

# Newborn Screening Quality Assurance Program

## 2021 Quality Control Report

In co-sponsorship with Association of Public Health Laboratories (APHL)  
Provided by the Newborn Screening and Molecular Biology Branch  
Centers for Disease Control and Prevention  
4770 Buford Highway NE, MS/F19  
Atlanta, GA 30341-3724  
Email: [NSQAPDMT@cdc.gov](mailto:NSQAPDMT@cdc.gov)

Volume 32, No. 1

Date issued: June 14, 2022

### 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 2021 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  $\mu$ L aliquots on Grade 903 filter paper (Cytiva (Cardiff, United Kingdom)).

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

T4, TSH, 17OHP and TGal, GALT consisted of DBS materials from three lots per analyte, with each lot containing a different concentration of analyte. The shipment for IRT, TGal, amino acids, SUAC, acylcarnitines, ALD, GAMT, and LSD 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  $\alpha$ -hydroxyprogesterone (17OHP2), 4-androstenedione (4AD2), cortisol (CORT2), 11-deoxycortisol (11D2), and 21-deoxycortisol (21D2); Second-tier Maple Syrup Urine Disease and Phenylketonuria (MSUD-PKUQC) by LC-MS/MS for the analytes alloisoleucine (ALE2), isoleucine (ILE2), leucine (LEU2),

phenylalanine (PHE2), tyrosine (TYR2), and valine (VAL2); Second-tier Methylmalonic/Propionic Acidemia and QC Material Production (cont.)

Homocystinuria (MMA-tHCY) by LC-MS/MS for the analytes malonic acid (MA2), methylmalonic acid (MMA2), ethylmalonic acid (EMA2), 2-methylcitric acid (MCA2), and total homocysteine (tHCY2). The shipment for these analytes consisted of DBS materials from four or five lots.

## QC Material Distribution

On January 12, 2021, we distributed DBS quality control (QC) materials to 502 participating 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 increased volume 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 numeric, 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 to the analyte you are reporting**
- **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 choose either manual entry or the pre-filled template. Both options cannot be used to submit QC data.**

## Participant Results

For the Set 1 QC materials, we compiled the participant results from five analytic runs from each QC lot and calculated mean values and standard deviations (SD). Data values outside 4SD limits were reviewed, and if considered to be “blunders”, removed from the data set. For linear regression analysis, 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 analysis, where mean activities differ based on method, we provided separate tables if sufficient data was submitted.

The reported QC data are summarized in tables on pages 4—103 which show the analyte by series of QC lots, the number of measurements (N), the mean values, and the standard deviations (SD) by kit or analytic method. In addition, we used 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.

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

For the purpose of our assessment, we first calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs for regression analyses. We then calculated the Y-intercept and slope using all analyte concentrations within a lot series (**e.g., lots A2005, B2005, and C2005**). 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, 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.

We assessed the majority of analytes as demonstrating acceptable performance, with slopes falling near or within the range of acceptability (range from 0.8 to 1.2). Analytes which demonstrated low slopes included **SUAC, C3DC + C4OH, C4, C14:1, and C18OH, and** were historically consistent with previous sets.

## 2021 Quality Control Data Summaries of Statistical Analyses

### 17 $\alpha$ -HYDROXYPROGESTERONE (17OHP ng/mL serum)

#### Lot A2005 – Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	436	22.0	2.2	4.5	-2.1	1.0
DELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	309	19.8	2.4	5.1	-4.1	0.9
GSP <sup>®</sup> 17OHP Neonatal PerkinElmer	540	24.1	2.0	5.8	0.0	1.0
LC-MS/MS non-kit	50	20.8	1.4	6.4	1.0	0.8
NeoMAP <sup>®</sup> 17OHP Interscientifica	30	22.4	1.8	2.2	-5.3	1.0
Neonatal 17OHP LabSystems	70	26.3	5.4	9.1	4.1	0.9
ZenTech ELISA Neonatal 17OHP	80	25.6	4.2	8.4	0.7	1.0

#### Lot B2005 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	436	48.1	4.2	9.7	-2.1	1.0
DELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	308	42.3	4.1	11.6	-4.1	0.9
GSP <sup>®</sup> 17OHP Neonatal PerkinElmer	540	50.7	3.5	11.0	0.0	1.0
LC-MS/MS non-kit	50	43.8	2.8	13.6	1.0	0.8
NeoMAP <sup>®</sup> 17OHP Interscientifica	30	44.1	4.6	4.7	-5.3	1.0
Neonatal 17OHP LabSystems	70	47.7	8.1	14.3	4.1	0.9
ZenTech ELISA Neonatal 17OHP	80	49.9	5.9	16.6	0.7	1.0

#### Lot C2005 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	436	96.2	8.1	19.2	-2.1	1.0
DELFI <sup>®</sup> A Neonatal 17OHP PerkinElmer	308	90.0	9.2	26.6	-4.1	0.9
GSP <sup>®</sup> 17OHP Neonatal PerkinElmer	540	99.0	8.2	24.7	0.0	1.0
LC-MS/MS non-kit	50	83.3	4.7	27.2	1.0	0.8
NeoMAP <sup>®</sup> 17OHP Interscientifica	30	99.4	8.6	22.0	-5.3	1.0
Neonatal 17OHP LabSystems	70	92.1	13.8	30.5	4.1	0.9
ZenTech ELISA Neonatal 17OHP	72	99.7	22.8	47.9	0.7	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

### THYROXINE (T4 µg/dL serum)

#### Lot F1900 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal T4 PerkinElmer	90	1.6	0.3	0.5	-0.1	0.9
DELFI <sup>®</sup> Neonatal T4 PerkinElmer	80	2.1	0.3	0.5	0.4	0.9
GSP <sup>®</sup> T4 Neonatal PerkinElmer	121	1.8	0.3	0.3	-0.1	1.0
NeoMAP <sup>®</sup> T4 Interscientifica	30	2.5	0.5	1.6	0.6	1.0

#### Lot G1900 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal T4 PerkinElmer	90	6.6	0.6	1.4	-0.1	0.9
DELFI <sup>®</sup> Neonatal T4 PerkinElmer	79	7.1	0.6	1.0	0.4	0.9
GSP <sup>®</sup> T4 Neonatal PerkinElmer	128	6.9	0.7	0.8	-0.1	1.0
NeoMAP <sup>®</sup> T4 Interscientifica	30	7.9	0.8	1.3	0.6	1.0

#### Lot H1900 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal T4 PerkinElmer	90	9.6	0.7	1.8	-0.1	0.9
DELFI <sup>®</sup> Neonatal T4 PerkinElmer	80	10.3	0.7	1.5	0.4	0.9
GSP <sup>®</sup> T4 Neonatal PerkinElmer	128	10.5	1.1	1.2	-0.1	1.0
NeoMAP <sup>®</sup> T4 Interscientifica	30	11.4	1.6	1.7	0.6	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

### THYROID-STIMULATING HORMONE (TSH $\mu$ IU/mL serum)

#### Lot F1901 – Enriched 25 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal hTSH PerkinElmer	498	26.8	2.3	6.5	0.3	1.1
DELFI <sup>®</sup> Neonatal TSH PerkinElmer	437	26.3	2.5	8.5	-1.1	1.1
DiaSorin Immunoassay TSH	30	28.1	3.2	3.6	1.2	1.1
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	640	27.9	2.4	4.5	-1.9	1.3
NeoMAP <sup>®</sup> TSH Interscientifica	40	31.3	2.9	4.4	-10.9	1.7
Neonatal TSH LabSystems	150	24.4	4.2	8.8	0.3	1.0
ZenTech ELISA Neonatal TSH	90	19.7	2.6	7.5	-6.8	1.1

#### Lot G1901 – Enriched 40 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal hTSH PerkinElmer	498	44.0	3.6	10.6	0.3	1.1
DELFI <sup>®</sup> Neonatal TSH PerkinElmer	438	43.8	3.9	13.9	-1.1	1.1
DiaSorin Immunoassay TSH	29	46.6	3.9	4.4	1.2	1.1
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	640	51.2	12.9	73.6	-1.9	1.3
NeoMAP <sup>®</sup> TSH Interscientifica	40	55.3	5.6	6.8	-10.9	1.7
Neonatal TSH LabSystems	150	39.9	5.6	14.5	0.3	1.0
ZenTech ELISA Neonatal TSH	90	38.6	5.4	12.9	-6.8	1.1

#### Lot H1901 – Enriched 80 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> Neonatal hTSH PerkinElmer	498	86.4	5.5	20.1	0.3	1.1
DELFI <sup>®</sup> Neonatal TSH PerkinElmer	438	87.5	7.0	28.3	-1.1	1.1
DiaSorin Immunoassay TSH	30	89.5	8.6	10.4	1.2	1.1
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	640	98.6	6.8	15.4	-1.9	1.3
NeoMAP <sup>®</sup> TSH Interscientifica	40	122.9	8.8	9.6	-10.9	1.7
Neonatal TSH LabSystems	150	78.4	10.6	28.3	0.3	1.0
ZenTech ELISA Neonatal TSH	90	80.7	10.2	30.1	-6.8	1.1

2021 Quality Control Data Summaries of Statistical Analyses  
**GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT U/g Hb)**

**Lot F2003 – Mean Activity 1.3 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	215	1.6	0.3	0.7	0.0	1.0
Microplate Rgt Kit Spotcheck® GALT Astoria-Pacific	56	0.9	0.1	0.1	-0.4	0.8

**Lot G2003 – Mean Activity 4.0 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	240	3.8	0.4	0.6	0.0	1.0
Microplate Rgt Kit Spotcheck® GALT Astoria-Pacific	66	2.7	0.3	0.8	-0.4	0.8

**Lot H2003 – Mean Activity 9.4 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	240	8.8	0.9	1.3	0.0	1.0
Microplate Rgt Kit Spotcheck® GALT Astoria-Pacific	66	6.8	0.5	1.3	-0.4	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### **Lot F2003**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	20	14.9	1.3	12.6	18.0
Perkin Elmer GSP Neonatal (U/dL blood)	97	0.8	1.0	0.0	4.3

#### **Lot G2003**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	20	85.2	12.5	59.0	102.6
Perkin Elmer GSP Neonatal (U/dL blood)	210	3.9	0.6	2.2	6.3

#### **Lot H2003**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	20	251.6	32.8	162.0	294.9
Perkin Elmer GSP Neonatal (U/dL blood)	210	15.6	3.1	4.5	23.0

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



## 2021 Quality Control Data Summaries of Statistical Analyses

### IMMUNOREACTIVE TRYPsinOGEN (IRT ng/mL blood)

#### Lot A2009 – Assayed 19.4 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELfIA® Neonatal IRT PerkinElmer	396	21.4	1.6	2.3	6.1	0.9
DELfIA® Neonatal IRT	198	21.1	2.3	3.3	5.7	0.9
FEIA IRT Labsystems	60	23.1	4.1	8.0	7.4	1.0
GSP® IRT Neonatal PerkinElmer, ng/mL	480	20.4	1.2	1.6	3.2	0.9
NeoMAP® IRT Interscientifica	40	28.9	2.0	5.5	17.2	0.8
ZenTech ELISA Neonatal IRT	66	35.9	4.9	12.8	20.0	0.9

#### Lot B2009 – Assayed 63.9 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELfIA® Neonatal IRT PerkinElmer	396	64.7	4.7	6.9	6.1	0.9
DELfIA® Neonatal IRT	198	61.8	5.5	7.4	5.7	0.9
FEIA IRT Labsystems	60	71.1	9.1	14.3	7.4	1.0
GSP® IRT Neonatal PerkinElmer, ng/mL	480	63.5	3.6	5.0	3.2	0.9
NeoMAP® IRT Interscientifica	40	67.2	4.9	6.2	17.2	0.8
ZenTech ELISA Neonatal IRT	66	107.1	14.2	17.2	20.0	0.9

#### Lot C2009 – Assayed 129.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELfIA® Neonatal IRT PerkinElmer	396	125.4	8.8	12.8	6.1	0.9
DELfIA® Neonatal IRT	198	121.0	9.5	12.8	5.7	0.9
FEIA IRT Labsystems	60	141.5	21.9	31.2	7.4	1.0
GSP® IRT Neonatal PerkinElmer, ng/mL	480	127.2	8.0	11.2	3.2	0.9
NeoMAP® IRT Interscientifica	40	120.7	16.4	27.5	17.2	0.8
ZenTech ELISA Neonatal IRT	65	177.1	12.7	30.1	20.0	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

### IMMUNOREACTIVE TRYPsinOGEN (IRT ng/mL blood) cont.

#### Lot D2009 – Assayed 231.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELFIA® Neonatal IRT PerkinElmer	396	212.8	13.9	20.8	6.1	0.9
DELFIA® Neonatal IRT	198	205.9	16.1	22.4	5.7	0.9
FEIA IRT Labsystems	60	232.4	40.9	61.8	7.4	1.0
GSP® IRT Neonatal PerkinElmer, ng/mL	478	220.1	13.7	18.1	3.2	0.9
NeoMAP® IRT Interscientifica	40	191.7	24.6	41.9	17.2	0.8
ZenTech ELISA Neonatal IRT	66	205.5	15.0	32.9	20.0	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	275.1	27.3	32.9	280.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	66	231.5	14.4	32.3	236.4	0.6
Derivatized - MS/MS non-kit	269	301.3	38.5	80.6	300.5	0.8
Non-derivatized - MS/MS MassChrom®	110	242.8	14.2	49.7	246.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	420	319.3	21.2	43.1	328.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	240	295.3	20.0	42.2	299.7	0.8
Non-derivatized - MS/MS non-kit	92	282.3	24.2	50.4	282.9	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	281.2	26.0	70.8	274.8	0.9

