

Newborn Screening Quality Assurance Program

2018 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 materials provide participants with external controls to assess method performance over time. The controls provide continuity and transcend changes in production lots of routinely used method- or kit-control materials. The external QC materials are intended to supplement the participants' method- or kit-control materials at periodic intervals to allow participants to monitor the long-term stability of their assays. NSQAP QC material is not a replacement for manufacturer kit controls or other daily QC, and should not be used for routine analysis. This report contains a summary of the 2018 Set 1 QC data submitted during the first half of the year by state, contract, and private laboratories in the United States; international participants; and manufacturers of screening test products.

QC Material Production

QC specimen lots were provided as 6-month supplies of DBS on filter paper. DBS QC lots were prepared from whole blood of 50% hematocrit. The materials were enriched with predetermined quantities of selected analytes and dispensed in 100 µL aliquots on Grade 903 filter paper (GE Healthcare Bio-Sciences Corporation (Westborough, MA)).

NSQAP provides QC materials for analysis of thyroxine (T4), thyroid-stimulating hormone (TSH), 17 α-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), eighteen acylcarnitines free carnitine (C0), acetylcarnitine (C2), propionylcarnitine (C3), malonylcarnitine (C3DC), butyrylcarnitine (C4), hydroxybutyrylcarnitine (C4OH), isovalerylcarnitine (C5), glutarylcarnitine (C5DC), hydroxyisovalerylcarnitine (C5OH), hexanoylcarnitine (C6), octanoylcarnitine (C8), decanoylcarnitine (C10), dodecanoylcarnitine (C12), myristoylcarnitine (C14), palmitoylcarnitine (C16), hydroxypalmitoylcarnitine (C16OH), stearoylcarnitine (C18), hydroxystearoylcarnitine (C18OH), 20:0-, 22:0-, 24:0- and 26:0-lysophosphatidylcholine for the detection of X-linked Adrenoleukodystrophy (XALD) and galactocerebrosidase (GALC), acid α-glucosidase (GAA), α-L-iduronidase (IDUA), α-galactosidase (GLA), β-glucocerebrosidase (ABG), and acid sphingomyelinase (ASM) for the detection of Lysosomal Storage Disorder (LSD). T4, TSH, 17OHP and TGal, GALT and XALD consisted of blood spot materials from three lots per analyte, with each lot containing a different concentration of analyte. The shipment for IRT, TGal, amino acids, SUAC, acylcarnitines, and LSD consisted of blood spot cards from four lots.

NSQAP also distributed certified QC materials for newborn screening analytes and disorders designed for second-tier testing by tandem mass spectrometry (MS/MS). These programs include Second-tier Congenital Adrenal Hyperplasia (CAHQC) by LC-MS/MS for the analytes 17 α-hydroxyprogesterone (17OHP2), 4-androstenedione (4AD2), cortisol (CORT2), 11-deoxycortisol (11D2), and 21-deoxycortisol (21D2); Second-tier Maple Syrup Urine Disease and Phenylketonuria (MSUD-PKUQC) by LC-MS/MS for the analytes 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); and guanidinoacetate methyltransferase (GAMT) by FIA-MS/MS for the analytes guanidinoacetic acid (GAA2), and creatine (CRE2).

QC Material Distribution

On January 9, 2018 we distributed dried blood spot (DBS) quality control (QC) materials to 480 participating laboratories.

QC Data Reporting Requirements

Participants used the QC Data Report forms located at https://www.cdc.gov/labstandards/nsqap_resources.html to report results. NSQAP required the following for each QC analyte; 1) laboratory information (contact name, laboratory code number, email, 2) analyte kit or method, 3) results of duplicate sample analysis from five independent runs in the analytic units and decimal places requested, and 4) at least nine data points for each lot of analyte. If these minimum requirements were not met, the data was not accepted unless the participant corrected their submission.

Participant Results

For the Set 1 QC materials, we compiled the participant results from five analytic runs from each QC lot, and calculated mean values and standard deviations (SD). Data values outside 4SD limits were reviewed, and if considered to be “blunders”, removed from the data set. For linear regression analysis, we could not include qualitative data, data submitted as inequalities or ranges, data submitted in unidentified units, or data from less than five analytic runs per specimen lot per analyte.

Several participants were required to resubmit their data because either the method was not entered from the drop-down menu as requested or data was reported in the incorrect units. To ensure that all results are appropriately entered in the CDC database, participants must convert their results to the requested units before entering them on the data report forms. For GALT analysis, where no conversion factor exists between units of U/g Hb and other reportable units, we included a separate table to provide participants with peer-group statistics. For LSDQC analysis, where mean activities differ based on method, we provided separate tables if sufficient data was submitted. For XALD analysis, tables are not provided for 20:0- and 22:0-lysophosphatidylcholine due to low participation.

The reported QC data are summarized in tables on pages 4—89 which show the analyte by series of QC lots, the number of measurements (N), the mean values, and the standard deviations (SD) by kit or analytic method. In addition, we used a weighted linear regression analysis to examine the comparability by method of reported (aggregated) versus enriched concentrations. Methods with less than three participants reporting data were not included in the tables.

Discussion

The enriched values of the QC specimen lots do not take into account the endogenous levels of the analytes. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, Gly, SUAC, acylcarnitines, 20:0-, 22:0-, 24:0- and 26:0-lysophosphatidylcholine, GALC, GAA, IDUA, GAL, ABG, ASM, and all Second-tier analytes, the non-enriched base pools were distributed as the first QC specimen lot in each series so that participants could measure the endogenous concentration of the series.

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

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.

Discussion (cont.)

For the purpose of our assessment, we first calculated the within-laboratory SD component of the total SD and used the reported QC data from multiple analytic runs for regression analyses. We then calculated the Y-intercept and slope listed in each table using all analyte concentrations within a lot series (**e.g., lots A1701, B1701, and C1701**). The Y-intercept is estimated by performing a weighted linear regression analysis on mean reported concentrations versus either 1) enriched concentrations, 2) assayed values (GALT, IRT), or 3) mean activity (LSD), and extrapolating the regression to the Y-axis. This parameter provides one measure of the endogenous concentration level for an analyte. For Phe, Leu, Met, Tyr, Val, Cit, Ala, Arg, Orn, Gly, SUAC, acylcarnitines, 20:0-, 22:0-, 24:0-, and 26:0-lysophosphatidylcholine, 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.

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 **Orn, SUAC, C3DC, C3DC + C4OH, C4OH, C5OH, C16OH and C18OH**, but were historically consistent with previous sets.

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1705 – Enriched 25 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	240	21.6	2.2	4.8	-1.0	0.9
Delfia Neonatal 17-OHP (A024)	229	22.7	4.3	8.1	-2.7	1.0
AutoDelfia	290	22.3	2.2	3.5	0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	339	21.6	2.2	4.6	0.3	0.8
Labsystems Diagnostics	70	34.7	2.0	25.9	19.5	0.6
Bio-Rad Quantase	30	32.1	4.6	17.0	8.5	1.0
TecnoSuma UMELISA	30	29.0	3.2	3.2	-0.7	1.2
PerkinElmer GSP Neonatal	510	22.8	2.0	3.3	1.9	0.8
Zentech	50	20.8	2.6	10.2	-15.1	1.4

Lot B1705 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	240	43.6	4.2	10.4	-1.0	0.9
Delfia Neonatal 17-OHP (A024)	229	44.5	6.2	16.3	-2.7	1.0
AutoDelfia	290	43.5	3.7	6.6	0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	339	42.3	4.0	8.6	0.3	0.8
Labsystems Diagnostics	69	47.4	5.2	8.2	19.5	0.6
Bio-Rad Quantase	30	61.6	6.3	34.1	8.5	1.0
TecnoSuma UMELISA	30	57.9	7.0	9.3	-0.7	1.2
LC-MS/MS	30	80.3	4.1	58.6	2.5	1.6
PerkinElmer GSP Neonatal	510	44.0	2.9	5.3	1.9	0.8
Zentech	50	50.7	6.1	15.8	-15.1	1.4

Lot C1705 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	239	88.7	9.5	23.8	-1.0	0.9
Delfia Neonatal 17-OHP (A024)	230	95.4	12.5	37.8	-2.7	1.0
AutoDelfia	290	87.7	8.1	13.4	0.2	0.9
AutoDelfia Neonatal 17-OHP (B024)	340	84.8	9.1	18.1	0.3	0.8
Labsystems Diagnostics	69	77.6	8.5	27.7	19.5	0.6
Bio-Rad Quantase	30	108.9	22.0	60.3	8.5	1.0
TecnoSuma UMELISA	30	117.1	16.4	19.1	-0.7	1.2
LC-MS/MS	30	158.0	15.0	103.9	2.5	1.6
PerkinElmer GSP Neonatal	510	86.0	6.6	11.5	1.9	0.8
Zentech	50	122.4	14.8	42.9	-15.1	1.4

2018 Quality Control Data Summaries of Statistical Analyses

THYROXINE (T₄ µg/dL serum)

Lot A1700 – Enriched 2 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	91	1.9	0.3	0.5	-0.3	1.0
AutoDelfia	186	1.8	0.4	0.5	-0.4	1.0
PerkinElmer GSP Neonatal	132	1.7	0.2	0.3	-0.7	1.1

Lot B1700 – Enriched 7 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	100	6.7	0.7	1.0	-0.3	1.0
AutoDelfia	186	6.8	0.7	1.5	-0.4	1.0
PerkinElmer GSP Neonatal	160	6.7	0.7	0.7	-0.7	1.1

Lot C1700 – Enriched 11 µg/dL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Delfia	100	11.0	1.3	1.5	-0.3	1.0
AutoDelfia	185	11.2	1.0	2.5	-0.4	1.0
PerkinElmer GSP Neonatal	160	11.6	0.9	1.2	-0.7	1.1

2018 Quality Control Data Summaries of Statistical Analyses

THYROID-STIMULATING HORMONE (TSH μ U/mL serum)

Lot A1701 – Enriched 25 μ U/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	600	24.3	2.6	6.8	1.6	0.9
AutoDelfia	880	26.3	2.4	5.5	0.6	1.0
Labsystems Diagnostics	140	24.0	2.6	6.7	-3.6	1.1
Bio-Rad Quantase	30	28.1	3.1	11.3	2.5	1.0
TecnoSuma UMELISA	30	24.0	4.5	7.0	-1.6	1.0
DiaSorin	70	24.3	2.9	5.3	2.0	0.9
PerkinElmer GSP Neonatal	590	23.4	2.2	5.1	-0.5	0.9
Trimaris Neonatal	30	29.3	3.3	3.7	7.8	0.9
Zentech	60	25.1	2.6	8.0	-3.4	1.1

Lot B1701 – Enriched 40 μ U/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	599	39.0	4.1	11.4	1.6	0.9
AutoDelfia	880	41.0	3.4	8.1	0.6	1.0
Labsystems Diagnostics	140	40.5	4.4	11.7	-3.6	1.1
Bio-Rad Quantase	30	44.0	4.6	17.4	2.5	1.0
TecnoSuma UMELISA	30	39.6	5.0	9.9	-1.6	1.0
DiaSorin	70	36.1	4.3	6.4	2.0	0.9
PerkinElmer GSP Neonatal	590	36.6	3.2	7.4	-0.5	0.9
Trimaris Neonatal	30	45.0	3.7	4.2	7.8	0.9
Zentech	60	39.1	4.1	12.0	-3.4	1.1

Lot C1701 – Enriched 80 μ U/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	600	75.4	6.7	20.9	1.6	0.9
AutoDelfia	880	82.1	7.1	16.7	0.6	1.0
Labsystems Diagnostics	140	84.7	7.8	18.7	-3.6	1.1
Bio-Rad Quantase	30	85.0	7.8	29.9	2.5	1.0
TecnoSuma UMELISA	30	80.6	10.8	16.0	-1.6	1.0
DiaSorin	69	71.9	9.3	13.6	2.0	0.9
PerkinElmer GSP Neonatal	590	74.9	6.5	15.8	-0.5	0.9
Trimaris Neonatal	30	79.4	6.8	7.0	7.8	0.9
Zentech	60	84.9	7.5	25.3	-3.4	1.1

