

# 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  
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### Introduction

The NSQAP Quality Control (QC) dried blood spot (DBS) materials provide participants with external controls to assess method performance over time. The controls provide continuity and transcend changes in production lots of routinely used method- or kit-control materials. The external QC materials are intended to supplement the participants' method- or kit-control materials at periodic intervals to monitor the long-term stability of their assays. NSQAP QC materials are not a replacement for manufacturer kit controls or other daily QC and should not be used for routine analysis. This report contains a summary of the 2021 Set 2 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 (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).

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 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 alioisoleucine (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 June 22, 2021, we distributed DBS quality control (QC) materials to 542 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 used is appropriate for the analyte you are reporting**
- **Convert results to the required 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. Only one option can be used to submit QC data.**

## Participant Results

For the Set 2 QC materials, we compiled results from five analytic runs for 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 required 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—104 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, C14:1, 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
AutoDELFIA® Neonatal 17OHP	378	23.1	1.8	3.9	-0.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	309	21.7	2.4	6.5	-2.8	1.0
GSP® 17OHP Neonatal PerkinElmer	648	24.0	1.9	3.4	1.2	1.0
NeoMAP® 17OHP Interscientifica	30	22.5	1.9	3.8	3.6	0.7
Neonatal 17OHP LabSystems	140	23.1	2.2	2.8	4.4	0.7
ZenTech ELISA Neonatal 17OHP	90	31.4	5.1	7.2	2.7	1.1

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELFIA® Neonatal 17OHP	378	48.9	3.4	8.8	-0.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	310	45.4	4.5	14.4	-2.8	1.0
GSP® 17OHP Neonatal PerkinElmer	648	50.4	3.4	6.6	1.2	1.0
NeoMAP® 17OHP Interscientifica	30	40.3	3.5	10.5	3.6	0.7
Neonatal 17OHP LabSystems	140	40.2	4.6	7.3	4.4	0.7
ZenTech ELISA Neonatal 17OHP	90	59.4	7.4	12.3	2.7	1.1

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELFIA® Neonatal 17OHP	378	96.1	7.8	19.1	-0.5	1.0
DELFIA® Neonatal 17OHP PerkinElmer	310	94.3	10.4	31.2	-2.8	1.0
GSP® 17OHP Neonatal PerkinElmer	648	96.0	6.8	13.7	1.2	1.0
NeoMAP® 17OHP Interscientifica	30	78.0	7.6	26.5	3.6	0.7
Neonatal 17OHP LabSystems	140	77.6	10.1	23.7	4.4	0.7
ZenTech ELISA Neonatal 17OHP	90	116.7	16.1	37.0	2.7	1.1

## 2021 Quality Control Data Summaries of Statistical Analyses

### THYROXINE (T4 µg/dL serum)

#### Lot A2000 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIATM Neonatal T4 PerkinElmer	80	1.6	0.4	0.4	-0.2	0.9
DELFIATM Neonatal T4 PerkinElmer	100	2.3	0.5	2.1	-0.2	1.5
GSP® T4 Neonatal PerkinElmer	146	1.6	0.2	0.3	-0.4	1.0

#### Lot B2000 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIATM Neonatal T4 PerkinElmer	80	6.8	0.7	1.5	-0.2	0.9
DELFIATM Neonatal T4 PerkinElmer	100	11.4	1.6	12.9	-0.2	1.5
GSP® T4 Neonatal PerkinElmer	172	6.6	0.5	0.7	-0.4	1.0

#### Lot C2000 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFIATM Neonatal T4 PerkinElmer	80	10.0	1.0	2.2	-0.2	0.9
DELFIATM Neonatal T4 PerkinElmer	100	15.8	1.7	17.2	-0.2	1.5
GSP® T4 Neonatal PerkinElmer	172	10.7	0.9	1.3	-0.4	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2101 – Enriched 25 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal hTSH	476	27.2	1.9	6.1	3.3	1.0
DELFI <sup>®</sup> A Neonatal TSH PerkinElmer	484	25.1	3.6	12.4	2.3	0.9
DiaSorin Immunoassay TSH	70	29.3	3.2	3.9	6.7	1.0
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	776	27.4	2.2	5.6	1.7	1.1
NeoMAP <sup>®</sup> TSH Interscientifica	30	30.4	3.1	5.6	-10.1	1.5
Neonatal TSH LabSystems	190	24.6	2.8	7.4	4.2	0.9
ZenTech ELISA Neonatal TSH	110	22.4	3.8	10.8	1.9	0.8

#### Lot B2101 – Enriched 40 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal hTSH	476	43.1	2.8	9.4	3.3	1.0
DELFI <sup>®</sup> A Neonatal TSH PerkinElmer	484	40.0	3.3	10.8	2.3	0.9
DiaSorin Immunoassay TSH	70	46.9	4.3	6.0	6.7	1.0
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	776	44.3	3.2	9.0	1.7	1.1
NeoMAP <sup>®</sup> TSH Interscientifica	30	48.1	4.1	7.8	-10.1	1.5
Neonatal TSH LabSystems	190	42.3	4.5	18.7	4.2	0.9
ZenTech ELISA Neonatal TSH	110	34.2	4.9	14.3	1.9	0.8

#### Lot C2101 – Enriched 80 $\mu$ IU/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
AutoDELFI <sup>®</sup> A Neonatal hTSH	476	81.2	5.0	18.4	3.3	1.0
DELFI <sup>®</sup> A Neonatal TSH PerkinElmer	484	76.4	5.5	20.1	2.3	0.9
DiaSorin Immunoassay TSH	70	83.0	6.4	8.9	6.7	1.0
GSP <sup>®</sup> hTSH Neonatal PerkinElmer	776	85.4	6.7	18.3	1.7	1.1
NeoMAP <sup>®</sup> TSH Interscientifica	30	113.2	6.8	12.3	-10.1	1.5
Neonatal TSH LabSystems	190	74.7	6.7	23.6	4.2	0.9
ZenTech ELISA Neonatal TSH	110	67.0	7.3	27.5	1.9	0.8

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

**Lot A2103 – Mean Activity 1.5 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	218	1.5	0.3	0.5	0.2	0.8
Microplate Reagent Spotcheck® GALT Astoria-Pacifi	50	0.6	0.1	0.2	-0.6	0.8

**Lot B2103 – Mean Activity 3.7 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	246	3.3	0.3	0.5	0.2	0.8
Microplate Reagent Spotcheck® GALT Astoria-Pacifi	50	2.2	0.3	0.4	-0.6	0.8

**Lot C2103 – Mean Activity 8.9 U/g Hb**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorescence GALT Neonatal PerkinElmer, U/g Hb	246	7.7	0.8	1.1	0.2	0.8
Microplate Reagent Spotcheck® GALT Astoria-Pacifi	50	6.2	0.6	1.0	-0.6	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 A2103**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
50hr Reagent Kit Spotcheck® GALT Astoria-Pacific, µmol/L blood	30	10.0	7.3	0.7	20.0
GSP® GALT Neonatal PerkinElmer, U/dL blood	112	0.7	0.7	0.0	2.3

#### **Lot B2103**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
50hr Reagent Kit Spotcheck® GALT Astoria-Pacific, µmol/L blood	30	39.7	29.2	1.9	69.0
GSP® GALT Neonatal PerkinElmer, U/dL blood	256	3.3	0.5	2.4	4.7

#### **Lot C2103**

<b>METHOD</b>	<b>N</b>	<b>Mean</b>	<b>All Lab SD</b>	<b>Min</b>	<b>Max</b>
50hr Reagent Kit Spotcheck® GALT Astoria-Pacific, µmol/L blood	30	121.1	90.7	5.4	232.0
GSP® GALT Neonatal PerkinElmer, U/dL blood	258	14.5	3.4	6.1	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	398	20.9	1.3	2.1	6.3	0.9
DELfIA® Neonatal IRT	210	19.8	2.1	3.5	4.2	0.9
FEIA IRT Labsystems	80	25.0	4.7	5.8	5.7	1.1
GSP® IRT Neonatal PerkinElmer, ng/mL	550	20.0	1.2	1.7	2.8	0.9
NeoMAP® IRT Interscientifica	30	28.5	3.8	12.7	11.6	1.0
ZenTech ELISA Neonatal IRT	40	36.6	5.8	8.7	47.4	0.8

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELfIA® Neonatal IRT PerkinElmer	408	62.8	4.4	6.7	6.3	0.9
DELfIA® Neonatal IRT	210	60.6	5.7	8.3	4.2	0.9
FEIA IRT Labsystems	80	73.0	6.4	12.9	5.7	1.1
GSP® IRT Neonatal PerkinElmer, ng/mL	550	61.6	3.9	8.1	2.8	0.9
NeoMAP® IRT Interscientifica	30	81.3	4.9	21.5	11.6	1.0
ZenTech ELISA Neonatal IRT	40	115.9	10.4	15.6	47.4	0.8

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
AutoDELfIA® Neonatal IRT PerkinElmer	408	126.5	8.6	13.1	6.3	0.9
DELfIA® Neonatal IRT	210	122.4	10.9	16.5	4.2	0.9
FEIA IRT Labsystems	80	153.4	16.7	58.0	5.7	1.1
GSP® IRT Neonatal PerkinElmer, ng/mL	549	124.7	7.8	10.4	2.8	0.9
NeoMAP® IRT Interscientifica	30	139.3	13.2	19.5	11.6	1.0
ZenTech ELISA Neonatal IRT	40	177.0	19.5	28.3	47.4	0.8

## 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	408	208.4	14.3	19.2	6.3	0.9
DELFIA® Neonatal IRT	210	207.4	16.9	29.1	4.2	0.9
FEIA IRT Labsystems	80	253.6	33.0	54.3	5.7	1.1
GSP® IRT Neonatal PerkinElmer, ng/mL	549	215.8	12.5	17.0	2.8	0.9
NeoMAP® IRT Interscientifica	28	245.7	42.7	64.0	11.6	1.0
ZenTech ELISA Neonatal IRT	40	215.2	16.5	22.7	47.4	0.8

## 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	253.5	25.7	53.9	263.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	231.6	16.3	51.9	248.3	0.8
Derivatized - MS/MS non-kit	270	276.2	29.9	72.1	290.0	0.9
LC-MS/MS non-kit	40	306.2	31.6	89.0	318.9	0.9
Non-derivatized - MS/MS MassChrom®	60	237.0	16.0	95.0	263.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	289.4	18.9	41.4	305.9	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	282	281.5	27.4	56.7	292.4	1.0
Non-derivatized - MS/MS non-kit	120	254.3	23.0	61.8	267.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	275.6	20.4	78.5	293.4	1.0

#### 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	416.1	33.3	81.5	263.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	425.0	21.9	93.8	248.3	0.8
Derivatized - MS/MS non-kit	270	484.0	41.6	93.5	290.0	0.9
LC-MS/MS non-kit	40	520.9	60.1	131.4	318.9	0.9
Non-derivatized - MS/MS MassChrom®	60	398.8	24.7	96.5	263.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	525.2	35.3	67.5	305.9	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	282	497.2	39.8	85.2	292.4	1.0
Non-derivatized - MS/MS non-kit	120	455.2	39.1	98.1	267.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	517.4	41.6	128.1	293.4	1.0

#### 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	533.8	33.9	92.7	263.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	558.5	23.6	110.6	248.3	0.8
Derivatized - MS/MS non-kit	270	637.5	53.1	132.6	290.0	0.9
LC-MS/MS non-kit	40	679.5	56.3	156.9	318.9	0.9
Non-derivatized - MS/MS MassChrom®	60	502.1	35.0	107.6	263.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	702.2	42.1	90.5	305.9	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	282	673.6	49.5	98.8	292.4	1.0
Non-derivatized - MS/MS non-kit	120	614.1	49.2	123.6	267.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	692.9	45.5	174.0	293.4	1.0

## 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	668.4	33.4	112.0	263.6	0.7
Derivatized - MS/MS MassChrom® Chromsystems	80	698.2	33.0	138.6	248.3	0.8
Derivatized - MS/MS non-kit	270	803.8	61.2	164.0	290.0	0.9
LC-MS/MS non-kit	40	859.1	102.3	223.3	318.9	0.9
Non-derivatized - MS/MS MassChrom®	60	561.0	44.2	202.1	263.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	434	885.0	54.2	112.3	305.9	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	282	854.2	63.4	139.5	292.4	1.0
Non-derivatized - MS/MS non-kit	120	768.8	60.5	147.5	267.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	50	878.7	70.9	212.8	293.4	1.0