#### Lot B2015 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	452.2	61.6	79.5	280.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	66	367.8	31.4	58.2	236.4	0.6
Derivatized - MS/MS non-kit	269	457.7	36.3	89.2	300.5	0.8
Non-derivatized - MS/MS MassChrom®	110	392.3	17.7	81.5	246.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	420	528.4	75.1	299.6	328.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	240	475.4	31.3	64.9	299.7	0.8
Non-derivatized - MS/MS non-kit	92	450.3	37.6	65.1	282.9	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	443.7	39.8	119.1	274.8	0.9

#### Lot C2015 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	565.2	39.4	45.9	280.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	66	481.0	44.0	83.8	236.4	0.6
Derivatized - MS/MS non-kit	269	615.6	52.1	120.2	300.5	0.8
Non-derivatized - MS/MS MassChrom®	110	529.7	24.2	100.3	246.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	420	687.8	47.7	97.7	328.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	240	636.1	42.5	85.2	299.7	0.8
Non-derivatized - MS/MS non-kit	92	608.6	53.1	106.4	282.9	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	617.5	81.5	178.6	274.8	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	748.4	55.7	65.4	280.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	66	604.3	31.5	97.5	236.4	0.6
Derivatized - MS/MS non-kit	269	775.3	69.7	153.8	300.5	0.8
Non-derivatized - MS/MS MassChrom®	110	669.6	34.7	129.1	246.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	420	877.8	54.0	122.5	328.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	240	803.8	53.8	106.3	299.7	0.8
Non-derivatized - MS/MS non-kit	92	778.5	72.3	136.3	282.9	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	806.3	82.0	222.9	274.8	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	6.5	1.1	1.7	6.9	0.6
Derivatized - MS/MS MassChrom® Chromsystems	66	18.2	28.8	72.9	20.0	0.8
Derivatized - MS/MS non-kit	279	7.3	0.9	4.5	5.5	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	38	4.0	0.4	0.6	4.1	0.5
Non-derivatized - MS/MS MassChrom®	110	6.9	0.8	1.7	10.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	6.6	0.7	2.7	5.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	270	6.1	0.7	1.2	5.5	0.9
Non-derivatized - MS/MS non-kit	102	7.1	2.0	3.7	4.8	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	7.6	0.8	1.9	6.2	0.9

#### Lot B2015 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	71.3	8.5	18.3	6.9	0.6
Derivatized - MS/MS MassChrom® Chromsystems	66	97.8	7.0	15.2	20.0	0.8
Derivatized - MS/MS non-kit	279	73.3	6.6	26.7	5.5	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	38	54.8	4.8	7.0	4.1	0.5
Non-derivatized - MS/MS MassChrom®	120	92.7	4.6	16.0	10.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	87.3	5.1	12.0	5.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	270	90.2	5.5	9.4	5.5	0.9
Non-derivatized - MS/MS non-kit	102	78.1	8.9	29.7	4.8	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	90.1	4.4	9.5	6.2	0.9

#### Lot C2015 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	127.4	14.2	24.8	6.9	0.6
Derivatized - MS/MS MassChrom® Chromsystems	66	174.1	12.6	28.4	20.0	0.8
Derivatized - MS/MS non-kit	279	143.5	10.5	52.5	5.5	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	38	104.2	8.3	14.2	4.1	0.5
Non-derivatized - MS/MS MassChrom®	120	170.5	11.3	33.2	10.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	167.2	10.7	24.3	5.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	270	173.6	10.4	16.7	5.5	0.9
Non-derivatized - MS/MS non-kit	102	150.0	17.2	57.6	4.8	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	174.6	12.1	20.0	6.2	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	194.3	21.9	38.4	6.9	0.6
Derivatized - MS/MS MassChrom® Chromsystems	66	246.0	12.9	34.9	20.0	0.8
Derivatized - MS/MS non-kit	279	216.4	16.7	85.8	5.5	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	38	155.1	10.6	14.6	4.1	0.5
Non-derivatized - MS/MS MassChrom®	120	244.8	10.6	49.0	10.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	253.5	14.0	33.1	5.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	270	261.0	16.5	28.8	5.5	0.9
Non-derivatized - MS/MS non-kit	102	231.9	25.8	91.8	4.8	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	263.0	10.8	23.9	6.2	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	18.4	2.2	3.1	19.5	0.7
Derivatized - MS/MS MassChrom® Chromsystems	56	15.5	0.9	2.2	16.0	0.8
Derivatized - MS/MS non-kit	299	15.8	2.8	7.7	14.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	14.4	1.5	2.1	13.3	0.9
Non-derivatized - MS/MS MassChrom®	120	15.3	1.2	2.0	15.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	15.6	1.7	2.0	14.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	14.6	1.5	2.1	14.4	0.9
Non-derivatized - MS/MS non-kit	162	15.9	2.1	4.5	15.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	13.9	1.7	3.5	16.2	0.9

#### Lot B2015 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	38.1	2.5	4.7	19.5	0.7
Derivatized - MS/MS MassChrom® Chromsystems	56	36.7	2.9	4.8	16.0	0.8
Derivatized - MS/MS non-kit	299	36.0	3.3	8.2	14.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	37.0	2.7	3.7	13.3	0.9
Non-derivatized - MS/MS MassChrom®	120	38.4	2.7	5.4	15.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	39.0	2.9	4.0	14.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	36.8	3.2	4.7	14.4	0.9
Non-derivatized - MS/MS non-kit	162	38.8	4.1	9.1	15.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	41.7	3.8	6.5	16.2	0.9

#### Lot C2015 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	85.9	9.1	11.8	19.5	0.7
Derivatized - MS/MS MassChrom® Chromsystems	56	97.4	6.9	12.9	16.0	0.8
Derivatized - MS/MS non-kit	299	96.9	8.1	21.6	14.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	97.3	5.2	9.3	13.3	0.9
Non-derivatized - MS/MS MassChrom®	120	106.1	6.8	14.2	15.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	105.5	7.5	10.5	14.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	98.4	7.5	9.7	14.4	0.9
Non-derivatized - MS/MS non-kit	162	104.3	10.7	23.7	15.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	106.0	9.6	19.6	16.2	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	188.0	12.0	21.1	19.5	0.7
Derivatized - MS/MS MassChrom® Chromsystems	56	219.2	14.7	32.2	16.0	0.8
Derivatized - MS/MS non-kit	299	226.7	19.2	49.7	14.7	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	235.4	15.7	23.3	13.3	0.9
Non-derivatized - MS/MS MassChrom®	120	244.4	15.4	34.0	15.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	248.5	16.4	25.5	14.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	229.1	16.9	25.3	14.4	0.9
Non-derivatized - MS/MS non-kit	162	243.8	23.7	49.7	15.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	242.0	14.6	43.0	16.2	0.9



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	333.5	26.8	53.1	331.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	46	309.3	17.8	27.8	316.0	0.6
Derivatized - MS/MS non-kit	229	357.6	24.1	114.4	354.3	0.9
Non-derivatized - MS/MS MassChrom®	110	237.9	17.5	34.3	239.4	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	358.1	27.1	65.2	356.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	232	331.8	29.6	64.6	336.1	0.8
Non-derivatized - MS/MS non-kit	64	273.3	35.2	82.6	274.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	282.1	36.9	84.9	276.5	0.7

#### Lot B2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	558.7	63.0	102.1	331.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	46	512.7	32.9	50.3	316.0	0.6
Derivatized - MS/MS non-kit	229	615.9	39.3	195.9	354.3	0.9
Non-derivatized - MS/MS MassChrom®	110	409.9	24.2	55.3	239.4	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	613.5	39.1	104.2	356.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	232	580.2	39.5	99.6	336.1	0.8
Non-derivatized - MS/MS non-kit	64	475.0	55.7	140.6	274.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	483.3	61.9	156.4	276.5	0.7

#### Lot C2015 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	758.3	73.7	111.3	331.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	46	709.6	31.7	52.0	316.0	0.6
Derivatized - MS/MS non-kit	229	878.7	57.5	283.3	354.3	0.9
Non-derivatized - MS/MS MassChrom®	110	581.9	33.9	78.8	239.4	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	865.0	64.4	145.7	356.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	232	810.9	61.5	141.1	336.1	0.8
Non-derivatized - MS/MS non-kit	64	677.8	84.9	197.4	274.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	709.9	92.1	243.2	276.5	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 900 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1009.0	94.8	136.6	331.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	46	882.7	46.9	105.6	316.0	0.6
Derivatized - MS/MS non-kit	229	1151.0	79.7	375.5	354.3	0.9
Non-derivatized - MS/MS MassChrom®	110	746.5	38.6	91.9	239.4	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	1128.4	71.6	193.2	356.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	232	1046.6	75.0	169.6	336.1	0.8
Non-derivatized - MS/MS non-kit	64	874.2	98.5	253.2	274.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	926.2	91.7	283.6	276.5	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	104.3	11.8	36.0	106.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	56	81.3	7.0	20.9	86.4	0.7
Derivatized - MS/MS non-kit	299	80.8	7.4	17.0	84.3	0.8
LC-MS/MS non-kit	36	96.3	9.2	33.2	97.9	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	89.6	5.4	8.4	90.5	0.9
Non-derivatized - MS/MS MassChrom®	120	87.8	5.0	22.1	93.7	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	90.4	5.6	10.9	91.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	84.5	6.0	11.4	87.4	0.8
Non-derivatized - MS/MS non-kit	172	84.7	5.7	11.7	87.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	80.2	7.3	14.3	78.5	0.8

#### Lot B2015 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	245.1	14.6	40.4	106.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	56	197.3	11.0	13.9	86.4	0.7
Derivatized - MS/MS non-kit	299	209.0	14.8	32.1	84.3	0.8
LC-MS/MS non-kit	36	250.4	27.6	70.3	97.9	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	226.4	12.2	26.9	90.5	0.9
Non-derivatized - MS/MS MassChrom®	120	214.7	8.3	36.3	93.7	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	226.5	13.3	24.6	91.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	214.5	13.9	26.3	87.4	0.8
Non-derivatized - MS/MS non-kit	172	218.0	16.4	33.2	87.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	196.0	13.0	31.2	78.5	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot C2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	358.2	18.5	29.4	106.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	56	307.7	13.9	20.2	86.4	0.7
Derivatized - MS/MS non-kit	299	331.9	25.1	55.5	84.3	0.8
LC-MS/MS non-kit	36	396.4	25.9	98.0	97.9	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	350.0	20.5	47.3	90.5	0.9
Non-derivatized - MS/MS MassChrom®	120	336.4	13.5	34.5	93.7	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	358.0	24.3	39.4	91.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	336.0	18.6	40.4	87.4	0.8
Non-derivatized - MS/MS non-kit	172	341.1	25.6	53.9	87.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	314.2	30.4	59.5	78.5	0.8

#### Lot D2015 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	631.0	47.8	66.4	106.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	56	514.3	24.3	59.0	86.4	0.7
Derivatized - MS/MS non-kit	299	570.6	41.7	92.4	84.3	0.8
LC-MS/MS non-kit	36	696.4	62.3	162.2	97.9	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	618.9	24.0	73.0	90.5	0.9
Non-derivatized - MS/MS MassChrom®	120	560.6	21.4	44.7	93.7	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	622.6	40.8	74.4	91.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	581.5	33.3	69.3	87.4	0.8
Non-derivatized - MS/MS non-kit	172	592.5	43.6	95.8	87.7	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	554.4	42.3	99.3	78.5	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	14.7	3.3	4.8	15.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	56	11.3	1.3	2.4	12.3	0.7
Derivatized - MS/MS non-kit	299	13.0	1.9	4.0	13.3	0.8
LC-MS/MS non-kit	24	13.8	1.5	3.7	13.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	46	10.9	0.9	1.0	9.7	0.8
Non-derivatized - MS/MS MassChrom®	120	9.6	0.7	2.0	9.4	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	10.8	1.0	1.6	9.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	9.6	1.0	1.4	8.9	0.8
Non-derivatized - MS/MS non-kit	172	12.0	1.0	1.9	11.2	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	9.2	2.1	5.4	7.1	0.9

#### Lot B2015 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	60.1	8.0	10.6	15.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	56	45.4	3.3	7.2	12.3	0.7
Derivatized - MS/MS non-kit	299	52.8	4.4	8.2	13.3	0.8
LC-MS/MS non-kit	24	53.0	8.2	17.5	13.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	46	50.4	2.8	2.9	9.7	0.8
Non-derivatized - MS/MS MassChrom®	120	44.7	2.7	7.9	9.4	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	49.6	3.7	6.8	9.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	45.7	4.0	6.4	8.9	0.8
Non-derivatized - MS/MS non-kit	172	53.1	3.9	7.4	11.2	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	50.0	8.4	30.9	7.1	0.9