2018 Quality Control Data Summaries of Statistical Analyses
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT U/g Hb)

Lot F1703 – Assayed 1.4 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit U/g Hb	298	1.3	0.3	0.8	-0.1	0.9
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	60	0.7	0.1	0.2	-0.4	0.7

Lot G1703 – Assayed 5.0 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit U/g Hb	313	4.3	0.4	1.0	-0.1	0.9
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	60	3.0	0.2	0.4	-0.4	0.7

Lot H1703 – Assayed 10.7 U/g Hb

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
PerkinElmer Neonatal Kit U/g Hb	311	9.6	1.1	2.5	-0.1	0.9
Astoria-Pacific Neonatal Microplate Reagent Kit U/g Hb	60	7.3	0.5	1.0	-0.4	0.7

2018 Quality Control Data Summaries of Statistical Analyses

GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (GALT) (cont.) METHODS REPORTED IN UNITS OTHER THAN U/g Hb (≥3 PARTICIPANTS)

Lot F1703

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	30	7.9	2.2	2.6	2.3	11.5
Perkin Elmer GSP Neonatal (U/dL blood)	64	0.6	0.1	0.8	0.0	2.1

Lot G1703

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	30	75.0	6.3	9.5	60.0	95.4
Perkin Elmer GSP Neonatal (U/dL blood)	197	3.9	0.4	0.6	2.4	6.0

Lot H1703

METHOD	N	Mean	Average Within Lab SD	All Lab SD	Min	Max
Astoria-Pacific 50 Hour Reagent Kit (µmol/L blood)	30	204.7	26.3	38.4	117.0	266.4
Perkin Elmer GSP Neonatal (U/dL blood)	198	16.3	1.2	2.8	6.8	29.7

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

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

2018 Quality Control Data Summaries of Statistical Analyses

IMMUNOREACTIVE TRYPsinOGEN (IRT ng/mL blood)

Lot A1709 – Assayed 18.3 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	240	17.7	2.1	2.9	-1.9	0.9
AutoDelfia	667	17.3	1.7	2.2	-2.1	1.0
PerkinElmer GSP Neonatal	359	17.6	1.3	1.5	-3.3	1.0
Zentech	30	34.7	4.8	7.2	51.3	0.8
Labsystems - FEIA	50	22.1	4.5	6.4	3.0	0.9

Lot B1709 – Assayed 63.7 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	240	57.7	5.7	8.8	-1.9	0.9
AutoDelfia	669	59.9	5.6	7.0	-2.1	1.0
PerkinElmer GSP Neonatal	380	60.8	4.7	5.8	-3.3	1.0
Zentech	30	126.3	10.1	23.8	51.3	0.8
Labsystems - FEIA	50	59.0	9.9	13.8	3.0	0.9

Lot C1709 – Assayed 132.9 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	240	119.1	10.8	19.2	-1.9	0.9
AutoDelfia	670	121.0	11.3	13.2	-2.1	1.0
PerkinElmer GSP Neonatal	370	122.1	9.0	10.7	-3.3	1.0
Zentech	30	189.5	16.4	16.4	51.3	0.8
Labsystems - FEIA	50	113.3	14.0	22.5	3.0	0.9

Lot D1709 – Assayed 227.1 ng/mL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Delfia	230	214.6	20.5	30.0	-1.9	0.9
AutoDelfia	669	219.4	20.3	25.7	-2.1	1.0
PerkinElmer GSP Neonatal	370	226.6	13.8	17.6	-3.3	1.0
Zentech	30	215.2	15.7	20.2	51.3	0.8
Labsystems - FEIA	50	206.5	27.6	40.8	3.0	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	639	219.2	25.0	52.9	229.8	0.7
Non-derivatized - MS/MS non-kit	150	238.4	23.2	55.7	252.6	0.7
Derivatized - MS/MS PE NeoGram Kit	40	223.8	19.5	50.5	234.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	709	249.9	18.8	41.4	262.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	197.2	22.9	44.9	203.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	185.9	21.4	45.0	194.5	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	205.5	18.8	50.9	215.5	0.6

Lot B1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	640	373.1	39.3	87.7	229.8	0.7
Non-derivatized - MS/MS non-kit	150	406.1	37.7	88.6	252.6	0.7
Derivatized - MS/MS PE NeoGram Kit	40	387.1	43.2	84.1	234.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	710	428.5	30.1	65.6	262.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	315.2	24.6	77.6	203.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	320.5	24.8	90.8	194.5	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	352.0	24.5	81.4	215.5	0.6

Lot C1715 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	637	518.6	51.2	121.6	229.8	0.7
Non-derivatized - MS/MS non-kit	150	556.1	58.1	135.0	252.6	0.7
Derivatized - MS/MS PE NeoGram Kit	40	540.4	50.4	117.7	234.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	710	601.4	42.7	90.2	262.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	449.6	36.2	106.2	203.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	453.4	35.7	120.4	194.5	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	480.7	31.8	106.1	215.5	0.6

Lot D1715 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	640	623.5	58.4	143.3	229.8	0.7
Non-derivatized - MS/MS non-kit	150	661.6	49.4	148.3	252.6	0.7
Derivatized - MS/MS PE NeoGram Kit	40	656.7	61.2	144.6	234.2	0.7
Non-derivatized - MS/MS PE NeoBase Kit	702	722.1	52.2	126.4	262.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	526.5	40.0	117.5	203.7	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	545.4	43.6	142.3	194.5	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	586.2	44.8	141.1	215.5	0.6

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	698	7.5	1.5	3.4	8.2	0.7
Non-derivatized - MS/MS non-kit	148	5.9	1.0	3.6	9.2	0.7
Derivatized - MS/MS PE NeoGram Kit	59	8.9	3.0	4.8	9.8	0.7
Non-derivatized - MS/MS PE NeoBase Kit	779	6.6	0.8	1.8	9.2	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	9.2	2.5	4.3	13.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	6.7	1.2	3.3	10.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	4.9	0.8	2.5	5.6	0.6

Lot B1715 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	698	70.6	8.9	23.8	8.2	0.7
Non-derivatized - MS/MS non-kit	150	74.9	6.9	22.8	9.2	0.7
Derivatized - MS/MS PE NeoGram Kit	60	78.4	9.6	14.4	9.8	0.7
Non-derivatized - MS/MS PE NeoBase Kit	779	79.4	5.1	9.7	9.2	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	83.8	8.0	16.0	13.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	83.3	6.7	19.7	10.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	58.5	5.0	20.4	5.6	0.6

Lot C1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	700	156.0	17.9	51.5	8.2	0.7
Non-derivatized - MS/MS non-kit	150	159.2	13.9	43.2	9.2	0.7
Derivatized - MS/MS PE NeoGram Kit	60	165.9	11.9	30.0	9.8	0.7
Non-derivatized - MS/MS PE NeoBase Kit	780	176.3	11.8	19.9	9.2	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	180.4	20.0	39.9	13.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	183.0	14.1	58.0	10.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	126.3	10.3	42.0	5.6	0.6

Lot D1715 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	700	204.6	22.9	70.5	8.2	0.7
Non-derivatized - MS/MS non-kit	150	204.4	17.3	52.5	9.2	0.7
Derivatized - MS/MS PE NeoGram Kit	60	221.7	14.6	42.0	9.8	0.7
Non-derivatized - MS/MS PE NeoBase Kit	779	224.3	14.0	24.9	9.2	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	221.1	22.8	44.4	13.8	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	227.6	16.7	69.5	10.8	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	169.5	14.6	55.2	5.6	0.6

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	735	10.8	1.6	2.5	11.2	0.7
Non-derivatized - MS/MS non-kit	219	12.2	2.0	3.4	13.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	13.0	2.1	3.0	11.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	844	11.3	1.3	1.7	12.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	98	12.7	1.4	2.0	13.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	11.0	1.3	1.6	11.6	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	10.9	1.3	1.6	12.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	12.6	1.4	2.4	14.1	0.7

Lot B1715 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	738	29.5	3.5	5.8	11.2	0.7
Non-derivatized - MS/MS non-kit	219	34.7	4.1	7.3	13.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	34.4	3.3	5.3	11.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	848	32.0	2.6	3.7	12.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	31.6	2.8	3.8	13.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	31.2	2.9	3.9	11.6	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	31.9	2.6	4.8	12.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	32.8	2.1	6.9	14.1	0.7

Lot C1715 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	739	85.1	10.1	17.9	11.2	0.7
Non-derivatized - MS/MS non-kit	218	99.3	11.1	18.3	13.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	97.7	5.9	13.6	11.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	847	94.5	6.5	10.2	12.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	91.3	9.7	13.4	13.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	90.5	7.6	8.9	11.6	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	91.8	5.8	14.5	12.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	85.8	5.0	12.7	14.1	0.7

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

Lot D1715 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	739	193.8	19.1	37.0	11.2	0.7
Non-derivatized - MS/MS non-kit	220	221.0	21.6	39.8	13.7	0.8
Derivatized - MS/MS PE NeoGram Kit	60	236.0	22.0	43.6	11.5	0.9
Non-derivatized - MS/MS PE NeoBase Kit	847	214.0	13.8	22.3	12.0	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	200.2	21.5	29.2	13.6	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	206.4	17.5	21.2	11.6	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	206.1	10.1	25.0	12.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	190.5	12.3	26.8	14.1	0.7

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	578	287.1	33.5	65.8	294.9	0.8
Non-derivatized - MS/MS non-kit	109	225.7	50.4	81.8	234.2	0.6
Derivatized - MS/MS PE NeoGram Kit	30	339.2	25.7	63.6	346.9	0.9
Non-derivatized - MS/MS PE NeoBase Kit	554	293.5	30.7	52.1	302.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	90	305.1	28.5	57.4	306.4	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	214.9	25.7	65.5	215.0	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	284.0	25.1	40.6	290.3	0.8

Lot B1715 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	579	527.3	58.2	115.5	294.9	0.8
Non-derivatized - MS/MS non-kit	110	412.6	56.6	126.9	234.2	0.6
Derivatized - MS/MS PE NeoGram Kit	30	632.1	35.2	119.2	346.9	0.9
Non-derivatized - MS/MS PE NeoBase Kit	557	547.0	48.5	93.7	302.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	90	490.2	35.8	108.4	306.4	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	377.9	34.2	117.0	215.0	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	521.3	34.6	66.5	290.3	0.8

Lot C1715 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	579	793.0	70.4	169.8	294.9	0.8
Non-derivatized - MS/MS non-kit	110	622.0	67.2	197.5	234.2	0.6
Derivatized - MS/MS PE NeoGram Kit	30	910.1	46.6	150.2	346.9	0.9
Non-derivatized - MS/MS PE NeoBase Kit	558	847.5	80.5	150.4	302.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	90	739.9	57.2	168.7	306.4	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	583.2	47.0	171.3	215.0	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	759.2	43.9	99.0	290.3	0.8

Lot D1715 – Enriched 900 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	580	981.5	94.4	217.9	294.9	0.8
Non-derivatized - MS/MS non-kit	110	755.9	91.9	239.2	234.2	0.6
Derivatized - MS/MS PE NeoGram Kit	30	1171.9	62.0	213.0	346.9	0.9
Non-derivatized - MS/MS PE NeoBase Kit	559	1031.8	90.6	185.3	302.6	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	90	886.1	56.8	202.9	306.4	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	99	724.6	55.2	212.5	215.0	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	964.7	51.4	166.2	290.3	0.8

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	756	82.8	9.0	15.5	90.1	0.7
Non-derivatized - MS/MS non-kit	290	97.3	7.5	16.0	105.4	0.8
Derivatized - MS/MS PE NeoGram Kit	60	87.6	6.7	9.4	90.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	98.3	6.8	11.9	104.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	99	86.9	13.7	24.6	95.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	94.6	6.2	16.0	102.3	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens Zentech	60	96.8	5.3	13.6	106.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	111.4	24.8	27.5	141.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	73.1	5.6	9.1	78.5	0.7

