Newborn Screening Quality Assurance Program

2022 Quality Control Report

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Centers for Disease Control and Prevention
4770 Buford Highway NE, MS/F19
Atlanta, GA 30341-3724
Email: NSQAPDMT@cdc.gov

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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 material is not a replacement for manufacturer kit controls or other daily QC and should not be used for routine analysis. This report contains a summary of the 2022 Set 1 QC data submitted during the first half of the year by state, contract, and private laboratories in the United States; international participants; and manufacturers of screening test products.

QC Material Production

QC specimen lots were provided as 6-month supplies of DBS on filter paper. DBS QC lots were prepared from whole blood of 50% hematocrit. The materials were enriched with predetermined quantities of selected analytes and dispensed in 100 µL aliquots on Grade 903 filter paper (Cytiva (Cardiff, United Kingdom)).

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 X-linked 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 DBS materials from three QC lots per analyte, with each lot containing a different concentration of analyte. The QC materials for IRT, LSD, and the materials that encompass amino acids, SUAC, acylcarnitines, ALD, and GAMT (MSMS1QC) consisted of DBS materials from four lots.

NSQAP also distributed certified QC materials for newborn screening analytes and disorders designed for second-tier testing by tandem mass spectrometry (MS/MS). These programs include Second-tier Congenital Adrenal Hyperplasia (CAHQC) by LC-MS/MS for the analytes 17 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, Homocystinuria (MMA-tHCY) by LC-MS/MS for the analytes malonic acid (MA2), methylmalonic acid (MMA2), ethylmalonic acid (EMA2), 2-methylcitric acid (MCA2), and total homocysteine (tHCY2). The QC materials for these analytes consisted of four or five lots.

QC Material Distribution

On January 11, 2022, we distributed DBS quality control (QC) materials to 555 participanting laboratories.

QC Data Reporting Requirements

Participants used the NSQAP Participant Portal at https://nbs.dynamics365portals.us/ to report results. Required input for QC data reporting included the following 1) analyte kit or method, 2) results of duplicate sample analysis from five independent runs in the analytic units and decimal places requested, and 3) ten data points for each lot and analyte.

Data processing for this set of QC revealed an increase of data entry errors. The following criteria are required for successful data entry. Refer to the QC Data Entry Instructions posted in the Portal for information on how to correctly submit QC data.

The majority of errors occurred when the "upload" option was chosen and the pre-filled data entry template was used to submit results. For successful data entry:

- **Fill in ALL the required data on the pre-filled template (Lab code number, method, method code, analyte, analyte code, analyte abbreviation, Lot Numbers, and replicate data for each lot)**
- **When entering the Lot Number, only use the 5-digit alpha numberic, not the full number stamped on the card. (Example: A2005 – one letter followed by four numbers)**
- **Enter all results to the correct decimal point per analyte**
- **Do not create exact duplicate rows of data**
- **Assure that the method you are reporting is applicable for the analyte**
- **Convert results to the requested units where applicable**

To avoid errors with the pre-filled template, use the manual entry option to enter all QC results. Participants are required to chose either manual entry or the prefilled template. Only one option can be used to submit QC data.

Participant Results

Results from five analytic runs from each QC lot, analyte, and method were used to calculate mean values and standard deviations (SD). Data values outside 4SD limits were reviewed, and if considered to be "blunders", removed from the data set. For linear regression analysis, we could not include qualitative data, data submitted in unidentified units, or data from less than five analytic runs per specimen lot per analyte.

To ensure that all results are appropriately reported, participants must convert their results to the requested units prior to data entry. 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 enzymes, 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 **and** show the analyte by series of QC lots, the number of measurements (N), the mean values, and the standard deviations (SD) by kit or analytic method. In addition, we used linear regression analysis to examine the comparability by method of reported (aggregated) versus enriched concentrations. Methods with less than three participants reporting data were not included in the tables.

Discussion

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.

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

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 QC series **(e.g., lots A2105, B2105, and C2105).** The Y-intercept is estimated by performing linear regression analysis on mean reported concentrations versus either 1) enriched concentrations, 2) assayed values (IRT), or 3) mean activity (GALT, LSD), and extrapolating the regression to the Y-axis. This parameter provides one measure of the endogenous concentration level for an analyte. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, Gly, SUAC, acylcarnitines, 20:0- 22:0- 24:0- and 26:0-lysophosphatidylcholine, CRE, GALC, GALC, GAA, IDUA, GAL, ABG, ASM, and all Second-tier analytes, participants measured the endogenous concentration or activity levels by analyzing the non-enriched QC lots. For CRN and MA, no results are shown due to insufficient data.

The majority of analytes demonstrated acceptable performance, with slopes falling near or within the acceptable range (from 0.8 to 1.2). Analytes which demonstrated low slopes included **SUAC, C3DC + C4OH, C14:1,** and were historically consistent with previous sets of QC materials.

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2105 – Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal 17OHP	376	23.3	1.9	4.0	-1.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	250	22.1	2.7	5.1	-1.1	1.0
GSP® 17OHP Neonatal PerkinElmer	612	24.3	1.9	3.6	-0.4	1.0
LC-MS/MS non-kit	50	21.1	2.0	5.1	0.7	0.8
Neonatal 17OHP LabSystems	180	21.9	2.3	5.4	3.6	0.8
ZenTech ELISA Neonatal 17OHP	60	23.2	3.5	7.9	-2.6	1.0

Lot B2105 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal 17OHP	376	49.2	3.8	8.1	-1.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	250	49.3	10.1	29.6	-1.1	1.0
GSP® 17OHP Neonatal PerkinElmer	612	50.2	3.7	8.4	-0.4	1.0
LC-MS/MS non-kit	50	41.6	3.4	9.8	0.7	0.8
Neonatal 17OHP LabSystems	180	41.8	5.6	14.5	3.6	0.8
ZenTech ELISA Neonatal 17OHP	60	46.0	6.6	10.3	-2.6	1.0

Lot C2105 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal 17OHP	376	98.8	7.7	18.5	-1.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	250	95.7	12.5	25.0	-1.1	1.0
GSP® 17OHP Neonatal PerkinElmer	611	99.6	7.6	17.2	-0.4	1.0
LC-MS/MS non-kit	50	82.4	6.0	17.8	0.7	0.8
Neonatal 17OHP LabSystems	179	78.4	12.6	38.1	3.6	0.8
ZenTech ELISA Neonatal 17OHP	60	97.6	13.1	34.3	-2.6	1.0

2022 Quality Control Data Summaries of Statistical Analyses

THYROXINE (T4 µg/dL serum)

Lot A2000 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal T4 PerkinElmer	80	1.7	0.4	0.6	-0.1	0.9
DELFIA® Neonatal T4 PerkinElmer	70	1.8	0.3	0.5	-0.1	0.9
GSP® T4 Neonatal PerkinElmer	119	1.7	0.2	0.3	-0.3	1.0
NeoMAP® T4 Interscientifica	30	3.9	0.5	0.5	2.0	1.0

Lot B2000 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal T4 PerkinElmer	80	6.4	0.5	1.4	-0.1	0.9
DELFIA® Neonatal T4 PerkinElmer	70	6.3	0.9	1.0	-0.1	0.9
GSP® T4 Neonatal PerkinElmer	164	6.7	0.7	0.8	-0.3	1.0
NeoMAP® T4 Interscientifica	30	9.5	0.8	1.2	2.0	1.0

Lot C2000 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal T4 PerkinElmer	80	10.0	0.8	2.1	-0.1	0.9
DELFIA® Neonatal T4 PerkinElmer	70	10.2	0.9	1.5	-0.1	0.9
GSP® T4 Neonatal PerkinElmer	164	10.6	1.0	1.1	-0.3	1.0
NeoMAP® T4 Interscientifica	30	13.1	1.7	1.8	2.0	1.0

2022 Quality Control Data Summaries of Statistical Analyses

THYROID-STIMULATING HORMONE (TSH µIU/mL serum)

Lot A2101 – Enriched 25 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal hTSH	426	26.9	2.0	6.1	3.1	1.0
DELFIA® Neonatal TSH PerkinElmer	430	28.0	2.7	22.3	2.7	1.0
DiaSorin Immunoassay TSH	70	29.1	2.8	4.5	9.7	0.9
GSP® hTSH Neonatal PerkinElmer	800	27.5	2.1	4.8	1.5	1.1
NeoMAP® TSH Interscientifica	30	32.8	2.9	5.2	1.2	1.3
Neonatal TSH LabSystems	160	23.5	4.2	9.7	1.1	0.9
ZenTech ELISA Neonatal TSH	100	34.3	4.4	19.8	11.0	1.0

Lot B2101 – Enriched 40 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal hTSH	426	42.6	3.0	10.0	3.1	1.0
DELFIA® Neonatal TSH PerkinElmer	430	44.6	4.3	33.2	2.7	1.0
DiaSorin Immunoassay TSH	70	46.8	3.6	5.2	9.7	0.9
GSP® hTSH Neonatal PerkinElmer	800	44.1	3.3	8.2	1.5	1.1
NeoMAP® TSH Interscientifica	30	51.2	3.3	5.5	1.2	1.3
Neonatal TSH LabSystems	160	39.2	5.6	13.7	1.1	0.9
ZenTech ELISA Neonatal TSH	100	51.2	5.7	22.2	11.0	1.0

Lot C2101 – Enriched 80 µIU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal hTSH	426	80.6	5.9	19.1	3.1	1.0
DELFIA® Neonatal TSH PerkinElmer	430	85.1	7.1	66.5	2.7	1.0
DiaSorin Immunoassay TSH	70	77.5	6.8	9.7	9.7	0.9
GSP® hTSH Neonatal PerkinElmer	798	85.6	6.7	16.4	1.5	1.1
NeoMAP® TSH Interscientifica	30	101.7	6.0	10.4	1.2	1.3
Neonatal TSH LabSystems	160	74.9	10.3	27.8	1.1	0.9
ZenTech ELISA Neonatal TSH	100	88.5	10.5	32.5	11.0	1.0

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot F2103 – Mean Activity 1.6 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	235	1.8	0.5	1.3	0.5	0.9
Microplate Reagent Kit Spotcheck® GALT Astoria-	60	0.9	0.1	0.1	-0.3	0.8

Lot G2103 – Mean Activity 4.2 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	236	3.9	0.7	1.2	0.5	0.9
Microplate Reagent Kit Spotcheck® GALT Astoria-	60	2.8	0.3	0.5	-0.3	0.8

Lot H2103 – Mean Activity 9.6 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	236	8.6	1.1	2.0	0.5	0.9
Microplate Reagent Kit Spotcheck® GALT Astoria-	60	6.9	0.7	1.6	-0.3	0.8

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

Lot F2103

METHOD	N	Mean	All Lab SD	Min	Max
GSP® GALT Neonatal PerkinElmer, U/dL blood	99	0.8	0.3	0.0	7.8

Lot G2103

METHOD	N	Mean	All Lab SD	Min	Max
GSP® GALT Neonatal PerkinElmer, U/dL blood	244	4.1	0.4	2.9	8.0

Lot H2103

METHOD	N	Mean	All Lab SD	Min	Max
GSP® GALT Neonatal PerkinElmer, U/dL blood	244	15.7	1.3	9.4	20.9

Several laboratories reported 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.

2022 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood)

Lot A2109 – Assayed 19.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal IRT PerkinElmer	110	19.4	1.4	1.6	3.2	0.9
DELFIA® Neonatal IRT	209	20.1	2.0	3.0	3.9	0.9
FEIA IRT Labsystems	90	24.2	3.2	4.4	0.3	1.2
GSP® IRT Neonatal PerkinElmer, ng/mL	598	18.3	1.1	1.5	0.7	1.0
NeoMAP® IRT Interscientifica	30	26.9	2.0	6.3	30.6	0.5
ZenTech ELISA Neonatal IRT	40	32.0	4.6	6.6	39.1	0.9

Lot B2109 – Assayed 65.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal IRT PerkinElmer	110	62.7	4.5	6.4	3.2	0.9
DELFIA® Neonatal IRT	210	63.2	5.6	8.9	3.9	0.9
FEIA IRT Labsystems	90	76.2	11.9	16.6	0.3	1.2
GSP® IRT Neonatal PerkinElmer, ng/mL	602	61.8	3.6	4.8	0.7	1.0
NeoMAP® IRT Interscientifica	30	69.3	5.2	8.3	30.6	0.5
ZenTech ELISA Neonatal IRT	40	107.7	9.0	10.1	39.1	0.9

Lot C2109 – Assayed 115.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal IRT PerkinElmer	110	113.7	8.0	10.0	3.2	0.9
DELFIA® Neonatal IRT	210	111.4	10.6	17.6	3.9	0.9
FEIA IRT Labsystems	90	148.9	20.2	35.2	0.3	1.2
GSP® IRT Neonatal PerkinElmer, ng/mL	602	113.4	7.1	9.9	0.7	1.0
NeoMAP® IRT Interscientifica	30	99.2	13.1	13.2	30.6	0.5
ZenTech ELISA Neonatal IRT	40	173.1	19.1	24.3	39.1	0.9

IMMUNOREACTIVE TRYPSINOGEN (IRT ng/mL blood) cont.