#### Lot C2015 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	139.3	10.5	14.1	15.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	56	113.4	7.6	19.2	12.3	0.7
Derivatized - MS/MS non-kit	299	133.8	9.9	20.2	13.3	0.8
LC-MS/MS non-kit	24	138.5	11.8	33.8	13.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	46	132.2	8.4	9.3	9.7	0.8
Non-derivatized - MS/MS MassChrom®	120	120.0	6.4	20.3	9.4	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	130.7	8.8	14.8	9.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	120.1	10.6	17.1	8.9	0.8
Non-derivatized - MS/MS non-kit	172	138.1	9.3	21.9	11.2	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	137.4	18.1	83.8	7.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	226.3	18.6	22.5	15.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	56	175.7	12.9	31.5	12.3	0.7
Derivatized - MS/MS non-kit	299	211.6	16.1	31.1	13.3	0.8
LC-MS/MS non-kit	24	219.2	29.6	53.4	13.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	46	217.7	10.2	11.6	9.7	0.8
Non-derivatized - MS/MS MassChrom®	120	190.4	9.2	27.9	9.4	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	214.0	13.4	23.6	9.7	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	195.9	15.2	26.5	8.9	0.8
Non-derivatized - MS/MS non-kit	172	224.5	15.2	33.6	11.2	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	230.6	23.6	144.4	7.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	157.7	25.9	45.9	154.8	0.7
Derivatized - MS/MS MassChrom® Chromsystems	36	175.8	6.2	30.6	175.7	0.7
Derivatized - MS/MS non-kit	239	123.1	12.1	58.1	120.9	0.6
Non-derivatized - MS/MS MassChrom®	110	185.3	11.5	32.1	185.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	166.1	12.2	26.0	164.8	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	154.6	9.0	19.4	153.9	0.7
Non-derivatized - MS/MS non-kit	84	149.6	19.7	40.5	146.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	162.6	10.4	43.7	158.3	0.8

#### Lot B2015 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	223.5	39.7	66.3	154.8	0.7
Derivatized - MS/MS MassChrom® Chromsystems	36	247.9	14.6	40.3	175.7	0.7
Derivatized - MS/MS non-kit	239	177.8	16.8	84.8	120.9	0.6
Non-derivatized - MS/MS MassChrom®	110	265.6	16.8	43.8	185.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	239.5	15.6	36.8	164.8	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	222.1	12.4	26.9	153.9	0.7
Non-derivatized - MS/MS non-kit	84	208.6	23.2	47.6	146.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	229.3	13.3	56.3	158.3	0.8

#### Lot C2015 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	276.7	43.9	71.7	154.8	0.7
Derivatized - MS/MS MassChrom® Chromsystems	36	323.3	13.4	53.1	175.7	0.7
Derivatized - MS/MS non-kit	239	239.4	23.3	112.1	120.9	0.6
Non-derivatized - MS/MS MassChrom®	110	341.3	20.2	55.6	185.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	312.5	21.8	48.5	164.8	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	288.3	15.9	32.9	153.9	0.7
Non-derivatized - MS/MS non-kit	84	269.6	20.4	74.1	146.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	308.2	20.0	78.1	158.3	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	363.1	55.5	83.2	154.8	0.7
Derivatized - MS/MS MassChrom® Chromsystems	36	394.3	17.8	68.1	175.7	0.7
Derivatized - MS/MS non-kit	239	301.6	28.9	142.2	120.9	0.6
Non-derivatized - MS/MS MassChrom®	110	422.8	23.5	66.5	185.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	360	392.4	25.0	60.3	164.8	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	359.9	19.7	43.2	153.9	0.7
Non-derivatized - MS/MS non-kit	84	344.6	28.0	90.6	146.2	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	390.2	18.7	97.0	158.3	0.8



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	35.2	1.7	3.7	37.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	35.4	2.3	4.7	38.2	0.8
Derivatized - MS/MS non-kit	309	36.5	2.9	5.5	37.7	0.9
Fluorometric manual Phe - non-kit	42	48.1	8.3	29.3	46.2	0.8
GSP® Phe Neonatal PerkinElmer	60	35.6	8.6	17.5	32.3	1.0
LC-MS/MS non-kit	24	36.6	4.9	8.0	44.3	0.9
NeoLISA® Phe Interscientifica	40	47.6	12.0	18.6	45.8	0.9
Neonatal Phe LabSystems	80	27.5	5.3	16.3	23.8	1.1
Neonatal® Phe Kit PerkinElmer	100	39.1	6.8	15.8	41.2	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	35.8	2.2	4.1	35.3	1.0
Non-derivatized - MS/MS MassChrom®	180	36.2	1.9	4.4	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	35.0	2.5	4.0	34.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	31.4	1.9	3.2	32.5	0.8
Non-derivatized - MS/MS non-kit	162	35.0	2.4	5.1	34.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	31.9	2.7	7.0	31.3	0.9

#### Lot B2015 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	176.6	8.8	28.9	37.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	165.0	9.9	18.1	38.2	0.8
Derivatized - MS/MS non-kit	309	179.8	13.3	28.4	37.7	0.9
Fluorometric manual Phe - non-kit	50	167.1	14.9	84.8	46.2	0.8
GSP® Phe Neonatal PerkinElmer	60	177.1	11.5	15.0	32.3	1.0
LC-MS/MS non-kit	24	192.2	35.1	49.1	44.3	0.9
NeoLISA® Phe Interscientifica	40	173.8	21.5	24.5	45.8	0.9
Neonatal Phe LabSystems	80	182.4	13.7	81.4	23.8	1.1
Neonatal® Phe Kit PerkinElmer	100	151.5	13.3	53.8	41.2	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	183.7	10.0	21.9	35.3	1.0
Non-derivatized - MS/MS MassChrom®	180	179.5	7.3	17.5	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	175.2	10.9	15.8	34.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	159.3	10.7	19.2	32.5	0.8
Non-derivatized - MS/MS non-kit	162	177.3	12.1	29.4	34.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	164.4	9.2	38.5	31.3	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot C2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	287.2	11.1	32.0	37.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	284.2	13.6	30.5	38.2	0.8
Derivatized - MS/MS non-kit	309	313.3	21.7	49.9	37.7	0.9
Fluorometric manual Phe - non-kit	50	278.0	23.8	141.0	46.2	0.8
GSP® Phe Neonatal PerkinElmer	60	318.4	40.5	58.6	32.3	1.0
LC-MS/MS non-kit	24	326.4	43.8	65.4	44.3	0.9
NeoLISA® Phe Interscientifica	40	302.5	38.3	49.9	45.8	0.9
Neonatal Phe LabSystems	80	335.7	23.2	162.6	23.8	1.1
Neonatal® Phe Kit PerkinElmer	100	249.9	24.2	91.8	41.2	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	313.7	18.4	39.6	35.3	1.0
Non-derivatized - MS/MS MassChrom®	180	312.3	14.4	30.2	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	308.7	19.4	30.9	34.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	277.6	15.5	29.4	32.5	0.8
Non-derivatized - MS/MS non-kit	162	312.7	21.2	56.4	34.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	292.5	21.3	68.7	31.3	0.9

#### Lot D2015 – Enriched 450 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	434.3	26.9	55.8	37.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	404.8	19.7	60.7	38.2	0.8
Derivatized - MS/MS non-kit	309	455.6	33.3	75.3	37.7	0.9
Fluorometric manual Phe - non-kit	50	410.4	31.2	208.1	46.2	0.8
GSP® Phe Neonatal PerkinElmer	60	476.4	33.8	55.1	32.3	1.0
LC-MS/MS non-kit	24	454.1	51.7	85.6	44.3	0.9
NeoLISA® Phe Interscientifica	40	436.4	42.6	55.2	45.8	0.9
Neonatal Phe LabSystems	80	509.8	34.0	267.1	23.8	1.1
Neonatal® Phe Kit PerkinElmer	100	358.7	25.9	131.4	41.2	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	473.1	21.6	53.0	35.3	1.0
Non-derivatized - MS/MS MassChrom®	180	450.9	18.5	56.4	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	455.2	26.9	41.5	34.4	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	404.8	22.9	43.0	32.5	0.8
Non-derivatized - MS/MS non-kit	162	461.9	31.3	79.3	34.3	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	430.3	25.4	102.5	31.3	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	64	0.5	0.4	0.1	0.6	0.4
Derivatized - MS/MS non-kit	130	1.1	0.3	1.4	1.2	0.5
Non-derivatized - MS/MS MassChrom®	30	0.5	0.1	0.2	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	0.6	0.1	0.4	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	191	0.2	0.1	0.1	0.2	0.2
Non-derivatized - MS/MS non-kit	100	0.5	0.1	0.4	0.5	0.6
Non-derivatized Labsystems Neomass AAAC Plus	30	2.7	1.2	2.8	2.8	0.3

#### Lot B2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	65	1.7	0.2	0.3	0.6	0.4
Derivatized - MS/MS non-kit	130	2.5	0.4	2.0	1.2	0.5
Non-derivatized - MS/MS MassChrom®	30	1.3	0.2	0.2	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	1.2	0.2	0.6	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	0.7	0.1	0.2	0.2	0.2
Non-derivatized - MS/MS non-kit	100	1.9	0.2	1.3	0.5	0.6
Non-derivatized Labsystems Neomass AAAC Plus	30	3.5	1.6	3.0	2.8	0.3

#### Lot C2015 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	65	4.9	0.4	1.0	0.6	0.4
Derivatized - MS/MS non-kit	130	6.4	0.7	3.9	1.2	0.5
Non-derivatized - MS/MS MassChrom®	30	3.4	0.2	0.3	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	3.1	0.4	1.0	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	2.4	0.7	1.7	0.2	0.2
Non-derivatized - MS/MS non-kit	100	6.1	0.6	4.4	0.5	0.6
Non-derivatized Labsystems Neomass AAAC Plus	30	5.9	1.5	2.9	2.8	0.3

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS MassChrom® Chromsystems	65	8.9	0.6	1.8	0.6	0.4
Derivatized - MS/MS non-kit	130	11.1	1.1	6.3	1.2	0.5
Non-derivatized - MS/MS MassChrom®	30	6.2	0.4	1.0	0.6	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	5.8	0.7	1.7	0.6	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	4.6	0.5	1.3	0.2	0.2
Non-derivatized - MS/MS non-kit	100	11.7	1.1	7.9	0.5	0.6
Non-derivatized Labsystems Neomass AAAC Plus	30	8.6	2.0	2.7	2.8	0.3

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	30.2	1.9	2.6	31.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	64	35.2	4.1	9.3	38.3	0.8
Derivatized - MS/MS non-kit	309	31.9	3.5	8.3	30.2	0.9
LC-MS/MS non-kit	24	28.7	3.4	4.6	35.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	29.2	1.5	2.1	27.2	0.8
Non-derivatized - MS/MS MassChrom®	180	32.9	2.1	4.1	34.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	34.1	3.3	5.0	31.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	29.5	2.1	3.7	29.6	0.8
Non-derivatized - MS/MS non-kit	162	31.4	2.8	5.2	28.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	46	29.6	3.6	4.6	24.3	0.9

#### Lot B2015 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	283.1	14.9	31.5	31.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	64	281.5	21.4	39.1	38.3	0.8
Derivatized - MS/MS non-kit	309	283.8	24.5	74.9	30.2	0.9
LC-MS/MS non-kit	24	270.5	28.7	38.1	35.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	280.7	14.6	21.6	27.2	0.8
Non-derivatized - MS/MS MassChrom®	180	296.8	18.3	35.4	34.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	302.5	18.9	30.2	31.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	266.6	15.0	28.6	29.6	0.8
Non-derivatized - MS/MS non-kit	162	284.5	18.1	44.0	28.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	46	275.6	28.8	42.4	24.3	0.9

#### Lot C2015 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	518.0	24.8	47.7	31.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	64	529.3	26.2	74.8	38.3	0.8
Derivatized - MS/MS non-kit	309	547.6	39.8	140.4	30.2	0.9
LC-MS/MS non-kit	24	509.5	41.3	64.0	35.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	520.6	30.0	39.9	27.2	0.8
Non-derivatized - MS/MS MassChrom®	180	564.5	26.6	51.5	34.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	575.5	38.7	63.3	31.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	499.4	27.3	50.6	29.6	0.8
Non-derivatized - MS/MS non-kit	162	546.5	34.6	92.4	28.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	46	533.4	74.8	100.3	24.3	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 900 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	772.6	35.1	56.5	31.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	64	759.7	43.2	127.4	38.3	0.8
Derivatized - MS/MS non-kit	309	802.3	59.9	200.1	30.2	0.9
LC-MS/MS non-kit	24	720.0	63.6	95.0	35.2	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	788.0	31.6	41.3	27.2	0.8
Non-derivatized - MS/MS MassChrom®	180	819.9	40.9	81.1	34.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	854.1	53.2	86.6	31.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	737.9	43.6	74.5	29.6	0.8
Non-derivatized - MS/MS non-kit	162	812.1	53.9	128.0	28.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	46	800.2	79.9	126.2	24.3	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	71.4	6.9	13.0	68.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	46	75.1	6.6	20.7	79.6	0.7
Derivatized - MS/MS non-kit	289	86.5	11.2	32.5	86.7	0.8
LC-MS/MS non-kit	32	82.0	8.1	16.5	82.4	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	74.2	4.9	5.4	75.4	0.9
Non-derivatized - MS/MS MassChrom®	120	63.1	3.9	13.4	67.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	76.2	5.7	12.1	76.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	72.4	4.0	7.5	74.7	0.8
Non-derivatized - MS/MS non-kit	152	64.0	4.3	8.8	66.8	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	56.4	5.4	19.1	55.2	0.7

