	62.5	85.1	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	595.2	36.7	58.5	80.9	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	39	602.4	73.8	84.5	108.7	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	556.6	26.0	54.4	112.5	0.7
Non-derivatized - MS/MS non-kit	280	659.5	53.0	119.1	103.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	669.1	36.4	67.9	108.8	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	658.2	30.5	91.4	112.9	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	298	595.1	32.3	88.8	101.5	0.8

METHIONINE (Met µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	12.4	1.9	3.0	10.6	0.7
Derivatized - MS/MS non-kit	549	15.5	1.8	3.8	13.5	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	15.2	1.0	1.1	21.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	13.6	1.0	2.0	11.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	9.6	2.5	2.7	4.8	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	11.0	1.5	2.7	9.4	0.7
Non-derivatized - MS/MS non-kit	280	13.4	1.6	4.5	11.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	12.5	1.0	1.7	9.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	14.1	1.0	1.9	10.6	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	289	11.4	0.9	1.5	9.4	0.7

Lot B1915 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	41.9	5.0	12.3	10.6	0.7
Derivatized - MS/MS non-kit	549	52.7	4.4	7.4	13.5	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	69.2	16.3	30.6	21.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	51.6	4.8	6.5	11.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	45.6	11.8	16.1	4.8	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	40.9	3.2	5.2	9.4	0.7
Non-derivatized - MS/MS non-kit	280	50.0	4.5	10.3	11.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	48.0	3.0	5.1	9.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	50.0	3.9	6.0	10.6	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	45.0	3.1	5.9	9.4	0.7

2020 Quality Control Data Summaries of Statistical Analyses

METHIONINE (Met µmol/L blood) (cont.)

Lot C1915 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	105.7	10.0	29.1	10.6	0.7
Derivatized - MS/MS non-kit	549	132.1	10.6	19.0	13.5	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	157.3	23.3	41.3	21.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	132.3	9.5	11.2	11.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	120.0	9.2	13.7	4.8	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	107.0	5.3	10.8	9.4	0.7
Non-derivatized - MS/MS non-kit	280	133.2	11.6	28.6	11.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	127.9	7.3	13.0	9.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	134.8	6.7	15.5	10.6	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	117.9	7.6	13.2	9.4	0.7

Lot D1915 – Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	174.2	15.9	41.9	10.6	0.7
Derivatized - MS/MS non-kit	549	217.5	17.4	31.6	13.5	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	233.5	17.7	18.8	21.3	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	219.3	14.6	14.3	11.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	219.8	28.1	36.7	4.8	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	174.9	7.6	16.1	9.4	0.7
Non-derivatized - MS/MS non-kit	280	217.4	18.5	46.5	11.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	213.5	12.8	23.9	9.7	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	224.6	7.7	16.4	10.6	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	289	195.7	11.6	20.4	9.4	0.7

2020 Quality Control Data Summaries of Statistical Analyses

ORNITHINE (Orn µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	222.9	22.3	62.8	210.1	0.6
Derivatized - MS/MS non-kit	439	175.3	14.9	85.9	165.0	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	173.3	13.8	19.8	162.6	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	269.6	31.8	45.4	259.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	234.4	24.9	49.8	220.7	0.6
Non-derivatized - MS/MS non-kit	150	189.1	20.9	53.0	177.1	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	530	223.1	12.4	26.2	208.4	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase 2	210	205.3	12.4	24.3	192.0	0.6

Lot B1915 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	248.9	24.7	57.7	210.1	0.6
Derivatized - MS/MS non-kit	439	196.5	30.6	137.3	165.0	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	202.5	21.3	25.7	162.6	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	303.4	64.1	97.3	259.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	253.8	20.6	46.7	220.7	0.6
Non-derivatized - MS/MS non-kit	150	219.1	21.2	58.6	177.1	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	530	246.2	13.3	28.0	208.4	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase 2	210	227.5	13.4	27.4	192.0	0.6

ORNITHINE (Orn µmol/L blood) (cont.)

Lot C1915 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	342.7	31.3	76.9	210.1	0.6
Derivatized - MS/MS non-kit	439	261.9	24.2	125.3	165.0	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	277.7	19.0	28.3	162.6	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	388.0	70.3	113.1	259.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	337.8	18.9	59.0	220.7	0.6
Non-derivatized - MS/MS non-kit	150	296.6	30.8	81.7	177.1	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	530	337.9	17.8	41.2	208.4	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase 2	210	306.9	20.1	40.1	192.0	0.6

Lot D1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	60	398.7	28.6	95.8	210.1	0.6
Derivatized - MS/MS non-kit	439	312.5	27.1	157.2	165.0	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	337.2	23.7	47.4	162.6	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	446.0	69.7	115.9	259.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	393.3	19.9	64.6	220.7	0.6
Non-derivatized - MS/MS non-kit	150	362.9	36.5	94.8	177.1	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	530	400.3	21.4	44.6	208.4	0.6
Non-derivatized - MS/MS PerkinElmer NeoBase 2	210	367.1	20.5	48.5	192.0	0.6

2020 Quality Control Data Summaries of Statistical Analyses

PHENYLALANINE (Phe µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	90	46.0	5.0	22.1	37.2	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	80	40.9	3.6	9.1	36.0	0.8
Derivatized - MS/MS non-kit	589	44.5	4.2	8.3	41.9	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	45.3	2.1	4.8	39.7	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	39.2	2.6	5.5	38.6	0.8
Fluorometric manual (e.g. Hill or Misuma)	108	58.0	10.7	33.0	57.2	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	30	45.0	4.2	7.2	42.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	46.7	4.8	9.3	48.2	0.8
Non-derivatized - MS/MS non-kit	310	42.4	3.2	9.8	40.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	46.7	2.8	28.9	43.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	48.8	2.7	6.1	46.3	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	37.5	2.3	7.9	37.0	0.8
PerkinElmer GSP Neonatal	80	44.2	8.2	22.1	38.8	0.9
PerkinElmer Neonatal Kit	140	35.6	6.5	30.0	34.0	0.6

Lot B1915 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	90	188.1	11.5	68.9	37.2	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	80	153.0	10.7	30.2	36.0	0.8
Derivatized - MS/MS non-kit	589	172.9	12.4	28.3	41.9	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	181.1	7.7	20.3	39.7	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	161.4	13.3	14.8	38.6	0.8
Fluorometric manual (e.g. Hill or Misuma)	110	195.4	16.7	97.7	57.2	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	30	183.2	15.6	25.9	42.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	173.3	8.4	20.2	48.2	0.8
Non-derivatized - MS/MS non-kit	310	173.9	13.6	33.2	40.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	175.4	9.7	31.0	43.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	182.7	9.1	21.0	46.3	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	150.2	9.6	33.0	37.0	0.8
PerkinElmer GSP Neonatal	80	163.2	12.1	63.5	38.8	0.9
PerkinElmer Neonatal Kit	150	120.2	10.2	85.1	34.0	0.6

2020 Quality Control Data Summaries of Statistical Analyses

PHENYLALANINE (Phe µmol/L blood) (cont.)

Lot C1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	90	348.2	19.0	128.2	37.2	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	80	274.8	15.7	53.1	36.0	0.8
Derivatized - MS/MS non-kit	589	303.2	22.5	53.5	41.9	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	316.4	13.0	36.3	39.7	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	286.9	27.6	28.2	38.6	0.8
Fluorometric manual (e.g. Hill or Misuma)	110	337.5	30.9	169.6	57.2	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	30	319.4	23.5	44.2	42.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	295.1	13.0	27.1	48.2	0.8
Non-derivatized - MS/MS non-kit	310	302.9	22.4	63.8	40.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	310.3	16.2	45.9	43.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	321.4	14.5	40.0	46.3	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	258.4	15.5	58.4	37.0	0.8
PerkinElmer GSP Neonatal	80	303.4	16.8	117.4	38.8	0.9
PerkinElmer Neonatal Kit	150	201.1	14.5	141.7	34.0	0.6

Lot D1915 – Enriched 450 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Ani Labsystems	90	525.5	28.1	202.2	37.2	1.1
Derivatized - MS/MS Chromsystems MassChrom Kit	80	406.3	22.8	81.7	36.0	0.8
Derivatized - MS/MS non-kit	589	444.0	32.6	79.1	41.9	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	480.7	24.0	55.0	39.7	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	410.2	25.2	33.3	38.6	0.8
Fluorometric manual (e.g. Hill or Misuma)	110	476.5	36.7	236.8	57.2	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	30	471.5	42.3	88.4	42.4	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	416.8	17.9	52.9	48.2	0.8
Non-derivatized - MS/MS non-kit	310	447.3	28.4	91.0	40.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	451.8	23.6	55.3	43.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	465.5	14.5	54.4	46.3	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	375.8	22.5	86.2	37.0	0.8
PerkinElmer GSP Neonatal	80	438.7	23.7	169.0	38.8	0.9
PerkinElmer Neonatal Kit	150	295.7	21.4	209.4	34.0	0.6

2020 Quality Control Data Summaries of Statistical Analyses

SUCCINYLACETONE (SUAC µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	79	0.4	0.2	0.3	0.5	0.4
Derivatized - MS/MS non-kit	224	0.7	0.2	0.5	0.7	0.5
Non-Derivatized - Labsystems Neomass AAAC Plus	30	1.3	0.8	1.2	1.5	0.3
Non-derivatized - MS/MS non-kit	70	1.5	0.3	1.3	1.6	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	450	0.5	0.1	0.3	0.5	0.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	234	0.2	0.1	0.1	0.2	0.2

Lot B1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	1.5	0.4	0.6	0.5	0.4
Derivatized - MS/MS non-kit	229	2.1	0.2	1.1	0.7	0.5
Non-Derivatized - Labsystems Neomass AAAC Plus	30	2.3	1.7	1.8	1.5	0.3
Non-derivatized - MS/MS non-kit	70	3.0	0.5	2.1	1.6	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	450	1.1	0.1	0.3	0.5	0.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	240	0.7	0.1	0.3	0.2	0.2

Lot C1915 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	4.2	0.6	0.9	0.5	0.4
Derivatized - MS/MS non-kit	229	5.9	0.7	2.8	0.7	0.5
Non-Derivatized - Labsystems Neomass AAAC Plus	30	4.7	1.3	2.1	1.5	0.3
Non-derivatized - MS/MS non-kit	70	7.2	0.8	4.9	1.6	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	450	2.7	0.3	0.7	0.5	0.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	2.1	0.3	0.6	0.2	0.2

Lot D1915 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	8.2	1.0	1.5	0.5	0.4
Derivatized - MS/MS non-kit	229	11.2	1.1	5.2	0.7	0.5
Non-Derivatized - Labsystems Neomass AAAC Plus	30	7.2	1.6	2.0	1.5	0.3
Non-derivatized - MS/MS non-kit	70	12.4	1.5	8.7	1.6	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	450	5.0	0.5	1.3	0.5	0.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	239	4.1	0.5	1.1	0.2	0.2

2020 Quality Control Data Summaries of Statistical Analyses

TYROSINE (Tyr µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	39.5	4.5	6.0	40.0	0.8
Derivatized - MS/MS non-kit	579	38.6	4.0	9.7	38.3	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	38.8	2.6	2.7	32.2	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	32.6	2.3	2.8	33.8	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	39.1	6.8	9.2	42.1	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	41.6	5.7	10.1	45.2	0.9
Non-derivatized - MS/MS non-kit	290	40.5	5.2	10.3	38.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	40.8	3.2	5.9	37.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	38.3	2.8	4.1	35.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	35.7	2.2	3.9	34.8	0.8

Lot B1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	293.2	21.5	35.8	40.0	0.8
Derivatized - MS/MS non-kit	579	293.5	21.6	58.2	38.3	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	291.2	15.2	18.4	32.2	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	271.5	21.0	22.5	33.8	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	309.5	52.0	81.0	42.1	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	301.5	16.7	35.7	45.2	0.9
Non-derivatized - MS/MS non-kit	290	302.2	22.7	47.4	38.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	306.4	18.7	33.4	37.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	289.0	15.8	23.3	35.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	270.3	15.2	23.2	34.8	0.8

TYROSINE (Tyr µmol/L blood) (cont.)