Lot D2109 – Assayed 214.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIA® Neonatal IRT PerkinElmer	110	198.8	15.4	18.0	3.2	0.9
DELFIA® Neonatal IRT	210	197.4	16.2	26.4	3.9	0.9
FEIA IRT Labsystems	90	262.2	34.5	48.8	0.3	1.2
GSP® IRT Neonatal PerkinElmer, ng/mL	602	203.3	12.6	18.1	0.7	1.0
NeoMAP® IRT Interscientifica	30	124.1	28.5	29.4	30.6	0.5
ZenTech ELISA Neonatal IRT	40	211.2	10.1	18.3	39.1	0.9

2022 Quality Control Data Summaries of Statistical Analyses

ALANINE (Ala µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	205.2	31.5	50.0	227.4	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	156.4	12.2	46.2	179.7	0.6
Derivatized - MS/MS non-kit	336	198.5	20.5	56.9	219.2	0.8
LC-MS/MS non-kit	30	393.3	105.6	343.3	412.3	0.9
Non-derivatized - MS/MS MassChrom®	110	162.8	10.0	34.2	186.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	414	219.3	18.0	45.1	245.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	286	213.7	14.1	52.2	235.2	0.8
Non-derivatized - MS/MS non-kit	107	199.2	40.0	19.1	211.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	60	140.0	15.0	67.4	160.0	0.6

Lot B2115 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	408.6	44.5	67.0	227.4	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	330.6	23.5	100.0	179.7	0.6
Derivatized - MS/MS non-kit	336	398.1	34.6	92.6	219.2	0.8
LC-MS/MS non-kit	30	620.2	130.0	396.1	412.3	0.9
Non-derivatized - MS/MS MassChrom®	110	343.2	16.1	78.3	186.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	414	461.6	34.9	81.4	245.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	286	424.7	29.1	84.2	235.2	0.8
Non-derivatized - MS/MS non-kit	110	412.0	29.0	82.1	211.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	60	309.5	36.5	149.4	160.0	0.6

Lot C2115 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	542.8	51.6	80.5	227.4	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	437.8	31.1	127.1	179.7	0.6
Derivatized - MS/MS non-kit	336	534.4	80.8	231.1	219.2	0.8
LC-MS/MS non-kit	30	757.4	78.3	347.2	412.3	0.9
Non-derivatized - MS/MS MassChrom®	110	442.4	31.7	97.0	186.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	414	614.0	45.2	105.1	245.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	286	571.6	37.2	100.5	235.2	0.8
Non-derivatized - MS/MS non-kit	110	550.5	39.2	93.4	211.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	60	409.9	41.8	194.1	160.0	0.6

ALANINE (Ala µmol/L blood) cont.

Lot D2115 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	669.6	52.7	74.4	227.4	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	529.3	37.9	154.7	179.7	0.6
Derivatized - MS/MS non-kit	336	661.9	59.9	163.4	219.2	0.8
LC-MS/MS non-kit	30	934.0	134.4	476.5	412.3	0.9
Non-derivatized - MS/MS MassChrom®	110	546.3	22.2	127.7	186.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	414	769.9	56.3	128.1	245.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	286	707.4	49.3	144.8	235.2	0.8
Non-derivatized - MS/MS non-kit	110	674.3	45.1	116.3	211.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	60	513.9	42.3	243.8	160.0	0.6

2022 Quality Control Data Summaries of Statistical Analyses

ARGININE (Arg µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	38	8.6	1.0	2.4	7.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	9.1	0.8	1.3	11.9	0.7
Derivatized - MS/MS non-kit	336	9.0	2.0	4.9	8.8	0.6
LC-MS/MS non-kit	30	12.7	2.5	7.3	13.3	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	5.8	0.5	0.6	6.2	0.5
Non-derivatized - MS/MS MassChrom®	120	9.6	4.0	9.5	14.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	7.7	0.8	1.9	8.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	8.8	0.8	2.0	10.0	0.8
Non-derivatized - MS/MS non-kit	120	10.8	1.6	5.4	9.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	9.6	1.0	1.5	10.7	0.8

Lot B2115 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	38	72.6	6.9	24.0	7.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	88.1	5.0	13.9	11.9	0.7
Derivatized - MS/MS non-kit	336	72.9	6.7	25.5	8.8	0.6
LC-MS/MS non-kit	30	107.9	18.5	38.2	13.3	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	60.5	6.2	7.6	6.2	0.5
Non-derivatized - MS/MS MassChrom®	120	94.5	6.5	20.6	14.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	85.1	5.7	11.2	8.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	93.3	5.4	13.3	10.0	0.8
Non-derivatized - MS/MS non-kit	120	86.9	7.4	22.1	9.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	95.4	7.5	14.1	10.7	0.8

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ARGININE (Arg µmol/L blood) cont.

Lot C2115 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	38	137.8	13.4	44.3	7.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	161.1	8.8	28.2	11.9	0.7
Derivatized - MS/MS non-kit	336	135.6	14.0	48.2	8.8	0.6
LC-MS/MS non-kit	30	182.3	25.1	48.6	13.3	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	111.5	10.6	13.6	6.2	0.5
Non-derivatized - MS/MS MassChrom®	120	172.0	9.7	40.9	14.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	161.7	10.4	22.5	8.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	179.3	9.6	27.1	10.0	0.8
Non-derivatized - MS/MS non-kit	120	165.1	12.6	35.9	9.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	178.1	12.2	25.9	10.7	0.8

Lot D2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	38	205.8	19.4	63.5	7.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	229.2	10.8	30.7	11.9	0.7
Derivatized - MS/MS non-kit	336	200.9	20.6	70.2	8.8	0.6
LC-MS/MS non-kit	30	285.3	36.3	87.9	13.3	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	166.0	14.4	20.2	6.2	0.5
Non-derivatized - MS/MS MassChrom®	120	234.4	13.7	59.4	14.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	235.7	15.8	31.3	8.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	256.8	14.2	35.2	10.0	0.8
Non-derivatized - MS/MS non-kit	120	245.4	17.9	53.0	9.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	259.7	17.2	39.6	10.7	0.8

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CITRULLINE (Cit µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	16.9	1.4	2.8	17.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	14.7	1.9	3.1	15.2	0.8
Derivatized - MS/MS non-kit	350	14.3	1.9	3.8	14.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	14.1	1.1	1.8	14.7	0.9
Non-derivatized - MS/MS MassChrom®	130	14.2	2.4	3.3	15.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	14.1	1.4	2.0	14.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	370	14.2	1.3	1.9	15.5	0.8
Non-derivatized - MS/MS non-kit	190	13.6	1.6	3.1	15.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	14.8	1.7	2.5	18.2	0.9

Lot B2115 – Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	34.4	1.8	3.3	17.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	35.7	3.1	4.9	15.2	0.8
Derivatized - MS/MS non-kit	350	34.3	3.7	8.2	14.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	36.1	2.5	3.0	14.7	0.9
Non-derivatized - MS/MS MassChrom®	130	35.9	2.6	5.0	15.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	36.6	3.3	4.3	14.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	370	36.3	2.6	4.0	15.5	0.8
Non-derivatized - MS/MS non-kit	190	35.8	2.9	8.4	15.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	43.1	3.8	6.9	18.2	0.9

CITRULLINE (Cit µmol/L blood) (cont.)

Lot C2115 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	86.7	6.1	10.4	17.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	96.0	6.2	13.2	15.2	0.8
Derivatized - MS/MS non-kit	350	92.0	9.3	22.8	14.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	100.3	6.0	9.4	14.7	0.9
Non-derivatized - MS/MS MassChrom®	130	98.0	6.7	12.0	15.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	99.9	7.1	10.3	14.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	370	99.5	6.4	10.9	15.5	0.8
Non-derivatized - MS/MS non-kit	190	100.2	7.9	19.8	15.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	111.3	7.0	16.2	18.2	0.9

Lot D2115 – Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	186.1	11.3	27.5	17.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	216.8	8.3	22.1	15.2	0.8
Derivatized - MS/MS non-kit	350	211.9	20.0	48.7	14.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	226.6	15.1	20.4	14.7	0.9
Non-derivatized - MS/MS MassChrom®	130	216.4	13.4	30.2	15.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	227.6	16.2	23.0	14.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	370	220.1	16.8	28.4	15.5	0.8
Non-derivatized - MS/MS non-kit	190	221.5	17.3	44.7	15.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	243.6	17.7	36.7	18.2	0.9

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GLYCINE (Gly µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	268.0	35.9	58.2	270.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	50	255.9	18.5	46.1	266.5	0.7
Derivatized - MS/MS non-kit	292	263.5	24.3	81.0	268.4	0.8
Non-derivatized - MS/MS MassChrom®	110	201.5	13.8	72.8	207.5	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	374	286.2	26.2	49.4	292.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	254	283.4	23.1	48.4	291.2	0.8
Non-derivatized - MS/MS non-kit	80	229.5	20.2	73.6	238.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	208.8	38.2	55.9	218.5	0.6

Lot B2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	517.0	39.0	86.1	270.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	50	503.1	20.7	90.4	266.5	0.7
Derivatized - MS/MS non-kit	292	523.3	45.5	155.4	268.4	0.8
Non-derivatized - MS/MS MassChrom®	110	373.3	19.4	88.8	207.5	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	373	569.2	89.1	45.8	292.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	254	546.9	38.0	89.1	291.2	0.8
Non-derivatized - MS/MS non-kit	80	462.3	27.3	109.7	238.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	418.1	61.6	92.5	218.5	0.6

GLYCINE (Gly µmol/L blood) cont.

Lot C2115 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	740.4	60.5	127.9	270.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	50	715.4	38.5	127.7	266.5	0.7
Derivatized - MS/MS non-kit	292	742.7	69.0	220.4	268.4	0.8
Non-derivatized - MS/MS MassChrom®	110	522.6	32.8	110.4	207.5	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	374	815.0	68.5	128.7	292.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	254	783.6	50.2	130.0	291.2	0.8
Non-derivatized - MS/MS non-kit	80	694.7	57.5	179.8	238.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	599.4	70.4	125.3	218.5	0.6

Lot D2115 – Enriched 900 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	992.6	70.1	147.9	270.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	50	927.1	40.9	151.4	266.5	0.7
Derivatized - MS/MS non-kit	292	998.3	84.4	302.5	268.4	0.8
Non-derivatized - MS/MS MassChrom®	110	675.5	32.3	143.9	207.5	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	374	1083.5	78.4	167.8	292.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	254	1021.4	70.5	175.9	291.2	0.8
Non-derivatized - MS/MS non-kit	80	884.5	54.4	225.1	238.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	774.3	155.3	226.8	218.5	0.6

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LEUCINE (Leu µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	75.5	6.6	15.8	81.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	60	72.8	24.1	55.6	82.1	0.7
Derivatized - MS/MS non-kit	342	68.5	7.0	18.4	78.0	0.8
LC-MS/MS non-kit	40	79.3	8.2	29.8	100.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	79.4	3.6	5.3	98.6	0.9
Non-derivatized - MS/MS MassChrom®	120	79.0	8.4	17.6	96.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	77.1	5.0	9.2	90.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	74.6	4.7	10.5	91.6	0.8
Non-derivatized - MS/MS non-kit	202	76.5	6.4	10.2	90.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	46	75.3	5.0	11.8	88.3	0.8

Lot B2115 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	224.5	14.4	30.6	81.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	60	197.6	11.3	14.9	82.1	0.7
Derivatized - MS/MS non-kit	342	212.2	15.2	38.4	78.0	0.8
LC-MS/MS non-kit	40	277.2	33.2	79.9	100.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	247.6	11.9	13.2	98.6	0.9
Non-derivatized - MS/MS MassChrom®	120	229.9	11.5	29.6	96.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	236.7	15.0	26.4	90.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	233.1	43.5	140.3	91.6	0.8
Non-derivatized - MS/MS non-kit	202	230.0	15.3	30.7	90.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	46	226.0	12.4	28.2	88.3	0.8

LEUCINE (Leu µmol/L blood) (cont.)