#### Lot B2015 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	226.5	18.1	29.2	68.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	46	222.4	15.0	61.4	79.6	0.7
Derivatized - MS/MS non-kit	289	238.0	20.8	53.1	86.7	0.8
LC-MS/MS non-kit	32	261.3	19.9	32.4	82.4	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	255.5	13.0	15.6	75.4	0.9
Non-derivatized - MS/MS MassChrom®	120	215.5	9.9	32.3	67.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	258.1	17.8	37.4	76.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	246.9	14.8	28.9	74.7	0.8
Non-derivatized - MS/MS non-kit	152	217.7	16.6	31.6	66.8	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	201.3	18.0	62.6	55.2	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot C2015 – Enriched 350 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	319.7	26.8	48.4	68.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	46	324.5	19.4	83.2	79.6	0.7
Derivatized - MS/MS non-kit	289	348.1	29.2	84.7	86.7	0.8
LC-MS/MS non-kit	32	400.5	20.1	36.1	82.4	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	373.0	22.7	30.1	75.4	0.9
Non-derivatized - MS/MS MassChrom®	120	316.1	14.0	39.2	67.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	386.8	27.5	62.6	76.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	365.7	22.0	36.0	74.7	0.8
Non-derivatized - MS/MS non-kit	152	324.6	27.2	53.6	66.8	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	308.9	45.8	93.0	55.2	0.7

#### Lot D2015 – Enriched 500 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	462.0	31.4	65.9	68.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	46	418.1	25.2	127.9	79.6	0.7
Derivatized - MS/MS non-kit	289	462.9	41.8	105.2	86.7	0.8
LC-MS/MS non-kit	32	530.2	28.4	57.8	82.4	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	514.3	19.5	29.2	75.4	0.9
Non-derivatized - MS/MS MassChrom®	120	417.1	16.1	49.4	67.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	448	526.2	36.7	92.2	76.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	492.7	29.1	55.4	74.7	0.8
Non-derivatized - MS/MS non-kit	152	431.5	30.7	67.0	66.8	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	424.0	71.7	131.3	55.2	0.7



## 2021 Quality Control Data Summaries of Statistical Analyses

### TOTAL GALACTOSE (TGal mg/dL blood)

#### Lot A2005 – Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
50hr Reagent Kit Spotcheck® TGal Astoria-Pacific	50	5.6	0.4	0.4	1.0	1.0
Fluorescence TGal Neonatal PerkinElmer	160	4.4	0.5	0.9	0.3	0.8
Fluorometric manual TGal - non-kit	58	5.5	0.9	2.2	0.3	1.0
GSP® TGal Neonatal PerkinElmer	240	5.2	0.5	0.8	0.1	1.0
NeoLISA® TGal Interscientifica	40	5.2	0.6	0.7	-0.4	1.0
Neonatal® HORM Kit PerkinElmer	110	4.7	0.8	1.1	0.4	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	110	6.7	2.7	5.5	2.0	0.8

#### Lot B2005 – Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
50hr Reagent Kit Spotcheck® TGal Astoria-Pacific	50	10.7	0.7	0.9	1.0	1.0
Fluorescence TGal Neonatal PerkinElmer	160	8.9	0.7	1.2	0.3	0.8
Fluorometric manual TGal - non-kit	58	10.4	1.1	2.3	0.3	1.0
GSP® TGal Neonatal PerkinElmer	240	9.9	1.0	1.4	0.1	1.0
NeoLISA® TGal Interscientifica	40	8.0	0.6	1.2	-0.4	1.0
Neonatal® HORM Kit PerkinElmer	110	9.1	1.0	1.4	0.4	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	110	8.9	3.2	6.6	2.0	0.8

#### Lot C2005 – Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
50hr Reagent Kit Spotcheck® TGal Astoria-Pacific	50	29.6	1.7	3.0	1.0	1.0
Fluorescence TGal Neonatal PerkinElmer	160	25.5	2.0	3.0	0.3	0.8
Fluorometric manual TGal - non-kit	58	31.1	1.6	6.8	0.3	1.0
GSP® TGal Neonatal PerkinElmer	240	30.2	2.8	3.8	0.1	1.0
NeoLISA® TGal Interscientifica	40	28.2	1.8	2.6	-0.4	1.0
Neonatal® HORM Kit PerkinElmer	110	26.3	2.1	2.8	0.4	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	110	25.7	8.5	22.2	2.0	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	18.79	1.95	2.75	18.3	1.4
Derivatized - MS/MS MassChrom® Chromsystems	86	14.84	1.35	4.77	14.1	1.0
Derivatized - MS/MS non-kit	329	18.52	1.67	3.38	17.3	1.4
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	18.97	1.24	1.67	17.5	1.3
Non-derivatized - MS/MS MassChrom®	130	14.32	1.01	2.86	13.4	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	16.02	1.22	1.98	14.7	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	312	15.88	1.00	1.90	14.7	1.1
Non-derivatized - MS/MS non-kit	164	16.93	1.73	2.74	15.8	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	14.44	1.68	3.30	13.5	1.0

#### Lot B2015 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	31.47	4.57	6.98	18.3	1.4
Derivatized - MS/MS MassChrom® Chromsystems	86	22.47	2.16	5.58	14.1	1.0
Derivatized - MS/MS non-kit	329	29.15	2.38	5.00	17.3	1.4
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	28.47	1.64	2.57	17.5	1.3
Non-derivatized - MS/MS MassChrom®	130	21.27	1.42	4.27	13.4	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	23.65	1.76	2.96	14.7	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	312	23.66	1.51	2.79	14.7	1.1
Non-derivatized - MS/MS non-kit	164	25.07	2.68	4.68	15.8	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	22.03	1.83	5.19	13.5	1.0

#### Lot C2015 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	47.51	6.06	10.87	18.3	1.4
Derivatized - MS/MS MassChrom® Chromsystems	86	34.15	2.44	7.10	14.1	1.0
Derivatized - MS/MS non-kit	329	45.40	3.75	7.50	17.3	1.4
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	43.48	2.77	3.94	17.5	1.3
Non-derivatized - MS/MS MassChrom®	130	33.21	1.96	6.26	13.4	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	36.84	2.62	4.74	14.7	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	312	36.13	2.37	4.19	14.7	1.1
Non-derivatized - MS/MS non-kit	164	39.19	4.19	7.84	15.8	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	33.86	2.81	7.14	13.5	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	60.86	5.63	8.94	18.3	1.4
Derivatized - MS/MS MassChrom® Chromsystems	86	43.45	2.81	8.16	14.1	1.0
Derivatized - MS/MS non-kit	329	59.57	4.78	10.29	17.3	1.4
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	57.67	3.21	5.22	17.5	1.3
Non-derivatized - MS/MS MassChrom®	130	42.37	2.35	7.34	13.4	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	48.10	3.66	6.26	14.7	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	312	47.48	2.92	5.62	14.7	1.1
Non-derivatized - MS/MS non-kit	164	50.23	4.14	9.09	15.8	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	43.91	3.59	9.64	13.5	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	10.96	0.70	1.12	11.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	11.13	1.06	3.65	11.2	0.8
Derivatized - MS/MS non-kit	329	11.95	1.16	2.62	12.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	10.58	0.65	1.03	10.5	1.1
Non-derivatized - MS/MS MassChrom®	130	8.50	0.49	1.36	8.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	8.97	0.57	1.07	8.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	8.34	0.44	0.90	8.4	0.8
Non-derivatized - MS/MS non-kit	142	10.71	1.12	4.26	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	9.12	0.89	3.32	8.8	0.9

#### Lot B2015 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	20.34	0.91	3.75	11.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	18.71	1.50	3.35	11.2	0.8
Derivatized - MS/MS non-kit	329	20.85	1.86	3.78	12.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	21.04	1.12	1.83	10.5	1.1
Non-derivatized - MS/MS MassChrom®	130	16.96	0.84	2.70	8.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	17.63	1.07	2.03	8.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	16.68	0.97	1.63	8.4	0.8
Non-derivatized - MS/MS non-kit	142	21.80	1.99	9.04	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	16.99	1.47	5.08	8.8	0.9

#### Lot C2015 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit RECIPE	30	28.42	1.54	4.27	11.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	26.86	1.33	2.66	11.2	0.8
Derivatized - MS/MS non-kit	329	30.41	2.60	5.69	12.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	31.49	1.64	2.25	10.5	1.1
Non-derivatized - MS/MS MassChrom® Chromsystems	130	26.05	1.21	3.87	8.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	26.81	1.69	3.31	8.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	25.33	1.39	2.73	8.4	0.8
Non-derivatized - MS/MS non-kit	142	32.89	3.27	13.23	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	25.66	1.67	6.88	8.8	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

### ACETYL CARNITINE (C2 $\mu\text{mol/L}$ blood) (cont.)

#### Lot D2015 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	38.26	2.15	5.91	11.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	76	33.62	1.89	3.04	11.2	0.8
Derivatized - MS/MS non-kit	329	38.77	3.30	6.77	12.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	42.41	1.82	2.82	10.5	1.1
Non-derivatized - MS/MS MassChrom®	130	33.65	1.69	4.55	8.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	35.44	2.18	4.39	8.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	33.31	1.93	3.52	8.4	0.8
Non-derivatized - MS/MS non-kit	142	42.88	3.57	16.15	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	50	34.96	2.48	11.14	8.8	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.14	0.09	0.11	1.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	66	0.97	0.12	0.23	1.0	0.7
Derivatized - MS/MS non-kit	329	1.12	0.13	0.23	1.1	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.09	0.09	0.11	1.1	1.0
Non-derivatized - MS/MS MassChrom®	130	0.93	0.06	0.16	1.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	0.98	0.08	0.13	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	1.15	0.08	0.13	1.1	1.0
Non-derivatized - MS/MS non-kit	152	1.15	0.11	0.27	1.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	1.00	0.11	0.40	0.9	0.9

#### Lot B2015 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	4.92	0.33	0.79	1.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	66	3.96	0.33	0.46	1.0	0.7
Derivatized - MS/MS non-kit	329	4.91	0.51	0.91	1.1	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	5.00	0.27	0.33	1.1	1.0
Non-derivatized - MS/MS MassChrom®	130	4.49	1.09	3.31	1.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	4.39	0.30	0.54	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	5.25	0.33	0.63	1.1	1.0
Non-derivatized - MS/MS non-kit	152	5.35	0.50	1.55	1.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	4.30	0.24	1.55	0.9	0.9

#### Lot C2015 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	8.29	0.49	1.23	1.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	66	6.98	0.82	1.19	1.0	0.7
Derivatized - MS/MS non-kit	329	8.80	0.92	1.71	1.1	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	8.89	0.54	0.57	1.1	1.0
Non-derivatized - MS/MS MassChrom®	130	7.79	0.42	1.18	1.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	8.01	0.59	1.03	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	9.47	0.55	1.14	1.1	1.0
Non-derivatized - MS/MS non-kit	152	9.56	0.83	2.62	1.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	7.91	0.67	2.90	0.9	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	12.45	0.73	1.80	1.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	66	9.69	1.14	1.67	1.0	0.7
Derivatized - MS/MS non-kit	329	12.44	1.29	2.23	1.1	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	12.99	0.62	0.69	1.1	1.0
Non-derivatized - MS/MS MassChrom®	130	10.90	0.55	1.25	1.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	11.82	1.50	4.85	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	13.63	0.83	1.64	1.1	1.0
Non-derivatized - MS/MS non-kit	152	13.83	1.16	3.42	1.1	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	11.41	0.96	4.17	0.9	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.02	0.01	0.02	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	0.13	0.16	0.40	0.1	0.8
Derivatized - MS/MS non-kit	299	0.03	0.01	0.02	0.0	0.6

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.30	0.04	0.13	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	0.48	0.06	0.19	0.1	0.8
Derivatized - MS/MS non-kit	309	0.33	0.05	0.13	0.0	0.6

#### Lot C2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.76	0.09	0.34	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	1.30	0.12	0.60	0.1	0.8
Derivatized - MS/MS non-kit	309	0.95	0.12	0.39	0.0	0.6

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.68	0.44	0.94	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	2.55	0.21	1.20	0.1	0.8
Derivatized - MS/MS non-kit	309	1.89	0.21	0.78	0.0	0.6



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	60	0.14	0.22	0.51	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.07	0.02	0.04	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	0.06	0.01	0.01	0.1	0.4
Non-derivatized - MS/MS non-kit	90	0.09	0.02	0.06	0.1	0.5
Non-derivatized Labsystems Neomass AAAC Plus	30	0.03	0.01	0.01	0.0	0.2

#### Lot B2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	0.44	0.04	0.33	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.45	0.05	0.17	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	0.44	0.03	0.11	0.1	0.4
Non-derivatized - MS/MS non-kit	90	0.58	0.06	0.34	0.1	0.5
Non-derivatized Labsystems Neomass AAAC Plus	30	0.25	0.06	0.11	0.0	0.2