Lot C1915 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	546.7	36.7	63.4	40.0	0.8
Derivatized - MS/MS non-kit	579	547.4	45.4	114.6	38.3	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	547.1	20.0	33.7	32.2	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	519.3	40.8	40.9	33.8	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	556.5	51.6	82.8	42.1	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	562.7	27.1	58.2	45.2	0.9
Non-derivatized - MS/MS non-kit	290	569.7	40.9	97.5	38.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	579.9	33.3	67.8	37.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	546.1	27.2	46.9	35.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	505.2	25.4	44.8	34.8	0.8

Lot D1915 – Enriched 900 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	798.0	38.9	82.8	40.0	0.8
Derivatized - MS/MS non-kit	579	804.1	67.0	180.1	38.3	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	830.8	52.1	76.6	32.2	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	748.2	48.6	63.8	33.8	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	823.8	79.3	163.4	42.1	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	803.6	43.6	82.6	45.2	0.9
Non-derivatized - MS/MS non-kit	290	840.4	62.9	147.6	38.1	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	740	855.8	50.3	93.1	37.9	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	807.2	27.3	36.7	35.5	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	744.3	37.4	68.5	34.8	0.8

2020 Quality Control Data Summaries of Statistical Analyses

VALINE (Val µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	95.3	8.9	20.1	88.6	0.9
Derivatized - MS/MS non-kit	529	100.0	9.8	28.3	91.9	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	96.7	5.2	9.6	83.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	80.6	6.5	6.8	71.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	97.3	10.7	15.5	89.9	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	82.2	6.9	14.5	77.8	0.7
Non-derivatized - MS/MS non-kit	250	83.9	6.4	13.4	76.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	96.9	5.9	14.1	86.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	99.5	5.1	11.1	90.0	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	94.3	5.3	7.9	85.7	0.9

Lot B1915 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	168.4	23.2	44.4	88.6	0.9
Derivatized - MS/MS non-kit	529	165.1	15.3	37.6	91.9	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	160.5	10.7	18.9	83.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	151.4	12.7	12.7	71.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	186.1	18.7	28.2	89.9	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	144.3	8.5	20.8	77.8	0.7
Non-derivatized - MS/MS non-kit	250	154.8	11.0	28.7	76.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	175.9	11.5	23.6	86.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	175.4	10.4	17.8	90.0	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	172.2	9.4	14.0	85.7	0.9

VALINE (Val µmol/L blood) (cont.)

Lot C1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	338.9	34.5	76.9	88.6	0.9
Derivatized - MS/MS non-kit	529	315.0	25.7	63.9	91.9	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	301.2	15.5	40.4	83.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	311.1	26.8	31.7	71.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	375.9	30.7	51.4	89.9	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	277.8	13.4	36.3	77.8	0.7
Non-derivatized - MS/MS non-kit	250	310.1	23.6	61.5	76.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	354.7	22.3	47.6	86.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	350.9	20.0	39.6	90.0	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	341.1	19.3	34.2	85.7	0.9

Lot D1915 – Enriched 500 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	70	520.1	43.4	99.5	88.6	0.9
Derivatized - MS/MS non-kit	529	488.8	35.2	92.2	91.9	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	502.5	33.5	83.1	83.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	502.4	32.2	66.6	71.6	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	594.4	52.8	104.8	89.9	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	426.0	19.9	60.1	77.8	0.7
Non-derivatized - MS/MS non-kit	250	494.7	33.7	95.9	76.2	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	568.6	33.5	73.0	86.7	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	554.3	24.4	41.2	90.0	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	544.8	29.6	63.6	85.7	0.9

2020 Quality Control Data Summaries of Statistical Analyses

TOTAL GALACTOSE (TGal mg/dL blood)

Lot A1905 – Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific 50 Hour Reagent Kit	30	6.1	0.5	0.8	1.4	1.0
Bio-Rad Quantase	50	7.0	1.1	1.3	-0.9	1.6
Colorimetric	59	8.0	3.1	5.4	0.7	1.4
Fluorometric manual (e.g. Hill or Misuma)	129	5.5	1.0	1.9	0.5	1.0
Interscientific Enzyme	30	4.4	0.4	0.5	0.1	0.8
Labsystems - FEIA	49	6.7	1.1	1.8	0.9	1.2
PerkinElmer GSP Neonatal	319	5.9	0.6	1.2	1.0	1.0
PerkinElmer Neonatal Kit	249	4.8	0.5	0.7	0.7	0.8
Siemens Healthcare Diagnostics	30	5.6	0.3	0.5	2.2	0.8
Zentech	60	5.9	0.7	1.0	2.5	0.8

Lot B1905 – Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific 50 Hour Reagent Kit	30	11.5	0.7	1.0	1.4	1.0
Bio-Rad Quantase	50	15.5	1.4	2.7	-0.9	1.6
Colorimetric	59	14.4	2.1	5.9	0.7	1.4
Fluorometric manual (e.g. Hill or Misuma)	130	10.5	1.0	1.6	0.5	1.0
Interscientific Enzyme	30	8.4	0.5	0.9	0.1	0.8
Labsystems - FEIA	50	12.7	1.7	3.0	0.9	1.2
PerkinElmer GSP Neonatal	320	10.9	0.9	1.7	1.0	1.0
PerkinElmer Neonatal Kit	250	8.8	0.8	1.2	0.7	0.8
Siemens Healthcare Diagnostics	30	11.5	0.5	0.9	2.2	0.8
Zentech	60	11.0	1.0	1.4	2.5	0.8

Lot C1905 – Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Astoria-Pacific 50 Hour Reagent Kit	30	31.0	2.4	3.9	1.4	1.0
Bio-Rad Quantase	50	47.3	4.1	9.8	-0.9	1.6
Colorimetric	59	43.0	4.6	16.8	0.7	1.4
Fluorometric manual (e.g. Hill or Misuma)	130	30.4	2.2	4.4	0.5	1.0
Interscientific Enzyme	30	25.2	1.7	2.3	0.1	0.8
Labsystems - FEIA	50	36.1	4.0	8.7	0.9	1.2
Other (Specify name and source)	90	35.1	1.9	7.9	-0.1	1.2
PerkinElmer GSP Neonatal	320	30.3	2.7	4.8	1.0	1.0
PerkinElmer Neonatal Kit	250	25.2	2.3	2.9	0.7	0.8
Siemens Healthcare Diagnostics	30	27.0	1.6	5.2	2.2	0.8
Zentech	60	25.8	2.4	4.9	2.5	0.8

2020 Quality Control Data Summaries of Statistical Analyses

FREE CARNITINE (C0 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	12.53	1.10	2.19	12.19	1.1
Derivatized - MS/MS non-kit	609	16.42	1.44	3.06	15.95	1.4
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	19.35	1.17	1.39	17.99	1.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	17.24	1.59	3.29	17.63	1.4
Non-Derivatized - Labsystems Neomass AAAC Plus	40	15.98	2.14	3.45	15.64	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	13.64	1.02	2.22	13.61	0.9
Non-derivatized - MS/MS non-kit	250	15.47	1.36	3.23	15.21	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	14.36	0.91	1.82	14.30	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	16.90	0.86	2.36	16.52	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	14.61	1.03	1.60	14.54	1.0

Lot B1915 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	22.85	1.66	4.66	12.19	1.1
Derivatized - MS/MS non-kit	609	29.72	2.39	5.75	15.95	1.4
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	35.50	1.74	2.57	17.99	1.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	32.82	3.17	4.61	17.63	1.4
Non-Derivatized - Labsystems Neomass AAAC Plus	40	27.98	3.89	5.82	15.64	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	23.25	1.57	4.37	13.61	0.9
Non-derivatized - MS/MS non-kit	250	26.62	2.30	5.68	15.21	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	25.01	1.61	3.15	14.30	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	28.40	1.65	4.29	16.52	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	25.24	1.70	2.70	14.54	1.0

FREE CARNITINE (C0 µmol/L blood) (cont.)

Lot C1915 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	32.56	2.77	6.36	12.19	1.1
Derivatized - MS/MS non-kit	609	42.37	3.66	8.67	15.95	1.4
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	51.81	3.14	3.76	17.99	1.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	45.42	4.84	7.82	17.63	1.4
Non-Derivatized - Labsystems Neomass AAAC Plus	40	37.32	5.03	8.77	15.64	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	31.93	1.98	5.77	13.61	0.9
Non-derivatized - MS/MS non-kit	250	36.79	2.87	8.16	15.21	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	34.31	2.11	4.23	14.30	1.0

Lot D1915 – Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	44.88	3.42	10.37	12.19	1.1
Derivatized - MS/MS non-kit	608	58.33	4.88	12.66	15.95	1.4
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	74.68	4.47	5.11	17.99	1.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	60.51	4.24	6.49	17.63	1.4
Non-Derivatized - Labsystems Neomass AAAC Plus	40	52.33	8.31	11.35	15.64	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	42.12	2.97	7.03	13.61	0.9
Non-derivatized - MS/MS non-kit	250	49.71	3.63	10.86	15.21	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	45.96	2.67	5.52	14.30	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	52.86	2.75	7.60	16.52	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	46.09	2.85	4.74	14.54	1.0

2020 Quality Control Data Summaries of Statistical Analyses

ACETYLCARNITINE (C2 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	8.70	0.67	1.75	8.38	0.8
Derivatized - MS/MS non-kit	569	12.02	1.20	4.56	11.61	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	12.80	0.75	2.18	12.13	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	9.41	0.46	0.59	9.25	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	9.73	0.87	1.54	9.44	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	7.48	0.46	0.75	7.37	0.8
Non-derivatized - MS/MS non-kit	240	9.34	0.72	2.51	9.04	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	7.95	0.48	0.85	7.84	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	9.82	0.53	0.78	9.51	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	279	7.50	0.46	0.71	7.37	0.8

Lot B1915 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	16.42	1.09	2.50	8.38	0.8
Derivatized - MS/MS non-kit	569	20.52	1.66	5.85	11.61	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	18.11	0.65	2.43	12.13	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	18.10	1.35	1.73	9.25	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	19.65	2.16	3.32	9.44	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	15.01	0.73	1.91	7.37	0.8
Non-derivatized - MS/MS non-kit	240	18.90	1.47	4.59	9.04	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	16.53	1.00	1.59	7.84	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	19.55	1.04	1.33	9.51	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	279	15.60	0.92	1.50	7.37	0.8

Lot C1915 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	24.13	1.51	3.54	8.38	0.8
Derivatized - MS/MS non-kit	569	29.31	2.51	8.03	11.61	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	24.13	1.05	3.13	12.13	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	27.11	2.14	2.17	9.25	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	29.13	3.44	6.00	9.44	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	22.46	1.23	2.58	7.37	0.8
Non-derivatized - MS/MS non-kit	240	28.26	2.25	6.79	9.04	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	24.65	1.46	2.35	7.84	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	29.32	1.47	2.10	9.51	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	279	23.00	1.30	2.45	7.37	0.8

ACETYLCARNITINE (C2 µmol/L blood) (cont.)