## 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	0.6	1.2	4.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	8.6	0.9	1.8	12.8	0.8
Derivatized - MS/MS non-kit	298	6.7	0.9	3.3	6.3	0.6
LC-MS/MS non-kit	30	11.1	2.6	7.9	11.3	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	4.2	0.5	0.8	4.6	0.6
Non-derivatized - MS/MS MassChrom®	50	6.1	0.8	1.3	12.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	5.4	0.6	1.4	4.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	294	5.7	0.6	1.1	4.6	0.9
Non-derivatized - MS/MS non-kit	120	7.9	1.1	4.1	7.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	5.9	0.8	1.1	6.8	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	74.4	4.1	8.2	4.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	101.7	5.2	15.1	12.8	0.8
Derivatized - MS/MS non-kit	298	68.2	6.3	26.5	6.3	0.6
LC-MS/MS non-kit	30	117.7	13.7	50.7	11.3	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	62.0	5.6	9.9	4.6	0.6
Non-derivatized - MS/MS MassChrom®	50	97.4	7.5	21.6	12.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	88.9	5.5	15.3	4.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	304	93.2	4.2	10.5	4.6	0.9
Non-derivatized - MS/MS non-kit	120	91.2	8.5	35.8	7.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	93.0	6.8	19.4	6.8	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	138.4	10.2	30.6	4.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	179.6	10.6	26.0	12.8	0.8
Derivatized - MS/MS non-kit	298	129.4	11.7	49.2	6.3	0.6
LC-MS/MS non-kit	30	217.2	26.5	76.5	11.3	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	116.9	7.4	18.8	4.6	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	50	171.1	12.6	40.3	12.3	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	444	171.2	13.2	40.9	4.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	304	178.9	8.2	20.8	4.6	0.9
Non-derivatized - MS/MS non-kit	120	177.7	17.1	68.0	7.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	173.1	10.3	30.7	6.8	0.8

#### 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	217.4	9.2	28.2	4.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	259.6	15.1	34.6	12.8	0.8
Derivatized - MS/MS non-kit	298	193.4	17.9	72.8	6.3	0.6
LC-MS/MS non-kit	30	326.2	45.2	110.9	11.3	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	174.1	9.5	24.3	4.6	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	50	240.3	20.5	65.7	12.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	260.5	14.1	60.8	4.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	304	272.6	13.6	32.8	4.6	0.9
Non-derivatized - MS/MS non-kit	120	263.4	24.1	101.3	7.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	259.0	15.0	46.0	6.8	0.8

## 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	20.8	5.1	7.8	18.9	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	14.8	1.4	2.0	14.9	0.8
Derivatized - MS/MS non-kit	310	15.1	2.0	4.5	13.9	0.8
LC-MS/MS non-kit	30	16.4	2.4	5.3	16.8	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	13.7	1.4	1.8	13.6	0.9
Non-derivatized - MS/MS MassChrom®	50	14.7	1.6	2.1	15.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	15.1	1.5	2.0	14.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	14.4	1.5	2.0	13.7	0.9
Non-derivatized - MS/MS non-kit	170	16.7	1.6	4.6	16.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	15.0	1.1	1.6	18.7	1.0

#### 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	37.6	2.8	4.5	18.9	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	36.9	2.5	3.9	14.9	0.8
Derivatized - MS/MS non-kit	310	35.0	3.7	9.3	13.9	0.8
LC-MS/MS non-kit	30	43.0	6.1	10.5	16.8	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	35.9	2.1	2.8	13.6	0.9
Non-derivatized - MS/MS MassChrom®	50	39.6	2.9	5.8	15.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	39.1	3.0	4.3	14.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	36.6	2.6	4.1	13.7	0.9
Non-derivatized - MS/MS non-kit	170	40.0	3.6	7.2	16.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	45.9	3.3	5.4	18.7	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	88.4	11.6	22.2	18.9	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	97.8	6.1	10.4	14.9	0.8
Derivatized - MS/MS non-kit	310	93.8	9.4	26.0	13.9	0.8
LC-MS/MS non-kit	30	113.5	10.4	13.6	16.8	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	98.5	5.7	6.8	13.6	0.9
Non-derivatized - MS/MS MassChrom®	50	102.3	7.4	14.6	15.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	105.8	7.5	11.3	14.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	98.9	6.6	11.6	13.7	0.9
Non-derivatized - MS/MS non-kit	170	105.1	8.5	18.8	16.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	116.3	6.8	9.6	18.7	1.0

#### 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	203.8	26.3	60.4	18.9	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	225.7	12.3	25.1	14.9	0.8
Derivatized - MS/MS non-kit	310	220.9	19.9	56.4	13.9	0.8
LC-MS/MS non-kit	30	263.5	24.2	32.0	16.8	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	230.0	12.5	13.3	13.6	0.9
Non-derivatized - MS/MS MassChrom®	50	238.9	20.0	39.0	15.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	248.0	16.6	24.3	14.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	234.3	13.3	25.1	13.7	0.9
Non-derivatized - MS/MS non-kit	170	241.7	16.9	46.6	16.7	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	258.7	18.1	28.1	18.7	1.0

## 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	292.7	23.5	42.9	300.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	286.5	14.7	56.0	291.9	0.7
Derivatized - MS/MS non-kit	248	319.7	31.7	109.6	328.2	0.8
LC-MS/MS non-kit	30	348.0	47.9	75.5	357.3	0.9
Non-derivatized - MS/MS MassChrom®	50	220.5	20.4	35.4	229.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	396	344.8	24.8	56.6	354.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	260	324.5	29.8	46.8	329.8	0.9
Non-derivatized - MS/MS non-kit	90	323.0	32.1	83.7	330.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	298.7	42.6	64.6	302.6	0.8

#### 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	534.2	29.7	70.8	300.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	513.6	32.8	95.5	291.9	0.7
Derivatized - MS/MS non-kit	248	587.9	56.8	200.1	328.2	0.8
LC-MS/MS non-kit	30	638.5	70.1	140.3	357.3	0.9
Non-derivatized - MS/MS MassChrom®	50	409.2	32.4	70.2	229.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	396	640.6	46.5	105.4	354.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	260	596.2	41.8	79.6	329.8	0.9
Non-derivatized - MS/MS non-kit	90	568.4	64.3	109.1	330.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	548.9	59.8	89.7	302.6	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	720.2	40.9	123.6	300.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	732.7	34.5	143.4	291.9	0.7
Derivatized - MS/MS non-kit	248	820.0	80.1	277.7	328.2	0.8
LC-MS/MS non-kit	30	875.2	84.9	160.4	357.3	0.9
Non-derivatized - MS/MS MassChrom®	50	565.0	52.8	97.3	229.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	396	904.4	57.3	144.1	354.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	260	847.5	57.6	114.3	329.8	0.9
Non-derivatized - MS/MS non-kit	90	800.7	84.0	157.3	330.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	771.9	90.2	110.6	302.6	0.8

#### 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	949.4	52.3	144.2	300.7	0.7
Derivatized - MS/MS MassChrom® Chromsystems	70	936.6	45.3	187.5	291.9	0.7
Derivatized - MS/MS non-kit	248	1063.8	107.3	363.0	328.2	0.8
LC-MS/MS non-kit	30	1146.3	148.4	197.8	357.3	0.9
Non-derivatized - MS/MS MassChrom®	50	726.6	70.0	134.8	229.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	396	1167.1	70.4	184.8	354.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	260	1102.9	78.5	154.4	329.8	0.9
Non-derivatized - MS/MS non-kit	90	1015.5	104.8	208.7	330.4	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	1016.2	102.4	145.6	302.6	0.8

## 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	81.9	4.6	6.3	84.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	89	73.1	5.7	11.3	80.0	0.9
Derivatized - MS/MS non-kit	298	77.5	7.8	20.8	84.8	0.9
LC-MS/MS non-kit	40	97.2	14.5	48.3	102.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	78.8	3.9	6.9	87.3	0.9
Non-derivatized - MS/MS MassChrom®	60	107.1	6.9	62.1	141.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	496	81.5	5.6	11.6	89.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	355	78.2	5.0	8.7	83.4	0.9
Non-derivatized - MS/MS non-kit	200	80.1	5.7	11.8	88.2	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	77.0	4.5	8.5	86.7	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	235.8	12.4	20.1	84.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	90	198.4	13.5	35.9	80.0	0.9
Derivatized - MS/MS non-kit	298	219.1	15.6	40.6	84.8	0.9
LC-MS/MS non-kit	40	247.4	31.3	72.1	102.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	223.4	10.2	13.3	87.3	0.9
Non-derivatized - MS/MS MassChrom®	60	246.5	14.4	61.5	141.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	496	229.3	17.0	33.7	89.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	217.1	11.8	23.4	83.4	0.9
Non-derivatized - MS/MS non-kit	200	220.5	16.1	28.5	88.2	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	219.4	14.4	30.1	86.7	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	354.0	13.5	18.9	84.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	90	310.7	16.5	58.5	80.0	0.9
Derivatized - MS/MS non-kit	298	344.5	24.5	58.5	84.8	0.9
LC-MS/MS non-kit	40	379.0	36.9	88.4	102.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	349.2	18.3	20.4	87.3	0.9
Non-derivatized - MS/MS MassChrom®	60	371.0	19.6	93.6	141.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	496	358.9	25.5	53.0	89.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	339.3	18.7	39.5	83.4	0.9
Non-derivatized - MS/MS non-kit	200	345.5	25.5	48.5	88.2	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	338.9	25.9	46.9	86.7	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	651.0	23.6	35.0	84.0	0.9
Derivatized - MS/MS MassChrom® Chromsystems	90	527.0	25.5	105.5	80.0	0.9
Derivatized - MS/MS non-kit	298	591.0	41.4	102.2	84.8	0.9
LC-MS/MS non-kit	40	655.1	74.6	133.2	102.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	596.0	30.3	39.2	87.3	0.9
Non-derivatized - MS/MS MassChrom®	60	479.0	37.0	180.9	141.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	496	613.0	42.6	90.8	89.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	590.9	31.3	71.9	83.4	0.9
Non-derivatized - MS/MS non-kit	200	586.0	42.0	87.2	88.2	0.8
Non-derivatized Labsystems Neomass AAAC Plus	30	575.2	30.7	70.9	86.7	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	11.8	0.7	0.9	13.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	9.8	1.4	2.4	10.3	0.6
Derivatized - MS/MS non-kit	308	12.6	1.5	3.0	12.8	0.8
LC-MS/MS non-kit	40	11.9	1.3	2.2	12.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	10.1	0.8	1.0	10.1	0.8
Non-derivatized - MS/MS MassChrom®	50	9.6	1.1	1.4	10.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	494	10.4	0.9	1.5	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	9.2	0.8	1.4	9.2	0.8
Non-derivatized - MS/MS non-kit	200	11.2	0.9	2.6	11.1	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	7.2	1.7	2.0	7.3	0.7

#### 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	52.9	4.6	5.0	13.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	42.0	3.3	9.8	10.3	0.6
Derivatized - MS/MS non-kit	308	54.9	4.8	10.1	12.8	0.8
LC-MS/MS non-kit	40	52.4	6.0	13.7	12.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	51.4	3.1	3.9	10.1	0.8
Non-derivatized - MS/MS MassChrom®	50	50.6	4.4	8.8	10.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	494	50.0	3.3	6.1	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	47.9	6.0	21.1	9.2	0.8
Non-derivatized - MS/MS non-kit	200	51.0	3.6	11.1	11.1	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	41.0	3.9	7.7	7.3	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	122.2	5.0	10.1	13.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	105.5	7.7	25.3	10.3	0.6
Derivatized - MS/MS non-kit	308	137.4	11.7	26.6	12.8	0.8
LC-MS/MS non-kit	40	135.5	9.7	24.9	12.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	136.4	7.8	10.7	10.1	0.8
Non-derivatized - MS/MS MassChrom®	50	128.6	10.7	20.9	10.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	494	133.7	14.9	56.0	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	123.4	7.6	14.9	9.2	0.8
Non-derivatized - MS/MS non-kit	200	133.5	9.0	28.8	11.1	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	109.6	12.3	19.3	7.3	0.7