#### Lot C2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	0.88	0.07	0.67	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.93	0.09	0.33	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	0.91	0.06	0.23	0.1	0.4
Non-derivatized - MS/MS non-kit	90	1.26	0.27	1.03	0.1	0.5
Non-derivatized Labsystems Neomass AAAC Plus	30	0.56	0.09	0.25	0.0	0.2

#### Lot D2015 – Enriched 5.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Non-derivatized - MS/MS MassChrom®	70	2.03	0.15	1.55	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	2.06	0.15	0.66	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	1.99	0.13	0.48	0.1	0.4
Non-derivatized - MS/MS non-kit	90	2.74	0.36	1.95	0.1	0.5
Non-derivatized Labsystems Neomass AAAC Plus	30	1.32	0.21	0.60	0.0	0.2

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.15	0.02	0.06	0.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.12	0.03	0.08	0.1	0.6
Derivatized - MS/MS non-kit	319	0.13	0.03	0.04	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.10	0.01	0.01	0.1	0.7
Non-derivatized - MS/MS MassChrom®	130	0.10	0.01	0.02	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	0.12	0.02	0.02	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	0.09	0.01	0.01	0.1	0.6
Non-derivatized - MS/MS non-kit	132	0.11	0.02	0.04	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.08	0.02	0.04	0.1	0.6

#### Lot B2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.89	0.09	0.13	0.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.68	0.07	0.09	0.1	0.6
Derivatized - MS/MS non-kit	319	0.80	0.10	0.16	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.80	0.04	0.06	0.1	0.7
Non-derivatized - MS/MS MassChrom®	130	0.74	0.05	0.10	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	0.76	0.05	0.09	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	0.72	0.04	0.08	0.1	0.6
Non-derivatized - MS/MS non-kit	132	0.85	0.09	0.29	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	0.67	0.06	0.24	0.1	0.6

#### Lot C2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.11	0.14	0.24	0.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	1.87	0.16	0.28	0.1	0.6
Derivatized - MS/MS non-kit	319	2.17	0.23	0.37	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.25	0.14	0.27	0.1	0.7
Non-derivatized - MS/MS MassChrom®	130	2.13	0.12	0.28	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	2.07	0.14	0.22	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	2.01	0.11	0.22	0.1	0.6
Non-derivatized - MS/MS non-kit	132	2.32	0.23	0.79	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	1.83	0.15	0.63	0.1	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	3.68	0.30	0.46	0.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	2.89	0.25	0.40	0.1	0.6
Derivatized - MS/MS non-kit	319	3.55	0.38	0.63	0.1	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	3.73	0.16	0.33	0.1	0.7
Non-derivatized - MS/MS MassChrom®	130	3.41	0.19	0.32	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	3.43	0.22	0.38	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	3.31	0.18	0.34	0.1	0.6
Non-derivatized - MS/MS non-kit	132	3.81	0.36	1.25	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	50	3.18	0.25	1.20	0.1	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.07	0.02	0.03	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	39	0.09	0.01	0.03	0.1	0.7
Derivatized - MS/MS NeoGram PerkinElmer	30	0.09	0.01	0.01	0.1	0.8
Derivatized - MS/MS non-kit	279	0.12	0.11	0.48	0.0	1.0

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.36	0.05	0.11	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	39	0.45	0.06	0.12	0.1	0.7
Derivatized - MS/MS NeoGram PerkinElmer	30	0.44	0.05	0.06	0.1	0.8
Derivatized - MS/MS non-kit	279	0.45	0.06	0.14	0.0	1.0

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.64	0.07	0.17	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	39	0.83	0.08	0.19	0.1	0.7
Derivatized - MS/MS NeoGram PerkinElmer	30	0.90	0.11	0.15	0.1	0.8
Derivatized - MS/MS non-kit	279	0.86	0.10	0.28	0.0	1.0

#### Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.54	0.21	0.40	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	39	1.90	0.16	0.42	0.1	0.7
Derivatized - MS/MS NeoGram PerkinElmer	30	1.95	0.18	0.26	0.1	0.8
Derivatized - MS/MS non-kit	279	2.60	2.15	10.26	0.0	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.09	0.02	0.04	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	0.10	0.03	0.08	0.1	0.8
Derivatized - MS/MS non-kit	329	0.08	0.02	0.03	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.06	0.01	0.01	0.1	0.9
Non-derivatized - MS/MS MassChrom®	120	0.11	0.02	0.09	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	468	0.06	0.01	0.01	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.06	0.01	0.01	0.1	0.8
Non-derivatized - MS/MS non-kit	162	0.08	0.01	0.03	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.07	0.02	0.02	0.1	0.8

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.48	0.06	0.07	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	0.48	0.05	0.06	0.1	0.8
Derivatized - MS/MS non-kit	329	0.48	0.06	0.09	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.49	0.03	0.05	0.1	0.9
Non-derivatized - MS/MS MassChrom®	120	0.52	0.04	0.11	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	468	0.45	0.03	0.05	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.43	0.03	0.05	0.1	0.8
Non-derivatized - MS/MS non-kit	162	0.55	0.05	0.13	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.47	0.06	0.12	0.1	0.8

#### Lot C2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.17	0.10	0.11	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	1.29	0.11	0.16	0.1	0.8
Derivatized - MS/MS non-kit	329	1.31	0.15	0.26	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.33	0.09	0.13	0.1	0.9
Non-derivatized - MS/MS MassChrom®	120	1.38	0.09	0.21	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	468	1.27	0.14	0.46	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	1.19	0.07	0.14	0.1	0.8
Non-derivatized - MS/MS non-kit	162	1.49	0.14	0.35	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	1.26	0.15	0.35	0.1	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.45	0.17	0.19	0.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	2.40	0.19	0.33	0.1	0.8
Derivatized - MS/MS non-kit	329	2.53	0.28	0.47	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.67	0.12	0.22	0.1	0.9
Non-derivatized - MS/MS MassChrom®	120	2.63	0.16	0.33	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	468	2.49	0.23	0.56	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	2.35	0.15	0.29	0.1	0.8
Non-derivatized - MS/MS non-kit	162	2.94	0.25	0.67	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	2.56	0.21	0.67	0.1	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.02	0.02	0.02	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	56	0.04	0.02	0.03	0.0	0.6
Derivatized - MS/MS non-kit	330	0.04	0.01	0.06	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS MassChrom®	100	0.02	0.00	0.02	0.0	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.02	0.01	0.06	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	288	0.01	0.00	0.01	0.0	0.6
Non-derivatized - MS/MS non-kit	132	0.02	0.01	0.04	0.0	1.2
Non-derivatized Labsystems Neomass AAAC Plus	42	0.01	0.01	0.02	0.0	0.6

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.33	0.04	0.07	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	56	0.34	0.05	0.08	0.0	0.6
Derivatized - MS/MS non-kit	330	0.40	0.05	0.12	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.34	0.02	0.03	0.0	0.7
Non-derivatized - MS/MS MassChrom®	110	0.29	0.02	0.15	0.0	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.31	0.07	0.29	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	298	0.31	0.02	0.04	0.0	0.6
Non-derivatized - MS/MS non-kit	132	0.59	0.06	0.59	0.0	1.2
Non-derivatized Labsystems Neomass AAAC Plus	42	0.23	0.03	0.19	0.0	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot C2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.86	0.09	0.18	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	56	0.98	0.11	0.23	0.0	0.6
Derivatized - MS/MS non-kit	330	1.12	0.12	0.30	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	1.01	0.06	0.07	0.0	0.7
Non-derivatized - MS/MS MassChrom®	110	0.93	0.07	0.32	0.0	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.86	0.14	0.52	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	298	0.89	0.06	0.11	0.0	0.6
Non-derivatized - MS/MS non-kit	132	1.73	0.16	1.71	0.0	1.2
Non-derivatized Labsystems Neomass AAAC Plus	42	0.81	0.11	0.43	0.0	0.6

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.81	0.15	0.35	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	56	1.88	0.17	0.43	0.0	0.6
Derivatized - MS/MS non-kit	330	2.21	0.23	0.51	0.0	0.7
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	2.05	0.09	0.16	0.0	0.7
Non-derivatized - MS/MS MassChrom®	110	1.88	0.13	0.56	0.0	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	1.74	0.23	0.82	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	298	1.81	0.13	0.24	0.0	0.6
Non-derivatized - MS/MS non-kit	132	3.50	0.29	3.66	0.0	1.2
Non-derivatized Labsystems Neomass AAAC Plus	42	1.73	0.17	0.86	0.0	0.6



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.03	0.01	0.02	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	76	0.06	0.03	0.09	0.1	1.1
Derivatized - MS/MS non-kit	339	0.02	0.01	0.01	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.04	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	0.07	0.02	0.02	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	400	0.05	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	281	0.37	0.04	2.26	0.5	1.0
Non-derivatized - MS/MS non-kit	154	0.04	0.01	0.02	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.06	0.04	0.07	0.0	0.9

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.62	0.05	0.13	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	76	0.64	0.08	0.12	0.1	1.1
Derivatized - MS/MS non-kit	339	0.29	0.04	0.13	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.44	0.03	0.06	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	0.59	0.07	0.13	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	400	0.50	0.04	0.07	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	296	0.90	0.08	3.37	0.5	1.0
Non-derivatized - MS/MS non-kit	154	0.43	0.04	0.15	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.48	0.16	0.26	0.0	0.9

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.12	0.09	0.24	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	76	1.23	0.13	0.20	0.1	1.1
Derivatized - MS/MS non-kit	339	0.58	0.07	0.26	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.81	0.05	0.12	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	1.12	0.15	0.24	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	400	0.94	0.07	0.12	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	296	1.81	0.95	6.87	0.5	1.0
Non-derivatized - MS/MS non-kit	154	0.84	0.11	0.34	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	0.76	0.14	0.20	0.0	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.63	0.26	0.75	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	76	2.91	0.25	0.49	0.1	1.1
Derivatized - MS/MS non-kit	339	1.44	0.15	0.64	0.0	0.6
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.98	0.11	0.28	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	2.77	0.25	0.56	0.1	1.1
Non-derivatized - MS/MS NeoBase™ PerkinElmer	400	2.32	0.17	0.31	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	296	2.89	0.21	6.48	0.5	1.0
Non-derivatized - MS/MS non-kit	154	2.05	0.23	0.74	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	48	2.19	0.70	1.46	0.0	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.29	0.04	0.06	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	56	0.43	0.06	0.10	0.4	0.7
Derivatized - MS/MS non-kit	339	0.41	0.05	0.10	0.4	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.67	0.05	0.06	0.7	0.9
Non-derivatized - MS/MS MassChrom®	100	0.37	0.03	0.10	0.4	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	0.48	0.04	0.08	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	0.55	0.04	0.10	0.6	0.6
Non-derivatized - MS/MS non-kit	140	0.56	0.06	0.14	0.6	0.8

#### Lot B2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.87	0.15	0.23	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	56	1.08	0.14	0.23	0.4	0.7
Derivatized - MS/MS non-kit	339	1.17	0.11	0.25	0.4	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.54	0.11	0.12	0.7	0.9
Non-derivatized - MS/MS MassChrom®	100	0.81	0.06	0.23	0.4	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	1.04	0.07	0.18	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	1.16	0.06	0.18	0.6	0.6
Non-derivatized - MS/MS non-kit	140	1.34	0.12	0.28	0.6	0.8

#### Lot C2015 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.35	0.12	0.24	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	56	1.85	0.19	0.38	0.4	0.7
Derivatized - MS/MS non-kit	339	1.97	0.17	0.45	0.4	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.40	0.16	0.19	0.7	0.9
Non-derivatized - MS/MS MassChrom®	100	1.28	0.11	0.38	0.4	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	1.62	0.11	0.28	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	1.79	0.12	0.33	0.6	0.6
Non-derivatized - MS/MS non-kit	140	2.13	0.20	0.47	0.6	0.8

2021 Quality Control Data Summaries of Statistical Analyses  
**HYDROXYISOVALERYLCARNITINE (C5OH  $\mu\text{mol/L}$  blood) (cont.)**

**Lot D2015 – Enriched 3  $\mu\text{mol/L}$  blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y- Intercept</b>	<b>Slope</b>
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.93	0.19	0.29	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	56	2.41	0.26	0.53	0.4	0.7
Derivatized - MS/MS non-kit	339	2.75	0.27	0.65	0.4	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	3.38	0.17	0.22	0.7	0.9
Non-derivatized - MS/MS MassChrom®	100	1.67	0.14	0.45	0.4	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	370	2.18	0.14	0.37	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	250	2.37	0.15	0.38	0.6	0.6
Non-derivatized - MS/MS non-kit	140	2.90	0.24	0.58	0.6	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.04	0.02	0.05	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	0.04	0.01	0.03	0.1	0.5
Derivatized - MS/MS non-kit	318	0.02	0.01	0.02	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.01	0.00	0.00	0.0	0.8
Non-derivatized - MS/MS MassChrom®	120	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	0.01	0.00	0.01	-0.1	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS non-kit	142	0.02	0.01	0.02	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.01	0.00	0.01	0.0	0.6