Lot D1915 – Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	33.44	1.91	3.93	8.38	0.8
Derivatized - MS/MS non-kit	569	39.74	3.07	11.85	11.61	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	32.41	1.72	4.32	12.13	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	36.46	1.96	3.52	9.25	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	40.72	4.48	7.68	9.44	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	30.58	1.59	3.01	7.37	0.8
Non-derivatized - MS/MS non-kit	240	39.45	3.27	10.23	9.04	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	33.99	1.92	3.44	7.84	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	40.56	1.65	3.20	9.51	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	279	32.14	1.78	3.64	7.37	0.8

2020 Quality Control Data Summaries of Statistical Analyses

PROPIONYLCARNITINE (C3 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.76	0.07	0.13	0.76	0.7
Derivatized - MS/MS non-kit	599	0.93	0.11	0.25	0.91	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.76	0.04	0.04	0.69	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.68	0.08	0.14	0.68	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.93	0.10	0.19	0.91	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.73	0.06	0.08	0.75	0.7
Non-derivatized - MS/MS non-kit	250	0.93	0.11	0.21	0.88	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	0.77	0.06	0.10	0.76	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.87	0.05	0.08	0.83	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	1.25	0.08	1.98	1.12	0.9

Lot B1915 – Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	3.73	0.29	0.65	0.76	0.7
Derivatized - MS/MS non-kit	598	4.37	0.39	0.96	0.91	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	3.77	0.15	0.20	0.69	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	3.59	0.35	0.58	0.68	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	4.76	0.46	0.81	0.91	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	3.57	0.22	0.52	0.75	0.7
Non-derivatized - MS/MS non-kit	250	4.45	0.48	0.93	0.88	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	3.82	0.23	0.39	0.76	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.21	0.22	0.31	0.83	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	4.42	0.28	0.82	1.12	0.9

Lot C1915 – Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	6.67	0.47	1.26	0.76	0.7
Derivatized - MS/MS non-kit	599	7.72	0.71	1.75	0.91	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	6.56	0.31	0.43	0.69	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete	30	6.54	0.57	0.80	0.68	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	8.60	0.86	1.64	0.91	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	6.33	0.40	0.92	0.75	0.7
Non-derivatized - MS/MS non-kit	250	8.02	0.80	1.62	0.88	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	6.89	0.40	0.68	0.76	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo)	50	7.64	0.46	0.63	0.83	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	7.90	0.47	1.06	1.12	0.9

2020 Quality Control Data Summaries of Statistical Analyses

PROPIONYLCARNITINE (C3 µmol/L blood) (cont.)

Lot D1915 – Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	9.69	0.67	1.51	0.76	0.7
Derivatized - MS/MS non-kit	599	11.30	1.06	2.75	0.91	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	10.02	0.48	0.77	0.69	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	9.44	0.54	1.37	0.68	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	12.53	1.66	2.72	0.91	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	9.11	0.79	1.52	0.75	0.7
Non-derivatized - MS/MS non-kit	250	11.78	1.11	2.42	0.88	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	709	10.00	0.55	1.03	0.76	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	11.13	0.39	0.91	0.83	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	11.59	0.71	1.49	1.12	0.9

2020 Quality Control Data Summaries of Statistical Analyses

MALONYLCARNITINE (C3DC µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	534	0.10	0.03	0.08	0.01	0.6
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.16	0.01	0.02	-0.07	1.5
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.12	0.02	0.05	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.07	0.01	0.03	-0.03	0.6

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	0.33	0.04	0.14	0.01	0.6
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.69	0.04	0.08	-0.07	1.5
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.45	0.05	0.14	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.26	0.07	0.12	-0.03	0.6

Lot C1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	0.91	0.11	0.39	0.01	0.6
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.91	0.11	0.21	-0.07	1.5
Derivatized - MS/MS Chromsystems MassChrom Kit	100	1.25	0.12	0.41	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.78	0.09	0.30	-0.03	0.6

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	540	1.94	0.21	0.80	0.01	0.6
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	4.42	0.22	0.67	-0.07	1.5
Derivatized - MS/MS Chromsystems MassChrom Kit	100	2.73	0.23	0.85	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.79	0.16	0.81	-0.03	0.6

2020 Quality Control Data Summaries of Statistical Analyses

MALONYLCARNITINE + HYDROXYBUTYRYLCARNITINE (C3DC+C4OH µmol/L blood)

Lot A1915 – Non-enriched 0.2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.06	0.01	0.01	0.02	0.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.11	0.02	0.03	0.03	0.3
Non-derivatized - MS/MS non-kit	120	0.21	0.03	0.13	0.08	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	0.15	0.01	0.07	0.05	0.4
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.14	0.01	0.03	0.06	0.4

Lot B1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.20	0.02	0.02	0.02	0.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.32	0.03	0.05	0.03	0.3
Non-derivatized - MS/MS non-kit	120	0.64	0.08	0.38	0.08	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	0.47	0.03	0.20	0.05	0.4
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.47	0.04	0.09	0.06	0.4

Lot C1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.39	0.04	0.06	0.02	0.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	0.65	0.06	0.10	0.03	0.3
Non-derivatized - MS/MS non-kit	120	1.25	0.14	0.77	0.08	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	0.96	0.07	0.41	0.05	0.4
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.94	0.07	0.19	0.06	0.4

Lot D1915 – Enriched 5.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.94	0.06	0.10	0.02	0.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	50	1.56	0.08	0.20	0.03	0.3
Non-derivatized - MS/MS non-kit	120	2.97	0.29	1.70	0.08	0.5
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	2.23	0.14	0.94	0.05	0.4
Non-derivatized - MS/MS PerkinElmer NeoBase 2	259	2.16	0.17	0.46	0.06	0.4

2020 Quality Control Data Summaries of Statistical Analyses

BUTYRYLCARNITINE (C4 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	84	0.08	0.02	0.03	0.06	0.7
Derivatized - MS/MS non-kit	589	0.14	0.03	0.10	0.11	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.13	0.05	0.08	0.05	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.03	0.05	0.05	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.09	0.02	0.02	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.08	0.01	0.02	0.08	0.7
Non-derivatized - MS/MS non-kit	220	0.13	0.04	0.11	0.09	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	0.11	0.02	0.04	0.08	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.09	0.01	0.01	0.08	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.08	0.01	0.01	0.06	0.7

Lot B1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.71	0.07	0.11	0.06	0.7
Derivatized - MS/MS non-kit	589	0.90	0.11	0.19	0.11	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.82	0.07	0.07	0.05	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.75	0.07	0.13	0.05	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.82	0.09	0.16	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.75	0.05	0.13	0.08	0.7
Non-derivatized - MS/MS non-kit	220	0.91	0.09	0.20	0.09	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	0.84	0.05	0.11	0.08	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.84	0.04	0.07	0.08	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.78	0.04	0.07	0.06	0.7

2020 Quality Control Data Summaries of Statistical Analyses

BUTYRYLCARNITINE (C4 µmol/L blood) (cont.)

Lot C1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.00	0.17	0.35	0.06	0.7
Derivatized - MS/MS non-kit	589	2.39	0.24	0.44	0.11	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.06	0.16	0.18	0.05	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.17	0.20	0.24	0.05	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.23	0.20	0.46	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.12	0.14	0.30	0.08	0.7
Non-derivatized - MS/MS non-kit	220	2.51	0.24	0.64	0.09	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	2.33	0.14	0.29	0.08	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.44	0.15	0.21	0.08	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	2.16	0.13	0.23	0.06	0.7

Lot D1915 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	3.36	0.25	0.54	0.06	0.7
Derivatized - MS/MS non-kit	589	4.04	0.39	0.76	0.11	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	3.92	0.31	0.40	0.05	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	3.72	0.27	0.48	0.05	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	3.87	0.37	0.63	0.06	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	3.50	0.21	0.43	0.08	0.7
Non-derivatized - MS/MS non-kit	220	4.30	0.40	1.07	0.09	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	710	3.95	0.22	0.44	0.08	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.02	0.18	0.33	0.08	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	3.67	0.21	0.32	0.06	0.7

2020 Quality Control Data Summaries of Statistical Analyses

HYDROXYBUTYRYLCARNITINE (C4OH µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.13	0.02	0.04	0.06	0.7
Derivatized - MS/MS non-kit	480	0.16	0.05	0.11	0.08	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.17	0.02	0.03	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.10	0.02	0.02	0.04	0.6

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.38	0.05	0.11	0.06	0.7
Derivatized - MS/MS non-kit	480	0.43	0.06	0.15	0.08	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.47	0.05	0.06	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.33	0.04	0.05	0.04	0.6

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.73	0.09	0.20	0.06	0.7
Derivatized - MS/MS non-kit	480	0.81	0.10	0.29	0.08	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.86	0.09	0.10	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.62	0.07	0.08	0.04	0.6

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.71	0.19	0.48	0.06	0.7
Derivatized - MS/MS non-kit	479	1.88	0.22	0.66	0.08	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.29	0.24	0.30	0.03	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.48	0.12	0.23	0.04	0.6

2020 Quality Control Data Summaries of Statistical Analyses

ISOVALERYLCARNITINE (C5 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.18	0.03	0.05	0.06	1.0
Derivatized - MS/MS non-kit	599	0.17	0.03	0.06	0.07	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.16	0.02	0.02	0.04	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.14	0.02	0.03	0.05	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.19	0.03	0.07	0.10	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.15	0.02	0.03	0.06	0.9
Non-derivatized - MS/MS non-kit	260	0.17	0.03	0.06	0.09	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.14	0.01	0.02	0.05	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.17	0.01	0.01	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.14	0.01	0.02	0.04	0.8

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.52	0.07	0.12	0.06	1.0
Derivatized - MS/MS non-kit	599	0.51	0.06	0.11	0.07	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.52	0.05	0.05	0.04	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.46	0.04	0.05	0.05	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.57	0.08	0.14	0.10	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.49	0.04	0.12	0.06	0.9
Non-derivatized - MS/MS non-kit	260	0.58	0.06	0.17	0.09	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.48	0.03	0.05	0.05	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.52	0.03	0.04	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.46	0.03	0.06	0.04	0.8

2020 Quality Control Data Summaries of Statistical Analyses

ISOVALERYLCARNITINE (C5 µmol/L blood) (cont.)