Lot B1715 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	759	161.9	15.5	27.3	90.1	0.7
Non-derivatized - MS/MS non-kit	290	182.2	16.0	29.8	105.4	0.8
Derivatized - MS/MS PE NeoGram Kit	60	174.2	14.2	19.9	90.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	850	182.0	11.6	20.3	104.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	149.8	15.3	22.0	95.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	172.8	8.8	23.2	102.3	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens Zentech	60	187.2	13.4	22.0	106.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	251.4	32.5	35.1	141.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	151.9	10.5	17.1	78.5	0.7

Lot C1715 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	759	284.9	25.5	51.4	90.1	0.7
Non-derivatized - MS/MS non-kit	290	305.8	22.0	47.4	105.4	0.8
Derivatized - MS/MS PE NeoGram Kit	60	307.3	23.4	30.5	90.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	310.5	21.2	34.1	104.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	274.3	24.1	36.7	95.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	128	286.5	14.8	35.3	102.3	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens Zentech	60	304.7	19.4	38.4	106.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	30	347.5	35.4	38.3	141.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	266.0	17.9	36.5	78.5	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 500 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	760	442.8	40.6	80.2	90.1	0.7
Non-derivatized - MS/MS non-kit	290	473.0	30.8	80.0	105.4	0.8
Derivatized - MS/MS PE NeoGram Kit	60	505.6	40.8	57.6	90.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	483.5	30.3	52.2	104.9	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	386.7	33.0	66.7	95.5	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	438.9	24.0	46.6	102.3	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	474.8	24.3	53.0	106.7	0.8
Zentech	30	525.3	49.5	59.1	141.0	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	432.7	31.1	71.6	78.5	0.7

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	736	15.7	2.5	3.4	16.2	0.7
Non-derivatized - MS/MS non-kit	280	14.0	1.7	2.8	14.0	0.7
Derivatized - MS/MS PE NeoGram Kit	49	16.0	1.9	2.0	14.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	865	12.9	1.2	2.0	12.2	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	100	14.3	2.6	5.5	15.0	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	10.4	1.2	2.0	8.5	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	13.2	0.7	1.6	13.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	14.8	1.6	3.0	14.9	0.7

Lot B1715 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	735	54.1	6.1	8.5	16.2	0.7
Non-derivatized - MS/MS non-kit	279	51.2	5.0	9.0	14.0	0.7
Derivatized - MS/MS PE NeoGram Kit	50	56.8	5.9	7.5	14.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	868	47.5	3.2	5.7	12.2	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	100	42.0	4.6	8.3	15.0	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	41.5	2.8	6.5	8.5	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	50.0	2.4	6.1	13.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	52.1	4.0	7.1	14.9	0.7

Lot C1715 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	739	126.4	12.1	19.2	16.2	0.7
Non-derivatized - MS/MS non-kit	278	119.5	10.2	19.2	14.0	0.7
Derivatized - MS/MS PE NeoGram Kit	50	133.7	11.7	15.5	14.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	867	116.1	7.6	13.7	12.2	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	100	101.9	11.4	21.0	15.0	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	102.4	6.1	16.4	8.5	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	116.6	6.9	13.4	13.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	121.9	7.9	16.4	14.9	0.7

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

Lot D1715 – Enriched 250 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	740	201.3	18.9	29.8	16.2	0.7
Non-derivatized - MS/MS non-kit	274	195.1	17.2	35.1	14.0	0.7
Derivatized - MS/MS PE NeoGram Kit	50	222.7	19.3	31.9	14.9	0.8
Non-derivatized - MS/MS PE NeoBase Kit	867	189.5	12.5	22.9	12.2	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	100	152.3	19.1	36.9	15.0	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	176.3	17.3	40.3	8.5	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	191.9	8.3	18.7	13.2	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	197.2	15.9	30.9	14.9	0.7

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	567	79.7	15.9	35.8	82.9	0.5
Non-derivatized - MS/MS non-kit	120	89.2	12.9	22.1	93.0	0.5
Non-derivatized - MS/MS PE NeoBase Kit	579	98.6	6.7	13.1	103.0	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	109.2	9.3	11.9	114.3	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	107.8	8.7	16.6	111.6	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	66.8	6.2	15.5	68.7	0.5

Lot B1715 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	565	140.7	28.3	65.6	82.9	0.5
Non-derivatized - MS/MS non-kit	120	153.1	16.5	35.1	93.0	0.5
Non-derivatized - MS/MS PE NeoBase Kit	579	176.9	11.2	22.7	103.0	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	187.5	16.3	21.0	114.3	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	185.6	11.9	29.3	111.6	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	122.0	11.9	20.8	68.7	0.5

Lot C1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	567	183.7	34.5	85.4	82.9	0.5
Non-derivatized - MS/MS non-kit	120	195.4	21.1	43.0	93.0	0.5
Non-derivatized - MS/MS PE NeoBase Kit	580	237.9	16.9	32.0	103.0	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	248.6	23.0	35.1	114.3	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	246.4	20.2	42.1	111.6	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	157.7	14.9	31.0	68.7	0.5

Lot D1715 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	565	237.6	38.0	103.1	82.9	0.5
Non-derivatized - MS/MS non-kit	120	251.3	25.5	57.5	93.0	0.5
Non-derivatized - MS/MS PE NeoBase Kit	580	302.8	19.0	41.3	103.0	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	310.0	29.5	42.8	114.3	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	100	313.4	26.3	61.1	111.6	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	213.0	21.8	39.9	68.7	0.5

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorometric Manual	68	49.7	9.0	18.4	53.0	1.1
PerkinElmer Neonatal Kit	268	35.1	8.7	21.1	37.0	0.7
Labsystems Diagnostics	94	30.9	4.3	23.0	26.4	0.9
Bio-Rad Quantase	40	45.1	17.6	19.5	48.5	1.0
PerkinElmer GSP Neonatal	49	25.1	7.5	15.9	28.5	0.8
Derivatized - MS/MS non-kit	778	33.0	3.7	6.4	35.7	0.8
Non-derivatized - MS/MS non-kit	328	34.6	3.4	5.7	37.5	0.9
Derivatized - MS/MS PE NeoGram Kit	60	37.1	3.4	5.1	38.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	879	32.6	2.7	4.6	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	100	36.1	4.1	7.8	40.5	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	36.0	2.5	5.4	39.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	31.7	1.9	3.4	35.4	0.8
Trimaris Neonatal	30	35.9	8.4	11.6	40.4	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	30.7	2.7	4.1	31.6	0.8

Lot B1715 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorometric Manual	70	164.1	12.9	22.9	53.0	1.1
PerkinElmer Neonatal Kit	270	105.4	14.9	48.4	37.0	0.7
Labsystems Diagnostics	100	101.9	12.6	55.8	26.4	0.9
Bio-Rad Quantase	40	154.7	18.9	18.9	48.5	1.0
PerkinElmer GSP Neonatal	60	110.6	13.6	57.3	28.5	0.8
Derivatized - MS/MS non-kit	778	118.5	11.3	21.2	35.7	0.8
Non-derivatized - MS/MS non-kit	329	127.4	9.6	18.2	37.5	0.9
Derivatized - MS/MS PE NeoGram Kit	60	133.0	10.6	18.1	38.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	889	119.6	7.7	12.8	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	100	117.0	10.6	31.0	40.5	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	128.0	6.5	15.2	39.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	120.4	9.1	12.0	35.4	0.8
Trimaris Neonatal	30	157.4	14.0	17.5	40.4	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	110.7	6.4	9.8	31.6	0.8

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

Lot C1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorometric Manual	70	288.4	18.4	36.5	53.0	1.1
PerkinElmer Neonatal Kit	270	185.4	20.0	81.5	37.0	0.7
Labsystems Diagnostics	100	208.2	27.0	115.1	26.4	0.9
Bio-Rad Quantase	40	247.1	30.8	48.0	48.5	1.0
PerkinElmer GSP Neonatal	60	208.2	18.4	105.0	28.5	0.8
Derivatized - MS/MS non-kit	780	213.2	19.5	39.0	35.7	0.8
Non-derivatized - MS/MS non-kit	325	226.4	16.1	29.2	37.5	0.9
Derivatized - MS/MS PE NeoGram Kit	60	234.7	17.9	28.2	38.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	890	215.7	13.9	24.0	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	100	215.5	17.1	55.8	40.5	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	225.2	12.1	22.3	39.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	210.8	15.2	25.7	35.4	0.8
Trimaris Neonatal	30	301.0	26.0	31.5	40.4	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	195.8	11.0	24.6	31.6	0.8

Lot D1715 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Fluorometric Manual	70	381.3	26.2	48.5	53.0	1.1
PerkinElmer Neonatal Kit	270	241.5	24.7	106.8	37.0	0.7
Labsystems Diagnostics	100	283.0	39.4	155.5	26.4	0.9
Bio-Rad Quantase	40	348.4	35.9	50.0	48.5	1.0
PerkinElmer GSP Neonatal	60	272.7	22.4	138.0	28.5	0.8
Derivatized - MS/MS non-kit	780	280.9	22.8	49.3	35.7	0.8
Non-derivatized - MS/MS non-kit	330	301.3	21.4	41.2	37.5	0.9
Derivatized - MS/MS PE NeoGram Kit	60	319.9	24.4	38.4	38.7	1.0
Non-derivatized - MS/MS PE NeoBase Kit	886	286.5	17.4	31.9	34.9	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	100	265.7	23.3	74.7	40.5	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	298.6	16.0	32.1	39.2	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	280.2	17.4	24.3	35.4	0.8
Trimaris Neonatal	30	388.7	31.8	35.9	40.4	1.2
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	268.9	20.3	43.7	31.6	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	229	0.7	0.2	0.4	0.7	0.5
Non-derivatized - MS/MS non-kit	99	0.9	0.3	1.2	0.9	0.4
Non-derivatized - MS/MS PE NeoBase Kit	519	0.5	0.1	0.3	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.5	0.1	0.4	0.5	0.3

Lot B1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	245	2.1	0.4	1.8	0.7	0.5
Non-derivatized - MS/MS non-kit	100	2.0	0.4	1.5	0.9	0.4
Non-derivatized - MS/MS PE NeoBase Kit	522	0.9	0.1	0.4	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.4	0.2	0.4	0.5	0.3

Lot C1715 – Enriched 7.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	245	4.7	1.0	5.1	0.7	0.5
Non-derivatized - MS/MS non-kit	100	3.7	0.5	2.2	0.9	0.4
Non-derivatized - MS/MS PE NeoBase Kit	526	1.9	0.3	0.6	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	90	3.0	0.4	0.7	0.5	0.3

Lot D1715 – Enriched 15 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	246	8.7	1.3	9.5	0.7	0.5
Non-derivatized - MS/MS non-kit	100	6.6	0.8	3.6	0.9	0.4
Non-derivatized - MS/MS PE NeoBase Kit	528	3.3	0.4	1.0	0.5	0.2
Derivatized - MS/MS Chromsystems MassChrom Kit	90	5.5	0.6	1.2	0.5	0.3

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	754	32.4	3.5	6.1	34.9	0.8
Non-derivatized - MS/MS non-kit	298	33.4	3.4	6.4	36.1	0.8
Derivatized - MS/MS PE NeoGram Kit	60	34.5	3.3	4.8	31.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	883	34.5	3.4	5.4	36.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	98	36.8	5.9	10.8	43.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	35.6	2.6	4.8	37.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	30.8	2.0	2.3	33.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	29.1	2.8	3.5	29.6	0.7

Lot B1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	757	183.3	17.9	31.3	34.9	0.8
Non-derivatized - MS/MS non-kit	298	189.5	15.2	30.0	36.1	0.8
Derivatized - MS/MS PE NeoGram Kit	60	187.3	14.3	21.0	31.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	890	197.4	13.1	21.9	36.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	193.0	15.7	37.5	43.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	203.8	11.9	29.5	37.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	184.0	11.2	17.3	33.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	172.7	12.3	16.1	29.6	0.7

