Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	2/4/2009
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Autism and Intellectual Disability Comprehensive Panel

ARUP test code 2014314

Creatinine, Urine	194 mg/dL		
Alpha-amino butyric acid, Plasma	10 umol/L		(Ref Interval: <=40)
Alanine, Plasma	**562 umol/L**	**H**	**(Ref Interval: 160-530)**
Allo-isoleucine, Plasma	<2 umol/L		(Ref Interval: <=5)
Alpha-aminoadipic acid, Plasma	<2 umol/L		(Ref Interval: <=4)
Anserine, Plasma	<5 umol/L		(Ref Interval: <=5)
Arginine, Plasma	104 umol/L		(Ref Interval: 35-125)
Argininosuccinic Acid, Plasma	<2 umol/L		(Ref Interval: <=2)
Asparagine, Plasma	52 umol/L		(Ref Interval: 20-80)
Aspartic Acid, Plasma	<5 umol/L		(Ref Interval: <=15)
Beta-amino isobutyric acid, Plasma	<5 umol/L		(Ref Interval: <=10)
Beta-alanine, Plasma	<25 umol/L		(Ref Interval: <=25)

H=High, L=Low, *=Abnormal, C=Critical

Citrulline, Plasma	29 umol/L	(Ref Interval: 10-45)
Cystathionine, Plasma	<5 umol/L	(Ref Interval: <=5)
Cystine, Plasma	35 umol/L	(Ref Interval: 10-65)
Ethanolamine, Plasma	8 umol/L	(Ref Interval: <=15)
Gamma-amino butyric acid, Plasma	<5 umol/L	(Ref Interval: <=5)
Glutamic Acid, Plasma	49 umol/L	(Ref Interval: 15-130)
Glutamine, Plasma	544 umol/L	(Ref Interval: 380-680)
Glycine, Plasma	261 umol/L	(Ref Interval: 140-420)
Histidine, Plasma	106 umol/L	(Ref Interval: 50-130)
Homocitrulline, Plasma	<5 umol/L	(Ref Interval: <=5)
Homocystine, Plasma	<2 umol/L	(Ref Interval: <=2)
Hydroxylysine, Plasma	<5 umol/L	(Ref Interval: <=5)
Hydroxyproline, Plasma	26 umol/L	(Ref Interval: 5-40)
Isoleucine, Plasma	74 umol/L	(Ref Interval: 30-120)
Leucine, Plasma	133 umol/L	(Ref Interval: 60-180)
Lysine, Plasma	131 umol/L	(Ref Interval: 85-230)

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Methionine, Plasma	28 umol/L	(Ref Interval: 15-40)
Ornithine, Plasma	50 umol/L	(Ref Interval: 25-110)
Phenylalanine, Plasma	69 umol/L	(Ref Interval: 30-82)
Proline, Plasma	275 umol/L	(Ref Interval: 90-350)
Sarcosine, Plasma	<5 umol/L	(Ref Interval: <=5)
Serine, Plasma	88 umol/L	(Ref Interval: 60-170)
Taurine, Plasma	56 umol/L	(Ref Interval: 30-130)
Threonine, Plasma	111 umol/L	(Ref Interval: 60-190)
Tryptophan, Plasma	67 umol/L	(Ref Interval: 25-80)
Tyrosine, Plasma	64 umol/L	(Ref Interval: 35-110)
Valine, Plasma	226 umol/L	(Ref Interval: 120-320)
C2, Acetyl	7.02 umol/L	(Ref Interval: 2.93-15.06)
C3, Propionyl	0.42 umol/L	(Ref Interval: <=0.82)
C4, Iso-/Butyryl	0.17 umol/L	(Ref Interval: <=0.42)
C5, Isovaleryl/2Mebutyryl	0.06 umol/L	(Ref Interval: <=0.24)
C5-DC, Glutaryl	0.05 umol/L	(Ref Interval: <=0.23)