Lot C1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.50	0.15	0.28	0.06	1.0
Derivatized - MS/MS non-kit	599	1.39	0.14	0.27	0.07	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.36	0.10	0.11	0.04	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.26	0.12	0.14	0.05	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.54	0.18	0.34	0.10	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.38	0.11	0.31	0.06	0.9
Non-derivatized - MS/MS non-kit	260	1.60	0.12	0.45	0.09	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	1.34	0.09	0.14	0.05	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.48	0.07	0.12	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	1.26	0.08	0.15	0.04	0.8

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.97	0.25	0.55	0.06	1.0
Derivatized - MS/MS non-kit	599	2.75	0.26	0.50	0.07	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.85	0.20	0.31	0.04	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.52	0.22	0.29	0.05	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.95	0.40	0.68	0.10	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.69	0.20	0.56	0.06	0.9
Non-derivatized - MS/MS non-kit	260	3.06	0.21	0.62	0.09	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	2.65	0.15	0.24	0.05	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.94	0.12	0.20	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	2.53	0.16	0.28	0.04	0.8

2020 Quality Control Data Summaries of Statistical Analyses

TIGLYLCARNITINE (C5:1 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	89	0.12	0.02	0.03	0.01	0.8
Derivatized - MS/MS non-kit	540	0.15	0.10	0.56	0.04	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.02	0.02	-0.01	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.16	0.04	0.13	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.09	0.02	0.04	-0.01	0.7
Non-derivatized - MS/MS non-kit	180	0.26	0.04	0.31	-0.01	1.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	0.09	0.02	0.06	0.01	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	250	0.10	0.02	0.06	0.01	0.7

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.43	0.06	0.12	0.01	0.8
Derivatized - MS/MS non-kit	540	0.44	0.05	0.13	0.04	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.35	0.04	0.06	-0.01	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.43	0.06	0.23	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.32	0.05	0.11	-0.01	0.7
Non-derivatized - MS/MS non-kit	180	0.92	0.09	1.08	-0.01	1.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	0.35	0.03	0.06	0.01	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	250	0.37	0.03	0.07	0.01	0.7

Lot C1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.26	0.14	0.38	0.01	0.8
Derivatized - MS/MS non-kit	540	1.29	0.12	0.38	0.04	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.08	0.11	0.17	-0.01	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	1.17	0.13	0.55	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.94	0.11	0.34	-0.01	0.7
Non-derivatized - MS/MS non-kit	180	2.76	0.20	3.20	-0.01	1.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	1.04	0.07	0.18	0.01	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	250	1.09	0.09	0.19	0.01	0.7

TIGLYLCARNITINE (C5:1 µmol/L blood) (cont.)

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.56	0.22	0.69	0.01	0.8
Derivatized - MS/MS non-kit	540	2.56	0.23	0.74	0.04	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.22	0.22	0.24	-0.01	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	2.25	0.26	0.99	0.08	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.99	0.15	0.42	-0.01	0.7
Non-derivatized - MS/MS non-kit	180	5.78	0.43	7.06	-0.01	1.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	600	2.10	0.13	0.31	0.01	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	250	2.22	0.15	0.33	0.01	0.7

2020 Quality Control Data Summaries of Statistical Analyses

GLUTARYLCARNITINE (C5DC µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.18	0.04	0.05	0.03	1.4
Derivatized - MS/MS non-kit	599	0.10	0.02	0.05	0.03	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.15	0.01	0.01	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.15	0.02	0.02	0.05	1.2
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.11	0.06	0.11	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.21	0.04	0.06	0.08	1.3
Non-derivatized - MS/MS non-kit	220	0.16	0.04	0.09	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	640	0.16	0.02	0.03	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.15	0.01	0.02	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.12	0.01	0.03	0.04	0.9

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.71	0.08	0.12	0.03	1.4
Derivatized - MS/MS non-kit	599	0.37	0.05	0.17	0.03	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.57	0.03	0.03	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.66	0.07	0.09	0.05	1.2
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.51	0.11	0.18	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.74	0.11	0.18	0.08	1.3
Non-derivatized - MS/MS non-kit	220	0.54	0.06	0.20	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	640	0.58	0.05	0.08	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.50	0.03	0.04	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.48	0.04	0.08	0.04	0.9

2020 Quality Control Data Summaries of Statistical Analyses

GLUTARYLCARNITINE (C5DC µmol/L blood) (cont.)

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.41	0.18	0.26	0.03	1.4
Derivatized - MS/MS non-kit	599	0.72	0.08	0.33	0.03	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.11	0.06	0.06	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.23	0.11	0.20	0.05	1.2
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.03	0.15	0.31	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.43	0.14	0.30	0.08	1.3
Non-derivatized - MS/MS non-kit	220	1.03	0.09	0.35	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	640	1.12	0.08	0.14	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.96	0.05	0.09	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	260	0.93	0.07	0.15	0.04	0.9

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	3.50	0.31	0.55	0.03	1.4
Derivatized - MS/MS non-kit	599	1.75	0.19	0.82	0.03	0.7
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.87	0.13	0.26	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	3.01	0.28	0.73	0.05	1.2
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.59	0.39	0.90	0.00	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	3.42	0.25	0.61	0.08	1.3
Non-derivatized - MS/MS non-kit	220	2.50	0.23	0.89	0.05	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	640	2.72	0.18	0.34	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.30	0.08	0.16	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	259	2.26	0.16	0.34	0.04	0.9

2020 Quality Control Data Summaries of Statistical Analyses

HYDROXYISOVALERYLCARNITINE (C5OH µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.40	0.05	0.11	0.39	0.8
Derivatized - MS/MS non-kit	580	0.39	0.05	0.10	0.37	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.39	0.05	0.05	0.36	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.25	0.03	0.04	0.23	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	0.39	0.04	0.06	0.38	0.5
Non-derivatized - MS/MS non-kit	200	0.60	0.04	0.13	0.59	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	570	0.45	0.04	0.10	0.45	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.64	0.04	0.05	0.61	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	240	0.57	0.04	0.10	0.58	0.6

Lot B1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	100	1.13	0.12	0.30	0.39	0.8
Derivatized - MS/MS non-kit	580	1.10	0.13	0.25	0.37	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.18	0.10	0.11	0.36	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.76	0.09	0.11	0.23	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	0.88	0.12	0.21	0.38	0.5
Non-derivatized - MS/MS non-kit	200	1.38	0.10	0.30	0.59	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	570	1.01	0.07	0.20	0.45	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.49	0.08	0.13	0.61	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	240	1.20	0.08	0.19	0.58	0.6

Lot C1915 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	100	1.89	0.20	0.53	0.39	0.8
Derivatized - MS/MS non-kit	580	1.84	0.19	0.40	0.37	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.95	0.13	0.15	0.36	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.31	0.16	0.23	0.23	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	1.42	0.14	0.35	0.38	0.5
Non-derivatized - MS/MS non-kit	200	2.16	0.17	0.53	0.59	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	570	1.57	0.12	0.28	0.45	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.40	0.14	0.24	0.61	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	240	1.82	0.12	0.26	0.58	0.6

HYDROXYISOVALERYLCARNITINE (C5OH µmol/L blood) (cont.)

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	100	2.65	0.22	0.71	0.39	0.8
Derivatized - MS/MS non-kit	580	2.63	0.26	0.56	0.37	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.90	0.20	0.27	0.36	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.87	0.14	0.35	0.23	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	60	1.92	0.16	0.29	0.38	0.5
Non-derivatized - MS/MS non-kit	200	2.99	0.22	0.72	0.59	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	570	2.15	0.13	0.36	0.45	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	3.35	0.14	0.22	0.61	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	240	2.44	0.17	0.33	0.58	0.6

2020 Quality Control Data Summaries of Statistical Analyses

HEXANOYLCARNITINE (C6 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	83	0.12	0.05	0.11	0.08	0.6
Derivatized - MS/MS non-kit	594	0.12	0.03	0.11	0.03	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.10	0.01	0.01	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.01	0.02	0.04	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.10	0.01	0.02	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.09	0.01	0.02	0.03	0.7
Non-derivatized - MS/MS non-kit	230	0.12	0.02	0.05	0.02	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.10	0.02	0.05	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.10	0.01	0.01	0.02	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.09	0.01	0.01	0.03	0.7

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.39	0.05	0.07	0.08	0.6
Derivatized - MS/MS non-kit	599	0.42	0.05	0.11	0.03	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.42	0.04	0.04	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.37	0.03	0.04	0.04	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.43	0.04	0.06	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.40	0.03	0.06	0.03	0.7
Non-derivatized - MS/MS non-kit	230	0.47	0.05	0.11	0.02	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.43	0.03	0.05	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.42	0.02	0.04	0.02	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.41	0.02	0.04	0.03	0.7

2020 Quality Control Data Summaries of Statistical Analyses

HEXANOYLCARNITINE (C6 µmol/L blood) (cont.)

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.70	0.08	0.16	0.08	0.6
Derivatized - MS/MS non-kit	599	0.80	0.08	0.19	0.03	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.69	0.04	0.05	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.68	0.08	0.08	0.04	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.81	0.07	0.09	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.79	0.06	0.12	0.03	0.7
Non-derivatized - MS/MS non-kit	230	0.92	0.08	0.22	0.02	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.85	0.05	0.09	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.84	0.04	0.08	0.02	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.78	0.04	0.08	0.03	0.7

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.56	0.11	0.29	0.08	0.6
Derivatized - MS/MS non-kit	599	1.98	0.20	0.45	0.03	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.73	0.13	0.20	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.63	0.12	0.14	0.04	0.6
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.96	0.19	0.24	0.03	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.86	0.11	0.21	0.03	0.7
Non-derivatized - MS/MS non-kit	230	2.30	0.19	0.57	0.02	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	2.05	0.10	0.19	0.03	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.05	0.08	0.15	0.02	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	1.87	0.09	0.20	0.03	0.7

2020 Quality Control Data Summaries of Statistical Analyses

OCTANOYLCARNITINE (C8 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.11	0.02	0.02	0.03	0.8
Derivatized - MS/MS non-kit	609	0.14	0.03	0.06	0.05	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.13	0.01	0.02	0.00	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.10	0.01	0.02	0.01	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.15	0.02	0.03	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.12	0.01	0.02	0.03	0.8
Non-derivatized - MS/MS non-kit	260	0.17	0.02	0.09	0.04	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.13	0.01	0.02	0.02	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.13	0.01	0.01	0.02	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.12	0.01	0.01	0.02	0.9

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.44	0.05	0.07	0.03	0.8
Derivatized - MS/MS non-kit	609	0.55	0.06	0.12	0.05	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.53	0.04	0.05	0.00	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.42	0.05	0.07	0.01	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.59	0.08	0.10	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.44	0.03	0.08	0.03	0.8
Non-derivatized - MS/MS non-kit	250	0.59	0.05	0.29	0.04	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.51	0.03	0.05	0.02	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.51	0.03	0.03	0.02	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.46	0.03	0.04	0.02	0.9

OCTANOYLCARNITINE (C8 µmol/L blood) (cont.)