Lot C2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	333.0	19.4	37.5	81.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	60	289.6	17.5	27.2	82.1	0.7
Derivatized - MS/MS non-kit	342	316.3	24.0	61.7	78.0	0.8
LC-MS/MS non-kit	40	378.0	40.3	72.7	100.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	358.4	15.9	19.9	98.6	0.9
Non-derivatized - MS/MS MassChrom®	120	327.4	18.0	43.5	96.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	346.6	22.6	38.7	90.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	328.4	21.3	42.3	91.6	0.8
Non-derivatized - MS/MS non-kit	202	330.2	22.2	40.7	90.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	46	328.0	17.7	47.7	88.3	0.8

Lot D2115 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	599.2	34.4	85.1	81.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	60	492.8	24.5	36.1	82.1	0.7
Derivatized - MS/MS non-kit	342	556.2	43.1	108.2	78.0	0.8
LC-MS/MS non-kit	40	670.4	83.4	174.7	100.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	599.1	35.5	36.5	98.6	0.9
Non-derivatized - MS/MS MassChrom®	120	543.1	28.5	72.8	96.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	599.7	34.9	63.0	90.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	560.3	36.2	70.5	91.6	0.8
Non-derivatized - MS/MS non-kit	202	566.2	33.8	81.5	90.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	46	564.5	26.9	73.6	88.3	0.8

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METHIONINE (Met µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	11.7	1.4	2.6	11.2	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	9.7	1.2	2.2	10.0	0.7
Derivatized - MS/MS non-kit	352	11.7	1.7	4.6	11.7	0.8
LC-MS/MS non-kit	30	8.0	1.7	2.1	8.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	9.4	0.5	0.7	10.1	0.8
Non-derivatized - MS/MS MassChrom®	130	7.8	0.9	2.6	7.7	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	9.3	0.9	1.7	8.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	8.4	0.7	1.2	8.2	0.7
Non-derivatized - MS/MS non-kit	192	9.4	0.9	1.8	9.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	7.5	1.5	3.5	6.5	0.7

Lot B2115 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	50.0	2.7	6.0	11.2	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	43.3	3.5	10.3	10.0	0.7
Derivatized - MS/MS non-kit	352	52.9	4.2	10.5	11.7	0.8
LC-MS/MS non-kit	30	43.3	6.7	22.5	8.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	52.3	2.7	3.9	10.1	0.8
Non-derivatized - MS/MS MassChrom®	130	40.4	2.1	9.3	7.7	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	47.4	3.4	5.7	8.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	44.1	2.7	4.7	8.2	0.7
Non-derivatized - MS/MS non-kit	192	49.1	3.6	10.5	9.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	39.2	5.0	11.1	6.5	0.7

METHIONINE (Met µmol/L blood) (cont.)

Lot C2115 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	124.8	7.9	17.4	11.2	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	108.0	9.2	28.9	10.0	0.7
Derivatized - MS/MS non-kit	352	130.0	11.1	25.9	11.7	0.8
LC-MS/MS non-kit	30	117.7	11.8	39.9	8.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	137.1	5.7	7.9	10.1	0.8
Non-derivatized - MS/MS MassChrom®	130	106.6	7.6	23.2	7.7	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	123.5	8.2	14.0	8.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	115.2	6.3	12.0	8.2	0.7
Non-derivatized - MS/MS non-kit	192	127.6	7.8	26.0	9.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	104.7	8.7	25.9	6.5	0.7

Lot D2115 – Enriched 250 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	204.6	12.2	21.4	11.2	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	173.9	13.9	43.6	10.0	0.7
Derivatized - MS/MS non-kit	352	213.5	17.3	37.1	11.7	0.8
LC-MS/MS non-kit	30	186.9	27.2	54.9	8.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	219.1	13.3	18.0	10.1	0.8
Non-derivatized - MS/MS MassChrom®	130	172.6	9.3	42.3	7.7	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	203.7	12.6	22.1	8.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	187.9	10.3	20.7	8.2	0.7
Non-derivatized - MS/MS non-kit	192	207.6	12.8	46.5	9.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	173.4	12.8	41.2	6.5	0.7

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ORNITHINE (Orn µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	126.3	15.7	22.8	132.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	179.9	12.5	39.8	195.1	0.9
Derivatized - MS/MS non-kit	272	102.3	9.7	47.2	108.3	0.6
Non-derivatized - MS/MS MassChrom®	100	173.3	12.4	36.5	188.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	372	149.7	11.1	19.5	161.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	276	144.1	10.5	33.4	156.4	0.8
Non-derivatized - MS/MS non-kit	100	129.8	12.1	29.2	142.5	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	154.1	13.9	28.7	166.4	0.8

Lot B2115 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	215.2	18.7	36.3	132.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	310.3	18.4	57.5	195.1	0.9
Derivatized - MS/MS non-kit	272	184.2	16.5	88.1	108.3	0.6
Non-derivatized - MS/MS MassChrom®	100	284.8	22.7	45.1	188.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	372	263.0	18.9	37.1	161.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	276	251.1	17.6	46.2	156.4	0.8
Non-derivatized - MS/MS non-kit	100	230.2	17.9	50.2	142.5	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	266.4	22.2	37.2	166.4	0.8

ORNITHINE (Orn µmol/L blood)(cont.)

Lot C2115 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	282.5	24.6	39.9	132.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	379.9	21.5	89.0	195.1	0.9
Derivatized - MS/MS non-kit	272	230.1	18.7	109.6	108.3	0.6
Non-derivatized - MS/MS MassChrom®	100	361.7	23.0	55.0	188.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	372	333.5	24.4	46.5	161.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	276	321.5	21.5	51.9	156.4	0.8
Non-derivatized - MS/MS non-kit	100	284.3	19.3	49.4	142.5	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	333.5	30.0	64.2	166.4	0.8

Lot D2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	350.4	30.1	48.7	132.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	464.6	31.7	94.4	195.1	0.9
Derivatized - MS/MS non-kit	271	289.6	23.9	135.8	108.3	0.6
Non-derivatized - MS/MS MassChrom®	100	416.2	28.2	73.9	188.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	372	407.1	28.7	58.6	161.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	276	385.3	23.8	56.4	156.4	0.8
Non-derivatized - MS/MS non-kit	100	344.0	22.8	64.3	142.5	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	406.9	34.8	74.8	166.4	0.8

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PHENYLALANINE (Phe µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	50	29.5	2.7	3.8	31.6	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	27.3	1.6	3.7	33.9	0.8
Derivatized - MS/MS non-kit	362	30.4	4.0	9.6	34.0	0.9
GSP® Phe Neonatal PerkinElmer	50	44.7	6.6	13.6	48.8	0.9
LC-MS/MS non-kit	40	31.6	4.5	6.1	31.4	1.0
NeoLISA® Phe Interscientifica	40	37.0	4.7	10.5	38.2	0.8
Neonatal Phe LabSystems	70	33.7	5.5	17.1	26.0	1.1
Neonatal® Phe Kit PerkinElmer	60	38.8	7.5	13.2	42.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	30.2	1.5	1.6	38.1	0.9
Non-derivatized - MS/MS MassChrom®	190	29.1	2.4	4.1	35.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	27.9	2.1	3.5	33.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	26.2	1.6	3.1	30.6	0.8
Non-derivatized - MS/MS non-kit	212	30.6	2.2	4.9	38.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	27.9	2.9	6.5	32.0	0.9

Lot B2115 – Enriched 150 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	50	174.1	8.5	12.3	31.6	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	169.2	7.1	19.7	33.9	0.8
Derivatized - MS/MS non-kit	362	174.5	13.5	31.3	34.0	0.9
GSP® Phe Neonatal PerkinElmer	50	196.0	18.9	23.0	48.8	0.9
LC-MS/MS non-kit	40	188.0	17.1	27.8	31.4	1.0
NeoLISA® Phe Interscientifica	40	164.0	11.9	37.1	38.2	0.8
Neonatal Phe LabSystems	70	186.5	21.4	45.4	26.0	1.1
Neonatal® Phe Kit PerkinElmer	60	168.6	14.6	29.2	42.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	185.9	9.8	15.1	38.1	0.9
Non-derivatized - MS/MS MassChrom®	190	172.1	7.6	15.2	35.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	169.9	10.4	16.2	33.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	157.6	8.8	17.9	30.6	0.8
Non-derivatized - MS/MS non-kit	212	179.6	11.1	24.0	38.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	172.7	11.6	38.0	32.0	0.9

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

Lot C2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	50	294.6	17.5	26.3	31.6	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	285.4	14.7	35.1	33.9	0.8
Derivatized - MS/MS non-kit	362	295.9	21.9	56.1	34.0	0.9
GSP® Phe Neonatal PerkinElmer	50	316.6	22.6	28.2	48.8	0.9
LC-MS/MS non-kit	40	341.9	29.5	71.8	31.4	1.0
NeoLISA® Phe Interscientifica	40	282.3	18.1	54.5	38.2	0.8
Neonatal Phe LabSystems	70	329.8	26.4	75.6	26.0	1.1
Neonatal® Phe Kit PerkinElmer	60	285.2	22.5	36.1	42.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	315.2	13.1	18.7	38.1	0.9
Non-derivatized - MS/MS MassChrom®	190	289.3	15.2	33.3	35.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	291.7	18.0	27.6	33.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	271.4	14.8	31.3	30.6	0.8
Non-derivatized - MS/MS non-kit	212	301.0	17.7	40.7	38.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	294.2	19.1	69.0	32.0	0.9

Lot D2115 – Enriched 450 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	50	440.9	31.0	41.1	31.6	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	406.9	15.8	41.5	33.9	0.8
Derivatized - MS/MS non-kit	362	433.2	33.4	82.8	34.0	0.9
GSP® Phe Neonatal PerkinElmer	50	462.9	27.8	36.3	48.8	0.9
LC-MS/MS non-kit	40	500.8	42.5	132.9	31.4	1.0
NeoLISA® Phe Interscientifica	40	407.8	36.9	81.1	38.2	0.8
Neonatal Phe LabSystems	70	525.7	51.1	102.1	26.0	1.1
Neonatal® Phe Kit PerkinElmer	60	403.7	25.7	53.4	42.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	444.9	24.0	28.9	38.1	0.9
Non-derivatized - MS/MS MassChrom®	190	413.2	20.6	56.5	35.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	414.9	24.5	73.8	33.7	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	389.4	22.3	45.1	30.6	0.8
Non-derivatized - MS/MS non-kit	212	426.3	24.3	68.8	38.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	430.0	23.8	101.0	32.0	0.9

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SUCCINYLACETONE (SUAC µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	70	0.5	0.1	0.1	0.7	0.4
Derivatized - MS/MS non-kit	150	0.6	0.2	0.4	0.5	0.6
Non-derivatized - MS/MS MassChrom®	40	0.6	0.1	0.1	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	340	0.6	0.1	0.3	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	258	0.3	0.1	0.2	0.3	0.2
Non-derivatized - MS/MS non-kit	90	0.4	0.1	0.3	0.4	0.5

Lot B2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	70	1.5	0.2	0.3	0.7	0.4
Derivatized - MS/MS non-kit	150	1.9	0.2	0.9	0.5	0.6
Non-derivatized - MS/MS MassChrom®	40	1.3	0.1	0.2	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	340	1.1	0.2	0.3	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	284	0.7	0.1	0.3	0.3	0.2
Non-derivatized - MS/MS non-kit	90	1.5	0.2	0.6	0.4	0.5

Lot C2115 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	70	5.8	3.5	8.3	0.7	0.4
Derivatized - MS/MS non-kit	150	5.9	0.6	2.9	0.5	0.6
Non-derivatized - MS/MS MassChrom®	40	3.6	0.2	0.7	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	340	3.0	0.4	0.7	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	284	2.3	0.3	0.6	0.3	0.2
Non-derivatized - MS/MS non-kit	90	5.1	0.5	2.9	0.4	0.5

SUCCINYLACETONE (SUAC µmol/L blood) cont.

Lot D2115 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	70	8.5	0.8	1.7	0.7	0.4
Derivatized - MS/MS non-kit	150	11.6	1.4	6.2	0.5	0.6
Non-derivatized - MS/MS MassChrom®	40	6.5	0.3	1.2	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	340	5.4	0.6	1.4	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	284	4.4	0.4	0.9	0.3	0.2
Non-derivatized - MS/MS non-kit	90	9.6	1.0	5.7	0.4	0.5

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TYROSINE (Tyr µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	26.3	2.6	2.7	21.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	60	28.2	1.9	3.7	30.2	0.8
Derivatized - MS/MS non-kit	362	28.2	3.0	7.7	28.6	0.8
LC-MS/MS non-kit	40	28.0	4.4	6.2	23.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	26.2	1.2	2.1	30.2	0.8
Non-derivatized - MS/MS MassChrom®	200	29.8	2.2	4.2	34.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	29.4	2.8	4.3	29.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	386	27.1	1.9	4.9	29.2	0.8
Non-derivatized - MS/MS non-kit	192	28.7	2.5	5.8	32.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	28.6	2.9	5.9	31.6	0.9

Lot B2115 – Enriched 300 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	250.4	14.2	18.5	21.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	60	278.7	12.7	31.5	30.2	0.8
Derivatized - MS/MS non-kit	362	278.0	20.0	50.5	28.6	0.8
LC-MS/MS non-kit	40	272.9	29.3	42.2	23.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	280.0	14.4	26.7	30.2	0.8
Non-derivatized - MS/MS MassChrom®	200	289.3	14.1	35.3	34.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	293.9	19.8	30.5	29.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	386	265.0	14.5	38.7	29.2	0.8
Non-derivatized - MS/MS non-kit	192	282.8	19.9	40.7	32.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	292.0	28.8	57.8	31.6	0.9

TYROSINE (Tyr µmol/L blood) (cont.)

Lot C2115 – Enriched 600 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	481.5	30.3	33.9	21.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	60	525.9	25.1	74.2	30.2	0.8
Derivatized - MS/MS non-kit	362	520.8	35.2	92.5	28.6	0.8
LC-MS/MS non-kit	40	536.6	40.7	47.0	23.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	528.2	25.4	45.7	30.2	0.8
Non-derivatized - MS/MS MassChrom®	200	544.5	30.9	68.5	34.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	558.1	36.9	56.5	29.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	386	503.4	27.9	78.7	29.2	0.8
Non-derivatized - MS/MS non-kit	192	526.7	31.6	70.4	32.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	536.8	40.1	87.1	31.6	0.9

Lot D2115 – Enriched 900 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	726.1	35.9	46.5	21.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	60	767.8	38.0	72.6	30.2	0.8
Derivatized - MS/MS non-kit	362	771.8	53.6	127.0	28.6	0.8
LC-MS/MS non-kit	40	796.6	64.6	71.6	23.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	764.7	40.3	71.6	30.2	0.8
Non-derivatized - MS/MS MassChrom®	200	785.0	41.9	104.4	34.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	821.8	51.5	80.6	29.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	730.6	38.7	107.2	29.2	0.8
Non-derivatized - MS/MS non-kit	192	767.9	48.3	105.8	32.3	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	794.7	48.4	136.8	31.6	0.9

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VALINE (Val µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	79.0	12.3	33.8	79.3	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	67.9	5.1	15.0	73.0	0.7
Derivatized - MS/MS non-kit	340	86.8	13.1	45.2	90.2	0.7
LC-MS/MS non-kit	40	72.6	6.6	8.7	85.9	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	68.9	3.2	6.2	78.5	0.8
Non-derivatized - MS/MS MassChrom®	120	57.8	5.3	12.0	64.5	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	72.4	5.7	10.8	78.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	69.2	3.7	6.2	76.0	0.8
Non-derivatized - MS/MS non-kit	170	66.3	5.3	10.6	73.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	60.1	5.2	9.3	67.1	0.8

Lot B2115 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	220.5	28.4	56.3	79.3	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	219.8	14.6	32.4	73.0	0.7
Derivatized - MS/MS non-kit	340	244.3	22.3	54.5	90.2	0.7
LC-MS/MS non-kit	40	274.3	29.2	40.2	85.9	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	258.4	14.9	25.1	78.5	0.8
Non-derivatized - MS/MS MassChrom®	120	204.7	11.8	28.3	64.5	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	267.1	19.4	39.7	78.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	251.3	15.1	23.5	76.0	0.8
Non-derivatized - MS/MS non-kit	170	235.9	16.5	38.8	73.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	232.5	19.7	32.8	67.1	0.8

VALINE (Val µmol/L blood) (cont.)

Lot C2115 – Enriched 350 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	314.8	36.8	88.6	79.3	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	303.9	21.8	35.4	73.0	0.7
Derivatized - MS/MS non-kit	340	336.4	28.3	69.1	90.2	0.7
LC-MS/MS non-kit	40	367.8	32.9	52.5	85.9	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	364.9	18.6	27.4	78.5	0.8
Non-derivatized - MS/MS MassChrom®	120	286.1	16.5	40.6	64.5	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	377.9	26.9	55.5	78.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	376	359.7	21.0	34.4	76.0	0.8
Non-derivatized - MS/MS non-kit	170	334.7	21.8	56.3	73.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	328.3	25.8	43.9	67.1	0.8

Lot D2115 – Enriched 500 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	426.6	46.3	92.9	79.3	0.7
Derivatized - MS/MS MassChrom® Chromsystems	50	411.2	21.7	47.8	73.0	0.7
Derivatized - MS/MS non-kit	340	453.7	36.3	95.4	90.2	0.7
LC-MS/MS non-kit	40	489.1	51.0	64.3	85.9	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	481.6	30.4	46.7	78.5	0.8
Non-derivatized - MS/MS MassChrom®	120	381.1	31.1	85.9	64.5	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	513.7	33.9	74.1	78.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	366	479.9	28.6	48.9	76.0	0.8
Non-derivatized - MS/MS non-kit	170	444.5	30.7	84.4	73.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	443.6	34.2	51.9	67.1	0.8

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TOTAL GALACTOSE (TGal mg/dL blood)

Lot A2105 – Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence TGal Neonatal PerkinElmer	170	4.2	0.7	1.0	0.5	0.8
Fluorometric manual TGal - non-kit	80	4.6	0.7	1.1	0.2	0.9
GSP® TGal Neonatal PerkinElmer	314	4.9	0.4	1.1	-0.1	1.0
NeoLISA® TGal Interscientifica	40	4.4	0.4	0.5	0.2	0.8
Neonatal® HORM Kit PerkinElmer	102	4.3	0.6	1.2	0.1	0.8
ZenTech Neonatal TGal Enzymatic Colorimetric	130	6.8	0.7	1.3	4.1	0.7

Lot B2105 – Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence TGal Neonatal PerkinElmer	170	8.5	1.0	1.6	0.5	0.8
Fluorometric manual TGal - non-kit	80	9.4	1.0	1.5	0.2	0.9
GSP® TGal Neonatal PerkinElmer	314	9.4	0.9	1.6	-0.1	1.0
NeoLISA® TGal Interscientifica	40	7.8	0.7	0.8	0.2	0.8
Neonatal® HORM Kit PerkinElmer	102	8.4	1.1	2.1	0.1	0.8
ZenTech Neonatal TGal Enzymatic Colorimetric	130	11.3	1.2	2.2	4.1	0.7

Lot C2105 – Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence TGal Neonatal PerkinElmer	170	24.0	2.1	3.1	0.5	0.8
Fluorometric manual TGal - non-kit	80	27.5	1.3	3.7	0.2	0.9
GSP® TGal Neonatal PerkinElmer	314	29.0	2.6	4.5	-0.1	1.0
NeoLISA® TGal Interscientifica	40	23.9	2.0	4.7	0.2	0.8
Neonatal® HORM Kit PerkinElmer	102	25.1	2.6	4.6	0.1	0.8
ZenTech Neonatal TGal Enzymatic Colorimetric	130	23.4	2.3	4.7	4.1	0.7

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FREE CARNITINE (C0 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	11.84	0.96	1.37	11.0	1.2
Derivatized - MS/MS MassChrom® Chromsystems	80	9.93	0.73	2.65	10.0	1.0
Derivatized - MS/MS non-kit	370	13.59	3.05	9.30	13.4	1.3
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	12.16	0.51	1.04	12.1	1.1
Non-derivatized - MS/MS MassChrom®	140	10.85	1.58	5.96	10.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	10.72	0.82	1.67	10.5	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	11.02	0.76	1.54	10.8	1.0
Non-derivatized - MS/MS non-kit	200	12.16	1.08	1.95	12.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	11.92	1.18	3.18	11.7	1.1

Lot B2115 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	22.67	1.44	2.62	11.0	1.2
Derivatized - MS/MS MassChrom® Chromsystems	80	20.25	1.56	5.85	10.0	1.0
Derivatized - MS/MS non-kit	369	25.62	5.58	2.40	13.4	1.3
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	23.31	1.21	1.66	12.1	1.1
Non-derivatized - MS/MS MassChrom®	140	17.64	0.93	2.30	10.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	20.48	1.46	2.99	10.5	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	20.91	1.43	3.00	10.8	1.0
Non-derivatized - MS/MS non-kit	200	23.29	2.08	3.95	12.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	22.86	2.15	6.30	11.7	1.1

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

Lot C2115 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	34.36	2.48	4.68	11.0	1.2
Derivatized - MS/MS MassChrom® Chromsystems	80	30.32	2.04	8.20	10.0	1.0
Derivatized - MS/MS non-kit	368	38.65	8.25	3.70	13.4	1.3
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	34.73	1.45	2.90	12.1	1.1
Non-derivatized - MS/MS MassChrom®	140	26.89	1.69	4.30	10.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	30.48	2.27	4.31	10.5	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	30.97	2.00	4.36	10.8	1.0
Non-derivatized - MS/MS non-kit	200	34.51	2.75	5.03	12.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	33.63	2.55	9.24	11.7	1.1

Lot D2115 – Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	48.86	3.60	6.84	11.0	1.2
Derivatized - MS/MS MassChrom® Chromsystems	80	40.45	2.24	9.98	10.0	1.0
Derivatized - MS/MS non-kit	370	54.62	5.44	12.11	13.4	1.3
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	46.11	2.73	3.29	12.1	1.1
Non-derivatized - MS/MS MassChrom®	140	35.32	1.92	4.95	10.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	41.31	2.95	5.89	10.5	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	41.66	2.53	5.72	10.8	1.0
Non-derivatized - MS/MS non-kit	200	45.91	3.40	7.14	12.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	45.83	3.62	12.21	11.7	1.1

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ACETYLCARNITINE (C2 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	8.30	0.70	0.91	7.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	7.34	0.46	1.32	7.2	0.8
Derivatized - MS/MS non-kit	354	7.99	0.80	2.05	7.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	7.58	0.43	0.67	7.6	1.0
Non-derivatized - MS/MS MassChrom®	140	5.86	0.40	0.90	5.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	6.08	0.48	0.80	6.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	5.68	0.41	1.01	5.7	0.8
Non-derivatized - MS/MS non-kit	180	6.66	0.54	0.91	6.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	6.01	0.54	0.85	6.0	0.8

Lot B2115 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	16.97	1.11	1.96	7.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	15.07	1.11	1.75	7.2	0.8
Derivatized - MS/MS non-kit	354	16.81	1.50	3.37	7.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	18.06	1.10	1.19	7.6	1.0
Non-derivatized - MS/MS MassChrom®	140	13.76	0.78	1.66	5.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	14.52	1.12	1.81	6.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	13.56	0.91	2.32	5.7	0.8
Non-derivatized - MS/MS non-kit	180	15.56	1.02	2.05	6.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	14.12	1.12	1.60	6.0	0.8

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

Lot C2115 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	26.06	1.98	2.75	7.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	23.07	1.40	2.10	7.2	0.8
Derivatized - MS/MS non-kit	354	24.92	1.93	5.06	7.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	28.26	1.71	2.35	7.6	1.0
Non-derivatized - MS/MS MassChrom®	140	21.56	1.14	2.32	5.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	23.02	1.75	2.77	6.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	21.63	1.42	3.60	5.7	0.8
Non-derivatized - MS/MS non-kit	180	25.17	1.51	3.64	6.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	22.27	1.60	2.77	6.0	0.8

Lot D2115 – Enriched 30 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	36.46	1.86	2.56	7.9	0.9
Derivatized - MS/MS MassChrom® Chromsystems	80	31.32	2.05	3.59	7.2	0.8
Derivatized - MS/MS non-kit	354	34.32	2.64	7.26	7.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	38.58	2.63	3.06	7.6	1.0
Non-derivatized - MS/MS MassChrom®	140	29.38	1.40	3.26	5.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	31.62	2.31	3.89	6.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	29.58	1.94	4.81	5.7	0.8
Non-derivatized - MS/MS non-kit	180	33.45	2.14	4.44	6.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	30.56	1.97	3.37	6.0	0.8

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PROPIONYLCARNITINE (C3 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.93	0.11	0.14	0.8	1.0
Derivatized - MS/MS MassChrom® Chromsystems	80	0.81	0.31	0.78	0.8	0.9
Derivatized - MS/MS non-kit	356	0.82	0.09	0.22	0.8	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.82	0.04	0.08	0.8	1.0
Non-derivatized - MS/MS MassChrom®	140	0.67	0.05	0.11	0.6	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.71	0.05	0.09	0.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	390	0.83	0.06	0.10	0.8	1.0
Non-derivatized - MS/MS non-kit	180	0.83	0.07	0.14	0.8	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.66	0.06	0.11	0.6	0.8

Lot B2115 – Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	4.51	0.22	0.34	0.8	1.0
Derivatized - MS/MS MassChrom® Chromsystems	80	4.17	0.77	1.73	0.8	0.9
Derivatized - MS/MS non-kit	356	4.34	0.39	0.76	0.8	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	4.61	0.23	0.29	0.8	1.0
Non-derivatized - MS/MS MassChrom®	140	3.71	0.28	0.52	0.6	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	4.01	0.26	0.41	0.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	400	4.68	0.28	0.54	0.8	1.0
Non-derivatized - MS/MS non-kit	180	4.55	0.28	0.56	0.8	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	3.75	0.27	0.62	0.6	0.8

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

Lot C2115 – Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	8.42	0.55	0.69	0.8	1.0
Derivatized - MS/MS MassChrom® Chromsystems	80	7.56	1.14	2.52	0.8	0.9
Derivatized - MS/MS non-kit	356	7.81	0.66	1.35	0.8	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	8.38	0.39	0.73	0.8	1.0
Non-derivatized - MS/MS MassChrom®	140	6.95	0.43	0.86	0.6	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	7.37	0.47	0.71	0.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	400	8.65	0.50	1.02	0.8	1.0
Non-derivatized - MS/MS non-kit	180	8.38	0.53	1.16	0.8	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	6.91	0.47	1.05	0.6	0.8

Lot D2115 – Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	12.47	0.74	0.94	0.8	1.0
Derivatized - MS/MS MassChrom® Chromsystems	80	11.14	1.55	3.34	0.8	0.9
Derivatized - MS/MS non-kit	356	11.52	1.10	1.97	0.8	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	12.17	0.79	1.21	0.8	1.0
Non-derivatized - MS/MS MassChrom®	140	10.07	0.50	1.31	0.6	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	10.79	0.68	1.11	0.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	400	12.56	0.72	1.45	0.8	1.0
Non-derivatized - MS/MS non-kit	180	12.09	0.77	1.47	0.8	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	10.15	0.56	1.43	0.6	0.8