#### 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	198.7	7.7	13.9	13.2	0.7
Derivatized - MS/MS MassChrom® Chromsystems	90	166.9	11.3	41.3	10.3	0.6
Derivatized - MS/MS non-kit	308	221.1	18.6	49.6	12.8	0.8
LC-MS/MS non-kit	40	215.0	22.2	39.9	12.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	218.2	13.8	18.9	10.1	0.8
Non-derivatized - MS/MS MassChrom®	50	206.1	19.7	35.9	10.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	494	210.7	11.8	23.1	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	200.7	11.5	22.6	9.2	0.8
Non-derivatized - MS/MS non-kit	200	213.1	17.5	47.8	11.1	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	176.6	14.8	26.9	7.3	0.7

## 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	144.4	13.3	25.7	138.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	163.0	12.0	33.8	164.1	0.9
Derivatized - MS/MS non-kit	266	98.7	10.3	43.1	102.0	0.6
LC-MS/MS non-kit	30	168.1	38.9	59.6	174.7	1.0
Non-derivatized - MS/MS MassChrom®	50	178.6	20.5	40.9	188.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	384	150.8	9.7	21.0	155.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	272	143.3	8.3	18.1	147.4	0.8
Non-derivatized - MS/MS non-kit	110	127.2	9.5	34.3	130.3	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	171.5	12.6	40.9	179.1	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	215.9	13.1	15.9	138.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	250.7	30.1	66.8	164.1	0.9
Derivatized - MS/MS non-kit	266	163.1	14.8	69.1	102.0	0.6
LC-MS/MS non-kit	30	280.8	42.7	74.4	174.7	1.0
Non-derivatized - MS/MS MassChrom®	50	292.9	35.1	68.5	188.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	384	243.8	16.0	32.1	155.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	272	229.3	12.1	28.0	147.4	0.8
Non-derivatized - MS/MS non-kit	110	207.4	20.0	54.8	130.3	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	284.9	22.1	71.4	179.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	296.9	22.5	57.6	138.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	333.3	37.6	87.2	164.1	0.9
Derivatized - MS/MS non-kit	266	215.0	17.6	91.6	102.0	0.6
LC-MS/MS non-kit	30	363.6	51.0	79.6	174.7	1.0
Non-derivatized - MS/MS MassChrom®	50	374.5	44.0	86.5	188.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	384	319.5	19.3	38.8	155.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	272	302.2	16.2	38.0	147.4	0.8
Non-derivatized - MS/MS non-kit	110	274.6	21.0	62.5	130.3	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	363.9	22.1	67.4	179.1	0.9

#### 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	395.0	15.0	68.5	138.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	70	418.2	25.9	85.9	164.1	0.9
Derivatized - MS/MS non-kit	266	269.0	23.5	109.7	102.0	0.6
LC-MS/MS non-kit	30	458.0	56.0	91.3	174.7	1.0
Non-derivatized - MS/MS MassChrom®	50	456.7	54.8	104.6	188.3	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	384	395.8	23.0	48.6	155.9	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	272	374.0	20.2	48.4	147.4	0.8
Non-derivatized - MS/MS non-kit	110	345.8	29.1	79.0	130.3	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	456.7	35.6	100.5	179.1	0.9

## 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	33.8	2.1	3.4	36.5	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	45.7	2.5	43.3	58.4	0.8
Derivatized - MS/MS non-kit	298	33.9	2.8	6.1	37.1	0.9
GSP® Phe Neonatal PerkinElmer	70	30.4	5.6	18.9	31.5	0.9
LC-MS/MS non-kit	30	33.1	2.6	3.5	33.5	0.9
NeoLISA® Phe Interscientifica	30	46.0	13.4	19.9	44.5	0.8
Neonatal Phe LabSystems	110	30.7	5.8	20.1	48.4	0.8
Neonatal® Phe Kit PerkinElmer	69	33.4	9.9	20.8	36.8	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	30.7	1.8	2.1	32.5	0.9
Non-derivatized - MS/MS MassChrom®	110	33.4	2.2	3.7	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	506	31.9	2.3	3.7	33.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	29.3	1.6	2.9	29.3	0.9
Non-derivatized - MS/MS non-kit	210	34.1	2.7	5.2	35.8	1.0
Non-derivatized Labsystems Neomass AAAC Plus	30	32.2	2.1	3.4	36.2	1.0

#### 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	173.9	11.1	24.7	36.5	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	185.6	8.3	40.5	58.4	0.8
Derivatized - MS/MS non-kit	298	177.0	13.0	27.1	37.1	0.9
GSP® Phe Neonatal PerkinElmer	70	171.9	15.6	28.4	31.5	0.9
LC-MS/MS non-kit	30	169.4	17.7	19.6	33.5	0.9
NeoLISA® Phe Interscientifica	30	160.6	18.1	33.5	44.5	0.8
Neonatal Phe LabSystems	110	190.1	11.3	128.6	48.4	0.8
Neonatal® Phe Kit PerkinElmer	70	146.8	14.1	63.1	36.8	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	171.0	8.6	11.0	32.5	0.9
Non-derivatized - MS/MS MassChrom®	110	184.4	10.7	16.0	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	506	177.1	10.3	18.0	33.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	160.8	8.2	16.0	29.3	0.9
Non-derivatized - MS/MS non-kit	210	185.1	11.6	25.0	35.8	1.0
Non-derivatized Labsystems Neomass AAAC Plus	30	185.1	16.2	28.8	36.2	1.0

## 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	281.4	13.7	33.2	36.5	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	312.8	18.8	62.9	58.4	0.8
Derivatized - MS/MS non-kit	298	305.0	21.0	43.4	37.1	0.9
GSP® Phe Neonatal PerkinElmer	70	314.9	21.9	33.4	31.5	0.9
LC-MS/MS non-kit	30	296.7	24.1	27.2	33.5	0.9
NeoLISA® Phe Interscientifica	30	280.4	24.5	66.5	44.5	0.8
Neonatal Phe LabSystems	110	289.9	19.3	143.3	48.4	0.8
Neonatal® Phe Kit PerkinElmer	70	253.7	22.2	110.2	36.8	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	300.9	16.2	16.9	32.5	0.9
Non-derivatized - MS/MS MassChrom®	110	312.0	22.4	37.7	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	506	310.3	17.8	32.8	33.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	282.3	15.2	27.4	29.3	0.9
Non-derivatized - MS/MS non-kit	210	325.4	22.0	47.3	35.8	1.0
Non-derivatized Labsystems Neomass AAAC Plus	30	320.3	29.3	40.0	36.2	1.0

#### 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	424.7	17.8	64.6	36.5	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	395.8	17.5	123.7	58.4	0.8
Derivatized - MS/MS non-kit	298	439.3	29.4	65.2	37.1	0.9
GSP® Phe Neonatal PerkinElmer	70	450.2	35.1	52.9	31.5	0.9
LC-MS/MS non-kit	30	435.4	44.4	47.5	33.5	0.9
NeoLISA® Phe Interscientifica	30	399.8	41.3	97.1	44.5	0.8
Neonatal Phe LabSystems	110	390.4	22.1	206.2	48.4	0.8
Neonatal® Phe Kit PerkinElmer	70	353.6	31.0	151.9	36.8	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	437.7	22.6	29.6	32.5	0.9
Non-derivatized - MS/MS MassChrom®	110	450.7	26.1	53.1	38.2	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	506	453.0	25.0	44.4	33.6	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	418.8	21.8	43.1	29.3	0.9
Non-derivatized - MS/MS non-kit	210	473.1	30.5	69.4	35.8	1.0
Non-derivatized Labsystems Neomass AAAC Plus	30	462.2	27.0	56.1	36.2	1.0

## 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	80	0.5	0.1	0.3	0.5	0.5
Derivatized - MS/MS non-kit	136	0.7	0.2	0.6	0.7	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	342	0.5	0.1	0.2	0.5	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	254	0.2	0.1	0.2	0.2	0.2
Non-derivatized - MS/MS non-kit	84	0.4	0.1	0.3	0.4	0.5

#### 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	80	1.8	0.2	0.5	0.5	0.5
Derivatized - MS/MS non-kit	138	2.0	0.3	1.0	0.7	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	342	1.2	0.2	0.3	0.5	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	268	0.8	0.1	0.3	0.2	0.2
Non-derivatized - MS/MS non-kit	84	1.6	0.2	0.8	0.4	0.5

#### 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	80	5.1	0.4	1.0	0.5	0.5
Derivatized - MS/MS non-kit	138	5.7	0.6	2.9	0.7	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	342	3.1	0.3	0.7	0.5	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	268	2.3	0.3	0.7	0.2	0.2
Non-derivatized - MS/MS non-kit	84	4.9	0.6	2.8	0.4	0.5

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot D2015 – Enriched 20 $\mu\text{mol/L}$ 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 MassChrom® Chromsystems	80	9.6	0.8	2.0	0.5	0.5
Derivatized - MS/MS non-kit	138	10.7	1.0	5.2	0.7	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	342	5.9	0.7	1.5	0.5	0.3
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	268	5.0	1.0	3.0	0.2	0.2
Non-derivatized - MS/MS non-kit	84	9.6	1.1	5.6	0.4	0.5

## 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	29.6	2.1	2.3	25.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	30.8	2.1	3.9	34.2	0.9
Derivatized - MS/MS non-kit	300	29.7	2.6	6.4	28.6	0.8
LC-MS/MS non-kit	30	33.0	4.1	8.1	29.7	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	26.7	1.9	2.6	27.3	0.8
Non-derivatized - MS/MS MassChrom®	100	30.5	2.1	3.9	35.8	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	484	32.4	2.8	4.3	31.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	28.6	1.8	3.2	25.9	0.8
Non-derivatized - MS/MS non-kit	180	31.2	2.7	6.4	30.5	0.9
Non-derivatized Labsystems Neomass AAAC Plus	38	30.3	2.2	2.9	34.9	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	273.6	12.4	20.5	25.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	291.8	18.5	47.0	34.2	0.9
Derivatized - MS/MS non-kit	300	276.3	20.1	52.8	28.6	0.8
LC-MS/MS non-kit	30	289.6	26.2	35.4	29.7	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	263.6	12.8	15.7	27.3	0.8
Non-derivatized - MS/MS MassChrom®	100	300.7	17.4	28.8	35.8	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	484	305.1	19.0	32.8	31.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	269.3	13.2	26.7	25.9	0.8
Non-derivatized - MS/MS non-kit	180	288.9	18.7	46.6	30.5	0.9
Non-derivatized Labsystems Neomass AAAC Plus	38	304.1	25.0	35.5	34.9	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	491.5	18.5	21.6	25.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	545.6	30.9	75.5	34.2	0.9
Derivatized - MS/MS non-kit	300	515.3	36.8	91.5	28.6	0.8
LC-MS/MS non-kit	30	558.7	46.1	65.2	29.7	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	507.5	23.1	27.2	27.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	100	563.4	31.1	53.0	35.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	484	581.8	35.1	64.7	31.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	513.6	25.3	52.6	25.9	0.8
Non-derivatized - MS/MS non-kit	180	556.4	35.4	82.9	30.5	0.9
Non-derivatized Labsystems Neomass AAAC Plus	38	568.2	47.1	52.2	34.9	0.9

#### 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	768.5	25.9	36.5	25.6	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	793.4	37.1	112.9	34.2	0.9
Derivatized - MS/MS non-kit	300	771.1	54.0	118.1	28.6	0.8
LC-MS/MS non-kit	30	825.5	74.0	99.0	29.7	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	737.7	34.5	53.1	27.3	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	100	810.9	53.5	96.5	35.8	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	484	858.3	45.8	88.7	31.3	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	766.0	39.2	82.6	25.9	0.8
Non-derivatized - MS/MS non-kit	180	812.6	54.2	125.8	30.5	0.9
Non-derivatized Labsystems Neomass AAAC Plus	38	824.0	45.3	75.3	34.9	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	67.1	4.4	11.8	63.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	90	65.7	4.9	13.0	70.7	0.8
Derivatized - MS/MS non-kit	288	86.0	12.5	34.2	87.6	0.8
LC-MS/MS non-kit	40	68.9	6.0	9.7	72.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	64.9	3.5	5.0	69.5	0.9
Non-derivatized - MS/MS MassChrom®	50	57.1	6.2	11.2	64.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	70.6	4.7	10.7	75.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	67.8	3.9	6.2	69.6	0.9
Non-derivatized - MS/MS non-kit	170	64.6	4.8	10.3	67.6	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	58.4	5.8	16.4	63.9	0.8