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.41	0.04	0.06	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	0.35	0.04	0.05	0.1	0.5
Derivatized - MS/MS non-kit	329	0.40	0.05	0.08	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.41	0.03	0.04	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	0.38	0.03	0.05	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	0.40	0.03	0.04	-0.1	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.39	0.02	0.04	0.0	0.7
Non-derivatized - MS/MS non-kit	142	0.43	0.04	0.08	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.33	0.04	0.07	0.0	0.6

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.70	0.07	0.09	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	0.63	0.05	0.07	0.1	0.5
Derivatized - MS/MS non-kit	329	1.01	0.80	4.09	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.81	0.05	0.07	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	0.77	0.04	0.10	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	0.79	0.05	0.08	-0.1	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.74	0.05	0.09	0.0	0.7
Non-derivatized - MS/MS non-kit	142	0.87	0.08	0.17	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.62	0.05	0.12	0.0	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.68	0.14	0.18	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	1.40	0.09	0.24	0.1	0.5
Derivatized - MS/MS non-kit	329	1.97	0.21	0.38	0.1	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.05	0.10	0.16	0.0	0.8
Non-derivatized - MS/MS MassChrom®	130	1.86	0.09	0.18	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	452	2.80	1.79	12.10	-0.1	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	1.81	0.09	0.23	0.0	0.7
Non-derivatized - MS/MS non-kit	142	2.21	0.21	0.42	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	1.58	0.11	0.27	0.0	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ 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	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	0.05	0.04	0.13	0.1	0.7
Derivatized - MS/MS non-kit	319	0.03	0.01	0.03	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.02	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS MassChrom®	178	0.03	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	480	0.03	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.03	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS non-kit	172	0.04	0.01	0.02	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.03	0.01	0.01	0.0	0.7

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.42	0.03	0.07	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	0.38	0.04	0.06	0.1	0.7
Derivatized - MS/MS non-kit	329	0.47	0.06	0.09	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.44	0.03	0.04	0.0	0.9
Non-derivatized - MS/MS MassChrom®	180	0.42	0.02	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	480	0.45	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.41	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS non-kit	172	0.51	0.04	0.21	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.38	0.03	0.07	0.0	0.7

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.80	0.04	0.09	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	0.71	0.07	0.11	0.1	0.7
Derivatized - MS/MS non-kit	329	0.91	0.09	0.16	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.84	0.05	0.06	0.0	0.9
Non-derivatized - MS/MS MassChrom®	180	0.81	0.04	0.09	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	480	0.86	0.06	0.09	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.77	0.05	0.08	0.0	0.8
Non-derivatized - MS/MS non-kit	172	0.98	0.09	0.40	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.73	0.06	0.13	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.95	0.11	0.34	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	76	1.69	0.15	0.22	0.1	0.7
Derivatized - MS/MS non-kit	329	2.26	0.25	0.43	0.0	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.14	0.10	0.16	0.0	0.9
Non-derivatized - MS/MS MassChrom®	180	1.99	0.11	0.22	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	480	2.13	0.14	0.20	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	1.90	0.12	0.21	0.0	0.8
Non-derivatized - MS/MS non-kit	172	2.42	0.26	1.02	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	1.83	0.15	0.35	0.0	0.7



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.05	0.02	0.04	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	74	0.03	0.01	0.03	0.0	0.5
Derivatized - MS/MS non-kit	328	0.03	0.01	0.02	0.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.02	0.00	0.00	-0.0	0.9
Non-derivatized - MS/MS MassChrom®	170	0.03	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.03	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.03	0.01	0.01	-0.1	1.1
Non-derivatized - MS/MS non-kit	162	0.04	0.01	0.03	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	0.03	0.01	0.01	0.0	0.7

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.39	0.04	0.07	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	74	0.26	0.03	0.04	0.0	0.5
Derivatized - MS/MS non-kit	329	0.48	0.06	0.12	0.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.44	0.03	0.03	-0.0	0.9
Non-derivatized - MS/MS MassChrom®	170	0.42	0.03	0.07	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.42	0.03	0.06	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.42	0.03	0.06	-0.1	1.1
Non-derivatized - MS/MS non-kit	162	0.51	0.06	0.13	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	0.35	0.02	0.04	0.0	0.7

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.77	0.06	0.13	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	74	0.50	0.04	0.07	0.0	0.5
Derivatized - MS/MS non-kit	329	0.98	0.11	0.22	0.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.87	0.06	0.07	-0.0	0.9
Non-derivatized - MS/MS MassChrom®	170	0.85	0.05	0.12	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.85	0.06	0.10	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.85	0.05	0.11	-0.1	1.1
Non-derivatized - MS/MS non-kit	162	1.05	0.14	0.27	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	0.70	0.06	0.09	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.90	0.17	0.34	0.0	0.8
Derivatized - MS/MS MassChrom® Chromsystems	74	1.25	0.10	0.21	0.0	0.5
Derivatized - MS/MS non-kit	329	2.52	0.29	0.61	0.0	1.0
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.31	0.10	0.11	-0.0	0.9
Non-derivatized - MS/MS MassChrom®	170	2.17	0.13	0.29	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	2.19	0.15	0.25	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	2.86	2.32	12.35	-0.1	1.1
Non-derivatized - MS/MS non-kit	161	2.67	0.70	0.35	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	48	1.84	0.10	0.23	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

### DODECANOYL CARNITINE (C12 $\mu\text{mol/L}$ blood)

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.07	0.04	0.10	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.15	0.16	0.47	0.1	0.6
Derivatized - MS/MS non-kit	317	0.04	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.02	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS MassChrom®	120	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.02	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS non-kit	134	0.03	0.01	0.03	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.02	0.01	0.01	0.0	0.7

#### Lot B2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.73	0.11	0.17	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.72	0.09	0.16	0.1	0.6
Derivatized - MS/MS non-kit	319	0.89	0.11	0.22	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.91	0.05	0.07	0.0	0.9
Non-derivatized - MS/MS MassChrom®	130	0.75	0.04	0.10	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	0.81	0.06	0.09	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	0.74	0.05	0.08	0.0	0.7
Non-derivatized - MS/MS non-kit	134	0.95	0.10	0.43	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.68	0.06	0.10	0.0	0.7

#### Lot C2015 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.41	0.23	0.35	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	1.38	0.13	0.26	0.1	0.6
Derivatized - MS/MS non-kit	319	1.71	0.19	0.40	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.70	0.12	0.13	0.0	0.9
Non-derivatized - MS/MS MassChrom®	130	1.47	0.09	0.19	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	1.57	0.12	0.17	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	1.43	0.09	0.14	0.0	0.7
Non-derivatized - MS/MS non-kit	134	1.84	0.17	0.83	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	1.33	0.13	0.21	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.02	0.21	0.38	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	1.99	0.17	0.38	0.1	0.6
Derivatized - MS/MS non-kit	319	2.54	0.28	0.56	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.64	0.16	0.22	0.0	0.9
Non-derivatized - MS/MS MassChrom®	130	2.17	0.14	0.27	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	430	2.35	0.16	0.23	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	280	2.14	0.16	0.25	0.0	0.7
Non-derivatized - MS/MS non-kit	134	2.78	0.28	1.31	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	1.99	0.16	0.34	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.11	0.05	0.12	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.09	0.03	0.08	0.1	0.7
Derivatized - MS/MS non-kit	327	0.07	0.02	0.03	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.06	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS MassChrom®	140	0.06	0.02	0.04	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	0.06	0.01	0.02	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.13	0.16	0.93	0.2	1.3
Non-derivatized - MS/MS non-kit	152	0.08	0.02	0.05	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.05	0.01	0.01	0.0	0.7

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.39	0.04	0.07	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.41	0.05	0.08	0.1	0.7
Derivatized - MS/MS non-kit	327	0.50	0.08	0.18	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.45	0.04	0.04	0.0	0.8
Non-derivatized - MS/MS MassChrom®	140	0.42	0.03	0.06	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	0.46	0.04	0.05	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.79	0.76	4.32	0.2	1.3
Non-derivatized - MS/MS non-kit	152	0.50	0.06	0.11	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.37	0.03	0.09	0.0	0.7

#### Lot C2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.06	0.11	0.25	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	1.09	0.10	0.15	0.1	0.7
Derivatized - MS/MS non-kit	327	1.38	0.14	0.23	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.24	0.09	0.11	0.0	0.8
Non-derivatized - MS/MS MassChrom®	140	1.99	2.58	9.37	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	459	1.28	0.10	0.13	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	2.22	2.16	12.30	0.2	1.3
Non-derivatized - MS/MS non-kit	152	1.40	0.17	0.33	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	1.05	0.08	0.25	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.07	0.13	0.53	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	2.02	0.17	0.27	0.1	0.7
Derivatized - MS/MS non-kit	327	2.70	0.31	0.60	0.1	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	2.53	0.11	0.17	0.0	0.8
Non-derivatized - MS/MS MassChrom®	140	2.33	0.15	0.31	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	460	2.57	0.19	0.26	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	3.97	3.31	18.65	0.2	1.3
Non-derivatized - MS/MS non-kit	152	2.78	0.30	0.61	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	2.12	0.19	0.59	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.06	0.04	0.09	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	76	0.07	0.02	0.05	0.1	0.4
Derivatized - MS/MS non-kit	339	0.04	0.01	0.02	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.02	0.00	0.01	0.1	0.4
Non-derivatized - MS/MS MassChrom®	100	0.02	0.00	0.01	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	0.03	0.01	0.03	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.02	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS non-kit	142	0.03	0.01	0.02	0.0	0.6
Non-derivatized Labsystems Neomass AAAC Plus	38	0.00	0.00	0.00	0.0	0.4

#### Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.21	0.03	0.04	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	76	0.27	0.04	0.07	0.1	0.4
Derivatized - MS/MS non-kit	339	0.29	0.04	0.06	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.30	0.03	0.03	0.1	0.4
Non-derivatized - MS/MS MassChrom®	100	0.24	0.02	0.05	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	0.27	0.03	0.06	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.26	0.02	0.03	0.0	0.5
Non-derivatized - MS/MS non-kit	142	0.30	0.03	0.08	0.0	0.6
Non-derivatized Labsystems Neomass AAAC Plus	38	0.20	0.00	0.00	0.0	0.4

#### Lot C2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.52	0.04	0.12	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	76	0.67	0.06	0.13	0.1	0.4
Derivatized - MS/MS non-kit	339	0.80	0.10	0.17	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	0.75	0.04	0.04	0.1	0.4
Non-derivatized - MS/MS MassChrom®	100	0.67	0.05	0.16	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	0.72	0.07	0.11	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.70	0.04	0.08	0.0	0.5
Non-derivatized - MS/MS non-kit	142	0.83	0.10	0.23	0.0	0.6
Non-derivatized Labsystems Neomass AAAC Plus	38	0.60	0.00	0.10	0.0	0.4

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit RECIPE	30	1.17	0.10	0.26	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	76	1.23	0.12	0.26	0.1	0.4
Derivatized - MS/MS non-kit	339	1.59	0.19	0.33	0.0	0.5
Non-derivatized - MS/MS MS2 Screen Neo Siemens	30	1.37	0.07	0.07	0.1	0.4
Non-derivatized - MS/MS MassChrom® Chromsystems	100	1.34	0.10	0.26	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	1.46	0.12	0.20	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	1.42	0.10	0.17	0.0	0.5
Non-derivatized - MS/MS non-kit	142	1.70	0.16	0.47	0.0	0.6
Non-derivatized Labsystems Neomass AAAC Plus	38	1.20	0.10	0.20	0.0	0.4



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.34	0.26	0.60	1.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	0.91	0.14	0.35	0.9	0.8
Derivatized - MS/MS non-kit	329	0.89	0.09	0.21	0.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.94	0.06	0.09	0.9	0.9
Non-derivatized - MS/MS MassChrom®	130	0.82	0.07	0.13	0.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	0.90	0.07	0.12	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	1.01	0.08	0.14	1.0	1.0
Non-derivatized - MS/MS non-kit	154	0.96	0.10	0.19	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	0.81	0.05	0.13	0.8	0.8

#### Lot B2015 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	4.51	0.29	0.78	1.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	3.95	0.30	0.48	0.9	0.8
Derivatized - MS/MS non-kit	329	4.19	0.39	0.90	0.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	4.63	0.28	0.33	0.9	0.9
Non-derivatized - MS/MS MassChrom®	130	4.08	0.25	0.53	0.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	4.30	0.30	0.45	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	5.00	0.34	0.63	1.0	1.0
Non-derivatized - MS/MS non-kit	154	4.70	0.44	0.87	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	3.86	0.26	0.62	0.8	0.8

#### Lot C2015 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	7.56	0.62	1.49	1.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	7.00	0.45	0.74	0.9	0.8
Derivatized - MS/MS non-kit	329	7.76	0.67	1.14	0.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	8.04	0.47	0.53	0.9	0.9
Non-derivatized - MS/MS MassChrom®	130	7.19	0.39	0.65	0.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	7.75	0.57	0.84	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	8.81	0.55	1.05	1.0	1.0
Non-derivatized - MS/MS non-kit	154	8.30	0.75	1.70	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	6.96	0.45	1.04	0.8	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