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MALONYLCARNITINE (C3DC µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.02	0.01	0.01	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	60	0.04	0.01	0.02	0.1	0.9
Derivatized - MS/MS non-kit	342	0.04	0.02	0.08	0.0	0.6

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.37	0.03	0.13	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	60	0.50	0.06	0.19	0.1	0.9
Derivatized - MS/MS non-kit	366	0.30	0.04	0.14	0.0	0.6

Lot C2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.09	0.09	0.47	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	60	1.42	0.11	0.54	0.1	0.9
Derivatized - MS/MS non-kit	366	0.85	0.10	0.39	0.0	0.6

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.25	0.13	0.76	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	60	2.71	0.18	1.07	0.1	0.9
Derivatized - MS/MS non-kit	366	1.70	0.19	0.79	0.0	0.6

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

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	0.04	0.01	0.02	0.0	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	0.05	0.01	0.05	0.1	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	334	0.05	0.01	0.01	0.1	0.4
Non-derivatized - MS/MS non-kit	110	0.07	0.01	0.05	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.02	0.01	0.01	0.0	0.2

Lot B2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	0.34	0.03	0.13	0.0	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	0.41	0.07	0.30	0.1	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	334	0.45	0.07	0.25	0.1	0.4
Non-derivatized - MS/MS non-kit	110	0.53	0.06	0.35	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.19	0.02	0.05	0.0	0.2

Lot C2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	0.70	0.06	0.27	0.0	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	0.86	0.14	0.59	0.1	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	334	0.92	0.06	0.26	0.1	0.4
Non-derivatized - MS/MS non-kit	110	1.11	0.11	0.79	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.39	0.03	0.11	0.0	0.2

Lot D2115 – Enriched 5.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	1.60	0.10	0.63	0.0	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	1.92	0.24	0.87	0.1	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	334	2.03	0.12	0.52	0.1	0.4
Non-derivatized - MS/MS non-kit	110	2.37	0.21	1.59	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.91	0.05	0.22	0.0	0.2

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BUTYRYLCARNITINE (C4 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.14	0.02	0.04	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.08	0.01	0.02	0.1	0.7
Derivatized - MS/MS non-kit	356	0.12	0.04	0.09	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.09	0.01	0.01	0.1	0.8
Non-derivatized - MS/MS MassChrom®	130	0.08	0.01	0.02	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	0.10	0.01	0.02	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	366	0.12	0.08	0.41	0.1	0.7
Non-derivatized - MS/MS non-kit	160	0.10	0.02	0.06	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.07	0.02	0.02	0.1	0.6

Lot B2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.88	0.05	0.07	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.72	0.06	0.10	0.1	0.7
Derivatized - MS/MS non-kit	356	0.86	0.13	0.32	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.87	0.05	0.08	0.1	0.8
Non-derivatized - MS/MS MassChrom®	130	0.77	0.05	0.09	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	0.79	0.06	0.09	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	366	0.85	0.18	0.91	0.1	0.7
Non-derivatized - MS/MS non-kit	160	0.92	0.10	0.53	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.69	0.07	0.15	0.1	0.6

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

Lot C2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	2.43	0.17	0.19	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	2.06	0.16	0.38	0.1	0.7
Derivatized - MS/MS non-kit	356	2.29	0.22	0.41	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.43	0.13	0.27	0.1	0.8
Non-derivatized - MS/MS MassChrom®	130	2.15	0.14	0.22	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	2.23	0.15	0.26	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	366	2.31	0.33	1.39	0.1	0.7
Non-derivatized - MS/MS non-kit	160	2.75	0.33	2.02	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	1.98	0.13	0.38	0.1	0.6

Lot D2115 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	4.21	0.30	0.51	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	3.36	0.18	0.43	0.1	0.7
Derivatized - MS/MS non-kit	356	3.82	0.35	0.69	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	4.05	0.24	0.44	0.1	0.8
Non-derivatized - MS/MS MassChrom®	130	3.58	0.22	0.45	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	3.70	0.24	0.41	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	366	3.70	0.47	1.89	0.1	0.7
Non-derivatized - MS/MS non-kit	160	4.74	0.55	3.70	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	3.27	0.21	0.55	0.1	0.6

2022 Quality Control Data Summaries of Statistical Analyses

HYDROXYBUTYRYLCARNITINE (C4OH µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.05	0.01	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	50	0.06	0.01	0.01	0.1	0.7
Derivatized - MS/MS non-kit	334	0.07	0.03	0.06	0.1	0.7

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.34	0.04	0.09	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	50	0.38	0.03	0.07	0.1	0.7
Derivatized - MS/MS non-kit	334	0.37	0.04	0.12	0.1	0.7

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.59	0.06	0.12	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	50	0.73	0.06	0.13	0.1	0.7
Derivatized - MS/MS non-kit	334	0.71	0.08	0.23	0.1	0.7

Lot D2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.50	0.18	0.33	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	50	1.71	0.10	0.33	0.1	0.7
Derivatized - MS/MS non-kit	334	1.71	0.18	0.58	0.1	0.7

2022 Quality Control Data Summaries of Statistical Analyses

ISOVALERYLCARNITINE (C5 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.06	0.01	0.02	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.07	0.01	0.02	0.1	0.9
Derivatized - MS/MS non-kit	356	0.07	0.02	0.05	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.06	0.01	0.01	0.1	1.0
Non-derivatized - MS/MS MassChrom®	140	0.12	0.01	0.18	0.1	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	0.05	0.02	0.04	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	403	0.08	0.06	0.41	0.1	0.9
Non-derivatized - MS/MS non-kit	192	0.06	0.01	0.02	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.07	0.02	0.02	0.1	0.9

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.43	0.03	0.08	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.52	0.05	0.07	0.1	0.9
Derivatized - MS/MS non-kit	356	0.51	0.05	0.09	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.54	0.03	0.05	0.1	1.0
Non-derivatized - MS/MS MassChrom®	140	0.57	0.04	0.15	0.1	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	0.47	0.04	0.07	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	406	0.55	0.15	0.89	0.1	0.9
Non-derivatized - MS/MS non-kit	192	0.54	0.04	0.08	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.52	0.05	0.12	0.1	0.9

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

Lot C2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	1.20	0.09	0.29	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	1.43	0.10	0.16	0.1	0.9
Derivatized - MS/MS non-kit	356	1.40	0.13	0.24	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.53	0.08	0.13	0.1	1.0
Non-derivatized - MS/MS MassChrom®	140	1.48	0.09	0.24	0.1	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	1.34	0.10	0.17	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	406	1.47	0.29	1.56	0.1	0.9
Non-derivatized - MS/MS non-kit	192	1.49	0.11	0.23	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	1.39	0.11	0.35	0.1	0.9

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	2.36	0.21	0.45	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	69	2.80	0.21	0.15	0.1	0.9
Derivatized - MS/MS non-kit	356	2.78	0.25	0.48	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.93	0.18	0.24	0.1	1.0
Non-derivatized - MS/MS MassChrom®	140	2.86	0.17	0.49	0.1	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	464	2.65	0.17	0.33	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	406	2.77	0.43	2.07	0.1	0.9
Non-derivatized - MS/MS non-kit	192	2.92	0.19	0.41	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	2.67	0.21	0.65	0.1	0.9

2022 Quality Control Data Summaries of Statistical Analyses

TIGLYLCARNITINE (C5:1 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	28	0.04	0.01	0.03	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	48	0.02	0.00	0.01	0.0	0.6
Derivatized - MS/MS non-kit	348	0.03	0.01	0.03	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.01	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS MassChrom®	90	0.01	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	400	0.01	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.01	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS non-kit	160	0.02	0.01	0.04	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.01	0.01	0.02	0.0	0.5

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	28	0.42	0.05	0.20	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	48	0.33	0.03	0.05	0.0	0.6
Derivatized - MS/MS non-kit	356	0.34	0.04	0.10	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.31	0.02	0.02	0.0	0.6
Non-derivatized - MS/MS MassChrom®	100	0.23	0.03	0.07	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	0.23	0.02	0.05	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	0.26	0.02	0.06	0.0	0.5
Non-derivatized - MS/MS non-kit	160	0.45	0.06	0.54	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.23	0.04	0.05	0.0	0.5

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

Lot C2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	28	1.18	0.10	0.56	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	48	0.92	0.07	0.12	0.0	0.6
Derivatized - MS/MS non-kit	356	0.96	0.11	0.27	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.90	0.05	0.05	0.0	0.6
Non-derivatized - MS/MS MassChrom®	100	0.73	0.07	0.19	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	0.70	0.06	0.13	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	0.76	0.05	0.18	0.0	0.5
Non-derivatized - MS/MS non-kit	160	1.32	0.18	1.53	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.68	0.07	0.10	0.0	0.5

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	28	2.45	0.31	1.27	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	48	1.83	0.14	0.21	0.0	0.6
Derivatized - MS/MS non-kit	356	1.92	0.19	0.52	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	1.79	0.13	0.14	0.0	0.6
Non-derivatized - MS/MS MassChrom®	100	1.48	0.12	0.38	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	1.39	0.10	0.26	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	1.51	0.11	0.33	0.0	0.5
Non-derivatized - MS/MS non-kit	160	2.57	0.30	2.75	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	1.35	0.11	0.14	0.0	0.5

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GLUTARYLCARNITINE (C5DC µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.03	0.01	0.01	0.1	1.1
Derivatized - MS/MS MassChrom® Chromsystems	70	0.04	0.01	0.03	0.0	1.3
Derivatized - MS/MS non-kit	357	0.02	0.01	0.02	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.04	0.01	0.01	0.1	0.9
Non-derivatized - MS/MS MassChrom®	134	0.07	0.02	0.03	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	0.04	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	354	0.03	0.01	0.04	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.04	0.01	0.02	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.09	0.05	0.10	0.1	0.8

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.61	0.05	0.13	0.1	1.1
Derivatized - MS/MS MassChrom® Chromsystems	70	0.66	0.08	0.14	0.0	1.3
Derivatized - MS/MS non-kit	362	0.30	0.06	0.17	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.47	0.04	0.05	0.1	0.9
Non-derivatized - MS/MS MassChrom®	134	0.62	0.06	0.09	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	0.50	0.04	0.06	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	0.42	0.04	0.09	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.49	0.05	0.13	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.50	0.11	0.17	0.1	0.8

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

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	1.20	0.10	0.21	0.1	1.1
Derivatized - MS/MS MassChrom® Chromsystems	70	1.30	0.16	0.28	0.0	1.3
Derivatized - MS/MS non-kit	362	0.56	0.06	0.24	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.92	0.07	0.08	0.1	0.9
Non-derivatized - MS/MS MassChrom®	134	1.18	0.12	0.20	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	0.99	0.08	0.12	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	0.84	0.07	0.15	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.95	0.08	0.24	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.92	0.17	0.28	0.1	0.8

Lot D2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	2.85	0.26	0.64	0.1	1.1
Derivatized - MS/MS MassChrom® Chromsystems	70	3.15	0.38	0.73	0.0	1.3
Derivatized - MS/MS non-kit	362	1.39	0.15	0.59	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.19	0.14	0.18	0.1	0.9
Non-derivatized - MS/MS MassChrom®	134	2.78	0.24	0.43	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	404	2.39	0.20	0.30	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	384	2.04	0.21	0.57	0.0	0.8
Non-derivatized - MS/MS non-kit	190	2.28	0.18	0.58	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	2.17	0.30	0.46	0.1	0.8

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HYDROXYISOVALERYLCARNITINE (C5OH µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.27	0.04	0.11	0.3	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	0.37	0.04	0.07	0.4	0.8
Derivatized - MS/MS non-kit	372	0.34	0.04	0.09	0.3	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.56	0.03	0.04	0.6	0.9
Non-derivatized - MS/MS MassChrom®	90	0.31	0.03	0.08	0.3	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	0.40	0.04	0.10	0.4	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	0.49	0.04	0.12	0.5	0.6
Non-derivatized - MS/MS non-kit	180	0.52	0.04	0.11	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	0.24	0.03	0.06	0.2	0.4

Lot B2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.85	0.07	0.41	0.3	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	1.13	0.11	0.18	0.4	0.8
Derivatized - MS/MS non-kit	372	1.08	0.12	0.26	0.3	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.45	0.07	0.16	0.6	0.9
Non-derivatized - MS/MS MassChrom®	90	0.75	0.05	0.17	0.3	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	0.97	0.07	0.23	0.4	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	1.11	0.08	0.23	0.5	0.6
Non-derivatized - MS/MS non-kit	180	1.35	0.09	0.27	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	0.61	0.06	0.14	0.2	0.4

Lot C2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.44	0.12	0.69	0.3	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	1.88	0.13	0.23	0.4	0.8
Derivatized - MS/MS non-kit	372	1.83	0.19	0.40	0.3	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.34	0.10	0.21	0.6	0.9
Non-derivatized - MS/MS MassChrom®	90	1.22	0.10	0.25	0.3	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	1.55	0.11	0.33	0.4	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	1.76	0.11	0.35	0.5	0.6
Non-derivatized - MS/MS non-kit	180	2.19	0.16	0.47	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	0.98	0.08	0.18	0.2	0.4