#### 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	226.1	12.2	26.7	63.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	90	227.8	15.1	42.7	70.7	0.8
Derivatized - MS/MS non-kit	288	244.6	21.0	49.3	87.6	0.8
LC-MS/MS non-kit	40	232.5	19.6	34.2	72.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	246.4	10.6	23.9	69.5	0.9
Non-derivatized - MS/MS MassChrom®	50	210.2	18.1	32.8	64.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	264.0	19.7	44.3	75.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	247.4	13.5	26.6	69.6	0.9
Non-derivatized - MS/MS non-kit	170	228.2	17.6	35.5	67.6	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	225.9	21.7	55.5	63.9	0.8

## 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	311.5	16.5	46.1	63.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	90	333.3	15.7	62.9	70.7	0.8
Derivatized - MS/MS non-kit	288	352.2	30.4	67.2	87.6	0.8
LC-MS/MS non-kit	40	339.1	20.2	56.6	72.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	369.3	18.9	41.7	69.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	50	296.0	27.1	47.0	64.5	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	486	388.3	24.8	59.5	75.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	369.4	20.4	41.7	69.6	0.9
Non-derivatized - MS/MS non-kit	170	339.9	27.8	58.3	67.6	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	336.5	36.6	80.1	63.9	0.8

#### 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	466.4	35.2	82.0	63.9	0.8
Derivatized - MS/MS MassChrom® Chromsystems	90	440.3	28.3	76.6	70.7	0.8
Derivatized - MS/MS non-kit	288	470.2	37.3	92.3	87.6	0.8
LC-MS/MS non-kit	40	454.2	33.3	78.4	72.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	491.0	23.6	47.0	69.5	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	50	392.2	37.7	72.6	64.5	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	522.2	31.2	79.1	75.5	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	502.9	26.1	52.9	69.6	0.9
Non-derivatized - MS/MS non-kit	170	454.6	33.6	79.6	67.6	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	444.2	38.4	100.1	63.9	0.8

## 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	38	5.5	0.4	1.0	0.4	1.0
Fluorescence TGal Neonatal PerkinElmer	160	4.6	0.6	1.0	0.6	0.8
Fluorometric manual TGal - non-kit	40	4.9	0.6	0.9	-0.1	0.9
GSP® TGal Neonatal PerkinElmer	308	4.8	0.5	1.0	-0.1	1.0
NeoLISA® TGal Interscientifica	30	4.8	0.8	1.0	-1.4	1.0
Neonatal® HORM Kit PerkinElmer	110	4.5	0.6	1.0	0.3	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	128	5.6	0.8	1.3	1.6	0.7

#### 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	38	10.6	0.9	1.5	0.4	1.0
Fluorescence TGal Neonatal PerkinElmer	160	9.2	1.0	1.4	0.6	0.8
Fluorometric manual TGal - non-kit	40	8.5	0.6	1.0	-0.1	0.9
GSP® TGal Neonatal PerkinElmer	308	9.5	1.0	1.7	-0.1	1.0
NeoLISA® TGal Interscientifica	30	7.7	0.9	1.1	-1.4	1.0
Neonatal® HORM Kit PerkinElmer	110	9.2	0.8	1.5	0.3	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	130	7.3	1.2	1.8	1.6	0.7

#### 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	38	31.1	1.9	3.3	0.4	1.0
Fluorescence TGal Neonatal PerkinElmer	160	25.5	2.0	4.0	0.6	0.8
Fluorometric manual TGal - non-kit	40	27.3	1.3	4.4	-0.1	0.9
GSP® TGal Neonatal PerkinElmer	308	28.6	2.5	4.3	-0.1	1.0
NeoLISA® TGal Interscientifica	30	29.9	4.6	5.4	-1.4	1.0
Neonatal® HORM Kit PerkinElmer	110	26.4	2.0	3.6	0.3	0.9
ZenTech Neonatal TGal Enzymatic Colorimetric	130	21.6	2.0	3.6	1.6	0.7

## 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	19.72	1.77	2.24	17.7	1.6
Derivatized - MS/MS MassChrom® Chromsystems	110	14.43	1.10	3.05	13.6	1.1
Derivatized - MS/MS non-kit	328	18.42	1.62	3.81	17.0	1.5
LC-MS/MS non-kit	30	19.39	1.40	4.92	18.0	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	16.96	0.99	1.50	15.7	1.2
Non-derivatized - MS/MS MassChrom®	80	14.67	1.10	3.97	15.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	476	15.96	1.12	1.93	14.8	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	16.10	1.12	2.15	14.8	1.1
Non-derivatized - MS/MS non-kit	180	16.54	1.18	2.16	15.3	1.2
Non-derivatized Labsystems Neomass AAAC Plus	40	16.18	1.48	2.54	15.0	1.1

#### 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	32.93	2.16	3.45	17.7	1.6
Derivatized - MS/MS MassChrom® Chromsystems	110	23.38	1.78	5.32	13.6	1.1
Derivatized - MS/MS non-kit	328	29.86	2.61	6.25	17.0	1.5
LC-MS/MS non-kit	30	30.45	2.02	8.59	18.0	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	25.76	1.33	2.31	15.7	1.2
Non-derivatized - MS/MS MassChrom®	80	22.82	1.22	5.86	15.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	476	24.27	1.76	3.14	14.8	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	23.97	1.51	3.10	14.8	1.1
Non-derivatized - MS/MS non-kit	180	24.94	1.79	3.52	15.3	1.2
Non-derivatized Labsystems Neomass AAAC Plus	40	24.54	2.48	4.23	15.0	1.1

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	45.63	2.24	2.61	17.7	1.6
Derivatized - MS/MS MassChrom® Chromsystems	110	36.02	2.72	8.42	13.6	1.1
Derivatized - MS/MS non-kit	328	47.36	3.75	9.68	17.0	1.5
LC-MS/MS non-kit	30	47.65	3.09	14.79	18.0	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	41.07	2.37	4.25	15.7	1.2
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	33.42	1.93	6.68	15.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	476	38.00	2.50	4.93	14.8	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	37.35	2.29	4.76	14.8	1.1
Non-derivatized - MS/MS non-kit	180	39.02	3.18	5.02	15.3	1.2
Non-derivatized Labsystems Neomass AAAC Plus	40	37.97	3.89	5.56	15.0	1.1

#### 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	69.08	3.03	7.69	17.7	1.6
Derivatized - MS/MS MassChrom® Chromsystems	110	47.04	2.98	10.39	13.6	1.1
Derivatized - MS/MS non-kit	328	63.13	5.11	13.42	17.0	1.5
LC-MS/MS non-kit	30	62.76	3.76	19.98	18.0	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	52.79	2.89	4.88	15.7	1.2
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	38.35	2.47	11.51	15.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	476	49.31	3.10	5.84	14.8	1.1
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	49.13	2.99	6.44	14.8	1.1
Non-derivatized - MS/MS non-kit	180	50.92	4.02	6.35	15.3	1.2
Non-derivatized Labsystems Neomass AAAC Plus	40	49.72	5.01	7.78	15.0	1.1

## 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	11.35	0.81	1.21	11.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	100	9.96	0.65	1.66	10.2	0.8
Derivatized - MS/MS non-kit	328	11.60	1.06	2.72	11.7	0.9
LC-MS/MS non-kit	30	14.92	1.26	7.80	14.7	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	9.95	0.51	0.81	10.0	1.0
Non-derivatized - MS/MS MassChrom®	80	9.05	0.57	2.59	10.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	472	8.79	0.52	1.00	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	8.30	0.43	0.92	8.2	0.8
Non-derivatized - MS/MS non-kit	170	11.03	0.83	2.95	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	40	7.81	0.56	1.19	8.0	0.8

#### 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	20.14	1.29	2.94	11.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	100	18.51	1.06	2.73	10.2	0.8
Derivatized - MS/MS non-kit	328	20.83	1.71	4.84	11.7	0.9
LC-MS/MS non-kit	30	30.20	1.57	15.51	14.7	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	20.02	1.07	1.55	10.0	1.0
Non-derivatized - MS/MS MassChrom®	80	17.53	0.92	2.86	10.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	472	21.97	15.58	92.92	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	16.54	0.79	1.77	8.2	0.8
Non-derivatized - MS/MS non-kit	170	21.36	1.90	5.54	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	40	15.71	1.06	2.24	8.0	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	27.46	1.62	3.41	11.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	100	26.76	1.33	3.44	10.2	0.8
Derivatized - MS/MS non-kit	328	29.75	2.13	6.48	11.7	0.9
LC-MS/MS non-kit	30	44.37	2.23	23.36	14.7	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	30.63	1.64	2.99	10.0	1.0
Non-derivatized - MS/MS MassChrom®	80	25.50	1.45	3.67	10.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	472	26.77	1.54	2.96	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	25.11	1.27	2.63	8.2	0.8
Non-derivatized - MS/MS non-kit	170	32.46	2.82	7.84	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	40	23.25	1.59	3.10	8.0	0.8

#### 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	38.43	1.80	3.11	11.1	0.9
Derivatized - MS/MS MassChrom® Chromsystems	100	34.41	1.72	4.99	10.2	0.8
Derivatized - MS/MS non-kit	328	38.87	2.85	10.32	11.7	0.9
LC-MS/MS non-kit	30	61.23	3.64	30.87	14.7	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	40.23	2.18	3.84	10.0	1.0
Non-derivatized - MS/MS MassChrom®	80	29.02	1.80	9.00	10.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	472	35.26	1.86	3.93	10.6	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	33.51	1.61	3.56	8.2	0.8
Non-derivatized - MS/MS non-kit	170	43.04	3.47	9.69	10.9	1.1
Non-derivatized Labsystems Neomass AAAC Plus	40	30.27	1.89	4.02	8.0	0.8

## 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	1.17	0.12	0.14	1.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	0.93	0.08	0.15	0.9	0.8
Derivatized - MS/MS non-kit	338	1.12	0.13	0.28	1.1	1.0
LC-MS/MS non-kit	30	1.54	0.15	0.76	1.5	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.02	0.05	0.08	1.0	1.0
Non-derivatized - MS/MS MassChrom®	80	1.29	0.07	1.02	1.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	0.96	0.07	0.12	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	1.11	0.07	0.13	1.0	1.0
Non-derivatized - MS/MS non-kit	180	1.15	0.10	0.26	1.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.87	0.06	0.12	0.9	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	5.14	0.30	0.42	1.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	4.22	0.29	0.59	0.9	0.8
Derivatized - MS/MS non-kit	338	4.85	0.49	1.08	1.1	1.0
LC-MS/MS non-kit	30	7.55	0.70	4.01	1.5	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	4.70	0.26	0.31	1.0	1.0
Non-derivatized - MS/MS MassChrom®	80	4.66	0.27	1.00	1.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	4.45	0.31	0.60	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	5.05	0.30	0.61	1.0	1.0
Non-derivatized - MS/MS non-kit	180	5.17	0.47	1.19	1.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	4.07	0.35	0.63	0.9	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	8.21	0.45	0.67	1.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	7.53	0.46	1.04	0.9	0.8
Derivatized - MS/MS non-kit	338	8.78	0.77	1.60	1.1	1.0
LC-MS/MS non-kit	30	13.17	0.90	6.98	1.5	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	8.55	0.52	0.76	1.0	1.0
Non-derivatized - MS/MS MassChrom®	80	8.07	0.52	1.52	1.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	8.03	0.50	0.94	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	9.16	0.54	1.06	1.0	1.0
Non-derivatized - MS/MS non-kit	180	9.36	0.77	2.17	1.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	7.23	0.54	1.01	0.9	0.8

#### 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	12.66	0.88	1.05	1.2	0.9
Derivatized - MS/MS MassChrom® Chromsystems	110	10.92	0.60	1.57	0.9	0.8
Derivatized - MS/MS non-kit	338	12.65	1.12	2.70	1.1	1.0
LC-MS/MS non-kit	30	19.51	1.80	9.88	1.5	1.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	12.36	0.66	0.93	1.0	1.0
Non-derivatized - MS/MS MassChrom®	80	9.66	0.69	3.69	1.6	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	11.63	0.68	1.36	0.9	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	13.45	0.92	1.77	1.0	1.0
Non-derivatized - MS/MS non-kit	180	13.52	1.12	2.91	1.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	10.25	0.59	1.28	0.9	0.8