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C5-OH, 3-OH Isovaleryl	<0.01 umol/L	(Ref Interval: <=0.07)
C6, Hexanoyl	0.02 umol/L	(Ref Interval: <=0.12)
C8, Octanoyl	0.05 umol/L	(Ref Interval: <=0.22)
C8:1, Octenoyl	0.10 umol/L	(Ref Interval: <=0.60)
C10, Decanoyl	0.04 umol/L	(Ref Interval: <=0.33)
C10:1, Decenoyl	0.03 umol/L	(Ref Interval: <=0.27)
C12, Dodecanoyl	0.02 umol/L	(Ref Interval: <=0.13)
C12:1, Dodecenoyl	0.02 umol/L	(Ref Interval: <=0.13)
C12-OH, 3-OH-Dodecanoyl	<0.01 umol/L	(Ref Interval: <=0.02)
C14, Tetradecanoyl	0.01 umol/L	(Ref Interval: <=0.06)
C14:1, Tetradecenoyl	0.02 umol/L	(Ref Interval: <=0.15)
C14:2, Tetradecadienoyl	0.01 umol/L	(Ref Interval: <=0.08)
C14-OH, 3-OH-Tetradecanoyl	<0.01 umol/L	(Ref Interval: <=0.01)
C14:1-OH, 3-OH-Tetradecenoyl	<0.01 umol/L	(Ref Interval: <=0.04)
C16, Palmitoyl	0.06 umol/L	(Ref Interval: <=0.12)
C16:1, Palmitoleyl	0.01 umol/L	(Ref Interval: <=0.04)

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C16-OH, 3-OH-Palmitoyl	0.01 umol/L	(Ref Interval: <=0.02)
C16:1-OH, 3-OH-Palmitoleyl	<0.01 umol/L	(Ref Interval: <=0.02)
C18, Stearoyl	0.02 umol/L	(Ref Interval: <=0.06)
C18:1, Oleyl	0.04 umol/L	(Ref Interval: <=0.18)
C18:2, Linoleyl	0.03 umol/L	(Ref Interval: <=0.10)
C18-OH, 3-OH-Stearoyl	<0.01 umol/L	(Ref Interval: <=0.02)
C18:1-OH, 3-OH-Oleyl	0.01 umol/L	(Ref Interval: <=0.02)
C18:2-OH, 3-OH-Linoleyl	0.01 umol/L	(Ref Interval: <=0.02)
Mucopolysaccharides mg/mmol CRT	5.1	(Ref Interval: 0.0-7.1)
	REFERENCE INTERVAL: Mucopolysaccharides mg/mmol CRT Access complete set of age- and/or gender-specific reference intervals for this test in the ARUP Laboratory Test Directory (aruplab.com). This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.	
Lactic Acid, Urine	39	(Ref Interval: 0-50)
Pyruvic Acid, Urine	10	(Ref Interval: 0-15)
Succinic Acid, Urine	**21 H**	**(Ref Interval: 0-20)**
Fumaric Acid, Urine	Not Detected	(Ref Interval: 0-4)

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2-Ketoglutaric Acid, Urine	7	(Ref Interval: 0-75)
Methylmalonic Acid, Urine	1	(Ref Interval: 0-5)
3-OH-Butyric Acid, Urine	2	(Ref Interval: 0-4)
Acetoacetic Acid, Urine	Not Detected	(Ref Interval: 0-4)
2-Keto-3-methylvaleric Acid, Urine	Not Detected	(Ref Interval: 0-10)
2-Ketoisocaproic Acid, Urine	Not Detected	(Ref Interval: 0-4)
2-Ketoisovaleric Acid, Urine	Not Detected	(Ref Interval: 0-4)
Ethylmalonic Acid, Urine	1	(Ref Interval: 0-4)
Adipic Acid, Urine	1	(Ref Interval: 0-35)
Suberic Acid, Urine	1	(Ref Interval: 0-3)
Sebacic Acid, Urine	Not Detected	(Ref Interval: 0-3)
4-OH-phenylacetic Acid, Urine	13	(Ref Interval: 0-25)
4-OH-phenyllactic Acid, Urine	Not Detected	(Ref Interval: 0-4)
4-OH-phenylpyruvic Acid, Urine	Not Detected	(Ref Interval: 0-2)
Succinylacetone, Urine	Not Detected	(Ref Interval: 0-0)
Creatine, Urine	15 mmol/mol CRT	(Ref Interval: 10-370)