Lot C1715 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	758	361.7	33.3	64.9	34.9	0.8
Non-derivatized - MS/MS non-kit	297	370.0	26.5	55.2	36.1	0.8
Derivatized - MS/MS PE NeoGram Kit	60	367.1	29.1	43.0	31.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	890	391.4	26.4	45.9	36.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	385.9	37.5	77.0	43.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	397.1	28.7	60.6	37.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	358.2	20.5	34.4	33.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	334.3	17.3	36.6	29.6	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 600 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	758	486.6	40.8	85.3	34.9	0.8
Non-derivatized - MS/MS non-kit	300	500.3	35.0	78.9	36.1	0.8
Derivatized - MS/MS PE NeoGram Kit	60	522.2	50.1	65.2	31.3	0.8
Non-derivatized - MS/MS PE NeoBase Kit	888	529.2	33.5	61.6	36.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	491.6	49.4	109.8	43.3	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	543.2	32.1	76.1	37.5	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	486.2	21.7	36.6	33.7	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	466.7	39.7	71.3	29.6	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	692	92.0	14.2	23.6	93.6	0.7
Non-derivatized - MS/MS non-kit	220	78.3	5.8	11.0	82.4	0.7
Derivatized - MS/MS PE NeoGram Kit	60	85.1	11.2	14.3	85.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	848	85.5	7.1	12.3	87.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	84.5	14.0	29.3	88.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	66.5	5.1	13.7	68.2	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	85.2	6.8	13.1	91.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	69.0	6.5	13.8	71.0	0.7

Lot B1715 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	695	232.5	29.3	46.4	93.6	0.7
Non-derivatized - MS/MS non-kit	220	226.7	18.4	36.8	82.4	0.7
Derivatized - MS/MS PE NeoGram Kit	60	225.4	33.2	44.0	85.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	850	250.9	19.3	34.1	87.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	213.9	19.1	83.6	88.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	189.7	11.7	34.4	68.2	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	257.2	28.0	39.5	91.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	203.1	13.9	41.3	71.0	0.7

Lot C1715 – Enriched 350 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	698	355.6	45.6	70.4	93.6	0.7
Non-derivatized - MS/MS non-kit	220	346.7	22.6	57.2	82.4	0.7
Derivatized - MS/MS PE NeoGram Kit	60	335.4	36.1	58.4	85.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	850	392.6	30.2	52.6	87.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	336.4	32.4	127.4	88.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	295.9	18.2	48.5	68.2	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	386.2	33.2	60.5	91.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	313.6	23.6	61.7	71.0	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 500 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	697	442.9	52.6	86.1	93.6	0.7
Non-derivatized - MS/MS non-kit	220	433.1	30.4	83.1	82.4	0.7
Derivatized - MS/MS PE NeoGram Kit	60	435.9	51.6	86.3	85.5	0.7
Non-derivatized - MS/MS PE NeoBase Kit	848	496.6	36.6	64.8	87.4	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	100	401.2	32.0	159.5	88.0	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	371.6	27.7	61.5	68.2	0.6
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	486.1	41.3	67.7	91.2	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	398.4	28.7	80.6	71.0	0.7

2018 Quality Control Data Summaries of Statistical Analyses

TOTAL GALACTOSE (TGal mg/dL blood)

Lot A1705 – Enriched 5 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Siemens Healthcare Diagnostics	40	5.9	0.3	0.4	2.3	0.8
Fluorometric Manual	140	5.4	0.9	1.4	0.5	1.0
Colorimetric	40	6.4	1.4	1.5	-0.4	1.3
PerkinElmer Neonatal Kit	309	5.4	0.8	1.0	1.4	0.8
Labsystems Diagnostics	70	9.2	1.5	8.5	4.6	0.8
Bio-Rad Quantase	120	6.6	1.1	1.6	-0.1	1.3
Interscientific Enzyme	30	5.4	0.6	1.1	0.8	0.9
PerkinElmer GSP Neonatal	209	6.1	0.6	0.9	1.2	1.0
Astoria-Pacific 50 Hour Reagent Kit	40	7.0	0.6	0.9	2.2	1.0
TecnoSuma UMTEST	40	7.3	1.2	1.5	0.9	1.3
Zentech	40	4.8	1.4	2.4	1.0	1.1

Lot B1705 – Enriched 10 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Siemens Healthcare Diagnostics	40	11.0	0.5	0.7	2.3	0.8
Fluorometric Manual	139	10.3	1.3	1.9	0.5	1.0
Colorimetric	40	11.6	1.7	2.7	-0.4	1.3
PerkinElmer Neonatal Kit	308	9.7	1.0	1.3	1.4	0.8
Labsystems Diagnostics	68	12.6	1.6	3.7	4.6	0.8
Bio-Rad Quantase	120	13.1	1.7	2.4	-0.1	1.3
Interscientific Enzyme	30	10.1	1.2	1.7	0.8	0.9
PerkinElmer GSP Neonatal	208	10.7	0.9	1.2	1.2	1.0
Astoria-Pacific 50 Hour Reagent Kit	40	12.0	1.0	1.6	2.2	1.0
TecnoSuma UMTEST	40	13.6	2.8	2.9	0.9	1.3
Zentech	40	14.3	1.1	2.7	1.0	1.1

Lot C1705 – Enriched 30 mg/dL blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Siemens Healthcare Diagnostics	40	26.5	1.3	6.2	2.3	0.8
Fluorometric Manual	140	29.8	2.4	4.5	0.5	1.0
Colorimetric	40	37.6	5.6	10.1	-0.4	1.3
PerkinElmer Neonatal Kit	306	25.9	2.1	3.0	1.4	0.8
Labsystems Diagnostics	70	30.1	3.8	14.3	4.6	0.8
Bio-Rad Quantase	120	39.6	5.7	7.7	-0.1	1.3
Interscientific Enzyme	30	28.6	2.8	3.4	0.8	0.9
PerkinElmer GSP Neonatal	208	29.9	3.6	5.0	1.2	1.0
Astoria-Pacific 50 Hour Reagent Kit	40	31.1	2.2	3.3	2.2	1.0
TecnoSuma UMTEST	40	39.1	4.2	5.0	0.9	1.3
Zentech	40	33.8	3.2	6.7	1.0	1.1

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	788	16.20	1.75	3.42	15.82	1.4
Non-derivatized - MS/MS non-kit	220	14.26	1.34	2.56	14.19	1.0
Derivatized - MS/MS PE NeoGram Kit	60	17.86	1.58	4.10	17.33	1.6
Non-derivatized - MS/MS PE NeoBase Kit	847	13.20	1.09	1.93	12.97	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	108	13.10	1.55	4.34	13.05	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	11.06	1.05	2.51	10.84	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	13.94	0.58	2.00	14.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	15.07	1.72	2.26	14.55	1.3

Lot B1715 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	788	29.05	3.16	5.66	15.82	1.4
Non-derivatized - MS/MS non-kit	220	24.59	2.30	4.21	14.19	1.0
Derivatized - MS/MS PE NeoGram Kit	60	33.41	3.11	7.84	17.33	1.6
Non-derivatized - MS/MS PE NeoBase Kit	845	22.36	1.64	3.05	12.97	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	23.09	2.28	5.83	13.05	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	19.12	1.39	4.11	10.84	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	24.59	1.61	3.51	14.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	26.97	2.49	4.21	14.55	1.3

Lot C1715 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	788	42.87	4.70	8.50	15.82	1.4
Non-derivatized - MS/MS non-kit	220	34.69	3.00	6.33	14.19	1.0
Derivatized - MS/MS PE NeoGram Kit	60	48.73	3.49	10.40	17.33	1.6
Non-derivatized - MS/MS PE NeoBase Kit	850	32.23	2.31	4.23	12.97	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	108	33.68	3.57	8.34	13.05	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	27.14	2.11	5.74	10.84	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	34.30	2.31	5.11	14.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	38.57	2.33	3.37	14.55	1.3

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	789	57.11	5.65	10.92	15.82	1.4
Non-derivatized - MS/MS non-kit	220	45.51	4.08	8.68	14.19	1.0
Derivatized - MS/MS PE NeoGram Kit	60	67.06	5.90	15.18	17.33	1.6
Non-derivatized - MS/MS PE NeoBase Kit	850	42.20	3.05	5.52	12.97	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	43.62	4.25	10.69	13.05	1.0
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	36.33	3.02	7.88	10.84	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	44.88	2.32	5.72	14.05	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	53.19	4.26	6.47	14.55	1.3

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	743	11.84	1.51	3.42	11.88	0.9
Non-derivatized - MS/MS non-kit	206	10.38	0.85	3.65	10.47	1.0
Derivatized - MS/MS PE NeoGram Kit	50	11.63	0.82	2.29	11.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	836	8.68	0.61	1.16	8.64	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	109	9.88	1.00	2.05	9.93	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	7.28	0.50	1.27	7.19	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	10.51	0.58	1.62	10.58	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	8.88	0.81	1.47	8.83	0.8

Lot B1715 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	740	20.76	2.37	5.12	11.88	0.9
Non-derivatized - MS/MS non-kit	203	20.29	2.05	6.51	10.47	1.0
Derivatized - MS/MS PE NeoGram Kit	50	18.48	1.06	2.79	11.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	835	16.93	1.07	2.15	8.64	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	17.65	1.40	2.70	9.93	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	14.28	0.95	2.58	7.19	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	20.92	1.46	3.47	10.58	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	16.54	1.09	2.12	8.83	0.8

Lot C1715 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	746	29.92	3.11	6.76	11.88	0.9
Non-derivatized - MS/MS non-kit	205	30.13	2.23	9.66	10.47	1.0
Derivatized - MS/MS PE NeoGram Kit	50	24.40	1.23	2.79	11.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	836	25.67	1.61	2.86	8.64	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	25.95	1.92	3.14	9.93	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	22.08	1.20	3.52	7.19	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	30.93	1.88	3.37	10.58	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	23.96	1.25	3.60	8.83	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 30 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	742	38.52	3.95	8.67	11.88	0.9
Non-derivatized - MS/MS non-kit	206	39.65	2.74	11.68	10.47	1.0
Derivatized - MS/MS PE NeoGram Kit	50	31.48	1.93	3.25	11.67	0.7
Non-derivatized - MS/MS PE NeoBase Kit	836	33.85	2.18	3.84	8.64	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	33.22	2.89	4.51	9.93	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	29.13	1.77	4.80	7.19	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	41.20	2.39	5.99	10.58	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	31.97	1.93	5.64	8.83	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	781	1.00	0.15	0.26	1.01	0.9
Non-derivatized - MS/MS non-kit	220	0.94	0.10	0.15	1.01	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.83	0.11	0.14	0.77	0.7
Non-derivatized - MS/MS PE NeoBase Kit	853	0.83	0.07	0.12	0.82	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.80	0.10	0.20	0.84	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.71	0.06	0.11	0.70	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.94	0.05	0.10	0.95	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.85	0.09	0.11	0.78	0.9

Lot B1715 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	786	4.48	0.60	1.00	1.01	0.9
Non-derivatized - MS/MS non-kit	219	4.47	0.45	0.66	1.01	0.9
Derivatized - MS/MS PE NeoGram Kit	60	3.72	0.29	0.50	0.77	0.7
Non-derivatized - MS/MS PE NeoBase Kit	859	3.80	0.25	0.46	0.82	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	3.59	0.34	0.61	0.84	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	3.35	0.22	0.54	0.70	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.51	0.24	0.47	0.95	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	4.16	0.36	0.59	0.78	0.9