## 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	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	77	0.04	0.01	0.03	0.0	0.9
Derivatized - MS/MS non-kit	316	0.03	0.01	0.03	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	0.03	0.04	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	0.48	0.06	0.20	0.0	0.9
Derivatized - MS/MS non-kit	328	0.34	0.06	0.20	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	0.86	0.11	0.18	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	1.38	0.13	0.56	0.0	0.9
Derivatized - MS/MS non-kit	328	0.94	0.12	0.45	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	1.76	0.21	0.35	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	80	2.68	0.21	1.12	0.0	0.9
Derivatized - MS/MS non-kit	328	1.87	0.21	0.88	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®	70	0.08	0.01	0.06	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.07	0.02	0.07	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	302	0.06	0.01	0.02	0.1	0.4
Non-derivatized - MS/MS non-kit	120	0.10	0.02	0.09	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.03	0.01	0.02	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	0.42	0.03	0.18	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.49	0.09	0.33	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	302	0.43	0.03	0.11	0.1	0.4
Non-derivatized - MS/MS non-kit	120	0.57	0.09	0.42	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.22	0.03	0.06	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	0.90	0.06	0.39	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.99	0.15	0.56	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	302	0.91	0.05	0.23	0.1	0.4
Non-derivatized - MS/MS non-kit	120	1.15	0.20	0.87	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.43	0.07	0.11	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	1.63	0.12	1.03	0.1	0.3
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	2.17	0.24	0.99	0.1	0.4
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	302	2.02	0.11	0.48	0.1	0.4
Non-derivatized - MS/MS non-kit	120	2.54	0.40	1.90	0.1	0.4
Non-derivatized Labsystems Neomass AAAC Plus	30	0.97	0.09	0.20	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	0.16	0.02	0.05	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	0.11	0.04	0.08	0.1	0.6
Derivatized - MS/MS non-kit	328	0.14	0.03	0.10	0.1	0.7
LC-MS/MS non-kit	30	0.12	0.02	0.05	0.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.10	0.01	0.01	0.1	0.7
Non-derivatized - MS/MS MassChrom®	80	0.17	0.01	0.22	0.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	0.11	0.01	0.02	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	348	0.09	0.01	0.01	0.1	0.6
Non-derivatized - MS/MS non-kit	170	0.12	0.02	0.04	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	0.08	0.02	0.02	0.1	0.5

#### 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	0.90	0.06	0.08	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	0.72	0.06	0.12	0.1	0.6
Derivatized - MS/MS non-kit	328	0.84	0.09	0.18	0.1	0.7
LC-MS/MS non-kit	30	1.03	0.13	0.38	0.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.78	0.05	0.07	0.1	0.7
Non-derivatized - MS/MS MassChrom®	80	0.91	0.05	0.40	0.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	0.76	0.05	0.09	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	0.70	0.04	0.08	0.1	0.6
Non-derivatized - MS/MS non-kit	170	0.79	0.07	0.14	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	0.65	0.06	0.10	0.1	0.5

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	0.15	0.19	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	1.95	0.15	0.33	0.1	0.6
Derivatized - MS/MS non-kit	328	2.19	0.20	0.41	0.1	0.7
LC-MS/MS non-kit	30	2.61	0.16	0.96	0.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	2.20	0.12	0.28	0.1	0.7
Non-derivatized - MS/MS MassChrom®	80	2.17	0.13	0.49	0.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	2.02	0.12	0.21	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	1.90	0.11	0.19	0.1	0.6
Non-derivatized - MS/MS non-kit	170	2.16	0.19	0.43	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	1.72	0.14	0.22	0.1	0.5

#### 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	3.75	0.33	0.45	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	3.20	0.21	0.50	0.1	0.6
Derivatized - MS/MS non-kit	328	3.64	0.32	0.65	0.1	0.7
LC-MS/MS non-kit	30	4.55	0.45	1.60	0.1	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	3.61	0.19	0.33	0.1	0.7
Non-derivatized - MS/MS MassChrom®	80	2.95	0.20	1.15	0.3	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	3.38	0.19	0.35	0.1	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	3.24	0.18	0.34	0.1	0.6
Non-derivatized - MS/MS non-kit	170	3.61	0.27	0.71	0.1	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	2.78	0.18	0.38	0.1	0.5

## 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**

<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	0.07	0.01	0.02	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.10	0.02	0.05	0.1	0.7
Derivatized - MS/MS non-kit	298	0.09	0.02	0.05	0.1	0.7

#### **Lot B2015 – Enriched 0.5 $\mu\text{mol/L}$ 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	0.38	0.03	0.04	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.48	0.05	0.13	0.1	0.7
Derivatized - MS/MS non-kit	298	0.47	0.14	0.47	0.1	0.7

#### **Lot C2015 – Enriched 1 $\mu\text{mol/L}$ 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	0.68	0.06	0.11	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	0.87	0.09	0.20	0.1	0.7
Derivatized - MS/MS non-kit	298	0.85	0.10	0.30	0.1	0.7

#### **Lot D2015 – Enriched 2.5 $\mu\text{mol/L}$ 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	1.65	0.15	0.21	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	70	1.95	0.16	0.42	0.1	0.7
Derivatized - MS/MS non-kit	298	1.94	0.23	0.62	0.1	0.7

## 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	0.08	0.01	0.02	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	0.08	0.01	0.02	0.1	0.8
Derivatized - MS/MS non-kit	338	0.08	0.01	0.03	0.1	0.9
LC-MS/MS non-kit	30	0.07	0.01	0.05	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.07	0.01	0.01	0.1	0.9
Non-derivatized - MS/MS MassChrom®	80	0.14	0.01	0.14	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	0.06	0.02	0.06	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	0.06	0.01	0.01	0.1	0.8
Non-derivatized - MS/MS non-kit	200	0.08	0.01	0.03	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.08	0.03	0.04	0.1	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	0.45	0.04	0.05	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	0.50	0.04	0.07	0.1	0.8
Derivatized - MS/MS non-kit	338	0.50	0.05	0.10	0.1	0.9
LC-MS/MS non-kit	30	0.61	0.08	0.25	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.50	0.02	0.04	0.1	0.9
Non-derivatized - MS/MS MassChrom®	80	0.60	0.03	0.20	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	0.46	0.03	0.05	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	0.44	0.03	0.06	0.1	0.8
Non-derivatized - MS/MS non-kit	200	0.52	0.05	0.10	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.54	0.05	0.10	0.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

### ISOVALERYLCARNITINE (C5 $\mu\text{mol/L}$ 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	1.13	0.08	0.15	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	1.28	0.13	0.20	0.1	0.8
Derivatized - MS/MS non-kit	338	1.36	0.13	0.25	0.1	0.9
LC-MS/MS non-kit	30	1.74	0.13	0.58	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.38	0.07	0.13	0.1	0.9
Non-derivatized - MS/MS MassChrom®	80	1.57	0.10	0.46	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	1.26	0.08	0.14	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	1.21	0.06	0.16	0.1	0.8
Non-derivatized - MS/MS non-kit	200	1.42	0.12	0.30	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	1.47	0.13	0.27	0.1	0.9

#### 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	2.25	0.10	0.17	0.1	0.7
Derivatized - MS/MS MassChrom® Chromsystems	110	2.53	0.15	0.32	0.1	0.8
Derivatized - MS/MS non-kit	338	2.64	0.23	0.48	0.1	0.9
LC-MS/MS non-kit	30	3.40	0.39	1.12	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	2.70	0.13	0.27	0.1	0.9
Non-derivatized - MS/MS MassChrom®	80	2.44	0.16	1.01	0.2	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	490	2.48	0.14	0.23	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	360	2.42	0.13	0.33	0.1	0.8
Non-derivatized - MS/MS non-kit	200	2.78	0.22	0.57	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	2.87	0.22	0.60	0.1	0.9

## 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	0.01	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	0.04	0.01	0.02	0.0	0.7
Derivatized - MS/MS non-kit	330	0.03	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS MassChrom®	70	0.05	0.00	0.09	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	426	0.01	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	320	0.01	0.00	0.01	0.1	0.6
Non-derivatized - MS/MS non-kit	150	0.03	0.01	0.03	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	30	0.01	0.01	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	0.33	0.03	0.04	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	0.38	0.04	0.10	0.0	0.7
Derivatized - MS/MS non-kit	330	0.40	0.05	0.09	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	0.34	0.02	0.02	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.39	0.03	0.19	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	0.29	0.03	0.07	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	0.48	0.37	2.20	0.1	0.6
Non-derivatized - MS/MS non-kit	150	0.57	0.05	0.81	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	30	0.32	0.03	0.09	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	0.91	0.06	0.15	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	1.04	0.08	0.25	0.0	0.7
Derivatized - MS/MS non-kit	330	1.15	0.11	0.26	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	0.99	0.05	0.06	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	1.02	0.07	0.28	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	0.86	0.08	0.20	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	0.90	0.06	0.13	0.1	0.6
Non-derivatized - MS/MS non-kit	150	1.68	0.17	2.40	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	30	0.96	0.10	0.27	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	1.78	0.11	0.24	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	60	2.04	0.14	0.53	0.0	0.7
Derivatized - MS/MS non-kit	330	2.32	0.24	0.54	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	2.02	0.09	0.16	0.0	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	1.70	0.13	0.77	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	436	1.74	0.12	0.36	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	340	1.85	0.13	0.27	0.1	0.6
Non-derivatized - MS/MS non-kit	150	3.38	0.27	4.72	0.0	1.1
Non-derivatized Labsystems Neomass AAAC Plus	30	1.91	0.19	0.56	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	0.04	0.01	0.01	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	98	0.04	0.01	0.03	0.0	1.2
Derivatized - MS/MS non-kit	337	0.02	0.01	0.01	0.0	0.6
LC-MS/MS non-kit	30	0.05	0.01	0.03	0.0	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.04	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	0.11	0.01	0.13	0.2	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	415	0.05	0.02	0.04	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	333	0.03	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.07	0.01	0.08	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.09	0.04	0.07	0.1	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	0.60	0.05	0.09	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	100	0.64	0.06	0.13	0.0	1.2
Derivatized - MS/MS non-kit	348	0.30	0.04	0.13	0.0	0.6
LC-MS/MS non-kit	30	0.38	0.06	0.20	0.0	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.44	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	0.68	0.06	0.13	0.2	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	0.50	0.05	0.08	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	0.40	0.04	0.07	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.53	0.05	0.14	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.51	0.13	0.16	0.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	1.07	0.10	0.15	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	100	1.18	0.12	0.27	0.0	1.2
Derivatized - MS/MS non-kit	348	0.57	0.07	0.26	0.0	0.6
LC-MS/MS non-kit	30	0.64	0.05	0.32	0.0	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	0.82	0.04	0.08	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	1.31	0.20	0.41	0.2	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	0.97	0.08	0.15	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	0.78	0.05	0.12	0.0	0.8
Non-derivatized - MS/MS non-kit	190	0.99	0.08	0.24	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.91	0.13	0.16	0.1	0.9

#### 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	2.64	0.20	0.48	0.1	1.0
Derivatized - MS/MS MassChrom® Chromsystems	100	2.95	0.25	0.62	0.0	1.2
Derivatized - MS/MS non-kit	348	1.45	0.18	0.65	0.0	0.6
LC-MS/MS non-kit	30	1.67	0.15	0.83	0.0	0.7
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	1.98	0.10	0.24	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	2.60	0.28	1.07	0.2	1.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer	416	2.34	0.15	0.31	0.1	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	1.95	0.14	0.29	0.0	0.8
Non-derivatized - MS/MS non-kit	190	2.37	0.20	0.52	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	2.22	0.19	0.24	0.1	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**

<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	0.30	0.03	0.07	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	100	0.43	0.05	0.07	0.4	0.8
Derivatized - MS/MS non-kit	348	0.40	0.05	0.10	0.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	0.68	0.03	0.06	0.7	0.9
Non-derivatized - MS/MS MassChrom®	50	0.36	0.03	0.08	0.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	0.52	0.04	0.18	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	312	0.54	0.04	0.14	0.5	0.6
Non-derivatized - MS/MS non-kit	160	0.63	0.06	0.14	0.6	0.8