### PALMITOYLCARNITINE (C16 $\mu\text{mol/L}$ blood) (cont.)

#### Lot D2015 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	11.27	1.07	2.74	1.3	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	10.00	0.74	1.15	0.9	0.8
Derivatized - MS/MS non-kit	329	11.14	1.26	1.86	0.9	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	12.09	0.59	0.82	0.9	0.9
Non-derivatized - MS/MS MassChrom®	130	10.38	0.67	1.01	0.9	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	446	11.39	0.78	1.13	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	12.80	0.82	1.55	1.0	1.0
Non-derivatized - MS/MS non-kit	154	12.23	1.11	2.22	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	48	10.16	0.54	1.71	0.8	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.04	0.04	0.08	-0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	75	0.02	0.01	0.04	0.0	0.7
Derivatized - MS/MS non-kit	326	0.01	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.01	0.00	0.00	0.0	0.8
Non-derivatized - MS/MS MassChrom®	100	0.01	0.01	0.01	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	469	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	300	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS non-kit	142	0.01	0.00	0.01	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.00	0.00	0.00	0.0	0.6

#### Lot B2015 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.18	0.02	0.03	-0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	86	0.18	0.02	0.04	0.0	0.7
Derivatized - MS/MS non-kit	327	0.26	0.21	1.04	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.19	0.01	0.03	0.0	0.8
Non-derivatized - MS/MS MassChrom®	110	0.12	0.01	0.04	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.17	0.02	0.03	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.18	0.01	0.03	0.0	0.7
Non-derivatized - MS/MS non-kit	152	0.20	0.02	0.06	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.13	0.01	0.04	0.0	0.6

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.66	0.09	0.15	-0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	86	0.68	0.05	0.14	0.0	0.7
Derivatized - MS/MS non-kit	327	0.78	0.08	0.20	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.73	0.04	0.09	0.0	0.8
Non-derivatized - MS/MS MassChrom®	110	0.45	0.03	0.17	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.65	0.05	0.14	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.71	0.04	0.11	0.0	0.7
Non-derivatized - MS/MS non-kit	152	0.79	0.09	0.25	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.55	0.04	0.11	0.0	0.6

2021 Quality Control Data Summaries of Statistical Analyses  
**HYDROXPALMITOYL CARNITINE (C16OH  $\mu\text{mol/L}$  blood) (cont.)**

**Lot D2015 – Enriched 1.5  $\mu\text{mol/L}$  blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y- Intercept</b>	<b>Slope</b>
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.57	0.23	0.80	-0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	86	1.00	0.10	0.21	0.0	0.7
Derivatized - MS/MS non-kit	327	1.19	0.12	0.29	0.0	0.8
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.15	0.06	0.16	0.0	0.8
Non-derivatized - MS/MS MassChrom®	110	0.68	0.06	0.25	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	470	0.99	0.08	0.21	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	1.07	0.07	0.16	0.0	0.7
Non-derivatized - MS/MS non-kit	152	1.21	0.12	0.35	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	50	0.83	0.07	0.17	0.0	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

### STEAROYL CARNITINE (C18 $\mu\text{mol/L}$ blood)

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.81	0.13	0.30	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	0.72	0.07	0.12	0.7	0.9
Derivatized - MS/MS non-kit	319	0.64	0.07	0.13	0.6	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	0.60	0.04	0.06	0.6	0.9
Non-derivatized - MS/MS MassChrom®	130	0.63	0.05	0.09	0.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	0.64	0.05	0.07	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	0.63	0.04	0.07	0.6	1.0
Non-derivatized - MS/MS non-kit	142	0.68	0.07	0.10	0.7	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	0.59	0.06	0.11	0.6	0.9

#### Lot B2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.59	0.19	0.25	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	1.64	0.13	0.24	0.7	0.9
Derivatized - MS/MS non-kit	319	1.53	0.16	0.29	0.6	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	1.52	0.09	0.11	0.6	0.9
Non-derivatized - MS/MS MassChrom®	130	1.60	0.10	0.23	0.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	1.57	0.11	0.16	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	1.60	0.10	0.18	0.6	1.0
Non-derivatized - MS/MS non-kit	142	1.68	0.17	0.23	0.7	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	1.44	0.14	0.25	0.6	0.9

#### Lot C2015 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	2.88	0.29	0.48	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	3.43	0.23	0.43	0.7	0.9
Derivatized - MS/MS non-kit	319	3.21	0.32	0.62	0.6	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	3.13	0.23	0.23	0.6	0.9
Non-derivatized - MS/MS MassChrom®	130	3.37	0.22	0.45	0.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	3.30	0.24	0.33	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	3.34	0.20	0.32	0.6	1.0
Non-derivatized - MS/MS non-kit	142	3.50	0.34	0.49	0.7	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	3.04	0.26	0.50	0.6	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	5.00	0.52	1.19	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	86	5.39	0.40	0.67	0.7	0.9
Derivatized - MS/MS non-kit	319	5.15	0.53	0.98	0.6	0.9
Non-derivatized - MS/MS MS2 Screen Neo Siemens	48	5.20	0.23	0.33	0.6	0.9
Non-derivatized - MS/MS MassChrom®	130	5.36	0.37	0.72	0.6	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	5.43	0.38	0.54	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	310	5.43	0.36	0.55	0.6	1.0
Non-derivatized - MS/MS non-kit	142	5.68	0.60	0.84	0.7	1.0
Non-derivatized Labsystems Neomass AAAC Plus	48	4.99	0.47	0.98	0.6	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.06	0.07	0.14	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	66	0.01	0.01	0.01	0.0	0.7
Derivatized - MS/MS non-kit	227	0.04	0.01	0.15	0.0	0.8
Non-derivatized - MS/MS MassChrom®	96	0.01	0.01	0.03	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	0.02	0.00	0.09	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	271	0.00	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS non-kit	92	0.01	0.01	0.01	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	0.00	0.00	0.00	0.0	0.5

#### Lot B2015 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.19	0.04	0.06	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	0.20	0.02	0.03	0.0	0.7
Derivatized - MS/MS non-kit	229	0.25	0.03	0.35	0.0	0.8
Non-derivatized - MS/MS MassChrom®	100	0.13	0.02	0.03	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	439	0.19	0.02	0.23	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	0.15	0.01	0.02	0.0	0.6
Non-derivatized - MS/MS non-kit	92	0.19	0.02	0.10	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	0.12	0.02	0.03	0.0	0.5

#### Lot C2015 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.58	0.14	0.23	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	0.72	0.06	0.11	0.0	0.7
Derivatized - MS/MS non-kit	229	0.83	0.08	0.70	0.0	0.8
Non-derivatized - MS/MS MassChrom®	106	0.49	0.05	0.13	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	439	0.65	0.06	0.43	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	0.58	0.04	0.07	0.0	0.6
Non-derivatized - MS/MS non-kit	92	0.70	0.09	0.40	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	0.48	0.06	0.09	0.0	0.5

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.17	0.16	0.23	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	76	1.09	0.09	0.17	0.0	0.7
Derivatized - MS/MS non-kit	229	1.29	0.13	1.11	0.0	0.8
Non-derivatized - MS/MS MassChrom®	106	0.74	0.07	0.22	0.0	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	440	1.01	0.08	0.72	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	290	0.89	0.06	0.11	0.0	0.6
Non-derivatized - MS/MS non-kit	92	1.09	0.16	0.66	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	48	0.73	0.10	0.15	0.0	0.5



2021 Quality Control Data Summaries of Statistical Analyses  
**24:0-LYSOPHOSPHATIDYLCHOLINE (24LPC  $\mu\text{mol/L}$  blood)**

**Lot A2015 – Enriched 0  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	40	0.07	0.01	0.06	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.15	0.03	0.08	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.07	0.01	0.02	0.1	0.6

**Lot B2015 – Enriched 0.25  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	40	0.25	0.02	0.09	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	0.40	0.05	0.13	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.26	0.18	0.27	0.1	0.6

**Lot C2015 – Enriched 0.5  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	40	0.45	0.04	0.13	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	0.64	0.07	0.19	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.36	0.07	0.11	0.1	0.6

**Lot D2015 – Enriched 2  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	40	1.70	0.10	0.38	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	210	2.15	0.19	0.48	0.2	1.0
Non-derivatized - MS/MS non-kit	30	1.29	0.22	0.37	0.1	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	0.03	0.01	0.04	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	228	0.10	0.02	0.04	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.06	0.01	0.03	0.0	0.6

#### Lot B2015 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	0.22	0.03	0.05	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	238	0.30	0.04	0.07	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.19	0.03	0.05	0.0	0.6

#### Lot C2015 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	0.43	0.04	0.08	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	238	0.54	0.07	0.12	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.35	0.06	0.09	0.0	0.6

#### Lot D2015 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS negative ion mode	60	1.72	0.13	0.26	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	238	1.94	0.19	0.36	0.1	0.9
Non-derivatized - MS/MS non-kit	30	1.31	0.20	0.29	0.0	0.6

## 2021 Quality Control Data Summaries of Statistical Analyses

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

Insufficient data reported for this analyte.

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2015 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	1.13	0.13	0.36	1.1	0.9

#### Lot B2015 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	5.55	0.46	1.70	1.1	0.9

#### Lot C2015 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	10.19	0.96	3.24	1.1	0.9

#### Lot D2015 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized – MS/MS non-kit	50	19.39	1.37	6.41	1.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

Insufficient data reported for this analyte.

## 2021 Quality Control Data Summaries of Statistical Analyses

### **GALACTOCEREBROSIDASE (GALC $\mu\text{mol/hr/L}$ blood)**

#### **Lot A2008 – Mean Activity 0.18 $\mu\text{mol/hr/L}$ blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	30	0.16	0.04	0.05	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	136	0.33	0.04	0.66	0.2	0.8

#### **Lot B2008 – Mean Activity 0.49 $\mu\text{mol/hr/L}$ blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	30	0.45	0.03	0.04	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	149	0.41	0.05	0.08	0.2	0.8

#### **Lot C2008 – Mean Activity 3.14 $\mu\text{mol/hr/L}$ blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	30	3.19	0.15	0.22	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	156	2.98	0.20	0.75	0.2	0.8

#### **Lot D2008 – Mean Activity 6.16 $\mu\text{mol/hr/L}$ blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	30	6.13	0.38	0.52	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	156	5.17	0.36	1.41	0.2	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2008 – Mean Activity 0.12 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	40	0.12	0.05	0.05	0.0	0.9
LC-MS/MS non-kit	30	0.07	0.01	0.02	-0.1	1.3
NeoLSD™ MSMS Kit PerkinElmer	154	0.10	0.03	0.06	0.0	1.0

#### Lot B2008 – Mean Activity 0.60 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	50	0.53	0.08	0.12	0.0	0.9
LC-MS/MS non-kit	30	0.65	0.06	0.18	-0.1	1.3
NeoLSD™ MSMS Kit PerkinElmer	184	0.55	0.06	0.10	0.0	1.0

#### Lot C2008 – Mean Activity 3.99 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	50	3.73	0.51	0.74	0.0	0.9
LC-MS/MS non-kit	30	4.89	0.31	1.84	-0.1	1.3
NeoLSD™ MSMS Kit PerkinElmer	184	4.05	0.42	0.59	0.0	1.0

#### Lot D2008 – Mean Activity 6.89 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Flow Injection Analysis (FIA)-MS/MS multiplexed enzyme reaction	50	6.29	0.45	0.87	0.0	0.9
LC-MS/MS non-kit	30	8.85	0.47	3.61	-0.1	1.3
NeoLSD™ MSMS Kit PerkinElmer	184	6.68	0.48	0.82	0.0	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2008 – Mean Activity 1.34 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	60	1.28	0.29	0.34	0.2	1.2

#### Lot B2008 – Mean Activity 2.10 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	74	2.44	0.33	0.50	0.2	1.2

#### Lot C2008 – Mean Activity 9.46 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	80	12.74	1.38	1.60	0.2	1.2

#### Lot D2008 – Mean Activity 18.71 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	80	21.76	1.62	2.02	0.2	1.2

#### GAA Fluorometric Method

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	24	0.45	0.33	0.07
B2008	30	0.66	0.50	0.16
C2008	50	2.91	1.31	0.36
D2008	50	5.51	1.82	0.54



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### **Lot A2008 – Mean Activity 0.09 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed	40	0.10	0.06	0.11	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	190	0.25	0.04	0.73	0.1	0.9

#### **Lot B2008 – Mean Activity 0.50 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	0.49	0.06	0.11	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	208	0.45	0.05	0.09	0.1	0.9

#### **Lot C2008 – Mean Activity 3.87 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	3.63	0.33	0.44	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	214	3.75	0.33	0.89	0.1	0.9

#### **Lot D2008 – Mean Activity 7.30 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
Flow Injection Analysis (FIA)-MS/MS multiplexed	50	6.94	0.56	0.64	0.0	1.0
NeoLSD™ MSMS Kit PerkinElmer	214	6.49	0.45	1.70	0.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### **Lot A2008 – Mean Activity 1.95 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	61	2.11	0.37	1.00	0.4	1.1