Lot C1715 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	789	7.98	0.96	1.60	1.01	0.9
Non-derivatized - MS/MS non-kit	220	7.81	0.74	1.16	1.01	0.9
Derivatized - MS/MS PE NeoGram Kit	60	6.58	0.51	0.85	0.77	0.7
Non-derivatized - MS/MS PE NeoBase Kit	860	6.89	0.47	0.77	0.82	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	6.67	0.72	1.12	0.84	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	6.10	0.39	0.70	0.70	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	7.98	0.48	0.66	0.95	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	7.58	0.55	1.07	0.78	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	786	11.41	1.34	2.49	1.01	0.9
Non-derivatized - MS/MS non-kit	220	11.10	0.90	1.54	1.01	0.9
Derivatized - MS/MS PE NeoGram Kit	60	9.79	0.98	1.34	0.77	0.7
Non-derivatized - MS/MS PE NeoBase Kit	857	9.84	0.61	1.11	0.82	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	9.13	0.89	1.67	0.84	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	8.75	0.57	1.12	0.70	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	11.53	0.61	1.01	0.95	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	11.17	0.81	1.97	0.78	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	695	0.04	0.02	0.05	0.05	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.04	0.02	0.02	0.05	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	98	0.04	0.02	0.03	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.01	0.01	0.01	0.01	0.4

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	708	0.35	0.06	0.15	0.05	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.65	0.08	0.11	0.05	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.41	0.06	0.18	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.22	0.03	0.05	0.01	0.4

Lot C1715 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	702	0.91	0.14	0.36	0.05	0.6
Derivatized - MS/MS PE NeoGram Kit	60	1.85	0.19	0.24	0.05	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	100	1.13	0.17	0.54	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.66	0.07	0.17	0.01	0.4

Lot D1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	701	1.74	0.25	0.70	0.05	0.6
Derivatized - MS/MS PE NeoGram Kit	60	3.65	0.29	0.57	0.05	1.2
Derivatized - MS/MS Chromsystems MassChrom Kit	100	2.18	0.28	1.11	0.05	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.30	0.16	0.38	0.01	0.4

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Non-derivatized - MS/MS non-kit	130	0.08	0.03	0.06	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	708	0.06	0.01	0.03	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	0.09	0.02	0.11	0.08	0.6

Lot B1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Non-derivatized - MS/MS non-kit	130	0.57	0.09	0.38	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	704	0.40	0.04	0.18	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	0.74	0.09	0.84	0.08	0.6

Lot C1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Non-derivatized - MS/MS non-kit	130	1.15	0.17	0.74	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	705	0.85	0.09	0.43	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	1.53	0.17	1.73	0.08	0.6

Lot D1715 – Enriched 5.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Non-derivatized - MS/MS non-kit	130	2.51	0.36	1.59	0.09	0.4
Non-derivatized - MS/MS PE NeoBase Kit	704	1.86	0.17	0.92	0.06	0.3
Non-derivatized - MS/MS Chromsystems MassChrom Kit	40	3.49	0.36	3.91	0.08	0.6

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	750	0.13	0.04	0.09	0.12	0.8
Non-derivatized - MS/MS non-kit	197	0.09	0.02	0.03	0.13	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.10	0.03	0.03	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	841	0.10	0.01	0.02	0.09	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.11	0.04	0.05	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.08	0.01	0.02	0.07	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.10	0.01	0.01	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.07	0.01	0.02	0.05	0.8

Lot B1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	755	0.94	0.13	0.23	0.12	0.8
Non-derivatized - MS/MS non-kit	200	0.94	0.09	0.14	0.13	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.81	0.09	0.13	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	0.83	0.06	0.12	0.09	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.71	0.10	0.15	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.75	0.05	0.13	0.07	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.95	0.10	0.16	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.81	0.08	0.10	0.05	0.8

Lot C1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	758	2.61	0.33	0.53	0.12	0.8
Non-derivatized - MS/MS non-kit	200	2.62	0.22	0.35	0.13	0.8
Derivatized - MS/MS PE NeoGram Kit	60	2.31	0.27	0.32	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	846	2.41	0.16	0.27	0.09	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.15	0.27	0.38	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	2.25	0.15	0.28	0.07	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	2.82	0.22	0.27	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	2.37	0.19	0.32	0.05	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	758	4.25	0.47	0.93	0.12	0.8
Non-derivatized - MS/MS non-kit	199	4.10	0.30	0.52	0.13	0.8
Derivatized - MS/MS PE NeoGram Kit	60	3.86	0.58	0.69	0.08	0.8
Non-derivatized - MS/MS PE NeoBase Kit	846	3.93	0.27	0.46	0.09	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	3.45	0.42	0.66	0.09	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	3.60	0.23	0.46	0.07	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	4.73	0.42	0.70	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	3.97	0.27	0.73	0.05	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	665	0.09	0.03	0.05	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.08	0.03	0.03	0.08	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	88	0.07	0.03	0.03	0.08	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	56	0.05	0.01	0.01	0.04	0.5

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	667	0.44	0.08	0.16	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.42	0.05	0.07	0.08	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.36	0.03	0.09	0.08	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.30	0.04	0.04	0.04	0.5

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	668	0.82	0.13	0.27	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	0.83	0.10	0.12	0.08	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	0.67	0.08	0.16	0.08	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.56	0.04	0.08	0.04	0.5

Lot D1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	663	1.84	0.23	0.65	0.09	0.7
Derivatized - MS/MS PE NeoGram Kit	50	1.86	0.20	0.24	0.08	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	90	1.50	0.11	0.36	0.08	0.6
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.34	0.12	0.28	0.04	0.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	769	0.08	0.02	0.04	0.09	0.9
Non-derivatized - MS/MS non-kit	258	0.06	0.01	0.02	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.07	0.03	0.03	0.06	0.8
Non-derivatized - MS/MS PE NeoBase Kit	880	0.06	0.01	0.01	0.05	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	102	0.08	0.02	0.03	0.09	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.05	0.01	0.02	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.07	0.01	0.03	0.07	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	54	0.06	0.01	0.02	0.05	0.9

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	788	0.51	0.07	0.12	0.09	0.9
Non-derivatized - MS/MS non-kit	260	0.50	0.04	0.08	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.45	0.05	0.08	0.06	0.8
Non-derivatized - MS/MS PE NeoBase Kit	877	0.44	0.03	0.06	0.05	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.47	0.05	0.07	0.09	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	0.43	0.07	0.11	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.53	0.04	0.05	0.07	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.47	0.05	0.06	0.05	0.9

Lot C1715 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	786	1.37	0.15	0.27	0.09	0.9
Non-derivatized - MS/MS non-kit	260	1.36	0.10	0.17	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	60	1.24	0.13	0.22	0.06	0.8
Non-derivatized - MS/MS PE NeoBase Kit	877	1.24	0.08	0.15	0.05	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.26	0.16	0.21	0.09	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.18	0.10	0.21	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.44	0.09	0.15	0.07	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.30	0.12	0.16	0.05	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	788	2.63	0.30	0.55	0.09	0.9
Non-derivatized - MS/MS non-kit	260	2.64	0.18	0.38	0.07	0.9
Derivatized - MS/MS PE NeoGram Kit	60	2.47	0.25	0.41	0.06	0.8
Non-derivatized - MS/MS PE NeoBase Kit	875	2.43	0.16	0.28	0.05	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.39	0.29	0.42	0.09	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.26	0.19	0.38	0.06	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.84	0.16	0.21	0.07	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	2.61	0.23	0.45	0.05	0.9

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	764	0.03	0.01	0.03	0.03	0.7
Non-derivatized - MS/MS non-kit	253	0.04	0.01	0.03	0.06	0.8
Derivatized - MS/MS PE NeoGram Kit	58	0.03	0.02	0.02	0.03	1.0
Non-derivatized - MS/MS PE NeoBase Kit	739	0.05	0.02	0.03	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	109	0.07	0.04	0.08	0.10	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	0.07	0.04	0.07	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.05	0.01	0.02	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	40	0.03	0.01	0.02	0.01	1.5

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	777	0.36	0.06	0.14	0.03	0.7
Non-derivatized - MS/MS non-kit	260	0.49	0.06	0.17	0.06	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.52	0.05	0.08	0.03	1.0
Non-derivatized - MS/MS PE NeoBase Kit	749	0.52	0.05	0.08	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.66	0.11	0.17	0.10	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.58	0.09	0.14	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.51	0.03	0.06	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.79	0.09	0.23	0.01	1.5

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	779	0.69	0.11	0.27	0.03	0.7
Non-derivatized - MS/MS non-kit	260	0.90	0.11	0.30	0.06	0.8
Derivatized - MS/MS PE NeoGram Kit	60	1.01	0.11	0.16	0.03	1.0
Non-derivatized - MS/MS PE NeoBase Kit	746	1.02	0.09	0.15	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.35	0.18	0.36	0.10	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	1.14	0.11	0.25	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.98	0.07	0.12	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	1.52	0.15	0.48	0.01	1.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	780	1.67	0.22	0.65	0.03	0.7
Non-derivatized - MS/MS non-kit	260	2.14	0.20	0.70	0.06	0.8
Derivatized - MS/MS PE NeoGram Kit	60	2.49	0.26	0.34	0.03	1.0
Non-derivatized - MS/MS PE NeoBase Kit	747	2.42	0.21	0.40	0.05	1.0
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.99	0.39	0.61	0.10	1.2
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	2.77	0.30	0.63	0.05	1.1
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.37	0.15	0.31	0.05	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	3.85	0.38	1.14	0.01	1.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	778	0.46	0.06	0.11	0.45	0.7
Non-derivatized - MS/MS non-kit	200	0.65	0.06	0.15	0.65	0.7
Derivatized - MS/MS PE NeoGram Kit	59	0.44	0.07	0.09	0.41	0.7
Non-derivatized - MS/MS PE NeoBase Kit	638	0.51	0.04	0.17	0.51	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.43	0.06	0.09	0.42	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.40	0.05	0.20	0.39	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.72	0.03	0.08	0.71	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.32	0.03	0.07	0.30	0.5

Lot B1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	778	1.15	0.14	0.25	0.45	0.7
Non-derivatized - MS/MS non-kit	200	1.35	0.12	0.30	0.65	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.09	0.13	0.18	0.41	0.7
Non-derivatized - MS/MS PE NeoBase Kit	636	0.98	0.07	0.31	0.51	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.97	0.11	0.25	0.42	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	0.82	0.08	0.36	0.39	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.54	0.08	0.15	0.71	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.82	0.10	0.19	0.30	0.5

Lot C1715 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	776	1.86	0.20	0.38	0.45	0.7
Non-derivatized - MS/MS non-kit	200	2.04	0.17	0.44	0.65	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.78	0.22	0.31	0.41	0.7
Non-derivatized - MS/MS PE NeoBase Kit	636	1.46	0.10	0.45	0.51	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.57	0.21	0.39	0.42	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.23	0.09	0.47	0.39	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.36	0.15	0.36	0.71	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.33	0.13	0.29	0.30	0.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	780	2.60	0.27	0.54	0.45	0.7
Non-derivatized - MS/MS non-kit	200	2.72	0.22	0.59	0.65	0.7
Derivatized - MS/MS PE NeoGram Kit	60	2.54	0.37	0.52	0.41	0.7
Non-derivatized - MS/MS PE NeoBase Kit	633	1.94	0.17	0.66	0.51	0.5
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.13	0.24	0.62	0.42	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	70	1.72	0.12	0.71	0.39	0.4
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	3.23	0.16	0.41	0.71	0.8
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.92	0.20	0.53	0.30	0.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	749	0.04	0.02	0.04	0.05	0.7
Non-derivatized - MS/MS non-kit	196	0.01	0.01	0.02	0.03	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.03	0.02	0.02	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	866	0.01	0.01	0.01	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.05	0.02	0.03	0.07	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.01	0.00	0.00	0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.01	0.00	0.00	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	49	0.01	0.01	0.01	0.03	0.6

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	764	0.41	0.06	0.13	0.05	0.7
Non-derivatized - MS/MS non-kit	200	0.42	0.05	0.10	0.03	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.37	0.08	0.08	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	879	0.38	0.03	0.05	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.36	0.05	0.07	0.07	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.36	0.03	0.06	0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.32	0.05	0.05	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.32	0.03	0.04	0.03	0.6

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	767	0.82	0.11	0.23	0.05	0.7
Non-derivatized - MS/MS non-kit	200	0.82	0.08	0.18	0.03	0.8
Derivatized - MS/MS PE NeoGram Kit	60	0.65	0.08	0.11	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	876	0.76	0.05	0.09	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	109	0.64	0.06	0.09	0.07	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.72	0.04	0.08	0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	0.65	0.07	0.09	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.62	0.05	0.06	0.03	0.6