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

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.05	0.20	0.92	0.3	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	2.76	0.22	0.38	0.4	0.8
Derivatized - MS/MS non-kit	372	2.64	0.28	0.56	0.3	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	3.20	0.19	0.35	0.6	0.9
Non-derivatized - MS/MS MassChrom®	90	1.68	0.17	0.44	0.3	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	2.10	0.15	0.48	0.4	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	2.37	0.15	0.45	0.5	0.6
Non-derivatized - MS/MS non-kit	180	3.01	0.22	0.65	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	1.38	0.08	0.29	0.2	0.4

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HEXANOYLCARNITINE (C6 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.06	0.01	0.05	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.03	0.01	0.02	0.1	0.6
Derivatized - MS/MS non-kit	340	0.03	0.01	0.04	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS MassChrom®	140	0.02	0.00	0.04	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	0.05	0.07	0.47	0.1	0.7
Non-derivatized - MS/MS non-kit	160	0.02	0.01	0.01	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.01	0.01	0.01	0.0	0.7

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.38	0.03	0.05	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.34	0.03	0.04	0.1	0.6
Derivatized - MS/MS non-kit	360	0.38	0.04	0.08	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens		0.40	0.02	0.03	0.0	0.7
Non-derivatized - MS/MS MassChrom®	140	0.39	0.02	0.04	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.38	0.03	0.04	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	0.46	0.16	1.02	0.1	0.7
Non-derivatized - MS/MS non-kit	160	0.39	0.04	0.07	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.37	0.04	0.06	0.0	0.7

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

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.69	0.06	0.09	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.64	0.06	0.09	0.1	0.6
Derivatized - MS/MS non-kit	360	0.73	0.07	0.14	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.78	0.05	0.07	0.0	0.7
Non-derivatized - MS/MS MassChrom®	140	0.73	0.05	0.09	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.76	0.06	0.09	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	0.89	0.26	1.69	0.1	0.7
Non-derivatized - MS/MS non-kit	160	0.79	0.06	0.10	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.71	0.06	0.10	0.0	0.7

Lot D2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.53	0.08	0.11	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	1.41	0.10	0.19	0.1	0.6
Derivatized - MS/MS non-kit	360	1.82	0.19	0.40	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.87	0.10	0.13	0.0	0.7
Non-derivatized - MS/MS MassChrom®	140	1.73	0.10	0.20	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	1.83	0.11	0.20	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	1.87	0.35	2.09	0.1	0.7
Non-derivatized - MS/MS non-kit	160	1.95	0.16	0.25	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	1.68	0.10	0.23	0.0	0.7

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OCTANOYLCARNITINE (C8 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.02	0.01	0.01	0.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	70	0.02	0.01	0.01	0.0	0.8
Derivatized - MS/MS non-kit	340	0.03	0.01	0.05	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.02	0.00	0.00	0.0	0.9
Non-derivatized - MS/MS MassChrom®	190	0.03	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.03	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	388	0.03	0.01	0.07	0.0	0.9
Non-derivatized - MS/MS non-kit	202	0.04	0.01	0.02	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.03	0.01	0.01	0.0	0.9

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.45	0.03	0.05	0.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	70	0.43	0.05	0.08	0.0	0.8
Derivatized - MS/MS non-kit	362	0.51	0.06	0.11	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.49	0.03	0.04	0.0	0.9
Non-derivatized - MS/MS MassChrom®	190	0.44	0.02	0.06	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.48	0.03	0.05	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	0.46	0.07	0.33	0.0	0.9
Non-derivatized - MS/MS non-kit	202	0.54	0.04	0.18	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.46	0.05	0.09	0.0	0.9

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

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.90	0.06	0.08	0.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	70	0.84	0.10	0.13	0.0	0.8
Derivatized - MS/MS non-kit	362	0.99	0.11	0.18	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.96	0.05	0.06	0.0	0.9
Non-derivatized - MS/MS MassChrom®	190	0.92	0.19	0.65	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.95	0.07	0.11	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	0.91	0.13	0.57	0.0	0.9
Non-derivatized - MS/MS non-kit	202	1.06	0.08	0.35	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.89	0.07	0.19	0.0	0.9

Lot D2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	2.20	0.16	0.21	0.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	70	1.99	0.17	0.24	0.0	0.8
Derivatized - MS/MS non-kit	362	2.39	0.25	0.48	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.32	0.16	0.18	0.0	0.9
Non-derivatized - MS/MS MassChrom®	190	2.13	0.11	0.31	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	2.32	0.15	0.25	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	2.15	0.23	0.80	0.0	0.9
Non-derivatized - MS/MS non-kit	202	2.55	0.18	0.81	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	2.17	0.13	0.39	0.0	0.9

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DECANOYLCARNITINE (C10 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.02	0.01	0.01	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	0.02	0.01	0.01	0.0	0.6
Derivatized - MS/MS non-kit	351	0.03	0.01	0.04	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.02	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS MassChrom®	190	0.03	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.03	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	386	0.03	0.00	0.02	0.0	0.8
Non-derivatized - MS/MS non-kit	182	0.05	0.01	0.04	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.02	0.01	0.01	0.0	0.7

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.32	0.02	0.03	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	0.26	0.02	0.08	0.0	0.6
Derivatized - MS/MS non-kit	362	0.42	0.06	0.12	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.40	0.03	0.03	0.0	0.8
Non-derivatized - MS/MS MassChrom®	190	0.38	0.02	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.38	0.03	0.06	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	396	0.37	0.03	0.06	0.0	0.8
Non-derivatized - MS/MS non-kit	182	0.47	0.04	0.09	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.36	0.03	0.06	0.0	0.7

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

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.65	0.05	0.09	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	0.57	0.05	0.17	0.0	0.6
Derivatized - MS/MS non-kit	362	0.85	0.10	0.23	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.81	0.04	0.05	0.0	0.8
Non-derivatized - MS/MS MassChrom®	190	0.76	0.05	0.10	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	0.76	0.06	0.10	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	396	0.75	0.05	0.12	0.0	0.8
Non-derivatized - MS/MS non-kit	182	0.92	0.08	0.17	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.72	0.06	0.11	0.0	0.7

Lot D2115 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.67	0.12	0.16	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	1.46	0.11	0.48	0.0	0.6
Derivatized - MS/MS non-kit	362	2.15	0.26	0.53	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.05	0.15	0.16	0.0	0.8
Non-derivatized - MS/MS MassChrom®	190	1.93	0.11	0.25	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	454	1.93	0.14	0.23	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	396	1.90	0.12	0.27	0.0	0.8
Non-derivatized - MS/MS non-kit	182	2.28	0.19	0.39	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	1.83	0.11	0.26	0.0	0.7

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DODECANOYLCARNITINE (C12 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.03	0.01	0.01	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.03	0.01	0.02	0.0	0.8
Derivatized - MS/MS non-kit	323	0.04	0.02	0.04	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.01	0.00	0.01	0.0	1.0
Non-derivatized - MS/MS MassChrom®	140	0.02	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	422	0.02	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	328	0.01	0.00	0.01	0.0	0.9
Non-derivatized - MS/MS non-kit	180	0.03	0.01	0.02	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.02	0.01	0.01	0.1	0.8

Lot B2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.80	0.07	0.10	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	0.83	0.08	0.17	0.0	0.8
Derivatized - MS/MS non-kit	340	0.91	0.11	0.22	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.02	0.06	0.11	0.0	1.0
Non-derivatized - MS/MS MassChrom®	140	0.84	0.05	0.11	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	422	0.91	0.07	0.10	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	338	0.86	0.06	0.11	0.0	0.9
Non-derivatized - MS/MS non-kit	180	1.03	0.09	0.41	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	0.87	0.07	0.17	0.1	0.8

Lot C2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.67	0.13	0.24	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	1.70	0.16	0.36	0.0	0.8
Derivatized - MS/MS non-kit	340	1.83	0.23	0.42	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.07	0.12	0.19	0.0	1.0
Non-derivatized - MS/MS MassChrom®	140	1.74	0.10	0.23	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	422	1.89	0.14	0.20	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	338	1.76	0.11	0.24	0.0	0.9
Non-derivatized - MS/MS non-kit	180	2.09	0.19	0.85	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	1.81	0.14	0.35	0.1	0.8

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

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.51	0.16	0.27	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	2.50	0.20	0.51	0.0	0.8
Derivatized - MS/MS non-kit	340	2.79	0.36	0.68	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	3.03	0.20	0.31	0.0	1.0
Non-derivatized - MS/MS MassChrom®	140	2.53	0.14	0.35	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	422	2.81	0.20	0.29	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	338	2.61	0.16	0.33	0.0	0.9
Non-derivatized - MS/MS non-kit	180	3.05	0.25	1.13	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	50	2.48	0.44	0.68	0.1	0.8

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MYRISTOYLCARNITINE (C14 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.04	0.01	0.01	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	0.06	0.01	0.02	0.1	0.7
Derivatized - MS/MS non-kit	362	0.07	0.03	0.08	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.05	0.00	0.01	0.0	0.9
Non-derivatized - MS/MS MassChrom®	140	0.04	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	0.04	0.01	0.01	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	0.04	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS non-kit	180	0.06	0.01	0.02	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.04	0.01	0.01	0.0	0.8

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	80	0.41	0.03	0.05	0.1	0.7
Derivatized - MS/MS non-kit	362	0.48	0.05	0.09	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.46	0.03	0.04	0.0	0.9
Non-derivatized - MS/MS MassChrom®	140	0.40	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	0.52	0.28	1.72	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	0.43	0.03	0.06	0.0	0.8
Non-derivatized - MS/MS non-kit	180	0.47	0.04	0.07	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	0.39	0.03	0.06	0.0	0.8

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

Lot C2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	1.11	0.09	0.13	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	1.19	0.09	0.13	0.1	0.7
Derivatized - MS/MS non-kit	362	1.38	0.14	0.26	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.36	0.08	0.09	0.0	0.9
Non-derivatized - MS/MS MassChrom®	140	1.20	0.07	0.15	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	1.31	0.11	0.15	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	1.28	0.09	0.16	0.0	0.8
Non-derivatized - MS/MS non-kit	180	1.39	0.11	0.22	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	1.17	0.07	0.12	0.0	0.8

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	2.25	0.17	0.23	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	2.25	0.17	0.24	0.1	0.7
Derivatized - MS/MS non-kit	361	2.76	0.29	0.47	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.63	0.18	0.19	0.0	0.9
Non-derivatized - MS/MS MassChrom®	140	2.34	0.15	0.35	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	2.60	0.19	0.26	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	2.52	0.16	0.31	0.0	0.8
Non-derivatized - MS/MS non-kit	180	2.71	0.22	0.42	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	2.31	0.18	0.34	0.0	0.8

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TETRADECENOYLCARNITINE (C14:1 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.01	0.00	0.00	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.04	0.01	0.03	0.0	0.4
Derivatized - MS/MS non-kit	338	0.04	0.01	0.04	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.02	0.00	0.00	0.0	0.4
Non-derivatized - MS/MS MassChrom®	100	0.02	0.00	0.01	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	0.02	0.01	0.01	0.0	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	391	0.02	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS non-kit	180	0.02	0.00	0.01	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.03	0.02	0.02	0.0	0.4

Lot B2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.17	0.03	0.04	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.23	0.02	0.04	0.0	0.4
Derivatized - MS/MS non-kit	352	0.25	0.03	0.08	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.26	0.03	0.04	0.0	0.4
Non-derivatized - MS/MS MassChrom®	100	0.18	0.02	0.03	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	0.21	0.03	0.09	0.0	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	0.26	0.18	1.04	0.0	0.5
Non-derivatized - MS/MS non-kit	180	0.24	0.03	0.07	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.21	0.02	0.04	0.0	0.4

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

Lot C2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.57	0.07	0.09	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.67	0.06	0.09	0.0	0.4
Derivatized - MS/MS non-kit	352	0.73	0.09	0.20	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.71	0.05	0.06	0.0	0.4
Non-derivatized - MS/MS MassChrom®	100	0.56	0.05	0.08	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	0.64	0.05	0.09	0.0	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	0.66	0.05	0.11	0.0	0.5
Non-derivatized - MS/MS non-kit	180	0.72	0.07	0.17	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.62	0.05	0.10	0.0	0.4

Lot D2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	1.23	0.11	0.16	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	1.30	0.11	0.16	0.0	0.4
Derivatized - MS/MS non-kit	352	1.50	0.20	0.43	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	1.33	0.18	0.25	0.0	0.4
Non-derivatized - MS/MS MassChrom®	100	1.14	0.09	0.19	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	1.29	0.10	0.16	0.0	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	398	1.64	1.06	6.25	0.0	0.5
Non-derivatized - MS/MS non-kit	180	1.42	0.12	0.33	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	1.25	0.07	0.18	0.0	0.4

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PALMITOYLCARNITINE (C16 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.69	0.07	0.11	0.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	0.61	0.06	0.07	0.6	0.7
Derivatized - MS/MS non-kit	360	0.72	0.11	0.36	0.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.70	0.04	0.04	0.7	0.8
Non-derivatized - MS/MS MassChrom®	140	0.57	0.04	0.08	0.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	0.66	0.07	0.13	0.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	368	0.73	0.06	0.15	0.7	0.9
Non-derivatized - MS/MS non-kit	190	0.68	0.07	0.13	0.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.67	0.07	0.09	0.7	0.8