#### **Lot B2008 – Mean Activity 2.53 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	65	2.99	0.43	0.61	0.4	1.1

#### **Lot C2008 – Mean Activity 10.39 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	80	12.05	0.76	0.87	0.4	1.1

#### **Lot D2008 – Mean Activity 22.87 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	80	24.36	1.99	2.13	0.4	1.1

#### **IDUA Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	21	0.24	0.29	0.16
B2008	40	0.30	0.27	0.07
C2008	60	2.44	0.93	0.30
D2008	60	7.08	4.77	0.54

## 2021 Quality Control Data Summaries of Statistical Analyses

### **α-GALACTOSIDASE (GLA μmol/hr/L blood)**

#### **Lot A2008 – Mean Activity 1.03 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	0.55	0.03	0.12	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	152	1.03	0.13	1.23	0.0	0.9

#### **Lot B2008 – Mean Activity 1.73 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	1.26	0.14	0.23	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	176	1.30	0.13	0.23	0.0	0.9

#### **Lot C2008 – Mean Activity 7.53 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	7.16	0.37	0.60	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	176	7.46	0.50	1.27	0.0	0.9

#### **Lot D2008 – Mean Activity 13.88 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	13.83	0.58	0.96	-0.5	1.0
NeoLSD™ MSMS Kit PerkinElmer	176	12.83	0.87	3.37	0.0	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### **Lot A2008 – Mean Activity 3.87 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	40	3.43	0.41	0.59	0.3	1.1

#### **Lot B2008 – Mean Activity 5.54 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	50	5.88	0.59	0.87	0.3	1.1

#### **Lot C2008 – Mean Activity 24.94 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	50	29.26	2.75	4.02	0.3	1.1

#### **Lot D2008 – Mean Activity 47.98 $\mu\text{mol/hr/L}$ blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	50	50.17	4.48	6.50	0.3	1.1

#### **GLA Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	50	0.98	0.40	0.23
B2008	50	1.73	0.65	0.37
C2008	60	6.73	2.84	0.74
D2008	60	13.07	4.87	0.90

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### **Lot A2008 – Mean Activity 0.47 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	0.38	0.08	0.13	-0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	162	0.60	0.18	0.71	0.2	0.7

#### **Lot B2008 – Mean Activity 1.01 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	0.76	0.07	0.26	-0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	166	0.74	0.19	0.29	0.2	0.7

#### **Lot C2008 – Mean Activity 4.57 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	4.31	0.32	1.26	-0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	172	3.54	0.47	0.99	0.2	0.7

#### **Lot D2008 – Mean Activity 9.24 μmol/hr/L blood**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>Average Within Lab SD</b>	<b>Total SD</b>	<b>Y-Intercept</b>	<b>Slope</b>
LC-MS/MS non-kit	30	8.28	0.98	2.76	-0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	172	6.34	0.76	2.01	0.2	0.7

2021 Quality Control Data Summaries of Statistical Analyses  
 **$\beta$ -GLUCOCEREBROSIDASE (ABG  $\mu\text{mol/hr/L}$  blood)**

**Lot A2008 – Mean Activity 2.08  $\mu\text{mol/hr/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	34	2.03	0.31	0.40	-0.2	1.2

**Lot B2008 – Mean Activity 1.97  $\mu\text{mol/hr/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	38	2.24	0.31	0.54	-0.2	1.2

**Lot C2008 – Mean Activity 4.60  $\mu\text{mol/hr/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	40	5.93	0.54	0.68	-0.2	1.2

**Lot D2008 – Mean Activity 8.11  $\mu\text{mol/hr/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidic Fluorescence	40	9.50	0.76	1.23	-0.2	1.2

**ABG Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	30	0.56	0.18	0.12
B2008	33	1.00	0.45	0.17
C2008	50	2.26	0.99	0.18
D2008	50	4.24	1.54	0.50

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2008 – Mean Activity 0.11 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
NeoLSD™ MSMS Kit PerkinElmer	112	0.14	0.03	0.30	0.0	0.8

#### Lot B2008 – Mean Activity 0.28 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
NeoLSD™ MSMS Kit PerkinElmer	127	0.19	0.05	0.09	0.0	0.8

#### Lot C2008 – Mean Activity 1.55 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
NeoLSD™ MSMS Kit PerkinElmer	142	1.35	0.15	0.31	0.0	0.8

#### Lot D2008 – Mean Activity 2.84 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
NeoLSD™ MSMS Kit PerkinElmer	142	2.18	0.22	0.70	0.0	0.8

2021 Quality Control Data Summaries of Statistical Analyses  
**2ND TIER 17  $\alpha$ -HYDROXYPROGESTERONE (17OHP2 ng/mL serum)**

**Lot F1911 – Non-enriched 0 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	117	1.11	0.48	1.08	1.6	0.9

**Lot G1911 – Enriched 10 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	208	9.84	1.31	1.98	1.6	0.9

**Lot H1911 – Enriched 50 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	208	47.58	3.92	11.10	1.6	0.9

**Lot I1911 – Enriched 100 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	206	97.13	7.18	13.46	1.6	0.9

**Lot J1911 – Enriched 500 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	208	466.45	32.39	63.17	1.6	0.9



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	102	0.62	0.22	0.45	1.4	1.0

#### Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	198	9.37	0.91	1.96	1.4	1.0

#### Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	198	48.85	3.88	13.60	1.4	1.0

#### Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	198	102.45	6.71	17.47	1.4	1.0

#### Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	198	485.50	33.01	76.86	1.4	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

### 2ND TIER CORTISOL (CORT2 ng/mL serum)

#### Lot F1911 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	100	4.15	2.04	9.09	2.2	0.9

#### Lot G1911 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	194	9.82	2.04	6.28	2.2	0.9

#### Lot H1911 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	45.42	5.30	12.52	2.2	0.9

#### Lot I1911 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	98.16	8.86	16.95	2.2	0.9

#### Lot J1911 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	465.79	35.61	61.06	2.2	0.9

2021 Quality Control Data Summaries of Statistical Analyses  
**2ND TIER 11-DEOXYCORTISOL (11D2 ng/mL serum)**

**Lot F1911 – Non-enriched 0 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	62	0.64	0.23	0.59	3.2	0.9

**Lot G1911 – Enriched 10 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	128	8.73	0.65	1.16	3.2	0.9

**Lot H1911 – Enriched 50 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	128	46.18	3.70	13.28	3.2	0.9

**Lot I1911 – Enriched 100 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	128	96.17	6.32	15.64	3.2	0.9

**Lot J1911 – Enriched 500 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	128	432.21	34.39	80.36	3.2	0.9

2021 Quality Control Data Summaries of Statistical Analyses  
**2ND TIER 21-DEOXYCORTISOL (21D2 ng/mL serum)**

**Lot F1911 – Non-enriched 0 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	69	0.79	0.43	0.77	-1.7	1.0

**Lot G1911 – Enriched 10 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	128	8.89	1.92	3.90	-1.7	1.0

**Lot H1911 – Enriched 50 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	42.37	4.75	14.64	-1.7	1.0

**Lot I1911 – Enriched 100 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	129	96.99	7.66	14.78	-1.7	1.0

**Lot J1911 – Enriched 500 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	485.67	48.84	81.00	-1.7	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

### 2ND TIER ALLO-ISOLEUCINE (ALE2 $\mu\text{mol/L}$ blood)

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	112	1.48	0.14	2.39	-0.5	0.9

#### Lot B2013 - Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	43.79	3.12	6.93	-0.5	0.9

#### Lot C2013 - Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	84.30	5.75	13.48	-0.5	0.9

#### Lot D2013 - Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	172.13	11.60	30.01	-0.5	0.9

#### Lot E2013 - Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	349.43	21.52	61.44	-0.5	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	20.46	1.56	3.87	16.8	0.8

#### Lot B2013 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	100.47	6.53	15.76	16.8	0.8

#### Lot C2013 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	176.90	12.09	30.01	16.8	0.8

#### Lot D2013 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	342.87	21.82	61.73	16.8	0.8

#### Lot E2013 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	677.32	40.97	124.3	16.8	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	58.90	3.51	15.81	60.8	1.0

#### Lot B2013 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	155.82	8.56	45.64	60.8	1.0

#### Lot C2013 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	251.21	13.82	81.69	60.8	1.0

#### Lot D2013 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	449.07	26.46	160.5	60.8	1.0

#### Lot E2013 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	822.90	44.39	252.1	60.8	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	140	33.47	1.91	5.79	33.2	0.9

#### Lot B2013 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	140	121.01	6.42	14.62	33.2	0.9

#### Lot C2013 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	140	207.64	12.14	29.31	33.2	0.9

#### Lot D2013 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	140	385.72	20.43	44.62	33.2	0.9

#### Lot E2013 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	140	735.58	36.29	87.89	33.2	0.9



## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	28.75	2.10	5.42	28.0	0.8

#### Lot B2013 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	111.46	6.34	16.51	28.0	0.8

#### Lot C2013 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	192.03	10.91	29.60	28.0	0.8

#### Lot D2013 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	359.34	22.76	52.54	28.0	0.8

#### Lot E2013 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	691.41	34.68	88.93	28.0	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2013 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	66.05	4.61	13.55	67.7	1.0

#### Lot B2013 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	163.02	9.47	31.04	67.7	1.0

#### Lot C2013 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	257.51	14.47	47.98	67.7	1.0

#### Lot D2013 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	449.14	28.19	87.70	67.7	1.0

#### Lot E2013 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	150	825.07	47.35	161.1	67.7	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

### **2ND TIER MALONIC ACID (MA2 $\mu\text{mol/L}$ blood)**

MA is not shown due to insufficient data.

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2014 – Non-enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	191	1.90	0.28	0.56	0.2	0.9

#### Lot B2014 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	4.59	0.50	1.05	0.2	0.9

#### Lot C2014 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	17.50	1.41	3.89	0.2	0.9

#### Lot D2014 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	196	43.71	3.25	8.53	0.2	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2014 – Non-enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	70	2.18	0.50	0.73	0.1	0.9

#### Lot B2014 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	70	5.21	0.63	1.21	0.1	0.9

#### Lot C2014 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	70	18.01	1.30	4.81	0.1	0.9

#### Lot D2014 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	70	47.60	3.08	12.25	0.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2014 – Non-enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	176	1.16	0.23	0.72	0.4	0.8

#### Lot B2014 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	176	2.49	0.41	1.03	0.4	0.8

#### Lot C2014 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	186	8.60	0.94	2.30	0.4	0.8

#### Lot D2014 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	186	21.18	2.21	5.94	0.4	0.8

2021 Quality Control Data Summaries of Statistical Analyses  
**2ND TIER TOTAL HOMOCYSTEINE (tHcy2  $\mu\text{mol/L}$  blood)**

**Lot A2014 – Non-enriched 0  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	206	7.43	0.68	3.22	7.4	0.7

**Lot B2014 – Enriched 10  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	206	13.58	1.07	5.35	7.4	0.7

**Lot C2014 – Enriched 50  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	206	40.25	3.21	15.77	7.4	0.7

**Lot D2014 – Enriched 100  $\mu\text{mol/L}$  blood**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	206	71.74	5.35	27.49	7.4	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 Walensky, M.D.

**Director**

National Center for Environmental Health

Patrick Breyse, Ph.D.

**Director**

Division of Laboratory Sciences

James L. Pirkle, M.D., Ph.D.

**Chief**

Newborn Screening and Molecular Biology Branch

Carla Cuthbert, Ph.D.

**Contributors**

Nicole Baird, Ph.D

John Bernstein, MS

Quan Bui, MS

Suzanne Cordovado, Ph.D

Paul Dantonio, MS

Katherine Duneman, MS

Sharon Flores, MS

Christopher Greene, Ph.D

Elizabeth Hall, BS

Laura Hancock, MS

Christopher Haynes, Ph.D

Miyono Hendrix, MS

Laura C. Hildreth, BS

Deborah Koontz, Ph.D

Francis Lee, Ph.D

LiXia Li, Ph.D

Tim Lim, Ph.D

Edgardo Lobo, MS

Daniel Mandel, Ph.D

Allison McCabe, BS

Joanne Mei, Ph.D

Kristina Mercer, Ph.D

Stanimila Nikolova, Ph.D

Kaila Pearson, MS

Gyliann Pena, MS

Kostas Petritis, Ph.D

C. Austin Pickens, Ph.D

Blanche Temate, Ph.D

Robert Vogt, Ph.D

Irene Williams, MS

Sophia Winchester, BS

Golriz Yazdanpanah, MS

Sherri Zobel, BS

**Production**

Vinay Anumula, MS

Kizzy Stewart

Joy Pressley

**ASSOCIATION OF PUBLIC HEALTH LABORATORIES SILVER SPRING, MD 20910**

**President**

Grace E. Kubin, PhD

**Chairman, Newborn Screening and Genetics in Public Health Committee**

Michele Caggana, Sc.D., FACMG

**Chairman, Newborn Screening Quality Assurance Quality Control Subcommittee**

Patrice Held, Ph.D., B.A. and Joseph Orsini, Ph.D.

**Chairman, Newborn Screening Molecular Subcommittee**

Rachel Lee, Ph.D.

**INQUIRIES TO:**

Irene Williams, Editor

Centers for Disease Control and Prevention (CDC), Newborn Screening Quality Assurance Program

Mailstop S110-3, 4770 Buford Highway, N.E., Atlanta, GA 30341-3724

E-mail: NSQAPDMT@cdc.gov