#### **Lot B2015 – Enriched 1 $\mu\text{mol/L}$ 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	0.83	0.08	0.14	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	100	1.17	0.11	0.16	0.4	0.8
Derivatized - MS/MS non-kit	348	1.15	0.11	0.26	0.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	1.56	0.07	0.13	0.7	0.9
Non-derivatized - MS/MS MassChrom®	50	0.85	0.07	0.18	0.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	1.13	0.08	0.38	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	1.13	0.07	0.24	0.5	0.6
Non-derivatized - MS/MS non-kit	160	1.46	0.12	0.29	0.6	0.8

#### **Lot C2015 – Enriched 2 $\mu\text{mol/L}$ 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	1.25	0.11	0.25	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	100	1.92	0.15	0.28	0.4	0.8
Derivatized - MS/MS non-kit	348	1.94	0.17	0.42	0.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	2.52	0.12	0.24	0.7	0.9
Non-derivatized - MS/MS MassChrom®	50	1.31	0.11	0.30	0.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	1.76	0.12	0.58	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	1.77	0.12	0.34	0.5	0.6
Non-derivatized - MS/MS non-kit	160	2.32	0.19	0.45	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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS ClinSpot® Complete Kit	30	1.85	0.14	0.30	0.3	0.5
Derivatized - MS/MS MassChrom® Chromsystems	100	2.67	0.19	0.35	0.4	0.8
Derivatized - MS/MS non-kit	348	2.75	0.27	0.60	0.4	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	3.41	0.19	0.31	0.7	0.9
Non-derivatized - MS/MS MassChrom®	50	1.74	0.13	0.43	0.4	0.5
Non-derivatized - MS/MS NeoBase™ PerkinElmer	382	2.33	0.15	0.74	0.5	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	2.41	0.15	0.52	0.5	0.6
Non-derivatized - MS/MS non-kit	160	3.14	0.23	0.60	0.6	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

### HEXANOYL CARNITINE (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	0.03	0.01	0.03	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	0.04	0.01	0.02	0.1	0.6
Derivatized - MS/MS non-kit	326	0.03	0.01	0.04	0.0	0.8
LC-MS/MS non-kit	30	0.02	0.01	0.01	0.0	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.01	0.00	0.01	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	0.06	0.00	0.12	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	471	0.01	0.00	0.01	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	332	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS non-kit	160	0.02	0.00	0.01	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.01	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	0.36	0.03	0.03	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	0.37	0.03	0.07	0.1	0.6
Derivatized - MS/MS non-kit	338	0.40	0.04	0.08	0.0	0.8
LC-MS/MS non-kit	30	0.47	0.06	0.12	0.0	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.40	0.02	0.06	0.0	0.8
Non-derivatized - MS/MS MassChrom®	80	0.44	0.03	0.11	0.1	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	472	0.40	0.03	0.04	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	0.37	0.02	0.04	0.0	0.7
Non-derivatized - MS/MS non-kit	160	0.39	0.04	0.08	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.39	0.03	0.05	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	0.62	0.03	0.07	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	0.67	0.05	0.12	0.1	0.6
Derivatized - MS/MS non-kit	338	0.78	0.08	0.13	0.0	0.8
LC-MS/MS non-kit	30	0.92	0.07	0.22	0.0	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	0.81	0.05	0.13	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	0.88	0.05	0.32	0.1	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	472	0.95	0.55	3.55	0.1	0.8
Non-derivatized - MS/MS non-kit	352	0.70	0.03	0.08	0.0	0.7
Non-derivatized - MS/MS non-kit	160	0.80	0.07	0.16	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.73	0.06	0.11	0.0	0.7

#### 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	1.57	0.12	0.16	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	1.54	0.09	0.28	0.1	0.6
Derivatized - MS/MS non-kit	338	1.97	0.18	0.31	0.0	0.8
LC-MS/MS non-kit	30	2.38	0.16	0.48	0.0	1.0
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	2.02	0.10	0.33	0.0	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	80	1.64	0.11	0.66	0.1	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	472	1.97	0.11	0.19	0.1	0.8
Non-derivatized - MS/MS non-kit	352	1.75	0.09	0.20	0.0	0.7
Non-derivatized - MS/MS non-kit	160	2.09	0.20	0.48	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	1.77	0.10	0.25	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

### OCTANOYL CARNITINE (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	0.7
Derivatized - MS/MS MassChrom® Chromsystems	119	0.02	0.01	0.01	0.0	0.7
Derivatized - MS/MS non-kit	327	0.02	0.01	0.02	0.0	0.9
LC-MS/MS non-kit	30	0.03	0.01	0.02	0.0	1.2
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.02	0.00	0.00	0.0	0.8
Non-derivatized - MS/MS MassChrom®	120	0.06	0.00	0.11	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	500	0.03	0.01	0.03	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	0.02	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS non-kit	200	0.04	0.01	0.03	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.03	0.01	0.02	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	0.40	0.03	0.04	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	120	0.40	0.04	0.09	0.0	0.7
Derivatized - MS/MS non-kit	338	0.48	0.05	0.11	0.0	0.9
LC-MS/MS non-kit	30	0.65	0.08	0.31	0.0	1.2
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.41	0.02	0.03	0.0	0.8
Non-derivatized - MS/MS MassChrom®	120	0.45	0.03	0.10	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	504	0.44	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	0.40	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS non-kit	200	0.52	0.05	0.30	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.39	0.03	0.09	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	0.05	0.08	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	120	0.76	0.06	0.16	0.0	0.7
Derivatized - MS/MS non-kit	338	0.93	0.09	0.22	0.0	0.9
LC-MS/MS non-kit	30	1.23	0.09	0.56	0.0	1.2
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.81	0.04	0.06	0.0	0.8
Non-derivatized - MS/MS MassChrom®	120	0.89	0.06	0.33	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	504	0.85	0.06	0.09	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	0.76	0.04	0.08	0.0	0.8
Non-derivatized - MS/MS non-kit	200	1.01	0.09	0.60	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.75	0.06	0.17	0.0	0.7

#### 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	1.82	0.11	0.14	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	120	1.79	0.11	0.34	0.0	0.7
Derivatized - MS/MS non-kit	338	2.28	0.20	0.43	0.0	0.9
LC-MS/MS non-kit	30	3.07	0.29	1.42	0.0	1.2
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.97	0.10	0.19	0.0	0.8
Non-derivatized - MS/MS MassChrom®	120	1.81	0.13	0.58	0.1	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	503	2.09	0.14	0.22	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	1.91	0.11	0.23	0.0	0.8
Non-derivatized - MS/MS non-kit	200	2.43	0.21	1.41	0.1	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	1.79	0.11	0.41	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	0.04	0.01	0.01	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	100	0.02	0.00	0.01	0.0	0.6
Derivatized - MS/MS non-kit	337	0.03	0.01	0.02	0.0	1.0
LC-MS/MS non-kit	30	0.11	0.01	0.06	0.1	1.4
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.02	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS MassChrom®	110	0.06	0.01	0.11	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	483	0.03	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.02	0.00	0.01	0.0	0.9
Non-derivatized - MS/MS non-kit	190	0.04	0.01	0.03	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.02	0.01	0.01	0.0	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	0.37	0.03	0.06	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	100	0.31	0.04	0.10	0.0	0.6
Derivatized - MS/MS non-kit	338	0.49	0.06	0.17	0.0	1.0
LC-MS/MS non-kit	30	0.75	0.07	0.22	0.1	1.4
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.42	0.03	0.03	0.0	0.9
Non-derivatized - MS/MS MassChrom®	110	0.46	0.03	0.11	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	0.42	0.03	0.06	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.40	0.03	0.06	0.0	0.9
Non-derivatized - MS/MS non-kit	190	0.53	0.05	0.16	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.39	0.03	0.06	0.0	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	0.04	0.15	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	100	0.61	0.06	0.17	0.0	0.6
Derivatized - MS/MS non-kit	338	0.99	0.10	0.30	0.0	1.0
LC-MS/MS non-kit	30	1.39	0.07	0.45	0.1	1.4
Non-derivatized - MS/MS MS2 Screening Neo (MS- Non-derivatized - MS/MS MassChrom®	50	0.88	0.06	0.07	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	110	0.94	0.05	0.29	0.1	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	486	0.84	0.05	0.10	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.81	0.05	0.11	0.0	0.9
Non-derivatized - MS/MS non-kit	190	1.08	0.13	0.31	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	0.78	0.07	0.09	0.0	0.8

#### 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	1.70	0.07	0.33	0.0	0.7
Derivatized - MS/MS MassChrom® Chromsystems	100	1.53	0.09	0.40	0.0	0.6
Derivatized - MS/MS non-kit	338	2.53	0.27	0.71	0.0	1.0
LC-MS/MS non-kit	30	3.62	0.33	1.19	0.1	1.4
Non-derivatized - MS/MS MS2 Screening Neo (MS- Non-derivatized - MS/MS MassChrom®	50	2.25	0.13	0.23	0.0	0.9
Non-derivatized - MS/MS NeoBase™ PerkinElmer	110	1.98	0.12	0.68	0.1	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	2.16	0.13	0.25	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	2.12	0.13	0.29	0.0	0.9
Non-derivatized - MS/MS non-kit	190	2.62	0.27	0.77	0.0	1.0
Non-derivatized Labsystems Neomass AAAC Plus	40	1.97	0.13	0.26	0.0	0.8

## 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 MassChrom® Chromsystems	110	0.04	0.01	0.03	0.1	0.7
Derivatized - MS/MS non-kit	324	0.04	0.01	0.03	0.0	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.02	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS MassChrom®	80	0.11	0.00	0.25	0.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	450	0.02	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	321	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS non-kit	160	0.02	0.01	0.01	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.02	0.01	0.01	0.0	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 MassChrom® Chromsystems	110	0.80	0.07	0.13	0.1	0.7
Derivatized - MS/MS non-kit	328	0.86	0.10	0.22	0.0	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.89	0.06	0.10	0.0	0.9
Non-derivatized - MS/MS MassChrom®	80	0.85	0.05	0.24	0.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	0.82	0.05	0.08	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	0.71	0.04	0.14	0.0	0.7
Non-derivatized - MS/MS non-kit	160	0.87	0.09	0.39	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.80	0.06	0.12	0.0	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 MassChrom® Chromsystems	110	1.50	0.12	0.26	0.1	0.7
Derivatized - MS/MS non-kit	328	1.71	0.19	0.45	0.0	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.75	0.11	0.21	0.0	0.9
Non-derivatized - MS/MS MassChrom®	80	1.54	0.10	0.25	0.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	456	1.59	0.10	0.14	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	1.39	0.08	0.28	0.0	0.7
Non-derivatized - MS/MS non-kit	160	1.68	0.19	0.74	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	1.54	0.12	0.21	0.0	0.8

## 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 MassChrom® Chromsystems	110	2.26	0.17	0.38	0.1	0.7
Derivatized - MS/MS non-kit	328	2.59	0.27	0.68	0.0	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	2.61	0.16	0.30	0.0	0.9
Non-derivatized - MS/MS MassChrom®	80	1.91	0.14	0.76	0.2	0.6
Non-derivatized - MS/MS NeoBase™ PerkinElmer	455	2.38	0.14	0.21	0.0	0.8
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	322	2.11	0.12	0.43	0.0	0.7
Non-derivatized - MS/MS non-kit	160	2.57	0.25	1.08	0.0	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	2.31	0.17	0.38	0.0	0.8

## 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	0.07	0.01	0.03	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	0.07	0.01	0.02	0.1	0.7
Derivatized - MS/MS non-kit	338	0.08	0.01	0.03	0.1	0.9
LC-MS/MS non-kit	30	0.07	0.01	0.02	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.06	0.01	0.02	0.1	0.8
Non-derivatized - MS/MS MassChrom®	80	0.10	0.01	0.12	0.2	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	0.06	0.01	0.01	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.05	0.01	0.01	0.0	0.8
Non-derivatized - MS/MS non-kit	170	0.06	0.01	0.02	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.06	0.02	0.03	0.0	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	0.40	0.03	0.05	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	0.43	0.04	0.07	0.1	0.7
Derivatized - MS/MS non-kit	338	0.50	0.05	0.10	0.1	0.9
LC-MS/MS non-kit	30	0.59	0.05	0.21	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.46	0.03	0.04	0.1	0.8
Non-derivatized - MS/MS MassChrom®	80	0.52	0.03	0.24	0.2	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	0.46	0.04	0.05	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	0.43	0.03	0.05	0.0	0.8
Non-derivatized - MS/MS non-kit	170	0.47	0.05	0.08	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.45	0.14	0.27	0.0	0.8