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Guanidinoacetic acid, Urine	22 mmol/mol CRT	(Ref Interval: 7-130)
Creatinine, Urine	14696.9 umol/L	
Creatine, Serum/Plasma	23.9 umol/L	(Ref Interval: 9.0-90.0)
Guanidinoacetic acid, Serum/Plasma	2.02 umol/L	(Ref Interval: 1.10-3.80)
FRAG X Specimen	Whole Blood	
Fragile X Allele 1	30 CGG repeats	
Fragile X Allele 2	Not Applicable CGG repeats	
Fragile X Methylation Pattern	Not Applicable	
Fragile X Interpretation	See Note This individual has a FMR1 allele with a CGG repeat size in the normal range; therefore, he is predicted to be neither affected with, nor a carrier of, fragile X syndrome (FXS). This test does not detect rare FMR1 variants causing less than 1% of FXS. This result has been reviewed and approved by [redacted]	

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BACKGROUND INFORMATION: Fragile X (FMR1) with Reflex to Methylation Analysis
CHARACTERISTICS OF FRAGILE X SYNDROME (FXS): Affected males have moderate intellectual disability, hyperactivity, perseverative speech, social anxiety, poor eye contact, hand flapping or biting, autism spectrum disorders and connective tissue anomalies in males. Females are usually less severely affected than males. FXS is caused by FMR1 full mutations.
CHARACTERISTICS OF FRAGILE X TREMOR ATAXIA SYNDROME (FXTAS): Onset of progressive ataxia and intention tremor typically after the fourth decade of life. Females also have a 21 percent risk for primary ovarian insufficiency. FXTAS is caused by FMR1 premutations.
Incidence of FXS: 1 in 4,000 Caucasian males and 1 in 8,000 Caucasian females.
INHERITANCE: X-linked.
PENETRANCE OF FXS: Complete in males; 50 percent in females.
PENETRANCE OF FXTAS: 47 percent in males and 17 percent in females >50 years of age.
CAUSE: Expansion of the FMR1 gene CGG triplet repeat.
  Full mutation: typically >200 CGG repeats (methylated).
  Premutation: 55 to approx 200 CGG repeats (unmethylated).
  Intermediate: 45-54 CGG repeats (unmethylated).
  Normal: 5-44 CGG repeats (unmethylated).
CLINICAL SENSITIVITY: 99 percent.
METHODOLOGY: Triplet repeat-primed polymerase chain reaction (PCR) followed by size analysis using capillary electrophoresis. Methylation-specific PCR analysis is performed for CGG repeat lengths of >100 to distinguish between premutation and full mutation alleles.
ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent; estimated precision of sizing for intermediate and premutation alleles is within 2-3 CGG repeats.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Rare FMR1 variants unrelated to trinucleotide expansion will not be detected. A specific CGG repeat size estimate is not provided for full mutation alleles. AGG trinucleotide interruptions within the FMR1 CGG repeat tract are not assessed.

PHENOTYPE	NUMBER OF CGG REPEATS
Unaffected	<45
Intermediate	45-54
Premutation	55-200
Affected	>200

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Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

Cytogenomic SNP Microarray

Normal (Ref Interval: Normal)

Test Performed: Cytogenomic SNP Microarray (CMA SNP)
Specimen Type: Peripheral blood
Indication for Testing: Fine motor delay, speech delay, autism spectrum disorder, learning disability, structural heart defect

RESULT SUMMARY
Normal Microarray Result (Male)

RESULT DESCRIPTION
No clinically significant copy number changes or regions of homozygosity were detected.

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INTERPRETATION
This analysis showed a normal result.

Health care providers with questions may contact an ARUP genetic counselor at (800) 242-2787 ext. 2141.