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.83	0.08	0.12	0.03	0.8
Derivatized - MS/MS non-kit	609	1.01	0.11	0.23	0.05	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.95	0.08	0.10	0.00	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.83	0.09	0.12	0.01	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.06	0.09	0.19	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.80	0.05	0.15	0.03	0.8
Non-derivatized - MS/MS non-kit	250	1.12	0.09	0.58	0.04	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.95	0.06	0.10	0.02	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.96	0.06	0.08	0.02	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.85	0.06	0.09	0.02	0.9

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.04	0.17	0.26	0.03	0.8
Derivatized - MS/MS non-kit	609	2.51	0.25	0.55	0.05	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.59	0.21	0.35	0.00	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.06	0.18	0.26	0.01	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.75	0.36	0.52	0.03	1.1
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.03	0.13	0.36	0.03	0.8
Non-derivatized - MS/MS non-kit	250	2.82	0.22	1.42	0.04	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	2.41	0.14	0.23	0.02	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.44	0.11	0.13	0.02	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	2.18	0.13	0.20	0.02	0.9

2020 Quality Control Data Summaries of Statistical Analyses

DECANOYLCARNITINE (C10 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	80	0.08	0.03	0.05	0.01	0.6
Derivatized - MS/MS non-kit	609	0.15	0.03	0.07	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.12	0.02	0.02	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.01	0.02	0.00	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.13	0.01	0.02	0.01	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.13	0.02	0.03	0.02	0.9
Non-derivatized - MS/MS non-kit	240	0.28	0.36	1.67	0.08	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.13	0.01	0.02	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.13	0.01	0.01	0.00	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.13	0.01	0.02	0.01	0.9

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.30	0.03	0.09	0.01	0.6
Derivatized - MS/MS non-kit	609	0.53	0.06	0.14	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.45	0.03	0.04	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.35	0.05	0.06	0.00	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.49	0.06	0.10	0.01	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.45	0.03	0.08	0.02	0.9
Non-derivatized - MS/MS non-kit	240	0.59	0.06	0.16	0.08	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.47	0.03	0.05	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.46	0.02	0.03	0.00	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.46	0.03	0.05	0.01	0.9

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.57	0.06	0.14	0.01	0.6
Derivatized - MS/MS non-kit	609	1.00	0.11	0.26	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.83	0.07	0.08	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.69	0.08	0.09	0.00	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.91	0.07	0.16	0.01	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.82	0.05	0.14	0.02	0.9
Non-derivatized - MS/MS non-kit	240	1.09	0.11	0.30	0.08	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	0.88	0.06	0.09	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.89	0.05	0.07	0.00	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	300	0.87	0.05	0.10	0.01	0.9

2020 Quality Control Data Summaries of Statistical Analyses

DECANOYLCARNITINE (C10 µmol/L blood) (cont.)

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	89	1.45	0.11	0.35	0.01	0.6
Derivatized - MS/MS non-kit	609	2.61	0.27	0.66	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.29	0.14	0.23	-0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.78	0.13	0.16	0.00	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.40	0.29	0.45	0.01	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.16	0.14	0.33	0.02	0.9
Non-derivatized - MS/MS non-kit	240	2.85	0.24	0.73	0.08	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	730	2.31	0.15	0.23	0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.36	0.10	0.13	0.00	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	299	2.26	0.14	0.23	0.01	0.9

2020 Quality Control Data Summaries of Statistical Analyses

DODECANOYLCARNITINE (C12 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.12	0.02	0.03	0.02	0.9
Derivatized - MS/MS non-kit	579	0.15	0.04	0.08	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.14	0.02	0.02	-0.04	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.11	0.02	0.03	0.02	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.12	0.02	0.03	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.11	0.01	0.01	0.00	0.9
Non-derivatized - MS/MS non-kit	210	0.16	0.02	0.07	0.00	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	700	0.13	0.03	0.13	0.00	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.13	0.01	0.01	-0.01	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	0.11	0.01	0.01	0.00	0.9

Lot B1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.85	0.08	0.15	0.02	0.9
Derivatized - MS/MS non-kit	579	1.03	0.15	0.37	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.03	0.10	0.11	-0.04	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.82	0.09	0.10	0.02	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.91	0.12	0.15	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.86	0.05	0.11	0.00	0.9
Non-derivatized - MS/MS non-kit	210	1.15	0.11	0.52	0.00	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	700	0.97	0.07	0.10	0.00	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.03	0.06	0.08	-0.01	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	0.87	0.06	0.08	0.00	0.9

Lot C1915 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.70	0.16	0.30	0.02	0.9
Derivatized - MS/MS non-kit	579	2.00	0.28	0.63	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	2.13	0.20	0.22	-0.04	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.60	0.15	0.16	0.02	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.73	0.16	0.19	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.71	0.11	0.20	0.00	0.9
Non-derivatized - MS/MS non-kit	210	2.28	0.20	1.14	0.00	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	700	1.93	0.12	0.19	0.00	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.04	0.13	0.17	-0.01	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	1.71	0.11	0.17	0.00	0.9

DODECANOYLCARNITINE (C12 µmol/L blood) (cont.)

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.59	0.25	0.45	0.02	0.9
Derivatized - MS/MS non-kit	579	3.13	0.43	1.16	0.02	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	3.43	0.34	0.45	-0.04	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.45	0.19	0.27	0.02	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.68	0.28	0.34	0.03	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.65	0.16	0.33	0.00	0.9
Non-derivatized - MS/MS non-kit	210	3.59	0.30	1.73	0.00	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	700	2.98	0.16	0.26	0.00	1.0
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	3.19	0.15	0.23	-0.01	1.1
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	2.64	0.15	0.23	0.00	0.9

2020 Quality Control Data Summaries of Statistical Analyses

MYRISTOYLCARNITINE (C14 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.13	0.02	0.02	0.05	0.7
Derivatized - MS/MS non-kit	599	0.17	0.04	0.09	0.06	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.16	0.02	0.02	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.11	0.02	0.02	0.04	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.13	0.02	0.03	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.13	0.01	0.02	0.04	0.8
Non-derivatized - MS/MS non-kit	230	0.17	0.02	0.06	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.14	0.01	0.02	0.04	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.15	0.01	0.01	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.14	0.04	0.15	0.04	0.8

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.42	0.04	0.07	0.05	0.7
Derivatized - MS/MS non-kit	599	0.54	0.06	0.14	0.06	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.51	0.03	0.04	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.38	0.04	0.06	0.04	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.46	0.06	0.07	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.44	0.03	0.07	0.04	0.8
Non-derivatized - MS/MS non-kit	230	0.53	0.05	0.10	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.48	0.03	0.05	0.04	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.49	0.03	0.03	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.46	0.03	0.05	0.04	0.8

Lot C1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.10	0.11	0.15	0.05	0.7
Derivatized - MS/MS non-kit	599	1.38	0.16	0.30	0.06	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.39	0.08	0.14	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.02	0.11	0.15	0.04	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.18	0.13	0.20	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.15	0.07	0.17	0.04	0.8
Non-derivatized - MS/MS non-kit	230	1.37	0.13	0.27	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	1.28	0.09	0.13	0.04	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.29	0.09	0.11	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	1.21	0.09	0.14	0.04	0.8

MYRISTOYLCARNITINE (C14 µmol/L blood) (cont.)

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	89	2.25	0.17	0.32	0.05	0.7
Derivatized - MS/MS non-kit	599	2.85	0.31	0.65	0.06	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	3.06	0.18	0.47	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.07	0.18	0.39	0.04	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	40	2.44	0.29	0.41	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.37	0.16	0.37	0.04	0.8
Non-derivatized - MS/MS non-kit	230	2.86	0.23	0.54	0.05	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	2.64	0.15	0.32	0.04	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.68	0.11	0.17	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	2.52	0.16	0.22	0.04	0.8

2020 Quality Control Data Summaries of Statistical Analyses

TETRADECENOYLCARNITINE (C14:1 µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	86	0.13	0.02	0.04	0.05	0.7
Derivatized - MS/MS non-kit	559	0.16	0.05	0.13	0.04	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.02	0.03	0.02	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.10	0.02	0.02	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.12	0.02	0.05	0.06	0.7
Non-derivatized - MS/MS non-kit	190	0.13	0.02	0.04	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	0.11	0.02	0.04	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.14	0.01	0.02	0.12	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	0.10	0.01	0.01	0.04	0.7

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.40	0.05	0.10	0.05	0.7
Derivatized - MS/MS non-kit	559	0.53	0.07	0.14	0.04	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.34	0.04	0.06	0.02	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	0.34	0.04	0.07	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.40	0.04	0.18	0.06	0.7
Non-derivatized - MS/MS non-kit	190	0.48	0.05	0.14	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	0.42	0.03	0.05	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	0.47	0.02	0.04	0.12	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	0.40	0.03	0.04	0.04	0.7

Lot C1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.16	0.12	0.28	0.05	0.7
Derivatized - MS/MS non-kit	559	1.52	0.18	0.35	0.04	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.07	0.11	0.13	0.02	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	1.01	0.11	0.17	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.17	0.14	0.57	0.06	0.7
Non-derivatized - MS/MS non-kit	190	1.42	0.14	0.46	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	1.23	0.08	0.15	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	1.32	0.08	0.13	0.12	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	1.16	0.08	0.13	0.04	0.7

2020 Quality Control Data Summaries of Statistical Analyses

TETRADECENOYLCARNITINE (C14:1 µmol/L blood) (cont.)