## 2021 Quality Control Data Summaries of Statistical Analyses

### MYRISTOYL CARNITINE (C14 $\mu\text{mol/L}$ 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	0.97	0.04	0.22	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	1.16	0.09	0.18	0.1	0.7
Derivatized - MS/MS non-kit	338	1.40	0.14	0.25	0.1	0.9
LC-MS/MS non-kit	30	1.65	0.09	0.58	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.28	0.08	0.11	0.1	0.8
Non-derivatized - MS/MS MassChrom®	80	1.34	0.08	0.38	0.2	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	1.29	0.09	0.12	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	1.22	0.07	0.12	0.0	0.8
Non-derivatized - MS/MS non-kit	170	1.33	0.16	0.23	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	1.21	0.37	0.70	0.0	0.8

#### 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	2.00	0.16	0.46	0.1	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	2.22	0.14	0.30	0.1	0.7
Derivatized - MS/MS non-kit	338	2.79	0.24	0.52	0.1	0.9
LC-MS/MS non-kit	30	3.30	0.23	1.20	0.1	1.1
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	2.54	0.16	0.23	0.1	0.8
Non-derivatized - MS/MS MassChrom®	80	2.10	0.16	0.85	0.2	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	486	2.59	0.17	0.22	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	2.47	0.15	0.27	0.0	0.8
Non-derivatized - MS/MS non-kit	170	2.63	0.25	0.47	0.1	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	2.46	0.75	1.49	0.0	0.8

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**

<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	0.03	0.00	0.01	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.05	0.01	0.04	0.1	0.4
Derivatized - MS/MS non-kit	336	0.04	0.01	0.04	0.0	0.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	0.02	0.01	0.01	0.1	0.4
Non-derivatized - MS/MS MassChrom®	80	0.04	0.00	0.05	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	465	0.03	0.01	0.01	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	356	0.02	0.00	0.01	0.0	0.5
Non-derivatized - MS/MS non-kit	166	0.03	0.01	0.02	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	40	0.03	0.01	0.02	0.0	0.5

**Lot B2015 – Enriched 0.5  $\mu\text{mol/L}$  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	0.23	0.03	0.03	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.26	0.02	0.07	0.1	0.4
Derivatized - MS/MS non-kit	338	0.29	0.04	0.07	0.0	0.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-	40	0.28	0.02	0.02	0.1	0.4
Non-derivatized - MS/MS MassChrom®	80	0.29	0.02	0.10	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	0.26	0.02	0.04	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	0.25	0.02	0.04	0.0	0.5
Non-derivatized - MS/MS non-kit	166	0.28	0.03	0.08	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	40	0.28	0.08	0.15	0.0	0.5
Derivatized - MS/MS ClinSpot® Complete Kit	30	0.23	0.03	0.03	0.0	0.4

## 2021 Quality Control Data Summaries of Statistical Analyses

### TETRADECENOYL CARNITINE (C14:1 $\mu\text{mol/L}$ 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	0.53	0.04	0.14	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	0.67	0.06	0.15	0.1	0.4
Derivatized - MS/MS non-kit	338	0.80	0.08	0.18	0.0	0.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	0.72	0.04	0.04	0.1	0.4
Non-derivatized - MS/MS MassChrom®	80	0.75	0.06	0.22	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	0.73	0.05	0.10	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	0.69	0.05	0.10	0.0	0.5
Non-derivatized - MS/MS non-kit	166	0.80	0.09	0.25	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	40	0.76	0.22	0.41	0.0	0.5

#### 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	1.14	0.07	0.26	0.0	0.4
Derivatized - MS/MS MassChrom® Chromsystems	60	1.28	0.12	0.28	0.1	0.4
Derivatized - MS/MS non-kit	338	1.61	0.16	0.38	0.0	0.5
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	40	1.31	0.05	0.08	0.1	0.4
Non-derivatized - MS/MS MassChrom®	80	1.21	0.11	0.50	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	1.47	0.10	0.19	0.0	0.5
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	358	1.41	0.10	0.22	0.0	0.5
Non-derivatized - MS/MS non-kit	166	1.59	0.14	0.49	0.0	0.5
Non-derivatized Labsystems Neomass AAAC Plus	40	1.54	0.44	0.84	0.0	0.5

## 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	1.05	0.09	0.16	1.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	110	0.79	0.07	0.12	0.8	0.8
Derivatized - MS/MS non-kit	338	0.94	0.09	0.19	0.9	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.89	0.06	0.07	0.9	0.9
Non-derivatized - MS/MS MassChrom®	80	1.16	0.07	0.98	1.5	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	476	0.89	0.07	0.10	0.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	350	1.25	0.92	5.03	1.1	0.9
Non-derivatized - MS/MS non-kit	180	0.89	0.08	0.14	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.86	0.07	0.10	0.8	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	4.50	0.32	0.65	1.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	110	3.96	0.29	0.57	0.8	0.8
Derivatized - MS/MS non-kit	338	4.38	0.37	0.72	0.9	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	4.38	0.28	0.37	0.9	0.9
Non-derivatized - MS/MS MassChrom®	80	4.47	0.35	1.12	1.5	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	4.31	0.31	0.52	0.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	4.68	0.36	0.64	1.1	0.9
Non-derivatized - MS/MS non-kit	180	4.32	0.40	0.72	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	4.27	0.30	0.51	0.8	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### 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	6.84	0.39	1.64	1.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	110	6.84	0.47	0.77	0.8	0.8
Derivatized - MS/MS non-kit	338	7.90	0.66	1.28	0.9	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	7.94	0.53	0.71	0.9	0.9
Non-derivatized - MS/MS MassChrom®	80	7.50	0.43	1.27	1.5	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	7.77	0.53	0.83	0.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	8.39	0.58	1.10	1.1	0.9
Non-derivatized - MS/MS non-kit	180	7.78	0.78	1.28	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	7.66	0.56	0.75	0.8	0.9

#### 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	10.55	0.58	2.60	1.1	0.8
Derivatized - MS/MS MassChrom® Chromsystems	110	10.29	0.71	1.43	0.8	0.8
Derivatized - MS/MS non-kit	338	11.61	1.00	2.08	0.9	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-Non-derivatized - MS/MS MassChrom®)	50	11.54	0.77	1.08	0.9	0.9
Non-derivatized - MS/MS MassChrom®	80	9.06	0.65	3.38	1.5	0.7
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	11.44	0.75	1.16	0.8	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	352	12.39	0.89	1.63	1.1	0.9
Non-derivatized - MS/MS non-kit	180	11.39	1.10	2.10	0.9	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	11.23	0.68	1.20	0.8	0.9

## 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	0.01	0.00	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	107	0.01	0.00	0.01	0.0	0.7
Derivatized - MS/MS non-kit	328	0.02	0.01	0.02	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.01	0.00	0.00	0.0	0.7
Non-derivatized - MS/MS MassChrom®	62	0.02	0.00	0.04	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	462	0.01	0.00	0.01	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	333	0.05	0.06	0.35	0.0	0.7
Non-derivatized - MS/MS non-kit	180	0.01	0.00	0.02	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.00	0.00	0.01	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	0.19	0.02	0.03	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	0.21	0.02	0.04	0.0	0.7
Derivatized - MS/MS non-kit	330	0.20	0.03	0.06	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.18	0.01	0.02	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.17	0.01	0.10	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	0.17	0.01	0.03	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	0.21	0.02	0.24	0.0	0.7
Non-derivatized - MS/MS non-kit	180	0.21	0.02	0.06	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.14	0.01	0.03	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	0.64	0.06	0.18	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	0.74	0.06	0.11	0.0	0.7
Derivatized - MS/MS non-kit	330	0.76	0.08	0.20	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.73	0.05	0.10	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.51	0.04	0.10	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	0.65	0.05	0.12	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	0.74	0.05	0.47	0.0	0.7
Non-derivatized - MS/MS non-kit	180	0.84	0.10	0.22	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.55	0.04	0.10	0.0	0.6

2021 Quality Control Data Summaries of Statistical Analyses  
**HYDROXPALMITOYLCARNITINE (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	0.99	0.08	0.25	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	110	1.13	0.08	0.16	0.0	0.7
Derivatized - MS/MS non-kit	330	1.18	0.14	0.32	0.0	0.8
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.11	0.07	0.17	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.68	0.05	0.29	0.0	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	474	0.99	0.06	0.19	0.0	0.7
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	362	1.16	0.09	0.84	0.0	0.7
Non-derivatized - MS/MS non-kit	180	1.27	0.14	0.34	0.0	0.8
Non-derivatized Labsystems Neomass AAAC Plus	40	0.84	0.05	0.16	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	0.72	0.05	0.08	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	0.66	0.06	0.09	0.6	1.0
Derivatized - MS/MS non-kit	318	0.64	0.07	0.15	0.6	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	0.56	0.03	0.05	0.5	0.9
Non-derivatized - MS/MS MassChrom®	80	0.70	0.05	0.30	0.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	0.62	0.04	0.06	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	334	0.61	0.04	0.13	0.6	1.0
Non-derivatized - MS/MS non-kit	160	0.63	0.05	0.09	0.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	0.60	0.05	0.07	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	1.57	0.13	0.28	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	1.60	0.13	0.19	0.6	1.0
Derivatized - MS/MS non-kit	318	1.54	0.15	0.32	0.6	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	1.45	0.10	0.12	0.5	0.9
Non-derivatized - MS/MS MassChrom®	80	1.77	0.10	0.57	0.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	1.57	0.11	0.15	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	1.54	0.09	0.28	0.6	1.0
Non-derivatized - MS/MS non-kit	160	1.56	0.14	0.25	0.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	1.52	0.14	0.22	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	2.81	0.20	0.68	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	3.37	0.30	0.48	0.6	1.0
Derivatized - MS/MS non-kit	318	3.21	0.29	0.62	0.6	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	3.06	0.22	0.28	0.5	0.9
Non-derivatized - MS/MS MassChrom®	79	3.49	0.21	0.76	0.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	3.32	0.22	0.30	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	3.27	0.20	0.57	0.6	1.0
Non-derivatized - MS/MS non-kit	160	3.28	0.31	0.55	0.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	3.21	0.31	0.38	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	4.71	0.36	1.38	0.7	0.8
Derivatized - MS/MS MassChrom® Chromsystems	100	5.53	0.38	0.59	0.6	1.0
Derivatized - MS/MS non-kit	318	5.24	0.48	1.09	0.6	0.9
Non-derivatized - MS/MS MS2 Screening Neo (MS-	50	5.00	0.33	0.43	0.5	0.9
Non-derivatized - MS/MS MassChrom®	80	4.68	0.35	1.70	0.8	0.8
Non-derivatized - MS/MS NeoBase™ PerkinElmer	466	5.47	0.35	0.47	0.6	1.0
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	342	5.39	0.32	0.96	0.6	1.0
Non-derivatized - MS/MS non-kit	160	5.38	0.53	1.00	0.6	0.9
Non-derivatized Labsystems Neomass AAAC Plus	40	5.28	0.48	0.71	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	0.01	0.00	0.01	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	96	0.02	0.01	0.01	0.0	0.8
Derivatized - MS/MS non-kit	252	0.02	0.01	0.02	0.0	0.7
Non-derivatized - MS/MS MassChrom®	62	0.02	0.00	0.05	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	435	0.00	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	298	0.00	0.00	0.00	0.0	0.6
Non-derivatized - MS/MS non-kit	140	0.01	0.00	0.01	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	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	0.22	0.07	0.09	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	0.22	0.03	0.05	0.0	0.8
Derivatized - MS/MS non-kit	258	0.20	0.03	0.08	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.19	0.01	0.16	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.15	0.01	0.02	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	318	0.16	0.01	0.03	0.0	0.6
Non-derivatized - MS/MS non-kit	140	0.18	0.02	0.11	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	0.13	0.01	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	0.66	0.15	0.20	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	0.78	0.08	0.16	0.0	0.8
Derivatized - MS/MS non-kit	258	0.72	0.10	0.24	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.52	0.06	0.18	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.59	0.04	0.07	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	318	0.59	0.04	0.08	0.0	0.6
Non-derivatized - MS/MS non-kit	140	0.66	0.10	0.43	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	0.50	0.05	0.11	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	0.94	0.20	0.33	0.0	0.6
Derivatized - MS/MS MassChrom® Chromsystems	100	1.18	0.11	0.23	0.0	0.8
Derivatized - MS/MS non-kit	258	1.12	0.16	0.42	0.0	0.7
Non-derivatized - MS/MS MassChrom®	80	0.67	0.06	0.36	0.1	0.4
Non-derivatized - MS/MS NeoBase™ PerkinElmer	444	0.91	0.07	0.12	0.0	0.6
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	318	0.93	0.06	0.18	0.0	0.6
Non-derivatized - MS/MS non-kit	140	1.02	0.14	0.65	0.0	0.7
Non-derivatized Labsystems Neomass AAAC Plus	40	0.77	0.08	0.18	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	30	0.06	0.01	0.02	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.16	0.04	0.06	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.07	0.01	0.03	0.1	0.8