Lot B2115 – Enriched 4 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	3.60	0.32	0.47	0.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	3.36	0.23	0.38	0.6	0.7
Derivatized - MS/MS non-kit	360	3.73	0.36	0.76	0.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	3.99	0.25	0.31	0.7	0.8
Non-derivatized - MS/MS MassChrom®	140	3.25	0.20	0.37	0.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	3.59	0.27	0.42	0.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	4.05	0.33	0.77	0.7	0.9
Non-derivatized - MS/MS non-kit	190	3.69	0.29	0.54	0.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	3.83	0.27	0.34	0.7	0.8

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

Lot C2115 – Enriched 8 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	6.57	0.46	0.65	0.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	6.23	0.40	0.66	0.6	0.7
Derivatized - MS/MS non-kit	360	6.80	0.62	1.36	0.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	7.36	0.37	0.57	0.7	0.8
Non-derivatized - MS/MS MassChrom®	140	6.08	0.38	0.70	0.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	6.70	0.52	0.76	0.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	7.40	0.54	1.33	0.7	0.9
Non-derivatized - MS/MS non-kit	190	6.82	0.54	1.01	0.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	7.08	0.45	0.66	0.7	0.8

Lot D2115 – Enriched 12 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	10.12	0.76	1.30	0.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	9.13	0.57	0.78	0.6	0.7
Derivatized - MS/MS non-kit	360	10.12	0.96	1.89	0.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	10.78	0.72	0.82	0.7	0.8
Non-derivatized - MS/MS MassChrom®	140	8.65	0.54	1.22	0.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	9.94	0.72	1.15	0.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	378	10.94	0.80	1.97	0.7	0.9
Non-derivatized - MS/MS non-kit	190	9.77	0.73	1.58	0.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	10.29	0.62	0.77	0.7	0.8

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HYDROXYPALMITOYLCARNITINE (C16OH µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.01	0.00	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.01	0.00	0.01	0.0	0.7
Derivatized - MS/MS non-kit	358	0.02	0.01	0.02	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.00	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS MassChrom®	100	0.00	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	0.01	0.00	0.01	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	353	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS non-kit	190	0.01	0.00	0.02	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.01	0.02	0.03	0.0	0.5

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.13	0.01	0.03	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.19	0.02	0.03	0.0	0.7
Derivatized - MS/MS non-kit	362	0.19	0.03	0.05	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.15	0.01	0.02	0.0	0.6
Non-derivatized - MS/MS MassChrom®	110	0.12	0.01	0.03	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	0.15	0.01	0.03	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	0.17	0.02	0.04	0.0	0.7
Non-derivatized - MS/MS non-kit	190	0.19	0.02	0.05	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.13	0.03	0.04	0.0	0.5

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.54	0.05	0.12	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.74	0.07	0.13	0.0	0.7
Derivatized - MS/MS non-kit	361	0.70	0.09	0.18	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.61	0.04	0.06	0.0	0.6
Non-derivatized - MS/MS MassChrom®	110	0.49	0.04	0.10	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	0.61	0.05	0.12	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	0.86	0.94	3.73	0.0	0.7
Non-derivatized - MS/MS non-kit	190	0.76	0.06	0.18	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.52	0.04	0.06	0.0	0.5

HYDROXYPALMITOYLCARNITINE (C16OH µmol/L blood) (cont.)

Lot D2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.83	0.11	0.19	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	1.09	0.09	0.17	0.0	0.7
Derivatized - MS/MS non-kit	361	1.07	0.14	0.30	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.88	0.05	0.09	0.0	0.6
Non-derivatized - MS/MS MassChrom®	110	0.70	0.04	0.16	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	442	0.89	0.07	0.17	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	408	0.99	0.07	0.21	0.0	0.7
Non-derivatized - MS/MS non-kit	190	1.10	0.09	0.24	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.75	0.05	0.09	0.0	0.5

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STEAROYLCARNITINE (C18 µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.53	0.08	0.09	0.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	0.51	0.04	0.06	0.5	0.8
Derivatized - MS/MS non-kit	352	0.50	0.06	0.12	0.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	0.46	0.03	0.03	0.5	0.8
Non-derivatized - MS/MS MassChrom®	140	0.46	0.04	0.09	0.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	0.48	0.04	0.06	0.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	356	0.50	0.04	0.08	0.5	0.8
Non-derivatized - MS/MS non-kit	180	0.51	0.06	0.07	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.45	0.04	0.05	0.4	0.7

Lot B2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.23	0.11	0.12	0.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	1.30	0.11	0.16	0.5	0.8
Derivatized - MS/MS non-kit	352	1.22	0.14	0.24	0.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	1.21	0.08	0.12	0.5	0.8
Non-derivatized - MS/MS MassChrom®	140	1.21	0.08	0.19	0.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	1.23	0.10	0.14	0.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	356	1.29	0.12	0.29	0.5	0.8
Non-derivatized - MS/MS non-kit	180	1.28	0.10	0.16	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	1.17	0.11	0.13	0.4	0.7

Lot C2115 – Enriched 3 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.77	0.29	0.30	0.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	2.90	0.21	0.38	0.5	0.8
Derivatized - MS/MS non-kit	352	2.70	0.28	0.49	0.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	2.76	0.15	0.25	0.5	0.8
Non-derivatized - MS/MS MassChrom®	140	2.79	0.18	0.47	0.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	2.83	0.23	0.30	0.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	356	2.92	0.24	0.54	0.5	0.8
Non-derivatized - MS/MS non-kit	180	2.89	0.25	0.41	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	2.67	0.23	0.25	0.4	0.7

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

Lot D2115 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	4.45	0.38	0.40	0.5	0.8
Derivatized - MS/MS MassChrom® Chromsystems	80	4.62	0.29	0.52	0.5	0.8
Derivatized - MS/MS non-kit	352	4.27	0.43	0.83	0.5	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	40	4.23	0.30	0.39	0.5	0.8
Non-derivatized - MS/MS MassChrom®	140	4.18	0.25	0.74	0.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	4.44	0.32	0.45	0.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	356	4.57	0.38	0.76	0.5	0.8
Non-derivatized - MS/MS non-kit	180	4.44	0.40	0.64	0.5	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	4.13	0.34	0.42	0.4	0.7

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HYDROXYSTEAROYLCARNITINE (C18OH µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.01	0.00	0.00	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.01	0.00	0.01	0.0	0.6
Derivatized - MS/MS non-kit	252	0.04	0.01	0.11	0.0	0.7
Non-derivatized - MS/MS MassChrom®	90	0.00	0.00	0.00	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	408	0.00	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	291	0.01	0.01	0.05	0.0	0.5
Non-derivatized - MS/MS non-kit	130	0.01	0.00	0.01	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.00	0.00	0.00	0.0	0.4

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.14	0.01	0.06	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.16	0.02	0.03	0.0	0.6
Derivatized - MS/MS non-kit	260	0.21	0.03	0.23	0.0	0.7
Non-derivatized - MS/MS MassChrom®	100	0.11	0.01	0.03	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	0.13	0.02	0.03	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	348	0.14	0.02	0.09	0.0	0.5
Non-derivatized - MS/MS non-kit	130	0.14	0.01	0.08	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.11	0.01	0.02	0.0	0.4

Lot C2115 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.59	0.06	0.25	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.65	0.06	0.11	0.0	0.6
Derivatized - MS/MS non-kit	259	0.74	0.09	0.51	0.0	0.7
Non-derivatized - MS/MS MassChrom®	100	0.44	0.03	0.12	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	0.52	0.05	0.09	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	348	0.55	0.07	0.22	0.0	0.5
Non-derivatized - MS/MS non-kit	130	0.55	0.05	0.31	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	50	0.41	0.04	0.05	0.0	0.4

HYDROXYSTEAROYLCARNITINE (C18OH µmol/L blood) cont.

Lot D2115 – Enriched 1.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	40	0.89	0.09	0.35	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.95	0.09	0.14	0.0	0.6
Derivatized - MS/MS non-kit	259	1.12	0.13	0.80	0.0	0.7
Non-derivatized - MS/MS MassChrom®	100	0.62	0.04	0.19	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	0.94	0.59	3.45	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	348	0.81	0.09	0.29	0.0	0.5
Non-derivatized - MS/MS non-kit	130	0.77	0.08	0.42	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	49	0.61	0.05	0.08	0.0	0.4

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

Lot A2115 – Enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	194	0.14	0.04	0.09	0.1	1.2

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	194	0.40	0.08	0.16	0.1	1.2

Lot C2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	194	0.68	0.10	0.25	0.1	1.2

Lot D2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	194	2.43	0.29	0.75	0.1	1.2

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

Lot A2115 – Enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.08	0.03	0.07	0.1	0.9

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.30	0.06	0.15	0.1	0.9

Lot C2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.55	0.12	0.41	0.1	0.9

Lot D2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	1.91	0.28	0.60	0.1	0.9

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

Lot A2115 – Enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	242	0.16	0.03	0.08	0.1	1.1
Non-derivatized - MS/MS non-kit	30	0.05	0.00	0.02	0.0	0.9

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	246	0.40	0.05	0.11	0.1	1.1
Non-derivatized - MS/MS non-kit	30	0.27	0.02	0.06	0.0	0.9

Lot C2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	246	0.67	0.11	0.24	0.1	1.1
Non-derivatized - MS/MS non-kit	30	0.49	0.05	0.12	0.0	0.9

Lot D2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	246	2.29	0.23	0.55	0.1	1.1
Non-derivatized - MS/MS non-kit	30	1.89	0.15	0.45	0.0	0.9

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

Lot A2115 – Enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	50	0.01	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	279	0.15	0.04	0.12	0.1	0.9
Non-derivatized - MS/MS non-kit	40	0.06	0.01	0.08	0.1	0.9

Lot B2115 – Enriched 0.25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	0.18	0.03	0.03	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	288	0.35	0.05	0.11	0.1	0.9
Non-derivatized - MS/MS non-kit	40	0.26	0.02	0.06	0.1	0.9

Lot C2115 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	0.36	0.04	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	288	0.54	0.07	0.12	0.1	0.9
Non-derivatized - MS/MS non-kit	40	0.47	0.04	0.08	0.1	0.9

Lot D2115 – Enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	1.53	0.17	0.25	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	288	1.99	0.22	0.37	0.1	0.9
Non-derivatized - MS/MS non-kit	40	1.80	0.14	0.30	0.1	0.9

2022 Quality Control Data Summaries of Statistical Analyses

CREATINE (CRE µmol/L blood)

Lot A2115 – Enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	40	222.5	20.6	64.7	224.7	0.9

Lot B2115 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	40	272.4	20.2	87.6	224.7	0.9

Lot C2115 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	40	412.5	20.1	117.1	224.7	0.9

Lot D2115 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	40	594.7	31.4	145.8	224.7	0.9

2022 Quality Control Data Summaries of Statistical Analyses

GUANIDINOACETIC ACID (GUAC µmol/L blood)

Lot A2115 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	80	1.2	0.1	0.4	1.2	0.7

Lot B2115 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	80	4.7	0.5	1.4	1.2	0.7

Lot C2115 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	80	8.2	0.7	3.0	1.2	0.7

Lot D2115 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	80	15.2	1.3	6.2	1.2	0.7

2022 Quality Control Data Summaries of Statistical Analyses

GALACTOCEREBROSIDASE (GALC µmol/hr/L blood)

Lot A2108 – Mean Activity 0.25 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	0.19	0.06	0.11	0.0	0.6
NeoLSD™ MSMS Kit PerkinElmer	140	0.24	0.05	0.14	0.0	0.9

Lot B2108 – Mean Activity 0.57 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	0.37	0.06	0.16	0.0	0.6
NeoLSD™ MSMS Kit PerkinElmer	140	0.52	0.06	0.20	0.0	0.9

Lot C2108 – Mean Activity 3.47 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	2.12	0.21	1.11	0.0	0.6
NeoLSD™ MSMS Kit PerkinElmer	140	3.18	0.19	0.83	0.0	0.9

Lot D2108 – Mean Activity 6.44 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	4.07	0.28	2.09	0.0	0.6
NeoLSD™ MSMS Kit PerkinElmer	140	5.77	0.37	1.57	0.0	0.9

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2108 – Mean Activity 0.19 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	0.32	0.12	0.36	0.2	0.8
LC-MS/MS non-kit	50	0.15	0.02	0.06	-0.2	1.2
NeoLSD™ MSMS Kit PerkinElmer	220	0.14	0.04	0.09	-0.1	1.0

Lot B2108 – Mean Activity 0.82 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	0.88	0.26	0.55	0.2	0.8
LC-MS/MS non-kit	50	0.81	0.09	0.33	-0.2	1.2
NeoLSD™ MSMS Kit PerkinElmer	220	0.73	0.13	0.28	-0.1	1.0