Lot D1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	2.23	0.21	0.48	0.05	0.7
Derivatized - MS/MS non-kit	559	3.05	0.35	0.85	0.04	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.06	0.20	0.24	0.02	0.7
Non-Derivatized - Labsystems Neomass AAAC Plus	30	1.96	0.17	0.24	0.03	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	69	2.17	0.29	0.92	0.06	0.7
Non-derivatized - MS/MS non-kit	190	2.74	0.26	0.88	0.04	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	610	2.37	0.17	0.36	0.04	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	30	2.24	0.07	0.20	0.12	0.7
Non-derivatized - MS/MS PerkinElmer NeoBase 2	270	2.25	0.15	0.22	0.04	0.7

2020 Quality Control Data Summaries of Statistical Analyses

PALMITOYLCARNITINE (C16 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.69	0.07	0.09	0.68	0.8
Derivatized - MS/MS non-kit	609	0.81	0.10	0.19	0.84	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.75	0.06	0.07	0.62	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.72	0.07	0.13	0.77	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.78	0.07	0.10	0.85	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.68	0.05	0.08	0.74	0.8
Non-derivatized - MS/MS non-kit	240	0.81	0.08	0.13	0.81	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.78	0.07	0.15	0.78	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.80	0.05	0.06	0.82	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.89	0.06	0.11	0.98	1.0

Lot B1915 – Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	3.82	0.42	0.61	0.68	0.8
Derivatized - MS/MS non-kit	609	4.32	0.36	0.74	0.84	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	4.11	0.21	0.26	0.62	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	4.15	0.36	0.75	0.77	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	4.55	0.47	0.71	0.85	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	79	3.85	0.22	0.40	0.74	0.8
Non-derivatized - MS/MS non-kit	240	4.42	0.35	0.62	0.81	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	4.26	0.29	0.52	0.78	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.39	0.25	0.27	0.82	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	5.06	0.34	0.60	0.98	1.0

Lot C1915 – Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	7.02	0.49	0.91	0.68	0.8
Derivatized - MS/MS non-kit	609	7.84	0.70	1.49	0.84	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	7.63	0.49	0.54	0.62	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	7.67	0.68	1.22	0.77	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	8.20	0.65	1.23	0.85	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	79	6.89	0.39	0.64	0.74	0.8
Non-derivatized - MS/MS non-kit	240	8.16	0.68	1.29	0.81	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	7.88	0.49	0.87	0.78	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	8.03	0.53	0.57	0.82	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	289	9.13	0.60	1.18	0.98	1.0

PALMITOYLCARNITINE (C16 µmol/L blood) (cont.)

Lot D1915 – Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	89	10.09	0.75	1.05	0.68	0.8
Derivatized - MS/MS non-kit	609	11.19	0.92	2.09	0.84	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	11.53	0.78	1.25	0.62	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	10.81	0.81	1.83	0.77	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	39	11.71	1.23	1.91	0.85	0.9
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	9.81	0.65	0.84	0.74	0.8
Non-derivatized - MS/MS non-kit	240	11.67	0.93	1.66	0.81	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	11.28	0.67	1.02	0.78	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	11.49	0.53	0.86	0.82	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	12.93	0.90	1.69	0.98	1.0

2020 Quality Control Data Summaries of Statistical Analyses

HYDROXYPALMITOYLCARNITINE (C16OH µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.11	0.02	0.04	0.01	0.9
Derivatized - MS/MS non-kit	599	0.12	0.02	0.05	0.01	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.11	0.02	0.02	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.01	0.02	0.00	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.08	0.01	0.02	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.08	0.01	0.02	0.01	0.7
Non-derivatized - MS/MS non-kit	210	0.15	0.15	0.61	0.10	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.10	0.01	0.06	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.10	0.01	0.01	0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.10	0.01	0.02	0.01	0.8

Lot B1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.24	0.04	0.07	0.01	0.9
Derivatized - MS/MS non-kit	599	0.26	0.04	0.08	0.01	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.23	0.02	0.03	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.20	0.03	0.04	0.00	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.20	0.02	0.05	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.18	0.02	0.04	0.01	0.7
Non-derivatized - MS/MS non-kit	210	0.39	0.48	2.05	0.10	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.21	0.02	0.05	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.21	0.01	0.02	0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.23	0.02	0.04	0.01	0.8

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.87	0.10	0.24	0.01	0.9
Derivatized - MS/MS non-kit	599	0.91	0.11	0.26	0.01	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.86	0.09	0.13	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.73	0.08	0.09	0.00	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.69	0.06	0.15	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.62	0.08	0.12	0.01	0.7
Non-derivatized - MS/MS non-kit	210	0.89	0.10	0.23	0.10	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	719	0.75	0.05	0.17	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.76	0.06	0.08	0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	289	0.79	0.05	0.12	0.01	0.8

Lot D1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.39	0.15	0.34	0.01	0.9
Derivatized - MS/MS non-kit	599	1.48	0.17	0.45	0.01	1.0
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.48	0.13	0.26	-0.02	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.17	0.10	0.13	0.00	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.12	0.13	0.26	0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.01	0.14	0.21	0.01	0.7
Non-derivatized - MS/MS non-kit	210	1.45	0.13	0.39	0.10	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	1.21	0.08	0.27	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.23	0.05	0.07	0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	1.27	0.09	0.21	0.01	0.8

2020 Quality Control Data Summaries of Statistical Analyses

STEAROYLCARNITINE (C18 µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.57	0.06	0.08	0.60	0.8
Derivatized - MS/MS non-kit	599	0.62	0.08	0.19	0.60	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.64	0.04	0.04	0.54	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.56	0.06	0.08	0.55	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	0.54	0.05	0.08	0.53	0.8
Non-derivatized - MS/MS non-kit	220	0.62	0.06	0.09	0.59	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	0.58	0.04	0.07	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.56	0.03	0.04	0.51	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.59	0.05	0.08	0.58	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	0.58	0.04	0.05	0.57	0.9

Lot B1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.41	0.13	0.19	0.60	0.8
Derivatized - MS/MS non-kit	599	1.46	0.15	0.33	0.60	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.54	0.09	0.10	0.54	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.38	0.12	0.13	0.55	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	1.38	0.10	0.23	0.53	0.8
Non-derivatized - MS/MS non-kit	220	1.54	0.14	0.22	0.59	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	1.47	0.09	0.14	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.37	0.09	0.11	0.51	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.53	0.15	0.28	0.58	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	1.50	0.10	0.15	0.57	0.9

Lot C1915 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	89	2.90	0.21	0.38	0.60	0.8
Derivatized - MS/MS non-kit	599	2.96	0.30	0.67	0.60	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	3.26	0.21	0.22	0.54	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	2.97	0.35	0.36	0.55	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	2.84	0.22	0.46	0.53	0.8
Non-derivatized - MS/MS non-kit	220	3.17	0.29	0.50	0.59	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	3.07	0.22	0.35	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.82	0.19	0.24	0.51	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	3.12	0.26	0.53	0.58	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	3.07	0.19	0.30	0.57	0.9

STEAROYLCARNITINE (C18 µmol/L blood) (cont.)

Lot D1915 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	4.74	0.35	0.56	0.60	0.8
Derivatized - MS/MS non-kit	599	4.82	0.49	1.07	0.60	0.8
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	5.68	0.48	0.73	0.54	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	4.69	0.51	0.63	0.55	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	80	4.61	0.32	0.68	0.53	0.8
Non-derivatized - MS/MS non-kit	220	5.20	0.42	0.75	0.59	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	720	5.02	0.29	0.44	0.55	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.74	0.24	0.33	0.51	0.8
Non-Derivatized - Labsystems Neomass AAAC Plus	40	5.09	0.58	0.94	0.58	0.9
Non-derivatized - MS/MS PerkinElmer NeoBase 2	290	5.02	0.33	0.46	0.57	0.9

2020 Quality Control Data Summaries of Statistical Analyses

HYDROXYSTEAROYLCARNITINE (C18OH µmol/L blood)

Lot A1915 – Non-enriched 0.1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.12	0.02	0.04	0.00	1.0
Derivatized - MS/MS non-kit	479	0.12	0.03	0.07	0.00	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.12	0.02	0.02	-0.03	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.09	0.02	0.04	-0.02	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.08	0.01	0.02	-0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.09	0.01	0.02	0.00	0.7
Non-derivatized - MS/MS non-kit	140	0.12	0.02	0.09	0.00	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	0.09	0.01	0.04	-0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	0.09	0.01	0.02	-0.01	0.8

Lot B1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.25	0.03	0.06	0.00	1.0
Derivatized - MS/MS non-kit	479	0.23	0.04	0.10	0.00	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.25	0.03	0.04	-0.03	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.20	0.03	0.05	-0.02	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.19	0.02	0.06	-0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.19	0.03	0.05	0.00	0.7
Non-derivatized - MS/MS non-kit	140	0.26	0.03	0.18	0.00	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	0.21	0.02	0.04	-0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	0.21	0.02	0.03	-0.01	0.8

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.87	0.08	0.21	0.00	1.0
Derivatized - MS/MS non-kit	479	0.76	0.10	0.34	0.00	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	0.89	0.07	0.14	-0.03	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	0.76	0.14	0.24	-0.02	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	0.65	0.06	0.20	-0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.67	0.12	0.20	0.00	0.7
Non-derivatized - MS/MS non-kit	140	0.92	0.10	0.65	0.00	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	0.73	0.05	0.16	-0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	0.71	0.05	0.09	-0.01	0.8

2020 Quality Control Data Summaries of Statistical Analyses

HYDROXYSTEAROYLCARNITINE (C18OH µmol/L blood) cont.

Lot D1915 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.53	0.14	0.33	0.00	1.0
Derivatized - MS/MS non-kit	479	1.37	0.17	0.65	0.00	0.9
Derivatized - MS/MS PerkinElmer NeoGram Kit	30	1.66	0.18	0.28	-0.03	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	1.34	0.24	0.36	-0.02	0.9
Non-Derivatized - Labsystems Neomass AAAC Plus	40	1.16	0.14	0.36	-0.01	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	69	1.12	0.11	0.23	0.00	0.7
Non-derivatized - MS/MS non-kit	140	1.59	0.18	1.15	0.00	1.0
Non-derivatized - MS/MS PerkinElmer NeoBase Kit	650	1.29	0.09	0.27	-0.01	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	280	1.24	0.09	0.16	-0.01	0.8

2020 Quality Control Data Summaries of Statistical Analyses

20:0-LYSOPHOSPHATIDYLCHOLINE (20LPC µmol/L blood)

Lot A1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	0.46	0.09	0.22	0.19	1.0

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	0.68	0.12	0.30	0.19	1.0

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	1.21	0.22	0.51	0.19	1.0

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	2.74	0.46	1.09	0.19	1.0

2020 Quality Control Data Summaries of Statistical Analyses

22:0-LYSOPHOSPHATIDYLCHOLINE (22LPC µmol/L blood)

Lot A1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	0.39	0.08	0.19	0.09	1.1

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	0.63	0.13	0.27	0.09	1.1

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	1.07	0.21	0.43	0.09	1.1

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS PerkinElmer NeoBase 2	120	2.74	0.45	0.98	0.09	1.1

2020 Quality Control Data Summaries of Statistical Analyses

24:0-LYSOPHOSPHATIDYLCHOLINE (24LPC µmol/L blood)

Lot A1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	30	0.31	0.04	0.05	0.06	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	170	0.45	0.09	0.21	0.11	1.1

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	30	0.45	0.05	0.06	0.06	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	170	0.67	0.12	0.31	0.11	1.1

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	30	0.82	0.09	0.10	0.06	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	170	1.11	0.18	0.43	0.11	1.1