**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	30	0.25	0.02	0.03	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.53	0.49	2.03	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.24	0.01	0.07	0.1	0.8

**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	30	0.46	0.02	0.05	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	0.62	0.08	0.14	0.2	1.0
Non-derivatized - MS/MS non-kit	30	0.41	0.03	0.09	0.1	0.8

**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	30	1.80	0.09	0.22	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	200	2.16	0.23	0.42	0.2	1.0
Non-derivatized - MS/MS non-kit	30	1.56	0.10	0.33	0.1	0.8

## 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	55	0.02	0.02	0.04	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	230	0.12	0.03	0.06	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.08	0.01	0.09	0.1	0.9

#### 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	58	0.21	0.02	0.04	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	230	0.29	0.05	0.08	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.26	0.01	0.13	0.1	0.9

#### 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	58	0.43	0.03	0.09	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	230	0.51	0.06	0.09	0.1	0.9
Non-derivatized - MS/MS non-kit	30	0.47	0.03	0.17	0.1	0.9

#### 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	58	1.75	0.10	0.34	0.0	0.9
Non-derivatized - MS/MS NeoBase™2 PerkinElmer	230	1.96	0.18	0.31	0.1	0.9
Non-derivatized - MS/MS non-kit	30	1.82	0.10	0.53	0.1	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	337.93	27.67	158.1	337.6	1.1

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	392.18	19.13	199.1	337.6	1.1

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	551.35	33.08	244.9	337.6	1.1

#### Lot D2015 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	50	769.53	60.40	330.63	337.6	1.1

## 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	70	1.51	0.13	0.72	1.5	0.7

#### 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	70	5.17	0.45	1.82	1.5	0.7

#### 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	70	9.01	0.67	3.09	1.5	0.7

#### 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	70	16.34	1.33	5.97	1.5	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

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

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	39.41	3.11	10.04	37.0	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 non-kit	30	79.74	5.55	18.04	37.0	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 non-kit	30	129.81	10.51	24.85	37.0	0.9

#### Lot D2015 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	30	222.34	11.01	35.19	37.0	0.9

## 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>
NeoLSD™ MSMS Kit PerkinElmer	87	0.16	0.06	0.11	0.0	1.0

#### **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>
NeoLSD™ MSMS Kit PerkinElmer	110	0.44	0.08	0.16	0.0	1.0

#### **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>
NeoLSD™ MSMS Kit PerkinElmer	116	2.88	0.37	0.74	0.0	1.0

#### **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>
NeoLSD™ MSMS Kit PerkinElmer	116	5.85	0.64	1.28	0.0	1.0

## 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	51	0.26	0.09	0.26	0.1	0.9
LC-MS/MS non-kit	30	0.09	0.01	0.02	-0.1	1.4
NeoLSD™ MSMS Kit PerkinElmer	148	0.11	0.03	0.05	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	60	0.68	0.16	0.32	0.1	0.9
LC-MS/MS non-kit	30	0.67	0.05	0.10	-0.1	1.4
NeoLSD™ MSMS Kit PerkinElmer	178	0.54	0.06	0.08	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	60	3.80	0.45	0.73	0.1	0.9
LC-MS/MS non-kit	30	5.31	0.45	1.61	-0.1	1.4
NeoLSD™ MSMS Kit PerkinElmer	178	4.03	0.41	0.50	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	60	6.46	0.54	1.01	0.1	0.9
LC-MS/MS non-kit	30	9.50	0.95	3.85	-0.1	1.4
NeoLSD™ MSMS Kit PerkinElmer	178	6.84	0.51	0.68	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
N/A						

#### 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	34	2.57	0.27	0.41	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	40	11.96	1.08	1.32	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	40	22.26	3.00	3.49	0.2	1.2

#### GAA Fluorometric Method

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	32	0.44	0.11	0.40
B2008	40	0.57	0.14	0.52
C2008	50	1.96	0.34	2.02
D2008	50	3.56	0.41	3.35

## 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	50	0.10	0.03	0.08	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	158	0.08	0.03	0.08	0.0	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	60	0.46	0.07	0.09	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	202	0.44	0.05	0.08	0.0	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	60	3.29	0.33	0.60	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	208	3.44	0.32	0.46	0.0	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	60	6.53	0.57	1.25	0.0	0.9
NeoLSD™ MSMS Kit PerkinElmer	208	6.70	0.53	0.77	0.0	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	21	2.39	0.26	0.35	0.7	1.0

#### **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	29	3.22	0.26	0.36	0.7	1.0

#### **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	40	11.52	0.66	0.82	0.7	1.0

#### **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	40	23.56	2.15	3.60	0.7	1.0

#### **IDUA Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	17	0.27	0.22	0.37
B2008	30	0.32	0.18	0.33
C2008	40	3.28	0.56	2.34
D2008	40	8.60	0.60	6.91

## 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	0.68	0.07	0.27	-0.4	1.0
NeoLSD™ MSMS Kit PerkinElmer	118	0.71	0.11	0.26	-0.4	1.0

#### **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	1.38	0.12	0.36	-0.4	1.0
NeoLSD™ MSMS Kit PerkinElmer	138	1.36	0.14	0.32	-0.4	1.0

#### **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	6.90	0.33	1.27	-0.4	1.0
NeoLSD™ MSMS Kit PerkinElmer	138	7.29	0.54	1.96	-0.4	1.0

#### **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	13.39	0.59	1.76	-0.4	1.0
NeoLSD™ MSMS Kit PerkinElmer	138	14.10	1.02	3.95	-0.4	1.0

## 2021 Quality Control Data Summaries of Statistical Analyses

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

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

#### **GLA Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	42	1.21	0.21	0.65
B2008	50	2.00	0.40	1.06
C2008	50	8.17	0.83	3.14
D2008	50	14.57	0.95	5.67

## 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	0.39	0.05	0.06	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	128	0.33	0.06	0.13	0.0	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	0.90	0.10	0.13	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	136	0.64	0.09	0.16	0.0	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	4.45	0.38	0.45	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	136	3.06	0.32	0.52	0.0	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	8.30	0.55	0.97	0.1	0.9
NeoLSD™ MSMS Kit PerkinElmer	136	6.30	0.63	0.99	0.0	0.7

## 2021 Quality Control Data Summaries of Statistical Analyses

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

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

#### **ABG Fluorometric Method**

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A2008	30	0.64	0.27	0.44
B2008	33	0.84	0.21	0.48
C2008	40	2.49	0.22	0.39
D2008	40	4.37	0.30	0.70

## 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	78	0.04	0.01	0.02	-0.1	0.9

#### 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	97	0.20	0.03	0.04	-0.1	0.9

#### 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	108	1.29	0.13	0.18	-0.1	0.9

#### 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	108	2.45	0.22	0.38	-0.1	0.9

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

**Lot A2111 – Non-enriched 0 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	104	1.28	0.43	1.33	0.3	0.9

**Lot B2111 – Enriched 10 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	210	8.99	1.04	2.69	0.3	0.9

**Lot C2111 – Enriched 50 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	210	46.52	3.16	12.45	0.3	0.9

**Lot D2111 – Enriched 100 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	210	95.28	6.69	26.39	0.3	0.9

**Lot E2111 – Enriched 500 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	210	471.57	28.38	127.05	0.3	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	86	0.70	0.25	0.63	0.4	0.9

#### Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	9.75	0.91	2.71	0.4	0.9

#### Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	46.33	3.35	11.96	0.4	0.9

#### Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	94.55	7.27	25.25	0.4	0.9

#### Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	468.15	31.10	122.13	0.4	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	85	2.05	1.01	1.53	0.0	1.0

#### Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	10.97	1.44	3.96	0.0	1.0

#### Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	45.36	4.20	13.89	0.0	1.0

#### Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	97.16	8.77	29.93	0.0	1.0

#### Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	200	487.04	33.36	138.68	0.0	1.0

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

**Lot A2111 – Non-enriched 0 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	52	0.74	0.29	0.77	3.5	0.9

**Lot B2111 – Enriched 10 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	10.21	0.80	3.55	3.5	0.9

**Lot C2111 – Enriched 50 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	46.96	3.14	15.08	3.5	0.9

**Lot D2111 – Enriched 100 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	94.71	6.67	30.78	3.5	0.9

**Lot E2111 – Enriched 500 ng/mL serum**

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	432.24	24.67	158.13	3.5	0.9

## 2021 Quality Control Data Summaries of Statistical Analyses

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

#### Lot A2111 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	52	0.31	0.15	0.35	-2.0	0.9

#### Lot B2111 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	9.73	1.06	3.42	-2.0	0.9

#### Lot C2111 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	40.39	3.33	12.81	-2.0	0.9

#### Lot D2111 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	89.08	7.09	27.83	-2.0	0.9

#### Lot E2111 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS non-kit	130	461.04	32.10	142.58	-2.0	0.9

## 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	106	0.68	0.16	0.40	-0.1	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	116	47.24	3.04	15.34	-0.1	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	116	89.30	5.31	20.69	-0.1	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	116	179.30	9.31	42.29	-0.1	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	116	365.08	25.54	83.08	-0.1	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	126	24.30	1.92	8.41	23.5	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	126	112.15	7.57	31.06	23.5	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	126	195.25	14.28	55.59	23.5	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	126	369.15	28.81	104.5	23.5	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	126	719.79	38.74	176.8	23.5	0.9

## 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	126	59.94	4.26	16.60	61.6	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	126	151.50	10.67	36.21	61.6	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	126	239.46	12.00	47.43	61.6	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	126	420.36	21.33	89.16	61.6	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	126	773.02	39.12	147.0	61.6	0.9

## 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	120	33.06	2.20	4.90	30.0	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	130	120.46	6.89	14.17	30.0	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	120	202.35	11.51	21.63	30.0	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	130	381.40	22.92	54.82	30.0	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	130	740.17	29.64	85.40	30.0	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	116	29.11	2.41	4.76	26.7	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	126	113.61	6.03	12.12	26.7	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	116	191.06	9.96	16.57	26.7	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	126	360.16	20.39	39.53	26.7	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	126	703.08	30.55	71.39	26.7	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	146	67.23	4.45	11.93	68.1	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	146	167.64	10.24	31.87	68.1	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	146	262.10	14.27	49.73	68.1	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	146	460.30	26.74	90.67	68.1	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	146	849.82	43.96	145.6	68.1	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	218	2.00	0.37	0.93	0.4	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	226	4.84	0.66	1.68	0.4	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	226	17.78	1.53	5.52	0.4	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	226	43.62	3.48	12.90	0.4	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	79	2.17	0.34	0.72	0.3	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	86	4.73	0.64	1.23	0.3	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	86	16.74	1.91	4.03	0.3	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	86	43.08	5.07	10.09	0.3	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	166	1.24	0.29	0.90	0.4	0.9

#### 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	166	2.56	0.45	1.05	0.4	0.9

#### 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	176	8.95	1.21	2.21	0.4	0.9

#### 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	176	21.90	2.82	5.49	0.4	0.9

## 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	246	7.23	1.08	3.53	7.0	0.6

#### 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	246	12.92	1.42	5.36	7.0	0.6

#### 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	246	37.85	4.05	14.75	7.0	0.6

#### 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	246	69.06	6.82	26.92	7.0	0.6

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