Lot C2108 – Mean Activity 5.70 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	4.53	0.58	1.04	0.2	0.8
LC-MS/MS non-kit	50	6.04	0.59	2.78	-0.2	1.2
NeoLSD™ MSMS Kit PerkinElmer	220	5.12	0.48	1.15	-0.1	1.0

Lot D2108 – Mean Activity 7.92 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	6.72	0.54	1.11	0.2	0.8
LC-MS/MS non-kit	50	9.61	0.75	4.97	-0.2	1.2
NeoLSD™ MSMS Kit PerkinElmer	220	7.62	0.62	1.68	-0.1	1.0

ACID α-GLUCOSIDASE (GAA µmol/hr/L blood) (cont.)
METHOD REPORT FOR DIGITAL MICROFLUIDICS

Lot A2108 – Mean Activity 1.40 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	30	1.25	0.25	0.29	0.3	1.0

Lot B2108 – Mean Activity 2.38 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	2.82	0.50	0.57	0.3	1.0

Lot C2108 – Mean Activity 14.02 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	15.25	1.49	1.71	0.3	1.0

Lot D2108 – Mean Activity 23.38 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	23.61	1.63	1.82	0.3	1.0

GAA Fluorometric Method

Level	N	Mean	Avg Within Lab SD	Total SD
A2108	30	0.8	1.0	0.4
B2108	30	1.7	2.0	0.4
C2108	50	6.6	9.3	0.8
D2108	50	10.3	12.4	1.3

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2108 – Mean Activity 0.12 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	0.40	0.11	0.55	0.3	0.8
LC-MS/MS non-kit	40	0.26	0.04	0.31	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	240	0.12	0.02	0.08	0.0	0.9

Lot B2108 – Mean Activity 0.62 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	0.79	0.20	0.59	0.3	0.8
LC-MS/MS non-kit	40	0.66	0.08	0.47	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	250	0.56	0.06	0.15	0.0	0.9

Lot C2108 – Mean Activity 4.98 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	3.92	0.47	0.71	0.3	0.8
LC-MS/MS non-kit	40	4.22	0.35	1.44	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	250	4.42	0.33	0.98	0.0	0.9

Lot D2108 – Mean Activity 8.47 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	6.76	0.53	1.01	0.3	0.8
LC-MS/MS non-kit	40	7.92	0.75	3.03	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	250	7.63	0.55	1.65	0.0	0.9

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2108 – Mean Activity 1.93 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	30	2.01	0.36	0.41	0.0	1.1

Lot B2108 – Mean Activity 2.76 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	55	2.94	0.34	0.45	0.0	1.1

Lot C2108 – Mean Activity 12.09 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	12.85	1.12	1.28	0.0	1.1

Lot D2108 – Mean Activity 22.86 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	24.32	1.79	1.96	0.0	1.1

IDUA Fluorometric Method

Level	N	Mean	Avg Within Lab SD	Total SD
A2108	20	0.18	0.18	0.16
B2108	38	0.26	0.22	0.09
C2108	60	3.65	2.22	0.57
D2108	60	9.23	6.78	1.2

2022 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA µmol/hr/L blood)

Lot A2108 – Mean Activity 1.57 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	1.00	0.11	0.68	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	170	1.01	0.13	0.41	-0.5	1.0

Lot B2108 – Mean Activity 2.54 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	1.91	0.13	1.26	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	170	1.96	0.26	0.77	-0.5	1.0

Lot C2108 – Mean Activity 11.03 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	10.28	0.64	5.50	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	170	10.14	0.59	3.04	-0.5	1.0

Lot D2108 – Mean Activity 19.86 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	18.73	1.61	8.65	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	170	18.52	1.12	5.43	-0.5	1.0

2022 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA µmol/hr/L blood)

GLA by the Digital Microfluidics method is not shown due to insufficient data.

GLA Fluorometric Method

Level	N	Mean	Avg Within Lab SD	Total SD	Avg Within Lab SD
A2108	40	0.78	0.36	0.16	0.36
B2108	40	1.62	0.86	0.18	0.86
C2108	50	8.24	5.05	0.63	5.05
D2108	50	15.88	8.15	0.73	8.15

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2108 – Mean Activity 0.68 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	0.72	0.09	0.43	0.3	0.8
NeoLSD™ MSMS Kit PerkinElmer	160	0.73	0.14	0.42	0.4	0.7

Lot B2108 – Mean Activity 1.23 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	1.18	0.16	0.67	0.3	0.8
NeoLSD™ MSMS Kit PerkinElmer	160	1.10	0.24	0.63	0.4	0.7

Lot C2108 – Mean Activity 6.15 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	5.63	0.53	2.64	0.3	0.8
NeoLSD™ MSMS Kit PerkinElmer	160	4.73	0.51	1.67	0.4	0.7

Lot D2108 – Mean Activity 11.68 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	50	9.42	0.98	3.98	0.3	0.8
NeoLSD™ MSMS Kit PerkinElmer	160	7.89	0.83	2.80	0.4	0.7

2022 Quality Control Data Summaries of Statistical Analyses

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

ABG by the Digital Microfluidics method is not shown due to insufficient data.

ABG Fluorometric Method

Level	N	Mean	Avg Within Lab SD	Total SD
A2108	30	0.66	0.24	0.15
B2108	40	0.83	0.37	0.15
C2108	50	2.82	1.04	0.32
D2108	50	4.72	1.60	0.36

ACID SPHINGOMYELINASE (ASM µmol/hr/L blood)

Lot A2108 – Mean Activity 0.17 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	0.12	0.02	0.14	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	126	0.08	0.02	0.07	0.0	0.8

Lot B2108 – Mean Activity 0.31 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	0.25	0.02	0.16	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	128	0.19	0.04	0.11	0.0	0.8

Lot C2108 – Mean Activity 1.46 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	1.41	0.10	0.66	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	128	1.16	0.11	0.39	0.0	0.8

Lot D2108 – Mean Activity 2.75 µmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	40	2.53	0.22	1.05	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	128	2.05	0.24	0.69	0.0	0.8

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	100	0.85	0.43	1.18	0.0	1.0

Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	9.22	0.98	1.96	0.0	1.0

Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	51.45	5.11	12.38	0.0	1.0

Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	104.84	9.37	26.76	0.0	1.0

Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	519.60	44.51	119.00	0.0	1.0

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	97	0.68	0.26	0.94	0.4	1.1

Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	11.80	0.91	4.11	0.4	1.1

Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	55.63	4.18	20.69	0.4	1.1

Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	113.02	8.46	41.23	0.4	1.1

Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	561.41	44.79	203.38	0.4	1.1

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER CORTISOL (CORT2 ng/mL serum)

Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	107	2.90	1.06	3.50	-1.3	1.1

Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	11.91	1.59	4.10	-1.3	1.1

Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	51.12	4.65	15.03	-1.3	1.1

Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	108.23	8.32	30.59	-1.3	1.1

Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	218	562.90	39.87	164.89	-1.3	1.1

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	73	0.29	0.15	0.36	2.6	1.1

Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	156	12.10	1.02	3.30	2.6	1.1

Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	156	57.12	4.78	15.91	2.6	1.1

Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	156	114.50	8.42	30.76	2.6	1.1

Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	156	542.35	37.37	172.76	2.6	1.1

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	76	0.16	0.12	0.31	-2.4	1.1

Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	166	11.15	1.12	2.68	-2.4	1.1

Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	166	48.58	3.93	12.23	-2.4	1.1

Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	166	106.68	8.91	25.13	-2.4	1.1

Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	166	551.56	39.21	129.73	-2.4	1.1

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	1.26	0.17	2.10	-1.8	0.9

Lot B2113 - Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	43.02	3.57	7.58	-1.8	0.9

Lot C2113 - Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	89.21	6.93	16.27	-1.8	0.9

Lot D2113 - Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	176.31	14.72	35.07	-1.8	0.9

Lot E2113 - Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	365.35	25.98	70.90	-1.8	0.9

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER ISOLEUCINE (ILE2 µmol/L blood)

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	19.19	1.78	4.29	14.1	0.9

Lot B2113 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	98.86	5.10	15.54	14.1	0.9

Lot C2113 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	184.48	9.08	31.60	14.1	0.9

Lot D2113 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	354.24	16.55	59.66	14.1	0.9

Lot E2113 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	706.85	33.39	109.5	14.1	0.9

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER LEUCINE (LEU2 µmol/L blood)

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	45.65	3.15	10.71	41.8	1.0

Lot B2113 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	136.74	7.43	46.28	41.8	1.0

Lot C2113 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	236.04	11.90	88.98	41.8	1.0

Lot D2113 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	434.19	17.96	155.7	41.8	1.0

Lot E2113 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	826.51	40.03	321.8	41.8	1.0

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER PHENYLALANINE (PHE2 µmol/L blood)

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	142	30.19	1.90	14.52	42.6	0.9

Lot B2113 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	131.65	25.75	80.02	42.6	0.9

Lot C2113 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	142	226.61	12.63	61.04	42.6	0.9

Lot D2113 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	434.33	20.48	109.2	42.6	0.9

Lot E2113 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	152	759.59	39.40	205.3	42.6	0.9

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER TYROSINE (TYR2 µmol/L blood)

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	132	26.68	1.84	3.48	20.8	0.9

Lot B2113 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	142	108.90	6.29	18.04	20.8	0.9

Lot C2113 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	132	188.44	13.48	28.26	20.8	0.9

Lot D2113 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	142	384.71	19.22	39.34	20.8	0.9

Lot E2113 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	142	734.56	33.02	78.56	20.8	0.9

2022 Quality Control Data Summaries of Statistical Analyses

2ND TIER VALINE (VAL2 µmol/L blood)

Lot A2113 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	58.06	5.05	13.45	52.7	0.9

Lot B2113 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	136.28	7.87	21.65	52.7	0.9

Lot C2113 – Enriched 200 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	223.56	15.76	40.47	52.7	0.9

Lot D2113 – Enriched 400 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	380.04	25.14	60.94	52.7	0.9

Lot E2113 – Enriched 800 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	172	735.28	35.84	110.7	52.7	0.9

2022 Quality Control Data Summaries of Statistical Analyses

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

MA is not shown due to insufficient data.

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2114 – Non-enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	245	2.04	0.54	1.29	0.4	0.9

Lot B2114 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	250	4.74	0.50	1.35	0.4	0.9

Lot C2114 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	250	17.65	1.45	4.13	0.4	0.9

Lot D2114 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	250	43.61	3.01	9.86	0.4	0.9

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2114 – Non-enriched 2 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	85	2.46	0.23	0.76	0.8	1.0

Lot B2114 – Enriched 5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	94	5.97	0.44	2.05	0.8	1.0

Lot C2114 – Enriched 20 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	94	22.54	1.16	6.93	0.8	1.0

Lot D2114 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	94	52.62	2.70	12.06	0.8	1.0

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2114 – Non-enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	170	1.09	0.18	0.77	0.2	0.9

Lot B2114 – Enriched 2.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	170	2.50	0.28	0.99	0.2	0.9

Lot C2114 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	180	9.23	0.88	2.27	0.2	0.9

Lot D2114 – Enriched 25 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	180	22.67	1.53	5.50	0.2	0.9

2022 Quality Control Data Summaries of Statistical Analyses

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

Lot A2114 – Non-enriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	240	7.64	0.80	3.62	7.6	0.7

Lot B2114 – Enriched 10 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	240	14.10	1.33	5.69	7.6	0.7

Lot C2114 – Enriched 50 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	240	39.63	3.45	15.15	7.6	0.7

Lot D2114 – Enriched 100 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	240	72.28	5.70	26.03	7.6	0.7

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
Rochelle P. Walensky, MD, MPH

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

John Bernstein, MS
Christofer Brown, BS
Suzanne Cordovado, Ph.D
Paul Dantonio, MS
Katherine Duneman, MS
Ernesto Gonzales Reyes, Ph.D
Christopher Greene, Ph.D
Laura Hancock, MS
Miyono Hendrix, MS
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
Allison McCabe, BS
Elizabeth McCown, BS
Joanne Mei, Ph.D
Stanimila Nikolova, Ph.D
Kaila Pearson, MS
Gyliann Pena, MS
Jose Perez, Ph.D
Kostas Petritis, Ph.D
C. Austin Pickens, Ph.D
Maryam Salehi, Ph.D
Blanche Temate, Ph.D
Robert Vogt, Ph.D
Irene Sofikitis Williams, MS
Golriz Yazdanpanah, MS
Sherri Zobel, BS

Production

Vinay Anumula, MS
Kizzy Stewart
Dion Cannon

ASSOCIATION OF PUBLIC HEALTH LABORATORIES SILVER SPRING, MD 20910

President
Denise Toney, PhD, HCLD(ABB)

Chairman, Newborn Screening Committee
Michele Caggana, Sc.D., FACMG and Joseph Orsini, Ph.D.

Chairman, Newborn Screening Quality Assurance Quality Control Subcommittee
Patrice Held, PhD

Chairman, Newborn Screening Molecular Subcommittee
Denise Kay, PhD and Richard Olney, MD, MPH

INQUIRIES TO:
Irene Sofikitis Williams, Editor
Centers for Disease Control and Prevention (CDC), Newborn Screening Quality Assurance Program
Mailstop S110-3, 4770 Buford Highway, N.E., Atlanta, GA 30341-3724 E-mail: NSQAPDMT@cdc.gov