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	30	2.12	0.22	0.32	0.06	0.8
Non-derivatized - MS/MS PerkinElmer NeoBase 2	170	2.92	0.39	0.93	0.11	1.1

2020 Quality Control Data Summaries of Statistical Analyses

26:0-LYSOPHOSPHATIDYLCHOLINE (26LPC µmol/L blood)

Lot A1915 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	40	0.36	0.04	0.12	-0.12	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	0.44	0.09	0.21	-0.08	1.3

Lot B1915 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	40	0.48	0.05	0.14	-0.12	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	0.58	0.09	0.23	-0.08	1.3

Lot C1915 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	40	0.75	0.10	0.22	-0.12	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	0.85	0.13	0.30	-0.08	1.3

Lot D1915 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS non-kit	40	2.91	0.31	0.86	-0.12	1.2
Non-derivatized - MS/MS PerkinElmer NeoBase 2	200	3.21	0.41	0.94	-0.08	1.3

2020 Quality Control Data Summaries of Statistical Analyses

CREATINE (CRE µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	185.46	33.80	50.20	181.16	0.9

Lot B1915 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	272.66	24.93	55.59	181.16	0.9

Lot C1915 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	426.77	44.70	90.90	181.16	0.9

Lot D1915 – Enriched 500 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	630.56	56.57	107.23	181.16	0.9

2020 Quality Control Data Summaries of Statistical Analyses

GUANIDINOACETIC ACID (GUAC µmol/L blood)

Lot A1915 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	70	1.36	0.16	0.61	1.26	0.9

Lot B1915 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	70	5.87	0.39	1.84	1.26	0.9

Lot C1915 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	70	10.06	0.69	3.30	1.26	0.9

Lot D1915 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	70	19.58	1.53	6.83	1.26	0.9

2020 Quality Control Data Summaries of Statistical Analyses

CREATININE (CRN μmol/L blood)

Creatinine is not shown due to insufficient data.

2020 Quality Control Data Summaries of Statistical Analyses

GALACTOCEREBROSIDASE (GALC µmol/hr/L blood)

Lot A1808 – Mean Activity 0.16 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.27	0.14	0.37	0.15	0.6
FIA-MS/MS multiplexed enzyme reaction	40	0.18	0.03	0.05	0.02	1.1
NeoLSD MSMS Kit	70	0.24	0.03	0.19	0.09	1.0

Lot B1808 – Mean Activity 0.39 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.41	0.10	0.26	0.15	0.6
FIA-MS/MS multiplexed enzyme reaction	40	0.43	0.02	0.05	0.02	1.1
NeoLSD MSMS Kit	70	0.48	0.03	0.23	0.09	1.0

Lot C1808 – Mean Activity 2.89 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	1.95	0.18	0.75	0.15	0.6
FIA-MS/MS multiplexed enzyme reaction	40	3.23	0.33	0.42	0.02	1.1
NeoLSD MSMS Kit	70	2.93	0.19	0.38	0.09	1.0

Lot D1808 – Mean Activity 5.58 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	3.70	0.34	1.47	0.15	0.6
FIA-MS/MS multiplexed enzyme reaction	40	6.07	0.34	0.71	0.02	1.1
NeoLSD MSMS Kit	70	5.58	0.30	0.61	0.09	1.0

2020 Quality Control Data Summaries of Statistical Analyses

ACID α-GLUCOSIDASE (GAA µmol/hr/L blood)

Lot A1808 – Mean Activity 0.16 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.26	0.05	0.14	-0.17	1.5
FIA-MS/MS multiplexed enzyme reaction	60	0.29	0.08	0.19	0.09	1.0
NeoLSD MSMS Kit	100	0.15	0.04	0.06	-0.09	1.1

Lot B1808 – Mean Activity 0.58 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.76	0.10	0.37	-0.17	1.5
FIA-MS/MS multiplexed enzyme reaction	60	0.65	0.15	0.32	0.09	1.0
NeoLSD MSMS Kit	100	0.50	0.04	0.07	-0.09	1.1

Lot C1808 – Mean Activity 4.98 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	6.89	0.78	3.10	-0.17	1.5
FIA-MS/MS multiplexed enzyme reaction	60	5.10	0.73	1.22	0.09	1.0
NeoLSD MSMS Kit	100	4.94	0.61	0.85	-0.09	1.1

Lot D1808 – Mean Activity 7.87 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	12.30	1.30	5.51	-0.17	1.5
FIA-MS/MS multiplexed enzyme reaction	60	8.12	0.60	1.48	0.09	1.0
NeoLSD MSMS Kit	100	8.24	0.52	1.13	-0.09	1.1

ACID α-GLUCOSIDASE (GAA µmol/hr/L blood)

Lot A1808 – Mean Activity 1.44 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	21	1.54	0.31	0.39	0.07	1.0
Fluorometric	60	0.45	0.18	0.52	-0.18	0.4

Lot B1808 – Mean Activity 2.43 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	41	2.38	0.48	0.60	0.07	1.0
Fluorometric	62	0.90	0.19	1.03	-0.18	0.4

Lot C1808 – Mean Activity 15.42 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	60	15.19	2.08	2.24	0.07	1.0
Fluorometric	80	5.96	0.80	7.01	-0.18	0.4

Lot D1808 – Mean Activity 28.23 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	59	26.21	3.09	3.59	0.07	1.0
Fluorometric	80	11.62	1.53	13.63	-0.18	0.4

2020 Quality Control Data Summaries of Statistical Analyses

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

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.17	0.06	10.00	-0.04	1.4
FIA-MS/MS multiplexed enzyme reaction	60	0.22	0.05	0.17	0.10	0.8
NeoLSD MSMS Kit	100	0.11	0.03	0.08	-0.03	0.9

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.50	0.09	0.14	-0.04	1.4
FIA-MS/MS multiplexed enzyme reaction	60	0.46	0.11	0.22	0.10	0.8
NeoLSD MSMS Kit	100	0.34	0.04	0.09	-0.03	0.9

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	5.88	0.77	1.50	-0.04	1.4
FIA-MS/MS multiplexed enzyme reaction	60	3.71	0.43	0.91	0.10	0.8
NeoLSD MSMS Kit	100	3.61	0.41	0.64	-0.03	0.9

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	12.20	1.60	3.78	-0.04	1.4
FIA-MS/MS multiplexed enzyme reaction	60	6.74	0.55	1.47	0.10	0.8
NeoLSD MSMS Kit	100	6.81	0.44	1.06	-0.03	0.9

2020 Quality Control Data Summaries of Statistical Analyses

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

Lot A1808 – Mean Activity 2.44 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	36	2.86	0.53	0.76	0.35	0.9
Fluorometric	30	0.10	0.03	0.04	-0.75	0.3

Lot B1808 – Mean Activity 4.23 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	53	3.43	0.77	0.94	0.35	0.9
Fluorometric	40	0.22	0.04	0.08	-0.75	0.3

Lot C1808 – Mean Activity 15.79 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	60	13.83	1.91	2.66	0.35	0.9
Fluorometric	50	3.32	0.41	0.83	-0.75	0.3

Lot D1808 – Mean Activity 30.52 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	60	26.87	2.50	3.38	0.35	0.9
Fluorometric	50	7.43	0.61	4.32	-0.75	0.3

2020 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA µmol/hr/L blood)

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	1.12	0.23	0.80	0.32	1.1
FIA-MS/MS multiplexed enzyme reaction	30	1.16	0.27	0.73	0.50	0.9
NeoLSD MSMS Kit	100	0.69	0.12	0.29	-0.04	1.0

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	1.70	0.18	0.93	0.32	1.1
FIA-MS/MS multiplexed enzyme reaction	30	1.65	0.23	0.73	0.50	0.9
NeoLSD MSMS Kit	100	1.22	0.12	0.28	-0.04	1.0

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	9.03	0.50	2.85	0.32	1.1
FIA-MS/MS multiplexed enzyme reaction	30	7.67	0.34	1.05	0.50	0.9
NeoLSD MSMS Kit	100	7.66	0.43	1.13	-0.04	1.0

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	16.66	0.87	5.32	0.32	1.1
FIA-MS/MS multiplexed enzyme reaction	30	13.98	0.62	1.69	0.50	0.9
NeoLSD MSMS Kit	100	14.63	0.74	2.22	-0.04	1.0

2020 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA µmol/hr/L blood)

Lot A1808 – Mean Activity 3.66 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorometric	40	0.84	0.14	0.31	0.11	0.2

Lot B1808 – Mean Activity 5.59 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	22	5.43	1.14	1.57	0.25	0.9
Fluorometric	40	1.41	0.12	0.35	0.11	0.2

Lot C1808 – Mean Activity 32.42 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	29.62	2.13	2.76	0.25	0.9
Fluorometric	50	7.65	0.81	3.43	0.11	0.2

Lot D1808 – Mean Activity 64.28 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	54.05	3.80	4.80	0.25	0.9
Fluorometric	50	14.66	0.96	5.77	0.11	0.2

2020 Quality Control Data Summaries of Statistical Analyses

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

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	0.84	0.25	0.58	0.19	0.9
FIA-MS/MS multiplexed enzyme reaction	29	0.56	0.16	0.23	0.06	0.8
NeoLSD MSMS Kit	100	0.46	0.09	0.19	0.04	0.7

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	1.04	0.21	0.61	0.19	0.9
FIA-MS/MS multiplexed enzyme reaction	30	0.84	0.11	0.14	0.06	0.8
NeoLSD MSMS Kit	100	0.74	0.13	0.27	0.04	0.7

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	5.08	0.48	1.95	0.19	0.9
FIA-MS/MS multiplexed enzyme reaction	30	4.49	0.45	0.50	0.06	0.8
NeoLSD MSMS Kit	100	3.78	0.46	0.73	0.04	0.7

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	10.10	0.96	2.64	0.19	0.9
FIA-MS/MS multiplexed enzyme reaction	30	8.80	0.77	1.07	0.06	0.8
NeoLSD MSMS Kit	100	7.52	0.73	1.37	0.04	0.7

2020 Quality Control Data Summaries of Statistical Analyses

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

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	26	2.40	0.46	0.52	0.09	1.0
Fluorometric	30	0.60	0.08	0.25	-0.48	0.5

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	26	2.41	0.35	0.46	0.09	1.0
Fluorometric	40	0.78	0.13	0.50	-0.48	0.5

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	6.86	0.64	0.81	0.09	1.0
Fluorometric	50	2.94	0.30	1.15	-0.48	0.5

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	10.98	0.92	1.43	0.09	1.0
Fluorometric	50	5.54	0.43	2.39	-0.48	0.5

2020 Quality Control Data Summaries of Statistical Analyses

ACID SPHINGOMYELINASE (ASM µmol/hr/L blood)

Lot A1808 – Mean Activity 0.16 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	40	0.15	0.02	0.03	-0.02	1.1
FIA-MS/MS multiplexed enzyme reaction	30	0.20	0.02	0.07	0.02	1.1
NeoLSD MSMS Kit	70	0.15	0.04	0.06	-0.01	1.0

Lot B1808 – Mean Activity 0.30 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	0.29	0.02	0.10	-0.02	1.1
FIA-MS/MS multiplexed enzyme reaction	30	0.34	0.05	0.08	0.02	1.1
NeoLSD MSMS Kit	70	0.29	0.07	0.08	-0.01	1.0

Lot C1808 – Mean Activity 1.45 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	1.67	0.17	0.76	-0.02	1.1
FIA-MS/MS multiplexed enzyme reaction	30	1.59	0.14	0.15	0.02	1.1
NeoLSD MSMS Kit	70	1.41	0.17	0.21	-0.01	1.0

Lot D1808 – Mean Activity 2.67 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	39	2.95	0.24	1.40	-0.02	1.1
FIA-MS/MS multiplexed enzyme reaction	30	2.94	0.21	0.25	0.02	1.1
NeoLSD MSMS Kit	70	2.64	0.37	0.50	-0.01	1.0

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER 17 α-HYDROXYPROGESTERONE (17OHP2 ng/mL serum)

Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	129	0.54	0.33	0.61	0.93	0.9

Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	9.44	1.08	2.60	0.93	0.9

Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	46.74	4.85	12.64	0.93	0.9

Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	94.84	8.02	23.76	0.93	0.9

Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	260	461.67	34.25	116.83	0.93	0.9

2020 Quality Control Data Summaries of Statistical Analyses

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

Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	127	0.41	0.22	0.43	1.04	0.9

Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	249	8.98	0.89	2.40	1.04	0.9

Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	47.78	4.83	12.74	1.04	0.9

Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	98.28	8.46	22.35	1.04	0.9

Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	260	471.63	39.66	107.90	1.04	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER CORTISOL (CORT2 ng/mL serum)

Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	142	1.50	0.87	1.60	0.45	0.9

Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	249	8.04	1.44	3.04	0.45	0.9

Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	259	45.22	4.23	10.16	0.45	0.9

Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	258	97.29	7.38	20.71	0.45	0.9

Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	260	468.37	39.36	103.57	0.45	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER 11-DEOXYCORTISOL (11D2 ng/mL serum)

Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	91	0.38	0.27	0.66	2.67	0.9

Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	189	8.64	1.00	2.96	2.67	0.9

Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	198	46.46	3.70	14.79	2.67	0.9

Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	199	95.17	6.98	30.31	2.67	0.9

Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	200	435.40	32.33	158.66	2.67	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER 21-DEOXYCORTISOL (21D2 ng/mL serum)

Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	99	0.33	0.23	0.41	-1.24	0.9

Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	199	8.08	1.11	2.51	-1.24	0.9

Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	199	42.4	4.12	11.92	-1.24	0.9

Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	199	93.91	7.74	24.53	-1.24	0.9

Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	200	466.49	38.2	124.1	-1.24	0.9

2ND TIER ALLO-ISOLEUCINE (ALE2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	110	1.73	0.25	2.64	5.74	0.9

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	91.26	9.71	18.94	5.74	0.9
UPLC	30	91.19	5.43	6.76	0.90	0.9

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	180.15	14.27	28.47	5.74	0.9
UPLC	30	180.80	11.40	16.82	0.90	0.9

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	353.33	24.23	58.42	5.74	0.9
UPLC	30	356.52	19.95	36.28	0.90	0.9

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	689.38	49.65	106.6	5.74	0.9
UPLC	30	724.04	26.22	69.85	0.90	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER ISOLEUCINE (ILE2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	12.80	2.96	16.06	12.61	0.9
UPLC	30	11.34	1.72	2.99	6.18	0.8

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	98.98	9.41	56.75	12.61	0.9
UPLC	30	88.00	6.88	13.23	6.18	0.8

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	193.91	13.26	98.79	12.61	0.9
UPLC	30	172.88	11.70	25.82	6.18	0.8

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	149	381.41	23.34	177.6	12.61	0.9
UPLC	30	338.34	18.03	49.89	6.18	0.8

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	734.13	48.96	324.5	12.61	0.9
UPLC	30	681.56	79.88	171.6	6.18	0.8

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER LEUCINE (LEU2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	75.84	8.84	16.77	83.72	0.9
UPLC	30	75.98	6.30	13.36	77.63	0.9

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	172.30	14.13	41.95	83.72	0.9
UPLC	30	165.80	11.27	19.53	77.63	0.9

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	268.88	18.62	83.49	83.72	0.9
UPLC	30	252.18	16.16	30.23	77.63	0.9

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	452.25	27.57	162.7	83.72	0.9
UPLC	30	413.43	20.68	49.16	77.63	0.9

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	795.92	47.25	308.9	83.72	0.9
UPLC	30	764.12	27.84	115.8	77.63	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER PHENYLALANINE (PHE2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	130	52.08	6.31	12.19	59.80	0.8
UPLC	30	50.41	3.71	11.76	50.13	0.9

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	140	141.27	8.83	17.96	59.80	0.8
UPLC	30	145.85	12.69	25.39	50.13	0.9

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	130	234.30	17.14	31.46	59.80	0.8
UPLC	30	239.94	16.12	39.40	50.13	0.9

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	140	409.75	21.64	40.08	59.80	0.8
UPLC	30	418.78	28.96	74.60	50.13	0.9

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	140	728.17	41.41	74.59	59.80	0.8
UPLC	30	803.84	52.05	131.8	50.13	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER TYROSINE (TYR2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	37.00	3.75	8.01	41.53	0.8
UPLC	30	38.50	2.84	7.46	36.05	0.9

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	130	120.91	7.90	22.01	41.53	0.8
UPLC	30	127.61	10.33	20.49	36.05	0.9

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	120	203.67	14.11	35.73	41.53	0.8
UPLC	30	214.11	15.62	35.73	36.05	0.9

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	130	371.02	20.91	62.65	41.53	0.8
UPLC	30	389.49	23.88	65.03	36.05	0.9

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	130	679.43	42.46	107.0	41.53	0.8
UPLC	30	757.37	53.11	135.4	36.05	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER VALINE (VAL2 µmol/L blood)

Lot A1913 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	100.98	10.23	26.83	105.43	0.8
UPLC	30	117.09	8.01	23.69	119.45	0.9

Lot B1913 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	189.35	15.36	41.57	105.43	0.8
UPLC	30	209.24	12.44	34.46	119.45	0.9

Lot C1913 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	280.11	17.22	52.79	105.43	0.8
UPLC	30	297.33	17.94	42.24	119.45	0.9

Lot D1913 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	434.47	28.27	87.15	105.43	0.8
UPLC	30	468.40	24.65	63.42	119.45	0.9

Lot E1913 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	150	771.97	56.53	155.6	105.43	0.8
UPLC	30	822.07	27.37	135.4	119.45	0.9

2ND TIER MALONIC ACID (MA2 µmol/L blood)

MA is not shown due to insufficient data.

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER METHYLMALONIC ACID (MMA2 µmol/L blood)

Lot A1914 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	260	2.33	0.33	0.64	0.61	1.0

Lot B1914 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	270	5.47	0.53	1.44	0.61	1.0

Lot C1914 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	270	20.17	1.74	4.28	0.61	1.0

Lot D1914 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	270	48.71	4.01	11.67	0.61	1.0

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER ETHYLMALONIC ACID (EMA2 µmol/L blood)

Lot A1914 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	80	2.65	0.33	0.91	0.38	1.2

Lot B1914 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	90	6.19	0.63	1.97	0.38	1.2

Lot C1914 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	90	24.2	2.17	8.85	0.38	1.2

Lot D1914 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	90	59.18	3.75	22.75	0.38	1.2

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER 2-METHYLCITRIC ACID (MCA2 µmol/L blood)

Lot A1914 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	200	1.24	0.23	0.49	0.35	0.9

Lot B1914 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	201	2.65	0.33	0.87	0.35	0.9

Lot C1914 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	210	9.68	0.98	2.18	0.35	0.9

Lot D1914 – Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	210	23.46	2.41	4.88	0.35	0.9

2020 Quality Control Data Summaries of Statistical Analyses

2ND TIER TOTAL HOMOCYSTEINE (tHCY2 µmol/L blood)

Lot A1914 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	230	15.38	1.90	8.06	16.62	1.0

Lot B1914 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	230	26.79	2.97	13.58	16.62	1.0

Lot C1914 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	230	66.39	7.39	31.36	16.62	1.0

Lot D1914 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC MS/MS	230	112.23	11.07	58.20	16.62	1.0

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

CENTERS FOR DISEASE CONTROL AND PREVENTION (CDC) ATLANTA, GA 30341

Director
Robert R. Redfield, M.D.

Director
National Center for Environmental Health
Patrick Breysse, Ph.D.

Director
Division of Laboratory Sciences
James L. Pirkle, M.D., Ph.D.

Chief
Newborn Screening and Molecular Biology Branch
Carla Cuthbert, Ph.D.

Contributors
Nicole Baird, Ph.D
John Bernstein, MS
Quan Bui, MS
Suzanne Cordovado, Ph.D
Paul Dantonio, MS
Katherine Duneman, MS
Christopher Greene, Ph.D
Elizabeth Hall, BS
Laura Hancock, MS
Christopher Haynes, Ph.D
Miyono Hendrix, MS
Laura C. Hildreth, BS
Samantha Isenberg, Ph.D
Matt Kilgore, Ph.D
Deborah Koontz, Ph.D
Francis Lee, Ph.D
LiXia Li, Ph.D
Tim Lim, Ph.D
Edgardo Lobo, MS
Daniel Mandel, Ph.D
Allison McCabe, BS
Joanne Mei, Ph.D
Kristina Mercer, Ph.D
Stanimila Nikolova, Ph.D
Kaila Pearson, MS
Gyliann Pena, MS
Kostas Petritis, Ph.D
C. Austin Pickens, Ph.D
Maryam Salehi, Ph.D.
Blanche Temate, Ph.D
Robert Vogt, Ph.D
Irene Williams, MS
Sophia Winchester, BS
Golriz Yazdanpanah, MS
Sherri Zobel, BS

Production
Vinay Anumula, MS
Kizzy Stewart
Dequnoas Lee

ASSOCIATION OF PUBLIC HEALTH LABORATORIES SILVER SPRING, MD 20910

President
Grace E. Kubin, PhD

Chairman, Newborn Screening and Genetics in Public Health Committee
Michele Caggana, Sc.D., FACMG

Chairman, Newborn Screening Quality Assurance Quality Control Subcommittee
Patricia R. Hunt, B.A. and Joseph Orsini, Ph.D.

Chairman, Newborn Screening Molecular Subcommittee
Rachel Lee, Ph.D.

INQUIRIES TO:
Irene Williams, Editor
Centers for Disease Control and Prevention (CDC), Newborn Screening Quality Assurance Program
Mailstop F-19, 4770 Buford Highway, N.E., Atlanta, GA 30341-3724
E-mail: NSQAPDMT@cdc.gov