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	765	1.89	0.24	0.49	0.05	0.7
Non-derivatized - MS/MS non-kit	200	1.95	0.19	0.45	0.03	0.8
Derivatized - MS/MS PE NeoGram Kit	60	1.49	0.16	0.23	0.06	0.6
Non-derivatized - MS/MS PE NeoBase Kit	876	1.82	0.11	0.21	0.02	0.7
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.45	0.14	0.23	0.07	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	1.76	0.13	0.23	0.01	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	50	1.65	0.17	0.28	0.00	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.47	0.11	0.17	0.03	0.6

2018 Quality Control Data Summaries of Statistical Analyses

OCTANOYLCARNITINE (C8 µmol/L blood)

Lot A1715 – Nonenriched 0 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	772	0.03	0.02	0.03	0.04	0.9
Non-derivatized - MS/MS non-kit	258	0.02	0.01	0.02	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.03	0.02	0.02	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	855	0.01	0.01	0.01	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	107	0.03	0.02	0.03	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.02	0.01	0.01	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.01	0.00	0.00	0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.01	0.01	0.01	0.00	0.7

Lot B1715 – Enriched 0.5 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	784	0.49	0.07	0.11	0.04	0.9
Non-derivatized - MS/MS non-kit	259	0.48	0.05	0.11	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.42	0.06	0.07	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	879	0.42	0.03	0.05	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.38	0.05	0.07	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.37	0.04	0.08	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.47	0.04	0.05	0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.35	0.04	0.05	0.00	0.7

Lot C1715 – Enriched 1 µmol/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	784	1.00	0.13	0.21	0.04	0.9
Non-derivatized - MS/MS non-kit	259	0.97	0.09	0.21	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.88	0.12	0.13	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	877	0.87	0.06	0.10	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.77	0.09	0.12	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	0.79	0.06	0.18	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.95	0.07	0.08	0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.73	0.05	0.06	0.00	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	785	2.34	0.29	0.47	0.04	0.9
Non-derivatized - MS/MS non-kit	260	2.33	0.19	0.50	0.03	0.9
Derivatized - MS/MS PE NeoGram Kit	60	2.12	0.27	0.33	0.02	0.8
Non-derivatized - MS/MS PE NeoBase Kit	875	2.16	0.15	0.24	0.01	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.77	0.24	0.31	0.04	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	130	1.92	0.12	0.34	0.01	0.8
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.35	0.15	0.24	0.01	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.83	0.15	0.23	0.00	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	742	0.03	0.02	0.03	0.03	1.0
Non-derivatized - MS/MS non-kit	245	0.03	0.01	0.03	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.03	0.02	0.02	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	856	0.02	0.01	0.01	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.02	0.01	0.03	0.03	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	118	0.02	0.02	0.02	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.02	0.01	0.01	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.01	0.01	0.01	-0.01	0.7

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	757	0.52	0.08	0.14	0.03	1.0
Non-derivatized - MS/MS non-kit	248	0.55	0.07	0.14	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.39	0.06	0.08	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	859	0.43	0.04	0.07	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	109	0.28	0.04	0.08	0.03	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	0.40	0.04	0.09	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.55	0.06	0.11	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.37	0.04	0.06	-0.01	0.7

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	758	0.97	0.16	0.28	0.03	1.0
Non-derivatized - MS/MS non-kit	247	0.97	0.10	0.22	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	60	0.74	0.07	0.10	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	857	0.80	0.06	0.11	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.56	0.09	0.22	0.03	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	119	0.74	0.06	0.16	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.00	0.08	0.18	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.67	0.05	0.07	-0.01	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	759	2.42	0.36	0.66	0.03	1.0
Non-derivatized - MS/MS non-kit	249	2.46	0.25	0.50	0.04	1.0
Derivatized - MS/MS PE NeoGram Kit	60	1.91	0.22	0.31	0.01	0.8
Non-derivatized - MS/MS PE NeoBase Kit	865	2.08	0.16	0.27	0.01	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.31	0.16	0.44	0.03	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	120	1.88	0.14	0.36	0.02	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.62	0.20	0.45	0.01	1.0
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.80	0.14	0.25	-0.01	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	725	0.04	0.02	0.03	0.03	1.0
Non-derivatized - MS/MS non-kit	205	0.01	0.01	0.01	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	59	0.04	0.02	0.02	0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	792	0.01	0.01	0.01	0.00	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.05	0.02	0.04	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.01	0.00	0.00	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.01	0.00	0.01	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	54	0.02	0.01	0.01	0.01	0.9

Lot B1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	734	1.02	0.15	0.27	0.03	1.0
Non-derivatized - MS/MS non-kit	206	1.14	0.13	0.34	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	60	0.99	0.13	0.15	0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	809	0.92	0.07	0.12	0.00	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.85	0.10	0.17	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.83	0.05	0.13	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.08	0.10	0.17	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.88	0.08	0.12	0.01	0.9

Lot C1715 – Enriched 2 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	734	2.06	0.29	0.54	0.03	1.0
Non-derivatized - MS/MS non-kit	207	2.26	0.24	0.68	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	60	2.01	0.20	0.30	0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	808	1.90	0.15	0.23	0.00	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.69	0.18	0.35	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	1.70	0.11	0.25	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.10	0.16	0.25	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.75	0.11	0.17	0.01	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	737	3.06	0.44	0.82	0.03	1.0
Non-derivatized - MS/MS non-kit	207	3.33	0.33	0.96	0.02	1.1
Derivatized - MS/MS PE NeoGram Kit	60	3.05	0.35	0.42	0.01	1.0
Non-derivatized - MS/MS PE NeoBase Kit	807	2.83	0.21	0.32	0.00	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.49	0.24	0.47	0.04	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	2.56	0.18	0.36	-0.01	0.9
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	3.18	0.22	0.47	0.01	1.1
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	2.66	0.19	0.38	0.01	0.9

2018 Quality Control Data Summaries of Statistical Analyses

MYRISTOYLCARNITINE (C14 $\mu\text{mol/L}$ blood)

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	764	0.06	0.02	0.03	0.07	0.9
Non-derivatized - MS/MS non-kit	205	0.05	0.01	0.03	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.06	0.03	0.03	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	837	0.04	0.01	0.01	0.04	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.06	0.02	0.03	0.07	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.03	0.00	0.01	0.04	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.05	0.01	0.01	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.04	0.01	0.01	0.03	0.7

Lot B1715 – Enriched 0.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	778	0.51	0.08	0.12	0.07	0.9
Non-derivatized - MS/MS non-kit	209	0.52	0.06	0.10	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	60	0.47	0.07	0.08	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	828	0.45	0.04	0.05	0.04	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.40	0.05	0.08	0.07	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	0.41	0.03	0.07	0.04	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.53	0.04	0.08	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	59	0.35	0.03	0.06	0.03	0.7

Lot C1715 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	771	1.40	0.18	0.30	0.07	0.9
Non-derivatized - MS/MS non-kit	210	1.44	0.13	0.26	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	60	1.34	0.13	0.18	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	826	1.29	0.10	0.13	0.04	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.10	0.15	0.25	0.07	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	1.15	0.08	0.18	0.04	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.43	0.11	0.21	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.99	0.06	0.13	0.03	0.7

2018 Quality Control Data Summaries of Statistical Analyses

MYRISTOYLCARNITINE (C14 $\mu\text{mol/L}$ blood) (cont.)

Lot D1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	774	2.71	0.34	0.53	0.07	0.9
Non-derivatized - MS/MS non-kit	210	2.79	0.26	0.51	0.06	0.9
Derivatized - MS/MS PE NeoGram Kit	60	2.66	0.31	0.40	0.05	0.9
Non-derivatized - MS/MS PE NeoBase Kit	828	2.53	0.21	0.29	0.04	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.07	0.23	0.42	0.07	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	2.25	0.17	0.32	0.04	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	2.79	0.18	0.34	0.06	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.99	0.15	0.34	0.03	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	796	0.81	0.12	0.18	0.81	0.9
Non-derivatized - MS/MS non-kit	216	0.79	0.08	0.14	0.83	0.9
Derivatized - MS/MS PE NeoGram Kit	59	0.73	0.09	0.13	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	0.74	0.07	0.11	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	108	0.74	0.11	0.18	0.72	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	0.67	0.06	0.11	0.64	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.78	0.04	0.09	0.85	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.89	0.11	0.14	0.82	1.0

Lot B1715 – Enriched 4 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	796	4.22	0.51	0.69	0.81	0.9
Non-derivatized - MS/MS non-kit	220	4.43	0.38	0.70	0.83	0.9
Derivatized - MS/MS PE NeoGram Kit	60	3.95	0.36	0.52	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	4.01	0.28	0.46	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	109	3.74	0.35	0.44	0.72	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	109	3.61	0.28	0.47	0.64	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.46	0.31	0.65	0.85	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	4.70	0.61	0.78	0.82	1.0

Lot C1715 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	797	7.64	0.82	1.26	0.81	0.9
Non-derivatized - MS/MS non-kit	220	7.91	0.64	1.09	0.83	0.9
Derivatized - MS/MS PE NeoGram Kit	60	7.02	0.53	0.96	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	849	7.36	0.55	0.80	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	6.91	0.68	0.86	0.72	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	6.48	0.52	0.93	0.64	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	7.80	0.54	1.07	0.85	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	8.51	0.74	1.33	0.82	1.0

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 12 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	797	11.06	1.13	1.84	0.81	0.9
Non-derivatized - MS/MS non-kit	220	11.41	0.90	1.79	0.83	0.9
Derivatized - MS/MS PE NeoGram Kit	60	10.56	0.94	1.42	0.68	0.8
Non-derivatized - MS/MS PE NeoBase Kit	847	10.77	0.77	1.21	0.70	0.8
Derivatized - MS/MS Chromsystems MassChrom Kit	110	9.92	0.99	1.18	0.72	0.8
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	9.58	0.76	1.41	0.64	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	11.31	0.63	1.34	0.85	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	12.66	1.13	2.25	0.82	1.0

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	730	0.02	0.01	0.02	0.02	0.7
Non-derivatized - MS/MS non-kit	210	0.01	0.00	0.01	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	59	0.02	0.01	0.02	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	833	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.02	0.01	0.02	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.00	0.00	0.00	0.01	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.00	0.00	0.00	0.01	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	49	0.01	0.00	0.01	0.01	0.7

Lot B1715 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	746	0.21	0.04	0.07	0.02	0.7
Non-derivatized - MS/MS non-kit	210	0.20	0.03	0.06	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	60	0.18	0.03	0.04	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	839	0.17	0.02	0.05	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.18	0.03	0.07	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.13	0.01	0.05	0.01	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.18	0.02	0.03	0.01	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.18	0.03	0.09	0.01	0.7

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	749	0.77	0.10	0.21	0.02	0.7
Non-derivatized - MS/MS non-kit	210	0.77	0.08	0.26	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	60	0.68	0.08	0.15	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	840	0.63	0.05	0.16	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.63	0.09	0.24	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.49	0.05	0.16	0.01	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.68	0.05	0.09	0.01	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.67	0.09	0.28	0.01	0.7

2018 Quality Control Data Summaries of Statistical Analyses

HYDROXPALMITOYLCARNITINE (C16OH $\mu\text{mol/L}$ blood) (cont.)