Cytogenomic Nomenclature (ISCN):
arr(X,Y)x1,(1-22)x2

Technical Information
- This assay was performed using the CytoScan(TM) HD Suite (Thermo Fisher Scientific) according to validated protocols within the Genomic Microarray Laboratory at ARUP Laboratories
- This assay is designed to detect alterations to DNA copy number state (gains and losses) as well as copy-neutral alterations (regions of homozygosity; ROH) that indicate an absence- or loss-of-heterozygosity (AOH or LOH)
- AOH may be present due to parental relatedness (consanguinity) or uniparental disomy (UPD)
- LOH may be present due to acquired UPD (segmental or whole chromosome)
- The detection sensitivity (resolution) for any particular genomic region may vary dependent upon the number of probes (markers), probe spacing, and thresholds for copy number and ROH determination
- The CytoScan HD array contains 2.67 million markers across the genome with average probe spacing of 1.15 kb, including 750,000 SNP probes and 1.9 million non-polymorphic probes
- In general, the genome-wide resolution is approximately 25-50 kb for copy number changes and approximately 3 Mb for ROH (See reporting criteria)
- The limit of detection for mosaicism varies dependent upon the size and type of genomic imbalance. In general, genotype mixture due to mosaicism (distinct cell lines from the same individual) or chimerism (cell lines from different individuals) will be detected when present at greater than 20-30 percent in the sample
- Genomic coordinates correspond to the Genome Reference Consortium human genome build 37/human genome issue 19 (GRCh37/hg19)

Variant Classification and Reporting Criteria
- Copy number variant (CNV) analysis is performed in accordance with recommendations by the American College of Medical Genetics and Genomics (ACMG), using standard 5-tier CNV classification terminology: pathogenic, likely pathogenic, variant of uncertain significance (VUS), likely benign, and benign
- CNVs classified as pathogenic, likely pathogenic, or variant of uncertain significance are generally reported, based on information available at the time of review
- Known or expected pathogenic CNVs affecting genes with known clinical significance but which are unrelated to the indication for testing will generally be reported
- Variants that do not fall within these categories may be reported with descriptive language specific to that variant
- In general, recessive disease risk and recurrent CNVs with established reduced penetrance will be reported
- For a list of databases used in CNV classification, please refer to ARUP Constitutional CNV Assertion Criteria, which can be found on ARUP's Genetics website at www.aruplab.com/genetics
- CNVs classified as likely benign or benign that are devoid of relevant gene content or reported as common findings in the general population, are generally not reported
- CNV reporting (size) criteria: losses greater than 50 kb and gains greater than 400 kb are generally reported, dependent on genomic content
- ROH are generally reported when a single terminal ROH is greater than 3 Mb and a single interstitial ROH is greater than 10-15 Mb (dependent upon chromosomal location and likelihood of imprinting disorder) or when total autosomal homozygosity is greater than 3 percent (only autosomal ROH greater than 3 Mb are considered for this estimate)

Limitations
This analysis cannot provide structural (positional) information associated with genomic imbalance. Therefore, additional cytogenetic testing by chromosome analysis or fluorescence in situ hybridization (FISH) may be recommended.

Certain genomic alterations may not or cannot be detected by this technology. These alterations may include, but are not limited to:
- CNVs below the limit of resolution of this platform
- Sequence-level variants (mutations) including point mutations and indels
- Low-level mosaicism (generally, less than 20-30 percent)
- Balanced chromosomal rearrangements (translocations, inversions and insertions)
- Genomic imbalance in repetitive DNA regions (centromeres, telomeres, segmental duplications, and acrocentric chromosome short arms)

Data Sharing
In cooperation with the National Institutes of Health's effort to improve understanding of specific genetic variants, ARUP submits HIPAA-compliant, de-identified (cannot be traced back to the patient) genetic test results and health information to public databases. The confidentiality of each sample is maintained. If you prefer that your test result not be shared, call ARUP Laboratories at (800) 242-2787 ext. 3301. Your de-identified information will not be disclosed to public databases after your request is received, but a separate request is required for each genetic test. Additionally, patients have the opportunity to participate in patient registries and research. To learn more, visit ARUP's Genetics website at www.aruplab.com/genetics.