Lot D1715 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	747	1.13	0.14	0.33	0.02	0.7
Non-derivatized - MS/MS non-kit	210	1.10	0.10	0.32	0.02	0.7
Derivatized - MS/MS PE NeoGram Kit	60	1.01	0.11	0.27	0.02	0.7
Non-derivatized - MS/MS PE NeoBase Kit	830	0.92	0.09	0.25	0.01	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.93	0.12	0.31	0.03	0.6
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.74	0.11	0.30	0.01	0.5
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.99	0.07	0.14	0.01	0.7
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.01	0.16	0.46	0.01	0.7

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	736	0.60	0.09	0.16	0.59	0.8
Non-derivatized - MS/MS non-kit	198	0.60	0.07	0.13	0.60	0.9
Derivatized - MS/MS PE NeoGram Kit	59	0.57	0.08	0.11	0.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	840	0.55	0.05	0.07	0.54	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	0.52	0.08	0.12	0.51	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	0.48	0.04	0.07	0.46	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	0.57	0.03	0.03	0.59	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.57	0.09	0.14	0.53	0.8

Lot B1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	739	1.44	0.19	0.26	0.59	0.8
Non-derivatized - MS/MS non-kit	200	1.50	0.14	0.23	0.60	0.9
Derivatized - MS/MS PE NeoGram Kit	59	1.46	0.15	0.20	0.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	840	1.41	0.12	0.16	0.54	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	1.27	0.18	0.24	0.51	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	1.20	0.08	0.18	0.46	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	1.51	0.09	0.12	0.59	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	1.38	0.19	0.41	0.53	0.8

Lot C1715 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	739	3.08	0.36	0.57	0.59	0.8
Non-derivatized - MS/MS non-kit	200	3.22	0.30	0.47	0.60	0.9
Derivatized - MS/MS PE NeoGram Kit	60	3.18	0.33	0.49	0.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	840	3.10	0.25	0.34	0.54	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	2.57	0.38	0.68	0.51	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	108	2.59	0.24	0.42	0.46	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	3.18	0.23	0.30	0.59	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	2.95	0.35	0.95	0.53	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot D1715 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
Derivatized - MS/MS non-kit	738	4.81	0.50	0.84	0.59	0.8
Non-derivatized - MS/MS non-kit	200	5.02	0.43	0.77	0.60	0.9
Derivatized - MS/MS PE NeoGram Kit	60	5.06	0.58	0.80	0.56	0.9
Non-derivatized - MS/MS PE NeoBase Kit	839	4.87	0.40	0.54	0.54	0.9
Derivatized - MS/MS Chromsystems MassChrom Kit	110	4.16	0.46	0.79	0.51	0.7
Non-derivatized - MS/MS Chromsystems MassChrom Kit	110	4.18	0.34	0.68	0.46	0.7
Non-derivatized - MS2 Screening Neo (MS-Neo) Siemens	60	4.97	0.30	0.36	0.59	0.9
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	4.79	0.56	1.52	0.53	0.8

2018 Quality Control Data Summaries of Statistical Analyses

HYDROXYSTEAROYLCARNITINE (C18OH $\mu\text{mol/L}$ blood)

Lot A1715 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	601	0.02	0.01	0.02	0.02	0.6
Non-derivatized - MS/MS non-kit	140	0.01	0.00	0.01	0.01	0.6
Derivatized - MS/MS PE NeoGram Kit	59	0.01	0.01	0.01	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	748	0.00	0.00	0.00	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.02	0.01	0.02	0.02	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.00	0.00	0.00	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	50	0.01	0.01	0.02	0.01	0.5

Lot B1715 – Enriched 0.25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	619	0.17	0.03	0.07	0.02	0.6
Non-derivatized - MS/MS non-kit	140	0.17	0.02	0.06	0.01	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.17	0.04	0.05	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	757	0.15	0.03	0.04	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.15	0.02	0.07	0.02	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	89	0.12	0.02	0.04	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.14	0.03	0.08	0.01	0.5

Lot C1715 – Enriched 1 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	616	0.64	0.10	0.23	0.02	0.6
Non-derivatized - MS/MS non-kit	140	0.62	0.07	0.20	0.01	0.6
Derivatized - MS/MS PE NeoGram Kit	60	0.67	0.08	0.15	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	760	0.60	0.09	0.14	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.56	0.08	0.25	0.02	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.46	0.06	0.13	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.51	0.10	0.28	0.01	0.5

Lot D1715 – Enriched 1.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Derivatized - MS/MS non-kit	613	0.93	0.12	0.33	0.02	0.6
Non-derivatized - MS/MS non-kit	140	0.90	0.10	0.29	0.01	0.6
Derivatized - MS/MS PE NeoGram Kit	60	1.01	0.13	0.26	0.01	0.7
Non-derivatized - MS/MS PE NeoBase Kit	759	0.89	0.11	0.20	0.00	0.6
Derivatized - MS/MS Chromsystems MassChrom Kit	100	0.83	0.11	0.35	0.02	0.5
Non-derivatized - MS/MS Chromsystems MassChrom Kit	90	0.70	0.10	0.19	0.00	0.5
Derivatized - RECIPE ClinSpot® LC-MS/MS Complete Kit	60	0.78	0.12	0.43	0.01	0.5

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1708 – Mean Activity 0.33 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	99	0.23	0.05	0.08	-0.02	0.8
FIA-MS/MS non-kit multiplexed enzyme reaction	59	0.38	0.21	0.28	0.10	1.0

Lot B1708 – Mean Activity 0.67 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	100	0.50	0.13	0.20	-0.02	0.8
FIA-MS/MS non-kit multiplexed enzyme reaction	58	0.66	0.38	0.38	0.10	1.0

Lot C1708 – Mean Activity 3.52 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	96	2.74	0.30	0.89	-0.02	0.8
FIA-MS/MS non-kit multiplexed enzyme reaction	60	3.68	0.80	0.82	0.10	1.0

Lot D1708 – Mean Activity 6.68 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	95	5.15	0.42	1.46	-0.02	0.8
FIA-MS/MS non-kit multiplexed enzyme reaction	60	6.37	0.56	0.73	0.10	1.0

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1708 – Mean Activity 0.15 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	109	0.18	0.05	0.08	-0.16	1.5
FIA-MS/MS non-kit multiplexed enzyme reaction	89	0.15	0.04	0.11	-0.08	1.1

Lot B1708 – Mean Activity 0.87 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	109	1.07	0.12	0.35	-0.16	1.5
FIA-MS/MS non-kit multiplexed enzyme reaction	100	0.84	0.11	0.18	-0.08	1.1

Lot C1708 – Mean Activity 5.66 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	109	8.18	1.31	3.14	-0.16	1.5
FIA-MS/MS non-kit multiplexed enzyme reaction	99	6.04	0.97	1.78	-0.08	1.1

Lot D1708 – Mean Activity 9.02 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y- Intercept	Slope
LC-MS/MS	109	13.42	1.28	5.76	-0.16	1.5
FIA-MS/MS non-kit multiplexed enzyme reaction	100	9.85	0.93	2.97	-0.08	1.1

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot B1708 – Mean Activity 2.00 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	2.99	0.42	0.46	0.58	1.2

Lot C1708 – Mean Activity 14.64 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	18.55	3.82	3.95	0.58	1.2

Lot D1708 – Mean Activity 24.65 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	29	29.75	2.71	2.82	0.58	1.2

Note: Lot A1708 is not shown due to insufficient data.

GAA FLUOROMETRIC METHOD

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A1708	30	0.72	0.6	0.3
B1708	30	2.02	1.7	0.6
C1708	40	11.36	12.2	4.1
D1708	40	17.39	16.8	2.6

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1708 – Mean Activity 0.12 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	108	0.23	0.08	0.31	-0.03	1.6
FIA-MS/MS non-kit multiplexed enzyme reaction	99	0.15	0.05	0.09	0.01	1.1

Lot B1708 – Mean Activity 0.60 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	0.90	0.17	0.56	-0.03	1.6
FIA-MS/MS non-kit multiplexed enzyme reaction	100	0.60	0.07	0.16	0.01	1.1

Lot C1708 – Mean Activity 4.38 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	6.84	1.05	3.36	-0.03	1.6
FIA-MS/MS non-kit multiplexed enzyme reaction	100	4.82	0.73	1.37	0.01	1.1

Lot D1708 – Mean Activity 8.04 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	110	12.83	1.60	6.32	-0.03	1.6
FIA-MS/MS non-kit multiplexed enzyme reaction	100	8.65	0.72	2.26	0.01	1.1

2018 Quality Control Data Summaries of Statistical Analyses

α -L-IDURONIDASE (IDUA $\mu\text{mol/hr/L}$ blood) (cont.) METHOD REPORT FOR DIGITAL MICROFLUIDICS

Lot B1708 – Mean Activity 2.85 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	1.65	0.36	0.77	-0.93	0.9

Lot C1708 – Mean Activity 14.01 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	30	12.27	1.37	1.44	-0.93	0.9

Lot D1708 – Mean Activity 25.98 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
Digital Microfluidics	29	23.51	1.52	2.15	-0.93	0.9

Note: Lot A1708 is not shown due to insufficient data.

2018 Quality Control Data Summaries of Statistical Analyses

α-GALACTOSIDASE (GLA μmol/hr/L blood)

Lot A1708 – Mean Activity 1.11 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	110	0.84	0.21	0.32	-0.29	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	70	0.87	0.10	0.29	-0.27	1.0

Lot B1708 – Mean Activity 1.78 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	1.53	0.17	0.45	-0.29	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	70	1.47	0.11	0.33	-0.27	1.0

Lot C1708 – Mean Activity 7.44 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	110	7.46	0.72	2.06	-0.29	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	70	7.20	0.48	0.89	-0.27	1.0

Lot D1708 – Mean Activity 13.52 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	13.66	1.08	3.50	-0.29	1.0
FIA-MS/MS non-kit multiplexed enzyme reaction	70	13.29	0.72	1.36	-0.27	1.0

Note: The Digital Microfluidics method is not shown for GLA due to insufficient data.

GLA FLUOROMETRIC METHOD

Level	N	All Lab Mean	Total SD	Avg Within Lab SD
A1708	30	0.73	0.5	0.2
B1708	30	1.28	0.9	0.4
C1708	40	5.03	2.5	0.6
D1708	40	9.43	3.8	1.0

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1708 – Mean Activity 0.68 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	0.79	0.24	0.33	0.15	1.1
FIA-MS/MS non-kit multiplexed enzyme reaction	78	0.69	0.30	0.41	0.07	1.0

Lot B1708 – Mean Activity 1.26 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	1.50	0.35	0.69	0.15	1.1
FIA-MS/MS non-kit multiplexed enzyme reaction	79	1.26	0.36	0.48	0.07	1.0

Lot C1708 – Mean Activity 5.88 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	108	7.22	0.85	2.59	0.15	1.1
FIA-MS/MS non-kit multiplexed enzyme reaction	79	5.95	0.93	1.54	0.07	1.0

Lot D1708 – Mean Activity 10.91 μmol/hr/L blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	109	12.31	1.28	3.73	0.15	1.1
FIA-MS/MS non-kit multiplexed enzyme reaction	80	10.63	1.61	2.85	0.07	1.0

Note: The Digital Microfluidics method is not shown for ABG due to insufficient data.

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1708 – Mean Activity 0.08 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	80	0.04	0.02	0.04	-0.09	1.3
FIA-MS/MS non-kit multiplexed enzyme reaction	50	0.03	0.02	0.04	-0.09	1.2

Lot B1708 – Mean Activity 0.22 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	79	0.18	0.05	0.06	-0.09	1.3
FIA-MS/MS non-kit multiplexed enzyme reaction	50	0.19	0.03	0.06	-0.09	1.2

Lot C1708 – Mean Activity 1.21 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	80	1.49	0.20	0.44	-0.09	1.3
FIA-MS/MS non-kit multiplexed enzyme reaction	59	1.35	0.23	0.49	-0.09	1.2

Lot D1708 – Mean Activity 2.04 $\mu\text{mol/hr/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	79	2.63	0.30	0.79	-0.09	1.3
FIA-MS/MS non-kit multiplexed enzyme reaction	60	2.46	0.38	1.09	-0.09	1.2

2018 Quality Control Data Summaries of Statistical Analyses

24:0-LYSOPHOSPHATIDYLCHOLINE (24LPC $\mu\text{mol/L}$ blood)

Lot A1710 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	29	0.26	0.08	0.10	0.26	0.9
Positive Ion Mode LC-MSMS	30	0.12	0.02	0.03	0.12	0.9
Negative Ion Mode LC-MSMS	40	0.08	0.02	0.03	0.08	0.6

Lot B1710 – Enriched 1.0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	30	1.13	0.19	0.30	0.26	0.9
Positive Ion Mode LC-MSMS	30	1.05	0.13	0.39	0.12	0.9
Negative Ion Mode LC-MSMS	40	0.67	0.09	0.18	0.08	0.6

Lot C1710 – Enriched 5.0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	30	4.58	0.68	0.89	0.26	0.9
Positive Ion Mode LC-MSMS	30	4.77	0.77	2.29	0.12	0.9
Negative Ion Mode LC-MSMS	40	3.03	0.34	0.94	0.08	0.6

Note: Tables for 20:0- and 22:0-lysophosphosphatidylcholines are not shown due to low participation.

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1710 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	30	0.16	0.05	0.13	0.14	0.9
Positive Ion Mode LC-MSMS	40	0.06	0.01	0.07	0.06	0.9
Negative Ion Mode LC-MSMS	43	0.04	0.02	0.03	0.02	0.8

Lot B1710 – Enriched 1.0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	29	1.00	0.17	0.18	0.14	0.9
Positive Ion Mode LC-MSMS	40	0.95	0.12	0.26	0.06	0.9
Negative Ion Mode LC-MSMS	50	0.83	0.10	0.16	0.02	0.8

Lot C1710 – Enriched 5.0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
FIA-MS/MS	30	4.58	0.77	0.85	0.14	0.9
Positive Ion Mode LC-MSMS	40	4.53	0.55	1.74	0.06	0.9
Negative Ion Mode LC-MSMS	50	4.15	0.45	0.76	0.02	0.8

2018 Quality Control Data Summaries of Statistical Analyses
2ND TIER 17 α -HYDROXYPROGESTERONE (17OHP2 ng/mL serum)

Lot A1711 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	144	1.1	0.5	1.5	-1.6	0.9

Lot B1711 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	9.7	1.4	3.1	-1.6	0.9

Lot C1711 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	43.3	4.3	11.9	-1.6	0.9

Lot D1711 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	90.3	8.4	23.6	-1.6	0.9

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	469.1	45.9	124.1	-1.6	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1711 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	144	0.8	0.4	1.1	-2.9	1.0

Lot B1711 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	10.2	1.0	2.6	-2.9	1.0

Lot C1711 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	42.3	4.1	10.6	-2.9	1.0

Lot D1711 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	90.4	7.9	21.6	-2.9	1.0

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	482.7	43.0	117.7	-2.9	1.0

2018 Quality Control Data Summaries of Statistical Analyses

2ND TIER CORTISOL (CORT2 ng/mL serum)

Lot A1711 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	1.4	0.8	1.6	-4.0	1.0

Lot B1711 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	8.6	1.2	2.5	-4.0	1.0

Lot C1711 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	41.4	4.6	10.4	-4.0	1.0

Lot D1711 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	85.4	10.2	22.0	-4.0	1.0

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	200	474.3	48.6	111.1	-4.0	1.0

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1711 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	110	2.0	0.6	2.7	-0.9	0.9

Lot B1711 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	9.8	1.0	3.4	-0.9	0.9

Lot C1711 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	45.3	4.6	11.1	-0.9	0.9

Lot D1711 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	89.7	8.8	21.8	-0.9	0.9

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	469.3	36.6	124.3	-0.9	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1711 – Non-enriched 0 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	91	1.2	0.8	1.6	-5.7	1.1

Lot B1711 – Enriched 10 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	9.2	1.5	3.4	-5.7	1.1

Lot C1711 – Enriched 50 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	46.3	5.1	12.1	-5.7	1.1

Lot D1711 – Enriched 100 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	89.7	9.0	22.9	-5.7	1.1

Lot E1711 – Enriched 500 ng/mL serum

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	523.2	47.4	125.1	-5.7	1.1

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	157	10.2	2.6	50.6	13.6	1.0
UPLC	40	0.2	0.1	0.3	12.7	0.9

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	158	108.9	11.3	85.8	13.6	1.0
UPLC	50	98.0	7.1	19.6	12.7	0.9

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	159	213.5	20.1	135.6	13.6	1.0
UPLC	50	203.6	27.3	38.7	12.7	0.9

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	158	410.5	33.5	213.5	13.6	1.0
UPLC	50	393.3	48.0	62.6	12.7	0.9

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	159	793.9	65.3	387.4	13.6	1.0
UPLC	50	731.0	79.3	126.6	12.7	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	147	45.9	4.3	43.2	43.8	1.0
UPLC	50	38.4	3.2	13.8	43.5	0.8

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	148	141.6	12.6	81.8	43.8	1.0
UPLC	50	124.9	8.9	30.2	43.5	0.8

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	236.4	17.5	135.6	43.8	1.0
UPLC	50	216.8	15.8	47.5	43.5	0.8

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	148	435.3	33.4	215.8	43.8	1.0
UPLC	50	388.3	20.6	74.0	43.5	0.8

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	826.9	70.4	393.1	43.8	1.0
UPLC	50	712.6	53.5	145.2	43.5	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	198.3	15.8	42.4	206.8	1.0
UPLC	50	181.2	12.1	42.4	186.1	0.9

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	310.5	24.6	77.1	206.8	1.0
UPLC	50	268.8	16.0	64.9	186.1	0.9

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	402.8	30.5	124.6	206.8	1.0
UPLC	50	361.9	25.7	92.4	186.1	0.9

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	150	621.9	50.5	210.4	206.8	1.0
UPLC	50	541.7	29.8	127.8	186.1	0.9

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	149	998.0	79.9	383.2	206.8	1.0
UPLC	50	869.7	55.2	225.7	186.1	0.9

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	130	79.0	6.5	25.9	83.9	0.8
UPLC	30	90.3	7.3	40.1	100.2	0.8

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	130	160.0	12.5	51.9	83.9	0.8
UPLC	30	178.5	19.0	78.1	100.2	0.8

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	130	237.1	19.7	79.5	83.9	0.8
UPLC	30	262.4	24.9	101.0	100.2	0.8

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	130	394.3	34.0	129.4	83.9	0.8
UPLC	30	435.8	33.5	126.4	100.2	0.8

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	130	686.5	51.2	222.2	83.9	0.8
UPLC	30	727.1	49.0	217.5	100.2	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	57.5	4.2	21.0	61.8	0.7
UPLC	30	71.6	8.6	34.7	76.0	0.8

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	134.7	11.5	47.8	61.8	0.7
UPLC	30	151.5	9.7	58.3	76.0	0.8

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	210.0	16.7	76.3	61.8	0.7
UPLC	30	234.0	24.8	81.2	76.0	0.8

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	361.8	27.4	129.9	61.8	0.7
UPLC	30	409.3	21.8	106.9	76.0	0.8

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	644.5	46.8	232.0	61.8	0.7
UPLC	30	702.5	54.0	212.1	76.0	0.8

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

Lot A1713 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	195.1	17.7	42.5	195.5	0.8
UPLC	40	183.6	11.9	46.0	192.6	0.8

Lot B1713 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	281.0	26.3	63.3	195.5	0.8
UPLC	40	265.1	14.2	66.2	192.6	0.8

Lot C1713 – Enriched 200 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	360.1	33.0	84.2	195.5	0.8
UPLC	40	346.0	18.4	82.0	192.6	0.8

Lot D1713 – Enriched 400 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	539.1	43.6	113.0	195.5	0.8
UPLC	40	519.4	39.0	98.5	192.6	0.8

Lot E1713 – Enriched 800 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	869.5	76.0	188.0	195.5	0.8
UPLC	40	790.4	55.9	194.0	192.6	0.8

2018 Quality Control Data Summaries of Statistical Analyses

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

Lot A1714 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	4.80	0.33	1.08	4.48	0.8

Lot B1714 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	8.55	0.41	0.91	4.48	0.8

Lot C1714 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	12.12	0.87	0.91	4.48	0.8

Lot D1714 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	22.44	0.75	2.98	4.48	0.8

Lot E1714 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	43.15	1.19	1.60	4.48	0.8

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

Lot A1714 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	169	0.49	0.28	0.55	0.19	0.8

Lot B1714 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	3.98	0.58	1.29	0.19	0.8

Lot C1714 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	7.79	1.06	2.35	0.19	0.8

Lot D1714 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	19.19	2.44	5.88	0.19	0.8

Lot E1714 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	210	38.79	4.55	10.83	0.19	0.8

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

Lot A1714 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	74	0.38	0.25	0.42	-0.11	0.9

Lot B1714 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	90	4.78	0.54	0.85	-0.11	0.9

Lot C1714 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	90	8.76	0.83	1.60	-0.11	0.9

Lot D1714 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	90	22.72	2.47	4.32	-0.11	0.9

Lot E1714 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	90	46.87	3.80	7.61	-0.11	0.9

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

Lot A1714 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	120	0.32	0.20	0.38	0.20	0.9

Lot B1714 – Enriched 2.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	2.50	0.51	0.83	0.20	0.9

Lot C1714 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	4.67	0.79	1.15	0.20	0.9

Lot D1714 – Enriched 12.5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	11.53	2.02	3.02	0.20	0.9

Lot E1714 – Enriched 25 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	140	23.10	3.64	5.51	0.20	0.9

2018 Quality Control Data Summaries of Statistical Analyses

2ND TIER TOTAL HOMOCYSTEINE (tHcy2 $\mu\text{mol/L}$ blood)

Lot A1714 – Nonenriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	6.45	1.06	3.48	5.44	0.9

Lot B1714 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	14.40	2.06	6.89	5.44	0.9

Lot C1714 – Enriched 20 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	22.19	2.92	10.28	5.44	0.9

Lot D1714 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	47.27	5.79	22.04	5.44	0.9

Lot E1714 – Enriched 100 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	189	93.11	12.14	47.17	5.44	0.9

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GUANIDINOACETIC ACID (GAA2 $\mu\text{mol/L}$ blood)

Lot A1612 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	30	1.09	0.23	0.50	0.70	1.1
Derivatized MS/MS non-kit	30	0.97	0.12	0.34	0.94	0.7

Lot B1612 – Enriched 3 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	30	3.39	0.37	1.33	0.70	1.1
Derivatized MS/MS non-kit	30	2.79	0.17	0.32	0.94	0.7

Lot C1612 – Enriched 5 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	30	6.10	0.50	2.77	0.70	1.1
Derivatized MS/MS non-kit	30	4.65	0.31	0.45	0.94	0.7

Lot D1612 – Enriched 8 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	30	9.12	0.92	4.17	0.70	1.1
Derivatized MS/MS non-kit	30	6.48	0.54	0.69	0.94	0.7

Lot E1612 – Enriched 10 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	30	11.74	1.68	6.11	0.70	1.1
Derivatized MS/MS non-kit	30	7.80	0.40	0.54	0.94	0.7

2018 Quality Control Data Summaries of Statistical Analyses

CREATINE (CRE2 $\mu\text{mol/L}$ blood)

Lot A1612 – Non-enriched 0 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	207.99	28.90	32.70	203.75	0.7
Derivatized MS/MS non-kit	20	203.65	8.70	9.20	211.73	0.8

Lot B1612 – Enriched 50 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	243.37	14.36	19.06	203.75	0.7
Derivatized MS/MS non-kit	20	248.49	12.72	14.51	211.73	0.8

Lot C1612 – Enriched 150 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	313.86	10.55	10.55	203.75	0.7
Derivatized MS/MS non-kit	20	330.76	22.32	28.55	211.73	0.8

Lot D1612 – Enriched 300 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	411.07	18.52	18.52	203.75	0.7
Derivatized MS/MS non-kit	20	453.54	24.29	24.29	211.73	0.8

Lot E1612 – Enriched 450 $\mu\text{mol/L}$ blood

METHOD	N	Mean	Average Within Lab SD	Total SD	Y-Intercept	Slope
LC-MS/MS	20	549.65	48.04	48.04	203.75	0.7
Derivatized MS/MS non-kit	20	539.43	18.77	22.27	211.73	0.8