This result has been reviewed and approved by [redacted]

INTERPRETIVE INFORMATION: CYTOGENOMIC SNP MICROARRAY

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EER Cytogenomic SNP Microarray	EERUnavailable
Autism/Intellectual Interp	See Note

Mildly elevated plasma alanine. Would repeat plasma amino acids and exclude lactic acidosis. No other metabolic abnormalities identifiable by this panel were detected. Genetic evaluation is recommended to assess the need for additional testing to exclude other rare metabolic disorders associated with autism and/or intellectual disability.

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INTERPRETIVE INFORMATION: Autism and Intellectual Disability Comprehensive Panel

MPS Screen, Urine: Mucopolysaccharides (Glycosaminoglycans) include: Keratan Sulfate, Heparan Sulfate, Dermatan Sulfate, and Chondroitin Sulfates 4 and 6. The excretion of Heparan Sulfate is variable. A normal mucopolysaccharides screen does not exclude Sanfilippo Syndrome (Mucopolysaccharidosis Type III).

Organic Acids, Urine: Results are reported in mmol/mol creatinine.

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VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Creatinine, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Alpha-amino butyric acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Alanine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Allo-isoleucine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Alpha-aminoadipic acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Anserine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Arginine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Argininosuccinic Acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Asparagine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Aspartic Acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Beta-amino isobutyric acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Beta-alanine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Citrulline, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Cystathionine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Cystine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Ethanolamine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Gamma-amino butyric acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Glutamic Acid, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Glutamine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Glycine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Histidine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Homocitrulline, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Homocystine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Hydroxylysine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Hydroxyproline, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

H=High, L=Low, *=Abnormal, C=Critical

Isoleucine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Leucine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Lysine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Methionine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Ornithine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Phenylalanine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Proline, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Sarcosine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Serine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Taurine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Threonine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Tryptophan, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Tyrosine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Valine, Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C2, Acetyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C3, Propionyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C4, Iso-/Butyryl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C5, Isovaleryl/2Mebutyryl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C5-DC, Glutaryl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C5-OH, 3-OH Isovaleryl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C6, Hexanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C8, Octanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C8:1, Octenoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C10, Decanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C10:1, Decenoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C12, Dodecanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C12:1, Dodecenoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C12-OH, 3-OH-Dodecanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C14, Tetradecanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C14:1, Tetradecenoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C14:2, Tetradecadienoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C14-OH, 3-OH-Tetradecanoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C14:1-OH, 3-OH-Tetradecenoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C16, Palmitoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C16:1, Palmitoleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C16-OH, 3-OH-Palmitoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C16:1-OH, 3-OH-Palmitoleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C18, Stearoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C18:1, Oleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C18:2, Linoleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C18-OH, 3-OH-Stearoyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
C18:1-OH, 3-OH-Oleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

H=High, L=Low, *=Abnormal, C=Critical

C18:2-OH, 3-OH-Linoleyl	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Mucopolysaccharides mg/mmol CRT	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Lactic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Pyruvic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Succinic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Fumaric Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
2-Ketoglutaric Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Methylmalonic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
3-OH-Butyric Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Acetoacetic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
2-Keto-3-methylvaleric Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
2-Ketoisocaproic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
2-Ketoisovaleric Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Ethylmalonic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Adipic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Suberic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Sebacic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
4-OH-phenylacetic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
4-OH-phenyllactic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
4-OH-phenylpyruvic Acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Succinylacetone, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Creatine, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Guanidinoacetic acid, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Creatinine, Urine	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Creatine, Serum/Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Guanidinoacetic acid, Serum/Plasma	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
FRAG X Specimen	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Fragile X Allele 1	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Fragile X Allele 2	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Fragile X Methylation Pattern	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Fragile X Interpretation	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Cytogenomic SNP Microarray	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytogenomic SNP Microarray	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Autism/Intellectual Interp	23-096-103231	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical